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(54) Title: METHODS FOR DETECTING TRISOMY 2 1

(57) Abstract: Methods for determining whether a subject, such as a fetus, has Down syndrome are described. In one embodiment, the methods include detecting one or more biomarkers in a biological sample, and determining whether the expression of the biomarkers is altered when compared to expression of the biomarkers in one or more subjects that do not have trisomy 2 1. In one embodiment, the biological sample is a blood sample, and the biomarkers are cell free plasma RNAs.

METHODS FOR DETECTING TRISOMY 21

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application Serial No. 61/565,761 filed December 1, 2011, which is incorporated by reference herein.

SEQUENCE LISTING

This application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. The ASCII copy, created on November 29, 2012, is named 42020201.txt and is 768,465 bytes in size.

BACKGROUND

Trisomy 21, also referred to as Down Syndrome and mongolism, is the result of a chromosomal abnormality. A human cell has two types of chromosomes. One type is the autosomal chromosomes (chromosomes 1-22), and the other type is the sex chromosome (the X and Y chromosomes). In a normal human cell there are 46 chromosomes, and they are present in the cell as 23 pairs. Thus each normal human cell has two of each autosomal chromosome (two copies of chromosome 1, two copies of chromosome 2, etc.) and one pair of sex chromosomes (an X and a Y chromosome for a male, or two X chromosomes for a female). A karyotype of a normal male is referred to as 46XY, and that of a normal female is 46XX. The chromosomal abnormality in a person having trisomy 21 is an extra chromosome 21. The karyotype of a male having trisomy 21 is 47XY+21, and the karyotype of a female having trisomy 21 is 47XX+21.

Trisomy 21 is typically caused by a meiotic nondisjunction event. With nondisjunction, a gamete (either a sperm or egg cell) is produced with an extra copy of the chromosome 21; thus, the gamete has 24 and not the normal 23 chromosomes. When combined with a normal gamete from the other parent, the resulting embryo has 47 chromosomes, with three copies of chromosome 21. An analogous process accounts for most

cases of trisomy 13 and 18. Trisomy 21 is the cause of approximately 95% of Down syndromes, with 88% resulting from nondisjunction in the maternal gamete and 8% from nondisjunction in the paternal gamete. The actual Down syndrome "critical region" encompasses chromosome bands 21q22.1-q22.3.

Since trisomy 21 is usually caused by nondisjunction in the gametes prior to conception, all cells in the resulting conceptus are affected. However, when some of the cells in the body are normal and other cells have trisomy 21, it is called mosaic Down syndrome (46,XX/47,XX,+21). This can occur in one of main two ways: in the first, a nondisjunctional event in a normal embryo during an early cell division results in a fraction of the cells having trisomy 21; in the second, a Down syndrome embryo secondary to nondisjunction loses the extra 21 chromosome with the result of a normal cell line. There is considerable variability in the fraction of trisomy 21 cells among mosaic trisomy 21, both as a whole and among tissues. Mosaicism causes 1-2% of Down syndrome.

Down syndrome is the result of a random event during the formation of sex cells or pregnancy. There is no evidence that it is due to parental behavior (other than age) or environmental factors. In 2006, the Centers for Disease Control and Prevention estimated the overall rate for Down syndrome in the United States was one per 733 live births (5429 new cases per year). Approximately 95% of these are trisomy 21. Down syndrome occurs in all ethnic groups and among all economic classes.

Maternal age affects the probability of conceiving a fetus with Down syndrome. At maternal age 20 to 24, the probability is one in 1562; at age 35 to 39 the probability is one in 214, and above age 45 the probability is one in 19 (Huether et al., 1998, J Med Genet 35 (6): 482-90. doklO.l 136/jmg.35.6.482. PMID 9643290). Although the probability increases with advancing maternal age, 80% of children with Down syndrome are born to women under the age of 35, reflecting the overall fecundity of that age group. Recent information suggests paternal age, especially beyond 42 years increases the risk of Down syndrome too.

A diagnostic test for Down syndrome is typically preceded by some form of screening test (history, ultrasound or blood protein measurement) as the current methods for diagnosis involves an invasive test- amniocentesis, chorionic villus sampling or percutaneous umbilical cord blood sampling (PUBS) - that is then offered to families who are screen positive, i.e. have an increased likelihood of having a fetus with Down syndrome. In the United States, the American College of Obstetrics and Gynecology guidelines recommend non-invasive

screening and invasive testing be offered to all women, regardless of their age, and most likely all physicians follow these guidelines. This recommendation is supported by some insurance plans that only reimburse invasive testing if the woman is >34 years old or if she has received a high-risk score from a non-invasive screening test. Amniocentesis, CVS and PUBS are invasive procedures that involve inserting instruments into the uterus, and therefore carry a risk of causing fetal injury or pregnancy loss. The risks of a loss from CVS and amniocentesis are often quoted as 1% and 0.5% respectively. In all likelihood, the fetuses lost as a result are otherwise normal.

There are several common non-invasive screening tests that can identify a fetus at high risk for Down syndrome. These tests are typically performed in the late 1st or early 2nd trimester. Due to the nature of screening, each test has a significant chance of a false positive that is suggesting the fetus has Down syndrome when in fact, the fetus does not. Screen positive tests must be verified by an invasive procedure before a diagnosis of Down syndrome is made. Common screening procedures for Down syndrome are given in Table 1.

Table 1: First and Second trimester Down syndrome screens

Screen	Weeks gestation performed	Detection rate	False positive rate	Description
Quad screen	15–20	81%	5%	Measures the maternal serum α feto protein, estriol, human chorionic gonadotropin (hCG) and inhibin-α.
Nuchal translucency/free β/ PAPP-A (1st Trimester Combined Test)	10–13.5	85%	5%	Uses ultrasound to measure Nuchal Translucency (NT) plus free β hCG and PAPP-A.
Integrated Test	10-13.5 and 15–20	95%	5%	The Integrated test uses both the 1st Trimester Combined test and the 2nd Trimester Quad test to yield a more accurate screening result.

Even with the best available non-invasive screening tests, the detection rate is 90-95% with a screen positive rate set at 2.5%. Screening tests more commonly used have screen positive

rates of 5- 7.5%. Inaccuracies may result from undetected multiple fetuses (rare with adequate ultrasound testing), incorrect dating of the pregnancy, normal variation in the ultrasound measurements or maternal protein levels that constitute the screen, or operator error. These ultrasound measurements and protein levels overlap in the healthy and disease groups broadly in all instances.

Confirmation of screen positive status requires a fetal karyotype that is normally accomplished by amniocentesis or chorionic villus sampling (CVS). Amniocentesis involves taking amniotic fluid from the amniotic sac, and CVS a placental biopsy, each to obtain fetal cells. The laboratory work can take several weeks but will detect over 99.8% of all numerical chromosomal problems with a very low false positive rate; however, these methods of confirmation have the risk of miscarriage of a healthy fetus.

The focus of noninvasive diagnosis of Down syndrome has been on the detection and separation of fetal DNA found in the mother's peripheral blood derived from chromosome 21. A few investigators have tried to use RNA based technologies with mixed success.

SUMMARY OF THE INVENTION

Provided herein are methods for determining whether a subject has trisomy 21. In one embodiment, a method may include screening a fetus for trisomy 21. The method may include

measuring a plurality of trisomy 21 biomarkers in a biological sample obtained from a first pregnant female, wherein the plurality of trisomy 21 biomarkers is chosen from any combination of SEQ ID NO:8-3,248, or a complement thereof. In one embodiment, the T21 biomarkers may be chosen from a sequence of at least 15 consecutive nucleotides selected from any combination of SEQ ID NO:8-3,248, or a complement thereof. In one embodiment, the fetus of the first pregnant female is between 8 weeks and 16 weeks post-implantation.

The method may also include identifying the fetus as having trisomy 21 if expression of the plurality of biomarkers is altered to a statistically significant degree in the biological sample compared to a biological sample from a second pregnant female carrying a fetus not having trisomy 21. The method may also include identifying the fetus as not having trisomy 21 if expression of the plurality of biomarkers is not altered to a statistically significant degree in the biological sample compared to a biological sample from a second pregnant female

carrying a fetus not having trisomy 21. In one embodiment, expression of a trisomy 21 biomarker is altered to a statistically significant degree if it is outside the 95% confidence interval for that trisomy 21 biomarker. In one embodiment, the method may further include recommending a genetic test chosen from amniocentesis, cordocentesis, and chorionic villus sampling, ultrasound, or a combination thereof.

In one embodiment, the plurality of trisomy 21 biomarkers may include at least 10 trisomy 21 biomarkers, wherein the pregnant mother having at least 6 biomarkers altered to a statistically significant degree is identified as carrying a fetus having trisomy 21. In one embodiment, the plurality of trisomy 21 biomarkers includes at least 10 trisomy 21 biomarkers, and wherein the pregnant mother having no greater than 4 biomarkers altered to a statistically significant degree is identified as carrying a fetus not having trisomy 21. In one embodiment, the first pregnant female and the second pregnant female may be matched with respect to a co-variable selected from, for instance, maternal age, gestational stage, maternal weight, diet, smoking, prior preterm birth, diabetes, use of prophylactic progesterone, ethnicity, or a combination thereof.

In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides encoded by chromosome 21, or from polynucleotides encoded by any of chromosomes 1-20, 22 or X. In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides that are up-regulated in the first pregnant female carrying a fetus with trisomy 21 compared to the second pregnant female carrying a fetus not having trisomy 21. In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides that are down-regulated in the first pregnant female carrying a fetus with trisomy 21 compared to the second pregnant female carrying a fetus not having trisomy 21.

In one embodiment, the method may further include obtaining the biological sample from the first pregnant female. The obtaining may include obtaining a blood sample. The blood sample may be processed to remove cells from the blood sample. The blood sample may be processed to obtain, and optionally isolate, cell-free plasma RNA. In one embodiment, the method may further include converting RNA polynucleotides present in the biological sample into cDNA molecules, and the measuring includes hybridization between a cDNA molecule and a complementary trisomy 21 biomarker. In one embodiment, the complementary trisomy 21 biomarker is in solution during the hybridization, and in one embodiment, the complementary trisomy 21 biomarker is immobilized on a solid support.

In one embodiment, a method may include detecting trisomy 21 in a fetus. The method may include detecting trisomy 21 biomarkers in a biological sample to yield an expression level of each detected trisomy 21 biomarker. In one embodiment, the biological sample includes plasma from a pregnant female. In one embodiment, the T21 biomarkers may be chosen from a sequence of at least 15 consecutive nucleotides selected from any combination of SEQ ID NO:8-3,248, or a complement thereof. In one embodiment, the fetus of the first pregnant female is between 8 weeks and 16 weeks post-implantation. The method may also include comparing the expression level of each detected trisomy 21 biomarker to the expression level of the trisomy 21 biomarker in pregnant females carrying a fetus without trisomy 21. In one embodiment, an expression level of a detected trisomy 21 biomarker that is outside the 95% confidence interval for that trisomy 21 biomarker indicates the expression level of the trisomy 21 biomarker is altered. In one embodiment, at least 10 trisomy 21 biomarkers are detected. In one embodiment, a fetus carried by the pregnant female is identified as carrying a fetus having trisomy 21 when at least 6 biomarkers are outside the 95% confidence interval. In one embodiment, the method may further include recommending a genetic test chosen from amniocentesis, cordocentesis, and chorionic villus sampling, ultrasound, or a combination thereof. In one embodiment, the pregnant female and the pregnant females used to establish the 95% confidence interval for each trisomy 21 biomarker may be matched with respect to a co-variable selected from, for instance, maternal age, gestational stage, maternal weight, diet, smoking, prior preterm birth, diabetes, use of prophylactic progesterone, ethnicity, or a combination thereof.

In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides encoded by chromosome 21, or from polynucleotides encoded by any of chromosomes 1-20, 22 or X. In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides that are up-regulated in the pregnant female carrying a fetus with trisomy 21 compared to the pregnant females carrying a fetus not having trisomy 21. In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides that are down-regulated in the pregnant female carrying a fetus with trisomy 21 compared to the pregnant females carrying a fetus not having trisomy 21.

In one embodiment, the method may further include obtaining the biological sample from the first pregnant female. The obtaining may include obtaining a blood sample. The blood sample may be processed to remove cells from the blood sample. The blood sample

may be processed to obtain, and optionally isolate, cell-free plasma RNA. In one embodiment, the method may further include converting RNA polynucleotides present in the biological sample into cDNA molecules, and the measuring includes hybridization between a cDNA molecule and a complementary trisomy 21 biomarker. In one embodiment, the complementary trisomy 21 biomarker is in solution during the hybridization, and in one embodiment, the complementary trisomy 21 biomarker is immobilized on a solid support.

In one embodiment, a method may include detecting trisomy 21 in a fetus. The method may include detecting trisomy 21 biomarkers in a biological sample from a pregnant female to yield a sample expression profile. In one embodiment, the biological sample includes plasma from a pregnant female. In one embodiment, the T21 biomarkers may be chosen from a sequence of at least 15 consecutive nucleotides selected from any combination of SEQ ID NO:8-3,248, or a complement thereof. In one embodiment, the fetus of the first pregnant female is between 8 weeks and 16 weeks post-implantation. The method may also include comparing the sample expression profile with a reference expression profile, wherein a difference between the sample expression profile and the reference expression profile is indicative of the presence or absence of trisomy 21 in the fetus. In one embodiment, the reference expression profile is from at least one second pregnant female carrying a fetus without trisomy 21, and a difference between the sample expression profile and the reference expression profile is indicative of the presence of trisomy 21. In one embodiment, the reference expression profile is from at least one second pregnant female carrying a fetus with trisomy 21, and a difference between the sample expression profile and the reference expression profile is indicative of the absence of trisomy 21. In one embodiment, the method may further include recommending a genetic test chosen from amniocentesis, cordocentesis, and chorionic villus sampling, ultrasound, or a combination thereof.

In one embodiment, the difference between the sample expression profile and the reference expression profile is statistically significant. In one embodiment, the sample expression profile includes at least 10 trisomy 21 biomarkers. In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides encoded by chromosome 21, or from polynucleotides encoded by any of chromosomes 1-20, 22 or X. In one embodiment, the trisomy 21 biomarkers may be selected from polynucleotides that are up-regulated in the first pregnant female carrying a fetus with trisomy 21 compared to the second pregnant female carrying a fetus not having trisomy 21. In one embodiment, the trisomy 21 biomarkers may

be selected from polynucleotides that are down-regulated in the first pregnant female carrying a fetus with trisomy 21 compared to the second pregnant female carrying a fetus not having trisomy 21. In one embodiment, the first pregnant female and the second pregnant female may be matched with respect to a co-variable selected from, for instance, maternal age, gestational stage, maternal weight, diet, smoking, prior preterm birth, diabetes, use of prophylactic progesterone, ethnicity, or a combination thereof.

In one embodiment, the method may further include obtaining the biological sample from the first pregnant female. The obtaining may include obtaining a blood sample. The blood sample may be processed to remove cells from the blood sample. The blood sample may be processed to obtain, and optionally isolate, cell-free plasma RNA. In one embodiment, the method may further include converting RNA polynucleotides present in the biological sample into cDNA molecules, and the measuring includes hybridization between a cDNA molecule and a complementary trisomy 21 biomarker. In one embodiment, the complementary trisomy 21 biomarker is in solution during the hybridization, and in one embodiment, the complementary trisomy 21 biomarker is immobilized on a solid support.

Also provided herein are articles. In one embodiment, an article includes a substrate and a plurality of different polynucleotides. In one embodiment, the polynucleotides are selected from any combination of SEQ ID NO:8-3,248, or a complement thereof. In one embodiment, the T21 biomarkers are selected from a sequence of at least 15 consecutive nucleotides selected from any combination of SEQ ID NO:8-3,248, or a complement thereof. The polynucleotides are immobilized onto a surface of the substrate. In one embodiment, the polynucleotides are immobilized on the substrate surface to form a microarray. In one embodiment, at least 10 polynucleotides are immobilized on the substrate surface.

Also provided herein are kits. In one embodiment, a kit includes an article having a substrate, a plurality of different polynucleotides immobilized onto a surface of the substrate, and packaging materials and instructions for use. In one embodiment, the polynucleotides are selected from any combination of SEQ ID NO: 8-3,248, or a complement thereof. In one embodiment, the T21 biomarkers are selected from a sequence of at least 15 consecutive nucleotides selected from any combination of SEQ ID NO:8-3,248, or a complement thereof. In one embodiment, the polynucleotides are immobilized on the substrate surface to form a microarray.

The term "and/or" means one or all of the listed elements or a combination of any two or more of the listed elements.

The words "preferred" and "preferably" refer to embodiments of the invention that may afford certain benefits, under certain circumstances. However, other embodiments may also be preferred, under the same or other circumstances. Furthermore, the recitation of one or more preferred embodiments does not imply that other embodiments are not useful, and is not intended to exclude other embodiments from the scope of the invention.

The terms "comprises" and variations thereof do not have a limiting meaning where these terms appear in the description and claims.

Unless otherwise specified, "a," "an," "the," and "at least one" are used interchangeably and mean one or more than one.

Also herein, the recitations of numerical ranges by endpoints include all numbers subsumed within that range (e.g., 1 to 5 includes 1, 1.5, 2, 2.75, 3, 3.80, 4, 5, etc.).

For any method disclosed herein that includes discrete steps, the steps may be conducted in any feasible order. And, as appropriate, any combination of two or more steps may be conducted simultaneously.

The above summary of the present invention is not intended to describe each disclosed embodiment or every implementation of the present invention. The description that follows more particularly exemplifies illustrative embodiments. In several places throughout the application, guidance is provided through lists of examples, which examples can be used in various combinations. In each instance, the recited list serves only as a representative group and should not be interpreted as an exclusive list.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Examples of normalization sequences. Peptidylprolyl isomerase A (SEQ ID NO:l); snRNA:U6:96Aa (SEQ ID NO: 2); snRNA:U6:96Ab (SEQ ID NO: 3); and snRNA:U6:96Ac (SEQ ID NO: 4).

Figure 2. Examples of T21 Biomarkers Selection: There are 3,143 mRNA biomarkers (Figure 2a) and 98 noncoding small RNA sequences (miRNA plus snoRNA) biomarkers (Figure 2b) selected from around 25,000 genes using Affymetrix microarray technique.

Figure 3. Examples of 3,143 T21 mRNA biomarker sequences. Each biomarker includes the following: SEQ ID NO, Chromosome location, Gene Symbol, Gene Accession Number, fold-change, and sequence.

Figure 4. Examples of 98 T21 noncoding small RNA biomarker sequences (miRNA plus snoRNA). Each biomarker includes the following: SEQ ID NO, Chromosome location, Gene Symbol, Gene Accession Number, fold-change, and sequence.

Figure 5. Examples of 15 T21 mRNA biomarkers confirmed by Real-time PCR in affected pregnancies. The X-axis is the subject number. The figures represent a graphic illustration of marker expression in trisomy 21 (the squares) compared to the normal range for chromosomally normal fetuses. The dotted lines demarcate the 95% confidence interval for normal.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

Provided herein are polynucleotides useful for determining whether a subject, or a subject's fetus, has trisomy 21 (T21), and methods for using the polynucleotides. The methods described herein, and other embodiments disclosed herein such as reagents and kits, are based in part on the surprising discovery of a plurality of molecular markers, the expression levels of which consistently differentiate between healthy subjects and subjects with T21. The molecular markers are derived from coding regions whose altered expression in an affected subject, as measured from an easily obtained biological sample, is indicative of the subject, or the subject's fetus, having T21. As used herein, the term "polynucleotide" refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxynucleotides, and includes both double- and single-stranded DNA and RNA. A polynucleotide can be obtained directly from a natural source, or can be prepared with the aid of recombinant, enzymatic, or chemical techniques. A polynucleotide can be linear or circular in topology. The terms cDNA, oligonucleotide, probe, and nucleic acid are included within the definition of polynucleotide and these terms are used interchangeably. The term polynucleotide also includes peptide nucleic acids (Nielsen et al., 1991, Science. 254:1497-500), and other nucleic acid analogs and nucleic acid mimetics (see, e.g., McGall et al., U.S. Pat. No. 6,156,501).

In one embodiment, a method provided herein includes detecting one or more T21 biomarkers in a biological sample. As used herein, a "biological sample" refers to a sample of tissue or fluid obtained from a subject, including but not limited to, for example, whole blood, blood plasma, serum, lymph fluid, synovial fluid, cerebrospinal fluid, urine, and saliva. In one embodiment, a biological sample includes serum. In one embodiment the methods provided herein are directed to non-invasive methods of detecting T21, and in such an embodiment a biological sample may be a fluid. In one embodiment, a biological sample includes blood plasma. In one embodiment, a biological sample includes whole blood. As used herein, "subject" refers to a prenatal or postnatal human. A prenatal human includes a fetus. Unless indicated otherwise, as used herein the term "fetus" refers to a human during prenatal development from the time of first cell division until birth. The fetus may be at any age after implantation. For instance, the fetus may be at 2 weeks post-implantation (PI), 4 weeks PI, 6 weeks PI, 8 weeks PI, 10 weeks PI, 12 weeks PI, 14 weeks PI, 16 weeks PI, 18 weeks PI, 20 weeks PI, etc. In one embodiment, the fetus is between 8 weeks and 16 weeks PI, or between 10 weeks and 14 weeks PI. A postnatal human refers to an individual at any stage of development after birth, including a newborn, a child, an adolescent, or an adult, and includes a pregnant human mother. In one embodiment where the subject is a pregnant human mother, the mother does not have T21. In the embodiment where the subject is a pregnant human mother, a method provided herein allows one to determine if the fetus carried by the pregnant mother has T21.

As used herein, a "T21 biomarker" is a polynucleotide that is indicative of T21 in a subject. A T21 biomarker is indicative of T21 when the expression level or quantity of the biomarker is altered more often in a subject having T21 compared to a healthy subject. A T21 biomarker having an altered expression level or quantity is one that is expressed at a greater level (e.g., over-expressed) or expressed at a lower level (e.g., under-expressed) when compared to a healthy subject. Whether the expression level or quantity of a biomarker in a subject having T21 is altered, e.g., greater than or less than the expression level or quantity of the biomarker in a healthy subject, is determined using routine statistical methods by applying accepted confidence levels, and is described in greater detail herein.

It should be understood that the term "biomarker," can, depending on the context, refer to the physical polynucleotide itself or to a graphical or numerical representation of the polynucleotide such as an amount of fluorescence present at a spot on a microarray, a band on

a gel image, a numerical value, and the like. For example, the amount of fluorescence at a particular spot on a microarray may be referred to as a T21 biomarker. This graphical or numerical biomarker reflects the existence of the underlying expressed polynucleotide in the test sample, which gave rise to an expression level.

In one embodiment, the detecting of one or more T21 biomarkers in a biological sample yields an expression level of each detected biomarker. In one embodiment, the detecting of two or more T21 biomarkers in a biological sample yields a sample expression profile. An "expression level" is any physical representation of the amount of a selected T21 biomarker, as determined from one or more biological samples from a subject. A "sample expression profile" is any physical representation of the amounts of a set of two or more selected T21 biomarkers, as determined from one or more biological samples from a subject. The subject may be one known to have T21, known to have T21 of a particular type (for instance, 47XX+21, 47XY+21, or mosiac), known to be free of T21, or the status of T21 in the subject may be unknown. In one embodiment, a sample expression profile for a subject may include information from a single biological sample that has been analyzed for T21 biomarker expression levels. In one embodiment, a sample expression profile for a subject may include information from multiple types of biological samples that have been analyzed separately for T21 biomarker expression levels.

The terms "normal" and "healthy" are used herein interchangeably to refer to a subject or subjects who do not have a chromosomal abnormality associated with T21. A normal or healthy sample refers to a sample or samples obtained from a normal/healthy subject.

One skilled in the art will appreciate that more than one sample from a subject may be examined. The expression level and/or sample expression profile may be represented in visual graphical form, for example on paper or on a computer display, in a three dimensional form such as an array, and/or stored in a computer-readable medium. An expression level and/or sample expression profile may correspond to a particular status of T21 (e.g., presence or absence of T21) or type (e.g., 47XX+21, 47XY+21, or mosiac), and thus provide a template for comparison to a patient sample. A control expression level and/or a control expression profile, also referred to herein as a reference expression level and a reference expression profile, can be obtained by analyzing a biological sample from at least one healthy subject, or multiple samples obtained from a group of healthy subjects, or from one or more subjects identified as having comparable T21 in terms of type. When multiple samples from a

group are used, the levels of expression of each detected T21 biomarker may be an average, consensus, or composite derived from the multiple samples. Similarly, comparable profiles can be obtained for age-matched and/or sex-matched subjects, and comparable profiles can be obtained for pregnant mothers at the same or similar stage of pregnancy. In one embodiment, expression levels and/or expression profiles can be obtained from a pregnant mother, and if the fetus is later determined to be healthy, such expression levels and/or expression profiles can be used as control expression levels and/or control expression profiles.

One skilled in the art will appreciate that multiple nontest factors may alter the marker level measured and may be mathematically adjusted by one of several well known and routine approaches. For example, the median level of each T21 biomarker may be determined at each gestational epoch in control women. If there is a statistically significant change with gestation, regression analysis of median on gestation weighted for the number of samples per epoch may be performed to determine the normal median curve that best fits the data. All results, both affected and unaffected pregnancies, may be expressed as multiples of the gestation-specific median (MoM) based on the fitted curve. In controls, potential co-variables may be examined, including maternal weight, smoking, prior preterm birth, diabetes or use of prophylactic progesterone and ethnicity, to see if they are significantly associated with the MoM. As the sample pool grows, it is likely other variables (such maternal medical diseases) may need to be considered. Plasma levels of fetal-placental derived sequences are specifically likely to decline on average with increased adiposity due to a fixed output being diluted into a greater volume of blood. If any co-variables are confirmed, the levels can be adjusted by, for instance, dividing the observed MoM by the expected median according to the co variable level found in unaffected pregnancies. Typically, the non-parametric Wilcoxon Rank Sum Test is used to select the subset of markers where there is a significant difference in the MoM distribution between affected and control pregnancies. As a large number of potential markers are to be tested, an extreme P-value of 0.005 may be used for an initial selection.

The risk of T21 may be modeled by the a priori risk of the disorder expressed as odds (a:b) multiplied by the likelihood ratio (LR) for the marker profile derived from multivariate Gaussian frequency distributions. All current aneuploidy and pre-eclampsia markers follow an approximately log Gaussian distribution over most of their range for both affected and unaffected pregnancies, and it is expected to be true for the T21 biomarkers disclosed herein. These Gaussian distributions are defined by the marker sequence means and standard

deviations after log transformation. For a single marker, the LR is calculated by the ratio of the heights of the two overlapping distributions at the specific level. For extreme results that fall beyond the point where the data fits a Gaussian distribution, it is standard practice to use the LR at the end of the acceptable range. The method is the same for more than one marker except that the heights of multivariate log Gaussian distributions are used. These are defined, in addition to means and standard deviations, by the correlation coefficients between markers within affected and unaffected pregnancies.

The method of numerical integration may be used to model the best combination of markers from the initial subset. This involves division of each marker operating range into up to 100 equal units, calculation of the volumes under the affected and unaffected multivariate Gaussian curves risk as well as the risk in the mid-point of the volume. This determines the distribution of risks in affected and unaffected pregnancies. These distributions will be calculated for all marker combinations and the sensitivity compared for a fixed specificity.

A second approach may be considered based on the well-known fact that a strong association does not guarantee effective discrimination between affected and unaffected. Nor does a high AUC guarantee good prediction of actual risk. Hence, model calibration via reclassification can be useful in order to accept only those markers least likely to have been identified at random. Prognostic models may be built for predictive accuracy after confirmed T21 with only non-T21 biomarker variables (age, race, maternal weight, gestation age, maternal comorbidities, etc) and then build prognostic models to include T21 biomarkers. Dimensionality of the models may be reduced by translating the RNA marker contributions into a few components or composite scores. Principal components analysis may be used to derive the principal components of the T21 biomarkers factors. For instance, leading components that explain more than 85 percent of the total variation in genetic predictors may be retained and included in a prognostic model. Models that are more complicated (more predictors) may appear to have better predictive performance even if that is not the case. Therefore, the model performance may be quantified with respect to calibration and discrimination. Calibration may be examined by comparing the observed with the expected frequencies while the discriminatory accuracy may be assessed using the receiver operating characteristic (ROC) curve estimation for survival data. The true positive fraction or sensitivity and the false positive fraction (1-specificity) may be discussed using the derived prognostic models. For instance, the discriminatory accuracy may be compared between the

models with and without validated genetic markers using the area under a ROC curve (AUC). Other validation techniques including cross-validation and bootstrap methods can also be carried to shed some insights about a model's adequacy. Alternatively, prognostic models can be constructed for T21 status (affected or unaffected) using logistic regression models. Modeling procedures may be similar to those previously described for routinely used Cox models.

In one embodiment, a T21 biomarker is RNA. In one embodiment, the RNA that is detected is cell-free, and is referred to herein as cell-free RNA. Cell-free RNA includes coding RNA (mRNA) and non-coding RNAs such as siRNA, miRNA, snoRNA, and snRNA. In one embodiment, cell-free RNA is from whole blood, blood plasma, or serum, and is referred to herein as cell-free plasma (CFP) RNA. CFP RNA includes coding RNA (mRNA) and non-coding RNAs such as, but not limited to, siRNA, miRNA, snoRNA, and snRNA. For instance, when the sample is blood, the CFP RNA to be detected is present in the plasma portion of the blood. Thus, in one embodiment, a biological sample is processed to remove cells prior to the detecting. In one embodiment, a biological sample is processed to minimize cell lysis. In one embodiment, the CFP RNA that is detected may be mRNA, non-coding RNA, or the combination thereof. Optionally, the CFP RNA may be isolated.

RNA may be obtained from a biological sample using routine methods. In one embodiment, RNA is obtained using a process based on a phenol/guanidium isothiocyanate/glycerol phase separation. Such a process may result in large quantities of CFP nucleic acid with total RNA yields of 1.5-30 ug or more from only 2 mL of plasma and full range of RNAs including not only mRNA but also small noncoding RNAs such as miRNA and snoRNA. This amount is more than enough for array technology and the performance of numerous PCR reactions using a clinically practical, single patient sample.

The RNA isolation method described herein allows for the isolation of 1.5 micrograms to 7 micrograms of CFP RNA from a 2 mL sample, which is more than enough for both microaarray gene screening and PCR validation. The method may include obtaining 2 mL or more of sample from a subject, such as plasma, and following the steps as described in Example 1.

The analysis of samples of blood obtained from pregnant mothers who later gave birth to healthy infants or gave birth to infants with T21 has led to the discovery of T21 biomarkers. Examples of T21 biomarkers are described at SEQ ID NO:8-3,248. Different

combinations of the T21 biomarkers listed at SEQ ID NO:8-3,248, or the complement thereof, allow the skilled person to predict whether the fetus carried by a pregnant mother has T21. Changes in the expression levels of these biomarker polynucleotides in a subject, as measured in a biological sample from the subject, thus may be used to indicate the presence, absence, or type or T21 in a subject, such as a fetus carried by a mother, or an infant, child, adolescent, or adult.

The panel of T21 biomarkers includes a subset encoded by chromosome 21 (SEQ ID NOs:3,028-3,065 and 3,238, see Figure 2A and 2B). That subset includes polynucleotides found to be up-regulated in a pregnant mother carrying a fetus that is T21 when compared to a pregnant mother carrying a normal fetus. That subset also includes polynucleotides found to be down-regulated in a pregnant mother carrying a fetus that is T21 when compared to a pregnant mother carrying a normal fetus. The panel of biomarkers includes a subset encoded by chromosomes other than chromosome 21, e.g., chromosomes 1-20, 22, and/or x (SEQ ID NOs:8-3,027, 3,066-3,227 and 3,239-3,248, see Figure 2A and 2B). That subset includes polynucleotides found to be up-regulated in a pregnant mother carrying a fetus that is T21 when compared to a pregnant mother carrying a normal fetus. That subset also includes polynucleotides found to be down-regulated in a pregnant mother carrying a fetus that is T21 when compared to a pregnant mother carrying a normal fetus. The panel of T21 biomarkers includes a subset that are mRNAs (SEQ ID NO:8-3,250) and a subset that are small non-coding RNAs (SEQ ID NO:3,251-3,248). An expression level of a T21 biomarker may include polynucleotide expression level information for one polynucleotide chosen from SEQ ID NO:8-3,248, obtained from a biological sample from a subject. A sample expression profile may include polynucleotide expression level information for two or more polynucleotides chosen from SEQ ID NO:8-3,248, obtained from a biological sample from a subject, for instance, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30. A sample expression profile may include polynucleotide expression level information for no greater than 30 polynucleotides chosen from SEQ ID NO:8-3,248, obtained from a biological sample from a subject, for instance, no greater than 30, no greater than 29, no greater than 28, no greater than 27, no greater than 26, no greater than 25, no greater than 24, no greater than 23, no greater than 22,

no greater than 21, no greater than 20, no greater than 19, no greater than 18, no greater than 17, no greater than 16, no greater than 15, no greater than 14, no greater than 13, no greater than 12, no greater than 11, no greater than 10, no greater than 9, no greater than 8, no greater than 7, no greater than 6, or no greater than 5.

The skilled person will recognize that detecting a T21 biomarker present in a subject may not require use of an entire nucleotide sequence disclosed at any of SEQ ID NO: 8-3,248. A nucleotide sequence used in a method provided herein is of a length that is at least substantially unique for a T21 biomarker to specifically hybridize with a RNA, such as a CFP RNA, present in a biological sample. A nucleotide sequence used in a method provided herein may be RNA, DNA, or RNA/DNA hybrid.

In one embodiment, a T21 biomarker present in a biological sample may be a polynucleotide that contains or consists of the sequence which defines the T21 biomarker target or complement thereof. The T21 biomarker may be identical to one of SEQ ID NOs:8-3,248, or can be a complement thereof, sense or antisense, as well as a sequence that hybridizes therewith under suitable conditions. In one embodiment, a T21 biomarker used to detect a RNA present in a biological sample, such as a CFP RNA, may be at least 15, at least 20, at least 25, at least 30, at least 35, or at least 40 nucleotides in length, and so on, of a sequence selected from SEQ ID NO:8-3,248, or the complement thereof. In one embodiment, a T21 biomarker may include a sequence selected from SEQ ID NO:8-3,248, or the complement thereof, that is from 15 nucleotides to the full sequence, from 16 nucleotides to 100 nucleotides, from 17 nucleotides to 50 nucleotides, from 18 nucleotides to 30 nucleotides, from 19 nucleotides to 25 nucleotides, or from 20 to 22 nucleotides. A T21 biomarker selected from SEQ ID NO: 8-3,248 may have perfect identity, at least 95% identity, at least 90% identity, at least 85% identity, or at least 80% identity with a sequence disclosed herein. A T21 biomarker selected from SEQ ID NO:8-3,248 may have perfect complementarity or at least 95% complementarity, at least 90% complementarity, at least 85% complementarity, or at least 80% complementarity with a sequence disclosed herein. A T21 biomarker may be continuous or it can have one or more bulges or mismatches upon hybridization. A T21 biomarker used to detect a RNA in a biological sample may also include one or more chemical modifications, such as a 2' carbon modification. A T21 biomarker may or may not form an overhang upon hybridization when detecting a RNA present in a biological sample.

"Hybridization" includes any process by which a strand of a nucleic acid sequence joins with a second nucleic acid sequence strand through base-pairing. Hybridization of polynucleotides is affected by such conditions as salt concentration, temperature, or organic solvents, in addition to the base composition, length of the complementary strands, and the number of nucleotide base mismatches between the hybridizing nucleic acids, as will be readily appreciated by those skilled in the art. Stringency conditions depend on the length and base composition of the nucleic acid, which can be determined by techniques well known in the art. Generally, stringency can be altered or controlled by, for example, manipulating temperature and salt concentration during hybridization and washing. For example, a combination of high temperature and low salt concentration increases stringency. The degree of stringency may be based, for example, on the calculated (estimated) melting temperature (T_m) of the polynucleotide. Calculation of T_m is well known in the art. For example, "maximum stringency" typically occurs at around T_m -5°C (5° below the T_m of the probe); "high stringency" at around 5-10° below the T_m; "intermediate stringency" at around 10-20° below the T_m of the probe; and "low stringency" at around 20-25° below the T_m. Maximum stringency conditions may be used to identify a polynucleotide present in a biological sample having strict identity or near-strict identity with a T21 biomarker selected from SEQ ID NO:8-3,248; while high stringency conditions are used to identify a polynucleotide present in a biological sample having about 80% or more sequence identity with a T21 biomarker. Such conditions are known to those skilled in the art and can be found in, for example, Strauss, W. M. "Hybridization With Radioactive Probes," in Current Protocols in Molecular Biology 6.3.1-6.3.6, (John Wiley & Sons, N.Y. 2000). Both aqueous and nonaqueous conditions as described in the art can be used.

Expression levels of any one or more of the T21 biomarkers described herein may be used to determine the presence, absence, or type of T21 in a subject. In one embodiment, expression levels of one or more T21 biomarkers encoded by chromosome 21 may be used to determine the presence, absence, or type of T21 in a subject. In one embodiment, expression levels of one or more T21 biomarkers encoded by the remaining 21 autosomes (chromosomes 1-22 exclusive of chromosome 21) and X may be used to determine the presence, absence, or type of T21 in a subject. In one embodiment, expression levels of one or more T21 biomarkers encoded by any combination of chromosomes 1-22 and X may be used to determine the presence, absence, or type of T21 in a subject. In one embodiment, expression

levels of one or more T21 biomarkers encoded by one chromosome selected from 1-22 and X may be used to determine the presence, absence, or type of T21 in a subject. In one embodiment, expression levels of one or more T21 biomarkers that are mRNAs (SEQ ID NO:8-3,250) may be used to determine the presence, absence, or type of T21 in a subject. In one embodiment, expression levels of one or more T21 biomarkers that are small non-coding RNAs (SEQ ID NO: 3,251-3,248) may be used to determine the presence, absence, or type of T21 in a subject. In one embodiment, the T21 biomarkers used may be those that are up-regulated in a pregnant mother carrying a fetus that is T21 when compared to a pregnant mother carrying a normal fetus. In one embodiment, the T21 biomarkers used may be those that are down-regulated in a in a pregnant mother carrying a fetus that is T21 when compared to a pregnant mother carrying a normal fetus. In one embodiment, the T21 biomarkers used may be a combination of those that are up-regulated and those that are down-regulated in a pregnant mother carrying a fetus that is T21 when compared to a pregnant mother carrying a normal fetus.

The number of T21 biomarkers used in an assay to determine the presence, absence, or type or T21 in a subject may vary. The skilled person will appreciate that, generally, the more biomarkers examined, the more accurate the determination of the presence, absence, or type of T21 in a subject; however, the skilled person will also appreciate that there is a minimum number of biomarkers useful for an accurate diagnosis of T21. In one embodiment, the number of T21 biomarkers evaluated in practicing a method provided herein may be at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30. In one embodiment, the number of T21 biomarkers evaluated in practicing a method provided herein may be no greater than 30, no greater than 29, no greater than 28, no greater than 27, no greater than 26, no greater than 25, no greater than 24, no greater than 23, no greater than 22, no greater than 21, no greater than 20, no greater than 19, no greater than 18, no greater than 17, no greater than 16, no greater than 15, no greater than 14, no greater than 13, no greater than 12, no greater than 11, no greater than 10, no greater than 9, no greater than 8, no greater than 7, no greater than 6, or no greater than 5. In one embodiment, the number of CFP RNAs detected varies depending upon whether the fetus or subject is normal or abnormal.

All the T21 biomarkers measured in a subject having T21 may not show altered expression levels when compared to a healthy subject. A subject may be considered to have T21 when at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% of the T21 biomarkers in a sample expression profile from the subject's biological sample show altered expression when compared to those T21 biomarkers in a control expression profile from a healthy subject. For instance, in an embodiment where 10 biomarkers are measured in a biological sample from a subject, such as a pregnant mother carrying a fetus with T21, the subject may be considered to have T21 when at least 6 of the biomarkers in a sample expression profile show altered expression when compared to those T21 biomarkers in a control expression profile from a healthy subject. Some of the T21 biomarkers in a subject not having T21 may show altered expression levels when compared to another healthy subject. A subject may be considered not to have T21 when no greater than 40%, no greater than 35%, no greater than 30%, no greater than 25%, no greater than 20%, no greater than 15%, no greater than 10%, no greater than 5%, or none of the T21 biomarkers in a sample expression profile from the subject's biological sample show altered expression when compared to those T21 biomarkers in a control expression profile from another healthy subject. For instance, in an embodiment where 10 biomarkers are measured in a biological sample from a subject, such as a pregnant mother carrying a normal fetus, the subject may be considered to have a normal fetus when no more than 4 of the biomarkers in a sample expression profile show altered expression when compared to the normal range for the population of healthy fetuses.

Whether the expression level or quantity of a biomarker in a subject having T21 is greater than or less than the expression level or quantity of the biomarker in a healthy subject is determined using routine statistical methods by applying accepted confidence levels. The expression level or quantity of a T21 biomarker in a biological sample is considered to be altered if the difference in amount of the biomarker in a test sample is increased or decreased to a statistically significant degree compared to the amount of the biomarker in a control sample. The term "statistically significant" refers to a result, namely a difference in numbers of positive results between a test and a control that is not likely due to chance. The minimum chance level for statistical significance herein is 95% probability that the result is not due to chance, i.e., random variations in the data. A 95% confidence interval means that if the procedure for computing a 95% confidence interval is used over and over, 95% of the time the

interval will contain the true parameter value. In one embodiment, the minimum chance level for statistical significance is 97% probability, 99% probability, or 99.9% probability. Various methods, as is known, can be used to calculate statistical significance. Examples include, but are not limited to, binomial probabilities, the Poisson distribution, chi-square, and t-test. The skilled person will recognize that one may use sufficient numbers of results to obtain a confidence interval of at least 95%, or higher, in order to determine statistical significance of a difference in expression level or quantity of a biomarker in a subject having T21 and the expression level or quantity of the biomarker in a healthy subject.

In one embodiment, a subject is considered to have T21 when comparison of expression of at least one T21 biomarker, or a plurality of T21 biomarkers, with the expression level of the at least one T21 biomarker, or a plurality of T21 biomarkers, in a biological sample from a subject not having T21 shows a difference, and that difference is indicative of the presence of T21 in the subject. In one embodiment, a subject is considered to have T21 when expression of at least one T21 biomarker, or a plurality of T21 biomarkers, is altered to a statistically significant degree in a biological sample from the subject compared to a biological sample from a subject not having trisomy 21. In one embodiment, a subject is considered to have T21 when comparison of expression of at least one T21 biomarker with the expression level of the at least one T21 biomarker in a biological sample from a subject not having T21 shows that the expression level or quantity of a biomarker in the subject is outside the 95% confidence interval for the biomarker. In one embodiment, a subject is considered to have T21 when comparison of expression of a plurality of T21 biomarkers with the expression level of the plurality of T21 biomarkers in a biological sample from a subject not having T21 shows that the expression level or quantity of the plurality of biomarker in the subject is outside the 95% confidence interval for the plurality of the biomarkers.

Accordingly, in one embodiment, a method provided herein includes measuring a plurality of T21 biomarkers in a biological sample obtained from a subject, such as a pregnant female. The plurality of T21 biomarkers measured may be selected from any combination of SEQ ID NO:8-3,248, or a complement thereof, or a portion thereof. The plurality of T21 biomarkers measured may be polynucleotides that hybridize to a sequence selected from any one of SEQ ID NO:8-3,248 under suitable conditions. In one embodiment, a method provided herein includes detecting T21 biomarkers in a biological sample to yield an expression level of each detected T21 biomarker. The T21 biomarkers may be selected from

any combination of SEQ ID NO: 8-3,248, or a complement thereof, or a portion thereof. The T21 biomarkers detected may be polynucleotides that hybridize to a sequence selected from any one of SEQ ID NO:8-3,248 under suitable conditions. The biological sample may include plasma from a pregnant female. In one embodiment, a method disclosed herein includes detecting T21 biomarkers in a biological sample to yield a sample expression profile. The T21 biomarkers may be selected from any combination of SEQ ID NO: 8-3,248, or a complement thereof, or a portion thereof. The T21 biomarkers detected may be selected from SEQ ID NO:8-3,248, or a complement thereof, or a portion thereof. The T21 biomarkers detected may be polynucleotides that hybridize to a sequence selected from any one of SEQ ID NO:8-3,248 under suitable conditions. The biological sample may include plasma from a pregnant female.

In one embodiment, such as one where the subject is a pregnant female, a method disclosed herein may include identifying the fetus as i) having trisomy 21 if expression of the plurality of biomarkers is altered to a statistically significant degree in the biological sample compared to a biological sample from a second pregnant female carrying a fetus not having trisomy 21, or ii) not having trisomy 21 if expression of the plurality of biomarkers is not altered to a statistically significant degree in the biological sample compared to a biological sample from a second pregnant female carrying a fetus not having trisomy 21. In one embodiment, such as one where the subject is a pregnant female, the method may further include comparing the expression level of a detected T21 biomarker to the expression level of the T21 biomarker in pregnant females carrying a fetus without T21, wherein an expression level of a detected T21 biomarker that is outside the 95% confidence interval for that T21 biomarker indicates the expression level of the T21 biomarker is altered. In one embodiment, such as one where the subject is a pregnant female, the method may further include comparing the sample expression profile with a reference expression profile; wherein a difference between the sample expression profile and the reference expression profile is indicative of the presence or absence of trisomy 21 in the fetus.

In one embodiment, such as one where the fetus is diagnosed as having T21, a method may further include recommending to the pregnant female a genetic test chosen from amniocentesis, cordocentesis, and chorionic villus sampling, ultrasound, or a combination thereof.

Amounts of T21 biomarkers in a biological sample may be determined in absolute or relative terms. If expressed in relative terms, amounts can be expressed as normalized amounts with reference to one or more normalization sequences present in a biological sample.

It is expected that this method will have a sensitivity (percent of fetuses or subjects having T21 correctly identified, also referred to as detection rate) of at least 98%, at least 99%, or 100% when enough T21 biomarkers present in a biological sample are detected. It is also expected that this method will have a specificity (percent of fetuses or subjects not having T21 correctly identified) of at least 98%, at least 99%, or 100% when enough T21 biomarkers present in a biological sample are detected.

Measuring the expression level or quantity of any single T21 biomarker or a plurality of T21 biomarkers may be accomplished by use of techniques that are known in the art and routine. In one embodiment, the expression level or quantity of a T21 biomarker or a plurality of T21 biomarkers may be monitored directly by detecting RNA present in a biological sample. RNA may be obtained from a biological sample using routine techniques known in the art. In one embodiment, the RNA is cell-free RNA obtained from biological tissue and/or fluid. In one embodiment, the RNA is cell-free plasma RNA obtained from whole blood, blood plasma, or serum. In one embodiment, the RNA is isolated. As used herein, the term "isolated" refers to a polynucleotide that has been removed from its natural environment.

Detecting one or more T21 biomarkers that are present as a RNA polynucleotide may be accomplished by a variety of methods. Some methods are quantitative and allow estimation of the original levels of RNA between the levels present in a test sample and a control, such as a control expression level for a T21 biomarker and/or a control expression profile, whereas other methods are merely qualitative. In one embodiment, a method for detecting one or more T21 biomarkers may include the use of polynucleotides that are in solution, and may be in any format, including, but not limited to, the use of individual tubes or a high throughput device, such as a PCR-card.

Quantitative real-time PCR (QRT-PCR) may be used to measure the differential expression of any T21 biomarker in a test sample and a control. In QRT-PCR, the RNA template is generally reverse transcribed into cDNA, which is then amplified via a PCR reaction. The primers used for amplification may be selected by determining which T21 biomarker(s) described at SEQ ID NO:8-3,248 is to be amplified, and then designing primers

using routine methods known in the art. The PCR amplification process is catalyzed by a thermostable DNA polymerase. Non-limiting examples of suitable thermostable DNA polymerases include Taq DNA polymerase, Pfu DNA polymerase, Tli (also known as Vent) DNA polymerase, Tfl DNA polymerase, and Tth DNA polymerase. The PCR process may include three steps (i.e., denaturation, annealing, and extension) or two steps (i.e., denaturation and annealing/extension). The temperature of the annealing or annealing/extension step may vary, depending upon the amplification primers and other parameters such as concentration. The temperature of the annealing or annealing/extending step may range from about 50°C to about 75°C. The amount of PCR product is followed cycle-by-cycle in real time, which allows for determination of the initial concentrations of mRNA. The reaction may be performed in the presence of a dye that binds to double-stranded DNA, such as SYBR Green. The reaction may also be performed with fluorescent reporter probes, such as TAQMAN probes (Applied Biosystems, Foster City, Calif.) that fluoresce when the quencher is removed during the PCR extension cycle. Fluorescence values are recorded during each cycle and represent the amount of product amplified to that point in the amplification reaction. The cycle when the fluorescent signal is first recorded as statistically significant is the threshold cycle (Ct). To minimize errors and reduce any sample-to-sample variation, QRT-PCR is typically performed using one or more normalization sequences.

Reverse-transcriptase PCR (RT-PCR) may also be used to measure the expression of a T21 biomarker. As described above, the RNA template is reverse transcribed into cDNA, which is then amplified via a typical PCR reaction. After a set number of cycles the amplified DNA products are typically separated by gel electrophoresis. Comparison of the relative amount of PCR product amplified in different samples will reveal whether the expression of a T21 biomarker is altered in a test sample.

Expression of a T21 biomarker may also be measured using a nucleic acid microarray (also referred to in the art as a DNA chip or biochip). In this method, single-stranded polynucleotides selected from at least a portion of SEQ ID NO:8-3,248, or a complement thereof, are plated, or arrayed, on a solid support. The solid support may be a material such as, for instance, glass, silica-based, silicon-based, a synthetic polymer, a biological polymer, a copolymer, a metal, or a membrane. The form or shape of the solid support may vary, depending on the application. Suitable examples include, but are not limited to, slides, strips, plates, wells, microparticles, fibers (such as optical fibers), gels, and combinations thereof.

The arrayed immobilized sequences are generally hybridized with specific DNA probes obtained from the test sample. As described above, RNA present in a sample, including T21 biomarkers, is generally reverse transcribed into cDNA. Fluorescently labeled cDNA probes may be generated through incorporation of fluorescently labeled deoxynucleotides during the reverse transcription step. The cDNA probes are hybridized to the immobilized nucleic acids on the solid support under highly stringent conditions. After stringent washing to remove non-specifically bound probes, the solid support is scanned using routine methods, for instance, by confocal laser microscopy or by another detection method, such as a CCD camera. Quantitation of hybridization of each arrayed element allows for assessment of corresponding RNA abundance. With multiple color fluorescence, separately labeled cDNA probes may be hybridized pairwise to the array. The relative abundance of the transcripts from the two sources corresponding to each specified T21 biomarker may then be determined simultaneously. Microarray analysis may be performed by commercially available equipment, following manufacturer's protocols, such as by using the Affymetrix GenChip technology, or Incyte's microarray technology.

Differential expression of a T21 biomarker may also be measured using Northern blotting. For this, RNA samples are first separated by size via electrophoresis in an agarose gel under denaturing conditions. The RNA is then transferred to a membrane, crosslinked, and hybridized, under highly stringent conditions, to a labeled DNA probe. After washing to remove the non-specifically bound probe, the hybridized labeled species are detected using routine techniques known in the art. The probe may be labeled with, for instance, a radioactive element, a chemical that fluoresces when exposed to ultraviolet light, a tag that is detected with an antibody, or an enzyme that catalyses the formation of a colored or a fluorescent product. A comparison of the relative amounts of RNA detected in a control sample and a test sample will reveal whether the expression of one or more T21 biomarkers or changed in the test sample.

Nuclease protection assays may also be used to monitor the altered expression of a T21 biomarker in a test sample and a control. In nuclease protection assays, an antisense probe hybridizes in solution to a RNA sample. The antisense probe may be labeled with an isotope, a fluorophore, an enzyme, or another tag. Following hybridization, nucleases are added to degrade the single-stranded, unhybridized probe and RNA. An acrylamide gel is used to separate the remaining protected double-stranded fragments, which are then detected

using techniques well known in the art. Again, qualitative differences in expression may be detected.

In one embodiment, expression of a T21 biomarker may be examined *in vivo* in a subject. One or more RNA polynucleotides may be labeled with fluorescent dye, a bioluminescent marker, a fluorescent semiconductor nanocrystal, or a short-lived radioisotope, and then the subject may be imaged or scanned using a variety of techniques, depending upon the type of label.

In one embodiment, the detection of a RNA, such as a CFP RNA, uses the nucleotides of a specific exon as described in SEQ ID NO: 8-3,248. Thus, if QRT-PCR is used to detect a specific CFP RNA, the primers used to amplify the CFP RNA will amplify all or a portion of an exon described in SEQ ID NO: 8-3,248. If a microarray is used to detect a specific CFP RNA, the arrayed immobilized sequence used to detect the CFP RNA will be based on all or a portion of an exon described in SEQ ID NO:8-3,248, or a complement thereof. A person skilled in the art will know which parameters may be manipulated to optimize detection of a RNA of interest using one or more of the polynucleotides listed at SEQ ID NO:8-3,248.

When determining whether the expression of a T21 biomarker or a plurality of T21 biomarkers are altered in a test sample compared to a control expression level or a control expression profile, it can be helpful to use a normalization sequence. A normalization sequence is a polynucleotide that can be used to normalize the relative amounts of polynucleotides, and/or data obtained from the polynucleotides, from one sample to the next. A normalization sequence can be RNA that has an expression level or quantity that is generally stable under the conditions studied. That is, the normalization sequence can have an expression level or quantity that is substantially unaffected by physiological circumstances present in a subject, and thus the normalization sequence can be used to normalize the amount of polynucleotides in separate samples for comparison. The separate samples can be from different subjects or the same subject at different time points, such as different time points in pregnancy. For example, the normalization sequence can be used to normalize the amount of RNA in QRT-PCR studies, such as by normalizing the amount of a RNA sequence of interest. The normalization sequences described herein can be used alone or in combination, and may be used to normalize samples to be assayed for T21 biomarkers. Thus, the normalization sequences provided herein can be for quantification of cell-free RNA, including CFP RNA, present in a biological sample.

It has been determined that previously reported normalization sequences utilized in other tissues for quantification of isolated RNA (e.g., mRNA: 18s RNA, RPLPO, and GAPDH; miRNA: miR-103, miR-146a, and miR-197) were either expressed inconsistently in control plasma samples or were altered by either pregnancy, gestational age or disease (see Dong and Weiner, WO 12/075150). The normalization sequences described can include cell-free plasma RNA sequences (including coding sequences, e.g., mRNA, and/or non-coding sequences, e.g., miRNA) that are substantially unchanged by a condition. In one embodiment, the normalization sequences are substantially unchanged during the course of pregnancy.

Normalization sequences appropriate for use in the methods provided herein may be identified as described in Dong and Weiner (WO 12/075150). In one embodiment, the normalization sequence includes a circulating RNA. Such a normalization sequence can be described as human (i.e., *Homo sapiens)* peptidylprolyl isomerase A (i.e., cyclophilin A, rotmase A), which is encoded by a PPIA coding region. The normalization sequence can be an mRNA for peptidylprolyl isomerase. An example of a peptidylprolyl isomerase normalization sequence can be found at accession number: NM_021 130 and/or NM_001008741. An example of a peptidylprolyl isomerase normalization sequence that may be useful for normalization of mRNA is depicted at SEQ ID NO: 1 (see Figure 1). In one embodiment, the normalization sequence may include miRNA. Such a normalization sequence may be a *Drosophila melanogaster* small nuclear RNA, such as snRNA:U6. The snRNA:U6 normalization sequence can be snRNA:U6 at 96Aa, 96:Ab, and/or 96Ac. Examples of these normalization sequences include snRNA:U6:96Aa (SEQ ID NO: 2 for miRNA), snRNA:U6:96Ab (SEQ ID NO: 3 for miRNA), and/or snRNA:U6:96Ac (SEQ ID NO: 4 for miRNA) (see Figure 1), and can be found at the following accession numbers, respectively: NR_00208 1 (snRNA:U6:96Aa); NR_002082 (snRNA:U6:96Ab); and NR_002083 (snRNA:U6:96Ac). Accordingly, SEQ ID NO:l may be used for normalization of mRNA, and SEQ ID NOs: 2-4 may be used for normalization of miRNA. More than one normalization sequence may be used.

Primers and probes for these sequences can be readily obtained by one of ordinary skill in the art. For example, sequences for the forward primer, reverse primer, and probe for SEQ ID NO:l (e.g., for an mRNA normalization sequence) may be: Forward primer: GCTTTGGGTCCAGGAATGG (SEQ ID NO:5); Reverse primer:

GTTGTCCACAGTCAGCAATGGT (SEQ ID NO:6); and Probe: AGACCAGCAAGAAGAT (SEQ ID NO:7). These polynucleotides may also be used as normalization sequences in the methods provided herein.

In one embodiment, a normalization sequence may be a polynucleotide that contains or consists of the sequence. The normalization sequence can be identical to one of SEQ ID NO: 1-7, or can be a complement thereof, sense or antisense, as well as a sequence that hybridizes therewith under suitable conditions. In one embodiment, a normalization sequence may include a sequence selected from SEQ ID NO: 1-7, or the complement thereof, that is at least 15 nucleotides, at least 20 nucleotides, at least 25 nucleotides, at least 30 nucleotides, at least 35 nucleotides, at least 40 nucleotides, at least 45 nucleotides, at least 50 nucleotides, or at least 55 nucleotides, to the full sequence. In one embodiment, the normalization sequence can include a sequence of SEQ ID NO:l, 2, 3, 4, 5, 6, or 7. A normalization sequence may have perfect identity, at least 95% identity, at least 90% identity, at least 85% identity, or at least 80% identity with a sequence selected from SEQ ID NO: 1-7. A normalization sequence may have perfect complementarity or at least 95% complementarity, at least 90% complementarity, at least 85% complementarity, or at least 80% complementarity with a sequence selected from SEQ ID NO: 1-7. A normalization sequence may be continuous or it can have one or more bulges or mismatches upon hybridization. A normalization sequence may also include one or more chemical modifications, such as a 2' carbon modification. A normalization sequence may or may not form an overhang upon hybridization when detecting a RNA present in a biological sample.

Provided herein is an article that includes a substrate and a plurality of individual polynucleotides. The individual polynucleotides may be selected from SEQ ID NO:8-3,248, or a complement thereof, or a portion thereof. The polynucleotides are immobilized onto a surface of the substrate. In one embodiment, the polynucleotides are immobilized on the substrate surface to form a microarray.

Provided herein are kits. A kit may include one or more polynucleotides for measuring the expression of at least one T21 biomarker, wherein alteration in the expression of the one or more T21 biomarkers in a subject relative to a control is indicative of the presence, absence, or type of T21. A kit may include one or more polynucleotides that are specific to a selected T21 biomarker

A polynucleotide present in a kit may have a sequence that is identical to a polynucleotide listed at SEQ ID NO: 8-3,248, or the complement thereof. In one embodiment, polynucleotide present in a kit may have a portion of a sequence that is identical to a polynucleotide listed at SEQ ID NO: 8-3,248, or the complement thereof. The polynucleotides to be used in the measurement of the expression of one or more T21 biomarkers can, depending upon the type of technique to be used. For example, the kit may include polynucleotides useful as primers for QRT-PCR. Polynucleotides useful as probes may be included in a kit and are optionally provided together with a solid substrate, such as but not limited to a bead, a chip, a plate, and a microarray. Polynucleotides may be immobilized on the surface of such a substrate. A kit may also further include a reverse transcriptase, a thermostable DNA polymerase , appropriate buffers and salts, or the combination thereof.

Additional reagents useful in the methods described herein, for example determining the presence, absence, or type of T21 in a subject, may be provided in a kit. Depending on the technique or procedure, the kit may further include one or more additional reagents such as, but not limited to, buffers such as amplification buffers, hybridization buffers, labeling buffers, or any equivalent reagent. Reagents may be supplied in solid (e.g., lyophilized) or liquid form, and these may optionally be provided in individual packages using containers such as vials, packets, bottles and the like, for each individual reagent. Each component can for example be provided in an amount appropriate for direct use or may be provided in a reduced or concentrated form that can be reconstituted.

A kit may further include materials and tools useful for carrying out methods described herein. A kit can be used for example in diagnostic laboratories, clinical settings, or research settings. The kit may further include instructions for use, including for example any procedural protocols and instructions for using the various reagents in the kit for performing different steps of the process. Instructions for using the kit according to one or more methods of the invention may include instructions for processing a biological sample obtained from a subject and/or for performing the test, and instructions for analyzing or interpreting the results. Instructions may be provided in printed form or stored on any computer readable medium including but not limited to DVDs, CDs, hard disk drives, magnetic tape and servers capable of communicating over computer networks. A kit may further include one or more normalization sequences.

It will be understood that generally, components of a kit are conveniently packaged or bound together for ease of handling in commercial distribution and sale.

The present invention is illustrated by the following examples. It is to be understood that the particular examples, materials, amounts, and procedures are to be interpreted broadly in accordance with the scope and spirit of the invention as set forth herein.

Example 1

T21 Cell Free Plasma Biomarker Confirmation Protocol

Presented here is an example of an assay that was used to confirm the microarray biomarker identification for those biomarkers identified as altered in pregnant mothers carrying a fetus that has trisomy 21. More than 1 million exon clusters and 1769 non-coding small RNAs were screened by Affymetrix GeneChip Human Exon ST and Affymetrix GeneChip miRNA Arrays, respectively. A total of 3143 mRNA biomarkers (38 encoded by chromosome 21, 3105 encoded by a chromosome other than 21) and 98 non-coding small RNAs (miRNA and snoRNA) were identified as informative. Fifteen of these markers (10 from a gene on chromosome 21 and 5 from one of the other autosomes) were selected for confirmation based on their predictive profiles. These data confirm that the microarray analysis functioned as designed and identified biomarkers that were informative of the trisomy 21 status of a fetus.

Blood Plasma Cell Free RNA isolation. A blood sample was taken from pregnant mothers at approximately 12-16 weeks of pregnancy. The blood sample was spun 200x g for 5 minutes, at 4 °C, to separate the cells from plasma. Plasma was transferred to eight tubes (250 microliters (ul) per tube). TRIzol LS (Invitrogen, Grand Island, NY, Cat. no 10296-010) (750 ul) was added to each tube, shaken vigorously, and incubated for 5 minutes at room temperature. Two hundred microliters of chloroform were added to each tube, shaken vigorously, and incubated for 10 minutes at room temperature. The tubes were centrifuged at 10,000 x g for 15 minutes at 4 °C. The resulting upper phase contained RNA, and the lower phase contained DNA and protein.

The upper aqueous phase (300ul/tube) was transferred to a new tube. Thirty microliters of 3M Sodium acetate (Ambion, Grand Island, NY, cat. No. AM9740), pH:5.5, and 3 volumes of 100% ice cold EtOH (Sigma, St. Louis, MO, cat. no. E702) (900 ul) were added and the tubes incubated at -20°C, overnight. After centrifugation at 12,000x g for 75 minutes (4 °C), all liquid was carefully removed. The pellet was washed with 50 ul per tube with ice cold 80% EtOH, and all the tubes from one patient were combined into one tube. This tube was centrifuged for 60 minutes at 12,000x g at 4 °C. All liquid was removed, and the tube was incubated at 37°C for 40 minutes.

The pellet was suspended in 20 to 40 ul of Diethylpyrocarbonate- (Sigma, cat. no. D5758) (DEPC) treated water, incubated at 56°C for 10 minutes to dissolve the RNA, then transferred to ice for 30 minutes.

RNA concentration. RNA concentration was measured by using a Qubit® 2.0 Fluorometer (Life Technologies, Grand Island, NY) as recommended by the manufacturer. Briefly, calibration of the Qubit® 2.0 Fluorometer was done using Standard #1 and #2. Working solution was prepared by diluting the Qubit™ RNA reagent at 1:200 in Qubit™ RNA buffer. Working solution (190 ul) and 10 ul of standard or RNA sample were mixed, then incubate at room temperature for 2 minutes. The RNA concentration was determined.

Reverse Transcription. Reverse transcription (RT) of the RNA was prepared using a Superscript® VILO cDNA synthesis kit (Life Technologies, cat. no. 11755050) and ERCC RNA Spike-in control mixes (Life Technologies, cat. no. 11755050) diluted 1:100. Each RT reaction contained Superscript® VILO™ MasterMix (4 ul), ERCC RNA Spike-in control (2 ul), 1,000 nanograms (ng) RNA, and H_20 to a final volume of 20 ul. The RT reaction was run using the following conditions: step 1 was 25°C, 10 minutes; step 2 was 42°C, 60 minutes; and step 3 was 85°C, 5 minutes. After the cDNA was produced the tubes were held at 4 until transfer to -20°C.

Preamplification. Preamplification of cDNAs to expand the signal were prepared by mixing a preamplification reaction in a 0.2 ml PCR tube as follows: cDNA, 100 ng; PreAmp Mix (ABI, cat. no. 4391128), 15 ul; probes, final concentration of 100 nM; H_20 to a final volume of 30 ul. The preamplification reaction was run using the following conditions: the reaction was held at 95°C for 10 minutes, and then cycled through 14 cycles of 95°C for 15 seconds followed by 60°C for 15 seconds. The reaction was then held at 99.9°C for 10 minutes, transferred to 4°C, and then stored at -20 °C.

Real-time PCR: PCR reactions were prepared by mixing 10 ul of a preamplified reaction, 45 ul of H_20, and 55 ul of TaqMan Universal PCR Master Mix (ABI, cat. no. 4440040). The thermal cycling reaction was run using the following conditions: the reaction was held at 50°C for 2 minutes, held at 95°C for 10 minutes, and then cycled through 40 cycles of 95°C for 15 seconds followed by 60°C for 1 minute.

Data analysis. For the initial analysis, the 95% confidence interval for expression (normalized to the described normalization sequences) of each of the fifteen (15) selected T21 markers at 12 weeks gestation was calculated (Figure 5, area between the dotted lines of each graph). Expression levels of the fifteen T21 biomarkers were then measured and plotted (squares) against the normal range for 10 affected pregnancies at 12 weeks gestation.

The complete disclosure of all patents, patent applications, and publications, and electronically available material (including, for instance, nucleotide sequence submissions in, e.g., GenBank and RefSeq, and amino acid sequence submissions in, e.g., SwissProt, PIR, PRF, PDB, and translations from annotated coding regions in GenBank and RefSeq) cited herein are incorporated by reference in their entirety. Supplementary materials referenced in publications (such as supplementary tables, supplementary figures, supplementary materials and methods, and/or supplementary experimental data) are likewise incorporated by reference in their entirety. In the event that any inconsistency exists between the disclosure of the present application and the disclosure(s) of any document incorporated herein by reference, the disclosure of the present application shall govern. The foregoing detailed description and examples have been given for clarity of understanding only. No unnecessary limitations are to be understood therefrom. The invention is not limited to the exact details shown and described, for variations obvious to one skilled in the art will be included within the invention defined by the claims.

Unless otherwise indicated, all numbers expressing quantities of components, molecular weights, and so forth used in the specification and claims are to be understood as being modified in all instances by the term "about." Accordingly, unless otherwise indicated to the contrary, the numerical parameters set forth in the specification and claims are approximations that may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the doctrine of equivalents to the scope of the claims, each numerical parameter should at least be construed

in light of the number of reported significant digits and by applying ordinary rounding techniques.

Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the invention are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. All numerical values, however, inherently contain a range necessarily resulting from the standard deviation found in their respective testing measurements.

All headings are for the convenience of the reader and should not be used to limit the meaning of the text that follows the heading, unless so specified.

What is claimed is:

1. A method for screening a fetus for trisomy 21 comprising:

measuring a plurality of T21 biomarkers in a biological sample obtained from a first pregnant female, wherein the plurality of T21 biomarkers comprise polynucleotides chosen from SEQ ID NO:8-3,248, or a complement thereof; and

identifying the fetus as i) having trisomy 21 if expression of the plurality of biomarkers is altered to a statistically significant degree in the biological sample compared to a biological sample from a second pregnant female carrying a fetus not having trisomy 21, or ii) not having trisomy 21 if expression of the plurality of biomarkers is not altered to a statistically significant degree in the biological sample compared to a biological sample from a second pregnant female carrying a fetus not having trisomy 21.

2. The method of claim 1 wherein the plurality of T21 biomarkers comprises at least 10 polynucleotides chosen from SEQ ID NO:8-3,248, or a complement thereof, and wherein the first pregnant mother having at least 6 biomarkers altered to a statistically significant degree is identified as carrying a fetus having trisomy 21.

3. The method of claim 1 wherein the plurality of T21 biomarkers comprises at least 10 polynucleotides chosen from SEQ ID NO:8-3,248, or a complement thereof, and wherein the first pregnant mother having no greater than 4 biomarkers altered to a statistically significant degree is identified as carrying a fetus not having trisomy 21.

4. The method of claim 1 wherein the T21 biomarkers are selected from polynucleotides encoded by chromosome 21.

5. The method of claim 1 wherein the T21 biomarkers are selected from polynucleotides encoded by any of chromosomes 1-20, 22 or X.

6. The method of claim 1 wherein the T21 biomarkers are selected from polynucleotides encoded by any of chromosomes 1-20, 22 or X.

7. The method of claim 1 wherein the T21 biomarkers are selected from polynucleotides that are up-regulated in the first pregnant female carrying a fetus with trisomy 21 compared to the second pregnant female carrying a fetus not having trisomy 21.

8. The method of claim 1 wherein the T21 biomarkers are selected from polynucleotides that are down-regulated in the first pregnant female carrying a fetus with trisomy 21 compared to the second pregnant female carrying a fetus not having trisomy 21.

9. The method of claim 1 wherein expression of a T21 biomarker is altered to a statistically significant degree if it is outside the 95% confidence interval for that T21 biomarker.

10. The method of claim 1 wherein the method further comprises obtaining the biological sample from the first pregnant female.

11. The method of claim 1 wherein the obtaining comprises obtaining a blood sample.

12. The method of claim 11 wherein the blood sample is processed to remove cells from the blood sample.

13. The method of claim 11 wherein the blood sample is processed to isolate cell free plasma RNA.

14. The method of claim 1 wherein the method further comprises converting RNA polynucleotides present in the biological sample into cDNA molecules.

15. The method of claim 14 wherein the measuring comprises hybridization between a cDNA molecule and a complementary T21 biomarker.

16. The method of claim 15 wherein the complementary T21 biomarker is in solution during the hybridization.

17. The method of claim 15 wherein the complementary T21 biomarker is immobilized on a solid support.

18. The method of claim 1 wherein the fetus is identified as having trisomy 21, the method further comprising recommending a genetic test chosen from amniocentesis, cordocentesis, and chorionic villus sampling, ultrasound, or a combination thereof.

19. The method of claim 1 wherein the fetus of the first pregnant female is between 8 weeks and 16 weeks post-implantation.

20. A method for detecting trisomy 21 in a fetus comprising:

detecting T21 biomarkers in a biological sample to yield an expression level of each detected T21 biomarker, wherein the biological sample comprises plasma from a pregnant female, wherein the T21 biomarkers are selected from SEQ ID NO:8-3,248, or a complement thereof; and

comparing the expression level of a detected T21 biomarker to the expression level of the T21 biomarker in pregnant females carrying a fetus without T21, wherein an expression level of a detected T21 biomarker that is outside the 95% confidence interval for that T21 biomarker indicates the expression level of the T21 biomarker is altered.

21. The method of claim 20 wherein at least 10 T21 biomarkers are detected.

22. The method of claim 21 wherein a fetus carried by the pregnant female is identified as carrying a fetus having T21 when at least 6 biomarkers are outside the 95% confidence interval.

23. The method of claim 20 wherein the T21 biomarkers are selected from polynucleotides encoded by chromosome 21.

24. The method of claim 20 wherein the T21 biomarkers are selected from polynucleotides encoded by any of chromosomes 1-20, 22, or X.

25. The method of claim 20 wherein the T21 biomarkers are selected from polynucleotides encoded by any of chromosomes 1-20, 22, or X.

26. The method of claim 20 wherein the T21 biomarkers are selected from polynucleotides that are up-regulated in the pregnant female carrying a fetus with trisomy 21 compared to the pregnant females carrying a fetus not having trisomy 21.

27. The method of claim 20 wherein the T21 biomarkers are selected from polynucleotides that are down-regulated in the first pregnant female carrying a fetus with trisomy 21 compared to the pregnant females carrying a fetus not having trisomy 21.

28. The method of claim 20 wherein expression of a T21 biomarker is altered to a statistically significant degree if it is outside the 95% confidence interval for that T21 biomarker.

29. The method of claim 20 wherein the method further comprises obtaining the biological sample from the pregnant female.

30. The method of claim 29 wherein the obtaining comprises obtaining a blood sample.

31. The method of claim 30 wherein the blood sample is processed to remove cells from the blood sample.

32 The method of claim 30 wherein the blood sample is processed to isolate cell free plasma RNA.

33. The method of claim 20 wherein the method further comprises converting RNA polynucleotides present in the biological sample into cDNA molecules.

34. The method of claim 33 wherein the detecting comprises hybridization between a cDNA molecule and a complementary T21 biomarker.

35. The method of claim 34 wherein the complementary T21 biomarker is in solution during the hybridization.

36. The method of claim 34 wherein the complementary T21 biomarker is immobilized on a solid support.

37. The method of claim 20 further comprising recommending a genetic test chosen from amniocentesis, cordocentesis, and chorionic villus sampling, ultrasound, or a combination thereof.

38. The method of claim 20 wherein the fetus of the pregnant female is between 8 weeks and 16 weeks post-implantation.

39. A method for detecting trisomy 21 in a fetus comprising:

detecting T21 biomarkers in a biological sample from a pregnant female to yield a sample expression profile, wherein the T21 biomarkers are selected from SEQ ID NO: 8-3,248, or a complement thereof; and

comparing the sample expression profile with a reference expression profile; wherein a difference between the sample expression profile and the reference expression profile is indicative of the presence or absence of T21 in the fetus.

40. The method of claim 39 herein the reference expression profile is from at least one second pregnant female carrying a fetus without T21, and wherein a difference between the sample expression profile and the reference expression profile is indicative of the presence of T21.

41. The method of claim 39 wherein the reference expression profile is from at least one second pregnant female carrying a fetus with T21, and wherein a difference between the sample expression profile and the reference expression profile is indicative of the absence of T21.

42. The method of claim 39 wherein the sample expression profile comprises at least 10 polynucleotides chosen from SEQ ID NO:8-3,248, or a complement thereof, wherein the difference between the sample expression profile and the reference expression profile is statistically significant

43. The method of claim 39 wherein the T21 biomarkers are selected from polynucleotides encoded by chromosome 21.

44. The method of claim 39 wherein the T21 biomarkers are selected from polynucleotides encoded by any of chromosomes 1-20, 22, or X.

45. The method of claim 39 wherein the T21 biomarkers are selected from polynucleotides encoded by any of chromosomes 1-20, 22, or X.

46. The method of claim 39 wherein the T21 biomarkers are selected from polynucleotides that are up-regulated in the first pregnant female carrying a fetus with T21 compared to the second pregnant female carrying a fetus not having T21.

47. The method of claim 39 wherein the T21 biomarkers are selected from polynucleotides that are down-regulated in the first pregnant female carrying a fetus with T21 compared to the second pregnant female carrying a fetus not having T21.

48. The method of claim 39 wherein the difference between the sample expression profile and the reference expression profile is statistically significant

49. The method of claim 39 wherein the method further comprises obtaining the biological sample from the first pregnant female.

50. The method of claim 49 wherein the obtaining comprises obtaining a blood sample.

51. The method of claim 50 wherein the blood sample is processed to remove cells from the blood sample.

52. The method of claim 50 wherein the blood sample is processed to isolate cell free plasma RNA.

53. The method of claim 39 wherein the method further comprises converting RNA polynucleotides present in the biological sample into cDNA molecules.

54. The method of claim 53 wherein the detecting comprises hybridization between a cDNA molecule and a complementary T21 biomarker.

55. The method of claim 54 wherein the complementary T21 biomarker is in solution during the hybridization.

56. The method of claim 54 wherein the complementary T21 biomarker is immobilized on a solid support.

57. The method of claim 39 wherein the fetus is identified as having trisomy 21, the method further comprising recommending a genetic test chosen from amniocentesis, cordocentesis, and chorionic villus sampling, ultrasound, or a combination thereof.

58. The method of claim 39 wherein the fetus of the first pregnant female is between 8 weeks and 16 weeks post-implantation.

59. An article comprising:

a substrate; and

a plurality of different polynucleotides selected from SEQ ID NO:8-3,248, or a complement thereof, wherein the polynucleotides are immobilized onto a surface of the substrate.

60. The article of claim 59 wherein the polynucleotides are immobilized on the substrate surface to form a microarray.

61. The article of claim 59 wherein at least 10 polynucleotides are immobilized on the substrate surface

62. A kit for diagnosis trisomy 21 in a subject comprising:

an article comprising a substrate and a plurality of polynucleotides selected from SEQ ID NO:8-3,248, or a complement thereof, wherein the polynucleotides are immobilized onto a surface of the substrate; and

packaging materials and instructions for use.

63. The kit of claim 62 wherein the polynucleotides are immobilized on the substrate surface to form a microarray.

Figure 1.

SEQ ID NO:1
GAACGTGGTATAAAAGGGGCGGGAGGCCAGGCTCGTGCCGTTTTGCAGACGCCACCGCCGAGGAAAACCG
TGTACTATTAGCCATGGTCAACCCCACCGTGTTCTTCGACATTGCCGTCGACGGCGAGCCCTTGGGCCGC
GTCTCCTTTGAGCTGTTTGCAGACAAGGTCCCAAAGACAGCAGAAAATTTTCGTGCTCTGAGCACTGGAG
AGAAAGGATTTGGTTATAAGGGTTCCTGCTTTCACAGAATTATTCCAGGGTTTATGTGTCAGGGTGGTGA
CTTCACACGCCATAATGGCACTGGTGGCAAGTCCATCTATGGGGAGAAATTTGAAGATGAGAACTTCATC
CTAAAGCATACGGGTCCTGGCATCTTGTCCATGGCAAATGCTGGACCCAACACAAATGGTTCCCAGTTTT
TCATCTGCACTGCCAAGACTGAGTGGTTGGATGGCAAGCATGTGGTGTTTGGCAAAGTGAAAGAAGGCAT
GAATATTGTGGAGGCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACCAGCAAGAAGATCACCATTGCT
GACTGTGGACAACTCGAATAAGTTTGACTTGTGTTTTATCTTAACCACCAGATCATTCCTTCTGTAGCTC
AGGAGAGCACCCCTCCACCCCATTTGCTCGCAGTATCCTAGAATCTTTGTGCTCTCGCTGCAGTTCCCTT
TGGGTTCCATGTTTTCCTTGTTCCCTCCCATGCCTAGCTGGATTGCAGAGTTAAGTTTATGATTATGAAA
TAAAAACTAAATAACAATTGTCCTCGTTTGAGTTAAGAGTGTTGATGTAGGCTTTATTTTAAGCAGTAAT
GGGTTACTTCTGAAACATCACTTGTTTGCTTAATTCTACACAGTACTTAGATTTTTTTTACTTTCCAGTC
CCAGGAAGTGTCAATGTTTGTTGAGTGGAATATTGAAAATGTAGGCAGCAACTGGGCATGGTGGCTCACT
GTCTGTAATGTATTACCTGAGGCAGAAGACCACCTGAGGGTAGGAGTCAAGATCAGCCTGGGCAACATAG
TGAGACGCTGTCTCTACAAAAAATAATTAGCCTGGCCTGGTGGTGCATGCCTAGTCCTAGCTGATCTGGA
GGCTGACGTGGGAGGATTGCTTGAGCCTAGAGTGAGCTATTATCATGCCACTGTACAGCCTGGGTGTTCA
CAGATCTTGTGTCTCAAAGGTAGGCAGAGGCAGGAAAAGCAAGGAGCCAGAATTAAGAGGTTGGGTCAGT
CTGCAGTGAGTTCATGCATTTAGAGGTGTTCTTCAAGATGACTAATGTCAAAAATTGAGACATCTGTTGC
GGTTTTTTTTTTTTTTTTTTCCCCTGGAATGCAGTGGCGTGATCTCAGCTCACTGCAGCCTCCGCCTCCT
GGGTTCAAGTGATTCTAGTGCCTCAGCCTCCTGAGTAGCTGGGATAATGGGCGTGTGCCACCATGCCCAG
CTAATTTTTGTATTTTTAGTATAGATGGGGTTTCATCATTTTGACCAGGCTGGTCTCAAACTCTTGACCT
CAGCTGATGCGCCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGATGTGAGCCACCGCACCCTACCTCA
TTTTCTGTAACAAAGCTAAGCTTGAACACTGTTGATGTTCTTGAGGGAAGCATATTGGGCTTTAGGCTGT
AGGTCAAGTTTATACATCTTAATTATGGTGGAATTCCTATGTAGAGTCTAAAAAGCCAGGTACTTGGTGC
TACAGTCAGTCTCCCTGCAGAGGGTTAAGGCGCAGACTACCTGCAGTGAGGAGGTACTGCTTGTAGCATA
TAGAGCCTCTCCCTAGCTTTGGTTATGGAGGCTTTGAGGTTTTGCAAACCTGACCAATTTAAGCCATAAG
ATCTGGTCAAAGGGATACCCTTCCCACTAAGGACTTGGTTTCTCAGGAAATTATATGTACAGTGCTTGCT
GGCAGTTAGATGTCAGGACAATCTAAGCTGAGAAAACCCCTTCTCTGCCCACCTTAACAGACCTCTAGGG
TTCTTAACCCAGCAATCAAGTTTGCCTATCCTAGAGGTGGCGGATTTGATCATTTGGTGTGTTGGGCAAT
TTTTGTTTTACTGTCTGGTTCCTTCTGCGTGAATTACCACCACCACCACTTGTGCATCTCAGTCTTGTGT
GTTGTCTGGTTACGTATTCCCTGGGTGATACCATTCAATGTCTTAATGTACTTGTGGCTCAGACCTGAGT
GCAAGGTGGAAATAAACATCAAACATCTTTTCATTA

SEQ ID NO:2
GTTCTTGCTTCGGCAGAACATATACTAAAATTGGAACGATACAGAGAAGATTAGCATGGCCCCTGCGCAA
GGATGACACGCAAAATCGTGAAGCGTTCCACATTTTT

SEQ ID NO:3
GTTCTTGCTTCGGCAGAACATATACTAAAATTGGAACGATACAGAGAAGATTAGCATGGCCCCTGCGCAA
GGATGACACGCAAAATCGTGAAGCGTTCCACATTTTT

SEQ ID NO:4
GTTCTTGCTTCGGCAGAACATATACTAAAATTGGAACGATACAGAGAAGATTAGCATGGCCCCTGCGCAA
GGATGACACGCAAAATCGTGAAGCGTTCCACATTTTT

Fig. 2A-1

Comprehensive Description of mRNA T21 Biomarkers

Biomarker ID	Chromosome location	Gene Symbol	RefSeq	Fold-Change
8	chr1	LMNA	NM_170707	Down
9	chr1	PLEKHN1	NM_032129	Down
10	chr1	B3GALT6	NM_080605	Down
11	chr1	ACAP3	NM_030649	Down
12	chr1	CPSF3L	NM_017871	up
13	chr1	---	---	Down
14	chr1	FLJ14100	AK024162	Down
15	chr1	MORN1	NM_024848	up
16	chr1	LOC100129534	NR_024489	up
17	chr1	RER1	ENST00000434662	Down
18	chr1	PANK4	NM_018216	up
19	chr1	PANK4	NM_018216	up
20	chr1	ARHGEF16	NM_014448	Down
21	chr1	WDR8	ENST00000378322	up
22	chr1	TP73	NM_005427	Down
23	chr1	DFFB	AB028912	Down
24	chr1	AJAP1	NM_018836	Down
25	chr1	NPHP4	NM_015102	Down
26	chr1	KCNAB2	NM_003636	up
27	chr1	CHD5	NM_015557	Down
28	chr1	RNF207	NM_207396	Down
29	chr1	PLEKHG5	NM_020631	Down
30	chr1	ZBTB48	NM_005341	Down
31	chr1	KLHL21	NM_014851	up
32	chr1	PHF13	NM_153812	Down
33	chr1	PHF13	NM_153812	Down
34	chr1	PER3	NM_016831	up
35	chr1	PARK7	NM_007262	Down
36	chr1	RERE	NM_012102	Down
37	chr1	CLSTN1	NM_001009566	Down
38	chr1	LZIC	NM_032368	Down
39	chr1	UBE4B	NM_001105562	up
40	chr1	UBE4B	NM_001105562	Down
41	chr1	C1orf187	NM_198545	Down
42	chr1	C1orf187	NM_198545	up
43	chr1	C1orf187	NM_198545	up
44	chr1	TNFRSF8	NM_001243	Down
45	chr1	VPS13D	NM_015378	Down
46	chr1	PRDM2	NM_012231	Down
47	chr1	PRDM2	NM_015866	up
48	chr1	DNAJC16	NM_015291	up
49	chr1	AGMAT	NM_024758	up
50	chr1	SPEN	NM_015001	Down
51	chr1	SPEN	NM_015001	Down
52	chr1	EPHA2	NM_004431	Down
53	chr1	ARHGEF19	NM_153213	Down
54	chr1	ATP13A2	NM_022089	up
55	chr1	ATP13A2	NM_022089	up
56	chr1	SDHB	NM_003000	up
57	chr1	PADI2	NM_007365	Down
58	chr1	PADI1	NM_013358	up

Fig. 2A-2

59	chr1	PADI3	NM_016233	Down
60	chr1	PADI3	NM_016233	Down
61	chr1	MRTO4	NM_016183	up
62	chr1	AKR7A3	NM_012067	Down
63	chr1	PQLC2	NM_001040125	Down
64	chr1	PLA2G2E	NM_014589	Down
65	chr1	VWA5B1	NM_001039500	up
66	chr1	KIF17	NM_020816	up
67	chr1	EIF4G3	NM_003760	Down
68	chr1	HSPG2	NM_005529	up
69	chr1	HSPG2	NM_005529	Down
70	chr1	HSPG2	NM_005529	Down
71	chr1	HSPG2	NM_005529	up
72	chr1	HSPG2	NM_005529	up
73	chr1	HSPG2	NM_005529	Down
74	chr1	HSPG2	NM_005529	up
75	chr1	CELA3B	NM_007352	Down
76	chr1	WNT4	NM_030761	up
77	chr1	C1QC	NM_001114101	Down
78	chr1	EPHB2	NM_017449	Down
79	chr1	ASAP3	NM_017707	up
80	chr1	ASAP3	NM_017707	Down
81	chr1	MYOM3	NM_152372	up
82	chr1	MYOM3	NM_152372	Down
83	chr1	GRHL3	NM_021180	Down
84	chr1	NIPAL3	NM_020448	Down
85	chr1	RUNX3	NM_001031680	up
86	chr1	MAN1C1	NM_020379	Down
87	chr1	C1orf135	NM_024037	up
88	chr1	C1orf135	NM_024037	Down
89	chr1	STMN1	NM_001145454	up
90	chr1	UBXN11	NM_145345	Down
91	chr1	PIGV	NM_017837	up
92	chr1	TMEM222	NM_032125	up
93	chr1	C1orf38	NM_004848	Down
94	chr1	TMEM200B	NM_001171868	up
95	chr1	MECR	NM_016011	Down
96	chr1	PTPRU	NM_133178	Down
97	chr1	MATN1	NM_002379	Down
98	chr1	SDC3	NM_014654	Down
99	chr1	SDC3	NM_014654	Down
100	chr1	SDC3	NM_014654	Down
101	chr1	FABP3	NM_004102	up
102	chr1	COL16A1	NM_001856	Down
103	chr1	COL16A1	NM_001856	up
104	chr1	CCDC28B	NM_024296	Down
105	chr1	EIF3I	NM_003757	Down
106	chr1	MARCKSL1	NM_023009	Down
107	chr1	KIAA1522	NM_020888	Down
108	chr1	YARS	NM_003680	Down
109	chr1	S100PBP	NM_022753	Down

Fig. 2A-3

110	chr1	FNDC5	NM_001171941	up
111	chr1	CSMD2	NM_052896	up
112	chr1	C1orf94	NM_001134734	up
113	chr1	LOC653160	BC021230	up
114	chr1	ZMYM6	NM_007167	Down
115	chr1	ZMYM4	NM_005095	up
116	chr1	PSMB2	NM_002794	up
117	chr1	EIF2C3	NM_024852	up
118	chr1	TEKT2	NM_014466	Down
119	chr1	TEKT2	NM_014466	Down
120	chr1	COL8A2	NM_005202	up
121	chr1	MAP7D1	NM_018067	Down
122	chr1	OSCP1	NM_145047	up
123	chr1	OSCP1	NM_145047	up
124	chr1	OSCP1	NM_145047	up
125	chr1	RSPO1	NM_001038633	Down
126	chr1	C1orf109	BC018109	Down
127	chr1	CDCA8	ENST00000373055	Down
128	chr1	POU3F1	NM_002699	up
129	chr1	MACF1	NM_012090	Down
130	chr1	PABPC4	NM_001135653	up
131	chr1	COL9A2	NM_001852	Down
132	chr1	EDN2	NM_001956	up
133	chr1	HIVEP3	NM_024503	Down
134	chr1	FOXJ3	NM_014947	Down
135	chr1	RIMKLA	NM_173642	Down
136	chr1	LEPRE1	NM_022356	up
137	chr1	ERMAP	NM_001017922	up
138	chr1	EBNA1BP2	NM_001159936	up
139	chr1	PTPRF	NM_002840	up
140	chr1	KDM4A	NM_014663	up
141	chr1	ST3GAL3	NM_174963	Down
142	chr1	ST3GAL3	NM_174963	Down
143	chr1	DPH2	NM_001384	up
144	chr1	DPH2	NM_001384	up
145	chr1	CCDC24	NM_152499	up
146	chr1	SLC6A9	NM_006934	up
147	chr1	RNF220	NM_018150	up
148	chr1	KIF2C	NM_006845	up
149	chr1	PTCH2	NM_003738	Down
150	chr1	HECTD3	NM_024602	Down
151	chr1	NASP	NM_172164	up
152	chr1	GPBP1L1	NM_021639	up
153	chr1	POMGNT1	NM_017739	up

Fig. 2A-4

154	chr1	FOXE3	NM_012186	Down
155	chr1	FOXD2	NM_004474	Down
156	chr1	RAB3B	NM_002867	up
157	chr1	ZCCHC11	NM_001009881	Down
158	chr1	GPX7	NM_015696	up
159	chr1	ZYG11A	NM_001004339	up
160	chr1	SLC1A7	NM_006671	up
161	chr1	FLJ40434	NR_002314	up
162	chr1	ACOT11	NM_015547	Down
163	chr1	C1orf175	NR_026782	up
164	chr1	TTC4	NM_004623	up
165	chr1	PPAP2B	NM_003713	up
166	chr1	ALG6	NM_013339	up
167	chr1	EFCAB7	NM_032437	Down
168	chr1	ROR1	NM_005012	Down
169	chr1	ROR1	NM_005012	up
170	chr1	CACHD1	NM_020925	up
171	chr1	DNAJC6	NM_014787	Down
172	chr1	INSL5	NM_005478	up
173	chr1	MIER1	NM_020948	Down
174	chr1	CTH	NM_001902	up
175	chr1	ZRANB2	NM_203350	up
176	chr1	LHX8	NM_001001933	Down
177	chr1	LHX8	NM_001001933	Down
178	chr1	ST6GALNAC3	NM_152996	Down
179	chr1	ELTD1	NM_022159	up
180	chr1	COL24A1	NM_152890	up
181	chr1	CLCA2	NM_006536	Down
182	chr1	BARHL2	NM_020063	up
183	chr1	BRDT	NM_001726	up
184	chr1	DR1	NM_001938	up
185	chr1	SLC44A3	NM_152369	Down
186	chr1	CNN3	NM_001839	Down
187	chr1	LPPR4	NM_014839	up
188	chr1	PALMD	NM_017734	Down
189	chr1	HEJ1	NR_033424	Down
190	chr1	WDR47	NM_001142550	up
191	chr1	ATXN7L2	NM_153340	Down
192	chr1	CYB561D1	NM_182580	Down
193	chr1	EPS8L3	NM_139053	up
194	chr1	FAM40A	ENST00000369794	Down
195	chr1	FAM40A	NM_033088	up
196	chr1	RBM15	NM_022768	Down
197	chr1	CHI3L2	NM_004000	up

Fig. 2A-5

198	chr1	CHIA	NM_021797	up
199	chr1	CHIA	NM_021797	Down
200	chr1	KCND3	NM_004980	up
201	chr1	ST7L	NM_017744	Down
202	chr1	MOV10	NM_020963	up
203	chr1	RHOC	NM_175744	up
204	chr1	ATP1A1	NM_000701	Down
205	chr1	TTF2	NM_003594	Down
206	chr1	PHGDH	NM_006623	up
207	chr1	PHGDH	NM_006623	Down
208	chr1	HMGCS2	NM_005518	Down
209	chr1	NOTCH2	NM_024408	up
210	chr1	HFE2	NM_213653	Down
211	chr1	PEX11B	NM_003846	Down
212	chr1	ACP6	NM_016361	Down
213	chr1	BOLA1	NM_016074	up
214	chr1	MTMR11	NM_001145862	Down
215	chr1	OTUD7B	NM_020205	up
216	chr1	C1orf54	NM_024579	up
217	chr1	ECM1	NM_004425	Down
218	chr1	ARNT	NM_001668	Down
219	chr1	SETDB1	NM_001145415	Down
220	chr1	ANXA9	NM_003568	up
221	chr1	FAM63A	NM_018379	Down
222	chr1	PRUNE	NM_021222	Down
223	chr1	PI4KB	NM_002651	Down
224	chr1	RFX5	NM_000449	up
225	chr1	RFX5	NM_000449	Down
226	chr1	CGN	NM_020770	Down
227	chr1	CGN	NM_020770	up
228	chr1	TDRKH	NM_001083965	up
229	chr1	CRNN	NM_016190	up
230	chr1	CRNN	NM_016190	up
231	chr1	SMCP	NM_030663	Down
232	chr1	PGLYRP4	NM_020393	Down
233	chr1	S100A8	NM_002964	up
234	chr1	S100A7	NM_002963	Down
235	chr1	---	---	up
236	chr1	DENND4B	NM_014856	up
237	chr1	CRTC2	NM_181715	Down
238	chr1	CREB3L4	NM_130898	Down
239	chr1	IL6R	NM_000565	Down
240	chr1	IL6R	NM_000565	Down
241	chr1	TDRD10	NM_001098475	Down

Fig. 2A-6

242	chr1	ADAR	NM_001111	up
243	chr1	ADAR	NM_001111	up
244	chr1	PYGO2	NM_138300	Down
245	chr1	SHC1	NM_183001	Down
246	chr1	DCST2	NM_144622	Down
247	chr1	ADAM15	NM_207191	up
248	chr1	ADAM15	NM_207191	Down
249	chr1	TRIM46	NM_025058	Down
250	chr1	MUC1	NM_002456	up
251	chr1	THBS3	NM_007112	Down
252	chr1	POU5F1P4	GU480875	up
253	chr1	PAQR6	NM_024897	up
254	chr1	SMG5	NM_015327	up
255	chr1	SMG5	NM_015327	Down
256	chr1	C1orf85	NM_144580	up
257	chr1	IQGAP3	NM_178229	up
258	chr1	IQGAP3	NM_178229	Down
259	chr1	BCAN	NM_198427	Down
260	chr1	NES	NM_006617	Down
261	chr1	NES	NM_006617	up
262	chr1	C1orf66	NM_015997	Down
263	chr1	HDGF	NM_004494	Down
264	chr1	INSRR	NM_014215	up
265	chr1	NTRK1	NM_001012331	Down
266	chr1	C1orf92	NM_144702	Down
267	chr1	FCRL5	NM_031281	up
268	chr1	OR6N1	NM_001005185	up
269	chr1	CADM3	NM_021189	Down
270	chr1	DARC	NM_001122951	Down
271	chr1	IGSF9	ENST00000198587	Down
272	chr1	DCAF8	NR_028103	up
273	chr1	LY9	NM_002348	up
274	chr1	F11R	NM_016946	Down
275	chr1	ARHGAP30	NM_001025598	Down
276	chr1	ARHGAP30	NM_001025598	Down
277	chr1	UAP1	NM_003115	Down
278	chr1	RGS5	NM_003617	up
279	chr1	FMO9P	NR_002925	up
280	chr1	MGC4473	NR_024160	Down
281	chr1	F5	NM_000130	Down
282	chr1	F5	NM_000130	Down
283	chr1	F5	NM_000130	up
284	chr1	PIGC	ENST00000367728	Down
285	chr1	TNFSF18	NM_005092	up

Fig. 2A-7

286	chr1	RASAL2	NM_170692	Down
287	chr1	FAM163A	NM_173509	Down
288	chr1	TOR1AIP2	NM_022347	up
289	chr1	---	---	Down
290	chr1	IER5	NM_016545	up
291	chr1	CACNA1E	NM_000721	up
292	chr1	CACNA1E	NM_000721	up
293	chr1	GLUL	NM_002065	up
294	chr1	RGSL1	NM_001137669	up
295	chr1	LAMC1	NM_002293	up
296	chr1	LAMC2	NM_005562	up
297	chr1	SMG7	NM_173156	Down
298	chr1	NCF2	NM_000433	up
299	chr1	B3GALT2	NM_003783	Down
300	chr1	NEK7	NM_133494	Down
301	chr1	CACNA1S	NM_000069	Down
302	chr1	CACNA1S	NM_000069	Down
303	chr1	CACNA1S	NM_000069	Down
304	chr1	CACNA1S	NM_000069	up
305	chr1	IGFN1	ENST00000412892	Down
306	chr1	LAD1	NM_005558	up
307	chr1	PRELP	NM_002725	up
308	chr1	REN	NM_000537	up
309	chr1	PLEKHA6	NM_014935	up
310	chr1	PLEKHA6	NM_014935	Down
311	chr1	NFASC	NM_001005388	Down
312	chr1	CNTN2	NM_005076	Down
313	chr1	TMCC2	ENST00000330675	Down
314	chr1	SLC26A9	NM_052934	up
315	chr1	IKBKE	NM_014002	up
316	chr1	LGTN	NM_006893	Down
317	chr1	DYRK3	ENST00000367106	up
318	chr1	PIGR	NM_002644	Down
319	chr1	CD55	NM_001114752	Down
320	chr1	CD46	NM_002389	Down
321	chr1	CD46	NM_002389	Down
322	chr1	PLXNA2	NM_025179	Down
323	chr1	CAMK1G	NM_020439	Down
324	chr1	TRAF3IP3	NM_025228	up
325	chr1	RCOR3	NM_001136223	Down
326	chr1	INTS7	NM_015434	Down
327	chr1	DTL	NM_016448	Down
328	chr1	ATF3	NM_001674	Down
329	chr1	USH2A	NM_206933	up

Fig. 2A-8

330	chr1	MARK1	NM_018650	up
331	chr1	MARK1	NM_018650	Down
332	chr1	MARK1	NM_018650	Down
333	chr1	C1orf65	NM_152610	up
334	chr1	TP53BP2	NM_001031685	up
335	chr1	TMEM63A	NM_014698	up
336	chr1	TMEM63A	NM_014698	Down
337	chr1	PYCR2	NM_013328	up
338	chr1	ACBD3	NM_022735	up
339	chr1	WNT9A	NM_003395	up
340	chr1	C1orf35	NM_024319	Down
341	chr1	OBSCN	NM_052843	Down
342	chr1	OBSCN	NM_052843	up
343	chr1	TRIM17	NM_016102	Down
344	chr1	EDARADD	NM_080738	Down
345	chr1	MTR	NM_000254	Down
346	chr1	RYR2	NM_001035	Down
347	chr1	HNRNPU	NM_031844	up
348	chr1	SCCPDH	NM_016002	up
349	chr1	ZNF669	NM_024804	up
350	chr1	NLRP3	NM_004895	Down
351	chr1	OR9H1P	AY358215	Down
352	chr1	TRIM58	NM_015431	up
353	chr1	OR2T12	NM_001004692	Down
354	chr1	ZNF672	NM_024836	Down
355	chr2	MYT1L	NM_015025	up
356	chr2	MYT1L	NM_015025	up
357	chr2	TSSC1	NM_003310	up
358	chr2	TTC15	NM_016030	up
359	chr2	SOX11	NM_003108	up
360	chr2	CMPK2	NM_207315	up
361	chr2	RSAD2	NM_080657	Down
362	chr2	ASAP2	NM_003887	up
363	chr2	ASAP2	NM_003887	up
364	chr2	ASAP2	NM_003887	Down
365	chr2	HPCAL1	NM_002149	up
366	chr2	HPCAL1	NM_134421	up
367	chr2	ATP6V1C2	AK127836	Down
368	chr2	GREB1	NM_014668	Down
369	chr2	RDH14	NM_020905	up
370	chr2	HS1BP3	NM_022460	up
371	chr2	HS1BP3	NM_022460	Down
372	chr2	APOB	NM_000384	Down
373	chr2	APOB	NM_000384	Down

Fig. 2A-9

374	chr2	KLHL29	NM_052920	Down
375	chr2	UBXN2A	NM_181713	up
376	chr2	CENPO	NM_024322	up
377	chr2	ADCY3	NM_004036	Down
378	chr2	DNMT3A	NM_175629	up
379	chr2	DTNB	NM_021907	Down
380	chr2	GPR113	NM_001145168	Down
381	chr2	C2orf28	NM_080592	up
382	chr2	CAD	NM_004341	Down
383	chr2	ZNF513	NM_144631	Down
384	chr2	NRBP1	NM_013392	Down
385	chr2	KRTCAP3	NM_001168364	up
386	chr2	SUPT7L	NM_014860	Down
387	chr2	PLB1	NM_153021	Down
388	chr2	LCLAT1	NM_182551	up
389	chr2	GALNT14	NM_024572	Down
390	chr2	SPAST	NM_014946	up
391	chr2	MYADML	NR_003143	up
392	chr2	MYADML	NR_003143	up
393	chr2	C2orf56	NM_144736	Down
394	chr2	SOS1	NM_005633	Down
395	chr2	KCNG3	NM_133329	Down
396	chr2	OXER1	NM_148962	Down
397	chr2	ZFP36L2	NM_006887	Down
398	chr2	EPAS1	NM_001430	Down
399	chr2	KCNK12	NM_022055	up
400	chr2	MSH6	NM_000179	up
401	chr2	RTN4	NM_207521	up
402	chr2	SMEK2	NM_001122964	Down
403	chr2	KIAA1841	NM_032506	Down
404	chr2	USP34	NM_014709	up
405	chr2	OTX1	NM_014562	Down
406	chr2	C2orf86	NM_001042692	Down
407	chr2	ARHGAP25	NM_001007231	Down
408	chr2	ANTXR1	NM_032208	up
409	chr2	GMCL1	NM_178439	Down
410	chr2	ADD2	NM_017482	Down
411	chr2	ADD2	NM_001617	up
412	chr2	CD207	NM_015717	up
413	chr2	VAX2	NM_012476	Down
414	chr2	ANKRD53	NM_001115116	up
415	chr2	MPHOSPH10	NM_005791	Down
416	chr2	RAB11FIP5	NM_015470	up
417	chr2	ALMS1P	NR_003683	up

Fig. 2A-10

418	chr2	INO80B	NM_031288	Down
419	chr2	MOGS	NM_006302	Down
420	chr2	AUP1	NM_181575	Down
421	chr2	LRRTM1	ENST00000433224	Down
422	chr2	FUNDC2P2	NR_003663	Down
423	chr2	TMSB10	NM_021103	up
424	chr2	KCMF1	NM_020122	up
425	chr2	TGOLN2	NM_006464	up
426	chr2	SH2D6	NM_198482	up
427	chr2	USP39	NM_006590	up
428	chr2	SMYD1	NM_198274	up
429	chr2	---	---	up
430	chr2	---	---	up
431	chr2	ARID5A	NM_212481	Down
432	chr2	ANKRD23	NM_144994	Down
433	chr2	FAM178B	NM_001122646	Down
434	chr2	ACTR1B	NM_005735	up
435	chr2	AFF3	NM_002285	up
436	chr2	LONRF2	NM_198461	Down
437	chr2	CHST10	NM_004854	Down
438	chr2	NPAS2	NM_002518	up
439	chr2	TBC1D8	NM_001102426	Down
440	chr2	RNF149	NM_173647	Down
441	chr2	IL18RAP	NM_003853	up
442	chr2	SLC9A2	NM_003048	Down
443	chr2	MRPS9	NM_182640	up
444	chr2	UXS1	ENST00000409032	Down
445	chr2	FBLN7	NM_153214	up
446	chr2	FBLN7	NM_153214	Down
447	chr2	IL1F7	NM_014439	Down
448	chr2	IL1F10	NM_032556	Down
449	chr2	SLC35F5	NM_025181	up
450	chr2	SCTR	NM_002980	Down
451	chr2	TMEM177	NM_001105198	up
452	chr2	EPB41L5	NM_020909	up
453	chr2	LOC84931	NR_027181	up
454	chr2	TFCP2L1	NM_014553	up
455	chr2	CYP27C1	NM_001001665	up
456	chr2	AMMECR1L	NM_031445	Down
457	chr2	LOC401010	NR_002826	up
458	chr2	MGAT5	NM_002410	Down
459	chr2	TMEM163	NM_030923	up
460	chr2	ZRANB3	ENST00000412849	up
461	chr2	---	---	Down

Fig. 2A-11

462	chr2	LCT	NM_002299	up
463	chr2	LRP1B	NM_018557	up
464	chr2	LRP1B	NM_018557	up
465	chr2	LRP1B	NM_018557	Down
466	chr2	ZEB2	NM_014795	Down
467	chr2	ZEB2	NM_014795	Down
468	chr2	KIF5C	NM_004522	Down
469	chr2	NEB	NM_001164507	up
470	chr2	CACNB4	NM_001005747	up
471	chr2	TBR1	NM_006593	Down
472	chr2	TBR1	NM_006593	Down
473	chr2	GRB14	NM_004490	up
474	chr2	ABCB11	NM_003742	up
475	chr2	LRP2	NM_004525	Down
476	chr2	METTL8	ENST00000375258	Down
477	chr2	SLC25A12	NM_003705	Down
478	chr2	DLX2	NM_004405	Down
479	chr2	ITGAV	NM_002210	Down
480	chr2	COL3A1	NM_000090	Down
481	chr2	COL3A1	NM_000090	up
482	chr2	COL3A1	NM_000090	up
483	chr2	COL5A2	NM_000393	up
484	chr2	NAB1	NM_005966	up
485	chr2	STAT1	NM_007315	up
486	chr2	MARS2	NM_138395	up
487	chr2	ALS2CR11	NM_001168221	Down
488	chr2	ALS2	NM_020919	up
489	chr2	BMPR2	NM_001204	up
490	chr2	PARD3B	NM_205863	up
491	chr2	PARD3B	NM_205863	up
492	chr2	INO80D	NM_017759	Down
493	chr2	KLF7	NM_003709	up
494	chr2	FZD5	NM_003468	up
495	chr2	FZD5	NM_003468	up
496	chr2	MAP2	NM_002374	Down
497	chr2	SPAG16	NM_024532	up
498	chr2	FN1	NM_212482	up
499	chr2	TMEM169	NM_001142310	Down
500	chr2	SMARCAL1	NM_014140	Down
501	chr2	RUFY4	NM_198483	Down
502	chr2	ARPC2	NM_152862	Down
503	chr2	GPBAR1	NM_001077191	Down
504	chr2	GPBAR1	NM_001077191	Down
505	chr2	STK36	NM_015690	Down

Fig. 2A-12

506	chr2	STK36	NM_015690	up
507	chr2	STK36	NM_015690	up
508	chr2	PRKAG3	NM_017431	up
509	chr2	WNT10A	NM_025216	up
510	chr2	FEV	NM_017521	Down
511	chr2	CRYBA2	NM_057093	Down
512	chr2	CCDC108	NM_194302	Down
513	chr2	ABCB6	NM_005689	Down
514	chr2	DNAJB2	NM_006736	Down
515	chr2	PTPRN	NM_002846	Down
516	chr2	DES	NM_001927	up
517	chr2	SPEG	NM_005876	Down
518	chr2	CHPF	NM_024536	up
519	chr2	STK11IP	NM_052902	Down
520	chr2	PAX3	NM_000438	Down
521	chr2	COL4A4	NM_000092	Down
522	chr2	COL4A3	NM_000091	up
523	chr2	COL4A3	NM_000091	up
524	chr2	SLC19A3	NM_025243	up
525	chr2	PID1	NM_017933	Down
526	chr2	DNER	NM_139072	up
527	chr2	TRIP12	NM_004238	Down
528	chr2	SP140	NM_007237	Down
529	chr2	SP140L	NM_138402	up
530	chr2	ARMC9	NM_025139	up
531	chr2	NGEF	NM_019850	up
532	chr2	SAG	NM_000541	Down
533	chr2	DGKD	NM_003648	Down
534	chr2	DGKD	NM_003648	up
535	chr2	ARL4C	NM_005737	up
536	chr2	COL6A3	NM_004369	up
537	chr2	RAMP1	NM_005855	Down
538	chr2	PER2	NM_022817	up
539	chr2	TRAF3IP1	AF242456	Down
540	chr2	TRAF3IP1	NM_015650	Down
541	chr2	ASB1	NM_001040445	up
542	chr2	HDAC4	NM_006037	Down
543	chr2	HDAC4	NM_006037	Down
544	chr2	NDUFA10	NM_004544	Down
545	chr2	GPC1	NM_002081	Down
546	chr2	SNED1	NM_001080437	up
547	chr2	SNED1	NM_001080437	Down
548	chr2	PPP1R7	NM_002712	Down
549	chr2	2-Sep	ENST00000429791	Down

Fig. 2A-13

550	chr2	---	---	Down
551	chr2	---	---	Down
552	chr2	---	---	Down
553	chr2	C2orf85	NM_173821	Down
554	chr2	FLJ40712	AK098031	up
555	chr3	ITPR1	NM_001099952	Down
556	chr3	ARL8B	NM_018184	Down
557	chr3	GRM7	NM_000844	up
558	chr3	CAMK1	NM_003656	up
559	chr3	IL17RC	NM_153461	Down
560	chr3	FANCD2	NM_033084	up
561	chr3	IRAK2	NM_001570	Down
562	chr3	TATDN2	NM_014760	Down
563	chr3	ATP2B2	NM_001001331	Down
564	chr3	SLC6A11	NM_014229	Down
565	chr3	SYN2	NM_133625	up
566	chr3	TMEM40	NM_018306	up
567	chr3	IQSEC1	ENST00000450726	Down
568	chr3	NUP210	BC067089	Down
569	chr3	NUP210	NM_024923	Down
570	chr3	NUP210	NM_024923	up
571	chr3	C3orf20	BC030599	up
572	chr3	EAF1	NM_033083	Down
573	chr3	COLQ	NM_005677	Down
574	chr3	TBC1D5	NM_001134381	Down
575	chr3	THRB	NM_000461	Down
576	chr3	TOP2B	NM_001068	up
577	chr3	AZI2	NM_022461	Down
578	chr3	CCR4	NM_005508	Down
579	chr3	UBP1	NM_014517	Down
580	chr3	PDCD6IP	NM_013374	Down
581	chr3	LRRFIP2	NM_006309	up
582	chr3	VILL	NM_015873	up
583	chr3	PLCD1	NM_001130964	Down
584	chr3	DLEC1	BC129824	up
585	chr3	XYLB	NM_005108	Down
586	chr3	ACVR2B	NM_001106	Down
587	chr3	SCN5A	NM_198056	up
588	chr3	CSRNP1	AB063301	up
589	chr3	XIRP1	NM_194293	Down
590	chr3	MYRIP	NM_015460	up
591	chr3	ZNF619	NM_001145082	up
592	chr3	ZNF621	NM_198484	up
593	chr3	CCK	NM_000729	Down

Fig. 2A-14

594	chr3	VIPR1	NM_004624	Down
595	chr3	VIPR1	NM_004624	up
596	chr3	C3orf23	NM_173826	Down
597	chr3	ZNF167	NM_018651	Down
598	chr3	LTF	NM_002343	up
599	chr3	LRRC2	NM_024750	up
600	chr3	ALS2CL	NM_147129	Down
601	chr3	NBEAL2	NM_015175	Down
602	chr3	SETD2	NM_014159	up
603	chr3	PTPN23	NM_015466	up
604	chr3	PTPN23	NM_015466	Down
605	chr3	SCAP	NM_012235	up
606	chr3	FBXW12	NM_207102	up
607	chr3	PLXNB1	NM_002673	up
608	chr3	---	---	up
609	chr3	SHISA5	NM_016479	up
610	chr3	COL7A1	NM_000094	up
611	chr3	COL7A1	NM_000094	up
612	chr3	COL7A1	NM_000094	Down
613	chr3	COL7A1	NM_000094	up
614	chr3	IP6K2	NR_027437	up
615	chr3	WDR6	NM_018031	Down
616	chr3	WDR6	NM_018031	Down
617	chr3	QARS	NM_005051	Down
618	chr3	CCDC36	NM_178173	Down
619	chr3	---	---	Down
620	chr3	---	---	Down
621	chr3	AMT	NM_000481	Down
622	chr3	RNF123	NM_022064	Down
623	chr3	MST1R	NM_002447	Down
624	chr3	RBM5	NM_005778	Down
625	chr3	SEMA3F	NM_004186	up
626	chr3	GNAT1	NM_144499	up
627	chr3	GNAI2	NM_002070	Down
628	chr3	GNAI2	NM_002070	Down
629	chr3	SEMA3B	NM_004636	Down
630	chr3	SEMA3B	NM_004636	Down
631	chr3	IFRD2	NM_006764	up
632	chr3	HYAL3	NM_003549	Down
633	chr3	CACNA2D2	NM_001005505	Down
634	chr3	MAPKAPK3	NM_004635	up
635	chr3	DOCK3	NM_004947	Down
636	chr3	TEX264	NM_015926	Down
637	chr3	PARP3	NM_001003931	up

Fig. 2A-15

638	chr3	ACY1	NM_000666	Down
639	chr3	TLR9	NM_017442	Down
640	chr3	TWF2	NM_007284	Down
641	chr3	DNAH1	NM_015512	up
642	chr3	SEMA3G	NM_020163	Down
643	chr3	NISCH	NM_007184	up
644	chr3	STAB1	NM_015136	Down
645	chr3	NT5DC2	NM_022908	up
646	chr3	PBRM1	NM_018165	up
647	chr3	ITIH3	NM_002217	Down
648	chr3	SFMBT1	NM_001005159	Down
649	chr3	RFT1	NM_052859	up
650	chr3	WNT5A	NM_003392	up
651	chr3	APPL1	NM_012096	up
652	chr3	FEZF2	NM_018008	up
653	chr3	MITF	NM_198159	Down
654	chr3	EIF4E3	NM_173359	Down
655	chr3	GPR27	NM_018971	Down
656	chr3	TFG	NM_006070	Down
657	chr3	ABI3BP	NM_015429	up
658	chr3	ZBTB11	NM_014415	up
659	chr3	FAM55C	NM_001134456	up
660	chr3	NFKBIZ	NM_031419	up
661	chr3	ALCAM	NM_001627	up
662	chr3	CD47	NM_001777	Down
663	chr3	CD47	NM_001777	Down
664	chr3	DZIP3	NM_014648	up
665	chr3	C3orf52	NM_001171747	up
666	chr3	ATP6V1A	NM_001690	Down
667	chr3	UPK1B	NM_006952	up
668	chr3	C3orf1	NM_016589	Down
669	chr3	POLQ	NM_199420	up
670	chr3	PARP14	NM_017554	Down
671	chr3	SEMA5B	NM_001031702	Down
672	chr3	PDIA5	NM_006810	Down
673	chr3	ADCY5	NM_183357	Down
674	chr3	ADCY5	NM_183357	Down
675	chr3	ADCY5	NM_183357	up
676	chr3	MGLL	NM_007283	Down
677	chr3	SEC61A1	NM_013336	up
678	chr3	RUVBL1	NM_003707	up
679	chr3	GATA2	NM_032638	Down
680	chr3	C3orf27	NM_007354	Down
681	chr3	ACAD9	NM_014049	Down

Fig. 2A-16

682	chr3	C3orf25	BC066975	Down
683	chr3	IFT122	NM_052985	up
684	chr3	PLXND1	NM_015103	up
685	chr3	ATP2C1	NM_014382	up
686	chr3	ASTE1	NM_014065	up
687	chr3	DNAJC13	NM_015268	up
688	chr3	---	---	Down
689	chr3	BFSP2	NM_003571	Down
690	chr3	BFSP2	NM_003571	Down
691	chr3	AMOTL2	NM_016201	up
692	chr3	EPHB1	NM_004441	Down
693	chr3	MRAS	NM_012219	Down
694	chr3	FOXL2	NM_023067	Down
695	chr3	GK5	NM_001039547	up
696	chr3	CHST2	ENST00000309575	Down
697	chr3	CHST2	NM_004267	Down
698	chr3	SLC9A9	NM_173653	Down
699	chr3	WWTR1	NM_015472	Down
700	chr3	EIF2A	NM_032025	Down
701	chr3	LEKR1	NM_001004316	up
702	chr3	SCHIP1	NM_014575	up
703	chr3	SCHIP1	ENST00000445224	up
704	chr3	SMC4	NM_005496	up
705	chr3	MECOM	NM_001105077	Down
706	chr3	LRRC31	NM_024727	Down
707	chr3	GHSR	NM_004122	up
708	chr3	ZNF639	BC026181	Down
709	chr3	MCF2L2	NM_015078	Down
710	chr3	EIF2B5	NM_003907	up
711	chr3	ABCF3	NM_018358	up
712	chr3	ABCF3	NM_018358	up
713	chr3	ECE2	NM_014693	Down
714	chr3	CLCN2	NM_004366	Down
715	chr3	SENP2	NM_021627	Down
716	chr3	RTP1	NM_153708	up
717	chr3	MASP1	NM_001879	Down
718	chr3	BCL6	NM_001706	up
719	chr3	LEPREL1	NM_018192	up
720	chr3	CLDN1	NM_021101	Down
721	chr3	ATP13A4	NM_032279	up
722	chr3	HES1	NM_005524	Down
723	chr3	GP5	NM_004488	Down
724	chr3	FAM43A	NM_153690	Down
725	chr3	ACAP2	NM_012287	up

Fig. 2A-17

726	chr3	MUC20	NM_152673	Down
727	chr3	MUC4	NM_018406	Down
728	chr3	MUC4	NM_018406	Down
729	chr3	TM4SF19	NM_138461	up
730	chr3	WDR53	NM_182627	up
731	chr3	NCBP2	NM_007362	up
732	chr3	LOC152217	NR_024388	Down
733	chr4	PDE6B	NM_000283	Down
734	chr4	GAK	NM_005255	up
735	chr4	DGKQ	NM_001347	up
736	chr4	IDUA	NM_000203	up
737	chr4	WHSC1	NM_133334	Down
738	chr4	WHSC2	NM_005663	Down
739	chr4	POLN	NM_181808	Down
740	chr4	RNF4	NM_002938	Down
741	chr4	TNIP2	NM_024309	Down
742	chr4	MFSD10	NM_001120	up
743	chr4	NOP14	NM_003703	Down
744	chr4	HTT	NM_002111	Down
745	chr4	RGS12	NM_198229	Down
746	chr4	DOK7	NM_173660	Down
747	chr4	LYAR	NM_017816	Down
748	chr4	D4S234E	NM_014392	Down
749	chr4	CYTL1	NM_018659	up
750	chr4	MAN2B2	NM_015274	Down
751	chr4	GRPEL1	NM_025196	Down
752	chr4	ABLIM2	NM_001130083	up
753	chr4	ACOX3	NM_003501	Down
754	chr4	ACOX3	NM_003501	up
755	chr4	FBXL5	NM_012161	Down
756	chr4	TLR10	NM_030956	Down
757	chr4	TMEM156	NM_024943	up
758	chr4	LOC401127	NR_026854	up
759	chr4	RHOH	NM_004310	Down
760	chr4	APBB2	NM_004307	Down
761	chr4	LIMCH1	NM_014988	up
762	chr4	GABRA4	NM_000809	Down
763	chr4	GABRA4	NM_000809	up
764	chr4	TXK	NM_003328	up
765	chr4	KDR	NM_002253	Down
766	chr4	SRD5A3	NM_024592	Down
767	chr4	HOPX	NM_001145460	Down
768	chr4	HOPX	NM_032495	up
769	chr4	LPHN3	NM_015236	up

Fig. 2A-18

770	chr4	TMPRSS11B	NM_182502	up
771	chr4	CXCL5	NM_002994	Down
772	chr4	ART3	NM_001130016	Down
773	chr4	PRKG2	NM_006259	up
774	chr4	HNRPDL	NM_031372	up
775	chr4	HPSE	NM_006665	Down
776	chr4	HPSE	NM_006665	Down
777	chr4	FAM175A	NM_139076	Down
778	chr4	WDFY3	NM_014991	Down
779	chr4	MMRN1	NM_007351	Down
780	chr4	ADH1B	NM_000668	Down
781	chr4	MAPKSP1	NM_021970	up
782	chr4	H2AFZ	NM_002106	up
783	chr4	MANBA	NM_005908	up
784	chr4	LEF1	NM_016269	Down
785	chr4	COL25A1	NM_198721	up
786	chr4	CFI	NM_000204	Down
787	chr4	LRIT3	NM_198506	up
788	chr4	ENPEP	NM_001977	Down
789	chr4	PITX2	NM_000325	Down
790	chr4	EXOSC9	NM_001034194	Down
791	chr4	TRPC3	NM_001130698	up
792	chr4	MGST2	NM_002413	up
793	chr4	SCOC	NM_001153484	up
794	chr4	UCP1	NM_021833	up
795	chr4	UCP1	NM_021833	up
796	chr4	NR3C2	NM_000901	Down
797	chr4	TMEM154	NM_152680	up
798	chr4	TRIM2	NM_015271	Down
799	chr4	DCHS2	NM_001142552	Down
800	chr4	RAPGEF2	NM_014247	up
801	chr4	TLL1	NM_012464	Down
802	chr4	TLL1	NM_012464	Down
803	chr4	PALLD	NM_001166108	Down
804	chr4	HMGB2	NM_002129	Down
805	chr4	VEGFC	NM_005429	Down
806	chr4	VEGFC	NM_005429	up
807	chr4	PDLIM3	NM_014476	Down
808	chr4	SORBS2	NM_001145671	Down
809	chr4	FAT1	NM_005245	Down
810	chr5	FLJ44896	AK126844	up
811	chr5	PDCD6	AK295082	Down
812	chr5	AHRR	NM_020731	Down
813	chr5	EXOC3	NM_007277	Down

Fig. 2A-19

814	chr5	CEP72	NM_018140	up
815	chr5	TPPP	NM_007030	up
816	chr5	NKD2	NM_033120	Down
817	chr5	CLPTM1L	NM_030782	up
818	chr5	SLC6A3	NM_001044	up
819	chr5	NDUFS6	NM_004553	up
820	chr5	NSUN2	NM_017755	Down
821	chr5	ADCY2	NM_020546	up
822	chr5	SEMA5A	NM_003966	up
823	chr5	CDH18	NM_004934	up
824	chr5	RNASEN	NM_013235	Down
825	chr5	DNAJC21	NM_194283	Down
826	chr5	DNAJC21	NM_194283	up
827	chr5	PRLR	NM_000949	up
828	chr5	EGFLAM	NM_152403	Down
829	chr5	SEPP1	NM_005410	Down
830	chr5	NNT	NM_012343	up
831	chr5	SNX18	NM_001102575	Down
832	chr5	PDE4D	AY245867	Down
833	chr5	SFRS12	NM_001077199	Down
834	chr5	MAST4	NM_198828	Down
835	chr5	SLC30A5	NM_022902	up
836	chr5	BDP1	NM_018429	up
837	chr5	MCCC2	NM_022132	Down
838	chr5	PTCD2	NM_024754	Down
839	chr5	POLK	BC050718	Down
840	chr5	IQGAP2	NM_006633	Down
841	chr5	F2R	NM_001992	Down
842	chr5	RASGRF2	NM_006909	up
843	chr5	ZCCHC9	NM_032280	Down
844	chr5	RASA1	NM_002890	Down
845	chr5	POU5F2	NM_153216	Down
846	chr5	GPR150	NM_199243	up
847	chr5	SLCO4C1	NM_180991	Down
848	chr5	GIN1	NM_017676	Down
849	chr5	FBXL17	NM_001163315	up
850	chr5	PJA2	NM_014819	Down
851	chr5	EPB41L4A	NM_022140	Down
852	chr5	EPB41L4A	NM_022140	up
853	chr5	DMXL1	NM_005509	Down
854	chr5	PRR16	NM_016644	Down
855	chr5	SNCAIP	NM_005460	up
856	chr5	ALDH7A1	NM_001182	up
857	chr5	MEGF10	NM_032446	Down

Fig. 2A-20

858	chr5	ISOC1	NM_016048	Down
859	chr5	ISOC1	NM_016048	up
860	chr5	ADAMTS19	NM_133638	up
861	chr5	ACSL6	NM_015256	up
862	chr5	PDLIM4	NM_003687	Down
863	chr5	RAD50	NM_005732	up
864	chr5	AFF4	NM_014423	up
865	chr5	ZCCHC10	NM_017665	up
866	chr5	C5orf15	NM_020199	up
867	chr5	SAR1B	NM_001033503	up
868	chr5	TGFBI	NM_000358	Down
869	chr5	FAM13B	NM_016603	Down
870	chr5	FAM13B	NM_016603	Down
871	chr5	REEP2	ENST00000254901	Down
872	chr5	ETF1	NM_004730	Down
873	chr5	ETF1	NM_004730	Down
874	chr5	CTNNA1	NM_001903	Down
875	chr5	CTNNA1	NM_001903	Down
876	chr5	SIL1	NM_001037633	up
877	chr5	NRG2	NM_004883	Down
878	chr5	SLC4A9	NM_031467	up
879	chr5	PCDHB18	NR_001281	Down
880	chr5	PCDHGA11	NM_018914	up
881	chr5	FGF1	NM_000800	up
882	chr5	PPP2R2B	NM_004576	Down
883	chr5	SPINK14	NM_001001325	up
884	chr5	SH3TC2	NM_024577	Down
885	chr5	ARHGEF37	NM_001001669	Down
886	chr5	CAMK2A	NM_015981	up
887	chr5	CAMK2A	NM_015981	up
888	chr5	DCTN4	NM_001135643	up
889	chr5	DCTN4	NM_001135643	Down
890	chr5	ANXA6	NM_001155	up
891	chr5	GRIA1	NM_000827	Down
892	chr5	FAM114A2	NM_018691	Down
893	chr5	MED7	NM_001100816	Down
894	chr5	LSM11	NM_173491	up
895	chr5	IL12B	NM_002187	up
896	chr5	IL12B	NM_002187	Down
897	chr5	CCNJL	NM_024565	up
898	chr5	GABRA1	NM_000806	up
899	chr5	SLIT3	NM_003062	up
900	chr5	SLIT3	NM_003062	up
901	chr5	DOCK2	NM_004946	Down

Fig. 2A-21

902	chr5	LCP2	NM_005565	Down
903	chr5	LCP2	NM_005565	Down
904	chr5	KCNMB1	BC025707	up
905	chr5	---	---	Down
906	chr5	---	---	Down
907	chr5	NKX2-5	NM_004387	Down
908	chr5	HMP19	NM_015980	up
909	chr5	NOP16	NM_016391	up
910	chr5	CDHR2	NM_001171976	up
911	chr5	HK3	NM_002115	Down
912	chr5	ZNF346	NM_012279	up
913	chr5	FGFR4	NM_002011	Down
914	chr5	FGFR4	NM_002011	up
915	chr5	NSD1	NM_172349	Down
916	chr5	MXD3	NM_031300	Down
917	chr5	B4GALT7	NM_007255	Down
918	chr5	GRM6	NM_000843	Down
919	chr5	ADAMTS2	NM_014244	up
920	chr5	---	---	up
921	chr5	RASGEF1C	ENST00000393371	up
922	chr5	GFPT2	NM_005110	up
923	chr5	GFPT2	NM_005110	Down
924	chr5	MGAT1	NM_001114618	Down
925	chr5	BTNL3	NM_197975	Down
926	chr5	TRIM52	NM_032765	up
927	chr6	SERPINB9	NM_004155	Down
928	chr6	PRPF4B	NM_003913	Down
929	chr6	RREB1	NM_001168344	Down
930	chr6	CAGE1	NM_001170692	Down
931	chr6	DSP	NM_004415	Down
932	chr6	GCNT2	NM_145655	Down
933	chr6	ERVFRDE1	NM_207582	up
934	chr6	TBC1D7	NM_016495	up
935	chr6	NUP153	NM_005124	Down
936	chr6	SOX4	NM_003107	Down
937	chr6	SOX4	NM_003107	Down
938	chr6	MRS2	NM_020662	up
939	chr6	FAM65B	NM_014722	Down
940	chr6	LRRC16A	NM_017640	up
941	chr6	HIST1H1T	NM_005323	Down
942	chr6	BTN2A3	ENST00000297020	up
943	chr6	ABT1	NM_013375	up
944	chr6	HIST1H2AL	NM_003511	Down
945	chr6	OR2B6	NM_012367	up

Fig. 2A-22

946	chr6	GABBR1	NM_001470	up
947	chr6	LOC554223	BC051362	Down
948	chr6	TRIM39	NM_021253	up
949	chr6	---	---	Down
950	chr6	---	---	Down
951	chr6	C6orf134	NM_024909	up
952	chr6	DHX16	NM_003587	Down
953	chr6	DHX16	NM_003587	Down
954	chr6	DHX16	NM_003587	up
955	chr6	MDC1	NM_014641	up
956	chr6	FLOT1	NM_005803	Down
957	chr6	CDSN	NM_001264	Down
958	chr6	---	---	Down
959	chr6	LTA	NM_000595	Down
960	chr6	BAT2	NM_080686	Down
961	chr6	C6orf26	AJ245661	up
962	chr6	C6orf27	NM_025258	up
963	chr6	C6orf27	NM_025258	Down
964	chr6	C6orf27	NM_025258	up
965	chr6	C6orf27	NM_025258	up
966	chr6	C6orf27	NM_025258	Down
967	chr6	VARS	NM_006295	Down
968	chr6	SLC44A4	NM_025257	Down
969	chr6	EHMT2	NM_006709	up
970	chr6	CFB	NM_001710	Down
971	chr6	CFB	NM_001710	up
972	chr6	C4A	NM_007293	Down
973	chr6	TNXB	NM_019105	Down
974	chr6	ATF6B	NM_004381	Down
975	chr6	PPT2	NM_005155	Down
976	chr6	PPT2	AF020544	Down
977	chr6	NOTCH4	NM_004557	up
978	chr6	NOTCH4	NM_004557	up
979	chr6	BTNL2	NM_019602	Down
980	chr6	HLA-DPB1	NM_002121	up
981	chr6	COL11A2	NM_080680	Down
982	chr6	RXRB	NM_021976	up
983	chr6	VPS52	NM_022553	Down
984	chr6	ITPR3	NM_002224	Down
985	chr6	IP6K3	NM_054111	Down
986	chr6	C6orf1	NM_178508	up
987	chr6	NUDT3	NM_006703	up
988	chr6	SPDEF	NM_012391	Down
989	chr6	SCUBE3	NM_152753	Down

Fig. 2A-23

990	chr6	DEF6	NM_022047	up
991	chr6	LOC100131043	AK124222	up
992	chr6	FGD2	NM_173558	Down
993	chr6	RNF8	NM_003958	Down
994	chr6	ZFAND3	NM_021943	Down
995	chr6	GLP1R	NM_002062	up
996	chr6	C6orf64	BC022007	Down
997	chr6	KCNK5	NM_003740	up
998	chr6	DAAM2	NM_015345	Down
999	chr6	TREML2	NM_024807	Down
1000	chr6	TREML4	NM_198153	Down
1001	chr6	TOMM6	NM_001134493	Down
1002	chr6	CCND3	NM_001760	Down
1003	chr6	TRERF1	NM_033502	up
1004	chr6	PPP2R5D	NM_006245	Down
1005	chr6	CUL7	NM_001168370	Down
1006	chr6	MRPL2	NM_015950	Down
1007	chr6	CRIP3	NM_206922	Down
1008	chr6	DLK2	NM_023932	Down
1009	chr6	TJAP1	NM_001146016	Down
1010	chr6	YIPF3	NM_015388	Down
1011	chr6	POLH	NM_006502	up
1012	chr6	CAPN11	NM_007058	Down
1013	chr6	HSP90AB1	NM_007355	Down
1014	chr6	GPR116	NM_015234	up
1015	chr6	TNFRSF21	NM_014452	up
1016	chr6	TNFRSF21	NM_014452	up
1017	chr6	OPN5	NM_181744	up
1018	chr6	PKHD1	NM_138694	Down
1019	chr6	LRRC1	NM_018214	Down
1020	chr6	LRRC1	NM_018214	up
1021	chr6	DST	ENST00000446842	Down
1022	chr6	COL19A1	NM_001858	Down
1023	chr6	OGFRL1	NM_024576	up
1024	chr6	KHDC1	NM_030568	Down
1025	chr6	MYO6	NM_004999	Down
1026	chr6	TPBG	NM_006670	up
1027	chr6	PNRC1	NM_006813	Down
1028	chr6	CCNC	NM_005190	up
1029	chr6	SIM1	NM_005068	up
1030	chr6	PREP	NM_002726	Down
1031	chr6	C6orf203	NM_016487	Down
1032	chr6	---	---	Down
1033	chr6	C6orf182	NM_001083535	Down

Fig. 2A-24

1034	chr6	AMD1	NM_001634	up
1035	chr6	TRAF3IP2	NR_028338	Down
1036	chr6	TSPYL4	NM_021648	Down
1037	chr6	HINT3	NM_138571	Down
1038	chr6	PTPRK	NM_001135648	Down
1039	chr6	LAMA2	NM_000426	Down
1040	chr6	LAMA2	NM_000426	Down
1041	chr6	MED23	NM_004830	up
1042	chr6	SGK1	NM_005627	Down
1043	chr6	AHI1	NM_001134831	up
1044	chr6	TNFAIP3	NM_006290	up
1045	chr6	NMBR	NM_002511	up
1046	chr6	VTA1	NM_016485	up
1047	chr6	ADAT2	NM_182503	up
1048	chr6	FUCA2	NM_032020	Down
1049	chr6	EPM2A	NM_005670	Down
1050	chr6	SHPRH	NM_001042683	up
1051	chr6	SHPRH	NM_001042683	up
1052	chr6	STXBP5	NM_139244	Down
1053	chr6	TAB2	NM_015093	Down
1054	chr6	LRP11	NM_032832	up
1055	chr6	PPP1R14C	NM_030949	Down
1056	chr6	IYD	NM_001164694	up
1057	chr6	MTHFD1L	NM_015440	Down
1058	chr6	SYNE1	NM_182961	up
1059	chr6	OPRM1	NM_000914	Down
1060	chr6	SNX9	NM_016224	up
1061	chr6	SYNJ2	NM_003898	Down
1062	chr6	EZR	NM_003379	up
1063	chr6	TAGAP	NM_152133	Down
1064	chr6	MRPL18	NM_014161	Down
1065	chr6	IGF2R	NM_000876	up
1066	chr6	IGF2R	NM_000876	up
1067	chr6	MAP3K4	NM_005922	Down
1068	chr6	PARK2	NM_004562	up
1069	chr6	T	NM_003181	up
1070	chr6	RNASET2	NM_003730	Down
1071	chr6	FGFR1OP	NM_007045	Down
1072	chr6	UNC93A	NM_018974	up
1073	chr6	KIF25	NM_030615	Down
1074	chr6	FRMD1	NM_024919	up
1075	chr6	SMOC2	NM_022138	up
1076	chr6	THBS2	NM_003247	Down
1077	chr6	WDR27	NM_182552	up

Fig. 2A-25

1078	chr6	C6orf208	NR_026780	up
1079	chr6	DLL1	NM_005618	Down
1080	chr7	ABCB8	NM_007188	up
1081	chr7	CYP2W1	NM_017781	Down
1082	chr7	CYP2W1	NM_017781	Down
1083	chr7	GPER	NM_001039966	up
1084	chr7	GPER	NM_001505	Down
1085	chr7	MICALL2	NM_182924	up
1086	chr7	MICALL2	NM_182924	up
1087	chr7	INTS1	NM_001080453	up
1088	chr7	INTS1	NM_001080453	Down
1089	chr7	MAD1L1	NM_003550	up
1090	chr7	NUDT1	NM_002452	Down
1091	chr7	EIF3B	NM_003751	Down
1092	chr7	C7orf27	NM_152743	Down
1093	chr7	C7orf27	NM_152743	Down
1094	chr7	IQCE	NM_152558	Down
1095	chr7	TTYH3	NM_025250	Down
1096	chr7	RNF216L	NR_023384	Down
1097	chr7	WIPI2	NM_015610	Down
1098	chr7	FSCN1	NM_003088	Down
1099	chr7	AIMP2	NM_006303	up
1100	chr7	ICA1	NM_004968	Down
1101	chr7	TMEM195	NM_001004320	Down
1102	chr7	TMEM195	NM_001004320	Down
1103	chr7	SP4	NM_003112	up
1104	chr7	C7orf30	AK127742	up
1105	chr7	OSBPL3	NM_015550	up
1106	chr7	CYCS	NM_018947	Down
1107	chr7	HOXA1	NM_005522	up
1108	chr7	CHN2	NM_004067	Down
1109	chr7	CCDC129	NM_194300	up
1110	chr7	FKBP9	NM_007270	Down
1111	chr7	ELMO1	NM_014800	Down
1112	chr7	ELMO1	NM_014800	Down
1113	chr7	STARD3NL	NM_032016	Down
1114	chr7	POU6F2	NM_007252	up
1115	chr7	GLI3	NM_000168	Down
1116	chr7	POLM	BC026306	Down
1117	chr7	AEBP1	NM_001129	Down
1118	chr7	POLD2	NM_001127218	Down
1119	chr7	MYL7	NM_021223	Down
1120	chr7	CAMK2B	NM_001220	up
1121	chr7	CAMK2B	NM_001220	up

Fig. 2A-26

1122	chr7	NPC1L1	NM_013389	up
1123	chr7	PPIA	NM_021130	up
1124	chr7	PURB	NM_033224	up
1125	chr7	CCM2	NM_001029835	Down
1126	chr7	RAMP3	NM_005856	up
1127	chr7	PKD1L1	NM_138295	Down
1128	chr7	COBL	NM_015198	Down
1129	chr7	POM121L12	NM_182595	up
1130	chr7	EGFR	NM_005228	Down
1131	chr7	EGFR	NM_005228	Down
1132	chr7	PSPH	NM_004577	Down
1133	chr7	NCRNA00174	NR_026873	Down
1134	chr7	STAG3L4	NM_022906	Down
1135	chr7	WBSCR17	NM_022479	up
1136	chr7	WBSCR17	NM_022479	Down
1137	chr7	CALN1	NM_031468	up
1138	chr7	TBL2	ENST00000437521	Down
1139	chr7	STX1A	NM_004603	up
1140	chr7	WBSCR28	AY372054	up
1141	chr7	ELN	NM_000501	Down
1142	chr7	ELN	NM_000501	Down
1143	chr7	LAT2	NM_032464	Down
1144	chr7	CLIP2	NM_003388	Down
1145	chr7	HIP1	NM_005338	up
1146	chr7	POR	NM_000941	Down
1147	chr7	YWHAG	NM_012479	up
1148	chr7	ZP3	NM_001110354	up
1149	chr7	UPK3B	NM_030570	up
1150	chr7	MAGI2	NM_012301	Down
1151	chr7	MAGI2	NM_012301	Down
1152	chr7	CROT	NM_001143935	Down
1153	chr7	ADAM22	NM_021723	up
1154	chr7	KRIT1	NM_194456	Down
1155	chr7	CDK6	NM_001259	Down
1156	chr7	CCDC132	NM_017667	Down
1157	chr7	COL1A2	NM_000089	Down
1158	chr7	SGCE	NM_001099401	up
1159	chr7	DYNC1I1	NM_004411	up
1160	chr7	TECPR1	NM_015395	Down
1161	chr7	BAIAP2L1	NM_018842	up
1162	chr7	SMURF1	NM_020429	Down
1163	chr7	ARPC1B	NM_005720	Down
1164	chr7	PDAP1	NM_014891	up
1165	chr7	ZNF789	NM_213603	Down

Fig. 2A-27

1166	chr7	ZKSCAN1	NM_003439	Down
1167	chr7	MCM7	NM_005916	up
1168	chr7	C7orf43	AK302342	Down
1169	chr7	GPC2	NM_152742	Down
1170	chr7	GPC2	NM_152742	up
1171	chr7	PILRA	NM_013439	up
1172	chr7	MEPCE	NM_019606	Down
1173	chr7	C7orf61	BC031966	Down
1174	chr7	C7orf51	AK124773	up
1175	chr7	LRCH4	AK074175	Down
1176	chr7	LRCH4	NM_002319	Down
1177	chr7	MOSPD3	NM_023948	up
1178	chr7	GIGYF1	NM_022574	Down
1179	chr7	ZAN	NM_003386	Down
1180	chr7	PLOD3	NM_001084	Down
1181	chr7	PLOD3	NM_001084	up
1182	chr7	ZNHIT1	NM_006349	up
1183	chr7	MYL10	NM_138403	Down
1184	chr7	CUX1	NM_181552	up
1185	chr7	CUX1	NM_181552	Down
1186	chr7	CUX1	NM_001913	Down
1187	chr7	PRKRIP1	NM_024653	Down
1188	chr7	RINT1	NM_021930	up
1189	chr7	SYPL1	NM_006754	Down
1190	chr7	FLJ36031	NM_175884	up
1191	chr7	PRKAR2B	NM_002736	up
1192	chr7	PRKAR2B	NM_002736	Down
1193	chr7	TES	NM_015641	Down
1194	chr7	MET	NM_001127500	up
1195	chr7	WNT2	NM_003391	Down
1196	chr7	CTTNBP2	NM_033427	Down
1197	chr7	SLC13A1	NM_022444	up
1198	chr7	GPR37	NM_005302	Down
1199	chr7	POT1	NM_015450	up
1200	chr7	FSCN3	NM_020369	Down
1201	chr7	MGC27345	ENST00000424840	Down
1202	chr7	CCDC136	NM_022742	Down
1203	chr7	KCP	NM_001135914	up
1204	chr7	IRF5	NM_032643	up
1205	chr7	TSPAN33	NM_178562	Down
1206	chr7	SMO	NM_005631	up
1207	chr7	ZC3HC1	NM_016478	up
1208	chr7	CPA2	NM_001869	Down
1209	chr7	MKLN1	NM_013255	Down

Fig. 2A-28

1210	chr7	LRGUK	NM_144648	Down
1211	chr7	SLC35B4	NM_032826	Down
1212	chr7	STRA8	NM_182489	Down
1213	chr7	CNOT4	NM_013316	Down
1214	chr7	CREB3L2	NM_194071	up
1215	chr7	TRIM24	NM_015905	Down
1216	chr7	KIAA1549	NM_020910	Down
1217	chr7	ZC3HAV1	NM_020119	Down
1218	chr7	TTC26	NM_024926	Down
1219	chr7	LUC7L2	NM_016019	up
1220	chr7	ADCK2	NM_052853	Down
1221	chr7	NDUFB2	NM_004546	up
1222	chr7	BRAF	NM_004333	up
1223	chr7	EPHB6	NM_004445	up
1224	chr7	OR6W1P	NR_002140	Down
1225	chr7	CLCN1	NM_000083	Down
1226	chr7	CUL1	NM_003592	up
1227	chr7	EZH2	NM_004456	Down
1228	chr7	PDIA4	NM_004911	Down
1229	chr7	ZNF746	NM_001163474	Down
1230	chr7	ZNF767	NR_027788	up
1231	chr7	SSPO	NM_198455	up
1232	chr7	SSPO	AK124542	up
1233	chr7	REPIN1	NM_013400	Down
1234	chr7	GIMAP8	NM_175571	Down
1235	chr7	ATG9B	NM_173681	Down
1236	chr7	AGAP3	NM_031946	up
1237	chr7	ABCF2	NM_007189	Down
1238	chr7	MLL3	NM_170606	up
1239	chr7	ACTR3B	NM_020445	Down
1240	chr7	DPP6	NM_001936	up
1241	chr7	PAXIP1	NM_007349	up
1242	chr7	NCAPG2	NM_017760	up
1243	chr8	DLGAP2	NM_004745	up
1244	chr8	DLGAP2	NM_004745	Down
1245	chr8	ARHGEF10	NM_014629	Down
1246	chr8	CSMD1	NM_033225	up
1247	chr8	CSMD1	NM_033225	up
1248	chr8	ERI1	NM_153332	Down
1249	chr8	TNKS	NM_003747	up
1250	chr8	RP1L1	NM_178857	up
1251	chr8	FAM167A	NM_053279	up
1252	chr8	NSAP11	AY176665	Down
1253	chr8	FGF17	NM_003867	Down

Fig. 2A-29

1254	chr8	FAM160B2	NM_022749	Down
1255	chr8	BMP1	NM_001199	Down
1256	chr8	PDLIM2	NM_021630	Down
1257	chr8	KIAA1967	NM_021174	Down
1258	chr8	KIAA1967	NM_021174	Down
1259	chr8	RHOBTB2	NM_001160036	Down
1260	chr8	RHOBTB2	NM_001160036	up
1261	chr8	TNFRSF10B	NM_003842	Down
1262	chr8	TNFRSF10D	NM_003840	Down
1263	chr8	CHMP7	NM_152272	Down
1264	chr8	LOXL2	NM_002318	Down
1265	chr8	SLC25A37	NM_016612	up
1266	chr8	NEFL	NM_006158	Down
1267	chr8	DOCK5	NM_024940	Down
1268	chr8	BNIP3L	NM_004331	up
1269	chr8	DPYSL2	NM_001386	Down
1270	chr8	CLU	NM_001831	Down
1271	chr8	PBK	NM_018492	up
1272	chr8	ELP3	NM_018091	Down
1273	chr8	PNOC	NM_006228	Down
1274	chr8	KIF13B	NM_015254	up
1275	chr8	PURG	NM_013357	up
1276	chr8	GPR124	NM_032777	Down
1277	chr8	GPR124	NM_032777	up
1278	chr8	PPAPDC1B	NM_001102559	Down
1279	chr8	WHSC1L1	NM_023034	up
1280	chr8	TM2D2	NM_031940	up
1281	chr8	C8orf4	NM_020130	Down
1282	chr8	ANK1	NM_020476	Down
1283	chr8	IKBKB	NM_001556	up
1284	chr8	VDAC3	NM_001135694	up
1285	chr8	THAP1	NM_018105	up
1286	chr8	SGK196	NM_032237	Down
1287	chr8	EFCAB1	NR_024605	up
1288	chr8	TOX	NM_014729	Down
1289	chr8	ADHFE1	NM_144650	Down
1290	chr8	ADHFE1	NM_144650	Down
1291	chr8	STAU2	NM_001164380	up
1292	chr8	ZFHX4	NM_024721	up
1293	chr8	TMEM55A	NM_018710	Down
1294	chr8	RUNX1T1	NM_175634	up
1295	chr8	PTDSS1	NM_014754	Down
1296	chr8	---	---	Down
1297	chr8	C8orf47	NM_173549	up

Fig. 2A-30

1298	chr8	POP1	NM_001145860	up
1299	chr8	NIPAL2	NM_024759	Down
1300	chr8	VPS13B	NM_152564	Down
1301	chr8	GRHL2	NM_024915	Down
1302	chr8	UBR5	NM_015902	Down
1303	chr8	KLF10	NM_005655	up
1304	chr8	SLC25A32	NM_030780	up
1305	chr8	RIMS2	NM_001100117	Down
1306	chr8	OXR1	NM_181354	up
1307	chr8	EBAG9	NM_004215	up
1308	chr8	KCNV1	NM_014379	up
1309	chr8	EXT1	NM_000127	Down
1310	chr8	MTBP	NM_022045	up
1311	chr8	FBXO32	NM_058229	Down
1312	chr8	RNF139	NM_007218	up
1313	chr8	KIAA0196	NM_014846	Down
1314	chr8	FAM49B	BC016345	Down
1315	chr8	ADCY8	NM_001115	up
1316	chr8	PHF20L1	NM_016018	Down
1317	chr8	TG	NM_003235	Down
1318	chr8	COL22A1	NM_152888	Down
1319	chr8	COL22A1	NM_152888	up
1320	chr8	DENND3	NM_014957	Down
1321	chr8	ZNF696	NM_030895	Down
1322	chr8	TOP1MT	NM_052963	Down
1323	chr8	RHPN1	NM_052924	up
1324	chr8	FAM83H	NM_198488	Down
1325	chr8	SCRIB	NM_182706	up
1326	chr8	NRBP2	NM_178564	up
1327	chr8	PARP10	NM_032789	up
1328	chr8	PARP10	NM_032789	up
1329	chr8	SPATC1	NM_198572	up
1330	chr8	OPLAH	NM_017570	up
1331	chr8	OPLAH	NM_017570	up
1332	chr8	ADCK5	NM_174922	Down
1333	chr8	SLC39A4	NM_017767	Down
1334	chr8	VPS28	AK091979	Down
1335	chr8	FOXH1	NM_003923	Down
1336	chr9	DOCK8	NM_203447	up
1337	chr9	SMARCA2	NM_003070	Down
1338	chr9	JAK2	NM_004972	up
1339	chr9	PTPRD	NM_002839	up
1340	chr9	FREM1	NM_001177704	Down
1341	chr9	PSIP1	NM_021144	Down

Fig. 2A-31

1342	chr9	ADAMTSL1	NM_001040272	up
1343	chr9	ADAMTSL1	NM_001040272	up
1344	chr9	RRAGA	NM_006570	Down
1345	chr9	TMEM215	NM_212558	up
1346	chr9	NOL6	NM_022917	Down
1347	chr9	ENHO	NM_198573	Down
1348	chr9	C9orf23	NM_148178	Down
1349	chr9	SIGMAR1	NM_005866	Down
1350	chr9	FANCG	NM_004629	up
1351	chr9	KIAA1539	BC004406	Down
1352	chr9	UNC13B	NM_006377	Down
1353	chr9	CD72	NM_001782	Down
1354	chr9	C9orf100	NM_032818	Down
1355	chr9	CA9	NM_001216	up
1356	chr9	RGP1	NM_001080496	Down
1357	chr9	OR2S2	NM_019897	up
1358	chr9	GRHPR	NM_012203	up
1359	chr9	ANKRD18A	AK093059	Down
1360	chr9	TJP2	NM_004817	Down
1361	chr9	MAMDC2	NM_153267	up
1362	chr9	C9orf41	AK299691	up
1363	chr9	GCNT1	NM_001097634	up
1364	chr9	PRUNE2	NM_015225	Down
1365	chr9	FLJ46321	NM_001001670	up
1366	chr9	---	---	up
1367	chr9	CTSL1	NM_001912	Down
1368	chr9	CDK20	NM_178432	Down
1369	chr9	SPIN1	NM_006717	Down
1370	chr9	SHC3	NM_016848	Down
1371	chr9	SHC3	NM_016848	up
1372	chr9	AUH	NM_001698	Down
1373	chr9	NOL8	NR_024020	up
1374	chr9	NOL8	NR_024020	Down
1375	chr9	ECM2	NM_001393	up
1376	chr9	C9orf89	AK128259	up
1377	chr9	BARX1	NM_021570	Down
1378	chr9	FBP2	NM_003837	Down
1379	chr9	HSD17B3	NM_000197	Down
1380	chr9	TDRD7	NM_014290	Down
1381	chr9	TMOD1	NM_003275	Down
1382	chr9	FOXE1	NM_004473	up
1383	chr9	NANS	NM_018946	Down
1384	chr9	TBC1D2	NM_018421	Down
1385	chr9	COL15A1	NM_001855	Down

Fig. 2A-32

1386	chr9	TGFBR1	NM_004612	Down
1387	chr9	STX17	NM_017919	Down
1388	chr9	C9orf5	NM_032012	up
1389	chr9	PTPN3	NM_002829	up
1390	chr9	PTPN3	NM_002829	Down
1391	chr9	AKAP2	NM_001004065	up
1392	chr9	ZNF483	NM_133464	Down
1393	chr9	DNAJC25-GNG10	NM_004125	up
1394	chr9	SUSD1	NM_022486	up
1395	chr9	SLC46A2	NM_033051	Down
1396	chr9	RNF183	NM_145051	Down
1397	chr9	RGS3	NM_130795	Down
1398	chr9	FLJ31713	AK056275	Down
1399	chr9	COL27A1	NM_032888	up
1400	chr9	COL27A1	NM_032888	up
1401	chr9	AKNA	NM_030767	Down
1402	chr9	TNC	NM_002160	Down
1403	chr9	TNC	NM_002160	Down
1404	chr9	TLR4	NM_138554	up
1405	chr9	CDK5RAP2	NM_018249	Down
1406	chr9	ARPC5L	NM_030978	Down
1407	chr9	SCAI	NM_173690	up
1408	chr9	RABEPK	NM_005833	Down
1409	chr9	GARNL3	NM_032293	Down
1410	chr9	GARNL3	NM_032293	up
1411	chr9	LRSAM1	NM_001005373	up
1412	chr9	ENG	NM_001114753	Down
1413	chr9	PTGES2	NM_025072	Down
1414	chr9	LCN2	NM_005564	Down
1415	chr9	CIZ1	NM_012127	up
1416	chr9	SLC27A4	NM_005094	up
1417	chr9	URM1	NM_030914	up
1418	chr9	ODF2	NM_002540	Down
1419	chr9	GLE1	NM_001003722	Down
1420	chr9	SPTAN1	NM_001130438	Down
1421	chr9	FAM73B	AK301241	Down
1422	chr9	TOR1B	NM_014506	Down
1423	chr9	USP20	NM_006676	Down
1424	chr9	USP20	NM_006676	Down
1425	chr9	USP20	NM_006676	up
1426	chr9	NCS1	NM_014286	up
1427	chr9	LAMC3	NM_006059	up
1428	chr9	LAMC3	NM_006059	up
1429	chr9	AIF1L	NM_031426	up

Fig. 2A-33

1430	chr9	NUP214	NM_005085	Down
1431	chr9	FAM78A	NM_033387	up
1432	chr9	POMT1	NM_007171	Down
1433	chr9	UCK1	NM_031432	up
1434	chr9	BARHL1	NM_020064	Down
1435	chr9	TSC1	NM_000368	up
1436	chr9	VAV2	NM_001134398	Down
1437	chr9	COL5A1	NM_000093	Down
1438	chr9	OLFM1	NM_014279	Down
1439	chr9	OLFM1	BC000189	Down
1440	chr9	KIAA0649	NM_014811	up
1441	chr9	GLT6D1	NM_182974	up
1442	chr9	CAMSAP1	NM_015447	Down
1443	chr9	SDCCAG3	NM_001039707	up
1444	chr9	NOTCH1	NM_017617	Down
1445	chr9	EGFL7	NM_016215	Down
1446	chr9	KIAA1984	BC007542	up
1447	chr9	C9orf86	NM_024718	Down
1448	chr9	TRAF2	NM_021138	up
1449	chr9	FBXW5	NM_018998	up
1450	chr9	LCNL1	NM_207510	up
1451	chr9	LCNL1	NM_207510	up
1452	chr9	ABCA2	NM_001606	Down
1453	chr9	C9orf139	BC132809	up
1454	chr9	C9orf140	NM_178448	up
1455	chr9	UAP1L1	NM_207309	Down
1456	chr9	NOXA1	NM_006647	up
1457	chr9	ENTPD8	NM_001033113	Down
1458	chr9	CACNA1B	NM_000718	Down
1459	chrX	GPR143	NM_000273	Down
1460	chrX	SHROOM2	NM_001649	Down
1461	chrX	CLCN4	NM_001830	up
1462	chrX	AMELX	NM_001142	up
1463	chrX	ARHGAP6	NM_013427	Down
1464	chrX	PRPS2	NM_001039091	Down
1465	chrX	PRPS2	NM_001039091	up
1466	chrX	GRPR	NM_005314	up
1467	chrX	CTPS2	AF226667	up
1468	chrX	CTPS2	AF226667	up
1469	chrX	SYAP1	NR_033181	Down
1470	chrX	PPEF1	NM_006240	up
1471	chrX	PHKA2	NM_000292	Down
1472	chrX	KLHL34	NM_153270	up
1473	chrX	PHEX	NM_000444	up

Fig. 2A-34

1474	chrX	IL1RAPL1	NM_014271	Down
1475	chrX	TAB3	NM_152787	up
1476	chrX	BCOR	NM_017745	up
1477	chrX	MED14	NM_004229	Down
1478	chrX	USP9X	NM_001039590	Down
1479	chrX	USP11	NM_004651	Down
1480	chrX	ZNF41	NM_007130	Down
1481	chrX	ZNF41	NM_007130	Down
1482	chrX	ARAF	NM_001654	up
1483	chrX	PORCN	NM_022825	Down
1484	chrX	WAS	NM_000377	Down
1485	chrX	WAS	NM_000377	up
1486	chrX	PQBP1	NM_001032382	up
1487	chrX	SLC35A2	NM_001032289	Down
1488	chrX	GPKOW	U66359	Down
1489	chrX	MAGIX	NM_024859	Down
1490	chrX	PRICKLE3	NM_006150	Down
1491	chrX	CACNA1F	NM_005183	Down
1492	chrX	CCDC22	NM_014008	up
1493	chrX	CCDC22	NM_014008	up
1494	chrX	FOXP3	NM_014009	Down
1495	chrX	AKAP4	NM_003886	Down
1496	chrX	KDM5C	NM_004187	Down
1497	chrX	FGD1	NM_004463	up
1498	chrX	FGD1	NM_004463	Down
1499	chrX	LAS1L	NM_031206	Down
1500	chrX	VSIG4	NM_007268	up
1501	chrX	VSIG4	NM_007268	up
1502	chrX	AR	NM_000044	Down
1503	chrX	AR	NM_000044	up
1504	chrX	NLGN3	NM_181303	Down
1505	chrX	TAF1	NM_004606	Down
1506	chrX	HDAC8	NM_018486	up
1507	chrX	CDX4	NM_005193	Down
1508	chrX	MAGT1	NM_032121	Down
1509	chrX	SH3BGRL	NM_003022	up
1510	chrX	SRPX2	NM_014467	Down
1511	chrX	ARMCX1	NM_016608	Down
1512	chrX	ARMCX2	NM_014782	up
1513	chrX	NXF4	NR_002216	up
1514	chrX	ESX1	NM_153448	up
1515	chrX	MORC4	NM_024657	up
1516	chrX	TEX13B	NM_031273	up
1517	chrX	VSIG1	NM_001170553	up

Fig. 2A-35

1518	chrX	COL4A6	NM_001847	up
1519	chrX	COL4A6	NM_001847	Down
1520	chrX	KCNE1L	NM_012282	Down
1521	chrX	ZCCHC16	NM_001004308	up
1522	chrX	AMOT	NM_133265	Down
1523	chrX	LRCH2	NM_020871	up
1524	chrX	IL13RA1	NM_001560	Down
1525	chrX	PGRMC1	NM_006667	up
1526	chrX	SLC25A43	NM_145305	Down
1527	chrX	RNF113A	NM_006978	up
1528	chrX	GRIA3	NM_007325	up
1529	chrX	XPNPEP2	NM_003399	Down
1530	chrX	AIFM1	NM_004208	Down
1531	chrX	SLC25A14	NM_003951	up
1532	chrX	MST4	NM_016542	up
1533	chrX	MBNL3	NM_018388	Down
1534	chrX	HS6ST2	NM_001077188	up
1535	chrX	NCRNA00086	NR_024359	Down
1536	chrX	MCF2	NM_005369	Down
1537	chrX	AFF2	NM_002025	up
1538	chrX	CXorf40A	NM_178124	Down
1539	chrX	HMGB3	NM_005342	up
1540	chrX	MAGEA10	NM_001011543	up
1541	chrX	DUSP9	NM_001395	up
1542	chrX	PLXNB3	NM_005393	Down
1543	chrX	PLXNB3	NM_005393	up
1544	chrX	PLXNB3	NM_005393	Down
1545	chrX	PLXNB3	NM_005393	up
1546	chrX	SRPK3	NM_014370	Down
1547	chrX	HCFC1	NM_005334	Down
1548	chrX	MECP2	NM_004992	Down
1549	chrX	FLNA	NM_001456	Down
1550	chrX	FLNA	NM_001456	Down
1551	chrX	ATP6AP1	NM_001183	Down
1552	chrX	PLXNA3	NM_017514	Down
1553	chrX	CTAG2	AJ223040	up
1554	chrX	GAB3	NM_001081573	up
1555	chrX	CLIC2	NM_001289	Down
1556	chrY	PRKY	NR_028062	Down
1557	chrY	---	---	up
1558	chr10	ZMYND11	NM_006624	Down
1559	chr10	DIP2C	NM_014974	Down
1560	chr10	WDR37	NM_014023	Down
1561	chr10	PFKP	NM_002627	Down

Fig. 2A-36

1562	chr10	PFKP	NM_002627	Down
1563	chr10	---	---	Down
1564	chr10	---	---	Down
1565	chr10	IL15RA	NM_002189	up
1566	chr10	FLJ45983	NR_024255	Down
1567	chr10	C10orf47	NM_153256	Down
1568	chr10	BEND7	NM_152751	up
1569	chr10	BEND7	NM_152751	Down
1570	chr10	HSPA14	NM_016299	Down
1571	chr10	HSPA14	NM_016299	up
1572	chr10	RSU1	ENST00000377921	Down
1573	chr10	CUBN	NM_001081	up
1574	chr10	STAM	NM_003473	Down
1575	chr10	CACNB2	NM_201590	Down
1576	chr10	PLXDC2	NM_032812	Down
1577	chr10	KIAA1217	NM_019590	up
1578	chr10	YME1L1	NM_139312	Down
1579	chr10	ARMC4	NM_018076	Down
1580	chr10	EPC1	NM_025209	Down
1581	chr10	PARD3	NM_019619	up
1582	chr10	CCNY	NM_181698	Down
1583	chr10	ZNF248	NM_021045	up
1584	chr10	RET	NM_020975	Down
1585	chr10	HNRNPF	NM_001098208	Down
1586	chr10	LOC439911	AK127450	up
1587	chr10	ZNF485	NM_145312	Down
1588	chr10	C10orf10	NM_007021	up
1589	chr10	ALOX5	NM_000698	Down
1590	chr10	WDFY4	NM_020945	Down
1591	chr10	FAM13C	NM_198215	up
1592	chr10	ZNF365	NM_014951	Down
1593	chr10	SIRT1	NM_012238	up
1594	chr10	MYPN	NM_032578	up
1595	chr10	SRGN	NM_002727	Down
1596	chr10	HK1	NM_033496	Down
1597	chr10	C10orf35	NM_145306	Down
1598	chr10	TYSND1	NM_173555	Down
1599	chr10	TYSND1	NM_173555	up
1600	chr10	NPFFR1	NM_022146	Down
1601	chr10	ADAMTS14	NM_139155	Down
1602	chr10	CDH23	NM_022124	up
1603	chr10	ASCC1	NM_015947	Down
1604	chr10	OIT3	NM_152635	Down
1605	chr10	TTC18	NM_145170	Down

Fig. 2A-37

1606	chr10	SYNPO2L	NM_001114133	up
1607	chr10	CAMK2G	NM_172171	Down
1608	chr10	ZMIZ1	NM_020338	up
1609	chr10	MAT1A	NM_000429	up
1610	chr10	TSPAN14	NM_030927	up
1611	chr10	CDHR1	NM_001171971	Down
1612	chr10	RGR	NM_002921	up
1613	chr10	GRID1	NM_017551	Down
1614	chr10	LDB3	NM_007078	up
1615	chr10	MMRN2	NM_024756	Down
1616	chr10	CFLP1	NR_028492	Down
1617	chr10	PTEN	NM_000314	up
1618	chr10	SLC16A12	NM_213606	Down
1619	chr10	FGFBP3	NM_152429	up
1620	chr10	PLCE1	NM_016341	up
1621	chr10	SORBS1	NM_001034954	up
1622	chr10	SORBS1	NM_006434	Down
1623	chr10	BLNK	NM_013314	Down
1624	chr10	DNTT	NM_004088	Down
1625	chr10	TLL2	NM_012465	Down
1626	chr10	TLL2	NM_012465	Down
1627	chr10	FRAT2	NM_012083	up
1628	chr10	MMS19	NM_022362	Down
1629	chr10	HPS1	NM_000195	Down
1630	chr10	GOT1	NM_002079	Down
1631	chr10	NKX2-3	NM_145285	Down
1632	chr10	ENTPD7	NM_020354	Down
1633	chr10	COX15	NM_078470	Down
1634	chr10	PKD2L1	NM_016112	up
1635	chr10	FAM178A	NM_018121	up
1636	chr10	LZTS2	NM_032429	Down
1637	chr10	PDZD7	NM_024895	Down
1638	chr10	BTRC	NM_033637	Down
1639	chr10	POLL	NM_001174084	up
1640	chr10	FBXW4	NM_022039	up
1641	chr10	KCNIP2	NM_014591	Down
1642	chr10	INA	NM_032727	up
1643	chr10	TAF5	NM_006951	up
1644	chr10	CALHM1	NM_001001412	up
1645	chr10	SH3PXD2A	NM_014631	Down
1646	chr10	OBFC1	NM_024928	up
1647	chr10	C10orf79	NM_025145	Down
1648	chr10	GSTO2	NM_183239	Down
1649	chr10	DUSP5	NM_004419	up

Fig. 2A-38

1650	chr10	ADRA2A	NM_000681	Down
1651	chr10	TCF7L2	NM_001146274	Down
1652	chr10	NRAP	NM_006175	Down
1653	chr10	ADRB1	NM_000684	up
1654	chr10	TDRD1	NM_198795	up
1655	chr10	FAM160B1	NM_001135051	up
1656	chr10	ATRNL1	NM_207303	up
1657	chr10	GFRA1	NM_005264	up
1658	chr10	PNLIPRP2	NM_005396	Down
1659	chr10	RAB11FIP2	NM_014904	Down
1660	chr10	EIF3A	NM_003750	Down
1661	chr10	GRK5	NM_005308	Down
1662	chr10	INPP5F	NM_014937	Down
1663	chr10	SEC23IP	NM_007190	Down
1664	chr10	TACC2	NM_206862	up
1665	chr10	FLJ46361	NR_003570	up
1666	chr10	PSTK	NM_153336	Down
1667	chr10	PSTK	NM_153336	Down
1668	chr10	METTL10	NM_212554	Down
1669	chr10	CTBP2	NM_022802	up
1670	chr10	DPYSL4	NM_006426	Down
1671	chr10	C10orf93	NM_173572	Down
1672	chr10	KNDC1	NM_152643	Down
1673	chr10	KNDC1	NM_152643	up
1674	chr10	KNDC1	NM_152643	up
1675	chr10	VENTX	NM_014468	Down
1676	chr10	ADAM8	NM_001109	up
1677	chr10	ZNF511	NM_145806	Down
1678	chr10	C10orf125	NM_001098483	Down
1679	chr10	ECHS1	NM_004092	Down
1680	chr10	PAOX	NM_152911	Down
1681	chr11	B4GALNT4	NM_178537	Down
1682	chr11	PKP3	NM_007183	up
1683	chr11	PKP3	NM_007183	up
1684	chr11	PKP3	NM_007183	Down
1685	chr11	SIGIRR	NM_001135054	Down
1686	chr11	LRRC56	NM_198075	Down
1687	chr11	C11orf35	NM_173573	up
1688	chr11	IRF7	NM_001572	Down
1689	chr11	CDHR5	NM_021924	Down
1690	chr11	CDHR5	NM_021924	Down
1691	chr11	SCT	NM_021920	Down
1692	chr11	EPS8L2	NM_022772	Down
1693	chr11	EPS8L2	NM_022772	up

Fig. 2A-39

1694	chr11	LRDD	NM_145886	up
1695	chr11	LRDD	NM_145886	up
1696	chr11	KCNQ1	NM_000218	Down
1697	chr11	SLC22A18	NM_002555	Down
1698	chr11	SLC22A18	NM_002555	up
1699	chr11	OR52A4	NM_001005222	up
1700	chr11	HBE1	NM_005330	up
1701	chr11	OR52B6	NM_001005162	Down
1702	chr11	FAM160A2	NM_032127	Down
1703	chr11	APBB1	NM_001164	Down
1704	chr11	CYB5R2	NM_016229	Down
1705	chr11	RPL27A	NM_000990	Down
1706	chr11	AMPD3	NM_000480	Down
1707	chr11	MICALCL	NM_032867	Down
1708	chr11	MICALCL	NM_032867	Down
1709	chr11	PDE3B	NM_000922	up
1710	chr11	PDE3B	NM_000922	Down
1711	chr11	SOX6	NM_017508	Down
1712	chr11	RPS13	NM_001017	up
1713	chr11	MYOD1	NM_002478	up
1714	chr11	---	---	Down
1715	chr11	GTF2H1	NM_005316	Down
1716	chr11	UEVLD	NM_001040697	up
1717	chr11	SPTY2D1	NM_194285	up
1718	chr11	NAV2	NM_182964	up
1719	chr11	NAV2	NM_182964	up
1720	chr11	LUZP2	NM_001009909	Down
1721	chr11	KCNA4	NM_002233	up
1722	chr11	PRRG4	NM_024081	Down
1723	chr11	PRRG4	NM_024081	up
1724	chr11	SLC1A2	ENST00000395750	Down
1725	chr11	PRR5L	NM_024841	up
1726	chr11	PRR5L	NM_001160167	Down
1727	chr11	EXT2	NM_000401	up
1728	chr11	CD82	NM_002231	up
1729	chr11	TSPAN18	NM_130783	Down
1730	chr11	TP53I11	NM_006034	Down
1731	chr11	SYT13	NM_020826	Down
1732	chr11	PEX16	NM_004813	Down
1733	chr11	PEX16	NM_004813	up
1734	chr11	AMBRA1	NM_017749	Down
1735	chr11	ARHGAP1	NM_004308	up
1736	chr11	PACSIN3	NM_016223	Down
1737	chr11	PACSIN3	NM_016223	up

Fig. 2A-40

1738	chr11	MADD	NM_130470	up
1739	chr11	MADD	NM_130470	Down
1740	chr11	OR4C12	NM_001005270	Down
1741	chr11	OR5AS1	NM_001001921	up
1742	chr11	TNKS1BP1	NM_033396	Down
1743	chr11	TNKS1BP1	NM_033396	up
1744	chr11	SLC43A3	NM_017611	Down
1745	chr11	RTN4RL2	NM_178570	Down
1746	chr11	SLC43A1	NM_003627	up
1747	chr11	SERPING1	NM_000062	Down
1748	chr11	ZDHHC5	NM_015457	Down
1749	chr11	ZFP91	NM_053023	Down
1750	chr11	GLYATL2	NM_145016	up
1751	chr11	MRPL16	NM_017840	Down
1752	chr11	GIF	NM_005142	up
1753	chr11	CD6	NM_006725	Down
1754	chr11	CD6	NM_006725	Down
1755	chr11	DAK	NM_015533	up
1756	chr11	CPSF7	NM_024811	Down
1757	chr11	C11orf66	NM_145017	up
1758	chr11	C11orf9	NM_013279	Down
1759	chr11	C11orf9	NM_013279	Down
1760	chr11	FEN1	NM_004111	Down
1761	chr11	MTA2	NM_004739	up
1762	chr11	MTA2	NM_004739	up
1763	chr11	MTA2	NM_004739	Down
1764	chr11	UBXN1	NM_015853	Down
1765	chr11	NXF1	NM_006362	up
1766	chr11	NXF1	NM_006362	Down
1767	chr11	SLC3A2	NM_001012661	up
1768	chr11	HRASLS5	NM_054108	up
1769	chr11	RCOR2	NM_173587	Down
1770	chr11	STIP1	NM_006819	up
1771	chr11	TRPT1	NM_001033678	Down
1772	chr11	PLCB3	NM_000932	up
1773	chr11	PRDX5	NM_012094	Down
1774	chr11	RPS6KA4	NM_003942	Down
1775	chr11	SLC22A11	NM_018484	up
1776	chr11	NRXN2	NM_015080	Down
1777	chr11	NAALADL1	NM_005468	Down
1778	chr11	TM7SF2	NM_003273	Down
1779	chr11	SCYL1	NM_020680	Down
1780	chr11	LTBP3	NM_001130144	Down
1781	chr11	SIPA1	NM_153253	Down

Fig. 2A-41

1782	chr11	KAT5	NM_182710	Down
1783	chr11	SNX32	NM_152760	Down
1784	chr11	EFEMP2	NM_016938	up
1785	chr11	CTSW	NM_001335	Down
1786	chr11	CCDC85B	NM_006848	up
1787	chr11	---	---	up
1788	chr11	---	---	Down
1789	chr11	BANF1	NM_003860	Down
1790	chr11	CATSPER1	NM_053054	up
1791	chr11	CATSPER1	NM_053054	Down
1792	chr11	RAB1B	NM_030981	up
1793	chr11	TMEM151A	NM_153266	Down
1794	chr11	B3GNT1	NM_006876	up
1795	chr11	SLC29A2	NM_001532	Down
1796	chr11	ADRBK1	NM_001619	Down
1797	chr11	SSH3	NM_017857	Down
1798	chr11	SSH3	NM_017857	up
1799	chr11	CARNS1	NM_001166222	up
1800	chr11	GPR152	NM_206997	Down
1801	chr11	PITPNM1	NM_004910	Down
1802	chr11	NUDT8	NM_181843	Down
1803	chr11	TBX10	NM_005995	Down
1804	chr11	LRP5	NM_002335	up
1805	chr11	MTL5	NM_004923	up
1806	chr11	CPT1A	NM_001031847	Down
1807	chr11	CPT1A	NM_001876	Down
1808	chr11	MRPL21	NM_181515	Down
1809	chr11	TPCN2	NM_139075	Down
1810	chr11	FGF19	NM_005117	up
1811	chr11	FGF3	NM_005247	up
1812	chr11	ANO1	NM_018043	Down
1813	chr11	CTTN	NM_005231	up
1814	chr11	INPPL1	NM_001567	Down
1815	chr11	STARD10	NM_006645	Down
1816	chr11	ARHGEF17	NM_014786	up
1817	chr11	RELT	NM_032871	Down
1818	chr11	OR2AT4	NM_001005285	Down
1819	chr11	SLCO2B1	NM_007256	up
1820	chr11	ARRB1	NM_004041	Down
1821	chr11	SERPINH1	NM_001235	up
1822	chr11	WNT11	NM_004626	Down
1823	chr11	B3GNT6	NM_138706	Down
1824	chr11	CAPN5	NM_004055	Down
1825	chr11	CCDC81	AK027167	up

Fig. 2A-42

1826	chr11	NOX4	BC051371	up
1827	chr11	C11orf70	BC054869	Down
1828	chr11	YAP1	NM_001130145	Down
1829	chr11	MMP20	NM_004771	Down
1830	chr11	MMP8	NM_002424	Down
1831	chr11	CUL5	NM_003478	up
1832	chr11	NPAT	NM_002519	Down
1833	chr11	NPAT	NM_002519	Down
1834	chr11	ATM	NM_000051	up
1835	chr11	NCAM1	NM_000615	Down
1836	chr11	DRD2	NM_000795	Down
1837	chr11	NNMT	NM_006169	Down
1838	chr11	CADM1	NM_014333	Down
1839	chr11	SIDT2	AK303023	up
1840	chr11	RNF214	NM_207343	up
1841	chr11	BACE1	NM_012104	up
1842	chr11	CEP164	NM_014956	up
1843	chr11	DSCAML1	NM_020693	Down
1844	chr11	UBE4A	NM_004788	Down
1845	chr11	CXCR5	NM_001716	up
1846	chr11	BCL9L	NM_182557	Down
1847	chr11	BCL9L	NM_182557	Down
1848	chr11	FOXR1	NM_181721	Down
1849	chr11	SLC37A4	NM_001164277	Down
1850	chr11	SLC37A4	NM_001164277	up
1851	chr11	HMBS	NM_000190	up
1852	chr11	H2AFX	NM_002105	Down
1853	chr11	NLRX1	NM_024618	Down
1854	chr11	USP2	NM_004205	Down
1855	chr11	GRIK4	NM_014619	up
1856	chr11	SORL1	NM_003105	up
1857	chr11	UBASH3B	NM_032873	Down
1858	chr11	OR8G5	NM_001005198	up
1859	chr11	OR8D2	NM_001002918	Down
1860	chr11	TBRG1	NM_032811	up
1861	chr11	ESAM	AY189281	up
1862	chr11	ROBO3	NM_022370	Down
1863	chr11	SLC37A2	NM_198277	Down
1864	chr11	DDX25	NM_013264	Down
1865	chr11	RPUSD4	NM_032795	Down
1866	chr11	SRPR	NM_003139	up
1867	chr11	KIRREL3	NM_032531	Down
1868	chr11	ETS1	NM_001143820	up
1869	chr11	C11orf45	NM_145013	Down

Fig. 2A-43

1870	chr11	C11orf45	NM_145013	Down
1871	chr11	NFRKB	NM_001143835	Down
1872	chr11	NFRKB	NM_001143835	Down
1873	chr11	PRDM10	NM_020228	up
1874	chr11	APLP2	NM_001642	Down
1875	chr11	APLP2	NM_001642	Down
1876	chr11	ST14	NM_021978	up
1877	chr11	ST14	NM_021978	up
1878	chr11	ACAD8	NM_014384	Down
1879	chr11	GLB1L3	NM_001080407	Down
1880	chr12	SLC6A13	NM_016615	Down
1881	chr12	NINJ2	NM_016533	Down
1882	chr12	CACNA2D4	NM_172364	up
1883	chr12	CACNA2D4	NM_172364	Down
1884	chr12	CACNA1C	NM_199460	Down
1885	chr12	PLEKHG6	NM_018173	Down
1886	chr12	LTBR	NM_002342	Down
1887	chr12	LTBR	NM_002342	up
1888	chr12	TAPBPL	NM_018009	Down
1889	chr12	IFFO1	NM_080730	Down
1890	chr12	IFFO1	NM_080730	Down
1891	chr12	NOP2	NM_006170	Down
1892	chr12	GPR162	NM_019858	up
1893	chr12	LPCAT3	NM_005768	up
1894	chr12	FAM90A1	NM_018088	up
1895	chr12	PZP	NM_002864	Down
1896	chr12	CLEC1B	NM_016509	Down
1897	chr12	TAS2R10	NM_023921	up
1898	chr12	DUSP16	NM_030640	Down
1899	chr12	EMP1	NM_001423	up
1900	chr12	C12orf36	NM_182558	Down
1901	chr12	MGP	NM_000900	Down
1902	chr12	RERGL	NM_024730	up
1903	chr12	PIK3C2G	NM_004570	up
1904	chr12	LDHB	NM_002300	up
1905	chr12	ETNK1	NM_018638	up
1906	chr12	SOX5	NM_006940	up
1907	chr12	IFLTD1	NM_001145728	up
1908	chr12	FLJ13224	NR_026806	up
1909	chr12	CPNE8	NM_153634	up
1910	chr12	GXYLT1	NM_173601	Down
1911	chr12	PPHLN1	NM_201515	up
1912	chr12	RAPGEF3	NM_001098531	Down
1913	chr12	RAPGEF3	NM_001098531	Down

Fig. 2A-44

1914	chr12	DDX23	NM_004818	up
1915	chr12	MLL2	NM_003482	up
1916	chr12	MLL2	NM_003482	up
1917	chr12	MLL2	NM_003482	up
1918	chr12	TROAP	NM_005480	Down
1919	chr12	KCNH3	NM_012284	up
1920	chr12	PRPF40B	NM_001031698	up
1921	chr12	PRPF40B	NM_001031698	up
1922	chr12	NCKAP5L	NM_001037806	Down
1923	chr12	---	---	Down
1924	chr12	METTL7A	NM_014033	Down
1925	chr12	SLC11A2	NM_001174125	up
1926	chr12	LETMD1	NM_015416	Down
1927	chr12	BIN2	NM_016293	up
1928	chr12	ANKRD33	NM_001130015	Down
1929	chr12	C12orf44	NM_021934	up
1930	chr12	KRT7	NM_005556	Down
1931	chr12	SPRYD3	NM_032840	Down
1932	chr12	ZNF740	NM_001004304	up
1933	chr12	SP1	NM_138473	Down
1934	chr12	AMHR2	NM_020547	Down
1935	chr12	ATF7	BC042363	up
1936	chr12	COPZ1	NM_016057	Down
1937	chr12	KIAA0748	NM_001098815	up
1938	chr12	ITGA7	NM_001144996	up
1939	chr12	MMP19	NM_002429	up
1940	chr12	CNPY2	NM_014255	up
1941	chr12	TIMELESS	NM_003920	up
1942	chr12	PRIM1	NM_000946	Down
1943	chr12	PRIM1	NM_000946	up
1944	chr12	LRP1	NM_002332	up
1945	chr12	LRP1	NM_002332	Down
1946	chr12	GLI1	NM_005269	Down
1947	chr12	B4GALNT1	NM_001478	Down
1948	chr12	CDK4	NM_000075	Down
1949	chr12	TSFM	NM_001172696	Down
1950	chr12	CTDSP2	NM_005730	up
1951	chr12	XRCC6BP1	NM_033276	Down
1952	chr12	MON2	NM_015026	up
1953	chr12	C12orf66	NM_152440	up
1954	chr12	GNS	NM_002076	up
1955	chr12	RPSAP52	NR_026825	Down
1956	chr12	PTPRB	NM_001109754	up
1957	chr12	ZDHHC17	NM_015336	Down

Fig. 2A-45

1958	chr12	C12orf50	BC038413	up
1959	chr12	CEP290	NM_025114	Down
1960	chr12	C12orf37	AK058107	up
1961	chr12	PLXNC1	NM_005761	Down
1962	chr12	NEDD1	NM_001135175	up
1963	chr12	SLC25A3	NM_005888	up
1964	chr12	APAF1	NM_013229	Down
1965	chr12	SCYL2	NM_017988	Down
1966	chr12	ANO4	NM_178826	up
1967	chr12	CCDC53	NM_016053	up
1968	chr12	C12orf42	NM_198521	Down
1969	chr12	HCFC2	NM_013320	up
1970	chr12	NUAK1	NM_014840	up
1971	chr12	POLR3B	NM_018082	Down
1972	chr12	POLR3B	NM_018082	Down
1973	chr12	SART3	BC041638	Down
1974	chr12	TCHP	NM_032300	up
1975	chr12	GIT2	NM_057169	up
1976	chr12	C12orf24	NM_013300	up
1977	chr12	RPL6	NM_001024662	up
1978	chr12	DTX1	NM_004416	Down
1979	chr12	DTX1	NM_004416	Down
1980	chr12	TBX3	NM_005996	Down
1981	chr12	C12orf49	AK298857	Down
1982	chr12	FBXW8	NM_153348	up
1983	chr12	NOS1	NM_000620	Down
1984	chr12	TAOK3	NM_016281	Down
1985	chr12	PRKAB1	NM_006253	Down
1986	chr12	CIT	NM_007174	Down
1987	chr12	PXN	BC052611	Down
1988	chr12	PLA2G1B	NM_000928	up
1989	chr12	MSI1	NM_002442	Down
1990	chr12	GATC	NM_176818	up
1991	chr12	---	---	up
1992	chr12	CAMKK2	NM_006549	Down
1993	chr12	---	---	up
1994	chr12	---	---	Down
1995	chr12	KDM2B	NM_032590	up
1996	chr12	KDM2B	NM_032590	Down
1997	chr12	CLIP1	NM_002956	up
1998	chr12	KNTC1	NM_014708	Down
1999	chr12	HIP1R	NM_003959	Down
2000	chr12	ZNF664	NM_152437	up
2001	chr12	FAM101A	NM_181709	Down

Fig. 2A-46

2002	chr12	NCOR2	NM_006312	Down
2003	chr12	NCOR2	NM_006312	Down
2004	chr12	NCOR2	NM_006312	up
2005	chr12	NCOR2	NM_006312	Down
2006	chr12	GPR133	NM_198827	Down
2007	chr12	SFRS8	NM_004592	up
2008	chr12	ULK1	NM_003565	Down
2009	chr12	EP400	NM_015409	up
2010	chr12	POLE	NM_006231	Down
2011	chr12	POLE	NM_006231	Down
2012	chr12	POLE	NM_006231	up
2013	chr13	ITGBL1	NM_004791	up
2014	chr13	SGCG	NM_000231	Down
2015	chr13	ATP12A	NM_001676	Down
2016	chr13	PABPC3	NM_030979	up
2017	chr13	FAM123A	NM_152704	up
2018	chr13	ATP8A2	NM_016529	Down
2019	chr13	PAN3	NM_175854	Down
2020	chr13	MTUS2	NM_015233	Down
2021	chr13	MTUS2	NM_001033602	Down
2022	chr13	OK	AB064667	up
2023	chr13	FRY	NM_023037	Down
2024	chr13	KL	NM_004795	up
2025	chr13	DCLK1	NM_004734	Down
2026	chr13	POSTN	NM_006475	up
2027	chr13	TRPC4	NM_016179	up
2028	chr13	UFM1	NM_016617	Down
2029	chr13	FREM2	NM_207361	up
2030	chr13	FOXO1	NM_002015	Down
2031	chr13	ENOX1	NM_017993	Down
2032	chr13	NUDT15	NM_018283	Down
2033	chr13	FNDC3A	NM_001079673	up
2034	chr13	FNDC3A	NM_001079673	up
2035	chr13	CCDC70	NM_031290	up
2036	chr13	NEK3	NM_002498	up
2037	chr13	KCTD12	NM_138444	Down
2038	chr13	MYCBP2	NM_015057	Down
2039	chr13	MYCBP2	NM_015057	up
2040	chr13	SCEL	NM_144777	Down
2041	chr13	SLITRK5	NM_015567	Down
2042	chr13	GPC5	NM_004466	up
2043	chr13	SLC15A1	NM_005073	up
2044	chr13	ZIC2	NM_007129	Down
2045	chr13	BIVM	NM_017693	Down

Fig. 2A-47

2046	chr13	ARGLU1	BC071587	up
2047	chr13	COL4A2	NM_001846	Down
2048	chr13	COL4A2	NM_001846	Down
2049	chr13	COL4A2	NM_001846	up
2050	chr13	RAB20	NM_017817	up
2051	chr13	CARS2	NM_024537	up
2052	chr13	CARS2	NM_024537	Down
2053	chr13	ING1	NM_198219	up
2054	chr13	ARHGEF7	NM_003899	Down
2055	chr13	ARHGEF7	NM_003899	Down
2056	chr13	ARHGEF7	NM_003899	up
2057	chr13	ARHGEF7	NM_003899	up
2058	chr13	PROZ	NM_003891	Down
2059	chr13	PROZ	NM_003891	Down
2060	chr13	CUL4A	NM_001008895	up
2061	chr13	GRTP1	AK300897	up
2062	chr13	TMCO3	NM_017905	up
2063	chr14	OSGEP	NM_017807	up
2064	chr14	METT11D1	NM_001029991	Down
2065	chr14	---	---	Down
2066	chr14	HNRNPC	NM_031314	Down
2067	chr14	---	---	up
2068	chr14	SUPT16H	NM_007192	Down
2069	chr14	---	---	Down
2070	chr14	SLC7A7	NM_003982	up
2071	chr14	MRPL52	NM_181304	Down
2072	chr14	SLC7A8	NM_012244	Down
2073	chr14	SLC7A8	NM_182728	up
2074	chr14	HOMEZ	NM_020834	Down
2075	chr14	EFS	NM_005864	Down
2076	chr14	MYH6	NM_002471	Down
2077	chr14	LRRC16B	NM_138360	Down
2078	chr14	FITM1	BC042179	Down
2079	chr14	RNF31	NM_017999	up
2080	chr14	IRF9	NM_006084	up
2081	chr14	IRF9	NM_006084	up
2082	chr14	TM9SF1	NM_006405	up
2083	chr14	LTB4R2	NM_019839	Down
2084	chr14	RIPK3	NM_006871	up
2085	chr14	KHNYN	NM_015299	up
2086	chr14	STXBP6	NM_014178	Down
2087	chr14	PRKD1	NM_002742	Down
2088	chr14	SCFD1	NM_016106	up
2089	chr14	SCFD1	NM_016106	Down

Fig. 2A-48

2090	chr14	HECTD1	NM_015382	Down
2091	chr14	PPP2R3C	NM_017917	up
2092	chr14	BRMS1L	NM_032352	Down
2093	chr14	FOXA1	NM_004496	Down
2094	chr14	SEC23A	NM_006364	up
2095	chr14	PNN	NM_002687	up
2096	chr14	PPIL5	NM_152329	Down
2097	chr14	ARF6	NM_001663	up
2098	chr14	ATP5S	NM_001003803	up
2099	chr14	MAP4K5	NM_198794	Down
2100	chr14	NIN	NM_182944	up
2101	chr14	SAMD4A	NM_015589	Down
2102	chr14	LGALS3	NM_002306	up
2103	chr14	PSMA3	NM_002788	Down
2104	chr14	DACT1	NM_016651	up
2105	chr14	SIX4	NM_017420	up
2106	chr14	SLC38A6	NM_001172702	up
2107	chr14	HIF1A	NM_001530	Down
2108	chr14	ESR2	NM_001437	up
2109	chr14	RAB15	NM_198686	Down
2110	chr14	RDH12	NM_152443	Down
2111	chr14	ZFYVE26	NM_015346	Down
2112	chr14	ACTN1	NM_001130004	Down
2113	chr14	DCAF5	NM_003861	Down
2114	chr14	---	---	up
2115	chr14	SLC10A1	NM_003049	Down
2116	chr14	SMOC1	NM_001034852	Down
2117	chr14	SLC8A3	NM_033262	Down
2118	chr14	MAP3K9	NM_033141	up
2119	chr14	MAP3K9	NM_033141	Down
2120	chr14	ZFYVE1	NM_021260	up
2121	chr14	COQ6	NM_182476	up
2122	chr14	LTBP2	NM_000428	Down
2123	chr14	LTBP2	NM_000428	Down
2124	chr14	MLH3	NM_001040108	up
2125	chr14	NEK9	NM_033116	Down
2126	chr14	ADCK1	NM_020421	Down
2127	chr14	NRXN3	NM_004796	up
2128	chr14	CATSPERB	NM_024764	up
2129	chr14	CPSF2	NM_017437	up
2130	chr14	CPSF2	NM_017437	Down
2131	chr14	CHGA	NM_001275	up
2132	chr14	ITPK1	NM_014216	up
2133	chr14	OTUB2	NM_023112	up

Fig. 2A-49

2134	chr14	IFI27	NM_001130080	Down
2135	chr14	SERPINA9	NM_175739	Down
2136	chr14	SERPINA13	NR_015340	up
2137	chr14	DICER1	NM_177438	Down
2138	chr14	GLRX5	NM_016417	Down
2139	chr14	C14orf132	NR_023938	up
2140	chr14	CYP46A1	NM_006668	Down
2141	chr14	EML1	NM_001008707	Down
2142	chr14	---	---	Down
2143	chr14	WDR25	NM_024515	Down
2144	chr14	DLK1	NM_003836	Down
2145	chr14	DIO3OS	BC065701	up
2146	chr14	WDR20	NM_181291	Down
2147	chr14	WDR20	BC030654	up
2148	chr14	CDC42BPB	NM_006035	Down
2149	chr14	TNFAIP2	NM_006291	up
2150	chr14	CKB	NM_001823	up
2151	chr14	XRCC3	NM_001100119	Down
2152	chr14	TDRD9	NM_153046	Down
2153	chr14	KIF26A	NM_015656	Down
2154	chr14	INF2	NM_022489	Down
2155	chr14	INF2	NM_022489	Down
2156	chr14	AKT1	NM_005163	up
2157	chr14	AHNAK2	NM_138420	Down
2158	chr14	JAG2	NM_002226	Down
2159	chr14	C14orf80	NM_001134875	Down
2160	chr14	IGH@	BC065733	Down
2161	chr14	IGHD	BC063384	Down
2162	chr15	NIPA1	NM_144599	up
2163	chr15	GOLGA6L2	BC129821	up
2164	chr15	SNURF	ENST00000401453	Down
2165	chr15	ATP10A	AB051358	Down
2166	chr15	HERC2	NM_004667	Down
2167	chr15	HERC2	NM_004667	Down
2168	chr15	TJP1	NM_003257	up
2169	chr15	KLF13	NM_015995	Down
2170	chr15	OTUD7A	NM_130901	Down
2171	chr15	C15orf55	NM_175741	Down
2172	chr15	THBS1	NM_003246	up
2173	chr15	GPR176	NM_007223	up
2174	chr15	BMF	NM_001003940	Down
2175	chr15	PLCB2	NM_004573	Down
2176	chr15	DISP2	NM_033510	up
2177	chr15	IVD	NM_002225	Down

Fig. 2A-50

2178	chr15	FAM82A2	NM_018145	up
2179	chr15	ZFYVE19	NM_001077268	Down
2180	chr15	PPP1R14D	NM_017726	Down
2181	chr15	RHOV	NM_133639	up
2182	chr15	VPS18	NM_020857	up
2183	chr15	INO80	NM_017553	Down
2184	chr15	RTF1	NM_015138	up
2185	chr15	RPAP1	NM_015540	Down
2186	chr15	TYRO3	NM_006293	Down
2187	chr15	TYRO3	NM_006293	Down
2188	chr15	JMJD7-PLA2G4B	NR_015346	Down
2189	chr15	SPTBN5	NM_016642	Down
2190	chr15	PLA2G4D	NM_178034	Down
2191	chr15	CAPN3	NR_027911	Down
2192	chr15	LRRC57	NM_153260	up
2193	chr15	CDAN1	NM_138477	Down
2194	chr15	CDAN1	NM_138477	Down
2195	chr15	UBR1	NM_174916	up
2196	chr15	UBR1	NM_174916	up
2197	chr15	ELL3	NM_025165	Down
2198	chr15	MFAP1	NM_005926	Down
2199	chr15	DUOX2	NM_014080	up
2200	chr15	DUOX2	NM_014080	Down
2201	chr15	C15orf48	NM_197955	Down
2202	chr15	C15orf21	NR_022014	Down
2203	chr15	ATP8B4	NM_024837	Down
2204	chr15	TMOD2	NM_014548	up
2205	chr15	GNB5	NM_006578	Down
2206	chr15	MYO5A	NM_000259	up
2207	chr15	ARPP19	NM_006628	Down
2208	chr15	PIGB	NM_004855	Down
2209	chr15	NEDD4	NM_006154	Down
2210	chr15	GCOM1	NM_001018090	Down
2211	chr15	TLN2	NM_015059	Down
2212	chr15	TPM1	NM_001018005	Down
2213	chr15	ANKDD1A	NM_182703	Down
2214	chr15	CILP	NM_003613	up
2215	chr15	IGDCC3	NM_004884	up
2216	chr15	IGDCC4	NM_020962	up
2217	chr15	RPL4	NM_000968	Down
2218	chr15	LCTL	NM_207338	Down
2219	chr15	MAP2K5	NM_145160	Down
2220	chr15	ITGA11	NM_001004439	Down
2221	chr15	SPESP1	NM_145658	Down

Fig. 2A-51

2222	chr15	TLE3	NM_005078	Down
2223	chr15	PARP6	NM_020214	Down
2224	chr15	HCN4	NM_005477	Down
2225	chr15	CD276	NM_001024736	Down
2226	chr15	PML	NM_033250	Down
2227	chr15	CYP11A1	NM_000781	Down
2228	chr15	C15orf17	NM_020447	up
2229	chr15	C15orf39	NM_015492	Down
2230	chr15	C15orf39	NM_015492	up
2231	chr15	CSPG4	NM_001897	Down
2232	chr15	ISL2	NM_145805	Down
2233	chr15	RCN2	NM_002902	Down
2234	chr15	TSPAN3	NM_005724	up
2235	chr15	ADAMTS7	NM_014272	up
2236	chr15	RASGRF1	BC040275	Down
2237	chr15	ARNT2	NM_014862	up
2238	chr15	KIAA1199	NM_018689	up
2239	chr15	AKAP13	NM_006738	up
2240	chr15	HAPLN3	NM_178232	up
2241	chr15	POLG	NM_002693	Down
2242	chr15	KIF7	NM_198525	Down
2243	chr15	IQGAP1	NM_003870	up
2244	chr15	CRTC3	NM_022769	Down
2245	chr15	MAN2A2	NM_006122	up
2246	chr15	VPS33B	NM_018668	Down
2247	chr15	LYSMD4	NM_152449	Down
2248	chr15	ADAMTS17	NM_139057	up
2249	chr15	LRRK1	NM_024652	up
2250	chr15	PCSK6	NM_138320	up
2251	chr15	TM2D3	NM_078474	Down
2252	chr16	SNRNP25	NM_024571	up
2253	chr16	ITFG3	NM_032039	up
2254	chr16	RGS11	NM_183337	Down
2255	chr16	RAB11FIP3	NM_014700	Down
2256	chr16	FAM195A	AK054811	up
2257	chr16	WDR90	NM_145294	Down
2258	chr16	RHOT2	NM_138769	up
2259	chr16	RHOT2	NM_138769	up
2260	chr16	CCDC78	NM_001031737	Down
2261	chr16	HAGHL	NM_207112	Down
2262	chr16	NARFL	NM_022493	Down
2263	chr16	MSLN	NM_005823	Down
2264	chr16	MSLN	NM_005823	up
2265	chr16	CACNA1H	NM_021098	Down

Fig. 2A-52

2266	chr16	UNKL	NM_001037125	Down
2267	chr16	CLCN7	NM_001287	Down
2268	chr16	CRAMP1L	NM_020825	up
2269	chr16	SPSB3	NM_080861	up
2270	chr16	SPSB3	NM_080861	Down
2271	chr16	HAGH	NM_005326	up
2272	chr16	HAGH	NM_005326	Down
2273	chr16	RPL3L	NM_005061	up
2274	chr16	TBL3	NM_006453	Down
2275	chr16	TRAF7	NM_032271	Down
2276	chr16	CASKIN1	NM_020764	Down
2277	chr16	CASKIN1	NM_020764	Down
2278	chr16	DCI	NM_001919	Down
2279	chr16	---	---	Down
2280	chr16	---	---	Down
2281	chr16	RNPS1	NM_006711	Down
2282	chr16	---	---	Down
2283	chr16	CCNF	NM_001761	up
2284	chr16	PRSS27	NM_031948	up
2285	chr16	SRRM2	NM_016333	Down
2286	chr16	---	---	Down
2287	chr16	PRSS22	NM_022119	Down
2288	chr16	TNFRSF12A	NM_016639	up
2289	chr16	ZNF263	NM_005741	up
2290	chr16	NLRC3	NM_178844	up
2291	chr16	TRAP1	NM_016292	up
2292	chr16	TRAP1	NM_016292	Down
2293	chr16	CREBBP	NM_004380	Down
2294	chr16	CREBBP	NM_004380	up
2295	chr16	ADCY9	NM_001116	Down
2296	chr16	ADCY9	NM_001116	Down
2297	chr16	CORO7	NM_024535	Down
2298	chr16	DNAJA3	NM_005147	Down
2299	chr16	NMRAL1	ENST00000404295	Down
2300	chr16	MGRN1	NM_015246	up
2301	chr16	ROGDI	NM_024589	up
2302	chr16	SEC14L5	NM_014692	Down
2303	chr16	NAGPA	NM_016256	Down
2304	chr16	C16orf72	NM_014117	Down
2305	chr16	CIITA	NM_000246	Down
2306	chr16	TXNDC11	NM_015914	up
2307	chr16	RSL1D1	NM_015659	Down
2308	chr16	CPPED1	NM_018340	Down
2309	chr16	MYH11	NM_002474	up

Fig. 2A-53

2310	chr16	ABCC1	NM_004996	Down
2311	chr16	ABCC1	NM_004996	up
2312	chr16	ABCC6	NM_001171	up
2313	chr16	ABCC6	NM_001171	Down
2314	chr16	XYLT1	NM_022166	Down
2315	chr16	TMC5	NM_001105248	up
2316	chr16	DNAH3	NM_017539	up
2317	chr16	VWA3A	NM_173615	Down
2318	chr16	POLR3E	NM_018119	Down
2319	chr16	CDR2	NM_001802	up
2320	chr16	ERN2	NM_033266	Down
2321	chr16	ERN2	NM_033266	Down
2322	chr16	SLC5A11	NM_052944	Down
2323	chr16	XPO6	NM_015171	up
2324	chr16	TAOK2	NM_004783	Down
2325	chr16	GDPD3	NM_024307	Down
2326	chr16	ITGAL	NM_002209	Down
2327	chr16	RNF40	NM_014771	Down
2328	chr16	ITGAM	NM_001145808	Down
2329	chr16	ITGAM	NM_001145808	up
2330	chr16	ITGAX	NM_000887	Down
2331	chr16	ITGAX	NM_000887	up
2332	chr16	ZNF843	NM_001136509	up
2333	chr16	ARMC5	NM_024742	up
2334	chr16	SLC5A2	NM_003041	Down
2335	chr16	GPT2	NM_133443	Down
2336	chr16	ABCC11	NM_032583	up
2337	chr16	ADCY7	NM_001114	Down
2338	chr16	SALL1	NM_002968	up
2339	chr16	RBL2	NM_005611	up
2340	chr16	OGFOD1	NM_018233	up
2341	chr16	NLRC5	NM_032206	up
2342	chr16	GPR56	NM_005682	up
2343	chr16	GPR56	NM_005682	up
2344	chr16	GPR97	NM_170776	Down
2345	chr16	KIFC3	NM_005550	up
2346	chr16	CNGB1	NM_001297	Down
2347	chr16	CNGB1	NM_001297	Down
2348	chr16	MMP15	NM_002428	Down
2349	chr16	CCDC113	NM_014157	Down
2350	chr16	PRSS54	NM_001080492	up
2351	chr16	PRSS54	NM_001080492	Down
2352	chr16	SETD6	NM_001160305	Down
2353	chr16	SLC38A7	NM_018231	up

Fig. 2A-54

2354	chr16	CMTM1	NM_181269	Down
2355	chr16	CDH16	NM_004062	up
2356	chr16	C16orf70	NM_025187	up
2357	chr16	NOL3	NM_003946	up
2358	chr16	E2F4	NM_001950	Down
2359	chr16	ELMO3	NM_024712	Down
2360	chr16	ELMO3	NM_024712	up
2361	chr16	FHOD1	NM_013241	up
2362	chr16	ZDHHC1	NM_013304	Down
2363	chr16	FAM65A	NM_024519	up
2364	chr16	C16orf48	BC008284	up
2365	chr16	SLC12A4	NM_005072	up
2366	chr16	DDX28	NM_018380	up
2367	chr16	PRMT7	NM_019023	up
2368	chr16	PRMT7	NM_019023	Down
2369	chr16	PRMT7	NM_019023	up
2370	chr16	PRMT7	NM_019023	up
2371	chr16	SMPD3	NM_018667	up
2372	chr16	COG8	NM_032382	up
2373	chr16	SF3B3	NM_012426	up
2374	chr16	HYDIN	AK299348	up
2375	chr16	AP1G1	NM_001030007	up
2376	chr16	DHODH	NM_001361	Down
2377	chr16	ZFHX3	NM_006885	up
2378	chr16	ZNRF1	NM_032268	Down
2379	chr16	BCAR1	NM_001170714	Down
2380	chr16	---	---	Down
2381	chr16	ADAMTS18	NM_199355	Down
2382	chr16	CDYL2	NM_152342	up
2383	chr16	PKD1L2	NM_052892	Down
2384	chr16	PLCG2	NM_002661	up
2385	chr16	CDH13	NM_001257	up
2386	chr16	NECAB2	NM_019065	Down
2387	chr16	LRRC50	NM_178452	Down
2388	chr16	KCNG4	NM_172347	Down
2389	chr16	ATP2C2	NM_014861	up
2390	chr16	ATP2C2	NM_014861	up
2391	chr16	KIAA1609	NM_020947	Down
2392	chr16	CRISPLD2	NM_031476	Down
2393	chr16	ZDHHC7	NM_001145548	up
2394	chr16	KIAA0182	NM_014615	up
2395	chr16	GINS2	NM_016095	Down
2396	chr16	C16orf74	BC009078	up
2397	chr16	KLHDC4	NM_017566	Down

Fig. 2A-55

2398	chr16	ZFPM1	NM_153813	Down
2399	chr16	IL17C	NM_013278	Down
2400	chr16	FAM38A	NM_001142864	up
2401	chr16	FAM38A	NM_001142864	Down
2402	chr16	FLJ40448	ENST00000333666	Down
2403	chr16	ANKRD11	NM_013275	Down
2404	chr16	SPG7	NM_003119	Down
2405	chr16	CDK10	NM_052988	Down
2406	chr16	CDK10	NM_052988	Down
2407	chr16	FANCA	NM_000135	Down
2408	chr16	AFG3L1	NR_003226	up
2409	chr17	FAM57A	NM_024792	Down
2410	chr17	MYO1C	NM_001080779	Down
2411	chr17	MYO1C	NM_001080779	up
2412	chr17	PITPNA	NM_006224	up
2413	chr17	PITPNA	NM_006224	up
2414	chr17	WDR81	NM_001163809	up
2415	chr17	WDR81	NM_001163809	up
2416	chr17	SMYD4	NM_052928	up
2417	chr17	TSR1	NM_018128	up
2418	chr17	SGSM2	NM_014853	Down
2419	chr17	MNT	NM_020310	Down
2420	chr17	KIAA0664	NM_015229	Down
2421	chr17	KIAA0664	NM_015229	up
2422	chr17	OR1G1	NM_003555	Down
2423	chr17	CAMKK1	NM_032294	Down
2424	chr17	CAMKK1	NM_032294	Down
2425	chr17	ATP2A3	NM_005173	Down
2426	chr17	ATP2A3	NM_005173	up
2427	chr17	ZZEF1	NM_015113	Down
2428	chr17	CYB5D2	NM_144611	Down
2429	chr17	MINK1	NM_015716	Down
2430	chr17	RNF167	NM_015528	Down
2431	chr17	INCA1	NM_001167986	Down
2432	chr17	KIF1C	NM_006612	Down
2433	chr17	PITPNM3	NM_031220	up
2434	chr17	BCL6B	NM_181844	Down
2435	chr17	DLG4	NM_001365	Down
2436	chr17	ACADVL	NM_000018	Down
2437	chr17	DVL2	NM_004422	Down
2438	chr17	DVL2	NM_004422	up
2439	chr17	GABARAP	NM_007278	up
2440	chr17	SLC2A4	NM_001042	Down
2441	chr17	KCTD11	NM_001002914	Down

Fig. 2A-56

2442	chr17	TMEM95	NM_198154	up
2443	chr17	PLSCR3	NM_020360	up
2444	chr17	CHRNB1	NM_000747	Down
2445	chr17	CHRNB1	NM_000747	up
2446	chr17	SENP3	NM_015670	up
2447	chr17	SHBG	NM_001040	Down
2448	chr17	EFNB3	NM_001406	Down
2449	chr17	CHD3	NM_001005273	up
2450	chr17	TRAPPC1	NM_021210	up
2451	chr17	CNTROB	NM_053051	Down
2452	chr17	CNTROB	NM_053051	up
2453	chr17	GUCY2D	NM_000180	up
2454	chr17	PER1	NM_002616	Down
2455	chr17	AURKB	NM_004217	Down
2456	chr17	PFAS	NM_012393	Down
2457	chr17	PFAS	NM_012393	up
2458	chr17	ODF4	NM_153007	Down
2459	chr17	NTN1	NM_004822	up
2460	chr17	WDR16	NM_145054	Down
2461	chr17	MYH13	NM_003802	Down
2462	chr17	MYH8	NM_002472	up
2463	chr17	MYH8	NM_002472	Down
2464	chr17	MYH4	NM_017533	up
2465	chr17	MYH1	NM_005963	up
2466	chr17	TTC19	NM_017775	Down
2467	chr17	NCOR1	NM_006311	Down
2468	chr17	TRPV2	NM_016113	Down
2469	chr17	RASD1	NM_016084	up
2470	chr17	RAI1	ENST00000395774	up
2471	chr17	DRG2	NM_001388	Down
2472	chr17	DRG2	NM_001388	up
2473	chr17	MYO15A	NM_016239	up
2474	chr17	LLGL1	NM_004140	up
2475	chr17	FLII	NM_002018	Down
2476	chr17	SLC47A1	NM_018242	up
2477	chr17	ULK2	NM_014683	up
2478	chr17	AKAP10	NM_007202	up
2479	chr17	USP22	NM_015276	Down
2480	chr17	---	---	up
2481	chr17	---	---	Down
2482	chr17	---	---	Down
2483	chr17	---	---	Down
2484	chr17	NOS2	NM_000625	up
2485	chr17	FLJ40504	NR_028334	Down

Fig. 2A-57

2486	chr17	VTN	NM_000638	Down
2487	chr17	SARM1	NM_015077	Down
2488	chr17	SPAG5	NM_006461	Down
2489	chr17	SUPT6H	NM_003170	up
2490	chr17	PIPOX	NM_016518	up
2491	chr17	PIPOX	NM_016518	Down
2492	chr17	PIPOX	NM_016518	up
2493	chr17	MYO18A	NM_078471	Down
2494	chr17	GIT1	NM_001085454	Down
2495	chr17	CORO6	NM_032854	up
2496	chr17	RAB11FIP4	NM_032932	up
2497	chr17	SUZ12	NM_015355	Down
2498	chr17	ZNF207	NM_003457	up
2499	chr17	SPACA3	NM_173847	Down
2500	chr17	TMEM132E	NM_207313	up
2501	chr17	C17orf66	NM_152781	Down
2502	chr17	SYNRG	NM_007247	Down
2503	chr17	GPR179	NM_001004334	Down
2504	chr17	PSMB3	NM_002795	up
2505	chr17	CACNB1	NM_000723	up
2506	chr17	RPL19	NM_000981	Down
2507	chr17	MED1	NM_004774	up
2508	chr17	CDK12	NM_016507	up
2509	chr17	PNMT	NM_002686	up
2510	chr17	ERBB2	NM_004448	Down
2511	chr17	MED24	NM_014815	Down
2512	chr17	NR1D1	NM_021724	Down
2513	chr17	CDC6	NM_001254	Down
2514	chr17	IGFBP4	NM_001552	up
2515	chr17	KRT27	NM_181537	up
2516	chr17	KRT16	NM_005557	Down
2517	chr17	SC65	NM_006455	up
2518	chr17	NT5C3L	NR_033465	Down
2519	chr17	ZNF385C	ENST00000436535	up
2520	chr17	DHX58	NM_024119	Down
2521	chr17	HCRT	NM_001524	Down
2522	chr17	STAT3	NM_139276	Down
2523	chr17	STAT3	NM_139276	up
2524	chr17	PTRF	NM_012232	Down
2525	chr17	PTRF	NM_012232	Down
2526	chr17	COASY	NM_025233	up
2527	chr17	PLEKHH3	NM_024927	Down
2528	chr17	PLEKHH3	NM_024927	up
2529	chr17	PLEKHH3	NM_024927	up

Fig. 2A-58

2530	chr17	CNTNAP1	NM_003632	Down
2531	chr17	VPS25	NM_032353	Down
2532	chr17	LOC388387	NR_027254	up
2533	chr17	MPP2	NM_005374	Down
2534	chr17	TMEM101	NM_032376	up
2535	chr17	ITGA2B	NM_000419	Down
2536	chr17	ADAM11	NM_002390	up
2537	chr17	GFAP	NM_002055	up
2538	chr17	MAP3K14	NM_003954	up
2539	chr17	ARHGAP27	NM_199282	Down
2540	chr17	SCRN2	NM_138355	Down
2541	chr17	SCRN2	NM_138355	Down
2542	chr17	FAM117A	NM_030802	up
2543	chr17	MYST2	NM_007067	Down
2544	chr17	---	---	Down
2545	chr17	TAC4	NM_170685	up
2546	chr17	ITGA3	NM_002204	Down
2547	chr17	PPP1R9B	NM_032595	Down
2548	chr17	PPP1R9B	NM_032595	Down
2549	chr17	MRPL27	NM_016504	Down
2550	chr17	CHAD	NM_001267	Down
2551	chr17	RSAD1	NM_018346	Down
2552	chr17	EPN3	NM_017957	up
2553	chr17	EPN3	NM_017957	Down
2554	chr17	ABCC3	NM_003786	up
2555	chr17	ABCC3	NM_003786	Down
2556	chr17	ABCC3	NM_003786	up
2557	chr17	WFIKKN2	NM_175575	Down
2558	chr17	UTP18	NM_016001	up
2559	chr17	KIF2B	NM_032559	Down
2560	chr17	TRIM25	NM_005082	Down
2561	chr17	SFRS1	NM_006924	Down
2562	chr17	EPX	NM_000502	up
2563	chr17	EPX	NM_000502	Down
2564	chr17	MPO	NM_000250	Down
2565	chr17	BZRAP1	NM_004758	Down
2566	chr17	BZRAP1	NM_004758	up
2567	chr17	TMEM49	NM_030938	Down
2568	chr17	USP32	NM_032582	up
2569	chr17	PPM1D	NM_003620	Down
2570	chr17	BCAS3	NM_001099432	Down
2571	chr17	BCAS3	NM_001099432	Down
2572	chr17	TBX2	NM_005994	up
2573	chr17	C17orf82	NM_203425	Down

Fig. 2A-59

2574	chr17	TBX4	NM_018488	up
2575	chr17	ACE	NM_152830	Down
2576	chr17	TACO1	NM_016360	Down
2577	chr17	CCDC47	NM_020198	up
2578	chr17	SMARCD2	NM_001098426	Down
2579	chr17	CD79B	NM_000626	up
2580	chr17	ERN1	NM_001433	Down
2581	chr17	GNA13	NM_006572	Down
2582	chr17	ARSG	NM_014960	up
2583	chr17	WIPI1	NM_017983	Down
2584	chr17	FAM20A	NR_027751	Down
2585	chr17	ABCA8	NM_007168	up
2586	chr17	SOX9	NM_000346	up
2587	chr17	COG1	NM_018714	Down
2588	chr17	TTYH2	NM_032646	Down
2589	chr17	CD300A	NM_007261	up
2590	chr17	CD300LF	NM_139018	up
2591	chr17	GRIN2C	NM_000835	up
2592	chr17	LLGL2	NM_004524	up
2593	chr17	LLGL2	NM_004524	up
2594	chr17	SAP30BP	NM_013260	Down
2595	chr17	ITGB4	NM_000213	Down
2596	chr17	ITGB4	NM_000213	up
2597	chr17	EXOC7	NM_001013839	Down
2598	chr17	FAM100B	NM_182565	Down
2599	chr17	QRICH2	NM_032134	up
2600	chr17	SPHK1	NM_021972	Down
2601	chr17	UBE2O	NM_022066	up
2602	chr17	RHBDF2	NM_024599	Down
2603	chr17	RHBDF2	NM_024599	Down
2604	chr17	RHBDF2	NM_024599	up
2605	chr17	RHBDF2	NM_024599	up
2606	chr17	TMC8	NM_152468	Down
2607	chr17	TK1	NM_003258	Down
2608	chr17	GAA	NM_000152	Down
2609	chr17	CARD14	NM_024110	up
2610	chr17	RNF213	NM_020914	Down
2611	chr17	RNF213	NM_020914	up
2612	chr17	NPTX1	NM_002522	Down
2613	chr17	C17orf56	BC064483	up
2614	chr17	C17orf56	BC064483	up
2615	chr17	TSPAN10	NM_031945	up
2616	chr17	CCDC137	NM_199287	Down
2617	chr17	HGS	NM_004712	Down

Fig. 2A-60

2618	chr17	HGS	NM_004712	Down
2619	chr17	SLC25A10	NM_012140	Down
2620	chr17	STRA13	NM_144998	up
2621	chr17	DCXR	NM_016286	Down
2622	chr17	GPS1	NM_212492	Down
2623	chr17	CCDC57	ENST00000392346	up
2624	chr17	CSNK1D	NM_001893	Down
2625	chr17	NARF	NM_012336	Down
2626	chr17	NARF	NM_012336	Down
2627	chr18	ENOSF1	NM_017512	up
2628	chr18	TGIF1	NM_003244	Down
2629	chr18	DLGAP1	NM_004746	Down
2630	chr18	EPB41L3	NM_012307	Down
2631	chr18	EPB41L3	BC008377	Down
2632	chr18	L3MBTL4	NM_173464	up
2633	chr18	KIAA0802	BC040542	Down
2634	chr18	FAM38B	NM_022068	up
2635	chr18	IMPA2	NM_014214	Down
2636	chr18	SLMO1	NM_001142405	up
2637	chr18	PTPN2	NM_002828	Down
2638	chr18	CEP192	NM_032142	up
2639	chr18	C18orf1	NM_181481	Down
2640	chr18	GREB1L	AK293321	up
2641	chr18	LAMA3	NM_198129	up
2642	chr18	DSC3	NM_001941	Down
2643	chr18	B4GALT6	NM_004775	Down
2644	chr18	C18orf34	NM_001105528	up
2645	chr18	MOCOS	NM_017947	Down
2646	chr18	MOCOS	NM_017947	Down
2647	chr18	KIAA1328	NM_020776	up
2648	chr18	SETBP1	NM_015559	up
2649	chr18	CXXC1	NM_001101654	Down
2650	chr18	ME2	NM_002396	Down
2651	chr18	TCF4	NM_001083962	Down
2652	chr18	ONECUT2	NM_004852	up
2653	chr18	FECH	NM_001012515	up
2654	chr18	---	---	Down
2655	chr18	---	---	Down
2656	chr18	MALT1	NM_006785	up
2657	chr18	CDH7	NM_033646	Down
2658	chr18	ZADH2	NM_175907	Down
2659	chr18	ATP9B	NM_198531	up
2660	chr18	NFATC1	NM_172390	Down
2661	chr19	BSG	NM_198591	Down

Fig. 2A-61

2662	chr19	BSG	NM_001728	Down
2663	chr19	PALM	NM_002579	Down
2664	chr19	MED16	NM_005481	Down
2665	chr19	C19orf6	NM_001033026	Down
2666	chr19	GPX4	NM_002085	up
2667	chr19	SBNO2	NM_014963	Down
2668	chr19	SBNO2	NM_014963	up
2669	chr19	C19orf26	NM_152769	Down
2670	chr19	C19orf26	NM_152769	Down
2671	chr19	CIRBP	NM_001280	up
2672	chr19	MUM1	NM_032853	Down
2673	chr19	APC2	NM_005883	Down
2674	chr19	APC2	NM_005883	Down
2675	chr19	APC2	NM_005883	Down
2676	chr19	PCSK4	NM_017573	Down
2677	chr19	TCF3	NM_003200	Down
2678	chr19	ATP8B3	NM_138813	up
2679	chr19	REXO1	NM_020695	up
2680	chr19	MKNK2	NM_017572	Down
2681	chr19	MOBKL2A	NM_130807	Down
2682	chr19	AP3D1	NM_001077523	up
2683	chr19	AP3D1	NM_001077523	Down
2684	chr19	AP3D1	NM_001077523	up
2685	chr19	DOT1L	NM_032482	Down
2686	chr19	PLEKHJ1	NM_018049	up
2687	chr19	C19orf35	NM_198532	Down
2688	chr19	SPPL2B	NM_152988	up
2689	chr19	GADD45B	NM_015675	Down
2690	chr19	ZNF77	NM_021217	up
2691	chr19	GNA15	NM_002068	Down
2692	chr19	NCLN	NM_020170	up
2693	chr19	NCLN	NM_020170	up
2694	chr19	CELF5	NR_033342	Down
2695	chr19	FZR1	NM_001136198	up
2696	chr19	MRPL54	NM_172251	Down
2697	chr19	DAPK3	NM_001348	Down
2698	chr19	EEF2	NM_001961	Down
2699	chr19	DPP9	NM_139159	Down
2700	chr19	C19orf30	NR_027148	Down
2701	chr19	TICAM1	NM_182919	up
2702	chr19	PLIN3	NM_005817	Down
2703	chr19	PTPRS	NM_002850	Down
2704	chr19	PTPRS	NM_002850	up
2705	chr19	ZNRF4	NM_181710	Down

Fig. 2A-62

2706	chr19	NRTN	NM_004558	Down
2707	chr19	FUT6	NM_000150	Down
2708	chr19	RFX2	NM_000635	up
2709	chr19	GTF2F1	NM_002096	up
2710	chr19	KHSRP	NM_003685	Down
2711	chr19	SLC25A23	NM_024103	Down
2712	chr19	DENND1C	NM_024898	Down
2713	chr19	CD70	NM_001252	Down
2714	chr19	INSR	NM_000208	up
2715	chr19	ARHGEF18	NM_015318	up
2716	chr19	EVI5L	NM_001159944	Down
2717	chr19	MAP2K7	NM_145185	Down
2718	chr19	SNAPC2	NM_003083	Down
2719	chr19	ELAVL1	NM_001419	Down
2720	chr19	CD320	NM_016579	Down
2721	chr19	KANK3	NM_198471	up
2722	chr19	HNRNPM	NM_005968	Down
2723	chr19	---	---	Down
2724	chr19	---	---	Down
2725	chr19	ADAMTS10	NM_030957	Down
2726	chr19	ZNF317	NM_020933	Down
2727	chr19	OR7D4	NM_001005191	Down
2728	chr19	COL5A3	NM_015719	up
2729	chr19	C19orf66	NM_018381	up
2730	chr19	DNMT1	NM_001130823	up
2731	chr19	ICAM4	NM_001544	up
2732	chr19	RAVER1	NM_133452	Down
2733	chr19	RAVER1	NM_133452	Down
2734	chr19	ATG4D	NM_032885	Down
2735	chr19	ATG4D	NM_032885	Down
2736	chr19	SLC44A2	NM_020428	Down
2737	chr19	QTRT1	NM_031209	Down
2738	chr19	LDLR	NM_000527	up
2739	chr19	LOC55908	NM_018687	Down
2740	chr19	RAB3D	NM_004283	Down
2741	chr19	EPOR	NM_000121	Down
2742	chr19	CCDC151	NM_145045	up
2743	chr19	ZNF44	BC136502	Down
2744	chr19	ZNF709	NM_152601	up
2745	chr19	MAN2B1	NM_000528	up
2746	chr19	C19orf56	NM_016145	up
2747	chr19	TNPO2	NM_001136196	Down
2748	chr19	ASNA1	NM_004317	up
2749	chr19	JUNB	NM_002229	up

Fig. 2A-63

2750	chr19	MAST1	NM_014975	up
2751	chr19	GCDH	NM_000159	Down
2752	chr19	CALR	NM_004343	Down
2753	chr19	NFIX	NM_002501	Down
2754	chr19	CACNA1A	NM_000068	Down
2755	chr19	CACNA1A	NM_000068	up
2756	chr19	---	---	Down
2757	chr19	DCAF15	NM_138353	up
2758	chr19	RFX1	NM_002918	Down
2759	chr19	DDX39	NM_005804	Down
2760	chr19	PKN1	NM_213560	up
2761	chr19	PKN1	NM_213560	up
2762	chr19	SYDE1	NM_033025	Down
2763	chr19	ILVBL	NM_006844	up
2764	chr19	NOTCH3	NM_000435	Down
2765	chr19	AKAP8L	NM_014371	up
2766	chr19	RASAL3	NM_022904	Down
2767	chr19	CYP4F22	NM_173483	Down
2768	chr19	CHERP	NM_006387	up
2769	chr19	CPAMD8	NM_015692	Down
2770	chr19	USHBP1	NM_031941	Down
2771	chr19	FAM129C	NM_173544	Down
2772	chr19	FCHO1	NM_001161357	up
2773	chr19	KCNN1	NM_002248	up
2774	chr19	PDE4C	NM_000923	Down
2775	chr19	LRRC25	NM_145256	Down
2776	chr19	---	---	Down
2777	chr19	C19orf60	NM_001100418	up
2778	chr19	COMP	NM_000095	up
2779	chr19	GDF1	NM_001492	up
2780	chr19	ARMC6	NM_033415	Down
2781	chr19	SF4	NM_172231	Down
2782	chr19	GATAD2A	NM_017660	up
2783	chr19	PBX4	NM_025245	Down
2784	chr19	ZNF254	NM_203282	up
2785	chr19	C19orf2	NM_003796	up
2786	chr19	SLC7A9	NM_014270	Down
2787	chr19	RHPN2	NM_033103	up
2788	chr19	GPI	NM_000175	up
2789	chr19	---	---	Down
2790	chr19	GRAMD1A	NM_020895	up
2791	chr19	FXYD5	NR_028406	Down
2792	chr19	FXYD5	NR_028406	up
2793	chr19	USF2	NM_003367	Down

Fig. 2A-64

2794	chr19	ATP4A	NM_000704	up
2795	chr19	HAUS5	NM_015302	up
2796	chr19	RBM42	NM_024321	Down
2797	chr19	ZBTB32	NM_014383	up
2798	chr19	MLL4	NM_014727	up
2799	chr19	U2AF1L4	NM_001040425	up
2800	chr19	U2AF1L4	NM_001040425	up
2801	chr19	LIN37	NM_019104	Down
2802	chr19	C19orf55	BC110893	up
2803	chr19	PRODH2	NM_021232	up
2804	chr19	APLP1	NM_001024807	Down
2805	chr19	COX7A1	NM_001864	up
2806	chr19	ZNF568	NM_198539	Down
2807	chr19	ZNF585A	NM_152655	Down
2808	chr19	DPF1	NM_004647	Down
2809	chr19	RASGRP4	NM_170604	up
2810	chr19	RASGRP4	NM_170604	Down
2811	chr19	RYR1	NM_000540	Down
2812	chr19	RYR1	NM_000540	Down
2813	chr19	RYR1	NM_000540	up
2814	chr19	MAP4K1	NM_001042600	up
2815	chr19	ACTN4	NM_004924	Down
2816	chr19	CAPN12	NM_144691	up
2817	chr19	CAPN12	NM_144691	up
2818	chr19	LGALS4	NM_006149	up
2819	chr19	ECH1	NM_001398	Down
2820	chr19	FBXO27	NM_178820	up
2821	chr19	FCGBP	NM_003890	Down
2822	chr19	ZNF546	NM_178544	Down
2823	chr19	MAP3K10	NM_002446	Down
2824	chr19	AKT2	NM_001626	up
2825	chr19	PLD3	NM_001031696	Down
2826	chr19	PRX	NM_020956	Down
2827	chr19	BLVRB	NM_000713	Down
2828	chr19	SPTBN4	NM_020971	Down
2829	chr19	LTBP4	NM_001042544	Down
2830	chr19	ADCK4	NM_024876	up
2831	chr19	C19orf54	NM_198476	up
2832	chr19	CYP2B7P1	NR_001278	up
2833	chr19	CYP2S1	NM_030622	up
2834	chr19	---	---	up
2835	chr19	AXL	NM_021913	up
2836	chr19	TMEM91	NM_001098821	up
2837	chr19	EXOSC5	NM_020158	Down

Fig. 2A-65

2838	chr19	ATP5SL	NR_030765	Down
2839	chr19	CEACAM5	NM_004363	up
2840	chr19	CEACAM3	D90278	Down
2841	chr19	ARHGEF1	NM_199002	Down
2842	chr19	GRIK5	NM_002088	up
2843	chr19	MEGF8	NM_001410	Down
2844	chr19	XRCC1	NM_006297	up
2845	chr19	CADM4	NM_145296	Down
2846	chr19	CADM4	NM_145296	Down
2847	chr19	ZNF45	NM_003425	up
2848	chr19	ZNF223	NM_013361	Down
2849	chr19	CEACAM19	NM_001127893	Down
2850	chr19	APOE	NM_000041	up
2851	chr19	NKPD1	ENST00000317951	Down
2852	chr19	MARK4	NM_031417	Down
2853	chr19	PPP1R13L	NM_001142502	up
2854	chr19	PPP1R13L	NM_001142502	Down
2855	chr19	OPA3	NM_001017989	up
2856	chr19	EML2	NM_012155	up
2857	chr19	QPCTL	NM_017659	Down
2858	chr19	SIX5	NM_175875	Down
2859	chr19	FOXA3	NM_004497	Down
2860	chr19	IRF2BP1	NM_015649	Down
2861	chr19	HIF3A	AK299699	Down
2862	chr19	CCDC8	NM_032040	Down
2863	chr19	PRKD2	NM_016457	up
2864	chr19	STRN4	NM_013403	Down
2865	chr19	BBC3	NM_001127240	Down
2866	chr19	CCDC9	NM_015603	Down
2867	chr19	CCDC9	NM_015603	Down
2868	chr19	PRR24	NM_178511	up
2869	chr19	DHX34	NM_014681	Down
2870	chr19	DHX34	D50924	up
2871	chr19	NAPA	NM_003827	up
2872	chr19	GLTSCR1	NM_015711	up
2873	chr19	LIG1	NM_000234	up
2874	chr19	CCDC114	NM_144577	up
2875	chr19	CYTH2	NM_017457	up
2876	chr19	CYTH2	NM_017457	up
2877	chr19	SULT2B1	NM_004605	up
2878	chr19	SPHK2	NM_020126	up
2879	chr19	FUT2	NM_000511	up
2880	chr19	PLEKHA4	NM_020904	Down
2881	chr19	PLEKHA4	NM_020904	up

Fig. 2A-66

2882	chr19	RUVBL2	NM_006666	Down
2883	chr19	DKKL1	NM_014419	Down
2884	chr19	ALDH16A1	NM_153329	up
2885	chr19	RCN3	NM_020650	up
2886	chr19	SCAF1	NM_021228	Down
2887	chr19	SCAF1	NM_021228	up
2888	chr19	CPT1C	NM_152359	up
2889	chr19	PTOV1	NM_017432	Down
2890	chr19	PNKP	NM_007254	Down
2891	chr19	AKT1S1	NM_032375	up
2892	chr19	TBC1D17	NM_024682	Down
2893	chr19	MYH14	NM_001077186	up
2894	chr19	POLD1	NM_002691	Down
2895	chr19	POLD1	NM_002691	Down
2896	chr19	SYT3	NM_032298	Down
2897	chr19	SHANK1	NM_016148	up
2898	chr19	SHANK1	NM_016148	Down
2899	chr19	SHANK1	NM_016148	up
2900	chr19	KLK1	NM_002257	Down
2901	chr19	KLK12	NM_019598	Down
2902	chr19	CD33	NM_001772	Down
2903	chr19	SIGLEC12	NM_053003	up
2904	chr19	ZNF701	NM_001172655	Down
2905	chr19	ZNF702P	NR_003578	Down
2906	chr19	PRKCG	NM_002739	Down
2907	chr19	TMC4	NM_001145303	up
2908	chr19	TSEN34	NM_024075	Down
2909	chr19	LILRA5	NM_021250	Down
2910	chr19	TTYH1	NM_020659	Down
2911	chr19	CDC42EP5	NM_145057	up
2912	chr19	LILRB4	NM_006847	up
2913	chr19	NCR1	NM_004829	up
2914	chr19	GP6	NM_001083899	Down
2915	chr19	RDH13	NM_001145971	up
2916	chr19	C19orf51	NM_178837	up
2917	chr19	PTPRH	NM_002842	up
2918	chr19	BRSK1	NM_032430	Down
2919	chr19	SUV420H2	NM_032701	up
2920	chr19	COX6B2	NM_144613	up
2921	chr19	SHISA7	NM_001145176	up
2922	chr19	U2AF2	NM_007279	up
2923	chr19	ZNF551	NM_138347	Down
2924	chr19	ZNF154	NM_001085384	Down
2925	chr19	ZSCAN18	NM_001145542	Down

Fig. 2A-67

2926	chr19	ZNF274	NM_016325	Down
2927	chr19	ZNF274	NM_016325	Down
2928	chr19	ZNF8	NM_021089	Down
2929	chr19	ZNF446	NM_017908	up
2930	chr19	ZNF446	NM_017908	Down
2931	chr20	C20orf96	NM_153269	up
2932	chr20	NRSN2	NM_024958	up
2933	chr20	SDCBP2	NM_080489	Down
2934	chr20	SDCBP2	NM_080489	up
2935	chr20	TGM6	NM_198994	Down
2936	chr20	SNRPB	NM_198216	Down
2937	chr20	IDH3B	NM_006899	up
2938	chr20	OXT	NM_000915	Down
2939	chr20	HSPA12B	NM_052970	Down
2940	chr20	ADRA1D	NM_000678	up
2941	chr20	RASSF2	NM_014737	Down
2942	chr20	RASSF2	NM_014737	Down
2943	chr20	C20orf7	NM_024120	up
2944	chr20	PCSK2	NM_002594	up
2945	chr20	MGC44328	BC033985	up
2946	chr20	C20orf12	NM_001099407	up
2947	chr20	SEC23B	NM_006363	Down
2948	chr20	SLC24A3	NM_020689	Down
2949	chr20	RIN2	NM_018993	up
2950	chr20	CRNKL1	NM_016652	up
2951	chr20	NKX2-2	NM_002509	Down
2952	chr20	CST8	NM_005492	Down
2953	chr20	PYGB	NM_002862	up
2954	chr20	ABHD12	NM_001042472	up
2955	chr20	GINS1	AK294593	Down
2956	chr20	NINL	NM_025176	up
2957	chr20	HM13	NM_030789	Down
2958	chr20	HM13	NM_178580	up
2959	chr20	DUSP15	NM_080611	up
2960	chr20	TSPYL3	NR_002781	up
2961	chr20	DNMT3B	NM_006892	up
2962	chr20	BPIL1	NM_025227	up
2963	chr20	BPIL3	NM_174897	Down
2964	chr20	BASE	NR_026760	Down
2965	chr20	NECAB3	NM_031231	Down
2966	chr20	AHCY	NM_000687	up
2967	chr20	CEP250	NM_007186	up
2968	chr20	CEP250	NM_007186	Down
2969	chr20	EPB41L1	NM_012156	up

Fig. 2A-68

2970	chr20	EPB41L1	NM_012156	Down
2971	chr20	DLGAP4	NM_014902	Down
2972	chr20	MYL9	NM_006097	Down
2973	chr20	SLA2	NM_032214	Down
2974	chr20	SLA2	NM_032214	Down
2975	chr20	C20orf117	NM_080627	Down
2976	chr20	VSTM2L	NM_080607	up
2977	chr20	TGM2	NM_004613	Down
2978	chr20	PLCG1	NM_002660	Down
2979	chr20	PLCG1	NM_002660	up
2980	chr20	ZHX3	NM_015035	Down
2981	chr20	PTPRT	NM_133170	up
2982	chr20	PTPRT	NM_133170	Down
2983	chr20	SGK2	NM_016276	up
2984	chr20	WISP2	NM_003881	up
2985	chr20	PI3	NM_002638	Down
2986	chr20	SEMG1	NM_003007	Down
2987	chr20	SNX21	AF258570	Down
2988	chr20	PCIF1	NM_022104	up
2989	chr20	ZNF335	NM_022095	Down
2990	chr20	CDH22	NM_021248	Down
2991	chr20	SLC35C2	NM_173179	Down
2992	chr20	EYA2	NM_005244	Down
2993	chr20	STAU1	NM_017454	Down
2994	chr20	B4GALT5	NM_004776	up
2995	chr20	TMEM189	NM_199129	Down
2996	chr20	DOK5	NM_018431	up
2997	chr20	PMEPA1	NM_020182	up
2998	chr20	PMEPA1	NM_199171	up
2999	chr20	ANKRD60	ENST00000457363	Down
3000	chr20	STX16	NM_001001433	up
3001	chr20	NPEPL1	NM_024663	up
3002	chr20	NPEPL1	NM_024663	Down
3003	chr20	TH1L	NM_198976	Down
3004	chr20	CDH26	NM_177980	up
3005	chr20	CDH4	NM_001794	Down
3006	chr20	SS18L1	NM_198935	up
3007	chr20	LAMA5	NM_005560	Down
3008	chr20	LAMA5	NM_005560	Down
3009	chr20	LAMA5	NM_005560	Down
3010	chr20	LAMA5	NM_005560	Down
3011	chr20	SLC17A9	NM_022082	up
3012	chr20	COL20A1	NM_020882	Down
3013	chr20	KCNQ2	NM_172107	Down

Fig. 2A-69

3014	chr20	KCNQ2	NM_172107	Down
3015	chr20	PRIC285	NM_001037335	Down
3016	chr20	GMEB2	NM_012384	up
3017	chr20	RTEL1	NM_016434	up
3018	chr20	RTEL1	NM_016434	Down
3019	chr20	RTEL1	NM_016434	Down
3020	chr20	RTEL1	NM_032957	up
3021	chr20	ZGPAT	NM_032527	Down
3022	chr20	SLC2A4RG	NM_020062	Down
3023	chr20	DNAJC5	NM_025219	Down
3024	chr20	UCKL1	BC033078	Down
3025	chr20	ZNF512B	NM_020713	up
3026	chr20	C20orf201	BC036837	Down
3027	chr20	MYT1	NM_004535	up
3028	chr21	CXADR	NM_001338	Down
3029	chr21	TMPRSS15	NM_002772	up
3030	chr21	ADAMTS5	NM_007038	Down
3031	chr21	C21orf7	NM_020152	up
3032	chr21	C21orf7	NM_020152	Down
3033	chr21	KRTAP19-3	NM_181609	up
3034	chr21	KRTAP6-1	NM_181602	Down
3035	chr21	OLIG2	NM_005806	up
3036	chr21	IL10RB	NM_000628	Down
3037	chr21	SETD4	NM_017438	Down
3038	chr21	CBR3	NM_001236	up
3039	chr21	MORC3	NM_015358	Down
3040	chr21	KCNJ6	NM_002240	up
3041	chr21	ERG	NM_004449	Down
3042	chr21	C21orf129	NR_027272	up
3043	chr21	PRDM15	NM_022115	Down
3044	chr21	ABCG1	NM_016818	Down
3045	chr21	ABCG1	NM_016818	up
3046	chr21	TFF3	NM_003226	Down
3047	chr21	TFF2	NM_005423	Down
3048	chr21	RRP1	NM_003683	Down
3049	chr21	PWP2	NM_005049	Down
3050	chr21	C21orf33	NM_004649	Down
3051	chr21	ICOSLG	NM_015259	up
3052	chr21	DNMT3L	NM_013369	up
3053	chr21	AIRE	NM_000383	up
3054	chr21	PFKL	NR_024108	Down
3055	chr21	PFKL	NR_024108	Down
3056	chr21	C21orf2	NM_004928	up
3057	chr21	TRPM2	NM_003307	Down

Fig. 2A-70

3058	chr21	POFUT2	NM_015227	Down
3059	chr21	SLC19A1	NM_194255	Down
3060	chr21	SLC19A1	NM_194255	up
3061	chr21	PCBP3	NM_020528	Down
3062	chr21	COL6A1	NM_001848	Down
3063	chr21	COL6A2	NM_001849	Down
3064	chr21	PCNT	NM_006031	Down
3065	chr21	DIP2A	NM_015151	up
3066	chr22	CECR1	CR456417	Down
3067	chr22	BCL2L13	NM_015367	up
3068	chr22	PRODH	NM_016335	Down
3069	chr22	5-Sep	NM_002688	up
3070	chr22	GNB1L	NM_053004	Down
3071	chr22	GNB1L	NM_053004	up
3072	chr22	ARVCF	NM_001670	up
3073	chr22	C22orf25	NM_152906	up
3074	chr22	DGCR8	NM_022720	Down
3075	chr22	ZDHHC8	NM_013373	Down
3076	chr22	THAP7	NM_030573	Down
3077	chr22	PPM1F	NM_014634	Down
3078	chr22	ZNF280B	NM_080764	up
3079	chr22	ZNF280B	NM_080764	Down
3080	chr22	IGLV2-23	ENST00000390306	Down
3081	chr22	GNAZ	NM_002073	up
3082	chr22	FBXW4P1	NR_033408	Down
3083	chr22	VPREB3	NM_013378	up
3084	chr22	SLC2A11	NM_030807	Down
3085	chr22	GSTT1	NM_000853	Down
3086	chr22	CABIN1	NM_012295	Down
3087	chr22	CABIN1	NM_012295	Down
3088	chr22	C22orf36	ENST00000446942	Down
3089	chr22	CRYBB3	NM_004076	Down
3090	chr22	LRP5L	NM_182492	Down
3091	chr22	MYO18B	NM_032608	up
3092	chr22	SEZ6L	NM_021115	up
3093	chr22	HPS4	NM_022081	Down
3094	chr22	HPS4	NM_022081	up
3095	chr22	TFIP11	NM_001008697	Down
3096	chr22	MN1	NM_002430	Down
3097	chr22	RASL10A	NM_006477	up
3098	chr22	ASCC2	NM_032204	Down
3099	chr22	GAL3ST1	NM_004861	Down
3100	chr22	FLJ20464	CR456348	Down
3101	chr22	SFI1	ENST00000433295	Down

Fig. 2A-71

3102	chr22	DEPDC5	NM_014662	Down
3103	chr22	C22orf24	AK294232	Down
3104	chr22	---	---	Down
3105	chr22	RBM9	NM_001031695	Down
3106	chr22	EIF3D	NM_003753	up
3107	chr22	---	---	up
3108	chr22	---	---	up
3109	chr22	---	---	Down
3110	chr22	CSF2RB	NM_000395	up
3111	chr22	CSF2RB	NM_000395	up
3112	chr22	C1QTNF6	NM_031910	Down
3113	chr22	CARD10	NM_014550	Down
3114	chr22	GGA1	NM_013365	Down
3115	chr22	TRIOBP	NM_138632	up
3116	chr22	TRIOBP	NM_138632	up
3117	chr22	GALR3	NM_003614	up
3118	chr22	PICK1	NM_012407	up
3119	chr22	CSNK1E	NM_152221	up
3120	chr22	SUN2	NM_015374	Down
3121	chr22	CACNA1I	NM_021096	up
3122	chr22	TNRC6B	NM_001162501	up
3123	chr22	TNRC6B	NM_001162501	Down
3124	chr22	ADSL	NM_000026	Down
3125	chr22	SGSM3	NM_015705	Down
3126	chr22	XPNPEP3	NM_022098	Down
3127	chr22	C22orf46	NM_001142964	up
3128	chr22	3-Sep	NM_145733	up
3129	chr22	WBP2NL	NM_152613	up
3130	chr22	NFAM1	NM_145912	up
3131	chr22	PACSIN2	NM_007229	Down
3132	chr22	SCUBE1	NM_173050	up
3133	chr22	SCUBE1	NM_173050	Down
3134	chr22	LDOC1L	NM_032287	Down
3135	chr22	SMC1B	NM_148674	up
3136	chr22	PPARA	NM_005036	Down
3137	chr22	PPARA	NM_001001928	Down
3138	chr22	CELSR1	NM_014246	up
3139	chr22	BRD1	NM_014577	up
3140	chr22	ALG12	NM_024105	Down
3141	chr22	MOV10L1	NM_018995	Down
3142	chr22	TRABD	NM_025204	Down
3143	chr22	SELO	NM_031454	up
3144	chr22	SELO	NM_031454	up
3145	chr22	SBF1	NM_002972	Down

Fig. 2A-72

3146	chr22	LMF2	NM_033200	Down
3147	chr22	KLHDC7B	NM_138433	Down
3148	chr22	CHKB-CPT1B	NR_027928	up
3149	chr22	ARSA	NM_000487	Down
3150	chr22	ARSA	NM_000487	Down

Fig. 2B-1

Comprehensive Description of Non-coding Small RNA T21 Biomarkers

Biomarker ID	Chromosome location	Gene Symbol	Sequence Type	Fold-Change
3151	chr1	ENSG00000201898	snoRNA	Up
3152	chr1	hsa-mir-181b-1 // hsa-mir-181b-2	miRNA	Up
3153	chr1	U44	CDBox	Up
3154	chr1	ACA16	HAcaBox	Up
3155	chr1	hsa-mir-186	miRNA	Down
3156	chr1	ACA26	scaRna	Down
3157	chr1	ENSG00000201791	snoRNA	Down
3158	chr2	hsa-mir-933	miRNA	Up
3159	chr2	ENSG00000212581	snoRNA	Up
3160	chr2	hsa-mir-216b	miRNA	Down
3161	chr2	hsa-mir-26b	miRNA	Down
3162	chr3	ACA4	HAcaBox	Up
3163	chr3	hsa-mir-569	miRNA	Down
3164	chr3	hsa-mir-944	miRNA	Down
3165	chr3	hsa-mir-548i-1 // hsa-mir-548i-2 // hsa-mir-	miRNA	Down
3166	chr3	hsa-mir-568	miRNA	Down
3167	chr3	hsa-mir-567	miRNA	Down
3168	chr4	ACA11	HAcaBox	Down
3169	chr4	ENSG00000202440	snoRNA	Down
3170	chr5	ENSG00000212363	snoRNA	Up
3171	chr5	ENSG00000201551	snoRNA	Up
3172	chr5	U95	CDBox	Up
3173	chr5	hsa-mir-581	miRNA	Down
3174	chr5	hsa-mir-548p	miRNA	Down
3175	chr5	U19-2	HAcaBox	Down
3176	chr6	ACA33	HAcaBox	Up
3177	chr6	hsa-mir-877	miRNA	Down
3178	chr7	hsa-mir-335	miRNA	Up
3179	chr7	hsa-mir-591	miRNA	Up
3180	chr7	hsa-mir-550-1 // hsa-mir-550-2	miRNA	Down
3181	chr7	hsa-mir-93	miRNA	Down
3182	chr7	ENSG00000207217	snoRNA	Down
3183	chr8	ENSG00000212342	snoRNA	Up
3184	chr8	HBII-276	CDBox	Up
3185	chr8	ENSG00000206853	snoRNA	Up
3186	chr8	hsa-mir-151	miRNA	Up
3187	chr8	hsa-mir-937	miRNA	Down
3188	chr8	hsa-mir-30d	miRNA	Down
3189	chr9	hsa-let-7d	miRNA	Up
3190	chr9	hsa-mir-31	miRNA	Down
3191	chr10	U108	HAcaBox	Up
3192	chr10	ACA19	HAcaBox	Up
3193	chr10	hsa-mir-607	miRNA	Down
3194	chr11	hsa-mir-548l	miRNA	Up
3195	chr11	ENSG00000201980	snoRNA	Up
3196	chr11	U99	HAcaBox	Up
3197	chr11	ENSG00000212277	snoRNA	Up
3198	chr11	ENSG00000206976	snoRNA	Up
3199	chr11	ACA54	HAcaBox	Up
3200	chr11	mgh28S-2409	CDBox	Up

Fig. 2B-2

3201	chr11	hsa-mir-129-2 // hsa-mir-129-1	miRNA	**Down**
3202	chr11	ENSG00000212551	snoRNA	**Down**
3203	chr11	U28	CDBox	**Down**
3204	chr12	hsa-mir-331	miRNA	**Up**
3205	chr12	hsa-mir-148b	miRNA	**Up**
3206	chr12	hsa-mir-148b	miRNA	**Down**
3207	chr13	ENSG00000199282	snoRNA	**Up**
3208	chr13	ACA27	HAcaBox	**Up**
3209	chr14	hsa-mir-654	miRNA	**Up**
3210	chr14	hsa-mir-541	miRNA	**Up**
3211	chr14	U93	scaRna	**Up**
3212	chr14	hsa-mir-543	miRNA	**Down**
3213	chr14	hsa-mir-432	miRNA	**Down**
3214	chr14	hsa-mir-376a-2 // hsa-mir-376a-1	miRNA	**Down**
3215	chr14	hsa-mir-493	miRNA	**Down**
3216	chr14	14q(II-4)	CDBox	**Down**
3217	chr15	ENSG00000199633	snoRNA	**Up**
3218	chr15	HBII-52-5	CDBox	**Up**
3219	chr15	HBII-85-3	CDBox	**Up**
3220	chr15	HBII-52-41	CDBox	**Up**
3221	chr15	HBII-85-4	CDBox	**Down**
3222	chr15	HBII-438A	CDBox	**Down**
3223	chr15	ENSG00000212604	snoRNA	**Down**
3224	chr15	ENSG00000212528	snoRNA	**Down**
3225	chr15	HBII-52-21	CDBox	**Down**
3226	chr17	hsa-mir-22	miRNA	**Up**
3227	chr17	U49B	CDBox	**Up**
3228	chr17	hsa-mir-1253	miRNA	**Down**
3229	chr18	ENSG00000199856	snoRNA	**Down**
3230	chr18	ENSG00000199856	snoRNA	**Down**
3231	chr19	hsa-mir-99b	miRNA	**Up**
3232	chr19	hsa-mir-520c	miRNA	**Down**
3233	chr19	hsa-mir-523	miRNA	**Down**
3234	chr19	hsa-mir-516a-1 // hsa-mir-516a-2	miRNA	**Down**
3235	chr19	U105	CDBox	**Down**
3236	chr20	hsa-mir-499	miRNA	**Up**
3237	chr20	U71b	HAcaBox	**Up**
3238	chr21	ENSG00000207147	snoRNA	**Up**
3239	chr22	hsa-mir-1286	miRNA	**Up**
3240	chr22	hsa-mir-185	miRNA	**Up**
3241	chr22	ENSG00000199783	snoRNA	**Up**
3242	chrX	hsa-mir-548m	miRNA	**Up**
3243	chrX	ENSG00000202231	snoRNA	**Up**
3244	chrX	ENSG00000200620	snoRNA	**Up**
3245	chrX	hsa-mir-98	miRNA	**Down**
3246	chrX	hsa-mir-450b	miRNA	**Down**
3247	chrX	hsa-mir-505	miRNA	**Down**
3248	chrX	hsa-mir-1277	miRNA	**Down**

Figure 3-1

8. chr1_LMNA_NM_170707_-1.58997
CCATGGGCAATTGGCAGATCAAGCGCCAGAATGGAGATGATCCCTTGCTG
ACTTACCGGTTCCCACCAAA

9. chr1_PLEKHN1_NM_032129_-1.66714
AGTGGGACCGGCTCTTGGTCCTGTACCCAACGTCCTTGGCCATTTTCTCC
GAGGAGCTGGACGGGCTTTGCTTCAA

10. chr1_B3GALT6_NM_080605_-1.56537
GGGCGGCGCTAGGCCTGGGCACGCTGGCGCTGTGCGGGGCGGCGCTGCTC
TACCTGGCGCGCTGCGCGGCCGAGCCCGGGGACCCCAGGGCGATGTCGGG
CCGCAGCCCGCCTCC

11. chr1_ACAP3_NM_030649_-1.55419
TGGATACACCTGCGGAACTGGAGCTCCGTGGGGCTGCCCGCCAGGGCGCC
CGGGGGACCAGGGGCAGCCTCGGCCTCGCGCATTTCCTCCGCCATGCGCG
CCAGAC

12. chr1_CPSF3L_NM_017871_1.7052
CAGTCCAGGAAGTCTGTTAGGCGGCCGTTCTGGGTGATGTAGGAGA

13. chr1_---_---_-2.08221
GATGGGCCACTCGGAGGGGGGCTCAC

14. chr1_FLJ14100_AK024162_-1.67072
CAGCGCCAGCGTGTAGCCTCCTCCCAGGATCCGGAGCAGGAGGGTGGCTG
TCTTTTGCGTTCAATCCGCTGGGCTGC

15. chr1_MORN1_NM_024848_2.10934
ATCTGTGAACTCGGCACAGCCCTGCT

16. chr1_LOC100129534_NR_024489_1.55634
CTCTGGGACTTTCGAGTCGGTTGGTGCACTTGCGGGGGCCCAGCAGGGGT
ACGTTCGTGACGGGCTATTTGGCAAAGACAGCCATTCTCCCCTTCTCCTC
CGGTAAGAGTCTTTGCCAGCACATTGCGCTTCTTGTCTCTGTGTGGCCTG
GTGTGGCCGGGCCGTGTAACCAAGCT

17. chr1_RER1_ENST00000434662_-1.51728
CTGTTTGCGGGGACGGTCGGTGCAGCTGCAAGGCTGGAGGCGGCCGGCAG
GTGCCCGGTGCTGGCTGCAGATGCGGCGCTAACCTTCTCTC

18. chr1_PANK4_NM_018216_1..75613
TATAGGTGATGGTGCGCATGGTCACGGGGTGGCCCCGGATAAAGAAGCCT
CCAAAGTACACGCGGTCCAGGCTGTGCAGCCGTGCGTGGAGGCAGGCCAG
CTGCCCAATGTCGTTGCTGATCATGTGCA

19. chr1_PANK4_NM_018216_1.62121
TTCGTTTTGGTGAGCAGAGCGCCAAGCCCCCAGAAGGTGCCGCCTCCAAT
GGAGCTGCCGCCGACCCACTCGAACCTGTCCTCCGTC

20. chr1_ARHGEF16_NM_014448_-1.65533
AGGACTACGCCCAGATGAACCACATCCAGGTGGAGAAGATAGAGCCGTCT
GAGCTCCCTCTGCCCGGGGGCGGCAACCGTAGCTCCTCCGTGCCCCACCC
CTTCCAGGTGACCCTGCTTCGCAACAG

Figure 3-2

21. chr1_WDR8_ENST00000378322_1.52292
CCCGTGTGATGCCAGACTGCACACAGCAAGGCTGCCACGTCCGTGGCCTC
GG

22. chr1_TP73_NM_005427_-1.85338
GCCGGTCCTCTCGCCCATGAACAAGGTGCACGGGGGCATGAACAAGCTGC
CCTCCGTCAACCAGCTGGTGGGCCAGCCTCCCCCGCACAGTTCGGCAGCT
ACACCCAACCTGGGG

23. chr1_DFFB_AB028912_-1.71896
GTGTCTTCTGCTGGACCGGCACCTTTTGTTTGTC

24. chr1_AJAP1_NM_018836_-1.75729
CCGTCTGCAGAGCGAGCGCTCAGACGGAGCCCCCGGGCAACTTGAGTGGC
GCCGATCGGCGGCGGAGCCTCTGGCAGAGCCCCCCGACCCGGCAGCGCGG
AGGGGACTCGCGTCCGTCCGCGTCGCGTCACCCCAAACCCTAAGCAGCGC
CGCCCCATCGGCGCGGAGCTCCGGCTGGAGGCAAGAGCCGCGCGCCGGGA
GACACGCACCGTGAGCGGCAGCGCCGCCGGCCTCCCTCCTCGCCGCCCCG
GAGGGCGAAGCCGCGGCTCCCCAGCCCTTTGCTGCGCCGCGACAG

25. chr1_NPHP4_NM_015102_-1.54678
TGGGTCTCACAGATGACGTTCGGGTCG

26. chr1_KCNAB2_NM_003636_1.55778
AATGAGGGAGTCAGCTCCGTGCTCCTGGGGGCCTCCAATGCGGACCAGCT
CATGGA

27. chr1_CHD5_NM_015557_-1.73201
CACACGCGGCAGAACTCCATGTGGTCGTCCTCCTCCTCCTCGCAGCCGCC
CTCCTCCTCTTCATCGTCGTCGTCCTTCGGCTCCCAC

28. chr1_RNF207_NM_207396_-1.96391
GGTGCGGCACAGCGCCGCCGAGGAGGAGGACGCTATCCACGCCCTCTTCG
GCAGCATGCAG

29. chr1_PLEKHG5_NM_020631_-1.91465
ACAGGCCTCGCAGAGGTTGAGGGGCCCCCGGCGGTGCAGCTGCTGGCAGT
CGGCGTGGTGACATAC

30. chr1_ZBTB48_NM_005341_-1.52777
CGGCTCCTTCGTCCAGCACAGTGTGAGGGTTCTGCAGGAGCTCAACAAGC
AGCGGGAGAAGGGCCAGTACTGCGACGCCACTCTGGACGTGGGGGGCCTG
GTGTTTAAGGCACACTGGAGTGTCCTTGCCTGCTGCAGTCACTTTTTCCA
GAGCCTCTACGGGGATGGCTCAGGGGGCAGTGTCGTCCTCCCTGCTGGCT
TCGCTGAGATCTTTGGCCTCTTGTTGGACTTTTTCTACACTGGTCACCTC
GCTCTCACCTCAGGGAACCGGGATCAGGTGCTCCTGGCAGCCAGGGAGTT
GCGAGTGCCAGAGGCCGTAGAGCTGTGCCAGAGCTTCAAGCCCAAAACTT
CAGTGGGACAGGCAGCAGGTGGCCAGAGTGGGCTGGGGCCCCCTGCCTCC
CAGAATGTGAACAGCCACGTCAAGGAGCCGGCAGGCTTGGAAGAAGAGGA
AGTTTCGAGGACTCTGGGTCTAGTCCCCAGGGATCAGGAGCCCAGAGGCA
GTCATAGTCCTCAGAGGCCCCAGCTCCATTCCCCAGCTCAGAGTGAGGGC
CCCTCCTCCCTCTGTGGGAAACTGAAGCAGGCCTTGAAGCCTTGTCCCCT
TGAGGACAAGAAACCCGAGGACTG

Figure 3-3

31. chr1_KLHL21_NM_014851_1.61569
ACATGAGTCCGTTTAGAGTCGCAGTCTTGGGGGCGAAGGACCAGGGCGGG
AGCTGGCCGCAGTCCACCAGCGACCACAGGTCGGTGTCCGGGTCGTAGCA
CTGCATCACCATGGTCTCCTTGCCAGCCAGGGAGCCGATGGCATAGAGCC
GGCCACGGCACGCAGTGGTGGAGCAGTTGTCCATGGGGTAGGTCATGGGC
TGCAGGGCCTCCCAGGAGTCAGTGGTGTGGTCATAGCGCTCGGTGCTGTC
GGCGGCCACCACGTACAGCAGTCCGTCCAGCACAGAGGAGCTGTGGTACT
CGCGGGCCTTCAGCATGGGCGCCACCTCCGCCCACTCATTCACGCTTGAG
TTGTACCTCCACACGCAGTCATAGAGCCGGGAGCCAT

32. chr1_PHF13_NM_153812_-1.62492
CACTGCTGGTACCATTGACAGCGACGGCTGGGACGCGGGTTTCTCAGACA
TCGCGTCCTCAGTGCCCTTGCCAGTCTCTGACCGCTGCTTTAGCCAC

33. chr1_PHF13_NM_153812_-1.5109
GGCCCGTGTTCATAACTCAGTTTCCTGTTTTGCACGATGTAAAAACCCTG
TCTTTTTGCACGATACAGCCAAAAGTATTGGCTGATTTCTTGCTGAGTGC
CCTCTTAGTTGGTGTGTGAGGTCTTGGTGGGCTCAGGCCAGCTGTTTGCG
AGTGTGGGAACTCATAGGTTCTGTCTTTGTCTCTTCCTTTCACCTCATTC
TGGTAGCAGCATAAAGGTTAGGCAATCACTGGGACCCGCATGGTGTTCCT
CCAAAGAATAGGGTAAAGGAGAGCTGGGAGGGAGCCCTCTCCGTTGGGTG
ACTCTTGTGTGCCCTTTAGACAGGCTGGCCTGCCGGTTCCACAGGGTACA
GTTAGGACTTGAGTCTTTCTTTTTCTGTTTTGAGTTGGTGAGTGAGTGAT
AGGGTAACATGGGCCTTCAGGATGACCCCTTGGAACTGTGCCGAGTTCCT
TAAATCTCAGCTGGGATCCTGGACCTGGGAGGCCCCTGTGAGGGCCAGCT
CTGGAAAAACCTGGGAGTTGATGCCGGAGGCTGTGGAAGAACTCTGCTCG
AGGGCAGGGTGCCCTGGAACACTGGTAGTTCTGGGGCTGGGAGGGAGAGG
GGCTCCGGCTTTCTCTGAAATGAACACTGCTCTTCAGCAGTTCAAGTACT
TGTTCTCAAAACATTTTCTAATTGATTGGTAGGTTTTCATAAGCATTGTT
TCTTTAAGGCATGGAAAGGGAAGAATGCTCAAGCAAGTCATGTTTGTTTT
CAGTGGGATGGGCCCGCGTTCTCACTGCTGGGGGCTTCCCCTTCATGTGG
CACCTTTGTGCCAGGCCACCAGGCAGACTCTTCCCACCTTCTCCCACTGA
AGCACCAAGGGGCTTGAACCGTAATTTGGCTAATCAGAGGCATTTTTTTT
GTCCTAGTATCTTTCACACTTGTCCAACCGTCTTATTTTTTTAAAAGTTC
TGTTGCTTGTATTAACACGAAACTAGAGAGAAATAGTTTCTGAAGCCAGT
TTATTGTGAAGATCCCCAAGGGGGAGGTTCGGTAGAGAAAAATAGTAAGC
TGGTTTAGAAACTGACGAGGGCAAACAGCCAGGACGCATTGGAGAGGAAT
TTGCCAAAGATCTACCCTGAGATAACGCCTGTCCAGTGTCTTCACCACGT
GAATAACCAGCGCTCCAAAGTGTTTTTCTGCTTTGAAAAAAAAAAATTCC
ACAAGCTTTTAAAGGTGCATTTAAGAATCCATGTGACTTTAGAATGGAAC
TGCCGGCCCTGGCAACTGTCACGTGTGCTAGAAGGTTCGATGCCTCTGGA
ATGCATGTGATACTCATCTCCATTTTGTTTCCTTGATTGCATTTTTGTTC
TTTTAGCAGATCTGTCCCTGTGGGTGGTGTCTAAGAAGTCGGACACCTTG
GTTTTTGTGTTAGATTGAGCTGGGCAGCTGCAATCAGCTTCTTTATATGC
AAATTAGGCACGACCCATCTGTGGTTCCTGGTTGGTGGCTAATGAAGTGA
GGGGAGGGAGGGATGTCACCCCAAAAGTAGGCCCTCCCATTGGCTTTGGC

34. chr1_PER3_NM_016831_1.59364
GAGTCCAACTCTGGACCCACCCCCTTCAG

35. chr1_PARK7_NM_007262_-1.55663
AGTACAGTGTAGCCGTGATGTGGTCATTT

36. chr1_RERE_NM_012102_-1.81991
CCCTCTCCCGGCTTCAGAAAGATGCTGTGGTGGCTGTGATGCCACCGGCA

Figure 3-4

GAGAGCATGCTGGGGGGTCACACAAAGCAGGAGTTGGAGATCTGCAACAG
GCCTGGGA

37. chr1_CLSTN1_NM_001009566_-1.56235
GCAGGTGGGCTTAATGCTGATCTTCACCAAAACATCTTCTGTGGCTCTTT
TCTTCCCACAGTCATAGGCAGTGACGGTCAGCTTATATTGATGTTCTTTC
CCGTA

38. chr1_LZIC_NM_032368_-1.50995
TCTGCTAACCTTGTCCGAAGCTGACCTGGTTGTTTCTTTGCAAACAATCT
GATGACCTCTGGGGTTTTAAAGGCCTGGCTGATAGCTGCCTGAATAG

39. chr1_UBE4B_NM_001105562_1.82295
ATGATCGAAGAGAAAAGCGGAGCCTCAGTGATAA

40. chr1_UBE4B_NM_001105562_-1.73628
CTTCTTTGCGGTTGTGGTTGCCGAAATCCTTAAGTCCTGGCTGTGGGCGG
GAGCTGCAGAGACTCTCTTACTTAGGGGCTTTC

41. chr1_C1orf187_NM_198545_-1.69394
CGGAACCTCCCTGAGAATCACATTGACCTCCCAGGCCCAGCGCTGTGGAC
GCCTCAGGCCAGCCACCACCGCCGGCGGGGCCCGGGCAAGAAGGAGTGGG
GCCCAGGCCTGCCCAGCCAGGCCCAGGATGGGGCTGTGGTCACCGCCACC
AGGCAGGCCTCCAGGCTGCCAGAGGCTGAGGGGCTGCTGCCTGAGCAGAG
TCCTGCAGGCCTGCTGCAGGACAAGGACCTGCTCCTGGGACTGGCATTGC
CCTACCCCGAGAAGGAGAACCGACCTCCAG

42. chr1_C1orf187_NM_198545_3.40239
GAAACACCGCGGTAAACTCTCCAG

43. chr1_C1orf187_NM_198545_1.67365
TGCCAAATTCCACCGGAACCGCAGGGTTACACGGAGGAAAGGGCGCTGTG
TGGAGCCCG

44. chr1_TNFRSF8_NM_001243_-1.68857
GCCTACCTGGAGAGCCTGCCGCTGCAGGATGCCAGCCCGGCCGGGGGCCC
CTCGTCCCCCAGGGACCTTCCTGAGCCCCGGGTGTCCACGGAGCACACCA
AT

45. chr1_VPS13D_NM_015378_-1.51903
GAGTAAACGATGGACCGTGCGGCTGGATATTTCTGC

46. chr1_PRDM2_NM_012231_-1.60425
CCCTGGCTGAGGTACCCGAACATGTGCTGCGAGGACTTCCGGAGGAAGTG
AGGCTTTTCCCTTCTGCTGTTGACAAGACCCGGATTG

47. chr1_PRDM2_NM_015866_1.6502
CGGCAGGCTTAGAGTCAGGCATCTGCTGCTTCGGTGGGGGCCCAACGCGC
ATGCTGGGCGCCCGGGTGATTGAGATCCAAAGAGAAGGGCACTGTAAGAC
AGGCCAGATGAACTGGCTCCTCGTCATGGGACTGGTACCTCAGATCTGAG
CATGGCCCTTGTTTTTGGCACGTAGCAGA

48. chr1_DNAJC16_NM_015291_1.74663
ACTTTTTAACATGCCCCTGTGAACAG

Figure 3-5

49. chr1_AGMAT_NM_024758_1.62486
GTCTGCACCGGCAGGCGCATCATGGAGCAGACGCCCACCGG

50. chr1_SPEN_NM_015001_-1.58454
GAATCTGGGGTGGTGGCAGTCTCCCCTGAGAAAAGT

51. chr1_SPEN_NM_015001_-1.67843
TCCCAGCACCCTCCCGAGGAGGAAGTGCATTATCACCTTCCTGTCGCTCG
AGCCACAGCCCCTGTGCAGTCAGAGGTACTAGTCATGCAGTCTGAGTACC
GACTGCACCCCTATACTGTGCCACGGGA

52. chr1_EPHA2_NM_004431_-1.58277
TAGCCGGCCGCCATGAAGTGCTCCGTATACTGCTGCATCTTGATGGACTC
CAGCCACTCGGACACCGTGCGGAAGGGCAC

53. chr1_ARHGEF19_NM_153213_-1.50471
CCCGCAGGCTCAGCGTGGCCAGGACGCCGCTGCCGCGTACGTCGGGGATA
TC

54. chr1_ATP13A2_NM_022089_1.5575
GGCCAGGGCCACGACACGGTAGCCAGCAGCTGTATAGCTCTGCAGCATCT
GGGCGAAGTCGGTGGGC

55. chr1_ATP13A2_NM_022089_1.70127
TGACCTGGTAGAAGGCTTGCTGGGTCTCGATCCAGATATAGCGCTGGCCC
TGGAAGAGGTAATACCGCAGCACCCG

56. chr1_SDHB_NM_003000_1.94039
CAGGCTCCGCCAAGGGTTGTGGCCGGCAACCGGCGCCTCAAGGAGAGGGC
GACCACCGC

57. chr1_PADI2_NM_007365_-1.62119
CTTGCTGTAGACCTTCTCATCACGGCAGTCCTCCTTGGGCAACCAGGGTG
TCTCTCGGTCACAGTTCACC

58. chr1_PADI1_NM_013358_1.72693
TGCGGAACTTCCTGAAGGCACAGC

59. chr1_PADI3_NM_016233_-1.80052
ATTTCTCGGCATCCCCTATCTTCACTGACACTGTGGTGTTCCGAGTGGCA
CCCTGGATCATGACGCCCAGCACTCTGCCACCCCTAGAGGTGTATGTGTG
CCG

60. chr1_PADI3_NM_016233_-2.07034
ACGTGTTTTGTGGATGCGGTGGCAGAGCTGGCCAGGAAGGCCGGCTGCAA
GCTGACCATCTGCCCACAGGCCGAGAACCGCAACGACCGCTGGATCCAG

61. chr1_MRTO4_NM_016183_1.74895
GGGTCGGAGCCCATCTGATGAATACA

62. chr1_AKR7A3_NM_012067_-1.61534
TGTACATCTCTGCCCAGGTATTCCCA

63. chr1_PQLC2_NM_001040125_-1.58841
GATTGGCGGAGACTCCTGCAACCTCATCGGCTCCTTCCTTGCTG

Figure 3-6

64. chr1_PLA2G2E_NM_014589_-1.70181
AGGAACACCAGCACGTGGGGAGATTTCAT

65. chr1_VWA5B1_NM_001039500_1.56451
GCCTTCTGTGAGGCCACGCACATCCCCATGGAGAAGCTCAAGTGGACGTC
CCCCTTCACCTGCCATCGAGTGTCCCTCACCACCCGCCCGTCTGAGTCCA
AGA

66. chr1_KIF17_NM_020816_1.57193
GCAGCTTAATGTGGAGTGGCCTTCCTTGGGCCACAGACCAGCCAGGGGTG
GGCAGTGCAGGAAGACCTGCTGTGGGACCCCTGTGCCACCCCATGGGGCA
GGGCAGTGCTTAGGAAGTGGGGCCAGTCAGACAGAGGCACAGTTCCTTCC
CAGCTGATATTGAGCTTC

67. chr1_EIF4G3_NM_003760_-1.9397
AACGGGTTTGAGGTTGTGAATTCAT

68. chr1_HSPG2_NM_005529_1.77804
GCAGTGGGAGATGCCGTGCGCCGTGAGGTTGAGGTCATGGAAGACGATCT
CCTCGCCCTGGATGCGCAGCTCCCGGACACA

69. chr1_HSPG2_NM_005529_-1.63266
CTTGCACACTGGGGTTACCCACGTAAC

70. chr1_HSPG2_NM_005529_-1.64188
CAGACCGATGTAGCCTGGCGGGCAGCGGCACTCCTCCACCTCGAGGGCGC
GGGGTCTGTTTGAGGGCCCCGGCTGGGCGACCTCCAGGCTGACTGCGCTG
ATGCTGGCCGCCAGCGGCACGGAGGAGAACGTGGCCCGGATCAGGAGCTC
ATCCAGGTCGGCCAGTGCCATCAGGAGGTGCTCGCGTGTGGCC

71. chr1_HSPG2_NM_005529_1.90474
GGCTGCTGGGCGTAGGATGCTCGGATCAGGAGGGTGTCGATGCCTGCCAG
TGCCATCAGCAGGTGCTCCCGTGTGGCTGGCTGCCCATCGGGCCGCTGCC
A

72. chr1_HSPG2_NM_005529_1.8463
ATGCTGCCACGCTCGTCACAGCGCACAATCTC

73. chr1_HSPG2_NM_005529_-1.61123
CGCTCCGGTCAGGACAGTCGCTCTCCTCGTCACAGTGGAAGCTGGCTGGG
ATGCACATGTTGGTAGAGACGCATCGGAACTGTGTGGGCCC

74. chr1_HSPG2_NM_005529_1.70291
GATGAACACCACACTGACAACCTGGTCTCCGGGAAT

75. chr1_CELA3B_NM_007352_-1.80825
CCCGCAGGAAGCCCACGGTGTTCACTC

76. chr1_WNT4_NM_030761_1.67577
GACCCCATGCACTGTCCTGTCACAGCCGCACTTCTCCAGCTCCCCACTGC
TGCACGCCCGCGTCACTGCAAAGGCCACACCTGCCGAAGAGATGGCGTAC
ACGAAGGCCGCCT

77. chr1_C1QC_NM_001114101_-1.65389

Figure 3-7

TGATCAGATTCAACGCGGTCCTCACCAACCCGCAGGGAGATTATGACACG
AGCACTGGCAAGTTCACCTGCAAAGTCCCCGGCCTCTACTACTTTGTCTA
CCACGCGTCGCATACAGCCAACCTGTGCGTGCTGCTGTACCGCAGCGGCG
TCAAAGTGGTCACCTTCTGTGGCCACACGTCCAAAACCAATCAGG

78. chr1_EPHB2_NM_017449_-1.80749
GCCACCGCCCATGGACTGCCCGAGCGCCCTGCACCAACTCATGCTGGACT
GTTGGCAGAAGGACCGCAACCACCGGCCCAAGTTCGGCCAAATTGTCAAC
ACGCTAGACAAGATGATCCGC

79. chr1_ASAP3_NM_017707_1.54419
CTTCTCGATGAAGGGGAACAGGCTCTGGGC

80. chr1_ASAP3_NM_017707_-1.81456
GTCACCCTGGCCCGATCGCGCTCCTTCTCC

81. chr1_MYOM3_NM_152372_1.63321
ATGACAACCAACTCTGAGGCCTTGGAGGGGACGCTGCTGCCTACCCTGCT
GATGGCTCTCACCCGGAACCGATAGCTCTGACCTTCGACGAGGCCTTGGA
TTGGGCACCGACAA

82. chr1_MYOM3_NM_152372_-1.79598
GACAGCTCGGAGGAGGCCGTCAGAGCCAGGGCTGCTGCCAGGGCGTAGTC
CGCGGCGCTGAACTCATGCT

83. chr1_GRHL3_NM_021180_-1.5746
TCTGCTGTATGTGCGGAGGGAGACTGAGGAGGTGTTTGACGCGCTCATGT
TGAAGACCC

84. chr1_NIPAL3_NM_020448_-1.7961
TCACAGATGTACGACTCCTCTTTGATTGCCAGTGTGGGCTACATTCTGTC
CACAACCATTGCTA

85. chr1_RUNX3_NM_001031680_1.78589
TGCTGAAGTGGCTTGTGGTGCTGAGTGAGCCTCGGGGGCTGGGTGTGCTC
GGTGTCACCCGCATGCGCAGCCGTTCCAGGTCCCCAAAGCGGTCAGGGAA
CGGCTTGGTCTGGTCCTCCAG

86. chr1_MAN1C1_NM_020379_-1.64768
CCATCCCGGGCGGCGCTCCGGACGCCCTCCCCTCACCGCGC

87. chr1_C1orf135_NM_024037_1.58907
TTAAAGTGCTGTACAGTTACCACAAAAATAAAATAGGAAACTAGCACCAT
TCTACCTCTCTTCTCTCCACACCTGGGTTGTGGGGAGATTTGCTAATCAC
TGAAAAAAAAGGGTCAAGAGTAATCATCCCAAGCTTAGGCTGATGTGGGT
TAAGATCAGCCAGAG

88. chr1_C1orf135_NM_024037_-1.53622
TCCAGGAAGGAGTGTTAGCATTTTGGTGCCTGGTTTGATTAAATGTGT

89. chr1_STMN1_NM_001145454_1.56006
AAGAGATCAGAGAATCTATGCGGAGAAGGTCTTCTTCTTCCAGTGTGGTT
GTAGTTGGCA

90. chr1_UBXN11_NM_145345_-1.86119

Figure 3-8

CCAGGACTGAATTTCAGGCTGGAC

91. chr1_PIGV_NM_017837_1.58258
AGGGAGCTCAATCCTGGTAGCAACACCCCTG

92. chr1_TMEM222_NM_032125_2.13592
TGGTTTTTCCCCATCATCGGCCAC

93. chr1_C1orf38_NM_004848_-1.52653
GTCAGCAGGTCATCCTGCACCTGCCCCTATCCCAGAAGGGGCCCTTCTGG
ACATGGGAGCCTAGTGCCCCTCGAACTCTGCTCCAGGTCCTACAGGATCC
AGCCCTGAAAGACCTCGTCCTCACCTGCCCCACCCTGCCCTGGCATTCCC
TGATCCTGCGGCCCCAGTATGAGATCCAAGCCATCATG

94. chr1_TMEM200B_NM_001171868_1.74809
GCGAGAGACGCGGCCCTCGGGGCTCC

95. chr1_MECR_NM_016011_-1.51333
CCTTGGCTGGATCCCCGTGGTGCCCATAGACAAGCGCCCGGACCCGGGCA
GGCTCGGCGGATGCGGAGTAGGAGGAGGCGGCAGGTCCGTGACAGCCAGA
AGC

96. chr1_PTPRU_NM_133178_-1.65407
CAACGCGGGCCAGAACGCGTCGTTCCAGTGCATGGCCGCGGGCAGAGCGG
CCGAGGCCGAACGCTTCCTCTTG

97. chr1_MATN1_NM_002379_-1.90946
TCTGGACTGGGGGGCGAGGCCAGGG

98. chr1_SDC3_NM_014654_-1.56844
GAGGCAGAAGCCTCCGTACGCCAGTGGTCCTTATAACAGCAGTGGTGGCC
GTAAAAGGGGGTGCTGCAGGGGTGCTGGGGGTGGCGGTGGCCACTGTGGC
AGGCACTGTGGCCACAGTCGGGTCCCCTGTGCTTGTGGCA

99. chr1_SDC3_NM_014654_-1.82338
TGTGCCCACAGGCTGGATGTTCGTGGTGGGCAGC

100. chr1_SDC3_NM_014654_-1.50388
CCCGAGTAGAGGTCATCCAGTTCATCATCGGGAAAGGAGTCATCATCCCC
AGAGCCCTCCAGGTCCACGGGTCTCTCGAAGTTCTCACTGCGCCAGCGCT

101. chr1_FABP3_NM_004102_1.61897
CCACCCCCAACTTAAAGCTGATCTCTGTGTTCTTGAAGGTGCTGTGTGTT
TTTAGGGTGAGAATGTCCCCATTCTTTTCGATGATTGTGGTAGGCTTGGT
CATGCTGGCCACCTGCCTGGTAGCAAAACCCAC

102. chr1_COL16A1_NM_001856_-1.60615
GGCAAGCCAGGGCTCCCCGAAGGCCCCGGAGCTCCAGGGTGGCCTCTCTC
TCCTGCAGGGCCCGGTGGCCCAACAGGCCCCATGGAACCACTCTTGCCAG
GTCC

103. chr1_COL16A1_NM_001856_1.59555
TGGGCGCAGTTGTCGAGGCCTGGCA

104. chr1_CCDC28B_NM_024296_-1.51723

Figure 3-9

CAGGCACACTACGGAGGGTCCCTGTGCCTACCAGCCACAGCGGCTCCTTG
GCCCTAGGACTTCCTCATCTGCCATCCCCCAAGCAGCGGGCCAAGTTCAA
GA

105. chr1_EIF3I_NM_003757_-1.58706
GGCGAAGATGGTTACGTCCGTATCCATTACTTCGACCCACAGTACTTCGA
ATTTG

106. chr1_MARCKSL1_NM_023009_-1.55206
TGGGGGGCGCTTGGAGCCGCCCCGGGCTCGCGCCGCAGGGGATAGTACGG
CGGGGTCG

107. chr1_KIAA1522_NM_020888_-1.65378
GGTCACGCCCTCGCTCCTGCAGATGGTGCGGCTGCGCTCCGTGGGTGCTC
CAGGAGGGGCTCCCACCCCAGCACTGGGGCCATCGGCCCCCCAGAAACCA
CTGCGAAGGGCCCTGTCAGGGCGGGCCAGC

108. chr1_YARS_NM_003680_-1.57318
GGCACAACCCTCCTAGAGGCGGGACGGTTTCCTGCCAATCACTGCTGGTT
TGCCCTCCCCCTGGTGTTGGCCCGGCTGACTCGGGGTAGGGGAGGTCGGG
GAGGGGGCGATAAAATGGCGCAGGGGGCGGAGTGAGGCGCAGTCGTTCGC
CCAGGCTTTGGCCCGGCTTCCGGAGGTGAAGAGCGGGAGGGACGAGGGGG
TCGGCGTTACCCGGCTTGGAGGGGGATGGGGGCGCCTGTTGCTTCTCCAG
GGGGTTGCGCACGCCGTCCGCCCCTTGGAGGGATTGGGAGGCCCACGCCC
TGCTGCGAGAAGGGCGCGTTCTAGCTCCTGAGGTGAT

109. chr1_S100PBP_NM_022753_-1.61614
TATCTCAGGAGTGTCATTGCTCAT

110. chr1_FNDC5_NM_001171941_1.50874
TCAGCTGGGACCTCGACCCGTTTGGG

111. chr1_CSMD2_NM_052896_1.52107
GTAAAAGTGATGTTGAAGCCCCTCTTCCCTGTGGAGTGGTCAGTCTGGAA
CTCGAGACGGGCCACGTGGCCACTGCTTGTGATGGAGGAGGGAAGCTGGT
TTCCTGAGAAGGTGCCCAGGACGGGCGCCTCGGCGGTGGCCCCATCCTTG
ATGACCAGGAAATCAAACTGAGGCTCCACGTCAATGTCGTTGAAGGCCAG
GTGGAT

112. chr1_C1orf94_NM_001134734_1.51371
AGTTCCTAAGCCTCACCAAAGAGCACTCGATCCTGGTCGAAGAGAGTTCT
GGGGAGCTGGAGGTACCCGGCAGCTCTCCCGAGGGGACCAGAGAGCTGGC
TCCCTGCATTCTTGCCCCTCCTCTAGTGGCAGGCAGTAATGAGCGCCCCA
GAGCCTCCATCATTGTCGGAGACAAGCTTCTGAAGC

113. chr1_LOC653160_BC021230_1.64843
AAGGCGGCCGCGAAGGCCACCGTGGCGGAGGCCAGCCCCGAGCTTGCCCA
GCGGTGCTCCAGGCAGGGAGGGGCCAGGCCCGCCAGCCAGGCGAAGGCGC
AGGCA

114. chr1_ZMYM6_NM_007167_-1.72728
TGGAGGAGGGCGGGCTTACAACCACTTGGCCCTGAGACAGGGGCACCGCC
GAAGAGTTTGTT

115. chr1_ZMYM4_NM_005095_1.52349

Figure 3-10

CTTCTGTAGTTGTATGAAAAAACAAATATTGTTAGCATAGTAGATAAATT
GTTATGAAATACCAGAAAAAAAAATCTGTATCTTTTACTGAGAACACCCA
ATACCCAGATAAATGACTGTATCAGGATTTCATTTGCATGTTAGTCCACA
GAGTTGCCCAGAACCCTAAATTTATTCATAAGAGAAAATATTGATTAATT
ATTGGTCATTCCTCATAAGTGTAGCTGTTGATGTGTGCGTCTGATTA

116. chr1_PSMB2_NM_002794_1.52264
GACTCCGAAGACAGTCAGCCAGGTTTCGGCGTGTGAAGTTAGCTGCTGCC
GTGGGAGACAATTCATATC

117. chr1_EIF2C3_NM_024852_1.63195
CATCTCAAGAACACATATTCTGGCCTACAGCTTATTATCGTCATCCTGCC
GGGGAAGACACCAGTGTAT

118. chr1_TEKT2_NM_014466_-1.62891
AGTGCCTGACCCTGCGGGAAAGCCGGCGAGACATTGATGTGGTGAAGGAC
CCTGTGGAGGATGAGCTGCATAAAGAGGTGGAGGTCATCGAGGCCACCAA
GAA

119. chr1_TEKT2_NM_014466_-1.62367
AGGATCTGCGCACAAAGCTCCTGAGCCTGAAGCTGTCCCATACCCGGCTA
GAGGCCAGAACCTACCGGCCCAACGTGGAACTCTGCCGGGACCA

120. chr1_COL8A2_NM_005202_1.93319
GGCAGTCCTGGCATCCCATAGCCAGTGGGGCCTATCAGCCCAGGGGGGCC
CCGGGTCCCTGGCTCCCCTTTGGCCCCTGATGGGCCCTGTGGTCCTGGCA
ACCCTGCTGCCCCTGGGACTCCCACACCGTCTACTCCAGGAGGTCCTTTT
GGGCCCACAGC

121. chr1_MAP7D1_NM_018067_-1.50888
GAAGGAGAAGAGTGCCCTAGCCCGGGAGCGCAGCCTCAAGAAGCGCCAGT
CGCTGCCCGCCTC

122. chr1_OSCP1_NM_145047_1.5327
GAACAGGCCCGGACACCGGCAACACAAAGCGACCGTTATTATTCTGAACT
TTG

123. chr1_OSCP1_NM_145047_1.7632
ATGAGGAGTGTCTGCCGGATCAGCTGGAACT

124. chr1_OSCP1_NM_145047_1.82644
CTCCCGGGATGTTCTGGGCCCGCAGCCGTTGGTCGAGGATGTAAAGCATC
TCCCCGCCCAAGTTCAAGAAGAGCAGCGGTAGCGTCCGCACCGACAT

125. chr1_RSPO1_NM_001038633_-1.58763
GCACTTGTTCATGTCGGGGTTGCGGGCGTCGAAGTATCCAGGTGGGCAGG
ACGGCAAGCAGACGCCCACCTGGCGGATGTCGTTCCTCTCCAGCAGGATG
AACAGCTTGGGTGAGCAC

126. chr1_C1orf109_BC018109_-1.56909
TTGTACAAGATCTTGGTGTTCGTCTTTTGAAATTCGGTCCCAGGCCTTGG
GCAAAGCTTGTATGTTTGCCAAG

127. chr1_CDCA8_ENST00000373055_-1.57627
ACGTGCCTGGCGACTTCTTCGGGTGGTCCCCGTCCGCCCTCCTCGTCCCT

Figure 3-11

ACCCAGTTTCTTGCTTC

128. chr1_POU3F1_NM_002699_2.02443
GGGTGGCGATGCGCCGCCCCCGCCA

129. chr1_MACF1_NM_012090_-1.50158
GTGCTAGAAGATAATTCTCAGCGGACCAAATGGAAAGTGATCAGCCCCAC
AGGGAACGAGGCAATGGTGCCGTCAGTCTGCTTCCTCATCCCCCCACCCA
ATAAGGATGCCATTGAGA

130. chr1_PABPC4_NM_001135653
GACTCTCTGAGTGGTAGTAGGGAGGCCACGAGAGGCCGGAGCATTAC

131. chr1_COL9A2_NM_001852_-1.81633
AGCCCTGGGGGACCTTTCATTCCGGGTGGACAGTTG

132. chr1_EDN2_NM_001956_1.51279
TGGAATGTGTGGACCGAGGCTCCCGCATGGCCTCCTGTTGTCGCTTGGCA
AAGAGGCTC

133. chr1_HIVEP3_NM_024503_-1.60027
CGGAGAGGTTCCTCGTCCGGGCTGGGAAGCGGGCAGAGGCCTCTGCCAGG
CAGCCCACAGAGCTGCTGCGGTCCAGCGGCGGGGTGGCAGAAGGCTCGGG
GTTGGTCGGTGCACGCGGGGACTCCAAGCGGGGGCTCCAGGACTGCGCTG
CCCGGCGTCCCTG

134. chr1_FOXJ3_NM_014947_-1.63938
GGCCGCTCCGTGCGTCTCCGCCCCCCCGGGAAAGGTCCCAACGGTGCCTA
CTGCGAGCGGTCGAGGCCCCGA

135. chr1_RIMKLA_NM_173642_-1.51239
TGGACCAGATCGCCGTCACCATCGTCGGCGGCCACCTC

136. chr1_LEPRE1_NM_022356_1.75998
CATCCTTGGGCTTCGATTCACTGC

137. chr1_ERMAP_NM_001017922_2.82256
GGAGAAGAGCCCGGTTGCATTTTG

138. chr1_EBNA1BP2_NM_001159936_1.75842
TCTCTGTCTGTGACAAGGGATTCATCGGATTCCGACTCCGAATCCGAGAG
CGGG

139. chr1_PTPRF_NM_002840_1.56328
CCCTTGGTGCTGAGTATCCAGCAAGAGTGACCGGGGTGAAGAAGCAAAGA
C

140. chr1_KDM4A_NM_014663_1.71205
GACATCTGAACAGCTGACCCCTGAGGAAGAGGCTGAGGAGACAGAGGCCT
GGGCCAAGCCTCTGAGCCAACTGTGGCAGAACCGACCTCCAAACTTTGAG
GCTGAGAAGGAATTCAATGAGACCATGGCCCAACAGGCCCCTCACTGCGC
TGTCTGTATGATCTTCCAGACTTATCATCA

141. chr1_ST3GAL3_NM_174963_-1.79626
AGTCACTGAGCGAGGACACAGCCTT

Figure 3-12

142. chr1_ST3GAL3_NM_174963_-1.58904
TTCTGGAAATCTGTGGCCACTCGAGTGCCCAAGGAGCC

143. chr1_DPH2_NM_001384_2.00366
TGCTGCGTGGATGTGCTGGGTGCTGAGCAAGCTGGAGCTCAGGCTCTCAT
ACATTTTGGCCCTGCCTGCTT

144. chr1_DPH2_NM_001384_1.51169
GAGGGTCTGTCCTTGTCAAAAGGCAGGTGCTAGACAGTCTAGACCAGGGT
TTCTCAAACTCGTACTTGACATTTGGGGCCAGATAATTCTTTGTTGTGGG
GCTGTCTGGTGTATGGTAGGGTGCTCAGCAGCATCCCTGGCCTCTGCCCA
CTAGACATCAGAAGCACTCCCCCAGTTGTGACAACCAAAAATATCTCCAG
ACCTTGGCAAATGTTATCTGTGGGGGAAAATTGCCCTCAATTGAGAACCA
CTGGTCTAGCTAGACCTGCACTGTCCAGTACAGTAGCCACTAAATACATG
TGGCTAAACTTAAATTTAAGTTAATTAAGATTAAAAGCTCAGTTTCTCAG
TCACATTAGTCATTCAAGTGTTCAGACAGCCACATGAGGGGACAGTGCAG
CTACAGGATATGCCATCATGGCAGAAAGTTCTATTGGTTGGACAGCGTTG
GTCTATACTGACTCTTATTTCTCAGGGAGATCACAGCAACCTAAATA

145. chr1_CCDC24_NM_152499_1.6653
CATCATCAAGGACCAACTGAACGTGTCCAACATTGACCAGGTGGCCAGAC
ACCTGA

146. chr1_SLC6A9_NM_006934_2.04373
GAGCCATTACTGCCCACAATGGGGATCTGCGCCTTGTCCGGGTGCAGTGG
CTGGACCTCGAAGCCGTCCTCAGGAGAGGGGGCTATGGTGGGGGCGTAGC
GCCCTGTCCGGTGCTCCAGG

147. chr1_RNF220_NM_018150_1.61889
TGGCTTCATCATGTGCAGCGGCAAAGAGAACCCGGACAGTGATGCTGACT
TGGAT

148. chr1_KIF2C_NM_006845_1.59041
CTGGGACAGAACAAGGCTCACACCCCGTTCCGTGAGAGCAAGCTGACACA
GGTGCTGAGGGACTCCTTCATTGGGGAGAACTCTAGGACTTGCATG

149. chr1_PTCH2_NM_003738_-1.52483
GACTGGAGCAGCAACGGGGCAAACTGATAGCGGGCGAAATGGGCAAGATT
CCAGCGGGCACAGGGCAGGGACTTGCAGGCTGCCTTCTGCCTTGTCTCCT
CCTCCTGGCCTAGAAGGTCCCGTGTGGA

150. chr1_HECTD3_NM_024602_-1.54226
ATCAGCTGTCCGATCCATTCATACTTGGCAAAGTCTCGGCAGGAGGGGTT
GGGTACATACATGTCCCGAGCCTCA

151. chr1_NASP_NM_172164_1.66088
CTCTATTCCGTTCGCTGGTTCGCCACCTCAGGGGAACG

152. chr1_GPBP1L1_NM_021639_1.52786
ATCAGAGGAATTATGTCGACGGCGGCTTACTCCAAATCTACCTTCTCCTC
TGGGTAGGTGCTCTCCGTGTTTTTCGAAGGTGGCAGTAG

153. chr1_POMGNT1_NM_017739_1.88933
GCTCGGGCCCCGCTAGGGCCCTCAC

Figure 3-13

154. chr1_FOXE3_NM_012186_-1.50319
AGCGCTTCAAGCGCGCCGAGCTGCCCGCGCACGCGGCCGCGGCGCCAGGG
CCGCCGCTCCCCTTCCCCTACGCGCCCTACGCGCCCGCGCCCGGCCCCGC
GCTGCTGGTGCCGCCGCCTTCTGCCGGACCGGGCCCCTCGCCGCCCGCGC
GTCTGTTCAGCGTCGACAG

155. chr1_FOXD2_NM_004474_-1.85894
CGGCTACGGCTACGGGCTGGCTCTCCCGGCCTACGGCGCACCCCCGCCGG
GGCCGGCCCCGCATCCGCACCCGCACCCGCACGCCTTCGCTTTCGCCGCG
GCAGCCGCCGCCGCTCCTTGCCAGCTGTCGGTACCCCCAGGCCGCGCCGC
CGCGCCTCCACCCGGACCTCCGACGGCCTCGGTGTTCGCAGG

156. chr1_RAB3B_NM_002867_1.54496
AGCTGGCCCTTCTCAGTGGGAACAACCCTCTCTTCCTC

157. chr1_ZCCHC11_NM_001009881_-1.55899
TGCGAGGCCCGCGAGCTACAGGCGCGCG

158. chr1_GPX7_NM_015696_2.09954
CTTTGCCCTCGCGACGCCGCCACCTCC

159. chr1_ZYG11A_NM_001004339_1.87509
GGTTCATTTCTTGCACCCGGGCCACACGCCCCGGAACATCGTCCCTCCTG
ACGCT

160. chr1_SLC1A7_NM_006671_1.73482
TTCCACGCATGAGAGCCCGGCCGGGGGCACAGGGTCTGGGCTGAGGGCTC
TAGCCCCTCAGCAGGCAGGTGGTCGGAGTTGCTAAACACCAGTCGCCAGC

161. chr1_FLJ40434_NR_002314_2.02739
GCTCGCAGGGTGCTGGCGTAGCCCGGTCGCGTCTGCACGCGGA

162. chr1_ACOT11_NM_015547_-1.68716
CTTGGCCACCTTCGTGGCCCGCCGAGAGATCACCAAG

163. chr1_C1orf175_NR_026782_1.53806
CCCAGAAATCATGCAAGGCATCTACATGCAGCTGAGCCACATCCAGGAGC
CTCGGGCCCGCCAGGTGGCCCTGCTGCCCGTCTCCCTCCTGGCTAGCTCC
TTCATGACCGAGGTTGTGGTGG

164. chr1_TTC4_NM_004623_1.54521
TCAGAATGAGGCTTTACTCCAGGCCATCA

165. chr1_PPAP2B_NM_003713_1.62573
CCGAGGCTGCTGCGGATAGTGGCGGGTCGGCCCCGGCTC

166. chr1_ALG6_NM_013339_1.6427
CAGTGGTTTTGTACTGTTGTTGCT

167. chr1_EFCAB7_NM_032437_-1.67128
TAGAGCTGCCTACTTAACTGTCTT

168. chr1_ROR1_NM_005012_-1.78883
TGCGCTGTTCTCGGAGTCCGACCCAGGGCGACTCACGCCCACTGGTGCGA

Figure 3-14

CCCGGACAGCCTGGGACTGACCCGCCGGCCCAGGCGAGGCTGCAGCCAGA
GGGCTGGGAAGGGATCGCGCTCGCGGCATCCAG

169. chr1_ROR1_NM_005012_2.02729
CCGGGAAGAGCCCGTGGATGTTCTG

170. chr1_CACHD1_NM_020925_1.69169
GTCCACCAGGAGCCGGTGACATACACAGCTATTGACCCTGGCCTGC

171. chr1_DNAJC6_NM_014787_-1.59491
TCTTGTGGCAAGCTATACCGGAAAAGCGGCATGTCAAAAATACTTTAGGT
TCTACATAGATCTCTTTCTCTCTTTTGTTTTGTTTGTTTGTTTGTTAAAG
TTCATTATTTATTTTACCTTTTACTGACAATGTGAAACTCGAAGAAAATG
TTCTCTTTTTAAATATACAGTCATAAACTGTTCAAGGTAACCATAACAAA
CTAGGTGTTATTTATTAACGTATTATAAAATAATGTTTGATCCAGTATGT
GCTTGTCTTATTTAAAATTGGAATGTGAGACATGTTGCTGTGACCTGT

172. chr1_INSL5_NM_005478_1.53679
GCACTCAAATCAGTCATGGAACAGCCATCAGTGCAACACAAAGTTTGTAA
ATCTTGTCTTGACATCACTGAATGCTTCTTTGACTTCCAAAGCTCTTCAG
TGGGCATCTGTCCACCCCAAAGACGGTCTTCCCCTGAGGCATCCACCTTC
GGAAGGTTTTGCGCTGGATTTTCCTCAGAAAACTCACGTTTATGTGGGAG
CTGGAAGGAGTTTCCTGTCTCA

173. chr1_MIER1_NM_020948_-1.81195
CATCTGTTGAATCTTCAAGTCCAG

174. chr1_CTH_NM_001902_1.7187
TGCAGGAAAAAGACGCCTCCTCACAAGGTTTCCTGCCACACTTCCAACAT
TTCGCCACGCAG

175. chr1_ZRANB2_NM_203350_1.59156
GATCCAGATGATGACCTGTGGCGT

176. chr1_LHX8_NM_001001933_-1.9064
GCGAACCGGCTGGAAAGAAACACCGAGTCACTCGTACAGACTCTTGGTCG
CAGAACTTGGCTTTCCGCTATTGGTCCTCCAGAACCGCTTGAAACAACTG
GCCCCAGCTGGCGCATCAGACCGCAGTGAGGAATGCCGCGGGGCGGGTGG
CGAAGGCAGGGTCTGCCCGCCAGTGGATTCCCGGGTGTCCCGCGTGGAGC
AGGCTTGCCCAGCTGGGAAGCCCATCAAACCTCAGTCTTGGCCCACAGTG

177. chr1_LHX8_NM_001001933_-1.57821
GCAAGGTATAAAACGGAGTCTGGGA

178. chr1_ST6GALNAC3_NM_152996_-2.11125
AGGCGCGCCCGCTGCTCGGTGGCAGGAG

179. chr1_ELTD1_NM_022159_1.69847
GGACCAGAGGACATCAAAATTGCAAAATGTGTCAGGTGATTACAGCGGCA
TGAGGTGTGGGTCTCATTTGAGTATGTCAGCTCACAGCCCTCTGAAGACC
AGCTGCCATTCATGGTATCAGG

180. chr1_COL24A1_NM_152890_1.8348
TTAGTCCTTGTTCACCCTGGTCACCT

Figure 3-15

181. chr1_CLCA2_NM_006536_-1.74649
AGACCCATGGCCTTCGACTACAAAAACATACTAACAAAGTCAAATTAACA
TCAAAACTGTATTAAAATGCATTGAGTTTTTGTACAATACAGATAAG

182. chr1_BARHL2_NM_020063_1.79784
CCTGCCCACTGGTAAGCATCTTCCTCTCTTACTCCTCTGCCTTCCAGAGT
TGGCTGCAAGGGAGGCCTAGTGGCCTGGAGCAGGGAGAGGACGGGCAGCA
GTCCGGGTT

183. chr1_BRDT_NM_001726_1.60205
TGGGAGGTCAAGTTAAGAGTCAAAA

184. chr1_DR1_NM_001938_1.84261
GCCTCGGGCTCTATAGAGCCGAGCCCGCTGGGTACCCGCCCGGTACCGCG
GCGAGGCCAGTGCCCCTGGATCTTGCCTCTGCTCCGACGCCGTTGGGGAC
CAGT

185. chr1_SLC44A3_NM_152369_-1.551
GGCGCAAACTTGGGGTCGTCCTCAGGT

186. chr1_CNN3_NM_001839_-1.95194
GAGGACTCGTTGACCTTCTTCACT

187. chr1_LPPR4_NM_014839_2.12424
GATCAAGGACAGCGTCACCCTCCTGCC

188. chr1_PALMD_NM_017734_-1.54334
AGTAAGTTCTAATCACAGTGCAGCATACAATGGCACCGATGGCCTGGCAC
CAGTTGAAGTAGAGGAACTTCTAAGACAAGCCTCAGAGAGAAACTCTAAA
TCCCCAACAGAGTATCATGAGCCTGTATATGCCAATCCC

189. chr1_HEJ1_NR_033424_-1.70023
TCATCAGATAGAACCCGGAATAGCTCAGCAAATTCAAGC

190. chr1_WDR47_NM_001142550_1.94302
CTTTCGACCTTGAAAGACTCCCTGG

191. chr1_ATXN7L2_NM_153340_-1.64813
AAGATCCCACCGGCAGCTGAACCTCCAGCTCACCTTGTCAACTCCCCGTT
ATCTGCTCCCCTGAGCCCATCCTCTACAGGCACCTGCCCCCGCCTTCCAG
GTCCAACCCTGAGA

192. chr1_CYB561D1_NM_182580_-1.54243
TTTCTCCTGGCACCCTGTATTCATGG

193. chr1_EPS8L3_NM_139053_1.55565
AAGGAGAGGGACTGAACAGATTCTTGACAAGCCTAGGCATAAATGCTCCA
GGTTTGGGAAAGAGGTAAAATAAATAGGTGGTTACTGGGGAGGCTCCAAC
ACAGCCAGAAGGGACACTGTTTGCTT

194. chr1_FAM40A_ENST00000369794_-1.60721
CTGTGTTCGCCCTGCAGTTTCCGCCTTGGCAGGAGGCCAGGCACAAGACT
GACATATGGGCTCAACCAGTGCCTGGCCTTGCCTGTGTCACCTTTGTCCA
GTG

Figure 3-16

195. chr1_FAM40A_NM_033088_1.58108
TTCTGTCCTGGATTACCCTCACTGCGTGGTGCATGAGCTGCCAGAGCTGA
CGGC

196. chr1_RBM15_NM_022768_-1.66492
GACATCGGGCACCAGACCCTTTGAGGGGTGCTCGGGATAGGACACCACCC
TTACTATACAGAGATCGTGATAGGGACCTTTATCCTGACTCTGATTGGGT
GCCACCCCCACCCCCAGTCCGAGAACGCAGCACTCGGACTGCAGCTACTT
CTGTGCCTGCTTACGAGCCACTGGATAGCCTAGATCGCAGGCGGGATGGT
TGGTCCTTGGACCGGGACAGAGGTGATCGAGATCTGCCCAGCAGCAGAGA
CCAGCCTAGGAAGCGAAGGCTGCCTGAGGAGAGTGGAGGACGTCATCTGG
ATAGGTCTCCTGAGAGTGACCGCCCACGAAAACGTCACTGCGCTCCTTCT
CCTGACCGCAGTCCAGAATTGAGCAGTAGCCGGGATCGTTACAACAGC

197. chr1_CHI3L2_NM_004000_1.52955
CATCAACCTCCTGTCCTTTGACTTCCATGGGTCTTGGGAAAAGCCCCTTA
TCACTGGCCACAACAGCCCTCTGAGCAAGGGGTGGCAGGACAGAGGGCCA
AGCTCC

198. chr1_CHIA_NM_021797_1.84664
TCTGTGCACGAACAGGTGGCCGACTCTGG

199. chr1_CHIA_NM_021797_-1.66316
CATTGGAGGCTGGAACTTCGGGACTGCCCC

200. chr1_KCND3_NM_004980_1.53114
GCCGGCTCGCCGAGCTGGAGAACTTTGCGAAG

201. chr1_ST7L_NM_017744_-1.57194
TTGCCGCTATCGCAGGCGCCAGGAG

202. chr1_MOV10_NM_020963_1.54724
CTGTACGACCGGAGTCTGGAGTCAAACCCAGAGCAGCTGCAGGCCATGAG
GCACATTGTTACGGGCACCACCC

203. chr1_RHOC_NM_175744_1.6431
AGAGAGGCCGCAGTCGATCATAGTCTTCCTG

204. chr1_ATP1A1_NM_000701_-1.54618
CCAGAAAGGATCCTAGACCGTTGCAGCTCTATCCTCCTCCACGGCAAGGA
GCAGCCCCTGGATGAGGAGCTGAAAGACGCCTTTCAGAACGCCTATTTGG
AGCTG

205. chr1_TTF2_NM_003594_-1.52546
GCTTTCTTAAGACCGGCGTCCGCGATGGCCCGAATAAAGGAAAGAGCTTC
TACGTGTGCCGGGCAGACACGTGCAGCTTCGTGCG

206. chr1_PHGDH_NM_006623_1.52432
CAGATTCCCCAGGCGACGGCTTCGATGAAGGACGGCAAATGGGA

207. chr1_PHGDH_NM_006623_-1.91442
CTTTGCCCAGTGCAAGAAGGGGGTGCGTGTGGTGAACTGTGCCCGTGGAG
GGATCGTGGACGAAGGCGCCCTGCTCC

208. chr1_HMGCS2_NM_005518_-1.78362

Figure 3-17

GACGCCGGGCATACTTTCGGCGATGCTGCTCGTCCACTCGCTCCAGGTAC
CAAGTACCTGGGAAAAGGCTGTTTGTGTCAC

209. chr1_NOTCH2_NM_024408_1.56525
ACTGTGACTGGGTGTTCGCTCAGCAGCATTTGAGGAAGCATAACTGTGCT
GTGAAGGGGGTGTGGGGTACTTGCCCACAGAGGCTGGGAAAGGATGATAG
GCTGGGAGAATGGTCTGAGCTACCTGCCCGTCCTGCTGGGGCATCATGGC
AGTGGGGAAAGCCACACTGGGCAAACGGGCCATTTCTGGAATCTGGTACA
TGGTGGGCAGGGGGCCCGCAACAGCTGGAGGGCAGGTGGACTGAGGCTGG
GGAGCCCCCGCTGGTTGGGCAATACTGCCTTTAGGGATGAGCTGGAAAGT
CACAATGGGGGGCAAGGGCTCCCGAGGGGTGGTTATGTGCTTCCCTTCAG
GTGGCCTGCTCTGGGGAGCTATGCCAGGATGGGTGCCCTCAGCTGGAGCC
AGGACCATACCAAACATCTCATTGTACTGGGTCTCATTCACCTCCATGCG
GTTCATCCAATCTGCTGGGACTGGGACTGGATGGAGCCTACTCAAGCTTC
CAGCACTGCCACTGCCTGGAGACACAATGTGGTGGTGGGATAGCAACTGG
CTCACTGAGGGAAGCACAGTGCTGGCCCCATGTGCCAAAGGCTGCATTTC
ATGAAGGTTAGAAAAAGATAGTGCATGCTGGGCATGGACTGGGGCAGGAG
GGGCGGCAGTGGCCAACATAGGGTTGGGTGAGGCCTGTAAGATCCCAGGG
GATGTAATCATTGGAGAGGATGTGGTGTCGGAAACATACGTGTGAGGAGA
TTCTAGGGAATCAACAGGGGATAAAGTTACTGAACTCTCAGACAGTTGGA
CCTTCTCACTCAGAGACTTCTTCCTCCTACTACCCTTGGCATCCTTTGCC
TCCTTGGCAAGGTTAGGGAGGCTAGTAGGCATGGTACTCTTGGCACTGGG

210. chr1_HFE2_NM_213653_-1.78466
TGCAAGATCCTCCGCTGCAATGCT

211. chr1_PEX11B_NM_003846_-2.06987
TGGACGCCTGGGTCCGCTTCAGTGCTCAGAGCC

212. chr1_ACP6_NM_016361_-1.50106
CAGCCAGCAAACAACGGGTGGACTCCAGATTCCGAAAAATGTTAGTGGA

213. chr1_BOLA1_NM_016074_1.52848
CCATGGCTGGCCGCGTTTGTTTGTGCCAG

214. chr1_MTMR11_NM_001145862_-1.74453
CAGAGGAGATAGCAGGTCGAGGGAGCCAACGAGAAGAGACTGCCAGCAGG
GAAGGACTGTCCCGCCAAGGACAGAGCTG

215. chr1_OTUD7B_NM_020205_1.76146
TGATCCTCAAGTACTTTCAGCCAG

216. chr1_C1orf54_NM_024579_1.67645
ATCAGGTGGTCTATTATTATACAG

217. chr1_ECM1_NM_004425_-1.62208
GACCGGGAGTATGCTGTGAAGACCCACCACCACTTGTGTTGCCGCCACCC
TCCCAGCCCTACTCGGGATGAGTGCTTTGCCCGTCGGGCTCCTTACCCCA
ACTATGACCGGGACATCTTGACCATTGACA

218. chr1_ARNT_NM_001668_-1.63693
TGAAATTCTCTGCCGGCCGGGGGGTAGGAGGGAATGTGTTGCCCTGGGAG
AATAGCTGTTGGGTGGCAGGGA

219. chr1_SETDB1_NM_001145415_-1.54115

Figure 3-18

CCAAACATGTGCACAAACCGGTTGGTGCAACATGGACTACAAGTTCGGCT
ACAGCTATTCAAGACACAGAACAAGGGCTGGGGTATCCGCTGCTTGGATG
ACATT

220. chr1_ANXA9_NM_003568_1.58627
TGGCACCGTCCCTCACCCAGGAGATCCTC

221. chr1_FAM63A_NM_018379_-1.55674
AGAGGATGTTCATGATGGCAAGGAGAGGGCAAGGGCCGTTAGTGCTCTGG
GTGATGATGGGTGTCTGTTCTCCTTTCCAAGGGATCCACT

222. chr1_PRUNE_NM_021222_-1.52633
AGTCCCGACCTCTACATGTTGTGCTGGGAAATGAAGCCTGTGATTTGGAC
TCCACAGTGTCTGCTCTTGCCC

223. chr1_PI4KB_NM_002651_-1.96109
ACAGCCAGACTTCGAGCTTCCAAG

224. chr1_RFX5_NM_000449_1.52635
ACCAAGGGAATTTTATCTTCTGCTTCTTTGGTATGCTGGGAACCGGGGCC
CCTTCCTCCTTTGGAAACAGTACCATCTCCCTGACCCTGGGCAAGTACTG
CCCCCTTTTCAGCCTCTCCCATTGGCCCTGGCCTCTCTGCCCCTCCAGCT
GAGTTGCCTTCC

225. chr1_RFX5_NM_000449_-1.6457
GCCACCAAGCCTTCGAGCTTTGATGTCAGGGAAGATCTCTCTGATGATCT
TGCCAAAGTTGGCTGTGCTGAGTGGGCGGCAACAGGCAAGACTCTCACAG
TACTTC

226. chr1_CGN_NM_020770_-1.50568
GGACCTGAAGACCCGGTTGGCCAGCTCAGAAGGCTTCCAGAAGCCTAGTG
CCAGCCTCTCTCAGCTTGAGTCCCAGAATCAGTTGTTGCAGGAGCGGCTA
CAG

227. chr1_CGN_NM_020770_1.70429
TTTGAAGCGTCAGGTGGATGAAGCAGAAGAGGAAATTGAGCGACTGGACG
GCCTGAGGAAGAAGGCCCAGCGTGAGGTGGAGGAGCAGCATGAGGTCAAT
GAACAGCTCCAGGCCCGGATCAAGTCTCTG

228. chr1_TDRKH_NM_001083965_1.75644
GCTGCTCCAGTCAGCCGTCGAGTGCGCCGCCTCG

229. chr1_CRNN_NM_016190_1.83382
CACACAGCGCCTTGGGTGAGTGCTGCTCCACTCCTGCCTTCCTGACTCAG
TGCTTGCCCCAGTCTGGGCCTGTCCTCCCGGTACTGTCTCTCCTGCCTCA
GGGTTGCTCACTTGCATCCATCTTTGACCACTGCCTGGCTGCGTCTGGGT
CTGTCCCTGTTCTCTAGCCCCTCCGTGGCTTACAGTTTGGCTTCTGTCCT
GCTCCACAGTCTCGGTGTGTGACCCTGCCTGTATCTGAGTGTGTCCTCCT
GTCACAGCCTGGCTGGTCTGGCTCCTGCCTTGACCGTGGATCTCAGTCCC
TCTGTTCTGGCCATTGGTGGACTCCTGTGTCTGGGTGCTGGTGCTTCCTG
TCTGGTGGCTGCTGTCCTGCTCCACGGTCTGGGTGGGTGTCTGGGTGTGT
GTCCCTGCCTGTATCTGAGCATG

230. chr1_CRNN_NM_016190_1.56819
CCCAGGTGGGATGAAACAAGTGGCTGTTAAGTGGTGTGAGGAGT

Figure 3-19

231. chr1_SMCP_NM_030663_-1.63367
TTGGAGACCAAGCCTGAAGTCTCACCCCTTAACATGGAGTCTGAGCCCAA
CTCACCGCAAACTCAGGACAAGGGCTGTCAAACCCAGCAGCAGCCCCATA
GCCCACAAAATGAGTCCAGGCCAAGCAAATGA

232. chr1_PGLYRP4_NM_020393_-1.87753
AAAGCCTGCCCAGGAGACAAGGTTCGGGCCACATCA

233. chr1_S100A8_NM_002964_1.55968
TTTGAACCAGACGTCTGCACCCTTTTT

234. chr1_S100A7_NM_002963_-1.50144
TGCCCCCGGAACAGGGCGCTGCTCCATGGCTCTGCTTGTGGTAGTCTGTG
GCTATGTCTCCCAGCAAGGACAGAAACTCAGAAAAATCAATCTTCTTATC
CTCATTCTTGTCCTTTTTCTCAAAGACATCGGCGAGGTAATTTGTGCCCT
T

235. chr1_---_---_1.65589
AAACATGGCCGTACAGTAACCTGCTATACATTCTTTCAGACACACACACT
CCAGCGTTTGTCCCTTATCACTCATTAA

236. chr1_DENND4B_NM_014856_1.52485
TGCACTAGGATGCGGGGTCTCTGTGGGGAAGGGAAGGGAACGTTGTGAAT
GAAGTGGGAGATGTGC

237. chr1_CRTC2_NM_181715_-1.7232
GAGCTGTATGGGTATGGGGGTAACCGCTGGTCAGTGGACAGTTTACTGGT
ATCCAGGG

238. chr1_CREB3L4_NM_130898_-1.53815
CTCAGGAAGATTTACTATAGCTAAGAGAAAACTGCAGCAGAAAGGGCGCG
GCTACCTACTTCTTAAATTCCGTTTGTGGACCCTCAGACTCTTAGTCCCC
TACTCCCAGATACAGCGGCCCTA

239. chr1_IL6R_NM_000565_-1.8999
CACTGTGTCATCCACGACGCCTGGAGCGGCCTGAGGCACGTGGTGCAGC

240. chr1_IL6R_NM_000565_-1.6486
CTGGGGTCTGACAATACCTCGAGCCACAACCGACCAGATGCCAGGGACCC
ACGGAGCCCTTATGACATCAGCAATACAGACTACTTCTTCCCCAG

241. chr1_TDRD10_NM_001098475_-1.95808
CAGCGACGACTTCTGGACCATCCCACCCCTG

242. chr1_ADAR_NM_001111_1.61072
ACAGGTTTGACTAGCGAACTGGGCATATTCTAACAGCCCGCTGATGGGGT
TCTTCAGCTGGCACTCTGTCAGTTTCTTGTAGGGTGAACACCGTGGCAAG
CCATGACTGTAGAAGGAGGGCATCTCCATGATGGCTCGAAACTCACCTGG
TGCTGCGCGGATACTATTCAAG

243. chr1_ADAR_NM_001111_1.5391
TGTCTATAGACATCCCCCTGCCTTTCCATGTCAATTAGCACAGCATTTAT
ATCTCGGGCCTTGGTAAGGCCAATATTTTTAGCCAAATTCAGGGCAGAGG
AGTCAGACACATTGAAGAGATAGTCGCAGATTTTCTCCTTG

Figure 3-20

244. chr1_PYGO2_NM_138300_-1.5545
CCTCACGGATGTAGACAGACTGGATCTCCTTGGTCTTGAGGCAGAGATCG
CAGGCCCAGACGGCAGAAGCTTCAGTGGTCAGCAGCCCATAGGCGCTCTC
AGTCATGCCTGTGCACTCACGGTGGAACCATTTCTG

245. chr1_SHC1_NM_183001_-2.06403
CTTAGCCTGGTTGGACCTCTGTGGCCCAGGAGTCACAGAAGTCCTGGGGA
GGGAGAGGGACAAGTGGCTTCCGCTCCCCAGCTCAGACCCAGACAGTTTC
AGGCCCCATCCC

246. chr1_DCST2_NM_144622_-1.74
AGTGGGGGCTCCTTTAGTGGCGGAGGATGTCTCAGGTGGTCTGTGGGGCT
CAGGGC

247. chr1_ADAM15_NM_207191_1.76776
CCTCCGCGCGCTGTTCCGCACTTGCTGCC

248. chr1_ADAM15_NM_207191_-1.51958
ACCGCCTCCGACAGTGTCCTCGCTCTACCTCTGA

249. chr1_TRIM46_NM_025058_-1.734
GCGGTACCGCCAGAGTGTGAGTGTGGGAGGTGCCATCCTGTGCCAGTTGT
GCAAGCCCCCACCACTAGAGGCCACCAAGGGCTGCACAGAGTGCCGCGCC
ACCTTCTGCAATGAGTGCTTCAAGCTCTTCCACCCCTGGGGCACCCAGAA
GGCCCAGCATGAGCCCACCCTGC

250. chr1_MUC1_NM_002456_2.04863
CATAGGATGGTAGGTATCCCGGGCTGGAAAGATGTCCAGCTGCCCGTAGT
TCTTTCGGCGGCACTGACAGACAG

251. chr1_THBS3_NM_007112_-1.95005
CAGCTACCATCTGCCGAGACTCGCCCACAGTCAGCAGGTCAATTA

252. chr1_POU5F1P4_GU480875_1.53487
TAACCGGTGCCAGAAAGGCAAGCAATCAAGCA

253. chr1_PAQR6_NM_024897_1.64319
GGAGAGGCCGGTGCACAGGAAGGAGTTGAGTGCGGCGGCAGGCACAAAGA
ACTGGTGCAGGTGGCCGTGCAGCCAGGAGGCCGGCATGGAGTAGGCG

254. chr1_SMG5_NM_015327_1.70652
ACCCTGACCCTGCTACTCGGTGCAGGCCACTCCAGGCCTTGCTTCTCTAA
CAGCCCCTGTGGCTGGCTCCAGAGCTGCCTGGTCCCCATAAAGGGGGCTG
AAAGGAGGATGGGTGATCCTTGAGGAGGGGAAGGGTCTGCAGAGAATCAC
TCAGACACCAGGTATTACCCAGCTCTTC

255. chr1_SMG5_NM_015327_-1.56704
GAGCAGGGGCCGATCCGTGTCAAAGTTAAAGCGTCTGTGGGCAGCTCGGA
GCGGGGGCAGGTTACGAAGAGCCATGTCCT

256. chr1_C1orf85_NM_144580_1.88445
TAATTTATGGACTGGTACTCTGAGTACTTCTTGTGGTGCAGCAGCAGAAC
CAAGCCGCCCCCTAGCAGCATGAGCCCTGGGGCACCCAGGGCCACTGCCA
TGATGCCCAGGACTAGTGGGGACAAGCCGTCCACTGGAGGGAAGCCCACA

Figure 3-21

CCCAG

257. chr1_IQGAP3_NM_178229_1.63493
CCTCCCGGGTCAGGTGAGAGGTGTTGAGGGGGCAGCCAGGAGGTTGCTCC
CAGATCCCCTGGAAGGTCTGCAGATGGAAGTAGTAGGCAGTGCCATCCTT
CATGTCATGTTGAACCCAGAAAGCTGTGT

258. chr1_IQGAP3_NM_178229_-1.64255
TGAGTTAGGTAGTGGTCATAGATGT

259. chr1_BCAN_NM_198427_-1.50729
CCAAGGCTCAACTGCCCTCTCTATCCTACTCCTTTTCTT

260. chr1_NES_NM_006617_-1.68783
ATTCTTCTGACAGGTCAGAGTCACGGCCACACTCCTCTTCTCCCTCCTCC
CCCTCCTCCTTTTCTGAGGGTGGGGCCTCAAGGCCCTCGGAAGCCAGGAC
AGCA

261. chr1_NES_NM_006617_1.56094
ACTTCTGGAGATCTCAGTGGCTCTTGATTCTCCTTTTCCAGAGCTGTCAA
TGACTCTAAGTTCTCTTGCAGA

262. chr1_C1orf66_NM_015997_-1.8072
GGCCCAGGAGAACCGTGTGGTGGCCTTCTT

263. chr1_HDGF_NM_004494_-1.88582
TGCCTCCTTGGGACGTTTAGGAGAG

264. chr1_INSRR_NM_014215_1.58918
AACTCAATGCATTCCCGTGGGCTGGCCAGCTCATTCACCGTCTTCAGGGC
CACGGGTGTGGACTCCTCTCCAGCCTCAAGTCCTCGTGCCAGCCCCTCAT
ATACCATCCCAAAAGAGCCCTGGCCCAGTTCCCGGATTATCGAGATCTGC
TCCCGAGGCAC

265. chr1_NTRK1_NM_001012331_-1.57078
TGCAGTGTCATGGGCAAGGGCCCCTGGCCCACATGCCCAATGCCAG

266. chr1_C1orf92_NM_144702_-1.8477
CTTCTGGCGCGGTGACCAAAAAGGGAGAGCGCGCGGCCAAAGAGAAGCCA
GCGACCGTTCTGCCTCCCGTG

267. chr1_FCRL5_NM_031281_1.69975
CAGTAGAGCAGCAGTGCCCCCGCAGCAAGGCCTGCTATGCTGAGCAGGCC
CCCGGCGACTCCTGTGGCAAAAGGGCCACTTCTGTTCGCGGTCA

268. chr1_OR6N1_NM_001005185_1.50843
AGACGTATCAGTGCAAGCCAAACTCAGCACAGGAGGGAAGTCACAAAAGA
CGTGCTGAATGCGATTGGGGCCACAGAATGGGAGGCGTGAAATCAA

269. chr1_CADM3_NM_021189_-1.62915
AGGAACCCAGAAACGGGATGGTTGTCGGCAAAGGTTGGGAGTGGCT

270. chr1_DARC_NM_001122951_-2.00183
CGGAGCTCTCCCCCTCAACTGAGAAC

Figure 3-22

271. chr1_IGSF9_ENST00000198587_-1.58205
CCGCACCGCTCGGCTCCACTCTCGCC

272. chr1_DCAF8_NR_028103_1.5063
GGTGATGGCGTCTCTGTCTCAGGTGATGCATAAGGAACCACAGCATGTGA
CTATCAAACAGGTCAGTTTGGTGCAAGCT

273. chr1_LY9_NM_002348_1.60679
TCTGTGAAGGTGTCTGAGAACTTCTCCTGTAACATCACTCTAATGTGCTC
CGTGAAGGGGGCAGAGAAAAGTGTTCTGTACAGCTGGACCCCAAGGGAAC
CCCATGCTTCTGAGTCCAATGGAGGCTCCATTCTTACCGTCTCCCGAACA
CCATGTGACCCAGACCTGCCATACATCTG

274. chr1_F11R_NM_016946_-1.72057
GCCAGAGTCCGGTAGCACCTGAGTAAGGCAAATGCAGATGATAGGCGGTG
AGCCGACCAGGC

275. chr1_ARHGAP30_NM_001025598_-1.72187
AAGACGACTCCGGGATCCAGACCCTTCTGCACCTTCAGATGGGAGCTCCA

276. chr1_ARHGAP30_NM_001025598_-1.69378
CCAAGAGAACAGGGGCATAGACAGCCGTCTGGACTGGGCT

277. chr1_UAP1_NM_003115_-1.63338
AACATTAATGACCTCAAACTCACGTTGTC

278. chr1_RGS5_NM_003617_1.87753
TTTGTCCAGGGAATCACGCCACTGC

279. chr1_FMO9P_NR_002925_1.60447
CATAGCTATGTCAATGTCCAGGGAAGCATTTTTAAATAGTAAATCAGAAA
CATGTAAACTAGTGAATACAATTTTCTATTTTTCATTCAGAAATTTGTTG
TCATAGATGCAGCCTTTATCTGGAAATCAGTGGGCAGCTCTGGTCAAGCA
CAGCATGGCGACCACTG

280. chr1_MGC4473_NR_024160_-1.50181
CCATTGGTCACTTAAGAGCACTAACCCCTCCCTGGTTTGAAGATGTTCTT
GACTTTAAATACAAACATCTGATATTCCAGCTTAGACTCCTCCACAAGAA
CTAGAGTGTCATCCTATTTTGGCTTCCAGCTCAGTCCCTCTGCTACAAGT
CTTGA

281. chr1_F5_NM_000130_-1.83401
TGGGGAAAGGGACATCTGACCAAAGTTTGGGGAAAGATCTGTCTCAC

282. chr1_F5_NM_000130_-1.51534
GGTCATCACGTTTCACCTCATCAGGATTTTCACAAAACTTGTTGATGTTG
TCCTCAAGGTACCAGCTTTTGTTCTCATCAAACACAGCAAACACAGCCTG
CTGTTCGATGTCTGCT

283. chr1_F5_NM_000130_1.69
GCTCAGGTCGGTAGCTCCAACTGATGCCCTGAGCAGCCACGTAGAACTGC
CTTAGCTGTGCCGCTTCTGTCCCTTGGCTCCCCCAGCCTACCCAGCTGGT
GCCCAAGA

284. chr1_PIGC_ENST00000367728_-1.58634

Figure 3-23

AGCCCGGGAATCTTAAGGCCGCCGCCGGGGTTGGAGGGTCTGCGACGCCC
AAAAGGGCAGCGCCCGCCCGCAGAGTGGGGCTGGGAGGGGACGGGGTAGG
GTAGGGTGACCCCAGGGTGCGCCTTCACTCTTCTGGCACCCCATTTGGCT
TTTTGG

285. chr1_TNFSF18_NM_005092_1.53468
TAGGAGATGAATTGGGGATTTGCTAGTAAAATGATAC

286. chr1_RASAL2_NM_170692_-1.64474
CACCGTCTGTCTTGTGGTCAGTCACCCTACACCGAGACAACAACGTGGGA
GCGGAAGTATTGCATCCTCACAGACAGCCAGTTGGTATTGCTCAACAAGG
AGA

287. chr1_FAM163A_NM_173509_-1.85161
TGATGAATGACCCTCCAACAGCCCCACATGGGTTGTTTCTGT

288. chr1_TOR1AIP2_NM_022347_1.53078
AATCGTAAAACTGTTAGTATCAGGAGAGCCCTTCGAGTATTCTCTCCGCT
CCACACCG

289. chr1_---_---_-1.50703
GTGTGGCAGTCCATCCATCTGTCAGCAGCCACTGCGGGCCTACTTGCTGG
GTGCCCAGCACCGCACTCACCACTGCAGGCGTGGCCAGGAGCGTGAGATC
CCCAGAGCCCATGGCCAGTGAGAGGCGGCCAGGGATAGGTACCCAGGGTA
TGCCACAGGAGTTTGCTGGGCTCACGGAGCTCTTTCACTGGTCAGAGA

290. chr1_IER5_NM_016545_1.53815
GCGCGTCACCAGAGTCGTTTCTCTTCGGAGTCTTAGGTGATCGAGGGTGT
GCCCAGGGGGCGGACTTGTTTGCGCCTCCCGTTCCCTCCCAATTTCCAAA
CGTGTCA

291. chr1_CACNA1E_NM_000721_1.60184
GCGCCAGCAGCAGATTGAGCGTGAGCTGAATGGCTACCGTGCCTGGATAG
ACAAAGCAG

292. chr1_CACNA1E_NM_000721_1.71496
ACATGGGCCGGGTCATCAGCCAGAGCGAGCCTGACCTCTCCTGCATCACG
GCCAACACGGACAAGGCCACCACCGAGAGCACCAGCGTCACCGTCGCCA

293. chr1_GLUL_NM_002065_1.72196
GGAGGCCGCAGTACTGCTCACACGCTCC

294. chr1_RGSL1_NM_001137669_1.64498
CAATCAACCACTAGGAGGGAGATCCTGAGCCACATGCAGAAAGTGGCTCT
GTTCAAACTCCAGAGCTATTGGCTTCCCAACTTTTACACCCACACCAAGA
TGACCATGGCCAAGGAGGAAGCATGCCATGGTCTGATGCAAGAGTACGAG
ACTCGCTTATACAGCGTTTGCTACACCCACATAGGAGGGCTCCCTCTGAA
CATGAGCATCAAGAAGTGCCACCACTTTCAGAAACGGTACTCAAGCAGGA

295. chr1_LAMC1_NM_002293_1.62817
GCACTCGGGCACGCGCTCGGAAGTCGGGGGTCGGCGCGGAGTGCAGGCTG
CTCCCGGGGTAGGTGAGGGAAGCGCGGAGGCGGCGCGCGGGGGCAGTGGT
CGGCGAGCAGCGCGGTCCTCGCTAGGGGCGCCCACCCGTCAGTCTCTCCG
GCGCGAGCCGCCGCCACCGCCCGCGCCGGAGTCAGGCCCCTGGGCCCCCA
GGCTCAAGCAGCGAAGCGGCCTCCGGGGGACGCCGCTAGGCGAGAGGAAC

Figure 3-24

GCGCCGGTGCCCTTGCCTTCGCCGTGACCCAGCGTG

296. chr1_LAMC2_NM_005562_1.65386
CCTGGCCCAGCAGTTGACAAGGGAGGCCACTCAAGCGGAAATTGAAGCAG
ATAGGTCTTATCAGCACAGTCTCCGCCTCCTGGATTCAGTGTCTCGGCTT
CA

297. chr1_SMG7_NM_173156_-1.6672
CGCCAGCACCCGCGGTGCCGCGGGGCCGCTCCGAGGAGCCTGAGAGACCC
ACGGAGGCTTCGCGGGAAGACGC

298. chr1_NCF2_NM_000433_1.54595
GGCTTTGGAACTAGGAGGAGCTGGGATGTCGGACTGCGGAGAGCTTTCCT
C

299. chr1_B3GALT2_NM_003783_-1.50362
AAAGATGCTATCGAACATGCGCACATCCCCCAACAGTCTGCCTCCTGCGA
TTGCTTTTCACAGTATCCAAAGTGTCCATCTGTCTGCTTGTCTTCGAGTT
ACCCTCCTTGTTCATATGGGTCCTAGTCTTCTGAAATTTTCCCTTTCTTT
CATTTTCTCTCTTTCGTTAAACAAAAGAGCTGTAGTTGCCCGTTCTGCTT
GTAGCACTGTTGACTCTTCCCGACAGTTGATGCATTGAAGCTTTTTACAT
CTGCTATTTTCCTGGCTGGACAATGCAGTGCTGTGTTCTCGTCTCA

300. chr1_NEK7_NM_133494_-1.51326
TATAAAACCAGCTAATGTGTTCATTACAGCCACTGGGGTGGTAAAACTTG
GAGATCTTGGGCTTGGCCGGTTTTTCAGCTCAAAA

301. chr1_CACNA1S_NM_000069_-1.69708
ATGGGCACGGCCTTCTCTTTCAGCTGCAGCTCAGCCAGGGGACGTGGTCG
GGGGCTCAGCGGGATCTCAGGCTCATCTTCCTCGT

302. chr1_CACNA1S_NM_000069_-1.50908
TTGCCACAGACGAAAAGGATGATGAAGTAAATGCACACAAGCATGCCAGG
GTAGGACGGCCCGCCGTAGGCCATGATCCCATTGTA

303. chr1_CACNA1S_NM_000069_-1.52931
AGAAGGATCCCAGCAAAATGAGGG

304. chr1_CACNA1S_NM_000069_1.68205
CAATGCCCCCGCCTTGGGGACTAGGCTG

305. chr1_IGFN1_ENST00000412892_-1.69711
CACAGTGAAGGCTCCGTGCTACCGGGAGCCCGACCTGAGCCAGAAGCCCC
GGTTCCTGGTGGGCCTGCGGTCCCACCTGCTGCCCCAGGGCTGCGAGTGC
TGCATGAGCTGTGCCGTGCAGGGCTCGCCCCGGCCCCACGTCACCTGGTT
CAAGAATGACCGCAGCCTGGAAGGAAACCCCGCGGTGTACAGCACTGACC
TGCTGGGCGTGTGCTCCCTCACCAT

306. chr1_LAD1_NM_005558_1.52523
CCGACTCAGTCTCCGGCGAGGTGGGATTTCCAGTTCCTTCTTGGAGACTA
GGGGTTTCTGTGTGGCCTGCACAGGGCTCAAGCTGTTCCTCCCCTCCTCT
GCCTCCAGCCTCTCCTGGATGGGGGCCTGTGCAGCCTCCACCACCTGCCG
CCTCTGCCTCCGCTCCTGCCGTGTTCTGAGGATGCTCTGGATGTCCTCGT
CCTCATCTTTGGAGGCTGGG

Figure 3-25

307. chr1_PRELP_NM_002725_1.53319
ATTCCCATCGTGAGTGAGCCCAGGTGAGGACATAGTCGGCTCCCGTTTGT
TGTAGGCCCTTCCCAGGTGCCTTCTCAGCTCCCTCATCTGTAAACCGAGG
AGGTGGATAAGATGCTCCCGGCCGGGCGCGGTGGCTCACGCCTGTAATCC
CAGCACTTTGGGAGGCCGAGGCGGGCAGATTATTGCCTGAGCTCAGGAGT
TCGAAACCACCCTGGGCAACATGGTGAAACCCCCGTCTCTACTAAAATAC
AAAAAAATTAGCCAGGCATAGTGGCGCGCGCCTATAATCCCAGCTACTGG
GAGGCTGAGGCGGGAGAATCGCTTGAGCCGGGGAGGCGGAGGTTGCAGTG
AGGCGAGATTGTGCCACTGCACTCCAGCTTGGGCGACAGAGTGAGACTCC
GTCTCAAAAAAGAAAAAAAAAAGATGCTCCTCTGAGGTCCCTCCGGCGCT
CATGTTCCGAGTCTGCAGCTCCACACTTTAAATCATACTCGAATGCAGGA
CAAGTCCTAAATATTTGCCCCTTCCCTTGCAGTAATTTATTTTCTGTATG
GACTGTCCCTCCCCCAGAGGCTTCCCCACCCTCCATTGCCTGGCCCAGGT
GAGCAGCTTGGCAGGTCTCCAAGTGGAACCCGGTCCAGACAGGGCTGCCT
CGACTTCACCTTTCCCCCTAACTTCCTCCAAGGGATGCTGCCCCTTCTCA
GCCCCCTGCGTGTGTATATTGGTGGGAGGCATAGAGGATGGATGTTCTAG
AAATGAGTAAGACACAGTGCCCACCCCCAAGTTAGGATGAAAAAAGTTCC
AGAGGTTTTTAAGAAATTGGATTAAGCTGGGTCCCTAACTTCAAGAAATT
CCCATTATGCTCCTTCTCACCTTTCTTTTTTGCTAATTATGGAAAATAGG
GCCCATTTCATCATAGCCTCCTTCCCCCGTGCTCCACTACAATCGCCGCA
TTCTTTCTAGCTGCAGCTGGTTTCTTCAAGGCTCCTGCTTAAAGTCCACA
CGTTATTATGGCCGAAAGCAACCTGGTGCTTCGGCCTGGATAAGAGCCCC
TTCTGCATCTTATTCACAGCTTGCAGCCTCAGCCCCTTTGATGAGGCCCT
CAGGGGAGAGGTCATTACCTTGATCCTGCAAACCCAGACTCGTTG

308. chr1_REN_NM_000537_1.65042
AGGAGGGCACCCAAACATTGGACGAACCAGTGTCAAAGACGACTTTGAAG
GTCTGGGGTGGGGTGCCGATGCCAATCTCGCCATAGTACTGGGT

309. chr1_PLEKHA6_NM_014935_1.89032
GAAGATCGGTGGAATCCTCCCAGGCTGTAATCCCTCAGAAACATGAGAAT
ATCCTAAGCACCTACAACAGTGCCTGGTACATAAAAGGTGCTCGATAAAT
ATTTGTTGAGTAAATTGTCATCTTTACTTGCATATGAACCAGTAACTGTC
CCAGCCATGAAGGAGTGCAGAGGAATTAGTAGGTGTTCTTGGGACCGCTG
GAAGTCAGGCTGAAGCCTCTGAGCGGCAACTCTAGCAGAGAGAAGGCCGA
GGGGCCACGGTGTCTTCAGTTTCCCTCCTTCCTCCTCTCTGGCTACATTC
GTCTCCAGGTGGGTGGAGCTGAGGAGGAATGCGTTTGCTTTTCTCTGTCT
TCCCCGCTGCCCTCCCGGGGCAGGTGGATCATGAGAGCGCCTAGCCTCAG
CCAGTCCTCGTCTGGGATGCCTGGGATAGGGGGATAGGCCTCCCAGATTA
AGGCCTCATCCCCCCTCCTCAAGGCGTACTCTCAGCTGGCCCACTGCACA
TTCCAGGGGGAACAGGGCAAGAAATATCATGGAACTGGGTAGGTAAGGCC
CCAAGGCTGACCACACCCTACATAAGACAAGTCCTTCTCTCTGCCCCTTA
CCCCAGGATGGCGAGGCAGACACCAGGCACAGACCTACTAACAGCCATCT
CCCAGGCAGTCGCTACTCAACCCCCTTCACCCAGATCCCCACACCAAGCA
TCTCCACTGAGGCTGCATGTGCTCCACTGGTGGGTCCTCCTAGGGATGAG
GTGGGAGGAGCAGAGGAGACAGTCTGGCACTGCACTGGGCACTAACCTAA
GGCTCCACCGGGGGAAACCAATCTGATATCCCCTTTCCATCTCCCTCCTT
CCTGCTTGACTTGCCAATGTGTCCTGCTGCTTCCCCCTCCTTCCACTCTG
AGGATCTCTCTCTCTCTCTCTCTCTCTCTCTTTCTGTCTCTCTCTCTC
TGCTACCCTTCCCAACCTGCCCTCAGACACTGCACAGACCTGCTGTTCTC
TAGCCACAGCCAGCACTGTTCCCTCTGGGAGCCAATGGCCTCTCCCCATC
TCTCATCACCTTGTCTTTGGCTCAAGCAGGGTGGTCAGTCTCCACCGGAC
CCCAGCGAGCACCCATAAGCAAAGCACTGGGTTTGTGTCAAAGCCCTGGG
TCCAGCTGAGGCAGTAGGGTGGGGCTGACGAGGATAGGGATGATGACAAG
TGCTGTCCTTGGTGTCAGGCTGGCTCCAGAGGCAGTGTCCATCTCCTCTT

Figure 3-26

CACCTCTAGTCCTCACATAAGATAGCCACAGGTGTGTTCTCCACCACGGC
ATGTCCCCCATCAGGGAATGTTCCACTGGAGTCACCACAACCCCAGCCAG
GGCAAGGCTGAGGCTCCCTGTGACTTGGACATTAATGAGGATGGTGCTCC
CC

310. chr1_PLEKHA6_NM_014935_-1.60138
CTGCCTCTACCTCTTGCCTGGTGGGCACAAGGCTGATGTCTCTGGGGGTG
TCCAGGGGCAATGTCTGGTGGGGGTCTTTCTTGCTTTGTTCATAGTTTGC
CTTGG

311. chr1_NFASC_NM_001005388_-1.68565
TGAATGCCACCTCGGCCTTTGGCCCCAACCTGCGCTACATTGTCAAGTGG
AGGCGGAGAGAGACTCGAGAGGCCTGGAACAACGTCACAGTGTGGGGCTC
TCGCTACGTGGTGGGGCAGACCCCAGTCTACGTGCCCTATGAGATCCGAG
TCCAGGCTGAAAATGACTTCGGGAAGGGCCCTGAGCCAGAGTCCGTCATC
GGTTA

312. chr1_CNTN2_NM_005076_-1.93825
GCGGGGGAGAGATCCTTATCCCCTGCCAG

313. chr1_TMCC2_ENST00000330675_-1.58053
TGAACCAGGTTGTTCAGCCCTTAATGAGCAGACACTCTGCATGTAGAG

314. chr1_SLC26A9_NM_052934_1.54099
TTGCCTGGGCAAAGAGGACTGCGTCATGTATGCTGGGAAAGACGTGCTTG
CATTCTAGACTCCCA

315. chr1_IKBKE_NM_014002_1.59217
AGGAACCACCTGCGCCTGGTTGGCTGTTCTGTGGCTGCCTGTAACACAGA
AGCCCAG

316. chr1_LGTN_NM_006893_-1.60914
CAGCAGGGGGCATCACCAGTCCAGGC

317. chr1_DYRK3_ENST00000367106_1.62428
CCTAGATCGGGGTATATGTTAAGGGATTACGAAAATCTAGGACTTTTTGT
GGGGCTTTTTATTAAAGGGGGGGAGCCCGGGAGCAATACCTTGGAAAGAA
GCCCTGTTGCTTAGAGCGGATAACCAACGGCTGAACTCTTGGGGTTTGC

318. chr1_PIGR_NM_002644_-1.84534
CCCGAGCGCCGCACCACTCAGGCCGACTTCTCCTGTGCAAT

319. chr1_CD55_NM_001114752_-2.96656
TGGTATGCGGTGGTGTGATCGTAG

320. chr1_CD46_NM_002389_-1.64987
CTGGCGCTTTCCTGGGTTGCTTCT

321. chr1_CD46_NM_002389_-1.71319
AGTAATTTGTGTTGTCCCGTACAG

322. chr1_PLXNA2_NM_025179_-1.59419
ACAGATTCTTTGCCATTGAATTTGACTCGGATCCTTGGCTCCTGAATGA

323. chr1_CAMK1G_NM_020439_-2.90371

Figure 3-27

GGACATCTATGAGAGCACCACCCA

324. chr1_TRAF3IP3_NM_025228_1.58977
GGCTTTGCCCGTGTGGAGTCCAAAGTCCTTCCCTAACGAAGTGGAGCCTG
AG

325. chr1_RCOR3_NM_001136223_-1.74582
TACTGGGGAAGAACCGATCGGCCAACGGCAGCGCCAAGAGCCCGGCAGGC
GGCGGCGGCAGCGGCGCCTCGTCCACCAACGGCGGGCTGCACTACTCAGA
GCCCGAGAGCGGCTGCAGCAGCGACGACGAGCACG

326. chr1_INTS7_NM_015434_-1.5333
CATCCAGTTCCTGTTCGCCATAGCCGGCAT

327. chr1_DTL_NM_016448_-1.86389
TGCTCTTCAATTCGGTGCTCCGCCAGCCCCAGCTTGGCGTCCTGAGAAAT
G

328. chr1_ATF3_NM_001674_-1.68623
GCGCGCACTGCACAGCTCTCTTCTCTCGCCGCCGCCCGAGCGCACCCTTC
AGCCCGCGCGCCGGCCGTGAGTCCTCGGTGCTCGCCCGCCGGCCAGACAA
ACAGCC

329. chr1_USH2A_NM_206933_1.5588
TGCTCCTGTTGTACGTCCTCGACTCCAATCACTATATACTGAACCTCCTT
CATGCGAGGCTATCACTCGATAC

330. chr1_MARK1_NM_018650_1.65373
CGCCGGGGCCGCTTGTTGCACCGCCCCGCGGCCTGCGGGAGCCGCTCGCC
CCGGCCTTGTGCTCGCGTCCGCACCCCTTTC

331. chr1_MARK1_NM_018650_-1.51347
CCGGACGCCATTGCCGACGGTGAACGAGCGGGACACGGAA

332. chr1_MARK1_NM_018650_-1.55067
TGCTGCTCCCGAGCTTTTCCAAGGAAAGAAGTATGATGGGCCTGAAGTGG
ATGTGTGGAGTCTGGGCGTCATTCTCTATACATTAGTCAGTGGCTCCTTG
CCTTTCGATGGCCAGAATTTA

333. chr1_C1orf65_NM_152610_1.67318
GGAGGTCTCAGGCCCCTTGGGCAGACGCTGCGCGTGCCCAGAGGGAGG

334. chr1_TP53BP2_NM_001031685_1.54605
CTGTATTTTCATCGGCCCCTCTGAAGCCTGAATGACCAAGGAACCATCCG
GCAGGGCTGGCTTCACCAGCAATTCAGGCCTTGAGGGCATCCGAGGCATA
GTAGACGACTGGATATAGGGACCTACTG

335. chr1_TMEM63A_NM_014698_1.69796
GCTGGATGCCAGCGGGACCTCAGACCTGGACTGCAGCATCTCTTTGGTTA
TCGGTTGTGTGTGTGCTCAGAAGGGAGGAGGCCTTCCCCTTGTTACATCT
CTCTCTCCATATATTCTCCCGGACTCATCAGTTTGGGGGGCGAAAAGTCC
ACCACATGGTCTTGGCGACAAA

336. chr1_TMEM63A_NM_014698_-1.73282
GCAGACGGAAGATGGCAGTCAGCC

Figure 3-28

337. chr1_PYCR2_NM_013328_1.67588
ATGGGTGCCCGTGGCGTACACTGTAGCGCCTTCCTGCACTACCACAGGTG
TGTTGGTCATGCAGCGAATCACTTTGGG

338. chr1_ACBD3_NM_022735_1.55344
CGCGACCGGATCCAGGTGGCGAGGGCGGTGGCAGCGGTGGCGGCAGCAGC
GGGGCGCCCTCCGCCCCAGGCCGCTCCTCCGGGTCCGGGCTGAGCGTGAG
GCCGTCGACGGACAC

339. chr1_WNT9A_NM_003395_1.83311
TCGGGTGCCTCATCGCAGGTACAGCGCTCCATGCGGCCCGCGCTGCACGC
CTTGGCCAGTGCGTGCGTCAGGCCAGCCGAGGAGATGG

340. chr1_C1orf35_NM_024319_-1.58168
TGCTTTCCGTCTGATCCTCCGCCCGCGGCTTCCTCCTGGCCGAGGCTGCC
GAGGTCCCGGGCCCGCCGCTCTCTACGCGGTGATG

341. chr1_OBSCN_NM_052843_-1.71786
TGGCAGCTGGACTCGTGACGGTCTGCGGTTCCAGCAGGGGCCCACGTGCC
ACCTGGCTGTGCGGGGCCCCATGCACACCCTCACACTCTCGGGGCTGCGG
CCAGAGGATAGTGGCCTTATGGTCTTCAAGGCCGAAGGAGTGCACACGT

342. chr1_OBSCN_NM_052843_1.54075
CAGACAGAACTGCGCGCTGCTGGAGCAGGCCTATGCCGTGGTGTCTGCCC
TGCCACAGCGCGCTGAGAACAAGCTGCACGTGTCCCTCATGGA

343. chr1_TRIM17_NM_016102_-1.71487
GGACCCATCGCTTACACTGTAGAAGGACACTTCCCCGGCTTCGAAGTCCA
GGAAGATGCCCATGTGGCTGGGAGGCTCCATCAGCATGACCGGGGTTAGG
GCAGAGAAGGTGGATAAGTACTTGGTCCCCTTGGACAGCTGCACCACCCA
GAAGCCGTTTTCGGGGCACTTGGGGACCCTGTCTTTCCGGCTCACGTTGT
CCCTGCACACACCCAGGGCCCACAACGCGTCCCCGGTGATGTTCATGCCC
ACCTCCCAGTAGTGCCTCCCAGAGGAGAAGGCCGTCTGGCCCACAGCACA
GGGGTAAGCCACAAATCGGTCCTTGCTGCAGAACCCACTGCCCTCCGGCG
AAGAGCCGAGGTAGCGCCTCTGGCGGCTCTCATACAGGAGGA

344. chr1_EDARADD_NM_080738_-1.612
TGAGCTCGTGGAAGAAGCGAAGGAGGAGAAGAAGAAGGGAGGGGAAGGCG
GAGGAGGGCAGGGGCGCGCAGAGCCACGGTTTGCTCCAGGCGCGTCGGAA
CCGCAG

345. chr1_MTR_NM_000254_-1.50152
TTCGCCGAGAACTGTGGGCCTACTGTGGCAGTGAGCAGCTGGACGTCGCA
GACCTGCGCAGGCTGCGGTACAAGGGCATCCGCCCGGCTCCTGGCTACCC
CAGCCAGCCCGACCACACCGAGAAGCTCACCATGTGGAGACTCGCAGACA
TCGA

346. chr1_RYR2_NM_001035_-1.55471
TTGTCAGGCATAGGATTTCACTAT

347. chr1_HNRNPU_NM_031844_1.80462
CAGCAGGCTAAGGAGATACCCATTCAAGAACTGACATGATTAAAAATTAA
GATATAAATGGGTGACTCACAATTTCATTAGCTTACAAAGATGGTGGAGT
TAACTACTACAAGCACACTAGTTATACAGTATTTTGTGGGAGAAGGGCAT

Figure 3-29

ACAGACATGGCTA

348. chr1_SCCPDH_NM_016002_1.79195
GCGACCGAGCAGAGGCCTTTCCACCTGGTGGTGTTCGGCGCGTCTGGCTT
CACCGGCCAGTTCGTGACCGAGGAGGTGGCCCGGGAGCAGGTGGACCCGG
AGCGGAGCTCCCGCCTGCC

349. chr1_ZNF669_NM_024804_1.52905
TTGCCCAGGTTGTTTCACATTGTTT

350. chr1_NLRP3_NM_004895_-1.63333
ACCTCACGTCACACTGCTGCTGGGATCTTTCCACACTTCTGACCTCCAGC
CAGAGCCTGCGAAAGCTGAGCCTGGGCAACAATGACCTGGGCGACCT

351. chr1_OR9H1P_AY358215_-1.53458
GGGTAGTAGGCTGATTTCATCTAGATAATTCCGGTCAACCACCCCAGCCA
ACACTGTAACTCCCTTCTTAGCCTGTTGACTTAAGAATAGGAGGAGAACA
AAGTGTCCAGGGGGCAATCTTAACTTCCAGTTTAATGGAATTTTTGTTGG
GTCTCCTGGTGGCAGTGCTCCTCCCTCTGGAACTAAGACCTCTAGGCCAG
CAGAAGATAATGTTG

352. chr1_TRIM58_NM_015431_1.61683
TGTAAAGCTGGATCCCGCCACGGCGCACCCGAGTCTGCTCTTGACCGCCG
ACCTGCGCAGTGTGCAGGATGGAGAACCATGGAGGGATGTCCCCAACAAC
CCTGAGCGATTTGACACATGGCCCTGCATC

353. chr1_OR2T12_NM_001004692_-1.72035
GGCCTCATTTTGCTGGTGTTTTAGG

354. chr1_ZNF672_NM_024836_-1.58401
CACAAGAGGAGGACATCCCATGCGGCTACTCCTGCCCAGCGT

355. chr2_MYT1L_NM_015025_1.53525
ATGAGAAGCATAATTGCCGGTGATATGTCCAGAACCATCACAGCCAGGCG
TGGGGCA

356. chr2_MYT1L_NM_015025_1.88847
TTCTGGAGGGACCCTATCTTTGTGCGGGCATCCGGACAGGCTGCGGTGAT
GTGGGTACAGCCCAGTTACGTGGCCGGTTC

357. chr2_TSSC1_NM_003310_1.59692
CCAGGGTCTTCACGGGTTCGGTGACATTTCGGGTGTCCCAGAACTTCACC
TTACAGTCGTCTCCGCAGCTGGCCAAGTAGTACTGCTTATTGGGATTAAA
GTCAAGGTCCCGCACCAG

358. chr2_TTC15_NM_016030_1.68554
GAGGACGCGGCACCCAGTAGCGGAGGGGCCCCGAGGCAGGACGCGGCCCG
CGAGGTCCCAGGCAGCGAAGCCGCGCGCCCGGAGCAGGAGCCTCCCGTTG
CGGAGCCGGTCCCGGTGTGCACCATCTTCA

359. chr2_SOX11_NM_003108_1.63354
GCAGCCGCCTCTACTACAGCTTCAAGAACATCACCAAGCAGCACCCGCCG
CCGCTCGCGCAGCCCGCGCTGTCGCCCGCGTCCTCGCGCTCG

360. chr2_CMPK2_NM_207315_1.69307

Figure 3-30

TGGCCGCCCGGGCAGTAGCAGAGCAGCCT

361. chr2_RSAD2_NM_080657_-1.55573
AGAGCCATTTCTTCAAGACCGGGGAGAATACCTGGGCAAGTTGGTGAGGT
TCTGCAAAGTAGAGTTGCGGCTGCCCAGCGTGAGCATCGTGAGCAATGGA
AGCCTGATCCGGGAGAGGTGGTTCCAGAATTAT

362. chr2_ASAP2_NM_003887_1.50833
AGGAACACGCCAAGCTCCATGGGATGATTCGGACTGAAATAAGCGGAGCG
GAAATTGCCGAAGA

363. chr2_ASAP2_NM_003887_2.27085
AAAATCCCACTGGCCAACGGACAT

364. chr2_ASAP2_NM_003887_-1.71023
GACAGCCTCCTCTGCTAACACCCTGTGGAAGACAAACTCTGTAAGTGTGG
ACGGTGGAAGCCGGCAGCGATCTTCGTCAGATCCGCCAGCTGTCCATCCA
CCG

365. chr2_HPCAL1_NM_002149_1.71281
CTGACGGGCGCCTCCACCTTGCTCCCTCCCTGGCTGCCGGCTTCCTTTTG
TCTTTCTGGGCGGCGATGAGCGCAGGGCCGGCGCAGCAGCTGCGGGCGCA
CGGAGGCCCGCGCTGCTAGTCACTCCTCCCGGCCTCGGCGCGCTTGTCCC
GGGCAGCGGCCCGGGCCCGCTGCAGCCGCCGCCGGCGCCGAACTTGGGCT
CGGGAAGC

366. chr2_HPCAL1_NM_134421_1.55652
CGCGGAGGCGATCCGCTCGTTCCTCCCAGGGCCATGGGGCGACGAGGAGA
GCCCTGGCCTCCCCGCGACCCGCACTGCGACCTGGGCCAGACGCGCCACC
TTCCCCGGTCGCGGTTTGCTTCTCTTTAAAATGAGGACAGCTCCTCCCTT
GGGGGCTGTGGTGACAGGTGAAATGAGAACGCACTGAAGACAGCTCTTGG
TCCAAAGCCCCGCACA

367. chr2_ATP6V1C2_AK127836_-1.53693
TCTTAAATTTGAGGAGCCGGAATCATGCCTTCCTCCTAATCTGCAGGGCC
TCTTTGGAGCTGCCCCCGCCAGCAGTGAAGGGTGCTTGTCGGCCAGGGCG
CCTCTCCCCGGGCGCCTGGCTGGAGGTGGCTGGAGCTGGGACGGGCAGGG
CCCTGGCTGGGGTGGTGGTTGGCAGCTCAGCTCTCCTCCCTTGGCTGCCC
TTGCTGAACCCACCCCTGACCTTTGTGGGCAGCTGCAGTGTCAGGCGGGA
GCTCGGGGCTCTTGCTCCAAGACTCTTGAGCTCCCAGGAAG

368. chr2_GREB1_NM_014668_-1.61911
GTCATCTGTCAGGACCGGAGCTCACTGCGCCAGACGGTCGTCCGCCTGGA
GCTCGAGGACGAGTGGCAGTTCCGGCTGCGCGATGAGTTCCAGACCGCCA
ATGCCAGGGAAGACCGGCCGCTCTTTTTTCTGACGGGACGACACATCTGA

369. chr2_RDH14_NM_020905_1.68789
TCCAGCTCCCGGACTATGAGCTCGCCCACCCCGCTGACGCCAGGCTCTGG
GCCGCACTCCGCGGCCTGGCGGAGCTCGCGGCGGAGCTGACCCGCCGCCT
CCTCGGCGCGCGCGCGGTCCCGGCAGCCCATGATCACCCGCGCTCCCAGG
CGCAGTAGCTCGGCGGCCGTGGCGCGGCCCAGGCCGCTGTTCGCCCCGGT
GATCAGCACAGTCTTCCCGTGCATGAGG

370. chr2_HS1BP3_NM_022460_1.53563
GAAAGGCCACTGACCAAGTCCAGACCCTGAGGACGACGAAGGCCTCGGGG

Figure 3-31

CAGAAGCCTGAGAGAATCATGCCCCACTGGCAGTGGGAGGCGGTGCAGGC
TGGGAGCCCTGCCCAGGCCCCAGGCTGAGCTGTGGGGAAAGCTATGACCC
AGTTTGCTGAGAGCTGCAATGACGAACATTGGCTCTG

371. chr2_HS1BP3_NM_022460_-2.08402
GTCCACGGATGACACGTCCTCCGAGGGGTCCTGTGGAGACAGCTTCCTGC
CCGGGCCAAAGAGCCCCTCATCAGGGTCCACCTCCTCGTCAAAGATGGTG
AGCCGGG

372. chr2_APOB_NM_000384_-1.57163
GAGAGTCTACCTCAAAGCGTGCAGTCAGTGCTTGAAAGGAAGGAATGACA
ATTCCAGCAGGTACAGAGAACTTAATGGAGGGAATCTCAATGGTCTGCTC
AGGCACGATGATGGTGGGCAACTCAAAGTCTGCGATCTTGTTGGCTACTG
CATTTAGATCCAAAGCAGCAATGCCATCTGAAACACTTTTTGGAAGCGTG
AACTGGGACACAGTTAACTGAGATTCAGGCACGGTTATCTCAAAAAAGGG
AATCAAGGAGTCTTCTGGTTGAGAATATTTTGTTAACACATCAACTTCAG
GGAATTTTACCTCGGGGAGTGTTGGTAGGTTGAGGGCAAATGATGAAGTT
CTCAGCTTCTTATAGATTTGTATTTCTCTGAAGTCAAGTTTGCACGATGG
AACCTGAAGATCTGTAAATGGGACATGGAACGTAGGCATGACAAGAACTG
AATTTAGATCATTTAGTTTCAGCCCAGGAATAATGAATTTATCAGCCAAA
ACTTTTACAGGGATGGAGAATGAATAGCCATTGGGGTTTTTGGTGTACAC
AAAGGCAGTTGAAACACGAAGATGCTGTCTCCTACCAATGCTGGTGGTTA
CATCCAGCTTTAGGAAATCCCATAAGCTCTTGTCATAGACTGGTAGGATG
ATATTTTTGAGGAACCTTAGGTGTCCTTCTAAGGATCCTGCAATGTCAAG
GTGTGCCTTTTCTTGGTCATTGGAAAGCTCGACCTGGCTCTGGAAAGACC
CAGAATGAATCCGGACTTCATTTTTCCATCTGATCTTCTGGTTCTTAGTG
TTAGCATTCAGGGCCACTTCCTGGCCAAGGTCAGGGAAATCATGGAAGGA
ACTGGGCTGACTTGCATGGACCTGAAC

373. chr2_APOB_NM_000384_-1.54093
TTTGCAACTGTAATCCAGCTCCAGTGGGGAGTTCAAAGGCATTCTCCATG
A

374. chr2_KLHL29_NM_052920_-1.60095
GAGCTCGTCCTGTCGAACCTGCAGGCAGACGTCCTGGAGTTGCTGCTGGA
GTTTGTCTACACGGGCTCCCTGGTCATCGACTCGGCCAACGCCAAGACAC
TGCTGGAGGCGGCCAGCAAGTTCCAGTTCCACACCTTCTGCAAAGTCTGC
GTGTCCTTTCTCG

375. chr2_UBXN2A_NM_181713_1.96962
ATCTCAAAGAAGTCCTCCGTTTTC

376. chr2_CENPO_NM_024322_1.53198
GGAGCAGGCGAACCCTTTACGTCCAGATGGCGAGTCCAAAGGAG

377. chr2_ADCY3_NM_004036_-1.54045
CGCAGCATGAAGTTATTGAAGGACTGGTTGTTGATGTTGGTGAGCGTATC
CTTCATGGCCAGCGCGAAGTCGGCCAGGTCAGC

378. chr2_DNMT3A_NM_175629_1.5394
CGTACTCTGGCTCGTCATCGCCTGCTTTGGTGGCATTCTTGTCCCCAGCA
TCGGACCCCACGGGCTCAGGCGTGGTAGCCA

379. chr2_DTNB_NM_021907_-1.6479
TGTCATTCATATTAGTCAGAGGGCGAGGAG

Figure 3-32

380. chr2_GPR113_NM_001145168_-1.59315
AATGAGCAGGGCTTTGATCACCCCCAGCAGAGCTTGGCGCTTCTCTGCTG
GGGGTCCCTCTGACAGCGAAGGTCTCAGCAACTTCAGCATGGCCATGGCT
AGTACCAGCCCATTCACGCCTATGATGGCCAGCACTGGCCCCACGAAGGT
GTATAACGCCCCTCCCTTCCCATCCAACCAGCATTCCCCCTCCCTCAGGT
ATTGCCCTTGAGGTAGGTAGAGCCCCAGGGTGACACCTGCCAACCCCAGT
GGGCACAGGTAGCCCAGGAGCACCATGAGGGGGAGAACTCGGTGCTTTGC
CAGCTGGTGAAAGACAAAGAGCAGCTGGTGGGCCAACACCAGGGCCTGCG
CCAGCATCCAGAAAAAGGTGGCCAGGTAGAGGAAATGACAGAGGAAGGCG
GCAGCAAGGCAGAGCGGGCTTCGGGGCCCTGGAGAGAGGAATGGGGCGCC
CAGGAAGCAAGTGTCTGCGGCCAGCAAGCAGAACACCATGTTGAGCAGGG
CGGCGTGGCGGAAATAGGAGATCTTGTTCCGCACCACGACTCTCCACACC
AGCCAGTACACACCCAGGCACACAAGCAGCGCCAGTATGGAAGCTCCCAA
GCCCACTTGAGTCAGCAGCGCCAGAGCGGGTTCTTCCGGAACAGTGTGTG
GGGACATGAGGACGGAGAAGGCAGTGAGGTGCTGGCAGAGGCACTGAGCA
GTGGGGCTGGCACTGGCCACCTGTGCCTGGCACCCTTCTTTGGACCAACC
CCCCCTGCCCTGGAAGAGACTGTGATCCCAGAAGACACAGTGAGGGGAAC
CATCTGTGTTCCCAAAGTCCATGATGACCTCTCCCTGGCTGAAGGCCCGG
TCACCTGCCATGATGGAAATGACAAGGACCAGGCCAGGAGTGGCATAGAG
GGAATCCCCCAGCCCTTGTCCATAGTTTGAGGGCAGAAGGTGGTCCAGTT
TTCGCAGCAC

381. chr2_C2orf28_NM_080592_2.22346
GGACCGGGCCGCTTAGGCCACGCCCGGGGAAGAGGGCCTGACGCGCTGCG
GGGCGGGGCCGCGGGGCCGGGTCGCGCGAGCAGCGGAGCACCAAGGGAAC
GGAAA

382. chr2_CAD_NM_004341_-1.52671
GCCCTCACCGATCCCTCCTACAAGGCACAGATCTTAGTGCTCACCTATCC
TCTGATCGGCAACTATGGCATCCCCCCAGATGAAATGGATGAGTTCGGTC
TCTGCA

383. chr2_ZNF513_NM_144631_-1.5257
GTGCCGCAGCATGTGACGTTTGAGGTTCATGCTCTGGTTGCAGCTGTAGT
TGCAAAGGCTACACCGAAAAGGTTTGTCACCAGAGTGGATGCGACCATGA
CGCTTGAGGTTGGCCAGATTGCCACAGGCATAAGGGCAGAGGGGGCACTT
GTAGGGCTTCTCTCCTGTATGGACGCGCTGGTGCCGTTTCAGGTTATCCA
GATGAGCAGAGGC

384. chr2_NRBP1_NM_013392_-1.58349
GAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTG
CCAGGAACAGTACCCTCAACTCAGCCGCTGTCACCGTCTCCTCTTA

385. chr2_KRTCAP3_NM_001168364_1.52402
TCTGCAGGGGAGGCTGCTCTATCTGGTTACTGCTGTGTGGCTGCACTCAC
TCTACGTGGAGTTGGGCCCTGCAGGAAGGACGGACTTCAG

386. chr2_SUPT7L_NM_014860_-1.62988
GGCAATAAGGTTGCGAAGACGTCGGTTGTGCTGAATCAACTGAATCGTAT
GGATGGTGAGACTACATGGCTCTGAGGGGATGTCCAGCATAGTGGGGGGC
TTCGGCTTGTTGGCTGAGGGTTGGTGCAGGGGTGGGTCATGGACTTCCAC
CAGACGGAACTCCCGTGGGAGCAAATCGAAGGAACTTC

387. chr2_PLB1_NM_153021_-1.76753

Figure 3-33

CGGCGGAGATGAGAACATCGGCACCGTTACCACCCTGGCGA

388. chr2_LCLAT1_NM_182551_2.21577
GAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAATGGA

389. chr2_GALNT14_NM_024572_-1.96877
GTGCAGGGCGACCCGAAACGTGGCAGGGAAGGACCGAGGGCAGCCAAGCT
GGACGCCCGCTCCAGCGGGAGAAGCGCGGTGG

390. chr2_SPAST_NM_014946_1.67641
CAAACGGGTATATGTGTCTTTACC

391. chr2_MYADML_NR_003143_1.5164
GGAGGTGCACAGCACACCTTCCTCCACTGGGAGAAAGGGGGCCCAATTCC
CACTCCCCCAAACACACACAAGTACACACTGACTAAGGCACAGCTAGGGC
GGGGGCGGGCAGAAGGCCCCTTGGGAGGACGTGGCGCCACAGCTGCAATG
GGTGTGGGGGTGTGGAGCTCATCACCGCTGGAGGTGCTTGGGGGCAGGAG
AAGAAAAGCCTCAGGGCTCCCCAGGAAATAGGAGAAGATGGTCGGGAAAT
AGGCAGATAAGAAAACCAACAGGAAACCTAGAAAAGAATTGAGAGGAAAG
AAACAAAAGAGAGAGTGGAAAAAGAGAAACGGGTGAAAACAGGTTGTGGG
CAACAGAACAAAACAAGAAGGAAACAGCAGAGGAAAGGGAAGAACATACA
TCAGAGAACTGGGAAAGTGCGATGAATT

392. chr2_MYADML_NR_003143_1.52451
ATTAAGTCACACGCCTGGAAAAGGCTGGGAACAGCGAGAGACAATGTCAG
TGTCCACTGGGTCTGGGCTTCTCCCTCCCAGGACCCGCCACCCCGTGGAA
CAGGAACATAGCACCGAGCAGGGA

393. chr2_C2orf56_NM_144736_-1.59119
GTTTTGCGACCACAAGCTTCATGATGTCTTAATTGCCCCAGGAACAGCA

394. chr2_SOS1_NM_005633_-1.53662
AATGGGCATTCTCCAACAGTGGTGGTCCATCTCTGTGCATGGATGGGTGT
GTGTGCTCCCTTTTGTAAGTTTTTGGAGGGAGTTTAGGGATATGTTGAGA
AGTGCTTTGTCGTGGAGGAACAGGCGGCCCAGCAATGGAATGAAGGTCCA
CTTCTTGTGTCAATGG

395. chr2_KCNG3_NM_133329_-1.90165
GCTCGAGTATCTCCGGCGCTGCTAGTAGCGCGCCCTCCGCCCGGCGGTAC
CTGCGGGTGGCCGGGGAGTCCTCGCCGGCGCCAGCGCTGAGCCCCACCGG
CTGGGAACGCGGCTGTGTCCGCGCCGCCGACCCTCGCGCCCGAGGGCTGC
GCACACCGAGGCCGCGGTGCCCTCTCCCAAGCCGCGGGGCCGACCCCCTG
AGGGCTGCGGGCGCCGAATGGAGCCGCCGGGGCGGAATAGCTCCCCGTCT
CCGGCGCTCCCTGCGGCCGCGAATCCGGCGGCCGCCCCGCCGCCGTCCAG
AGGCGAGAGGCAAAGTGAGCGGGTTCGGAGGCGGC

396. chr2_OXER1_NM_148962_-1.74045
TTCAGGTAGCGGTTGAGTGCGATGGCTGTGAGGAAGACAACGCTGGCCGT
GCGGTTGGTGGACAGCAT

397. chr2_ZFP36L2_NM_006887_-1.54393
CGCCCCCGGTGCCGTACAGCAGAGCGG

398. chr2_EPAS1_NM_001430_-1.53409
ATTGGTTACCACCCTGAGGAGCTGCTTGGCCGCTCAGCCTATGAATTCTA

Figure 3-34

CCATGCGCTAGACTCCGAGAACATGACCAAGAGTCA

399. chr2_KCNK12_NM_022055_1.6987
TCGTTGAGGTGCGAACGGCGGCAGCAG

400. chr2_MSH6_NM_000179_1.62899
TGTCGCGACAGAGCACCCTGTACAGCTTCTTCCCCAAGTCTCCGGCGCTG
AGTGATGCCAACAAGGCCTCGGCCAGGGCCTCACGCGAAGGCGGCCGTGC
CGCCGCTGCCCCCGGGGCCTCTCCTTCCCCAGGCGGGGATGCGGCCTGGA
GCGAGGCTGGGCCTGGGCCCAGGCCCTTGGCGCGCTCCGCGTCACCGCCC
AAGGCGAAGAACCTCAACGG

401. chr2_RTN4_NM_207521_1.58875
TCCACGCACCACACCACTGGAGGCGCTCTCCCTTCACTGCGGTTGGGTCA
ATGTGGACGTTTTCCACTCGGCCAGCTCC

402. chr2_SMEK2_NM_001122964_-1.52853
CCACGTAAGTGGAGGAGACGTGCCCGGTGCCTCGGTCGTCCCATTGCCGG
TCTTCGTTCAGGGTATAGACCTTCACTCGCCGCC

403. chr2_KIAA1841_NM_032506_-1.67706
CTGCCCGGCGCCTTTGTCCGCTCTGCGCCCCTGGAGTTTCTGTGCCTCCA
CGGGCGGGAGCGGGGCGCGAAGGTCTGGGGGTGCCCCGAGGACGCGCCGC
GTAGTGAGCCTCC

404. chr2_USP34_NM_014709_3.03899
TTCAGGTCCTTTTGTTCCCATGTA

405. chr2_OTX1_NM_014562_-1.76038
TGATGTCTTACCTCAAACAACCCCCATACGGCATGAACGGGCTGGGCCTG

406. chr2_C2orf86_NM_001042692_-1.60558
GTTCTCTGCCGTCTTCTCTCAGTTC

407. chr2_ARHGAP25_NM_001007231_-1.52759
CTGAACTGTGCTGTTAACAAGATGAGTGTGGACAACCTGGCTACTGTGAT
TGGTGTGAATCTCATCAGGTCGAAGGTCGAAGACCCTGCCGTGATCATGA
GAG

408. chr2_ANTXR1_NM_032208_2.49
AGGGTCAAGAACAACCAGCCAGCC

409. chr2_GMCL1_NM_178439_-1.56413
GCGCGGCGCGACCGGACGCTGCGGGCGGGGAAGAGGATGGAGACTGTGGC
GTCCGCTGCAACGGTTGGGGCTGCGCGT

410. chr2_ADD2_NM_017482_-1.68719
GCAAACACGTTTCCCCGCCAGTCAGGGGCAGCCT

411. chr2_ADD2_NM_001617_2.06957
CCCAGCCGACTCTTCTGCATAGGCCCAAAGGTGCTCCCGGCCCACTGCAC
GGAGCCCACCTCATGGGGCCGGTGCTTCTCCTGCTCCAGGAGGATGAGGT
TCTCCACTCCCCC

412. chr2_CD207_NM_015717_1.57065

Figure 3-35

ATGCACAAGACACAGGAAGATAGGAAATGCAGAAGGAGGAGGAGGTGCCG
GAGAGGTGAGGACAGGGGCTGGATGGACGCTGGGTGGAAGGCAGGGCTC

413. chr2_VAX2_NM_012476_-2.21429
CTCCTCAGCCTCCGAGGCCTTTGCCACCTCCAACATTCTGCGGCTGCTGG
AGCAGGGCCGGCTGCTCTCTGTGCCCAGGGCCCCTAGCCTCCTGGCGCTG
ACCCCTAGCCTGCCAGGC

414. chr2_ANKRD53_NM_001115116_1.58629
CCAGCAAGGAGTCCGACCAGACGGCAATCGACCAGACGGCGATCGGGAGC
TACTACCAGCTGTTCGCAGCGGCTGTGGGCAACGTGGAATGGCTGCGATT
CTGTC

415. chr2_MPHOSPH10_NM_005791_-1.6796
GCAGGTCTGGCGTCGACGGACCCTGGAGCGGTGTCTGACGGAAGTCGGCA
AAGCCACGGGTCGGCCCGAGTGC

416. chr2_RAB11FIP5_NM_015470_1.54358
CTGAGTCGGGTCCTTGGCTTCTCTCAAGCCAAACCAGCTACTCTTGGCCT
TTTCCTCCCCACTGGATGAGTGATGTGGGGAGGCCCCCAGGATGGGACCC
CCCTTTTCCCCCAGAGAGCTTCGGCGACCCAACTCGCT

417. chr2_ALMS1P_NR_003683_1.51336
AAACAGTGGCCGAAGGCTTGTTATGTGCTGTGCCTGGACTTGGCATGAAG
GCACCAGATGTCAGAAGCGAGGCTGCTGCCCA

418. chr2_INO80B_NM_031288_-1.82249
TCTGCTCCAGAAGGCGCGGAGTCAACCTTCCCCTATGCTGCCGCTGCCTG
TAGCTGAGGGCTGCCCACCTCCCGCCCTCACAGAGGAGATGCTGCTGAAG
CGCGAGGAGCGGGCGCGGAAGCGGCGGCTCCAGGCGGCGCGGCGGGCAGA
AGAGCACAAGAACCAGACTATCGAGCGCCTCACCAAGACTGCGG

419. chr2_MOGS_NM_006302_-1.90447
GTGGACTGCTCGTTGTACTAGGAATTCTGGAGGCACCCGGGCTCGGGCCT
CATCCCCCAGTATCTGCTCCCTCCCAATCCAGCCATCAGCATTTAGCAGC
CCCAGCCAGTGGCCAAGGGCTTCCCGGGTGAGGGAGGGATCCCACCGCTG
AACCACCAGCTGGTGAAAGCCTTCATCCCAAAGGAAGCCTCGTGGGAAGA
ATGACCGGGAGGGCACTGCTGTAAAAAGAGGTACGGGTGGAAAGAGGGCT
GGGTCCACCTTCTGCTCAGACCCTTCCACCCCGATGTCTGGCAATACCAG
CCCTTGTCCGTAGAAGTAGCCAATTCCACCAAGGAGGCCGCTGAGGGCAG
CCTGACCCAAAACCTGCTCGCCAGAGCTCAGGCCCTTCTCCTTCAGCTGG
AAGGTCTTCTCAAAGCGCTCTCTAAAGCCTTCAGCATGGCTCTCCAGGGC
CTGGGTCAGTAGACTGCCTGCCAGTCTTGGCAGGGCTTGATTTCCTCCTG
CCTGGGCACTGCCTGATTCAAACACAAACTCTATGGAAATGGGAATTTTC
AGGGTCACCTGC

420. chr2_AUP1_NM_181575_-1.71301
CCACCCATCCAGCCTGTTGTGAGTTGGGTGAGGGCTGCCCCCAGTCTCCG
TCCTGCGGCTCTGG

421. chr2_LRRTM1_ENST00000433224_-1.98827
CAGAGAGCGGGCTCACTCATGCTTTGCGGGCGGC

422. chr2_FUNDC2P2_NR_003663_-1.70221
CGACAGCGCGCCACTCCGCAGCGTAACCTCGCAGATCCCCTGCGTGTG

Figure 3-36

423. chr2_TMSB10_NM_021103_1.52673
AGAGCCACCTGCAAGATGGACACGAGCCACAAGCT

424. chr2_KCMF1_NM_020122_1.52353
TTTATACTATGGTGGGGAAGCTTTCTCTGTAGAGCAGCCACAGTCTTTTA
CTTGTCCCTATTGTGGAAAAATGGGCTATACGGAGACATCTCTTCAAGAA
CATG

425. chr2_TGOLN2_NM_006464_1.617
GGATAGCGCTTCCGCCCTCTAATGCTCTCGCGAGATCCGCGCGCGGGGCC
CCTCTCCAGTCCCGCCCCTGCTGCGCGCGTCTCTCAGTCTCCCGCTGCCG
CCAAGACGAAGGGCGGGATTTAGGGGGCAGCTGCTGATGTCGGCGCTCGC
CTTCGGCT

426. chr2_SH2D6_NM_198482_1.592
AGCCTTGGTACTCGGGGAACTGTGACCGCTATGCTGTTGAGAGTGCCCTG
CTCCACTTACAAAAG

427. chr2_USP39_NM_006590_1.91377
TGTCCGGCCGGTCTAAGCGGGAGTCTCGCGGTTCCACTCGCGGGAAGCGA
GAGTCTGAGTCGCGGGGCAGCTCCGGTCGCGTCAAGCGGGAGC

428. chr2_SMYD1_NM_198274_1.60075
TGCGGGCAGGGCTGACCAACTGGCATGCTGGTAACATTGAG

429. chr2_---_---_1.6146
TAATTGTAATCTTGTAGACAGTAA

430. chr2_---_---_1.6036
GCATATCTTTACTCTGACACTGTCA

431. chr2_ARID5A_NM_212481_-1.5755
GTCCTTTGTGGGTGCCAGCGGCTGTCCT

432. chr2_ANKRD23_NM_144994_-1.66486
GGGTGCGGGGATGCGCCACGTGGGCCTGCAGGGCCTCCCGGATGCCGCGC
TGCCAGTCTCGAGCCAGCTGCACCGGG

433. chr2_FAM178B_NM_001122646_-1.60765
ATGTCCTGGCAGCTAACAACTACCCCGGCCAGCAT

434. chr2_ACTR1B_NM_005735_1.60033
GAGAGCACGATGTTGGCGAACAGCGTCCGGCGCAGGTCCATGTCGGACTT
GTGTATGGCGAAGGCCACCACCTCATGGAGCCCCTCACTCTCATCCCCGA
CAAGGTCCGGCTGGAACAGCAGC

435. chr2_AFF3_NM_002285_1.85297
TATTGTGTCCAGAGGATACAAGCT

436. chr2_LONRF2_NM_198461_-1.99517
CAGAGGGCACACTCAAAGTCAGTTAC

437. chr2_CHST10_NM_004854_-1.61588
TCGAAACGGGCATACAGGCGTCGGATGTCTCGTTTGCTGATGCCCAGGAA

Figure 3-37

ATAGTGCTCCACCTTGGTTCTGTTATACACGGTAATGCCCGGAGGGATAG
TCGGGTATGACACCAGGTGGTCAATGCCAGCCTCTTTTAAGATGTATGGG
GCATCGTCCTCCAGGGTCTCGTGGTGTCCAATCA

438. chr2_NPAS2_NM_002518_1.87962
ATCGTCCTGCGACCTCACACAGCAGCTCCTGCCTCAGACCGTTCTGCAGA
GCACGCCCGCTCCCA

439. chr2_TBC1D8_NM_001102426_-1.6895
TCGGCTCCTGCAGATCGGGGTCGAGGTCAAAGACCTCATTATCCAGCAGC
CTTCGCAGCGTCACGTCGGCCAGCTG

440. chr2_RNF149_NM_173647_-1.96842
TAGGAGATGGGTCCTCCATGCCGAGAGTCACTCCTGCCGGCTT

441. chr2_IL18RAP_NM_003853_1.71848
GTAGCCTGTTGTGTCAAGATGATTTTAGAAGTTAAGCCCCAGACAAATGC
ATCCTGTGAGTATTCCGCATCACATAAGCAAGACCTACTTCTTGGGAGCA
CTGGCTCTATTTCTTGCCCCAGTCTCAGCTGCCAAAGTGATGCACAAAGT
CCAGCGGTAACC

442. chr2_SLC9A2_NM_003048_-1.65419
TCTGGAGGGCATCGGAACCTGGAAGCCGGAAAGCCCGATTTGGGAGTGAG
AAGC

443. chr2_MRPS9_NM_182640_1.5573
GACTACTTACTACTGATCCACGTGTGAGGGAACGGAAGAAGCCAGGCCAA
GAGGGAGCCCGCAGAAAGTTTACGTGGA

444. chr2_UXS1_ENST00000409032_-1.55502
TCAAAGCTCAATCCAGACGTCAGTCTGTATGGGAAACCTTCTCACCATCC
TTGGTCAGAAATAATCCCTTGCCTGCACCACTAGTCCACAACAGCTCAGC
GCTGCCTTGTCCAGAGATTCACACATGC

445. chr2_FBLN7_NM_153214_1.57907
GAGGGCAGCGTGGCCGGCGACTCCGCCTTCAGCCGCGCGCCGCGCTGTGC
GCAGGTGGAGCGGGCTCAGCACTGCAGCTGCGAGGCCGGATTCCACCTGA
GCGGCGCCGCCGGCGACAGCGT

446. chr2_FBLN7_NM_153214_-1.79473
ATCACGCTCTTCCGCATGGCCACAGCCTCTGCCCCCGGCCGAGCTGGGCC
CAACAGCCTGCGGTTTGGGATCGTGGGTGGGAACAGCCGCGGCCACTTTG
TGATGCAGCGTTCAGACCGGCAGACTGGGGATCTGATC

447. chr2_IL1F7_NM_014439_-1.9666
CTCCCCACCATGAATTTTGTTCACA

448. chr2_IL1F10_NM_032556_-2.41794
TCCCTCCCCATGGCAAGATACTACAT

449. chr2_SLC35F5_NM_025181_1.5382
GACTCTCACACTGTTCGCTGTCTTC

450. chr2_SCTR_NM_002980_-1.65381
ATTTCTGCTGGTGAGCATCCGGAGGAATCTCGGGCATTCCACCTCCACCA

Figure 3-38

TCCGGCCCGGCACAGAAGAGGGC

451. chr2_TMEM177_NM_001105198_1.57991
GGACACTTCCAGCTTGTGCAGACACCACCCTGCCATTGAGTCTGGAGGGC
CCTGTTGGAGCCTTTGGACCTATAGCTCACGGCCAGAAAAATCACTGGCT
TTGGAATTAAATAGCTTAGATTGTACTATAACCACTACTTATGAACTCAG
GGACTATGAGGGACTATTCAGGGGCTATGAATCTGAGCCTTTGTTTCTTG
AACTGTAAAGTGGAGATGATGTAAACCGCCTTGCA

452. chr2_EPB41L5_NM_020909_1.77174
CTCTGCCTGTGAGTCCTTCCATTTCCTC

453. chr2_LOC84931_NR_027181_1.51039
CAGCTAAGGAAAGACCGGAATCGTCCGAGCCCTTTG

454. chr2_TFCP2L1_NM_014553_1.63259
AATGTCTCTGAGAAAGGCCGTGCACATACATTGTGGCATCTACCATGCCA
ATGCGCCAGTGCAGAGACAGGA

455. chr2_CYP27C1_NM_001001665_1.58405
AAATGCACAGGATACTGCCAGTCATTAAATATTGAGTCTAGCACAATGTA
TGAAGCATAAAAATTCACTGCCACTGGTTTTTAAACAGCTGTTTCCCCCA
AAGAAAGGGCAACTTCTGGTATGCACCAGTAAAATAGCAACCTTTTTACA
TTACTTTGCATAAAGATTTACAAGTGTCCCAGGACCTGGGAGGCCAGTCT
ATAACAAGACAGCCTTTAGCGACATCGCTTTCCTTCTCCACGGTGATCAG
CGAACACAAATACCCACTGTGTGTCGGCGAGCTGGTCTGCTACATCAG

456. chr2_AMMECR1L_NM_031445_-1.56105
AGTAATAGAAGTAACTGGACCAGGAAGAGGAGGCATCTGCTCCAATGATG
TCATAGCCATTGGTGGCCACGGGGGGGGTGGGACTGGTCATGCAGCCGTGT
G

457. chr2_LOC401010_NR_002826_1.5068
CTCTTAAGCAGCATACGGCACTGCTT

458. chr2_MGAT5_NM_002410_-1.59222
AGAATTCCGGTGGATGAGACTACGGATCCGGCGAATGGCTGACGCATGGA
TCCAAGCAATCAAGTCCCTGGCAGAA

459. chr2_TMEM163_NM_030923_1.88745
CGTCGCTGAACTGGCCGCTCTCGCT

460. chr2_ZRANB3_ENST00000412849_1.51692
TTTGGGGTCGTGGCTGCCTATCTGGAGTGCT

461. chr2_---_---_-1.53311
CAGTCAGGAAACGAAGCAAGGCTTGGGCTGAGTGAATTTTCTATTCTACA
GGGTATCCAAAGAGGTCCTTTGTTGGCATTTAACAGGCCGGTGGACTTGG
TCTGGAGCATCCCGGATTGCTTCTCGCACCTGTCTGG

462. chr2_LCT_NM_002299_1.53419
GTGCCCATGACAGAAATACCTTATAATGGGTGATCTGACTGGCATGGA

463. chr2_LRP1B_NM_018557_1.53043
CTGTCTCCGGTGTATTCCGGCTGGCAGTGGCAGTAAGGCTGGTTTCCAGC

Figure 3-39

AGTCACAATGCAGGTTCCTCCATTTTGACAAAAATCCTCACAGACTGTCT
TACCACAGTTTGGCCCAGT

464. chr2_LRP1B_NM_018557_1.65117
GTGGTCGCCCGGTAAGGAAGCCTGCGCTGGAGACTGCTC

465. chr2_LRP1B_NM_018557_-1.83068
TTGGAGCCTGGAATCGAGCGGCGTCATTTACAAATGT

466. chr2_ZEB2_NM_014795_-1.65297
GAGTCAGAGTACCCCTGAGGGGTAATGCTCTGCAAGTAAGCCCGGTTCAT
CAGCAGCTCGGTGGGTTCCAAGTGCCCTTTCTCGCGCGCCTCGCGCTCCG
CCGCTTCCCGCTCCTCCGCCTCCCGCTTGCAGTAGGAATACCTGTGATTC
ATGTGCTGCGAGTACGAGCCCGAGTGTGAGAAGCGCTTGCCACATTTATC
ACACTGATAGGGCTTCTCGCCCGAGTGAAGCCTTGAGTGCTCGATAAGGT
GGTGCTT

467. chr2_ZEB2_NM_014795_-1.67899
CTGGCGTGCCAAGGCGAGACAGCTCCTCAGGGGCTTCTGGGTAAATAATG
GCTGTGTCACTGCGCTGAAGGTACTCCTCGATGCTGACTGCATGACCATC
GCGTTCCTCCAGTTTTCT

468. chr2_KIF5C_NM_004522_-1.58491
CCCGGTTTGAACATCGTTCTTTCAGAAGTGCTGAAAATGCTGCAAAGTTG
GATAAGTGGAAATGTGGCTGCCCCTCTCCTCACTACTTCCTCTCTGATCG
TTCTGAAGCTTGCATTGGGAATGGCTGCTTTCTCTAACCATTTTCAGCTT
GAGTGGGTATTGCTGAAGAAATCCAACATCATTCCAGCAGTTGAAAAAGG
AAGCCTTCGGGAGAAAGTGCTTGTCAAAATTTTGTTCTTTGTGCTTGTGT
ATGAGTAAGTTGCCATGAATAAGTTATTATTTTAACCCATAATTGGCGAC
TGTTTATATGAATTCTTTCTTTGGCACCAAATAGGTTTCATCTTCTTAGG
CACAATTAGAAAAAATCCACATAGATGGATATTTTACATTTAGTTATTGC
TTTATCCAAATACATGAATCTAAAGCTGAATCAACCCTTACTTCCAGTTG
TGCTTATTAAGAAGATCAATTTCCAAGTAGTAAAGTTTTCAGGGAAACTG
ACTGTGCTGCTATTTGTTTTGACAAATTTGGGGGTAAGTCAATGACAACC
AAACCAATCTCGGTGGAAACTCCTATCCTATCATGTTGTGTGCCCAAGAT
GAGTGAGCTGGCACTGTGCCCTGAAGCTTTCACCACTGTAATGAAATATA
TGCCAGGGGAGACTTTGGGCTTTTCTCATGACTGTGTGGGTCGAAGGTAG
CTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TATGTGTGTAAAGTGCTAAGAACTGTGCATTGACATCCAAACATTTCTTG
TACAAAATTTCCCTAGCAAAGCAAACCTGCTTTGACTTAATTTATTTGTT
AAATGTTGCACTTTGTTTATGTATGTTTTGTTTTTGGTGGGGAATAAGGA
GAGAGAGGACGACAAATTCTATTGAAGTATTTATTTTGTGAAGATGGCAA
TTTTGCATTTGTTTAAATTTTTTTCATTCTTTAATTTTGTTATCAGTGCC
AGCCCAATATACCTGCTCTACCATTATTTGCGGTCTGATAAAAGGGTCCT
TG

469. chr2_NEB_NM_001164507_1.51098
GGCTGCCTTGATAGGAATGGCATCTACCCGCATGTCATAACCTTTCCTCT
TGGCTTCTTCTAGGCCAAGCTTATA

470. chr2_CACNB4_NM_001005747_1.6418
CGTAACCTTTCAGTGACGGCCCCACTAACACCACCGGACGCATTGACGGT
ACAACATCGTAAGGAGGAATGTGCTCCG

471. chr2_TBR1_NM_006593_-1.52652

Figure 3-40

GGGTCTATATGCATCCGGATTCCCCCAACACTGGGGCTCACTGGATGCGC
CAAGAAATCTCTTTTGGAAAATTAAAACTTACGAACAACAAAGGAGCTTC
AAATAACAATGGGCA

472. chr2_TBR1_NM_006593_-1.5473
TGCCGCACACCAACGGGCTGCTGTCGCCGC

473. chr2_GRB14_NM_004490_1.6184
TGGGCGGCCAGCGGCGAATCCCGGGCAGCC

474. chr2_ABCB11_NM_003742_1.55701
AGTGGTGACTAGTTTGTAGTAGGCTCCTTTTTGGGCCATCAGTTCTTCAT
GGGTCCCCTTTTCAATCA

475. chr2_LRP2_NM_004525_-1.53571
CATCAGAGGCATCAAAACAATCTGTTTCTTGATCACAATACCAATGTTGA
GGAATACAGCGCCCAGATGCGCATTGGAACTCACTGCT

476. chr2_METTL8_ENST00000375258_-1.84193
AGAACCTCCCAGGGCGAAGGTCGGGGCCGAGAAGCTTGTGAGTACCGGGG
CAGTGAGGGAGGGATCCCTAAGTGCAGGGCGCACACACGGGGCGGAGACC
TGGAGGCGGCAGCACCGCGCCCCCAGGGCTCTGCCCAGCTAGCCACTCGC
AGCACAGAGA

477. chr2_SLC25A12_NM_003705_-1.5299
CTGTAGAGTCCAAAGAAGCCCTCATAACGCAAGACTTTCTTAAAACAGTC
AAAGCTGTTTTTGTACATTAGCTCCCCAACAACAGAGCCAGAGCCACGCT
GGTTTTGCATTCGGGTCTTCACCAGATCTATAGGAT

478. chr2_DLX2_NM_004405_-1.62083
GACCGGGAGGTCAATAACTGCAGCGTCCGAGCTGAGCCCAGGGGAGCGGG
CGAGGAGAAAGAAGCCTCAGAGCGCCCGGGAAGCCTCGCGCGCCTGGGAG
GCTTCCATCTCCCGGGACC

479. chr2_ITGAV_NM_002210_-1.53465
TCTTCTCGTGGGAGCTCCCAAAGCAAACACCACCCAGCCTGGGATTGTGG
AAGGAGGGCAGGTCCTCAAATGTGACTGGTCTTCTACCCGCCGGTGCCAG
CCAATTGAATTT

480. chr2_COL3A1_NM_000090_-2.01573
CTACTCGCCCTCCTAATGGTCAAGGACCTCAAGGCC

481. chr2_COL3A1_NM_000090_1.84352
AAAGGTCCAGCTGGGATACCTGGAT

482. chr2_COL3A1_NM_000090_2.43773
CTTCCCTGGTGCTCGTGGTCTTCC

483. chr2_COL5A2_NM_000393_1.81995
GCTGTCCTTGTAAACCCTGTGGTCC

484. chr2_NAB1_NM_005966_1.58143
GGAGGAACATTTAAGCTGATGGAAGTGGAAGTGGAAGTTGCTGTACATTG
GCAGCAAGGCCTCCGAGTTAGCTTTTGAATGCAGTTAACTGGTTTCTCTT

Figure 3-41

AACTGTGGAATTCATTGAAAAGTCAGACTCCGAGTGGTCGTTCCAGGATA
TCTT

485. chr2_STAT1_NM_007315_1.55122
TCATTCGTTCTGGTGCCAGCATTTT

486. chr2_MARS2_NM_138395_1.5302
TTTTCTACGTGAACGCGGCGCCGCACATCGGGCACCTGTACTCGGCACTA
CTGGCGGACGCCCTATGCCGCCACCGTCGCCTCCGAGGTCCCAGCACGGC
CGCCACGCGATTCTCCACTGGTACCGACGAGCACGGGCTGAAGATTCAGC
AGGCAGCAGCTACCGCGGGCCTGGCCCCGACCGAGCTGTGCGACCGAGTC
TCTGAGCAGTTCCAGCAGCTTTTCCAGGAGGCCGGTATCTCCTGCACAGA
TTTCATCCGCACCACGGAGGCCCGGCACCGGGTGGCTGTGCAGCACTTCT
GGGGGGTGCTTAAGTCCCGCGGTCTGCTCTACAAGGGCGTCTATGAAGGT
TGGTATTGCGCTTCCGACGAGTGCTTCCTGCCTGAGGCCAAGGTCACCCA
GCAGCCGGGCCCATCGGGGGATTCGTTTCCTGTATCTCTCGAGAGCGGGC
ATCCAGTCTCCTGGACCAAGGAAGAAAACTACATTTTCAGGCTTTCCCAG
TTCCGGAAGCCACTCCAGCGGTGGCTGCGGGGCAACCCTCAGGCGATCAC
CCCCGAACCATTTCATCACGTAGTTCTTCAGTGGCTGGACGAGGAGCTGC
CCGACCTGTCCGTGTCTCGCAGAAGTAGCCACTTGCACTGGGGCATTCCG
GTGCCCGGGGATGATTCGCAGACCATCTATGTATGGCTGGATGCCCTGGT
CAACTACCTCACTGTAATTGGCTACCCAAATGCTGAGTTCAAATCTTGGT
GGCCGGCCACCTCTCATATCATAG

487. chr2_ALS2CR11_NM_001168221_-1.65998
CTGGAGGTGGTGCAAGATTCATAAACAT

488. chr2_ALS2_NM_020919_1.57709
AACTGCTCCTCAGGTGTAGTTATCT

489. chr2_BMPR2_NM_001204_1.61342
CCTAGTGAAAAATGATGGAACCTGTGTTATTAGTGACTTTGGACTGTCCA
TGAGGCTGACTGGAAATAGACTGGTGCGCCCAGGGGAGGAAGATAATGCA
GCCATA

490. chr2_PARD3B_NM_205863_2.30173
ACCTGTTCGGCCCGGCCCGGCGTG

491. chr2_PARD3B_NM_205863_1.61202
GATGTCACCGGACGAACCCAGGAAGAGCTTGTGGCCATGCTCAGGAGCAC
CAAGCAGGGGGAGACAGCATCGCTGGTCATTGCCCGCCAAGAAG

492. chr2_INO80D_NM_017759_-1.53597
CACTGTAGGGAGACGGCACATGCTCACTATCATAATGGCTTCCATGGGGT
GAGGAGTGTGAGTGATCACTGCTGTATTGCTGTCGTGAGGTGATTAGGTC
ATCTGCCTTGCTCAGCAGCTGGGCAGGATGTGGCCTCTGGGAGGCATGGC
TGCCGTCATGAAGTCCATGAAACTGTCCTGGGAAGGCTCTCTCCCCAAGT
GCACTCTGGCTGATCAGAGTGGCAGAAGTAAGGCCAACGTTGGCTGGGGC
AGAGAACTGCCCCTGGATCTGCCCTGCCAGGGGTGTAGGTGGGTTTGACA
AGGTAGCAGAACGGAGCAGGTTCTCATCCAGCTCTAGACTAGAAAAATTA
TCATGTACTATACGCCCATTCAATAGCTCCCCTAGGTCTGTGTTCACCTC
TCGGCTCAAGGATTGTATTCCTGAAGCTCCAGTACCTGTGGAGAACACCC
CTATTCCTCTATCTGACAACTCCTGGACTGGCACACCATCTGACTGGGCA
AGGACCCCAATGGTACTCAGGCACTCGAGAGAAGTTACAGCCTGCA

Figure 3-42

493. chr2_KLF7_NM_003709_2.07352
AGGCAGACATCCAGTGGCCCTTTTGTT

494. chr2_FZD5_NM_003468_1.59884
TGAGCATGAGCACCCAGTACTCGGGCTTGGCGCGCGGCTGGCCGGTGTCG
TGGCCCGGGCAGGCGCAGGTGAGCGCCGCCTCCCAGCTCTCGCGGTAGTG
CTGCTCGTACAGGTAGCAGGCCACCACAATGCTGGCGGGGACCGTGTAGA
GCAGCGTGAAGATGCCGATGCGGATCATGAGCTTCTCCAGCTTGTCCGTC
TTGGTGCCGCCCTGCTTGATGACGCTGCGGATGCGGAAGAGCGACACGAA
GCCCGCCAGCAGGAAGAGCGTGCCCACCAGCAGGTAGAGCACCAGCGGGC
CCAGCACGAAGCCGCGCAGCGAGTTCAGGTTCTGGTTGCCCACGTAGCAG
ATGCCGGCCACTGGGTCCCCGTCCACGGAGCTCAGCGCCAGTGCCGTGAT
GGACTTGACGCTGGGGATGAGCCACGCAGCCAGGTGGAAGTACTGCGCGT
AGCCCGCGATGGCCTCGTTGCCCCACTTCATGCCGGCGGCCAGGAACCAG
GTGAGCGACAGGATGACCCACCAGATGGAGCTGGCCATGCCGAAGAAGTA
GACCAGGAGGAAGACGATGGTGCACAGTGCAGGGCCCGTGGTCTCGTAGT
GGATGTGGTTGTGCTCGCGGCTGCAGGCCACGCTGGCATGGCCCACGACC
AGACGCACCAGGAAGCCCAGCGACACGCACAGGTAGCAGGCTGACAGGAA
GATGATGGGGCGCTCAGGATAGCGGAAGCGTTCCATGTCGATGAGGAAGG
TGGCCACTGTGGTGGACGTGGAGATGAAGCACAGCACCGACCACAGGCCT
ATCCAGAAGGTGGCGAACGTGCGCTCGTCGGCACTGAAGGACGGCTGGTA
GCAGGGTACCGCGCAGTTGGGCACCTGGCCCGTCCGCACCTTGTTGTAGA
GCGGGTGTGACTCCTTCAGAATGGGCACGAAGGGCTCGCGACACTTGCAC
ACGAACGGGCCCCCAGCGGGGCATTCGCCCCCCGAGGCCGGCGCCCCTGG
CGGGCCTGGAAGGGTGGGCTTGGCTGGGAAAGGCCTGGGGGGCGCCGTGG
TGGCCTCGCTGCGGTTGTAATCCATGCAGAGGACCTCGGCGTCGCGGCCC
AGCACCGGGAGGCGGTCGCAGCTCATGCGCTCGGGCCAGGCGAAGCCGTA
CTGGCGCATCAGCGGCGAGCAGCCGGCCTTGGCGCGCTCGCACACCGAGC
GGCAGGGCGGCAGCGGCTTGTGGTAGTCGGGCAGACAGATGGGCGTGTAC
ATAGAGCATAGGAAGAAGCGCAGGTCCGGCGAGCATTGGATCTCC

495. chr2_FZD5_NM_003468_1.63305
CCACGGATCCCGCCGAGAAGAGCAGACAG

496. chr2_MAP2_NM_002374_-1.62057
AAACAGAAGTTCAGGCCCACTCTCCCTCCAGGAAATTCATTTTAAAACCT
GCTATCAAATATACTAGACCAACTCATCTCTCCTGTGTTAAGCGGAAAAC
CACA

497. chr2_SPAG16_NM_024532_1.67506
AGACATCCTAGTCTCCTGTGGCGAGGACCGACTCTGGAAGGTGTTGGGCC
TTCCAAAATGCAATGTGCTTCTCACGGGATTTG

498. chr2_FN1_NM_212482_1.72009
AGTGGAGGCGTCGATGACCACAGGGGAGCTCCGAGCATTGTCATTCAAGG
TGTACAGGTAGATCTTGTAGTCAGTGCCTGGTTGTAA

499. chr2_TMEM169_NM_001142310_-1.55341
GCCGCTACGTCACCTTAACTGGGACCATCACACGAGGGAAGAAAAAGGGT
CAGATGGTGGACATCCATGTCACATTGACAGAGAAAGAGCTGCAGGAACT
GACCAAACCTAAAGAGTCATCAAGGGAAACGACGCCTGAAGGAAGAATGG
CCTGCCAGATGGGAGCTGACCGTGGGCCCCATGTGGTCCTCTGGACGCTG
ATCTGCCTGCCTGTGGTTTTCATCCTTTCTTTTGTTGTCTCTTTCTACTA
CGGCACTATCACCTGGTACAACATCTTCCTCGTGTATAATGAGGAAAGGA
CCTTCTGGCACAAGATCTCGTATTGCCCTTGCCTCG

Figure 3-43

500. chr2_SMARCAL1_NM_014140_-1.50733
AGGACCTGTGCCAGCAGTTCCAACTGTCGGAGAGGCATGCTGTGGCCGTG
CTGTCCATCACCGCTGCCAATATGGGCCTCACCTT

501. chr2_RUFY4_NM_198483_-1.82726
TCAGACTTGGGCTCCGGAAGGCTGAG

502. chr2_ARPC2_NM_152862_-1.56657
GGCGGCTCGGCAGGCGGGTTCAGGCTTCGGGG

503. chr2_GPBAR1_NM_001077191_-1.62597
TCGAAGTCTATGGGCTCCTGCTGCCCGCCGTGGGTGCTGCTGCCTTCCTC
TCTGTCCGCGTGCTGGCCACTGCCCACCGCCAGCTGCAGGACATCTGCCG
GCTGGAGCGGGCAGTGTGCCGCGATGAGCCCTCCGCCCTGGCCCGGGCCC
TTACCTGGAGGCAGGCAAGGGCACAGGCTGGAGCCATGCTGCTCTTCGGG
CTGTGCTGGGGGCCCTACGTGGCCACACTGCTCCTCTCAGTCCTGGCCTA
TGAGCAGCGCCCGCCACTGGGGCCTGGGACACTGTTGTCCCTCCTCTCCC
TAGGAAGTGCCAGTGCAGCGGCAGTGCCCGTAGCCATGGGGCTGGGCGAT
CAGCGCTACACAGCC

504. chr2_GPBAR1_NM_001077191_-2.19928
TGACTCCTACCAGAGCATCCGTCCAGCTCAGCCATCCAGCCTGTCTCTAC
CGGGCCCCACTTCTCTGGATCAGAGACCCTGCCTCTGTTTGACCCCGCAC
TGACTGAATAAAGCTC

505. chr2_STK36_NM_015690_-1.80946
TTGGCAAATCAGCTAACTGAAGACAGCAGCCAGCTCAGGCCATCCCTCAT
CTCTGGCCTGCAGCATCCCATCCTGTGCCTGCACCTTCTCAAG

506. chr2_STK36_NM_015690_1.53168
GCAGCAGCCTGTCTATTGGGACAGCTTGGTCAGCAAGGGGTGACC

507. chr2_STK36_NM_015690_1.57742
CCATCGTCTCGTTTCTCTCAGTTGCCCTCCTGAGTGACCAGCCACTGTTG
ACCTCCGACCTTCTCTCTCTGCTGGCCCATACTGCCAGGGTCCTGTCTCC
CAGCCACTTGTCCTTTATCCAAGAGCTTCTGGCTGGCTCTGATGAATCCT
ATCGGCCCCTGCGCAGCCTCCTGGGCCACCCAGAGAATTCTGTGCGGGCA
CACACTTATAGGCTCCTGGGACACTTGCTCCAACACAGCATGGCCCTGCG
TGGGGCACTGCAGAGCCAGTCTGGACTGCTCAGCCTTCTGCTGCTTGGGC
TTGGAGACAAGGATCCTGTTGTGCGGTGCAGTGCCAGCTTTGCTGTGGGC
AATGCAGCCTACCAGGCTGGTCCTCTGGGACCTGCCCTGGCAGCTGCAGT
GCCCAGTATGACCCAGCTGCTTGGAGATCCTCAGGCTGGTATCCGGCGCA
ATGTTGCATCAGCTCTGGGCAACTTGGGACCTGAAGGTTTGGGAGAGGAG
CTGTTACAGTGCGAAGTACCCCAGCGGCTCCTAGAAATGGCATG

508. chr2_PRKAG3_NM_017431_2.68922
CTGCGCAGTGCGTGCTCCAGCCCG

509. chr2_WNT10A_NM_025216_1.52694
CAGCCGCTTCCACCGCGCCACGCTCATCCGGCCGCACAACCGCAACGGCG
GCCAGCTGGAGCCGGGCCCAGCGGGGGCACCCTCGCCGGCTCCGGGCGCT
CCCGGGCCGCGCCGACGGGCCAGCCCCGCCGACCTGGTCTACTTCGAAAA
G

Figure 3-44

510. chr2_FEV_NM_017521_-1.61447
CCCCCTGCTAAGTGCGGCAGGTGGAGTAAACTCTGGATTAGAGGACGGTT
GACGGAGGCTCCCGGGCCCTCCCCGGGATGCCGATGGGATCG

511. chr2_CRYBA2_NM_057093_-1.93468
TGGGTAGCGGATGAAGAACCCGGGGGCTGGACCCGGCCTAGCTCTGGACC
CGGCTGCCAGGGGCTCGCAGTCTTCCCGCGCTCCC

512. chr2_CCDC108_NM_194302_-1.50179
GCCAGGCGTGACCCCTAGCGGCATGTCGGAGAGGCT

513. chr2_ABCB6_NM_005689_-1.52597
TAGAATATAGGCACCAACACATTGAGTGCCCGTTCCAAACCCATGAGCCC
CAGGCAGATGAGCACCACCAGCTGCAGAGCTGGACTCCCTCGAGGCCACA
GGTAGCCACTCAGGAGG

514. chr2_DNAJB2_NM_006736_-1.52381
GCGGGAGGCACAGCACCGACGGCAGGGGCGGCCCAAGGCCCAGCACCAAG
ATCCAGGCTTGGGGGGGACCCAGGAGGGTGCGAGGGGTGAAGCAACCAAA
CGCAGTCCATCCCCAGAGGAG

515. chr2_PTPRN_NM_002846_-1.58955
TTTCCGAGCTCCGGGCGCTCGCTCCCGGGCCGGAGCCGCAGCGACGCTGG
CGGGAGCCTGC

516. chr2_DES_NM_001927_2.04907
TGTCAGACCTGACCCAGGCAGCCAACAAGAACAACGACGCCCTGCGCCAG
GCCAAGCAGGAGATGATGGAATACCGACACCAGATCCAGTCCTACACCTG
CGAGATTGACGCCCTGAAG

517. chr2_SPEG_NM_005876_-1.74118
AGTCCCAGCCAGAACCGCCGTTCTTCTGACACTGG

518. chr2_CHPF_NM_024536_1.87563
CTACGGCCAGCCCTGCCCAGCGAG

519. chr2_STK11IP_NM_052902_-2.34265
GGAACTCTGTCGCCCCTTGTTGGTGT

520. chr2_PAX3_NM_000438_-1.60935
CGGCCCTACAATTGCTCAGAGATGCCCAGTCTCATACATTTAATGGCAAC
AGAGTGAGAGCTTCCCCTGCCCCCTACAACAGAGCACAATTCACAGTTCT
AGAATCCCAGGGGCTGAAAGTGGTTAAGAAAGAAAGATTTACAAAACAGA
AAAACTAAGCAGAATAGAAATGTTTGTTTTGATTCCTAGTGTCCCTCTGG
TCTTTCAGTTCCATGTCGTTACTCAGGCGCAGAGACACCGCGCATGAAGG
GACCTTGAT

521. chr2_COL4A4_NM_000092_-2.72976
CTGGTGGACCAGGAAATCCCAGTC

522. chr2_COL4A3_NM_000091_1.50266
AAAAGGTCCACCTGGAACTGCAGGA

523. chr2_COL4A3_NM_000091_1.56054
AGCTGCCTGCAGCGATTTACCACAATGCCATTCTTATTCTGCAATGTCAA

Figure 3-45

TGATGTATGTAATTTTGCATCTCGAAATGATTATTCATACTGGCTGTCAA
CACCAGCTCTGATGCCAATGAACATGGCTCCCATTACTGGCAGAGCCCTT
GAGCCTTATATAA

524. chr2_SLC19A3_NM_025243_1.50783
GTTGCAATAGCTTCTACGGCCCCATTATAGATGGAAGAATCTTGGGATGG
CGCCTTGTAATCCCACAGGATTTGAACATAGTTCAAAACCTGGTTAAAAC
CTGCTGTGGCGAAAGCCCACCATAGAGACCAGTAG

525. chr2_PID1_NM_017933_-1.51033
TTTTGGCAGAGGAGACGCTGGCGAGACTGTCGATCGCGCCGGGGGGCGAG
GGGCTGGGGTCCCGCTTTACATCTGGGGTCGGTGTCCGCGGGATGTGCGT
CCTGG

526. chr2_DNER_NM_139072_1.67871
GGTGACAAGGGTTGCTGGCACAAGGATCT

527. chr2_TRIP12_NM_004238_-1.50011
GTGCCATAACTCATCATGCTTTTTTGCATTTCTAGGGGAAGTTTTCGTTG
GAGCTGTTTGGGCTCTTCCTCTTTTACCA

528. chr2_SP140_NM_007237_-1.51187
TAATAGCAAAGCCGACGGCCAGGTGGTCTCCAGTGAAAAGAAGGCGAACG
TGAATCTGAAAGACCTT

529. chr2_SP140L_NM_138402_1.77768
CCTTTACTTCCAGTGACCTGTGGT

530. chr2_ARMC9_NM_025139_1.80393
TCCACCATGTTACGAGCCTCCTTGGCACC

531. chr2_NGEF_NM_019850_1.7183
CCAGCTCCTTGTGAGCATCCAAAGCAGTGCACTCCCGCTCAGACCTCTCT
TCTAC

532. chr2_SAG_NM_000541_-1.83634
GAAGTCGCCACTGAGGTCCCATTCCGCCTCATGCACCCTCAGCCT

533. chr2_DGKD_NM_003648_-1.63673
ATGGCATACGAGGCCAAGCTCCCCCGGCAGGCCTCCTCCTCTACCGTCAC
CGAAGACTTCAGCGAG

534. chr2_DGKD_NM_003648_1.51529
ATCCGAGAAATAGCTCAGTCTCACCGGGACATGGAGCAGGAACTGGCCCA
CGCCGTCAATGC

535. chr2_ARL4C_NM_005737_1.97128
GGGCGGACAGCAGGACCGGCTCTTC

536. chr2_COL6A3_NM_004369_1.77433
AATGCCTTGTTCTCCTATCAGCCCTGGAGGACC

537. chr2_RAMP1_NM_005855_-1.53731
TGCATGGCCGCTACTTCAGGAGCTGCCCCATCTCAGGCAGGGCCGTGCGG
GACCCGCCCGGCAGCATCCTCTACCCCTTCATCGTGGTCCCCATCACGGT

Figure 3-46

GACCCTGCTGGTGACGGCACTGGTGGTCTGGCAGAGCAAGCGCACTGA

538. chr2_PER2_NM_022817_1.57273
GGAACACGCCCACATCGTGAGGCGCCAGGAACTCCACAAACTTGGCATCG
CTGAAGGCATCTCTTTTACAGTGAAATATGGATGCAACCTGGTCAGAGAT
GTACAGGATCTTCCCAGACACCAGG

539. chr2_TRAF3IP1_AF242456_-1.5399
TTGCTAAGGCCGCGCAGCCCTAGTGACCGAACGCCCTGCGGCGGCCGCGC
AGGCGCTGTGGTGGGCTCCGGTGCACTGTGGGATGGAAACCGGAGCGGCG
CGTCCT

540. chr2_TRAF3IP1_NM_015650_-1.5616
TTGAAAGAAGACCGCAAGCCAAGAGAAAAGGACAAGGACAAGGAGAAGGC
CAAGGAGAATGGCGGAAACAGACACAGAGAAGGGGAGAGAGAGAGAGCCA
AAGCCCGGGCCAGGCCAGACAACGAGCGACAGAAAGACAGAGGCAACAGG
GAGCGGGACAGAGACTCCGAGCGCAAGAAGGAGACAGAGAGAAAGAGTGA
GGGGGGGAAAGAGAAGGAGAGACTGAGAGACAGGGACCGAGAGCGCGACC
GGGACAAAGGGAAGGACAGGGACAGACGGAGAGTGAAAAACGGGGAGCAC
TCCTGGGA

541. chr2_ASB1_NM_001040445_1.50429
GGTGAACGGGCACCTAGAGAGTACCCAGATCCTTCTCGAAGCTGGCGCGG
ACCCCAACGGAAGCCGGCACCATCGCAGCA

542. chr2_HDAC4_NM_006037_-1.52528
GTCAACTGAATTCGGCAGCTCGGCCGCCTGTTGCCACAGGCTCCTTTCTT
CCACGGCGTCCCTTGCGGGACCCGCCAGAGTGTGCTTGGCTTCCGCGTGT
CCGTGTGTCTGCGCGTCGCCGGCGTCTGTCCCGTGTTCCCTGTGAGGCTG
CCACGCCCAGGCGTGCATGTGCGTCTCGAGACCTGTGGGCCTGGGCGGCA
GAAAGGCTTCCCGTGGCTGTTGCAC

543. chr2_HDAC4_NM_006037_-1.60593
TGCCGGTTGAGGGGGTTCGTGCCATA

544. chr2_NDUFA10_NM_004544_-1.73584
CCCGGGCGGACGCGGACGTCGCTGCCAGCTTC

545. chr2_GPC1_NM_002081_-1.60477
TCCCGGACGCCCTTGACCCATGCCCTCCCAG

546. chr2_SNED1_NM_001080437_1.69277
GAGGGATGAGTGCCGAGCTCACCCGTGCAGAAATGGAGGGTCCTGCAGGA
ACCTCCCAGGGGCCTATGTCTGCCGGTGCCC

547. chr2_SNED1_NM_001080437_-1.511
GGTGGACGCCTGCGACTCCAGCCCCTGCCAGCATGGAGGCCGGTGTGAGA
GCGGCGGCGGGGCCTACCTGTGCGTCTGCCCAGAGAGCTTCTTCGGCTAC
CACTGCGAGA

548. chr2_PPP1R7_NM_002712_-1.77798
TCGAGTCTGAAGAATCCGGCGATGAAGAAGGGAAGAAACACAGCAGTGGC
ATCGTGGCCGACCTCAGTGAACAGAG

549. chr2_SEPT2_ENST00000429791_-1.55248

Figure 3-47

GCCGGCGACAGTGGCTCCGACACGGGCAGGCCCGGGCGCGGGAGTGGGGA
TTCCGGTGACCCCTTGTTGACCCTGCGGGAATTCCTCTGCACTGTCGTCG
GTGCTGGGCCTCGGGGCGTCGAGTGCGGTCGAG

550. chr2_---_---_-2.10908
AATTAGGCTGAGTGCAGTGGCTAACACC

551. chr2_---_---_-1.63544
GACTAAATTTGCTCTAAAGTAAGTTTGTAACAATTTACATTTCCAAAGTG
TACTCTTCTCTCC

552. chr2_---_---_-1.6091
GGGGATCCTCATGGTCTTCGGCCTGGCACCCGCCCAGGGGCTGAGACAGT
G

553. chr2_C2orf85_NM_173821_-1.5748
CGTCTGGGTTCTGCTACCTGAGCACAGCCTGGTCCCGGGATGCCTGGACG
GCGGTGGTGTCCAGTACCTGCT

554. chr2_FLJ40712_AK098031_1.5274
TGGCTCCTGTTCTACGCCTTGTCAGGGAAGATGTGGGTTCGCCCCAGGTG
CTCCAGAAAGGTCGTGTTCTCTATGGAATGAAGACGGGTGGGCATAAGCG
TGGGTCCGGGGCCACCCTCTGTCGTCCGCCGGCGTGTTTCTCATCCAGCC
ACGTCTCGGAAGGTCTGTGACTGCTGAAAACATTCTGTGCATGAACGTTG
GGGAAGGAAACCCACCCAGAGGAGGGGCAGGCGCCACCCCAGGCGTCAGA
GCACCAAGCCGCAGAGAACGGAGGCAGCAGGTGCCCGGGACACACCGGGG
AGACCGCAGGAGCAGCCCGTGTCTTCTGTGGCTCAGTCCCGCGAGAAACT
GGAGGCCAGCGCTTCACAGCTCCCATTTGCAGAGACCAGCTCCCGTGAAT
GA

555. chr3_ITPR1_NM_001099952_-1.50078
TTCTGAACCCCGTCAATGCTGGTCAGCCCCTACATGCTAGCAGCCATCAA
CTGGTAGATAACCCAGGCTGCAAT

556. chr3_ARL8B_NM_018184_-1.76633
AGTCATATGATCCGCTCGGCTTCCTGGGTCTGGCTGCTGCCGCCCGCCGG
TGTCCGCCCGTGTCGCGCCGGGGCACCAAGGAGCCGTTGGAGGGTCCGGG
CGGAGGCCCGCTCGTGTGGAAGTCGTCGACGCCGCCGCTCGTCCGTCCTC
CCGTCCGTTCTCGCTC

557. chr3_GRM7_NM_000844_1.6624
CCTAAGTGCATCAGTGGCGCTGGGGATGCTATAC

558. chr3_CAMK1_NM_003656_1.89838
ATGAGGTAGAGGTGGCCCCCACTCTCATAGATGTCATCCAGGGCTACAAT
GTTGGGGTGCTTGATC

559. chr3_IL17RC_NM_153461_-1.78718
AGAACCTCTGGCAAGCCGCCCGACTGCAACTGCTGACCCTGCAGAGCTGG
CTGCTGGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCT

560. chr3_FANCD2_NM_033084_1.53013
TATTTGATAGTCATCCTGTTCTGCATGTATGTT

561. chr3_IRAK2_NM_001570_-1.66362

Figure 3-48

TACGTGATCACAGACCTGACCCAGCTGCGGAAGATCAAGTCCATGGAGCG
GGTGCAGGGTGTGAGCATCACGCGGGAGCTGCTGTGGTGGTGGGGCATGC
GGCAGGCCACCGTCCAGCAACTTGTGGACCTCCTGTGCCGCCTGGAGCTC
TACCGGGCTGCCCAGATCAT

562. chr3_TATDN2_NM_014760_-1.7251
CTTGGGGACCGAAGGACTGTCATTGACAAA

563. chr3_ATP2B2_NM_001001331_-1.72536
CGCCGGGCGGGTGGTAGAAGGACAGCCCCAGGGAGATGATGGCGGCAATC
TCCAGGATGATGAGCGTCACGTCCTGCAGCGCCTCCCACACGAGCTGCAG
GAAGGTTTTTGGCTTCTTTGGAGGTATAAAGTTTTGCCCAAAAATTTGCT
TTCTCTTTTCCAGGTCTGGAGCGGTGCCCGGCAAAC

564. chr3_SLC6A11_NM_014229_-1.61946
TGGCCTTTATTGCGTACCCCAAGGCGGTCACCATGATGCCTCTCTCCCCG
CTGTGGGCCACCTTGTT

565. chr3_SYN2_NM_133625_1.53411
TACAAACTGTGGGTGGACACCTGC

566. chr3_TMEM40_NM_018306_1.73131
GGCTCCGTCGATGTTTTCCGGTTGCTCTGGGTTGCTGGTCCTCA

567. chr3_IQSEC1_ENST00000450726_-1.77926
GCCACAAACAGCCGCAGCCTGGCTG

568. chr3_NUP210_BC067089_-1.57248
CAACAGCCCAGATAAGGAATGAAAACCAACAGTGGGGACCGATGGCCCAA
GCT

569. chr3_NUP210_NM_024923_-1.54406
GCTGTGGTTCCTGATGCCTCGTGAAC

570. chr3_NUP210_NM_024923_1.87894
GGCCAAGGACGAGGCTGCTCTGTCCCA

571. chr3_C3orf20_BC030599_1.77009
CAGGAGACCCTGAACAGGTTTCAG

572. chr3_EAF1_NM_033083_-1.53291
GACGCCAGCGCCAGAAGCTCGGATCGCGGCTGCACCGGGAGAGCGCCGAT
CTGGGTGCGAGGCA

573. chr3_COLQ_NM_005677_-1.55952
CCCTTTGGTCCTGTCTTGCCAGGAAGC

574. chr3_TBC1D5_NM_001134381_-1.74806
AGAGACCTTATTTATATTCAGGGGAGCACC

575. chr3_THRB_NM_000461_-1.5755
GTGCCCTGGAGCCGGTTGGGTTGAGCGCCCCTGCCCGGGGAAGGTAGCCT
GCGGGCTCTTGCC

576. chr3_TOP2B_NM_001068_1.71006

Figure 3-49

TCCTAGCCCGACCGGTTCGTGGCAGAGAA

577. chr3_AZI2_NM_022461_-1.59825
CAGAAGCCAGGCTACGTAGGGCCGCCCCCAAGGCCGCCGAGTTTCGATTC
CTTAGTGTTTGG

578. chr3_CCR4_NM_005508_-1.50515
ATAACTCGTGCTCACAGGAAGCCACGCACCCTTGAAAGGCACCGGGTCCT
TCTTAGCATCGTGCTTCCTGAGCAAGCCTGGCATTGCCTCACAGA

579. chr3_UBP1_NM_014517_-1.51108
GGCCTCCGCGTCCAGGGCGAAGGAGCC

580. chr3_PDCD6IP_NM_013374_-1.64996
TATCTGCCTTAAGTCGAGAGCCGACCGTGGACATATCTCCAGATACTGTT
GGGACCCTCAGTCTTATTATGCTGGCACAGGCTCAAGAAGTATTT

581. chr3_LRRFIP2_NM_006309_1.5946
CCTGGACTGCTTCGGGCTGAACTTATTCTTGATGAA

582. chr3_VILL_NM_015873_1.55135
GCACCAGCGCCACGATCAACGGGGGCCTGCGCCGGGAACAACTGATGC

583. chr3_PLCD1_NM_001130964_-1.57598
TGGTGATGACAGCAGTCTGGCGGCTGGCCACGTCCCGGCTCACGCCATGG
ATCTCCACTGT

584. chr3_DLEC1_BC129824_1.57596
GGTGTCTCCCACATGTCTACTATGGCAAAAAACATTACCATCCCCACCCA
TACCACAGCATCCCCTAGAGAGAGTGAGGTGCAGGGACCCGAGGGCCAGG
TTAGCACAGCGCTGGCCCCAGCATGGAGGGAAGCCCTGTGGGCCACGGTA
GGCTAGAAGGGAATTCGAGCTGGGCATGAAAAGGATGCTCCGGGGCCATT
GTTAGTGGGTTTGGGGCTGAGATGAGTGATCCTGCCTCTGGTCCCAGCAT
CCAGCTGCCTCGTTGTCTATCCTGGGAGGGTGTGGTGCTTCGGACACGTT
GAGGGGCTTTGTCAGCATCAGGAAGGCCTTTGCTTCTTGCACCCAGGCCC
AGCTGAGACAGGCCCCTGAGTCCTGGCTCATGTTCTGGCAGCAACTTCAC
TTTTCCTAAGGAGGGGAGGAGGCAGCAGGGAAGCAACCCTGGGTTTTCAG
AAGGTCCTTCTGATGGCTAGGCTA

585. chr3_XYLB_NM_005108_-1.69199
TCTTTGGTCAGTAGCTTTGCTGCTTCCCTGTTCCTTGGCTCTTACTCCCC
TATTGACTACAGTGA

586. chr3_ACVR2B_NM_001106_-1.88369
CTCGCCCTCCTCTGGGGATCGCTGT

587. chr3_SCN5A_NM_198056_1.67235
TGAGCCGCGGGCTTGCTTCTCTGCCATGCGCTTCTCGATGGCTGCCAGGG
ACTCCCGTGTGAACCTGCGGAAGCTGCTGGTGCCCCGAGGTAATAGGAA

588. chr3_CSRNP1_AB063301_1.61569
AGCGTTTCCACCCTCACGCTTTTACTGCAGCCGGTCTTCTCGACTGGAAT
GC

589. chr3_XIRP1_NM_194293_-1.58612

Figure 3-50

GGTGTTTGTGGTCTGTAGCAGCTGTGGTCTCAGGGTTCGTCGTTCCTCTG
GAGGTTCTTGTTCAAATTGGTTCTGTTCTGCTGGC

590. chr3_MYRIP_NM_015460_1.84272
GGCCCAGAGCTCTGACCAAGGCCCCATAGCTGCCTCCCCATCCTCTGCAC
TCTCCCCCAACCCTGAGGCCATGTGCTCTGACTCGGAGACCTCCTCCGCA
G

591. chr3_ZNF619_NM_001145082_1.55451
GATATTCCAGCTGGAGCAAGGAGA

592. chr3_ZNF621_NM_198484_1.59112
ATGGGCCAGCCTCGACCCTGCGCAGAGGG

593. chr3_CCK_NM_000729_-1.66127
GGTACTCATACTCCTCGGCACTGCGACGGCCAAAATCCATCCAGCCCATG
TAGTCCCGGTCACTTATCCTGTGGCTGGGGTCCAGGTTCTGCAGGTTCTT
AACGATGGAC

594. chr3_VIPR1_NM_004624_-1.52046
GCAGGGCGTCCTGGGCTGGAACCCCAAATACCGGCACCCGTCGGGAGGCA
GCAACGGCGCCACGTGCAGCACGCAGGTTTCCATGCTGACCCGCGTCAGC
CC

595. chr3_VIPR1_NM_004624_1.53645
GCTTCCAAGCCGAAGTCTCCCTGGTCTGA

596. chr3_C3orf23_NM_173826_-1.6452
TTTGCCACCTGAGACCTATGAGGAG

597. chr3_ZNF167_NM_018651_-1.72627
GTGTCCGGCTTCGGTGCCGAGTGCCACCGCGAGTGGGCCGAGACGCGGAG
GGAGGCGCGGCCGGAGCTCGGGTCGCCGACGCTGGCCAGGACCGCGCTTC
TTCCCGGCG

598. chr3_LTF_NM_002343_1.78491
AGGGCCACGCACTTTTCTCATATTCCTTTGCCATTGGAAGCATTTTGTGG
CCTCGGGTTGGGATACGGCGCACCACTGAACACT

599. chr3_LRRC2_NM_024750_1.69728
AGGCATTTCTACCCGGCTGTGGTAAGCGGAGGTTCTCCTCTT

600. chr3_ALS2CL_NM_147129_-1.66276
CTGAGGGTTTATTGGTCAGGGCCCAGGCAGATGTCATGTGCCCCTGTTGT
CCCCACGCAGGCCCACAGACATCACAGGAGAATGATTTACAAGCCACTTG
GGGCCTGCTGGCAGTGAGGGTTTACCCACCCCCCGCCCCAGCTTGCTCCA
GTGCCGCCGTTTACGTCATGGGTACGTGGCCTGCAGTTCACGGATCTCCA
GGCCCATCCTGTTGACTGCATACCCAGTGAGGCT

601. chr3_NBEAL2_NM_015175_-1.6203
CATACACACTGTACGCCGCGGACAGTTTGTAGCGGCACTACGGCCTCTGG
GTGCCACATTCCCTGGACCTATTTTCCACCTGGCATTGGGGTCCGA

602. chr3_SETD2_NM_014159_2.06264
TACACTGACAGACTGTTGGTTTGA

Figure 3-51

603. chr3_PTPN23_NM_015466_2.06921
TAGATAGCATCCAGGCGCCCATCCC

604. chr3_PTPN23_NM_015466_-1.83244
ACACAGCCCCACGGCCAAACCCCA

605. chr3_SCAP_NM_012235_1.952
AGGAAGAAGTCAGACACCAGCCCC

606. chr3_FBXW12_NM_207102_1.51175
GATCGCAAGTTTCCAGGTGGCAGCTCATCTGAAGTGCCCTATCTGGATGG
GAGCCAGTGATGGATATATGATTGTCTTTACCAGTGGACCATACTTGTTA
CTCTTCAGCATCACTGGCTTCCTGCTGCAACGATTTGAGGACCATCAGGC
AGCCATCA

607. chr3_PLXNB1_NM_002673_1.71047
GGATTCTTGGCGTCTGTACCACGTCCAGATTCTGGCCACGGACGCATATC
TCAC

608. chr3_---_---_1.52448
AGATTGGGGAGAACTGTGAACACAACCAGCCCA

609. chr3_SHISA5_NM_016479_1.5989
CTGACATGGGGTCGTTGTAGCCAGGGCGAAACCTCAGCGCCGAGCCCAGC
TGCTCCACCGGCTCTACACTGGCAGGCA

610. chr3_COL7A1_NM_000094_2.58823
CTCCCTTCTCGCCTCGAGGACCGGCAGGCCCTG

611. chr3_COL7A1_NM_000094_1.54306
CTTGGACTCCGGTAGCTCCTCTGGGCCCAG

612. chr3_COL7A1_NM_000094_-1.92914
TCCAGGACGTCCAGCAACCCCTGGCAGCC

613. chr3_COL7A1_NM_000094_1.51099
GCCAGTCTGTAAGCTGTGGCTCCAGTGACCCCTACCCAGGTGATCCGTAG
AACGTCGCTGGAAGCATTGAGGATCTGCAGCCTCGACACAC

614. chr3_IP6K2_NR_027437_1.61768
TGGAGGACAAAAAGCAGGCGGCAAGTATT

615. chr3_WDR6_NM_018031_-1.60013
CAAACCTGTAGCACCTGACCGACGAATCAGTGGGCATGTGGGCATCATCT
TCAGCA

616. chr3_WDR6_NM_018031_-1.69703
CAGAAGCTGCAGGCGGACGAACATCTGACCAAAGAGGTGTGGT

617. chr3_QARS_NM_005051_-1.53972
GAGACGCCGGGTATCCCTGAGTCGGGAGGCCAAGCCATATAACAGGATCC
CGGTAGCTTTGTCAATGGTGGAACCCAGGGTCTGC

618. chr3_CCDC36_NM_178173_-1.58545

Figure 3-52

ACTAACTGCAAGAACTGGGCTGTTACTAAAACAGGTGCCAAGAACCATGG
TTCCAGCGTCCCAGGCCATAAGATTCCCAGTGACAGGGACCTGGTTTCCC
AAGGAGCCTCACAGCTCACATCATTGGAGATA

619. chr3_---_---_-1.74658
GAGGTTGCAATGAGTGGAGGTTGCAATGAGCTGAGATTGCACCACTGCAC
TCCAGCCTGGCCAACAAGAGCGAAACTCCATTTAA

620. chr3_---_---_-1.53917
GGGCCACTGCACACCAGCCTGGGGGACAGAGTAAGACTCCATCTCAC

621. chr3_AMT_NM_000481_-1.68027
GCGAGCAGTGCTGGCGTGTGTGCAGGTGCGAGTCAGTGTGACTGTCCCGG
TACTGCACTGGCAGACTCCAAC

622. chr3_RNF123_NM_022064_-1.70291
TATGGCCTACTTCCCAGCCATCAGCCTCTCTTTCAAGGAGTCCGTGGCCT
TCAACTTTGGCAGCCGTCCTCTGCG

623. chr3_MST1R_NM_002447_-1.74381
ATAAATACATGTTGCAGGACTGCCCTCACTGGCTCACTCTGTGGAGTGAG
GGACCTAATGGGCCCCATTTACCTATTGCCTCTGAAAGTTAAAGGGCAGG
AACAAGGTGGAGGGCCACTGCCCTCTGGCCTGGCATGGCCCAGAGGCAGC
TTGGGGTTAGCTCAAGGCAGCTAAGCAGGTCCAGCCCAAGAAC

624. chr3_RBM5_NM_005778_-1.51467
CAGTGACCGATCCGAAGATGGCTACCATTCAGATGGTGACTATGGTGAGC
ACGACTATAGGCATGACATCAGTGACGAGAGGGAGAGCAAGACCATCATG
CTGCGCGGCCTTC

625. chr3_SEMA3F_NM_004186_1.51787
ATCCAGCACCCGTCAAGACCATGACCATCTCTTC

626. chr3_GNAT1_NM_144499_1.5271
CACCTACGAGGACGCCGGCAACTACATCAAGGTGCAGTTCCTCGAGCTCA
ACATGCGGCGCGACGTGAAGGAGATCTATTCCCACATGACGTGCGCCACC
GACACGCAGAACGTCAAATTTGTCTTCGACGCTGTCACCGA

627. chr3_GNAI2_NM_002070_-1.63841
ATCATCCACGAGGATGGCTACTCCGAGGAGGAATGCCGGCAGTACCGGGC
GGTTGTCTACAGCAACACCATCCAGTCCATCATGGCCATTGTCAAAGCCA
TGGGCAACCTGCAGATCGACTTTGCCGACC

628. chr3_GNAI2_NM_002070_-1.56396
CCACCGACACCAAGAACGTGCAGTTCGTGTTTGACGCCGTCACCGATGTC
ATCA

629. chr3_SEMA3B_NM_004636_-1.5992
TGTGGAATGGCGAGAGGAGTGCAACTGGG

630. chr3_SEMA3B_NM_004636_-1.91312
CTGAAGGTGATCTCGGTCCCCAAGGGCA

631. chr3_IFRD2_NM_006764_1.50464
ATTCACTGGCGGTGCTGCGGGCCTCACTGGCTGCCTCATCGTCACTGGAA

Figure 3-53

CCCGAGTCAGCTTGGGCACTG

632. chr3_HYAL3_NM_003549_-1.57782
GCCTCCTCCAGGCGATGTCGGACAAAGGCC

633. chr3_CACNA2D2_NM_001005505_-1.73487
CCACTGCAGCGGTGTGACGTCATAGTTATGCTGCCCCACGGAGAAAGTAA
ACACGCGCAC

634. chr3_MAPKAPK3_NM_004635_1.57505
AGTGCCTTGGCCACTATGCGGGTAGACTACGACCAGGTGAAGATCAAGGA
CCTGAAGACCTCTAACAACCGGCTCCTCAACAAGAGG

635. chr3_DOCK3_NM_004947_-1.74356
AACAAGAAACATGGCGCGAGACCGGCATTTCCTTTGTGACCTCAGTCACC
CGCCTCATGGAACGTCTTCTTG

636. chr3_TEX264_NM_015926_-1.52674
AGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACCAGGAAGACCAG
ATCCATTTCATGTGCCCACTGGCACGGCAGG

637. chr3_PARP3_NM_001003931_1.61908
GGACACTGAGTTGGAGCTGGATGGCCAGCAAGTGGTGGTGCCCCAGGGCC

638. chr3_ACY1_NM_000666_-1.59792
TCTCTGAAGTACTAACACAAGGACA

639. chr3_TLR9_NM_017442_-1.81051
TGCACCAGGAGAGACAGCGGGTGCAG

640. chr3_TWF2_NM_007284_-1.54162
TTTTTCACTGTGGCCCGCGTGGCCGCGTACA

640. chr3_DNAH1_NM_015512_1.78059
CCACCATCATGGTGTATGCAACCATCACCTCCCAGCTGCTGCCCACTCCA
GCCAAGTCCCACTACACCTTCAACCTGAGGGACCTCTCCAAGGTCTTCCA
AGGCATGCTCATGGCTGACCCGGCCAAGGT

642. chr3_SEMA3G_NM_020163_-1.66875
GGGGCCAGAGCTACCCCCATGGAGCAGGAGGCCCCCTAGCAGCCAGCAAA
TGGCCCAGGCCGAGGG

643. chr3_NISCH_NM_007184_1.76023
TGAGCTGCCTGTCGAGCTCACCGGCTAG

644. chr3_STAB1_NM_015136_-1.60813
GAGTGTGTCTACATCCATGACCCAACGGGGCTCAATGTGCTAAAGAAGGG
CTGTGCCAGCTACTGCAACCAAACCATCATG

645. chr3_NT5DC2_NM_022908_2.10164
GGACTGGTAAGGATTGAGGCCGTAGGATGGGCTCGAGTGTGGCGGTGTCC
CCAGGGCCCCAGTGAGCAAGTGGGTGTGCTGGGAACCTGGCCACAAGTGA
A

646. chr3_PBRM1_NM_018165_1.58677

Figure 3-54

GATGAAGACACAGTCGCCAACCTTCAGCCACATGTCATTGTAATGGAGCT
GCTCAAAGTAGTGGCAACCTGGTTCACCATTGGACA

647. chr3_ITIH3_NM_002217_-1.91317
AATCCTGGAAGATATGCAAGAGGAAGACTATCTGAATTTCATCCTGTTCA
GTGGAGATGTGTCCACATGGAAAGAGCACTTAGTCCAGGCCACGCCCGAG
AACCTCCAGGA

648. chr3_SFMBT1_NM_001005159_-1.66781
AACACTTATCCAGAACCATCCGTGGACCGAAGAGGTTAGGACAGCATTCC
AGTTTGATACAGGTTTGCCGGCAGAA

649. chr3_RFT1_NM_052859_3.27036
GCCGGGCCGCGTGGCCCAGCACCT

650. chr3_WNT5A_NM_003392_1.65362
GTCTGCACGGTCTTGAACTGGTCGTAGCCACGGCCGCAGCACATGAGCTC
GCAGCCATCCATGCCCTCCGACGTCTTGTTGCACAGGCGGCCCTGCGTGC
CCAGCGAGCCGGTGCTCTCATTGCGCACGCAGTAGTCAGGGCTGGGGTCG
ATGTAGACCAGGTCTTGTGTGGTGGGCGAGTTGAAGCGGCTGTTGACCTG
TACCAACTTGCCCCGGCTGTTGAGCCGCATGGCCGCCGCGCTGTCGTACT
TCTCCTTCAGGGCATCACCCACCTTGCGGAAGTCTGCCAGCTGCAGCCAG
CATGTCTTCAGGCTACATGAGCCGGACACCCCATGGCACTTGCAGGCCAC
ATCAGCCAGGTTGT

651. chr3_APPL1_NM_012096_1.55967
CAGTTTTACTTCACGCAGGGTGGAAATTTAATGAGTCAGGCCCGTGGGGA
TGTAGCAGGAGGCCTGGCCATGGACATAGACAACTGTTCAGTGATGGCTG
TGGACTGTGAAGACAGACGATATTGTTTTCAGATCACC

652. chr3_FEZF2_NM_018008_1.51762
TTGCCGCAAAATTCGCAGACGAAGGGCTTGTAGCCCGCGTGGATGCGGAT
ATGCGTGTTGAGCGTGGAGCTGCGGTTGAACGCTTTGCCGCACTGGTTG

653. chr3_MITF_NM_198159_-2.23534
CGGGGAGCAGCGCACCCAACAGCCCC

654. chr3_EIF4E3_NM_173359_-1.53635
AGAGGCGGGACTAGAACGTGGGTAGCTTGAGGTCCGGACCAACGTGCTGT
CCCACTGCATGACACGCAACACAGACGACTTGGGGTGGCAG

655. chr3_GPR27_NM_018971_-1.70997
GCCACGACTGGACCTTCCACGGCCCGGGCGCCACCGGCCAGGCGGCCGCC
AACTGGACGGCGGGCTTCGG

656. chr3_TFG_NM_006070_-1.59708
GCGGCGGTCGCGAAGGGCAACCGAGGGGGCCGTGACCACCGCCTCCCCGC
GACGCCCCAGTCCAGTGGCCTCGCGTCCGCCCATTCAGCGGAGA

657. chr3_ABI3BP_NM_015429_1.5074
AGGGAGTCGCTCAAGTAAATCTTGTATCTGAGAGAGTTGCACAGCTGCAC
TCCTACAAATTTTTTATACCATGTCCTTTTGACATATTGTTTGCCCTTAC
ACTCTGAGTAAGAGTCTGA

658. chr3_ZBTB11_NM_014415_1.61615

Figure 3-55

GGAGCGGCGGCACCGTAGGGAGAAACGGCTGCGCCTTTGGCGAGCGCTCT
TCGACGGCT

659. chr3_FAM55C_NM_001134456_1.72037
CTAACAGTCTAGAACTATCTCAAG

660. chr3_NFKBIZ_NM_031419_1.59345
GCGGCCTCATGACCAGCCCGCTCAACCTGAGCTACTTCTACGGCGCGTCG
CCGCCCGCCGCCGCCCCGGGCGCCTGCGACGCCAGCTGCTCGGTCTTGGG
CCCCTCGGCGCCCGGCTCGCCCGGCTCCGACTCCTCCGACTTCTCCTCTG
CCTCGTCGGTGTCCT

661. chr3_ALCAM_NM_001627_1.54862
ATAGTAAAATTATCATTTCCCCTGAAGAGAATGTTACATTAACTTGCACA
GCAGAAAACCAACTGGAGAGAACAGTAAACTCCTTGAATGTCTCTGC

662. chr3_CD47_NM_001777_-3.51447
ATTAAGGGGTTCCTCTACAGCTTT

663. chr3_CD47_NM_001777_-1.9829
AGCCCAGCAACAGCGCCGCTACCAGGGGCCACAT

664. chr3_DZIP3_NM_014648_1.5506
GCCTTGAGTACCTTGCCTCCAGTCCAGCT

665. chr3_C3orf52_NM_001171747_1.64059
CTGGTCTCTGTCTGAAAGCAGTGCTCTACCAAGTCCTGGAGATGAAGGGA
ATTCACTCTGTTTTGCAGAAAAGATTCTGTGGATTAATACAGAAGCACCA
GCAACACCAGAGGGGTGGAGACTCCTTTCTCTCCCGATTCTACAGTCTGG
CTCTAAGCCCAGTAAAACAGCTCCCGAGCACTGCTTCAGCTGGGTCCAGT
CTTGACA

666. chr3_ATP6V1A_NM_001690_-1.63818
GCAGCTTTGAGACTAGTGCCTATGTGTGTTATTTGTTTCCCTGTTTTTTT
GGTAGGTCTTATATAAAACAAACATTCCTTTGTTCTAGTGTTGTGAAGGG
CCTCCCTCTTCCTTTATCTGAAGTGGTGAATATAGTAAATATACATTCTG
GTTACACTACTGTAAACTTGTATGTAGGGTGATGACCCTCTTTGTCCTAG
GTG

667. chr3_UPK1B_NM_006952_2.1123
CATCTTGTATCACAGCAGCAACAC

668. chr3_C3orf1_NM_016589_-1.50848
ATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTATGGCTGGCGCT
GGGGTTGGAGAACTGCAGTGTTTGTGAC

669. chr3_POLQ_NM_199420_1.52914
ATGAATGATTTTGCCTGGTCCCAGTTAATTTTGATTTTTCAGCCCTTTCA
TCTTGATCTCCTCCATCTTGATCACCTTGGTGGTGCTCATCAAGTACTGG
ATCACTTAGTTCTAATGCTCTAGGAGATACTACAGTATGATTCTTCTCTT
GGACAGGAAATATATCCACATTGTCCAAAGCTTCAACCATCTGAACAGAA
TCCATTTCTGAAAATATAATAGATTCATCATTGGAACAAGTCAACTGCTG
GTGGGTATCTTGATTCTCATTTACATTTGATTTTTTAATTAGGTCTTCTT
GTAGACACAGAGAATCACTAAAATGGTTTGATGTTACTTCTGAAGGAAGG
GGTTCTTTCATTTGCATATCAGGTAATTGTTCTTTTACTAGATAGTCATC

Figure 3-56

ACTGAAGCTATCAAATAGTAAACTATCACTCATATTCAAACTTGTTTCAG
GAACTGGAAGACATTCTCCTTCTACACCAGTGGGAGTTCTCTTTTGAGGA
ATCAGAAGTATAACTGGTTTCACAGTTTCTTGTGTTTGATAACCTTGAAG
AAAACTATTTAATTGTGAATCAGTAACAGAAACTTCATTCTTTTTTAAAA
AAAGACCATTTTCCTCCAATAGTATTGGAGAATGGAAAATCGGGCTTTCT
GGAGTCAGGATATCAACCCCATGTGAATCACTGCTTTGTTTCATAGTACC
TACAGTCTTAAGGTCCAAATGATCTATCTTAGTCGCTCCTAGAGGGTGC

670. chr3_PARP14_NM_017554_-1.53311
TAAGCATTATGGTGGCCTGGCCGCTGCGCTCTCAAAAGCAGCTGGCCCTG
AGCTCCAGGCCGACTGTGACCAGATAGTGAAGAGAGAGGGCAGACTCCTA
CCGGGCAATGCCACCATCTCCAAGGCAGGAAAGCTGCCCTACCACCACGT
GATCCATGCAGTGGGGCCCCGCTGGAGCGGATATGAGGCCCCGAGGTGTG
TGTACCTATTAAGGAGAGCTGTGCAACTCAGTCTCTGTCTAGCCGAAAAA
TACAAGTACCGATCCATAGCCATCCCAGCTATTAGTTCTGGAGTCTTTGG
CTTTCCCTTAGGCCGATGCGTGGAGACCATTGTTTC

671. chr3_SEMA5B_NM_001031702_-1.73102
CCCACGATGAGCTGGTTCCCGGAGGGGTCCAAAGCCAGCTGGGAGAAATC
CCGGGCTCCAGGGTAGGTGAAGTTAGAGACCCACGGCTGCAGGT

672. chr3_PDIA5_NM_006810_-1.54911
ACTTCAGACGGCTCCTGAAGAAGGAAGAGAAGCCGCTCCTGATCATGTTT

673. chr3_ADCY5_NM_183357_-1.56098
ATGCGGTCGGGTACACCGGTGCTGTCCATGCGGCTGGCCACGTTCACGGT
ATTGCCCCAGATGTCGTACTGAGGCTTTCGT

674. chr3_ADCY5_NM_183357_-1.53153
GGCCTCCAGCTCAACGTAGAACTCGGAGAAGTTGGCGATGGAGGCGAACA
TGACCGCCACACACTCACAGGACTGATAGTAGAGCTCATCATTGCGCCGC
TCGC

675. chr3_ADCY5_NM_183357_1.59184
GGTCGTCACCGCTCAGCGGAGGATCGTCGTCGTCGTCGCTGCGCCAGCGG
CTGGCCAGGCGCTGCTGCTGCTGCGGGGTCACCGCCCCCCCCGGGTTTCTT
GGTGGAGCCGCGGGCAGAGCCCCCGGGGGCATGGGGGTAGCCATTCGCGC
GGGAATCGGCCTCGCCCCACGCAGAGCGGTGTTCGGGGCCTCCCCGGGGC
GCCGGCGCCGCAGTCTTCTGCGCCGCGTAGCCCGGG

676. chr3_MGLL_NM_007283_-1.9294
AAGCCCAGGGTAGTCTTTCTGCAT

677. chr3_SEC61A1_NM_013336_1.57586
GCTGTGGACCGCTATCACCCTCTTTATCTT

678. chr3_RUVBL1_NM_003707_1.6445
AATGGCCCTGCGGAAGTTCTCCATCAGCA

679. chr3_GATA2_NM_032638_-1.63578
CAGAGCCTGGGCGGCACGCCGAGCGGCCGCAT

680. chr3_C3orf27_NM_007354_-1.55094
GGCTGTCACCAGAGAGCCCGACGGCTTCAAGGAACAC

Figure 3-57

681. chr3_ACAD9_NM_014049_-1.5433
CCTGCAGGCAGTGCTCTCTAACAG

682. chr3_C3orf25_BC066975_-1.64183
GCCTCTGAAGGCGTGATGCTGGGCTTGTTCTCCAGCCACCTCTTTACATC
ACCAAAGGACTCTAGCTCCTGCCGCAG

683. chr3_IFT122_NM_052985_2.45923
GCCCGAGCCGTAAGGGAAGCCGTG

684. chr3_PLXND1_NM_015103_1.59837
GGCGCGGCGAGTGCATGGGGCGAGGCGCGGCCGGGAGCCGGGAGCCCGGA
GGCGGCGGGAGGCGGGGGGCGGGCCCGGGCCGCGATGCGCTTCCTGCCCG
CGCCAGCCGCCCCCGACCCCGGCGCCCGGGCCCGGGTCAGCCTCGCCGCG
CAGCCC

685. chr3_ATP2C1_NM_014382_1.53848
CTTGGAGTAGAACCAGTGGATAAAGATGTCATTCGTAAACCTCCTCGCAA
CTGGAAAGACAG

686. chr3_ASTE1_NM_014065_1.53524
CTGGCTCCTGCACGTGAGAGTCCAATCTCAAGAGCGGGAATCGGAAGTCT
CCCGGTGTGACGTCTCTGGGAAGTACAGTTCCGTGATGCCGGTGGCGC

687. chr3_DNAJC13_NM_015268_1.71641
TGGTATTTTGGCAACGCAGACAAAGAAAGGAGTGGCCCGTATGGATTTCA
TGA

688. chr3_---_---_-1.73935
CGCGATCGTGCCACCGCAGCGAGACC

689. chr3_BFSP2_NM_003571_-1.73221
CTGCAGACAGAAACTATCCAGGCCGGAGCAGATGACTTTAA

690. chr3_BFSP2_NM_003571_-1.55464
CAAACAGTTGGCAGGGTGTGAGCTGGAACAAATGGATGCTCCCATTGGCA
CTGGTCTGGACGACATCCTTGAGACGATCAGAATTCAGTGGGAGA

691. chr3_AMOTL2_NM_016201_1.66302
GCGGTGGCTAAGAACATGCACATTCTTGAATGTCCTCTGCATGGTGCCTG
GCCTTCTGGATGGTTTCGGACAAAACTTTATGTGCTAGGTGGGAGTGGGA
AAAGGAGTGGGGGAAGGATAAAGCCATCTTTGGACACCCACTCCCACTGT
GGATAACCACAGCGTGTGGCCGAACAAAGCTGATTAGAACACAGCCCTAC
CTCGGGAGGCTGCCATCTGCCAGGCCCTCCTTCCCCTCCCAGCCTTCAAG
AAATGTTATCTATGAAAGGGGAAAAATGCCAGCCACATCCTCATTCCAAC
TCTATCCTTAATGCAGCTTCACAAAATTCCTAAATTCTATCTTGGGTCCT
TGAAGAGATTGGACTATGACTTGGGTGGCCCC

692. chr3_EPHB1_NM_004441_-1.54447
AATGGACACCAGAACGGCTACTGCAGAGCTGGGCTGGACGGCCAATCCTG
CGTCCGGG

693. chr3_MRAS_NM_012219_-1.52558
CACCTAACTGCACTGAAACCATTTCTAACCACAACCCTTGGCCCAAGGAC
TTGGTACAGGAAGGGAGAAGGGCAGGTGGGCAGGGAGCAGACAGGGTCTG

Figure 3-58

GCTTTGCCCAGAGGGCACGGGCTTTCCCACCTCTCAAAGAGACAAGGAAG
CCACCTGTAAGCAGAAGCAGCATCCAAGTGCCCCTGGCCCCCCCATGTGT
TGATTCAACCCGGTTCCTCCCCCTCTCTCGGTGGGTGTGTTGTTT

694. chr3_FOXL2_NM_023067_-1.55016
GAGGCTGCGGTAGCGGCCACGAGTTGTTGAGGAAGCCAGACTGCAGGTAC
TTGGGGGGCGCCAGGTAGCCGTAGCCGTCG

695. chr3_GK5_NM_001039547_1.55938
TTCTGCACGCTGGAGCCGCAGACCCGCGCCGCCCGGTCATAGACGTGGCA
GCGGATCACAGAACTGCCCACATCCAGCCCCAGCACGAAGCCGGGGTACC
GCGGCTCCTGCGCTCTCTGCTCCGGGTCCGTGAGCAGC

696. chr3_CHST2_ENST00000309575_-1.63861
CCGACAGGGGATTTCTGCCCAAACTTCATCACCAACTCTTTCTGAGAGCA
AAAACATGGGGCCGAGTCCGGCAGCTGCACGCAGAATCCAACTCTCTGGC
AGCTCTCGGCACCGACGAGCTCCAGATCCCGCGTTCGCATCCCGGCGCTT
TGCGCGCAGAGCTAAGCCTTCGGACCCGTGGACTGCA

697. chr3_CHST2_NM_004267_-1.64137
TCCTTTGGTCCAGTCGGAGGCTGCGGAGCGGCGGGGGTTGCCTGCGCTGT
CCGCCCGGGCATCCTCCCGGTGATGGAAGCAGCCGCCGC

698. chr3_SLC9A9_NM_173653_-2.36624
TCGGCAGACAGGAAGGCACTCCAA

699. chr3_WWTR1_NM_015472_-1.52356
CGCTCGGGTGAGTCCCGAGATTGCGGAGCTGGAGCCGAGGCTTGGCTGAC
AAATCCCGACCCGACTCTGTGCCTGGCAGTCTAAGGGCTTCGGCTCTCAC
ATCCCCCGAGCTGGCCTAAGGCGCTAGTGCTGGGCGAAA

700. chr3_EIF2A_NM_032025_-1.60712
TGATTTTGTATTATCACCTGGACCCCAACC

701. chr3_LEKR1_NM_001004316_1.57353
CTTTTCTTCAGGAGACAGTGCGTAGAGAATGTGAAGAACGCTTTGAACTG
ACAGAGGCTTTGAGTCAAGCCAGAGAACAGCTCCTGGAGCTCAGTAAGCT
TCGTGGAAGTTTACCATTCTCACCGTGTTCCCTCAGCAAGGGCAGCCTAA
CCTCCCCTGCTGCAGCAGTCAGTAATCATGGAGAGAGAAGCCTTGCAAGA
CTGAACTCTGAAAAAGGAATCCAAATTCCCAACCTGCGCGGGGTGTCA

702. chr3_SCHIP1_NM_014575_1.73501
GATGACCGCTCTCCGGCCCGGGAACCGGGGGACGTAAGCGCCAGGACCCG
CAGCGGCGGCGGCGGGGGCAGGAGCGCCACCACCGCCATGCCGCCCCCGG
TGCCCAACGGCAACCTCCACCAGCACGACCCCCAGGACCTCAGGCACAAT
GGCAACGTGGTGGTGGCTGGCCGGCCGAGCTGTTCCCGGGGCCCCCGCCG
GGCGATCCAAAAGCCCCAGCCGGCTGGGGGCCGGCGCAGTGGCCGCGGCC
CGGCGGCTGGGGGGCTCTGCCTTCAGCCCCCAGACGGCGGGACGTGCGTC
CCCGAAGAGCCCCCGGTGCCACCTATGGATTG

703. chr3_SCHIP1_ENST00000445224_1.54769
CCCGCCGGTGGATGCTCCGCGCCTGCCCTCCGCAGCCTCGCTCAGCAGTC
CTGCGTTGGGGTCTGCGCCCTAGGATGCACTGAG

704. chr3_SMC4_NM_005496_1.60186

Figure 3-59

TTCATTGGCTTTAGTATTTGCTCTTCACCACTACAAGCCCACTCCCCTTT
ACTTCATGGATGAGA

705. chr3_MECOM_NM_001105077_-1.67398
GTTTCATGGGGATAGTCTTCGCTCTTCAT

706. chr3_LRRC31_NM_024727_-1.93913
GAAGTTGATGGGGGTAGTTCCCAATAAGACATCTTCCTG

707. chr3_GHSR_NM_004122_1.89073
AGGCACAGGGAGAGGATAGGACCCGCGAGAGAAAGCCTGAGCGCGCGCTG
AGACCCA

708. chr3_ZNF639_BC026181_-1.82341
GTGCGGCCGCGGAGCCTAGGCCAGGGGCCTGGCGCTCAGGGCGTGGGGCG
CGCGGGGAGGGAGAGGGGTCGGCCCAGCACAGCGTCCGGGAGCGCTAGGG
CCGGAGCAGCGCTGCCCGCCGCCGTGCGTCCGCGGGAAGGAC

709. chr3_MCF2L2_NM_015078_-1.70546
TCCCCGGGAGTTCAACTCTGTCTCCGTATAAGGTTCCTCAGACGTTCTCA
GAGGACGAGCTAGAGG

710. chr3_EIF2B5_NM_003907_1.58829
TCGTGGCGACCACAAGTCCTATCACGCCACAAGAATCTCGGCTTGTTCAC
CTACAAATGAAGGCCGACGATACTTGCAGACCGAGTCTGACATCTATGGG
ACCC

711. chr3_ABCF3_NM_018358_1.66824
TAGAGAAGGCCGAGGCTCGACTTAAGGCAAAGCAGGAGAAGCGCTCAGAG
AAGGACACGCTCAAGACCAGCAACC

712. chr3_ABCF3_NM_018358_1.58829
GACATGGACTGGTCTCTCAGACCCCTGGGCCACCATGTAGGCCACCACTC
CAGGCCGTGGACTTCCCCCAACTTGGGGACAGCCTTATTCCCAAATGTCT
CTATCCTTTTGACTGGAGCATCTTCTGCACAACCTTGGGAGCCCATCCAA
GGGTTGGTGAGGACTG

713. chr3_ECE2_NM_014693_-1.58101
TACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACC
GAGGGGTGAGCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGG
ATTCGGAGGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAA
CAGCCTCTGGGACCAAAACCAGGCCATACTGA

714. chr3_CLCN2_NM_004366_-1.66957
TTCCAGACTGCCAAGACCCGGAAGATGAAGGCACTGAAGGTGGCAGCGAA
GAAGCCCCGCCAGTAGTTCCGCACTGCAAAGAAG

715. chr3_SENP2_NM_021627_-2.95524
GCAAGGGTCTGAGGCGTCCCCATTG

716. chr3_RTP1_NM_153708_1.52982
ACCGCGGAGAGTTCTGCGAGGCCTGCCAGGAGGGCATCGTGCACTGGAAG
CCCAGCGAGAAGCTGCTGGAGGAGGAGGCGACCACCTACACCTTCTCCCG
GGCGCCCAGCCCCACCAAGTCGCAGGACCAGACGGGCTCAGGCTGGAACT
TCTGCTCTATCCCCTGGTGCTTGTTTTGGGCCACGGTCCTGCTGCTGATC

Figure 3-60

ATCTACCTGCAGTTCTCTTTCCGTAGCTCCGTA

717. chr3_MASP1_NM_001879_-1.51342
CTTTCTTCTTCAGCGGGGCATAAGCCTTCTGGCAGGTGCTGTGGTCAACA
ATCGGGATTTCA

718. chr3_BCL6_NM_001706_1.58506
AAACTTCCGGCAAGTGTCCACAACATGCTCCATCTGCAGGTACATAGCCG
TGGCCATCACAGCCATGATGTTGCCCTCCCGCAAATTGAGCCGAGATGTG
TA

719. chr3_LEPREL1_NM_018192_1.54456
TGAGAGGCGGAGGCCGTGCCTGGC

720. chr3_CLDN1_NM_021101_-1.65806
AAGGCACGGGTTGCTTGCAATGTGC

721. chr3_ATP13A4_NM_032279_1.54701
AGGTAGAGCCGGAGGAACCGCAATTGTGATGACGTCAAGGGCTTTCCTCA
CCAC

722. chr3_HES1_NM_005524_-1.56921
AATTCCTCGTCCCCGGTGGCTGCTACCCCAG

723. chr3_GP5_NM_004488_-1.58257
GATTTCGGTGGAACTGCAGCTCCGTCAGGGCGCCCAGGCTGTTCAACAGC
CCCGAATCCAGAGACACAAGGCGGTTCGAGTGGAGCAGAAGTCTCTCGAG
CTTAGCCTGTGCTCCAAGCAACCCCTTGGGCAGGTGGGTCAGGTTGTTTC
CCGATAAATCCAACAACTTCAGGTTCTCCAGATTCGTGAAGAGACTGGCA
GGAAGGAAATCGAGCTGATTCTGGTTCAGAGCGAGCTCCTGCAGGTTAAC
CAGTTTCTGAAACATGTTTTGGTCAATGCCCCTTAGCGCATTGTGGTCCA
AAAACAACTGCTCCAGGAGCACCATCTTATCCAGCAGCGCACCTGGAAGA
TGCGTGATTTTGTTGCGCGACAGCCTCAGGGTTTTCAGTTTTATCAGGTC
ACTGAAGGTGCCGGGGGCAACGGCGGAAATGTGGCTGTCGGAGATCATGA
GGCGCTGCA

724. chr3_FAM43A_NM_153690_-1.8246
AGCGCAGCCGCAGCGCGCCCAAGCTTGGCTCCATCACCGAGGACCTGCTC
GGCGAACAGCTGGAGCAGGAGCTGCAGGAGGAAGAGGAAGAGGAGCAACC
CGAGGGCTGC

725. chr3_ACAP2_NM_012287_1.5409
GGCCGCGCTGGGACGCAGACGGCTACGGCGGGCGCACGGCCGCGACTAGC
GTTGCGCGGAGCTGCGAAGGGCGC

726. chr3_MUC20_NM_152673_-1.64391
AATGGAGGTTTCCTCCTCCTGCGGCTGAGTGTGGCTTCCCCGGAAGACCT
CACTGACC

727. chr3_MUC4_NM_018406_-1.77539
AATCGTAAGTCCCGTCGTCCCTGCTG

728. chr3_MUC4_NM_018406_-1.52305
CCCCACGCTAATCACCCTTTTCTCTCCTCAGCCCCACCCCACTACCCCAC
CAGGAAAGAAAACACCGATACACCCGTTGCTCTGCTTCTCATCAGCCTGA

Figure 3-61

GCTGAGTGGCGGGAGGGATGGGAGGAGACATGGGGGAATGGGAACAGGTC
ACACTGGAAATGGGTGGGCCACCCTCCTAGCCGGGTTCCTGGGTCCTCTC
CTCCCTCCCCAGGGGCTGCCCCTGTCCCACCAGAGCTTTGGGCTGCTGGG
AAGAATGGGGAAGAAAGGGCCCCAGAGGGAGCGACCTTGGGGCTGTA

729. chr3_TM4SF19_NM_138461_1.63302
GCTGTTGATGACATGAACGACCAC

730. chr3_WDR53_NM_182627_1.56799
GTCCACATGACACCAGGCTCTGAGGCCTCTGAGGCCGAAAAGCCACTGAG
GAGCAGATATTGGAATGTCTCTTCAAGGATCTGATAACTTTCTTGTTTTC
CAAGTCTAGGATTTTGATTGCCCCAGAGTCGTCAGCAGAAGCCAGCAGGT
TTTCCGTTTGATTCAATGAAAGACAATTGATTTCTTCTTCATTCACATGA
AAATGGTCCAAGGAATCTTTGAGGGACCTGACATCCAGTACACTAATGGT
TTCTCCATGTGAGGCATAGAGCTTGGTGGGACAGGAGGGAGAAAATAAGA
CACTGGTAACATCATCAGCCCCTTGGAACCGCGTGTGTCCTAATGGAG

731. chr3_NCBP2_NM_007362_1.52302
CCTTAAAGCCTGCGTCCCAGTCTGTGCGAATGATTCGGTCATCCAGACGC
GTCCCATTTATGTACCGCATGGCGTTTTCCGCA

732. chr3_LOC152217_NR_024388_-1.74721
AACGTCTGTCAGAGTCGCGGCCTATCCGACGTGCGGCGCAGCTCACGGCC
TTCGCACTGCTGCAGGCCCAGCTGCGGGGCCAGGACGCGGCCCGCCGCCT
GCAGGACCTCGCGGCTGGGCCCGTGGGCTCCCTGTGCCGCCGCGCTGAGC
GATTTAGAGACGCC

733. chr4_PDE6B_NM_000283_-1.70857
GAGCCTGCTGACTGCGATGAGGACGAGCTGGGCGAAATCCTG

734. chr4_GAK_NM_005255_1.52773
GGTTGGTGAAGAGCCGCTCTGTCCCACCCCGCAGAATGTCCAGGAAGCCG
CCATACGGCTGGTCGTACTCCGCCAGCG

735. chr4_DGKQ_NM_001347_1.60531
CGCCGGCCAGCACGTCAGAGGAGCCGCACGTCTTCCTGCAGAC

736. chr4_IDUA_NM_000203_1.74924
GGTCTACGTCACGCGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCG
AGTGGCGGCGCCTGGGCCGGCCCGTCTTCCCCACGGCAGAGCAGTTCCGG
CGCATGC

737. chr4_WHSC1_NM_133334_-1.66928
CTGGTCCGGCTGATGGGGGTTTGCTCAGCACTGTGCCA

738. chr4_WHSC2_NM_005663_-1.6484
CCCAGGGGTCCGAGTCGAGGCTGGCGAGCTGGAT

739. chr4_POLN_NM_181808_-1.85472
TGCTCCATAGACCACCGCGTACACCACCTTCTTGGTTTGCTCTCTGTCTG
CGTGTGTCACCTGTTCCACGGGCACATC

740. chr4_RNF4_NM_002938_-1.51516
CCGGCGGTGGCGCCTGCGGACCTAACTAG

Figure 3-62

741. chr4_TNIP2_NM_024309_-1.87732
CGTCCACTAGGGACGGCGCGGCGTCCCCCTCCAGCGCGGCCAGGCGGGCG
CGGAGGCGAGCGATGAGGGCGTCGCGGGCAGCGAGCTGGTCCTGCAGGCG
GCGCAGCCGCTGTCCGGCCTCGTGGTACAGGGTGCAGAGCGCGGCAGCTG
C

742. chr4_MFSD10_NM_001120_1.64038
TCCACTGGCATCCCGATGGCGGTGGCAAACCAGTCC

743. chr4_NOP14_NM_003703_-1.63088
CCTGAGGGCCCGTGCGCGAGACACCCCGGGCAGTCCCACGTCGTGGCGCG
TCTTCCGGCCCAGGATCTGGAACTTCTGCCTGTTAACTTTCAC

744. chr4_HTT_NM_002111_-1.67491
TTCTCTCACCTGCTGAAGGTGATTAACATTTGTGCCCACGTCCTGGATGA
CGTGGCTCCTGGACCCGCAATAAAG

745. chr4_RGS12_NM_198229_-1.83802
GGGACCCATGGCAGCCGAGACCTCCCAGTCAACAGAATCATCGATGTGGA
TCTTGTAACTGGCTCGGCGCCCG

746. chr4_DOK7_NM_173660_-1.58568
GTCACTTGGACGTCAGCGCCAGCAGCCGGCTCACCGCATGGCCAGAGCAA
TCCTCGTCGTCAGCCAGCACGTCACAGGAGGGGCCTAGACCAGCAGCTGC
CCAGGCCGCCGGGGAAGCCATGGTGGGTGCCTCAAGGCCACCCCCCAAGC
CGCTGCGTCCGCGGCAGCTGCAGGAGGTTGGCCGCCAGAGCTCCTCGGAC
AGCGGCATCGCCACTGGCAGCCACTCCTCTTACTCCAGCAGCCTCTCGTC
CTACGCGGGCAGCAGCCTGGACGTGTGGCGGGCCACAGATGAACTGGGCT
CACTGCTCAGCCTGCCAGCAGCGGGGGCCCCCGAGCCCAGCCTGTGCACC
TGCCTGCCCGGGACAGTCGAGTACCAGGTGCCCACCTCCCTGCGGGCCCA
CTATGACACACCACGCAGCCTTTG

747. chr4_LYAR_NM_017816_-1.61555
TTCCGAGTGCCTCCGCTTCCTCTTCCCTGCGCCCACGTGTGCCTCTTCCT
CACTGGCGCTGTCCTTGCGCTGCTTCTTCTTCTTGCTCCTCTTCCCTGCA
GAGCCATTGGCCTCAGGGACTTCCTCCCCACCAGCCTCAAGGTCAGCCTC
CTGTCCCTTTTTGCGCTTCTTAGGCTTCTGATTCC

748. chr4_D4S234E_NM_014392_-1.67578
TCCTCACCTGCGTCGTCTTCCTGGTTGTCTACAAGGTGTACAAGTATGAC
CGCGCCTGCCCCGATGGGTTCGTCCTCAAG

749. chr4_CYTL1_NM_018659_1.54257
AATGAAAGAGTGGGTCCTGTCAGCACTACGTAAAATATATATCTTAAGAG
CATTAATTTCTTTTTAAATGAAAGACAGTGAAGAAAGTCTGTGTTAGAAA
AAGGCATAATAGAAGCTTGGTTAAATGTAAGCAGGTTTCTATCAAGAAAG
AATAAAAGTACCATTACTCCATTAAACCAGTAATAAAAACATACTATTGT
GCAAGTTCTCAAAATAGTTGTTCATAAAAGTGAAGCTTGTTAGTCCTTTT
CTTCTTTTTAGTGACCAAATCAACATGCTGTGTATCTAACCATCCTGGCA
AGACATGAGTCAAGGGAATGAGAAGCATGGTTGCTAACTCTATGCTCAAA
GGAGGT

750. chr4_MAN2B2_NM_015274_-1.51658
CCAACCTGATGCACAGCATCTGGGA

Figure 3-63

751. chr4_GRPEL1_NM_025196_-1.63813
TGTGCACAACAACCGGGGAGATGGC

752. chr4_ABLIM2_NM_001130083_1.80389
CTGGCTGCTTGTCGACACGCCGGATGCCAGATGGAG

753. chr4_ACOX3_NM_003501_-1.60488
TCGCCGTCGGCTCTGCCAATCGGTGAGTCC

754. chr4_ACOX3_NM_003501_1.53023
CAGGAGGAGCGATCACGTCTACCAGGGCAACTGCA

755. chr4_FBXL5_NM_012161_-1.51538
AGTGTGGGGCGGTGAAGACGTCCACTTCTTCAGGAA

756. chr4_TLR10_NM_030956_-1.9921
TTACCACTTATTTCCTCATATGAAT

757. chr4_TMEM156_NM_024943_1.59995
GTGTATATTGATCTCACTGATGCACTGTGGAAGTAAC

758. chr4_LOC401127_NR_026854_1.53595
CTCTGTCATCAGGACCCTCCGTCCACGTCCCCTGTGCGGCCAGCGTCAGA
G

759. chr4_RHOH_NM_004310_-1.69105
TGTTTGAGTGCGCCGTCCGAACTGCCGT

760. chr4_APBB2_NM_004307_-1.51123
AAAGGTTGCTTGTGACAGGTCCAGCCAAGAAGACAGTGAAACTAACTCAC
GCATCATTCATTCCAAGGACGCAGCGTTAGTTCACTAGGAGGGGTGGGGC
CACACTCTTCTCTGTGTGTGTGTGAAGTTAAGTAATGTTCACAATATTTA
CAATAAGAAAAAGACCTTCCACTGCGCATGATGTAACTTACAGCAAAAAA
AATTATTCATGCTTCTTTTCATATCACATGATGGTGGCAAGACGAGAGAA
CATGCTTGTCTAACACTGCTTGGTTAAGGGTAAATTCTCTGAAGACAAAG
CATCAGCAACTGGATGGAAGGTCGGATGGCGGAGTTCATTTTCTTTAGTG
TAGCTAGTCAATCTTCAGGTAAATAGCCGAGTCCTTTTGCATGTGCAG

761. chr4_LIMCH1_NM_014988_1.68458
TGGGATTCCGAGCGCAGCGACTCCCTCTCTCCTCCTCGCCACGGCAGAGA
TGATTCCTTCGACAGCCTGGATTCCTTTGGCTCTCGCTCTCGGCAGACGC
CTTCACCAGATGTAGTC

762. chr4_GABRA4_NM_000809_-1.93464
AACAGGTCCAAAGCTGGTGACATA

763. chr4_GABRA4_NM_000809_1.6815
GGAAGCGCAGGAGGGCGAAACTGACCCCGGCGGACAGAGCGATCGCGGGT
A

764. chr4_TXK_NM_003328_1.88144
GGCTTTCGTTTTGACGGCTGCACACGGCCCGTGTT

765. chr4_KDR_NM_002253_-1.6859
TTCCTCACTGGAGTACACGGTGGTGTCTGTGTCATCGGAGTGATATCCGG

Figure 3-64

ACTGGTAGCCGCTTGTCTGGTTTGAGCCTTCA

766. chr4_SRD5A3_NM_024592_-1.59461
AGTAGATGAGACTTCTCCAAGCTGCTTCACAAGCAAACTAACCGAAAAAC
CGAAAATATACAAACAGCTTCACACACACACACACACACACACACACACA
CACACACACACAAAGGAAGATCATCAATGGCTGCGGTAGCCTAGTAGGAA
TGGACTATATAAT

767. chr4_HOPX_NM_001145460_-1.59536
GCGGCAGTAGAGAAAAGTAATCGAAAGCCAAGCACGGCAGACTATCATGG
GGGTAGCCTTCTCTTTGGGGGCTACTTTCTGGGTGCCATATTT

768. chr4_HOPX_NM_032495_1.53803
CACTGAAAGTATGCCGAGGTTACGTCTCTCCTGGTTATTCAGGTTTGATG
TTCAGGCTGGGACTTCTGAGAGTCTCATGGAACTTTCTCGTCACTATCTT
CTCGTCCCTGACCTCTCTCCTAGCCAAGCAAGCTTCTTCACCAAGATAGG
ATAAGAGAGATGTGGCTGAGAGAAGACGGGGAAGAGAAAAGGGACCCTGA
GTCTTCTCA

769. chr4_LPHN3_NM_015236_1.81509
TCCAGACCCGTGTCCAGGAACCTATAAATACCTTGA

770. chr4_TMPRSS11B_NM_182502_1.51696
AGAGGCTCCACAGTAGTGACGGCCTTTCCATTGCATGCTGGCCTGCCATG
GCCATGCCCCCTCCAGGGAGCTTTTTCCATTCACAATTTTGTTGCCAGTT
ATGATACTGTTGGCTACTTGTCTCCCA

771. chr4_CXCL5_NM_002994_-1.509
GCTAGGGCCTCGAGGATGTCGCTATATATTTTTATAACTAAATGATAAAT
TTATATTCAAATTGTTTGAATACGTTTCCAAAACTTTCAGAGTACAAGTC
ATTGTTAAGTTTGCCTTTACTTTAAAAACTAAAAGAATACATTTCTATAT
AAACTAGCAGTCAGGAATTTGCCTGTTTTCTAGCTTCTTCATCTATCTAA
AATATATATTTAGCTACCAGAATTATGGTACTCCTAATAAAATACTTAAT
AAATAGCATATAAAATCAAAGTTTAAAAGTAAATGATGGCAGTTTGCCAT
ACTAAAAAGATAAAGAATGTCTAAAATTATAGGAAGATAAGATATTAGCC
CTCATAGAACTTAAACTTTTAGAAATTCTGAATAAGGAAATATATTCTAC
ATAGATAAGGTGTGAAACACTCAGCTTTCTAAAGTGAAATAATTAAATAG
TATCCCACAATCAAGAGTAAGGAAATTCTCTAACATATTCCCCAAGAAAC
ATTAAAATATTTCCTATTTCTTATAAAAGTGAAGATAACAGTGTATTTCC
ATCAACAGAATTCTTATGAAACATCATTTCCACATTAAATCCACAGCCTT
CTCAGTTAATATCTTAAGGAATATTTCTTGGAAATATAATAGTCACCTAC
AATTCAAGACACTTTGAAAGATTAACAGCCAGTGATTCCTGGCTCACACT
ATAGTCAATTGCCAAAACTTCAATAGCATAGCAGATAAAATAACAGCAAA
TAGCAGAGGTACTATGCTAAACACTTCATTAGCTGAGCTGAAAGCTTAAG
CGGCAAACATAGGTTTTCCTCACACTCTTCAAAGTGAGGAATCCAGGAAG
AAAGCTAACTACTGGAAAAACAAATAAACAAACAACAACAAAATCTTTCC
TTCTTGTCTTCCCTGGGTTCAGAGACCTCCAGAAAACTTCTCTGCTGAAG
ACTGGGAAACTTTTCCATGCGTGCTCAT

772. chr4_ART3_NM_001130016_-2.84552
TGTGAAAATCCTTGAACCCACCCAAATACCTG

773. chr4_PRKG2_NM_006259_1.67395
ACTCCCTTGCTGATAGTTTCTCCCATACATGCATTCCACCATGTCTTTGA
TCTGCTGAGGATCCAGTCTTTTCAGAAACTGATTTTTATTAAGGGCATCT

Figure 3-65

GT

774. chr4_HNRPDL_NM_031372_1.93741
TTCGACCAAACTCATACCTTTCTACCAAAATCCTTGAG

775. chr4_HPSE_NM_006665_-1.74998
ATTCCAACCGTAACTTCTCCTCCACATCAGGAGGGATGGATCCATATTTG
CAAAT

776. chr4_HPSE_NM_006665_-1.68768
GGAGGATGAGGAACCGCGGGTCCGTGGCCAGGTTGGCGTCAATGGTGACG
GACAGGAACGA

777. chr4_FAM175A_NM_139076_-1.71858
GTCCGAGTCCGTGTTGAGGTGCTGGAAAGCGAGTGCGCCGAGCACAAAGC
CCGAGAGCACCGCCGACGTA

778. chr4_WDFY3_NM_014991_-1.99942
TCCGCAGGGGAAACAAAACTGCACA

779. chr4_MMRN1_NM_007351_-1.88325
TTGATACACACCAACCAGGCTGAAAGT

780. chr4_ADH1B_NM_000668_-1.93148
CACCAGCAGACTGTGAGTCTTTGTG

781. chr4_MAPKSP1_NM_021970_1.55121
GAACCCCCTTCTCTCGCAGGATCAATCTCC

782. chr4_H2AFZ_NM_002106_1.57595
GATTTTAGGTGTCGATGAATACGGC

783. chr4_MANBA_NM_005908_1.64682
GCCAATAAAGTGCCCCCATCGTGTGCCCTTGCTGATCCACTATCTCGCTG
CGACTACGGCGGTAGAATTCAGTTTCTGTTTTGACACACTGGGCC

784. chr4_LEF1_NM_016269_-1.62267
CCGGGATGATTTCAGACTCGTTCACCAAGGAAGACTTGATGTCAGCTAAA
TCGCCTTCCTCTTCGGGATGACTGATCTCGGCGAAGATCTTTTCCTTCTG
AG

785. chr4_COL25A1_NM_198721_1.80687
AGTCTTGAGGTGATCCAGGGTATCAGGCAGCAGATGAATGGAAGGGGCCC
CTTTGGCGGATTCGAGAGCGGCGATCCTCGCCTGGAGGTCGTTGGTTTTC
ACACCCAGGTACAGGCAAGACACCACGGCCACCACTGACAGGAGGGCCGC
CAGGACGGCACACGGGGGCATGGTCCGGGCACAATGCTGTTCG

786. chr4_CFI_NM_000204_-1.89773
TAAAAATATCCAGTGAGATTTGCT

787. chr4_LRIT3_NM_198506_1.52982
AGGTTCCAGACCAGAGTATTATTGCTAA

788. chr4_ENPEP_NM_001977_-1.63448
TTCGACTGCCGGACTTCGTCAACCCAGTCCACTACGACCTGCACGTGAAG

Figure 3-66

CCCCTGTTGGAGGAGGACACCTACACGGGCACCGTGAGCATCTCCATCAA
CCTGAGCGCTCCCACCCGGTACCTGTGGCTGCACCTCCGGGAGACCAGGA
TCACCCGGCTCCCGGAGCTGAAGAGGCCCTCTGGGGACCAGGTGCAAGTC
CGGAGGTGTTTCGAGTACAAAAAGCAGGAGTACGTGGTGGTCGAGGCGGA
GGAAGAGCTTACCCCCAGCAGTGGAGATGGCCTGTATCTCCTGACCATGG
AGTTCGCCGGCTGGCTGAACGGCTCCCTCGTGGGATTTTATAGAACCACC
TACACGGAGAACGGA

789. chr4_PITX2_NM_000325_-2.11604
AGTCCTTGGCTACTGCCCCGCCGAGCCCCCGTAGCCGCCGCTGCCCGCTC
CGGGTCGCGCTCTAGGCGCGGAGTTTCC

790. chr4_EXOSC9_NM_001034194_-1.64966
TTTGGCAAATACGTGTAGACCTACATTTATTAAATCATGATGGAAATATT
ATTGATGCTGCCAGCATTGCTGCAATCGTGGCCTTATGTCATTTCCGAAG
ACCTGATGTCTC

791. chr4_TRPC3_NM_001130698_1.56947
CGTTGCTGAGCTCTAGGGCCGTAAGCACCGGGTCCTCGCTGGACAATGAG
AGGTAAGCCGGGCTGGCCAGCCCCTTGTAGGCATTGATCCTCGAGCGTGA
GTGGCTGAAGGAGTCGTGCCTCTGCTTCTCCATGCAGTCCCCGCACTTGC
AGAAATAGTCGTGCGGCCGCTCGATCCTGGCACCCTTCATCAGCAGCATG
TGCACCACTTCGTATTTCTGGCAGTGCGCCGCCAGGATGATGGGGGTGAT
GTCCGGCGAGAAGCGCGTGCCGTCCTCGTCGTAAGCGTAGAAGTCGTCGT
CCTGCAGCTCCTGCTCACAGGGGCTCAGAGTGAGACGCTTGCTGGCCGCG
AAGCCAGGGTGGTTGAGGATGGCCTCTACGATGCGCACGTAGCCCTTGCT
GATGGCGAGCAGCAGGGCGTCGCCAATGCGCGCCAGGTTCTCCTTCTTGA
GCAGCAGCTCGGTCACCTCCAGGTGCTCGTTGCCCACAGCCAGCTGCAGC
GCGTTCTGGCCCATGTAGTCCACGCAGTTGACGTTCAGCG

792. chr4_MGST2_NM_002413_1.68029
TTTTGCTACTTGTCTGGGTCTGGTG

793. chr4_SCOC_NM_001153484_1.79071
GTTGGAACTCCAACACACACTTGA

794. chr4_UCP1_NM_021833_1.60059
CCTGGACCGTGTCGTAGAGGCCGATCCTGAGAGAGGCGGAGCTGATTTGC
CGCTGAAGCCCCGCAGGCAGCCCGCTGTAGAGTTTCATCCGCCCTTCTGT
TTTTACCACAGCGGTGATTGTTCCCAGGACACCTTTATACCTAATAACAC
TGGACGTCGGGCATTCACCTTGGAC

795. chr4_UCP1_NM_021833_2.10941
GGAGCCGGACTTTGGCCGTGTCCAGCGGGAAGGTGATCACGTCCGCCAAG
CACGCCGCTATTCCAGCTGAGAAGAGCTGGACCCCCAGGGTCGGGTGTAC
GTCCGAGGCTGTCAGGC

796. chr4_NR3C2_NM_000901_-1.629
GGTCCGTCTCTCGCCGTCTACCTGTTGCAGCGCTTGCCACCGCCACGAAA
CCCCTGCTGCGGAGCCCCCCTAAATCCAACCACATCCAGGCCAGCGAGTG
CCGCTCTC

797. chr4_TMEM154_NM_152680_2.044
CGACGGGAACGAGCGCGATCACCAGGGCGAAGACTAGGGCTGC

Figure 3-67

798. chr4_TRIM2_NM_015271_-1.64877
GGCCAGTTCAAAAGTCGTTTTGGCATACGGGGACGCTCTCCGGGGCAGC

799. chr4_DCHS2_NM_001142552_-1.74539
ACCGCTTTCGGAATCAATGGCAAAAGATGGTCCACACTCTGCGGTGTGGA
CCATCTTTGATTGCAGGGAGCCGAGATTGCAGGGAGCCGAGAGTTGGACT
ACAGTGTAGCGCAGCCAGGCGTGATCACTGCCTGCCTCGTCGGCATCGGA
GGCGCTGACCCACATGACTACAGTGCCAGGGGCCGCGGCCTCGGACACTG
AGGCCTTGTAATGCTGTTGGCTGAAGAGAGGTGGTTGGTCATTGAGGTCA
GCGACCCGGAGTAGCAGCGTCTCCTCCGTGCTCAGCGGCGGGGACCCCGC
GTCCGTGGCCACCAGTAGTAACTCATACAGATCGCGGCTCTCTCTGTCCA
GGGGCCCCTCCACGCAAAGGAAAAATACCCCTGGGGGGCCGCCGGGTAGC
AACGCGAAGTCTCCCTCTCCGCCTTCCAAGGACAGAGAGATGCTCCCGTC
TCCAAGACCCACACCAAGCTCCCCTGTGGCCTCATCTTCCTTCTCCCAGT
CACCGTCCGCGTCAGACACCGAGACGCGAGCCACGTAGTCGCCCGGTCGG
GCGCCTTCAGAGACACGGGCGACGCCTCCCTCTGTGAGAAAGAGCACGTG
AATTGCTGGCCGGTTGTCATTCACGTCCAGCACGGCGATGGACACGCGCA
CCGTGGCAACCTCAGGCTCGGCGCCTCCATCGCGGGCCTCCACCACCAAC
TGGTGCCAGGCCTGTGCCTCGCGGTCCAGAGGTCTCCACACTCGCACCAC
GCCGCTCAGCTCCTCCACCGCGAAGTAGGCCGCGTCGCCCAGTGCCCCGC
CGCCGCTACCCGCCCCAGGCACTTGCCGGGCGCGGACGCTGTAGCGCACG
AAGCCATTGGGCCCCAGGTCGCGGTCGGTGGCGCGCACGCGACAGACCTC
GGCGCCCGGCTGGGCGTCCTCGCGCACCGCGGCGCGGTACTCGTCCTGCT
CAAAGACCGGCGGGTTG

800. chr4_RAPGEF2_NM_014247_1.7067
GAAAGGAGGGCAGGTATCGAGAGCCCCCGCCCACCCCTCCCGGCTACATT
GGAATTCCCATTACTGACTTTCCAG

801. chr4_TLL1_NM_012464_-1.69221
GCGGCTCGCGCTCGGCCGCGGAGTCCTGGCAG

802. chr4_TLL1_NM_012464_-1.88988
AGAGACGGGTACTGGAGAAAATCA

803. chr4_PALLD_NM_001166108_-1.66196
AGTTCAACAGATTCTGACAGTGAA

804. chr4_HMGB2_NM_002129_-1.67567
TTCTGGTTCGTTCTTCTTCTTTGAGCCTGTTGGCCTGCCAGGGCCCTT

805. chr4_VEGFC_NM_005429_-1.88934
GTCTTGCTGAGGTAGCTCGTGCTGGTGTTCATGCACTGC

806. chr4_VEGFC_NM_005429_1.76825
TCCCGTGGCATGCATTGAGTCTTTCTCCACT

807. chr4_PDLIM3_NM_014476_-1.63566
GAAAGGTTTGGGCCGAATATTATGCTTGTGTTCAA

808. chr4_SORBS2_NM_001145671_-2.02377
TACCAGTGACTTCTCCGAGTCGGGAGCTAGAAAGAGGCTTCCGGCCAGGT
TCCCTTGGAACAGGTG

809. chr4_FAT1_NM_005245_-1.71778

Figure 3-68

CCCGAGCAGGGACCGGGCCTGCCGGG

810. chr5_FLJ44896_AK126844_1.74085
CAGCAAACATCCAGGCGGCGGCAGCAGCTCTCAAGGTACACTTGTCCTGT
GAGCCGCAGAG

811. chr5_PDCD6_AK295082_-1.51523
ACCTGGGCTGCTTTGTATCCGACCCGCTTGGGTACCCGCTTGTGTTTCCT
TTGTCTGTGGGTCCGTATCACTTTGCTCCCTTCTGGAATTCCACTTAGAT
GAGCGTCGGCCCTTTCATCCCTCTCCCTCCGTCTCTGTACCTTTTCACAT
CTCTCCGTGTATGTTTGCTCTATTC

812. chr5_AHRR_NM_020731_-1.57705
AGATGATGCTATCCTGGGGAGGCTGCT

813. chr5_EXOC3_NM_007277_-1.55276
GTGGATGTCGGCACCCTGGAGCCATTGCTTTCTCCACACGTGGTCTCTGA
GCTGCTTGACACGTACATGTCCACGCTCACT

814. chr5_CEP72_NM_018140_1.51479
ACTTCAAACAAGTGTGAAGAGGCTGTGTGGCGAGATTGTGGAACTGAAGC
AGCACCTGGAGCACTACGACAAGATCCAGG

815. chr5_TPPP_NM_007030_1.64933
CTGCGTGCTTGTAGCCGGACACATAGCCTGACTCGTCCACCAGATCCACG
CGGCCAGCCTTGCCCTTGCCCTTGCCAGAGGGGTCGAAGCGCTCCTTGTG
GGAGCCCGTGAACTTGGTGGTGTCCGTGAGCCTCGACACTGTGGGCGACG
AGATG

816. chr5_NKD2_NM_033120_-1.5654
ACCATCTATGAGGTCGTGGATGCCTCGGTCAACCACTCCTCGGGCAGCAG
CAAGACCCTCCGTGTGAAGCTAACCGTCAGCCCTGA

817. chr5_CLPTM1L_NM_030782_1.61338
CCAGGGCAGATGTGCCACTGACTTCAA

818. chr5_SLC6A3_NM_001044_1.56041
GCCTGGGCTTTGCACGCGAGTCCTGGCGCCGAGAGCGTTCCGCGAAGCCT

819. chr5_NDUFS6_NM_004553_1.62612
GAAACAAAAACCGGCACATGCGGTTACTGT

820. chr5_NSUN2_NM_017755_-1.50117
TCCTGAGATAATGAAGCCGTTCATTCTTGGGCACAAAAGTTCGAATGGAG
GCCTTTCCCCGCCATCCGCATAAGACGATGGGACACTGCAGAGCGTCTGG
ATTC

821. chr5_ADCY2_NM_020546_2.08882
CAAGCCCTTTGCACACCTACATCACAGGGACAGCATGACCACAGAGAACG
GCAAGATCAGCACCACG

822. chr5_SEMA5A_NM_003966_1.69989
GTGGATGACAGTCGCATCGTGGGATTGCTGCTGGTACCGCTGGCAGTAAG
TATAGACGAGCAGGGTGAGGAGGCAGCCGAGGATGGAGCTGCTCAGCCCC
ACGGCGATCATGTGGAACATGT

Figure 3-69

823. chr5_CDH18_NM_004934_1.59702
AGATCTGTAACTGGCTCCCTGTTTC

824. chr5_RNASEN_NM_013235_-1.51325
TTTGACTTTGGGACTATTTGCTAGGAGGTGGCGAAGTTTCACATAACTCT
TCCACAGTTT

825. chr5_DNAJC21_NM_194283_-2.79749
GGAGTTTGGAGATGGATCGGATGA

826. chr5_DNAJC21_NM_194283_1.54368
TAAAGACAGTGATGAGGCCGAGGACGCTGAGCTCTATGATGACCTTTACT
GCCCAGCATGTGACAAATCGTTCAAGACAGA

827. chr5_PRLR_NM_000949_2.5952
CTTGGGCTTGCCGCTGTTCTCTCT

828. chr5_EGFLAM_NM_152403_-2.15216
TCCTTGGGCCTTCGGGATGGAGCCCT

829. chr5_SEPP1_NM_005410_-1.94538
TCTCTGTTCCTCCCGATGGGAGGA

830. chr5_NNT_NM_012343_1.73877
TAGACATCCTTATCAGCACAGCACT

831. chr5_SNX18_NM_001102575_-1.71985
CCGGCCCGCTACGCCAATGTGCCCCCCGGGGGCTTCGAGCCCCTGCCTGT
CGCG

832. chr5_PDE4D_AY245867_-1.62764
CTCATGGGCAAGGTTCTAACACGCAGGAGCGCTTTCTTCCTTCATACTGA
ATTTACTCCAGTACTAGGCTGTTAGGAAGTGACAGTTTCTTCTGTGTCTT
GCAATGCCAAGGGAGGAACTGAATTCTGAATTGATTCTTCATCTGGGTCA
CAAGGGAAACCAGCATAGTGAAAGAGTCACTTGATCTCTTTTTTGCAATT
CCATAGTAACAGCTTTAAAGGTTTCTGACACTCGAAGAGCGCAGGTAGAG
AGAGAGAAAAAGAAAATGACCGGGAGGTACTGTAACACGGGAGAGCTGTC
AAGGAAGTTCCATTTCAGGGCAAGCACAGGAAAACACTCCTCTCCGTGGA
GCAAAGAAGTCAGCC

833. chr5_SFRS12_NM_001077199_-1.55515
TAGATCCCATAATAGATCACGTTCAAGACAGAAAGACAGACGTAGATCTA
AGAGCCCACATAAAAAACGCTCTAAATCAAGGGAGAGACGGAAGTCAAGG
AGTCGTTCGCATTCACG

834. chr5_MAST4_NM_198828_-1.88175
TTGACCACATATTATCCCCTCCACC

835. chr5_SLC30A5_NM_022902_1.58612
TGCCAATATCTTATCATCTCCCTCTAAG

836. chr5_BDP1_NM_018429_1.5504
ACTGAAAAGCCATCGACTCCAGTCCAGACAAGA

Figure 3-70

837. chr5_MCCC2_NM_022132_-1.7595
TGTGGGCCGTCCTGAGGTTAGCCCTGCGGCCGTGTGCCCGCGCCTCTCCC
GCCGGGCCGCGCGCCTATCACGGGGACTCGGTGGCCTCGCTGGGCACCCA
GCCGGACTTGGGCTCTG

838. chr5_PTCD2_NM_024754_-2.27983
TCAGCCGTCGCACCTTCCAGCCAC

839. chr5_POLK_BC050718_-1.69381
TTTTGATATGGTGTCCTTAGTTTTTA

840. chr5_IQGAP2_NM_006633_-1.76575
ATAATTGATGTGATCCGGAACCAGCCAGGGA

841. chr5_F2R_NM_001992_-2.23496
CAGAGACTCTCACTGCACGCCGGAGGGCGCCCTTCCTCGCTCGCGCCCGC
GCGACCGCGCGCCCCAGTCCCGCCCCGCCCCGCTAACCGCCCCAGACACA
GCGCTCGCCGAGGGTCGCTTGGACCCTGATCTTACCCGTGGGCACCCTGC
G

842. chr5_RASGRF2_NM_006909_1.67061
CGTGCCAACGCCATCGAGAAATGGGTGGCAGTGGCGGACATCTGCCGATG
CCTGCACAACTACAACGGCGTGCTGGAGATCACCTCGGCCTTAAACA

843. chr5_ZCCHC9_NM_032280_-1.86918
GCGAATGGTCACAGTTGGTCGCTGGGCAAAG

844. chr5_RASA1_NM_002890_-1.55375
GGACGAAGGTGACTCTCTGGATGGACCAGAATACGAGGAGGAAGAGGTGG
CCATACCGTTGACCGCTCCTCCAACTAACCA

845. chr5_POU5F2_NM_153216_-1.79093
GGCTACCCCTGCAGAGTAGAGACGTGTATAGTGGGGGATATCCACTGGGA
GCCCCAGTCCCAGGTGAAAGCACA

846. chr5_GPR150_NM_199243_2.18525
GCCGCCAACGTCCCTGCAGCCAGGCGCGCCCCCGGCCGCCCGCGCCTGGC
CGGGGGAGCGTCGCTGCCACGGGATCTTCGCGCCCCTGCCG

847. chr5_SLCO4C1_NM_180991_-1.53661
ACAGTTATAGGAGTACCGGCCATAAAGGTAAAAATAATTACAATAAAGAA
AATGCAAAGGAATATGGGCAGTTTCGCACAATGAGTTTCACATTTTCCAG
CTTTAGCTTCAAAACCAAAAGTTTCTGCAGTGGATGTTATT

848. chr5_GIN1_NM_017676_-1.54891
ATTCTCTTATGTAGGGCTTAAGGTGGGACATTTTGATAGGT

849. chr5_FBXL17_NM_001163315_1.54394
GAGCATGCAGGGCCCGCGGAAGAAGCAGTCCCGGCTCCG

850. chr5_PJA2_NM_014819_-1.57018
ACTGTCATTTGAAGGTGGGGCATCAGGATCAGGCTCAGAGGAAGGAGCTG
CAGATGCTTCAATAACCGCAGGTGGGAAATGACGGCGGCACACAGGGCAT
G

Figure 3-71

851. chr5_EPB41L4A_NM_022140_-1.56167
TAAGGGTTAACTTGGATTCATCCAGGAGCAAAACTTCGCAGTAAAATTCT
TCCGGAACAGCGCAGAAACAGCCCAT

852. chr5_EPB41L4A_NM_022140_1.58578
CGGTTGTGGTCGTCTCCAGCCAGGAGAGAAAGCTACCACCGAGGCGCCCA
GCCGCCCCCTCCACTCAAGCGCGATGCATTAATTTATTGTCCGCGCCGTG
GCG

853. chr5_DMXL1_NM_005509_-1.50023
TATATCCTGCATGCAGTGCTCCTTA

854. chr5_PRR16_NM_016644_-1.50909
GACTGACAGCTCCAAAACGGACACGCTGAATAGTAGCTCAAGTGGCACAA
CAGCCTCCAGCCTAGAGAAGATCAA

855. chr5_SNCAIP_NM_005460_1.59747
ATGGTCAGTTGGAGTGCGTACGCTGGATGGTGAGCGAAACAGAAGCCATT
GCAGAACTGAGTTGTTCTA

856. chr5_ALDH7A1_NM_001182_1.55599
CGTTGTTAGCAGGGCAATAGGTCGTAATAAC

857. chr5_MEGF10_NM_032446_-1.52007
GAACTTGCAGAACTCCCTCGGAGACGCAGGTTGCAGTGGACATTGGGATT
GTTGCTTGAAAAATTAAAATTTGAATATTTTCTCTCTCATTTGCATCATA
CAGCTCTACCTAGGATTGTACAGTTTACCATAAAATTTACTTCATGAAAG
TGGGAATCACTGAACATGTAGAAGACAAGGAACATATTGTTAACTCCTGA
TTCTTAACTTTATTCAACTGGACTCAGAATTGTAGGGATAATATGAATGC
AGGAGGAAACATTCTGTCAGGCGGTATGACTGGACAGACTTTGAATATAC
TCTAAAAGTGGACAGAAAATTTACGAAAATCTTAGATTTTGTTTAGAATG
AGAAAATATACAATTAGAATTATTTTAGAAATAGTAGGAAGTATTGCAGA
AGTCAATACACAAATGTGCCAGGCAGAGGTGGTTTTCTCTGTTTGACTCT
CAACCAACTTCAGATCTATGACATTATTCTGATCACTGGCTCCATCATAC
ATATTCACCACTTGAGATTCATAACATATCAATAGTTATTTCATAAATAT
AGAAATGAAATAATTTTATTTTTGACAGACTGGATGGAATGAGTGTGTAA
TGATTGATAAAGGTTGTAAATTTTAAATGCAAGATGACGCTTACGTTCTG
TAAACCATTAGTAATACATGCTGTAATATAGAATTAGTGGAACATTTTGA
TTAATCTTTCCCTAGAAGTGACTGAAATATTTTTGTGCATATTTGAGAAA
GGGAACTTTCCTTTTATTAATTGTCAATTTAGAGAAACTATGCTTAAGCT
GGTCTTTTGCATTGCTAATGTGACATGTACCCAACTTTTCATTAATTTGT
ATTTCCATTTTTAAATTGCATATTCTATGTTTTGTAGTGTTTGGATTGTT
AATGAAAAAATATTATATGTTCGTTATTCCTTGTATTATTGCCACTTATC
TTTTGCTTGATAAAAATGCGTTGTTCTTTTTTCTTTTGGAGGGACAAGAT
GAAAATATATAATTTGAATTGATTAAAATTGGTCGTTACTAAAATAGTAT
AGTAACCACAAGTGATTGGCTTATAAATGAAGTAGAAATGCTTTTTAATA
TTCCAAAATAGAGTTCCTTTTGATCTGTTGGTGCTGAGCCTTGGTTAAAC
CAGGGAGAAGGGGAGCAGAAAGGAAACGTTGTTACTGATGAGTACCACAG
ACTCATCTTAAAAAAAACTCTCATTATGGTGATCATAGAATTGACCATCC
AAACTGGGACACTCTTGAGAGTAAATGGAGGGCATTATTAATAATTATCT
TGTAATGAACTTAAATCTGGACTGTTCCAGGCAAACCAGACTTATCTTGC
AATATGAGAATGCTGACACAATGCAGGAAAGCCAGTTTCCCTTTTGTTGA
TCTACTTGACCAAGCAAAGGGGCTGAAAAACTGAATAAGGAAACAACTTT
ATAAGAGAAACAGTGGTCTTCAATCTTTTAAAGACATGAAATCCTATATG
GCATTCTGTCTCAGTGAGTCAGTTAACAAATACGTATGTGCAACCCTTCT

Figure 3-72

GCTAGTAGTGCACATAAGTGATTATCCCTGCCAGGTATCGAGTTGGAATA
TCCAGTTATTTCATGTCACACATCGGCACGTATGATGGTGGTTTGGTCAG
ATGGATAATACAGCAGACACACTTAGAACACTCACTGCACTGGTGGCTGT
TCATTTTGAGGAACTCCAAAGTCAATTCAAGGAAATAAGGAATGACCTGG
AACAGGCCTTAGAAACAATTGATTTATTCCAATAGTTAACCACTGGCTGG
CTCCCAACTCTAGGTGATAGGCATCTAATTGAGACATGTGTGAGTCAATA
GCCATCGGGGTCCTT

858. chr5_ISOC1_NM_016048_-1.56305
TTCGCGCGACCCTCGTCGGTGCCACACGGGGCGGGCTACGAGCTGCTCAT
CCAGAAGTTCCTCAGCCTGTACGGCGACCAGATCGAC

859. chr5_ISOC1_NM_016048_1.59153
TGCATCCAACAAACTGCCCTGGAGCTAGTTGGCCGAGGAGTCGAGGTTCA
CATTGTTGCTGATGCCACCTCATCAAGAAGCATGATGGACAGGATGTTTG
CCC

860. chr5_ADAMTS19_NM_133638_1.7216
TGCCGAGCCGGATGGCGACGAAGTGTTGCTGCGGATCCCGGCCTTCTCTC
GGGACCTGTACCTGCTGCTCCGGAGAGACGGCCGCTTCCT

861. chr5_ACSL6_NM_015256_1.60918
AAGCCTGAGAAATCAGCCACCACGTTCCCATGGGTGAGCATCGCACCTTT
TGGGTTCC

862. chr5_PDLIM4_NM_003687_-1.66894
GGTTACTTCTTTCTGGACGAGCGGCTCTACTGTGAGAGCCACGCCAAGGC
GCGCGTGAAGCCGCCCGAGGGCTACGACGT

863. chr5_RAD50_NM_005732_1.51955
TTCAGGGTTCAGCAGTACAGCCGAGACTCGACTCTGTGCCTCCCTCCCCA
GTGCAAATGCATGCTTCTTCTCAAAGCACTGTTGAGAAGGAGATAATTAC
TGCCTTGAAAATTTATGGTTTTGGTATTTTTTTAAATCATAGTTAAATGT
TACCTCTGAATTTACTTCCTTGCATGTGGTTTGAAAAACTGAGTATTAAT
ATCTGAGGATGACCAGAAATGGTGAGATGTATGTTTGGCTCTGCTTTTAA
CTTTATAAATCCAGTGACCTCTCTCTCTGGGACTTGGTTTCCCCAACTAA
AATTTGAAGTAGTTGAATGGGGTCTCAAAGTTTGACAGGAACCTTAAGTA
ATCATCTAAGTCAGTACCCACCACCTTCTTCTCCTACATATCCCTTCCAG
ATGGTCATCCAGACTCAGAGCTCTCTCTACAGAGAGGAAATTCTCCACTG
TGCACACCCACCTTTGGAAAGCTCTGACCACTTGAGGCCTGATCTGCCCA
TCGTGAAGAAGCCTGTAACACTCCTCTGCGTCTATCCTGTGTAGCATACT
GGCTTCACCATCAATCCTGATTCCTCTCTAAGTGGGCATTGCCATG

864. chr5_AFF4_NM_014423_1.55307
TCTGAGCCTCTCTCGTGTGCTTTTCTGGCACATTTTTCTTTTCCCCCTTG
GGCGGCTCTGTTTCTTTGTAAGGCTTTCCTGGTATTCTAGTCAAAAGATT
CAGGTCAATCT

865. chr5_ZCCHC10_NM_017665_2.68571
CTTGGCCTTTCTTTCTACATTGGTT

866. chr5_C5orf15_NM_020199_1.91736
AAATATGTGAGTTGAGTACGGTTGGGCTCGGTGAAT

867. chr5_SAR1B_NM_001033503_1.79194

Figure 3-73

ACATTAGAGTTTGTTTTATTGCAT

868. chr5_TGFBI_NM_000358_-1.62816
CAGCGGGGACATGCTCACTATCAACGGGAAGGCGATCATCTCCAATAAAG
ACATCCTAGCCACCAACGGGGTGATCCACTACATTGATGA

869. chr5_FAM13B_NM_016603_-1.58079
CCTTCTATGATTGGCTGTAACATCTGACCCCTTCGCTTGGTGGATGGAGA
TC

870. chr5_FAM13B_NM_016603_-1.60893
AAGAATAAGTTCAAGGGTTGCTTC

871. chr5_REEP2_ENST00000254901_-1.53101
CTGGGCTGGACTCCCGTGCTCCTCAGG

872. chr5_ETF1_NM_004730_-1.61858
TGCTACTTTCCGAACATAGTTATGTCGCTTTTCCATTCTTAA

873. chr5_ETF1_NM_004730_-1.62628
GGACTGAAAGGCGGTTTACTCGTGACTTAATG

874. chr5_CTNNA1_NM_001903_-1.68488
GGGAGACAAAGCAGCGCCCGTCTGCTTCGGGCCTCTGGAATTTAGCGCTC
GCCCAGCTAGCC

875. chr5_CTNNA1_NM_001903_-1.59557
GGTGCAGAATCTCGGCGGGGAGCTTGTTGTCTCTGGG

876. chr5_SIL1_NM_001037633_1.6204
TCTCCGTGACCAGGTCGTAGAGCAGTGTGACCACGCGCACGGCGAGCACC
TCCGTGCCCTTCTCCTGCACCAGGGTCCTCAGGACCTGCAGCCCCCCGAG
CTTCAGGAACTGCCGCTGGG

877. chr5_NRG2_NM_004883_-2.17795
GCGGCGAGTCCGAGCGCAGCGCGTCGTGCGCCCCAC

878. chr5_SLC4A9_NM_031467_1.51669
ATTCCAGTGGTCAGTTCGTCGGGCCAGCAACCTTCATGACCTTCTGGCAG
CCCTGGATGCATTCCTAGAGGAGGTGACAGTGCTTCCCCCAGGTCGGTGG
GACCCAACAGCCCGGATTCCCCCGCCCAAATGTCTGCCATCTCAG

879. chr5_PCDHB18_NR_001281_-1.73783
TCCTGAAGCCGGTGATTCCCAATCTCCTGTCCCGCGACAGCGA

880. chr5_PCDHGA11_NM_018914_1.77239
GCGGGGACCGCAGTCGGCTGCTGCTGCTGCTGTGCATTTTCCTGGGGACG
CTGCGGGG

881. chr5_FGF1_NM_000800_2.48238
CTGCTGCTTGTGGCGCTTTCAAGA

882. chr5_PPP2R2B_NM_004576_-1.55693
CTTTGACGGTCAAGTAGTCCCTGGTCATGATATACCTCCCACTGTGGCTG
AACTTCACATCCGAAATCGAAGAGATAATTTCAGAGAAAAATGATCTGTT

Figure 3-74

GCTTGGATCTTCCGGC

883. chr5_SPINK14_NM_001001325_1.61712
GTGGCCACCACGTGGAATTATTAAG

884. chr5_SH3TC2_NM_024577_-1.87828
CGATACAGTTGGATCCTTGGAAGGAGTTT

885. chr5_ARHGEF37_NM_001001669_-1.54222
TCCAGGGGAATCTGTGTAATGTGCCTTTTCCCTCTCCAAATGCCTAGAAC
CATGGCACTGTGTCTTATTTATTTAACCGTTGGGCTGTCTCATACTAAAC
TTGCAAAGATATTTGCCTATGAACTGAACAAGACTTCCAGGAGTTGAAGT
CTGGTTCACAAGGGTACCC

886. chr5_CAMK2A_NM_015981_1.53857
TGTGGAAGTGGACGATCTGCCATTTGCCATCCCGGCGGTGCCAGACACGG
GTCTCCTCCGACTGGGCGGTGCGTGGGATGCCGCCAGCGTCCAGGTACTG
CGTGATGCGGATGTAGGCGATGCAGGCTGACTCGTC

887. chr5_CAMK2A_NM_015981_2.00608
TGGGGAGAGATATCCAGGAGTCCCT

888. chr5_DCTN4_NM_001135643_1.51752
TTCATGTAGCGAAGGTTGGGAATTGACATGATTCTCACTTC

889. chr5_DCTN4_NM_001135643_-1.55134
CTGCCATGCCCACATCTCTAGACGTCCAGCGACAAAATCCACATGCCAGG
TAATAGGCTTTCTTCATGGTGGTCTTGGCTGGGTCATCTGGAAGCTGTGT
GGAGATGCTCGTGGCCCGAGTAGA

890. chr5_ANXA6_NM_001155_1.6084
GAGGCCTCGGGTCGCAGACGGACGCACGGGCGCAGGGACTCGAGGACGCA
GCGCTCGCTGGATCGGAGCCCGTTAGCCCAGCAGCAACCGCAGCGCGGGG
CGGACCGGGAGGACAGCCGTGGGC

891. chr5_GRIA1_NM_000827_-1.692
GCTCAAGAAGAACGCCAATCAGTTTGAGGGCAATGACCGTTACGAGGGCT
ACTGTGTAGAGCTGGCGGCAGAGATTGCCAAGCACGTGGGCTACTCCTAC
CGTCTGGAGATTGTCAGTGATGGAAAATACGGAGCCCGAGACCCTGACAC
GAA

892. chr5_FAM114A2_NM_018691_-1.50751
GTAGCTGAAAGGCGTCCTGGATGTAGGA

893. chr5_MED7_NM_001100816_-1.58538
CTCGTTTTATACTCCCAGGGCTCCTTATTAAAATATCTAAAAGGTCCAAG
AAATTAATAAGGATAGACATATTAAGTTTTCTCAGTTCTTTCTTGTGATC
AAACTGCATAGGATGAAGCCGTTCGATGCCCTGACTTTCCAAAGGGCGGA
TGATAAGATCAT

894. chr5_LSM11_NM_173491_1.6406
GAGCGCATCCAGCGCCTCCGCCGTCTCATGGTGGCCAAAGAGGAAGGGGA
CGGGGCCGCAGGAGCGGGCCGGAGGGGTCCGGGTCGGAGCAGGAAGGCGC
CACGCAACGTGCTCACG

Figure 3-75

895. chr5_IL12B_NM_002187_1.52748
AGAGAGTGTAGCAGCTCCGCACGTCACC

896. chr5_IL12B_NM_002187_-1.60397
TCTGCTGCTTTTGACACTGAATGTCAAATCAGTACTGATTGTCGTCAGCC
ACCAGCAGGTGAAACGTCCAGAATAATTCTTGGCCTCGCATCTTAGAAAG
GT

897. chr5_CCNJL_NM_024565_2.06112
AGGTAGACGGCCAGGTGCCGGGCTGCAGGGCAGAGCTGGCAGTGGCTGCT
CAGCAGGGTCAGGATGTCCACGAAGAACCGGCGGCTCTTC

898. chr5_GABRA1_NM_000806_1.51047
GCGTGTAACCGAAGTGAAGACTGATATCTTCGTCACCAGTTTCGGACCCG
TTTCAGACCATGATATG

899. chr5_SLIT3_NM_003062_2.00581
TGGAGTCCGAGAGGTGGCAGGCAG

900. chr5_SLIT3_NM_003062_1.5941
CTTCTACAAACGAGGAGCCGTCCGTGCACTGGAAGACGTATTTCCGCCGC
TTGCTGCGGGTGGGCTGGCAGCACTGGGGCCCACAGCCCCCACGACATTC
CATGATGGGCACCTTGGAGGCTGTGGCACATGATGCATAACCTTTCTGGC
GGCGGATCACCTCTCGGACTACTTGT

901. chr5_DOCK2_NM_004946_-1.55177
GTGCTGCAGAGCACCCAACCATTGCCAAGTCGGTGGAGAACTTCGTGAAC
CTGGTCAAAGGCCTCCTGGAGAAGCTGCTGGATTACCGGGGTGTGATGAC
AGATGAGAGCAAAGACAACCGCATGAGC

902. chr5_LCP2_NM_005565_-1.51014
TGGTTTATCTTTCTAAGAGCAGCTTCTGCCTCTGGTCGGGTAATATAAGA
AACGTACCACTCTTCATTTA

903. chr5_LCP2_NM_005565_-1.56424
TTGAGAGAAGTATGGTGGCAGGGAGGCACTCTGTGGAAAACTGCTG

904. chr5_KCNMB1_BC025707_1.59879
GACAGGGACAGTTAGGAACAGGCTCACACAC

905. chr5_---_---_-1.66528
TTTTTCGGCAAGTCTCGCTCTTGTGCCCCAGG

906. chr5_---_---_-1.78717
CATGGCTCACTGTAACTTCTGCCTCCCGGGTT

907. chr5_NKX2-5_NM_004387_-1.66293
CTTTTCGGCTCTAGGGTCCTTGGCTGGGTCGGGGTCGCTGTAGGCACGTG
GATAGAAGGCGGGGGCGGCGGGAAAGGCAGACGCACACTTGGCCGGTGAA
GGCGCGCGGCCCAGCTCTGCGCGCAGCTCTGGGAGGCCCGGCGCAGCCGC
CTCGGGCCCAGCGTAGGCCTCTGGCTTGAAGGCGGCCAGCATGCAGGAGG
AGGGCGCC

908. chr5_HMP19_NM_015980_1.9626
CCCAGCCTCCCTGGATGCTTACTACTCCTCCCAGGACCCCAATTCCAGAA

Figure 3-76

GCCGCTTCTACACAGTCATCAGCCACTACAGCGTGGCCAAGCAGAGCACT
GCCCGGGCCATCGGGCCGTGGCTGTCAGCAGCCGCTGTCATCCATGAGCC
CAAG

909. chr5_NOP16_NM_016391_2.37281
ATTCGATCCGCGGCGCTGCCTTCC

910. chr5_CDHR2_NM_001171976_1.50095
GATTCAGGGAACAATGGCGTCATCCTGTTCTCCATCCTCCGAGTAGACTT
CATCTCTAAGGACGGGGCCACCATCCCTTTCCAGGGTGTCTTCTCGATCT
TC

911. chr5_HK3_NM_002115_-1.76406
CAAGCCCGTCTGGTGACAAGGGAAAGAGAAGCTGAAGCCAAGCTGCAGAC
CCTGTTTGTTCACAGGCTGCGCATCCAGG

912. chr5_ZNF346_NM_012279_1.56737
GTCGTGGCCCAGTCGCACTACCTGGGGAAGACCCACGCAAAGAACTTAAA
GCTGAAGCAGCAGTCCACTAAGGTGGAAG

913. chr5_FGFR4_NM_002011_-1.84236
TGACCTCCAGCAACGATGATGAGGACCCCAAGTCCCATAGGGACCCCTCG
AATAGGCACAGTTACCCCCAGCAA

914. chr5_FGFR4_NM_002011_1.75407
GGCGTCCACCACATTGACTACTATAAGAAAA

915. chr5_NSD1_NM_172349_-1.58945
GTTAAATCACTCACCCAGGCCAGACTTCTTTCTCAGCCTCCTGCCAAGGC
CTTTTTATATGAGCCAACAACTCAGGCCTCAGGAAGAGCTTCTGCAGGGG
CTGAGCAGACCCCAGGGCCTCTTAGCCAATCCCCGGGCCTGGTGAAGCAG
GCGAAGCAGATGGTCGGAGGCCAGCAACTACCTGCACTTGCCGCCAAGAG
TGGGCAATCTTTTAGGTCTCTCGGGAAGGCCCCAGCCTCCCTCCCCACTG
AAGAAAAGAAGTTGGTAACCACAGAGCAAAGTCCCTGGGCCCTGGGAAAA
GCCTCATCACGGGCAGGGCTCTGGCCCATAGTGGCTGGACAGACACTGGC
ACAGTCTTGCTGGTCTGCTGGGAGCACACAGACATTGGCA

916. chr5_MXD3_NM_031300_-1.55748
TGGGGGGGTCGCTTCTTCCTCCTGTGGATGGGGCCTGGACTGCGATGCGG
GCACAGGGACGCATAACCATGCTCGGCC

917. chr5_B4GALT7_NM_007255_-1.61457
GCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGAGGACGACGAG
TTCTACCGGCGCATTAAGGGAGCTG

918. chr5_GRM6_NM_000843_-1.50701
GAGGAATCCTACCCAGGCCTGAGTGCCTCCATCCAGATGCACAGCCCCAG
GTCTCCTCTTGCTGAGACAGCTCCTCCTCCACTCCAACCCCATGTTTCAT
TCTGGGGTCTACACGTTCTTCCACACTGCCCAATCCCCAGGTTATGGGGG
TTGACTGAGGGGAGGAAATCTCCCGCAAACCAGGCAAAGCCCAGGGCTTC
ATCATCCTCTTTGGACTTCGGATGAGAGAATAAGTTTAGTCCCTTTCTAG
AGCTAGAACCTTCTCGGTGGCTGTTTCCCACCATGGGAAGCGAGTCTGGT
CTGTGGTGAGGAAGCATGAAGCTCACATGCTGGAATCGGGGTAGAGCTGG
GTCCAGTTCCTTCTCAAGGCCAGCCCCACCGACGCGGAGCATGGTCTTGG
CAAACTCCCTGCCACTGACTGTTCACCGTGGACCCGGG

Figure 3-77

919. chr5_ADAMTS2_NM_014244_1.50764
TCTGCAGCGTCTCCCGGCCGTCCTCGTCTCTGTACTCCCACTCCACGCCC
ATGGCAATGAAGGTTTTGGAACTGGCATCCACGTCATTC

920. chr5_---_---_1.50354
GAAGATAAATTTGGAACGTTTTCAAAGGGAAAGCAAAATTCGTGAAAATA
CTTAT

921. chr5_RASGEF1C_ENST00000393371_1.59387
CATTCTCCGTCTTCTCATGGCCTCTCAACTCTCCTGCAGGACCCATCTCT
TGTCTACTCCTC

922. chr5_GFPT2_NM_005110_1.58757
TGCCCACGGTGTTGGTGACGCCCAC

923. chr5_GFPT2_NM_005110_-1.87153
TCTCGGGCTCCTTCGCGGCTCGAGGGGGTCTGCCCGTTCGGACGCTGGGG
CTCCT

924. chr5_MGAT1_NM_001114618_-1.64635
CACCTGGTCACTGCTCCACCTCATGCTGAGAGGAGCCTGTGTGTCAAACC
CCAGGGGAAAAAGGGACAGGCAGATCGAATTCTGTCTTCTA

925. chr5_BTNL3_NM_197975_-1.62107
ATCAGTTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAA
TCTAAGCAGATGCCACAGTATCGAGGGAGAACTGAGTTTGTGAAGGACTC
CATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTCAGTTCCCAGATTTACGATGAGGAG
GCCACC

926. chr5_TRIM52_NM_032765_1.53292
CACATCTGGCGAATTATCTGGACCATGTTGGCCAGCTGCAAGTTGGGACG
AAAGCTGCGACGTGTAAAGCTCTTTCGGCACTGGGGGCAGGTGAACTGCC
CTGGAAGGGGCAAGGAAGGAGGCGGGTGGATGTCAGGATACAGCTCTTCA
TCTTCGTCCTCATCGTATGCTTCCAGTATTTCTTCTTCTCGGTAGACATC
AATTCTCAGGTCAGGTCTCAAGCCTCCTAGGTA

927. chr6_SERPINB9_NM_004155_-1.51858
CATCTGGGTTGCGGTGTTTCCCTTTGCCCCTAGGAGAACCATGGCCAGGG
CAGAGGAGATGCTCACAGGAGAACAGAACACGTTGTGCGAAGGGTTATCT
TGACACAGTATCTTTAAAAGGCGTATGGCAAAAGTACCA

928. chr6_PRPF4B_NM_003913_-1.51482
GCAGATCACGCTTGCGAAGGCGGTCTCGATCACGCGGTGGTCGTAGACGA
AGGAGCAGAAGCA

929. chr6_RREB1_NM_001168344_-1.62594
GGGATGGCAACTGCGGTCACCCTGCTAAAGTCGGGGCGGGGGCGGCGGTC
CTCCCCCTCACCCCCCCCAGTCCGAGCGCCGCCGCCGCCGCCGCCGCCGC
CGCCGCGGCCGCTCAGTAACACGTCCC

930. chr6_CAGE1_NM_001170692_-1.70698
GTGGGAGGGAGAACGCTTTCCAACCTCCTCCACCAAGGACTCTCACAAAC
TCGCAATCGGGCTCCCGGAGTGCTGGAACGCCCCTGTGTGACGTCCGCCC

Figure 3-78

GCGCCGGGGGAACTCCGCAGAGACAGGTGCAGCCCGCGAGGCCCGAGCGA
CCCTACTGTGGGTGCGGTGTCTTCCCAGAGAGTGGTGAAGTTAGGAAGGT
ACGACCCCCTAGGCCGAACAGCCTGTGGGCTAGCTGGCGCCTCCTGCCGC
AGTAAACACAAAGTGG

931. chr6_DSP_NM_004415_-1.78259
CTGGCCTCATACACCTCAGGACTGGAAACTCTGCTGAACATACCTATCAA
GAGGACCATGATTCAGTCCCCTTCTGG

932. chr6_GCNT2_NM_145655_-1.54032
TTGAGCCCGCCAAAAAGTTATGAGAAGCTGAACAGTTCCAGTGAAAGGTA
TTTTAGGAAAACTGCCTGTAATCACGCCTTAGAGAAAATGCCAGTCTTTT
TGTGGGAAAATATATTACCATCACCTTTGCGAAGTGTCCCTTGC

933. chr6_ERVFRDE1_NM_207582_1.58767
GAGTGGCTCGTTCCCGTAAACTGGAGGCTTGATTTAGGAGTTGTCTGATG
TTGTCTTGTACTTTTCCTGATTGATTTACCCAAAAGCAACATTTTTCATC
TAAGGCCAAACAAATTCCTCCCTGTGCTGCCGTTAACATGTCTAGTCCTC
GACGATTTTGAAGGACTACGGCTGCTAAAGAGTCGATTTGTTCTTGCATG
GTCGTTAAGGCTTTAGCCATGGTGTCAATGTTGTTGGCTATTTCCTTTGA
GAGCTGGCTATAGGTGAGGGAAGCTTTTGTGATTCCAGCAATTCCGGTTC
CCGTACCAGCTAGAATGCCGAGTCCCGCGAGAAGGGGAATGAAATGGATT
GCCCTCCTCACCCTGGGCAACGGGGAATTCCCATAGATTGGTATTGGAAG
AGAGAGATTGCCAGGGGCTATGAAGATGTCTGGGGTTACATAGCCTATGG
TACAAGTTCCAGTCCAGTTACTGGGGAGGCATTGGTGAATCGACTGGCCA
CAAATATAAAAGGCTCCTTGAGTTTTAAGGCATGTAGAGATATGGAAATG
AAATAAGGGGGTGAGGGAGGTTCCAAAAAATTCTGAGACTGCTGATATGC
CCAGGTAGCTGGTGGCTATAGTCATGCCTGCTAAGACTTGGACGCAGGGT
GTTTGGCTCTGGTTAGCTCCCTTGGTTTTATTTTCCCAAAAAAGAGAATT
TCGAGTTTGGTCCAATAGAACCCATTCCGCTGTAGAGCTGAGGTTGGAAA
TTTGCAGACATTGGTTATAATCAGCAGGCCGGAACCAGAAGTTTC

934. chr6_TBC1D7_NM_016495_1.95117
GTTGAGACTAAGTGGTCCGGGAGAAGCAGAGGAAGCCGTGCCCTGTGCGC
TGACCGA

935. chr6_NUP153_NM_005124_-1.63622
TTCTCTATTTTGTCCGGGTGTCATATTTT

936. chr6_SOX4_NM_003107_-1.53255
TGGGGTTAGCAAACCGCACGCCAAGCTCATCCTGGCAGGCGGCGGCGGCG
GCGGGAAAGCAGCGGCTGCCGCCGCCGCCTCCTTCGCCGCCGAACAGGCG
GGGGCCGCCGCCCTGCTGCCCCTGGGCGCCGCCGCCGACCACCACTCGCT
GTACA

937. chr6_SOX4_NM_003107_-1.73779
GGTGAAGCGCGTCTACCTGTTCGGCGGCCTGGGCACGTCGTCGTCGCCCG
TGGGCGG

938. chr6_MRS2_NM_020662_1.62326
CGGCGCAGCTTTGCGGGCCCGACCGGCTCCGCGTGGCAG

939. chr6_FAM65B_NM_014722_-1.67492
CACCTGAGGACTGTCGGCGGCAAGCCTCAGATGG

Figure 3-79

940. chr6_LRRC16A_NM_017640_1.87246
GCTTCTCAAGCCCTAAAAACAAAC

941. chr6_HIST1H1T_NM_005323_-1.65751
AAAGGGCCTCGGTGATCAACTTGGACACAGAGAGGTTCGGCACTTTGCGA
CTTGCACTTATCAAGCCAGCCGGCTTCCTCCCTCGCTTCTTGGTTGGAAG
TTTCTCCATAGCGGCTACACCAGCACTGGCAGAAGCTGCAGGCACGGTTT
CAGACA

942. chr6_BTN2A3_ENST00000297020_1.67118
AGTTCCCCAGTCTCACAGCCATGGAAACAAGCCCTGGCCATCTCAGCAGC
CACTGCACAATGCCTCTGGTGGAA

943. chr6_ABT1_NM_013375_1.50942
ACGTGAACGGGCTCGCCTGGCAACTGCCCAGGACAAGGCCCGCTCCAACA
AAGGGCTCCTGGCCAGGATCTTTGGAGCCCCGCCACCCTCAGAGAGCATG
GAGGGACCTTCCCTTGTCAGGGACTCCTGA

944. chr6_HIST1H2AL_NM_003511_-1.9978
ACCCGCTCTTCTCGTGCCGGTCTCC

945. chr6_OR2B6_NM_012367_1.78215
GCCTTGGGGGCTACTGAATATCTT

946. chr6_GABBR1_NM_001470_1.51155
AAGAGCACAACAAGAGTGATATAGGAGGAGAAAACTATGGCAAGAGAGGC
AAAGGCAAAGGCTGCATCCTGCTGGCTGGACAGAATCATGGTGACAGGAG
CAGTGATGAGGCACAG

947. chr6_LOC554223_BC051362_-1.60794
CCCAGCGCTGGGCATTCCCCATCTTTGCA

948. chr6_TRIM39_NM_021253_1.60328
GACAAGTCTGTTAGAGGCTGGGGCCTC

949. chr6_---_---_-1.64494
AACATGAAGATATCCTCCCAGGGTTGAAGT

950. chr6_---_---_-1.57912
ACATTGTAGCTCCATCACCCAGGCTGGAGTGCAGTGGCATGAACATGGCT
CACTGCAGCCTCCACCTCCTGGGTTTAAAGGATCTTCCTGCCTCA

951. chr6_C6orf134_NM_024909_1.77956
TGGAGTTCCCGTTCGATGTGGACGCGCTGTTCCCGGAGCGGATCACGGTG
CTGGAC

952. chr6_DHX16_NM_003587_-1.54294
TGGTGTCAGGTTCTGTTTACGTCCTTCT

953. chr6_DHX16_NM_003587_-1.50795
ATGTCCACAGGAAACCTGCGTCCGGGGATTCGAAACACAGGGGCGTCATC
AAAGAAGGTGGAAAAACGGGCAGTGTCCATTGTGGCTGAAGCCACCAGGA
CCTTGAGCTCAGGTCGGAAGCGAGCAACATCC

954. chr6_DHX16_NM_003587_1.56169

Figure 3-80

TCCGGTCTTCCTCGGCCATCTTGAGGCGCTTCTGAGCCTCT

955. chr6_MDC1_NM_014641_1.78904
AGGAACTTGACTGTCCGGCGGATGCGATCAGTGACCAGGTGGGAAGCCTC
TGCCGCTGAACCAGCCAGACTTCCCCCCAGTGCCAGCACAGCCCGCTCTC
CCCGAGCATCCACCACTCCTGTGAAGA

956. chr6_FLOT1_NM_005803_-1.68388
GACAAGGCACAAACTATTTGGCAAGGAGAGATGAGGGGTGGGACCTCACT
GTCAATGGACATGCTCAGGGAGGCCAGTGGGTTACATGCAACAGGAGGAT
CATTCAGGCAACTTCAGCTATGAGGCTGG

957. chr6_CDSN_NM_001264_-2.186
CATCCAGGGTGCCCGAGACGAGCCCAT

958. chr6_---_---_-1.67875
ATACAAAATTTAGCCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGG
AGGTGGAGATTGCAGTGAGGCGAGATTGAGCCACTGT

959. chr6_LTA_NM_000595_-1.57145
GCCCGTGCTTCGTGCTTTGGACTACCGCCCAGCAGTG

960. chr6_BAT2_NM_080686_-1.54523
AAAGGGAGTCTGCCGAACAGTCGTCTGGGCCCGGACCAAGCCT

961. chr6_C6orf26_AJ245661_1.57672
TTTCTTTAGTCTCAAAACAAGAGACTAGGA

962. chr6_C6orf27_NM_025258_1.51891
AGAAGGACAGGGACTACAGTGCTAGGCTGAGGGGCAGCCCTGTGCAGGCG
CCGCCCCGCTGCGTCCTGGCCAATCAGCTCCAGGGAGAAGGGTCTAGGGG
TGGACAGCAGCGTGGGCGACAGCGAGGCTGCGAGGAGACCTCGCTCCGGA
GGTCCCACGGGCTCCAAGGGCACCTGGCCTAGTTCGGCACCCTCTGGGAC
CCCTCGAAGGATGACGTGGGAGAAATGCGGCTGAGGATCCCCA

963. chr6_C6orf27_NM_025258_-1.80749
CCATCCTCCATGGGGATCCCAAAGTG

964. chr6_C6orf27_NM_025258_1.56676
TGCTGATGTCTCCGTGGATCCGGACTGTGATCTTCTGGAGCAGCCCATCC
ACGCTGAACACAAGTGG

965. chr6_C6orf27_NM_025258_1.55098
GATGAGTTCCAAAGTAGCCAGAGGTGAGGAGTGTGAAGCCCAGCCAATTC
CTGGGGCAGCTCAACTCCTCGCAATCGGAGCAGGTAGGATCGGCCA

966. chr6_C6orf27_NM_025258_-1.92598
CATGAAGTGCAGCCCCGAGGCGCTGGCGAGCCAGGGTGTGGTCAAGGGCC
CTGGCTGCCACCACGGTCTCCCGCAGAGCCCCTACCAGGCGCGCGCGTCC
CTGACCCAGTCGCTCAGCATCAAAGTGCAGGTCGGGGTCATTCCTGGAAG
TTGGCAGGAAGTCCTGGGCTGCATTGGCACGAGACACCTC

967. chr6_VARS_NM_006295_-1.51869
CACGAAGGGCAAACTTGGTGGCATTCCAGAGCTTGTTGCAGAAGTGGCGG
TAACCCAGTATCCGGTTCA

Figure 3-81

968. chr6_SLC44A4_NM_025257_-1.66027
ATCCCCACCACGATGTAACCTAGAATGAAGAGCAGGAAGAGGACGCAGCA
GATGACATC

969. chr6_EHMT2_NM_006709_1.71193
AGCACATGGCAGATCTCCACGGAGCCCTTCTGGGCGGCTGCATGCAGGGG
CGTGCGCTTGCTCTGCTGGTCGCTCTGGAAGTTGG

970. chr6_CFB_NM_001710_-1.55321
GGGTACTGCTCCAACCCGGGCATCCCCATTGGCACAAGGAAGGTGGGCAG
CCAGTACCGCCTTGAAGACAGCGTCACCTACCACTGCAGCCGGGGGCTTA
CCCTGCGTGGCTCCCAGCGGCGAACGTGTCAGGAA

971. chr6_CFB_NM_001710_1.56309
TCCAGGCAGTGTACAGCATGATGAGCTGGCCAGATGACGTCCCTCCTGAA
GGCTGGAACCGCACCCGCCATGTCATCATCCTCATGA

972. chr6_C4A_NM_007293_-1.83691
CTCCGCGTGCGGAAGAAGGAGGTGTACATGCCCTCGTCCATC

973. chr6_TNXB_NM_019105_-1.54129
GCGTTTCCCATTCTGGAGTCCAAAGAGCAGGAACTTGTACTTGCGGGCCG
GGTCCAGCCCCGAGACGGCGACCGCTCGGAGGTCTCCGCTCACAGGCACT
GCCTGGGGCTGCCCCTGCGCGTCCCTGTACTGTACCAGGAAGGAGTCAAA
GGGGCCCTGGGCCACCGTCCATGAGAGGCCCACTGAGTCCGAGGTCA

974. chr6_ATF6B_NM_004381_-1.71734
ACCAGGGACATCTTGGGCCGGGAGGTCTTGTTGTGGCTGATGGCTG

975. chr6_PPT2_NM_005155_-1.65263
CACGGACTACTTGAAGTGGCTGTTCCCCA

976. chr6_PPT2_AF020544_-1.80981
CCACCCACCAGTCTGAGCTGCTTCTG

977. chr6_NOTCH4_NM_004557_1.5147
CAGCCAGCATCAAGGGTGTGGTCCCGTCCTCTGTGCGAGCGTCCACTGCA
GTTTGTCTGCTACGGAGCAGA

978. chr6_NOTCH4_NM_004557_1.66674
CCCAGGGGTGATCCTGCTGTGGCCT

979. chr6_BTNL2_NM_019602_-1.67289
TCCCTCCATGTGGATGCTAGGGGCAGACCCC

980. chr6_HLA-DPB1_NM_002121_1.52372
CCTGGATAGTCCTGTCACCGTGGAGTGGA

981. chr6_COL11A2_NM_080680_-1.59386
TCCCACCACTCCTGGAGGACCAGGG

982. chr6_RXRB_NM_021976_1.63874
TCTGTCCCCGCAGATTGCACATAGCCGTTTGCCAGC

Figure 3-82

983. chr6_VPS52_NM_022553_-1.51953
GATCTGATAGTTGGTCATGGGTTTCCTGAAGGAATAAATCTTCTGGAGGA
TAAACTCTCGGATCTTCGTCACTGC

984. chr6_ITPR3_NM_002224_-1.65611
CATGTTCCTGCGCGTGCTCATCCACCTCACCATGCACGACTATGCGCCGC
TGGTCTCGGGTGCCCT

985. chr6_IP6K3_NM_054111_-1.74972
CGCTTGTTCTCTGGGTACTCGGAGCACAGGCGGGTCAGGTGGGCCTGGTG
GCATTGCAGGCCCCACGGGTTGAAGCT

986. chr6_C6orf1_NM_178508_1.55842
AGTCGTATGCTCATCGTCCCAGGTCAAGGGGGCATGCCAGGGTGGGGAGG
GCGTCAGGCCGCTGCTAGGATGCGGGCCAGCAACAGCGGACAGGAGGTGG
TTCCCACGGCGCTGGGAGGCTCAGGCCGGAGGTGGGGGTGTTGGGGGATG
CGGATGGGCCGCCCCGCGCCCGAACATCCTGGAAGCCCGTCACCCGAGGC
GTG

987. chr6_NUDT3_NM_006703_1.81983
CAAAAATTCCAACTAATCTTCCCA

988. chr6_SPDEF_NM_012391_-1.58467
GCACGAACTGGTAGACGAGGCGCTGGGAGATGTCTGGCTTCCGGATGATG
CCCTTCTTGTAATACTGGCGGATGGAGCGGCTCAGCTTGTCGTAGTTCAT
GGCGGGACGGTTCTTGC

989. chr6_SCUBE3_NM_152753_-1.60981
TACCACGGCCAGACGGAGCAGTGTGTGCCATGCCCAGCGGGCACCTTCCA
GGAGAGAGAAGGGCAGCTCTCCTGCGACCTTTGCCCTGGGAGTGATGCCC
ACGGGCCTCTTGGAGCCACCAACGTCACCACGTGTGCAG

990. chr6_DEF6_NM_022047_1.83249
CTCTGCTTGCCCACCGTGACTCCTCCCTAAAGCGCCTGACCCGCTGGGGA
TCCCAGGGCAACAGGACCCCCTCGCCCAACAGCAATGAGC

991. chr6_LOC100131043_AK124222_1.67895
GTGCTGCCTGTTGGTTTCTGGTGAACTCATTTCCCCTTTCCCTGTCTTTG
TTCCCACAGAGGCCGTCAGCTGATCTTTACCGTGGTCTCTTCTGTC

992. chr6_FGD2_NM_173558_-1.63758
CCAGAGAAGAAGATCGTCCAGGAGCTGCTGGAGACAGAGCAGGCCTATGT
GGCGCGCCTCCACCTGCTA

993. chr6_RNF8_NM_003958_-1.64327
TCTTCGTCACAGGAGACCGCGCCGGTGGCCGGA

994. chr6_ZFAND3_NM_021943_-1.56042
AGGCAGCATACGTCCCAGGGACAGTGGGTTTGGATCTGTCTAGAACAGCG
GTTTGTGGCTGTGGCCCAGCTCCGAGAGTGATATTTGCTCTGGTAGGTGA
GGGCCTGAGGGTACATTTCTC

995. chr6_GLP1R_NM_002062_1.77439
CTGTGTCCCTCTGGGAGACGGTGCAGAAATGGCGAGAATACCGACGCCAG
TGCCAGCGCTCCCTGACTGAGGATCCACCTCCTG

Figure 3-83

996. chr6_C6orf64_BC022007_-1.5229
GCTGCCTTTAGAGTCGCTGCTGCTTCCGCCTTCTCTCCTGGGGTTTGTGC
GCCCTGACTGGCAGCAGGGGGTTGGGCCGCCAGACCCGCCCGTTTCCGCG
CCGCCCGAAACTCAGCTAACCGCTGTTCCAT

997. chr6_KCNK5_NM_003740_1.66307
TCATGGCCTTCTTCCCGATCTGCTTGATGAGGTCGTTGTAGGTCTCTTCC

998. chr6_DAAM2_NM_015345_-1.80422
CCCCCCGCAAGAGGAGCCACCATGGCCTGGGCTTCCTGTGCTGCTTCGGG
GGCAGTGACATCCCCGAAATCAACCTCCGGGACAACCACCCTCTGCAGTT
CATGGAGTTCTCCAGCCCCATCCCGAACGCAGAGGAGCTCAACATCCGCT
TTGCAGAGCTGG

999. chr6_TREML2_NM_024807_-1.70191
CAAGTAGACTTCCACATAGGGCTCTGGTCTTCCAGGTGGGTCACGTGTAG
AAGGATCGCTGCACATGCTGTAGC

1000. chr6_TREML4_NM_198153_-2.52607
TCCTGTTAGTGCTCCTGATCTGCA

1001. chr6_TOMM6_NM_001134493_-1.66157
CAGACCGGAGGTGCGTCATTCACCGGCGACGCCGATACGGTTCCTCCACC
GA

1002. chr6_CCND3_NM_001760_-1.8326
GTGCCGGGTGCCTTCGCAACACAGCAGCTC

1003. chr6_TRERF1_NM_033502_1.76472
GAACAGCACAAATTCAGAAGATTC

1004. chr6_PPP2R5D_NM_006245_-1.65386
GTCCCAGCAATAGCACGCCGCCCCCCAC

1005. chr6_CUL7_NM_001168370_-2.27433
CTGGCACAGGTATCTGAGGAACAC

1006. chr6_MRPL2_NM_015950_-1.53541
ATCCCCGGCTCCATTACTTGTAAGGGAATTGGG

1007. chr6_CRIP3_NM_206922_-1.63288
TCAGCATGACTCCCAGCAGTCAGGGTCTTGTGGCAACGCTGGCACCTCAG
ACACGGTCGGTGCCAATT

1008. chr6_DLK2_NM_023932_-1.91104
GGGTCCAGCCTTGCGCTCGCAGTCACGCCCATGGAAG

1009. chr6_TJAP1_NM_001146016_-1.80238
AGCGGTACCGGCTGGACTGCAACCTGGCTGT

1010. chr6_YIPF3_NM_015388_-1.69562
TGGGGGAAGTTGACCATCTTGATAG

1011. chr6_POLH_NM_006502_1.53766

Figure 3-84

GAGAGACTGACTAAAGACCGAAATGAT

1012. chr6_CAPN11_NM_007058_-1.65863
TGAGAGGGCACGCTTACTCTGTGAC

1013. chr6_HSP90AB1_NM_007355_-2.19655
CATCTCCCGAGAAATGCTCCAGCAG

1014. chr6_GPR116_NM_015234_2.05788
CACGTAGGTTGGATTATCCTGTTC

1015. chr6_TNFRSF21_NM_014452_1.51783
ATGGCCATTGCAGTAGTAGATCCATTTCTCCCGGTTCTGGGTTGGAGTCA
TGGATTTCTTCAGCCCTGCCTTTTCCACAATGGCACTGGGATCCTGCCGG
GGCCCCTTTTTCAGAGTCCTCGAGCTTTTCCGGATACTGCACACCACAAT
CACCACAAGCACCAGCAGCAGGAAAAGCACAATCATCCAGGGCAAATGCT
CATTGATGTCAAAATGCTTGTGTAGGTTCTGTCTAGGATGTCCCC

1016. chr6_TNFRSF21_NM_014452_1.55214
GAGAAGGGAGCCCGCGATCATCGTGGCTGTGGCTCG

1017. chr6_OPN5_NM_181744_1.58889
CTGCACACCGTAACCACAGTCAGGAA

1018. chr6_PKHD1_NM_138694_-1.79411
CCTGAATAGTTTCCGGGTGTACTGAATGAAGGCAGA

1019. chr6_LRRC1_NM_018214_-1.70378
GCTCCCGCTCCAGGTTCCTTGAAGCACTTCCGACCGCGAAGCCCGGCGCG
AGAAGCGAGCTAACCCAAGAGCCAACAACGAGCGCGGA

1020. chr6_LRRC1_NM_018214_1.92541
ACCCAGCTGCGAAGACTAGAAGAA

1021. chr6_DST_ENST00000446842_-1.60396
ATCAGCAGGAGAAGCCGTCTCATCATTTTCCTCTTGCAGTGTGTCGTAGT
CCTCAGGGTGCAGGCAATCACGATCATCACCATCAAGAAGCAAAGAATCA
TGGTCATCATCTTCAAACAAGGGAGTATC

1022. chr6_COL19A1_NM_001858_-1.69103
TGAACCTGGAATTGGGCTGCCAGGGAGTC

1023. chr6_OGFRL1_NM_024576_1.64618
ACCTGCTCGGCGGGGTCAGCTTCCGCGAGCCCACCACCGTGGAGGACTGC
GACTCCACCTGGCAGACCGACTCGGA

1024. chr6_KHDC1_NM_030568_-1.82262
TCGAGACCACAGGGGGGTCAGGTAGCCAAGGCTGGGCTTTGACGGTAGGA
ATGAAGGAGGTGAGGGTGGCGCGCCGCAGGCCTGGGCCACTCCCTGAGTA
GGGCGGCG

1025. chr6_MYO6_NM_004999_-1.70183
GTTTAAAGCTTTGGGCTTAAATGAAAATGACTACAAGTTTGGGTTA

1026. chr6_TPBG_NM_006670_1.79078

Figure 3-85

TCCTCGGCGCCGTTCCTGGCTTCCGCCGTGTCCGCCCAG

1027. chr6_PNRC1_NM_006813_-1.77316
TGACTGTCGTCTCCGTCCCGCAGCGGGAGCCGCTCGTCCTGGGTGGCCGC
CTTGCGCCGCTTGGCTTTT

1028. chr6_CCNC_NM_005190_2.33242
AGTGGGAGCTCTGCCAAAAGTTCC

1029. chr6_SIM1_NM_005068_1.85752
GGATTTTGACTTTGAGCTGGAGAGCCGGGATTTGGCCCCCTTTCTGTTGT
CAGTCA

1030. chr6_PREP_NM_002726_-1.57301
CTTGGTGTCAACGTGGGAAAGCCCTTGAGGTTTTCTGTCGCTGTCAGGAG
GAAGCACGAAAACT

1031. chr6_C6orf203_NM_016487_-1.80979
GGAGGCCTGCAGTCCGCGCGGCCGCG

1032. chr6_---_---_-1.63023
AGGGTCTCCCTAAGTTGCTCAGGCTGGTCTTGAACTCCTGGGCTCAAGGG
ATCCTTCCACCTCAGCCTCCCAAAGTGCTGGAATATGAGGTGTG

1033. chr6_C6orf182_NM_001083535_-1.54534
TACACTGAGACTTCGTCACACATAAAACAAGCACGACAAAGAAAGAGGGC
GCGAAGGGACTCCTGGAAGAAATTGAGTCTACATTTAAGATCACCCTAAA
AGTAGTGACGGCCTCTTCATTACTCCAAA

1034. chr6_AMD1_NM_001634_1.8733
GAATTCGTGACCTGATACCAGGTT

1035. chr6_TRAF3IP2_NR_028338_-1.63217
CATCCTCGTCCAGCTGCGACTCAGCGCCTTCCACGTCCTGTTTGTATTT

1036. chr6_TSPYL4_NM_021648_-1.52794
TCCTTTTCCACTGCTGCCGAGATGGCGCGTTTTTTAGTCGTCAC

1037. chr6_HINT3_NM_138571_-1.74031
AGACTGCGCGGGCCCGGTAGCCCTGGAGAGGCCGAGGCTCTAGGCCGCGA
GGGGC

1038. chr6_PTPRK_NM_001135648_-1.61665
TCAGGGGCGAAAGCGTCGCCAGCGTCGCCGGCC

1039. chr6_LAMA2_NM_000426_-1.50214
AGCCCAAGATGAGGTGTACCTGCACCCATCTGAAGAACATACTAATGTAT
TGTTACTTAAAGAAGAATCATTTACCATACATGGCACACATTTTCCAGTC
CGTAGAAAGGAATTTATGACAGTGCTTGCGAATTTGAAGAGAGTCCTCC

1040. chr6_LAMA2_NM_000426_-1.82087
CCCTGGAACTGAGGGGCGTTCAACCTGTATCATGCCCAGCCAACTA

1041. chr6_MED23_NM_004830_1.61785
ATACAACGAGTTCTCTCTTGCTGAAATCTTTGTAAAAATGGTCCAACAAG

Figure 3-86

ATGGTATACATAAAGCAACTGGAATTCGGTCTTCACTATAGGAAGAAGTA
C

1042. chr6_SGK1_NM_005627_-1.55968
CCCTTTCCGATCACTTTCAAGAAGTGAAAGTCAGATGGTTTAGCATGAGG
ATTGGACGACGGGCCAAGGTTGATTTGCTGAGAAGGAC

1043. chr6_AHI1_NM_001134831_1.63331
GGAGCCGACACCCGGAGCAGTGCAAATCAACTCCCCCAGCCTAGCGGCGC
GTGCGCGAAGTGAGGCGGCCACGCAGCCACCTAACCCGCCAGCGACCCGT
GTCCTGAAAGCAAGCCGCGGCTCTGT

1044. chr6_TNFAIP3_NM_006290_1.59031
CAGAGATGTGAAGCCAGATCCTCAT

1045. chr6_NMBR_NM_002511_1.59749
GCTTCGGGAACTGCCAGCAACACGGAGACCACCCAGATACCCATGGCCTT
CACACAGGTCCGCAGCAATGCCCCTGACGTCTGCAT

1046. chr6_VTA1_NM_016485_1.59155
TGTAGCAAGTAATACTATCCAACCTACTCCACAGACTATACCTGCCATTG
ATCCCGCACTTTTCAATACAATTT

1047. chr6_ADAT2_NM_182503_1.54452
TCCACTTTTCGGTCTCCTCTGCCGACACCGAGCACGCGCCGCTTGCAGCT
GGCTT

1048. chr6_FUCA2_NM_032020_-1.67726
GCAGGCCGGCTGTCCTCTCTGCAGGCTCCCGCGGCCTCGGGAGCGCTGTT
CTTCCGTCTCTGCCGCTGAGTATGCCGCGCCG

1049. chr6_EPM2A_NM_005670_-1.76823
AAATCTTCTTGTGCCCGGGCCAAGGC

1050. chr6_SHPRH_NM_001042683_1.52347
CCATCACGCAAGGTAGGTGGTATCCCTGGGTGCCTGGCTATCAACAATTC
CAT

1051. chr6_SHPRH_NM_001042683_1.51934
AGAAGGTGGTACATCACTATCAGCATGATTTAGAGATTCAGCACAGTCCT
CTGTTTCATGTTCTTGGTTGAATTCAGAGATACATGTACTTTTAGACATA
GCAACATCAGTTATTCCAGAGTCGCTAGTAGCTGGACAGTGACCTTGTGA
ATCGGGATTGATAAATGGTTGACTTTTTCCTTTTTTTGTGGATGGAACAA
GCTTTTTCCTCAATTTACTGCGATTTCTCCTGGACTTATAATAATAATAG
TAAGGATCATCATCATCATCAGAGGTGTCTGATGGCAAGTATTC

1052. chr6_STXBP5_NM_139244_-1.52636
ATGGCACCTTGACTATATGGAATGTAAGGTCCCCTGCTAAACCAGTACAG
ACAATCACTCCACATG

1053. chr6_TAB2_NM_015093_-1.64639
CATTTTAACCCCAGCGCTATTCATAACTTT

1054. chr6_LRP11_NM_032832_1.52345
CATCCTGCCCAGCCTTGCTAAGTGGAGGCGCATC

Figure 3-87

1055. chr6_PPP1R14C_NM_030949_-1.54828
AGGACTCGGCGCCCGTGGCCACGGCGG

1056. chr6_IYD_NM_001164694_1.56649
GACCTCAAGCGCAAACCTCTGGACCAGATCATG

1057. chr6_MTHFD1L_NM_015440_-1.50137
GTAACAGACATAAACCTGGGGAAGCTGGTGCGAGGGGATGCCCAT

1058. chr6_SYNE1_NM_182961_1.7308
GCTGGGTGATTGTCTCCAGGCTGCTTGTCTCCAGGAGGTCAGGTGCCACC
AGTCTGCCAGACATCTGCAGCAGCCACTTTTCGACCTCTTGGAGCTCACT
GTTGTAGTCTTCATGGTCTTTGACTTTCGCCTCCAGACTGAAGACA

1059. chr6_OPRM1_NM_000914_-1.57438
TGGGAGGGGGCTATACGCAGAGGAGA

1060. chr6_SNX9_NM_016224_1.61187
CGGTCCGGGAAGCGTATCATAACCACCTGGGAGTTGCCAAGAAGCAGACA
GTCTCCCAGTGTCTGACTCTCGGATATTTGGATTTGACTGGTGTGAGGCA
AAGTGAAAAAGGGATGGGGGAAATGGAGATGGCACGGGCTCCTCAGAGCG
TGGTAGCCGACTGT

1061. chr6_SYNJ2_NM_003898_-1.64893
GCTCTGGGCTTCTTGCCACGCGGGCGACACGCCTATGATCAATTTTG

1062. chr6_EZR_NM_003379_1.81071
TACAGGGCCTCGAACTCGTCGATGCGCTGCTTGGTGTTGCCCTGCCGGAT
CTGCCGCAGCGTCTTGTACTTGTCCCGGCCTTGCCTCATGTTCTCGTTGT
GG

1063. chr6_TAGAP_NM_152133_-1.55405
GTCCAGGGGTGGATTTCACTCCCGTGTGG

1064. chr6_MRPL18_NM_014161_-1.56511
CCCTGTCAACCAGCTCCGAGCCGGCAGCGAAACCTGAAGTGGACCCTGTG
GAAAATGAAGCTGTCGCCCCAGAATTCACCAACCGGAACCCCCGGAACCT
GGAGCTTTTATCTGTAGCCAGGAA

1065. chr6_IGF2R_NM_000876_1.60112
TCTGAGCTCCTTAAGTGGCAGGGCGGGATTCACAGCTGCTTACAGCGAGA
AGGGGTTGGTTTACATGAGCATCTGTGGGGAGAATGAAAACTGCCCTCCT
GGCGTGG

1066. chr6_IGF2R_NM_000876_1.52362
AGTTGTTGTCACGTACTCCAAAGGTTATCCGTGTGGTGGAAATAAGACCG
CATCCTCCGTGATAGAATTGACCTGTACAAAGACGGTGGGCAGAC

1067. chr6_MAP3K4_NM_005922_-1.53231
GGAGGCCAGCCAGTCGGTCTAATTTGAAAG

1068. chr6_PARK2_NM_004562_2.12239
GGGCAGTGTGGGGATTGGCATTCA

Figure 3-88

1069. chr6_T_NM_003181_2.72746
GGCCCCTTGGACCGAGACCTGCGACGGCTC

1070. chr6_RNASET2_NM_003730_-1.57902
TGGGTATCACTCCATATACTCTGG

1071. chr6_FGFR1OP_NM_007045_-1.70357
CAAGTGCACAGACAACACCAAGTAAG

1072. chr6_UNC93A_NM_018974_1.7288
GCACATACCTCACGATCACGGGAAACACACATGCAGAGAAGGCGGGAAAG
CGTGGCAAAGACATGG

1073. chr6_KIF25_NM_030615_-1.63798
GACCAAGCCTGCAGTGCCACCCTCCCCAGGGAGCAAACAGAGGCAGGAAG
GGCAGGAAGGAGCCGCAGAGCTTCTCAAGG

1074. chr6_FRMD1_NM_024919_1.70939
CCATTCCCAGGGTCGGCTCCTGCTGACTGCATGCAGGCCTCTCAGGACTG
GGTTCCATACATCGCGCCC

1075. chr6_SMOC2_NM_022138_1.57358
CCAGTGTCACAGCTACACGGGATACTGCTGGTGCGTCACGCCCAACGGGA

1076. chr6_THBS2_NM_003247_-2.12969
AGATTGAGGTTGGGCCAGCCGTCCAGGTCCGAGTCCTCCCCGCAGATGAG
CCCGTCGCCCGCGTAGCCTGTCTGGCACTCGCACTTGTACATGGGGTCGC
TGAAGTGGCCCAGGTAGATGCACTCCGCGTGCTTGTGGCAGTTGTGTGTC
TTGTCCTTGCATGGGTTTTCGGGCTCA

1077. chr6_WDR27_NM_182552_1.61206
CACAGCAGGTGTCCCAGTCAGGCTGGCATCAAAAACGAGTAACAGATGGT
TGGCCAACCCACAGGCCA

1078. chr6_C6orf208_NR_026780_2.03932
CTCCCGCTGAAGCGGGTTCCAAGGCCACCGTGAGGGGGACCATCCATCCA
G

1079. chr6_DLL1_NM_005618_-1.7637
ATCACCGAGGTCCACACACTTGGCA

1080. chr7_ABCB8_NM_007188_1.80171
TGCTGTCGACACGCCTCACGCTGCTGCTGATGGTGGCCACACCAGCCCTG
ATGGGAGTGGGCACCCTGATGGGCTCAGGCCTCCGAAAATTGTCTCGCCA
GTGTCAGG

1081. chr7_CYP2W1_NM_017781_-1.57817
GGAGGAGCTAGACCGCGTGCTGGGCCCTGGGCGGACTCCCCGGCTGGAGG
ACCAGCAGGCTCTGCCCTACACAAGCGCCGTGCTCCACGAGGTGCAGCGG
TTCATCACGCTCCTGCCGCACGTGCCC

1082. chr7_CYP2W1_NM_017781_-1.98657
GGCACTGGCGCCAGAGGCTTCCTTGGGGCGGGGGGAGGGCACCTCAGCCC
CTGAAGACAAGCAGCACTGCAGTGGCAAAAATGGAAACACTGACCCGGTG
CGGTGG

Figure 3-89

1083. chr7_GPER_NM_001039966_1.57243
CTGCTCAGGCATTCGGCAGGTCCAGCAGAGGTACACCTCCTGCAGCGGGT
TCCAAGTGCACCTCCAGCCTGATGGGCCTGACCAAGGA

1084. chr7_GPER_NM_001505_-1.59193
TTAGTCGGGTGCCAGGACAATGAAA

1085. chr7_MICALL2_NM_182924_1.5681
TGGTTTGCCCTGAAGGTGAGGTTTCTTCTCCTCCTCCTTCCAGCTCTGCA
CTCGGGCTTCCTGGCCAGGGGGCTCCGGCCGAAGCCAGTTGTCACAAACG
TCGAGGCTGGCAGG

1086. chr7_MICALL2_NM_182924_1.63141
GATAGTGGAGGCTTCCGGGCTGGGGCGGGCGAGGGCAGCTTGGCCGCCTG
GACTGGAGCCTTCTTCCCTGACGGCTCCTCCTCAGAGTCCTCCGAGGCCC
TCTTCACGCCTGCCA

1087. chr7_INTS1_NM_001080453_1.82146
GCAGCAGGCGGATGAAGGACAGAAGGCAGTCCCACAGCGCCCCCTGGTGC
TCGCTGCGGAACACGTGCGGCTGCAGCAGCTCCAGCAGGCCCAGCACGTG
CAGGAAGCAGCTCAGGTGGTTCTGCTGCCGGAACTCCT

1088. chr7_INTS1_NM_001080453_-1.59237
TGATGTTCTGCTCCAGAGTCTGGGGGTCGTGGGCCACTGCCTGGTCCAGG
AACTGGAGGAGTTTGCTCATGCTGGACACGGGGATGCCAAACGACTGCAC
GAACA

1089. chr7_MAD1L1_NM_003550_1.70242
TGAGGTGGGACTTCGAACGGATCTGCTCTGCTCTT

1090. chr7_NUDT1_NM_002452_-1.51489
GCTGCTGAACAGCCGCAAACCATCTTCACCTGGGGGCATTGAGTGGCGCA
GAGCCGGGTTTCATCTGGAATTAACTGGATGGAAGGGA

1091. chr7_EIF3B_NM_003751_-1.528
CGGCCTCCGGCCCGTCCGAGTCGCCCTCGCCGCCGGCCGCCGAGGAGCTG
CCCGGGTCGCATGCTGAGCCCCC

1092. chr7_C7orf27_NM_152743_-1.77414
GACAGCTGCCCCATGGCGGTCACTGCACTCGCTCGGACATAACTCTCAGG
GTCCT

1093. chr7_C7orf27_NM_152743_-1.71184
TGGGTCAGGAACTCGAGGGCGGAGTCC

1094. chr7_IQCE_NM_152558_-1.69843
TCCACAAACCTCCACCCACATCGCCAA

1095. chr7_TTYH3_NM_025250_-1.61972
GGCAGGCGCACGACAGCCTCTACCGCGTCCACATGCCCAGCCTGTACAGC
TGTGGCAGCAGCTACGGCAGTGAGACCAGCATCCCGGCCG

1096. chr7_RNF216L_NR_023384_-1.55587
ATATGGAAAATCTCACCAGCCAGGATGAGGTACCCAGAGATACC

Figure 3-90

1097. chr7_WIPI2_NM_015610_-1.74053
TACTTACGTGCCTTCATCCCCAACGAGACTT

1098. chr7_FSCN1_NM_003088_-1.58523
CCTGCCCACATGGCGGCTCCTGCCAACCCTCCCTGCTAACCCCTTCTCCG
CCAGGTGGGCTCCAGGGCGGGAGGCAAGCCCCCTTGCCTTTCAAACTGGA
AACCCCAGAGAAAACGGTGCCCCCACCTGTCGCCCCTATGGACTCCCCAC
TCTCCCCTCCGCCCGGGTTCCCTACTCCCCTCGGGTCAGCGGCTGCGGCC
TGGCCCTGGGAGGGATTTCAGATGCCCCTGCCCTCTTGTCTGCCACGGGG
CGAGTCTGGCACCTCTTTCTTCTGACCTCAGACGGCTCTGAGCCTTATTT
CTCTGGAAGCGGCTAAGGGACGGTTGGGGGCTGGGAGCCCTGGGCGTGTA
GTGTAACTGGAATCTTTTGCCTCTCCCAGCCACCTCCTCCCAGCCCCCCA
GGAGAGCTGGGCACATGTCCCAAGCCTGTCAGTGGCCCTCCCTGGTGCAC
TGTCCCCGAAACCCCTGCTTGGGAAGGGAAGCTGTCGGGTGGGCTAGGAC
TGACCCTTGTGGTGTTTT

1099. chr7_AIMP2_NM_006303_1.58641
GAGTCCCGCCAAGATGATATTTTAAAACGTCTGTATGAGTTGAAAGCTGC
AGTTGATGGCCTCTCCAAGATGATTCAAACACCAGATGCAGACTTGGATG
TAACCAACATAATCCAAGCGGATGAGCCCACGACTTTAACCACCAATGCG
CTGGACTTGAATTC

1100. chr7_ICA1_NM_004968_-1.90822
CTCTCTCTCTACTCCCCGGGGTCTCTCCTCGACCCCCATCTCCTGGGGTA
TCCCCCGCTCGGAT

1101. chr7_TMEM195_NM_001004320_-1.7536
GATGAACAGCATATACTGAAGGGGGTATG

1102. chr7_TMEM195_NM_001004320_-1.56531
AGGCACCTCTTCTAATGTTTGGAATGAAGTTTCACTGGGTTTCATCGTGT
AAAACAACATGCGAAATCCCTGGGAAAC

1103. chr7_SP4_NM_003112_1.61533
CTAATGCCACGATAGGTGCTGTTAGTCCTGACCAACTCACACAAGTGCAT
TTGCAGCAAGGCCAGCAGACTTCTGATCAAGAGGTACAACCTGGCAAGAG
GCTTCGAAGAGTTGCCTGTTCCTGTCCT

1104. chr7_C7orf30_AK127742_1.67959
CGTGCAGCGGCTTCCCGTAGGAGCAGCGTTCTGCCGGGCTTGCCAGACCC
CAAACTTTGTCCGCGGCCTGCAC

1105. chr7_OSBPL3_NM_015550_1.55727
AGCCGCCGCCACAGTAGATGCTTTCATGCCATTTCCCAAACAGCCGATGA
ACCGCTTTTCCACTCCTGTCAAACACTGTGCCTTCAATCTCATGGG

1106. chr7_CYCS_NM_018947_-2.13251
CACAACGAACACTCCCGCTCCGAAGCCGGACGTCCCCACTCTCTAAGTCC
AAGGACACGCCGGTC

1107. chr7_HOXA1_NM_005522_1.67333
TTCCTGATTTAACGCGTAGGGGCTGTAAGGCGCACTGAAGT

1108. chr7_CHN2_NM_004067_-1.52699

Figure 3-91

GCAGCGACGCGAGGGGCGCGCGGA

1109. chr7_CCDC129_NM_194300_1.5327
ACCAACAGTGGCTGCGGGACTTTCCAGCACCTAGCCTGGGCATTCCCACA
GCCCAGAGGGAGCTCGTCCCAGACAACCAAGAGGAAAAGAAGGGAAACAA
GAAAGAGATGGAGACCCATCATTGTGGCCAACGACCCCACGAAGAGGGAA
TAGCGGTCCACGCACGGGACCCAGCCTCCGATCAAGCCCAGCAGGCGCCG
GGTGCGCCTGTGCTGGGAGGCAGAGCCCACGCCCACCCGGAACCGCGCCG
GCCAGCGAGGTCCGTGCGCAGCCCCGGCTGCCGCCTGCGCTTCTCCCTCC
ACACCTCACCGTTAGCAGAGGGAGCCGGCTCCGGCCTCAGCCAGCCCCAG
AGACAGGCCCCCACAGCACAGCGGCGGGCTGAAGGGCTCCTCGAGCGTGG
CCAGAGCAGACGCCGAGGCTAAGGAGGTGCCGAGAGACAGCGAGGGCTGC
TAGCACATTGTCACCTCTCAATACTGGAACTCAGAATAAGAGGTCTCCAC
TGTTCTGAGTTATGGGAGAAAGATGGGTGTATGGTAGACAGAATAGTGCC
TCCCCACAACAAAGATGTCAACATGTTACTGTGTGTGTTAAAAGGGACTT
TGTAGGTGTGAGTAAGTTGAAGATCTTGAGAAGAAAAGATTATCCTGGGT
TTTTTGGGTGGGGCCAATGTCATAAAAAGGTCCAGATAAGAAAGAGGCAG
AAGAGTCAGGGTCAGAGGAGGAGCCATCATGATAGGAGCAGAGAAGCAGA
GTCAGGAGAGTTGATGCTACACTGCTAACTTTGAAGATGAAGAAGCCACG
AGCTATGGAATGGAGACAGCCTCTGAAAGGCAAGGAGATGGATTTCCTTT
AGAGCTTCCAGGAAGGAGTGCAGGCCTGCTAACAGATACGTTT

1110. chr7_FKBP9_NM_007270_-1.5466
CTCCGACGCGGAGCTGCAGATCGAGCGGCGCTTCGTGCCCGACGAGTGCC
CGCGCACCGTGCGCAGCGGCGACTTCGTGCGCTACCACTACGTGGGGACG
TTC

1111. chr7_ELMO1_NM_014800_-1.57919
GGAGGTTAAAGGTGAGCACTTGTAGAACATACAGCTGGTGCGCCATCTCA
TTGTTGATGGCCCGCT

1112. chr7_ELMO1_NM_014800_-1.55517
TAGGCGCCCGGCCATTCTATGGCCACCTTGACGATGTCCGCGGGTGGC

1113. chr7_STARD3NL_NM_032016_-1.54067
TGTCTTCTCTTTAGGGATGGTGAGGTTGGAAAAAGGCTCCTGTAACCCTC
CTCCAG

1114. chr7_POU6F2_NM_007252_1.52788
TGTCTCAAAGTCCCGTCCGGCAGGCTTCCTCTTCTTCCTCCTCATCCTCC
TCTTCTTCAGCTTTGAGCGTGGGCCAGTTAGTCAGCA

1115. chr7_GLI3_NM_000168_-1.75086
ATCTGTAGGGCTCAGCCCACGGGTTGCTGAGATCATGGAGAGCGATGGGC
TGCTGTGCAAGGAGCGGATATAGTCCATGTAGGGATTAATGTAGGGATGT
GGAGGGCTGAAGGGAGACTCGGAAGCAGCAGTGGGGTTCCGGTGTGGGGA
GATCCTAATGAAGGGCAGGTCCGGATACGTAGGGCTACTAGATAAGGCGG
AAGT

1116. chr7_POLM_BC026306_-1.66942
GCTGCCCCTGTTTGCCTCCCCGTGCATGGTGTGGACTGTGTTGTCATTCC
CAGGGCAGGACATTCCTGGGGTAGGTCCGAGCCCTGC

1117. chr7_AEBP1_NM_001129_-1.62485
GGAAGGCCCCTGGTATGGACACTGA

Figure 3-92

1118. chr7_POLD2_NM_001127218_-1.64826
AGGAGGTTGCCAGCGAGGATAACCCGGGAGACGTGGGCGGCGCTGCA

1119. chr7_MYL7_NM_021223_-1.81949
TTTCTCGTCTCCATGGGTGATGATGTA

1120. chr7_CAMK2B_NM_001220_1.60826
CGTAGGCCTCAAAGTCACCGTTGTTGACGGCCTCGATGAGCTGCTCCGTG
GTCTTAATGATCTCCT

1121. chr7_CAMK2B_NM_001220_1.92361
CGGACGGGCTCGGCGTGCGCTCGGCTGCGCTC

1122. chr7_NPC1L1_NM_013389_1.52293
AGGAGACAGCGAAGGTGGGCACAAGGCAGAGGCTGAGCATGAAGAGCCCC
TCAGGGAGGATGGTCAGGTACTGCTCATAAAACACATTGGTGATC

1123. chr7_PPIA_NM_021130_1.70245
GGAGGCCAGGCTCGTGCCGTTTTGCAG

1124. chr7_PURB_NM_033224_1.53014
GAATTCGCTCTTGAGCGCGCGCCGCGGCCCGCCGCCCTCCTCGGCGCCAG
CCGCCAGCTGCTCGGGGCTGCTAGGGCCCAGCTGCGCGTAGTGTTCTATG
AAGTCGCCCAGCGAGTCGCGGAACTCGGCGGCCACCGCCATGGACAGCGT
GAGGCGGCTCTTGGAACCGCCC

1125. chr7_CCM2_NM_001029835_-1.59049
CAGCTCTGATGACCGGTCGGCACCCTCAGAGGGGGATGAGTGGGACCGCA
TGATCTCGGACATCAGCAGCGACATTGAGGCGCTG

1126. chr7_RAMP3_NM_005856_1.50339
CATCACCGGCATCCACAGGCAGTTCTTCTCCAACTGCACCGTGGACAGGG
TCCACTTGGAGGACCCCCCAGACGAGGTTCTCATCCCGCTGATCGTTATA
CCCGTCGTTCTGACTGTCGCCATG

1127. chr7_PKD1L1_NM_138295_-2.41038
TGGGGGTGCGAGGAATGCCAGGCG

1128. chr7_COBL_NM_015198_-1.63226
CACCCTCACGTGACCCATGCCCATGGTGGGGGGCTGGTTTCTCCCCTCCC
CTAGGGGGTTCCGGCCCTCATGGTGGGCAGACTTCTGCTGGGGCGATATT
GGCTTGGGGTCTGCTTG

1129. chr7_POM121L12_NM_182595_1.65797
TGATGCTTGGCCTTCCGTGCTGGTCCAGCCCGCCCCATCCGCCATCTGGG
ACTTCTGGGAGGCGACAACGCCTTCCTGCGGCAGCTGCAGTAGGGTCTCC
TTCGCCCTCGA

1130. chr7_EGFR_NM_005228_-1.65192
GAAGCCACGTGCAAGGACACCTGCCCCCCACTCATGCTCTACAACCCCAC
CACGTACCAGATGGATGTGAACCCCGAGGGCAAATACAGCTTTGGTGCCA
CCTGCGTGAAGA

1131. chr7_EGFR_NM_005228_-1.52259

Figure 3-93

CAGGCTTGGCCTGAAAACAGGACGGACCTCCATGCCTTTGAGAACCTAGA
AATCATACGCGGCAGGACCAAGCAACA

1132. chr7_PSPH_NM_004577_-1.50554
CCAGGGCCTCCACCGAACGCTCTCTTGAGA

1133. chr7_NCRNA00174_NR_026873_-2.17412
AGGGCCGCCGGAAAGCCGAAGGTGGGTCCGGGAGGCCTGAACGCAGGGAA
GCCTGGGGCCTACAACGGCTGCCAGGAGCTGGGCAGGAGCTGGGCCGAAC
GTGGTTGTCGTGAGGCAGGAGCTGGGCCCGTGGAGGTGGCCGGGAGAGCT
GGGCCTGGAGAGGCCGACGGGAACCAGTTCTGG

1134. chr7_STAG3L4_NM_022906_-1.57138
GGGTCACAAGGGAGATGTCCGCCCCCAGTCGTAGCCTCGGACGGTTTCTG
AGCG

1135. chr7_WBSCR17_NM_022479_1.56721
ACTTGATCGCGGTAGCCGGCTTCGTGCTCTTCCTGGCCAAGTGCCGGCCC
ATCGCGGTGCGCAGCGGAGACGCCTTCCACGAGATCCGGCCGCGCGCCGA
GGTGGCCAACCTCAGCGCGCACAGCGCCAGCCCCATCCAGGATGCGGTCC
TGAAGCGCCTGTCGCTGCTGGAGGACATCGTGTACCGGCAGCTGAAT

1136. chr7_WBSCR17_NM_022479_-1.8708
TGTGGACCTGGTACTGAGGAGCAAGACTGTCCAGTTCTCCTCCACATCTC
CCATCCCAGAATCAGGATCTGG

1137. chr7_CALN1_NM_031468_1.65283
AAGGCAGTAAGAACGGAAGCGGTGAGGGGTGCAGCTGAAGACCGCCAGGG
CTGCACCCCACTTAATGGCTTTCCCCTCATGCCTTGGGGGGGTCTCCACT
GGGTGGAGGAAGGAAGCCAGGGTGGGATGGAAAGCCCCCTCTTCTGTGGC
AACCCTGAAGTCAGCCTCTTGGAACTGAGGGTTGACCTCAGCA

1138. chr7_TBL2_ENST00000437521_-1.64046
AAGAACTCGGGGATGAGAAGTCAACATCTGTTGAGTCCTG

1139. chr7_STX1A_NM_004603_1.75168
GCGGAGCTCCTGGGTTCGGTCCTTCAT

1140. chr7_WBSCR28_AY372054_1.8162
GCAGTGGTGCCGGCTCAGCTCGTTGCAGCC

1141. chr7_ELN_NM_000501_-2.05716
CCCGGCTTTGGTGTCGGAGTCGGAG

1142. chr7_ELN_NM_000501_-1.50109
GCCGCTGGGCTCGGAGGACTCGGAGTCGGAGGGCTTGGAGTTCCA

1143. chr7_LAT2_NM_032464_-1.64253
CAAGCTGTTGCAATTCTACCCCAGCCTGGA

1144. chr7_CLIP2_NM_003388_-1.85244
AGCGAGCCCGGCTGCTCGTGGAGAGCGTGCGGAAAGAGAAGGTGG

1145. chr7_HIP1_NM_005338_1.59938
CTATTCTGGCCGTGGCAGTTTCAATAGCAGCTGAAGTGGCCGCCATCTCC

Figure 3-94

TTGTCCACCAGGTCCCCCAGCTCCTCCTGCTTGATGTCCAGTCCCCTGGG
CA

1146. chr7_POR_NM_000941_-1.56851
TCATCGTGTTCTACGGCTCCCAGACGGGGACTGCAGAGGAGTTTGCCAAC
CGCCTGTCCAAGGACGCCCACCGCTACGGGATGCGAGGCATGTCAGCGGA
CCCTGA

1147. chr7_YWHAG_NM_012479_1.65396
GCGGGCCACGTTCACAGATAGACAGATTCACCCGAAATGAGAATGAGGGC
CTTAAGGCTGCCGAAAACAAATGGGTGGAAATAGCAACGTTGTTTCCGTC
AATTCCAAATGTGCACTGGCTGCGTGAGACAAGCCAATCTCCAATTCCTA
TGCTTTTTTCATTAAAAAGAAAAAACTATCTCGAGAGGAAAAAGTTCTGG
TCAAATAGGAGTTCAGTGTTTGTTATCTGGTAACAGTTTTTTTATCTTCC
TACAATTACTTGGGGAAGGAGTGTCTTCGGGGAGGAAAAACTGACACACT
GACAAGGCTCCCGAAATTGGACAGAATGGTTAAGGATATAGCTCTTCCTT
TTGGGTTTTTCTACCAGTAGGCTTCTAGCACCTGAATTTTCACACACTGC
ACCACAGACCTTCTCCAAACGCCTCTCCGACCCCACAGCTTCTGCACCCA
GCTGCGTCCGCCAGCACGAGGCGCAGTAGGAAACGCCCCAGTGCAGAGTG
GGTGACGGCAGTGTGATCCCTGAGGAGGGAGCTGCAGCAGCTTCAGAAGC
GGGATGTTCTCTGAAAATACCAACACGATCCATGACATACAGACCTGAAT
TTTCTCTATTTTTGTGGCGTTTCACGTTTCTCTCAAGAGGATTAATAATT
TTGGTGGTGGATTTACGTTAAGAGGAAAGAAGGACCAAAAAAAAAAAATC
CCACAGCCACCTGACCTGAAGTCGCTTTCATTCTCATTTAGCCTAGGAGA
CCGATCAACAGCAAAACCAACCTGGATAAGGCTGAATAAGGATGTTAAAG
CCCAAACAACTAGCAAAGGAAAAGTACACAATCGATGGCTTGATGTTACA
TATGGCTGTAATGTAGAAATACTGTAAACTGCAATTTAGTGTTAATACTG
TCAACTAATCAGAGACTTCGGAAAACTGGCAAGGCCTAAACCATAAGGAT
GAATGAGACCTCAGGTTCTAAGTCTGTCAGTCTGGGATTTACACTGTTCC
ATGTCTGTAGGCTACACCCTGGAAAACATGCAGAGCCGAGACAGATGAGA
TAGAAAGTACCCAAAACGAGAGACGAGAGCGTATGTACATAAAAATCCTT
ACTGGAACCACAGAACTTACTGAATGAGGGCCATTCCTCTTTAAGTTTTC
TTTTCATCTGAAAACCCTATTATCTAGCAATAAGTTAAATTAGAGACAGA
CAGCTCCACTTGCATGAATCTACAGAACAGTCCAGACGCCAGTGTGAGGC
TGCTATTCCAATACCAGCACAGCTAGCCTGACTTTCCACTAGTGGTATTT
TGGCAAAAATGTCAAAGAGGCGATCAAAGACAGGACAGGTCGTGGGTTTC
TCCCTGGGAAGGTCATCCCTCCCTTTCCCTCCCCCACCCGACCCCCAACT
CATGGGAAAAAAATAAAGACTGCAGTAGTAGCATCCGCGTGCGCT

1148. chr7_ZP3_NM_001110354_1.50485
GTGGAGCCAGCCATCCTGAGACGTCCGTACAGCCCGTACTGGTGGAG

1149. chr7_UPK3B_NM_030570_1.50857
ACCCTGGGGGCAGCCTCACCTAGGGCTGCA

1150. chr7_MAGI2_NM_012301_-1.65325
AGTCCGACAGAGGGTACTGCCTGGTGTCGGGGGAGTGCTGCCTGTAGTCC
AGTAGGGGAGGCTGCCTGTAGTCCAAGGGTGGGGGCTGCTGGTAGTCCCC
TCCTGGGGGTTGCCTGTAATCCAGCGGGGGCTGCCTGTAGTCTGTGAATG
GAGGCTGTCGGATGTCTGGTTTCACATCTTGCCTTGCTTTCACTTC

1151. chr7_MAGI2_NM_012301_-1.81861
CTCCCCCGAGGATTCTGAAGCCAAA

1152. chr7_CROT_NM_001143935_-1.78193

Figure 3-95

TGCTGTGTCGAGGCCGAGCTTTTGTCTTTGAT

1153. chr7_ADAM22_NM_021723_1.53247
TGTGTGCCGAGAAGCAGTAAATGATTGTGATATTCGTGAAACGTGCTCAG
GAAAT

1154. chr7_KRIT1_NM_194456_-1.72614
CATTACAAAATGTGGTGGCTTGAGTAACA

1155. chr7_CDK6_NM_001259_-1.68359
ACTGAGGTTAGAGCCATCTGGAAA

1156. chr7_CCDC132_NM_017667_-2.53303
ATCAAATCTCTCATGACCCGACAG

1157. chr7_COL1A2_NM_000089_-1.72357
GGCTCCAAAGGAGAGAGCGGTAACAAGGGTGAGCCC

1158. chr7_SGCE_NM_001099401_1.61967
GTTGGGGACCCATATAGGACTCCATCACTATATGGTGTCCTTTGGATATA
TCGAAGCCATCCAGGTCGGTCTGGGTAACCCA

1159. chr7_DYNC1I1_NM_004411_1.59799
ATGTCTCCCTCCTCGAAATCAGTGAGCACTCCCAGTGAAGCTGGAAGCCA
AGACTCAGGCGATCTGGGGCCATT

1160. chr7_TECPR1_NM_015395_-1.53775
ACAAAATCCTTCATCGTTTTGGACCCATGG

1161. chr7_BAIAP2L1_NM_018842_1.87794
AGGTGCTCTCCGTGAGCCGGTTCACCTCCTCGG

1162. chr7_SMURF1_NM_020429_-1.66906
GGCGTCTGTAGTGAACCTCGCACATCAGGGTTTCGAAGCCGCTGTGCCTG
AAGTCTTTGATCTTGACTTGGGGACTCCACGAACCTGCAATTCCCTCCTC
CAGCAGCAGCACCGGTGCTATCTGTGTAAGGGGCTGGTTCCTCCATGAAG
CAGCTGAGCGGCCTCCCAGGCCCGGAGTCTTCATACACCGT

1163. chr7_ARPC1B_NM_005720_-1.50503
CCGTATTGTGACCTGCGGCACAGACCGCAACGCCTACGTGTGGACGCTGA
AGGGCCGCACATGGAAGCCCACGCTGGTCATCCTGCGGATCAACCGGGCT
GCCCGCTGCGTGCGCTGGGCCCCCAACGAGAACAAGTTTGCTGTGGGCAG
CGGCTCTCGTGTGATCTCCATCTGT

1164. chr7_PDAP1_NM_014891_1.56451
GCGCCTCGAACTGACACCGGAACCGGAAATAGCTTGGGCTCGACTTCTTC
CTCC

1165. chr7_ZNF789_NM_213603_-1.60546
TGAAAAAGCTAACTCCAAAACAGAAATTTTCTGAAGATTTAGAGTCATAT
AAGATATCAGTGGTAATGCAGGAATC

1166. chr7_ZKSCAN1_NM_003439_-1.68833
CCTCATGAGGGTAGTCCCAGAGACCAGGCGATGGCATCTGCACTATTCAC
AGCGGATTCC

Figure 3-96

1167. chr7_MCM7_NM_005916_1.65028
TGTTCATCTTCACAATCCGATGGG

1168. chr7_C7orf43_AK302342_-1.80484
CTCCACCAAGTCCCGGACAGCAGGGCTGCTGGGGCTGCTCTTGCGGGAGA
GGGGCCG

1169. chr7_GPC2_NM_152742_-1.58695
TCCAGCGAGGCGTCCGCTGCCATGCGAGAGTCTCCGCAC

1170. chr7_GPC2_NM_152742_1.50568
GTGTGAACCAGAAAGGAGCCGCTGTCCTCCACCAGGCCTCGGAAGGTGGC
CTCAGTCTCCCTGATCAGCCTCTGCTCTGTCTCACTGGAACAGCAGGTGT
ACTCCT

1171. chr7_PILRA_NM_013439_1.50731
CACAACCGGCCTCAGGGTCACACAGGGCAAACGACGCTCAGACTCTTGGC
ACATAAGTCTGGAGACTGCTGTGGGGGTGGCAGTGGCTGTCACTGTGCTC
GGAATCATGATTTTG

1172. chr7_MEPCE_NM_019606_-1.66063
GGAGGCTTCAAACATCCGGCCTTCAAGAGGCGCAGGCGGGTGAATTCGGA
CTGTGACTCTGTGTTACCCTCCAACTTCCTCCTGGGGGGCAATATCTTTG
ATCCCCTGAACC

1173. chr7_C7orf61_BC031966_-1.50713
TTGCCAAGCCCGTCTAACCCATCGGAAGA

1174. chr7_C7orf51_AK124773_1.68416
CCGCGAGCGTGACGGGAAGCTGCTGGAGGTGATCGAGCGCAAGCGCTGCG
TGTGCAAGGAGATCAAGGCGCGCCACCGCCCGGACCGAGGCCTCTGCAAG
CAGGAGAGCATGCCCATCCTCCCCAGCTGGCGGCGGGGACCCGAGCCCCG
CAAGTCCGGCACCCCGCCCTGCCGCCGGCAGCACACGGTCCTCTGGGACA
CCGCCATCTGA

1175. chr7_LRCH4_AK074175_-1.78956
CCCGAGCGCAGGACGGTACCGCCGTGTCC

1176. chr7_LRCH4_NM_002319_-1.51994
CGAACCCCTACAAATATAGATCCTCTCTACAAAATAGAGATAATTTAGCC
CCCCCATAGCAGCTGTTGGGGGGGGAAGGGGAGGGCACAGGAGGAAGGGG
GAGACTCCAGCTCCTGCCACCCCTCACGGGGTACAGAGGGCAGGGGCAGG
GCCGGCGGGGACATGAAGGCACCGTCAGCACTGAGAGGTGGGGACTCGTG
GGGCTACTGGAGGGAGGCCAGAGGCTGGGGGCCCAGGGTCTGGGGGCACC
AGAGTGGGGCCTCTGAGGTCAGTGTCTGTGAAGGGGGTGCACTAGTGTCT
TTGGTTGGGGCTGAAGGCACCGCAGGTGGGGTCGGGTGGAGCAGGGACCT
TATAAAT

1177. chr7_MOSPD3_NM_023948_1.56261
TTCTTGCTGACGGGGATTGTGTCTGTGGCCTTCCTGCTGCTCCCACTCCC
GGACGAACTCGGCAGCCAGCTGCCTCAAGTCCTGCACGTCTCCCTGGGAC
AAAAGTTGGTGGCCGCCTA

1178. chr7_GIGYF1_NM_022574_-1.72964

Figure 3-97

TGGGGGGTTTGAGCGCCTGGAGCTGCTGCAGGAATGCCGTGAGCTGCTGC
TGCTGCTGCTGTGGCGGCGGCGGTGGTGGCGGTGTCAGGTCCCCCAGAGC
TGCCTTTTCTCGGAGCGCGCACTGTGGGAGCTGGCGG

1179. chr7_ZAN_NM_003386_-1.76667
GACTTTGAAGACAACGCCCATCCCTTCTGTGACTGGGTCCAGACTTCCGG
GGATGGTGGACACTGGGCCCTCGGACATAAAAATGGACCCGTCCATGGCA
TGGG

1180. chr7_PLOD3_NM_001084_-1.618
CGGCCCCACGAGCTTCACAGCTGAGAAGTGGTCCTGGAGCTGCGGCCAGG
AGTCAGCGATGTGGGGTTCATGGAAGACCTC

1181. chr7_PLOD3_NM_001084_1.61252
AGAATTGAGGAAGCGCTTCCCCGTGCCCACCTCAGGGTACTGCTCCGCCA
GCCCCCACTCGGGCCAGCAGAAGCTCTCTGCAGAGAAGAGCAGGCGGCTG
CCACTCTGGACGAACTTCTTCAGCAGCTCTGTGGGGCTGCCGGCCAGAAT
CACGTCGTA

1182. chr7_ZNHIT1_NM_006349_1.74487
GGCCGAGGGCCCTAACTACCTGACGGCCTGTGCGGGACCCCCATCGCGGC
CCCAGCGCCCCTTCTGTGCTGTCTGTGGCTTCCCATCCCCCTACACCTGT
GTCAGCTGCGGTGCCCGGTACTGCACTGTGCGCTGT

1183. chr7_MYL10_NM_138403_-1.57381
CCTCCTCACTGAAGCGGTCTGCCTGGGTCATAAGTTTTTCTT

1184. chr7_CUX1_NM_181552_1.57071
TCCACTCCGTGACATCGCTCCAGGACCCGCTGCAG

1185. chr7_CUX1_NM_181552_-1.80284
AGCGCTTATTTGGGGAGACCATCTTAGGGCTCACCCAAGGCTCTGTCTCT
GACCTCCTTGCCCGCCCCAAACCCTGGCATAAGCTCAGTCTGAAAGGACG
AGAGCCCTTCGTC

1186. chr7_CUX1_NM_001913_-2.99357
GCCGCTGAGCACCGCCTGGAGAAG

1187. chr7_PRKRIP1_NM_024653_-1.93073
CAGCCGCCTCCTCGGTGCGACCACCGAGGCCCAAGAAAGAGCCGCAGACG
CTCGTCATCCCCAAGAATGCGGCGGAGGAGC

1188. chr7_RINT1_NM_021930_1.6504
GCTCTGAAAGTGGTGACGAAAGGAAGAACCTCGAGGAGA

1189. chr7_SYPL1_NM_006754_-1.72049
CTCAGTAACTGCAGGAGGACAATT

1190. chr7_FLJ36031_NM_175884_2.8759
CGGAACCGGCCGGCGCGCCTGGCC

1191. chr7_PRKAR2B_NM_002736_1.58201
CCGCCACCACACGGAGCAGACGCGCGCCGGGAGCCGCGGGCCGGGCCAGC
CGGGCCGCCGGGGCCCAGTGCGCCGCGCTCGCAGCCGGTAGCGCGCCAGC
GCCGTAGGCGCTCGCTCG

Figure 3-98

1192. chr7_PRKAR2B_NM_002736_-2.48921
CCGCGGACGCAGGGGCGTTCAATG

1193. chr7_TES_NM_015641_-1.75869
CGGAAGTTCGACGGCGCCGGGCGAGTGGCTGTTGAGCGGCGCCGCGGGAG
TTCCGCAGGTTTCCCGTGTTCGCAGCGGAGCCGGAGGCCAGCTGAACCCG
GCCGTGGGATCCCGGATAGGAGGAGGAG

1194. chr7_MET_NM_001127500_1.61943
TTCACTGCATATTCTCCCCACAGATAGAAGAGCCCAGCCA

1195. chr7_WNT2_NM_003391_-1.67728
CACACTTGGTCATCCGGGTGACATGGGAGGTGTCGTAGCCTCTCCCACAG
CACATGACTTCACAGCTGTCCATGCCCCGGGAAGTCAGGTTGCA

1196. chr7_CTTNBP2_NM_033427_-2.04154
GAGGCACCTGGTCTACAGGATGAGGCACTAACGGGGTTTATGGAAGAGCA
AAAGGCAATGGTGGTAGGAATGACAAGGGAACTGTCTGAACATGCAGGTT
GGTTCAGTCCGGG

1197. chr7_SLC13A1_NM_022444_1.89826
GGTCTCATTACTCATAGCAGGAGC

1198. chr7_GPR37_NM_005302_-1.65829
TAGCAGAAGCAGTAGCCGCGACATGCGGGCGAGAAGCGCGCCCGG

1199. chr7_POT1_NM_015450_2.03955
TTAAGTTGATTCAGGGGTGTATATATAT

1200. chr7_FSCN3_NM_020369_-1.54745
GGGAAGTTCTCTCTGGGAACATCT

1201. chr7_MGC27345_ENST00000424840_-1.50258
AGTTTCCACCCCATTGACAGGCTTGGAGTCTTGAGTACCATCTGGGTGGG
TGGAGCTGGCACTGGCACGAAACCTC

1202. chr7_CCDC136_NM_022742_-1.50489
TCCTGGAGGATGAACGGCTAGCCAGCGCCCA

1203. chr7_KCP_NM_001135914_1.79989
GGCACATGCCTTGGGCTCGCAGCTCACGCTGCCCTCCCAGCAAAGGCAGA
GGTGGCAGGCAGCAGTGGGCGATGGGAAGCGCTCCCCGCTGGCAAA

1204. chr7_IRF5_NM_032643_2.22332
CCGAAGGCGTGGATGAAGCCGATCCGGCCAAGTGGAAGGCCAACCTGCGC
TGTGCCCTTAACAAGAGCCGGGACTTCCGCCTCATCTACGACGG

1205. chr7_TSPAN33_NM_178562_-1.63121
GATCGTGGTGGGTGTCCTCATGTTCCTGCTCACCTTCTGTGGCTGCATTG
GGTCCCTCCGCGAGAACATCTGCCTC

1206. chr7_SMO_NM_005631_1.57211
GGGCCCGGATTCTCTGGGCGCACAGGTCGCCTGAGCCGCCTCCG

Figure 3-99

1207. chr7_ZC3HC1_NM_016478_1.55138
CCCTCTTCCGGGGCAATCCCCTCAT

1208. chr7_CPA2_NM_001869_-1.61417
TCCTGTTGGACAAAGAGAATGAAGAAATGCTTTTTAATAGGAGAAGAGAA
CGGAGTGGTAACTTCAATTTTGGGGCCTACCATACCCTGGAAGA

1209. chr7_MKLN1_NM_013255_-2.56066
GGCGGCCGCTACGGTGCTGACAAG

1210. chr7_LRGUK_NM_144648_-1.70209
TACACAGACAGCACGAGGCAGCCCGGCAAGCTCTAATGGGAAGGATACGC
CCTGATCACACACTC

1211. chr7_SLC35B4_NM_032826_-1.86375
ATTTGCGTAGGGTCACGACGAGCGTGACGGTGAGGGAGGCGCATTCTGTG
GTGAGGATAAACACACCCCGG

1212. chr7_STRA8_NM_182489_-2.58319
TGAAGAAAACAGCAATCCCCATGAC

1213. chr7_CNOT4_NM_013316_-1.53901
TCTGGTGCTGTAGGCCAGTCACTGGATGTCTGTGGGGAGCTGGGGAAAGG
AGGAAGCCCACTTGGGATAGGGTTGGGATGGCGAAAATTGTCTGAGAATA
ACGACTGTGACTCTGTTACTGCCCCTTCAAAAGGGGACCGTGCACTGTGA
TTGGATGAA

1214. chr7_CREB3L2_NM_194071_1.56077
GCTGGTCTCATTCGAGATAATGAAATGGGGAAGATCCACATCCGGCCTGG
ACTCCAGCCCTGACACCCTGAGCAGGGAGGAACCTCTATCCCAGCCCCCC
AGCTCCCCAGCCGAGCCCGGGCTGGATGACTCCTCTGGGGGAGAATGTTC
CTCGTAGATCAGC

1215. chr7_TRIM24_NM_015905_-1.55129
AGTCATTCGTTGCCCAGTTTGCAGCCAAGAATGTGCAGAGAGACACATCA
TAGATAACTTTTTTGTGAAGGACACTACTGAGGTTCCCAGCAGTACAGTA
G

1216. chr7_KIAA1549_NM_020910_-1.50515
GGAAGTTCTGCACGGTGCTCTGTTTCTGGGAGAGCCGGAGGAGCTCCTCG
CGGATT

1217. chr7_ZC3HAV1_NM_020119_-1.65069
ATTGGCTGGCTTGGTGACAGAAGAAGGAGTGGAGAGGCGTCGGATGGGAA
AGGAATC

1218. chr7_TTC26_NM_024926_-1.7009
ACTCCAAAACCGCCTCCTCTTCCACT

1219. chr7_LUC7L2_NM_016019_1.51829
GCATCGCAGACATCGATCTCGCTCC

1220. chr7_ADCK2_NM_052853_-1.67616
CTTCTGAAAGCCACCGAGACCTCAGGCCCAACCTACATCAAACTGGGCCA
GTGGGCCAGCACCCGGCGCGATCTGTTTTCGGAGGCTTTCTGTGCCCAAT

Figure 3-100

TTTCCAAGCTGCATGTCCGAGTGACGCCCCACCCGTGGACTCACACTGAG
CGCTTCCTTCGGCAGGCTTTTGGGGATGACTGGGGGAGCATCCTCTCTTT
TGAGAACCGGGAACCTGTGGGCTCAGGCTGCGTGGCCCAGGTGTACAAAG
CATACGCCA

1221. chr7_NDUFB2_NM_004546_1.64234
TGTCCGCTCTGACTCGGCTGGCGTCTTTCGCTCGCGTTGGAGGCCGCCTT
TTCAGAAGCGGCTGCGCACGGACTGC

1222. chr7_BRAF_NM_004333_1.78599
TCCTTTCTCGCTGAGGTCCTGGAGATTTCTGTAAGGCTTTCACGTTAGTT
AGTGAGCCAGGTAATGAGGC

1223. chr7_EPHB6_NM_004445_1.72936
AAAGAACTGGAATAACCCCTTGCAGAA

1224. chr7_OR6W1P_NR_002140_-1.8289
ACAATGGAGAGGAAACCAACCACCCA

1225. chr7_CLCN1_NM_000083_-1.81741
GGGCAGAGCTCGCCCCACAAAGAAGAA

1226. chr7_CUL1_NM_003592_1.60429
GCGCCGTGTCGCACGCAGCTCCAGGCGGGGCAGCCCCGGTAGCTGAGGGA
CGCAGCTAGACCTTGGCGGGACGG

1227. chr7_EZH2_NM_004456_-1.62084
CATCAGCTCGTCTGAACCTCTTGAGCTGTCTCAGTCGCATGTACTCTGAT
TTTACACGCTTCCGCCAACAAA

1228. chr7_PDIA4_NM_004911_-1.56213
GGACCCTGGATCATGCCCCTTTGCCCCCAGCCCTTGGTTTGCAGGGAGGC
CGCCTGGCGATGCCCAGCCTGAAACAGCACCCCTGGCAGGGCTGCTCAGT
GGCAGCTCTCACTTTGTGCTCAACAGGAAGCAATCAGAAACACATACCAG
AAGCCAAATCTACGCCAACAATTTCTCAGACAACGAAAAAGCAAAGAGCA
AAATCAACATGATTTGGAAAAGGAATTTTAAACCTTAAATTAAAAAAAGA
AAACATTTTCACACAGAAGAATTATCTGCTTTGAGAAATAAAGAAATTAG
AAGGTGTAAAAAAAAATTTTTCAAACCCCAAATAATGATAAAAATAGATG
TATCCTCTGTAAAAATCTGGACTAAACTATTCAGTCATTCATGGTTATTC
AGTATTCAGAGCATGAAGTGAAACACCAAAGTATAAAAAATTAAAAAAAA
AAAAAAAGGAATCCGAGATACTGTCGTTTGTTGCCGGCC

1229. chr7_ZNF746_NM_001163474_-1.74959
CGGCCCGGCAGACGAAGGCCCGTGAGGCT

1230. chr7_ZNF767_NR_027788_1.75099
CCCGCGGCCCAGATAAAGTCGTCGCCGCTGCT

1231. chr7_SSPO_NM_198455_1.50714
CTGTATTCACCCTGGACTGTGCCAACCAGTGCCCACACAGCTGTGCCGAC
CTCTGGGACCGCGTTCA

1232. chr7_SSPO_AK124542_3.0903
CACCTCCAAAGTCAAGGCCCGGGA

Figure 3-101

1233. chr7_REPIN1_NM_013400_-1.68569
GGCCCGGTGGAGATGCCGTCGACCGCCCCTTCCAG

1234. chr7_GIMAP8_NM_175571_-1.64096
GAAGAGGGTCGCTCTCCGGCCATTCTCCCCTCACC

1235. chr7_ATG9B_NM_173681_-2.12454
TCTTGTTGTACTCGGCCCCAGAGG

1236. chr7_AGAP3_NM_031946_1.62752
CCCAGAAGGTAGTGGCCTTGCGAAAGAAGCAGCAACTGGCCATCGGGCCC
TGCAAGTCACTGCCCAACTCGCCCAGCCACTCGGCCGTGTCCGCCGCCTC
CATCCCGGCCGTGCACATCAA

1237. chr7_ABCF2_NM_007189_-1.70669
CAGGGATGGGCACTTCACGCTTCCCAATAGCAGAGAGCAGCA

1238. chr7_MLL3_NM_170606_1.55568
GAAAGGCAGCCGTTGCCTTCCGTCAGGAGCCCTATGTCTCAGTTCAATAT
ATGCTTGGCCCAGTATGTTGTGCTGCTGA

1239. chr7_ACTR3B_NM_020445_-1.8831
AGGACTATGAAGAGTACGGGCCCAGCATCTGCCGCCACAACCCCGTCTTT
GGAGTCATGT

1240. chr7_DPP6_NM_001936_1.88159
AGCGCTTCGGGGAAATCCGTGCAGCAGCA

1241. chr7_PAXIP1_NM_007349_1.57279
CCTGGACAGGCTCGAATCCAGTGAAAAGCACAAAAGGGGTCAATTCTGGA
GTTAGCTTTTTAGTGGGAGGTGGTACGTCTTCAAT

1242. chr7_NCAPG2_NM_017760_1.53218
GGTTTTTAATGGTCCCGTGGATCATTTTGATG

1243. chr8_DLGAP2_NM_004745_2.04934
TGGAAACGGCCACAGATTCTGACACGGAGAGCCGCGGTCTGCGGGAATAC
CACTCTGTCGGGGTGCAAGTG

1244. chr8_DLGAP2_NM_004745_-1.54735
GCCCGACAGACAACGCCAGGAAGCCCGGAGGCGCCTCATGGCCGCCAAGC
GAGCGGCGTCCTTCCGGCAGAATTCCGCCTCCGAGCGCGCGGACAGCATC
GAGA

1245. chr8_ARHGEF10_NM_014629_-1.66553
TAACCCGTTTAAAGGAGCACTATGAGAAAAAGATGAGAGATTTGATGGCA
AGCACGGTGGGCGTGGTGGAGATTCAGCAGCTCA

1246. chr8_CSMD1_NM_033225_1.76466
AGACAGGTTTGCTCGGATTCCACCTGCCGTCTTTGGTACAGCGAATAGTG
GCGGATGTGACTGCTTCCATGACATAGCCTGGGTTACACTGATAGCTCAC
AGTCTTGTTGAAGGTGAAGTCGGTCCCAAACTGGATGCCATTTGCTAGTG
TGCCTGGATCCCC

1247. chr8_CSMD1_NM_033225_1.50042

Figure 3-102

AGACATCGAGTTTCGCTGCCGCTCCAGAGCCCATTTGCCAAGCACTCTCT
GACATGAGACCCCACAAGCGTGTAGCCGGTGTTGCACGTAAATATAGCTG
TGGCCCCATAAACTGTCAACG

1248. chr8_ERI1_NM_153332_-1.50424
ATGGATTATGATGGGCGGCCTCACTGTGGTCTTGATGACTCTAAGAATAT
CGCCCGAATAGCAGTTCGAATGCTTCAGGATGGGTGTGAACTCCGAATCA
ACGAGAAAATGCATGCAGGACAGCTAATGAGTGTGTCCTCTTCCTTACCA
ATAGAGGGCACTCC

1249. chr8_TNKS_NM_003747_1.7731
CTGACGATATCAGAGCTTTGCTGA

1250. chr8_RP1L1_NM_178857_1.62139
GGCTGAGGCGTGTCCCTGGCCTCTTCCCCCAGGCTGGCAGCCCCAGATTT
TGAGCAGGAGTCGGATGTGTGGGGAGGTATGGGGGCCGGCGAGCATGTCC
TGGACCCCGCGT

1251. chr8_FAM167A_NM_053279_1.52782
GCTATAGCTTCATCGATGCTCTGAAAGCCTTCCAGCTTGCCAGTGGACAG
GGGTCTGGCACCTTGGCTGGCACTCCTGGCAGAAGGGGGGTGCTGCCCAG
CCTCTCTCAGGGGGAGCAAGGGCTCCTGCCCCCCACGCTCCCCCTCCTCC
AAGCTCGCCTGTGGCTCCGCAGCCGGCCTCGGGAAGGGCCAGGTATGCTC
CTCCAGCCTGGCCTGCCATTCCAGGTAGGAGGGCCTGCGGGTCTCCAGCC
TCAGTTTCTCGGTGAGGGCCTTCA

1252. chr8_NSAP11_AY176665_-1.79576
TCATCGCCATCTGTCCCACCGGACACCCC

1253. chr8_FGF17_NM_003867_-2.01784
TGCTGATTCTCTGCTGTCAAACTC

1254. chr8_FAM160B2_NM_022749_-1.54277
CACGAGGGGATCATCCACAGCCTGGTCCTGCGCAACCTTGAGGGCCGCCC
TTACGTGGCCTGGGGCTCA

1255. chr8_BMP1_NM_001199_-2.21043
GGCCGCTGGACTTGGCCGACTACACCTATGACCTGGCGGAGGAGGACGAC
TCGGAGCCCCTCAACTACAAAGACCCCTGCAAGG

1256. chr8_PDLIM2_NM_021630_-2.01836
GCCCGCCAGCGCTACTCCGCACCTGCCACCCT

1257. chr8_KIAA1967_NM_021174_-1.59886
CAAGAAACGCAAACAGCGGGCTGGTGGAGAGCCCTGGGGTGCTAAGAAGC
CAAGGCATGACCTGCCTCCTTACCGGGTCC

1258. chr8_KIAA1967_NM_021174_-1.56872
CCATAACCGTTTCTCAGCCACTGAAGTAACCAATAAGACGCTGGCGGCAG
AGATGCAGGAGCTGCGAGTCCGGCTGGCGGAGGCCGAGGAGACCGCCCGG
ACGGCGGAGCGACAGAAGAGCCAGC

1259. chr8_RHOBTB2_NM_001160036_-1.58793
GGCCGACTGGTGTCTCCACCACATCTGCACCAACTACAACAACGTGTGCC
GCAAGTTCCCCCGAGACATGAAGGCCATGT

Figure 3-103

1260. chr8_RHOBTB2_NM_001160036_1.71348
GCAGAATCGACTCCAATGCCTTTCAGGAAAGGACTCGGCACTTCTCTGAC
TGCGGAGGCCCTGACCCTGCCAGCTGGCTCCGAGGGCAACACAGGGGCCT
GGCCTCTAGAGGGCTGGTGATTGAGGGGCCCGGGCTGGCGGCAAAGAGGG
GTTTGGTCTCGGGGCTTAAATGGCACCAGACTCTTGCTTTTGCCCATCTG
GAGACTGCAGGCTCCCTTCCTTACCCTCAGAGAGTGCTTATGGTGGGTGT
TTTTGCGGGGCTGCAATAGGGGCCAAAAGTCAGGGAAAGGGGCACTGACC
TGTAGTGAAAGGCCACAGGACACAGCCTTATTACTGCTGGGGTGGGATAA
GGGGAAGGAGAAGAGGGAGAATGGAGCAGGAGGAAAAGCAGAGTTGGTCT
AGAGAGGAGGAGGGCGGGGCTGGAGGAATGTGGGGGATTGAAACTAGCTC
CCAGCCCCCATGGGGCAGCAGCTGGGCCACAATTGCCCCTTTCCGTTTTC
TAACCCCGACTCAGATTTCACCACCCACACTCTTTTTAGGTGTAAAAGAT
GGAGTCCCACGGAGGAGGGGCAGAGCCAGGAGGCAGTGGGGCTGTGGGCT
CAGAGCTCAGGAGTCGCCTTACCTGAGAGAGATGTTCTAGCTGAGAGGGC
CTGGCCCTGGGGTGGGCTCCAGGAAAACGCTGGTTAGGCCTGGGATTGAG
CTAACCTGAAACA

1261. chr8_TNFRSF10B_NM_003842_-1.78974
CTGTCCACACGCTCAGGGTCCCCAC

1262. chr8_TNFRSF10D_NM_003840_-1.55362
CGATGAAGACGACGAACTTAAGGATCTTGGGGTCCAGGAGCCATGGTCTG
GTTCCCGACGCTGTCCTGGCT

1263. chr8_CHMP7_NM_152272_-1.82523
TGTAAAGAAGAAGCCCGCCGGGCATGCCGAGCAGGAA

1264. chr8_LOXL2_NM_002318_-1.57966
AAGCCAAACATGCCGCAGACCACGCGGGAATTCTTGGCCGTCCAGTGCTT
GTCACAGATCTGCTTCCAGGTCTTGCCCTC

1265. chr8_SLC25A37_NM_016612_1.5047
AATCAGCTGCATCCGGACGGTGTGGAGGACCGAGGGGTTGGGGGCCTTCT
ACCGGAGCTACACCACGCAGCTGACCATGAACATCCCCTTCCAGTCCATC
CACTTCATCACCTATGAGTTCCTGCAGGAGCAGGTCAACCCCCACCGGAC
CTACAACCCGCAGTCCCACATCATCTCAGGCGGGCTGGCCGGGGCCCTCG
CCGCGGCCGCCACGACCCCCCTGGACGTCTGTAAGACCCTTCTGAACACT
CAGGAGAACGTGGCCCTCTCGCTGGCCAACATCAGCGGCCGGCTGTCGGG
TATGGCCAATGCCTTCCGGACGGTGTACCAGCTCAACGGCCTGGCCGGCT
ACTTCAAAGGCATCCAGGCGCGTGTCATCTACCAGA

1266. chr8_NEFL_NM_006158_-1.78799
TCGTTGGTGGCATCTTCCGCCGCCAGGCGCAGGTCGCGGAT

1267. chr8_DOCK5_NM_024940_-1.74757
TCTGGAGGTCACTCTGACCCCTGAAGTAGAGCTCCGGAAAGCC

1268. chr8_BNIP3L_NM_004331_1.54255
TTTGAAGAAAAGTGCGGACTGGGTATCAGACTGGTCCAGTAGACCCGAAA
ACATTCCAC

1269. chr8_DPYSL2_NM_001386_-1.53389
AAGTACTGAGTGTGATCCGGGATATTGGCGCCATAGCCCAAGTCCACGCA
GAAAATGGCGACATCATTGCAGA

Figure 3-104

1270. chr8_CLU_NM_001831_-1.57837
GTATGAATTCTGTTGGCGGGTGCTGGAAGGCCGGGCTATGGAAGTGGATG
TCCATGGCCTGCTGAGCCTCGTGTATCATCTCAAGGAA

1271. chr8_PBK_NM_018492_1.55944
TTCATTAGGTACACATTTACCCCAGTACCA

1272. chr8_ELP3_NM_018091_-1.85931
CCTGGTGGACCTGATTCTGATTTT

1273. chr8_PNOC_NM_006228_-1.63517
GGAAGGGGCGCTCCTCCCAGCTGTACCGGCCACTGCAACCCAT

1274. chr8_KIF13B_NM_015254_1.65326
TTGTTGCTGCCTAGACTGTATGATGGA

1275. chr8_PURG_NM_013357_1.87876
TAGGCCAGAGCCCCCTACATTCTTGCCTCCGCGGCCGCGGCCGCCGCCGC
CTCCCCTTCGCCTGGCTCTTTCCA

1276. chr8_GPR124_NM_032777_-1.52919
GCTGAGCGCCTTTCCCAGGGAGGTGGGGGGCGCCGGGGCAGGGCTGCACC
CCGTGGTATACCCCTGCACGGCCTTGCTGCTGCTCTGCCTCTTCGCCACC
ATCATCAC

1277. chr8_GPR124_NM_032777_1.55189
AGCCTTGGCGCCTTCTACATCCCTGTGGCTTTGATTCTGCTCATCACCTG
GATCTATTTCCTGTGCGCCGGGCTAC

1278. chr8_PPAPDC1B_NM_001102559_-1.93427
TCCTCCGGCTGGATGAGTCTCTGGAACGGGGGGAGCAGCTC

1279. chr8_WHSC1L1_NM_023034_1.50906
GCACTGCTGCACTCATCGCACTGATGCCACGGACACTCCCACTTTC

1280. chr8_TM2D2_NM_031940_1.67906
TTGCATGCACGTAATCAAAACGGGCAAAAGACATTTCTTCATCAAGTTTT
CTGGGGTTCGGTTTCACCCTGCTGACCCCTTTCCAAGCCAATTAAACTGA
AGCACAGCAGGTCAAACGGACAGCCACCAAAATG

1281. chr8_C8orf4_NM_020130_-1.7
GAGCTGAATTCCGGAAGATCCCCACATCG

1282. chr8_ANK1_NM_020476_-1.7657
GCACCACTTGGGTGAAGGTGTTCTTGGCCTCCTGCACCTGCTCTTCTTGG
CCTTGCTGCCTCCGGTCCCTGTCGGCCTGGGAGCTCTCAGCCTCGGGCTG
TTCTGTCCACGTGTGCTC

1283. chr8_IKBKB_NM_001556_1.53985
CCGGCGCCTTGTCTGCACACTGGAGGTCCTCCATTACAGAGGCCCAGCGC
ACATCGCTGGCCCCACAAACGTTCAGGGGTACAGCCA

1284. chr8_VDAC3_NM_001135694_1.589
TGGTTTCATAAGAGCCTGAGAGAG

Figure 3-105

1285. chr8_THAP1_NM_018105_1.51384
TCTCAGTGTCGCTGCGCTCGGTTGGATTCCCTCGCTTCTTTTGTAGCTTT
GGCCAACAGTTACAGTGATGGTGGCCTCCCTCGGGGGTGACTAGTGTGCC
CGTTTTGTTG

1286. chr8_SGK196_NM_032237_-1.60992
GTTTCCCGACCAGTCCCTGGGCGCCAACTAGAGTATGGACTGACCAGGTA
CCTG

1287. chr8_EFCAB1_NR_024605_1.73958
GGCACAGTTAGGTCGTGCCCTGATAAGGGGGTACACAAGGGGAACTCCAG
GCA

1288. chr8_TOX_NM_014729_-1.8937
CATAGTCCTGGCTCGGCTCTGTCAT

1289. chr8_ADHFE1_NM_144650_-2.04037
CCAGTGCCCAACTCATTCTCATAC

1290. chr8_ADHFE1_NM_144650_-1.58474
GCCAACTACCTCAGGAACCGGGAGTGAAACTACTGGGGTTGCCATTT

1291. chr8_STAU2_NM_001164380_1.54357
GAGTTTGATTTCTTGCAGTCCTGAGCGATGGAGCCCGGGGGTGCCTGGTT
ATTGTCCGCTTTCTCTCTCAGATG

1292. chr8_ZFHX4_NM_024721_1.81599
AACTGCCTCATTGGGAGCCAGGACTTGT

1293. chr8_TMEM55A_NM_018710_-1.6799
CGAGCCGGGGTTGCGGCCTCGGCGGAGTGGTGGCTACTGCTGCT

1294. chr8_RUNX1T1_NM_175634_1.98047
TTGACAATATTCAAAGTTCCCTTTTTTCCGGCAGTCACCTATTACTAA

1295. chr8_PTDSS1_NM_014754_-1.56407
CATTTGGAACTCCCCGTGAGGAGGTCGAGGCGCACAGGGCAAGCAGGAAG
AGGCGAGGGCACTTGGGGGTCATTATTTGA

1296. chr8_---_---_-1.56944
ACTCCAGCCGGGGTGACAAGAGCAAAACT

1297. chr8_C8orf47_NM_173549_1.52756
CCCTCAACAAGGCCGGCGACAGCAGCA

1298. chr8_POP1_NM_001145860_1.86993
CCCTCCTGCAAAACGGCCCAACTACGTTAAGCTTGGCACTCTGGCACCTT
TCTGCTGTCCCTGGGAGCAGTTAACTCAAGACTGG

1299. chr8_NIPAL2_NM_024759_-1.50873
AACGGAGCGATCAGAGTAATGGGAGCAAATCCATAGGCTGCAAAGTTCCC
CGTCTCTCCCACGGCCATCAGCAGGACACCACCCCACCACAGCACACTCT
TGAAGTATGGCCTTGGG

Figure 3-106

1300. chr8_VPS13B_NM_152564_-2.13266
AGGGGACGCGGCGGTACTCTGGCGT

1301. chr8_GRHL2_NM_024915_-1.85349
GGGAGGGCCCCATGACCTACCTCAACAAAGGACAGTTCTATGCCATAACA
CTCAGCGAGACCGGAGACAACAAATGCTTCCGACACCC

1302. chr8_UBR5_NM_015902_-1.53142
CGATCCCGTCCTGTCCGAATAACTCGAGTCTGCCGGCGGGAATCTCGAGC
TCCAGCTGATGACCTACCAGA

1303. chr8_KLF10_NM_005655_1.5094
GCGTCCTCGTGTGGGCCTTCAGATGGGAACTTTTAAAGTATGTCTTGCCA
CATCCTGGGTGGCTACAGATGTGACTCCTTATCCTTGATGAATCAATCTG
AGGAGTGAC

1304. chr8_SLC25A32_NM_030780_1.60763
CCCGCTATCAGGTTCTCATACCGGACGTGGCGGAATACCGT

1305. chr8_RIMS2_NM_001100117_-1.50307
TCATCGTCTGGGGAGATTATGGCCGCATGGATCACAAATCTTTTATGGGA
GTGGCCCAGATACTTTTAGATGAACTAGAGCTATCCA

1306. chr8_OXR1_NM_181354_1.59228
GCGGCAGCATGGACTACCTGACGACGTTCACCGAGAAGAGTGGGCGCCTT
CTGCGGGGCACGGCCAACCGCCTGTT

1307. chr8_EBAG9_NM_004215_1.62428
CTGAATTAGGTGACTTAGATACCTGGCAGGAAAA

1308. chr8_KCNV1_NM_014379_1.62704
GCCACAAAGTTGGGGACACGCCGGAAGCTTTGGTCCCGCGAG

1309. chr8_EXT1_NM_000127_-1.5776
CTGTCACAGCGAGAATCCTTGTGCTTTTGCCAGTCTTTGCCATGCTTGCA
GGTGGTGAGGAGCACAACGTCCTCCCCGTTATGGACGTGATATAAGGCAT
TCCTGGTGTCTGATCCTATC

1310. chr8_MTBP_NM_022045_1.63955
CCTTTTGACTTATTATCACTTCCACATTTTTCTGGGGAGCAGATTGTACA
GAGAGAGAAACAGTTAGCTAATGTTCAAGTTTTAGCTTTGGAAGAATGCC
TAA

1311. chr8_FBXO32_NM_058229_-1.79144
TGCTGAGGTCGCTCACGAAACTGCCGCTCTTCTCATCCAGGAAGCGCTTC
CAGCCGTCGGCCGTCTTCACCCAGTTCT

1312. chr8_RNF139_NM_007218_1.68566
AGCAGGTGCGGATGGCCCATCAGCAGGTCTGGGCGGCGCTCGAAGTGGCG
CTCCGGGTGCCCTGCCTTTACATCATCGACGCCATCTTCAACTCCTACCC
GGATTCCAGCCAAAGCCGGTTCTGCATCGTGCTCCAGATCTTCCT

1313. chr8_KIAA0196_NM_014846_-1.69519
AAAAAATGCAGTTGTATGAGCAACTGAGTTTCTTTTCATCTTCAAATTCA
TTTGTGATGGTGGGAAGATCTAAGGACAATCCTTCCATTGAAGAAGTAG

Figure 3-107

1314. chr8_FAM49B_BC016345_-1.70028
ATGGGGTACTTGTTAAGGCTCCCAGAAGA

1315. chr8_ADCY8_NM_001115_1.64372
TCTCTAGGAAATGGCGGGCCACATGGCTGGGTAAGATATTCCGGAGCATG
TTCTCATTGTGTTCCCTCAGCTCCTTCATCTCATTGATCTCCTCTTTGGC
CTGTACTCGCCAAAGGAAGTCCA

1316. chr8_PHF20L1_NM_016018_-1.56225
CTGGGCTTGTTCCGGGAAGCGAAAAGACCAAGATCAAATAATAGCTGGGG
TGGAGAAAAAAATAGCTCAAGACACAGTTAATCGAGAAGAAAAGAAATAT
GTACAGAACCATAAAGAACCACCTCGTT

1317. chr8_TG_NM_003235_-1.68953
TGAGGCCAGTCAGGACGGACTGGGATGCG

1318. chr8_COL22A1_NM_152888_-1.71332
TTTCCCGGGAAGCCGATCTCTCCAGGCAAAC

1319. chr8_COL22A1_NM_152888_1.72489
CCTTGCAAACCAGGAGGTCCATCCCT

1320. chr8_DENND3_NM_014957_-1.55187
AAGGGGAAAATCTACGTGATTGACGCCGAGAGGAAGACCGT

1321. chr8_ZNF696_NM_030895_-1.92377
CCAGCCGCTCTCGGGCGCGGCGTGGGGGAGGCGGCCCTGCAGGTGCGTAC
CCGGGGTCCGACACGTGCGGGGCTTCCTGCGAGCTGAGTCCCCGCTGC

1322. chr8_TOP1MT_NM_052963_-1.56057
GTCAGCCTGTCGAAGAGGTCGTCCCG

1323. chr8_RHPN1_NM_052924_1.56745
AGCCTGCTTGGGCCGCTCCTGCTGGCCTCCACAGGCCGTGAGCTGTCAGT
GTCT

1324. chr8_FAM83H_NM_198488_-1.65708
AGCGGAATGAGTCCTGCTTGGCCAGGCCAGGCTCCTCCGGGCCCTCGCGC
TCTGGGCCGTTGCCGCCGCTGCCCGGGCCTGGCACCGGGACCTTGGTGGG
GAAGGCTGCTGGGACGCGGAAGGCCGAGGGGAGCAGGTCGCCGGCAGGTG
CCCGGCCCCCGGGAGCCAGCACGTCGTCTTCGTAAGCCTCCGCTTCCATG
GGCGCCGGTAGGCCGTCGTCGCCCCCATCCTCGCCGTGGCAGCCGCTCAA
GTAGGAGGCCAAACGCCAG

1325. chr8_SCRIB_NM_182706_1.63388
AGCTTGTCACCCACACGGACTCCAGCCCGGGCCGCAGGGCCTTCCTCGGA
CACCCGAGAGAT

1326. chr8_NRBP2_NM_178564_1.62982
AGGCCTGGGTCCCACGGTACTTGAGGAAG

1327. chr8_PARP10_NM_032789_1.75828
CGAACGACGCGGATGCTGCTGCGGGCAGCGTCCAGGGTGTCGTAGAAGGC
CCGCACCA

Figure 3-108

1328. chr8_PARP10_NM_032789_1.70144
GGGCTCGTGGTGGAGCTGGCCGCAGGCTC

1329. chr8_SPATC1_NM_198572_1.68932
CCAGAGCCTCTCAGCATGGCGTTTGCAGGAGCACCCCTCCAGACCTCCAC
CCCTATCGGAGCCATGGGCACACCTGCTCCCAAGACGGCCTTCTCCTTCA
ACACTT

1330. chr8_OPLAH_NM_017570_1.71484
CCAGAACCGGGAGACTTAAGGCATCTT

1331. chr8_OPLAH_NM_017570_1.57903
GGCGAGCGGGCTGTGGCTGGGTGCTGGTGGGCAGACACCATCAGAGCACA
GTCCGTGCCCTGGTAGCGCAGGTGCA

1332. chr8_ADCK5_NM_174922_-1.6357
TCTCCACCGCGGTAGTGGGGGCGCCCCTGCTCCTCGGAGCCCGCTATGTC
ATGGCAGAGGCACGGGAGAAGAGGAGGATGCGGCTCGTGGTGGATGGCAT
GGGGCGCTTT

1333. chr8_SLC39A4_NM_017767_-1.55632
TCTCAACCCCTGGCGCCCTTCCGTCTCCCCAGGCCCCTGTCCTGCTTCCC
CAACTACAGGGGTGCACGCAGAGGGGTCCCCAACAGTGGTCCCCCATCCC
CAG

1334. chr8_VPS28_AK091979_-1.53688
GCTCGCGTGTCCACGGGTGCGGGAGGCCCCACGGCTCACGGGCCCCAACC
CCTCCTCAGCCACAGCTGTCACTTGGGCCTCCTCACTGTACTCTGTTCCC
AAACCCAGCAGGCCTCCTGGGTGAACGAGGTCCTGGCTGCCCAGACAGCT
GTGTGGGAACTGAAGGGTGGGCCCACACCCACACTCTCTCCCGAGGCCAG
GACCCCGCCAGAACGCACCCTGTGCTCATCCCCCCGACAGGAGTCCAGGT
GGCCTGGGGGCGTCCCCGCATGCTGCCCACCCCTCATTCCTAGTTAAAGG
GGTTCCCTTCTGCCCAGCAAGTCAGAGTGCTG

1335. chr8_FOXH1_NM_003923_-1.57342
CAGCTTCAGTCTGCGGGAGGGAGCGGCCTGAATCACCAAGGCGATCATGG
CCAAGTAGGTGTAGGGGGGCTTGTCATGTCGCAGGTACCTC

1336. chr9_DOCK8_NM_203447_1.56007
ACAGTTAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCG
AGAATTCCGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCG
ACAGCATCG

1337. chr9_SMARCA2_NM_003070_-1.70788
GCCCCTAGATCTGACAGTGAAGAG

1338. chr9_JAK2_NM_004972_1.57025
ACATCCACCTCTTCTATATATCAG

1339. chr9_PTPRD_NM_002839_1.5227
TGGTGGAGGTTGCCAACTTACCAAAATACTAGTGGAACTTGGGCTGGTGC
AACTAATGTCTTGAGGAGGAG

1340. chr9_FREM1_NM_001177704_-1.54403

Figure 3-109

AAATGCAAGCTTGAGTGAGTGCCAGGGACTCCATCAGAGGCGGCCATCTT
G

1341. chr9_PSIP1_NM_021144_-1.69277
TGGGTAGTTTGTTTGTGGGTGGCTTTACAGCTCCATCA

1342. chr9_ADAMTSL1_NM_001040272_1.7928
ACCCAGGTGCGAATAGTCAGGTGCCAGGTGCT

1343. chr9_ADAMTSL1_NM_001040272_1.64742
GAGTCAGCCTGTGGACCCTGTGCACAGCTACCTGTGGCAACTACGGCTTC
CAGTCCCGGCGTGTGGAGTGTGTGCATGCCCGCACCAACAAGGCAGTGCC
TGAGCACCTGTGCTCCTGGGGGCCCCGGCCTGCCAACTGGCAGCGCTGCA
ACATCACC

1344. chr9_RRAGA_NM_006570_-2.47286
GGAGCGAGGCGCGGCCTGCGAGTC

1345. chr9_TMEM215_NM_212558_3.37937
TGGGACCACGAGACCATCGTCTAA

1346. chr9_NOL6_NM_022917_-1.84132
CTCACTTCGGGCCTCCACAGTCTGCACCAGGCCTTCACCCAGCACAGCAA
AGTCCTCCAGGATTGCTTCAACATTGGGCACCATTACTAGCTCCCCACCT
CGAGACATCACCATGCGCCCCTTTGTG

1347. chr9_ENHO_NM_198573_-1.56128
TGAGTTGAGCCTGGTGCGCGCCCGCGGGAGGGTCCGGGGCAGCGGGATGC
TCGGCGCCGACTAAGGCTTGG

1348. chr9_C9orf23_NM_148178_-1.77823
GAAGCCGCCTCACGCACGATCCGGAGCCAA

1349. chr9_SIGMAR1_NM_005866_-1.64136
AGACGACCTGGGTCAGCACCGCTGCGACAGCCAGGAGCAGCG

1350. chr9_FANCG_NM_004629_2.11481
CTCAGGTGTGGCCCGGAAGAGCAGCTCGA

1351. chr9_KIAA1539_BC004406_-1.98645
TGGATTATGAGGGGCCTCGGTCAC

1352. chr9_UNC13B_NM_006377_-1.65885
ACCCTGATAGTGCCGTCGATGACCGAGATAGTGACTATCGCAGTGAGACC
AGCAACAGCTTCCCACCTCCTTACCATACAGCTTCCCAGCCCAACGCTTC
TGTGCACCAGTTCCCTGTGCCGGTGCGATCGCCACAGCAGCTGCTACTTC
AAGGCAGTTCCCGGGACTCTTGTAATGACTCTATG

1353. chr9_CD72_NM_001782_-1.76267
AGGCCTCAGGTTAGGAAGGAGGGGCACAGGTTCTTGTTGGCATGAG

1354. chr9_C9orf100_NM_032818_-1.60631
TGAGGAGAGCAATGATTCTGTGAATTTTTGGGGAATTTGTGGCAGGAGGG
AGGAATGGGGACATAGGTTGGGAGCCACTGAGTGGACATTTCTT

Figure 3-110

1355. chr9_CA9_NM_001216_1.92745
CAGAGGTAGCCGAGACTGGAGCCTAG

1356. chr9_RGP1_NM_001080496_-1.8215
TCAGGATGTCCGGTTTCCCCAGGATGAG

1357. chr9_OR2S2_NM_019897_1.52425
AAAGCTGTCCAGGACCAGTGGGACTGAGGAGGTAGTGAAGCAGA

1358. chr9_GRHPR_NM_012203_1.71892
GAGACCGGTGCGACTCATGAAGGTGTTCGTCACCCGCAGGATACCCGCCG
AGG

1359. chr9_ANKRD18A_AK093059_-1.80455
AACATGGGGCAATTCCACGCAGGGTCCATGGAGGGAGCAGAAAGCAGCCG
CAATGAAGAGCCACGGTGG

1360. chr9_TJP2_NM_004817_-1.60228
CTCCGGCTTGGGAGTCAGATCTTCGTAAAGGAAATGACCCGAACGGGTCT
GGCAACTAAAGATGGCAACCT

1361. chr9_MAMDC2_NM_153267_1.53112
TGCAAGCTGAAATCACCTTTAAGAAGCCCATGCCTACC

1362. chr9_C9orf41_AK299691_1.58913
CGTAGTAGCGGAAGGCATTAATGAT

1363. chr9_GCNT1_NM_001097634_1.63333
TGAGGACGTTGCTGCGAAGGAGACTTTTTTCTTATCCCACCAAATACTAC
TTTATGGTTCTTGTTTTATCCCTAATCACCTTCTCC

1364. chr9_PRUNE2_NM_015225_-1.53974
CATTTCTTCATCCAGCCTAGCCCTGGCATCCTCCTTCTTGGGGTTGCACC
ATTCAAGTACACAATCATATAGTCTTCAGCTACCATCAAC

1365. chr9_FLJ46321_NM_001001670_1.53275
GATATTTCGCAGGCCATGAATCCCATTGATTCTTGTGCTCGTCATCACGG
ACCACCAATCCCATCTGCTTTACCACCGGAAGATTGCACTGTGACTCAGT
CTAAATCAAGTCTCACCATCTTGAAGACTTTTCCGGAAATGTTATCTCTA
GGTGGCTCTGGTGGGTCATCCACCTCTGCCCCAACAATCAAAGGCATTGA
CCATTCACACCTTGCATCTTCAGAATTCACCTGGTGGCAGCCTCATGCCA
AGGACTCTTTTTCCTCTAATTTTGTGCCATCTGATTTCATGGAGGAGCTT
CTTACCCTTCATTCTTCTGAGGCCTTTTTAGGGGGGCACTCTGTGGCCAA
CCTCATAGAGCCTGTTAACATCTCA

1366. chr9_---_---_1.67897
AGTTAACCACGTGTGCAGTCCGCGGCTTCTCAGAAAGAAGAGTACACACT
GTTATGATCTTTCTCTCCAGGCATGCCAGCCTGCATTTCATAGTTTGATT
GAAATTGTGCCATCCAGTCTGTCTCTTCACAAACAAATGGAATATTCTGA
GCTGCCAGCATTTGGAGGCGCACAGCTTGCATCTTTTTATGAAGAAAAAT
AAACACTGTGTATCGTAACAACCAAGTCATGATGGATAAAACATGCCTGC
GATCGAGAACCACTTGCACGGCCCACGCCACAGACTCGAGGCAGGTGGGG
AACGGCTGGACAGTGATGGAGAACAGGCTGCGGGCGGCTGGCCGAGAGAG
ATGAGTGGGAGCCGCGTGTGGACGTGCCATCAAGGAGAACTCTCTTTTCT
GGTTGCATCCCCGCCATTCCTGAAGAACACAGGCACGTGTTGTTTACTCC

Figure 3-111

ATTGGTGACAATTAGTGGTGGCGTCCGGTTCCCTTTGTGCTTCCAGTCAT
TACTCAAATGCTTCAAACTTGTCCCATCTCCTGGACATCCTTAGGTTGTT
TTGTGGACTAGAAAGAATTTCAAACCACTCACATGTGATTTGCCAACTCA
TTCCTTTGGACAACTGCTTTTCATAGCCCCAAAGTCCTGGAGCAGTGGTG
CTCAGGGTGTGGTCCCTGGGAGCATCAGCATCAGCATCAGCATCCGTCAG
GGAACTTGGGAAAAATGAAAATGCTTAGGCCCAGCCCCAGAGCTGCTAAA
GGGGGATGGGCAAAGGACAAAGGGCAAAGAGCTCACGTCAAGTGAATTTA
CACCCATTTACACACTTTCTAGAAGTTTCATCCAGTGAGGTCTACTTAGG
TCTCTTTGGCCGGAACGGTGTCATATGGCCGCTACTCACTGCAAGGAAGA
CTAGGGAACAGAGCTTTTGAGTTGGGCCCGTTA

1367. chr9_CTSL1_NM_001912_-1.93405
CAGCCCTGGCAACGAGAGCGTCTACCCCGAACTCTG

1368. chr9_CDK20_NM_178432_-1.50642
GGTGCCCAAGATGCGAAGCACATAGCAAAGCTGTTCAATATCGTTCTTGC
CCGGGAAAAG

1369. chr9_SPIN1_NM_006717_-1.5592
TGTATCTTATAAAATACGATGGATTTGACTGTGTTTATGGACTAGAACTT
AATAAAGATGAAAGAGTTTCTGCGCTTGAAGTCCTCCCTGA

1370. chr9_SHC3_NM_016848_-1.63067
TCAGTCTAGTATCAAGAAAGCCCCCTGGAGGAGGCATCTTGCTTGGGATG
CTGTTGTAGTATGGGTGGTCTGAGCCATCTCCCTCCTCTTCCGTCCATGG
CTCATCCAG

1371. chr9_SHC3_NM_016848_1.92669
CCCTCCGTGGGCTCGCTGCATCCGCCCG

1372. chr9_AUH_NM_001698_-1.55344
GCCCTGGGCCCAGATCGCCGGGCCCGCTCGC

1373. chr9_NOL8_NR_024020_1.51523
ATTAGTTACTCAGGATAGAGGGCAAAGAGATTATATACAAAAAGTATTTT
CAAGGACTATCTTGTTCTTCCTTTATAAGAAGTTGAATTTAATTTTTGAA
GTAATTACTTAGGAAGAAATGCAGAGGAGTTCCACAGAAAAAGATGGCAA
CCAGAATGATATTCCGTCAGCCAGATTTTTAAAATTCCTTCACTCTGAAA
TTTCTTCTTTGTCAGCTAAAACTGTTTTCTGGGTCAGTTTCCTTAGGTGA
GCCTTGTTCACATTCAGTATCAAAACCAGC

1374. chr9_NOL8_NR_024020_-1.68577
TGATTTAGAAGGAGTAATGGAATCACAAGTTCTTTTTTGTGCAGCCTGTT
GCTGTGTTAAGGGTGGTCTCTCTATTACCCTCCTGGGCCTTGTACTCATG
GCCAGAGACCCAGTGGAACTCTCATCCTTCTGCACTTTTATTATCTTCTT
GGGAGGGCCATGAAAGTCAGAGAACTCTCCTCGCCGTTTCTTACT

1375. chr9_ECM2_NM_001393_1.69215
GTAGGACAGAGAGCACCCGCTTGGCAGGCGCA

1376. chr9_C9orf89_AK128259_1.74118
TCCATCTCCGCCTCAGGGGCTTCTCCACCCCAAGTCTGGCTCCATTCCTG
GCCTTCTGTTGGTGACAGACCCCCCCCCTAAGGTGCTCGTTTGGGGGCTC
TTCAGGCAGCACCTCAGCCTGGCACCCCCACTCCCCTGCGCAGCCCCCAG
GCCTCAGGACCCCACCCCTCTGAGGCCCAGGGGAGCCCTGTTCACGCTGG

Figure 3-112

TTTCTC

1377. chr9_BARX1_NM_021570_-1.55327
TGTCCGGCGTGGAAAGGTACTTCTGCTTCTCGAAGCGTTTCTCCAGGCC

1378. chr9_FBP2_NM_003837_-1.57747
CTCCCGGCAGGAAACCTTGCTTACTTCTGA

1379. chr9_HSD17B3_NM_000197_-1.78964
GAAGGCACCGCTGTAGAAGGCCCAGGCCGGGATCAGGCTCAGAAAGCCCG
C

1380. chr9_TDRD7_NM_014290_-1.53238
CAAAGACTATTCTGCTGCTCAGGAATTAATGGAAGATGAGATGAAGGAAT
ATTACAGTAAGAATCCTAAGATCACACCAGTCCAGGCTGTGAATGTTGGG
CAGTTGCTGGCCGTAAATGCCGAGGAGGACGCCTGGTTAC

1381. chr9_TMOD1_NM_003275_-1.61068
CATTCCCAAGTGCCGGAGTGGTGTCTAG

1382. chr9_FOXE1_NM_004473_3.92692
TGACTGCCGAGAGCGGGCCGCCGC

1383. chr9_NANS_NM_018946_-1.66161
ACCCGTGCTTCATCATTGCCGAGATCGGCCAGAACCACCAGGGCGACCTG
GACGTAGCCAAGCGCATGATCCGCATGGCCAAG

1384. chr9_TBC1D2_NM_018421_-1.54554
GGTGCTGGCGTCAGAGGCCAAGGGCTGCTCCTCCCTCTGAGGCTCCCCAC
TCTGTGGAGAATCTTCCCCTGGAGGTTCATGGCCTGTTCCCTGGGCCTGC
TTGTTGCCACGGATGTTGTGCATT

1385. chr9_COL15A1_NM_001855_-1.70625
AACCTGGAATGCATGGAGCCCCAGGA

1386. chr9_TGFBR1_NM_004612_-1.74065
TGGAGGCGGCGGTCGCTGCTCCGCGTCCCC

1387. chr9_STX17_NM_017919_-1.50995
GTGCTGTCCCTCCCTTGTAATTATGAAAAGTTCTTTGGTTTCTGGGGTGA
ATTCTACCCATGTATAATGAGGAATTCTCTCATAACCTTTTTTGTCTTGT
CTGTCATCTCTGTTCATCCCTTCCTATAACCTCTAGGTAAAAAGAAAAGA
AAAAAAGAAATTTCGAGATATTTTCAACATTGTTAGAGTTTGGGCTAAAA
TGAGCAAGGAGAAAAAAACCACCAAGAACATTTCCTGGGGCATGTTCCAG
TTTTGAGGGGTGATATATCTGCCAGATAGGGGGTATCTGACCCAGTCTTC
TTTTCAGCTGGTCTCTGGGGGGAGCTGAGAACTCGCTTGCTACCTCACAT
CCTTTTCCCCAGACTTTTTATCTCCTATGCATCCCTTTGCTTTCTATAGC
TGGTGTTTCTTCCCCAAAATGGCGTTCCCATGCTTACCTTTCTCACATTC
TAGACAATGATGGACAAAGACGCATGCAAGACTCAGACCCGGGGAATGGT
GTGGTGCTAATCTCAACACCTGACATTCACAGCAAGCATGGCCCAGCCCA
ACTGCATGTCTA

1388. chr9_C9orf5_NM_032012_1.53733
GGAGGTGGACAACGTTGGAGCGGATTCTCCCCTGTC

Figure 3-113

1389. chr9_PTPN3_NM_002829_1.50999
GGCCAACCCTCCAGAAGCTGGGTTTCCCATGGTTCAATTACTAGAAGCTC
TTTTCTCAGAAGGCCAAACATTCGGAATATTTAGATGACACTGTCCCATC
TCCCCTTGGGAAAATCATAAGGTTTCAAGTGGAGGAGCTTGAAGTAGCAG
CAATACATGTAGGAGATTCAGTAGTCGGTGATTCCAGTCC

1390. chr9_PTPN3_NM_002829_-1.60776
TTCACGTAACTTGCATTAATATAATCTTCATTTCCCTGCAATAATACCCG
GGTGGTGTCAT

1391. chr9_AKAP2_NM_001004065_1.6374
CTCTCTGGGCGATGAAGGACAATGGTGGTAGGGCCACTTAGAGAGCAGTA
GGGCCCAGGCTGGTGCAGCCTACATGGCACAGGATATTTCCCTGCACCAG
TTTCCCACCTGTCACTTGCAGCATCAGAGGGTGTTGCATTAACTCCATTT
TCTCCAGCAGCCATAAAATGAATGGCGTTTCTCTCCATATTTGCCCAGAA
GAGGCAGTTATGATTCCACTTCTCCTACATTTAATTATTTTTAATTGAGA
ACAACTCATGATCACAATTCATAAAATCCATATTTTAAGACAATAGTTCT
TCATGTCACAAACACAATCTATTCTACATGAGGAGGCTGAGAAAGGGGAA
GAGAAAAACAAACCAAATGGATGATGTTAGCTTTAGGATCGTGTCTGCTT
ATAATATTCACTGATCTGCAGTTTATGAGAACACATTTTCACAGTTATGT
TTCTTCATAGGAAAACTATATTTAGTGGGCAACAACTATTTTTATGATGG
GATGGGGGAGTATATACACGTATAGAATCTGTACGCGTTGAACAACTTGG
TTCAAGATGGTGGGGGCATTTTTAGAGCGGCAATAATTGAAAAAAAAGGC
GAACTCTGCCTTGGAGAGGTAGATGATAAGAAATAAAAAGGTGTTTATAA
CTATTTTGTATTATAAAGTGGGCCTTAGAGATAGGAAGAAGAATGATGGA
TTCCTTTTGGATCAATCAGAAAGGAAACACGAAAGAAAAGTCAGGAAGGT
AGAGAGAGAAAAAGGGAGGGAAGGAGAAAGAATGGGAATAAAATAAGGAG
GTAAGAGATACTATTTTTGCTGAGCAACCAGTGTGTTTCAGGATGATACA
AAGAAAAATATAGAATAGAAATAAGTGCAGGCTTGGAATCAGCTACAAAT
CCTAAAGATGGGGTGTGTGTGGATGTGTGTGTGTGTGTGTGTACACCATT
GTGTGTTTGTAAAATGTGTATGTTCATGAGTAAGGGTGTGTGTGTGTGTG
TATTAAAATTCCAGAGTGACCGTGGCACTTGGGTGTACAGGTAATTCCTC
CAGAGCTGTTTGCTGGCTTCAGGAGTGGAGTGAGAATTTCTTTTTTATGA
AAAGGGATATAAAGGCACCGAGCTGATGCAGTATTTGTA

1392. chr9_ZNF483_NM_133464_-1.53398
TGTTACTCAGAAGTAGCTGGACCCAGGAAAGCTCTGAGTCAACTCTGGGA
GCTCTGCAATCAGTGGCTGAGACCAGACATTCACACGAAAGAACAGATTT
TAGAGCTTCTGGTGTTTGAGCAGTTCCTGACCATTTTGCCTGGGGAGATC
AGGATTTGGGTAAAGTCACA

1393. chr9_DNAJC25-GNG10_NM_004125_1.50013
TGGGGGCGCCGCTGCTCTCTCCCGGCT

1394. chr9_SUSD1_NM_022486_1.88348
TCCATATCAGCTGTCTTGATGCTTC

1395. chr9_SLC46A2_NM_033051_-1.63407
GGCCAGTGGCGAGCAGAGCCAGGG

1396. chr9_RNF183_NM_145051_-1.68711
CTGAGGTGGGCCAGACATTCCACGCAGAAGGAGTGGCAGCAATCCAGCAT
TTTGGGGGTATGGAACGTGTTGTTGAAGGGGTTCCAGCAGACGGGGCACT
CAGCCTCAAG

Figure 3-114

1397. chr9_RGS3_NM_130795_-1.59839
CTGCAAGGTGTGCTCGGAGCGCCGCTACCGC

1398. chr9_FLJ31713_AK056275_-1.50636
CAGAATCCTTTGCTGGCCGGAAGAGTTCACCATATTGGTGAACCTCAGTA
TCATGGCCTTTCACCATCTTCCTGTTCCCACGTGGCAACCAAGGGAGGGA
ATGTGGTCTCCCTCCCTCCCTGATGGCCAGCGCCCCCTGCCCTCCAACCA
CGGCCAGCCCCACAAGGTGAAGGGCCCCAGGGCAGACACTTGGAGGTAAA
CGGAGGTGGCAGTCCGTAGTTGCCTCAGACCAGGGAGCCCAGAGGAGAGG
CTGAGAGAGGGCCTGCTACAGCTGCCAAGGGTGGTTGGGGACCCCTGAAA
AATTAGAAGGGGCCCCGCAAGGTCAGACCAGCTAAAAGTCCTTACGTGGT
AAGCATATGTACATTGCAGGCCTGCTGCTTCCTGGACCAACTCTTCCATG
GCCCTGGGTGTCACCCAGTGTTTCTGGAGCCTCTGAGTGGTGCCCGCTGC
CTGGCAGCAGCCCCTGGAGGTAGGCACTTCCTGGCATCATGGCAGATCTG
GCATCCTCT

1399. chr9_COL27A1_NM_032888_2.89049
GGGCTCTCCGGGAATCCAGGACCT

1400. chr9_COL27A1_NM_032888_1.72379
AAAATCAGGGAAGCAAGGCGAGAAGGGCCGCACTGGAGCC

1401. chr9_AKNA_NM_030767_-1.76262
CATCCTGGGTCCTAATGGGCCGGCAGTGGGGACAGGAGACTGTGCCATTG
CCTTTTGGGACCGCCTTAGGGGACAGAACATGGTATTCGTGGC

1402. chr9_TNC_NM_002160_-1.62625
CCGTTTGCGCCTGCCTTCAAGATTTCTGAAGTTGCTTGGTCTCAGCTTCA
TCTCAGCAAACTGGATTGAGTGTTCGTGGCCCTTCCAGTGGAACCAGTTA
A

1403. chr9_TNC_NM_002160_-1.65092
ACCCCGCGGATGGTGATGGTATAATGAGTGGCTGCTTTGAGCCCAGGCAG
GTCTGTGGACCTCAGTCCTCCTGGGACGGTGAGGTTCTGGGCTGCCTCTA
CTGTGTCAGCCTCCTGCACCTGAATGAAAAAGTACTCATAGGCCCCTTC

1404. chr9_TLR4_NM_138554_1.82936
CTGGACCTGAGCTTTAATCCCCTGAGGCATTTAGGCAGCTATAGCTTCTT
CAGTTTCCC

1405. chr9_CDK5RAP2_NM_018249_-2.98263
ACCCAGCATTGGGGTTGATGCCAT

1406. chr9_ARPC5L_NM_030978_-2.28225
GGAACACGCTGTCCTCGCGCTTCC

1407. chr9_SCAI_NM_173690_1.69087
GTTTTCGAGGCGGTTTCTCCACTGTG

1408. chr9_RABEPK_NM_005833_-1.58337
TGGAAATCCTCCATCTCCCCGGCATGGTCATGTGATGGTGGCAGCAGGGA
CAAAGCTCTTCATCCACGGAGGCTTGGCGGGGGACAGATTCTATGATGAC
CTCCACTGCATTGATATAA

1409. chr9_GARNL3_NM_032293_-1.76703

Figure 3-115

GCTGATGGAGCCATCCAAAGGGCTGGAAGATTCAGAGTGGAAAATGGCTC
TTCA

1410. chr9_GARNL3_NM_032293_1.96339
TGACCTTCCATCAGTGCCCGTGTTTGACAGAACT

1411. chr9_LRSAM1_NM_001005373_1.539
ACCGCGGTGCGCTGAAGCTAGAGATTCCGAAAGGGGGTTCGGGTAGTTCG
CTCCGGAGAAGTCTGAGAAGGGTGGCTCCGGTGATCCCAGCCCTAGCTGT
TTC

1412. chr9_ENG_NM_001114753_-1.60735
GGACCCTCAGGATGTGCGCCTCCTTGTGGCCGGCCACGCCTTCCAAGTGG
CAGCCCCGGACCAAGGCTGGAGTACGCGGCCGCCACTCGAGCGTGCGGCC
CATGTCCTGG

1413. chr9_PTGES2_NM_025072_-1.56721
CTGAGCGCTCTGCGTGGAGGTCCTGGGCGCGCAGGTGCCACCGCGCCGTG
TGGTACAGCCCCA

1414. chr9_LCN2_NM_005564_-1.61881
TGACTACTGGATCAGGACTTTTGTTCCAGGTTGCCAGCCCGGCGAGTTCA
CGCTGGGCAACA

1415. chr9_CIZ1_NM_012127_1.58777
TTTGAGGCGGGTTGAGCGCCGAGGTAGTGGGGGCTGGGAGGGTCGAGCCG
TCACCTTGCTGGGTGTTTTGTCCTGGGTGTTGGGCTGGGAGGGTGGGCGG
CCGCTGGAGGTGAACAGGGCTGTCAAAGCGTTCCGGGCGTTGA

1416. chr9_SLC27A4_NM_005094_1.5855
GGCTTGCCGGCTTCGGGGAAGGTGCGGCAGGCGGTGCTGCGGCCTGGCAC
AGCAGGTTTGGGGTGCGGGAGGCGGGCGGGGTAGGAGCGCGGCGGGCGGG
GCCGGGCGGCGGGCGGGGCTGGCGGGGCGGCCGGGCCATGCAGGGCGCAG
AGCCGGCTAAACCCTGCTGAGACCCGGCTCCGTGCGTCCAGGGGCGGCTA

1417. chr9_URM1_NM_030914_1.53329
GCTGCTTACAGCTCATTCTGCTGGGGGTAGAGATGAGGGGAGGGAGTAAG
TTAAACCTTGGACTAGCAAGTAGAAGCCTGGGGGGATGCGTGTGCCTCAG
TTTCCTCCTCCACAACTGAATATAGTGGCTGAAAACTGGGGAGATACTTG
ATGGCGCGAATGTCCGTTTTCTCTCCCTTCCCACCTCCTGCAGGAAGCAG
GACGGGGCAGGCAGCACCTGGTAGGCACAGTGCTTTGCCCCTCCTCCCCT
TCCCTTCTGGAAGTCTTGGGGCCTCAGTGCTTGCAACAGCCGGCCTTGGG
CAAATAA

1418. chr9_ODF2_NM_002540_-1.51442
AAACAAATGACCTGCACGGACATCAACACCCTGACAAGGCAGAAGGAACT
TCTCCTGCAGAAGCTGAGCACATTTGAGGAGACCAACCGCACCCTCCGAG
ACCTCCTGAGGGAACAG

1419. chr9_GLE1_NM_001003722_-2.47657
CTCCCCTGCAACACCAAATGGAAC

1420. chr9_SPTAN1_NM_001130438_-1.9208
TGTGCTCTCACTTTCCACTGTAACCTTAAGCCTGCTTAGCTTGGAATAAG
ACTTAGGAGAAAATGGTGCTTCACTAACCCGCTTCCGGTCCAGTCACAAT

Figure 3-116

CATCATGTCACTGTGGGGACCCAGATCTGTGTCTTGAAGCAGCTGCCCTC
ATTCCGACTTCAGAAA

1421. chr9_FAM73B_AK301241_-1.66768
TGAGCTATGCCCTGCGGCCCGAGACCTGGGCCACAACACGGCTGGAGCTG

1422. chr9_TOR1B_NM_014506_-1.52893
GCCCGCCGAGCACTCTTGATCTGAGCTGACCTGTGTGTGTGTGTGTGGGG
GGGTGGGGCCTTCACCTAAGACCTCTGCAGCAGACCTGGACAGACAGGCC
CCTCCCGCCTGTCCATCGCTCTAGCTGCTAATACAGCCCTGGCTGTGGAA
TCCTTCACCGTCTCAGCTGGTATCAGCCCCAGCCTGCCTTGTGCCATATC
TCAGCTTGGATCTCTGCTAGAGTCCCCCCAACCATATATCATAGAGTTGA
ATCACAATGAGACCGTTGGCTTTGAATTTGAGTCGTTGGTTCCCATGGTG
AGATGCTTGTTAAGACTTTATACTTGGGTCAATCTCTCACTTTATTTTGT
AGAACCATTTGAAATCCTAGGATGTGCTTGTTCTGGAAGGATGACATGGG
CCCAGACTGAACAAGTCAGCTTGATGATCTTAAATGATGGAAGTATAGGA
CGTTGCTTATTTTAAAACAAGGGAAGGACACAAAATGGAATGACTGCTTA
GTCCTTTCTCAGATACTCTTAAAACAATTTTTTATTGTTAAATTTGTGGT
AATACATGGTCACAACCGTGGATCAAACAAGGTCAGTCTAAAGTGGCAGG
TCCTAGGTGTGACCTGATACCACCACCCTTTGTGGCAGCACCGGGCTGGA
CTGCCCTGATCCCTGGGACGTGAGACTTAGCTT

1423. chr9_USP20_NM_006676_-2.42163
TTTGCCCTCACCTTGACTCCATAG

1424. chr9_USP20_NM_006676_-2.12787
TGGGGGCCTGTCGTCACCCTGGAAGACTGCCTTGCTGCCTTCTTTGCCGC
TGATGAGTTAAAGG

1425. chr9_USP20_NM_006676_1.5256
GGTCCCTCCATGGCACTCTGGGTCCTCTCCTCACTCTCCAGAGACCCTCA
CATGTCCTTTTGAACATCCAAAG

1426. chr9_NCS1_NM_014286_1.76639
AGCCCGAAGTTGTGGAGGAGCTGACC

1427. chr9_LAMC3_NM_006059_1.68419
ACAATGGAGCCCAAATGGGGTCCTCCTGAGCC

1428. chr9_LAMC3_NM_006059_1.59808
AGAAGACCAAGCAGGCGGAGAGGATGCTGGGAAACGCGGCCCCTCTTTC

1429. chr9_AIF1L_NM_031426_1.84931
GTCGGGCGAGCTCAGCAACAGGTT

1430. chr9_NUP214_NM_005085_-1.73415
TTTCGATCCCTGGGACCAACCGCATCCTCAG

1431. chr9_FAM78A_NM_033387_1.8297
GCTGGTTTCGGGTCTAAATGCCCATCCTCACCCTTCTCCCAAGACAACCG
GGAAGAAGGGCTCAAGAGACTCTCGCGGGCGACCCCAACCCTCCCTCCAC
CTCTGGCAGAAGAGGAAAAGTCCGGTAGAAAAGAGATCCTGCTTTCTTTC
TCCGATTGGTTTTCTTCCTTTCAATTCAGCTTAAGGCAAAAGTTTGGCAA
AGCAAGTCTACATAAGGCCGCATGACAGAGGGCGGAGGGACCTGGGGGGA
AGGCCGGCCAGCGCCACAAATCGGCAGCAGTGTGGATCTGTCTCTTTGAT

Figure 3-117

CGGGGGCTGGAGCTTCCCTCCTAATCAGCTCCCCCTCCTCCTGCCCCTGA
GCCCCCAAAAGAGGAGTTTTTTTAAAAAACGGAAAAAGCAGTGTTTCAGG
GAATCTGTTACAAGTGAGCGACTGAAACTGAGAAAAAGGAGAGGCAAGGA
GACCAGAGGTCACCCTGAGGGCGCACGTGGGGTCTGTCTGTCCTGCTTAG
ATCTCCCCTCTCCCTGAAAGGAAGCAGGTGCCGAGAGCCGGGGAGGCCTT
CCCGGGGGCATCAGCACAGTGAGATCCGCCCGCTGGAGAGGGTAGAATGG
TTGTATCTTGCTGAATGACTGAAGAGTGAGTCTGAGTTTTGTTTTCAGCG
GTATTATTATTTGTGAGTCTAACCTAGCGGGT

1432. chr9_POMT1_NM_007171_-1.73004
CTGGCTAACACTGACAGGGGTCGCTTGTTCCTGTGCAGT

1433. chr9_UCK1_NM_031432_1.63027
GGCAGGCAGAACTCCTCGAAGGCCGGCTTCACGAAGGTGGTGTACTGCGT
CAGAATCT

1434. chr9_BARHL1_NM_020064_-1.62373
AAATGGAAGCGACAGACGGCCGTCGGGTTGGAGCTGCTGGCGGAGGCAGG
CAATTACTCAGCGCTCCAGCGGATGTTCCCGTCGCCTTATTTCTACCCGC
AGAGT

1435. chr9_TSC1_NM_000368_1.91741
TCCAAAGTGGGTCCAGTCGACAGA

1436. chr9_VAV2_NM_001134398_-1.54381
CCAAAGTCTCGCACATCGAAGAGGTCAAAGGGGTCAAACAGCTCGCTGTT
CCTTAATCCAAATTTATCGTGGCAGACTTTCAGGA

1437. chr9_COL5A1_NM_000093_-1.93374
AGGCAAGGATGGACTCCCAGGACACCC

1438. chr9_OLFM1_NM_014279_-1.85192
TGCCAGGTCGTTGGAGGTGGCAGCG

1439. chr9_OLFM1_BC000189_-1.86046
AGAAGACACTGAACGAGCTTCCCTTGTTTTGCCTGGAAGCCCACGCT

1440. chr9_KIAA0649_NM_014811_1.61233
TGCTTATCAGCACTCTGCAGCGCGACGGGGCTGCTCGGGGCACCAGCGAT
GAGCGCGCCGCACAGAGGGGCCACAGGGCAGAGGGATGCCACGACGCCAG
GCCGGCTGCCAAGCCCACCGTGCACAAGGAGCCACCCGCGTTGGCTGTCT
GTGG

1441. chr9_GLT6D1_NM_182974_1.80835
ATGATGTAGAAGATCACTCGGTAGCCTGTCATGAAGTGCTTATTTGCGGA
GTGTAGGAACGGCCTCAGGTACTCCTCTGCAA

1442. chr9_CAMSAP1_NM_015447_-1.68489
AGTCGCTGCACGACTCTTCCCGGTGCACCGACTTCGGCCGCGGCTTCTTC
GGCTTTGACTTGGGCTTGCCGAGCCCCTGCTCCTCTAGGATCTGCTGCTG
CTTCCTCCGCAGGTACTCCTGCTTGATGAGCTCGCGCCGCGCCTT

1443. chr9_SDCCAG3_NM_001039707_1.68196
AAGCATTTAGTGCTCATCGCCGTCCCTCTGAGGGGGGCCGTCAGAAAGGC
AACTGGGACCTGACAGACCCGGGCACATACTTGAAATTCCTGAA

Figure 3-118

1444. chr9_NOTCH1_NM_017617_-2.3553
AGGCACACTCGTGGGTGACGTCGCCCGTGGGGCGGCAGGTGCCCCCGTTC
TGGCAGGGCGAGGGGCTGCAGGGCACGTAGGGCCGCTCGCAGTTGGGGCC
AGTGTGGGTGGCGCGGCAGACGCAGCGGTAGGAGCCGACCTCGTTGTGGC
AGGTGCCTCCGTGGCGGCAAAGCCCGGGCTTCTGGCCACACTCGTTGACA
TCCTGCCGGCAGGT

1445. chr9_EGFL7_NM_016215_-1.91466
TCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATC
CCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTACGAGCTCCCTGC

1446. chr9_KIAA1984_BC007542_1.95638
CTGGGGAGAAGGCTTGACTATTTGA

1447. chr9_C9orf86_NM_024718_-1.76111
ACCCTGGGGGTGGCGACTACGAGGAG

1448. chr9_TRAF2_NM_021138_1.79469
GTATCTACCTGAACGGCGACGGCACCGGGCGAGGAACACACCTGTCCCTC
TTCTTTGTGGTGATGAAGGGCCCGAATGACGCCCTGCTGCGGTGGCCCTT
CAACCAGAAG

1449. chr9_FBXW5_NM_018998_1.79269
CTTGGAGCAGGACGCGAACTGGTACCCGGAATGGGAGAAGCTGAGGTGCA
GGACCTGGTCTGTGTGTTCCCGCAGCGTCTGCACCTCCACGCAGGGCACC
GTGTCATACAGCCGCTGGAACTCCTCGTACCAGGA

1450. chr9_LCNL1_NM_207510_1.57868
GGCACCTGGTACATGGTCGGGGTGGTGTCAGATG

1451. chr9_LCNL1_NM_207510_1.72642
CGAGCGCCCGAGCTGTTTCCCGAAGGCGCCCAGAAGATGCAGCTACTGGC
GCCCCAAGT

1452. chr9_ABCA2_NM_001606_-1.55001
GTACCCAATGAGGGCGATGGCCGTGGAGAGCTTCCGCTTGTTGCCGCCGC
TGTAGGTGCCAGCCGGCTTGTCTGCGTACTTGGTCAGCTCCAG

1453. chr9_C9orf139_BC132809_1.62232
GCTTGCTCCTTGAGGACCCTGGGCAGGGTGGCTGCCATGGGGCCCAATCG
TGCGTGGGAACCTGCGAGCTGGCAAACGGGGCTCGGGGGTTTTGCCCAGA
AATGGGTCAGAACGAAAGCCTCTCAGA

1454. chr9_C9orf140_NM_178448_1.61595
TCCGCGCTGGAGCTCGGTTCCAGCGCCGCG

1455. chr9_UAP1L1_NM_207309_-1.51149
ACGTCATGACCAGCGAGTTCACTCTGGGGCCCACGGCCGAGTTCTTCAGG
GAGCACAACTTCTTCCACCTGGACCCCGCCAACGTGGTCATGTTTGAGCA
GCGCCTGCTGCCTGCTGTGACCTTTGATGGCAAG

1456. chr9_NOXA1_NM_006647_1.60021
CCAGGTGGAGCAAGTTGGCAAACAGGCTCCT

Figure 3-119

1457. chr9_ENTPD8_NM_001033113_-1.58945
GAGCACGCTGGTGGCCTCCACCAGGAGGAGAATGAGTGCCGTGAGGCCTG
AGACCC

1458. chr9_CACNA1B_NM_000718_-1.72596
GAACTCGGCCAAGGCGCGCTCGGTGTGGGAGCAGCGGGCCAGCCAGCTAC
GGCTGCAGAACCTGCGGGCCAGCTGCGAGGCGCTGTACAGCGAGATGGAC
CCCGAGGAGCGGCTGCGCTTCGCCACTACGCGCCACCTGCGGCCCGACAT

1459. chrX_GPR143_NM_000273_-1.64915
GCCGAGAAGGTCGCAGGCAGCGGCAGCGCGCAGGATGCGGACCGAGGCCG
GCGGGGACGTCGCGGGGGACCCGGGGCCCGCGGGCCGGCGGCCGGGCAGC
AGCTGCAGAAGGCCCAGCGCCAAGCGGAGCCCGCCGCTGCCCAGGCAGAG
CGCGTGGAAGGCCCGCGGCTGGAAGCTCAGCACGAGCTGCGTGGCTGCGT
CCCGCGTGGGGCAGCAGAAGGTCCCTAGGCGCG

1460. chrX_SHROOM2_NM_001649_-1.99571
TCGCCCCCCAGAAACTGACGGACAA

1461. chrX_CLCN4_NM_001830_1.63447
TGGGTCCGCTCACGACCGTCCTGTTTCTTGCTCC

1462. chrX_AMELX_NM_001142_2.29346
CAGCAGCCCGTGATCCCCCAGCAACCAATGATGCCCGTTCCTGGCCAACA
CTCCATGACTCCAATC

1463. chrX_ARHGAP6_NM_013427_-1.64718
CGCCGCCGGTGCGCTCCAAGTGCCCCGGCG

1464. chrX_PRPS2_NM_001039091_-1.62552
GCCTCCCGCGTCGCTGTCGCTGTTGCCTCCGCC

1465. chrX_PRPS2_NM_001039091_1.5182
TCTTGGCCGAAGCAATCCGAAGGACACACAATGGGGAATCCGTGTCCTAC
CTG

1466. chrX_GRPR_NM_005314_1.61388
TCCCGGAAGCGACTTGCCAAGACAGTGCTGGTGTTTGTGGGCCTGTTCGC
CTTCTGCTGGCTCCCCAATCATGTCATCTACCTGTACCGCTCCTACCACT
ACTCTGAGGTGGACACCTCCATGCTCCACTTTGTCACCAGCATCTGTGCC
CGCCTCCTGGCCTTCACCAACTCCTGCGTGAACCCCTTTGCCCTCTACCT
GCTGAGCAAGAGTTTCAGGAAACAGTTCAACACTCAGCTGCTCTGTTGCC
AGCCTGGCCTGATCATCCGGTCTCACAGCACTGGAAGGAGTACAACCTGC
ATGACCTCCCTCAAGAGTACCAACCCCTCCGTGGCCACCTTTAGCCTCAT
CAATGG

1467. chrX_CTPS2_AF226667_1.56591
TGAAAACAGTTCTTCTTATTCCCAGTCTCATTGTTCCTCCCAAATTGCCA
GGGTTGTGCTCGGGCATATCAA

1468. chrX_CTPS2_AF226667_1.65171
TCCCCAGGTAATCACCACGCCTCTCTTTATTGATCA

1469. chrX_SYAP1_NR_033181_-1.59634
CTCCGGCTGGCGTGCAATTTAATTTCGACTTTGATCAGATGTACCCCGTG

Figure 3-120

GCCCTGGTCATGCTCCAGGAGGATGAGCTGCTAAGCAAGATGAGATTTGC
CCTCGTTCCTAAAC

1470. chrX_PPEF1_NM_006240_1.52107
TGGAAGAATTCTATGCCTGGCTCCCAATCGGTACAATCGTTGACAATGAA
ATCCTGGTCATCCATGGTGGGATATCAGAGACCACAGACTTGAATTTACT
CCACCGTG

1471. chrX_PHKA2_NM_000292_-1.69895
GTGAGGACGGCAATGCTGATGTCCTGCCCACTGGCCTCGTAGATGAGTTT
TGTGAGCTCCTCTGG

1472. chrX_KLHL34_NM_153270_1.64657
GGCGGTGGCTGCACACCATCACCTGGAAGAACCGAGTTGCCGGTGGACTC
CGGGGGTGCTGGATGTCCGACGGCGCAGATGCGGCGTCCCGGGAGTGCAG
GGCGAGGACTC

1473. chrX_PHEX_NM_000444_1.60166
TCAATCAGTAGAAGGCGGGACACCGAAGCCATACAGAAAGCCAAAATCCT
T

1474. chrX_IL1RAPL1_NM_014271_-1.60319
TCTGACTGATAAGCCACCCAAGCTTTTGTATCCTATGGAAAGTAAACTGA
CAATTCAGGAGACCCAG

1475. chrX_TAB3_NM_152787_1.76514
CAGGTGTACCGTGGCATCTCGCACTGC

1476. chrX_BCOR_NM_017745_1.63262
CAGAAGGGTCTCGCCAGCGTTCTTATTGACAATAAGTCTCCGTGCTTCCG
GCGGCATAGGGCGAGACTGGGTGGTCTCCTGAGGGGAACTTGAGCATGGC
AGCTGTGTGGACTGGGAGGCTGGTAGCAGTTGCTGCAAGCGGTCGAAGGG
CTTTGGCTCCTGCTTGGCTGGTGACAGATCATAGTCCGAACTGGGCTCCG
G

1477. chrX_MED14_NM_004229_-1.77095
GGGCTTGGCGCAACGGCACACGATGCGGTCCTCGAGCCTCCCGGGCGCTC
GGTCACCGCGCCGAAACGGGAGCGGGCAGAGTCGCCACCGCCTA

1478. chrX_USP9X_NM_001039590_-1.7447
ATGAACATGAGTCGCCTCCACCTGAAGATGC

1479. chrX_USP11_NM_004651_-1.68722
AAGAAAGATGGCACTTGGCCCAGCGCACA

1480. chrX_ZNF41_NM_007130_-1.67292
GCCTCTGACTTGGGAATTTGGTAC

1481. chrX_ZNF41_NM_007130_-1.59949
ACCATGGGGGAGAGTCCCCATTAGCTGCCAT

1482. chrX_ARAF_NM_001654_1.51627
ATGGCTTCCGTTGCCAAACCTGTGGCTACAAGTTCCACCAGCATTGTTCC
TCCAAGGTCCCCACAGTCTGTGTTGACATGAGTACCAACCGCCAACA

Figure 3-121

1483. chrX_PORCN_NM_022825_-1.71849
GCACATCTGTGGACCCTCATAACCCTCTTAAGACCCCTCTCAGGGTGCCA
CTGATGGGGGATGAGGGAAGGCCCTCTCTCTACTCCTTGA

1484. chrX_WAS_NM_000377_-1.99128
GCCGCCCAGCTCCGGGAATGGACCA

1485. chrX_WAS_NM_000377_1.64743
TGAGTTACTTGCTGCCCTGTGCTCCTCCCCGCAGGACATGGCTCCCCCTC
CACCTGCTCTGTGCCCACCCTCCACTCTCCTCTTCCAGGCCCCCAACCCC
CCATTTCTTCCCCACCAACCCCTCCAATGCTGTTATCCCTGCCTGGTCC

1486. chrX_PQBP1_NM_001032382_1.8001
ATCGTAGCGGCGACACGAGAGAGACGGGCGGTGTGACAGCCTT

1487. chrX_SLC35A2_NM_001032289_-1.68555
CGGAGGGTGGCGACTTGGGTCCTGCAGATGCCCAACACCCTCCACCCCAG
TCCCCCTCCCTTGTGTCCCCCCATTGCTG

1488. chrX_GPKOW_U66359_-1.62855
TCCTTTTCCCAGGCCGGCGCGCTGCTTGCTGGGAA

1489. chrX_MAGIX_NM_024859_-1.56628
CGGGGACGTCGTGCTCCACATCAACGGAGAGTCAACGCAGGGCCTCACCC
AT

1490. chrX_PRICKLE3_NM_006150_-1.58043
CAGTGATGGTCACCGGGAAGATGCGCACGATGCCACGCCCCAGATTCTCC
CGCTTCCGCTGCTGGCTAAAGGCTCGGAGCTCTTTCTTT

1491. chrX_CACNA1F_NM_005183_-1.5471
CCTCCTCATCGAAGCGGGAGAGGATGGACTCCTCGTCGCTATAGAGAGAG
CTGGTTCCCTGTGCCAGCAGGTCACTGGCAGCATTGTCCATCTCATCCAG
CGTCAGGCGACACGCATCTGCAATCTCCTGCTTGGCCAGGGCCACGAAAC
GTGGGTCTCGAGCAAAGAGGCC

1492. chrX_CCDC22_NM_014008_1.50984
ATGTGTCCCGGCTGGCCTACACCCAGCGCATCCTGGAGATCGTGGGCAAC
ATCCGGAAGCAGAAGGA

1493. chrX_CCDC22_NM_014008_1.60718
GAAGATCCGGGAGGACTACCGAGCCCTCCGCCAGGAGAACGCTGGCCTCC
TAGGCC

1494. chrX_FOXP3_NM_014009_-1.57884
AGCGGATGAGCGTGGCGTAGGTGAAAGGGGGTCGCATGTTGTGGAACTTG
AAGTAGTCCATGTTGTGGAGGAAC

1495. chrX_AKAP4_NM_003886_-1.70611
CTTTATCTTCTACATTCAGGGTGGACACATCGACAAAGCATAT

1496. chrX_KDM5C_NM_004187_-1.51918
GATAAACTGGAGGGCATCAACTGGGGGAGGTTGTAGTGTAGGAGTTTGGG
TGAGGGGGCCCGAGCCCATCTGTTTGGACTTGAGGGAAAGTGGCTTGGGG
TTAGAGTCGGGGGAGGATCAGAATGTCTTGCCCAAGGTTAAGAAGCTGGT

Figure 3-122

GGAACTTGATTTCAGAACCCAGAGCTCCCTGGCTTCAGCCCTAGTGCTCC
TGCCAGCACTACAGCTGCTCCACTGACTGGTGATGGAAGCACTGTCTTCC
CCGTCTAAGA

1497. chrX_FGD1_NM_004463_1.73267
GTGGTGCTGTGGACTGGGACCGCAGGGCAAGACCCGGTGGCCTGGAGCAG
CGCCCAGGCTGGTGTCCGAGGGTCCGACAAACTGGGGATCCAGTGGGCCG
CCAAGAGCCGAACCTGAG

1498. chrX_FGD1_NM_004463_-1.85574
TTCCGAGGCTCCAGGGTCCGAGTCGGCACAGGCCGGCGGAGCGGCGCCCG
GCGGGTTCGTGGCCGGGTGTTCGGGCTCCGA

1499. chrX_LAS1L_NM_031206_-1.71343
AGGCGACCACGATGCCGTGGGCCGAGAGTGGCAACGACCCTTTCC

1500. chrX_VSIG4_NM_007268_1.5031
GGCCAGAAACTCATAATCCAGAGGAACTGTGTCCAGCAGGCGGGCGTAGT
TGCCATTGATCTGGGCGATGATCTGGTACTCCTGTCCTATGCAGGGCTCA
TCAGAGTAGTTGTTGCCCAGATTCTGGGAAGTTGGCTCATCACTGGAGCA
GCCACTTGCGAAGATGGCCACCCTCATGGTTTCTCCAGAGTCGTTGGCC

1501. chrX_VSIG4_NM_007268_1.74093
ACTTCACACGTGTAGTGGCTCCGGTCATCCATCTCCAGGGTGCTCAATTG
GAGGGATACATCTCCTGGAACCTTGTGGCTCACATGCAGGCGGCCCTGGT
ACTTTGCCTGCTGGATATGGTCTCCAGAAGAGTCACGTAGAAAGATGGTG
ACAGGGTCTGAGCCACGTTGTACCAGCCACTTCACCAAGACTTGGGTGTA
GCCTTGCAGGGGGTCATAGGTGCAGGGAAGATTCACATCCCCTTTCCAAG
GTCCTGTTACACTCTCTGGCACTTCCAGGATGGGACGGC

1502. chrX_AR_NM_000044_-1.64178
GGTAACTCCCTTTGGCTGCGAGCGGGCGAGCTAGCTGCACATTGCAAAGA
AGGCTCTTAGGAGCCAGGCGACTGGGGAGCGGCTTCAGCACTGCAGCCAC
GACCCGCCTGGTTAGGCTGCACGCGGAGAGAACCCTCTGTTTTCCCCCAC
TCTCTCTCCACCTCCTCCTGCCTTCCCCACCCCGAGTGCGGAGCCAGAGA
TCAAAAGATGAAAAGGCAGTCAGGTCTTCAGTAGCCAAAAAACAAAACAA
ACAAAAACAAAAAAGCCGAAATAAAAGAAAAAGATAATAACTCAGTTCTT
ATTTGCACCTACTTCAGTGGACACTGAATTTGGAAGGTGGAGGATTTTGT
TTTTTTCTTTTAAGATCTGGGCATCTTTTGAATCTACCCTTCAAGTATTA
AGAGACAGACTGTGAGCCTAGCAGGGCAGATCTTGTCCACCGTGTGTCTT
CTTCTGCACGAGACTTTGAGGC

1503. chrX_AR_NM_000044_1.50372
CCTGGATGGATAGCTACTCCGGACCTTACGGGGACATGCG

1504. chrX_NLGN3_NM_181303_-1.58918
GCAGACATTGCACCCCTATAACACCTTTGCCGCAGGGTTCAACAGTACCG
GGCTGCCCCA

1505. chrX_TAF1_NM_004606_-1.6285
CAGCAGCTACCATCACTGCTGCCGCCAT

1506. chrX_HDAC8_NM_018486_1.53135
AGCCCATATTCTATGGAGTCCGGATGATCATCATCGCCCTCTTGGCTGAC
CTTCTGGAGATGCTGCAGATAAGCATCAGTGTGGAAGGTGGCCATCTCCT

Figure 3-123

CCATGGAGGCCACTTTAGGCTTAAC

1507. chrX_CDX4_NM_005193_-1.563
TGTACCCGGGCACTCTCATGAGCCCTGGGGGCGACGGCACAGCTGGGACA
GGCGGCACAGGGGGCGGTGGGAGTCCGATGCCAGCCTCCAATTTCGCTGC
GGCACCGGCTTTCTCGCACTATATGGGGTATCCTCATATGCCCAGC

1508. chrX_MAGT1_NM_032121_-1.54316
TTGGAGAGCAGTGAACATGACGATAACGGAGTAATTTCTCGGTGGGGCTT
TCACAAGGCGACGGAACTTGTCTCCATTCATTCTTATTACAGGTC

1509. chrX_SH3BGRL_NM_003022_1.53262
GCCAACCGCTGTTTCAGCCCCTAGCTGGATTCCAGCCATTGCTGCAGCTG
CTCCACAGCCCTTTTCAGGACCCAAACAACCGCAGCCGCTG

1510. chrX_SRPX2_NM_014467_-1.87704
TCCCATATTTCTGCTTCCCCTCACTTTTAGAAGTTAATTGATGGCTGACT
TCTGAAAGTCACTTTCCTTTGCCCTGGTACTTCAGGCCATATACATCTTT
TCTTGTCTCCATAATCCTCCCTTT

1511. chrX_ARMCX1_NM_016608_-1.68893
CGTGGCCGCTGGTGTGGTTATCGGGGCTGGTGCCTGCTACTGTGTATACA
GACTGGCTTGGGGAAGAGACGAGAACGAGAAAATC

1512. chrX_ARMCX2_NM_014782_1.5925
TTGGGTACCGCTCCAGTCGCTGATGTGGCTTTCGGTATAGCCCCAGTGTG
AGCCCCAGGGGTTGCTTTCTTGGCAGCTGATGTTCCAGGAACCACCGCTG
TT

1513. chrX_NXF4_NR_002216_1.51506
GTAGGTAGGTGGGTAGGAGGATCATGAAGGCTCTAGTTTTTTCTT

1514. chrX_ESX1_NM_153448_3.34522
AATTCAGGCGTGCTGCAAGTCTCT

1515. chrX_MORC4_NM_024657_1.55007
TGGGCAATGAATCCTCGGTAATAATCAT

1516. chrX_TEX13B_NM_031273_1.87287
TGCTGATGGAGTTCGGAGTCTCTCCTGTCTCTTGGGGGCTCTTGAGGGTC
TATTCCCTGGGCCTCC

1517. chrX_VSIG1_NM_001170553_1.54836
TTCTAAGCCCCTTTGTAGCGTTCAAGGAAGACCAGAAACTGGCCACACTA
TTTCCCTTTCCTGTCTCTCTGCGCTTGGAACACCT

1518. chrX_COL4A6_NM_001847_2.35608
TGCGGGATGGTGATGTCCTGGCTGT

1519. chrX_COL4A6_NM_001847_-1.51173
GGCCAGCTGCTCCAATTGTGGTACGGCCTGGGTTTCCTTGGTCCCCCTTC
AGCCCTGGAAATCCCTGAGGCCCTAGGGCT

1520. chrX_KCNE1L_NM_012282_-1.65193
TGGAAGGTGGGAGGCGCGCCCAGGGATGAGCGAGATGAGGAGGGCGCGAA

Figure 3-124

CCAGCAATCT

1521. chrX_ZCCHC16_NM_001004308_1.63565
GGCAACATTGAGTGGCGGACAACACTTTTTGGCATCTCTCCAATTCAGCT
GTTAGCATCTCCTAGTGTCTTCTTCACAGCTAACAGCTTTGGCTACTTGC
TCATGACACTCCGTCTCTGA

1522. chrX_AMOT_NM_133265_-1.71241
TCTTATTTGTCCTTCTTAGCAGCT

1523. chrX_LRCH2_NM_020871_1.50683
TTATCACTTCCAATTCCAGAGTCAGGGCCATGATTTTTATT

1524. chrX_IL13RA1_NM_001560_-1.77535
TTATATTCCCTCCAATTCCTGATCCTGGCAAGATTTTTAAAGAAATGTTT
GGAGACCAGAATGA

1525. chrX_PGRMC1_NM_006667_1.73176
CATGAGATTTTCACGTCGCCGCTCAACCTGCTGCTGCTTGGCCTCTGCAT
CTTCCTGCTCTACAAGATCGTGCGCGGGGACCAGCCGGCGGCCAGCGGCG
ACAGCGACGACGACGAGCCGCCCCCTCTGCCCCGCCTCAAGCGGCGCGAC
TTCACCCCCGCCGAGCTGCGGCGCTTCGACGGCGTCCAGGACCCGCGCAT
ACTCATGGCCATCAACGGCAAGGTGTTCGATGTGACCAAAGGCCGCAAAT
TC

1526. chrX_SLC25A43_NM_145305_-1.62131
TGGCTACGTGGAGGCGGGACGGCCGACTGACAGGCGGCCAAAGGCTGC

1527. chrX_RNF113A_NM_006978_2.257
TGATCCACCGCCTTTCCTGGAGAA

1528. chrX_GRIA3_NM_007325_1.80422
GTAGACCTAGCCTATGAAATAGCCAAACATGTAAGGATCAAATACAAATT
GTCCATCGTTGGTGACGGGAAATATGGTGCAAGGGATCCAGAGACTAAAA
TATGGAACGGCATGGTTGGGGAACTTGTCT

1529. chrX_XPNPEP2_NM_003399_-2.50596
TTAGTGGTCTCCACCCTTGCCATCC

1530. chrX_AIFM1_NM_004208_-1.90343
TCTGCCTCGGGCTTCGGACGCACACGGTCCGCACCAAGGGCACCAGCTTC
TGCTTCAAAGCACCCGCCGC

1531. chrX_SLC25A14_NM_003951_1.91727
TCTGGCATCGGTGGTTTTACTTCTTCGATTGAACCCTGCTTCCTCGACCC
CCCTGGGAGGCCGCCTTCTTCAGGCGCCTCCCTTCTCTCCACGAGCTCGC
TCTGA

1532. chrX_MST4_NM_016542_1.73503
TACCACCGTACGAAAGAAGCCTGATC

1533. chrX_MBNL3_NM_018388_-1.54346
TGCAGGGATAAATGCCGGCTGTGGGAGCTGCA

1534. chrX_HS6ST2_NM_001077188_1.74538

Figure 3-125

CAGCGTCGCCTGAGGACGTGCATCCGCCTGCGGCGGCCCCGGGACAGCAG
CGCGAAAAGCGGGGCGCACGC

1535. chrX_NCRNA00086_NR_024359_-1.73023
GGCCTGATGACATGCCCCCTTGTCC

1536. chrX_MCF2_NM_005369_-1.94235
TCTTGCCTCTCCGGGGATTTGCTTC

1537. chrX_AFF2_NM_002025_1.53583
GTCACCTGGAGATGACGTCCTGGGCGGCTCTGCCCCTTCTATCCAGCAGC
AGCACTAATGTCCGGAGACCCAAG

1538. chrX_CXorf40A_NM_178124_-1.93942
GGCCCATGCTGCGGGAGCCTGTGTG

1539. chrX_HMGB3_NM_005342_1.85097
TGGAGGCAGCTAGCGCGAGGCTGGGGAGCGCTGAGCCGCGCGTCGTGCC

1540. chrX_MAGEA10_NM_001011543_1.59332
TCTTCAGGCATGCAGCGCTGACGCTTTGGAGCTCGAGGCAT

1541. chrX_DUSP9_NM_001395_1.92895
TGTCTTGACGGGATCACTGGGGCTC

1542. chrX_PLXNB3_NM_005393_-1.50615
CGTACCCCTGTGGCGACGAGCACACCCCCAGCCCCATTGCTGGCCGCCAG
CCCCTGGAGGTCCAGCCTCTGCTGAAGCTCGGGCAGCCGGTCAGCGCCGT
GGCAGCTCTCCAGGCAGATGGGCACATGATAGCCTTC

1543. chrX_PLXNB3_NM_005393_1.76505
CAGCTCACCATCCGAGGTCAGCACCTCCAGACAGGTGGCAACACCAGTGC
CTTCGTGG

1544. chrX_PLXNB3_NM_005393_-1.51889
AGGGCCTCAACCTGGGCATCAGCAAGGAGGAGGTGCGCGTGCACATCGGC
CGCGGCGAGTGCCTGGTGAAGACGCTCACGCGCACCCACCTGTACTGCGA
GCCGCCTGCGCAC

1545. chrX_PLXNB3_NM_005393_1.84469
GACAGCAGCAAGCCGGATCCACCAACACCGCAGCGCCTTATGACCCCGGA
ACCGAGCCAGCCACTGAGGGGAGCTGGCAGAGCCTGGGGGCACAGGGTGC
AAAGCCAGGCACTGTGCCCAGCAGTGGGCTCCCTGCCTGCCACCTCCCCT
GCCAGCCCACCCACCTTCCCCCCACCTGAGATTGTTTCTAATTTATAAGG
ATCCCCCTCCTTCCCCCTCTCCCCATTGTATTTATTTGCCTGCTGGAAAA
TCACA

1546. chrX_SRPK3_NM_014370_-1.59009
GCCAGCACGGGCGGTGGTGGGGACAGCG

1547. chrX_HCFC1_NM_005334_-1.68402
CACCAGGAGGCGAGTCCCGTCACACACGAAGCCATAGGCTGCACACCCAG
GGGGAATGTCCCCCCTCACGGCTGGGATGAACCACTGGT

1548. chrX_MECP2_NM_004992_-1.51053

Figure 3-126

ATGGGTACTGGAAAGCTGTCGGTCAATTCTGCTGTTCACAAATTCACTGA
AAGAGGCCCCCATCTTCATAATGTTCAAGTACAGACAAAATTGAAATTGA
GGTCACACCCCAAAACTGGGCCGGACACAGCTGGTGAGAATCCTGCAGCT
TAAGGCTTTCCCTCCAACCTCCTGTCAACCTGACCCCAAGGCAGGGGCAG
CATGAGAGCTGCAGGGCCCCTGCCTGCCAGGGCGATAAACCGCCAAGGCT
GCCTGCTGAAAGGCGACTGACTCGTGATGCCTTTGGGAAAGACGAGGGAA
TGAGGAAGAAAGGGGGAAATAGAGAGAAAACCCTAAGGAGCCTCAGGCCC
CACTGGCAGCTCTGGAATAAACTGGAAGGGAAAGAGGCTGGGCAACTGCC
TCTTTGAGGGAGCTGCAGGTGGGGCCCGAATGAAATAAAGTGACGCTTGA
AATGCTGTGTTCCCAACCACGACTGCCCCATCGGCCCTGAATGAACTGTC
ATGGGTGACAGGGGGGCCTGGTGGGCCACGCACTCCTCTTACCAGGACCA
GATGACGCCCAGGTGACGGGGAAGCAGCTCTGGACAATGATTCCAGAAGC
CACATTACATTTGACTAAGTATAATACATAAAAACCCAACTGACCAAAAT
AAACATCTTCTCAGTGACAACCTGGTCGGATGCTGCGCTCTCGTGGATAA
GTGTCCTTTGGTAGTGCCAGGAGTTCGAGGCCACTATGGGGGCAGGAGCC
TTCTGTCCTTGGAGGAAGAGTTCTGGAGGACTCACCCTCTCTTCTGACCC
CCCTTCCCTTCCTGGGGAAGAGTCAGAAGTGAAGCTGGGGGGGTCATCAG
CAGAGCAGGTGGAAGGGATCAGGGATCAGGGATTGGGCTGATGGGAGTTT
GGTTGCAGGACTTGCTTTTACAGCATAAGGAAATGGACACATATATGCTA
GAAAGTCCAACTATGAGACTCTACAAACAGAACGGGGCAAACTCCCTCAC
TTCTAACCATTCCAGAAGAGACAAACACGGTTTTTTCTTAAGCTACTGAT
TGGAACTGTCAACTATGGTTCCTGATCACTAAAGACTGGCAAGGAAGTGC
TAGACAGTTTCTATGATGTTTCACTCCTTCATGATTACACCATAGTAAGG
AAGCCAGGGACAATAACTGAAATACACAAGACAACACACACTTGACAGTT
CATGGCAGCAGCTCACATGGGACATGCCTGTGGGTGTTTCTGGAAGCATA
AGACTGCTGTCTCATTTGCTACTTTGATAAGGTACTTCTCAGTTGGACAG
ATTTAGATATAAGAGACATCTCTGTAAACACAGAAAAGGATATACCAATA
TGATGAAGATATGCAGCTAGATAAGGACTTCCTGAACAGAGGTTAAAAAG
ATGGGATCCCACATGAAAACTGATCAATTAAAAACCCACAGCAAGCCCAT
GCCTCTAAGCCCCTACACCACAGCTATGGACCAGACAGACAGTGAAATGT
GTGGTGTTCTGGCCCCCTGTCTGCATCGAGCAAAAGCAAAACATTGCCAT
TCAAGAAGAACTCCGAGGGAAAAGGGGGAGCAGAGGAAGGGCTGGGGACC
CAGGTACTGGTCCCAGCTCGGGTCTTGGGAGTTCTGCATTGGTACCGCTA
CTGCCCTGCTGCACTACGCTAGACTCTGGACTTCTGAGTGAGGTCAAGGT
CGGCTGGCATGGAGCCCCTGTTGGGCCACTCGATGACTGGCAGGCCACAG
GAGGCCTCTGTGCTTTCCTCAACTACCAAATCGGGCCCAGCTCCTCCAGT
CCACTTCTCTAGAGTAGAAGGGTGAAAAGGCTCGTTGTTCAGGGTGGGAA
ATGCCTTTTGCTTTTTCTTACCAGGGAAGAGGGGGCTACCTAGGAGAGCA
AGACCTTGCTGCTCTCTTGCTCTTCACAGACAGGCCAGGTCGGACTCAGC
AGAGCCCAAGGCCTCCTCAGGGCTCAAAACAGGGTGGGGCTGGTACTGGC
AGCAGGAGGACAAAGGGCAGGCAGAGTTCTGGGGACTGGAGCCGACAAGT
GTGGTTGGGCACCGCGGCTGCCTGGAAGAGAAGGGATGAACTAGGAAGGA
GGAGGATGGAGGAAGGGAAAGAAGTGAAAGGATGAAATGAACAAAAGGCA
GAAATGGAAGGGGAGAAGAGAAACCAATCAGGAAGTCCTTATAAAATTGC
AGCAAACACTTAGAGTTTCGGAGCTTCGTGGGAACCCTATGTGCTGAGCC
CACTTTAAAACAAGCGCAGGTATATATACAAATCCAGGTAGTTCTCAACA
CTGTCACATCTGGTGGCTTGAGGGACTAA

1549. chrX_FLNA_NM_001456_-1.5789
GGCCGCCGTACTTGATGGAGATGAGGTAGCTGCCAGGTGCCATGGGGGTA
TAGGTGACGCGGTAGCCCTCAGGGCACTCCTGGCAATCCATCTTCACCTT
GGAGGGGCCGTCAATGGTCACCGACAGGGCACCAGCTCCCGCATTGCTCG
TGTTCACG

1550. chrX_FLNA_NM_001456_-1.53179

Figure 3-127

CGGGCACGCCGTCATAGGTCACCTCCACCTCATAGGGCCCTTCCTCACGG
GGCAGGAAGCGCACCACACTGTTGTCAGCCCCCAGGCCTGGCTCCACCTT
GCAGGGCACCGCTGCACCCGAGGGGCCCACAATCTTGGATGCCACTTTGC
CTTGACCACCAGCACCCTTTGATTTGA

1551. chrX_ATP6AP1_NM_001183_-1.69995
CGCTGGTGCTGTGGTCGAGTGACCG

1552. chrX_PLXNA3_NM_017514_-1.66922
AGCGCCCAGGTCCCAGTGAAGGTTCTCAACTGTGACAGCATCACCCAGGC
CAAAGATAAGCTGCTGGACACTGTGTACAAGGGCATTCCGTACTCCCAGC
GTCCCAAAG

1553. chrX_CTAG2_AJ223040_1.62655
AGGTCAGGGCCCACGAGGATGCGGAGGCAGA

1554. chrX_GAB3_NM_001081573_1.68816
TGGTTTCCTCAGTGGCTACGGCATTAGTGTTTGGGTCATCTCTTGGCAAA
GAGGAGCTGGCAGCATGGGCGGTAAGAAGGGAGCTGGCAGAGGATGGCTG
CAGGGAGGAGGGCGTGTAAGAGAGGCTCT

1555. chrX_CLIC2_NM_001289_-1.52797
CTTTGTCTTCAGGACACGTGTGGGTAAATTCTTCACGGGCATAGGCATTG
TGGAGATAACGCCAGACTC

1556. chrY_PRKY_NR_028062_-1.81549
ACGCGGCCACCGAGCTGGAGGAGGCGGCGGGCGTGAGACCGGGAATGCTT
GGGGCCCCCGCCTTCCTCGCAGCCATCCAGCACTCGGTGCACGCCCCGCG
AGGCCAGCGGCTGCTCCCTCCCGGGGCTATTGCTGCTAG

1557. chrY_---_---_1.95935
GTAGTGCAATCTCCAGTGGTCTTCA

1558. chr10_ZMYND11_NM_006624_-1.52942
TGCGGCGGCGCCTGACAATGCCCCCTCGCGCCCCGGCCTCGGCGCCCGCT
CCCGGCTCCAGCGCGCCTG

1559. chr10_DIP2C_NM_014974_-2.35308
ATGCCATGCCAGAGCCCGACGTCCTTCTTGAAATC

1560. chr10_WDR37_NM_014023_-1.52948
CTGACAAGGACGAGCCCGACCTCGATGGGGATGTGTCCAGCGACTGCCCC
ACCATCCGCGTCCCACTGACATCCCTCAAGAGCCACCAGGGCGTGGTCAT
CGCCTCCGACTGGCTGGTTGGGGGGAAGCAGGCTGTGACTGCCTCCTGGG
ACCGGACGGCAAACCTGTACGACGTGGAGACGTCCGAGCTCGTTCACTCT
CTG

1561. chr10_PFKP_NM_002627_-1.71126
ATGGTGGACGGAGGCTCAAACATCGCAGAGGCCGACTGGGAGAGTGTCTC
CAGCA

1562. chr10_PFKP_NM_002627_-1.71467
GGTGAGTGCCTTGGCCTGCGGTGCGGACTGGGTGTTCCTTCCAGAATCTC
CACCAGAGGAAGGCTGGGAGGAGCAGATGTGTGTCAAACTCTCGGAG

Figure 3-128

1563. chr10_---_---_-1.88101
CAGGAGAATCACTGGAACCCAGGGGGTGGAGG

1564. chr10_---_---_-1.5545
CACGAGAATCGTTTGAGCCTAGGAGGTGGAGGTTGCACTGAGCTAAGATC
GTGCCACTGCACTGCAGCCTG

1565. chr10_IL15RA_NM_002189_1.60813
TGGGAGCCCGGGACAATAGCTGCTGTTGTGGCCGCTGTGTTGTTTGA

1566. chr10_FLJ45983_NR_024255_-1.7135
AGGGACGGCTTCTTCTATCTCGAATTTTTGCATTTGTAGGGAATTTTATG
GGGTAGAGGAGCGAAGAGGGAACAATGTCTCCAATTCAAATAAAACCCCA
AATTAAGCTCTCAGCCCCATCGGTGGGATAGCCTGCGGGGGAACCCACTC
CCTCTCCTGGCAGCATTGCCCTGGGGGCGAGCAGAGAGTGGATTTGGAGT
CTTCTTTTCCCGCCTGACCCCTGCTCGCCCGAGCAGCATTTTCGGG

1567. chr10_C10orf47_NM_153256_-1.69473
GCATCACCGTGCAGTTCGCGGGCCGCGGCT

1568. chr10_BEND7_NM_152751_2.16421
TGGGAGCATATAAGGGAAATTGGA

1569. chr10_BEND7_NM_152751_-1.9592
AGAGGAGTTCAAACGTGGAGGCCAGACTAAATCCAGGTCCTGGGGCTCTT
CTTTTAGTTTCTCTCCTTCTTTGCCAACTCGCTGATAGATCCGCCCAGTG
CTGTCGTT

1570. chr10_HSPA14_NM_016299_-1.74906
TGGCGGCCATCGGAGTTCACCTGGGCTGCACCTCAGCCTGTGTGGCCGTC
TATAAG

1571. chr10_HSPA14_NM_016299_1.66511
TGGACGAATCAGGAGCCAGTAGATT

1572. chr10_RSU1_ENST00000377921_-1.64904
ACAACAACAAAGCACGTGGGCGATGACAGCAAGCGCAGAGGCGGAAAGGC
AA

1573. chr10_CUBN_NM_001081_1.53346
CGACACTGATGCGGTGACCGTGGTGTGGAAACCCCCAGCACTGATGCTAG
AATCAGAGACGAATCTCAGCGTCAGGGCGCTGCTGAAGGATGTGATAGGA
TGGGGCATGTCGGTGCCACAGTAACGGC

1574. chr10_STAM_NM_003473_-1.57919
TCCCCGGGGACACCTCGGCACGCAGCGGAG

1575. chr10_CACNB2_NM_201590_-1.71741
TGCTTGACAGACGCCTTATAGCTCCTCAAACTAAATACATTA

1576. chr10_PLXDC2_NM_032812_-1.57172
CCAGTTTAACAGATGTGGCCCCTGTGTATCTTCTCAGATTGGCTTCAACT
GCAGTTGGTGTAGTAAACTTCAAAG

1577. chr10_KIAA1217_NM_019590_1.50407

Figure 3-129

TACCACAGGGGCTGTAAGACCTAGTGACCCTCCTAAGTGGGAAAGAGGAA
TGGAGAATAGTATTTCTGATGCATCAAGAACATC

1578. chr10_YME1L1_NM_139312_-1.57523
AAGATATGTTTTGCTCGTTCATAT

1579. chr10_ARMC4_NM_018076_-1.83283
AGTTTGGTGATACCCCCGTGCTGCCTCAC

1580. chr10_EPC1_NM_025209_-1.52769
AAACGGCCCCGGCCAGCGGGATCATGGAGAACCGGGGGTTCGGTCCCCAC
TCGCCAACCGCTGCCGGG

1581. chr10_PARD3_NM_019619_1.60548
ATAGGTCCGCCGACGATCTTCTACATCTTCATCTTGCTTTGCTTGCTGAA
ATTCTTGCCTCAGACGCTGTATCCGATCATGATTGCTAGGAG

1582. chr10_CCNY_NM_181698_-1.70166
GAAATCGTGCAGTGAACCTGTCCCCTCCGGTCACAACATCAAGAGCTGAA
CTGGGACTAGAAGTCATCGCCCCAGAGCTTTTTGCTA

1582. chr10_ZNF248_NM_021045_1.55149
TCCCTGATGGATAATGAAAGCTGAATTGTCACAGAAGATTTCCCCATATT
CATTATATTCATAAGGATTGTCCTTTGTAAGAGCTCTCTGATGTCCAAAC
CTTAAATTCATGCAGAAGGACTTCCCGCAAATACTGCATCCATACGGCTC
CATTTCCAAA

1584. chr10_RET_NM_020975_-1.7483
ATGTCAGACCCGAACTGGCCTGGAGAGAGTCCTGTACCACTCACGAGAGC
TGATGGCACTAACACTGGGTTTCCAAGATATCCAAATGATAGTGTATATG
CTAACTGGATGCTTTCACCCTCAGCGG

1585. chr10_HNRNPF_NM_001098208_-1.74941
TCAGGGTGGGTGTCAGGTGATCTTGGGTGTGGCTT

1586. chr10_LOC439911_AK127450_1.55195
ACCATGGATGGCCTATTATTATTAT

1587. chr10_ZNF485_NM_145312_-1.60204
CTAATTACTCAGTTGGAGCAAGGGGCAGAGCCCTGGACTGAGGTGCGAGA
GGCTCCATCAGGCAC

1588. chr10_C10orf10_NM_007021_1.59324
AATGCCACCACAGGACGTATGAGTTGTAGCCAGCAGAGTGCCCCAGTGGT
GCCAGGTGACAGTCCCCCGGAATACATTAGTGCATTTGCTAAGACTCCAT
GTGTTCTCTTGGGCCTCACAGAACATGGGCTTTGAGGGTGGGAGCCAAGA
GGCAGACTTGGGAGTGCCCGAGGCCTTGTTCTGAAACACCTGGGGGGCTG
ACACCCCCACTACCCTCACACCCCTACCACCAGTTTCCCCACCAGCGATG
ATGGTAGCTACTCAGCCAGTGGGCTCCTATATGCGGTTACACGTCAGAAT
GGCC

1589. chr10_ALOX5_NM_000698_-1.69909
CACCGACTGCCAAGGGCGTGGTGACCATTGAGCAGATCGTGGACACGCTG
CCCGACCGCGGCCGCTC

Figure 3-130

1590. chr10_WDFY4_NM_020945_-2.52241
TGCATCCCGGGGTCGTGTGCATCATG

1591. chr10_FAM13C_NM_198215_1.66655
AGATGGAGCATCGTGGCGACAGCAGTGGGTTATCACCATCAGTGATGTGA
TAGAGCAGCCTGCTGGTCCCCACAGAGTGGAGGTCTTCTGGTGCACTGTC
GGCCTCATTCT

1592. chr10_ZNF365_NM_014951_-1.64175
GACATCTCCTCAAATAGGAAGCCCAAATG

1593. chr10_SIRT1_NM_012238_1.52124
TCCTCGATGTCCTAGGTGCCCAGCTGATGAACCGCTTGCTATCATGAAAC
CAGAGATTGTGTTTTTTGGTGAAAATTTACCAGAACAGTTTCATAGAGCC
ATGAAGTATGACAAAGATGAAGTTGACCTCCTCATTGTTATTGGGTCTTC
CCTC

1594. chr10_MYPN_NM_032578_1.52893
ACTCTCTGCTCATTGACCCACTCACTCAGCGCGACGCAGGGACCTATAAG
TGCATCGCTACCAACAAAACCGGGCAGAAT

1595. chr10_SRGN_NM_002727_-1.53443
AGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGACTACTCTGG
ATCAGGCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCT
TCCTAACGGAAATGGAACAGGATTACCAACTA

1596. chr10_HK1_NM_033496_-1.70354
ACCACAACCTGACACTGGGCAAGATGGCCCACCTGTGGCATCCCAGGTTC
CTGCCCTGTAAAGAGGAGTCTGG

1597. chr10_C10orf35_NM_145306_-2.01764
TGCAGCCCATCAGGGACCCACAGC

1598. chr10_TYSND1_NM_173555_-1.93868
CACACGTGGTCTGCAGCATTACGGGCGTGCCATT

1599. chr10_TYSND1_NM_173555_1.54243
GCGTCGGTAAGCAGCAGTGGGCCGGCCACGTTGCTGAGCACCCCGCAGCT
CAGCGTGTTGAGAAAGATG

1600. chr10_NPFFR1_NM_022146_-2.97308
CGCCCATTCCGCAGCGGGAGGCGGC

1601. chr10_ADAMTS14_NM_139155_-1.63735
GGCATGTGTCACCCCCTGAGGAGCTGTGCCCTCAACCATGAGGATGGCTT
CTCCTCAGCCTTCGTGATAGCTCATGAGACCGGCCACGT

1602. chr10_CDH23_NM_022124_1.60452
GAGGTCTACGCCACGGACAAGGATGAGGGCCTCAACGGGGCGGTGCGCTA
CAGCTTCCTGAAGACTGCGGGCAACCGGGACTGGGAGTTCTTCATCATCG
ACCCAATCAGCGGCCTCATCCAGACTGCTCAGCGCCTGGA

1603. chr10_ASCC1_NM_015947_-1.54185
GTGTCTTTCTGCAATATCGTGAGGGAAGCCGAGGCCCTGAATCATCAAAG
AGA

Figure 3-131

1604. chr10_OIT3_NM_152635_-1.99702
ATCACAGGCACCTCCGTGTCACCCGTGG

1605. chr10_TTC18_NM_145170_-1.50631
AGCTCCTCCTGTCCGACGGGTAAGAGGAGGCCTTGGAGGAATCATTTCCT
T

1606. chr10_SYNPO2L_NM_001114133_1.61102
GCTTGGCCTATGGCCCCCGGAGTTTGAACAGTGTCCCCAGGAGAGAAGTT
GAGGTGCTCGAACCCCGTCTGGGCT

1607. chr10_CAMK2G_NM_172171_-1.74901
TCCATCCCCTCCACGAGGTTACCAAGGGCCTCAGGCT

1608. chr10_ZMIZ1_NM_020338_2.35344
AGCCTTGGAGGAGCACTGGCAGTT

1609. chr10_MAT1A_NM_000429_1.57429
CTTCGTCCAGGTACTTGGCCGGCACCACGGCCCTGATGACTTGCTCCTTC
AGGGCCCTGCGCATCTCCTCCAGCGTGATGTCTTCGTTGTGCTGCACAGA
GATGACGATGGTGTGGATGCGCACAGGGATGACTGCGCCA

1610. chr10_TSPAN14_NM_030927_1.93021
GGAGTTGTCTTCCTTGGAGTCGGGCTGTG

1611. chr10_CDHR1_NM_001171971_-1.65621
ATTCTCAGAAATCCTCCCTAGACCATTTTCCCTCTC

1612. chr10_RGR_NM_002921_1.64528
GCCCACTGGCTTCGGGGAGCTCGAGGTGCTGG

1613. chr10_GRID1_NM_017551_-1.65387
TCCCCCGGGCGCGCGGCTCATCCACCCGGGCCCGGGGCGAGGCCGAGGGC
AGCGCGAAGCGGGGAGGCG

1614. chr10_LDB3_NM_007078_1.61439
CCAGCTACAGTGAGGGCCCCGCCGCCCCTGCACCCAAGCCCCGGGTTGTC
ACCACTGCCAGCATCCGGCCTTCTGTCTACCAGC

1615. chr10_MMRN2_NM_024756_-1.533
GCACCTTCTGCTTGACCTGGTACACT

1616. chr10_CFLP1_NR_028492_-1.8177
AGGACTGCCGCTACGCCCCTTATGACGCCACCAAG

1617. chr10_PTEN_NM_000314_1.80698
GGTCTCTCCCCTTCTACTGCCTCCAACACGGCGGCGGCGGCGGCTGGCAC
ATCCAGGGACCCGG

1618. chr10_SLC16A12_NM_213606_-1.50877
TGACATGAGTAAAAAACTGTACTCTTGCTGCAAACAGCAACAGAGGCAAG
TCTGTGCCCATTCTTTGGTCAAAGATGAATAGGGAGACACCCGCTTAATG
TCTTCTTTCT

Figure 3-132

1619. chr10_FGFBP3_NM_152429_1.51836
GGCGACAGCGACGCTCGCAGCTTCGGAGGA

1620. chr10_PLCE1_NM_016341_1.51476
AGAGCAACCTCGAACAGTCATCAAAGCACCCCGCGTCAGCACTGCACAGG
ATGTCATT

1621. chr10_SORBS1_NM_001034954_1.58938
ATCGTCTATATTGAGGAGGTCCCCAAAGCGCTCATTAGTGATAAACTGAT
GGTGCGTCGGAATGACGCCTGTGTGGCGTCGAGCTGCAATA

1622. chr10_SORBS1_NM_006434_-1.97691
TGCATGGAAGTTGGAAGAATATAT

1623. chr10_BLNK_NM_013314_-2.16545
GTGAACCGGCCTGGTTTCCTGCTCTACTGGAGGCGGCTCGTAGCTGTCAT
CAGCGTTCTCCTCGGCGGGCATCACGTACATCTCTGAG

1624. chr10_DNTT_NM_004088_-1.56211
TGAGAAGAGACTATTCAGATAGCACCAACCCAGGCCCCCCGAAGACTCCA
CCAATTGC

1625. chr10_TLL2_NM_012465_-1.50536
CGTAGCCGTCGTAGGCTTCCATGTAGTCGTAGCCGCAGTCGGCCTCCTCC
TCAACCTCAAAGGTCCGGAATGTCAGCTCCACGCCGTAGCCGTCCTCTGC
CACGATCACCCAGTCACAGCGGGCCTCGCTCGGGTAGTTGTTGTCC

1626. chr10_TLL2_NM_012465_-1.56871
CACTTCAAACTGAAGGGAGATCCGGTACTGAGCGGGGGCCACCACCTGCC
AGACACAGTTTTTGTTTGTGGGATACTCCTTCGGCCACCCAGGGCTGGTG
ATGGTTCCATTCAGCTTGGTAATGAAACCGCCACAGG

1627. chr10_FRAT2_NM_012083_1.73937
ATGCGGTCAGGTCCGCTGCGGCCTCCCCCGGGCCCAGGGGCGCTTGCGGG
GCCCGTGGCTGCAACCGCGGCGACGGCTCGTTGGAGTCTCCGCACGGCTT
CCTTGATGAGGTTTCCCGAGAGCACGAGCTGCTGGAGGAGCCGATGCGGG
TCGTCGTCGCCGGCGCGTGCCCCGGCTTGGGTCCATCGGCGCTGCTGCAA
GCGGC

1628. chr10_MMS19_NM_022362_-1.64374
TCAGAAACTTGGTGACGAGGGTGTCCACGTGAAGACTCATGACTTGGGGT
GCTTCCAG

1629. chr10_HPS1_NM_000195_-1.82461
CACTCTGCCCTATCCTCAGGATGGCCACTGCAGACAGGAGGCTCTCGTCA
TGGGGAACAGTGGCAAGCAAGGGTGGCTGGAGGACAGGATGCAAAGGCAG
ACTGCGGCCACCTTG

1630. chr10_GOT1_NM_002079_-1.66834
AGGGTGCTGGCCACAATTCGTGCTCCCTGGGCGGGGGGATTGGACCAAGT
AATCCGCACGATCTTCTCCATCTGG

1631. chr10_NKX2-3_NM_145285_-1.54898
TGTTACCAAGCCCGGTCACCTCCACCCCTTTCTCAGTCAAAGACATTTTG
AATCTGGAGCAGCAGCACCAGCACTTCCATGGTGCGCACTT

Figure 3-133

1632. chr10_ENTPD7_NM_020354_-1.56908
CAGGTCTGAGTCCCGACAATCCATTTCTGGATCCCTGCCTGCCAGTGGGA
CTCACAGATGTGGTGGAGAGGAACAGCCAAGTCTTACATGTCCGAGGAAG
AGGAGACTGGGTGTCTTGTGGGGCAATGCTGAGCCCCC

1633. chr10_COX15_NM_078470_-1.68126
AGCAGACGAGGCCACAGAGGGCAAGAACACGTCCTTTCATGCCACGGCTG
AGCCAGCCCTTTCTCCAAAAGTAGGCAGCAGGCAGGATGTACACAAGGCC
TACAAGGCGACCCCACATTCGGTGTGAGTACTCCATGTACCAGATGAACT
TGA

1634. chr10_PKD2L1_NM_016112_1.74124
CAGGTGCCCACTCTCAGCTAGAGGAAGAGGGAGCAGAGGCACAGCCCAGC
CTAGCCAGCAGAGAGCAAATGGAAAGGCGTCTGAGAGCAGCTGTTTCCAC
ACAGCCTGGGCTCCTGCCTTTTGTAGGGGGATGTCTGTGCCTGCTGGGGA
GGGAGCGGATGAGAGGACAGGGTGGGGAAGGACCATCAATCCTGTCAGGA
G

1635. chr10_FAM178A_NM_018121_1.51677
ATTCTTCTTCATTTAGTCGGTGAAGTTAGTTGTT

1636. chr10_LZTS2_NM_032429_-2.06102
TCAGCTGCTGACAAACCCCTGGCATTTAG

1637. chr10_PDZD7_NM_024895_-1.51034
AAGGTCAGATAGCTCTGGGAGCGCGTGATGGGGGGCCGGGGTCGGCTGAG
GGCCAGCAGCAAAGCCGTCTTGGGAGACTCAGAGAGCGCAGAGTCAAGGC
GGCGGCCGGGATGGGGGCCGTCCGAGCGGATGGCGGTGTCCCTGAGGATG
ACTGTGGGCCGCACGCTGCACCAGGTCTCCACCCGGCCTCCCGCATCGGG
CTCCGTCTGCATGGCTGTGTCCGCCCGCCCCCAGCCTGGGCCGCGGCTGC
CGGGCTCCTCCTGCCCGAGGCAGATGTCCATGCGGTCCGACGGCAGGGAG
CCCGAGCTGTAGGGGGCGCTGGAGGCGCACGAAGAGACGCTGGAGCTGCT

1638. chr10_BTRC_NM_033637_-1.61429
GGATCCGGGCGCTGCGTTGGCTGCGGCCTGGCACCAAAGGGGCGGCCCCG
GCGGAGAGCGGACCCAGTGGCCTCGGCG

1639. chr10_POLL_NM_001174084_1.54158
CCCAGCTCCCCAGATGTTGGAGAAGAGCTCCAAGACAGGCACGCTCTCAC
TGATATGGTCCAGCTTCCGCAAATGCCCGCTCTCCAGGATCTCTATGATT
TTCTCAGCC

1640. chr10_FBXW4_NM_022039_1.54426
CGGCAGCGCCCCAGTCTCCAGTTCTGAGACACCTTCACTCGTTCCTTCAC
TGG

1641. chr10_KCNIP2_NM_014591_-1.93736
CCTGGCGGCCTACTGTGCTGTCGGGGCTGGGGAAGTCCGGGCTGAGGCTG
AGTCTGGGAATGGGCCCGGGGTCTGAGGTCTACCCGGAGGTCCTGGAGCA
GGAGAGGGAACACTAGGCAGCAGGTGAGCGCAGAGCCGGAGGCAGAGCGG
AGCTGAGCGCGGAGCCGAGCCGAGCTGCCTCTCTCCTCCCGCCCCCTCCC
CGCGGCTGTCACCGCCTCCTCCCCTCTTTGGCGCTGCCGGGATTGGCT

1642. chr10_INA_NM_032727_1.51108

Figure 3-134

TGAGCTTCGGCTCGGAGCACTACCTGTGCTCCT

1643. chr10_TAF5_NM_006951_1.93853
ACGCTGCTACCTCCGCAGGCGGGGGACGGCGCAGGCGAGGGTAGCGGCGG
CACTACCAACAACGGCCCCAACGGCGGCGGCGGGAACGTTGCGGCGTCGT
CGTCCACTGGCGGGGATGGCGGGACCCCCAAGCCCACGGTGGCTGTCTCC
GCCGCTGCCCCGGCGGGGGCGGCCCCGGTGCCCGCCGCTGCTCCGGACGC
CGGCGCTCCGCATGACCGAC

1644. chr10_CALHM1_NM_001001412_1.52347
GAACTCAGGTGTGCCTGACCCAAAGCTTTGCTCTTCATCACATTTGTACC
TCCTGATACCTCCGGGCCTTCTCTTCCCACTGGAAGTGCTGCCACCCACC
AACATACACCTTGTTTTTTGCTCATCCTAATCCTCCCTGACTTCAGGGCC
CATACCAACTCCTACCTCCTGGAAGAGCCCTCCCAGCCCACCTTGGCCCA
CAAAGATCTGAGCAACTCCTCCCAAATAATTAAGAGGAGGGAAACTGGAC
CCCAGAAGTGGGAATAGAGGGAAGGATGGATAAAAAAGGATGGAATCATG
CCAAGATCAAAATGAATCCTTAGATGCTTGGGACTTATGTCTCAGAGCTG
AGGGCGGTGCTGAGAAACCTATCTGTA

1645. chr10_SH3PXD2A_NM_014631_-1.73104
ATTCTCTGCGTGGTGGAGGTCTTGTCCGTAGGTTC

1646. chr10_OBFC1_NM_024928_1.5962
AGTCCTGCTGAATGATCCGGTGGATCTTTCTGTGCAGG

1647. chr10_C10orf79_NM_025145_-1.58854
GACTTCCAGAACTCCTCCCATCATGTCCA

1648. chr10_GSTO2_NM_183239_-1.52891
AGCGGTGGCGAGCCACAGGGCGGCGACCGTGAGCTCCGGGAGCTGCGCAA
ACCACCTGGAGA

1649. chr10_DUSP5_NM_004419_1.58241
AAGGTCACGTCGCTCGACGGGCGCCAGCT

1650. chr10_ADRA2A_NM_000681_-1.81702
CTGGCCGTGGTCATCGGAGTGTTCGTGGTGTGCTGG

1651. chr10_TCF7L2_NM_001146274_-1.75844
CGGCTACCCCTTCATCATGATCCCCGACCTGACGAGCCCCTACCTCCCCA
ACGGATCGCTCTCGCC

1652. chr10_NRAP_NM_006175_-1.53161
AGGTCCTCGGGCAGTGCTGTGAACTTGTGATACTGTGTCCTGTAGTCGTG
GTCGCTGGCCAGAGCCT

1653. chr10_ADRB1_NM_000684_1.59948
TGAAGAAGATCGACAGCTGCGAGCGCCGTTTCCTCGGCGGCCCAGCGCGG
CCGCCCTCGCCCTCGCCCTCGCCCGTCCCCGCGCCCGCGCCGCCGCCCGG
ACCCCCGCGCCCCGCCGCCGCCGCCGCCACCGCCCCGCTGGCCAACGGGC
GTGCGGGT

1654. chr10_TDRD1_NM_198795_1.62918
CAGGAGGGCGCACTGGGGATTGGAGGCGAGGGAAGTGCAGGGCGCATCCC
AGGCGGCAGGGCTCCCAGCATCGGCAGTCGCCAT

Figure 3-135

1655. chr10_FAM160B1_NM_001135051_1.56598
AATCTTGGGCCTTGGATCAACTGCCCACCCTTGAACCAATCCTGGTGGCC
CCAGGCTGATTGGCAGACCTGAATCACCTATCCCATGCCCAGAACTTTGG
CTTGACCAGGCTCATCCAAAACAAGGG

1656. chr10_ATRNL1_NM_207303_1.52664
CTTCGAGAACGACAGCAGATGGCCAGCCGTCCCTTTGCTTCTGTTGATGT
AGCTCTGGAAGTGGGAGCTGAACAAACAGAGTTTCTGCGAGGGCC

1657. chr10_GFRA1_NM_005264_1.54844
TAATTCGTCTTGCAGGAGTCCTGCAAATTCAAACAGTTGGGCTTCTCCCT
CTCTTCATAGGAGCACACAGGCACGATGGTCTGTCGCCTCCGCTCTGTGC
AGGCGATGTCCCGGCAGGAGCAGAAGAGCATTCCGTAGCTGTGCTTGGCC
GGGACCTTGTCAAAGAACTGCCGGAGGGCCTTGTGGCACTTGCGGCGGTT
GCAGACATCGTTGGACACGCTGGTGGTGCACGGGGTGATGTACGCCGACC
TGTACTTCTTGCAAATGTCGTCGAGGTTGCAGGCCT

1658. chr10_PNLIPRP2_NM_005396_-1.50573
GTCCCGGGCAATGTACACCCAAGCCGTGCAAAACATTCGGGTTGTTGGGG
CGGAGACAGCTTTCTTAATACA

1659. chr10_RAB11FIP2_NM_014904_-1.5263
AGATTGATTGCCACCTGCCCTAAAAATTTATCCAGACCCACCAGGGACCT
GTGCATAACTATAAGGAAAAGAATGTATTTCTCTGGACTTCCCTGAATTA
GCAATCCAGGTAGCTCGAAAGAGGCCTCCTCCTTCCAAACTGGCTCAAGG
GTTTTCTCAGCTACAGAGGTGGAGTACTTTTCCTTGCCCAGCTGAATTAT
AGTGTATGTGTCATTGGTACCACTTTTGCCTTTTGGCTTCAGATCTTTGG
CTTGGAGCACTGTGACCTGCACGTGGGTTGGAAACCACTTTTGGGCTTGC
TCGGACAGCA

1660. chr10_EIF3A_NM_003750_-1.66764
ATCTGAGTGGAGGTCCTCTTCGGTCCCTGTCGTCTCTTAGATCTCGTCTT
TCTCTTAGATCACGCCGGTCA

1661. chr10_GRK5_NM_005308_-1.50573
GTGCAGCCACTGTTAAGCCATGTGTTCCAAGGCATTTTAGCGGGGAG

1662. chr10_INPP5F_NM_014937_-1.75138
AGAAGGTGTTATTGGGAAAATTCA

1663. chr10_SEC23IP_NM_007190_-1.51002
AGAAAACCTAACGGTGGCAGCGGCGGCGCCTCCACTTCCTCATCGGGCAC
TAACTTACTTTTCTCCTCCTCGGCCACGGAGTTCAGCTTCAATGTGCCCT
TCA

1664. chr10_TACC2_NM_206862_1.57467
TCAGTCTCCCACCAGACGGTGCAGCAGCTGGTTCTGGAGAAGGAGCAAGC
CCTGGCCGACCTGAACTCCGTGGAG

1665. chr10_FLJ46361_NR_003570_1.58816
TGAAGAGAGATGAGCTACCCACACCTTCTATGTCTT

1666. chr10_PSTK_NM_153336_-2.49907
TGAAGACCGCCGAGAACATCAGAG

Figure 3-136

1667. chr10_PSTK_NM_153336_-1.75455
GACCATCCACCTGATGGGAAGAAAGCTAGAAAAGCCCAACCCTGAGAAAA
ATGCTTGGGAACACAACAGCCTCACAATTCCGAGTCCAGCATGTGCTTCG
GAGGCCA

1668. chr10_METTL10_NM_212554_-2.01
CCTGGACGGCCGTTGGGGCCGCCAT

1669. chr10_CTBP2_NM_022802_1.55069
GCCTCCGCAGCTGCATTTCGGTCCTGCA

1670. chr10_DPYSL4_NM_006426_-1.57334
TCGTGTTTGGGGAGCCCATCACCGCCAGCCTGGGCACCGACGGTTCACAC
TACTGGAGCAAGAACTGGGCCAAGGCCGCAGCCTTCGTCACATCACCCCC
TGTCAACCCAGACCCCACCACGGCGGACCACCTCACCTG

1671. chr10_C10orf93_NM_173572_-1.61758
ATACTGTAGCTGTCTGCAGGTAACAAACTGCAGAAAGTGAACTGCGGGTA
ACGAGGCACTGCCGGTGTGATTTACACGTCCAATAATGGGACTGGTGGAG
GATGTTCTGGATCATCAGCATCATGAAATTTTACGCCGTCCGTAA

1672. chr10_KNDC1_NM_152643_-1.84703
GGCCCTTCCGGGAGTACGAGCTGTGGGCCCTGTGCCTGGCCTGCCTCCGC
GCACTGCAGACACGCCCTGAGCACCCAG

1673. chr10_KNDC1_NM_152643_1.70014
CTCCAGCGAGGCATGGACAGCCGGAAAATCCTTGCCCACCTCAGAGCTTC
CATCTGCC

1674. chr10_KNDC1_NM_152643_1.77961
GCTTCAGCGGTGCCGACATTTCCACACTCGCCGCAGATAGCAGGGCCAAC
TTCCACCAGGTCTCCAGCGAGAAGCACTCACGGAAGATTCAGGACAAGCT
ACGGAGGATGAAGGCTACATTC

1675. chr10_VENTX_NM_014468_-1.51491
GCATCAAGGAGGCCGCCGGGTCCTCAAATCTGC

1676. chr10_ADAM8_NM_001109__1.59171
CGAAGCGTTCCTGGCAGCGGCAGCCCTGGACGTTCTCATCATGGTCCATG
CCCAGGTTGTGGCCCATCTCATGGGCCATGGTACAGGCCACGC

1677. chr10_ZNF511_NM_145806_-1.98709
ATACCCTCTACCATCTGCTTTGGTCAGGGTGCCGCTCGAGGATTTAAAA

1678. chr10_C10orf125_NM_001098483_-1.82831
CCGTGCCCCATCCGCGCCAGCGCGTAGAGCAGCTCGGGGGACAGC

1679. chr10_ECHS1_NM_004092_-1.57035
TGCTTGCTTGGCGTCCTGGGCTGAGATCCGGTCACCAGTGAGGACCATCT
CCATCGCCAGCGACTTCCCAACAGCACGGGTGAGTCTCTGGGTGCCGCCC
GCAC

1680. chr10_PAOX_NM_152911_-1.76867
AGCTGGCTGCTGAGTACGGGCTGCTGGGGGAGAAGGAGCTGTCCCAGGAG

Figure 3-137

AACCAGCTGGTGGAGACCGGGGGTCACGTGGGCCTGCCCTCCGTGAGCTA
CGCCAGCTCCGGGGCCAGCGTGA

1681. chr11_B4GALNT4_NM_178537_-2.14147
AGACGAGGTGCAGCGCCGAGCCTTCCTCTT

1682. chr11_PKP3_NM_007183_1.87529
ACGGTAACTTCCTGCTGTCGGCCCTG

1683. chr11_PKP3_NM_007183_1.62285
CCCTCAGCAGTCAAGTACCTCATGGCTTCAGACCCCAACCTGCAGGTGCT
GGGAGCGGCCTACATCCAGCACAAGTGCTACAGCGATGCAGCCGCCAAGA
AGC

1684. chr11_PKP3_NM_007183_-1.5604
GTGGAACCTTTCATCCAGCGACCACCTGAAGGACCGCCTGGCCAGAGACA
CGCTGGAGCAGCTCACAGACCTGGTGTTGAGCCCCCTGTCGGGGGCTGGG
GGTCCCCCCCCTCATCCAGCAGAACGCCTCGGAGGCAGAGATCTTCTACAA
CGCCACCGGCTT

1685. chr11_SIGIRR_NM_001135054_-1.64299
CATCCTTGGACACCAGGCAGTAGAAGTCTGTGCGGGCACTGTAGTTTCGC
GAGCCGAGATCCGAGACGTCCACTTCGCTGCTCCGGCTCTCTCCCAGCGA
GACCCCACTGGTGTGCGGTGGAGCTGATGGCTCTCCAAAGACAGGCCCC

1686. chr11_LRRC56_NM_198075_-1.73478
CTGCCCAACCTGGACCAACTGAAGCTG

1687. chr11_C11orf35_NM_173573_1.5999
TGTTTTCAGAGAGGTCGCTTGGGTCCATCAGAGTCTCTG

1688. chr11_IRF7_NM_001572_-1.6864
GGTGTCACAGTTCCGAGGCAGCAGGCAGGCTGGGGTGGAGGGGCTGGCGG
AGCCTGGGGGTCCGCCCACCTCCCAGTACACCTTGCACTTGCCCATGCGC
CGGGCCCACAGCTGTGGCCCCCGAAGCTCCAGGTGCAACCCAGGGGCCAC
GTGCCGCAGCAGTTCCTCCGTGTAGCGCAGCTGCTTCTGGTCCGGGAGCT
CGGCAGGGCTGGGGAATGCTACCTGCTGGGGGTCTGTGGCCCGGACAGCT
GGGTCTGGGGGGCCGTATAGGAACGTGCAGCTCGGGT

1689. chr11_CDHR5_NM_021924_-1.60791
GGTGTTTGAGACCACCGGCTCCCAAGTGCGTCGCCTTGGGGGTTTGCATC
GGCTCCTCAGCCTCCCCAGGCAATCTCTGTGTAGGGTCGGGAGCGGGAGG
TCTGAGATGAGCCGGGTGCCTGAGATCTC

1690. chr11_CDHR5_NM_021924_-1.96419
GGGCATCGGCTGAGAGGTTCCTGCCT

1691. chr11_SCT_NM_021920_-1.6198
TGCAGGATGGGCATGTTGGACCCTGACGGGCAGAGCAGACCCGCGCT

1692. chr11_EPS8L2_NM_022772_-2.06692
TTTCCGCCGTCGGGAGTCGCAGGAG

1693. chr11_EPS8L2_NM_022772_1.71556
CGGCAGTGGTGGAAGCTGCGCAGCCGCAGCGGCCAGGCGGGGTACGTGCC

Figure 3-138

CTGCAACATCCTAGGCGAGGCGCGACCGGA

1694. chr11_LRDD_NM_145886_1.6019
GGCCAAGCCCATGCGTCGGATGCTGTCCTGGTAC

1695. chr11_LRDD_NM_145886_2.21766
CAGCTGCACGGTGACCGGTTGGAGGAAGCTGGGGGGACCGCTCTGTGACA
GGCACAGCAGGGGGCTCACTGCAGCCTCTGGTTCTCCCAGGAGGGCCTGC
AGCTCTCGGCCAGCCATGCGCACCA

1696. chr11_KCNQ1_NM_000218_-1.60969
CTGGAAGTGAGCATGCCCCATTTCATGAGAACCAACAGCTTCGCCGAGGA
CCTGGACCTGGAAGGGGAGACTCTGCTGACACCCATCACCCACATCTC

1697. chr11_SLC22A18_NM_002555_-1.69507
CCCGGATCAACTGGACTTTTGCCCCCTGCTCCGCCA

1698. chr11_SLC22A18_NM_002555_1.70448
GTGTTCGACCTGAAGGCCATCGCCTCCCTGCTGCGGCTGCCAGACGTCCC
GAGGATCTTCCTGGTGAAGG

1699. chr11_OR52A4_NM_001005222_1.82938
TATATGGGGAATACATGTATTAAA

1700. chr11_HBE1_NM_005330_1.74107
ACAGAAGGCTTTCTCTCAAGGCCA

1701. chr11_OR52B6_NM_001005162_-1.50362
TGCTGATGTCTTGCTCTCTACCACCAC

1702. chr11_FAM160A2_NM_032127_-1.52192
CCAGGCTGAAGGACCAATTGTGCCGCCTGCCGGGCCCTGGTTGGACTGTG
TGCATGCCGCAGGAGTAACTCCC

1703. chr11_APBB1_NM_001164_-2.55423
GGGAAGGTCAACGTCCCCTCCTCA

1704. chr11_CYB5R2_NM_016229_-1.65883
CCAGCAATCATTCCCAGGTGATCGGCCAGTGTTTTTTTAGGCTCACTCGT
CTGGTCTGGTCTGATTCCAAGATTCC

1705. chr11_RPL27A_NM_000990_-1.51299
CCTGGTGGCTCCATCGGCCGCGTTCATCAGTCAGCACGACCCGACCTCAG
TGGCGTCCTCACAACACAGACCGGACCTTGGGTCTT

1706. chr11_AMPD3_NM_000480_-1.68106
CCTCCCTGCTGAGGCGGCCCTCCCTCCTCCCGCGGGGCCCTCCTGGCCGG
GGATCCGCAGCGCTGCGCCCTCTGAACGCCCGGCCCCCGCGCCTGCTGCG
GGGCGCGGCCTGGCCGGGCCCTGGCCCCGGCTGGCCTCAGTGCCCAGCAG
CCCCGCTCCGCTCTGCCCAGCGCGTCCCCTTTGCTCCA

1707. chr11_MICALCL_NM_032867_-1.51302
GCCCAATCGGCCATCCAAGGTCTTTCCTGCA

1708. chr11_MICALCL_NM_032867_-1.81435

Figure 3-139

GATTGAAGATGTCCCCACACTCCT

1709. chr11_PDE3B_NM_000922_1.50196
GCGACACTGAGTCTCCAGTCCCGAGAGGTGCCCGAGGGAAAAGGAGGCGG
CAGCTAAACTGGTCCTGGAGAGAA

1710. chr11_PDE3B_NM_000922_-1.51176
TTGAACAGGAAGTATCACTGGACCTGATTTTAGTAGAAGAGTATGACTCA
TTAATAGAAAAGATGAGCAACTGGAATTTTCCAATTTTTGAACTTGTAGA
AAAGATGGGAGAGAAA

1711. chr11_SOX6_NM_017508_-1.52522
CAATGGGGCTAGGGATGCTGCTTTTGTTTGGCAGATTGACAGGGCTGGTT
TTGCTGGCTGGGAAGAGGTTCTGGGTGGGAGACGTTGGGGACTTTACAGG
CTCTGCTGTCTTGGGTCGGGATGAGAGATTCAGA

1712. chr11_RPS13_NM_001017_2.63185
GATCTGTGAAGGAGTAAGGCCCTT

1713. chr11_MYOD1_NM_002478_1.57584
GGCGACTCCGACGCGTCCAGCCCGCGCTCCAACTGCTCCGACGGCATG

1714. chr11_---_---_-2.95742
AAATAGCAGCCACCGCTCCCTGGCA

1715. chr11_GTF2H1_NM_005316_-1.52756
CTTGTTGTGAGTCAAGTGATCAGT

1716. chr11_UEVLD_NM_001040697_1.5265
AGGCCGGTCCCGAGCTAGGTCCCAGGACTCC

1717. chr11_SPTY2D1_NM_194285_1.65377
AACAGGTTTGTCGTGGCCCTCACGAAGTGAGGGTTGGGAGCTATTGCCAG
ATCCTGCCTTGATCCTCTCTCCTGGCATGGATTTGGATGAAGACAAAGCG
AGGTGTTTCTCATTGGCCATGCTGGGTCTTGATTTCTTCTCAGCATGAGG
AAGGGGCATTCCTTTGGAAGAAGGATGCCTGTCTCCAGAACCTTTGCTAA
GTTTTGTGCCCACACTTTCTTTCTGAGAGGGTGCCTTTTTGGACACAGTT
GGAGGTAGTTTTCCATCTGTCTCAAGTTTTTTTCTCCTATGCTTTCGTTC
AAGGAATTCTCGCTCCCTAAGTTCTTCTGCGGTCATAGGTCGCTCTTCTG
ATTTCTTCACTACCTTGATTTCCACTGGTTCAAACTGCTTTTTCTCAGCC
AGCCTGAGTAAATCAGTGAAGTTCATGGGTGGTGGGGCACTTTTAAGGGG
GACCTTTGGTTTGCTTTCAACTTTGGGAGGTTCTTGCTCTTCCTCATACT
CCTGCTCTGACTCTGCGTGATTGTACTCGAGGAATTCATTCTCTTCTTCC
ATTTCATACTCTCGGTCGGTTCCTTGGCTGG

1718. chr11_NAV2_NM_182964_2.32863
CAGCAGGTGCCAGTCACTCCCCAAGC

1719. chr11_NAV2_NM_182964_1.62677
GACCCGCACCTTGATAGGAACACTTTGCCT

1720. chr11_LUZP2_NM_001009909_-1.54861
GAAAGAGCAAAATGATCCGAGACCTCCAGAATG

1721. chr11_KCNA4_NM_002233_1.62111

Figure 3-140

AAGCTGCTCTGCCGGTAGTGGGCTTTCTTCT

1722. chr11_PRRG4_NM_024081_-1.50055
TTGTCTCCATTGCCGCCTTCTGTGGAGGATGCAGGATTACCTTCTTATGA
ACAGGCAGTGGCGCTGACCAGAAAACACAGTGTTTCACCACCACCACCAT
ATCCTGGGCACACAAAAGGATTTA

1723. chr11_PRRG4_NM_024081_1.69674
AAAAATCTATGTCTCTCCCATCTCAC

1724. chr11_SLC1A2_ENST00000395750_-2.16516
CTGACATCTAACCTCTCCTCCCTG

1725. chr11_PRR5L_NM_024841_1.56959
TGTGCGCGACTCGGGGTGATTCACGCCGGGGA

1726. chr11_PRR5L_NM_001160167_-1.53357
TGACCCGCGGCTTCGCTCCCATTCTGCCCGTCGAGTTCCACAAGATGGGC
TCCTTCCGCAGGCCTAGACCGCGCTTCATGAGCTCCCCCGTGCTCAGCGA
CCTTCCCCGATTCCAAGCAGCTCGGCAGGCTC

1727. chr11_EXT2_NM_000401_1.55382
ATGTCCTGCGCCTCAGGGTCCGGTGGTGGCCTGCGGCATCCCTTGCGGTG
CCAGAAGCCGTGGGACGA

1728. chr11_CD82_NM_002231_1.54902
CGCAGTGATCCTGGGCTTCGGGGTGTGGATCCTGGCCGACAAGAGCAGTT
TCATC

1729. chr11_TSPAN18_NM_130783_-1.81885
CTCCTGGACCACCCTCAAGCTTCAG

1730. chr11_TP53I11_NM_006034_-1.97715
CAGATGGGGGATTGAGGCTTCGGCCTGAGGGCACTGCCCATTGGCGGCAC
CACCTGTGGG

1731. chr11_SYT13_NM_020826_-1.56586
GTGCCACATGGCAATCTGCCGGCGAGGGTTTTTGAGCA

1732. chr11_PEX16_NM_004813_-1.73297
CTGTCCAGTGGAACGATAGGGGGTGAAGTCTGGAGGCCAGCCTTGAACCA
GAGCAGCAGGAGCATCCGCAGTACAGCC

1733. chr11_PEX16_NM_004813_1.8836
TGGCCAGCTGGACGAGGGCGATGACAAGCCAGCGGCCCACTTCACCCCAC
ACCTTGGCAGCTCCCATCTCCATGAACACCTCCACGCACTCCAGCA

1734. chr11_AMBRA1_NM_017749_-1.65883
TGGATGCCAGAAGAGCGGGAGGACAGCATGTGCAGGAAATTGTGGAGGAG
AGGCGTCCGGCGAACTGGCTGTGATTGCAGGAGGGCACGCTGACGGTAGT
GGGATAATTCTGTTCCATCTATG

1735. chr11_ARHGAP1_NM_004308_1.69754
TGCACTTCCCGGACCACTTGGGTGTTGGCCGACCTCCGGAAGATGCCCTC
GGTGGTG

Figure 3-141

1736. chr11_PACSIN3_NM_016223_-1.6357
TGAAGAAAAGAAGCCGCTGGCGCTCGGCGGCCTGGCAGGTCTCAAAGGCC
TGTTCCATGTCCTCCATGTAGCGTGGAGTGTAGCGATGCAGCTCTGCCAG
CGTCTGCTCATACTGAG

1737. chr11_PACSIN3_NM_016223_1.59676
GCGTTCCACCCGTTCCTGCAGTTTGCGCAGCTGCTCCTGGGAGACGGCGC
TGTCTGCCTTTGCGTGGCTCTCCCTCGTCTGGGCGGTCTTCTCATCCTTC
CGGGCTGCGTGGTAGCTTTTCTTGGAA

1738. chr11_MADD_NM_130470_1.53854
ATGCAGAAGTGCTGCCTATCCTGCCAGAACCAGAATCACTAGAGCTGAAA

1739. chr11_MADD_NM_130470_-1.78974
ACAGCATGGAGCGCGCTGCCGCCCGACAGCAAAGCATCAA

1740. chr11_OR4C12_NM_001005270_-1.74792
AGTGTGTAGACCACGGGATTTAACATTGGGACCACCATAGTATAAAATAC
AGCAACAGCTTTATCAATGGGCAGAGTGGTCACTGAGCGCAGATACACAA
ATATACAGGGCACAAAGAATAAGACAACTACTATGATGTGAGAAATACAG
GTGGAGAGGGCTTTACACCTCCCCTCCAAGCTATTGTTC

1741. chr11_OR5AS1_NM_001001921_1.64401
TAAATCGTTTAAGAATAGTCAATA

1742. chr11_TNKS1BP1_NM_033396_-1.54077
GCTGCCATAGGTGCCGAGTGACACATCTCTCTTCTGAAACTCCCAGTCCT
GCTCATCGGCATCCTGGCTGCTGTACCTACCATGGTGGTCCCTCTTCCCC
AAATCTTGGCCCTGCTCGTTGGCATCTTGGCTGGCATAAGCACCCAGAGA
ATCTCTCTTCCCAAATTCCCAGTCCCCAAGGCTTACATCTCGACTACTGT
AGGTACCCAGTGAATCTCTCTTTCCGAATTCCTGGTCCTGGAGTTCTGCA
TCCCGGCTGGAGTAAGTGCCCTGGGAATCC

1743. chr11_TNKS1BP1_NM_033396_1.50036
CCTCGTCAGGCAGGGCTGCACTTGGAGCTGATGGAGTCACAGCGGGGCAG
GGAGAAGCCTGGGAAGCTTCAGGAGTCTGGGCTTCCAGAAGCTGTGAGTG
GCAGGGAGAACTCTTATCAGGCGGGT

1744. chr11_SLC43A3_NM_017611_-1.5322
TCTCTCCCAGTTTCACACTCCCAGAGC

1745. chr11_RTN4RL2_NM_178570_-1.7762
CTTGTTCGCGGACCTGGCCAACCTGAGCCACCTCTTCCTCCACGGGAACC
GCCTGCGGCTGCTCACAGAGCACGTGTTTCGCGGCCTGGGCAGCCTGGAC
CGGCTGCTGCTGCACGGGAACCGGCTGCAGGGCGTGCACCGCGCGGCCTT
CCGCGGCCTCAGCCGCCTCACCATCCTCTACCTGTTCAACAACAGCCTGG
CCTCGCTGCCCGGCGAGGCGCTCGCCGACCTGCCCTCGCTCGAGTTCCTG
CGGCTCAACGCTAACC

1746. chr11_SLC43A1_NM_003627_1.57846
CCTGGCCACCAGTCACAAGGTACTCCAGCATCTTGTTCACAGCAGCCATG
TAGAAGATGATCCGCAGCTGGGTCATGCCCATGGTGAGGAGGCTCCACAG
GAAAGTGGGGGAGCAGAGGCTCTTGCGTAAGGGGACAGACC

Figure 3-142

1747. chr11_SERPING1_NM_000062_-1.94349
GGCCGTGTTGGGGGATGCTTTGGTA

1748. chr11_ZDHHC5_NM_015457_-1.60695
CCCGGCACTGAGGGCAACGGCCGCGCGCCGGCTCCGAGACGAGCGACGCC
TGGCGGGAGCGCG

1749. chr11_ZFP91_NM_053023_-1.50779
AACAACGGCCCCCTGAGGCGGTCGCGG

1750. chr11_GLYATL2_NM_145016_1.64626
GCTTCTTTCCCTCAAGAAGATGAT

1751. chr11_MRPL16_NM_017840_-1.53442
CGCAGGAGCGGCGCACTAGCGCGAGCCAGCA

1752. chr11_GIF_NM_005142_1.53304
CTTCAAGTTGTAGGCTCCGGCCAGATTCATGGCAATCAGGATGCTGGGGT
TTGGGTAGGCTGATGAAGTCACCGAGTTCTCCATGAGTACTTGTATTCCA
TTGACCAAGGGCTCCTGT

1753. chr11_CD6_NM_006725_-1.83003
CGCCGAGGCCGTGTGCCGAGCACTGGGCTGCG

1754. chr11_CD6_NM_006725_-1.5572
AGCAATAGCTATCAACCGGTCCCCATCACCATC

1755. chr11_DAK_NM_015533_1.52623
GGGGACGCTCCTTATCGTGAAGAACTACACTGGGGATCGGCTCAACTTCG
GCCTGGCCCGGGAGCAGGCCCGGGCTGAAGGCATCCCGGTGGAGATGGTG
GTGATTGGGGACGACAGCGCCTTCACTGTCCTGAAGAAGGCAGGCCGGCG
GGGGCTGTGCGGCACGGTGCTTATACACA

1756. chr11_CPSF7_NM_024811_-1.51165
GGCTCCCGGAGAATCAGAAACTCATACGTTTTCTTGGACAAAGCACCATT
CTCTATGGAGACCAGGGGCCT

1757. chr11_C11orf66_NM_145017_1.5669
TGGCCAGAGGCTCCAAGCGGGAAACAGCCTTCAGCCGAGGGAATGAAAGG
A

1758. chr11_C11orf9_NM_013279_-1.88897
TGGAGAATTCGATGTCCATCACCTCC

1759. chr11_C11orf9_NM_013279_-1.72821
AGCCTTCCACAGAGTCTCCACACCCACCAG

1760. chr11_FEN1_NM_004111_-1.62646
GCTAAGCGCAAGGAGCCAGAACCCAAG

1761. chr11_MTA2_NM_004739_1.57668
CAGATCTTTGACGATAGTTGCCAGGGGCAGCCGCACCAGAGGGTGAATCT
TCAATGGAGTCTTGGCGGCCTTAGGAAGTCGAAT

1762. chr11_MTA2_NM_004739_1.60269

Figure 3-143

TGCTGAATATACCGGTCTGTGGTTTTCCA

1763. chr11_MTA2_NM_004739_-1.5577
GTGGGTGGCTGGTAATGATTCAAATTGCCGAGAAAGAAAAAGTTCCCGGT
GCTTCAGTTGATGGCGCTGCTGCTCAGACACCCCTGGCTGCTTTGA

1764. chr11_UBXN1_NM_015853_-1.64058
GGCTGCTAACTCCTCGGCCTTTTCCCTCCGCCTCTCCTCAGCAGCCCGGC
GCATCTCATCTTCCTGTAGCCGCTGTCGTGCTGCTGACAACTCTTGCCCT
TGTCTCCTGCGCTGCCGTTCCCGTTCCAATGC

1765. chr11_NXF1_NM_006362_1.74827
GTGAAGGGCACACTGCACTTGCTCTGAATCATGCTCAG

1766. chr11_NXF1_NM_006362_-1.73435
GCTGTACGACTTCCCCTCGTCCGCCAT

1767. chr11_SLC3A2_NM_001012661_1.64419
AGCTGAATGAGTTAGAGCCCGAGAAGCAGCCGATGAACGCGGCGTCTGGG
GCGGCCATGTCCCTGGCGGGAGCCGAGAAGAATGGTCTGGTGAAGATCAA
GGTGGCGGAAGACGAGGCGG

1768. chr11_HRASLS5_NM_054108_1.56479
ATCTGAGGCCATTGACAAAGTGCTCACAGTTCCCTTCAATCAGGCTGTAC
TGCACGATCTTGTTGACCATCTTTTTTGTACGCTGGATGATCTTGTCCAC
CGGCAAGGGCAGGTACGTCCCATCTAGCTTGTTATTGACCTTCCAGGAGC
AGCCATGCAGCACATCCTCCAGACGACTGTATTTCACCACGGCCCGATTG
CTAAAGATGGAAGTAATGCTGCCCACCTCA

1769. chr11_RCOR2_NM_173587_-1.68323
AGAGGTCGCCACTGAGGTTAGGAGAGGCAGGAGGTCAGCGTGGCTAGGGT
CCGGCGGGGTGGGAGCCCACCTGGTAGCCCCAGCGCTCTCCACGACCCCC
ACGAGCCAGGGCGTCAGAAAAGTTTGTGCAGAAGTGGGGGACGCAAGGGA
TGAGCGCAAGGTCCGGTGCGGCTGGGGCGTGATTACTATGTACGCCCCTC
AGGGT

1770. chr11_STIP1_NM_006819_2.594
AAGCCAAGCGAACCTATGAGGAGG

1771. chr11_TRPT1_NM_001033678_-1.65074
GCCCCGCACCCCAGATCGCTGGTGCGCCCCGCAGGGTGGTCCGGGAGGCA
GGGCCGACGTGCCGACGGACCGGGCGGAAGCG

1772. chr11_PLCB3_NM_000932_1.54289
ATACCACTACGTCTGCCTGCGGAACGAGGCCAACCAACCGCTGTGCCTGC
CGGCCCTGCTCATCTACACCGAAGCCTCGGACTACATTCCTGACGACCAC
CAG

1773. chr11_PRDX5_NM_012094_-1.75249
GGGTGTGCTGTTTGGAGTTCCTGGGGCCTTCACCCCTGGATGTTCC

1774. chr11_RPS6KA4_NM_003942_-1.69529
CATGATGCTGTCGGGGCAGGTCCCCTTCCAGG

1775. chr11_SLC22A11_NM_018484_1.52652

Figure 3-144

GGCTGCCAGAATCCGCCCGGTGGCTGATTATTAAGGGCAAACCAGACCAA
GCACTTCAGGAGCTCAGAAAGGTGGCCAGGATAAATGGCCAC

1776. chr11_NRXN2_NM_015080_-2.05511
GCACGAAGGGGGATCGGGTGGCCACG

1777. chr11_NAALADL1_NM_005468_-1.5159
CAGCCCCACGGATGATGCCCAGGACGTTGGAAGAGTTCCTCAGCTCCAGG
CGGTTGTAGACGCTCACATTCACCTGG

1778. chr11_TM7SF2_NM_003273_-1.59242
GCTCCTGGCGGCCCGTTCGGGCCCCGCGCGCCTGCTGGGTCCACCCGCGT
CCCTGCCGGGGCTGGAGGTGCTGTGGAGCCCACGGGCGCTGCTGCTGTGG
CTCGCCTGGCTCGGCCTGCAGGCGGCGCTCTACCTACTGCCGGCGCGCAA
G

1779. chr11_SCYL1_NM_020680_-1.65668
AGATGGGACGACGAAGACTGGGGCAGCC

1780. chr11_LTBP3_NM_001130144_-1.8942
GGCACTGGCGCTGCGCGGGACTGTACTCGGCAGGGGGCGTGCAGGCACAG
CGGTAGCCGCCGCGCGTGTTCTCACACACTCCGTTCCGGCAGTTGGACTC
GTCCAGGCACTCGTCC

1781. chr11_SIPA1_NM_153253_-1.57879
ATCAGAACTTCTTCGGGATGGACGAGTCGCTGGGCCCGGTGGCAGTGAGC
CTGCGGCGGGAGGAGAAGGAGGGCAGCGGAGGGGGCACCCTGCACAGCTA
CCGCGTCATCGTGCGGACCACGCAG

1782. chr11_KAT5_NM_182710_-1.61033
GAGATAATCGAGGGCTGCCGCCTACCCGTGCTGCGGCGGAACCAGGACAA
CGAAGATGAGTG

1783. chr11_SNX32_NM_152760_-1.58123
GGCACTGGCCGACTACGAGAATGCCAACAAGGCGCTGGACAAGGCGCGCA
CCAGGAACCGGGAGGTGCGGCCCGCCGAGAGCCACCAGCAGCTGTGCTGC
CAACGCTTCGAGCGCCTCTCCGACTCCGCCAAGC

1784. chr11_EFEMP2_NM_016938_1.68486
CACAGGAGCGGTTGTTAGGCCCCAGCTGGAAGCCCGGCTCGCACTGGCAG
CGGAAGGAGCCAGGCAGGTTCACGCAGCGGTGCTGGCAGTAGCGGTAGCG
GCACTCGTCTATGT

1785. chr11_CTSW_NM_001335_-1.72625
AATTGCGCAGTACCTGGCCACTTATGGCCCCATCACCGTGACCATCAACA
TG

1786. chr11_CCDC85B_NM_006848_2.2583
GGCTGGAGCGGAGGGACTTGCTGGGGGTTGGATTGG

1787. chr11_---_---_1.70841
GCTGGCTTTCTAGAGTGTGTGGGGGAGAGCGTGGGGAGCAGCAGTGACTG
TTAATGCAGGAACGGTAATTTCTGATGGTGGT

1788. chr11_---_---_-1.72477

Figure 3-145

GATGGAGACCATCCAGGCTAGTACGGTGAAACCCCA

1789. chr11_BANF1_NM_003860_-1.54652
AGTCTGATCCCTCCGAAAACCGTACTTCCGGCGCTGTCTCGGAGGCCTCC
CGTCCCCTCCCTTGTCCGTCTTCTAACTCTTCCCCACGCCAGGTCCGTCA
AGCCTAAGTCCTTGAGTTCCGGGTCCGGGCAGCAGAGAAAGGAAGTCCTC
TCCCTGGAGGCCTATCTCCCTCAGAACTGCGCGAGAAGCGAGACCTTAGA
AGGCAGGGCTTCCCGCGAAGGACCGGAAAGGAGCGCCTACTAAGGACGCC
GTCGAGGTCCGGGGCGCCTCAACTCTATAGCTCTA

1790. chr11_CATSPER1_NM_053054_1.80643
TGAGGATGGCTGCGATGGACGGCAAGGACTGGCCCAGGG

1791. chr11_CATSPER1_NM_053054_-1.54697
CAGAAGTCAAAGAAGTACGAGAGGCCCAGGGCGATGATCTTGAGCA

1792. chr11_RAB1B_NM_030981_1.56338
CTTTCCCCAAGGTAGCACATCTGGCTCACTCCCCA

1793. chr11_TMEM151A_NM_153266_-1.80213
CGAGGACGGCGCTGGCGACGGCGGGGAGGTGCCCGCGCTCATCCCGGACG
GCGAGCCGC

1794. chr11_B3GNT1_NM_006876_1.65306
TACTGCCGAAAGCGCTCGTCGAAGGTGGGCACCTTGCCTCCTGCCACGTA
GAATGGCTCCCAGGGGTCCTGCCAAGGTACCACGTAGGCGGGCCGCAGCA
AGCTCTCTTCCGGCAGGTTGACCCAGCGGGAATAGTTG

1795. chr11_SLC29A2_NM_001532_-1.52964
CACCATGGCTGTGATGGCGGGGAAGACGGACAGG

1796. chr11_ADRBK1_NM_001619_-1.61279
ACTACGCTCCCTGCTGGAGGGGTTGCTGCAGAGGGATGTCAACCGGAGAT
TGGGCTGCCT

1797. chr11_SSH3_NM_017857_-1.51321
TGGAGCAGGCGATCCGTGCTGAGCTGTGG

1798. chr11_SSH3_NM_017857_1.79602
TGAAGTCCCGCCAGTCAGTGGTTACCCTCCAGGGCAGTGCCGTGGTGGCC
AACCGGACCCAG

1799. chr11_CARNS1_NM_001166222_2.00888
CTCGTGGAGTCAGACCCCAACCACTTTGC

1800. chr11_GPR152_NM_206997_-1.85264
CTGTGGCTCAGTGGGCGTGAAGCTGCCCGGCCGCTCCTCGCAGAGAGCTG
CCGCGAAGGACGAGAGCACGGAGCGCAGCAGGGTCCGGAGGTCGGCACTG
GCCATGAGGCA

1801. chr11_PITPNM1_NM_004910_-1.56943
ACTTCTGGTAGCGGGGCACGGTCAGTGGGGCGATGGCCTGGAACTTCGGG
GCCAGCAGGGGCTCGAGGCGTGAGGCGCAGGGGTCAGCCGCGTGGAAGAG
GTTGTAGATCTGTTCACAGG

Figure 3-146

1802. chr11_NUDT8_NM_181843_-1.74187
GGATCCAGTGGGCCTACACCAGCAAGCACT

1803. chr11_TBX10_NM_005995_-1.87699
AGGACACAATCTGGCGCATCCACTGGGCACCCTTGGCTGGCGAGTCGGG

1804. chr11_LRP5_NM_002335_1.95497
CCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAG
GCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACC
CCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGACAGCTGCCCGC
CCTCGCCCGCCACCGAGAGGAGCTACTTCCATC

1805. chr11_MTL5_NM_004923_1.74018
GAACGCGTGCAGGACGGGTTCCTTGGGGTCCGCCGGGCCCAGGTACGCTT
CTTTGAAGACGTGGAACTCGTCCTCCTCGTACTTCACGGGGGCCTTCAGG
CCGATGTTCTCCGAA

1806. chr11_CPT1A_NM_001031847_-2.2427
AACTTGGTCCTTGACTTATAATCC

1807. chr11_CPT1A_NM_001876_-1.51495
AGTCGCATGACTCAGTGGTGCAGGAGCGCACGGTCTCCGTCCTCCCCTCT
CGGAAGAGCCGGGTCATGGAGGCCTCGTATGTGAGGCAA

1808. chr11_MRPL21_NM_181515_-3.26011
CAATGCTGTTTATCCGGAGGACAG

1809. chr11_TPCN2_NM_139075_-1.50658
TCCAGACCTCGCTGTTTCGGAGGCGGCTG

1810. chr11_FGF19_NM_005117_1.73765
GGTCGTGGCCCTAGATCCTGGACGCAGCGCTCCTGCTCTGACGGCGCGGC
GGCTCCGGGCCGGCAGCCTTATATAGTAGCGCCTTACGGGCCCCACGGGT
AGGTGCCCAAGACACCCGAGCATTTCTTATCGGGATTGCATCAAGCCTCC
GC

1811. chr11_FGF3_NM_005247_1.65956
GCAGCCCACTCTGTAGCTGCCGCAC

1812. chr11_ANO1_NM_018043_-1.54078
GGCCAGCCGGGCATCCTGACCGATGGGCACCCTCTCCCAGG

1813. chr11_CTTN_NM_005231_1.89937
TTTCGGCGGCAAATACGGTATCGACAAGGACAAAGTGGATAAGAGCGCCG
TTGGCTTTGAGTATCAAGGCAAAACGGAGAAGCACGAGTCC

1814. chr11_INPPL1_NM_001567_-1.89343
CCCACCGGATGACCGGGATGCCTCAG

1815. chr11_STARD10_NM_006645_-1.51178
GGTCCTAGTCCGGCTCTCCTGGGTCCTCCGCGGAGGCTCCGACAACGTCG
ACGCGGCTGCAGATGCTGACGC

1816. chr11_ARHGEF17_NM_014786_1.55795
GATCCAGCGCATGGGTGCCCAACAAGATGATGGAAGCGATGCCCCCCCTG

Figure 3-147

GAAGCCCTGACTGGGCAGGGGATGTGACCCGAGGGCAGCGGTCCCAGGAG
GAGCTCTCAGGCCCTGAGTCCAGTCTGACAGATGAAGGCATTGGGGCAGA
CCCTGAGCCTCCTGTTGCAGCATTTTGCGGCCTGGGTACCACAGGGATGT
GGCGACCTCTTTCCTCATCCTCGGCCCAGACGAACCACCATGGCCCTGGG
ACTGAGGACAGTCTGGGCGGGTGGGCCCTGGTGTCGCCTGAGACCCCTCC
CACACCAGGTGCCCTCCGCCGACGACGCAAAGTCCCACCTTCAGGTTCTG
GTGGGAGCGAATTGAGCAATGGGGAGGCAGGGGAGGCCTACAGGTCCCTG
AGTGACCCAATTCCTCAGCGCCACCGGGCTGCCACCTCTGAAGAGCCTAC
TGGGTTCTCTGTGGACAGCAACCTCCTGGGCTCACTGAGCCCCAAGACAG
GGCTCCCTGCCACCTCAGCCATGGATGAGGGCTTGACCAGTGGTCACAGT
GACTGGTCTGTGGGCAGTGAAGAGAGCAAGGGATATCAGGAGGTTATTCA
GAGCATAGTTCAGGGGCCTGGCACCCTGGGGCGTGTGGTGGACGACAGGA
TTGCTGGCAAAGCCCCCAAGAAGAAATCCCTGAGTGACCCCAGCCGCCGT
GGGGAGCTGGCTGGGCCTGGATTCGAGGGCCCTGGAGGGGAGCCCATCCG
AGAAGTTGAGCCCATGCTGCCTCCATCCAGCAGCGAGCCCATCCTTGTAG
AGCAGCGGGCAGAGCCAGAAGAACCTGGTGCCACCAGGAGCCGGGCACAG
TCTGAAAGGGCCCTACCTGAGGCTCTGCCTCCCCCTGCCACTGCCCACCG
AAACTTTCACCTTGACCCCAAGCTGGCTGACATTCTGTCCCCGAGGCTAA
TCCGCCGAGGCTCCAAGAAGCGCCCAGCTCGGAGTAGTCACCAGGAGCTT
CGGAGAGACGAGGGCAGTCAGGACCAGACTGGCAGCCTGTCTCGGGCCCG
GCCCTCCTCCAGACACGTTCGCCATGCCAGTGTGCCCGCCACATTTATGC
CTATTGTGGTGCCTGAGCCACCAACTTCTGTTGGTCCCCCTGTGGCTGTG
CCAGAACCCATAGGCTTCCCTACCCGAGCCCATCCCACGTTGCAGGCACC
ATCGCTCGAGGACGTCACCAAGCAGTACATG

1817. chr11_RELT_NM_032871_-1.85591
AGGGCACATTATGCAGGCCCTGCCCCCCAGGCACCTTCTCAGCTGCATGG
GGCTCCAGCCCATGCCAGCCCCATGCCCGTTGCAGCCTTTGGAGGAG

1818. chr11_OR2AT4_NM_001005285_-1.84918
GGATGCCCAATAGATAGAAGACGGGTGAGCCATCCACTGATTCATTACAG
GCTGTGGCATCC

1819. chr11_SLCO2B1_NM_007256_1.50553
TCAGCCTGCCGCTCTTCTTTATCGGCTGCTCCAGCCACCAGATTGCGGGC
ATCACACACCAGA

1820. chr11_ARRB1_NM_004041_-1.67029
GTGCATTAGGGTGAAGGGCAGTTCCACGGCCACGTCG

1821. chr11_SERPINH1_NM_001235_1.78101
CTGGCACTGCGGAGAAGTTGAGCCCCAAGGCGGCCACGCTTGCCGAGCGC
AGCGC

1822. chr11_WNT11_NM_004626_-1.61071
TCGGAAAACTTGGCCCCCATGAGGAGCCCGTAGCTGAGGTTGTCCGCACA
TCCTCCCCAGCGGTTCCCGGGCCCGGGTGGCTCACCTGGGACGGGGCCGC
AGGAGCAGCCGGGCAGGTCGCCGGAGGTGCAGGCCCGGGCGATGGCGTGG
CTGATGGCGGCGGCCGACAGCGCATACACGAAGGCCGACT

1823. chr11_B3GNT6_NM_138706_-2.07469
GACCGGGGACACCGGGTCTCCTGA

1824. chr11_CAPN5_NM_004055_-1.59533
CGGCCTGGTAAAGGGCCACGCATACGCCGTCACTGATGTGCGCAAGGTGC

Figure 3-148

GCCTGGGCCACGGCCTACTGGCCTTCTTCAAGTCAGAGAAGTTGGACATG
ATCCGCC

1825. chr11_CCDC81_AK027167_1.50471
CTCTGGACTTATAAGCGCTTAACATAAACAACAACAAGAAAAGTATCGTG
GTAGCCTTGCCTATGAGCCTGCAGTTTTTAATTTGTCTGAGTCCTGGACC
TCAGCCTAGATGTAACCTTG

1826. chr11_NOX4_BC051371_1.52899
AAGCAACTTGAGGGGCGAGGTGAGGTCTTACTCTCTGGGT

1827. chr11_C11orf70_BC054869_-1.51475
GACTTGGGTGGCTACTACTTCAGGTTCTTGCCTCAGAAAACCTTCCAGTC
TCTGAGCTCTAAGGAGATCACCAGCCGGCTCCGC

1828. chr11_YAP1_NM_001130145_-1.61108
GCGGGGACTCGGAGACCGACCTGGAGGCGCTCTTCAACGCCGTCATGAAC
CCCAAGACGGCCAACGTGCCCCAGACCGTGCCCATGAGGCTCCGGAAGCT
GCCCGACTCCTTCTTCAAGCCGCCGGAGCCCAAATCCCA

1829. chr11_MMP20_NM_004771_-1.9639
CCACAGCGAGGCTTCTTGATCACGTTCATTGTGGTCTGGTCTAACTTCCC
GGTGACTTGGAGGCCAAAGAACGCTTGTAGC

1830. chr11_MMP8_NM_002424_-1.51474
AGTATTTCTCCACGGAGTGTGGTGATAGCATCAAATGTCAAACTGGGGTC
ACAGGGTTTGGGTGTGCTTGGTCCAGTAGGTTGGATAGGGTTGCTT

1831. chr11_CUL5_NM_003478_1.52211
CTTTAGTAGCTTTCCCAAAACTCAAACGGCAAGTTTTGTTGTATGAACCT
CAAGTCAACTCACCCAAAGACTTTACAGAAGGTACCCTCTTCTCAG

1832. chr11_NPAT_NM_002519_-1.5601
TTGGATCTTGGAAATTCCGTATTGTTGAATGAGGGCCAGACAAAGTGGTA
CTTT

1833. chr11_NPAT_NM_002519_-1.66235
CAATACAAGCCGGGCTACGTCCGAGG

1834. chr11_ATM_NM_000051_1.5505
CTGTTTTACTGACGTTGATAGCTGTGGTT

1835. chr11_NCAM1_NM_000615_-1.59676
TGGAGGGCATCGTCACCATCGTGGGCCTGAAGCCCGAAACAACGTACGCC
GTAAGGCTGGCGGCGCTCAATGGCAAAGGGCTGGGTGAGATCAGCGCGGC
CTCCGAGTTCA

1836. chr11_DRD2_NM_000795_-1.69656
GGGACGGGTCGGGGAGAGTCAGCTGGTGGTGGC

1837. chr11_NNMT_NM_006169_-1.95219
GAGGAGAAGTTGAGACAGGCGGTCAAGCAGGTG

1838. chr11_CADM1_NM_014333_-1.51224
AACCACCTGATAGTCGTGGCTGGCTTGCTGGCCATAGCAGTGCAGTTGAC

Figure 3-149

TTCAATCTCCTCACCTTCCACCGCAGTGTCTTTCTGGATATCGATCATCA
GATTACGTGGTGGGA

1839. chr11_SIDT2_AK303023_1.54895
TCTCTGTGGCTGATCTGGCGTCCACACC

1840. chr11_RNF214_NM_207343_1.50862
TCTCCAGCAAATGGGGTTGAAGGAGTCCGAGTGGATCAGGATGATGATCA
AGATAGCTCTTCCCTGAAGCT

1841. chr11_BACE1_NM_012104_1.80092
TCGGGCCCTCTGGGCTCGCACTGGCCCACGTCCGTCCCTGGCGCCTGCCC
CCAAGTCTGGGTGGTGCTGGTGGCTTCTCAGGAGAGGGAGCTTGGGGGCA
TCAGGACGCCAGGGCCTGCAGGGCCCTGGGCCAGCCCCCGGGTCCGGGCT
GTGGAGAGCGGTCAGGGGAGATCCGCAGAGCACGGGAGCAGGGGAGAGGC
TGGGATCCGGAGCCCGCTACATCGG

1842. chr11_CEP164_NM_014956_2.25342
CCAGCAACCACTGGGAATAGAAGACAAGGATGACAGCCAGTCCAGCCAAG
ATGAGCTGCAGAGCAAGCAGTCCAAAGGCCTGGAGG

1843. chr11_DSCAML1_NM_020693_-1.72384
GTTCTTGTATTCAATGTCGAAGCCCGTGATGATGCTGTTCCCGTCGAATC
GCTGGGTCCAGCGCAGGTTCATGCTCCGGGCCTT

1844. chr11_UBE4A_NM_004788_-1.53688
TAGTCCCCTCACCATGGACCAGATCCGGCCAAACACAGAACTAAAAGAAA
AAATCCAACGGTGGCTTGCAGAGAGGAAACAACA

1845. chr11_CXCR5_NM_001716_1.57815
CTCACCGTGGCTAAGAGTGTCCTAGGAGTATCCTCATTTGGGGTAGCTAG
AGGAACCAACCCCCATTTCTAGAACATCCCTGCCAGCTCTTCTGCCGGCC
CTGGGGCTAGGCTGGAGCCCAGGGAGCGGAAAGCAGCTCAAAGGCACAGT
GAAGGCTGTCCTTACCCATCTGCACCCCCCTGGGCTGAGAGAACCTCACG
CACCTCCCATCCTAATCATCCAATGCTCAAGAAACAACTTCTACTTCTGC
CCTTGCCAACGGAGAGCGCCTGCCCCTCCCAGAACACACTCCATCAGCTT
AGGGGCTGCTGACCTCCACAGCTTCCCCTCTCTCCTCCTGCCCACCTGTC
AAACAAAGCCAGAAGCTGAGCACCAGGGGATGAGTGGAGGTTAAGGCTGA
GGAAAGGCCAGCTGGCAGCAGAGTGTGGCCTTCGGACAACTCAGTCCCTA
AAAACACAGACATTCTGCCAGGCCCCCAAGCCTGCAGTCATCTTGACCAA
GCAGGAAGCTCAGACTGGTTGAGTTCAGGTAGCTGCCCCTGGCTCTGACC
GAAACAGCGCTGGGTCCACCCCATGTCACCGGATCCTGGGTGGTCTGCAG
GCAGGGCTGACTCTAGGTGCCCTTGGAGGCCAGCCAGTGACCTGAGGAAG
CGTGAAGGCCGAGAAGCAAGAAAGAAACCCGACAGAGGGAAGAAAAGAGC
TTTCTTCCCGAACCCCAAGGAGGGAGATGGATCAATCAAACCCGGCGGTC
CCCTCCGCCAGGCGAGATGGGGTGGGGTGGAGAACTCCTAGGGTGGCTGG
GTCCAGGGGATGGGAGGTTGTGGGCATTGATGGGGAAGGAGGCTGGCTTG
TCCCCTCCTCACTCCCTTCCCATAAGCTATAGACCCGAGGAAACTCAGAG
TCGGAACGGAGAAAGGTGGACTGGAAGGGGCCCGTGGGAGTCATCTCAAC
CATCCCCTCCGTGGCATCACCTTAGGCAGGGAAGTGTAAGAAACACACTG
AGGCAGGGAAGTCCCCAGGCCCCAGGAAGCCGTGCCCTGCCCCCGTGAGG
ATGTCACTCAGATGGAACCGCAGGAAGCTGCTCCGTGCTTGTTTGCTCAC
CTGGGGTGTGGGAGGCCCGTCCGGCAGTTCTGGGTGCTCCCTACCACCTC
CCCAGCCTTTGATCAGGTGGGGAGTCAGGGACCCCTGCCCTTGTCCCACT
CAAGCCAAGCAGCCAAGCTCCTTGGGAGGCCCCACTGGGGAAATAACAGC

Figure 3-150

TGTGGCTCACGTGAGAGTGTCTTCACGGCAGGACAACGAGGAAGCCCTAA
GACGTCCCTTTTTTCTCTGAGTATCTCCTCGCAAGCTGGGTAATCGATG

1846. chr11_BCL9L_NM_182557_-1.50694
GTCCTGGTAGAAGACACCCTGTCTAGAATGGCCCTTGGTCCTGGAGGTGG
GGCGCAAAAGGCCTCAGCCAGGGAACTGCCCTGCCACCTCCCGAGGCAGG
AAAGGAAGTGAGAAAAGGAGAAGTTTTTTTACTCCTGGGGCCAAAGTAGG
GGGACAAACACCCAGTCGTATATGGCTTCAGCTCTGACCAAAGGCGGATA
GGGAGCTCTCCTGGGTAGGAGCAGGGAGCCAAGGGGGAGGCAGTGGCTGT
GCCTGGGTGGGCACAGACAGATCTGGTACATGGCCCTGAGCCCTGGGCAG
AGGGACAACCTTGCCGGTGAGTGGGCAGGCAGAGAGGAGGCGGCAGGATG
CTGTTTCCCCGATTCCATCCTCAGGGAGTGGAGACTGGAGGGGAGGTGCA
CTGACTCAGATGAACTGTTCTCCCCCTTCTTTGATAAGAAGTAGGTGGCA
GCAGCCTCTGGAAAAGTCAGGGCCCTGGAGGTTACCTGGCCCAGGGCTAC
TACAGCCACAGGCCCCAGTGGCACCATGCCACCCCTTCCATGGCTCCACT
CAAGGGGGCCACACAGCCACCGCCTCTTCCTCCTTTCCTTCATCCCAAAC
TGGGACAAAAGACTTCAAGTTCTGGCTAAGATGTAGCAGCAGCGGATGCC
CGGGCATCCAAAGTGGAAA

1847. chr11_BCL9L_NM_182557_-1.67636
ACACAGTGGGGCTACGGCCCCTGTGCGTGCCCAGGGCCCAGCCAGGTACT
CGGTACTGGAGCACGGA

1848. chr11_FOXR1_NM_181721_-1.59599
TCCAGATTATGAGCCCAACCTCTGGATGTGGGTAAATCCCAACATTGTGT
ATCCCCCTGGAAAGCTGGA

1849. chr11_SLC37A4_NM_001164277_-1.5684
TCCAGGTTGCGGAGTCCAACATCAGCAGGTTCATTGTGGATGAGCA

1850. chr11_SLC37A4_NM_001164277_1.79734
ACCACAGTTCCTGCTTGCCGCTCTCACAGTTCCCAGATCTGCTGAGTTGG
GTTTTTTCTGCTCCCTCCTCCACCCAGCCTCCCAGGCTCCCTTTATAGCC
GCCTTCTGGACAATCATTAAGCCTGGGGAG

1851. chr11_HMBS_NM_000190_1.9804
CTGCAGAGAAAGTTCCCGCATCTGGAGTTCAGGAGTATT

1852. chr11_H2AFX_NM_002105_-1.56224
CCACGGTGGCGCTGGTCTTCTTGGGCAGCAGCACGGCCTGGATGTTGGGC
AGGACGCCTCCCTGGGCGATCGTCACGCCGCCCAGCAGCTTGTTGAGCTC
CTCGTCGTTGCGGATGGCCAGCTGCAGGTGGCGGGGGATGATTCGCGTCT
TCTTGTTGTCGCGGGCCGCATTGCCCGCCAGCTCCAGGATCTCAGCGGTG
AGGTACTCCAGCACTGCCGCCAGGTACACTGGCGCGCCGGCGCCAACGCG
CTCGGCGTAGTGGCCCTTCCGCAGCAGCCGGTGTACACGGCCCACTGGGA

1853. chr11_NLRX1_NM_024618_-1.51054
CGGCAGGCACCTAGCTATGTGACCACTGGCCCTAAACCTTTTCCCTCTGT
GGCCTCCTGGCTTGCACTGCTCCCTCTAGAAAGATTCCTTCAGGTCTGGA
GGCAGAGGAATGGGCATAGCTGAGCCAGTTGCCCTCCTAGGGCATGTTTG
ACCAGGACTGAGTCTGGAATCTCCAAGTTAAAGATGGTGAATCAATGCTT
CGGGCTTGGAGATGGAACATGCCTCCTCTCCATTCAGCTAGAAGGACCAA
AGCATGTGGCATTTGGATGGCCAGAGTGCCCTGAAGCACCACTACCAACC
TTGCCTCCCCCTCCTCTCAAAGAGCCTCTGACTGTGTCACCAAGGGGCTC
ACATCTTATG

Figure 3-151

1854. chr11_USP2_NM_004205_-1.62203
TGCCTGACTCTCTCCCACCTCCGCCGGGGGCCCAGAAGGGACCTCCCCGG
GAAATCGGCGCCACCCAGCG

1855. chr11_GRIK4_NM_014619_1.56927
GCCCTACGAGTGGTACAGCCCACACCCATGTGCCCAGGGCCGGTGCAACC
TCCTGGTGAACCAGTACTCCCTGGGCAACAGCCTCTGGTTTCCGGTCGGG
GGGTTCATGCAGCAAGGCTCCACCATCGCCCCTCGCGCCTTATCCACCCG
CTGTGTCAGTGGC

1856. chr11_SORL1_NM_003105_1.7969
CCAACTTGGGCGATGTGACCGATTTGAGTTCGAATGCCACCAACCGAAGA
CGTGTATTCCCAACTGGAAGCGCTGTGACGGCCACCAAGATTGCCAGGAT
G

1857. chr11_UBASH3B_NM_032873_-1.95475
TGGCTCAGTACGGCCACCCCAGTCCG

1858. chr11_OR8G5_NM_001005198_2.19468
ATCTATGTAGTCACAGTGCTGGGG

1859. chr11_OR8D2_NM_001002918_-1.91784
CGGGTAGTATGGACTGTGGCCCACAG

1860. chr11_TBRG1_NM_032811_1.57732
TGGATTTTCTCATCCAGCCATCCACAACCTG

1861. chr11_ESAM_AY189281_1.66167
GTGTCTACTGTGCCTACAGGCTCAGCCACTCTCCCTCCCCCAGCTCGCAT
TCTCCAAATGCCCCTCACATGCACCCATTCTTCTAACCTGAA

1862. chr11_ROBO3_NM_022370_-1.55327
GTCTCTGAGCCTGTCCGTACACAGG

1863. chr11_SLC37A2_NM_198277_-1.55027
GGCCTGGTCAATGGCCCATACGCGCTCATCACCACTGCTG

1864. chr11_DDX25_NM_013264_-1.66194
CAGGTCACAATTGTTGTGAACTTTGATCTCCCTGTAAAACAAGGAGAGGA
GCCGGACTATGAGACCTACCTCCACCGCATAGGGCGGACGGG

1865. chr11__RPUSD4_NM_032795_-1.54093
ACCGTAGGGCTTATTGATGACCACAAGGTTCTTGTCCTGGTGGAGAATTC
CTCGGGTCAGTGCCTTAGCAAGCACGTTGGGGTGGACTCGCTGCAGCTGC
CGTGTGAACCGCACTATTTCTTGCACTCTCCGCTGAACAGCG

1866. chr11_SRPR_NM_003139_1.53151
TGGTGGGAGTACTGTAATCCAACACTTCTTTGTTAGCAC

1867. chr11_KIRREL3_NM_032531_-1.51396
AGACGTCAACCGTGCGGCTGAGGTTGGTGCTGCCCAGGGCGTTGGTCACC
TCACAGGAGACGGGCTCTGAGAAGTACGTGTAGTCCACTGTGGTCCTGTA
CACCTCTCCAGATG

Figure 3-152

1868. chr11_ETS1_NM_001143820_1.69523
ACTATCGTAGCTCTCTATGCTTTCA

1869. chr11_C11orf45_NM_145013_-1.60413
GCAGCAGGTTTGCACAGGGTGCCAGTTAGGGAGGAGAAGGCAGCGAGGAA
CCCCGCA

1870. chr11_C11orf45_NM_145013_-1.56761
TCTCGCACGATCCGGCCAAGAGATGGCGGGGTGGCGGGAGGGGCGCTCTG
GCGACCCCGGAAGCGAGAAGCAGGCCTCTGCAGGGCCAGGGATGAAGGTG
CAAGGGAAAGCCCTGGGACCTG

1871. chr11_NFRKB_NM_001143835_-1.87462
CCGTGCTGGGACGCACCACATAGTCAGTTCTT

1872. chr11_NFRKB_NM_001143835_-1.50259
TTGATAGCAGGAATTGCCAGCGGAGAGGGGGCCTGTGAGAGAGGTGCGAC
CCCTTCAGTACTGCTTAGCGGCTCGGCCAGGTCCTCTGCCTCTGATTTGA
TCGTTTTTATTTTCTTCTTCTTCTTTTCCTCTTTTTCCTTAACCTTTTTT
TTAAGGACAGCCAAGTCATATAAGG

1873. chr11_PRDM10_NM_020228_1.51367
ACAGGCGGCACTTGAACGTGAAGCTGTCGTAGTCTGTGGACGTGATGCGG
GGCTTGAACGTCTTGGAGCGGCTGATGCGGTCGGCTTTCTTGGCCTCCCT
CTCAGGATTATGCATCCTCTGCATGTGTTCCCGTAGTTTGTC

1874. chr11_APLP2_NM_001642_-1.94365
CGCGCGCTAGAGCGACCCGGCGAGGG

1875. chr11_APLP2_NM_001642_-1.54066
CACCTGGCCCGAGTGGAAGCTATGCTGAATGACCGCCGTCGGATGGCTCT
GGAGAACTACCTGGCTGCCTTGCAGTCTGACCCGC

1876. chr11_ST14_NM_021978_1.53329
GCTGTACAGCGGAGTCCCATTCCTGGGCCCCTACCACAAGGAGTCGGCTG
TGACGGCCTTCAG

1877. chr11_ST14_NM_021978_1.6611
ATGCCCGGGGCAGTTCACGTGCCGCACGGGGCGGTGTATCCGGAAGGAGC
TGCGCTGTGATGGCTGGGCCGACTGCACCGACCACAGCGATGAGCTCAAC
TGCA

1878. chr11_ACAD8_NM_014384_-1.55174
CTGCCGGCGTTTCGGGGCGCGCCTCGGCTGCCTGCCCGGCGGTCTCCGGG
TCCTCGTCCAGACCGGCCACCGGAGCTTGACCTCCTGCAT

1879. chr11_GLB1L3_NM_001080407_-1.61719
GTCGACCCAGGTTAGGAAGCCCGAGGTCGGGGCGTTACCCCAAGGGCCCT
CCCGCTTCCCCTCCGAGGGCAGAGAGGCGTCCGCGCCCGGACGCACTGCG
GGAACACCTGGAGCGCCGGCGGAGCTCGGCTGTCCCCGCGGGAGGGAGCC
CGACGCGCATCCTTGGGACCCGGACCCGGCGCCCGCGCCTCGGGACGGAT
TTCTGCCTCGGCTGCAGGCGCAGCGCGCAGACCTGAGCCT

1880. chr12_SLC6A13_NM_016615_-1.64899
ACAGACGCGTGAGGTTTGGGTACAGGTAAAACTGAATTCCTTGGGCTGCC

Figure 3-153

CCAGGCAACGTCACCCCTCGAATTAACAGGACCACCAGCATGAGGTAAGG
A

1881. chr12_NINJ2_NM_016533_-1.58364
ACCAGGGTGGTGTAGTAGTGAGAGGATGGTCCCTGCTCCAGCACCGCCTT
CAGCCGCATGGCGTTGGACATGAACAGGGCCACGTCCAG

1882. chr12_CACNA2D4_NM_172364_1.58858
AGATAGAGCTTCCCTCCCAGTGGACCCTGCTTAGCAAGTTGGAATGTTCC
CACAAGTTCCAACCCTAAGGATTTCACTCCAGGGACAGAGTCAAGTAGAT
TCTTTTGTAAATCATTGGCCAGAAAAGAGCACAACCACTGCTCTTTTTCA
CTATTTTACAGCTATTTTTGCCGTCCCCTGAATGTACATCAATTTCCATG
CAGCAATTGGATGTCTCAGCCTATTGGCTTTTCATAGATGCAAACTTTCC
TTTAGGGCTTTGTAAAGAAGTTTTGGGAAGTTCTTCAATAGCAGCAGTTT
GGGGACATCACGTGTAGCCCTGTCGATATTTCCTGAATGGATTTCATTCC
TTTCTCAGTCTTGACCATTCCCTTACCCAACCCCCACCCCAACACAGTCA
AAACCTTTTCGAGCAGCAGCTAGGAAGGTGAGTGGCCTCCCACCATGAGC
CTCACTTTGGGGAATCTATGCTTTAGTTGGGGCATATTCTTGCCTTAGCC
TCATCTCTGCATTTGGCCTCATTCTGCTGCTGCTTCTCAGTACCCAGAAG
TCCTTGGGTTCTACCAGAGACCACTCCGACAGAAAGGGTCAGAAACAACT
GACCCTTTCTTGGCTGGGTCTGGACTCTGGAGTACAGGAAGAACTAAATT
ATTTTGTCTTGGTCCAAGCTGAGCTCACGCTGGCTTCCCGAAGAGGAGAC
AGGAAGGTTAGGTCAGAAGTATGCTCATGTTGAGACCTAGGGCAGATGGT
ACCGGGCACCATGAAGCATCTTGA

1883. chr12_CACNA2D4_NM_172364_-1.90761
CAGCAGGAGTAGGGGCGGCGAGGCTGAGGTGTCCGAGGCGC

1884. chr12_CACNA1C_NM_199460_-1.55599
GAGGCTACGATTTGAGGAGGTTGAGGGGGAAGACAGGAGGGAAAGAAAAG
TCCTACAACTGTCAGGAATGGGGCACCTTTCCCT

1885. chr12_PLEKHG6_NM_018173_-1.82454
GGATGCGGGGGCCCCACATCATTCAGC

1886. chr12_LTBR_NM_002342_-1.659
TGCCACACCCTCTAACAGGGGCCCAAGGAACCAATTTATCACCCATGACT
G

1887. chr12_LTBR_NM_002342_1.52887
AGCAAACCTGAGGCCTCCCGGCAGACCCACCCACCCCCTGGGGCTGCTCA
GCCTCAGGCACGGACAGGGCACATGATACCAACTGCTGCCCA

1888. chr12_TAPBPL_NM_018009_-1.55007
GACACAGACCCAATCCCTGAGCTTCCTGCTGGGGTCCTCAGCCTCCTTGG
ACTGTGGCTTCTCCATGGCACCGGGCTTGGACCTCATCAGTGTGGAGTGG
CGACTGCAGCACAAGGGCAG

1889. chr12_IFFO1_NM_080730_-1.65271
CAGGTGCCGGTTCATGTCGTTCTTGGCCGTGGCC

1890. chr12_IFFO1_NM_080730_-1.58429
CGACCAGATGGTGCCGGGCATGAAGCGGGCCGACGAGGAATAGGTGGTGG
AGGTGGAGGTGGAGGACGACGAGAGGCTGGCCGCGGAGGGCGCGAGGGGG
CCGGCCGGGGAGCGCGCGGGCGAGCCCAGCACGCGCGCCGAAGGGCTGCA

Figure 3-154

GACAGCGGCCGGCCGGGCGCCCAGCTGCAGCCCCAGGGGCCGGATGGGGC
TGACGAAGCCGGTCTGCACTGCCTGGTCGCGACGA

1891. chr12_NOP2_NM_006170_-1.73489
CCTCCAGGGGCACAACACATGTCCAGGATCCGCTCATGTTCCTGGGGTGC
CAAGGCCATGACGGGCAACATGCTGGAGGCTCCCTGCAGCATGTAGTGCC
CAGCCAGGT

1892. chr12_GPR162_NM_019858_1.76452
GCTCTGCTTCCTAGCGGGCACACACATACTCATGGCAGCTGTGCCCCTCA
CCACCTTTGCCGTGGTGCAGCTGCGTCGTCAGGCTTCCTCCGACTATGAC
TGGAACGAGAGTATCTGCAAGGTCTTCGTGTCCACCTACTACACCCTGGC
GCTGGCCACCTGCTTCACGGTCGCCTCCCTCTCCTACCATCGCATGTGGA
TGGTGCGCTGGCCCGTCAACTACCGCCTCAGCAACGCCAAGAAGCAGGCA
CTGCATGCCGTCATGGGCATCTGGATGGTCAGCTTCATCCTCTCCACACT
GCCCTCCATTGGCTGGCACAACAACGGCGAGCGCTACTATGCCCGCGGCT
GCCAGTTCATAGTCTCCAAGA

1893. chr12_LPCAT3_NM_005768_1.66112
TGATCTTTCCCTCCGTCAAAGTAGTCAACAGCCAAAC

1894. chr12_FAM90A1_NM_018088_1.53738
CCGCCATGTTTTCAAGCCCGAGGCCAGCT

1895. chr12_PZP_NM_002864_-1.57643
GTGCTGCAGGGGGCGATATACTCAGCAACCACAG

1896. chr12_CLEC1B_NM_016509_-1.64893
GAATCAAAGCCATCACACGCCACCAGGAGG

1897. chr12_TAS2R10_NM_023921_1.64379
AATACTATCATGAAGGGAAGAACCATATTTGTTCTGCTCTTCAACCAGAG
AAATATGTAGTTGGAAAAATTTGCTATCTTCAGGAAATAGAAGATGCTGA
GGCTGGTGGCAAACCACATACTTGATTGATTACCAATTACCCAAAAGTAA
CTAATATATTCAATTAGGTTACCGGAGGCATATATATTTGGAGAGAATAT
CTGTATAAATCCATCTGTAATTATTATCCATATCAGAAAAATTCTTGAAA
TAGCTAAGCCGGTGAGAATAAAGCC

1898. chr12_DUSP16_NM_030640_-2.11458
AGAGTCGGCACAGGGTGGACTGAGGGGCGTCTCGCTTTTCTGTCC

1899. chr12_EMP1_NM_001423_1.52527
CCAGTACACCAGCAGAGGAAACTTATAACCTCGGGAG

1900. chr12_C12orf36_NM_182558_-1.5277
AGGAACCTAAAGAAGCTCTCCCTCT

1901. chr12_MGP_NM_000900_-1.66468
TACGGGATGTTAGTGGAAGGCTGTGAGG

1902. chr12_RERGL_NM_024730_2.32543
CCTGTTCCTTCACCACCCAAGACA

1903. chr12_PIK3C2G_NM_004570_1.53093
TAGTGGAAGTACCTCAAAGCAGCAATACGAGTCTGGCCTCTTTTT

Figure 3-155

1904. chr12_LDHB_NM_002300_1.50599
AGGTGTCTGAAGAAATAAGCTCCCA

1905. chr12_ETNK1_NM_018638_1.62731
TGGCCAATTACATCCACGTCCCTCCCGGCTCCCCGGAGGTGCCCAAGCTG
AACGTCACCGTTCAGGATCAGGAGGAGCATCGCTGCCGGGAGGGGGCCCT
GAGCCTCCTGCAACACCTGCGGCCTCACTG

1906. chr12_SOX5_NM_006940_1.57403
TTCCTGCCGCCTGTTGCGCATGATTGCCTTGTATTCACCAATGCGCAGCT
TTTTGCCATCCACCAGGCAGGTGCGCTTTGGCCTGGGCTTGTACTTATAG
TCA

1907. chr12_IFLTD1_NM_001145728_1.50526
ATGGTTAAACAATTGCACGTGCTCTTCTTTTGTGAGTTCTGTACCCAAAA
TAACTTTGTTTACAAAAAGAGAAATCTAAGGCAAATAGCAATTTTATCCA
TTGAATAATACTAACCATCTGCTTGTTTTCTGCAGGGATTTGGAAGGCAG
GAGTGGTAGGACTTGTGATTTCATCAAGCATCTATAATTCACCAATTCTA
CAGCAATACAAATTTTGGATCCTTTTTCCATATAGAAATGTGATGTCTTC
ACCCTCTCATGGAATAGCAGGGAGGTTGCAGAGCAGGCCTCAGGGATTTG
AGTTCTCTTTTGCTTTTCTAGTAGCTGGTTGAGGGTG

1908. chr12_FLJ13224_NR_026806_1.59113
CATCCCTCCGGAGTTGAGCAAACAACGCCACGCCGCGTGCGCTCCGGCAG
AGCCCAGCACTGACCCCCAAAGGCCGATTTAAAGACCCTCGGCCGCCAGC
TCGGAAGCGGATGGCAACTTAGTTTCCGAGCGAATGGCGTTTATTGTCCA
CCCTAGTCCGAGGGCTGCAGTCAACTAAACCACGAGGTTTCACAACGGCG
CCCGACCCTGCCCGCGCCTCGCGCCCACGCGGACGCACCGACCCCGGCCG
CTGCGCGGTGGCCAACGAGTCGCTTTCCTCTCGGGCCTTTCGGCCGCCGG
GCTCCTTTCCGCGAGAGAACACTGCGGCGGAGAAAAGTCATTGTCACCTT
CAACGTGGATCCCTCAACTCCGGCGACTCCTCAATTATGCCCAGGCTCCA
CTCACTTCCCCGCCCCGAGACTTTCGGTTTGCCTCAAATA

1909. chr12_CPNE8_NM_153634_1.72556
CCTCCACCCGCGTGGCCGGGATGGCAGCGCTCAGCTGGTTCAAGTCC

1910. chr12_GXYLT1_NM_173601_-1.57859
ACCGCCGCCCGTTCCTTCTTCCAGGGACACGGCGAGCTGGCTGAAAGCGT
AAAGGAGCGAGCAGAAGCCGCAGGCCACACACAGCACCACGACGCGCAGG
TAG

1911. chr12_PPHLN1_NM_201515_1.52519
AAATTTGATTCCTAAAAGGACTCA

1912. chr12_RAPGEF3_NM_001098531_-1.60087
AGGGTTGTGGCTTCGGCAGTGGTGCAGCATCCGCGCGGCTCT

1913. chr12_RAPGEF3_NM_001098531_-1.58517
GGGCCACAGCTTCGGCCAACTCCTCCTCCATCTCATGAGTTCTCACGGGC
TCGGGCTCGGGCCCGGGGAACCGGTAGAATTGGGCATCTCGGTC

1914. chr12_DDX23_NM_004818_1.5421
CTGAGTCTGAACCGCCCAACGCGGCCTCAACGTCGCGGAGCCGTCGCCAT
CTTTCCCGTTTCCTGGTCGCGGAGATGAACACCC

Figure 3-156

1915. chr12_MLL2_NM_003482_2.13744
TGGACAAGCAGGAGTTGTGAGTCCCCAGA

1916. chr12_MLL2_NM_003482_1.50959
GAAGAGCCCTCATGTGGCAAAGACATGGCCTGGGCAGGGCCTGGTGCAGA
CAGTAGGGAATGCT

1917. chr12_MLL2_NM_003482_1.53531
CTGCACCTTGTTGATGCGGTGAGCTGCCCGGTTATCTTTGGCCTT

1918. chr12_TROAP_NM_005480_-1.81444
CCAGTGGCTGCGTGGTGTCTCCCCT

1919. chr12_KCNH3_NM_012284_2.75488
AGGAAGAGCTTTGCCATCCCCTGC

1920. chr12_PRPF40B_NM_001031698_1.71961
CGGCTCCGGGTGCGGACACCGCCAGCT

1921. chr12_PRPF40B_NM_001031698_1.95591
TCCACACCAAAGGCCGAAAGCATGGCAGGA

1922. chr12_NCKAP5L_NM_001037806_-1.98698
CCTCCAGTTGTCGGGGTGGGCACATGAGAGGGTCCGAGGAGCTGCCGGCT
GCCCTAGTATTGGGGAAGGTCCAG

1923. chr12_---_---_-1.59096
TCCCTCATGCTTGAGTCCCCTGGGGCCACCTTGAGGCAGCCTATCCCAAT
GCATCCCCGCCCCGCTATCCGGGTGGGGCGCAGAAGAGAGGGGAGCCCTT
CTCCGCTCAGTCTCC

1924. chr12_METTL7A_NM_014033_-2.12772
GAGCAACCGCACCCAGCTTAAGGTTT

1925. chr12_SLC11A2_NM_001174125_1.59276
ACACAAAGCCCAGATAAGCCACGCTGACCACAGCAGCCACCACATATAAT
GCCACATGCCCTAGGTCCCGGACATAAACCACTACAAAGTACATATTGAT
GGAACAGATGATAAGGACCAAGATTCCTCCTGC

1926. chr12_LETMD1_NM_015416_-1.58678
TGTGTGGGGCTCGGCAGTCACCCCTGGACATTTTGTCACCCGGAGGCTGC
AACTTGGTCGCTCTGGCCTGGCT

1927. chr12_BIN2_NM_016293_1.68465
GGTACCATGGAGACTTGAAGCTGGTCT

1928. chr12_ANKRD33_NM_001130015_-1.58855
CAGCCGAAGCCCAGTCCTTCAGGACACCAAAGTCTGGCCCTTCCTCTCTG
GCGATACCAGGAGCTCA

1929. chr12_C12orf44_NM_021934_1.51029
GGAACGCGGGCGCTCCTCCAGCTTCCGAGTCCAGCCAGCCTGGGCGCGGG
GCGCCGCCCCCGAGACACCCGAGGAGTCCGTTCCTCCCTGGTTACGTGGA
CTGTGGAG

Figure 3-157

1930. chr12_KRT7_NM_005556_-1.65774
GCTGGACGCCGACCCCTCCCTCCAGCGGGTGCGCCAGGAGGAGAGC

1931. chr12_SPRYD3_NM_032840_-1.51863
GTCCCACAGACTCTGACATCATGTAGCCGGCCCCATTCATCCTCGTAACT
GTCCACCATCATGACGCTGTCGTCCTCACGGCCCAGCTCAGCGTTGAGGT

1932. chr12_ZNF740_NM_001004304_1.50667
CAGCAAGCAGGCCGAGAATGGCGAGCGGGCAGGTAGCCCTGATGT

1933. chr12_SP1_NM_138473_-1.74974
ATGCCCAACCCCAAGCCGGTCGGAGGACCCGGCGGGAAGCATGCACCTGC
CCCTACTGTAAAGACAGT

1934. chr12_AMHR2_NM_020547_-2.30255
GGCTGCCTTGGCCCATCCTCAAGA

1935. chr12_ATF7_BC042363_1.64464
ATAAAAATAGCCTAGGTCTGAATAC

1936. chr12_COPZ1_NM_016057_-1.65001
GTGATCCTAGAGAGTGATCCCCAGCAGGTGGTACACCGGGTGGCATTAA

1937. chr12_KIAA0748_NM_001098815_1.68972
GATCTTCCTGTGAGAATTGCCCCAAATCAGAGTCTTGCTGGAGGAACTGC
TTCTCTTCTTTCACTTTGTCCATCACTTCCAACACAACTTGGTCCAAACT
GTTCCTTTTGGGGGTGTTGTGGGGTGGTGGTGGCCGGTCTCGGGGGCATG
TGTACAGACACATCTTGGAGATGGCTTTCCGAAGGCGGTCTCTGGGTGAC
TGGGGTTCAGGCTCTCGGGACAGAATCCTGATGGATGGCACATCAGTTGG
ATGGTTGCAATTCCAGAACATGTGGGATGGTGTGAACTTTTGGACAGGTG
TCTTAGACACATAGGAGTAGAGACA

1938. chr12_ITGA7_NM_001144996_1.56206
GCTCAATGAAGACACGGGCTCGTGCAGAGACTGGAT

1939. chr12_MMP19_NM_002429_1.57993
TCGAGGCGAGTAGACAGCAGCATCCAGGTTTCCGGGGAGCCCCTCCCAAA
GGGCAGACACTCGGAACAAGGGGCCCGGTCCTGAATCTGATACAGTCCAC
ACATAGTCCCCCTTGAAAGCATAGGTCTTCCCACGGG

1940. chr12_CNPY2_NM_014255_1.64526
TAAGCGGGACTCCAGCGTGCTGCGGTGCGAGCCCCAATCAGACACCGA

1941. chr12_TIMELESS_NM_003920_1.52136
GAGGGCTCGAGTCTTCTTTTCTGCCATCTCTCGCTGGCGCAACACCTCCA
GTTCTGCAAAATCTGCACTCCGCTCCTGAGCTAAGCGTCCCTGCCCTACT
C

1942. chr12_PRIM1_NM_000946_-1.6573
CCACCGTAGTTGAGCCAGCGATAGTACTGAGAGTAGGGAAAGAGCCTCCG
GTAATAAAGTTTAAGCAGCTCGGGCAGCTCGGTGGGGTCAAACGTCTCCA

1943. chr12_PRIM1_NM_000946_1.51607
GCGGAACTCGCCACGGTAAGGATTACCACAGGAATTGGCGGGAACAGCA

Figure 3-158

1944. chr12_LRP1_NM_002332_1.63177
GGACGGACGATGGGCCCAAAAAGACAATCAGCGTGGCCAGGCTGGAGAAA
GCTGCTCAGACCCGCAAGACTTTAATCGAGGGCAAAATGACACACCCCAG
GGCTATTGTGGTGGATCCAC

1945. chr12_LRP1_NM_002332_-1.62093
GCCATGGCAGTCGCCACTCCCTGGCCAGCACGGACGAGAAGCGAGAACTC
CTGGGCCGGGGCCCTGAGGACGAGATAGGGGACCCCTT

1946. chr12_GLI1_NM_005269_-1.64525
GCAGCACCACCTCGACTTCTGCCCCCATTGCCCACTTGCTATGGGCCTCT
CAAAGTGGGAGGCACAAACCCCAGCTGT

1947. chr12_B4GALNT1_NM_001478_-1.68145
GCTCACTGACCCAAAGATTTGCACCGTGTGGGTCTGACCTCATCATGTGG
AGTGCAGAGGGCCCTGATGACATGTGTGTGATGAGGACCATGACCCTTGA
ACCC

1948. chr12_CDK4_NM_000075_-1.62522
CCACATGTCCACAGGTGTTGCATATGTGGACTGCAGAAGAACTTCGGGAG
CTCGGTACCAGAGT

1949. chr12_TSFM_NM_001172696_-1.54583
AAGGCCTGATTGGGCTGTTGCAGGAAGGAAACACAACTGTATTAGTAGAG

1950. chr12_CTDSP2_NM_005730_1.68802
GGTGGAACACGCAAGACTCACGGAATAGGCGGGCCCGGAACACCCCACAC
CGGTCCAGCAGGTCTGTCACAGGGTCGGCATA

1951. chr12_XRCC6BP1_NM_033276_-1.70423
GCCCTTCTTCCCTGCGGAGGGAGGGCCTGGGCGGTCGCGTTGGCGGGAGG
GAGGTTACCTTTCCCAGTCTCGCTCTGGCCGCCTGAGCCAGGAGGAAGCA
GCGGCGAGGTCTGCGGGAG

1952. chr12_MON2_NM_015026_2.00601
GGGCGACTCGGCTAATGGCGTCGGCGAGTCTTAG

1953. chr12_C12orf66_NM_152440_1.56331
CATGATGGCATCCAAAAGGCCAACGAGCTCTTCAGCATTGATGAACTTCT
GTGTGCTGAGGGTGTACATCTTCTCATAGAAGTCTGCCATCTCCATCCGA
GCCTGAACAAAGAAGCAGAGCTGCTCTGACAGGTGGGAAAGGAGTTCTTC
CACGTGAGGAGCAGTCCCACCCAGGGCACCACGGCCAGTCACCACCTTCT
TCAGCTCATTATGCAATGAAGTATAGATGGTGCGGATGGAATCCTTCC

1954. chr12_GNS_NM_002076_1.61041
AGCTGAAGGGCGAGAGGCCGACCAGCCGAAGGAATAAAAAGCCGTGCCTT
GAAGGCCGGTGGCTGGAGTCAGACGTTTTCTCCCTAGGCGCGATCACGT

1955. chr12_RPSAP52_NR_026825_-1.68076
TGAGCCTTCCAGTCTTCAGTAGAAAC

1956. chr12_PTPRB_NM_001109754_1.51743
CGTATGTGGTGTTGTCTATCCGAAAGGTAGGGCACAACGCGGCCCCCAGG
GTGTCACTGCTATAGATGAGGCTAAAGTTACAGGGTGAGCCCAAAATTCT

Figure 3-159

CCACTGGATAGACACAGAATGGCTGGAGGCCTTGGACTCCGCCAGGGTGA
AGTTACATCTCT

1957. chr12_ZDHHC17_NM_015336_-1.60326
CCTTTTTCGATCATTCAATGCATAGTGCATTGCCCCTTGGGATATATTTG
G

1958. chr12_C12orf50_BC038413_1.84154
GATGACAAAATATCTGGAGGAGTA

1959. chr12_CEP290_NM_025114_-1.50564
ATAGCCTCTTTCCGAGATTCCCTGAGCTCCTGTCTTAATTCTTCATTTCT
TCCGGTAAGCTGATCAACTTGGGCTTTCAA

1960. chr12_C12orf37_AK058107_1.52047
TCCCATGAGCATGAGAGAAGAAGCAATGCACGCTCCGGCAGATTCCT

1961. chr12_PLXNC1_NM_005761_-1.63953
GCCTGCACTTCGTGGACGCCTTTCTCTGGAACGGCAGCATCTACTTCCCC
TACTACCCCTACAACTACACGAGCGGCGCTGCCACCGGCTGGCCCAGCAT
GGCGCGCATCGCGCAGAGCACCGAGGTGCTGTTCCAGGGCCAGGCATCCC
TCGACTGCGGCCACGGCCACCCCGACGGCCGCCGCCTGCTCCTCTCCTCC
AGCCTAGTGGAGGCCCTGGACGTCTGGGCGGGAGTGTTCAGCGCGGCCGC
TGGAGAGGGCCAGGAGCGGCGCTCCCCCACCACCACGGCGCTCTGCCTCT
TCAGAATGAGTGAGATCCA

1962. chr12_NEDD1_NM_001135175_1.59867
GTGTGCTGCCTCCGAAAAGTTTGCCTCGTCTCCACAAGTCTGTCTCCTTT
TTTGTCAACCTCAAGTA

1963. chr12_SLC25A3_NM_005888_1.61399
TCTGGCGCACATCACTATATTTGGCTGCCTCTGCCAGTGCTGAATTCTTT
GCTGACATTGCCCTGGCTCCTATGGAAGCTGCTAAGGTTCGAATTCAAAC
CCAGCCAGGTTATGCCAACACTTTG

1964. chr12_APAF1_NM_013229_-1.56737
CTATGACTGGGGAACTAGTACACACCTATGATGAGCACTCAGAGCAAGTC
AATTGCTGCCATTTCACCAACAGTAGTCATCATCTTCTCTTAGCCACTGG
GTCAAGTGACTGCTTC

1965. chr12_SCYL2_NM_017988_-1.61359
GCCAAAGGTTCTACCAAAACTGCC

1966. chr12_ANO4_NM_178826_1.67299
TTTACAGGACACCCAGGTGCCTACTTGA

1967. chr12_CCDC53_NM_016053_1.83338
CGGTGGACCCCGAGTTCACCCACAAACCCCTCCCAGATGGGGCCCGCCCA
ACCCGGTAATCACGTCTCAACTT

1968. chr12_C12orf42_NM_198521_-2.17071
CTGCAGGGTCCCTATCCCGGGGCGCC

1969. chr12_HCFC2_NM_013320_1.60072
CAATAAGAAAGCACCTTTAAATTGA

Figure 3-160

1970. chr12_NUAK1_NM_014840_1.66381
CTCGGCCAGAAAACCTCTCGGTGGCCCGCTTGACTTTGCCGTAGGTGCCT
TTGCCCAGGGTCTCCTGCAGCTCGTAGCGGTGCTTCAAGTTGTGCTTGTG
GTGATGCCGCTTCACCCCGTGCG

1971. chr12_POLR3B_NM_018082_-1.57448
ATATTGAATATACCCGAGGCAGCCAGAGGATCATCCGCAATGCCTTACCT
ATCGGCAG

1972. chr12_POLR3B_NM_018082_-1.58164
TGTTTGTGGCTTGATCGTCCCCCAGGAAGAC

1973. chr12_SART3_BC041638_-1.57266
CACAGGGTCGTGGCGAGGATTCAATGAGATAACGTTTGCAAGGCAATGGG
CAGGCAGTAAGCACTCAAATCCGACAGGAGCTACTGTCACGAAAAGCGGG
TTTGCAGCCTTGGC

1974. chr12_TCHP_NM_032300_1.72673
GATGGAAGCCTTCCGGCAGAAGGCA

1975. chr12_GIT2_NM_057169_2.23206
GCTGCTCCGGAGCCGTTTCGACAT

1976. chr12_C12orf24_NM_013300_1.73277
CCCGCACACGGCTCGCGGTCTCGGCGCCGCGGAGATGCCCGGCCAGG

1977. chr12_RPL6_NM_001024662_1.63788
CCTGTGGCGTCCAGTGAGGATGATCAGAATGGTCCCGGGGGGTAATGCTGG
CTCGCAGTTTTCTCACGTGCTGACTGAAGGGTTTTTTGCCGTGGCTCAAC
AGCTTTCGAGGCACATCTTCAGTAGGATAA

1977. chr12_DTX1_NM_004416_-1.73007
CATCCTGGCCTCGCAGCGCCGCAAGGCGCCCCCCGCGCCCCCGCTGCCGC
CGCCGCCGCCACCTGGAGGGCCTCCAGGCGCGCTTGCCGTGCGCCCCAGC
GCCACCTTCACAGGCGCCGCGCTCT

1979. chr12_DTX1_NM_004416_-1.66559
TGACCGGGATACTGCTGTGCGCGGCCGGGCTGCCCGTGTGCCTGACGCGG
GCCCCCAAGCCCATCCTGCACCCGCCGCCCGTGAGCAAGAGCGACGTGAA
GCCCGTGCCTGGCGTGCCCGGGGTGTGCCGCAAGACCAAGAAGAA

1980. chr12_TBX3_NM_005996_-1.52529
CGATGTCCCTACAGTGGAGGCGGCTGGAGAAGAAGCCTGGGCGAAGCAGT
TGAAAGCTGCTTGTTCACTGGAGGACTCATCAGAGGTCCCATT

1981. chr12_C12orf49_AK298857_-1.89207
TGAGGAAGTAGACGAGCGACAGCCCGAAGACCAGGGCGAGCAC

1982. chr12_FBXW8_NM_153348_1.63834
CACAGCCTCATCACGGCCAACGTGCCTTACCAGACGGTAATGCGAAACGC
CGACCTGGACAGCTTCACTACTCACAGGAG

1983. chr12_NOS1_NM_000620_-1.72363
TCGTACGTTCGCAGGGTGACTCCAAAAATATC

Figure 3-161

1984. chr12_TAOK3_NM_016281_-1.66063
CAATGAGGACACGTAGTGGCCGGTCTCGTCGAACAAAGTCAT

1985. chr12_PRKAB1_NM_006253_-1.5717
AAAGCGCGATTGCGAGAGCTCGGCAACCCTGCCGACTCAGCCGGAACCGG
CTCCCGGCCCGAGGGGCGTGGTGTCCTGGTGCTCCGACTCCTTCCGCAGG
CTCCTTGGGACCCGCGGTTCCGGGAGTCCCTTGCTCAGGGTCCCTTTC

1986. chr12_CIT_NM_007174_-1.72679
CTCCTTTCTGCGGCTGGATGGCGGGGCCAGCAGGCTCATGGCACTGGGCT
GGTGCTCTGGCGACCGCACGATGGCGGACATGGCGATCTGCTGCCTCGCG
GTGGCTGGCGTGGATGGGTGTGGGTGGTCCGTTGCTTTGCGGTGGGCAG

1987. chr12_PXN_BC052611_-1.54772
ATACCTCCGAAGCCCATGGCTGCTCCCATGTGGCAGCCAAGGCCTCCTCT
GGGCACGAAGGGCTGGCTGGTGGCCCCTGGGGCTCCCCAGGCTCTTGGAG
AGCTGTGCTCCCAGCACAGGGTACAGTGTGGCAGCGGGGAGCCCCAGAGA
GCTCACTTGTGATGGTCGGCAGGTGCCTCCAATCTCG

1988. chr12_PLA2G1B_NM_000928_1.59088
GCTACAGGTGATTGCCGAGCCAGAGCACGAGTATGAATAGGTGTGGGTGT
ACGGGTTGTCCAGCAGAAATTTACAGCTGTCCAGCTTCTTGGCCTGGTCA
TAGCAGTTGTCATGTG

1989. chr12_MSI1_NM_002442_-1.70004
GCCTGAGAGAGCGGGCCTGCCGTGGCCAC

1990. chr12_GATC_NM_176818_1.64441
TCACGGCTGCGGTGATCGAGCACCTGGAGCGTCTAGCGCTTGTGGACTTC
GGCAGCCGCGAGGCAGTGGCGCGACTGGAGAAAGCTATCGCCTTCGCCGA
CCGG

1991. chr12_---_---_1.56638
CACACCATGGCACTTGACCCATAGCAACTGTTGAAAAACCACAATGGCAC
GGTTACTAAATAAGCGAGGCATAGCCTTCTCCGGCTTAG

1992. chr12_CAMKK2_NM_006549_-1.68311
GGTCTGGAAATTCCAGGGCCTGACTCTTGATCTTACTGTGTAAACACATG
ATCCGCTCGTCCATGAATGGGCA

1993. chr12_---_---_1.78479
AATTATGGTACATGAAAATAATCT

1994. chr12_---_---_-1.50279
AGCTATTTGGGAGTCTGATGCATAAGAATAGCTTTAACCCAGGAGGCAGA
GGTAGCAGGGACCCGAGATCAT

1995. chr12_KDM2B_NM_032590_1.69001
GAGATCCCGCATCTGGGCATCCTTTAGTCCCTCCACCCACTGGACATCCA
GGGTCCGGAGCAGCGGACAACTGGAGCTGCAAAGGGCCGAGACCGCGATC
CAT

1996. chr12_KDM2B_NM_032590_-1.8136
CTGTGCATGACGTGGGCTGCCCCATCGTCCAGGGGTAGCGAGTCAGGCGG

Figure 3-162

GGGGCTGATGGGGGGTGGCCGGATCACATGGCGCTCCATCTGGATACACT
TGGGCGGG

1997. chr12_CLIP1_NM_002956_1.73563
CTGAACAGAGACTGCCTCCTCTGA

1998. chr12_KNTC1_NM_014708_-1.82785
AAGCCATCTCCAGTATCCATTCTT

1999. chr12_HIP1R_NM_003959_-1.68986
CCTCATAGACACCTGCAGGGAGTGCGGGGCCCGGGCTCTGGAGCTCATGG
GGCAGCTGCAGGACCAGCAGGCTCTGCGGCACATGCAGGCCAGCCTGGTG
CGGACACCCCTGCAGGGCATCCTTCAG

2000. chr12_ZNF664_NM_152437_1.69962
GCGCCCTGCGTCCGGCAGAGGAGGCGAG

2001. chr12_FAM101A_NM_181709_-1.72831
GGGCGTCCCCAGCTAACACCCATCCACGCA

2002. chr12_NCOR2_NM_006312_-1.67328
CATCCCGGTACAGCAGCGGGTACACAGCACTCCGGGAGTGCCCTGGCTCC
GTCATGCCCTCCGGTGGGGACACAGGTTCAATACCGTCCTCACCACCACC
CAAGACCGACGTCTTGTTTGGCTCTG

2003. chr12_NCOR2_NM_006312_-2.308
AGCTCACAGGGCTGACGGGCTCCACCCCTTCG

2004. chr12_NCOR2_NM_006312_1.50283
TTCTGTCCAGCGAGAACTCTCATTCAGCTCCATG

2005. chr12_NCOR2_NM_006312_-1.68826
ATTCCCGGGCTGGAACTCAGACAGCAGGGAGGGCCTCCGCCGCTGGGGCT
GGATGATGGAGCCGGGCGACAGGTGGGAGGCATAGTCGCGGGAGTGGTGC
TGGTACTCCAGGAGCCCGACGTC

2006. chr12_GPR133_NM_198827_-2.08522
ACCCGGCCAGGCATGGCCTCCACCAAGCTCAGCCCTTGGGACAAGAGCAG
CCACTCTGCCCACCGCGTCGACCTGTCAGCCGTGTGA

2007. chr12_SFRS8_NM_004592_1.52198
CCGCGGCCCACTCGGCGCACTCAGCCAGCGTCTCCCCTGTGGAGAGTCGG
GGCTCCAGCCAG

2008. chr12_ULK1_NM_003565_-1.88141
CATCACCCTTTCCTCGATGCCAGCCCCTCGGTCAGGA

2009. chr12_EP400_NM_015409_1.52185
AGAACGACACATTGGATACAGAAG

2010. chr12_POLE_NM_006231_-1.70128
GCACGGACGCAGAGGCACCCGGGGCC

2011. chr12_POLE_NM_006231_-1.50482
ACCAGCTGTTTATTGACCACACAC

Figure 3-163

2012. chr12_POLE_NM_006231_1.69921
GCACAATCTGCCACGGAAGGTCCAGGATGCTGCGGGCAGTTCTTCGCAAG
AAGCTCCCCAGCCCCGTGGCAGGACCATCCCGGATGGCCCCGGGCCTGAG
CACACCCTCTGCCGACTCCAGACGCTGCCTCTTCCTGCGGGCGAGGCGCT
GCCGGGCCTGCAGCTGCCACTTCTTCTTGTGGAACCGGAGCCAGACA

2013. chr13_ITGBL1_NM_004791_2.28431
GCAATTGCAACTCCGGCTGGAGCCCCGGACCTGCAAGCCTGGGTGTCCGT
GGGTCCGTCTGCCCAGCCAT

2014. chr13_SGCG_NM_000231_-1.67771
TTAGAATCCCCCACTCGGAGTCTAAGC

2015. chr13_ATP12A_NM_001676_-1.56649
ATTATGGTTACTGGTGATCATCCCATCACAGCCAAAGCTATTGCCAAGAG
TGTGGGGATCATTTCAGCCAACAGTGAAACAGTGGAAGACATTGCACATC
GCCTCA

2016. chr13_PABPC3_NM_030979_1.98426
GAAACTTTGACTGCCTCCAGGTTGG

2017. chr13_FAM123A_NM_152704_1.65484
ACTCTGCGGACCAGCACTTTGGAAACCGGGATTTTTGTTCTGGGCATCTC
ACTCCTGGAGGGTTGCTGGTGCACCACGGGATGGCTAGATGGAAGGTTGG
TCAGGTGCTTGATGCTAATAGGGATCTTAGAGTCCTTCAGCAAGCTGCCT
GGTGTTCGCAGTGGACAGGTGATGGTGCCTGGAGATACGGGCTTTAACCG
GGACAGGGAGGACGTCTCCTCGTTGTCCTTCCCTCCAGGAAGGGTTGCTG
GACTTCCGTCCGGGTCAGCATAGAGATCATAGAGCGCGTCCCCGCT

2018. chr13_ATP8A2_NM_016529_-1.7484
TGTCCCGGGCCACGTCTGTTGGAGACCAGCTGGAGGCACCCGCCCGCACC
ATTTACCTCAA

2019. chr13_PAN3_NM_175854_-1.5137
ATTCACATTTGGGAAACGAACAGGAGATGAGCAA

2020. chr13_MTUS2_NM_015233_-1.68042
AAGGTAGCCAAGGGAACCACATGGAAGTTGTGACAGCTCCCAGCGGCGCG
CCCCTTTCGTGTGTGCCGGTACCTCGGCTTAGGAGTTGCCCGCTGACACC
TTGAATGA

2021. chr13_MTUS2_NM_001033602_-1.61907
AAGATCTCACCGCCAGCCATGATGCTGCTCTCCTAGAGATGGAAAATAAC
CACACAGTTGCCATCACAATCCTGCAGGATGACCACGACCACAAAGTCCA
AG

2022. chr13_OK_AB064667_3.69709
AGGCGGCCCACTAGAAGGCGGCAG

2023. chr13_FRY_NM_023037_-1.66425
CGGAGCTAAAAGAATTACGGCACAAAGAGCAGAACCCATATGTGGTTCAA
AGCATTATCAGCTTAATAATGGGCATGAAATTCTTTCGAATTAAGATGTA
TCCAGTGG

Figure 3-164

2024. chr13_KL_NM_004795_1.77432
TCGTTTAACGACCGCACAGCTCCGAGGTTTGGCCTCTATCGTTATGCTGC
AGATCAGTTTGAGCCCAAGGCATCCATGAAACATTACAGGAAAATTATTG
ACAGCAATGGTTTCCCGGGCCCAGAA

2025. chr13_DCLK1_NM_004734_-1.71156
ATAAGTGATTACACCTGCTGCCCA

2026. chr13_POSTN_NM_006475_1.7366
GTGCCAGCAAAGTGTATTCTCCATCTGGCCTCAGAGCAGATGCCAAGCCT
AATTGGGCCACAAGATCCGTGAAGGTGGTTTGCTGTTTTCCAGCCAGCTC
AATAACTTGTTTG

2027. chr13_TRPC4_NM_016179_1.95759
TCATGCCATGCTATTTCTTCGTCT

2028. chr13_UFM1_NM_016617_-1.53831
TAAGATCACGCTGACGTCGGACCCACGGCTGCCGTACAAAGT

2029. chr13_FREM2_NM_207361_1.50537
GCTCTAGGCCGAGAATGGTATATACATACGATCTATACAGTGAGATCGAA
AGACAATGCCAATCGAGGTATTGGCAAAAGAAGTGTGGAGTACCATTCTC
TGGTGAGTCAAGGAAAGCCCCAATCCACCACCAAGAGCCGGAAGAAGAGA
GAGATCAGGAGCACACCCTCACTGGCATGGGAGATTGGTGCTGAAAACAG
TCGAGGAACAAACATCCAGCACATTGCCCTGGACCGCACCAAGAGGCAGA
TCCCCCATGGGAGAGCACCTCCAGATGGCATCCTCCCCTGGGAGCTCAAC
AGCCCCAGCTCTGCAGTCAGCCTGGTCACTGTGGTGGGAGGCACCACGGT
AGGGTTACTCACCA

2030. chr13_FOXO1_NM_002015_-1.75089
GCGGGTGCTGCGACAGCGGCCCGGGCGGCGGGGGCTGCGGTGGCGCTGGG
TGCAGGCAGCCCGCCTCCGGGCCCTGGAAGTCCCCGCACAGCCCCCCGGT
GGCGGCCGC

2031. chr13_ENOX1_NM_017993_-1.69058
GGGGCAGGAACACTTTGATGGCTGAGTGCAGGGTCCCCTCGGAGGTCATC
AGATT

2032. chr13_NUDT15_NM_018283_-1.51483
TGACGGCCAGCGCACAGCCGCGCGGGCGGCGGCCAGGAGTCGGAGTCGGA
GTCGTGGTGACCAGCTGCAAGCATCCGCGTTGCGTCCTCCTGGGGAAGAG
GAAAGGCTCGGTTGGAGCTGGCAGTTTCCAACTCCCTGGA

2033. chr13_FNDC3A_NM_001079673_1.59847
TCACTTTAAATGATCTCAAGCCAGCC

2034. chr13_FNDC3A_NM_001079673_1.55148
TGAATCTTTACTTGTGCAGACTCCAGCTGTGCCTCCTGGCCCATGCCTCC
CTCCCAGATTACAGGGTAGACCCAAAGCAAA

2035. chr13_CCDC70_NM_031290_1.57579
CAGGACTGAAAGGGCACAGACAGGTCACTGCCAGCATTGTTGGGGCAAGC
CTGCAAGCACGCATCACTGGGGATCTGACATGACAA

2036. chr13_NEK3_NM_002498_1.50175

Figure 3-165

CTGGACAAGCCGAGCTACGATGCCTCGAGAGAGAAGCGTTGTAGCCGAGG
GGCGATGTGAGGGATTCCTTTTAAACATCTGCTTGACTAGGAACTGAAGT
TCATAGGAGTAATGAGACGGCAGTGGACTGATGCACCCTTGACATACTTT
GAGG

2037. chr13_KCTD12_NM_138444_-1.56355
AGTGGCAGGAAGCCGCGCTGCACTCAGGAGCTGCAACCGCCTTCCCCGGA
GCCCCGGAACCCGGACGCTCGCTCAGCCCTGCGCCCCGCCGCCGCCGCCG
CCGCCACCGCCGCCACCGCCACCGCCGCCACCTCCTAGAGCCGCGCGGAG
CCGAGCGGTGCGAGCGCGCCGCTGTG

2038. chr13_MYCBP2_NM_015057_-1.50558
GTTGTGACCTGAAGGTCCCGTCTTCACTACCTTGTACATGCCTGGCCCTC
CTCGCAAGAATGGCATATCTTGTTCTTGCATTGTT

2039. chr13_MYCBP2_NM_015057_1.59083
TGGCACCAGTATCTCGTCCACACTGTCCTTTATTATTTACACCAAATGTC
CACACCTCTCCATTCTTCATTAAAACACAAGTGTGAGCTTTGCCCATAGC
TAC

2040. chr13_SCEL_NM_144777_-1.87986
GAACCAGGTGTTCACCCTCCAATACCTCCAAAGCCCAGTTCTC

2041. chr13_SLITRK5_NM_015567_-1.61686
GGCGGGAAAGCCACCACTTGCGGAGCCCCGCCTACAGCGTCAGCACCATC
GAGCCCCGGGA

2042. chr13_GPC5_NM_004466_1.73634
TGTGGTGATGTTACTTCCCGGGATTTG

2043. chr13_SLC15A1_NM_005073_1.69122
ATCTGATCGGGCTGAATTTCAAGAGCTCC

2044. chr13_ZIC2_NM_007129_-1.62194
AGCCCGCGGACCGACCCCTACTCGGCGGCGCAACTCCACAACCA

2045. chr13_BIVM_NM_017693_-1.53612
TGCTATCCGACGACCTGTCGCCGGGCACCGCAGCATCCTCGCTCGCTCCG
ATGGGACGAGGGACGCC

2046. chr13_ARGLU1_BC071587_1.52993
GAGTGTGCTCCTCGGCTGCCATACGCGCCAGCTTCC

2047. chr13_COL4A2_NM_001846_-1.61467
CATAGGACCCCGAGGATCCAAAGGTGCAGTGGG

2048. chr13_COL4A2_NM_001846_-1.88239
AGCCCCCGGGATTGCAGGAATCCCCCAGAAGATTGCCGTCCAACCAGGGA
CAGTGG

2049. chr13_COL4A2_NM_001846_2.30006
GCTCCTGCCTGGCGCGGTTCAGCACC

2050. chr13_RAB20_NM_017817_1.52657
GGTCTCGACTCTGCAGATTGGGCTTTGCAGAGGATTCCTGTTTCCCACCT

Figure 3-166

CCCCACCCCTCTGACAGAGACTGAGGAGACCACACACGTTGACCTCCTCT
TCATAGCCAGCCATCATTTCCACTCCAACATTCTGCTGCGGGTGTCATTC
TGGAAAATAATTCCTTGCTGTTCCTTGCTCCTTTCAGATCACAG

2051. chr13_CARS2_NM_024537_1.57192
CTCCCACAGCATCGCTTCCCTGACGGAG

2052. chr13_CARS2_NM_024537_-1.61879
GGCCTGGGCCGCGCGTAGTCCTCAACAT

2053. chr13_ING1_NM_198219_1.53069
GCGCGCGCTGATCCGCAGCCAGGAGCTGGGCGACGAGAAGATCCAGATCG
TGAGCCAGATGGTG

2054. chr13_ARHGEF7_NM_003899_-1.6725
CCGAGCCCCGGAGCGAGAGCGAGTGCCTGAGCAA

2055. chr13_ARHGEF7_NM_003899_-1.73309
ATCAGGAACACTGAAGAGCCCTCCCAAAGGATTTGATACGACTGCCATAA
ACAAAAGC

2056. chr13_ARHGEF7_NM_003899_1.58192
CTGAAAGTCATTGAAGCTTACTGCACCAGCGCCAAAACAAGGCAAACACT
CAATTC

2057. chr13_ARHGEF7_NM_003899_1.73955
GCACTGCCGCATCCACCTAGAGGTGTTTGCTCTTGTCCGCTGTCTGAGTA
CTGTGATTCTCAGATGAGTTTGCTGCGTTTTGGGAGGACACAGACGGTTC
TGTATAGGCTAGTTCAGTAACAACAAAATACACTGTTTTGTCTTCCCTCA
AAGAGAGATCTTACTAGAACCTGTAAATAGAATGTATTATTTATTATAAG
TCACTGCAGCTGATGAAAACAGATGGAGGCCATGCTGCAGGCTGATACTG
ATGGGTGGAGTTTTGTCATCAGGCCAGCCTCATCCCGAGGTCTCCTCCAC
CATTGGCCGTAGCCAGCAGGCTTCAGTGCTCACCGAAAGTAAAATCCCCT
CCTTCAGCAAGAATAAAGCAATATACACCTTAGGTTCCACTAAGTAACAT
AGGCATAAGCAGGGAACGTTTCCCCCACTGTGTTCCAGTGCAGAGGAGAC
GAAGCCTGTCCTCACCGCGGCTCGCTGGGCCCAGGCTGGCTCTGGAAAGC
CTGTGCGGTCCTGGGCAGGAAGCCCGGCCCGTGGAGCAGGTTTTCGTTCT
GCTTCAGCAATAAATAAGGGTGACCACAGGGACTTTGCTTTTGGTTTCCT
TTCCTGTGAAAAGGTTGGTTTTAAAGTGAGATACACTTTTCCGTAGAACA
AGTGTTCTATCTTTAAAAACCCAAATTGCAGCACCGTGGATTACTGGTCT
CAGAACAACTCATTGCGCATCAGATTTGACTCTCTGATTTTCTGTCTATT
GGCCAAATTGCCCTTTAACTGCACCTGAATCCTTTGTGTACTGATGCCTT
TGAGCTGGGCACCTTGGGAGAGTGTTGTGTTGCTGTTTACGGTTCTTCCT
TGCCCTTGCTAATTACAGTCTCTGGTGCCCAGCAAGCCCCTTTGGCTTCC
TTCCGTGACTGGTCACGTTGTCTGCCTGGGCTCAGCGTGGACCTGCCCCA
TGCTGCAGAACCTGGCCTCACCTGGACTTTTCACTAGAATTGCCAGCTTC
CTCAACTTAGCAGATCATTCACTCATGCGGGCACAAGCAAAGATCAACAC
TTTCTTTTTTGGTAAGCTTGAGTTTTACAAGTTATTTTTTGGTGATGCGT
AAGACATTGCAGTGGGAAACCATTCAACTTGAGTTTATTGGAGTTTGCTG
TTGTAGCAGGTTTTAACTCAGGAACAACTCTTGTCTGATCTCTCCGCCCC
TCTGCCGGGAGGCGACATTAACTGTCCTCTCGGAGCCGGTAGCGTTGCTG
TCCGAGTCCCCAGGACGGATCTCCTGCAGACCTGCCTTAATGCTCAGATC
GAAGTATTTCACAAGAATACTTGTGTTTTTAACAGCCCTTCCCCTGGACG
GTGCGGCCATGAGGGCCTCATGTTACGGCATTGCCTTTTCTTTCTGTGGA
TCCAGTATCTTCCTCGGCTTTTTAGGGAGCAGGAAAAATGCGTCTGAGAG

Figure 3-167

CAACTCTTTTTAAAAACCTGCCCTGTTGTATATAACTGTGTCTGTTTCAC
CGTGTGACCTCCCAAGGGGGTGGGAACTTGATATAAACGTTTAAAGGGGC
CACGATTTGCCCGAGGGTTACTCCTTTGCTCTCACCTTGTATGGATGAGG
AGATGAAGCCATTTCTTATCCTGTAGATGTGAAGCACTTTCAGTTTTCAG
CGATGTTGGAATGTAGCATCAGAAGCTCGTTCCTTCACACTCAGTGGCGT
CTGTGCTTGTCCACATGCGCTGGGCGTCTGGGACCTTGAATGCCTGCCCT
GGTTGTGTGGACTCCTTAAT

2058. chr13_PROZ_NM_003891_-1.67905
CCTCGCCCTCCATCGTGTGGAGCCCTCAG

2059. chr13_PROZ_NM_003891_-1.64508
GGCCTCCAAAGCAAACGACGTTCTGGTGAGGTGGAAGCGTGCGGGCTCCT
ATCTTCTGGA

2060. chr13_CUL4A_NM_001008895_1.57931
CCCTATAGACCTCACAGTGAACATACTCACAATGGGCTACTGGCCAACAT
ACACGCCCATGGAAGTGCACT

2061. chr13_GRTP1_AK300897_1.86636
GAAATACCGCCCACGTTTGCCATGCTGCACCCAGAGTGGCCCCGAGCCTC
CACTCCCTCTTAGGAAACTACTGACTCCCAGGCCTGAGCCTCTCCTGGCG
TCTTGGCTTCCTCAGAAGGCCTGTCAGGTACAGCTCCCACAACGCCCTCA
TCAGGACCTGAGTCTATACGGCCTGCGCCAGGTCCAGGACCCAGTGGGGA
GGCCGGGCCTCGGGAAGCCACACTTCTGGCACCACACACAGCAGATGAGT
ACAGCCATTAGGACCAGGAGCAGCGTCCGCAGTGCCAGGGCCAAGAAGAC
AGGGCCGCCATAGACAGGAAAGCCCTCGGAGGCC

2062. chr13_TMCO3_NM_017905_1.72925
GCGAAGAGCGGGCGTCATCTCTCGGGAG

2063. chr14_OSGEP_NM_017807_1.51497
TCTCATCTGTAGCAAAAAGCCGGGCTCCACGTTCCTGGCACATTGTTGCC
ATCATCTCCTGTAGCCTCACATTA

2064. chr14_METT11D1_NM_001029991_-1.76123
GGATGGTGGCTTTGCAGCAGTCTCC

2065. chr14_---_---_-1.60752
AAGGAACAGATATGATTGCTAGGCAACAGAGTGAAGGTGCATTTCAGAGA
ACTG

2066. chr14_HNRNPC_NM_031314_-1.62938
TGAGTAGAGGGGACGGAGAAGGGTGTTCTGTTACTGAC

2067. chr14_---_---_1.50697
TCTTGCCTTGTTACTCCCTTTACATCTGGAAGGTGTAAAAACCACTTG

2068. chr14_SUPT16H_NM_007192_-1.66328
CACTCTCCCAATGACCCGGAAGTATCGACCTCAAAGATGCCCTTTCCGCT
TCCGGGTCCCAACAGCGTTAGGTTTTTTTTTTGTTTGTTTGTTTGTTTTG
TTTTTTTCCAACCCTCTTTCGGATGGACGGGGGAAAGAGAGAAAGAAAAA
CGAGGGAAAATCAACAAAATGTGCGATGCAAAGAGTCGATTTTCGCGGGG
TTTGTCAACTTCGCCACTGCCGCACGCGAATCGACGTCGT

Figure 3-168

2069. chr14_---_---_-1.72679
AAAGAAGTGAAAGCAGGATCTCGGCCAGGCACAGTGGTTCACACCTGCAA
TCCCAGCACTTTGGGAGGCTGAACCAGGCGGATCACCCGA

2070. chr14_SLC7A7_NM_003982_1.93388
GAGAGGAAACCCTTCACCAGCTTCC

2071. chr14_MRPL52_NM_181304_-1.66984
TATAGATAGGGACCGTGGACTCGGG

2072. chr14_SLC7A8_NM_012244_-1.5316
CAGCGACGGCGTTGGATGCCAGCAGCTCCTGGGGGGACATTGCAGTGACA
TAAGCGACATTGGCAAAGACATACACAAATGTGACCAGTGGGATGGAG

2073. chr14_SLC7A8_NM_182728_1.89285
GCAAAAGGGGTGAGGCATGTCCCTCC

2074. chr14_HOMEZ_NM_020834_-1.65585
AGGTACTGCGTTGTCCCGAAACCACTTTAGTTGCCCATGCTTCAAGGCAT
AGCGTGTGTCACCAAACCACTGAATGATCTCAGGCCGAGGTAAACCAGTG
ATCTGTTCTAACTTTTGGTAATCCTCACGCCGTGCCCACTGGCACTGTAA
AAAAAAGGATTTAAGGATAGCCAGCTGCTCT

2075. chr14_EFS_NM_005864_-1.70128
GTTGGCGGGCACAATGCCCTGCTGGCCGTGTAGGGAGCAGAGGCACCAGC
CGTCCAGTCCACCAGCGCCCTCTCTCTGCAGGACCCGTAGGACATCCCCT
CGGCGGAAGGACAGCTCCTGGGGGGACTCAGCGGTGTTGTCATACAGTGC
CCGGGCCA

2076. chr14_MYH6_NM_002471_-1.78985
GGTGGAGAGCCGACACCGTCTGGAAGGATGAGCCCTTTTT

2077. chr14_LRRC16B_NM_138360_-1.54502
CGGACTCTGAGGACCGTGCGGCCAGGACTCTCGGAGGCACCGCTGCCTCC
ACTCCAGAAGAAGAGGCGCCGGGGCCTGTTTCACTTTCGCCGGCCCCGGA
GCTTCA

2078. chr14_FITM1_BC042179_-1.51452
AAAGGGCACGGCAAGGAGAGAACGAGTGATGATGTGTAGGGTTGGGGAGA
GTGCAGTGATGGGAGCACAGACCAGGGTGGGAGATGGAGCTTGGGGTCTC
AATAGTCTCCCTTCTTTGCC

2079. chr14_RNF31_NM_017999_1.50571
ATACTCATCCAAGACAGCAGGCACTG

2080. chr14_IRF9_NM_006084_4.15274
CAAGCAGGACTTCCGGGAGGACCA

2081. chr14_IRF9_NM_006084_1.73382
CCACCGAAGTTCCAGGTAACACTGAATTTCTGGGAAGAGAGCCATGGCTC
CAGCCATACTCCACAGAATCTTATCA

2082. chr14_TM9SF1_NM_006405_1.61685
CCTGAGGGTTATGGTAGGGTCCCACTTTGTTGACATACAGAATAACAGGG
TCGCCGGCCTTGTAGTGTGTCACGCCTTCCACCC

Figure 3-169

2083. chr14_LTB4R2_NM_019839_-1.50313
GGACCGCGTATGCCAGCTGTGCCACCCGTCGCCGGTCCACGCCGCCGCCC
ACCTGAGCCTGGAGACTCTGACCGCTTTCGTGCTTCCTTTCGGGCTGATG
CTCGGCTGCTACAGC

2084. chr14_RIPK3_NM_006871_1.60968
AGTCCTTCTAAGCCGGGAGTCTCAGGCCCGGCTTGGGGCAGCTCAGCCAA
TGAAGGCCGGTT

2085. chr14_KHNYN_NM_015299_3.05619
ATGCCTCTCCTCCGAGGGTGCCCA

2086. chr14_STXBP6_NM_014178_-1.52928
CAGCCACGTTGCCCGGCGGTGTTGGTGAGGCTCGATGCCGGCGTGCACGG
CAAGCGCGAATTCGGAACCTGGCGCCCTTGAC

2087. chr14_PRKD1_NM_002742_-1.61657
GTTGGCGTCCTCGTGGTCTGGGTCTGGATCTTGCATCTCGCCACTGTCGT
TCTGGCACTCTGCCATTGCCATCTCTGCATCTTGGACCATTGCTTCTTCC
ATATCATCCATGAGCCCACTGTTC

2088. chr14_SCFD1_NM_016106_2.19068
AGCAGCCAGTATTCGGGAAAGGCAGACAG

2089. chr14_SCFD1_NM_016106_-1.54149
TTGGAAGATGATATGTTTGTATTA

2090. chr14_HECTD1_NM_015382_-1.58856
CAATCCTTCGGGTACATTCCGCAGATACATCCAGGTAGTATGTTATGGCA
CGGGCTGTCACCTCTAATACA

2091. chr14_PPP2R3C_NM_017917_2.00666
TGCACTTTGCTCCAGCCTTTTCACC

2092. chr14_BRMS1L_NM_032352_-1.64522
TGCCAGTCCATTCCCGAGGGGATAAGAAGGAGACCAACCATCACGATGAG
ATGGAGGTGGACTACGCCGAAAATGAGGGGAGCAGCTCCGAGGACGAGGA
CACTGAGAGCTCGTCGGTCTC

2093. chr14_FOXA1_NM_004496_-2.16142
AGCTGGCCGGTCTTCCCGTGCACACCCCGATGGAGGGGCGAGTCGGCGCT
GGGGTTAGAGGCGCCAGAGGGGTCCTTGCGGCTCTCAGGGCCGCC

2094. chr14_SEC23A_NM_006364_1.52946
TGGCATTGGAAATCTGGAGTGAAGAATTTCCTGTGCATCATCCACTGGGG
CTTGCAGAAGGTGGCGGAAATTTTCATACTCAGGCATATCCTGGTATCCT
GACTTCCGCCACTGTG

2095. chr14_PNN_NM_002687_1.60916
GGATAAGAATTCCCGGTCCGACAGAAAGAGGTCTATATCAGAGAGTAGTC
GATCAGGCAAAAGATCTTCAAGAAGTGAAAGAGACCGAAAATCAGACAGG

2096. chr14_PPIL5_NM_152329_-1.57598
TTCACCAAATTTGTAGATGAGGGGAAAGCCACTGTTCGGTTAAAGGAGCC

Figure 3-170

TCCTGT

2097. chr14_ARF6_NM_001663_1.69888
GGATCCTCATGTTGGGCCTGGACGCGGCCGGCAAGACAACAATCCTGTAC
AAGTTGAAGCTGGGCCAGTCGGTGACCACCATTCCCACTGTGGGTTTCAA
CGTGGAGACGGTGACTTACAAAAATGTCAAGTTCAACGTATGGGATGTGG
GCGGCCAGGACAAGATCCGGCCGCTCTGGCGGCATTACTACACTGGGACC
CAAGGTCTCATCTTCGTAGTGGACTGCGCCGACCGCGACCGCATCGATGA
GGCTCGCCAG

2098. chr14_ATP5S_NM_001003803_1.65023
GGTCTCTGAGCAGCGACTCACCTGTGCAG

2099. chr14_MAP4K5_NM_198794_-1.69322
GGCGGCCCCGTCTTTGTTGAGCGCGGAGCCCG

2100. chr14_NIN_NM_182944_1.63472
TAGGCGTCGCAGTGGACCTCAGGTGCTGCAT

2101. chr14_SAMD4A_NM_015589_-1.56681
TGGGCAGACGGAACCCGCGCCAGTACCAGATCCCCTCTCGGAACGTCCCT
TCCGCCCGCCTGGGCCTCTTGGGCACCAGTGGATTCGTCAGCTCCAACCA
GCGCAACACCACAGCTACC

2102. chr14_LGALS3_NM_002306_1.97707
CGCCAGCAGCCGTCCGGAGCCAGCCAACGAGCG

2103. chr14_PSMA3_NM_002788_-1.50935
AGTAGCAGGTTTGTTGGCAGATGCTCGTTCTTTAGCAGACATAGCAAGAG
AAGAAGCTTCCAACTTCAGATCTAACTTTGGCTACAACATTC

2104. chr14_DACT1_NM_016651_1.58303
TTAAGAATTCGAAACAGGCGTGTCTGCCCTCTGGCGGGATACCTTCTCTG
AACAATGGGACATTCTCCCCACCGAAGCAGTGGTCGAAAGAATCAAAGGC
CGAACAAGCCGAAAGCAAGAGGGTGCCCCTGCCAGAGGGCTGCCCCTCAG
GCGCTGCCTCCGACCTTCAGAGTAAGCACCTGCCAAAAACGGCCAAGCCA
GCCTCGCAAGAACATGCTCGGTGTTCCGCCATTGGGACAGGGGAGTCCCC
TAAGGAAAGCGCTCAGCTCTCAGGGGCCTCTCCAAAAGAGAGTCCTAGCA
GAGGCCCTGCCCCGCCGCAGGAGAACAAAGTTGTA

2105. chr14_SIX4_NM_017420_1.60881
GGATCTGGACAATGCCATACTGGTTAATTTGCACTGGTGTAGTAAAAGTC
ACTACAGACCCTCCATCTTGGGAAGCCACTGTTTGAATGCCTTCTCTTTT
CACCTCAGTGCTGGGTATCAGGCCTGGGAATGAGACAGGGACACTGGGGC
TGTAGGACGTGGTGGTTGCTGAGTTAGCAGAACTCTGGAGGACTTTGAAT
TCCTTCACGTCCTGGGAAGTAGACCCCAGTATGTCAGTCATGGATATACC
ATTGCTCACAATGTTTGATGACATTTTTGGTGGGTTCAATGCCACTGCCT
GTGTATTTCCCACATTTAATCCATTAAGGATAACTCCACTGGGTCCCTGA
ATAAAAGAATTTCCATTAAGGAAGACAGGTGAAGTACTTGCAGGTACCAA
GCTTCCATTCAACAGAACTCCAGAAGAGCTTAATGATATCTTAGCATTTC
CAATTTGTTGCATATATACTGGCTCCATATGACTGGAAAGGCTGAGGTTG
GTGATGCCATCAGATGAACTGGAGAGTGGGTGAGGAGATAAATCCTCATG
TCCCTTGCTGG

2106. chr14_SLC38A6_NM_001172702_1.61225

Figure 3-171

AAGGGCCGGGCTCAAAGCTCCGCCTCTGGCGCGACCGACGACTGGAGCGC
AGGGCA

2107. chr14_HIF1A_NM_001530_-1.68166
GGCCGCCCGCCGTGAAGACATCGCGGGGACCGATTCA

2108. chr14_ESR2_NM_001437_1.51473
CATCAGGAGGTTAGCCAGGCGCATGGATTGCTGCTGGGAGGAGATGCCGC
TCTTGGCAATCACCCAAACCAAAGCATCGGTCACGGCGTTCAGCAAGTGA
GCCAGCTTCCGGCTGCTGTCAGCATCCTGGGTCGCTGTGACCAG

2109. chr14_RAB15_NM_198686_-1.55538
GATGGTGGAGATGTGCGAGGAGTGGAAC

2110. chr14_RDH12_NM_152443_-1.53583
CTTTGCTGGTGGAGTGTGTAGAACAAATGTGCAGCTTCCTGGCAAGGTAG
TGGTGATCACTGGCGCCAACACGGGCATTGGCAAGGAGA

2111. chr14_ZFYVE26_NM_015346_-2.04816
TGCAGCCTGGTGGACAATTTCTTGGA

2112. chr14_ACTN1_NM_001130004_-1.68934
TGTTGCATGGCATGCATGGTGTTCTCGGGCACCCGGTTCTCCAGCCACGG
GATTGTGCGGCGGATCCAC

2113. chr14_DCAF5_NM_003861_-1.57716
CATCATGGAGGATAACTTGCTCAT

2114. chr14_---_---_1.52075
TCATTTGAACCAAGAAGGCAGAAG

2115. chr14_SLC10A1_NM_003049_-1.67966
AGGCTGTGCAAGGGGAGCAGTCCTCCCCTTTGTAGGTGCCATTTCCCAGA
GCTCCTGGAATTGTTTCTTCAGTTGTGGCAGCTGTGTAG

2116. chr14_SMOC1_NM_001034852_-1.78077
GAGAGCGACGCCAGGGCCAAGACTACAGAGGCGGATGACCCCTTCAAGGA

2117. chr14_SLC8A3_NM_033262_-1.50021
CTCCCGAGCGGAGTGGGCAAGGGAGGGGGGTGAGGAAGGTACGCGATGCC
CCCGCCGCCCGGCGCCTCACCGGTCGCAGCGGCTCATCGCCCCCGCGGGC
TGCCCGCCGGCCGCAGCCGCGTCCGGGGCATGTCAGTCCGCCGCCGCCGC
CCTCCCGCCGGGGTTCGTGGGCTCGCAGCTGTCAGGGAGCTGCGG

2118. chr14_MAP3K9_NM_033141_1.65681
AAGTGGAAATGTGGAGATTCTGATGGGGTACTTAAACCATTAGCTTTCTC
A

2119. chr14_MAP3K9_NM_033141_-1.67357
CTGAATGGGCGGGTAGCAACTGGGGTCCTCGCCGCCGGGCTGGCAGCGGC
TGGAGAAGGCGCTGCGCGGGGTCACGTAGTTGCTGGG

2120. chr14_ZFYVE1_NM_021260_1.61819
GATAGGATTTCAGCACAACGGGCCCTTTCCAGTCATGACAGACAGAGATG
TCCAGGCTCTTGAGGAGAAACAAAAGTTCCTTTGACTTCTCTTGCAAGGA

Figure 3-172

CCAAAGAGATAAATTTTTTCTTTACGATCTGTTGAAATATTTATATAGAC
TTTTAAAAACAACTAACAGTTCATCCTGTGCTCAGTTTCCCTGGAAGGTT
TCTCATGATCGCCCCTCCGAGAGCTAGAGGGGTTGTGTGTCTGGGAACAA
AGGATTAAGACACTTTAAAATAAGCAATGAAAATCCTAGTGCGACACTCA
GAAGCAGATGGTGGGCTTGAGGGGGCCGAGGGGTGGGAGGCAGATGCTTC
GATTGAGGAGCTGGGTGCCGCCTTTTGGGAAAGCCGAGTGGAGACAGAAG
CATCGGGACAGGAAGCCCTGCTGGAGAAGGCTCAGTTCCTTCCTTGCTGT
TCCCTGGGGGACCAGGGACAGCACGGCCCCTGCATTTCTACTTCTCAGGG
CCGAAGACCCGACCTCTGACCCTCCACCCACTCCGGTGACCTGCACGCTA
AGTTGGGTGGTCTCTGACTAAAACAGGCTTAAGCCAAGAATTGGGACTCG
ACTCCCAGGAGACCTAGGGAGAATTCCCTTCAGGCTGTTTCAGGCAGGAA
GGACCAGGGAGGCTCACTCCCCAGGCAGCTGACAGGCATGGAGGGAAGAG
CCAAGGACAGGAGAGGCTTCCAAGGCTCCAAGAGCAGCAGAGGAAGGGGC
CAGCCACGTGGTGGCCATGGACCTGGCTCGGCTCATGAGGAAGACGTGCT
GCCACTGCCACCTCACCCTGTGCGGAGGAGACTGTGCGAAGTCTTCACAG
CCAGCAGCAGCCTCGATACGCCCCGAGTGCCTTTCATATGTATATATGAG
AGAGAGATATACACATATATATTCATTATTTTTAACTGAAATAAATGCAA
CGGATTCAGGTTCATTCCCCTTTGCGATAAGTTGCAAGGTCCCCTGCCCT
GAGGGGTCCACACCTTCGGGCCTGCCGCCAGGCTCACCCCCACTGAGGGA
AAGTGGCCCTGGATGCGGAGAGGAGAGGACACACACCACAGCAGGTGACT
GGGAGGAGGGCCTACCTCGCAAGACTGTTT

2121. chr14_COQ6_NM_182476_1.574
CAGACACCTTGAGTTCCTTGGTTTGGTCCACGTCCCATGAACATGCAGCA
GAGCTAGTTAGCATGGATGAGGAAAAATTTGTGGATGCCGTTAACTCTGC
CTTT

2122. chr14_LTBP2_NM_000428_-1.62114
TACGCAGGCCATGTGGGCCGCATCCAGCTGGAAGCCCTCAAAACAGTCAC
AGGTGTAGCCCTCCCGCACGCGCACACAGCGGCCATTCTCACAGCCGTTC
AGGATGCCGCACTCCTCCGCCTGAAGCCCTTCGAAGCCGGCTGGG

2123. chr14_LTBP2_NM_000428_-1.89516
CAGCCGCTGCCGGGTAGCTGCCCCCAGGGCGCCGCAGTCGATTCGCGTCT
CCACCAGCCGGCTCGTATCTCCCT

2124. chr14_MLH3_NM_001040108_1.54614
GAATCATTCCTTTGGTGAAACGATAGGGATACAAGATGTTGTGAATTTTA
ACTGCTAAGCTCTCAGCCTGGCCACTGCTTACATCAACAGCAA

2125. chr14_NEK9_NM_033116_-1.75906
CTGCACGCACACGCAGGAGGAGTCAGTGGTGTTCCCTTCCCAGCACAGGT
TACTGCAGGATTCAGCCGAGGTGA

2126. chr14_ADCK1_NM_020421_-1.545
GTTCCAGAGCTTCGATGACACCCCTCTGGGGACGGCCTCCCTGGCCCAGG
TCCACAAGGCAGTGCTGCATGATGGGCGGACGGTGGCCGTGAAGGTCCAG
CACCC

2127. chr14_NRXN3_NM_004796_1.84423
TCGAGAGGAGAATGTGGCCACTTTCCGAGGCTCAGAGTATCTGTGCTACG
ACCTGTCTCAGAACCCGATCCAGAGCAGCAGTGATGAAATCACCCTCTCC
TTTAAGACCTGGCAGCGTAACGGCCTCATCCTGCACACGGGCAAGTCGGC
TGACTATGTCAACCTGGCTCTGAAGGATGGTGCGGTCTCCTTGGTCATTA
AC

Figure 3-173

2128. chr14_CATSPERB_NM_024764_1.73218
CAGTAACCAGATATGGAGATTGCAA

2129. chr14_CPSF2_NM_017437_1.52353
CAGATATAGATTCCAGTGATGAGAGTGATATTGAGGAAGATATTGACCAG
CCATCAGCTCATAAGACGAAGCATGACTTGATGATGAAAGGTGAAGGCAG
TCGTAAAG

2130. chr14_CPSF2_NM_017437_-1.56256
ATGGCCCACCAGAGGCCAGTCAAGATCTGGCAGAGTGCTGTCGCGCCTTT
GGTGGGAAAGATATTAAAGTGTACATGCCAAAGCTACATGAAACAGTTGA
TGCCACTAGTGAAACTCACA

2131. chr14_CHGA_NM_001275_2.283
GCTCTTCTGCTCTGCGCCGGGCAAG

2132. chr14_ITPK1_NM_014216_1.73589
CAATGACGGCGTGCTGCCCTGTCTGGTTGTTGATGATGATGTCGATGCCG
AAGAGTGACACGCCCAGTGCCTGCCGCAGGGCCCGGGAGAGCTCCCGGAT
GACCTCGTCGCTCGGCCGCTCGAACACGCCCTCGATCTTGTCCAG

2133. chr14_OTUB2_NM_023112_1.53365
GGGAACACATGACATGATTTGTGAATATCATCATCTTTGCCAGACAAGTC
TCCAGGGGATCCCTGTTTCCCAACTGAAAGGTGTGAACGGACACACACAC
AGCCTGGATGACGCCTTGGCTGTTCTA

2134. chr14_IFI27_NM_001130080_-1.778
CAGCGAGGAGCCAACTATCCCAAA

2135. chr14_SERPINA9_NM_175739_-1.55125
CATTGGCCGGGGACACACAGTAGATTGGAGCACAGAGGCCAACAGCAAAG
AGTACTCCATAAAGGTAAGA

2136. chr14_SERPINA13_NR_015340_1.51258
TGATGACTTTCCACACGGAAACAGGAAG

2137. chr14_DICER1_NM_177438_-1.50092
AACTGCGCTCGATCTGGATTCCAGTGATCCTCTGCAGTGCCCACCTGCCT
CCAGGGAGCGACTGAAGAAGCCGACTGCCGGGGGAACACCTGGATTCATG
AACCAAAGCAGCCTCAAGTTTCATGTTGTCAAGGCAGGGTATCAGAATCT
TTCTGAGGGCAAAGTATTATTAACAAATAAAAATATCAGTATTTTAAAAG
ACAATTACAGGAGTGTTAGAGGTCATTCTAAATTTCATCACTTCACGTAA
TATAAAAGAAAAAAGAAAAGAAATATAACAAACATTTTAAAAACATAATT
AAGAGTTCAGTTAACAAATCTGTTTCATACTTTCACAAACAGTAAAAATG
CCACAGACAAAAATGACCTATTTAAGTTGTGCGAGTATATGACACATTGC
AGGCATTATAATTATCTTTTTCAAATTCCATAAATCAAAACAGCAGCAAG
GCCAAACCACATTTTTTTCCTCTCTGTTAAGCATATTTTCTTGAAATGAG
GTAAAGCATGGTACCAAGTGCAATGCTTATCTGTGCTACATGAACAGAAC
AGAAGGGAAAAAGCTATTATAAAACGCAGCATAGTTAGGACTGCGGAAAG
CATATTATAAAAGAAATTTTAAAAAATTTACAAATGAAGGTTCATGTTAA
CTAACTTGCACACAATCATCATAAGGAATTTCTGCAGTTGCTTTTTCAAG
ACACGCCTCCCCAGTCCTTTACACACGTGCTCAGGGCACAACCACACCCC
ACTGGTAGGTTTTCCATATTACATTCGGTCTCACATTGCAATCACAGGAA
CACAGGGTGGCACACAGGGCTCTAAA

Figure 3-174

2138. chr14_GLRX5_NM_016417_-1.58231
GGTGGTCTTCCTCAAGGGGACGCCGGAGCAGCCCCAGTGCGGCTTCAGCA
ACGCCGTGGTGCAGATCCTGCGGCTGCACGGCGTCCGCGATTACGCGGCC
TACAACGTGCTGGACGACCCG

2139. chr14_C14orf132_NR_023938_1.54305
TGGGCGTGGTGTATGCCTTCACCTTC

2140. chr14_CYP46A1_NM_006668_-2.13217
GGAGCAGGCCACACTCAAGCCACTGGACCCCGTGCTGTGCACCCTGCGGC
CCCG

2141. chr14_EML1_NM_001008707_-1.52971
TGGAGGAACCAATCTCTGTGCTGTGGATGACTCCAACGACCATGTGCTCT
CTGTATGGGACTGGC

2142. chr14_---_---_-1.52496
CTTGTATTCACAGGAAGGCAGTGGGAGATTGACTGCCAA

2143. chr14_WDR25_NM_024515_-1.71332
CCTTGCACCCGAGAGAGCCCGTGTTCCTGGCACAGACCAATGGCAACTAC
CTGGCCCTTTTCTCCACTGTGTGGCCCTACCGGATGAGCAGACGGCGGC

2144. chr14_DLK1_NM_003836_-1.62143
CCCCTTTGTGACCAGTGCGTGACCTCTCCCGGCTGCCTTCACGGACTCTG
TGGAGAACCCGGGCAGTGCATTTGCACCGACGGCTGGGACGGGGAGCTCT
GTGATAGA

2145. chr14_DIO3OS_BC065701_2.7671
TCCTGCCCGAAGCCTCAGGAGGTC

2146. chr14_WDR20_NM_181291_-1.52824
GCCGGGAGCTGTACTTCTATATCTACAAGGGGGTCCGCA

2147. chr14_WDR20_BC030654_1.53672
TGCCCTGCCTCCGGTGCCGGTGGATGGGGGAGGGACTGGCCTCTGACTGC
GGGGTTGCACCATGGCGGCGGTCG

2148. chr14_CDC42BPB_NM_006035_-1.5992
GCCGGACCACGCGGTGCTGCTTCTCCAGCCCCCGCAGCCGCTGCGTGGAG
TCCTCACGCTCTTGGCGAAGCGCCACTGTGTCCTCAAGCTGTCGCTCGAG
C

2149. chr14_TNFAIP2_NM_006291_1.55271
GCCAAGGCCGAGAGCATCACGCTGGACTTGG

2150. chr14_CKB_NM_001823_1.68294
CATTTCTGGGCAGGCATGAGGTCGTCGATGGCCTGGCCCTGCTCCAGCCG
CTGCTCCATCTCGATGAGCAGCTTCACTCCGTCCACCA

2151. chr14_XRCC3_NM_001100119_-1.59666
TTCTGGGATTCAGGTCCAGTAGATCCAAATCCAT

2152. chr14_TDRD9_NM_153046_-1.51245

Figure 3-175

TTTTGCAATGCCTTTCCGGCAGCATCTCGATGGATATAG

2153. chr14_KIF26A_NM_015656_-1.6051
GTCGGCCGAGTACCTGGCGGCCCTGGAGCGAGCCACGGCGGCCCTGGAGC
AGTGCGTGAACCTGTGCAAGGCGCACGTCATGATGGTCACCTGCTTCGAC
ATCAGCGTTGCAGCCAGTG

2154. chr14_INF2_NM_022489_-1.86065
CTGGAACAGCCCTCGCAAGCAGCAG

2155. chr14_INF2_NM_022489_-2.00013
TGCAGGAGATCCCGTGGGCAGCACGCGCTGTCCCGCCTCTGAGCCCGGCC
TTGATGCTACAACAG

2156. chr14_AKT1_NM_005163_1.92755
AGCCTCACGTTGGTCCACATCCTGCGGCCGCTCCTTGTAGCCAATGAAGG
TGCCATCATTCTTGAGGAGGAAGTAGCGTGGCCGCCAGGTCTTGATGTAC
TCC

2157. chr14_AHNAK2_NM_138420_-1.51484
AAGAATTTCTGCTGGCTCCTCATCTGAACAGCTGTCTGCAAGCTGGTGGC
CAGAAGGAACTTCAAATGTGAGTGTTTGCTGTCCCAGTACATTGACGCTG
GAAGAGATCATCTCAAATGGTTCTCCAGTGTCAGGCTGGAGATCTCCAGA
AATGGAGTCTACTCCTGGGGTGGCTTGTATGGGAGCCTCTTCTGTGCCCT
CCTGAGTCCTAGAGTGTTGAGTCA

2158. chr14_JAG2_NM_002226_-1.61726
GTGAGTGCAAGTACGACCCTCCCAGCCGTCC

2159. chr14_C14orf80_NM_001134875_-1.92359
CTCCTCTTCCGTGTGCTCTCGCCACTCCCTGCGGGC

2160. chr14_IGH@_BC065733_-1.57536
ATGCGACGACCACGTTCCCATCTTGGGGGGTGCTGTCGAGGCTCA

2161. chr14_IGHD_BC063384_-1.70774
AGGGGCTGGCGCATCTTCCTGCACACAGAAGAGTCCAGGGTGGGTCCTTT
CTGCTCTCTGGTAGCCACAGATGAGGTACAGAGGCTGCTTCCCTTCTCTG
CAGGTACAGGGCGTCCTGCTC

2162. chr15_NIPA1_NM_144599_1.55895
GCCCACCACACAATGTCTGTTAAATAGGAAG

2163. chr15_GOLGA6L2_BC129821_1.83284
GGGCACTGCTGGGCGTTCTTCATCCCACAAA

2164. chr15_SNURF_ENST00000401453_-1.56419
AAACTCCTGGATCAATCTAGACTCCTGCCTCAGCCTCCCAAGTGCCTGTT
AGTACAGGCTTGA

2165. chr15_ATP10A_AB051358_-1.59393
CTCCATCCTGGACGGCGAAACGACCTCGGGAGACCCCGGTTAGGACCTTA
CTCCAGGGATCAACTGGAATCAAAATCCAA

2166. chr15_HERC2_NM_004667_-1.55604

Figure 3-176

TCCCATCAGCCGTCACAGCAAAGAGGGTCTGTTCCCCTCCGATTAACTGC
ACGGGTCTGAGAGTTGCAAGGGCTTCACAGGGAGTGGGAACTTTGACTTT
TGCGCCTTCAATGCCCCCGAGCTGGCCCCTGTGATTATGTCCCCAT

2167. chr15_HERC2_NM_004667_-2.41978
TCAAGAAATCAGCTCGTTTTTTGT

2168. chr15_TJP1_NM_003257_1.77638
TTTTGTCATGTTCACTGAATTGAT

2169. chr15_KLF13_NM_015995_-1.51836
CATGCGCTCACTCTTCGGTGCCCGGCCGGGCCGGCGCCTCGCAGACGCGG
AGCCGCGCGGGTGACGGCACAGGCGGCTGCGCGCCCAGCCCAGCCCAGCC
CAGCCCGAGGAGAGGGCGCGCCGCGCCCCCGCCCCCCGCCCGCTCTCCCG
AGGCCGTGGGTGCGGATGCGCGGCTGACGACTCGCAGCAA

2170. chr15_OTUD7A_NM_130901_-2.09875
ACGTGCTGGCCGACGCACCAGACTCCTCCTTGCTGCCCTTGCGCGACTTG
GCCTTCTTCTCCTTGCCCCGCTCGGCCGAGTCCCCGTTCTTGCCATTGGC
GGAGTTGGCGCGGCCCATCTTGCCGTGCA

2171. chr15_C15orf55_NM_175741_-1.70798
GCATTGCCGGGACCGGATATGAGCATGAAACCTAGTGCCGCCCCGTCTCC
ATCCCCTGCACTTCCCTTTCTCCCACCAACTTCTGAC

2172. chr15_THBS1_NM_003246_1.56705
TGCAAAAAGGTGTCCTGCCCCATCATGCCCTGCTCCAATGCCACAGTTCC
TGATGGAGAA

2173. chr15_GPR176_NM_007223_1.68922
CAGCCCACTCGACAGGAATGGAAACACAGAAGGAGGCATTCGATGGTCAA
GGAGGGCGCTCTCCGCTCCCGCTGCCTCCTTCAACCGCGGGTCCTCCGCC
CCTCGAGGGCTAGGGCATCCCTCTCCAGTCCCCTCGGGCTGACGCACTCG
ACCCCTCTCCTTAGCGGGAGGAGAACGTTTGGCCGAAGCTATTTTTCAGT
CCTGTTGGCTTCGAGGCTGGATGGCGATGTGAAGCCAACGTAATGCCC

2174. chr15_BMF_NM_001003940_-1.5891
TCGGGGGCTGGACGCCCAGACTCGATTGGGAAGGA

2175. chr15_PLCB2_NM_004573_-1.55249
GCACGCGCCCGTCCACGCCCTCAGGGCCCTCGCCCGGCGCGGCTCCGGCG
CTCTCCTCGCGGGGCAGGCT

2176. chr15_DISP2_NM_033510_1.63704
GGCTGGAGCCCGAAGGTATTTCTCCAGATCCACAGGGAGAGGTCTCACCC
TCCAGCTGTGGATGTTAAACCCTGCCAGATGTCCCAGCCTTGATCTGTCT
GCTCCTACTCCTCACATCTGGAGGATTCCAGCAGGAGGGGTTTTGGAGGG
GACCTGCTTGCGACCTGCTGAGGGCTTGTCTGCTCCCACAGCACCATCTA
AGACCCCTCCTCTAGAAGTGGGGAAGGCCAGATGTGTAGCTTCGGGTATC
AGAGGAGGCTGACCTGGCCCCCATCCCAAGTTACAAGAACTTCAGTGAGA
CTAAGGGACCCCCATCCTAGGGATCTTGTCAGGGTTCCTTACTGACCAGA
GGAGCCCGCAGCAATCTCCACAGCCTCCTGGGTCTCACCCCTTTCATGGG
CTCTTCATCAGGACACTTCCCTCTCTTTTGGGAGCTTCTCTGGGCAGAAT
TGGGCTGGGACCTCTCTCCCCAACTGCCCTGCTCTCCTCATACTCACCGG
TTTGACCAGAAATTCTCCAAATCCAGCCATAGATGGCTGCTGGGTGTGCA

Figure 3-177

GCAGGAGAAGGAGGATGGTCAGCCTTGGAGCATCTCTCAATTACGGGACA
G

2177. chr15_IVD_NM_002225_-1.57874
GGAACCTGGGCGTATTGGGCATCACAGCC

2178. chr15_FAM82A2_NM_018145_1.56693
TCTGTGAACGTGGCTCCCGAGGAGGCCGTGAAGTAGACAGAGCTGGAGCC
AGTGGAGTCACTCCTCTCCCGGACAAACGG

2179. chr15_ZFYVE19_NM_001077268_-1.6445
GTGGCCCAGGGAGCACTAATTCCAAG

2180. chr15_PPP1R14D_NM_017726_-1.90245
TCTGAGGCCGGCTGAGTCTCCGGAGTTTCTTG

2181. chr15_RHOV_NM_133639_1.51407
CGTGCGGATCTCGGGCAGCCATTTCTCTGTGATGTTTTGAAAGGAGCTGG
GCTGCACCACGCTGAAGCACGCCAGGAAGACATCGGTATCCGGGTAGCAA

2182. chr15_VPS18_NM_020857_1.61777
ACCACTTCAAGGAGGCGATCTGCAGCTCACTTAAGGCCTACAACCACCAC
ATCCAGGAGCTGCAGCGGGAGATGGAAGAGGCTACAGCCAGTGCCCAGCG
CATCCGGCGAGACCTGCAGGAGCTGCGGGGCCGCTACGGCACTGTGGAGC
CCCAGGACAAATGTGCCACCTGCGACTTCCCCCTGCTCAACCGCCCTTTT
TACCTCTTCCTCTGTGGCCATATGTTCCATGCTGACTGCCTGCTGCAGGC
TGTGCGACCTGGCCTGCCAGCCTACAAGCAGGCCCGGCTGGAGGAGCTGC
AGAGGAAGCTGGGGGCTGCTCCACCCCCAGCCAAGGGCTCTGCCCGGGCC
AAGGAGGCCGAGGGTGGGGCTGCCACGGCAGGGCCCAGCCGGGAACAGCT
CAAGGCTGACCTGGATGAGTTGGTGGCCGCTGAGTGTGTGTACTGTGGGG
AGCTGATGATCCGCTCTATCGACCGGCCGTT

2183. chr15_INO80_NM_017553_-1.61017
ATGGTGTTCTGAATTGGGGTCCCGGTTAGCAAAAGCCGATTCCGACACTG
GAACTGTAAGAGGATCTTCCAA

2184. chr15_RTF1_NM_015138_1.51037
ATCCCACAACAAGGAACGGCGTTCCAAGCGGGATGAGAAACTAGACAAGA
AATCTCAAGCCATGGAGGAGCTAAAAGCAGAGCGAGAAAAACGAAAGA

2185. chr15_RPAP1_NM_015540_-1.56852
GTCCCCAAAGAGCGGGTAAATAGCTAAGCCACTCTTCACTCCCAGTACAG
ACCTTCAGAAGCCCCAGATATCAGGATGTAATGGTAGGGCTCACTGCTCT
AAAACAGCTCAAACAACCTGCTCCCAGGAAGGCAAGCCTTCTGCTCCTTG
GTCTCCTGCCTACCATTAGGACACAATGTTCTTCGTCTGGCCAGACATCT
GTTGAAAGGCTGGATACAGGACAACGTACCCAT

2186. chr15_TYRO3_NM_006293_-1.75836
CGCGCTGCTGACGGCGGCGACCGCGGCCGGAGGCGGGCGCGGGTCTCGGA
GGCGGTCGCCTCAGCACCGCCCCACGGGCGGCCCCAGCCCCTCCCGCAGC
CCTCCTCCCTCCCGCTCCCTTCCCGCCGCCTCCTCCCCGCCCTCCTCCCT
CCTCGCTCGCGGGCCGGG

2187. chr15_TYRO3_NM_006293_-1.63533
TGTGGTAGTCCTCCCAAGCTGTGCTGGGAAGCCCGGACTGACCAAATCAC

Figure 3-178

CCAATCCCAGTTCTTCCTGCAACCACTCTGTGGCCAGCCTGGCATCAGTT
TAGGCCTTGGCTTGATGGAAGTGGGCCAGTCCTGGTTGTCTGAACCCAGG
CAGCTGGCAGGAGTGGGGTGGTTATGTTTCCATGGTTACCATGGGTGTGG
ATGGCAGTGTGGGGAGGGCAGGTCCAGCTCTGTGGGCCCTACCCTCCTGC
TGAGCTGCCCCTGCTGCTTAAGTGCATGCATTGAGCTGCCTCCAGCCTGG
TGGCCCAGCTATTACCACACTTGGGGTTTAAATATCCAGGTGTGCCCCTC
CAAGTCACAAAGAGATGTCCTTGTAATATTCCCTTTTAGGTGAGGGTTGG
TAAGGGGTTGGTATCTCAGGTCTGAATCTTCACCATCTTTCTGATTCCGC
ACCCTGCCTACGCCAGGAGAAGTTGAGGGGAGCATGCTTCCCTGCAGCTG
ACCGGGTCACACAAAGGCATGCTGGAGTACCCAGCCTATCAGGTGCCCCT
CTTCCAAAGGCAGCGTGCCGAGCCAGCAAGAGGAAGGGGTGCTGTGAGGC
TTGCCCAGGAGCAAGTGAGGCCGGAGAGGAGTTCAGGAACCCTTCTCCAT
ACCCACAATCTGAGCACGCTACCAAATCTCAAAATATCCTAAGACTAACA
AAGGCAGCTGTGTCTGAGCCCAACCCTTCTAAACGGTG

2188. chr15_JMJD7-PLA2G4B_NR_015346_-1.67739
CGTGCGGAGCGAGTTACGAGAATTCCCGGCCGCTGCA

2189. chr15_SPTBN5_NM_016642_-1.51343
TGTGTGTTTCCTGCCGTGGCGGCCCCGCAGCCTCTCACACCGGGCTCCCG
TGAGGTCAAGGAGGGCTATGGAAGCTACTTT

2190. chr15_PLA2G4D_NM_178034_-2.32415
ATTCCCTTGGCTGGTGCTGGTCCT

2191. chr15_CAPN3_NR_027911_-1.70532
ACAAACCCTTGTCCCTTTGCCATGTGGAGGAAAGTGCCTGCCTCTGGTCC
GAGCCGCCTCGGTTCTGAAG

2192. chr15_LRRC57_NM_153260_1.54957
AGAGAGTTGCCCAAAGGTAGACGGCAGCTCTCTAAGGTGATTGTTGTTTA
GGCTTAGCGTCTCTAGTTTTTTCAGATTGCATATCTCATCAGGCA

2193. chr15_CDAN1_NM_138477_-1.96639
TTTATCTCGGAGATGAGGTGGGAGGG

2194. chr15_CDAN1_NM_138477_-2.06309
AGCTGGACTTAGTTCAGGGTCGCTGTCCTTGGCAGTCACCATCCTCCGGG
CAGTGAGGAGCTGAAA

2195. chr15_UBR1_NM_174916_1.70514
TGCATACAGGTAAGAATCTTCAAAAAAGATCGAAAACCTTCAAGGAACTG
CATTCTTAATCTTTCTGTCCATATTGTGGGTTTGCTGATCAGGATATAC

2196. chr15_UBR1_NM_174916_1.55054
ATGGCAGTGGTATGCAACTGGGCCTCTGCGAGCTCACAGTCAAGAGCTCT
TTGTAGGCTGTATATGACGTGGTCATATGAATGGTGTTCA

2197. chr15_ELL3_NM_025165_-1.83761
CCTCGGTGGCCTTGGAAAGCAATCAC

2198. chr15_MFAP1_NM_005926_-2.02478
TTGATGGCAGCGACGGTGATTCCCGAAACTTGA

2199. chr15_DUOX2_NM_014080_1.5551

Figure 3-179

CTTCTTCACGCTCTCTTTGAGTTTCTTTTGTAGCTTCTTGTGTTCTCGGC
CCCGGAAATAGGCCA

2200. chr15_DUOX2_NM_014080_-1.56715
AGTACGGTGCGGTTGTGGAGCGACGGCAGGCCGGCTATGCCCCGCGTGGC
TGCGTTGCTGAGCCGGCGCGGGTTGGGCAGCTGCGGCTCCTCCAGAGCCT
GATACACACCGTCGGCGTAATTGGCTGGTACGCGGCGCTGCAA

2201. chr15_C15orf48_NM_197955_-1.53651
TTGGGAAACTGTGGACCCTACTGTACCTCAAAAG

2202. chr15_C15orf21_NR_022014_-1.54467
TCTGGAAGTGTTAGTTGCAAAGAT

2203. chr15_ATP8B4_NM_024837_-1.50316
AATGTGTCTTTTCCAGCCCTGATGTTGGGGGTGGATTTTTAGCTCGCATA
TTTTTTCCAGATGTGATAAGCTCTCCATAGCCTTCTTGGTGAGCAAAAGC
ATAGCCAGACCTTCTTGAGCTTGACCTGCGGGTCCGAGGCCTTCGGCTAC
TTGGAGGCCTTGCCTTCTTTTGAGCCTTCTGCCACCGGCG

2204. chr15_TMOD2_NM_014548_2.00493
TGGATACCAGTTTACCAAGCAAGGGCCACGAACAAGGGTGGCA

2205. chr15_GNB5_NM_006578_-1.51614
ACACGAAGGTGTTTCCAGTTTCTGAGGGGGCCAGGTCCAAGCAGAGGACG
TCAGCCCCATGTCCGTGGAAGCTCTGCAGCAGCTGCCCGCTCTCCACGTC
CCACAGGGCACATGTGCCATCGCCGCT

2206. chr15_MYO5A_NM_000259_1.55999
TTTGTGTAGAGCTCCGACGCAGCCAT

2207. chr15_ARPP19_NM_006628_-1.65286
TAGCAACAAGGGACGGCTTCCGTTGAGGAAGGTCTTGCGGAGTGGGAATG
TGG

2208. chr15_PIGB_NM_004855_-1.71324
ATACTCATTAACCCACCTGAAAAC

2209. chr15_NEDD4_NM_006154_-1.76332
CCAGGAGCCCGAACACCTCCACCGCGCAAGTTGC

2210. chr15_GCOM1_NM_001018090_-1.96973
TGCTGCGCTCCACGTCCACGGTCACCCTGCTCTCGGGCGGCGC

2211. chr15_TLN2_NM_015059_-2.15536
TGCAGAAGGCCTCCGGGTAGCAACCAACGCAGC

2212. chr15_TPM1_NM_001018005_-1.54027
AGAGTTGGATCGTGCCCAGGAGCGTCTGGCAACAGCTTTGCAGAAGCTG

2213. chr15_ANKDD1A_NM_182703_-1.87358
TGCCCTGCATTCGGCTGCTGGAGGATCCCACCCTGACTGTGTGCAGCTCC
TCCTCAGGGCTGGGAGCACCGTGAATGCCCTCACC

2214. chr15_CILP_NM_003613_1.51834

Figure 3-180

AGGCCCTAGGGTTGGACAAGAAGCCAGTTCTAGGCTCCAGGTTAATCACG
GAGATCACAACCCCCTGGATCTGCTCACTAGGCAAGAACCTCTCACTCCG
GTAGGCCCTCACCTTAACAAAGCACCGCCTGCTTTCAGGAACATCCAGGT
TAAAGAGCCTCCTCTCACGAATCTCCAGGTTGCCCACCAGGAAGGTTCTG
TCTTCTCTTTTGTTCCTCCTTTGATTTTCAAATTTGAAATCACCTTCCTC
CTCCCACAGCCCTGTGTCTGGATTGAGTGACCAGAGTTTCACTGTGGATA
TGTGCTCTGGCATCTTGACCTGGGTCGAGTCAAGGTGGACCTTCACTTTG
CCAGCATTAAGTGGCTCTGAGGTGACCTCATCTCTGAAGTCCACAGAGAA
CATGCCATACGTCCGAAGGGGGAAAGTGTCTCCTTCGTCATTGATGAAGT
TCAGGTCAGTCTGGGCAGCTGTGGCTGTGGAAATATTCCGGGGATCCAGG
AAGGTCACACTGGCCTTCACTTTTCCTATGTAGGGCTCCCCATTCTGCCT
GTAGAAACTCCTGGATGGAATCTCCAGTTCAGCCATGGGGTCTTCACCAA
CCACTTCCCCCAGGGGGATGATGTTGGTCTCCATGGCTTCCAAAGTGATG
GGCTTTTTCCGACGAAGCATCTTGATTTCATGGAACACGGCACTCCCCTT
CTTGTTGAAAGGTAGCACTTTGGTGGTGTTGACAAACTTCTGCAGCCTGT
CCACAAATGTGAGCACCAGCCTCTCAGTGTCCTGGGGGACATGGAGGGTG
AAAGTGCCCTTGTAGCCAGTCATGCTTACACGGCTGTTCCCCATGTACAC
ATGGCCAAAGCGCATGGGCTCCCCATTGTCAGCAGCACTGACACGGCCCC
GCACGATGCTCCGAGTTTCCGTACACCGCTGGCAGCTGCACTCCTTGGCC
ACCTTGGTGGGTAGCGTGTAGCCACTGCACTGGATCTCCCTTTCCTCTGT
CTTGGAGATGCCACAGCAGTTCTGCACAGCATCACGGCACCTGATCCCAT
TATCCTGCTGCCCTGCACAAGTCTTAACAGGGCAGCGTCCCA

2215. chr15_IGDCC3_NM_004884_2.6461
GCGGAGACGCGGCGCGCTGCACAG

2216. chr15_IGDCC4_NM_020962_1.67489
TTTATGGCGTCGTACACCAGAGCCTGCAGCAACAGCGTCTGCCCAGTTCC
AGCAGGGGGCAGCAGGGCCCGGGTCAGAGCCGGCCGGGGGCCTGCCTGGG
GCAGCTCACAGCCTGCCCAGGAACCAGCCCAGCTCAGCCCGCTTGGTTGA
GCCCAG

2217. chr15_RPL4_NM_000968_-2.49299
TGTTCCGGCGCATGGTCTTTGCAT

2218. chr15_LCTL_NM_207338_-1.5048
CGAGGATCACTGAACGTGATCCAGTGCTTCACACGGTCCC

2219. chr15_MAP2K5_NM_145160_-1.5001
GTGAAGCCCTCCAATATGCTAGTAAACACAAGAGGACAGGTTAAGCTGTG
TGATTTTGGAGTTAGCACTCA

2220. chr15_ITGA11_NM_001004439_-2.59387
GAGGATGGGGATGATTACGAATTC

2221. chr15_SPESP1_NM_145658_-1.55538
ACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTG
ACACCTTCCCTTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGT
TCCGGTCGCATGGCAGAGTGCTACGGACGACGCCT

2222. chr15_TLE3_NM_005078_-2.16688
GGCTTGGTGTGGTGCAGCACCTCC

2223. chr15_PARP6_NM_020214_-1.98349
GTGCAGACATGGTCGGACACAGGGCACACCCAGATGTTCCCATGCTT

Figure 3-181

2224. chr15_HCN4_NM_005477_-1.6158
GTCCAGCGCCACGGTCTCGAAGGCCCTTCGCATCATGGGGTACTCCTCCA
GCACCTCATTGAAGTTGTCCACGCTCAGCGAGTAGAGGCGGCAGTAGGTG
TCGGCCCTCACGCTGGCTGT

2225. chr15_CD276_NM_001024736_-1.70976
CTCAGGCGGATTCTCCGGCGCGGCCCGCCCCGCCCCTCGGACTCCCCGGG
CCGCCCCCGGCCCCCATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGC
CAGGCTGGGCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGC

2226. chr15_PML_NM_033250_-1.78289
TGGAGCCCATGGAGACCGCCGAGCCACAGTCCTCGCCAG

2227. chr15_CYP11A1_NM_000781_-1.5285
GCAAAGCGGAACAGGTCATCACTGAT

2228. chr15_C15orf17_NM_020447_1.52981
GAGTCTGGGCGGTTCGGCGAGGCCCCCAGCATGCCTTTTCTCCGCAGAAC
GGCCTTGGCCAG

2229. chr15_C15orf39_NM_015492_-1.88585
CCTGTGATGTATGGCAAGCTGCCCCGCTTAGAGACAGACTCCGGGCTCGA
GCACAGCCTGCCCCACTCTGTTGGTAACCAGGATCCCTGCACCTACAAGG
GGTCCTACTTCTCCTGCCCCATGGCAGGTACTCCTAAGGCCGAGTCTGAG
CAGTTG

2230. chr15_C15orf39_NM_015492_1.62297
CCTGCTGACCAACTGCCTGTTCTACCGCTCGCCAGCAGAAGGCCCTGAGA
AGATGCAGGACTCCAGCCCTGTTGAGCTCCTGCCCTTCAGTCCCCAGGCT
CACTCCTACCCAGGCCCACCACTGGCAGCACCCAAACCTGTCTACCGCAA
CCCTCTGTGCTATGGGCTCTCAACTTGTCT

2231. chr15_CSPG4_NM_001897_-2.01214
CTGAGGGTCTGACTGCTGAGTGGC

2232. chr15_ISL2_NM_145805_-1.66435
GCATCAAGTGCGCCAAGTGCCAGGTG

2233. chr15_RCN2_NM_002902_-1.76833
GGAGCTGCACTACCCGCTGGGCGAGCGCCG

2234. chr15_TSPAN3_NM_005724_1.51879
AGCAGCCAATTAGCCCAATGATGAAAAGCAGGGCTCCTACAGCTATGATC
ACTACAGCAGGGATGAGCGTGTACACATCTTCAAAGAAGTGGTCATAGTC
ATCATAAGTGATGAAGACATAGGCTCCCA

2235. chr15_ADAMTS7_NM_014272_1.64148
GTGGAGACATGATGAAAGGTCGTTTCCCAACGGGCTCACAGTCATTGCCG
CTTCCGTCA

2236. chr15_RASGRF1_BC040275_-1.81052
TACCTGGGAGTGTTAGACCTCAGCCCAGTACTTTGCCCACTTGTGGATGC
CCAGTGGCCAGCCCACGGGTCTTCCTGCCCTAGCCCCAATCC

Figure 3-182

2237. chr15_ARNT2_NM_014862_1.52982
AGTGGACAAAGTAGCGGGCAGTTCCAAGGGCGGCCCTCGGAAGTCTGGTC
GCA

2238. chr15_KIAA1199_NM_018689_1.65752
GGCGTCAGTGACTGCACAGCCACAGCTTACCCCAAGTTCACCGAGAGGGC
TGTCGTAGACGTGCCGATGCCCAAGAAGCTCTTTGGTTCTCAGC

2239. chr15_AKAP13_NM_006738_1.54681
AATGGAGAGGGTTAAAAACATGCAAACTGCCACTTTCAACCTTTGCCAGT
ATTCCCTCTACCCCCGTGAGAGCTATCTGGGGGGAAG

2240. chr15_HAPLN3_NM_178232_1.56956
CAATGACCTCACAGCGGTAACGCCCATAGTCCTCCAGCCGCAGATCCTGG
ATCTCCAGCGAGACGTCATGCTCTTTGTCCTGCCGCAGGTGCACGCGGCC
TTGGTAGTCCCCAAAGGAGCGGTGCCTCAGCCCGATGGCCACCAGCACGT
CCTTCTCTGGGGCCCCGTTCTCCGACAGCTTCCACCATTTGACACGCACA
CGCCGCGGGGAGACCAGGGCCGGCTCGTAGCGGTAGCGGCAGGGCAGGAT
CACACTGGCCCCTTGGTAGGTGAACAGGGTCTCCTCGGGTGTCTCCA

2241. chr15_POLG_NM_002693_-1.58315
TGGATGTCCAATGGGTTGTGCCGCAGCTGCC

2242. chr15_KIF7_NM_198525_-1.75381
GCTCTGGGCCGCAGCGACCCTCCTGCGGAACTCCTGGAGCCGAGACCGCT
CGCCAGCATCCTGGAGCTCCTTGCCCTCGAGCTCCCGCAGCTGCCTCTGG
CCTTCACTCAGCTCGGCCCGCACCTGCTCTGCCTCCTGCTCCAGCTCCCG
GATACGCTGGCTGTGCTGG

2243. chr15_IQGAP1_NM_003870_1.6869
AGCTGCAGTCTGGAGTGGATGCTGC

2244. chr15_CRTC3_NM_022769_-1.94296
TGGACACCACCGACCACCACTTTGGCAGT

2245. chr15_MAN2A2_NM_006122_1.60817
GGCGGAGACCGCACTCATCTTACACCGCAAGGGTTTTGACTGCGGCCTGG
AGGCCAAGAACTTGGGCTTCAACTGCACCACAAGCCAA

2246. chr15_VPS33B_NM_018668_-1.78117
TCTGCCCAGGAACCGGAGGGCTGAGATCTCAGAGAATGTACAACCACCCA
AGA

2247. chr15_LYSMD4_NM_152449_-1.84191
ACGGGGCCAGCCTTCGCGTCCGAGCTCAGGGG

2248. chr15_ADAMTS17_NM_139057_1.61703
TGTCTGCCCCACACTCGGTGCCATCCAGGGGAGGGTCCAGCTTGGTCTTG
CAGGATGTGTCTCCTTCTACCAGGCACCACAGTCCAG

2249. chr15_LRRK1_NM_024652_1.51147
ACACGGGCGGCAAGCCGTCCACGCGGGGCGGTGACCCTGCAGCGCGGTCC
CGCAGGACGGAAGGCATCCGCGCCGCGTACAGGCGGGGAGACCGCGGCGG
CGCCCGGGACCTGCTGGAGGAGGCCTGCGACCAGTGCGCGTCCCAGCTGG
AAAA

Figure 3-183

2250. chr15_PCSK6_NM_138320_1.547
TATCCCGCTGCTGCACGGTGTCTGCCCACAGCAGGGACCCAACAAATATG
CATCCAGTGAACAAAGGGACGAAGGCCCCTCAGCAGCTCTGTAAATGGGC
TCCTGTCCACAGTGGGGTGATGCAACATGCCCTC

2251. chr15_TM2D3_NM_078474_-1.56399
TTAGAGCCAGAGCCGTAGACCACTTATAGCCTCCAGTCCAATTGCAATAT
AGCATTTTGG

2252. chr16_SNRNP25_NM_024571_1.52135
AAGTCAACTCCCAAATAGCCCTAGAATACGGCCAGGCAATGACGGTCCGA
GTGTGCAAGATG

2253. chr16_ITFG3_NM_032039_1.51321
TAGCCTAGCCCTCCCGAGCCTCCCTGGGGGTCCACTGTCCGCCAGCCTGC
CGACCGCAGACCACCGCTCAGCCTTCTTCTTCTGGGGCCTCCACGAGCTG
GGGA

2254. chr16_RGS11_NM_183337_-1.52714
GGGCGTCTCGTCTGGCCGGAGCATGAGGCTACGGGGGTCGCGCAGCGGGT
AGATGTAGCCATGCTGCACCAGGAC

2255. chr16_RAB11FIP3_NM_014700_-1.62354
CAGTGAGGCGGAGCTGTCCCCAGAGACCCTATGCAACGGGCAGCTGGGCT
GCAGTGACCCCGCTTTCCTCACGCCCAG

2256. chr16_FAM195A_AK054811_1.66976
CCTGGCTCAGCCCGACTGCCCTCCT

2257. chr16_WDR90_NM_145294_-1.64131
GCGGGCAGGGCAGTGTGCGGCTCTGGCGGCTGCGTGGCGGGGTGCTGCGT
TCCTGCCCCGTGGACTTAGGGGAGCACCACGCGCTGCAGTTCACCG

2258. chr16_RHOT2_NM_138769_1.65158
ACAGATGGTCTGCTGGCCACATCGCTGGACGCCACCTGTGACGTTGCCTG
CTTGATGTTTGAT

2259. chr16_RHOT2_NM_138769_2.04405
CTCAAGTTTGGAGCCGTTTCCGTGGTTGTAGCAG

2260. chr16_CCDC78_NM_001031737_-1.69963
CTCCTGATGCTCCAGCGCCCACTTCACTTCCCCCTG

2261. chr16_HAGHL_NM_207112_-2.73131
CTGCGGCCACGAGCACACGCTTAG

2262. chr16_NARFL_NM_022493_-1.9644
TGAGACGGCCCGATGAAGTCATCCAGGTCCGTCAGCTGCAGCGCCCCGCT
GAAGGGCGACGCCAT

2263. chr16_MSLN_NM_005823_-1.82199
CTGCGCCCCTGGACGGAGTCCTGGCCAACCCACCTAACATT

2264. chr16_MSLN_NM_005823_1.50613

Figure 3-184

ACCCCGAGTCTGTGATCCAGCACCTGGGCTACCTCTTCCTCAAGATGAGC
CCTGAGGACATTCGCAAGTGGAATGTGACGTCCCTGGAGACCC

2265. chr16_CACNA1H_NM_021098_-1.53782
GGGGAACGTGAGTCCCTGCTGTCTGGCGAGGGCAAGGGCAGCACCGACGA
CGAAGCTGAGGACGGCAGGGCCGCGCCCGGGCCCCGTGCCACCCCACTGC
GGCGGGCCGAGTCCCTGGACCCACGGCCCCTGCGGCCGGCCGCCCTCCCG
CCTACCAAGTGCCGCGATCGCGACGGGCAGGTGGTGGCCCTGCCCAGCGA
CTTCTTCCTGCGCATCGACAGCCACCGTGAGGATGCAGCCGAGCTTGACG
ACGACTC

2266. chr16_UNKL_NM_001037125_-1.56896
GTTGCGCCGCCTGTCCCGGCTATTGTGGTAGTGTGGGCACGCATAGCCCT
GGCGGCACAGGCGTGGCGGCTTCGGGCACTGCTCCGTCTTGTAGCTGCCC
AG

2267. chr16_CLCN7_NM_001287_-1.86318
GTGTGATTGATCCGCCGCTCCTCCTCCAGGAACAGCTGGTTCTCACTGTT
GTCATAGTCCAAG

2268. chr16_CRAMP1L_NM_020825_2.07158
TGCTCCGCACCGATGCAGGAGAAG

2269. chr16_SPSB3_NM_080861_1.58479
CCAGCCCAGCTTGTTGTGTAGCACCTGCTTGAGGCCCGGCGGCAGCGGCA
GACCCTCCAGCGTGTCTCCCGAGTCTGGCCGCAGCTGGCGCAGGCGGTGG
CAGCACAGGTACTGGAGGGAAGTGGCGCTGGCACAGGAGCGGGTGACCTT
CATGCTGCTCCGGGCCGCCGTGGAGCACACCATCGGGTAGA

2270. chr16_SPSB3_NM_080861_-1.69691
TGCCCATCAGAGTCGTAGCCCCAGTTAGTGGAGCCTG

2271. chr16_HAGH_NM_005326_1.55933
TACATGTAGTTGTCGGTCAGGGCAGGCAG

2272. chr16_HAGH_NM_005326_-1.66576
GGACTGCAAAACACCGGCGTCGGCGCGTCGCAGCCAATCAGCGCCCGCCT
CGCGCTGCCCTCAGCCAATCAGCGTCCACCTCGCACCGTCCGCCAACCAA
TCAACGCGCTCGCGCTCAACTTGTTTTGTCCGCGAGCCCCGACTGCCACG
GGCCGGGAGACGGGCCTGGGAGCGGCGGCGGCGGCCCGAGAGCTGCGCCG
GGAGAGCTGTGCCGCGAGCCTCCGCCTCTTTTTTGGCACCGCACAGTGGA
TCCCTGGAGGCCGAGCGCCACGCCGCCCGGGTACCCGGCAGATCGCGAGG
TGGAAC

2273. chr16_RPL3L_NM_005061_1.7689
TTTGCCGACCCTGCAACTTGATGGATCTGCTGGCACCAACCAGATTGATA
AACTGGCTCATCTGATCTTGTGGCCACCACCCAGGAGCTGACTCAGCGCA
AGAAGACAGCTGACTCCCTGTGATTTCCTCCCTGACCAATCGGCTCTCCT
GGCTCACTGGCTCTCCCCACCCGCCAAGTTATCCTTAAAAACTCTGCTCC
CCGGCACTCCAGCAGCCTGGGCGACAAGATCAAGACTCTCTCAAAAAAAA
AAAAAAAAAAAACCTCTGCTCCGCAAATGCTCAAAGAGATCGATTTGAGT
AATAATAAAACATAAAACTCCGGTCTCCCGCACAGCCAGCTCTGTGTGAA
TTACTCTTTCTCTATTGCAATTCCCCTGTCTTAATGAATCGGCTTTGTCT
AGGCAGCAGGCAAGGTGAACCCCTTGGGCGGTTACACAGCGCTCTGAGAC
CTCGCAGGAAGAGTCGCCTCCGGCCTTTGTTA

Figure 3-185

2274. chr16_TBL3_NM_006453_-1.65837
CCTGGATGTGTTCCGGAAGGGGTGGCTCTTTGC

2275. chr16_TRAF7_NM_032271_-1.93549
ACAACATGATCTGCACGCAGACCCTGCTGCGTCACCAGGGCAGTGTCACC
GCGCTGGCTGTGTCCCGGGGCCGACTCTTCTCAGGGGCTGT

2276. chr16_CASKIN1_NM_020764_-1.50433
GGCGGGGCCCTCATCCAGGAGGTAC

2277. chr16_CASKIN1_NM_020764_-1.74792
GTCCCCCGGGCCGGACTCAGAGACGGACTT

2278. chr16_DCI_NM_001919_-1.50151
GCGCGGAGCAGAACGCGCGCCGGGACTCGCACAGAAGCCACCAGCG

2279. chr16_---_---_-1.50489
GCTCTCTGCCAGCCCGCACAGCAGTGGAAGGCAGGCAGGGCTGAATAAAG
GGTCTG

2280. chr16_---_---_-2.18269
GTGTGGGAGGTTGATTGTAAAGAAAA

2281. chr16_RNPS1_NM_006711_-1.544
GTGTCTGCGCCGAGAAGGACTTGGAGA

2282. chr16_---_---_-1.52339
CTGACCCAGGCTAGGTTGATTTTTTC

2283. chr16_CCNF_NM_001761_1.52816
AATTTTCCCAGATAGGCTAGCCAGAAAAAACTTCAAGTCCTCTGTAACAT
CTGAGGTGACCAAGAGGCAGAAGAGCAGAGCAGTCGGGGGCCGTGTCCTG
GCTGATCCCAACTGCAGCTCTGCTGTGGGGGCCCGTGGGAGGGAGGCAGA
CCCCTGGGCTTTCCTGCTGGCCACGGAGACTCTGCTCCTGCATGGAAAGG
GAGCCTGGGAGCCAGCAGCCCACGCCTGGGGAGCCTGCCTGGGGCCATGT
GACCATGGCCTCTCCCTGGGAACGGGCTGACCACAACACACCCTGCTGCC
ATCCACTTCTGTTTACTCTGCAAATGTAAGAAAGAACCACTTGGCCAGAA
GTGTCCCCCAGATGCTTTTTTTTTTTTTTTTTGGAGACAGTTTTGCTCT
TGTCTCCCCGGCTGGAGTGCAGTGGCATGATCTCAACTCTCAACTCACTG
TAACCTCCGCCTCCCGGATACTCCTGCCTCAGCCTCCTGGGTAGCTGGGA
TTACAAGCACCCAACCACGCCCAGCTAATTTTTGTATTTTCGGTAGAGAC
GGGATTTCACCATGTTGGCCAGGCTAGTCTCGAACTCATGACCTCAAGTG
ATCCGCCCACTTCGGTCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC
GGCGCCTGGCCCCCAAATGCTCTTGAACCGGAAACCCAGGGATGGGAGAT
GCTCACTGAGCTGCTGCTTTTATGTGTGCTGGTGCTATGTGTGTTCATGT
CCGCGGCAGCTGTCTTTTTGCTACTATAAGGGAATTCTGGCCACCCTGGG
TGGGGTGTGGTCGGGGTGAGAACCCAAGCGTTGGAACTGTAGACCCGTC

2284. chr16_PRSS27_NM_031948_2.31448
TGTTGCTGCCTTGGCCCTCTGAGAC

2285. chr16_SRRM2_NM_016333_-2.30865
TCCCCTTCCCCTGCTAAGCCTGGCC

Figure 3-186

2286. chr16_---_---_-1.64523
ACTGCACGGCGCGGGCGATACCGTTGCAGGGGTTGCATGCCACGGTGCCC
TCGGCGCCCGGGGCCCGGCACGAGGTCTAAACATCGC

2287. chr16_PRSS22_NM_022119_-1.68138
AGGTATCCTGGCCGCATTGAGGATGG

2288. chr16_TNFRSF12A_NM_016639_1.55107
CCTGGAGCGCGGACCTGGACAAGTGCATGGACTGCGCGTCTTGCAGGGCG
CGACCGCACAGCGACTTCTGCCTGGG

2289. chr16_ZNF263_NM_005741_1.68647
CATGAGTGCGGAGACAGCTTCTCTCACAGCTCCAATCGGATTCGCCACCT
GAGAACGCATACGGGAGAGAGACCCTATAAATGTTCTGAATGTGGAGAAA
GCTTCTCTCGGAGTTCCCGTC

2290. chr16_NLRC3_NM_178844_2.56084
GGGCCTTGGCACCTCCATCACCAATACTATTACTGG

2291. chr16_TRAP1_NM_016292_1.56727
CCAGGCCAGGCTCGCTTGCGCGCAGCTGATTCAGCTTC

2292. chr16_TRAP1_NM_016292_-1.57838
GGGTTGATCTCCAGCGTGGGCTGCAGGAGCTGTGCGCGCTCCTCCTGGGT
CTTGGCCAGCTGCTGCATGCGCAGGAAGTGGCGGGCAGCCCCCATCTCCA
GCACGGTGACCATGGCAGGGTGGGTGTCCAGTCGGAGGGTCAC

2293. chr16_CREBBP_NM_004380_-1.90778
GGTGAGACGTGGTGTGGCGAAGGCTGGGGCTGTATCCGTGGTGACGGGCT
GGAATGT

2294. chr16_CREBBP_NM_004380_1.62939
CTGTGCCGTTACTGCTACTCTCTT

2295. chr16_ADCY9_NM_001116_-1.58738
AAGCAGGCTTCATCCCGGAAATGGTAGCCAAAGGTCTCGAAAAGGACAGA
GTAGGCCACCCCCAGACACAAACTCAGGTACAAAGGTAAGTGCATGACGG
TATAGAGCAAAAAGAGCACTTCGATGCACATGGAGAAGCTCCCCACTTGA
GATAAGCAAGTATCTGTGGGCCGGGCTGTGGCCGTAAGGTTGGAGCTGTC
GCCGCGTCCTGAGACAGGCGTCAAGACCTGGAACTGCGCAGCCAGGGTCA
GGGCGAACACCAGCAGGGTGAGAGCCAGCGAGGTCCACGCGTAATGCCGG
GCGTACAGCTTGGTGAAGGTAAACAGAAAGAAGCCCACACACACCAGGAG
GAAGCACAGCGCGGGGGCGACCATGACGATCAGTCTGGATCTCATGTGGA
CCGCAAAATAGATGCTCCACAGAAGGCAGGCGAAGCCGATGTAGAAGAGC
GCATACCGGAACCGGCGCTGGGTCTGCGGGAAGCAGCGCTCCAGGCAGGC
CTCCTCCAGGTTCACCGAGTCGAACTTGGGGTCCCACCAGCGGCTGGAGG
CCCTCTCGAACAGCTGGGGCAGCTTCTTCTGCCTGCGCAGCCGGCCTCCG
CCGCCCACTCGCCGGGGGACGCCCCCGGAGTCCCCAGAGCTGCTGCAGCT
AGAGGAGATGCTGTATTTGCAGTGCTTGGGGTGGCTGTTGGAGGACAGCT
GCTTGGGGTTGATCTTGACGCGCACGCTGTT

2296. chr16_ADCY9_NM_001116_-1.60522
GGCTCCGGGACCGCTTTGCTCGCTCGCCTTCCGCGCCTCTCGCCCCGAGG
GTGGCCTCCGCGCCGCGCGGCTTCTCCTCCTCGCGCGCTCGCCTCCTCCA
GCTGCGGCTCCGGAGGGAAGTTCAGACCTTGAGCGCTCCCAGCCCCGCGA

Figure 3-187

GCCGCCTGCGCACAAACAACTCCGCTGGCGGCGCGGAGCCCTCCATCCTG
CAGGAGCCGCGCTCCGATGCGTCAAA

2297. chr16_CORO7_NM_024535_-1.66064
CCAGGGCGCTGGAGAAGAACCGCGTGTCCCACAGCTTCACTTCGCGCTCA
CGCAT

2298. chr16_DNAJA3_NM_005147_-1.53488
TCTTGCAGGGCTAAAACTCTAATTTGGAATTGAATATTGTGGATATCTTA
GTTAAAGGCCATGCTTACAGCTTAGAAATGAAGCCTTAAGCTGCATCAAG
TTACGAAGTGATTAATTTCCTTCTCAGCAAACCTCCGGGAGGTTCCAGAA
TGAGTTCTTCCTGACAGGTTGTCTTCACTGGGAGCGTGGGGCCCCCAGGC
CCCACCAGCACCGTCCTCCCCTAATGAGGGGCCCTGCCGAGGCATCAGCT
GCTCTGCTCAGTTAGTTTTTATTCCCGGGGTACCAAGCAGCTGCACAGTC
GGTGCCTGGGAGGCACGTAGAGGCCCAGAGAGTCCCTGGGGGTTCTGCTC
TGACCGTGTGGGTGGTGATCCTTGTCAGGATGTACAGTCCTTGCTCCCAC
CCCATCCGGGATGGCCGCCTGTCCCTGACTATTGAGTCCTGTTGTTGTAA
GCCAGGCATGGAGGGCTCCTGCCCTTCTGCTGAGCCACAGCCCATTGCAG
CACTGTGCTGGCCAGACTTCAGCTGCCTTGGGAACTGAAGCCCTGCCACT
GTTGCTAGTCA

2299. chr16_NMRAL1_ENST00000404295_-1.54004
GCCTGGGCGGGACAAGTTCCAGGAGCCCGGGACCCCGATTCTGCGGCCGA
GTCCACTGCAGAGGCGGGGATGGAGCTGCGCGCTAGGCGCCAACTC

2300. chr16_MGRN1_NM_015246_1.53425
GGCTCCGAGCATGAGGTCCGCCTCCTGGGCGAGACCCAGCAGTGGACAGC
ATGGTCCTCACACCCAGCTCCCTGCACACCCAGGCCAGCCACCCCTCCCG
CTCGTGCACAGGCACGCAGATGCGCTCACACGTACACACACACAAATGCA
CGCCCACTTGCACATGCTCACGCACATGTTCACACATGCACACTCACGCT
CACACATGCTGTCACGCATACACACACGCACATACTCCTGCACATGTTCC
CATGCATGTGTGTGCACTCGGACCGAGCATC

2301. chr16_ROGDI_NM_024589_1.56702
CAGAAGGGTCTGTAGCTCCAGTAGCTGGAGAACACGGAGAT

2302. chr16_SEC14L5_NM_014692_-1.85763
AGGGTGTTCAAGGCGGGACACACCAGGCTAGAGATCCGCGATCGGGCC

2303. chr16_NAGPA_NM_016256_-1.7757
GTTGGACCCGGTCCATCCGGCATCAC

2304. chr16_C16orf72_NM_014117_-1.73622
AGGACTTTCTCTCTGGGTCCCCTTCCAAAACGCAGCCACCGCCGTCACCA
ATCTCTACAA

2305. chr16_CIITA_NM_000246_-1.51602
TGACCGCGTTCTGCTCATCCTAGACGGCTTCGAGGAGCTGGAAGCGCAAG
ATGGCTTCCTGCACAGCACGTGCGGACCGGCACCGGCGGAGCCCTGCTCC
CTCCGGGGGCTGCTGGCCGGCCTTTTCCAGAAGAAGCTGCTCCGAGGTTG
CACCCTCCTCCTCACAGCCCGGCCCCGGGGCCGCCTGGTCCAGAGCCTGA
GCAAGGCCGACGCCCTATTTGAGCTGTCCGGCTTCTCCATGGAGCAGGCC
CAGGCATACGTGATGCGCTACTTTGAGAGCTCAGGGATGACAGAGCACCA
AGACAGAGCCCTGACGCTCCTCCGGGACCGGCCACTTCTTCTCAGTCACA
GCCACAGCCCTACTTTGTGCCGGGCAGTGTGCCAGCTCTCAGAGGCCCTG

Figure 3-188

CTGGAGCTTGGGGAGGACGCCAAGCTGCCCTCCACGCTCACGGGACTCTA
TGTCGGCCTGCTGGGCCGTGCAGCCCTCGACAGCCCCCCCGGGGCCCTGG
CAGAGCTGGCCAAGCTGGCCTGGGAGCTGGGCCGCAGACATCAAAGTACC
CTACAGGAGGACCAGTTCCCATCCGCAGACGTGAGGACCTGGGCGATGGC
CAAAGGCTTAGTCCAACACCCACCGCGGGCCGCAGAGTCCGAGCTGGCCT
TCCCCAGCTTCCTCCTGCAATGCTTCCTGGGGGCCCTGTGGCTGGCTCTG
AGTGGCGAAATCAAGGACAAGGAGCTCCCGCAGTACCTAGCATTG

2306. chr16_TXNDC11_NM_015914_1.53969
TGCTCCCAGTCGCCGGCTTTATACCGCCGCCGCCGCCTCGGGCCCGAAGG
CCCGGCCCGGCCCGTTGCTCCCCAATCCCGCAGCTCGCCGCACCCGCTAA
CCCGGACGCTCCA

2307. chr16_RSL1D1_NM_015659_-1.57037
GGACTTGCAATGCGTCAAGAGAGCGTCCACTGCCTTTCTAAC

2308. chr16_CPPED1_NM_018340_-1.9323
GAACTCCTCGACGGTCTCGGCCGTGGGGGTGTTGCCAATGTCATGGTTGC
CGCTGACAAGGACCAGTGGGATGGCCCTGTCCACTGCCCTAAGCACTCGC
TTCAGGTCCTCCGT

2309. chr16_MYH11_NM_002474_1.63116
CCTCCTCGCTGAAACCCATGATTGCCATGGCCTCCACGGTTTCCTGGAAC
ATCTCATCATCCTGGGCTGCTGGGATGGGCACAAAGCCATTGGAGAGGAA
GGTGTAGTTGTTGAAGCCCTCC

2310. chr16_ABCC1_NM_004996_-1.85201
GGCCGTGTACTCCAACGCTGACATTTACCTCTTCGATGATCCCCTCTCAG
CAGTGG

2311. chr16_ABCC1_NM_004996_1.56126
TGGCATGCTGGTGACGGACAGTGCAGGGAA

2312. chr16_ABCC6_NM_001171_1.60354
AGTCCATCACGGAGCGCAGGCGGTGGGCAATGAGCAGCACAGTGCACTGT
GCAAACCAGCTCCCGAGCATGGCCTGCATCTGCAGCTCCGTGCCAGGGTC
CACGGCAGCAGTAGCCTCGTCCAGGATGAGGATCTGGGTCTTCCGGAGAA
GGGCACGTGCCA

2313. chr16_ABCC6_NM_001171_-1.75416
ACTGCAGGGTCGTCCGCCCACAGGCTCAGCCAGTAGCCCCGGCAGAAGGA
GGCCACTTGCTGGCAGAGGAAGAGGAAGAGTGCGTAGAGGCAGAGGGGGG
TGCCCACGGCACGCAGGTAGGCCAGGT

2314. chr16_XYLT1_NM_022166_-2.17594
CTCGAGGGGGCAGAACCGAGTCAC

2315. chr16_TMC5_NM_001105248_1.53422
AAATATCAATCATTGGCATTCTTTGTTACTATTGGCTCAACACCGTGGCC
CT

2316. chr16_DNAH3_NM_017539_1.56661
GACACTGATGGTGGCCGGTTGGTAGACCTTCAGCAGATCTTTCA

2317. chr16_VWA3A_NM_173615_-1.87723

Figure 3-189

GCAGAACCAAAGGTCACTCTTTCC

2318. chr16_POLR3E_NM_018119_-1.75207
CTGCTTCCCCGGATGAGCAGAAGGTGTTT

2319. chr16_CDR2_NM_001802_1.5106
GCAAAGCTGGGTGCCGGTTTCTCCTGGTCACACTTTCCCGGGCTCCTTCT
CCCTTGGCCAGATGACTTCAGCTCCTCCACTTGGCTCTGGAGGTGATCAA
TGTTGGTTTGCAGGCATTCAATCGTTTCAGTCAGG

2320. chr16_ERN2_NM_033266_-1.71109
GAAGAACTGGAGTTGCTTGGCTCT

2321. chr16_ERN2_NM_033266_-2.19261
TGCGGCAGGGAGAGGCATGAACCAGC

2322. chr16_SLC5A11_NM_052944_-2.48992
TGAGCTGGTTCACAGAGCCACCCT

2323. chr16_XPO6_NM_015171_1.82949
AAGGTTTGGCCACGGAAGCAGCAAGATGTTAGAGAGGGCTCGGCACACCA
ACACCTGG

2324. chr16_TAOK2_NM_004783_-1.77626
GTGCGGTTCTTACAGAAGCTCCGGCATCCCAACACCATTCAGTACCGGGG
CTGTTACCTGAGG

2325. chr16_GDPD3_NM_024307_-1.59483
ATGAGCTCTTCGTTCTTCCCTTTGATCTCTACGCTCATGGGTGTCCTTGG
AAACCTCTGGAACAGGTCCTCCAGACGAACCATGC

2326. chr16_ITGAL_NM_002209_-1.62746
CACCTCTATGGCAGCAACGCCTCCCTGGCCCA

2327. chr16_RNF40_NM_014771_-1.72826
CATCTCACGGCTGCGGCGCAAGCTGGAAAAGCAGAGGAAGGTGGAGGTCT
ACGCAGATGCCGACGAAATCCTCCAGGAGG

2328. chr16_ITGAM_NM_001145808_-1.61529
CAGCGCTCACAGCGATCCTGGCGCCTGGCCTGTGAGTCTGCCTCCTCCAC
CGAAGTGTCTGGGGCCTTGAAGAGCACCAGCTGCAGCATAAACCACCCCA
TCTTC

2329. chr16_ITGAM_NM_001145808_1.73246
TCTCGAGTACGTGCCACACCAAGGAGCGCTTGCCCTCTCACTCCGACTTT
CTGGCTGAGCTTCGG

2330. chr16_ITGAX_NM_000887_-1.96552
TTAAATGACATTGCATCGAAGCCCTCCCAGGAACACATATTTA

2331. chr16_ITGAX_NM_000887_1.65622
ACTGAGCGGGGGTCAAGACCTCACCCAGGATGGACTG

2332. chr16_ZNF843_NM_001136509_1.55789
TGCGGAAGGAAAGATTTCAGATCCC

Figure 3-190

2333. chr16_ARMC5_NM_024742_1.55536
TCCCAGCCTGACAAGCTTTCCACTCACAG

2334. chr16_SLC5A2_NM_003041_-1.94986
CTGCGCGGACTCATGCTGGCGGTCATGCTGGCCGCGCTCATGTCCTCGCT
GGCCTCCATCTTCAACAGCAGCAGCACGCTCTTCACCATGGACATCTACA
CGCGCCTGCGGCCACGCGCCGGCGACCGCGAGCTGCT

2335. chr16_GPT2_NM_133443_-1.5723
TGGAGTCCATGAACCCGCAGGTGAAGGCGGTGGAGTACGCCGTGCGGGGA
CCCATCGTGCTCAAGGCCGGCGAGATCGAGCTCGA

2336. chr16_ABCC11_NM_032583_1.58133
GGCAGAAGTTCCAGGTCCCGATTCAGGGAGCA

2337. chr16_ADCY7_NM_001114_-1.69374
AGCGGGACCCCTACCTCAAGGAGATGAACATCCGCACCTACCTGGTCATC
GACCC

2338. chr16_SALL1_NM_002968_1.60971
TCGGCACAGCACCGGCCACAGACGTGGGCATCCTTGCTCTTAGTAGGGCG
ACTCGGTTGACC

2339. chr16_RBL2_NM_005611_1.76693
GCGCTTCGCCGTTTGAATGGCTGCGGGCCC

2340. chr16_OGFOD1_NM_018233_1.56179
AAGGGCGCCGGATTGCCTTCATCCTGTACCTGGTTCCTCCCTGGGACAGG
AGCATGGGTGGTACCCTGGACCTGTACAGCA

2341. chr16_NLRC5_NM_032206_1.69645
TTGTCTCAGGTTAACCTCTGTGAGGACGATGATGCCAGTTCCCTGCTGCT
GC

2342. chr16_GPR56_NM_005682_1.53355
GGTGACTTCCAAGAGTGACTCCGTCGGAGGAAA

2343. chr16_GPR56_NM_005682_1.77118
GAGGGTCTGGCACATCCTTAATCCTGTGCCCCTGCCTGGGACAGAAATGT
GGCTCCAGTTGCTCTGTCTCTCGTGGTCACCCTGAGGGCACTCTGCATCC
TCTGTCATTTTAACCTCAGGTGGCACCCAGGGCGAATGGGGCCCAGGGCA
GACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCA
CAGCAGCAGCTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCC
CCCCAGTCCTCCCTCCATCTTCCCTGGGGTTCTCCTCCTCTCCCAGGGCC
TCCTTGCTCCTTCGTTCACAGCTGGGGGTCCCCGATTCCAATGCTGTTTT
TTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGTTTGTC
TACTGCACAAGCCTCGGCCTGCCCCTGAGCCAGGCTCGGTACCGATGCGT
GGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATT
GCCCTTGCTCACCCTGACCAAGCACACGCCTCAGAGGGGCCCTCAGCCTC
TCCTGAAGCCCTCTTGTGGCAAGAACTGTGGACCATGCCAGTCCCGTCTG
GTTTCCATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTGGTGACAC
TGGCCTAGGGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAAT
AGCTCCAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAAC
ACACACGGGTAGATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGAC

Figure 3-191

CGACCTGGTCACTCCTCCTGCCAACATTCAGTCTGGTATGTGAGGCGTGC
GTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCATCATTCCTGC
CTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTT

2344. chr16_GPR97_NM_170776_-1.5834
GACATGGGGGTTGGCCATCTTCACCCCGTTGGGCCTCTCCACCGTCTACA
TCTTTGCACTTTTCAACTCCTTGCAAG

2345. chr16_KIFC3_NM_005550_1.78194
GCAGCAGTGGGAAGCCGCGCACCTGCCGCTTGAGCCCATTGTAGTCGTTG
GTGAGGGTCCGCAGTGCCGGCTGCA

2346. chr16_CNGB1_NM_001297_-1.52488
AGTGCCAGGTGTACTCGTACCAGGTCTTGACGCGGTTCTGCACGGACTTG
GGGATCTTGTAGAAATTCATGTACTTCACCGTGCTGTCCATGCAGCTGCG
GTAGTAGGTCTGTCC

2347. chr16_CNGB1_NM_001297_-1.51536
CAGAGGTGACGTCAGGGTCAATGAGTTTCTCCTTCACTTTCTCTGTCCGC
TCCTTGAAGAGCTTCACCAGCTCCTGGAGCCGGTCGTTGATGATGGCGCT
ATTTGTGCTGGCCGT

2348. chr16_MMP15_NM_002428_-1.51028
ACTGGCTGCGGCTTTATGGCTACCTGCCTCAGCCCAGCCGCCATATGTCC
ACCATGCGTTCCGCCCAGATCTTGGCCTCGGCCCTTGCAGAGATGCAGCG
CTTCTACGGGATCCCAGTCACCGGTGTGCTCGACGAAGAGAC

2349. chr16_CCDC113_NM_014157_-1.59106
AAATATTACGCTAAACTGGAGCCCAGGGATCAGCGACCTCCACGATTATC
AGAA

2350. chr16_PRSS54_NM_001080492_1.6111
TCCCCAGAGAGACCCGCCGCGGACACCATGGGCAG

2351. chr16_PRSS54_NM_001080492_-1.52704
AATGGTCCTCAGAGTTCGTCCATGAACTGTTCCTGCTCAAGGAGAAATGA
ACTCAGGCTGGCCTGACACAGTAGAGTTCA

2352. chr16_SETD6_NM_001160305_-2.33325
TGGCGACCCAGGCGAAGCGTCCACGG

2353. chr16_SLC38A7_NM_018231_1.54066
AGGGTAGGAGGTGAGCACGCTCAGGATGATGAAGGCTCGGGCAACGGCCA
CGGCCATGTCCTCCGAGGGATAGGACAGGAGCACGTCAGGATCCACAG

2354. chr16_CMTM1_NM_181269_-1.52667
CGGCGCCCTAGCAGATGCACGTGTCTGTCGAATCGCTGCCTCCGAGCCCA
CCCCCGAGCTCGCATGCTGTCACCCATTC

2355. chr16_CDH16_NM_004062_1.87314
ACAGTCGCCTTCAGGGGCACGCTGTCTGCTGGTTGATCCGGGTCCTTCTT
CCTTGACATGGTCCAGTGGGTGAAAA

2356. chr16_C16orf70_NM_025187_1.70269
CCTGGAGGTAGTGCCCGAACGCTCTCTGGGGAACGAGCAATGGGAATTC

Figure 3-192

2357. chr16_NOL3_NM_003946_1.70152
TGTGCTTGCGGAGCCGTCCGGCGGCTGGGATCGAG

2358. chr16_E2F4_NM_001950_-1.60431
GGGCCCAACAACACTGGACACCCGGCCACTGCAGTCTTCTGCCCTGCTGG
ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGTAAC
AGCAGCAGTTCGTCCGGACCCAACCC

2359. chr16_ELMO3_NM_024712_-1.94064
CCGCGAGGACAAGCACGAGTGCCCCTTTGCCCGGGGCAGCATCCAGCTGA
CGGTGCTGCTGTGTGAGCTGCTCCGTGTTGGGGAGCC

2360. chr16_ELMO3_NM_024712_1.55246
ACAGCCCAGGACTTCTCACCCATGTTCTTCGGCCAAGACCAGAGCTTCCA
CGAGCTCTTCTGTGTGGGCATCCAGCTGTTGAATAAGACCTGGAAGGAGA
TGCGGGCTACACA

2361. chr16_FHOD1_NM_013241_1.54661
GTTGCCCACCGCTAGGAGGGTAGCCAGGATGCAGCGGAAGGTGGCATTCT
GTACCAGCTGTTCCATACCCA

2362. chr16_ZDHHC1_NM_013304_-2.47839
GGAACAAGGATCCCAAAGCCGATCACAGCAAAGAAGAGGTACAGCAGCCA
GGCCACAATCTGGAGCGGGTGAGGGGGCCAGCTCCACCCATTCCGGCGGG
ATCGCTGGCCCTGCAGCTCAGGGGAGGGTCCGCTGGGCTGTGCCGGTGCC
GTCCACACACTCTTCTCAGGGGCCGTCTTG

2363. chr16_FAM65A_NM_024519_1.58711
TGGACCTGGTGTACACGGCGCTGAAGCGGGGCCTGA

2364. chr16_C16orf48_BC008284_1.60025
CGGCCGCCTGTAGTTGTCAGGACAGAGCGTCGGGTCTGGGGGGATGGGCC
CCGAGATGCGGGACGGGCCCTCGCACAT

2365. chr16_SLC12A4_NM_005072_1.72978
TGCAGGCACCAAAGAGAACCACACT

2366. chr16_DDX28_NM_018380_1.75173
TTCCGCCCCGGTGCTAATTATTCTTAGG

2367. chr16_PRMT7_NM_019023_1.62728
TCCACAAGAACTCAACTGGCAAGGCTGCTTTTCTGTGCTAAAACTGGGGA
GCTAGTGGGCACC

2368. chr16_PRMT7_NM_019023_-2.35811
CCCACAGAGCCACCGTCTATGCACAG

2369. chr16_PRMT7_NM_019023_1.76761
CCCGCTGTGGGAGTACCCATGCCGCAGCCTCT

2370. chr16_PRMT7_NM_019023_1.732
AGAGCCACGCAGCGGTGCTATGGATGGAGTACCACCTGACCCCGGAGTGC
ACGCTCAGCACTGGCCT

Figure 3-193

2371. chr16_SMPD3_NM_018667_1.57718
CCGAAGACACCATCAGTCGCATGGCTACTGGCAGGTGGTCCGTCAGGCC

2372. chr16_COG8_NM_032382_1.54785
AAGGACAGCCCAAAGTACATGCACTGGCCCAGCAGAGAGTCCAGGTGGCC
GCCTATGCCCCGGTAAAGGTCGGTCTCCAGCACCTGCAGGAATTGTGAGA
CCTTCTGTAGCACCCAGCCATGGAAGATGGCACTCTCATTCACAGTGTGC
TCACCCATGGCAGGGGGCAGCAGTGGGTCCTCGTCTGAGAAGATGGCACG
GTACTGGGTGATGATATCAAAGAGATGGACACGGGAGGCCTCGATGGTTT
TTGTAATATGGAAATAGGGATCATCATTAGGAATGGCAGTCAGGATGGAC
CGGAGCCAAGCATCTCGGGCCTGAAGA

2373. chr16_SF3B3_NM_012426_1.58426
TGGCATTAGAGAAGCTCGGTGCTGTCTTCAATCAAGTAGCCTTCCCACTG
CAGTACACACCCAGGAAATTTGTCATCCACCCTGAGAGTAACAACCTTAT
TATCATTGAAACGGACCACAATGCCTACACTGAGG

2374. chr16_HYDIN_AK299348_2.28651
GCTTGAAGCCGCCCGCACTCTCCAT

2375. chr16_AP1G1_NM_001030007_1.51212
CCCGAAACCTCGAATGAAACCAGCAGCTCCGGG

2376. chr16_DHODH_NM_001361_-1.61215
AAGAACAAGACCTCAGTGGACGCCGCGGAGGACTACGCAGAAGGGGTGCG
CGTACT

2377. chr16_ZFHX3_NM_006885_1.57222
TTGGTAGTTGTGGAGTAGTTACACA

2378. chr16_ZNRF1_NM_032268_-1.67595
ACAGAGCGCCCCTGCTCCAGGGAGGAGGCTCACCGGACCCTGGGGCAGAG
CTGAGCTTGGGACACCAGCGGGAACAGGGCACCCCTTCTGCA

2379. chr16_BCAR1_NM_001170714_-1.60551
ACTGCCCATCTGGCGAGTCCTGGGAGGTGAACTTAGGGGGTGAGGGCAGG
GGTCGTGACTGGATGCTGCTGGTCTTGTCAGTGGGGTTGGGGTGCAGGGT
GCCACCCCCCTCAGGCCCCGGGGCAGTGGCCTTGGTCCGTCTGAAGAGCA
GTGAGGCATTGCCGTGCAGGAAGGAGGCCAGCTGCTTGGCGTCCTCGGGC
ACAGCCCGCGAGCAGGCCACCAGCCGGTCCAGGTCCTCAAGGGTGGCTCC
AGAGCCTCCCCGGCCAGCGTCGAGGGCCTGACCATGTGCCACCAGCGTCT
GGTGCACGTCCTCCATCTTCTGCAGCTGCCGGCTAAGCTTGGCATGCAGG
GCACGGTCAGATGTGTGGGCAGCATTGCCCACCGCGCTGCGGGCAAACTC
CAACAGCTCGTGGACGGCACTCTGGACAGCGGCCACAGCAGCCTGCAGGT
CCTGCACCAGCGGCTCCTGTGGCTCAGAGGGGCTACGCCAGCTCCCAGTC
GCACCGGCGCTGCCTGCCAGGTCCAGAAGGTGGGCAACGGTGGCGCTCAC
ACCCTGCTGCAGCCGTGCCAGGGCCTCCACAGCAACTTCCAGCTCCAGGG
GTTCCCGGCCCGGCCCTGCCACCTCCAAGGAGGACGCAGACTGGCTGCTG
CGTGTGCTGCCGGTGCTGGAGGCCGACAGGCGCTTGCCCTCTGCCGGGGC
TTCACGTTCAGCTGGGGGAGGCACCGCATACACACCACTGTCGACCACGC
CACCATCAGCCACCTCAGGAGGAAGCACCCGTTCACGGGGCACATCGTAC
AGGGTGCCCGGGCCAGGCCGCCGCAAGCCAGGGGGCACGTCGTAGAGGTC
AGGAGCCGGGGGCGGCACGTCATACACGTCCTCGGCCGGCGGGGAGTCTG
GAGGGGGCGCAGCCAGTACCAGTGGGGTGCGGGCCGGGTCAAAGGGCTTG
GCCTTGGCGAAGGCGGGGGGCACATCGTAGGTCTCCTCACGCAGCAGTGG

Figure 3-194

GCCATCGGGCACATCCTTGCTCACCGATGGAGGAACGTCGTA

2380. chr16_---_---_-1.6411
CCTGGGCTGAAGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTA
CAGGTGTGAGCCCCCACACCCGGCCTGCATT

2381. chr16_ADAMTS18_NM_199355_-1.51797
AGACCAGCGTCTCATTTGTGGGCCCTGGCGCGTACAGACGTTCCGGGCGG
TTGAAAGAGCGCTGGTATTCAAACGTGGTCCCAGCGAAGGGGAACTCCCC
AGGCCAGTCGATGCTCCAGCCCCCGGTGAGGTAATACTTTTGACTGAGGC
TTCGAACTGCGAGGTAACTGGAGGAAACCTGCAGCTCCTGGATTTCGATG
CTTCGGGCGCCAG

2382. chr16_CDYL2_NM_152342_1.66094
GATGCCATCTCCTTGACCCGCAGCATGACCTCCTGGCTGAACGTGGTGGG
CCAGAAGACCTGCGACACCAGCCCCCTGC

2383. chr16_PKD1L2_NM_052892_-1.81683
TGCTCTGTTGGGGTGTTGTCCAAATA

2384. chr16_PLCG2_NM_002661_2.82399
TGATTTCTCCCGATTCCTTCCTTC

2385. chr16_CDH13_NM_001257_1.56445
CTGGCTGGCGAGGCAGAGCCTCTCCTCAAAGCCTGGCTCCCACGGAAAAT
ATGCTCAGTGCAGCCGCGTGCATGAATGAAAACGCCGCCGGGCGCTTCTA
GTCGGACAAA

2386. chr16_NECAB2_NM_019065_-1.61641
GCCGGCGCGCACAGGCTGCTCCGGGAGCCGCCGCAGCAGGGCCGGGCGCT
GGGCGGGCTGCTGCGCTGGGTGGGCGCCAGGATGGGCGAGCCCCGGGAGT
CGCTGGCCCCCGCCGCCCCCGCGGACCCCGGCCCAGCCTCGCCGCGCGGG
GGCACCGCCGTCATCCTGGAC

2387. chr16_LRRC50_NM_178452_-1.58373
GCCCACAATCACCTGGAGACCGTGGAGGACATTCAGCATCTACAAGAGTG
TTTGAGGCTTTGTGTCCTTGACCTTTCGCACAACAAGCTGAGTGACCCGG
AGATCCTGAGCATTCTGGAAAGCATGCCCGATTTG

2388. chr16_KCNG4_NM_172347_-1.62379
TGCCTCAGTACGTCCTCCCTGTGCAGCTTGGC

2389. chr16_ATP2C2_NM_014861_1.72844
AGGAGTATGAGGACGCCGTCAGCATCGC

2390. chr16_ATP2C2_NM_014861_1.62912
GTCAGGGGCGATCGTGGCCATGACTGGGGATGGGGTGAACGACGCAGTGG
CCCTGAAGTCTGCAGACATTGGGATCGCCATGGGGCAGACAGGGACGGAC
GTCAGCAAAGAGGCCGCCAAC

2391. chr16_KIAA1609_NM_020947_-1.82219
AGTTCTCCTGAGCCGACAGCTGCGGGCTGTTGTACGTGGTGCACGTGGGC
TTGGCTCTGCTGTGTCCTTTCCCAAAATCAACATCCACCCAAAGCCCAAA
GTAATTGTGCTGCCCC

Figure 3-195

2392. chr16_CRISPLD2_NM_031476_-1.64504
ATTTGGACTGCTACACGACCGTTGCTCAGCTGTGCCCGTTTGAAAAGCCA
GCAACTCACTGCCCA

2393. chr16_ZDHHC7_NM_001145548_1.59572
ACAAATGCCCACAAGGGTTGGGTCCAGCCCAGTTTTCACTGTGCAGGCAG
ATGGTCGGCAGTCACTGGATT

2394. chr16_KIAA0182_NM_014615_1.58433
TCAGAAAGGGAGCGGCTCCAGGCAGAACTGGACCACTTACGAAAGTGCCT
TGCCTTGCCTGCAATGCACTGGCCTAGG

2395. chr16_GINS2_NM_016095_-1.5372
CTGGAGGTTCGTGCGGAGTTTGTACATGTGGTT

2396. chr16_C16orf74_BC009078_1.55113
AGGAGCCCTTGTCACATCTCACAGAACCATGAGTCGGGAAACAGATTTTG
GGAAATGCTGATCATAGGCTAGTTGGCCTCTGGGTCCAGTTGTCAGCCTT
TACCATGTGGCCCAGCCAGCTGCAGCCTCATTCCCGGCCACCAGCCCCCA
CTCTCCACAGCGCTCCAGCCTCCACTCTCCAAAGTGCTCACACTTCCCCA
GACTCCCTAGGCTCCTGGGGCCCCTTCGTGCCTTTGCATATGCTGCTCCC
CCCGCCTGGGATGCTCTTTCTTCCTCTGCCTGAGTAACAAGCTCCT

2397. chr16_KLHDC4_NM_017566_-1.89021
TGTCTTCGTCGTCGACCCCACCCTCGGCGCCCTCAACCTCCTCACTGTCC
TCTTCCGAGTCCGTCTCCTCCAG

2398. chr16_ZFPM1_NM_153813_-1.61055
GCCTCGCCCCTGCGCGCTCGCCCGGCCCCGCGGCCGACGGCCCCATCGAC
CTGAG

2399. chr16_IL17C_NM_013278_-1.71931
CACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCC

2400. chr16_FAM38A_NM_001142864_1.62182
GCGCGGGAGGCGCGTGCCAGGCAGGG

2401. chr16_FAM38A_NM_001142864_-1.66227
TGCGCCAGTAGGCAGGGAAGTCCTGGAACTGGAAGGTGTAGACGGCGATG
AGGACCAGCATGGTGTAGGCCACCACGAGCCACCAGAAGGCCTTGAGCAG
CTTCCGCCACAGGCTGTAGTAGAC

2402. chr16_FLJ40448_ENST00000333666_-1.50689
AAACCAGGCTGAGCCGGGGATCAGGCCACCTCCGCAGGGACCCACTGCTG
CCTCTTCCAGGAGCCCAGGAGACCCAGTGGGTCTCCTGCCCCCGACTCCA
ACTCCCTCCTGGCAGGACACACCCAGCTCACAGTGGCCTTTCCATCCTGG
GAAAGGGAGTGAGAGGAGGCTCAGGCCAGGGACCCGCCCAGCTCTGGCCG
GCAACCGCCCTTCAGCCTTTCCTGAACCACTGTGTGGGCCCCAACCCATC
CGCTGCCTGCCGGAGGGAGCCCATGGGGAATGGACTATTCTTGCCACCCC
TATCCATGGCAGGGGAGGGGCTCAGCATGGCTCTTGCCCACCCAGAAGAA
GGTGCAGGGGGCCTGGCGTGGTGGTTCACACCTTTGGGAGGCCGAGGTGG
GTGGATCACCTCAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGA
AACCCTGTTTCTACTGAAAATACAAAAATTAGCCAGGCGTGGTGATGGGC
ACCTGTAATCTCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTTCAC
TTAAACCCA

Figure 3-196

2403. chr16_ANKRD11_NM_013275_-1.50951
TCTGCTCCCCATTGGCGCCCGCGGTGAAGGGCAGCTTCCGCTTGCTGGCT
CGCTCCCTCACCTCCTTCCCGCCATCGCCACGCTCCAGTTTTGGGGTCTT
GGTTAGAGAAACTTTATCTTTATC

2404. chr16_SPG7_NM_003119_-1.64644
TCCCGAGTGAGCATGGAACACTTCGAGTTCCCAGGGTTATAGACAGTCGT
TCCCAGTGTGGCTGAGGCCACCCAGAGGCAGCAGAGCATTCAGACTCCAA
ACAGACCCCTGTTCATGCCGACGCTTGCACGACCGCCCCAGTTCCTGTGG
CTCCCTCGGAATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGA
TTGTCCTATCTCCAGCGGCCCTG

2405. chr16_CDK10_NM_052988_-1.54842
TGTGGGCTGCATACTGGCCGAGCTGCTGGCGCACAGGCCTCTTCTCCCCG
GCACTTCCGAGATCCA

2406. chr16_CDK10_NM_052988_-1.52393
TGGGCACGCCCAGTGAGAACATCTG

2407. chr16_FANCA_NM_000135_-1.67174
GAGCACACGTCCACACATGGTCCTC

2408. chr16_AFG3L1_NR_003226_2.21725
TTTATTGGCGTTGGGCCAGCAAGG

2409. chr17_FAM57A_NM_024792_-1.50244
GGACCAAATTGTGCCCTGGGTAGCCTCAGACTTTGGGTATTGATAAGCCG
ATGGATTTGAGTTTTTCTAAAGAATATTCATATTACCTCCTTCTTCTAAC
TTGCCCTATTTGCAAAAGCACTTTTGTAGTAACAACTATTGGGTCCTGTC
AGACCTCCACGGACAGCAAAGTGGTTTTAATGCAAGCCCAAGGATCCTTC
TTAAGGTCTTATCTCAAGAGCTCTGGGAGGTGGAAGCATGGGGTGGGATC
GGTGGACCAGGGTGGTAAGTGTCTGCACATC

2410. chr17_MYO1C_NM_001080779_-1.55965
GCACTCGGGGGCTGATCTCATCTGT

2411. chr17_MYO1C_NM_001080779_2.01933
TCCCGAACCTGCTGGAGTTATCGTTCCGGAGG

2412. chr17_PITPNA_NM_006224_1.56216
AAAGTAAGTCAGGGAGTCCCAGCAGGGACTGTAAAAGAACTTGGGAAGCT
ATACACATGCCCACGATACTGACCCTGTCCCGGACCTCTCTGCATGAGAA
GGCCAGAGCCCAGCACCCCTCCTACAGAGGCACTGCTGCTTCTGTTGGGG
CTGTGACCCTGGAATTCTGATGGAAGCAGCTGGTCTGAAGGGGCATGGCA
CACACTCAGGTACTACCCCTGGAGCTGAACCTTTATCATAAGTCCCTCTG
AGTGCTAGTCAGTTTGGAGGTGGGTGAGGAGGAAAGGGGGTACTTAAAAG
AAGCCAACACTGTTGCCCAGCAGCAACACCATCCGTGGGGATGGAACAGA
CCAGGGACATCCTCCTTTATGTTTATGTGGGCTGCAATTCCAGATCCAGG
CTGACCTCAGCTCATAATGGATGCTTTTCAACTGGGGCAACAGGTGGAGG
TGGGAGGAGCCCTTGTTAGGGCTAAAGTGATATGTGTGGGTCTCAAGAGC
CAAAGGAAGGAGACTAACAGCTGCTGACCCTCAGACCACATAGACAACTG
TCTGCCTAGAATGTCAGTTTGTTTCTTTCAAGATAACCCGCATCTGGACT
TCCCCTAGTTGATGAATGAAGGAACATCTTTAAGCACAAATATAATGAAT
AGCTAACACAGAGCTTATAGGAAAACACTGACATTTTTCTCCAGTAGGAA

Figure 3-197

TGCCTCTTCTCCAACTTTCCAAGTCAGATAAATGCTACCAGCAGTTGAGA
TGCTACCCAGATGCATTACTAAAGACCCCTCAAGGTGAGGAGACTTACAC
AGAGGAAGGTGTCTGTAACAAGACATCTGGTTCCAAAGGGACC

2413. chr17_PITPNA_NM_006224_1.56005
GGTTCTGCAGTAGGGGTAAGCATTCCAGGCTTTCTCGTGTATATTCAGGG
CTCCCTCTGGGGCCAGCATTCGAACAAACGTGGGT

2414. chr17_WDR81_NM_001163809_1.5095
AGCCGACTGAACAGCCGTAAGGAGGCGGGGCTGCTGGCCGCGGTGACGCT
GACTCAGAAGATCATCGTGTACCTCTCAGACACCACACTCATGGACATCC
TGCCCCGGATCAGCCATGAGGT

2415. chr17_WDR81_NM_001163809_1.7519
CGACTGGGCGGTGGGCTGAACCCTGGGCTTGTCCGTGCCCTGGCCATCAG
CCCCAGTGGCCGTAGTGTCGTGGCCGGCTTCTCCTCAGGCTTCATGGTGC
TCCTGGACACCCGCACAGGCCTGGTTCT

2416. chr17_SMYD4_NM_052928_1.51185
GATTTCATCGTCCCATGGGCCACAGTGCAGCGACAGAACCTCCTCAGCTT
TCTGTATTGTGCTCAGGGCTTCGGGTACTGCA

2417. chr17_TSR1_NM_018128_1.60072
TGAGGCTCGGAAGCGCCTGAATCCACAGTGAAATATGAGCTCTTCCTTGG
CTTTCACAGGTTCAGTGTTGCCAGGGTCACGCCT

2418. chr17_SGSM2_NM_014853_-1.65557
TCTGGAATGCGACCGGAGCACTTGCTCTGAGGAATCCCAGGGTGACTCTG
TCGGGGAAGAATCCGGTCACAGCCTCCCCTCAGAGACAGGCCTCAGTTCG
AGGGCAGCCCATTATCTGTCGCAGACATCTGCCATGTCCCTGAGACTGCG
GGAGGCAGGGGATGCATGGGTGTCCCCATCTGTCCCTGGTGAGAAGCAAG
GC

2419. chr17_MNT_NM_020310_-1.56603
TCTGCCGCAGCACGCGGTCAATCTCCAGTACGTCCATCCACTGGCTCAGC
TCGTGCTTGAGCTCTGCCAGCCGCTGCTGCGTGGCAATCTT

2420. chr17_KIAA0664_NM_015229_-1.75481
CAGGTCGCCGTCGGTGAAGACACTCAGGAAGGACAAGGAGTTGCAGTCAA
CCCCGTTGAAGGCATCGGATGGGTCCAGGCTCTTGAGCAGGTCTCGGACA
TGG

2421. chr17_KIAA0664_NM_015229_1.59639
AAAAGCCCGTGTCCTGAATGACAATGACTTCCTGGCCGGTGGTCTCATCT
CCCGGGCCGGCCTCGTCAAGCCCATTTTCCCTGGGTGGCTCGGCCGCCGC
CGCCTCCTTCTTCAGGCTCTCTGGGCAGTCCCCGTTTAAGAGCA

2422. chr17_OR1G1_NM_003555_-1.57814
ACTGTGTCCTTCTGGGCCGAGTGGGTTGAGGGAGAACTGAAATCAACACA
AAAAGAAGTCCCAAAGAAGAGAGAGACCACGGAGAGATGAGAGCTGCAGG
TGGAAAAGGCTTTCCGCTTCCCCTGAGCTGATGGGATCTTCAGGATGGTC
GAGAAAACGTTCGTGTAAGAGATAATCAGGCAAAGCACACAAATGAGTCC
TGTGAGACCCC

2423. chr17_CAMKK1_NM_032294_-1.53213

Figure 3-198

GACGTGCGTGCGTGGAGGTCATGCAGCACGATGGGGGAGGGGCGGGAGTG
GGGCTGCAGTCCCCAGCCCCCTGCCTGCGGGGGCGGCTGTTGCATGAG

2424. chr17_CAMKK1_NM_032294_-1.50498
TTGATGTCTGGCACCCCAATTCTCGTCTCGGGATTCTTGTCTAAC

2425. chr17_ATP2A3_NM_005173_-1.7768
GGGGCGGCACGAGCAGGATGAGGAAGTGCAGGGCCATGGACATGGCCACA
GCCACCAGCAGCCAGGGGTTCATCCAGGGCGGCATCCGCAGCAGCGACTG
GTTCTCCGAGACG

2426. chr17_ATP2A3_NM_005173_1.61746
AGTGCCAGGCATGTAGTGATGACAGCCGGGAGGCCCTCGGGGATGGCCGC
CACCGCCAGGGCCACGGCGATCTTGAAGTAGTAGACAGCGCCACGCAGCC
AGGAGCCACCGTGGGCCGGGTCGGCGAAGTGGCCGATGTTGATGACCCA

2427. chr17_ZZEF1_NM_015113_-1.86398
TTCAACAGCGCAAGGTCACACAGGT

2428. chr17_CYB5D2_NM_144611_-1.67372
CGGCACTGACCCAGGTAGAAGCTGCGATCACCAGAGGCTTGGAGGCCAAC
AAACTACAGCTGCAAGAGAAGCAGACATTCCCGCCGTGCAACGCGGAGTG

2429. chr17_MINK1_NM_015716_-1.50268
CAGCGGCAGCGGCGCATAGAGGAGCAGA

2430. chr17_RNF167_NM_015528_-1.6608
ACCGGAAGTCCTTCATCTCAAGCATCCAATGCTGAAAGCGGCCTGATTTT
CTCTACCGGAAGCCCTTTTCCAGAGGCTGGGAACACGGCCCACCTAGCAG
GAAGTCCCACCTCCTTGAGCTCCGCCACCCTTCCCGAAGTTTTTCTGTCA
CCTG

2431. chr17_INCA1_NM_001167986_-1.52357
TGGCAAAGGGGATGAGGTTGACTCCATCATCCTGC

2432. chr17_KIF1C_NM_006612_-1.53591
AAAAGCACAACTCTTATCCCCAGCCACCCCAACCCTACCCAGCCCAGCGG
CCCCCAGGGCCCCGCTACCCCCCATACACTACTCCCCCACGAATGAGACG
GCAGCGTTCTG

2433. chr17_PITPNM3_NM_031220_1.56505
GACGACCATCTTCACAGGATAGACACCAACCCCCAGGCGCCGGGGCCGCG
GCACATTGTATGTGATGCGACCACTGCTGTTGGTGATCTCTGTGTCCAGG
TGTACCCAGCGGCCTGAGGATGGCTCTGCCATT

2434. chr17_BCL6B_NM_181844_-1.59533
TAAGAAGAGAAGCCGCGGCCCCTGC

2435. chr17_DLG4_NM_001365_-1.63733
TCTGGTTTATACTGAGCGATGATCGTGACCGTCTGACCCGCATTCTTCAG
GGCAATGGCAGCCTGCTCATGGCTGGCATTTCGGAGGTCCACACCGTTGA
C

2436. chr17_ACADVL_NM_000018_-2.00644
GACTGTGGCCGCTTTCTGTCTAACCGAGCCCTCAAGCGG

Figure 3-199

2437. chr17_DVL2_NM_004422_-1.67578
GGGCATCATGACCACCATCATGGGGTTGTAGGGGAGGGCCATGCCAGGGG
GCGGTCCATAGGGATGGAGCCCTGGGTGGGCTCGGAGATTAGGGGCACCC
CCAGTTGAGCCTCTGGATGGAGGAGGGCCCCCATCGCTAGTCCCACTTGC
TTCCCCACCCCGCCGAAGGCTGCCCCCTCGGCTGGAGGGCTCAGACTCAC
TGCCACTGCCGGACTTGGACTCG

2438. chr17_DVL2_NM_004422_1.85014
CCCAGTACGGGAGAGAAGCAAAGGGGAAAAAGCACGGATCTGCGAGGGTG
GCGGCGGGGGGCGGGCCGCGGGGTGCGACTCAAAGCCCCGGTCTCAGCGG
CCGCCGCGCGCCACCGCCACCGACGCCGCGAGCTTCCTCCAGGTAC

2439. chr17_GABARAP_NM_007278_1.67312
GGGTATTTCTTTCGGATCTTCTCGCCCTCAGAGCGGCGCTTCTCGAACGG
ATGCTCTTC

2440. chr17_SLC2A4_NM_001042_-1.67497
GAGATTGCTCCCACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACT
GGCCATTGTTATCGGCATTCTGATCGCCCAG

2441. chr17_KCTD11_NM_001002914_-1.59617
GGAGGCGGCCACTACTTCATCGACCGGGATGGCAAGGCCTTCCGGCACAT
CCTCAATTTCCTGAGGCTGGGCCGCCTGGACCTGCCCCGTGGGTACGGAG
AGACAGCGCTGCTCAGGGCAGAGGCTGACTTCTACCAGATCCGGCCCCTC
CTGGACGCGCTGCGGGAACTGGAGGCCTCTCAGGGGACCCCTGCACCCAC
AGCTGCCCTGCTCCACGCAGATGTAGATGTCAGCCC

2442. chr17_TMEM95_NM_198154_1.52937
TGAGGTGTCCATGAACAAAGTCACA

2443. chr17_PLSCR3_NM_020360_1.67118
GAATTCGAGGCCAGAAGGCACCCCTGGCAGTGGCAAGAAGGGGGCAGCAG
ACCCCAAGGCCACGGGGCCAGGCGAGGGGAAGAGGGCGAAGCCGGGAGCT
GGGGCAGGTACCTGGGCGGGCACTGGCGCCTGCCCGGGCCCAGGATGTAG
CGCCGGCTCCGGGTACCCAG

2444. chr17_CHRNB1_NM_000747_-1.5751
GGGAGATTATCCACAAGCCCTCTCGGCTAATCCAGCCTCCAGGCGATCCT
AGGGGAGGGAGGGAAGGACAGCGCCAGGAAGTCATCTTCTACCTCATCAT
CCGCCGCAAGCCTCTCTTCTACCTGGTCAACGTCATTGCCCCATGCA

2445. chr17_CHRNB1_NM_000747_1.9236
CATGGTAGTGGACCGCCTCTTCCTGTGGACTTTCATCATCTTCACCAGCG
TTGGGACCCTAGTCATCTTCCTGGACGCCACGTACCA

2446. chr17_SENP3_NM_015670_1.63236
CAATAGTTTCTTCTATGATAAACTCCGTACCAAAGGG

2447. chr17_SHBG_NM_001040_-1.74705
ACTGGCTACCTCGCGCCTGCTGCTGTTGCTGCTGTTGCTACTACTGCGTC
ACACCCGCCAGGGATGGGCCCTGAGACCTGTTCTCCC

2448. chr17_EFNB3_NM_001406_-1.84933
TACCCTCAGATCGGGGACCGGCTAGACCTGCTCTGCCCCCGGGCCCGGCC

Figure 3-200

TCCTGGCCCTCACTCCTCTCCTAATTATGAGTTCTACAAGCTGTACCTGG
TAGGGGGTGCTCAGGGCCGGCGCTGTGAGGCACCCCCTGCCCCAAACCTC
CTTCTCACTTGTGATCGCCCAGACCTGGATCTCCGCTTCACCATCAAGTT
CCAGGAGTATAGCCCTAATCTCTGGGGCCACGAGTTCCGCTCGCACCACG
ATTA

2449. chr17_CHD3_NM_001005273_1.72377
GTACGGGGCGGCCTTCAGCGCCGCACC

2450. chr17_TRAPPC1_NM_021210_1.61494
AGCCCGGGCGGAGAAGAAGGGCAGAGAGCGAACATAGGAGTCCAGTCGGG
AGCGAAAGAGCTCA

2451. chr17_CNTROB_NM_053051_-1.61639
GCTGGAACCGGCATGAGGCTGAGCGGACAGAGGTTCTCAGGGGACTTCAA
GAGGAACACCAGG

2452. chr17_CNTROB_NM_053051_1.5096
GAAAGGCCATTCCCTGAGGAAGATCCTGGACCTGACGGGGAGGGCCTCCT
AAAGCAA

2453. chr17_GUCY2D_NM_000180_1.5853
AGAAATTCCCAGGGGATCAGCACATAGCTATCCGCCCAGCAACCAAGACG
GCCTTCT

2454. chr17_PER1_NM_002616_-1.50474
TGATACGGCAGAAGACGGACTTCTCCTGGGTAA

2455. chr17_AURKB_NM_004217_-2.07165
GGCTCCCATGGGCACGGAAGCGGGGAACTTT

2456. chr17_PFAS_NM_012393_-1.54596
ATGTGGCTGTTTGGTTGCCCCTTACTGCTGGATGATGTTGCTCGGGAGTC
CTGGCTCCTTCCTGGCTCCAATGACCTGCT

2457. chr17_PFAS_NM_012393_1.64396
CCGGAAGCGGCCAGACACCTTCAGCCTGGGCGTGTGTAATGGCTGTCAAC
TGCTGGCTCTGCTCGGCTGGGTGGGAGGCGACCCCAATGAGGATGCTGCA
GAGATGGGCCCTGACTCCCAGCCAGCCCGGCCAGGCCTTCTGCTACGCCA
CAACCTGTCTGGGCGCTACGAGTCTCGCTGGGCCAGCGTG

2458. chr17_ODF4_NM_153007_-1.57743
ATCTGGATCTTCGAGTTGGAAAGGAATGTATCCATCCCCATAGGCTGGAG
CTATTTCATTGGTTGGCTGGTGCTTATCCTATACTTCA

2459. chr17_NTN1_NM_004822_1.50742
GCCTTCTGCGGCAGGCGGACAGATCCTCGGCGCGGCA

2460. chr17_WDR16_NM_145054_-1.76348
CAGGCCGACTGATGTATGTCATTAACAATGCTCACAGGATCGGCGTCACC
GCCATCGCCACCACCAGTGACTGTAAAAGGGTCATCAGTGGCG

2461. chr17_MYH13_NM_003802_-1.89148
GGTTCCCAAGTGACAGTCAGTGTC

Figure 3-201

2462. chr17_MYH8_NM_002472_1.92519
TTCTTAGCACCTTTCTTCGCGCTGCTAT

2463. chr17_MYH8_NM_002472_-1.89492
GAAGCCCAGGATGTCAATGGCACT

2464. chr17_MYH4_NM_017533_1.55268
CTTCCTCTAGGGAAGTCTGTAGTTCACTCTTCTCATGATCAAGTTGTTTC
TTTACTTTCTCCAGTTCATGGATATGCTTTCCACCCTCTGCAATTTGCTC
TG

2465. chr17_MYH1_NM_005963_1.57432
TTTGGAGAGGTTGACGTTGGATTGTT

2466. chr17_TTC19_NM_017775_-2.27135
GGCGCAGCCACACACGACCTCGGTCCCGTACTTCGCGCGCTCTCCTGCAC
CGCCGCCGCCATCTCGCTCAGGAGCTCCTCCACAACCGCCGGCAACACTA
CGGCCATCGCGCCGCAGGACACGCCCTCCACGACCGGCGGACCGCCGCGA
CGCTCCAGCTGACTGCGCCTACCTGTGGAGGATCCTGACCCCCCGCCGGG
GCAGGGCGAGACGGAGTGACGTCGGGGCGCGTCATCGCGCGTGCGGACGC
AGGGATGTCCTGCTCAGTCGTCAGGGCCCGGCCAATCCGGAGGGCGCTCG
GCGCGTGGTCGGGGGCCAGGAGCGCGTCTGGCCTGCAGTGCGCAGAGGAC
GCGGCGGGAGCATGTTCCGGCTCCTGAGCTGGAGCC

2467. chr17_NCOR1_NM_006311_-1.82707
TGAATGAGGTGATGGGTCCCCTTCCTCTC

2468. chr17_TRPV2_NM_016113_-1.54317
ACTGGGCTTCATGGGAGCAGACGCTGCCTACGCTGTGTGAGGACCCGTCA
GGGGCAGGTGTCC

2469. chr17_RASD1_NM_016084_1.62733
CATGGCGAAGAGCGCGCGGAACATCTGGTCCAGGCT

2470. chr17_RAI1_ENST00000395774_1.9276
CCGTGCGATGCCCGCGCAGGGGCGGG

2471. chr17_DRG2_NM_001388_-1.55249
CGCATCCACCGGTCACTCGCCAGCCA

2472. chr17_DRG2_NM_001388_1.72456
AGCACCAAGTACAGTCCGCAGCGGGTGGGCCTGACCCACACCATGGAGCA
TGAGGACGTCATCCAGATCG

2473. chr17_MYO15A_NM_016239_2.46421
CAGGCAGCCGCCGAGGCTTTTCCAGG

2474. chr17_LLGL1_NM_004140_1.8566
CTTGCTCGGCCCACGTGGCCAGTGTCCCCGCCAAGCTGTGGGCCCGCATT
GTGAGC

2475. chr17_FLII_NM_002018_-1.60781
TTGAGGATGAAGCAGAACTCGGAGTTGAGGAGGCT

2476. chr17_SLC47A1_NM_018242_1.69063

Figure 3-202

TTGTACTGCCCCAGATCGTAACTGGAGTTGCAGCCAACCTTGTCAATGCC
CTCGCCAACTATCTGTTTCTCCATC

2477. chr17_ULK2_NM_014683_1.82513
GCGAAGGCCCCGTGTCCCACGAGATCCCTCTTGCTGTACTCGAAGTCACC
CACCACCT

2477. chr17_AKAP10_NM_007202_1.58467
GGTTCAGGCTCAGATTCTCGGATGA

2479. chr17_USP22_NM_015276_-1.53966
GGAAGGACACATACGTGGTGATCTTCCGCCGCAGCTTG

2480. chr17_---_---_1.54803
ACACAAATATAGTTTCTACGACAACAGGCCAGGTCAGAGTGAAGCCTAAT
GAACAAACAAA

2481. chr17_---_---_-2.01647
GAGGTGGAAGGATCGCTTGGGCCCAGGAGACAGAGGGTGCAGTGAACTGT
GCTCCAGCCTGG

2482. chr17_---_---_-1.50496
AGCCTCAGCGACCTCATATTGCATGGAGCTCTTTCTTTATAAATGTTTGC
CTAAGGTGATTCCTATGTGTTTCAAAGGGTCTGACGTTTCAT

2483. chr17_---_---_-1.55967
GCATCCACAGGCTGACATGGACCGTGGAGGGGTGGCACTGTTTAAGCAGC
CCAGCACACCACTTTCTGGTGTGGTGGCT

2484. chr17_NOS2_NM_000625_1.86797
TGGGCGGCGGCACCCAAACACCAAGGTCA

2485. chr17_FLJ40504_NR_028334_-1.59125
AGCTGCTCCGTCCGCAGGGTGTAACAGGCCTCCA

2486. chr17_VTN_NM_000638_-1.55567
ACTGAGCGATGGAGCGTGGGTAGGGAGGGTCCACAGTGTCCACTCGCCGT
GTGCGAAGATTGACTCGGTAGTACTTGT

2487. chr17_SARM1_NM_015077_-1.62872
TGCCGTTGCTCGACTCTAACCGCTTGGAGGCGCAGTGCATCGGGGCTTTC
TACCTCTGCGCCGAGGCTG

2488. chr17_SPAG5_NM_006461_-1.69999
AATTGGTGGCCATAGGCTGGCAGTTGGAGTCCAGCTGGCCTGCCAGGGCC
TCCTGGAGCACTTTGGTCTCTGTCTCCGCACGCCGAAGTGAGCGGGTAAG
GTGGGTCACCTCC

2489. chr17_SUPT6H_NM_003170_1.98957
GACCCGGACACCTGCCTCTATCAAT

2490. chr17_PIPOX_NM_016518_1.54156
AAGATCTCTGGGACGCCATTGTGATTGGGGCGGGGATCCAGGGCTGCTTC
ACTGCATACCA

Figure 3-203

2491. chr17_PIPOX_NM_016518_-1.67188
CCATGGACAAAGCCGGATAATCCGAAAGGCGTACCTGGAAGACTTTTACA
CCCGGATGATGCATGAGTGCTATC

2492. chr17_PIPOX_NM_016518_1.60243
CGGGTTCAAGCTGGCCCCTGTGGTGGGGAAGATCCTGTATGAATTAAGCA
TGAAATTAACACCATCTTATGACTTGGCACCTTTTCGAATCAGCCGTTTC
C

2493. chr17_MYO18A_NM_078471_-1.51848
GCTCCCGCTTCTCTCGCAGAACCTTCTGCTTGTCCT

2494. chr17_GIT1_NM_001085454_-1.68511
AGGGAGGCCATCTCGGTCACAGCCAAATGGATCT

2495. chr17_CORO6_NM_032854_1.63033
CACGTCCAGGATGTTGCGCTTCGTGACCCGGAGCTCGCGGTGCTTGGGGG
GCACATAGCCGTCCCTCAGCGAAATGAGCACGGGTTCGGC

2496. chr17_RAB11FIP4_NM_032932_1.73699
ATCAACTTCCGGCTGAGGCAGTACATGGACAAGATTATCCTCGCCATCCT
GGACCACAATCCCTCCATCCTCGAGATCAAACACTAA

2497. chr17_SUZ12_NM_015355_-1.70269
CATTTGCAGCTTACGTTTACTGGT

2498. chr17_ZNF207_NM_003457_1.54632
TTACATGAACATACCACCCTAGTAAAGGCAAGTTCTGTAAGCTTACATTG
CTATTTG

2499. chr17_SPACA3_NM_173847_-2.26646
ACCTCACTGAATGGGTGGATGGCT

2500. chr17_TMEM132E_NM_207313_1.58728
GGGCCCCTTGGAGATCTTGCAGCTGGACTTTGAAATGGAGAACTTCACCA
GCCAGTCAGTCAAGCGGAGGATCATGTGGCACATTGACTACCGTGGCCAC
GGCGCCCTGCCTGACCTGGAGCGGGCAGTCACTGAGCTGACGGTCATTCA
GCGGGATGTGC

2501. chr17_C17orf66_NM_152781_-1.5446
CTTTCTGGAACCTTGTGGGCTCTGCCTTCACATTGGTCTTAGGTGCCTCA
TATACAGAGAGAACCTTGTTTTTCAGCTTGTTTTGGATCCAGGGATCAAT
TGAGGCACAAAGG

2502. chr17_SYNRG_NM_007247_-1.53785
TGTTTCCATGCTGGGAGTTACTTGTTTTTGAAGAAGCAGGCAACTCTTGG
AAATCACTGAATGAGTCATCAAGGGATCCTGACTTAG

2503. chr17_GPR179_NM_001004334_-1.7482
TGGGGTTGGAGCTAGAGCTGGCAGCAGAGCTGGAGCCAAGGTGGAGGTGG
GAGATAGCATCCTTGGCTCT

2504. chr17_PSMB3_NM_002795_2.11946
GTCATTGCCGGGTTGGACCCGAAGAC

Figure 3-204

2505. chr17_CACNB1_NM_000723_1.92188
GATTGATGGTGTCAGCATCCAGAGCGACCAACTGAAGGGTCCGGGCCAGC
TCGAAGATTCGCTCGATTTCACTCTGCACC

2506. chr17_RPL19_NM_000981_-1.71199
GAGGCTCGCCTCTAGTGTCCTCCGCTGTGGCAAGAAGAAGGTCTGGTTAG
ACCCCAATGAGACCAATGAAATCGCCAATGCCAACTCCC

2507. chr17_MED1_NM_004774_1.66212
ACCATGTCTTCAACTGTCTCTGCAATGAGGGACAGTGCTGGGGTGTCGGC
TTGAATGGTTTCAGCTTTCCTCCGAATAGCCCTCATCGTCACAGGGATGG
A

2508. chr17_CDK12_NM_016507_1.60505
GTTGTCCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGGAAA
CGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAAC

2509. chr17_PNMT_NM_002686_1.64607
AGCGGCGCAGACCGTAGCCCCAATGCGGGCGCAGCCCCTGACTCGGCCCC
GGGCCAGGCGGCGGTGGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCT
ACCTCCGCAACAACTACGCGCCCCCTCGCGGGGACCTGTGCAACCCGAAC
GGCGTCGGGCCGTGGAAGCTGCGCTGCTTGGCGCAGACCTTC

2510. chr17_ERBB2_NM_004448_-2.00116
CCACTGCCCACTGACTGCTGCCATGAGCAGTGTGCTGCCGGCTGCACGGG
C

2511. chr17_MED24_NM_014815_-1.79751
ATGTCTTCGCGGTGTCTCTTCTTCTGGCGGGTGGACGCCTGTCCCTTGTG
GGAGGAGTAGGAACTGAGGGCACACCACACGGCCAG

2512. chr17_NR1D1_NM_021724_-1.57152
CCACTTGTAGACTCCCAGGGGGGCTCCCATTATAGAAGGAGGAGGAGGAT
GACGACGAGGAAGATGAGGAA

2513. chr17_CDC6_NM_001254_-1.50506
TATTGCTAATACCCTGGATCTCACAGATAGAATTCTACCTAGGCTTCAAG
CTAGAGAAAAATGTAAGCCACAGCTGTTGAACTTCCCACCTTATACCAGA
AATCAGATAGTCACTATTTTGCAAGATCGACTTA

2514. chr17_IGFBP4_NM_001552_1.54977
CGGGCCGAGGATGCGGCGCAGCGCCTCGGCGGCCAGGCTTGCTCCCCTCC
GGCACGCCTGCTAACTTCCCCCGCTACGTCCCCGTTCGCCCGCCGGGCCG
CCCCGTCTCCCCGCGCCCTCCGGGTCGGGTCCTCCAGGAGCGCCAGGCGC
TGCCGCCGTGTGCCCTCCGC

2515. chr17_KRT27_NM_181537_1.64686
GTTTGAAGAGTGCGTTTCATCTCGATAAGCTCATTCCGGGCTGAGGTGGT
GGCGCCAGCGTCGTCAGAGATCTGCT

2516. chr17_KRT16_NM_005557_-1.6885
CTCGCGGGAAGAATAGGATTGGCCA

2517. chr17_SC65_NM_006455_1.56127
CTGCTGCATGACGCTGTCCTTGGGGTCGAAGAGCATGTAGCTGGCGGCGC

Figure 3-205

TGCGGGCAGCCTGGCGCACATCATT

2518. chr17_NT5C3L_NR_033465_-1.50126
CCCGAGACCCGAGAGAACCACTGACCCCTGCGCCACGCTGGGCCCGAGGG
GAGCCCGGGGCTCGCTCGGGCGCGCGTGTGAGGCGG

2519. chr17_ZNF385C_ENST00000436535_1.77503
AGACATCACAGAGCGTGTACGATGGCCGCTTTCTTTCTCGCTTGGGCTTA
GGTGGTTCTGGGGGCCGAGGGAGGCACTCAGCAGCTCCAGATATGGGGGT
CT

2520. chr17_DHX58_NM_024119_-1.73662
TGCGCCTGTGGCAGAGGTTGTACTGTTTGCAAGGCTGTTGGCTGTGCTCC
TGCAGCTGGGGGCAGCAGTTCTGGGGTGACATGATGCACCACGTGTCC

2521. chr17_HCRT_NM_001524_-1.54434
CAGCCGCCCCGGACGACAACAGCGCGGGCGGCAGCAGCAGCAGCAGCAGC
AGTAGCGTCACGGCGGCCCAG

2522. chr17_STAT3_NM_139276_-1.52388
CTCCGCATCTGGTCCAGCGCAGTGAGCATCTGTTCCAGCTGCTGCATCTT
CTGCCTGGTCACTGACTGGTTGTTTCCAT

2523. chr17_STAT3_NM_139276_1.51635
GTGGCTGCAGTCTGTAGAAGGCGTGATTCTTCCCACAGGCACCGGGCCAC
AATCCGGGCAATCTCCATTGGCTTCTCAAGATACCTGC

2524. chr17_PTRF_NM_012232_-1.81938
CGCTGTCGCTCTTGTCCACCAGCACGGCGTCCGACTCCTCGGTGATCT

2525. chr17_PTRF_NM_012232_-1.6167
CAGCACCAGCACGCCGTTCACCTGGTCCGACTTGATCAGCTCTTCTGAGC
CGGCCCCCGACGGCTCCTCCGCTGCCTGAGCCCCAGCGGAGGAAGGCTC

2526. chr17_COASY_NM_025233_1.52216
CCAGCCCTGTGACAAGGGTTCCTGTCCAG

2527. chr17_PLEKHH3_NM_024927_-2.36528
CCACCCTCAAGGCCAGGGTGTGGG

2528. chr17_PLEKHH3_NM_024927_1.52777
CGCCAGGGCGCGCAGCGTGTCGTCGGGTGGGGGCGGC

2529. chr17_PLEKHH3_NM_024927_1.7433
GTGGGAGTCGATGGCCACAGCACAGGCACCAGCCCCCGGACAGTGCACGG
TACACAGCAGCTCCTGCCGTTGGCTCAACGCGGAAATCTCCGCCAGCGAG
GGCACCAGCTCTCTGCCGCGCGTCCGGCCCAGCGCTTTCCGGATGAAGCG
CGCATATTCCGCCAGTTCCGAGTCCGG

2530. chr17_CNTNAP1_NM_003632_-1.83042
GTACCGCACCCTATCAACTTCGGAGGCCCTCACAACTTCGTTCAAGTGCC
CGGTTTCCCACGCCGTGGCCGCCTGGCAGTCTCATTTCGCTTCCGCACCT
GGGACCTCACCGGGCTTCTCCTTTTCTCCCGTCTGGGGGACGGGCTGGGC
CACGTGGAGCTGACGCTCAGCGAAGGGCAGGTCAACGTGTCCATCGCGCA
GA

Figure 3-206

2531. chr17_VPS25_NM_032353_-1.65292
TGGCGATGAGTTTCGAGTGGCCGTGGCAGTATCGCTTCCCACCCTTCT

2532. chr17_LOC388387_NR_027254_1.84849
GTGTCCCGTCCCAGCAGATGGTGAA

2533. chr17_MPP2_NM_005374_-1.75734
TGCTTGTCAATCGCTAGCCCGGCTCTTAAAGCGGCAAGGCCTCTCCGCGA
GGGGGCGGAGGTCCGGAGGAGAGGGGAGGTGAGGAGAACGCGGAGGCCGG
CACAACTCGGAGGAAGTAGTCTTTCCCAGCAGCTGGTACGGGGGCAGCCA
GGTAGTGGTTTGGGAGACACCGCACAGAC

2534. chr17_TMEM101_NM_032376_1.66712
CAGCCCTCTCAGCGTACAGCATGAGCTGGCTGAAGCAGCCCCAAAAGGGG
CAGCGTGTGAGCAGCACCGAACCCAACTGCATGATCAG

2535. chr17_ITGA2B_NM_000419_-1.62364
TCCAAGTGGGGGCACCGACGACATATT

2536. chr17_ADAM11_NM_002390_1.82987
AGCAGCTGGACACAAGGGTCCGCCAGGAGCCA

2537. chr17_GFAP_NM_002055_1.59465
TGAGGAGACGTAGGAGCGGCGAGCAGCGGAGGTGATGCGTCTCCTCTCC

2538. chr17_MAP3K14_NM_003954_1.53613
CCATGCAGAATCCTTCGTGAGTGGAGGTATTCCAGACCCTCCAGGGCCTG
GCCCAGGTAGTACAGGGCCCGGTCCTCTGGGAGACA

2539. chr17_ARHGAP27_NM_199282_-1.62455
AGAGGTGCTGGAAGAGCATCCGCAGAGTGTCGTGGTTGGGAGCGGGCAGC
GAGCGCACCA

2540. chr17_SCRN2_NM_138355_-1.82454
AAGCTGGCCGCTCAGAACATGGCCAAGGAGCGTGAAGGGATTGCTCCACT
TTACCACCACT

2541. chr17_SCRN2_NM_138355_-1.53618
CCTGGTGTCCACGGTAGAGGGTATGCCGACGATCTAC

2542. chr17_FAM117A_NM_030802_1.72498
GCAGCTGGAAGGGGATCGTGGCCCTGAGCGGC

2543. chr17_MYST2_NM_007067_-2.01781
AGCCCGCCGGAGCCACCGTTCCTGCTGCTGCCGCCGCTGCCCGAATCGGA
ACCGTCGGGCCGCAGCCGC

2544. chr17_---_---_-1.60961
CCTGTGATTTCTGTCATTATACTCTTCTCCCCAGTTTG

2545. chr17_TAC4_NM_170685_1.51321
CAAAGAACTGGCTTGCCTTGCCCGTCTTCACCTCCTG

2546. chr17_ITGA3_NM_002204_-1.52001

Figure 3-207

TGCTACGTGCGAGGCAATGACCTAGAGCTGGACTCCAGTGATGACTGGCA
GACCTACCACAACGAGATGTGCAATAGCAACACAGACTACCTGGAGACGG
GCATGTGCCAGCTGGGCACCAGCGGTGGCTTCACCCAGAACACTGTGTAC
TTCGGCGCCC

2547. chr17_PPP1R9B_NM_032595_-2.20495
TCCTCCAGAACCCGACGCTGTGCAGTCTCCTTTT

2548. chr17_PPP1R9B_NM_032595_-1.75301
TGCCGTTGAAGCGCACCACGACGTCCAGCTTCCGGTCCTGCAGGCCGGCG
CGCTCCTGCCTCAGCAGCCGCCGCGCCGCGCTCCTTGTCGCCGCCTGCGC
GCTGGGGCGCTCCGTTCGAACAGCTTCCG

2549. chr17_MRPL27_NM_016504_-1.73202
TGTAGCCGGAGTGGGGCTTAGCAAGGATGTAA

2550. chr17_CHAD_NM_001267_-1.63251
TTTTCCGACAGGTAGAGCCAGCGCAGGTCCTTGGCTCCCTGGAAGGCGCC
TGCGCGCAGCTCACGGATCTTGTTGTTGTTGAGCTGCAAGATGAAGAGGT
TGACCAGCGGGGAGAGCAACCCCCGGGGCAGCTCAGTGACCTTGTTGTGG
TCCAGGTAGAGGTAGGTCAGCTCGGTCAGGTCGTCGAAGGCACCTGCGCG
CAGCACGCGGATGTCGTTATGGGACAGGTACAAGTAGATAAGTTGCTTGA
GGCCGCGGAAGGCACCGGCGGCCACCTCGCGGATCTGGCAGTGCTGCAGG
TGCAATGACACGAGGTTCGGC

2551. chr17_RSAD1_NM_018346_-1.83163
GGCCCATGGACGATTTATGCCCCAGGGGGCTGGAGGCCACACCCGGGAGG
CTCGGATCCAGACACTGGA

2552. chr17_EPN3_NM_017957_1.63621
CTGTGACCTCGCCACAGTGGCCCTCAGCCCTCCACCTCCGGCGGGGGCG

2553. chr17__EPN3_NM_017957_-1.982
TGGGGCTGACCCTTGGGGAGCCTCCCTGGAGACCTCCGACACACCTG

2554. chr17_ABCC3_NM_003786_1.72519
GAGTGCTGGTGACGCACGGCATTAGCTTCCTGCC

2555. chr17_ABCC3_NM_003786_-1.6421
ATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACT
CCCACTTTTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAAC
CGCAGCCGGGATTTTGAGATCATCA

2556. chr17_ABCC3_NM_003786_1.53615
GCTGCTACCCCTACATCATCTCCAACCG

2557. chr17_WFIKKN2_NM_175575_-1.8418
CTGCCGCCCATCCGCTATTCCCACGCCGGCATCTGCCC

2558. chr17_UTP18_NM_016001_1.50916
ATACCATGGATTTTTCTCCGAGAAGTGGATACTTTGCCT

2559. chr17_KIF2B_NM_032559_-1.75544
ACTGCAACCCTGCTCAGTGCTCCGGGCGC

Figure 3-208

2560. chr17_TRIM25_NM_005082_-1.92263
CAAAGGGGCAGCCTTCAGATCCAAGTG

2561. chr17_SFRS1_NM_006924_-1.5115
TCCATCGTGCATCTTAAGGGCTCCAATCGTCAAAAATAGGAAAAAAAAAA
TCTTTGGAATAGCCAATTAAGTTGAATAAAAAAATCCACACGAATGCGGT
TTGGTTGGGGCAGGAATCCACTCCTATGTTCCTGGTAATCTGATCCCGCT
CCATGAATCCTGG

2562. chr17_EPX_NM_000502_1.67623
GTGCTCTCCGGGACCAGGCCGAGCGCTGCAGCGACAAGTACCGCACCATC
ACTGGACGGTGCAACAACA

2563. chr17_EPX_NM_000502_-1.61402
TCCGGGCTGTCTCCAACCAGATTGTGCGCTTCCCCAATGAGAGACTGACC
TCCGACCGTGGCCGAGCCCTCATGTTCATGCAGTGGGGCCAGTTCATTGA
CCATGACCTGGACTTCTCCCCGGAGTCCCCGGCCAGAGTGGCCTTCACTG
CAGGCGTTGACTG

2564. chr17_MPO_NM_000250_-1.62169
GCCGTTGCGCTTGACCCCGGGCGTCCAGCCGTAGGGAAGAGAGAAGCCGT
CCTCATACTCCGCCGGCAGCCAGCGCACAAAGGCACGGTTGGAG

2565. chr17_BZRAP1_NM_004758_-1.56312
GCAGGCGGAAAGCCTGGAGTTCCTGTGCCAGGAGGCTGAACTGCTCGGTT
TGGCTGCGGCACTGTTCTTCGAGCTCTCGAACCCGGG

2566. chr17_BZRAP1_NM_004758_1.89554
AGCGTCTCCCGCTGGTTGCGCAGCGCGATCTGCCTCTGCAGCCGCAGCAC
CTCCCGCTGGGACTCGCGCAGCAGCCGATCGAAGTCCCGCACGTGGAGCC
ACTGGG

2567. chr17_TMEM49_NM_030938_-1.65147
GACGTGAGCGGGTTCCGGTTGTCTGGAGCCCAGCGGCGGGTGTGAGAGTC
CGTAAGGAGCAGCTTCCAGGATCCTGAGATCCGGAGCAGCCGGGGTC

2568. chr17_USP32_NM_032582_1.5741
CGTAGCTGAGGAATCCGATCCGTGACTCCTTGGCA

2569. chr17_PPM1D_NM_003620_-1.76989
CCAGCGGTGGCAGCCCGAGAGGCTCGCGACCCTCTCCCGGACGCCGG

2570. chr17_BCAS3_NM_001099432_-1.71042
GCTGGAGACTAGCGTTAACCGGCGGG

2571. chr17_BCAS3_NM_001099432_-2.69101
TGATGGCATTGTGGCCCACTTCCCT

2572. chr17_TBX2_NM_005994_2.26475
CGGGGCTGCACGTCTCGGCACTGGGCCCGCACCCGCCCGCCGCGCATCTG
CGCTCCCTCAAG

2573. chr17_C17orf82_NM_203425_-1.84958
AGCTGACCGCGAACTCCTGCGTGGGGTGCTCCTGGGGCGGGAGGGGCGCG
CTCAGCCTCGCTCTCCCCGGGACTCTCACGCTCAAG

Figure 3-209

2574. chr17_TBX4_NM_018488_2.13679
GACCTGGGCGAGTGACTCGTTGTGTGCTGTGCCCGCAG

2575. chr17_ACE_NM_152830_-1.53074
TGACAGTCACCCATGGGACAAGCAGC

2576. chr17_TACO1_NM_016360_-1.50304
GACAGTGTAGGGTCATTAGCTGTTGAGCCGCCCCGGGCGGGCCCAAGCCT
TTGGATCTCAGGTGACCGGCACAGGCGGCCGCGGGGTCCGGAACTGCTTG
TTCCGGCAGTGGAAGAGACGCGCCGGCGTTGGCCGCTGCTGCTAGCAGCT
TGAACCCCAGGGTC

2577. chr17_CCDC47_NM_0201981.70784
GGCCTCATCATCCGGGCCAGGACATTCAGTAAGTCTT

2578. chr17_SMARCD2_NM_001098426_-1.63562
AGGTCTCGGCGCTGGGAACGGAGCCATTCCTGGATGAAGTCCTGGGGGTC
GGTGCTAAAACTGAGCATGAAATC

2579. chr17_CD79B_NM_000626_1.51439
TGGCTATGAAACGTGGGCTCTGCCAGATCCGCGAACAAGCACTAC

2580. chr17_ERN1_NM_001433_-1.53695
GCAACCCCCTCGTGTACCATTGAGGGAGAGGCATA

2581. chr17_GNA13_NM_006572_-1.8927
AGTTGAAATTCTCGACGCCGGTCATAGGCATTCTGTATGCCGCTGTCTGC
CCATAATGCTCTTATAGCAGGAAGATATTGTAAGAAAACCCTTGTTTCCA
CCATTCCTTGGGCTGCCATGGGGGCCCGGGTATCAAACGACATCATCTTA
TCTCCATGTTGTTGGTTTGAGTTGTCTCCCCAGGGAATATGAAGCTT

2582. chr17_ARSG_NM_014960_1.53299
GGGCTGTACTGATACTCCAGGCTACAACCACCCTCCTTGTCCAGCGTGTC
CACAGGGTGATGGACCA

2583. chr17_WIPI1_NM_017983_-1.53728
CAATTGCACTCCATTCTTCCGCCTTCCTTGTTTTCTCCAAAACCACCTGA
TAGGGGGGATGTCCTGATTTCTGA

2584. chr17_FAM20A_NR_027751_-1.72319
AGATTTCCCAGTGCACTCAGGAGATCGTCGGTGGCCTTGATGAAGCCAGT
GCTTTTTGGGAAAAACGGAGCAAGGCAACGCACGACAGAAGCGGTGCACC
AAGGAGTAAAGATTCAGTTCCATGGGCCCCACTTGCTGTTTGAGAAAATG
TCCTGCTTCCTTCCTAGCTGACTTGACTCCCAGCAGTAACAGGT

2585. chr17_ABCA8_NM_007168_1.54754
GGCCCAAGTTTGTTGACACACACTG

2586. chr17_SOX9_NM_000346_1.58112
GCCGCAGGCGGCGCCCCCACAGCAGCCGGCGGCACCCCCGCAGCAGCCAC
AGGCGCACACGCTGACCACGCTGAGCAGCGAG

2587. chr17_COG1_NM_018714_-1.77579
TGGTATGTACAGTCCTTCCTGTTT

Figure 3-210

2588. chr17_TTYH2_NM_032646_-1.75616
GCGTGGACTACATCGCTCCCTGGTGGGTCGTGTGGCTGCACAGCGTCCCG
CACGTCGGCCTGCGCCTGCAGCCCGTGAACAGCACCTTCAGCCCCGGCGA
CGAGAGTTACCA

2589. chr17_CD300A_NM_007261_1.89402
TGGCATTGTTGCTGCTTCTGTTGGT

2590. chr17_CD300LF_NM_139018_1.88627
GCCAAGAGTGAGGCGGCCACCAAAAGCAGC

2591. chr17_GRIN2C_NM_000835_1.55577
GAGCCTCCGCTGATGCTGAGGATGGGCACATGGGTCTGGGAGGAGATGAA
GTCAAGGATCTGGGCCACCGCCTCGGTGTCCACGTTGTCCTCAAAGACAA
TGCCGTGGACGTGGGCAGCACCCAGGAGGCCGCAGATCTGGGTGAGGAGG
CTGCTGGGGTTGGTGGTGTTGACCCCAACTGTGAGCGGCTGGATCTCCAG
GGGTAGGTCCAGGAAGCTCTGGGGGGTGAGGCGGGCACGGAACTGGGCCT
GGGGCGGCCCTGAGCTGCTAAACACCACAGCCACCGTCATGCCCTGCTCG
CCCTGCCCCGGACCCAGCCCTGCCCAGGCACCGAAGAGCGAGGTGAGCAA
CAG

2592. chr17_LLGL2_NM_004524_1.55428
GCTCTACCTGGGCACCGAGAGTGGCAACGTGTTTGTGGTGCAGCTGCCAG
CTTTTCGTGCGCTGGAGGACCGGACCATCAGCTCGGACGCGGTGCTGC

2593. chr17_LLGL2_NM_004524_1.5534
CGGCAACTGGCGTTCACATCGAGCCGCCGTGGGGTGCAGCCT

2594. chr17_SAP30BP_NM_013260_-1.51103
ATATGTTTGATCCCCATGGCTGGTCTGAGGACTCCTACTATGAGGCATTA
G

2595. chr17_ITGB4_NM_000213_-1.56108
GCTGCCTATGGCACCCACCTGAGCCCACACGTGCCCCACCGCGTGCTAAG
CACATCCTCCACCCTCACACGGGACTACAACTCACTGACCCGCTCAGAAC
ACTCACACTCG

2596. chr17_ITGB4_NM_000213_1.54562
GCCAGCCACCGCATTCCGGGTGGATGGAGACAGCCCCGAGAGCCGGCTGA
CCGTGCCGGGCCTCAGCGAGAACGTGCCCTACAAGTTCAAGGTGCAGGCC
AGGACCACTGAGGGCTTCGGGCCAGAGCGCGAGGGCATCATCACCATAGA

2597. chr17_EXOC7_NM_001013839_-1.51201
TGGTCCAGGCAGGACAGCGTCTTCTCAACATTCTCCTGCAGCCGCTGCAG
ATTCTCCGTCTGCTTG

2598. chr17_FAM100B_NM_182565_-1.69136
TCAGCGGCAGTCCCCGAACGTTGGGCCGGCCCAGCCCCGCCCCGCGCTGT
TGTTTGTGGTGTCGGCCGGGCCGCGGGAGTCGAACCACAACATTCGCCGG
GCGGGCGGCGGCGGAGCGGGCGGCGGAGCGGCGGCAGCAGCGGTGAGCGC
GAGCCC

2599. chr17_QRICH2_NM_032134_2.06834
AAGCTGAGCTCCTCGGCGGCGTCCTT

Figure 3-211

2600. chr17_SPHK1_NM_021972_-1.77499
TCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCA
CCGCCAGAAGAGCCCTTATGA

2601. chr17_UBE2O_NM_022066_1.54965
ATCTGGTTCTTCAAGTCGTAGACCTTCCCCAGCCAGCAGTCATAGGCAAT
GTAGTCCCCATACATGA

2602. chr17_RHBDF2_NM_024599_-1.51772
ACTTCTCGCAGAAGCGGCTGGTGAAGGGGAAGCAGGTGAGGTGCTCGATC
CAGGGCCAGTTAATGGGGTAGATGTACAGCCACAGCACGAGGGCGGCGAA
GAGGCCGGCAAAGGCCAGCAGTGACACCAGGATGAGTGCCCGCTTGCGGT
ACTTGTCGCTGGTGCCGAAGGTGATGTAGGGCAGGAAGGCGAAGGCCAGC
AGCAGGCCACTGAGGAAGCCGAAGAT

2603. chr17_RHBDF2_NM_024599_-1.67
CTCTTGCGGCGTGGCAGGTGGGAGTAGCCAGAACGGACACTGGTGAAGGA
GGTGAGGGACAGGACTCCGGGGGTCAGCGGTGGGTGCGGGGCGTGGGGCC
TGTCCATCTCCTCCGGGTGGCGGAA

2604. chr17_RHBDF2_NM_024599_1.61328
AGCATGCTGTCCTGCTCGCCAGGGGCCTGGGTCTCTTTCTCGGGTGGCGG
GATGGTGATGGAGAGGTTGGGTGGCTTCCGGCTCTGCAGGCGGCTGCTGG
ACACAGAGGACACGCTCCCGCCATTCTTGTCAGC

2605. chr17_RHBDF2_NM_024599_1.50926
TCGAGTCTGAGTTTGCCCGCGGCTTCCTGGGTCTTGCTGTGAAGGGCTTT
AGAGCATGTTCTTGTCTTCTCCTTGCTCTGTACAGATGCTCCGGTGTCAA
GCCTCAGTCTGTGGAAGGGTGGCTGGACAGACAGGTGGCTGGAAGGACAG
ATAGACAGCTCCAGGC

2606. chr17_TMC8_NM_152468_-1.65371
CCGCGGTCGGTGTCATCGGAGCGGGCCCCTGGGGTGCCGGAGCCGGAGGA
GCTGTGGGAGGCAGAGATGGAGCGGCTGCGCGGCTCTGGGACGCCCGTGC
GCGGGCTGCCCTATGCCATGATGGACAAG

2607. chr17_TK1_NM_003258_-1.6364
GCCCCTCGTCGATGCCTATGACAGCCACGCCCAGGGCCTCCTGGGCCACG
TCTCGGAGCAGGCAGGCG

2608. chr17_GAA_NM_000152_-1.80986
GAGGCCCGCGGCTGTTGCTACATCCCTGCAAAGCAGGGGCTGCAGGGAGC
CCAGATGGGGCAGCCCTGGTGCTTCTTCCCACCCAGCTACCCCAGCTACA
AGCTGGAGAACCTGAGCTCCTCTGAAATGGGCTACACGGCCACCCTGACC
CGTACCACCCCCACCTTCTTCCCCAAGGACATCCTGACCCTGCGGCTGGA
CGTGATGATGGAGACTGAGAACCGCCTCCACTTC

2609. chr17_CARD14_NM_024110_1.61885
ACCAGGCTTGGCATGGTCTGAACTGGAAACCCTGAGAATGTTTCTGCAGT
GGGACAGGAGGGACGTCTTCCCATGCCTTCCCTAGAACCGGAGGCCCCGG
ACTTCTCTGGAAAACCGCCTGTCTGCAGGCCCGATTCAAATCTATGGGGG
CTGCACTTCCCTTTTACATTTTGATGTGTCAAAGGCTTTTGGAGTGACCA
AAAGCACAGAGGCAGCGGGTGGGGCGCCTGGGTGGTCCCCAAGGTCGCTG
CCACCCTTGCCCGGGGCAGAGGCAGAAGCCCACATATGCTGTGACGCTGG

Figure 3-212

CCACCTTTT

2610. chr17_RNF213_NM_020914_-1.52324
GATGCGCCTCAGTGTCTTTTTAAAGAAGCAAGAAGAGAGCCAGTTTCACC
CTCTGGAGTGGTTGGCAAGGGAAGCCTGCAACCAGGACGCTCTCCAGGAG

2611. chr17_RNF213_NM_020914_1.51297
GAGCCCGGATCTTGTGCTGCTTTTCTCACTGACGTGTTGCCTTTTTTCTT
TACAAAATCTGCTTTGATACTTAGGACCTCTCTGGACTAATTTCTCTTCC
TAGACAGCTCAGCACAGCTATTGATATGTTAGAGGCAGTATCCTTAATAT
TCATTCTAAATGAGTTAACGACTTAACTTGAAATTGGGCCTAAGGAGTGA
GAACTACAAAAATACAAAATGCTTGTCCAGGACTCAGCCATGCACACCTT
GAGCAGCGCCGGCAGGAGGCACGGAAGGAACTGTGCTCCGTTCTCCTCAC
TGTCATGGTGCCACCAGTGTCTGATGAAGGGCAGAGTGACCCAGACTGCA
GGCAGTAACTGACTTCACACAGTCCCTGGCATTTAGTCATCTGTGATTGT
TTTATCACTCTGGACTGTGCAGAGCCACCTGCCACCGAGATCTGCATTCC
GACTG

2612. chr17_NPTX1_NM_002522_-1.99297
CGCTGCTCCGGAGCTCCTCGGCGCCGCCGGCGGCCACGGACGCGGCGCAC
ATGTCGGCGTCCACGGGCACCGAGGTGCAGATGAAGCGCGTCGGCCCGAA
ATC

2613. chr17_C17orf56_BC064483_1.80375
GGCCTTGTTGGTCACAGGTCCCGGGCTGCCCATGCTGAGCTCCTGCAGCC
ACGGCCGGGTGCGGAGGAGGATGTGCTCCT

2614. chr17_C17orf56_BC064483_1.56481
CAGGTAGCCCGGACACGGGACATCATCATCGGACGTCCCCTTCAGGAGAA
TCGGGA

2615. chr17_TSPAN10_NM_031945_1.5768
GACCGCCACGCACAGGGATACAGGGGGCGCCTCCGCCCGGCTAAAAAGCG
CGGCCTGCGCCGCCGCCGCCGCCTGATTTCGCTCGGGCTTCGGGTGACTT
CGCCGCAGGACCTACCCAGCTCGCTCACTTCGCTCGCTCCGCGTCCCCCA
TGCCAGCCCCCAACGCAGGGCGCCCGGCGAAGCCACGGGACTGGCGGGAG
GAGCACGCGGGGCCGGAGGAAATCCTGAAGCTGACC

2616. chr17_CCDC137_NM_199287_-1.5645
AGGGAGAGGAGCCCGACATCGCAGTCCCCAAGTTCAAACAGAGG

2617. chr17_HGS_NM_004712_-1.57096
ACAAGAACCCACACGTCGCCTTGTATGCCCTGGA

2618. chr17_HGS_NM_004712_-1.76679
TTCTTCCAAGTACTCCACCATCCCCAAGTTTGGCATCGAGAAGGAGGTGC
GCGTGTGTGAGCCCTGCTACGAGCAGC

2619. chr17_SLC25A10_NM_012140_-1.63942
ATGCAGAACGACGTGAAGCTGCCCCAGG

2620. chr17_STRA13_NM_144998_1.95127
CGTCCACACGGAGCGCGTCTTCTGCCTGGGCCTGCCGCACGCCGCGGACT
GCTG

Figure 3-213

2621. chr17_DCXR_NM_016286_-1.83997
CCAGCACCCGGCGGCCCGCGAGGAACAGCTCC

2622. chr17_GPS1_NM_212492_-1.64928
GCTCGGCCTCCTCGTCAGTGACAGATCTGTACT

2623. chr17_CCDC57_ENST00000392346_2.72322
CCCAGCTCTGCACGGAGCCTGTTC

2624. chr17_CSNK1D_NM_001893_-1.7079
GAGAGGTATCTTGTCGGCCTGTGAGGTCGGACGAGGAGATGTTGACGGGG
GCCCCGCGGTGCAGCCGCATACTCACTTTCCGCTCTCTCTCCATGCCGGA
GACGGG

2625. chr17_NARF_NM_012336_-1.62911
CTGGGTCCGATACGCCGAGCGGGTGCTGGGTCGCCCCATCACTGCCCACC
TCTGCACCGCCAAGTCCCCCCAGCAGGTCATGGGCTCTTTGGTGAAGGAT
TATTTCGCCAGACAGCAG

2626. chr17_NARF_NM_012336_-1.59156
TGCTGCATACCACGTACCAGAGCCAGGAGCGTG

2627. chr18_ENOSF1_NM_017512_1.61269
CATCCTTCAGCGCCTGGGCACAGAG

2628. chr18_TGIF1_NM_003244_-2.74608
ACAGCGCCGAGGTGCGCCGAGCAG

2629. chr18_LGAP1_NM_004746_-1.66258
GCAGGTACTGGCAGGAGCGTTCTTGCTGACACGACTCGGACTTCACCATG
GCCTGGTCCATGTTCACCGAGGCCTTCTGGTAAACCTCCCGGGCCCGGCT
CACGGTGAGCGTGGAGGACCAGGCGCTCTT

2630. chr18_EPB41L3_NM_012307_-1.62262
GGGAGATGTGGGGGCACAATGGGTGGATGGGGGTGACAAGGGACATGAGT
CAGTGCCAAGCCCAG

2631. chr18_EPB41L3_BC008377_-2.19421
AGAAAAAAAGTAGCGCAAGGGCAGAGAGAGGTAGG

2632. chr18_L3MBTL4_NM_173464_1.89251
TTTTCATGCTCTGGAAAGGACTGA

2633. chr18_KIAA0802_BC040542_-1.59022
CTCCAGGCCCGAGAGACCAGCAAACCGTCGCCCTCCGTCCCGTTGGGCCC
CACATTCCCCCACTGCCTCACAGCCTCAGTCACCCGGAGACCCGACGTCC
TTGGAGGAGCATG

2634. chr18_FAM38B_NM_022068_1.56109
GCAGGCCGACCCACTCTGTAGGATCGATAGGAGCGCTGTAGAGCAGAGAC
TTGTTCAACTCATTAAAGGG

2635. chr18_IMPA2_NM_014214_-1.78255
CCCCCCGGAGTACTTCAGAATGCAA

Figure 3-214

2636. chr18_SLMO1_NM_001142405_1.66963
CGGGACGGAAAAGCACGTCTGGCTGCGAGGGCACACAGGGCCGGGGAGGA
GGATTAGGCTGGACTGATCGCGGGTCGCAGGTGACCCCGGGACCAGATGT
CCCTCCCCTCATGAGCGTGCAACAGGGAGCAGCCCCAGCCAGCCCCACCG
CCGCCGTCTGCGTGGATGGA

2637. chr18_PTPN2_NM_002828_-1.74605
GCTGGCGCGAGCAGAGCCTGCGCCGGCGGAGAGGCTCAGGCCCCGCACGA
TCCGGGGAGAGCGCTGGCGCTGCGGCGCATGCGCGCTGCGCGCCGCGCCC
CGCCCCCACGCCAAGCCCTGTCGGCCGTGGGGAAAGTACCTGGAGCGTCG
GACGTCA

2638. chr18_CEP192_NM_032142_1.60929
CAAAGAATCTACTCCTTAAACCTGG

2639. chr18_C18orf1_NM_181481_-1.79165
TGGCCTTCAGACAGCGCCGCACCGCGGCTGGGC

2640. chr18_GREB1L_AK293321_1.65378
GAGAAGGGCTTCGAAGATAAACTGAGCTCCATTCCCCTGGCATGAAACTT
TCAGATTCCCCTGCCTCTAGAAATTGTC

2641. chr18_LAMA3_NM_198129_1.52417
TGTCACCCGGGATGATGATGTACTTTGTGTTACTGAATATTCCCGTATTG
TACCTTTG

2642. chr18_DSC3_NM_001941_-1.51645
ATTCGGGCATACATGCAGACCAGGTGGTTTTCAGCATGTTCAAAGAACAA
AGAGATGGTTAGAGGTTTTATAAACAGGGAAGTGATACTGGTTGCTCTTT
GAGAAAGTTTATCGGCACTAGTAAAGTCTTGGGGAGGTAGCAGGTTTTGA
TCGGTGAGTGAGGGAGTGAGCAAAACACAGTGGGTGTTTCAGTAGCCGTT
AGATAAAACTGGCTTCTGGATACAGCAGGAAATTTCAGCAACTAGGCTTA
CAGAGAATTCCA

2643. chr18_B4GALT6_NM_004775_-1.61091
GGCCGGACTCGGGGCCACTGTCCA

2644. chr18_C18orf34_NM_001105528_1.50895
TAACCATCGTTTTCGCATGTGCCATCTGTCAAAGTCTGGAAGAAACCTAA
GATGTGTTGCATTAAA

2645. chr18_MOCOS_NM_017947_-2.00852
AGCTGTGGACCTTCGCGGGTTCCCG

2646. chr18_MOCOS_NM_017947_-1.54982
TGTACCTGATGCATGCATCATTGGATTTATCCTCCCCATGTTTC

2647. chr18_KIAA1328_NM_020776_1.53288
CTGGATGGTTCCTACTTGAGCATAGCCAGACCACAGACCTACTATCAAAC
CAAGCAAAGACCTAAGTCTGCAGTCCAGGATTCAGCTTCAGAATCCCTTA
TAGCATTTAGGAATAATTCTTTGAAACCAGTAACCCTTCATCATCCCAAA
GATGATCTAGATAAGATACCATCAGAGACCACAACATGTAATTGTGAATC
TCCAGGGAGAAAACCTGCAGTCCCAACAGAGAAAATGCCACAAGAAGAAT
TGCACATGAAGGAATGTCCACATCTTAAGCCTACTCCTAGTCAATGCTGT
GGTCATAGACTTGCTGCAGATCGTGTTCATGACAGCCATCCTACAAACAT

Figure 3-215

GACCCCTCAACATCCTAAGACACATCCAGAATCATGCAGTTATTGTCGGC
TTTCTTGGGCATCTCTGGTGCATGGTGGTGGGGCACTGCAACCCATTGAA
ACTT

2648. chr18_SETBP1_NM_015559_1.56423
AGCCAGCCGCAGTTGACAGTGTTACAATTCCACCAGCCCCAGTGTTATCT
CTCCTTGCTGCATCTGCAGCAACGTCGGATGC

2649. chr18_CXXC1_NM_001101654_-1.85371
GGCGCAGCCGGCACTTCTGCCGGATCTTGTTGGGGCCCC

2650. chr18_ME2_NM_002396_-1.60559
TGTTCTCCCTGACCACTTTGGTTGATGTATTTTTTCCATGCGTCTCCACA
TCTGTTGGGGTAGACGTGTTGATTGATTGCATTGCCCACCAGCACCCTAC
AGTCAGATAGTTGTGATGCTTTAATTCTAACATACAGCCCGTACCACATC
CAGGAGATGTAAAAAGTGTGTTTGTGAATGTCTTCACTTGTACTCTAATT
CAGACTTGCCAAAGTATTTGCTATTTACTATTATGGGTAATACTCTTCTC
TGGCCTAGTTCTTACAGAGCTACT

2651. chr18_TCF4_NM_001083962_-1.65595
ATACTGTCTGTCCCGTTGGCAGGAGGCGTACAGGAAGAGGTGCTGTAATG
GTTTGTACCACTACGATGGAAAGTGGACATCGGAGGAAGACTGGAATTGA
TGTCTGC

2652. chr18_ONECUT2_NM_004852_2.18775
CCAGCGCCTGTCCGGCAACGTCAG

2653. chr18_FECH_NM_001012515_1.55002
GCCACACCAGTCGGTAGGGGTTGCAGTACTCCAGCCTTTCCATGACTTTT
TGGACAGTGGCGCTTAC

2654. chr18_---_---_-1.65323
AGTTAGCTGGGTATGGTGGCATGCACCTGTAGTCCCAGCTACTCGGGAGG
CTGAAGCAAGAGAATCACTTGAATCTGGG

2655. chr18_---_---_-1.6646
AACTACTGGAAATCTGGCTGGGCGTGGTGGCTCAAGCCTGTAATCCCAGC
ACTTTGGGAGGCTAAGGAGGGCAGATCACCTGA

2656. chr18_MALT1_NM_006785_1.59923
GAAGGACAAGGTTGCCCTTTTGAT

2657. chr18_CDH7_NM_033646_-1.53955
CGCTCCGAGCTCAAGCGCTGGATAGGCTCACCAACAAACCCGTGGAGCCC
GAGTCGGAGTTTGTCATCAAAATTCAGGATATCAACGACAATGAACCCAA
ATTTTTGGATGGCCCATACACGGCAGGAGTTC

2658. chr18_ZADH2_NM_175907_-1.5539
TTCAATCAGAACGGGCCCATGGGGTTTCAGCGCAACGGTGACAGCGGCAG
CAGTCTTCAGGGCACTAAAGGTTAAGAGGGA

2659. chr18_ATP9B_NM_198531_1.50251
GAAAGATGAGAACATCCCTGGCACGGTCGTTCGGACCAGCACTATCCCAG
AGGAACTTGGGCGCCTGGTGTATTTATTGACAGACAAAAC

Figure 3-216

2660. chr18_NFATC1_NM_172390_-1.51052
CAGAGCACGGACAGCTATCCGGTCGTGGGCGGGAAGAAGATGGTCCTGTC
TGGCCACAACTTCCTGCAGGACTCCAAGGTCATTTTCGTGGAGAAA

2661. chr19_BSG_NM_198591_-1.71653
TGAAGCAGTCGGACGCGTCTCCCCAAGAAAG

2662. chr19_BSG_NM_001728_-1.69445
GCTGTGAAGTCGTCAGAACACATCAACGAGGGGGAGACGGCCATGCTGGT
CTGCAAGTCAGAGTCCGTGCCACCTGTCACTGACTGGGCCTGGTACAAGA
TCACTGACTCTG

2663. chr19_PALM_NM_002579_-1.8097
CGAGTCTCCAACACGCCCCTGAGGACGGTTGACGGCTCCCCCATGATGAA
GGCAG

2664. chr19_MED16_NM_005481_-1.61387
CACACCATTGTGCAGCCAGGACAGGGCCACAATGGGGTCCCCCTCCACTA
GGCTGCCCACTGAGCTCTCCCAGCTATTAGCCAGGTGGTCCGCCATGCTC
CAGCACTTGATCTGCCCGTCGGCATCTGCTGACAGGA

2665. chr19_C19orf6_NM_001033026_-1.67787
CCTCCCAGCGTCGCGCCCTAACGACCCGCAAGTGTCCGAGGGCGCCT

2666. chr19_GPX4_NM_002085_1.94507
GCCTCGGCCGCCTTTGCCGCCTACTGAAGCCGGCGCTGCTC

2667. chr19_SBNO2_NM_014963_-1.50935
GCATATATTAGCAGGGGTCTGCCCCACGGAGCCCCCGAGACGCGGGGCCC
TGAGCACCTGGGGTTTCCTGAGTTTCTAGCTCTTGGGACCACCCGGTTTC
ACGGATTTCAAGGGTTTGGGCCCACTGAGCCCTTGTGGG

2668. chr19_SBNO2_NM_014963_1.80259
CCCGGCGCACGCAGCCCTCGGGGATCTTGAT

2669. chr19_C19orf26_NM_152769_-1.52302
GTTGAGGCGCTGGTGGACGTCCCAGCAGCGCTTGCAGAGGAGCAGGACGC
CAGACAACACCACCAGCGTGCCCCCCACGAACAGCGACAT

2670. chr19_C19orf26_NM_152769_-1.60215
GCGTCCAGTGGCATTGTCCCACGACGTCGTCAGGGCTACTG

2671. chr19_CIRBP_NM_001280_1.61994
CAAGTCGTCAGACAACCGATCCCGTGGGTACCGTGGTGGCTCT

2672. chr19_MUM1_NM_032853_-1.6484
GGGCCTCGTACTGCCTCATGGAAAATCCTCCGGAGCCGCC

2673. chr19_APC2_NM_005883_-1.51501
GCGCAAGGAGATGCGCGTCCTGCACGTGCTGGAGCAGATCCGGGCCTACT
GCGAGACC

2674. chr19_APC2_NM_005883_-1.67286
CCATCGAGCCGCAGATCTGCCAGGCCACCTGTGCTGTTATGAAGCTGTCC
TTTGATGAGGAGTACCGCCGTGCCATGAACGAGCTAG

Figure 3-217

2675. chr19_APC2_NM_005883_-1.64986
AGTCCACCCTGAAGAGCGTGCTGAGCGCCCTGTGGAATCTGTCTGCACAC
AGCACAGAGAACAAGGCGGCCATCTGCCAGGTGGATGGCGCCCTGGGCTT
CCTGGTGAGCACCCTGACCTACAAGTGTCAGAGCAACTCGCTGGCCATCA
TCGAGAGCGGCGGCGGCATCCTCCGCAATGTGTCCAGCCTCGTCGCCACC
CGTGAGGACTACAG

2676. chr19_PCSK4_NM_017573_-1.97687
CAGAGACCACGATGCCCTGGCCTGACAGCCCCTGACTCCAGGCCTGCAGG
ATGCTCAGGTCTGGTTGGGCCTCGCTGTT

2677. chr19_TCF3_NM_003200_-1.73902
GCCCTTCCCGTTGGTGACAGGCAGCGGGAA

2678. chr19_ATP8B3_NM_138813_1.9636
TCATGTTGATGTCGTTGGCACCGTCCCCGATGG

2679. chr19_REXO1_NM_020695_1.57345
CTCGTCCCCAAAGAGGTCGGCGTGGCTCAGGGCCCGCTTCTTCAGCTTGG
GGGCGTCCTGGGAGGCGCCCTCGTCTAGTGAGCGGGCTTTCCGCTCCACT
AG

2680. chr19_MKNK2_NM_017572_-1.55208
CACTCATTCACAGTAACGGTTCTGACCAGTCCTCCAGGTCGCACGTGGAT
GCGACAG

2681. chr19_MOBKL2A_NM_130807_-1.81615
CTTCTCGGATTCCTCCAGGAACAGTGGAGAAGACAAGGCAGGAATCAGCT
CTCAGAATTCCACACCAAGGCCTTCTGGGCTCCCCCGGTCTTCCCACGGA
CGAGACACAAGTGACCC

2682. chr19_AP3D1_NM_001077523_1.7133
TTCACCAGGAGGCAGACATGGTGGCCCTGGATGGAGCGGCTGTACATGGA
GGCGCAGGAGTCCACTCGCTCCA

2683. chr19_AP3D1_NM_001077523_-1.61027
TGCAGACTGCCCCGGATGTCACAGGT

2684. chr19_AP3D1_NM_001077523_1.60999
GGTGCTTGGGACGCCGCTGCTCCTCCTCGTGGAAGACGGCCCTGGGCCTC
TCGTCCTCTGACTCGCTGTCCGAGAGTGGCTCATTGATCCAGGCGTCCA

2685. chr19_DOT1L_NM_032482_-1.62776
CCCGCCCGCGCTGCAGAAGCTTCTA

2686. chr19_PLEKHJ1_NM_018049_1.8275
TCTTGGGGCCCCTCATGCCCAGCTCGGCCGCCATCTCGGCCGGCTGCCGG
GACAG

2687. chr19_C19orf35_NM_198532_-1.77032
CGCACCACGCGGTAATACAGGGCGTCCCCGCTCTCTGCGCAGGGTGAGCT
GTCTAGGAGGCGGAAGCTGTGGCCGGGGTGGCAGGGCCCGGGGTGGCCCC
CCATGAGCCGGGCACGGAGCCGGGCATAGATGGTACGGAGGCCCTGCAGC
TGCCGCGCAGCCAGTGCAGTGTGCACAGCCTCCGGGCTGTGCAGATCGCG

Figure 3-218

GAGGGAGAGGCCCAGTGGGGCGTCAGCCGGGCCAAAGGTCAGCTCTGCAG
GGAGACAGGCTGGTCCCACTGCAGCCTGGCTCTTGTCCACACTGTGGGAC
CCCAGAAAGGGTCTCCGAGGCGGCTGTACTTGGATG

2688. chr19_SPPL2B_NM_152988_1.66173
CTATGGCGTTGGCCTCCTTGTGACATTCGTGGCACTGGCCCTGATGCAGC
GTGGCCAGCCCGCTCTCCTCTACCTGGTGCCCTGCACGCTGGTGACGAGC
TG

2689. chr19_GADD45B_NM_015675_-1.76585
CAACCCAACCCACGAGGACCATCGGGGGCAGAGTCGTTGGAGACTGAAGA
GG

2690. chr19_ZNF77_NM_021217_1.63584
CCACTTCCTCAAAGATCACGCAGTC

2691. chr19_GNA15_NM_002068_-1.5001
GGAGAGCCTCGCATTGTTTGGGACTATCCTGGAACTACCCTGGTTCAAA

2692. chr19_NCLN_NM_020170_1.74361
AGGAAGCGGGCGAGGTGCTGGAGAAC

2693. chr19_NCLN_NM_020170_1.53937
GGAGGAGGCAAGTTTAACTACCAGGGAACCAAGCGCTGG

2694. chr19_CELF5_NR_033342_-1.99571
GCGGACGCTCCGGCGCATGCAGCAGATGGTGGGCCAGCTGGGCATCCTGA
CGCCGTCCCTCACATTGCCCTTC

2695. chr19_FZR1_NM_001136198_1.55132
AAACCCACCCGCAAGATCTCCAAGATCCCCTTCAAGGTGCTGGACGCGCC
CGAGCTGCAGGACGACTTCTACCTCAATCTGGTGGACTGGTCGTCCCTCA
ATGTGCTCAGCGTGGGGCTAGGCACCTGCGTGTACCTGT

2696. chr19_MRPL54_NM_172251_-1.71571
TGGGAGCTCCTAAACCCCGCCACTTCCGGAAGACTCCTGGCCCGGGATTA
TGCCAAGAAA

2697. chr19_DAPK3_NM_001348_-1.63996
TGCCGGCACTTCCGCACGATCGCAAA

2698. chr19_EEF2_NM_001961_-2.06193
ATGGGGATGCAGGCGTGGTCCTCCTCCAGGTCCTTCAGGCAGATCTCCAG
GTGCAGCTCGCCGGCGCCCGCGATGATATGCTCTCCCGACTCCT

2699. chr19_DPP9_NM_139159_-1.63083
ATTAGCCCCATGAGCGAGAGGAAGCCCCCGTAGGACCAGCCATGGATGGC
AACTCGGCTCAGGTCGATGAAGCCATACTTCTCGGCCACGAAC

2700. chr19_C19orf30_NR_027148_-1.51158
ATCAAGGGAAACGATCCTTATTGCCTCACCATTTCCCACGTGAAGTCTGT
ATTGACATTCTCATAG

2701. chr19_TICAM1_NM_182919_1.52679
TCTACAGAAAGTTGGAGTGGCGTCTGGTCTTTGACAGAGCAGGGGTTTTT

Figure 3-219

GACCGGCTCCAGAATAGGCAAGGGGAGAGACTGGGGGCCTGCAGACCCCT
CGGTGCACTCCACTGGGTAGTTGGTGCTGGTTTCTGGAGCTGCGGGGGTA
TCAGGGAGGCCAGTGGAGGTTGCATCTGGGGCCACTTCGGGAAGCCCAGG
AGGTGGGCTGCTTGGCAGCTCTGGTGGGCTGGCAATCTCCCCCGATGGCG
GCCAGCTCATCTCCTCAGGCTCCTGGCAGCCACCGGGGACAGGCTCGGGC
ACCAAGCTGGCCTG

2702. chr19_PLIN3_NM_005817_-1.52187
AGGTGTGTTCTGGGCCACATATTCCACCATGTGGTCCAGGGCCTCGCGGG
CGCTGGCGACACGCTCACGGCTCTGGGCCAGAATGCTGCTGGACAGGTCC
TGGAAGGAGTGGATGCTGGAAAACGTGGCCTGGAGGTCCTCCACCTGGCG
GCGGGCCTGCTGCACCTGGTCCTTCACATTGGTGGGGAGGCCCTGAATGC
TGGACCCCAGGGAGGTACAGGTGGCCTGCAGTTGCTGGGCAATGTCCCGG
AACATGGTGAGCG

2703. chr19_PTPRS_NM_002850_-1.55442
GGCTCCAGGACAGCGTGATGCTGGTCTCCGACCTGGCCTCGGCCCGCAGG
TTCATGGGCT

2704. chr19_PTPRS_NM_002850_1.52792
TTCACCGTGATCTGAGCAACCGCCTCAATGACGCCCAGGCTGGACATGGC
CACGCAGGTGTAGTTGGCCGAGTCCTTGACATCTGTGAGTTCCAGCACGT
TCCGACCCACGGGCATGTCATCCTCGGGGGTCAGGTCCTCGGCCCCCTGC
ATCCACTTCACGTATGGCATGGGCGAGCCCACGGCCACGCAGGTGATGTT
CACGTTGCCCCCTGGCATGATCTCGTGGCTCATGGGCAGGAT

2705. chr19_ZNRF4_NM_181710_-1.59415
CCCTGGTCGTATCAGCCTTCTTTGTCCTGAACCACCTGTGGCTCTGGGCC
CAGGCCTGCTGCAGCCACAGACGGCCGGTGAAGACGTCTACCTGCCAGAA
GGCCCAGGTCCGCACCTTCACGTGGCACAACGACCTGTGTGCCATCTGCC
TGGATGAGTATGAGGAGGGCGACCAACTCAAGATCCTGCCCTGCTCCCAC
ACCTACCACTGCAAATGCATTGACCCCTGGTTCTCCCAAGCCCCCCGGCG
CTCCTGCCCCGTGTGCAAACAGTCGGTGGCCGCCACAGAAGACAGCTTTG
A

2706. chr19_NRTN_NM_004558_-1.51808
CCGGATGCGATGGAGCTGCGCGAGCTGACGCCCTGGGCTGGGCGGCCCCC
AGGTCCGCGCCGTCGGGCGGGGCCCCGGCGGCGGCGCGCGCGTGCGCGGT
TGGGGGCGCGGCCTTGCGGGCTGCGCGAG

2707. chr19_FUT6_NM_000150_-2.03672
TGACCGCGTCTGCCTGTGGATACACCT

2708. chr19_RFX2_NM_000635_1.57015
CCGGCCTCAGCACGTCGGGGATGAGAATCTCCACCAGCGCCTGGTAGAGG
ATGTGGTCGCAGCTCCTCATCCACCTGAGGATGGGGTCGCACTGACACAG
GGAGATAAGCTTGTCCTTGGGCA

2709. chr19_GTF2F1_NM_002096_2.18617
CTGGCATCACTGGCATCGGACGACATCTCCAGGTCGTCCTCCAGGTCGTG
GATGCGCAGCTCGCTCGCCTTCCTGCGGCCACGTTTCTCCTTCTCCTCCT
CATCCTCGTCCTGGTCCTGATCCTTGAGCCGCCGCT

2710. chr19_KHSRP_NM_003685_-1.63252
CTGGGGTGGGTACTGGTGAGGAGGG

Figure 3-220

2711. chr19_SLC25A23_NM_024103_-1.68231
GGCCAGCCCCTGGCGCAACTCGTGCACGTCCACGCGGCCATCCTTGTTAC
TGTCCAGCTCCTCGAACAGGCGACCCCAG

2712. chr19_DENND1C_NM_024898_-1.74735
TAACCCTCAAAGCACTTCTTAAGA

2713. chr19_CD70_NM_001252_-1.51862
CGGGAGAGCAGATTCCCACGGCCAGGGTGGTGGGGTGGTGCCTGGAGGCC
GTCGTGGAGGAGCAGATGGCCAGCGTCACCTGGATGTGTACCATGTAGAT
GCCATCACGATGGATACGTAGCTGCCCCTTGTCCAG

2714. chr19_INSR_NM_000208_1.58221
GGCCGCAGAGAACGGAGGTAGCTCTTCAGGTCTCCGTGAGCCATCAGCTC
CATCACCACCAGCGTGGGCTGGCCCTTGGACACCA

2715. chr19_ARHGEF18_NM_015318_1.50299
TCCAGAGCCTGATCTGCAGGCAGCTGGGCAGCGCCAACGGCCAGGCGGAA
GACGGAGGCAGCTCCACAGGCCCGCCCAGGAGGGCTGAGACCTTCGCGGG
CTACGACTGCACAAACAGCC

2716. chr19_EVI5L_NM_001159944_-1.57566
GGACATGCCCGTCAAGAACCAGTACTCCGAGCTGCTCAAGATGTCCTCGC
CGTGCGAGAAGCTGATCCGCAGGGACATCGCCCGCACCTACCCGGAACAT
GAGTTCT

2717. chr19_MAP2K7_NM_145185_-1.84624
CAACAGGACAGTTTCCCTACAAGAACTGCAAGACGGACTTTGAGGTCCTC
ACCAAAGTCCTACAGGAAGAGCCCCCGCTTCTGCCCGGACACATGGGCTT
CTCGGGGGACTTCCAGTCCTTCGTCAAAGA

2718. chr19_SNAPC2_NM_003083_-1.59785
CTCTTTCTGAGGATCCCGTCATGGGGGAAGGTCCTTGAGATGATGCTCAG
CTGTGGGGCGGGCCTCTAAGATGCCCCATACTTTGGGGGTCTCAGAAATG
GAACCCCCGTTGTACAGGGGTTGGGTGGGGGTTGCAGGACTCCACTCACA
AGCCTCCTGATGTCAAGGACAGGCGGACAGGGCTGGCCTCCCCCAGTCCC
CAAGCCCCACTGTGCCTTGTTGTCTGCTGGGGGGCCATAGCTGGCACTGC
CCACCGTAAAGGCCCTCGCACATTTTCCCCCTTCCTGTACACCTCGGGGC
CAG

2719. chr19_ELAVL1_NM_001419_-1.66236
AATCTCTGCGCCTGGTGGTGAACGGGGCCTCCGAACCGTCGCGCTGGCGA
GTGGTACAGCTGCGAGAGGAGTGCCACGTTTTTGTTCTGGTTGGGGTTGG
CTGCAAACTTCACTGTGATGGGCTCAGAGGAACCTGGGGGTTTATGACCA
TTGAAACTGGTAATTGCCTCTTCTGCC

2720. chr19_CD320_NM_016579_-1.90294
GCGCAGTTTCTTGTCAGTTCCCCC

2721. chr19_KANK3_NM_198471_1.66576
TAGGTGTAGTGAGCCAGACGAGGCAGC

2722. chr19_HNRNPM_NM_005968_-1.55697
GTTACTGGTTGCGTCGGGTCACGTGGGCGCGCAGGCGCAGCGCGGTGCAG

Figure 3-221

CCCGTTCGCTCACACAAAG

2723. chr19_---__---_-1.79322
GGCCTCAAATGATCCCCCCTTCTTGGCTTCCCAA

2724. chr19_---__---_-1.5313
TTATATGTTTAGTAGAGTCGGAGTTTCAC

2725. chr19_ADAMTS10_NM_030957_-1.59145
TGGCAGGCCTCCAGTACAGGTGGGCGCGGCTGCGGGCATGCGCTGTCGTC
CAGCGCCTTCTCCTCCGCGGCAGAGACGCGGCGCTGGCACACGACCGAGC
GGCTGCGCACGCCTGCATCGCAGCTGCGGCTGCAGAGCGACCAGTTCCCT
ACAAC

2726. chr19_ZNF317_NM_020933_-1.65701
GAGAGAAGTCCACTGAATACGCTCACTTGTTCGAAGTCTTTGGCATGGAC
CCTCATCTCACTCAGCCAATGGGAAGGCACGCTGGCAAGAGGCCCTATCA
CCGCCGCGACTATGGGGTAG

2727. chr19_OR7D4_NM_001005191_-1.67213
ATACACCTGAGTGAGGCACCCCATGTAGGAGATGTCTTTGCTCCGTGCCT
GGATGCTCACTAGCAT

2728. chr19_COL5A3_NM_015719_1.94928
GTGGCTGCTGTCGTCTGGTTGAAAGACAGCTCCTCTCCATTGGTGCCAAG
GAAGCGGGCGGAGTGGCTGTAGTCACCCGTGGCTTCGTCCAGCCAGGCAG
CTGCATTCTGGCAGGAGTAGGTGAAGTTCTGGCGAGCTGTGGCACTCAGC
AGTTTCAGGAAGTTCAGCTGCACGACATTCACTGGGGACCCGTCGGCGTC
CACGTAGGAGA

2729. chr19_C19orf66_NM_018381_1.54893
GTGCTCACCCCAAGAGCCGGAAGCAGAACCACCTGCCCAAAGTGCTCCAC
CCCAGCAACCCTCACATTAGCAGTGGCTCCACTGTGG

2730. chr19_DNMT1_NM_001130823_1.51162
CATCTCTGGGATGTTATCATCGACTTCCTCATCGTCATCTGCCTCCTTCA

2731. chr19_ICAM4_NM_001544_1.82431
TTCTATGCCGGCTGAGCGAGAAAAAGAGGAATATGAAACAATCTGGGGAA
ATGGCCATACATGGTGG

2732. chr19_RAVER1_NM_133452_-2.11889
GTGACCATTAGGCCCGGGGCTGAG

2733. chr19_RAVER1_NM_133452_-1.5947
CTGGAGGGACGCGGATGGGCCCAGGTTGTTGAGCAGCTGCAGGATGTTGG
GCTCGGGGAGGAGTCCCT

2734. chr19_ATG4D_NM_032885_-1.58597
CTCCCAGCCGGTACCATGGGCCTGCCCGCTGGATGCCCCCACGCTGGGCC
CAGGGTGCCCCTGAGCTGGAGCAGGAACGCCGGCACCGGCAGATTGTGTC
CTGGTTCGCCGACCACCCCCGGGCCCCCTTTGGCCTACACCGGCTGGTGG
AGCTTGGGCAGAGCTCAG

2735. chr19_ATG4D_NM_032885_-1.60939

Figure 3-222

TGCTGTACCTGGACCCTCACTACTGCCAGCCCACTGTGGATGTCA

2736. chr19_SLC44A2_NM_020428_-1.51904
CCTGGAGAGGAATGACGGCTCGGCCGAGAGGCCTTACTTCATGTCTTCCA
CCCTCAAGAAACTCTTGAACAAGACCAACAAGAAGGCAGCGGAGTCCTG

2737. chr19_QTRT1_NM_031209_-1.53228
CGAGACGTGCCTGGCTTCGCCATCGGGGGCCTGAGCGGGGGTGAGAGCAA
GTCGCAGTTCTGGCGGATGGTGGCGCTGAGCACC

2738. chr19_LDLR_NM_000527_2.26488
TCTGGGCGACGTTGCTGGCAGAGGAA

2739. chr19_LOC55908_NM_018687_-1.78949
TCACGCTGACAAGCAGAGCCACATCCTATGGGCCCTCACAGGCCACGTGC
AGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGACAGATC
CAGGAGAG

2740. chr19_RAB3D_NM_004283_-1.58281
GGTCGTCGGCGAGCCTCCGGCCATCCTCAGCAGGCACAACACGTTCGTCC
TCCAGGTCACACTTGTTCCCCACCAGGATGACCTGGGCGTTGTCCCAGGA
GTA

2741. chr19_EPOR_NM_000121_-1.52433
TGGGAGAGCAGCGCGAGCACGGTCAGCAGCACCAGGATGACCACGAGGAT
GAGGGAGAGCGTCAGGATGAGGGGGTCCAGGT

2742. chr19_CCDC151_NM_145045_1.75571
CACTTGCATCGCCCGCAAGGCGCGCTCCAGCTGGTCCTTGGCCTCGGCGT
GCCGCCGCTCCTCCTTCTTGAGACGCTCCTGCGCCTCGG

2743. chr19_ZNF44_BC136502_-2.81123
TCCCCTGGTTTTTGTACTGCTCTT

2744. chr19_ZNF709_NM_152601_1.62152
CAAGTTAACAAAGGTTTCTTGCATC

2745. chr19_MAN2B1_NM_000528_1.57819
GGCGCTCAGGTTACGTCCGGAATCCTCTCCTACGGCAAA

2746. chr19_C19orf56_NM_016145_1.97388
GAGGCCGCACATGCTGAAGATCATGCCCAGCAGGTTCATGTAGTCCGGCG
TCGGGTCGTCCAAGGCCGGGTTACATTCGCTCGGCG

2747. chr19_TNPO2_NM_001136196_-1.62678
AGCGGCGGCAACTCGCGCTGCGGCTTCTCCA

2748. chr19_ASNA1_NM_004317_1.68029
GCAGTCCAGCTCTCCAAGGGGCGTGAGAGTGTTC

2749. chr19_JUNB_NM_002229_1.52475
GGAACAGCCCTTCTACCACGACGACTCATACACAGCTACGGGATACGGCC
GGGCCCCTGGTGGCCTCTCTCTACACGACTACAAACTCCTGAAACCGAGC
CTGGCGGTCAACCTGGCCGACCCCTACCGGAGTCTCAAAGCGCCTGGGGC
TCGCGGACCCGGCCCAGAGGGCGGCGGTGGCGGCAGCTACTTTTCTGGTC

Figure 3-223

AGGGCTCGGACACCGGCGCGTCTCTCAAGCTCGCCTCTTCGGAGCTGGAA
CGCCTGATTGTCCCCAACAGCAACGGCGTGATCACGACGACGCCTACACC
CCCGGGACAGTACTTTTACCCCCGCGGGGGTGGCAGCGGTGGAGGTGCAG
GGGGCGCAGGGGGCGGCGTCACCGAGGAGCAGGAGGGCTTCGCCGACGGC
TTTGTCAAAGCCCTGGACGATCTGC

2750. chr19_MAST1_NM_014975_1.5419
AAGAAGCGCAGCTCCCTCTTCCGGAAG

2751. chr19_GCDH_NM_000159_-1.54594
TGCCTGCAGCTCGGCCGCTTGAAGGACCAGGACAA

2752. chr19_CALR_NM_004343_-2.58735
GCAGAGCTGGCCGCGCCAAATAAT

2753. chr19_NFIX_NM_002501_-1.68021
CCAAGCGCCCCAAGTCCATCGATGACA

2754. chr19_CACNA1A_NM_000068_-1.69833
TAGGCTGGCTGTTGGGCATGTCGGTAGGGGGGCCTTGTTCCGGACTCCAT
GTGCCCGTCTTCTGGAACATCTCCTGGGCACGCTGGGTCACCCAGGACGG
GCTCTCCTTGAGGCCGCTTTCGTGAGCCAT

2755. chr19_CACNA1A_NM_000068_1.8194
GGAGGGGAGGGCGTTCTGGCCAGGTCCCCCTTCCTGCGTTGGGGACGGGG
GCTCCATGCGCTGGAACATGAGGGGTGTCCGGTC

2756. chr19_---_---_-1.67308
CCGCAGCTTCTTCCTCTTAGTCATTTTATCTTCCCCTTGAGAAAT

2757. chr19_DCAF15_NM_138353_1.59933
GCTCCCTGAAGGTTCTGGCGGACAGCGAGCGATATACGTGGATCGTGCTG
TGA

2758. chr19_RFX1_NM_002918_-1.50032
CCTGCTGGGTACCATGGACCGTCAGGGAGACCTGGCCACCTTTGCTGCCT
GGGGCTGCGCTCTGCACCACCA

2759. chr19_DDX39_NM_005804_-1.86295
GGAGGTGAAGCTGCATGCGGGCGGCTCCG

2760. chr19_PKN1_NM_213560_2.17963
AGGCCAATAACCCCTCGGAGCAGGA

2761. chr19_PKN1_NM_213560_2.11473
TGCTTCGGAGGAACCCAGAGCGGAGGCTGGGATCTAGCGAGAGAGATGC

2762. chr19_SYDE1_NM_033025_-1.72959
GGAGCCCGCCGGCGAGATCTGGTACAA

2763. chr19_ILVBL_NM_006844_1.67905
GGCAGCGGTCCCTCGGGCTGAGGCTCCCAGGCTCCTGCAAAGAGGTTGGC
CAGGTAATTCTCTAAATAC

2764. chr19_NOTCH3_NM_000435_-1.60353

Figure 3-224

AGTCGTAAGTGAGGTCGCCACTCTGCCTGCAGGTGCCCCCGTTACGGCAT
GGTGAGGGTGCACAGGGCACCGCGGGGTTCTCACATAGTGGCCCTGTGTA
GCCAGC

2765. chr19_AKAP8L_NM_014371_1.60369
CGGTTCCGGTTGTGATCCATGGTCTTCAGATGCTTCTGGATGATCCCAAA
CTGCATGGGAATGAAGAGGTCGCAGGCTGCACAATGGGCTGCCTCCACCT
TCTTCACAAAATGCTCCATGGCAATTT

2766. chr19_RASAL3_NM_022904_-1.5298
TTTGGGTGCTCAGCGACTCCACGAGGCGGGACAGCACTTTCTGCTCCTCA
CGCAGAGCGGCCACCTCGCACTGCAGC

2767. chr19_CYP4F22_NM_173483_-1.58833
CTTGGTCAGCATCTATGGAACCCACCA

2768. chr19_CHERP_NM_006387_1.5107
GGAAGTCGTCCTGCATGAAGCGGGGCGGGAAGCGGTTGAAGTTGTGGGGG
TGCGGAGGCTGGTTGAACTGCGGGTGCTGCTGGTGGGGCGGGAAGGGCCC
CCGGAAGTGTGGGGGCCGCTGCATGCGGAAGGGTGGCTCGCGCTGGCCCC
CGCCCCAGGGCGGCTGCTCGTGCTGGCTGTTCCAGGGGCCCTCGAACTGG
CTGTT

2769. chr19_CPAMD8_NM_015692_-1.51295
CTGTTTCCAGGAGAGCAACCACCACGTAGGCTGTCAGCGGGACAGTGCCG
TGGATCCC

2770. chr19_USHBP1_NM_031941_-1.56871
AGAGACCCAAGGATCTGGGTGCTGGAATGGCTGCGGAGGCGCCGAAGCAG
GGGGTGAGC

2771. chr19_FAM129C_NM_173544_-1.81621
CTTGGAAGTGCCTGTGAGCTTCCCGCTGTTCCTGCAGCACCCCTTCCGCC
GGCACCTCTGCTTCTCTGCAGCCACCAGGGAGGCACAGCATGCCTGGAGG
CTGGCCCTGCAGGGTGGCATCCGGCTTCAGGGC

2772. chr19_FCHO1_NM_001161357_2.35228
GCACCATGAAACGCCATTCTTCAC

2773. chr19_KCNN1_NM_002248_1.51321
ACAGCTACAATGGCAGCGTGGGGCGGCCGCTGGGCAGCGGGCCGGGCGCC
CTGGGACGAGACCCTCCGGACCCTGAGGCCGGCCACCCCCCACAACCCCC
GCACAGCCCGGGCCTCCAGGTGGTAGTGGCCAAGAGTGAGCCAGCCCGGC
CCTCACCCGGCAGCCCCCGGGGGCAGCCCCAGGACCAGGACGATGACGAG
GATGATGAGGAAGATGAGGCCGGCAGGCAGAGAGCCTCGGGGAAACCCTC
AAATGTGGGCCACCGCCTGGGCCACCGGCGGGCGCTCTTCGAGAAGCGGA
AGCGCCTCAGCGACTATGCCCTCATTTTCGGCATGTTTGGCATCGTCGTC
ATGGTGACGGAGACCGAGCT

2774. chr19_PDE4C_NM_000923_-1.54937
GCCCTCCTCCCACACGAGAGCCCATTTTCCAG

2775. chr19_LRRC25_NM_145256_-1.55463
TACGTAGAGACACCGGAATCCTAGCCCTGACCTCAGCCCTGTGGTCGCCC
TCGCCTCCACCGCCAGTGTTTATTATTA

Figure 3-225

2776. chr19_---_---_-1.6492
ATTCTGCAAGACCCCTCTGCCATGCCAGGGCACGCCCATTCCAGCTGGAG
TCGTGGGGCTGGGCACAGGGGAATTTTTCCAGAGCTGAGCCTGACGTCTG
CTCTGAAGAATGCTTAGAAGGTTCCCAGACACCAGA

2777. chr19_C19orf60_NM_001100418_1.71608
GGGATGCGCCGAGGGAGATGGGAAACGGGGCGGATGGCGCCCAGCCCAGC
CCTAACTGCCAGCTGGCTGGGGTTGCGCCCCACTGCGCTGCTGACCTTCC
TGCAGTTCCAGACACCTCCCACAATAAAGAGCTC

2778. chr19_COMP_NM_000095_1.55335
GCTCTGGCCCTGTCCGGACGCGCCGAGGGCAGCCAGGGTGAGCAGAAGAA
CGCAGGCGGTGTCGGGGACCAT

2779. chr19_GDF1_NM_001492_1.71949
CGGAGCGCAGGGCGGTCCAGCCCAGCGCGC

2780. chr19_ARMC6_NM_033415_-1.93019
TGCTGATCCGAAACCTGGTGGCCCACGGCCAGGCCTTCTCGAAGCCCATC
CTGGACCTGGGGGCTGAGGCACTCATCATGCAGGCCCGATCTGCCCACCG
TGACTGTGAGGACGTGGCCAAGGCCGCCCTGCGGGACCTGGGTTGTCATG
TCGAGCTCC

2781. chr19_SF4_NM_172231_-1.96425
GAGGGGCGCTGGGCGCACTGGTCGGGGCGT

2782. chr19_GATAD2A_NM_017660_1.60544
GCCCTCGCTCCAGCTGAACGCCTCCATTGCTGCTTGTTCTGGAGACCCCC
GCCCCCGCACCTTCCAGACTTAGCAGAAGAACAAACTGAAGAACAGACCC
AGCCAGAGAAGCAGGGATTCCAGAAGCTGCCCATTAAGGGAGAAGGA

2783. chr19_PBX4_NM_025245_-1.73628
GCCGCGAACGCAGGGTCATCACTGCCTCACAGGTGCTCTGCTTCAACTGC
ATCTGGATGGCGCTGAACTTGCCGTGAATGGCGCCGACCATGCGCTCAAT
CTCCTTAGGGGAGACAGGCCTCATCCTGCTCTGCTCCTGGAGGAGGTTGG
TGACGTGCGTGGTGAACTCAC

2784. chr19_ZNF254_NM_203282_1.53601
GCCTTTAATCGGTCCTCGCACCTCACCACAGATAAGATAACT

2785. chr19_C19orf2_NM_003796_1.76957
CCAAACGTAAACGAAAGAACAGCACTGGCAGTGGCCACTCTGCCCAGGAG
CTGCCGACCATCAGGACGCCTG

2786. chr19_SLC7A9_NM_014270_-1.72777
TTTTGGAGACTGGTGGTCTTAGGCTCTTGGCTCTGGATCGACTTCTCATC
CTCTCTCCGCTTTCTCAGGCCAGTAT

2787. chr19_RHPN2_NM_033103_1.71034
CCGCACGGCTTTCAGGATCTGCTGATTCAAAGCAGCTCTTTGATTCTGCA
ATTTACTCCGGCCGGTTTG

2788. chr19_GPI_NM_000175_2.15044
CCGCCCGGGAGCGGATGTTCAATG

Figure 3-226

2789. chr19_---_---_-1.59044
ACCACCTCCTTCATGCTCCTCTGTGATCACCTCTCCAAGTCCCGGTGTCA
GGAGCCTTCTCTGTGGCCGCCCTGGAGAGACTTGAGCCTGGGACGTGACG
TGCTGGGCTGTGAAGCTTTCTGAGAAGGGAAACCTGTGGCCTGACCTGCC
TGAATGCTGCAC

2790. chr19_GRAMD1A_NM_020895_1.50347
GAGAAGCTGCACCAAGGCATCACAGTCTCAGACCCTCCCTTTGACACCCA
GCCCCGGCCCGATGACAGCTTTTCCTGA

2791. chr19_FXYD5_NR_028406_-1.64043
CCATCCACGCCCACATCTCTCTGCCTCCTCTCCTGGGCTACAGTGGGCCG
CTCTGCCTCGCTCCCGCCCGCCT

2792. chr19_FXYD5_NR_028406_1.77655
CACTTTTTCCTCTGAGCGCGGGAGGCGTTACTCACTCTTCCTCCTTCCCC
TCCTCGCCGACTCCCGGGCTCTGGGCCCCTGGGGGAGGGAAGAGGCCTCC
TATCTACTCCTCTGCCCCAGTCCCCTCCTTGCGTCAGTCCCAGTGAGGGA
TAAGCGCCTGGCGGAAGGCGCAGGGAGGTGTTTCTCTGCTTCAGGAGTGC
CCGCCGGCCCTTGCAGCTGCTGGAAGACCCATTTATCTCATG

2793. chr19_USF2_NM_003367_-1.5151
CCTGCGATTACATCCGGGAGTTGCGCCAGACCAACCAGCGCATGCAGGAG
ACCTTCAAAGAGGCCGAGC

2794. chr19_ATP4A_NM_000704_1.51902
GGCTCGTTGACCAATCTGTCACGCTTTGGGTTGCGTGGACGCAGGTGCAT
GATGTCACTCTCGGCCTTTTCATATGC

2795. chr19_HAUS5_NM_015302_1.68064
GAGACCCAGGAACAGGTCCGCCTGCTCATCAAGGGAAACTCGGCCAGCAA
GACCCGC

2796. chr19_RBM42_NM_024321_-1.57612
AGTATGTGGGCTCGCGCCCCATCAAGCTTCGCAAGAGCATGTGGAAGGAC
CGGAATCTGGACGTGGTCCGCAAGAAGC

2797. chr19_ZBTB32_NM_014383_1.61286
GGGACAGGGCTAAAAAGCCAGATCCAGGCCTGAAGAAACATCAGGAGGAG
CCAGAGAAACCCTCAAGGAATCCTGAGAGAGAACTGG

2798. chr19_298_MLL4_NM_014727_1.52634
GTGGTCACCACTCCTGTTAAGGCCGAGGTGTCCCCTCACGGGGCTCCAGC
TCTGAGCAACGGGCCACAGACACAGGCTCAGCTACTGCAGCCCCTGCAGG
CCTTGCAAACCCAGCTCCTGCCCCAGGCACTACCGCCACCACAGCCACAG
CTGCAGCCACCGCCGTCACCACAGCAGATGCCTCCCCTGGAAAAAGCCCG
GATTGCGGGCGTGGGTTCCTTGCCGCTGTCTGGGGTAGAGGAGAAGATGT
TCAGCCTCCTCAAGAGAGCCAAAGTGCAGCTATTCAAGATCGATCAGC

2799. chr19_U2AF1L4_NM_001040425_1.5963
GGAGAGGTCCTGCCAGGAACATCTG

2800. chr19_U2AF1L4_NM_001040425_1.56371
GTTCTGGGAAATGGGCCGCAGATGCATGAAGTTGCAGAAGCCACCTCGGG

Figure 3-227

TACATTCC

2801. chr19_LIN37_NM_019104_-1.55083
CTGCAGATCCCGCATCCCATCTCCACTG

2802. chr19_C19orf55_BC110893_1.8734
ATTCCCCACCAGCTCTGATGGCCTCTCTCCCTTCTCGGAGACCTTCATCC
CTGACTCCAGCAAGGGCCTTGG

2803. chr19_PRODH2_NM_021232_1.92186
CCAGCAGCGAGAGCGCAGGGTTCAGTGAGGTGTACTCCGCATCCACCAGG
AGCCGCACGTGCTGG

2804. chr19_APLP1_NM_001024807_-1.8514
ACCTGCGTGCGGAGCAGAAGGAACAGAGGCACACGCTGCGCCACTACCAG
CATGTGGCCGCCGTGGATCCCGAGAAGGCACAGCAG

2805. chr19_COX7A1_NM_001864_1.58916
CCTTGTCCTCTTCCGCCGGAGTCACCTCCCTTCTCCGCCCAAGGACACGC
GTAGTCCTCCTCTGTCCAGGAACCCCAGGCCCCACCCGCTGCGCGCAGCG
TGACAGCTGGGGACGCGGCGGGGCTGGGGCTGGGGCTGGGGCTGGGTTGC
GGGGAGTCCTGCTCCTCGGATTCGTCCACCACGGAGGAGG

2806. chr19_ZNF568_NM_198539_-1.62745
TCGGCGCTTTAGGCGTCTGTCACAGACCTATCTGCGGGTCGCCTTCACCC
AGCATCTCAGAAACTGCGCGCGGGATGAACATTCGGGTGTTTC

2807. chr19_ZNF585A_NM_152655_-1.66749
CACTGGGTCTCAACCCTTTTTCTGTAGGGTGTCTGAAGCTTGGCAGTCAT
CTGTGAACTCAAGCAGAGCTGCTCTGAAGAGATGGGCTGGAGTCTAGAGG
AAAATCTGGC

2808. chr19_DPF1_NM_004647_-1.98608
GGGTGAGACCCGCCCAGCTGGCACC

2809. chr19_RASGRP4_NM_170604_1.53752
AGCTGTCGCAGAAGGTAGGCTTTCGGAAGGTGACCTCATGGAAGGTGTGC
AGGAAGGCCAGGCCCAACTTGGAGCAGATGGCGCTGGCCCGGAGCAGGTA
CCCTGTCAG

2810. chr19_RASGRP4_NM_170604_-1.53031
GTCTTGCAAGAGTAGGGCTCAGCTCCTCCCCTTGCCCAGGACTCCAGCTT
CTCAGCCCCTAGGGAGCTGGGGCCTCCTCGGTGCTTGGGAAGGAAAGA

2811. chr19_RYR1_NM_000540_-2.09495
AGAGACAGGTGCCATGGTGTCCTCCA

2812. chr19_RYR1_NM_000540_-1.75739
GGTGACCGAGCTCCTGGCAGGCATGCCCGACCCCACCAGCGACGAGGTGC
ACGGCGAGCAGCCGGCCGGGCCGGGCGGAGACGCAGACGGCGAGGGTGCC
AGCGAGGGCGCTGGAGACGCCGCGGAGGGCGCTGGAGACGAGGAGGAGGC
GGTGCACGAGGCCGGGCCGGGCGGTGCCGACGGGGCGGTGGCCGTGACCG
ATGGGGGCCCCTTCCGGCCCGAAGGGGCTGGCGGTCTCGGGGACATGGGG
GACACGACGCCTGCGGAACCGCCCA

Figure 3-228

2813. chr19_RYR1_NM_000540_1.53354
CTGTTTCACATGTACGTGGGTGTCCGGGCTGGCGGAGGCATTGGGGACGA
GATCGAGGACCCCGCGGGTGACGAATACGAGCTCTACAGGGTGGTCTTCG
ACATCACCTTCTTCTTCTTCGTCATCGTCATCCTGTTGGCCA

2814. chr19_MAP4K1_NM_001042600_1.65275
GCTGGGAGCAGTAGGATCATCCACTGGGCGTGTCTCCA

2815. chr19_ACTN4_NM_004924_-1.5058
CTCTCTGCAGTCCTCCGGGGTGGGTGGGTGGGCAGGGAGGGGCTGGGGCA
GGCTCTCTCCTCTCTCTCTTTGTGGGTTGGCCAGGAGGTTCCCCCGACCA
GGTTGGGGAGACTTGGGGCCAGCGCTTCTGGTCTGGTAAATATGTATGAT
GTGTTGTGCTTTTTTAACCAAGGAGGGGCCAGTGGATTCCCACAGCACAA
CCGGTCCCTTCCATGCCCTGGGATGCCTCACCACACCCAGGTCTCTTCCT
TTGCTCTGAGGTCCCTTC

2816. chr19_CAPN12_NM_144691_1.51232
TGCCAGCCTCAGCTCGTAGGAGTTCATGGTTCCAGA

2817. chr19_CAPN12_NM_144691_1.94952
TGTGTGTGCCCGTGATGGAATACGCGTGTCCCTTTACCAGGCCCTCTTCT
GTGCGGTACTCACCCCGATCA

2818. chr19_LGALS4_NM_006149_1.53391
GGAAGGCCGAGAGGCGATGGGCAAAGTCAAAGAGGTGCTGGCCATTGGCG
TAAAC

2819. chr19_ECH1_NM_001398_-1.8016
GTTGAAGGTCTCCTGGTATCGAGTGATGATGTCACGGAGGTACCAGCTGA
TCCGGGCCACATCATCTCCTTTGGGCTGCAGGATGTCCGAAGCCATGTCC
AT

2820. chr19_FBXO27_NM_178820_1.86042
AGGCACGGTTGTCCTGTTTTCCTCCACCACCCAGCCGTCCCCACCGTGTT
GCACCATCCACTTTCGGAGGCCTT

2821. chr19_FCGBP_NM_003890_-1.51382
GTTTGGAGTCAACGTCACCATCCCATCCTGGAAGAAGATGTGGACCTGGC
CCACAGCCTCCGTTTTGCCATGGCAGATCTGGACTTCGGCAACTACACGG
TACCAGGGGATGGTATTCTGTAGTCCTGGGCAGCGGGAAGAGAGCTCATA
GACACCAGGAGAGGTGGTGGCACCACGGGCCCCATCAAAGGTGGTGAGGT
TGGCACCCACAGACAGGACACAGAGACCACGGGTGGCCCAGCAGTTCCGG
GCTTCAGCCTTGACCTCACATACACGGCCTGGTGGGCAGCCAGCTGCCTG
GCATGTCAGGCCAGAGCTTGAGGAAC

2822. chr19_ZNF546_NM_178544_-1.52126
TAGGGATGTGTCCATAGACCTCTCCCAAGAG

2823. chr19_MAP3K10_NM_002446_-1.53896
TGGAGGCAGCAGCGTGCCCCCTTCCCCCTACTCGACCCCGTCCTACCTCT
CAGTGCCACTGCCTGCCGAGCCCTCCCCGGGGGCGCGGGCGCCGTGGGAG
CCGACGCCGTCCGCGCCCCCCGCTCGGTGGGGACACGGCGCCCGGCGGCG
CTGCGACCTGGCGCTGCTAG

2824. chr19_AKT2_NM_001626_1.5717

Figure 3-229

TCACTGGGGCTTGTGTGGATTAAAACCTGAATCTCCAACCGCCCAACAGC
CCAGGCCTGGGCGGGAGGTGGAGTCTTCCAAATGCGAGTCTGGGCACAAA
GGTG

2825. chr19_PLD3_NM_001031696_-1.77241
CCTGCAGAGGAGCCCGCCAATGAGCTGCCCATGAATGAGATTGAGGCGTG
GAAGGCTGCGGAAAA

2826. chr19_PRX_NM_020956_-1.74361
ACCAGCTCCACCTCGGGGATCTTAAGCTGCACAGCGGTGGACTCAGCCTT

2827. chr19_BLVRB_NM_000713_-1.5655
TGTACGCCCCAGTTAGTGGCTGGTCTC

2828. chr19_SPTBN4_NM_020971_-1.73252
GCGGGCGCAGCGGGAACAGCGGGCGGCGCGCATGACCTGTCCAG

2829. chr19_LTBP4_NM_001042544_-1.69478
CGAATGCCGGAACCGGTCCTTCTGCGGTGCCCACGCCGTGTGCCAGAACC
TGCCCGGCT

2830. chr19_ADCK4_NM_024876_1.71184
AGGCCCATCCTGGTAAAACTTTTG

2831. chr19_C19orf54_NM_198476_1.5494
CTCTTCTCCAGGCCGAAGACATGACGGGGAGCAGGCC

2832. chr19_CYP2B7P1_NR_001278_1.59404
CCGGGGAAAAATCGTCATCATGGACCCAGTCTACCAGGGATATG

2833. chr19_CYP2S1_NM_030622__1.50459
CAGAAGAGTTCAACCCAGACCGTTTCCTGGATGCAGATGGACGGTTCAGG
AAGCATGAGGCGTTCCTGCCCTTCTC

2834. chr19_---_---_1.55297
ACAGCGCCCAGAGCCCGGATAGAGAGACACGGCCTCACTGGCTCAG

2835. chr19_AXL_NM_021913_1.50775
TGCCATCTGCACGAGGTCAGAGCTGGAGGATTTCCTGAGTGAAGCGGTCT
GCATGAAGGAATTTGACCATCCCAA

2836. chr19_TMEM91_NM_001098821_1.54112
GACAGCCCTAGTCTTCGTGAGCTTCAACAGCCTCTGCTGGAGGGCACAGA
ATGTGAGACCCCTGCCCAGAAGCCTGGCAGGCATGAGCTGGGGTCCCCCT
TAAGAGAGATAGCCTTTGCCGAGTCCCTGA

2837. chr19_EXOSC5_NM_020158_-1.84107
AGCTCTTGGAGTAACGCCTCTGCAGCGATTCCCGGTAGAAACGGAAGACG
TGTTGCGAAGC

2838. chr19_ATP5SL_NR_030765_-1.65332
GGCTGTGTCCCGAGGCTGCTCCTCC

2839. chr19_CEACAM5_NM_004363_1.5623
ATTTCCCCTCTAAACACATCTTACAG

Figure 3-230

2840. chr19_CEACAM3_D90278_-1.54331
CCTGTCCCAAGCAAACCTGGGCAGACCCAGCCTTGACCAAGAATAGGAGG
GGA

2841. chr19_ARHGEF1_NM_199002_-2.0426
CCGGACCGAGAGAATCCTCAGTGACCTCCTGCCCTTCTGCAGACCAGGCC
CCGAGGGCCAGCTCGCTGCCACGGCCCTTC

2842. chr19_GRIK5_NM_002088_1.76533
TTTAGCTCGATGGTCCTCCTCCTTGGGGCACCGGCCCCCCTCCCACCACT
TGCGCTTCAGGATCTCCAGCCGGTTGTTCTCCTGAAGCTGCAGGATGGCC
AGTGTGATCTCATCCCGGAACGGGG

2843. chr19_MEGF8_NM_001410_-1.50166
GCGCCTCCCAGTGGTCGGTACTCACATGTAGCTGCGGTGCTTGGTGGCAG
CGTCCTGTTGGTGGCTGGGGGGTACAGCGGCCGGCCCCGTGGGGACTTGA
TGGCGTACAAGGTGCCC

2844. chr19_XRCC1_NM_006297_1.75617
TGCTGTCCCGGGTCCAGTCTGGCCGATACTTGGCCCCAAGCTCTAGGGCC
TTATCTCGCAGCTCGGAGCGGAAGG

2845. chr19_CADM4_NM_145296_-1.5958
AGCTCCTTGCGGTCCCGGTACCAGCGCAGGGTGGCAGCCGGACGGGACCG
CGGAACGAGGCAGCTGAGCTCCACC

2846. chr19_CADM4_NM_145296_-1.61654
TAGTACCGTGAGCGTGGCAATCTGGTGGTGGGTGTCTTCTGTGTAGAGCT
GGCAGAAATAGCCCCCCTCGTCCTCCAGGCGGGCATCTGAGAGCCGGATC
CGCACCCGGCGTGGGGAGAACTCCTCAAGCTGGAAACGCTCATCCT

2847. chr19_ZNF45_NM_003425_1.55566
GTGCCAGAAAATTGGAGGCCCGACAGAAGCCCTTCCCACACTCCTCACAT
TGATAGGGTTTCTCTCCAGTGTGGCACCTCTGATGGGCTTGAAGCTGTGA
ACCTACACTGAAGCCCTTCCCACACTCTGCACACTGATATGGTTTCTCTC
CAGTGTGAACTCTCTGATGCACCTGAAGGCTGGAGAACTGACTGAAGGCC
TTACCACACCTCTCGCATTTATAGGGTTTCTCTCCTGTGTGGATTCTACA
GTGTACATTAAGATCTGAGCTCCGACTGAAGCCCTTCCCACATGTACCAC
ATTTGTAGGGTTTCTCTCCAGTGTGGCCTCTTTGATGGGCCAGAAGATTT
GAGGCCTGGCTGAAGCCCTTGCCACACTCCTCACATTTATAGGGTTTTTC
CCCTGTATGGACTCTAAAATGAATGTTAAAATCTGAGCTACGACTGAAGC
CCTTACCACATGCATCACACTGATACGGTTTCTCTCCAGTATGGCCTCTT
TGATGGTCCAGCAGATTTGAGGCCCGGC

2848. chr19_ZNF223_NM_013361_-1.53328
TTAACCAGGCCTCAAGACTCTACCATAAAGAGCTCTCAGTTCTTTGAACA
GGGTGATGCCCACTCCCAGGTTGAGGAAGGACTATCTATAATGCACACAG
GACAGAAACCTTCCAATTGTGGGAAGTGTAAACAATCCTTCAGTGATATG
TCCATCTTTGATCTTCCTCAGCAAATACGCTCAGCAGAGAAGTCTC

2849. chr19_CEACAM19_NM_001127893_-1.9218
GGGCCAGGGATCTCTGTCCATCTTGTGCTCGGCTGTATCCCCAGTGCCTT
CAGTGACGCCCAGCACATG

Figure 3-231

2850. chr19_APOE_NM_000041_1.5091
GCGCAGCCTGCAGCGGGAGACCCTGTCCCCGCCCCAGCCGTCCTCCTGGG
GTGGACCCTAGTTTAATAAAGATTCACCAAGT

2851. chr19_NKPD1_ENST00000317951_-1.6288
GCGCTGTTGGCCCGGTGGGCAGCGTGGGGGGTATCGCGGGTAGG

2852. chr19_MARK4_NM_031417_-1.71403
ACGACGGGCCGGAGGTGGACATCTGGAGCCTGGGAGTCATCCTGTACACC
CTCGTCAGCGGCTCCCTGCCCTTCGACGGGCACA

2853. chr19_PPP1R13L_NM_001142502_1.66173
AGAGACCAATGTTTCCCACCCAGACCCCAAGACTGCTGGGAGAGATGGTG
TCAGCAGTGACTCCCAGGAATATCCAGTGGTGTGGTGGCCCATCCCAGGC
CCGGCTGGGCAGGTGGCTGGCTTGCTGGGGGATGTGATGATGGTGGTAGG
CATGGGAGGCACTTTGGACGGGAT

2854. chr19_PPP1R13L_NM_001142502_-2.0965
AGGAGGCGCGGGAGAGTCTGACCACAGCGACTCCAG

2855. chr19_OPA3_NM_001017989_1.54883
GGGCGAACTGACGATGACTTAGGTAGTAAAGGGACAGGCCGGTCCCTAGC
AAAGGCAACTGAAGAGGACAGCGAGGGAGGACCGGATAAAAGGACAGTAG
CAGTAGGTCCAGGACTGGGGACTGGTGACCAAGTGACTGAGCCTGAAAGC
CAGAATGGACTAGCCCTGGTCAAGACCGGTTTTTCCTCCCAAAAGGCCAC
GTCCTGCTGGAACAGACCACAGAATGCCGGGCTGGGAGGCGTTTCCCTGG
AAGACCCAGCATAGCCATGCCAGTGGGGTGCGCCATAGGTGGAAGAAGAG
GGGGGTTATGTTGGATCGATCCACTCAGGGAGGGGAGGATGTCAATGACA
GGTACTAAGATGGATTAAGGTCAGGAGCCGCAGGGTGGTGACTCATTGGA
GCTAACGCAGTCCAGGATTCAC

2856. chr19_EML2_NM_012155_1.6142
CAGACCACCCGCCACTGTAGCACAC

2857. chr19_QPCTL_NM_017659_-1.79077
ATTGATCGGAAGCCTCCCCGAAGCCCGGCTGCGGAGGGTGGTGGGACAAC
TGGATCCACAGCGTCTCTGGAGCACTTATCTGCGCCCCCTGCTGGTTGTG
CGAACCCCGGGCAGCCCGGGAAATCTCCAAGTCAGA

2858. chr19_SIX5_NM_175875_-2.03722
AGGACCTGGGAGACGAGCATGCTGGTGGGGAAGGTGGCGGTGAGGATGAT
CTTGCCCTGCTGCAGGGCCACACCCGTCACGATGGGGCTGCCAG

2859. chr19_FOXA3_NM_004497_-2.21903
CCCGGCTATAAAGCGTGGCCGCCTCCCGCGGCGCTCGGGACAGCCGTACC
CCGGGCGGTCGGACGGGCGGGCGCCGGTGGGAGCTCGGGCCGTGCCCGCT
GAGAGATCCAGAGCGCTCCGTTCCC

2860. chr19_IRF2BP1_NM_015649_-1.62451
CGACACACGGCCTCGCTGAAGTCCCACACCATGGCCCACGGCATCTTGGG
CAGGTCGCACAGGTAGCACCACTGGCGGCGGGACGCCTGCACAGA

2861. chr19_HIF3A_AK299699_-1.54623
CCACCACGCCCGACAGTAAATATGTTTTGAA

Figure 3-232

2862. chr19_CCDC8_NM_032040_-2.00324
CTGGAGGTCTCGAAGTCGCTGAACTCGCTGTCGCTGGCGTTGCTGCTGTC
GTACGTGCCCACGACCAGCCGGGGCGGAGGAGTCACCATCTGCTGCACTC
TCCTCCTCACTCGGGGCTCCTTGGGCTTTTTGGGGGGCTGGGGCGGGTGC
GGGGTGCTCTTCTCCATGATGCGGGCCACGTCCTCCAGGGTGCGGCCCTC
TTCTTCCAGGAACTGGGTCAGCCGCTCCCGAAATTCTGCTTCCTTGGTGG
CGGGCTTAGAGATGACTCTCCAGACGCCCCCAGCCAGCCTGACCTCCCGG
GGGATGAGCAAATAGTCGACGTCCTCCCC

2863. chr19_PRKD2_NM_016457_2.25433
CAGTAGCGGTGGCGGCGACTGCAGC

2864. chr19_STRN4_NM_013403_-1.52208
CCTCCATGTCATACAAGACGGTGTCGCCAGAGCGGAAGGAGGCCACGATG
TGGGCAGGCTCGGTGCTGGTGAAGGCCACTGAGGTG

2865. chr19_BBC3_NM_001127240_-1.50654
CATTCCGGTATCTACAGCAGCGCATATACAGTATCTTACAGGCTGGGCCA
TCCCTCCCCACTCCCAGACTCCTCCCTCTTCCGAGATTTCCCCCCCTCCC
TGACTCCCCGTCTTCCCCCCAGCGCTTGGCCCTGGGGACTAAGGCTGGGG
CGGCTTCAGCCAAAATCTCCCACCCCCCAAATGAATGCCAGTGGTCACAC
GTGCTCTCTCTAAACCTATGCAATGGGATTGATGGGGCGGGGGGCGGTCA
CGGGCAGAGCACAGGATTCACAGTCTGGGCCCCTCCTGGCCACCCCCTGA
TGAAGGTGAGGCAGGCATGCCCACCACCCGCCGGCTGGCTCAGGGAAGAT
GGCTGGGCGCCGGGCTGGAGCAACCGGCAAACGAGCCCCACTCTCTGGCT
CCAGGAGGCTAGTGGTCACGTTTGGCTCATTTGCTCTTCACGGGC

2866. chr19_CCDC9_NM_015603_-1.54316
TGCGGTCGCAGAGGCCGACGGAGCCGGAGTCGCGGACGCCGC

2867. chr19_CCDC9_NM_015603_-1.77411
CTGCCCATGAACCATCCCACCGCTATG

2868. chr19_PRR24_NM_178511_2.06407
TGCCGTGCTGCTCGCCGTGTACTACGGTCTCATCTGG

2869. chr19_DHX34_NM_014681_-1.73727
CATGGTTGCTCACTCCCGTAATAAAAAAATA

2870. chr19_DHX34_D50924_1.7116
GCCCCATCAGAGGGGACGTGCTGGGTGT

2871. chr19_NAPA_NM_003827_1.55512
AGAGAGAGAAACCGGCCTCATGACTCAGCTGGTCAGGAGATAGGGGGCCA
GATGCTGACCCCAAATCCCCGGCAGCACCCCTAGCAAATAGGTCTGTATC
AAAGATTCTGTACAGCTGGTTTTGGGGGTGAAGGGCACCTATGGGGGCTT
AAATAAATGGACAGGGGGCAAGGGATGTAGCGAGAACAGAGGGTGACTGT
CCGGCCAGCAGCCTGGGCCTCTGGCGCCCCTGCATGCTGACCCCCGGTGC
CACCTGCCCACTGTGGCCCGCGGCACTCCCCAGATGGGAAAGGAGGGAAG
CTCTCCAGCAAG

2872. chr19_GLTSCR1_NM_015711_1.64555
CCCAGCCGCCTGAGGGACCGCTGCCC

2873. chr19_LIG1_NM_000234_1.65424

Figure 3-233

TTCCTGAATGGTCCGTTTCGGGAGCTGCT

2874. chr19_CCDC114_NM_144577_1.97674
TGGGCATGTAGGAAGGCCTGCACT

2875. chr19_CYTH2_NM_017457_1.59792
CTTGGTGGAGAATGAACTGCTGCAGAACACACCCGAGGAGATCGCCCGCT
TCCTGTACAAGGGCGAGGGGCTGAACAA

2876. chr19_CYTH2_NM_017457_1.61124
TTCTATGGAGCTTTCGCCTACCCGGAGAGGCCCAGAAAATTGACCGGATG
ATGGAGGCCTTCGCCCAGCGATACTGCCTGTGCAA

2877. chr19_SULT2B1_NM_004605_1.55662
GAAGAACCACTTCACGGTGGCCCAGAGCGAAGCCTTCGATCGTGCCTACC
GCAAGCAGATGCGGGGGATGCCGACCTTCCC

2878. chr19_SPHK2_NM_020126_1.57931
TGGGGCCGCCACCTACGAAGAGAACCGTGCCGAGGCCCAGCGCTGGGCCA
CTGCCCTCACCTGTCTGCTCCGAGGACTGCCACTGCCCGGGGAT

2879. chr19_FUT2_NM_000511_1.96182
CTCCGATGGGTAGGAATTGTCACATACCCATGTGACCCGATAGGAGGCAA
AAGAAATGAGACTTCTGGGATTAGTTTAGCCTCAGATTCTGCAGCTGAGA
AGTTGATCAGCCACCTCTGAAGGACATGCAGCTTGCAGAAAATTAGGGTG
GTGTTACCAAGGTGAAAAGGGGAAATGGCTTTAGAGTAGACAACAGAGAT
GCCCTGAGGGGTTGTGTAGGTTGTTCACTGCAGGAAGTCCCCTGGTTAAG
AAGGCAAGTGGGGTTTAAACAGACCCACAGTCTACTCATCAAACCAGGTG
TCCTTGGCATTGTGTCCACCCAGAGAGC

2880. chr19_PLEKHA4_NM_020904_-1.87589
TAGCCAGGGCTTGGGAGAGGCTGAGAACCCGCTCC

2881. chr19_PLEKHA4_NM_020904_1.60682
GAAGCCAGCCTCGGATGTGCACGGGAAGGTTGGGATCCCTCCTGAGCGCA
TTGCCTCTCTTCCCAAAGGCGTGGAT

2882. chr19_RUVBL2_NM_006666_-1.88431
ATCCGGGGCACCAGCTACCAGAGCCCTCACGGCATCCCCATAGACCTGCT
GGACCGGCTGCTTATCGTCTCCACCACC

2883. chr19_DKKL1_NM_014419_-2.15196
TGCCCCAAGCACCATATGGAAATAA

2884. chr19_ALDH16A1_NM_153329_1.71428
GGGCACTGTCTGGATCAACGCCCACGGCCTCAGAGACCCTTCGGTGCCCA
CAGGCGGCTGCAAGGAGAGTGGGTGTTCCTGGCACGG

2885. chr19_RCN3_NM_020650_1.50881
GCGGCTGAGCAAAGCGGAAATCCTGGGTAATTGGAACAT

2886. chr19_SCAF1_NM_021228_-2.02151
AGAAGATGAGTCTCGAGGGAAGACAGAGGAGTCGGGGGAGGATCGGGGCG
ATGGTCCGCCAGACAGAGACCCCA

Figure 3-234

2887. chr19_SCAF1_NM_021228_1.56263
GGCTTGTCGGGAAGGCAAGGTCTCGGTGGAGGTGGTGACCGCTGGTGGAG
CCGCCCTCCCGCCGCCCCTGCTGCCGCCCGGCGACTCGGAGATCGA

2888. chr19_CPT1C_NM_152359_2.06268
ACTTCCTGTATGTCACACCCACGCCTCTGCAG

2889. chr19_PTOV1_NM_017432_-1.5233
TCCTACAAAGCATCGTGTGAGATCCGCGTGCTTATG

2890. chr19_PNKP_NM_007254_-1.58043
GTGTTGTCGATGGCGACCCGTTTCCCTTGCTTCAGGGCTGTCTCACACGT
GGTCACACAGCGCTG

2891. chr19_AKT1S1_NM_032375_1.58855
TCATCTGATGACCGCGCCTCTGTCCTCTTCTCCTTGAAGCCCCAGACGGG
CACAGACACAGGCAGGGACTTGGCGTACTGCTGTGTGGGTAGGGCT

2892. chr19_TBC1D17_NM_024682_-2.29864
GGGCCTACCTGGTTCTGGTGACCCAGGCTGGAGGTTCCCTGCCCGCACTG
CACTTCCACCGCGGGGGCACCCGCGCCCTGCTCCGCGTCCTCAGCCGCTA
CCTGC

2893. chr19_MYH14_NM_001077186_1.76583
GAAGGCAGCTGTACTTCGGGCAGTGGAGGAACGTGAGCGGGCCGAGGCAG
AGGGCCGGGAGCGTGAGGCTCGGGCCCTGTCACTGACACGGGCA

2894. chr19_POLD1_NM_002691_-1.76563
CTCCGCGCCTTCGGGGTCACCGATGAGGGGTTCTCTGTCTGCTGCCACAT
CCACGGCTTCGCTCCCTACTTCTACA

2895. chr19_POLD1_NM_002691_-1.71864
ATCAGGACCCCCACCGGGGACGAGTTTGTGAAGACCTCAGTGCGGAAGGG
GCTGCTG

2896. chr19_SYT3_NM_032298_-1.64916
TGCCAGTGCTCCACGGGCTTGCGGGGATTGGCCAGCATCTCTGCCCAGTG
CTCGCGGCCGTGCGGGTCGGCAGCGTCGGGGCCCACACGGCACACGCCGA
TCACCTCGTTGTGCCCGATG

2897. chr19_SHANK1_NM_016148_1.54542
GGCGGGGGAATGTCCTCCGAACCAGGCACAGACAGGCTGCGGCTGAATTT
CATGGCTGGGGGTGCTAGGTAAGGTCTGTCATCT

2898. chr19_SHANK1_NM_016148_-1.64396
GATTTTTGCCGGAGCATCAACCCAGGTCCTGGAGGCAGGAAAGAAGGACG
CTCGTAACTTGGCTGGGCA

2899. chr19_SHANK1_NM_016148_1.72824
TGTAAACTCGGGTCTTGTATCGGAA

2900. chr19_KLK1_NM_002257_-1.5498
GTGCTGAAATGGTACAGAGCCGCCTGCCAGGGCTGGGAATGCTGCTCACA
CTCCCAGCCTCCCACAATCCGGGACTGAATCGGGGGC

Figure 3-235

2901. chr19_KLK12_NM_019598_-1.56537
CAGCGGTTGCACAGTCATTGGGCAGGGGCAGGGGTTGAACGCTGCTGGTT
ACGCGGACGGGCAGGCGCAGCCGCAGCAGCCGGAGGTCGTGCTCGTGGCT
CGTCGAGGCTCCCAGGTAGCCGGGATGGGTCACAGAGAAGCCGCTGTGCC
GGATCTGCTCGGTCCAGTCGAGCTGGCTGA

2902. chr19_CD33_NM_001772_-1.73972
GGGCAGGAATGACACCCACCCTACCACAGGGTCAGCCTC

2903. chr19_SIGLEC12_NM_053003_1.50856
ATCGACCGTGGGTATCCTCTTGCACTTTTCCACTTGGGGTGTTTGTGGCC
ACTGGAATATCCCATGGTATATCGGCCCCTTCCTTGAACCAGGATCCATA
AACAGGGCTAGAGGCAGTCCAGTTGTAATGGGGGTAAAGGACACTGCAGG
GCACAGAGACACACAGACCCTCCTGCACAGTCACCGACTCTGGCACCTCC
AGCCTGTATCTTGACAGTAGGTCCTGG

2904. chr19_ZNF701_NM_001172655_-1.68737
GAGTAGTACAGAGCGACATGATCA

2905. chr19_ZNF702P_NR_003578_-1.53927
ACACTACTGCTAACATGGCCAAGCACATGGATGCTCCAGCATTTTCTCAG
CTTCCTGCTTTGTTTTCTTGATCTGTCCCCATGTTATGGGGGTGGATGTC
AGTGTGACTCCAGTCGGCCCTTGCTCCATCTTTGCATTCAAATTCAGCTG
GCTCACGACTCCTACTGGAGGGACCAGGTCCACGGTTGGCCAACGTGGGT
CCTGCTAGTCTCCCATTTCAT

2906. chr19_PRKCG_NM_002739_-1.60407
TGAACGTGCACCGGCGCTGTGTGCGTAGC

2907. chr19_TMC4_NM_001145303_1.85257
GCGCGCCGTGCCAGGAAGACTTTATTCT

2908. chr19_TSEN34_NM_024075_-1.52351
TAAGGTGGTCTACACCTCCCTGCAATGG

2909. chr19_LILRA5_NM_021250_-1.67137
CAAGGTCCAGGAGAGCTTGTGGTCTCCTTCCTCAGTCAGAATGAACCTGT
CGAATCTCAGCCGTGAGCCACACTG

2910. chr19_TTYH1_NM_020659_-1.54125
AATCCAAGCGCTTTGTGCAGTGGC

2911. chr19_CDC42EP5_NM_145057_1.50916
TAGAGGCCGATGACGTCGTTCAGCTCGAGGTCCGCGTTGGGGCGGCAGCG
GGCCTGGGGGGGCTGCGTCCCGGGGCGGGGTTCCGCGTCGGGCTTGGCGG
CAGCCGCCTCCGGGCGCGCCGCGTCCATGACGCCCAGCACCGCGTCCAGC
AT

2912. chr19_LILRB4_NM_006847_1.61288
CTCACCCACAAGGTCCGTCTCAACA

2913. chr19_NCR1_NM_004829_1.53593
GGTTCATCCTGGACCCGAAGTGATCTCGGGAGAGAAGGTGACCTTCTACT
GCCGTCTAGACACTGCAACAAGCATGTTCTTACTGCTCAAGGAGGGAAGA
TCCAGCCACGTACAGCGCGGATACG

Figure 3-236

2914. chr19_GP6_NM_001083899_-1.73151
ATAACCCGCGGCTGTGAACATCCTGTCGGCCTCCATC

2915. chr19_RDH13_NM_001145971_1.72752
AGGTGGAGCCATGGATGCCCGTGTGTCTGCCCAGCTCTGTCCTGGCCACG
CCGGGGTGCAGGGCGTTGACAGTCACACCAGAGC

2916. chr19_C19orf51_NM_178837_1.7788
GTCAGGCCCTCAAGGGCTGGGTTGCTGGCTTCAAGAGGCTGGGCCAGGAT
GTCAAGGGGCGGAGTTCCGGGTTCCACAGCTGGGAC

2917. chr19_PTPRH_NM_002842_1.88347
TCAACGGCCGACTCTCTCTCATCTTCCTTACAAAGCTGAAGGGCCCAAGG
AGACCCTCGGACTGCAGCTGCCGGAGCAGGACGTCCAGGGCAATGAGGGT
TCCTGTGCGACCCACG

2918. chr19_BRSK1_NM_032430_-1.51845
CCCAGCCGTCGGTTCAAGCGAGTGGTGGAGACCATCCAGGCACAGCTCCT
GAGCACTCATGACCAGCCCTCCGTGCAGGCC

2919. chr19_SUV420H2_NM_032701_1.52579
CAGCATCATGTACTCAACCCGCAAGCGGAGTGCTCAGCTGTG

2920. chr19_COX6B2_NM_144613_1.66707
AAGCGCGGGTCGAAGGGCGGCGTCGACCATTTCC

2921. chr19_SHISA7_NM_001145176_1.73958
GGTCCCAGAGTGGGTGGTCATCTCTGGTGATGA

2922. chr19_U2AF2_NM_007279_1.6513
AAACCTTTGACCAGAGGCGCTAAAGAGGAGCACGGTGGACTGAT

2923. chr19_ZNF551_NM_138347_-2.55324
ATGGAGAATGAGGCGATAGCTTCT

2924. chr19_ZNF154_NM_001085384_-1.64536
CTGGAGCTGTAGGGAAAGAACTTCCCACATTCACTGCACTCATAAGGCCT
CTCCCCAGTGTGAACTCCCCGATGTTGAAGGAGTGCAGACCTTTGGCTAA
AGGATTTCCCACATTCGCTGCACTTATAAGGCCTTTCTCCAGTGTGAACC
CTATGGTGTTCAATGAGGCTAGAGTTTTGGCTAAATGACTTCCCACATTC
GCTGCACTCATAAGGCCTGGATCCACTGTGAACTTTCTGGTGTTTTATGA
GACTGGAATGATATGTAAAAAACTTCCCACATTCACTGCACTCATAAGGC
CTCTCCCCAGTGTGAACTCCCCGATGTTGAAGGAGTGCAGACCTTTGGCT
AAAGGATTTCCCACATTCACTGCACTCATATGGCCTTTCCCCAGTGTGAA
CTCTCCGATGTTTAATGAGGTTAGACTTGTTGCTAAATAATTTTCCACAT
TCATCACATTCATGAGGTCGTACTGCAGTGTGAACTCTCCGGTGCTGAAT
GAGACTAGAGCTTTGCCTAAAGGACTTCCCACACTCTCGACATTCATAAG
GCTTTTCTCCAGTGTGAAGTCTCCAATGGTCATTGAGACTGTAGCTTTTG
CTAAAGGATTTCCCACATTCACTGCATATGTAACATCTTTCTGTAGTGAG
GGTTCTCTGCTGCTGAACAAGTGTGTGTTTACCGCTGAATGCTTTTGTGT
GTTCTCCACAGTTGTAATGAGTTTTTCCTCTGTGACTGATGGCCCCACCG
TCGCTTTTGCTATTTGATTGCTCCCCAGTGTGAGCAGCCTGTTGATGGAG
AAATCCCAACTTGGCCAGGAAGTCCTTCCCAACTTCTCTGCAGGTGGAAG
GCTCCCCTGACACATGGAATGTGCAGGTCTTCACAAACAAGGCTCTGCCC

Figure 3-237

ACATTGCTTCTGAAATGTTTTTCTCCAAGGTGCTGCTTCTGATGATGAAC

2925. chr19_ZSCAN18_NM_001145542_-1.84156
TTCCCGCGGGACAAGCCCGGCTCGTCAGCCCCA

2926. chr19_ZNF274_NM_016325_-1.71033
ACCCCGGAAGAGTGGGGACTGCTGGACCTCAAACAGA

2927. chr19_ZNF274_NM_016325_-1.64252
ACAGAGGACCGAGTACCGCGATGTGAT

2928. chr19_ZNF8_NM_021089_-1.69066
TCACGCAAGGAAGAGGGCCTGCCTGAAGAGGAGCCATCCCATGTCACGGG
AAGGGAAGGATTCCCGACAGATGCTCCTTATCCCA

2929. chr19_ZNF446_NM_017908_1.67224
ACTTGCAGCACAGTCCCCTGAGGGGAACCATGGACACCAAGAACCAGCCT
CCACATCCT

2930. chr19_ZNF446_NM_017908_-1.61837
GGCTTCGACTGGAAGTCAGTGTTCGTCATCCACCACCGGACACACACGAG
TGGGCCAGGTGTGCAGTCCCCGGGGCTAGCCACCGGGGAAAGCACAGAGA
A

2931. chr20_C20orf96_NM_153269_1.55122
AATCAGAAATTCCCACCTGGCCCAGCAGCACCAACCAGAAAGAAGGGAAG
AAGAGAGGAAAAAACCACAGGAAGAAAGAAAGGAGGGAGGGAGGGAGAGG
AGGAAGGAAGGAGGAGGGAAGGGAAGGGGGGAAGAAGGGAGGGAGGGAGG
GAGGGAAAGAAAGAGGGAGGAAGGGCAGAGGGAGCAGGGAGACTGTAGAT
CAGGGTCTGAATGGAGATCCGGTCCTGGAAGTAAATGATCCAAGGCTCCA
GGTGCTGGGA

2932. chr20_NRSN2_NM_024958_1.60197
ACATGGCCTAAGATGTGGGTCCTGGATCCTTCCCCCCTTCTCACCATAAC
CCCCTCTCA

2933. chr20_SDCBP2_NM_080489_-1.58249
ACCACGACAATCTTATCGCCTGATGCCTTCTTCACCACCTGATGGGCTTT
GTGCGAGCTCCACCCAGCACAGTCACGCCCGTCAATCTGCAGG

2934. chr20_SDCBP2_NM_080489_1.90367
CTTGGTCCACTTTTAGGTCCTCTAGAGATGGGTACAGG

2935. chr20_TGM6_NM_198994_-1.69947
CAGCAACAACGACCGAGGTGTGGTGCAAGGACAGTGGCAGGGCAAGTACG
GCGGCGGCACCAGCCCGCTGCACTGGCGCGGCAGCGTGGCCATTCTGCAG
AAGTGGCTCAAGGGCAGGTACAAGCCAGTCAAGTACGGCCAGTGCTGGGT
CTTCGCCGGAGTCCTGTGCACA

2936. chr20_SNRPB_NM_198216_-1.99303
TAGGGCCTTGGTGGGCGCATTCCCGG

2937. chr20_IDH3B_NM_006899_1.55368
CCTTCATGGAACTCAGCACCTGCT

Figure 3-238

2938. chr20_OXT_NM_000915_-1.54708
AGCCTCGCTTGCTGTCTGCTCGGCCTCCTGGCGCTGACCTCCGCCTGCTA
CATCCAGAACTGCCCCCTGGGAGGCAAGAGGGCCGCGCCGGACCTCGACG
TGCGCAAG

2939. chr20_HSPA12B_NM_052970_-1.52888
CGGCCAACGAGCTGCGGGCCCGGGATCGCGGCGGCTGGACGGGGC

2940. chr20_ADRA1D_NM_000678_1.68894
AAATATCGGTCTCCCGTAGGTTGCTGTAGTCGGCCAATTCGTAGGCCTGG
CAGGTGGCGCCCTCGGCCACCTCGTGTGGGACG

2941. chr20_RASSF2_NM_014737_-1.78082
TGAATGAAGCTTTTAAGTACCGGCATCTCGAACTTTATATACTG

2942. chr20_RASSF2_NM_014737_-1.64645
GAATGCGTTCGTTGTCATCCTGCATCTGCAGGCGAATGGGCCGGCGCAGG
CCCCAGGAGATGTTCAGGAGCCCCTCCACAATGAACTCGT

2943. chr20_C20orf7_NM_024120_1.64578
GAGGTTCCGCAACTGTGTCATTTGG

2944. chr20_PCSK2_NM_002594_1.53051
TGGGAGCTGGGATACACAGGGAAAGGTGTTACCATTGGAATTATGGATG

2945. chr20_MGC44328_BC033985_1.50122
CTGAGGCATTCTTGGGCCACATAGCAGTTGACTGCCCTCTCCACCATCTT
TTCACAAGTGTTAATCCCAATAAACACCCATCCTCTTC

2946. chr20_C20orf12_NM_001099407_1.64146
CCAGTAAAGTGGCGGTGCTCTCTCTTCCT

2947. chr20_SEC23B_NM_006363_-1.86575
CATCATGATCCAGCCCATTCTCTA

2948. chr20_SLC24A3_NM_020689_-1.65097
TGTTCGGCGTCCACCTGAACAAGTGGCAGCTG

2949. chr20_RIN2_NM_018993_1.62771
AGCAGAGGGCGGTGCAAAGACCTTGAGCGGCGGCCGGCC

2950. chr20_CRNKL1_NM_016652_1.63089
CCTCCTTGCGGCAGCGCGTGGAGTGCGGCGTCCTGGAGCTGCGGATGAGG
TGGGTAACGCCGTGCTGACTAGCAGCGACGCAAGGA

2951. chr20_NKX2-2_NM_002509_-1.53119
ACTGAAGGCCCTCGGTGCTGGCCAGCCAGCGCGTGTACGGGTTGTCGCTG
CTGTCGTAGAAGGGGTTCTTCAGGGGCAGGCTCTGCACCGCGTCCAGGGC
GCCCTGCCCCAGCGGCCCGGCCCTCTTGGCTGGCTCGGGCCCCTCGTTCT
CTTCCTCCGGACCTTCGGCCACAGAGCCCTCCTCATCGTTGGTGTCC

2952. chr20_CST8_NM_005492_-1.71703
TGCCGGTGGCTCTCCCTGATCCTCCTCACCATTCCCCTGGCCCTGGTGGC
CAGGAAAGACCCAAAAAAGAATGAGACAGGGGTGCTGAGGAAATTAAAAC
CCGTCAATGCCTCAAAT

Figure 3-239

2953. chr20_PYGB_NM_002862_1.5954
CCTGCGCAGGATGTCTGTGATCGAGGAGGGGGACTGCAAGCGGATCAACA
TGGCCCACCTGTGTGTGATTGGGTCCCATGCTGTCAATGGTGTGGCGAGG
ATCCACTCGGAGATCGTGAAACAGTC

2954. chr20_ABHD12_NM_001042472_1.88953
GGCACCACCGGGTCGTCCTCAGCGTGCAGGATGAGCAGGGGAC

2955. chr20_GINS1_AK294593_-1.86833
TATATGAGGTCACTGGGAGGAGAT

2956. chr20_NINL_NM_025176_1.50748
GGTAATGAGACCAAGCCTTGCTCGGTTTAACCCGAGTGGAAGACTCTAGA
AGTAGCGCGGGCTCATGACTGAAGAGGCCAAGCTGGAATTCCTCAAGACT
CACTTTGCCG

2957. chr20_HM13_NM_030789_-1.54943
TGGAGTCGGATCCCGAACGCACCCTCGCC

2958. chr20_HM13_NM_178580_1.82886
AGCTAGCTGGCCCTCGCCGCCGGCGC

2959. chr20_DUSP15_NM_080611_1.64366
GGAAATGGTGGTGGAGCCGCCGCTG

2960. chr20_TSPYL3_NR_002781_1.66159
GGCGCCCTCCTCCTTGTTCGCGTCCTCGGC

2961. chr20_DNMT3B_NM_006892_1.53587
CTTCTTCACCAGTGACACGGGGCTTGAATAT

2962. chr20_BPIL1_NM_025227_2.21424
GAAGCTTCAGGGGACCACGTCTGT

2963. chr20_BPIL3_NM_174897_-2.71704
ATGCTCCCCAAGATGGTCAACAAG

2964. chr20_BASE_NR_026760_-1.70416
TGCTGAATGTCTCCGGCCTCTTTGTTCTCCT

2965. chr20_NECAB3_NM_031231_-1.78152
CGGGCGCGAGCTGGGGGTGCCGCG

2966. chr20_AHCY_NM_000687_1.67789
TGATGCGGCGCCCATTCTTCAACCGATACCGGTCCAC

2967. chr20_CEP250_NM_007186_1.56152
CAAACAGTCAGAATCACTCAGTGAACTGATCACTCTTCGGGAAGCCCTGG
AGTCAAGTCACCTGGAAGGGGAGTTACTGAGGCAAGAGCAAACGGAAGTG
ACCGCAGCGCTGGC

2968. chr20_CEP250_NM_007186_-1.79376
GGCGAGAAATGCTTTGCAGGTCGACCTGGCGGAGGCAGAGAAGAGGAGGG
AAGCCCTGTGGGAAAAGAACACTCACCTGGAGGCTCA

Figure 3-240

2969. chr20_EPB41L1_NM_012156_1.71145
GGAGGGAGTTCATAGCAACCACTCCCTCCATCACCACGGAGACCATATCG
ACCACCATG

2970. chr20_EPB41L1_NM_012156_-1.59478
CTGCTTGTGCCAGGGACTATTCTCAGGCTGAAGAAGGTGGGAGGGGAGGG
CGGAACCTGAGGAGCCACCTGAG

2971. chr20_DLGAP4_NM_014902_-1.52501
GCCTAGTGGCGTATAAGAAGACCCCGCCACCGGTCCCTCCACGCACCACT
TCAAAGCCGTTCATCTCAGTCACAGTCCAGAGCAGTAC

2972. chr20_MYL9_NM_006097_-1.78265
GGCCCAGTTCCACGCACCCAGCGAGCCCAAGCGCCTTCTCCGCACCAG

2973. chr20_SLA2_NM_032214_-1.68138
GCGGTGAGATGTACAGCCAGCCATTGTCAAGGCAGTGGATCCTGTAGTGT
CTGATCCGGTCCCAGGATGCAGGGCGGCTGAGGCGGACTGACAGAGAGTA
A

2974. chr20_SLA2_NM_032214_-1.71325
ATGGGAGACTTTGGCCACGTGGACGCTGGGGATGTTATACTCTCTGCCTG
AGACTTCAGACAGCACCGTCCACCAGTCTCCA

2975. chr20_C20orf117_NM_080627_-1.77835
GGTCGGGCTTAGAGTCCAAGTCACCAGTGCGGAAAGCCTCTCGGATCCTG
GGCTCCCATTCCGGCAGGTCCCTGAAGTCA

2976. chr20_VSTM2L_NM_080607_1.53014
TCCTGGCGAGTCCTTCCTGTTCAGCTCCCTGTGCGACCCTCCAGGGATGC
AGGGGATCCAGGATTCTCTGCCCTGTCACACGGCGAGTCAGAAGGGAGGG
GCCTTTCCCTCGGACCCATGGCCCCAGGCAGAGTTTTGCACCAGCAGGAC
C

2977. chr20_TGM2_NM_004613_-1.7682
GGCCAATGATGACATTCCGGAAGCCCTTCACAGCCTTCAGCTTGTCGCTC
TCGAAGTTCACCACCAGCTTGTGGAGGCCCATGTGGAGCGGCA

2978. chr20_PLCG1_NM_002660_-1.60742
AGAACAGTGTGTGGAACTCGCAGCTGGATGCAGTATGCCCGGACACCATG
AACAACCCTCTTTCCCACTACTGGATCTCCTCCTCG

2979. chr20_PLCG1_NM_002660_1.52742
CCAAGAAGGACTCGGGTCAATGGAGACAACCGCCTCTAG

2980. chr20_ZHX3_NM_015035_-1.55953
GCAGGGAAGGTGCCTAGAGTCCCCAC

2981. chr20_PTPRT_NM_133170_1.56486
CGGGGTCACCTGGGCGCTGCCCAT

2982. chr20_PTPRT_NM_133170_-1.50314
TCGTGTGAGGAGCACTCGGATCTCATACTCAACATCGGGGTCCAGATGCC
ACAGCTTATAGTTGGGAGAGTCGACTATGTGGGTCTCTGCCCACGTGCCT

Figure 3-241

GTGGTGGTGCGATATTCCACTTCCTTCAGGATGATGGGGCCATCCCCGAT
GATGGAGTTGGCATTTGGCTTGATCCACAGGTAT

2983. chr20_SGK2_NM_016276_1.55274
TGCAGGGGTTGCTTACCTCGGGTAGGAAACCCTCAGGCGGTGGCA

2984. chr20_WISP2_NM_003881_1.71146
GGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGG
TCTGCCAGCCCGGGG

2985. chr20_PI3_NM_002638_-1.86552
AGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCACACTGT
CCATTCTTCCTCCCATTCAGGATGCCCACGGCTGGAGCTG

2986. chr20_SEMG1_NM_003007_-1.56968
CCGTGTAGTTTCAGATTCTTGGTCCATGGATGACACCACCTGCCCATGCT
TCCTTGAATTAGGCTTTCCTAACCTGAAGCGCCTTCAAACTTCCAATA

2987. chr20_SNX21_AF258570_-1.50761
GTGGGGAGGTACAGCTGGGAGTGTGGGGGATGGGGAAGGATGGGGAGGGA
ACGGGCCCGTGGACAACTTGCATTTGCCCTGACACCCA

2988. chr20_PCIF1_NM_022104_1.97923
ACCCTTTGGGGCTGAATGCGACCCCACTGCCCCAAGACTCAAGCTTGGTG
GAAACTCCCCCGGCTGAGAACAAGCCCAGAAAGCGGCAGCTCTCGGAAGA
GCAGCCAAGCGGCAATGGTGT

2989. chr20_ZNF335_NM_022095_-1.79686
AGCTGCTTGCGTGTCGGCACCGTAC

2990. chr20_CDH22_NM_021248_-1.62363
GGACAGCTCCAGAGTCGGGGAAGCGCCATGGTTCCTGCGCAGAAAGGATG
CGGGTTGGGGCCGGCAGATCCTGCCAGGA

2991. chr20_SLC35C2_NM_173179_-1.90441
TGGAGGGATATTCCCGAGAGGCAGAG

2992. chr20_EYA2_NM_005244_-1.58862
TGGTCACCACCACTCAACTAATTCCTGCCCTGGCCAAAGTCCTGCTATAT
GGCCTGGGGTCTGTGTTTCCTATT

2993. chr20_STAU1_NM_017454_-1.66248
ACCATTTATTGATGACAAACACTT

2994. chr20_B4GALT5_NM_004776_1.6692
GCTCGGGTGTCAGGTTGACAGTTATGTTTTTATACAAGGCGTCGTATGTG
ATGTTTGCAAAGTAGTTCAGGTTGTTGAGGCCATCCAGCCCTTGCCGTTC
TTTTGA

2995. chr20_TMEM189_NM_199129_-1.60107
CGCAGCCAGCTCGCGGGCCCCGGCGTGCTGCGCGCCCCAGCGGCAACAAG
ACGCCTCGTCCTCGTCCA

2996. chr20_DOK5_NM_018431_1.60355
ATGGCGAATGTGCCTTGCAGATTACATATGAGTATATCTGTCTTTGGGAC

Figure 3-242

GTCCAGAATCCCAGAGTCAAACTCATCTCTTGGCCGCTAAGCGCCCTGCG
GCGGTATGGACGTGATACTAC

2997. chr20_PMEPA1_NM_020182_1.60121
AACAAAGAGCGTTTGCAGTTGCACGTGCAGGAGACATTGGGCTGCCCGGC
GGCGGCGGCGGCGGTGCTGTTGACCCCCATCAAGCGGTGCAT

2998. chr20_PMEPA1_NM_199171_1.63228
AGACCAGAGCGAATTCATCCTGAAGAACTCAGAGAAAGCCGGTGCAGGAA
GTGGGTTCCCGCTCTCCCTGCACAGGCACAGTGATGCTGCCAGAGCTCTC
CCAGAAAGACCAGGAGGCTTGTTCTGGAGAAGTCAAGCCCAG

2999. chr20_ANKRD60_ENST00000457363_-1.72117
CTATCCGGTGGAGGAGGACCATCTGCCTCTCGCTCAGTGTGTGGTTCAGG
CGGTGTGCAATGGAGATGGGGGTCTCCCCCTTGGCATCTCTGTCGTGGAT
GGAGGCCCCGTGCTGGAGCAGGAGGATTATACAGTCTGACCGGCCCAT

3000. chr20_STX16_NM_001001433_1.79353
TACAATAAAGCAATCACGCAGATT

3001. chr20_NPEPL1_NM_024663_1.70784
GCTTAGCGAATGCCACAGACGGCGTGCGGCTAGCAGCCCGCATCGTGGAC
ACACCCTGCAATGAGATG

3002. chr20_NPEPL1_NM_024663_-1.83018
TGCCGGGGATGAAGCGAGACTGCGGG

3003. chr20_TH1L_NM_198976_-1.59108
CAGAACATTCCAGAACCCGTTGTGGAAAAACCCTTTCAAGAAGCTGTTTT
AAGAGGCTCGGGCAGCGTCTTGAAAATGGGCACCGCTGGGAG

3004. chr20_CDH26_NM_177980_1.52102
TGGAACAGGAGTTGCAACCTGATTTGCTGGACTCTTTGGGTTCAAAAGCG
ACTCCGTTTGAGGAAATATATTC

3005. chr20_CDH4_NM_001794_-1.74629
GTACACAGTCATCGTTCAGGCCACAGATATGGAAGGAAATCTCAACTATG
GCCTCTCAAACACAGCCACAGCCATCATCACGGTGACAGATGTGAATGAC
AACCCGCCAGAATTTACCGCCAGCA

3006. chr20_SS18L1_NM_198935_1.73425
GCGCAGCCGGAGTATCCACCTCGATGACCACGGGCTGAG

3007. chr20_LAMA5_NM_005560_-1.62141
TGTGGCGTCCACTGCCCGGTTCAAAGCCTCTCGCAGGTCCATGAGGCCGG
CCTCGTGCTGGGCCAGCCGGTCGCGGGTTTGTGTGGCCAGTGCCT

3008. chr20_LAMA5_NM_005560_-1.64973
GGCCGCCTAGCCGCCGTGCGTCCTGCCCGAGGCTTGT

3009. chr20_LAMA5_NM_005560_-1.80768
GCCACACGCGGCCGGCGTTGATGAGGACTTCCACGGGGAAGGTGGGGTGG
GCTGGCTGGTAGCCGTGCAGCAGGAAGGCATAGCGGCCCAGCGTGGGCAC
ATGGGTGGTGAAGACCACGGTGGC

Figure 3-243

3010. chr20_LAMA5_NM_005560_-1.57872
GAAGTGAAAGTAGCCGGGGGCACAGCGATCACATGTGGCCCCCTCGAAGC
CCACTCGGCACCTGCACTGGCCTGTGTCAGGGTCACAGCGGTCATCGGCC
ACTCCAGGGCT

3011. chr20_SLC17A9_NM_022082_1.66355
TGCAGCCACCCCCAGACGAGGCCCGCAGGGACATGGCCGGGGACACCCAG
TG

3012. chr20_COL20A1_NM_020882_-1.60443
CGCCGCCTCCACGGAGCTGCACAACCTGGCCTCCCGCACAGAGTACCTGG
TCTCCGTGTTCCCCATCTATGA

3013. chr20_KCNQ2_NM_172107_-1.65418
GCTGACTTTGAGGCCCGGGGTCAGGTCCTCGGTCACAAACTCGCAGGGGC
AGCTCTTGTCATCCACAATGTCCTCTCCGGGGAGGCTT

3014. chr20_KCNQ2_NM_172107_-1.6123
TAGAGCGTCCGGGGCAGCATCCACA

3015. chr20_PRIC285_NM_001037335_-1.51146
CGTGCAGCAGCTTCCGTAGCGCAGCCGGGGGCAGGTTCTCGTACAGCCGG
GCCTGCTGCAGGGACTCGGGCCTGGCGACAGTGTCCAGCAGCCCGTCCTC
CCCGACGGTCACCATCACCTTCTGGCTCTCGTCCAGAAGCTCCCGTAGGA
T

3016. chr20_GMEB2_NM_012384_1.5036
CCGTTCATGCGGATGGCTCTCTTCCAGTCCTTCAGGGTGGACTTCCCGGC
CAGGTGCACAAATTCCTTTGGGCTGATTACATGCTCGTCGT

3017. chr20_RTEL1_NM_016434_1.64624
GCGAGAACACCTCCGAGACGGCATCTCTGCCCGCAAGATTGCCGAGAGGG
CGCAAGGAGAGCTTTTCCCGGATCGGGCCTTGTCA

3018. chr20_RTEL1_NM_016434_-1.73565
CCATCGGGCGAGTGATCCGGCACCGCCAGGACTACGGAG

3019. chr20_RTEL1_NM_016434_-1.5622
AGAAGATGCTGTCAGCGAGGCCAAGTCGCCTGGC

3020. chr20_RTEL1_NM_032957_1.77706
TCATGGGAGAGACATCGCTGGGCAGCAGGCCACGGGAGCTCCGGGCGGGC
CCCTCTCAGCAGGCTGTGTGTGCCAGGGCTGTGGGGCAGAGGACGTGGTG
CCCTTCCAGTGCCCTGCCTGTGACTTCCAGCGCTGCCAAGCCTGCTGGCA
ACGGCACCTTC

3021. chr20_ZGPAT_NM_032527_-2.07489
ACCATGCCAGCAAGAGTGCCAAGCGGGCCCTGAGCCTGCGGCTCTTCCAG
ACTGAGGAGAAGATCGAGCGAACCCAGCGGGACATCAGGAGCATCCAGGA
GGCTCTCGCCCGCAACG

3022. chr20_SLC2A4RG_NM_020062_-1.6397
GACCTGGCCAGTGACCAGTCCTCTCCGTCCACC

3023. chr20_DNAJC5_NM_025219_-1.50814

Figure 3-244

TTTGTCTTCTGCGGCCTCCTCACGTGCTGCTACTGCTGC

3024. chr20_UCKL1_BC033078_-1.65358
TGTGGGGCCAACAGTTGAGCGGGAGCACGCGCCCGGG

3025. chr20_ZNF512B_NM_020713_1.52743
GGTTGGAGCCTTCTGGCCCAAGGATGAAGCCAGAGACAGGAAGTGTTCTG
CAACCCCAGTCCCCAAAGTGCTCCTGGAACTTGTCTCCCTACTACTGCAG
GCCAAG

3026. chr20_C20orf201_BC036837_-1.91016
AGGCTGGGGCGCGTCGCACACTCTC

3027. chr20_MYT1_NM_004535_1.75205
TCCAGCAAGCAGAAAGGCATCCTGAGTCACGAAGAGGAGGACG

3028. chr21_CXADR_NM_001338_-1.52528
CTGTAAAAAATGCCTCTTCTGAGTA

3029. chr21_TMPRSS15_NM_002772_2.04411
AAAAGCCCCACTCGTTCTTGTCTCCCTCCTGGTCCAGTTGGGGTAGAAAT
GT

3030. chr21_ADAMTS5_NM_007038_-1.70689
CATTGCTTAAACGCAGAAGGCCTTTGGGAGAGAGGACATCCTTTTGCTAA
CTTCCGGTTTCCATCCTGGCACTGCACCGTTCTGGTGTGCCAAC

3031. chr21_C21orf7_NM_020152_1.66934
GGGGCTGGCAACAGCTTCGTAATCCTGGCTTCCTGCTTTCTGGGTCAAAG
CCCTGGTGGTGTGTTCTTGATATCGGTCCATCTAGTGGCGTTGTTTGATT
CCTCCCACCTTGCTGATCATTCGTAGTGTAGC

3032. chr21_C21orf7_NM_020152_-1.56427
CTTTCCAGAATTAGACCAGCAGCTAC

3033. chr21_KRTAP19-3_NM_181609_1.50703
CTCCATAGTATGATGGGCGGTAGCAGCCATA

3034. chr21_KRTAP6-1_NM_181602_-1.58962
ATAGCCACAGAACCCATAGCCAGGGGTGCCATAGTAGTT

3035. chr21_OLIG2_NM_005806_1.70868
AGGAGGACCCTGCGAAAGCTGCGACGACTATCTTCCCCTGGGG

3036. chr21_IL10RB_NM_000628_-1.85914
TGGTACCACCTCCCGAAAATGTCAGA

3037. chr21_SETD4_NM_017438_-1.5844
GTGGGCTATGATTCAGCAGGTCCAGGTACGGAGCGAGTGCACAGGTGTCC
GGCTCTGCAGAAAGGCATTCCCGCTGCCTGGGCCTCAGGTACACGGCTCT
GGTGTTGACGGTGCACCAAGCCCA

3038. chr21_CBR3_NM_001236_1.62271
AGGAAAGGTTCCACAGTGAGACACTCACAGAAGGAGACCTGGTGGATCTC
ATGAAAAAGTTTGTGGAGGACACAAAAAATGAGGTGCATGAGAGGGAAGG

Figure 3-245

CTGGCCCAACTCACCTTATGGGGTGTCCAAGTTGGGGGTCACGGTCTTAT
CGAGGATCCTGGCCAGGCGTCTGGATGAGAAGAGGAAAGCTGACAGGATT
CTGGTGAATGCGTGCTGCCCAGGACCAGTGAAGACAGACATGGATGGGAA
AGACAGCATCAGGACTGTGGAGGAGGGGGCTGAGACCCCTGTCTACTTGG
CCCTCTTGCCTCCAGATGCCACTGAGCCACAAGGCCAGTTGGTCCATG

3039. chr21_MORC3_NM_015358_-1.51471
CAGTTGGATTATATGGGAATGGCTTCAAGTCGGGTTCTATGCGTCTGG

3040. chr21_KCNJ6_NM_002240_1.63358
CTCATGGAAGCTGTTGTAGTCAACTTCGTAGAACCCGTCCTCCAGGGTCA
GGACAGGTGTGAACCGGTAACCCCACAGGATCTCACTGGTGATGTAGGAG
CTTCGAGC

3041. chr21_ERG_NM_004449_-1.73034
TGATATGAGCTGCTGGGTCCGGGACAGTCT

3042. chr21_C21orf129_NR_027272_2.12425
TTCCCAGGGATCCACAATCTTCTA

3043. chr21_PRDM15_NM_022115_-1.80098
TTGGAACCGAGCTGGTGTCAGTGGTGGTGGTGGCCAGCTTCCCCAGAACC
AGCTCCATGATCCGCTCATCTGGCGTTGCACTCACAGGCTCATCCGGAGG
GACCTCGGTAATGATCTCTGCCA

3044. chr21_ABCG1_NM_016818_-1.56682
CGGGAAGTTCAATAGTGGTGAGTTGGTGGCCATTATGGGTCCTTCCGGGG
CCGGGAAGTCCACGCTGATGAACATCCTGGC

3045. chr21_ABCG1_NM_016818_1.50559
CTCGCTGATGAAAGGGCTCGCTCAAGGGGGTCGCTCCATCATTTGCACCA
TCCACCAGCCCAGCGCCAAACTCTTCGAGCTGTTCGACCAG

3046. chr21_TFF3_NM_003226_-2.06491
CAGGCCCACGTACTCCTCAGCAGA

3047. chr21_TFF2_NM_005423_-1.61198
ACAGACTTCGGGAAGAAGCACCAGGGCACTTCAAAGATGAAGTTGGAGAA
GCAGCACTTCCGAGAGGCGCATTCCTCGGGGCTGATGCCCGGGTAGCCAC
AGTTTCTTCGGTCTGAGACCTCCATGACGCACTGA

3048. chr21_RRP1_NM_003683_-1.65067
AGAAAATAAAATGCCGCGCAGCCCTTG

3049. chr21_PWP2_NM_005049_-1.51772
CACCCAGTTCTCCTGTGTGGCGGTGGATGCGAGCGGTGAGATCGTCTCTG
CAGGGGCGCAGGACTCCTTTGAGATTTTCGTGT

3050. chr21_C21orf33_NM_004649_-1.56874
GGGCTGAAGTCCAGATCTTTGCTCCTGACGTCCCTCAGATGCACGTGATT
GACCACACCAAGGGGCAGCCGTCCGAAGGC

3051. chr21_ICOSLG_NM_015259_1.66018
AAGCCCCGCATGTTCAAGAAGACGGTGTCATTCTGCAGAGCCTGGTCCAG
CAGGCTGTTGTCCGTCTTATTGATCCAGTACACGTTGGGCCTGGGGTAGC

Figure 3-246

CGTTTATGGATGTACACGTGAAGGTGAGCTCATCCTGGGAGGGGCTGTGG
GGGGCGCTGACGACGGGCACGCTGAAGTTT

3052. chr21_DNMT3L_NM_013369_1.55931
GATGAGCAGCGTCTCTCCGGAGCAGCAGATGGAGCAGTAGGATTGGTACC
CGTCATCGTCGTACAGGAAGAGGGCATCCA

3053. chr21_AIRE_NM_000383_1.65147
CTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGCACCTG
CCGGCT

3054. chr21_PFKL_NR_024108_-1.5023
GGCAGCGGCCTACAACCTGGTCCAGCACGGCAT

3055. chr21_PFKL_NR_024108_-1.74183
CTGCTGGAAGCCACGCCTGACACGCCGGCCTGCGTGGTCACCCTCTCGGG
GAACCAGTCAGTGCGGCT

3056. chr21_C21orf2_NM_004928_1.75963
ATCTTTTATTAGGGAGGACAGCCTGCAAAATCCTCCCTTTAAGAGCCCAG
GCCAGCCTAGAACCTCCAGACCACAGAAGGGGAGTCCTGGGGACAGGACT
GGTGTAGACAGGCATCTCCACCGCCCCGGTTAGCCAGTACCTAACACCCA
CTCCTGCCCTCGGCCGATGTGGCAAA

3057. chr21_TRPM2_NM_003307_-1.71273
CGCGGCCGCCATGGACCCCATGGGAGA

3058. chr21_POFUT2_NM_015227_-1.59857
AAGCCGCCCCCGACAGAATATCGGCCGCCGATTGTCCGGGCCAGAACT

3059. chr21_SLC19A1_NM_194255_-1.88962
AGGCCAGCACGTCCGCGGTGACCGGGACCAGTCCCCTCCGGGCTGGCACA
AGTGTGGGAGCA

3060. chr21_SLC19A1_NM_194255_1.61846
GGTGATGAAGCTCTCCCCTGGCCGTATCTGCGCCATGAAGCCGTAGAAGC
AAAGGTAGCACACGAGGTGCCGCCA

3061. chr21_PCBP3_NM_020528_-1.79444
CACCGGCATGCAGTGGTAATTATTTTAGAAATATTGTTCCTTGGTGTCAG
CGTAGCTGTCTGTCTTAGGAGCTGGGTCGGCGTTCCGACAGCACTTCCTG
TCCGCCCTTCTCCTCTGCCATCCAGAACCGTCCAGAACTGTTGCCTGAGA
CCCCTCCTCTCTCACACAGCCCTGCCATGCTGACTCGGTTTCCCCTCAGA
GCCATTGTTGTCTGGGCTCGAGTTTCTGCCCCAGGTTGTGTGCTGGAATC
GGGGGGTGGCTCTCCTGCCACCCATGGGGAGCGCCAGGAGAGGAGGGTCA
TGGAGGATGTTGGGGCTCTGACCCCAGGAGTGGGGTGGAGGGCGGAGCCT
GCTGGGGGCCCTGCCTTCACAGAGATGCCGCGTGCT

3062. chr21_COL6A1_NM_001848_-1.72796
ACCCCAGGCACGCGGGGACCAAGAGGAGAC

3063. chr21_COL6A2_NM_001849_-2.29693
GGTATCAAGGCAACAGTGGAGCCCCAG

3064. chr21_PCNT_NM_006031_-1.53564

Figure 3-247

TGGACAGGCGGCAGGCCCGCAGAGCCACAGCTCACACACGGGTGCCCGGG
GCCCACCCACAGCCTCGCATGGATGGTGGCGCCAAGGCCCAGGTCACCGG
CGACGTGGAGGCCTCCCATGATGCTGCTTTGGAGCCGGTTGTCCCTGACC
CACA

3065. chr21_DIP2A_NM_015151_2.21109
CTCTGCCCGGACGCTAGCCGGCCTGG

3066. chr22_CECR1_CR456417_-1.56252
ATGCGCCCGTGTTTCATCTATGGATAGAGCTGAGCCGAAGAAAGACATTG
CCACAGCCAACAGCAAGAAGCACAGGGCTGGCCGCT

3067. chr22_BCL2L13_NM_015367_1.52874
CCGGCCGTGACGAAGGCACGCCGGGGTGACCTCACCCTCCAACATGGCGG
CGGCGGTAGATTAGGGCCGCGGGTCGGAGCACTCACCGCCGCTGGGGGAC
CCTGTCGGAAGCAACTGCCG

3068. chr22_PRODH_NM_016335_-2.2049
CAGCGGGACGAAGCGGGGAATGCA

3069. chr22_SEPT5_NM_002688_1.51817
AGAGCGCGCCCTTCGCCGTTATAGGCAGCAACACGGTGGT

3070. chr22_GNB1L_NM_053004_-1.5278
CGGCAAGCGTCCAGCGTGGCTGGCCCCCGGCCAGGATGCTGCTCCGGCAG
AAGCCCACACTCTCCAAGCACACGGAGTCCACGACAGCGCTCCTGCCCTC
CGCGAGGTCCCACAGGCAC

3071. chr22_GNB1L_NM_053004_1.79942
TGAGAAGAGGAGCGGGCGCCCCTGAGCCTGGGCTCCTTCGCAGAAGTGCA
GCGCATGCACCGGTGACTGGGTGCCTCGGAGGACAAACT

3072. chr22_ARVCF_NM_001670_1.9024
CAGCTGTTGCCAGGCCATTGGCAGGGGCTGCCCACTGCCCATGCCACCAC
TGA

3073. chr22_C22orf25_NM_152906_1.67726
TCCTGGAGGCTGTGGAACGGAGCCA

3074. chr22_DGCR8_NM_022720_-1.67628
CCTCTCCGCTCCCGTGTGGGCCCGCAG

3075. chr22_ZDHHC8_NM_013373_-1.96808
TCTGATGCCTTCTCGGGCGCTTTGCGCTCCCTGAGCCTCAAGGCCTCGAG
CCGGCGGGGCGGGGATCATGTGGCCCTGCAGCCCCTGCGCTCTGAGGGGG
GGCCCCCCACGCCCCACCGTAGCATTTTTGCCCCCCATGCACTGCCCAAC
CGCAACGGCAGCCTGTCCTATGACAGCCTGCTCAATCCTGGCTCGCCTGG
TGGCCACGCCTGCCCTGCCCACCCAGCAGTTGGCGTGGCCGGATACCACT
CACCCTACCTGCATCCTGGGGCAACGGGCGACCCGCCACGGCCCCTACCC
CGCAGCTTCAGCCCCGTGCTGGGCCCCCGCCCCCGGGAGCCCTCGCCTGT
GCGCTACGACAACCTGTCCAGGACCATCATGGCATCCATCCAGGAGCGCA
AGGACAGGGAGGAGCGTGAGCGCCTGCTGCGCTCCCAGGCCGACTCACTC
TTCGGCGACTCAGGCGTCTATGACGCTCCCAGCTCCTACAGCCTGCAGCA
GGCCAGTGTGCTGTCCGAGGGCCCCCGAGGTCCCGCGCTGCGCTATGGCT
CCAGAGACGACCTTGTGGCTGGGCCCGGCTTCGGTGGCGCCCGCAACCCT

Figure 3-248

GCCCTGCAGACGTCACTGTCCTCGCTGTCCAG

3076. chr22_THAP7_NM_030573_-2.1191
TGGGCAGCCCCTCGGTCAGTCCAGCAGCCCC

3077. chr22_PPM1F_NM_014634_0.0108929_-1.65471
TGGGAATCCCCGAGCCAGGCGACGTGCAGGGTCGCTCCTGCAATGAGCGC
ACACA

3078. chr22_ZNF280B_NM_080764_1.51776
TAAATTTAGCCCAGTCCAGGAACTGGACAGACACCACTTGTTTGGCCCTT
TTCAGTTAAAACTATGGGTCCAGTACAGTTCAAATTATAGATATTAGGGC
TTCTTCCCCTTGGGAAACTTGCTTTACAGCTGTGGCTGAGAATATGGCCA
GTTCATTCTCCACTAACGGCTAGCCAGAAGGGAGAGGAGAGGGAATGAAT
CAAATTCACCTTTAGATCACAGAACAGGAAGTCAGCTAGTACCAGGCACC
ATTCTATTAATTTTATTGCTATTTCACCTCAAACCAATGATACATGACGG
CTGTTTGATGTCTGCAGGGGCCCTTCACCAAACAAAACCATTTTACTTTG
AATGGTTTGGCTTCCTTGGATGTTTTCAGGTAGGTAAAGATACTCTGAAG
CAGTGTTCCTTTTGACCTGGCCCCAAGACTAGAATGAA

3079. chr22_ZNF280B_NM_080764_-1.62397
GCACTTCTGGGAATTCGGCAGCAAGTGGGCCAGGGCATAACAAAGCCATT
CCAGTCTGACTAGAGTTAACCATGAAATGCTGAATGCATGGAAAAAGCTG
TAAAGAAAACTAAGTATTTCAAAAATTCTATGAATTCTGTATATAGAAAA
AAGAGCTTTCAAGCTTAGGAGTAACATGAAATACCAAAACAATAAATAGG
TGCCAGGG

3080. chr22_IGLV2-23_ENST00000390306_-1.51815
ATGTTGGGAGTTATAACCTTGTCTCC

3081. chr22_GNAZ_NM_002073_1.57979
GATGTCGGCAAAGCTCAGAGGAAAAAGAAGCAGCCCGGCGGTCCCGGAGA
ATTGACCGCCACCTGCGCTCAGAGAGCCAGCGGCAACGCCGCGAAATCAA
GCTGCTCCTGCTGGGCACCAGCAACTCAGGCAAGAGCACCATCGTCAAAC
AGATGAAGATCATCCACAGCGGCGGCTTCA

3082. chr22_FBXW4P1_NR_033408_-2.0292
CGCGGCTCGGCACCAACCTGATGACC

3083. chr22_VPREB3_NM_013378_1.69361
ACTAAAGCCGTAGCCAACAGAGCAGTAGTAATCCGCGTCGTCTTCAGGCT
GCACGGGACTAATGGTGAGGACACAGGCATTGTGGGCCTCATCCTTGGCT
GCCGAGAATCGATCGGGGATGTCAGCAGGCCGGTGGTGATCCTCCTCCGA
GCGGTAGTAGA

3084. chr22_SLC2A11_NM_030807_-1.58596
AGCGCCCCTAAGGAGCTCCGAGGAGCTGTGGCCATGAGCTCAGCCATCTT
TACGGCTCTGGGGATCGTGATGGGACAGGTGGTCGGAC

3085. chr22_GSTT1_NM_000853_-1.63824
TTTAATCAGATCCACGATGCGCAGCTCGAAGGGAATGTCGTTCTTCTTGG
CAAAGATGTAAACAGCGCGGCAGGGC

3086. chr22_CABIN1_NM_012295_-1.61133
TCCCCGTGGACGAGATTGACCGGCCGGGCAGCTTTGCCTGGCACATGAAC

Figure 3-249

CGCTCCATCGTGCTGCTGCTCAAGGTGCTGGCCCAGCTGCGGGACCACAG
CACCCTGCTGAAGGTGTCCTCCATGCTTCAGCGGACCCCAGACCAGG

3087. chr22_CABIN1_NM_012295_-1.8232
GAGAGAACTTCTTTCCTGTGACAGTGGTGCCCACAGCCCCTGACCCTGTG
CCAGCTGACTCTGTCCAGCGGCCCAGTGATGCTCACACCAAGCCTCGCCC
TGCACTAGCTGCCGCCACAACTATTATCACCTGCCCTCCGTCA

3088. chr22_C22orf36_ENST00000446942_-1.61101
CGAGGGAGCCGTGCTCCACTGACGCCAATCCCAGGGAGTAGGAACAAGCC
AGGTCAGCGTGTTCTTCTTCCTCTCACTCTCCAAGCGAGACTGCGCCTGC
GGG

3089. chr22_CRYBB3_NM_004076_-2.09985
TGGCGGAACAGCACGGAGCACCCGAACAGGCTGCAGCTG

3090. chr22_LRP5L_NM_182492_-1.58127
AGCGTGGCCTGACAGCGTACGGCCGGCACAAGAGAGGCTCGAC

3091. chr22_MYO18B_NM_032608_1.50685
TGCAGTCCTGGTTGAGCTGTACTCTGTCCCTGGCCACAGATACTATGAGG
ACTCCTTCTCGACA

3092. chr22_SEZ6L_NM_021115_1.54245
TTTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCACACGGAGTTGG
TGCGGGGAGCCAGAATCACCTACCAGTGTGACCCCGGCTATGACATCGTG
GGGAGTGACACCCTCACCTGCCAGTG

3093. chr22_HPS4_NM_022081_-1.51515
ACTCTGGGCTAGTGGACGATCAGGTTCTAGAAAAAATGCCAACTTGGAAG
CTTGTGGCACCAATTCAAGCTGGGATGGAACAGCAGGAGATATGAAATAC
CTCAGGCTCAGTATGGCAGAGAGGGAGCCAAGCCCGTCCCGGCCCCAACA
CTACCGATTAAATACAGTTCTTTATCAAGTGCTCTGGGTCTGCCGACCTG
AAGAACTAAC

3094. chr22_HPS4_NM_022081_1.57661
AGGACTCTGCTGGTGTCAGCCTGG

3095. chr22_TFIP11_NM_001008697_-1.64223
TGCTCATAGGGCTCAAACTCAGGAGTGCTAGAAGTCAGGCCTCGGGCTTG
TCTCTCTCT

3096. chr22_MN1_NM_002430_-1.62117
GCCGGGCACCGACAGAGCGGTCCCTCCCCCCGCCCCCCGGAGTCCCCGCG
CCCCGCAGCCCGAGCCTCCACCGAGCACGATCCGCTCG

3097. chr22_RASL10A_NM_006477_1.68775
CAAGTCGTAGACGGCGCCGTCGAGCAGCACCGCGGGTCGGTAGAGGCGCG
GCCCGTCCGTGGGCCGGTGGCGCTCGGGGTAGTCACCGAACAGGAACTGG
CGGATGATGGCCGTCTTGCC

3098. chr22_ASCC2_NM_032204_-1.52926
CATGCGGAGGAAGGTGAGAAAAACACTTCGATGGAGGCGCTTCTGCATGT
CAACAACCTCAGGGGCTGAGGCCACCCCCTCGTCGAATTTGCGGGGGACA
TAGCGCAGGTAGGAGTCCAGGCACTTCTGTAGAGTCTCGTCAAAGATCAC

Figure 3-250

3099. chr22_GAL3ST1_NM_004861_-1.66466
AGCCTGAGTTCCAGTGAGCCATGACT

3100. chr22_FLJ20464_CR456348_-1.63528
AAATTCCCAGAAGTCGCCTGCGACCGCCTCCCTGCTTCAAACACCAGAGA
GGGCCCGGGGTCCTGGCCGGAGACAGGCCGAACCTCCGGAGCTGCTTCTG
CACCCGGTACATT

3101. chr22_SFI1_ENST00000433295_-1.61301
GTGCTCCTCACTGTTTGACTGACCTTGATGGGATCCTGAACGTCTCAGAG
GCTGCTCCCCTGTGACATGGACCCTGGCGACCTGTACACCAGCGTCACCA
GGGTTGTTCTGCAGGTCAAAAGAGACAATGTGGGTGAAGCAGTCCCCTGG
CGTCAGGTACCTTTTGTCG

3102. chr22_DEPDC5_NM_014662_-1.75851
GCTCCGCCCAGTCAGCCGAGAGCAGCAGCGTTGCCATGACTCCC

3103. chr22_C22orf24_AK294232_-1.5053
CAATGGAATGTACCCAGGAGCCCCTAATCCCCCATTGATTTAGTGTTCGG
GCTTGGTCAGCAGTCTTCTTGTCCCACTGCAGGCATGTGCAGCCCCGGCT
CTTTCTGAGTTAAGCCAGGGACTGAAATGGGTCGGCAGAATGCTCATCTG
TTGGGCGCTTTATGGTTTATAAAGCCCTTTCCCTTCTGTGCCCTCCTCAC
AACCCCATGGAGACTCTGCACGGCCCCTCCAGCTCTTAGAGGCTGCATTT
TGCGCAGTGAAGGCCACATTAAATATTAACAGGGCAGCTCCTGGCCCCGC
TGTGACGTCAATTACGGGGCCGCTTGGTGAGGGCTGCGGATGCCTTTCCA
AGGTGAAGCGGTGACCG

3104. chr22_---_---_-2.06888
TGCAAGCTCCACTTTCCAGGTTCACACCAT

3105. chr22_RBM9_NM_001031695_-1.63709
GAGGTACCGCTCGGACTGCACCATATACTGTCCGCCCTCTGCCCCTCAAA
TGGGCTCCTCTGAAAGCGGCTGCCGTGGTGGCTGCAGTAG

3106. chr22_EIF3D_NM_003753_1.98995
GAAGGTGCCATCAGGGAGGCTGTAGACACGGATGAC

3107. chr22_---_---_1.54494
GACGGAGGAAGTCAGAGATCTGAAGCACAAGAAGGATCTGATGTGCTGTT
GCTATCTTGGAGATGGAGGGGGCCATGTGACAAGGAATGCAGGTGGC

3108. chr22_---_---_2.23328
TTGCTTTCTGCCACCATTGCAAGTTT

3109. chr22_---_---_-2.11021
CGATCTCCTGATGTCAAGTGATTCTCCGCCTCGG

3110. chr22_CSF2RB_NM_000395_1.56755
GTGCTTCTTTGACGGGGCCGCCGTGCTCAGCTGCT

3111. chr22_CSF2RB_NM_000395_1.59974
AGGGGCTCGGCAGCCTCCACACCAGGCACCACTGCCAGATTCCCGTGCCC
GACCCCGCGACCCACGGCCAATACATCGTCTCTGTTCAGCCAAGGAGGGC
AGAGAAACACATAAAGAGCTCAGTGA

Figure 3-251

3112. chr22_C1QTNF6_NM_031910_-1.815
ACGGGAAGGAGATACCTGCCCCTGCCACCGGGACCCCGTCCCACCAGCCT
TGGGGAGCAGTGGGTAATGGAGGACCAGCAGCACCTGAACACCCAGAACA
CAGGCCCCCATGAGCTCTGGGTCTGCTTTAAAACCTATGTACACATCTCT
CCCCGCCTGGGCTGGACTGGCCAGTCACTGAGGGCAGGGGCAGGGCCTGT
GTCTGACCCCCTCACCCTTCCCGGGACCCAGCACAGAGTGAGTGCTCAGT
GTTTAATGAATGAATAAATGAACGGTGGCTGCAGTGGTGCAGGCCTGAGC
AAGAGAAGAGGGGGAAGGGGTAAAGAGAACATAGCACGGGGAGCCCTGGA
GGGATGAGAGAATTTAAGAATGTTGGAATTGGCCAGGCACGGTGGCTCAC
ACCTGTAATCCCAGCATTTTGAGAGGCCGAGGCGGGTGGGTCACCTGAAG
TCAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCCATCTCTACT
AAAAATACAAAAATTAGCCAGGCATGGTAGCAGGCGCCTGTAATCCCAGC
CACTAGGGAGGCTGAGGCAGAAGAATCGCTTGAACCCGGGAGGCAGAGGT
TGCAGTGAACTGAGATTGCACCACTGCACTCTAGCCTGGGCAACAGAGCA
AGACTCTGTCTCAAGAAAAAAAAATGTTGGGAGAATTCTAGAATGTGGGG
AGGATTCCAGAATGTTCAGAAAGTACTAGAATATTGAGAAAGTCCTAGAA
CCTGGTTGCTCCAGTGTGGTTCATAGACTGACCCCATCAGCATCACCCAG
GAACATATGAGAAACACAGAATCCTGGACCCACTCAGACCTGCTGAGTCA
GAATCTGCATTTAACACGAACCCCGGGTGATTCGCATGCATTTCCAAGTT
TGAGAAGTGCTGGGCTACGAGGCTGGGAAAGTTCTAGAATATTTAGGTTA
GCAAGCTTCTTAAAATAGGTCCAAGAGAGAAGAGAGGAGCAGAAATAGGC
TGGGAGGGATGATGGCAGCCAAGATAGAAGCAGGGTCTCCCCAGAATGC

3113. chr22_CARD10_NM_014550_-1.7749
TCTTCCTCACGCTGCCGGCGGAGGATGGAGCCGGCACTGGGGGGGAAGGG
CAGGATGGAGAGCCGATTGATCTCCTTT

3114. chr22_GGA1_NM_013365_-1.76003
GTGTATGACCAGCACGGCTTCCGCATCCTCTTCCATTTTGCCCGGGACCC
ACTGCCAGGGCGCTCCGACGTGCTGGTGGTGGTGGTTTCCATGCTGAGCA
CCGCCCCCCAGCCCATCCGCAACATCGTGTTCCAGTCAGCTGTCC

3115. chr22_TRIOBP_NM_138632_1.6692
TCACTGTGCCCGTTTTACAGACAAGGCCACTGAGCTCTGAGAGGTTATGT
GACTTGCCCAAGGTCACCCCGCCTGCAGGTCTCAAAGGTGGGATTTGA

3116. chr22_TRIOBP_NM_138632_1.57501
GAGAATGCACCGTCCGCCTAGGACAGCGGTTCTCAACGGGGTCCATTTTG
TCCCCCTTGGGGACATTTGGCTGTGTCTGGGAATACTTCTGGTTGTCACA
ACTAGGACAAACTAACTCTCTAGAAAAAACGTGTGTGTG

3117. chr22_GALR3_NM_003614_1.85609
CACTGCCTGGCCTACGCCAACTCCTGCCTCAACCCGCTCGTCTACGCGCT
CGCCTCGCGCCACTTCCGCGCGCGCTTC

3118. chr22_PICK1_NM_012407_1.55489
GCAGCCTTGGACGGCACAGTGGCAGCTGGCGATGAGATCACCGGTGTCAA
TGGCAGGTCAATCAAAGGGAAAACTAAGGTGGAGGTGGCGAAGATGATTC
AGGA

3119. chr22_CSNK1E_NM_152221_1.71868
GAAGCCACGGGCTCGGCGGCACTGCGGAGCCGGTTGGCAGTGGCCCCCGT
GGGTGGGCCAGGGGGCAGGGCTCGGGTCGCGGACCCCCGTAGCTGCCCCA
TCCTCTCCTCGCGTTCGTGTT

Figure 3-252

3120. chr22_SUN2_NM_015374_-1.5018
AGTGCTGTTGGGTGACAAGGCCTTGGGCACATGCTCTAAGGTAACGGCTG
TGGGGCGGATGCGGGCAGAGAGGCGGACCACGGCGAAGCCTTGTGGCCC

3121. chr22_CACNA1I_NM_021096_1.53169
TGAGCCGGCATGCCACCTTCGAGAACTTCGGCATGGCCTTCCTCACACTC
TTCCAGGTCTCCACGGGTGACAACTGGAA

3122. chr22_TNRC6B_NM_001162501_1.50322
TTAAGCCAACCAACGGCCGCCAGCCCAATTGGCAGCTCTCCATCGCCACC
AGTCAATGGTGGCAACAATGCCAAAAGGGTGGCAGTGCCGAACGGACAAC
CGCCAAGC

3123. chr22_TNRC6B_NM_001162501_-1.86355
ACTCGCCCTCTCATCCTGTTGGGCC

3124. chr22_ADSL_NM_000026_-1.58304
TTTGCACCGACATACGCCTCCTGGCAAACCTCAA

3125. chr22_SGSM3_NM_015705_-1.57194
CGGGAGGTCGAGAGAGACTTTGCCTCCGTGTATTCCCGTCTGGTGCTCTG
TAAGACCTTCAG

3126. chr22_XPNPEP3_NM_022098_-1.7258
TTTCCTGGCGACGCGGCCCTGCAGGCGGTTGCGTTCCCCGTCGTTACCCT
CTTTCTCTTCCCGACGCGTGAGTTAGGCCGTA

3127. chr22_C22orf46_NM_001142964_1.71596
CAGACTCGCCCTGCCTTGGACATGTGTCAAGAGATGGAGCAGCTGCTGCT
TCACTCACAGGAAAGGTTGGTGTCACTGGAGCCTGTCATCAGTGTGAGGT
CTCGCCCCACCTCCATGACCTTAACCACCTCTCTTCCAAACTTACTTTCA
GCTGAGAGGCTGCAGTTCTGCCCCCAGAGAGCTCCTGCCTGATCCTTCCC
ACCAAACACTGAGAATGTGCACTTGGAAGTC

3128. chr22_SEPT3_NM_145733_1.74979
AGGAGAGCATGCCTTTTGCTGTGGTGGGAAGTGACAAGGAGTACCAAGTG
AATGGCAAGAGGGTCCTCGGCCGAAAAACTCCATGGGGGATCATC

3129. chr22_WBP2NL_NM_152613_1.62022
TGGCGGTGAATCAGAGCCACACCGAGAACCGCCGCGGAGCCCTCATCCCT
A

3130. chr22_NFAM1_NM_145912_1.51962
AAACAGGCCCGGAGTTCATTCAAATCCAGCCTCTGGGAGCAGGGGCCTTG
CCACTCGGTTATGTGAGCCTGCTAAAGCCCTCCTTGCCATGTGTGCTTGC
AGGCGGGGGCCCAGAACCAAGTTGGGAGGCCACTGGCTGTCCTGTGGGAC
CAGAGAAGTCTGGTGCCACCCTAGCAGGGCCAAGGGACTTCTTCTGGACG
TCAGTCTGTGCCCAGCCTCTACCACCAGCTTTCCCTTCCCTGCAGGGAGG
GGCATGACCTGCAGAACCAAAGGTGCTTCTGTGAGCCAGTAGCCCAGTGC
TGCTTGGGGGCAGGGGCGGGGCCTGTGCCTTGGGTTCCCCCCCCTCCCTG
GGCACATTTGGGGTTGGGGCAGCCCACACGGTGGGGTGGGAAGATTGACC
TGCCCATTTTACAAATGAGCAAAGGTGGGAGAACTCAGGGAGACATGGGG
GAGCAGAGGGAGGAAGCAGAGCCCAACAGCCCGGGGCACCCGGACCCCAG
CCACTGCCTGCCTGTGGATGGGTTTCTGGCCACGGTGCAGGGCTACTGCG

Figure 3-253

AGGAGGAAATGAGGGTGATGTGGGCACCTGAAACAGCAGAAATGGCTCAG
GGCCAGGCACTGGGGAGCCACTGTCCCCATGGGGCTTGAGCTTCTGCCTC
AGAGGGACCTTCCGGCTGCCATTGAGGGTCCCAGCACCAAACCCCACAGC
TGGACCACTTGGGACCTCAATCCACAGGGGGCCAGGGCTGCGGCCTATGG
CAGATAAAGATAGAGGAGGAGGGCTGGATGAAGCCACAGGTGGTGGGCAC
AGGATAGGCCAGACAGAAGGGACTTTGGGGGACTCCACCTTGGGTAGAAG
GAGGGACAGCTGAGGTCCTGTGGTGGAGAAGGCCTGGAGCAGAGGGTGAC
CAAGGAGATGACAGAGTGCACGTACAGGGCCAGGCCAATGGGAGTGGGAA
CCCTTGGGAGAGGGAGCTTCAGGCCATTCATTCAGTTCCTGTTTAGCCAG
CACCCTCCTCCCCTCATCTGTCCCTCTGCCCTCACCCCAACATGCCAGAA
TCTCCTTCCTCTCCAGCTTGTACCCAAGCCCTCTCTGCTCCATGCCCCCA
GCCTGCTGACCACCTCTCAGCCATGTCCTGGGCCTCCAGATCTGTCCCTG
ATCCTAGTCTTGCCTCTGAGGGGTCCATCATCCTTGTCTGTCCCCCAGAC
CTCCCACGCCAGCCCCTGCTCCCACCCTGCCTGGCTGCCTCGTGCCTCTG
GCCCAGCTGGGTAGGTAGGGATTTGCATAGCTGCTCCCCAGCTCCTCCAT
ACCTCGGCTCCCCACACAGCACTGCTAGGCGCCCCTGCAGGGTCCTCCCT
CAGCTCAGAGGCTGCCCTACTGGCTGAGGTGCAGGCTGGTGCCAAGAGAG
CATGCTGCTCTGTCAGCATGAGGCAGTGAGCAGGGCTCTGGGCAAGGGTG
GCATCCAGGAAAGCCCTTGAAGACTGAGGGGCGCTTTGCTGGTTGGGCCA
AGGGAGGAAGGGCCTGCCTGGCAGAAGGAACAGCCTGGGCAAAGGCCCCA
AGATGGGAAAGCCTTGGTGGTTGGGGCATAGAATGGGGGGGCAGTGGGGC
CGGCCAAGACAGGAAGGGCCTTGAATGTGAGGGTGAAATGATGGGGTGTC
CCTGGGGGCCTTACTCCCAACTCAGATCAAGTCCTTTGGTGGCAGGGGCT
GCCCCGGTCCTCTGACCCAGGGCAAGCTCTATGAGCGGTGGAGCCCA

3131. chr22_PACSIN2_NM_007229_-1.53684
ATGCCCGGCCCGTGATTGGCTCGGAACCACCTCAGGTCCTCCACTGCATC
AGCTGCTCTGATGCTC

3132. chr22_SCUBE1_NM_173050_1.80422
CCTGGTGGTTCTCCGAGGCGTACAGGCGCCCATCGCGCACGATGTCCTCT
ATGAGTTGCTGGTAG

3133. chr22_SCUBE1_NM_173050_-2.42049
AGCAGCGGCTGCCTGGCGGTCTCCTTTGCTCGTGCCTGG

3134. chr22_LDOC1L_NM_032287_-1.64354
TAAAGATTCCGTGCTCGGGCAGGCAGGGCTGGCGCTGGACTAGTCCCGTT
GGAAGCTGGATGCAC

3135. chr22_SMC1B_NM_148674_1.55407
CCTTAAGTTCTTTATAACGATCCAG

3136. chr22_PPARA_NM_005036_-1.96443
CAGTGTCATGTGAGGACGTGCTTC

3137. chr22_PPARA_NM_001001928_-2.25239
CTGGCAAGTTCGATGTTAGCTCCCGGGACACTCAGCAGCGATGGTGAGCA
TTTTGGTTTCCTTAAGGCCCAGCAAGACTTCCAGGGACATCTCTGGTGAA
GCCAGAATGGAGACACCCGTGACCTCAGGCTGAAAGTCACTCGACATTGG
TCTCTTGTGTTGATAGGGAAGGAAATCAGGCATTCCTATTTCTTTAAATA
ACAAAACCACTAATTGCCACTCAATGCTGGAATATTTTGGGTCACCTAAT
CATAGATTTCTCAGGGCATCAATACTCAAATATAGGCTGATTATGCCCCA
GTTCAAATGGGAACTATTAACAGAGTGCATTTCTTGCTTGCTGGGTTTCA
ACAGACATCAGCCAAAAGAACAAAAGAGATGTCAGGACAGATTCCAGGAG

Figure 3-254

TGTCGGAGCACATGTGTGGCACCCGCTCCCTCTGGCAGCGAATGTAGGAA
GTCGCCAAATTTACCCACTCTTCAACAAGTCATTGTTTAAACACGGTTTT
TCATTTTCTCAACTTTTAATAGCAAAAAGTGCCAAAGTCCTCAGAGACCT
AACAGCCTTGGTCTACCGTGCTGACCAGGGTGAAGGCACGGCGAGGGACT
CCTCCCAGACGTGCCTCTTGTGTGCCAGCTGGCTGTGGCTCGGGAGCAGA
CGCAGGCCTCTCCATTGTCCAGGGGAGCCTGGCGGCGCATCCCTCCTCTC
CCACCTCCTGGCACTTCCAGCTGGGTGTCCCACATGTTGGATTCCGTCCC
CACCACACTTCCAGAGACCGGAGAACTGTGCAGGGCCTAAGGCCGTTTGG
ATGAATTGTCAAAACAAGATGCTTCCAGTTACAGCGGCAGGAGCGGGACT
GGGAGCACGGGCTGACGGCTGCTGGTGCCTTTCTTCCCACCTCGCTTGCC
TGTTTCCGCTTGACCCTTCCTCCAGCTCCGATGAGAAGAGTATAAAGCAT
CTTCCTAACGGGTGTGTTTGCTATACGAACATAATGGACGTGAAGTGGGG
CAGAAACCCAGAACTCAGCATTCAAGGATGCCCAGGAGAGCTGTCCCTGT
TTTAAAGAGCTGTGTTTTGTTTTGTTTCGCATTTAGAGAGCAGACAAGGC
ACCCTTCTGCTGCGCTGATACGTTTCTTA

3138. chr22_CELSR1_NM_014246_1.63828
GCACTGGCCGTTGGTCTTATTACAGTCGGGATCAAAGCCTTTGCTGACGG
CACAGTGGCA

3139. chr22_BRD1_NM_014577_1.55933
CGAGGCGGCGGCATCAGTGGAGATCCACATGCTGCTCT

3140. chr22_ALG12_NM_024105_-2.37648
GCGGCTGCCACGTCAATGTGCAGA

3141. chr22_MOV10L1_NM_018995_-1.682
TTTAATGTTGCAATCACCAGACCCAAAGCTTTGCTGATAGTGCTGGGAAA
CCCCCAT

3142. chr22_TRABD_NM_025204_-1.88137
GTGCATCCTAGCCCGCCCGAGGCCCCTGCCACCCCCCATGGGGGTCTGGG
CCCGGCCTCGCCTGCCCTCCTGGGCCAGTCACCCCTCCCCCAGCCCACCC
AAATAAAGGATTATT

3143. chr22_SELO_NM_031454_1.68749
GCGCTCGGGGCTTCGCTCGCGGCTGCCCGACTCTTGCCCCTCGGTCGCTG
TTCCCCGTCGCCGGCGCCCCGCTCTACGTTGTCGGGCGCCGCCAT

3144. chr22_SELO_NM_031454_1.66373
CGGGGCCTGCTTCACCCGCGTGCAG

3145. chr22_SBF1_NM_002972_-1.53843
ACTCTGGTTCTAGAAACTCGCCTGCAGCCGCTGGCTGGACCAGCACACGC
TGACGGGGCCGGACTATTTACAGGCCCATTGCGGGCTGTACCTTGGCCAC
CTCCCGGCACGGTGCTCAGCTGTGACGCCAAAATAAGTTAGGG

3146. chr22_LMF2_NM_033200_-1.53863
TGCAGCAGGCGCAAGACCAGGCTTGTGAACCACGGGCTGTGC

3147. chr22_KLHDC7B_NM_138433_-1.59663
CTACCTGCGCACCTGCATGTGTTCAACCCCCGGGAGAACACCTGGCGGCC
CCTGACCCAGGTGCCCGAGGAGGCCCCGCTTCGGGGCTGCGGTCTCTGCA
CCATGCACAACTACCTGTTTCTGGCGGGGGGCATCCGTGGCTCCGGTGCC
AAGGCCGTCTGCTCCAACGAGGTCTTCTGCTACAACCCTCTGACCAACAT

Figure 3-255

CTGGAGCCAGGTTCGGCCCATGCAGCAGGCCCGAGCCCAGCTCAAGCTGG
TGGCCCTGGACGGGCTGCTCTATGCCATCGGTGGCGAATGCCTGTACAGC
ATGGAGTGCTACGACCCGCGAACAGACGCCTGGACCCCACGCGCGCCACT
CCCCGCAGGCACCTTCCCTGTGGCCCACGAGGCTGTGGCCTGCCGTGGGG
ACATCTACGTCACCGGGGGTCACCTCTTCTACCGCCTGCTCAGGTACAGC
CCCGTGAAGGATGCTTGGGACGAGTGCCCATACAGTGCCAGCCACCGGCG
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TGCGGGGCGTGGGCGCCGCCGTGATGCGCTACAACACAGTG

3148. chr22_CHKB-CPT1B_NR_027928_1.57625
TTGGAGACCAAGTAAAGGCAGAAGAGGTGCCTGTCGATCCCTGCCCCGGT
CATGGCCAGGCGGTACATATTCTGGTGCTTCTTAGCAGCCTTCTGGAAGA
GATCTCGCAGGTCTGC

3149. chr22_ARSA_NM_000487_-1.62594
TCAGAGAGCTGGAGGCGTGGCAGGCAGGGTCTGCAGTGGTATCACTGTGG
GCA

3150. chr22_ARSA_NM_000487_-2.28437
TGACGGCCGCCTCCTGAAGCTCCA

Figure 4-1

3151. chr1_ENSG00000201898_snoRNA_1.17744
TTTAGAATGTCAAAATTGATTTTGTAATAGTCAGGACAGGATAAACAGTCGCTATATTAAGACCATGTACGTGTC
CCTAGACCTAGTTCTTTCCCTACGTCTGTTTTTATAAATGCTGGTGATAAAC

3152. chr1_hsa-mir-181b-1 // hsa-mir-181b-2_miRNA_1.16141
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3153. chr1_U44_CDBox_1.14249
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3154. chr1_ACA16_HAcaBox_1.10574
TTGGCCCTTATCGAAGCTGCAGCTGCTTCCGCATAGCTGCTGTGGTCAAAAAGGAGCCCAGAGTGACAGTTTTCC
TTGACGGTCGCCGTTCTGTTTGTTGTAACTGATCTGCAACATTTTGGGAAAATACAGTT

3155. chr1_hsa-mir-186_miRNA_-1.26223
GCCCAAAGGUGAAUUUUUUGGG

3156. chr1_ACA26_scaRna_-1.20014
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3157. chr1_ENSG00000201791_snoRNA_-1.14915
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ACTCGATTCCATAATAAGACAGAGACGCTTGGTCTCAAACAT

3158. chr2_hsa-mir-933_miRNA_1.39658
UGUGCGCAGGGAGACCUCUCCC

3159. chr2_ENSG00000212581_snoRNA1_1.12901
TTATCAGCTGGGATAATCTTTACCTGTTCCTTCTTTTGGAGGGCAAATTAGGACATGATTGGGGTTCACATAGTAT
GCGATTAACGTCTCTGAGTAATCAGGACTTCCAGTACCCTGATTGTGCCTATCTGAT

3160. chr2_hsa-mir-216b_miRNA_-1.29243
AAAUCUCUGCAGGCAAAUGUGA

3161. chr2_hsa-mir-26b_miRNA_-1.27088
UUCAAGUAAUUCAGGAUAGGU

3162. chr3_ACA4_HAcaBox_1.12488
TACCAAAAGTTAGCTTTTTGGGGGGCAGGTTTTTAAGTAACCTTTGCCAACTTGGGCTATTTGGAAGAGTAAAAG
ACCACACTCCACAGTGGGCTATACCACTTAGTATAGTTCGCTACTATTTTGTGGCCTACATG

3163. chr3_hsa-mir-569_miRNA_-1.34492
AGUUAAUGAAUCCUGGAAAGU

3164. chr3_hsa-mir-944_miRNA_-1.25927
AAAUUAUUGUACAUCGGAUGAG

3165. chr3_hsa-mir-548i-1 // hsa-mir-548i-2 // hsa-mir-548i-3 // hsa-mir-548i-4_miRNA_-1.20759
AAAAGUAAUUGCGGAUUUUGCC

Figure 4-2

3166. chr3_hsa-mir-568_miRNA_-1.18586
AUGUAUAAAUGUAUACACAC

3167. chr3_hsa-mir-567_miRNA_-1.16603
AGUAUGUUCUUCCAGGACAGAAC

3168. chr4_ACA11_HAcaBox_-1.14069
GCGCTCACTAAGGCTCGGTCCTCTCCACGTGGTCCTGACCTGTCCTCTGTGAGCAAGAGAAACAGGACTGGTTTG
GGGGTGTCCTGTCTCAGTGGACACAGGACACCACGGTTTTCAGTACAACA

3169. chr4_ENSG00000202440_snoRNA_-1.14053
TAGCATATGATGGAAAAATCTTAATCTTCTGAGACTTGTGATGTCTTCAAAGGAACCACTTCAATGCAA

3170. chr5_ENSG00000212363_snoRNA_1.14444
GTGACATGTATGTTTTTGTTTAACTTGTATACAAAGGCTTATGGATAGGTGCAAAAATAAATTCTCTTTTGCAACC
CAGAACTCATTGTTCAGTGTGAGTTTTGATACATATAAGAAGGGATATT

3171. chr5_ENSG00000201551_snoRNA_1.13479
ATACCTAAACCCAAGAATCACTTTCTTATAGTGATGATTTAAACAGATGCAAACAGCGAGCACATCTTGTCACCTT
TGCGGGACTGTGGCTGTGCCCCTCGCAGTAAATTTGGAGGTTCTACATCC

3172. chr5_U95_CDBox_1.12758
GCGGTGATGACCCCAACATGCCATCTGAGTGTCGGTGCTGAAATCCAGAGGCTGTTTCTGAGC

3173. chr5_hsa-mir-581_miRNA_-1.26672
UCUUGUGUUCUCUAGAUCAGU

3174. chr5_hsa-mir-548p_miRNA_-1.17659
UAGCAAAAACUGCAGUUACUUU

3175. chr5_U19-2_HAcaBox_-1.13734
TTTCCAGCAGTAGTCAGCCATCCGGACAGAACCGTTCCTGTGATGGTGTTACACTGCTGGGAGAGGAATGTCTT
GTCTTCATCCGGTTGCCTGCGCCACTGTTCTGGTGGCGTCTGGCACTGGTGCAAGACAGAGCTGTGCTTCCCCGA
GAGTGTGCTAAGCATTCACTTTGGCTGCTTAGTTCTAGTCTGGGAGCAGACAGAG

3176. chr6_ACA33_HAcaBox_1.1639
AAGCCAGCCAATGAATCTGCTTACCTGATTGTGTTTGTGCAGACATACTTTAAAAACTGGCAATAGTAAAGCCAT
GTTACGAGCCTTAAGGACATTGAAGTCGTTAAGGTCCCTGAGAATGGCTATAACAAAT

3177. chr6_hsa-mir-877_miRNA_-1.31816
UCCUCUUCUCCCUCCUCCCAG

3178. chr7_hsa-mir-335_miRNA_1.32246
UCAAGAGCAAUAACGAAAAAUGU

3179. chr7_hsa-mir-591_miRNA_1.13852
AGACCAUGGGUUCUCAUUGU

3180. chr7_hsa-mir-550-1 // hsa-mir-550-2_miRNA_-1.29982
AGUGCCUGAGGGAGUAAGAGCCC

Figure 4-3

3181. chr7_hsa-mir-93_miRNA_-1.19393
CAAAGUGCUGUUCGUGCAGGUAG

3182. chr7_ENSG00000207217_snoRNA_-1.14222
TGGGTTTGGATTATGACAGGCCCATCCCCCTGGACCTCTCATAGTGCCCCATGCCAGAGCAAACTGTGGCCCCGA
ACCATTGCCTGGCTTCTGTACCCGTGGGCCACTGGCACTGAAGAGGGTTACACAGTG

3183. chr8_ENSG00000212342_snoRNA_1.13696
TCTCGTGGTAGTTTTCTTTTTGGCACATTTGTTAAGTTTTCAAATGGGCCTAACACTGCCACATGTATTATACTGGA
GTTGGCAAAGGCCTGTGACAATGAGATATCTCTCAAGCCTTTCACGCCTTTCCTCTATCAGAGAATGGCTCCCAC
ATGT

3184. chr8_HBII-276_CDBox_1.13068
ACAATGATGACTTAAATTACTTTTTGCCGTTTACCCAGCTGAGGTTGTCTTTGAAGAAATAATTTTAAGACTGAGA

3185. chr8_ENSG00000206853_snoRNA_1.12239
AGCCTCCTGGTGTTTAACACAGCTGTGTTCTTATACTGACTGTGTAGAAAGAGAAGGAAATAAACCTTACCCCAT
ATGCATTTCATCCCCGGACCCTGCACCTCGTCTATATTGTGAATAGGGAAATATGG

3186. chr8_hsa-mir-151_miRNA_1.11986
UCGAGGAGCUCACAGUCUAGU

3187. chr8_hsa-mir-937_miRNA_-1.20015
AUCCGCGCUCUGACUCUCUGCC

3188. chr8_hsa-mir-30d_miRNA-1.15544
CUUUCAGUCAGAUGUUUGCUGC

3189. chr9_hsa-let-7d_miRNA_ 1.30382
AGAGGUAGUAGGUUGCAUAGUU

3190. chr9_hsa-mir-31_miRNA_-1.24627
AGGCAAGAUGCUGGCAUAGCU

3191. chr10_U108_HAcaBox_1.18615
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AGATGGCAAAGGCTTGTGACGGAGATATCTCTCTTAAGCCTTTCCTGCATCAGAGAATGGCTCCCACATGT

3192. chr10_ACA19_HAcaBox_1.08483
GTGCACATTTCATTGACCTGCTTTCTTTTATGTGAGTAGTGTTATTTCTTATGTGCTATACAAATAATTGAAGGCTA
ATTAGCAGTATAACTATAAATAGTAATGCTGCCAGTCTCCTTCAGACAAAA

3193. chr10_hsa-mir-607_miRNA_-1.20511
GUUCAAAUCCAGAUCUAUAAC

3194. chr11_hsa-mir-548l_miRNA_1.231
AAAAGUAUUUGCGGGUUUUGUC

Figure 4-4

3195. chr11_ENSG00000201980_snoRNA_1.16939
ATTGCACGTTGTTGGAGCTTGGAGTTGGTGCTCTAACTGGCTGATAAACTTGCAAGTGTAGGTAGTATGCTATGT
GAGGGGCAAATTTTTCAGTAACATGACAAAGGTCTTTGGCCTAGTGAGTAGAGTTTGACAATAATCCTCGCTGCA
AGT

3196. chr11_U99_HAcaBox_1.13188
CCTCCTTTTCTTGGCGGGGATCGGGCTTGTGGTGCCGCTCCCCGTAATGTACGGAGGAAGAGGGAAAGGGCTCT
GGCCCCCTCGGCGTCATGTCTTCGGTGCTGGCGGCTTCCCATCCGCTGGTTCTATCCTCAAACGCCGGGACACCG

3197. chr11_ENSG00000212277_snoRNA_1.12722
ACAGATGATGAACTCATTGACAGACATACAGAGACTGTGTGCTGATTGTCATGTTCTGACTTA

3198. chr11_ENSG00000206976_snoRNA_1.12188
GGCCTCCTGGGATCCCATCTGGAAAGTGCTTAGTATTCTGCCTGCTTCACAAAGGGAGGGAAAGCAAACGTGGT
GAGGCACCCTTTCCATTCCAGCTTGCTCGGTAGCTGGTGATTGGAAGACACTCTGTGACAGCG

3199. chr11_ACA54_HAcaBox_ 1.11476
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CATGACTGACTGACTGGTGGCTTTCAGTTTCAGGTCTTGGAGACAAAT

3200. chr11_mgh28S-2409_CDBox_1.10388
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3201. chr11_hsa-mir-129-2 // hsa-mir-129-1_miRNA_-1.28449
AAGCCCUUACCCCAAAAAGCAU

3202. chr11_ENSG00000212551_snoRNA_-1.1303
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CATAAGGAGGAGGCACAACATTCTCCCTAGAGCCTGAAGCTGGCTCTTGGTGTTTCATGACTACAGCAGCCATTT
GCCACTGATGACTGTTCTCTTCCAGGAGAATAAGAAGGAGAAGATGCAGTTTGG

3203. chr11_U28_CDBox_-1.12887
GTCAGATGATTTGAATTGATAAGCTGATGTTCTGTGAGGTACAAAAGTTAATAGCATGTTAGAGTTCTGATGGCA

3204. chr12_hsa-mir-331_miRNA_1.22856
CUAGGUAUGGUCCCAGGGAUCC

3205. chr12_hsa-mir-148b_miRNA_1.22081
AAGUUCUGUUAUACACUCAGGC

3206. chr12_hsa-mir-148b_miRNA_-1.1608
UCAGUGCAUCACAGAACUUUGU

3207. chr13_ENSG00000199282_snoRNA_1.12355
TGGCAAGCCTCCAGCGTGCGTGGGTCTGTGGTGATGTGTGCATTCCTACACTGCTTGCCAGAACAGTATTGAAAT
AGTGGAGCGTTTGTCCTGCTCCATCCAGAGCAAGGTTATAGAAATTTCAGACAATT

3208. chr13_ACA27_HAcaBox_1.10612
TACCCCCTTTTCACTTTGCCAGTTGGACTTATGTCTTTATTGGTCATTCAAGTGGGGCAAAGGAAATATCCTTTTA
AAACTCAGGCAAACTGGGTGTTTGTCTGTATCCTGTCAGAGGAAACAAAT

Figure 4-5

3209. chr14_hsa-mir-654_miRNA_1.2714
UAUGUCUGCUGACCAUCACCUU

3210. chr14_hsa-mir-541_miRNA_1.19625
UGGUGGGCACAGAAUCUGGACU

3211. chr14_U93_scaRna_1.12552
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AGAGGAAGCTGAGGCATGCCTGCTCGAGAGCCAGCTGTTCCATGTGCAATTTTCCTCTGATAGTTTCTGGTCACT
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3212. chr14_hsa-mir-543_miRNA_-1.26569
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3213. chr14_hsa-mir-432_miRNA_-1.26277
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AUCAUAGAGGAAAAUCCACGU

3215. chr14_hsa-mir-493_miRNA_-1.15138
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3216. chr14_14q(II-4)_CDBox_-1.126
TGAGCCAGTGATGAAAACTGGTGGCATAGAAGTCAAGGATGCTGAATAATGTGTGTCTAGAACTCTGAGGTTCA

3217. chr15_ENSG00000199633_snoRNA_1.30231
ATGCAGGTACTGTTACAATATGACTGAAGTGATTTGTTGTCATTTCCCCTGCTTAAAGCCCTTGATATATAACTAT
CTCTGTCTAACTCATTCTGAAGTAAGACAGAGATGCTTGGTTTCATTTTT

3218. chr15_HBII-52-5_CDBox_1.14086
GGATCGATGATGAGAACCTTATATTGTCCTGAAGAGAGGTGATGACTTAAAAATCATGCTCAATAGGATTACGC
TGAGGCCC

3219. chr15_HBII-85-3_CDBox_1.13418
TGGATCGATGATGAGTCCCCCATAAAAACATTCCTTGGAAAAGCTGAACAAAATGAGTGAGAACTCATACCGTC
GTTCTCATCGGAACTGAGGTCCA

3220. chr15_HBII-52-41_CDBox_1.11431
GGGTCAGTGATGAGAACCTTCTATTGTCCTGAAGAGAGGTGATGACTTAAAAATCATGCTCAATAGGATTACGC
TGAGGCCC

3221. chr15_HBII-85-4_CDBox_-1.14266
TGGATCGATGATGAGTCCCCCCAAAAAAACATTCCTTGGAAAAGCTGAACAAAATGAGTGAAAACTCATACCGT
CGTTCTCAGCGGAACTGAGGTCCA

3222. chr15_HBII-438A_CDBox_-1.14261
GGATCGATGATGAGAATAATTGTCTGAGGATGCTGAGGGACTCATTCCAGATGTCAATCTGAGGTCC

Figure 4-6

3223. chr15_ENSG00000212604_snoRNA_-1.13849
TGCCCCTGACCTGGGAAGAGAGGGGCCTGGCTGGTGGTATCCATCTCATACCAGCTAGGGATGAAGAAACCGC
TTGCTCATCCCAGCCTGGCTCCTGGTCTATGCCCATGCCTGGTTCGTGCCTTGGACATATCA

3224. chr15_ENSG00000212528_snoRNA_-1.11412
AAGACAACGTAAATATATGTATAAAGAGTATCTTCAGGAGACGTAATAATGTAAAAATCATGCTCAATAGAATTA
AGCTGAGGCTC

3225. chr15_HBII-52-21_CDBox_-1.11103
GGGTCGATGATGAGAACCTTATATTTTCTGAAGAGAGGTGATGACTTAAAAATCATGCTCAATAGGATTACGCT
GAGGCCC

3226. chr17_hsa-mir-22 miRNA_1.21361
AGUUCUUCAGUGGCAAGCUUUA

3227. chr17_U49B_CDBox_1.12667
CTGATGATACTTGTAATAGGAAGTGCCGTCAGAAGCGATAACTGACGA

3228. chr17_hsa-mir-1253_miRNA_-1.13437
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3229. chr18_ENSG00000199856_snoRNA_-1.13078
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TGCCACTGATGATTGTTCTTGTCTTCCTCTGGGAGAGTAAGACGGAGAGCATGCAGTCTGAGTG

3230. chr18_ENSG00000199856_snoRNA_-1.12167
AAGACTATACTTTCAGGGATCATTTCTATAGTTCATTACTAGAGAAGTTTCTCTGAATGGGTAGAGCACTGGAAA
CCATGAGGAGGAGGCACAGTGTTCTCTCCTGAGCATGAAGCTGACTCTTGGTGTTGCTTCACTGCACCTGCCATG
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3231. chr19 hsa-mir-99b miRNA 1.22661
CAAGCUCGUGUCUGUGGGUCCG

3232. chr19_hsa-mir-520c_miRNA_-1.22238
CUCUAGAGGGAAGCACUUUCUG

3233. chr19_hsa-mir-523_miRNA_-1.19767
CUCUAGAGGGAAGCGCUUUCUG

3234. chr19_hsa-mir-516a-1 // hsa-mir-516a-2_miRNA_-1.13252
UGCUUCCUUUCAGAGGGU

3235. chr19_U105_CDBox_-1.10671
CCCCTATCTCTCATGATGAACACATATGCCTCTGAGCTGCTGTGATTTCTGGCTTCAAAGTAAACGCTCTGAAGAA
GAGATGGGG

3236. chr20_hsa-mir-499_miRNA_1.2299
AACAUCACAGCAAGUCUGUGCU

Figure 4-7

3237. chr20_U71b_HAcaBox_1.17112
TCCCTGTATTCGAAAGTGATCGTGGGCTGCCTTTGCCCTGGTCATTGATAGTGCAGGGAGAGGAATCAATGAAA
GCGCTTCCCCGTGTTTGAAGGGTCCACTCCTATCCCTTCCAAACTCTGGAGCTTTCGTACATGC

3238. chr21_ENSG00000207147_snoRNA_1.18521
GCCCGCCTTGGCCTCCCAAAGTGCTGGGATTCTTACATCGACTGCATAGAAAGAGGAGAGAACATAACCTACCT
ACCCCGTACATACTTCAGCCCAGGTCCTGTGCCTCATCTGTAATATGAATGAAGAGACATGG

3239. chr22_hsa-mir-1286_miRNA_1.29375
UGCAGGACCAAGAUGAGCCCU

3240. chr22_hsa-mir-185_miRNA_1.17568
AGGGGCUGGCUUUCCUCUGGUC

3241. chr22_ENSG00000199783_snoRNA_1.15181
CCGCAGTGACAGCAATATTTTTCATCCACAGTTCACCTCATGAATGTTGTCACTTTGGGTCTGAGTGA

3242. chrX_hsa-mir-548m_miRNA_1.1709
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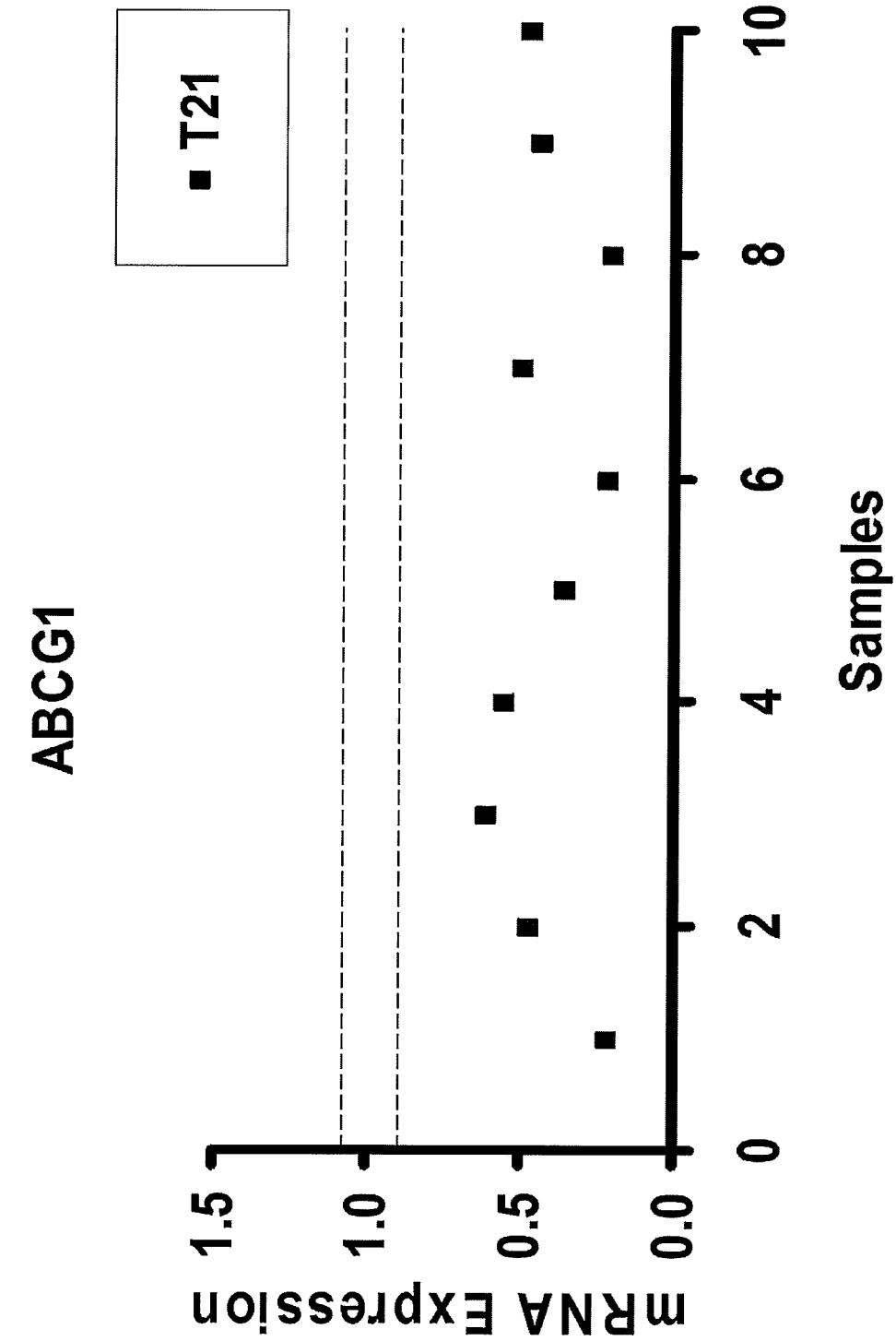
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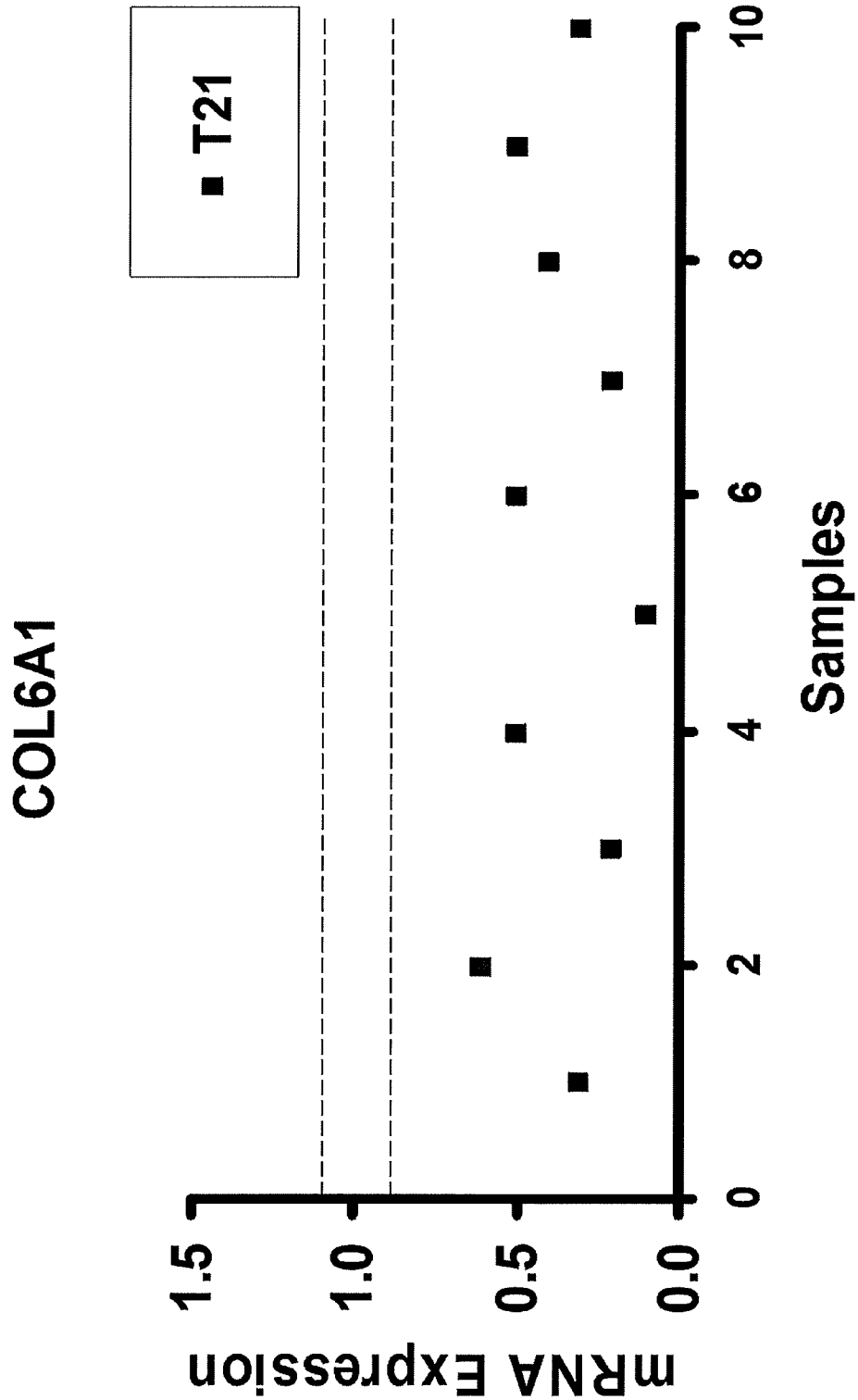
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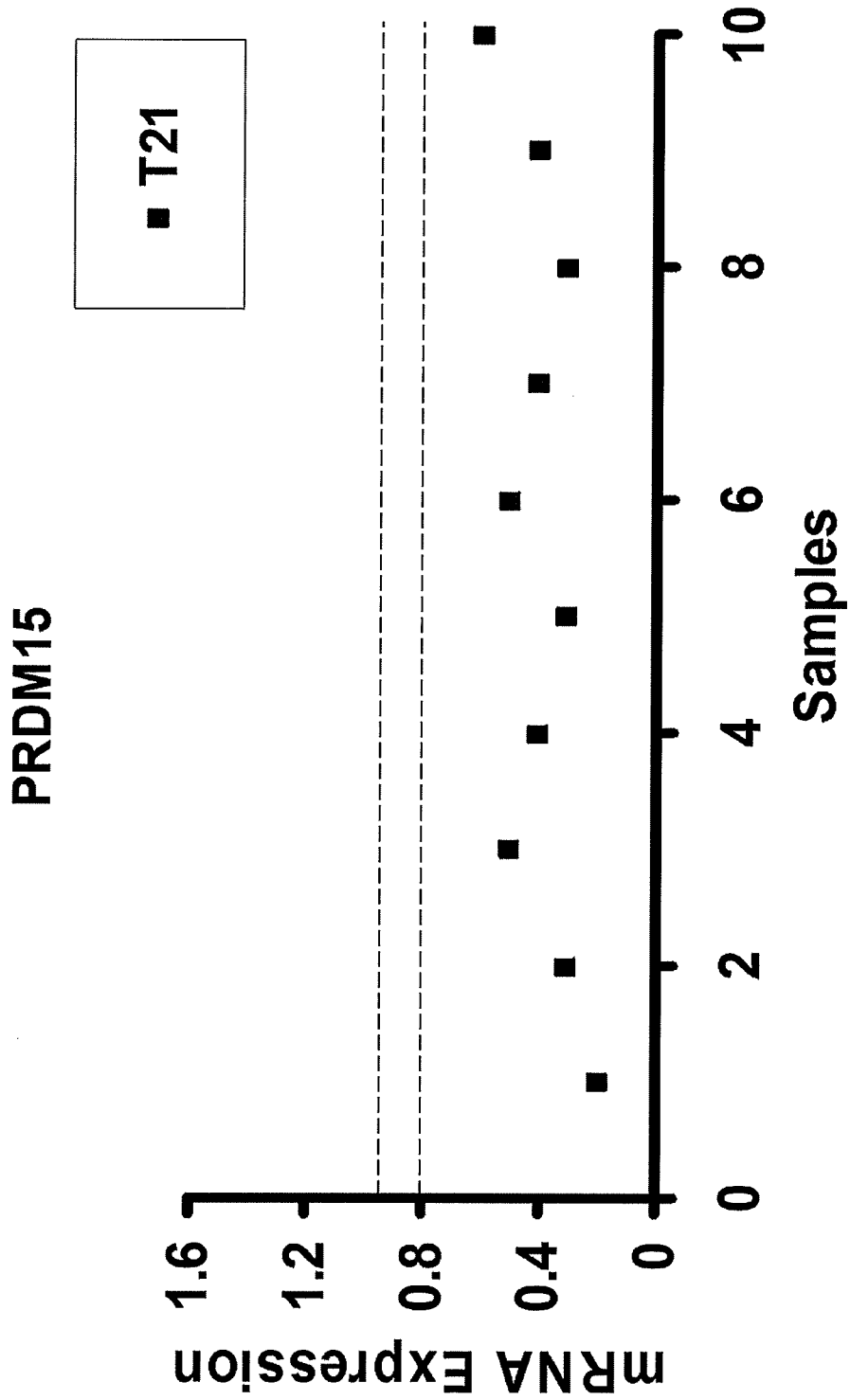
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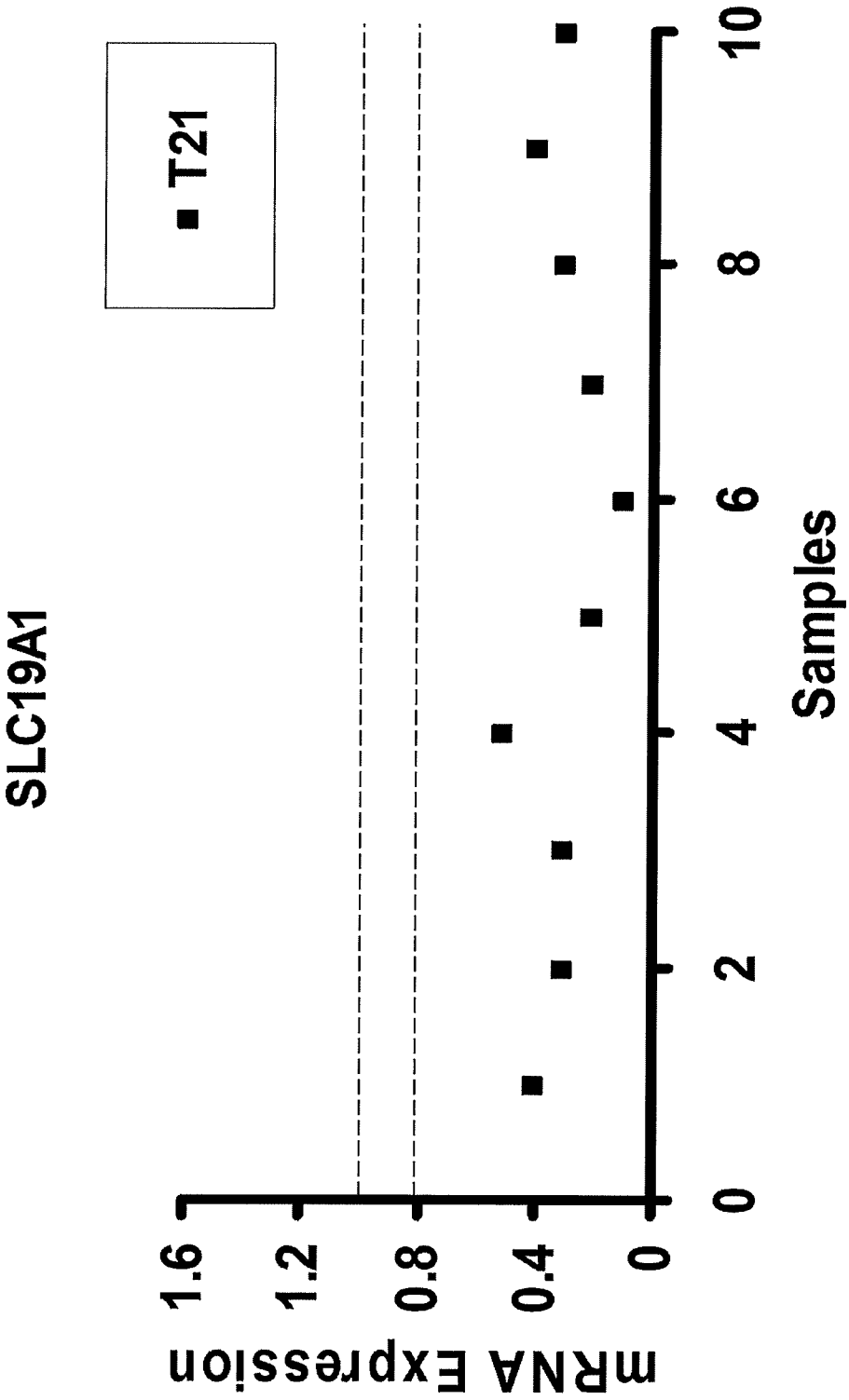
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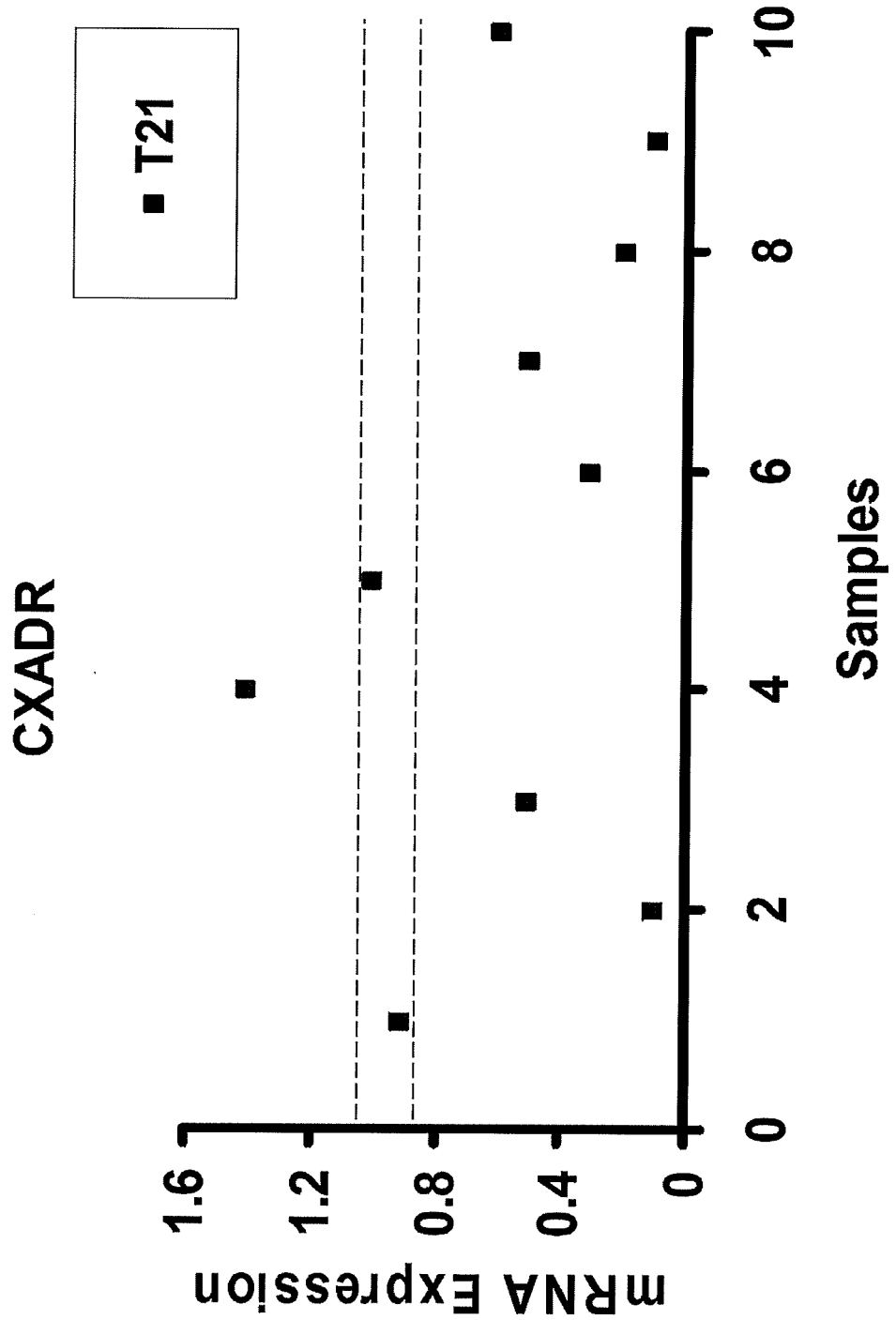
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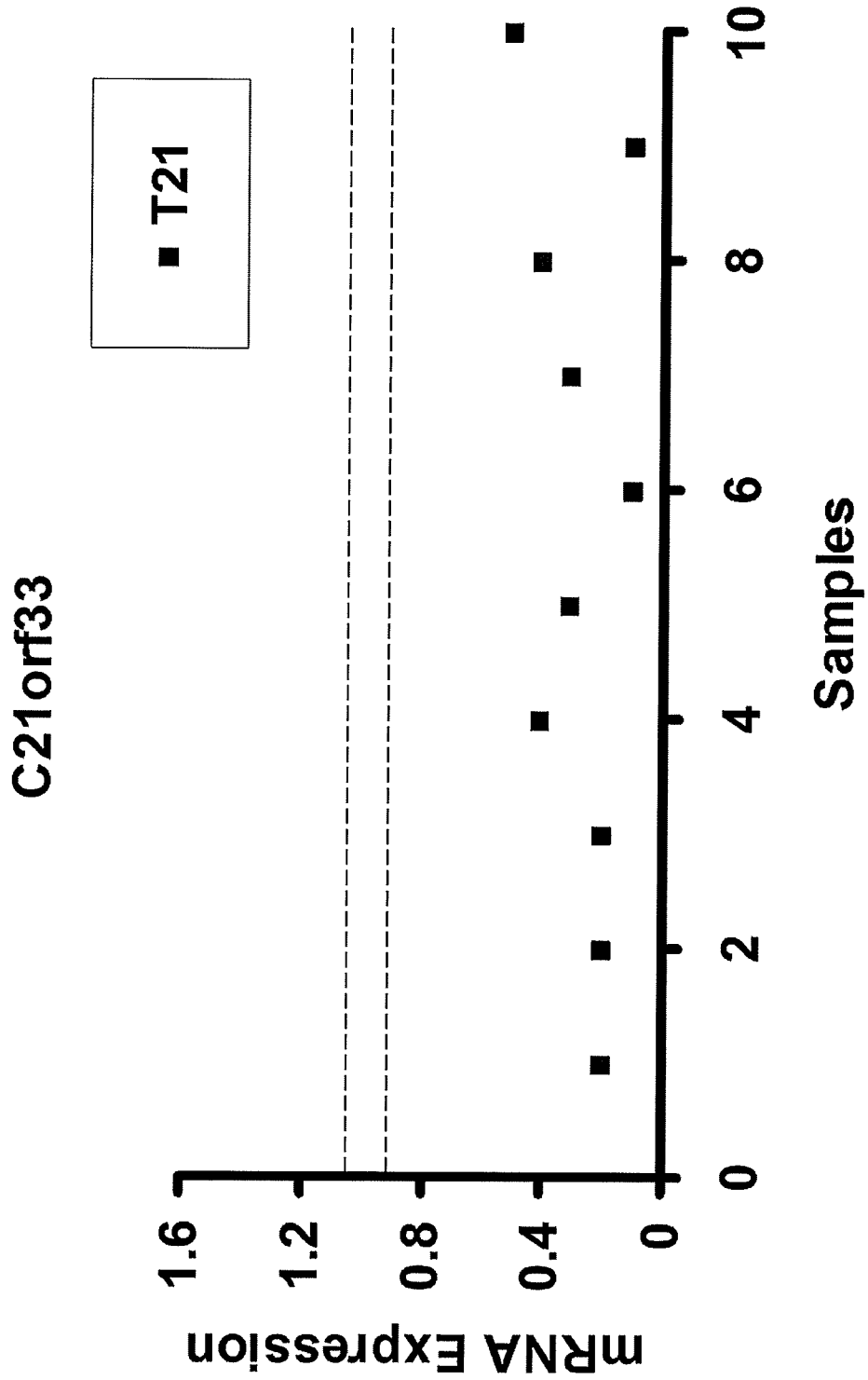

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0.0
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8
10
Samples

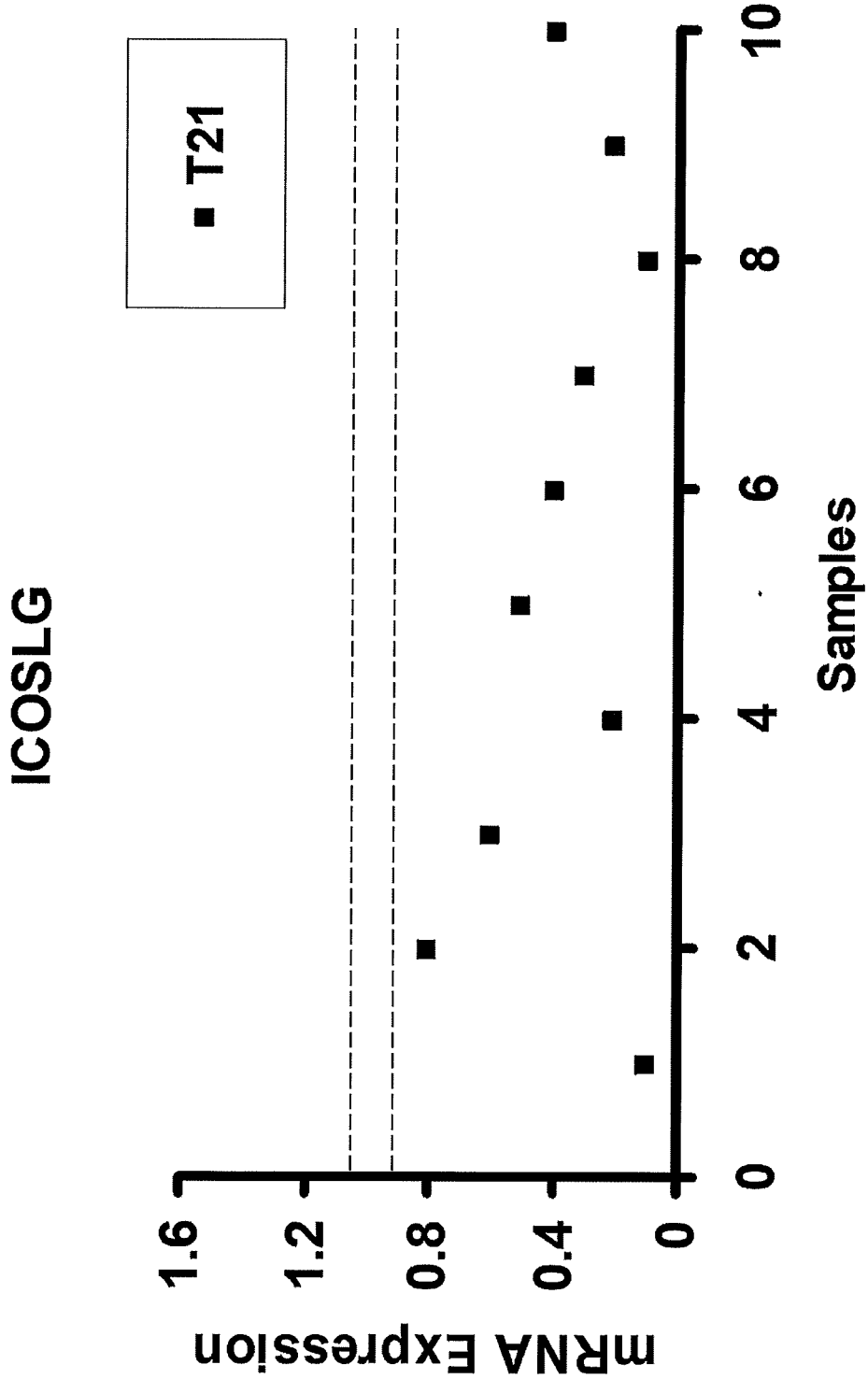

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T21
mRNA Expression
1.5
1.0
0.5
0.0
0
2
4
6
8
10
Samples

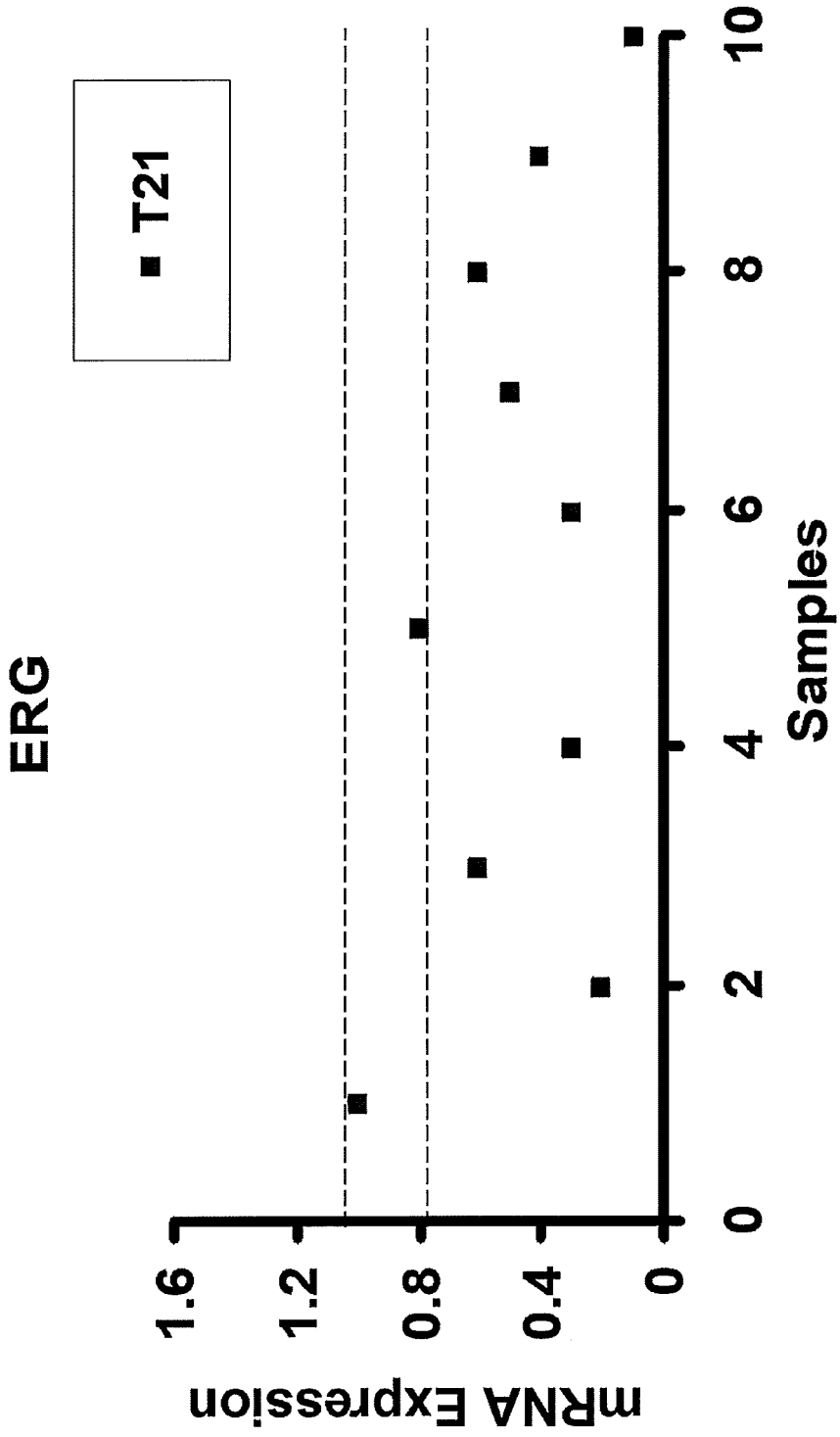

PRDM15
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

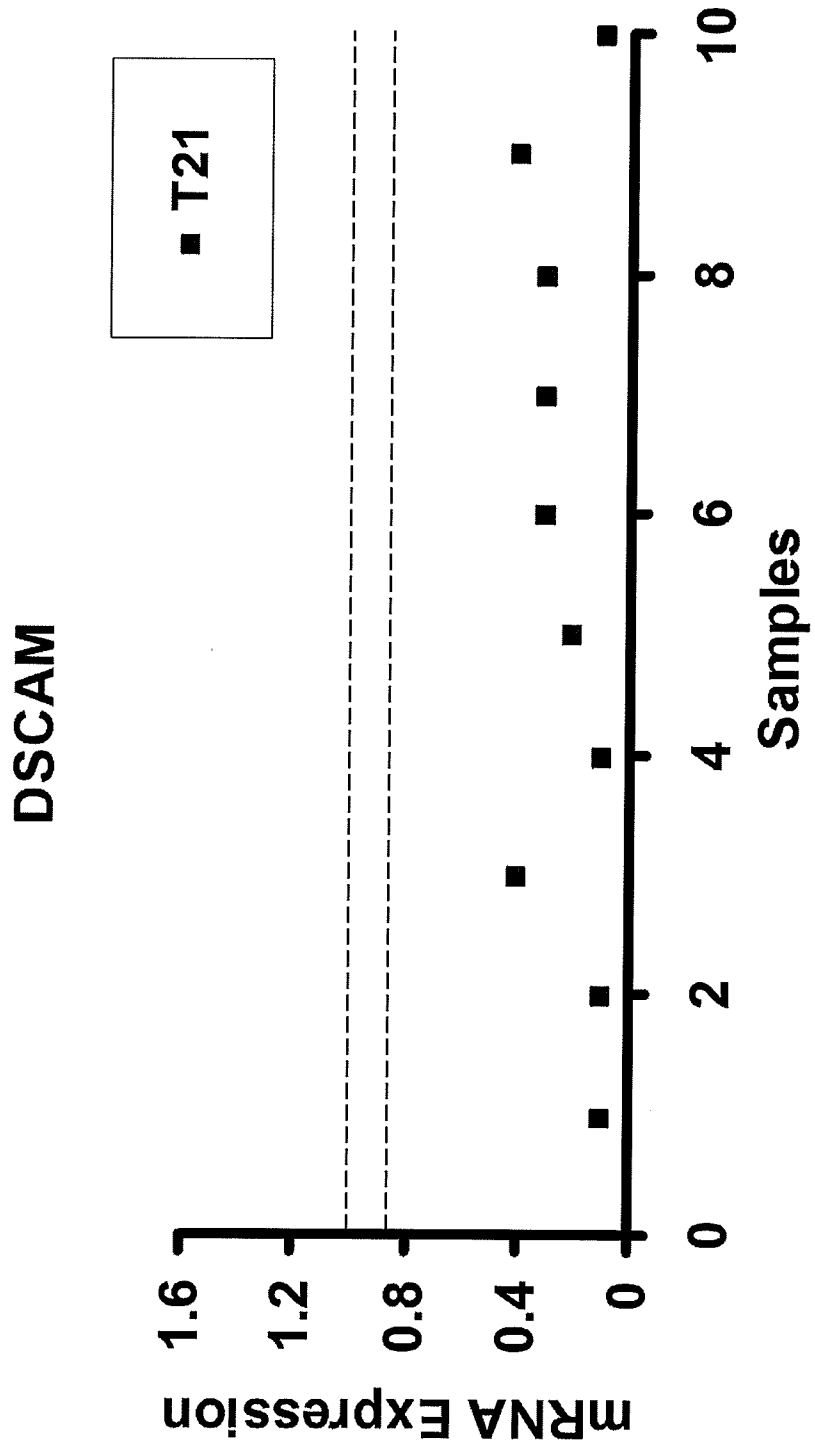

SLC19A1
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

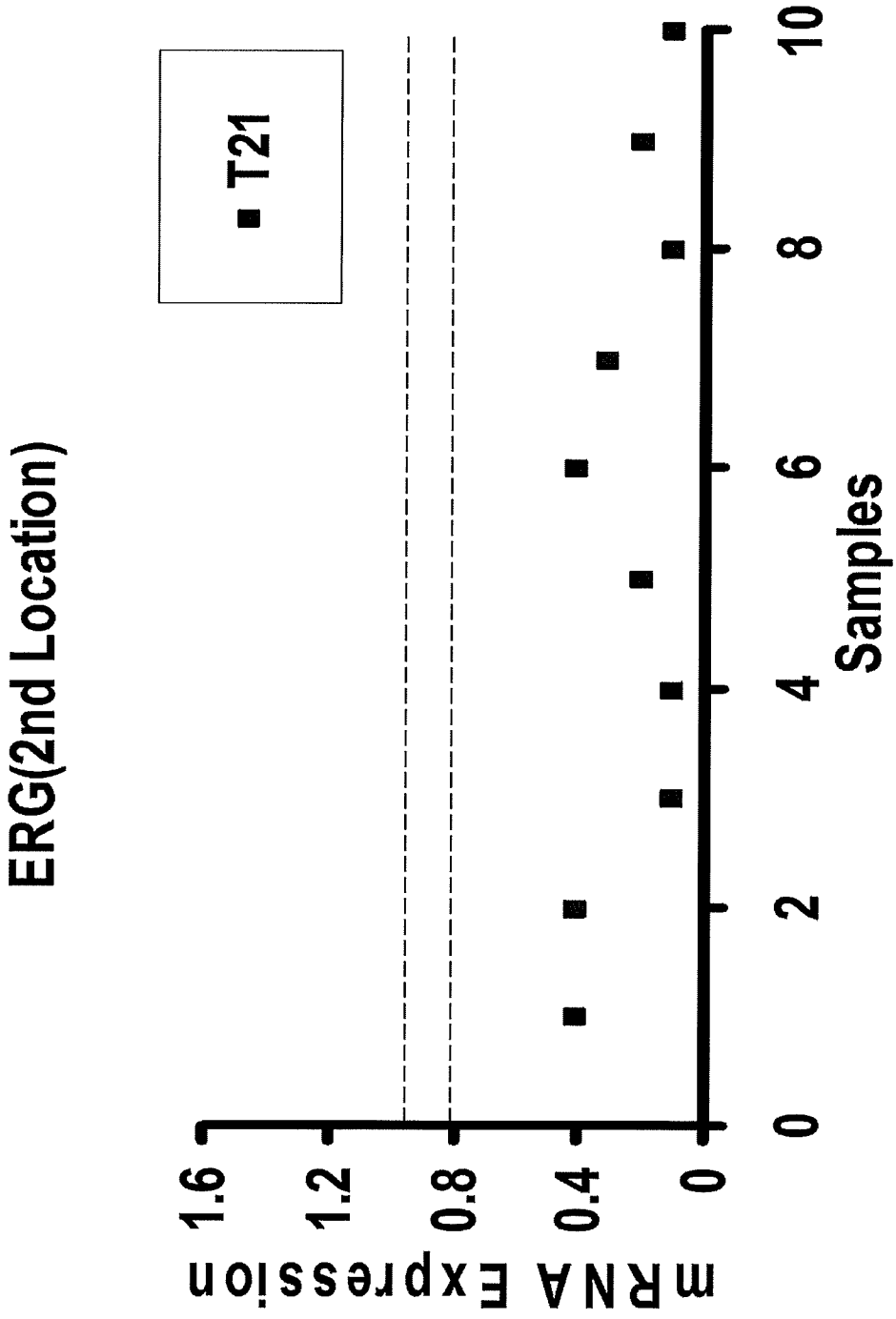

CXADR
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

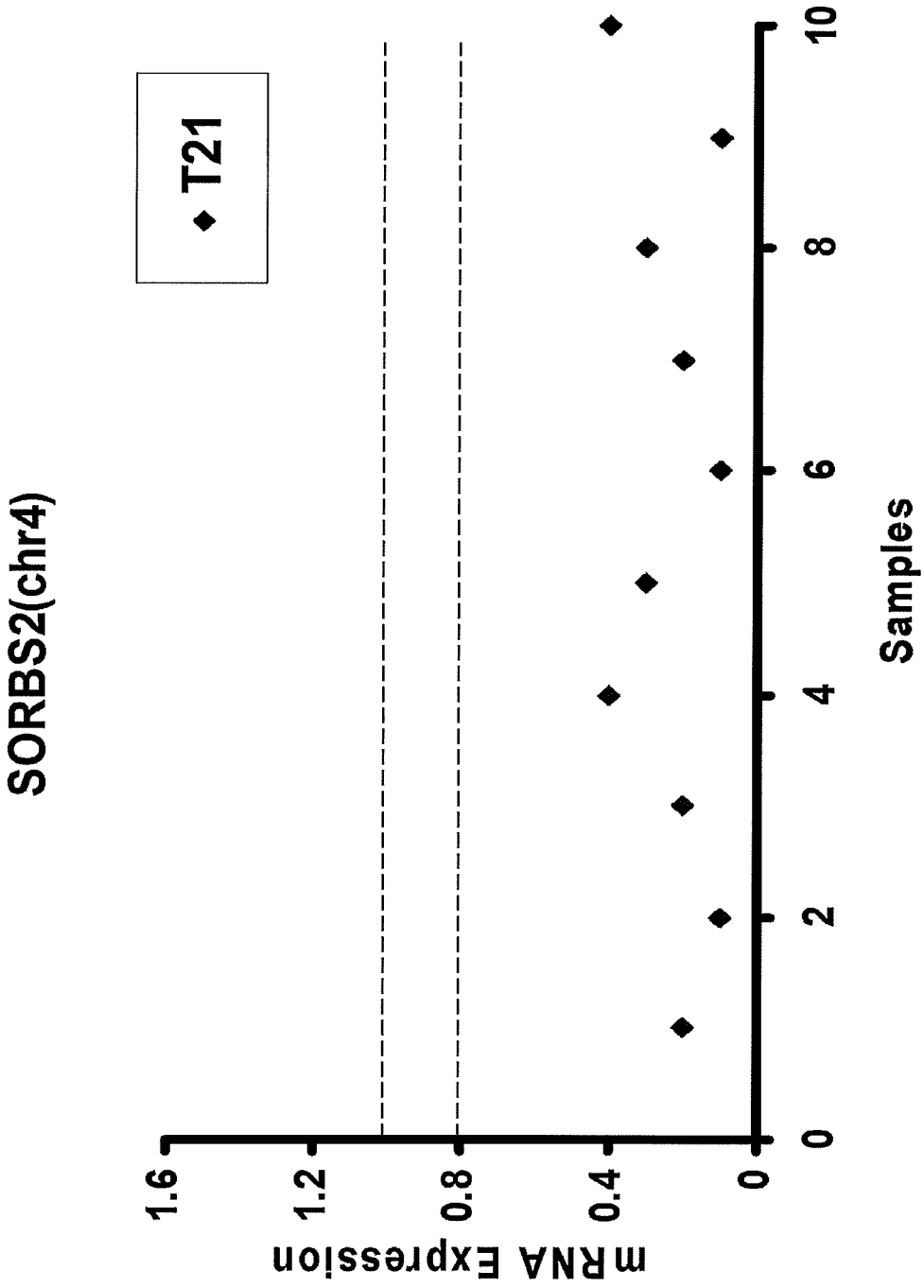

C21orf33
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

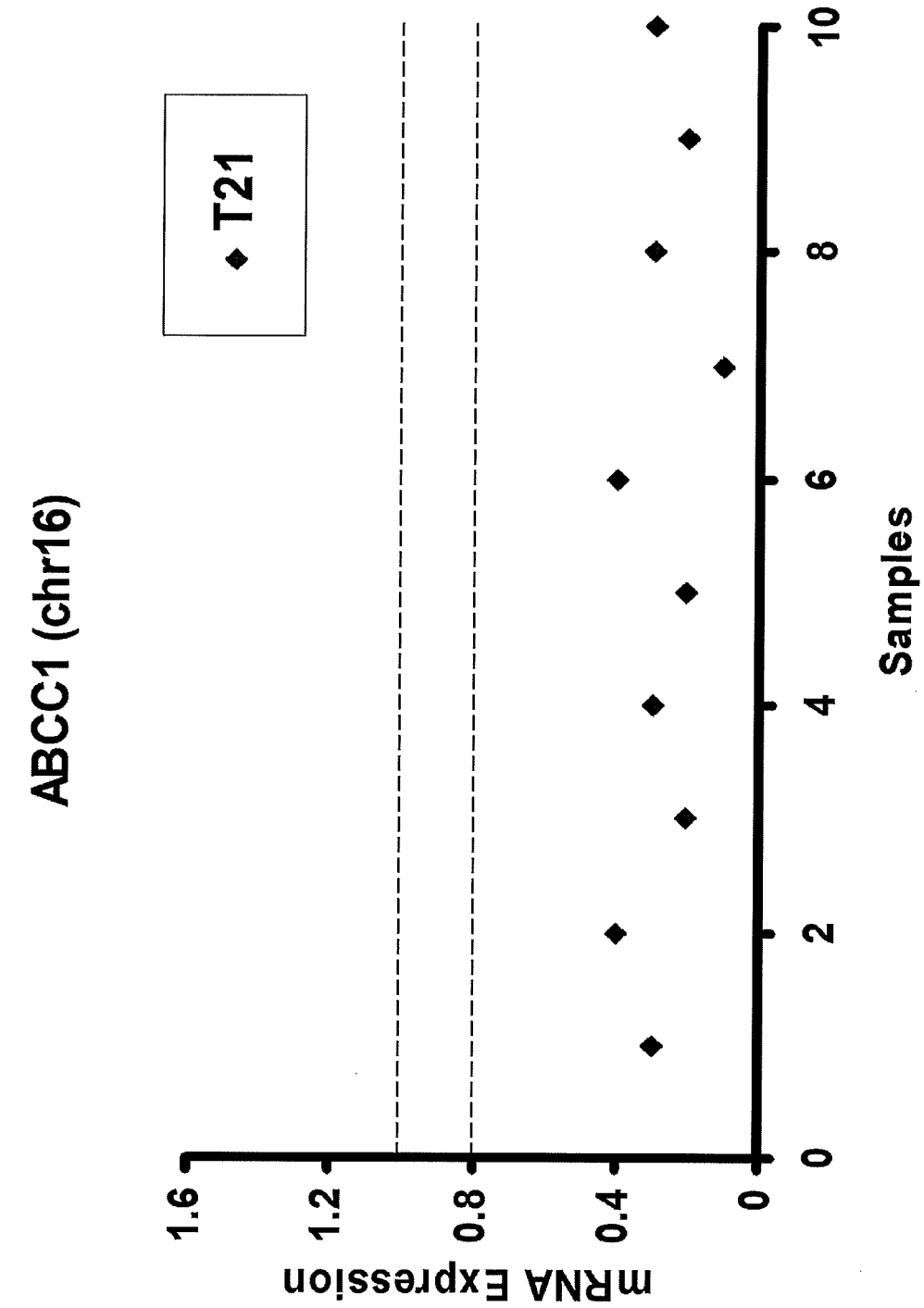

ICOSLG
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

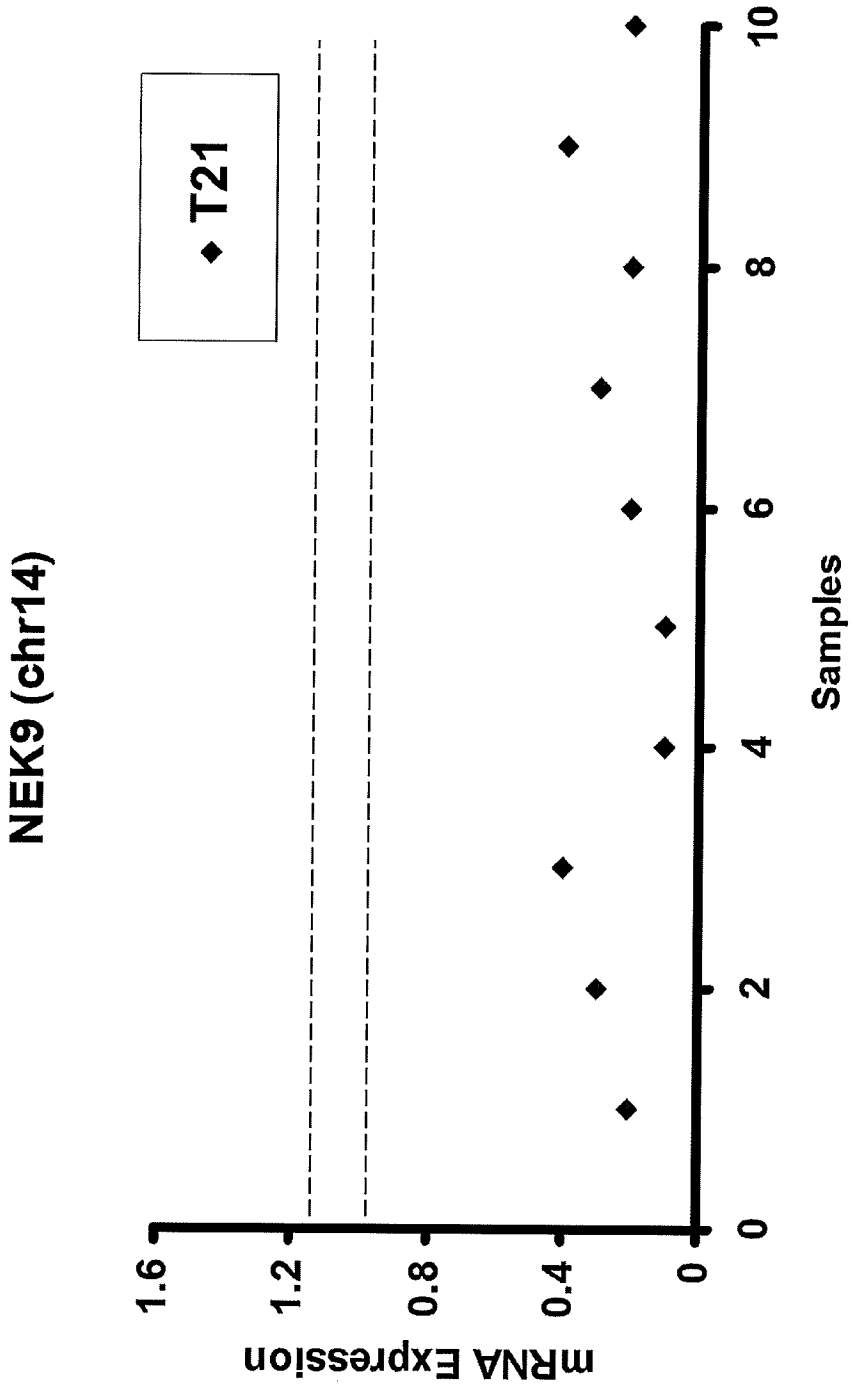

ERG
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

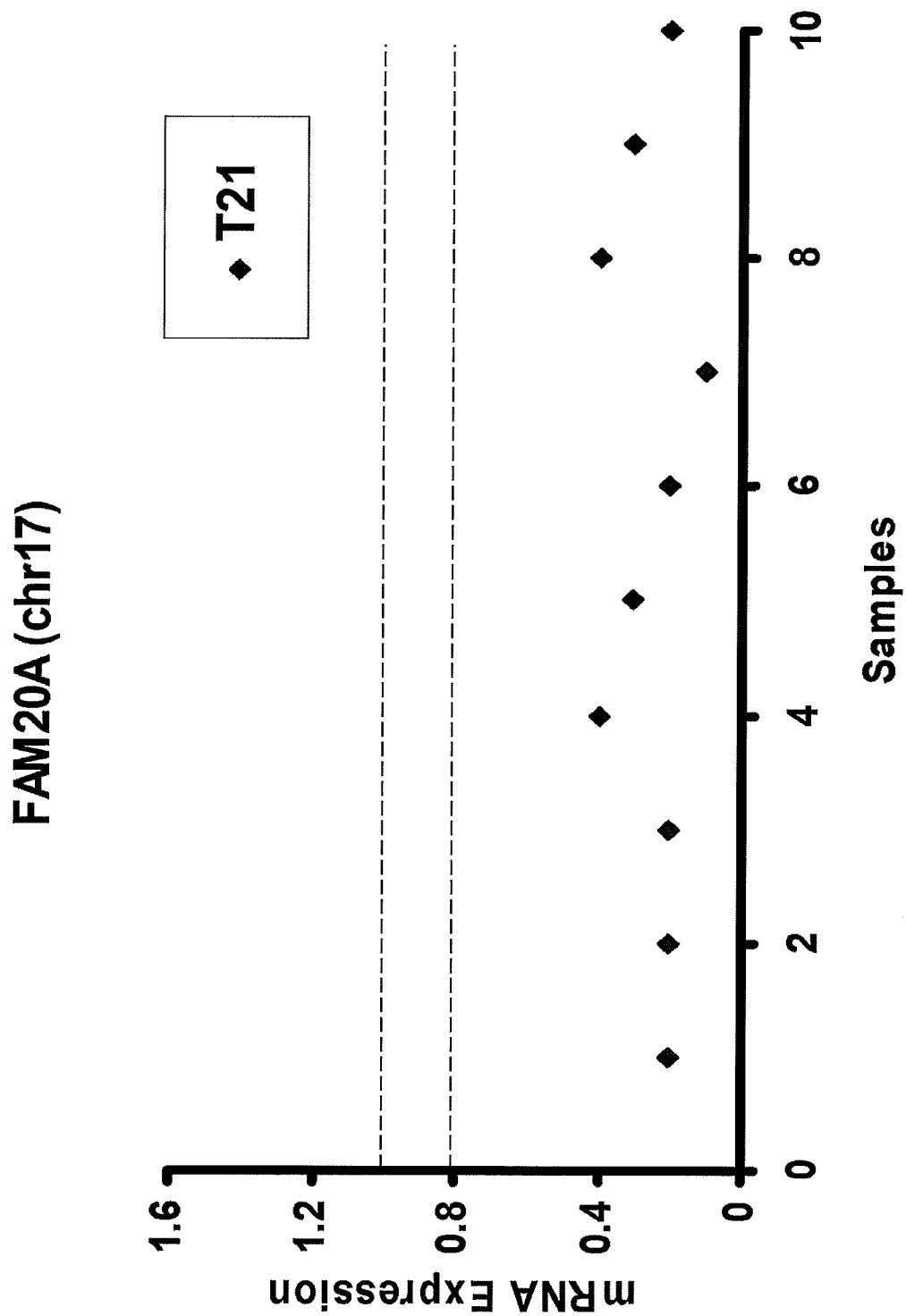

DSCAM
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

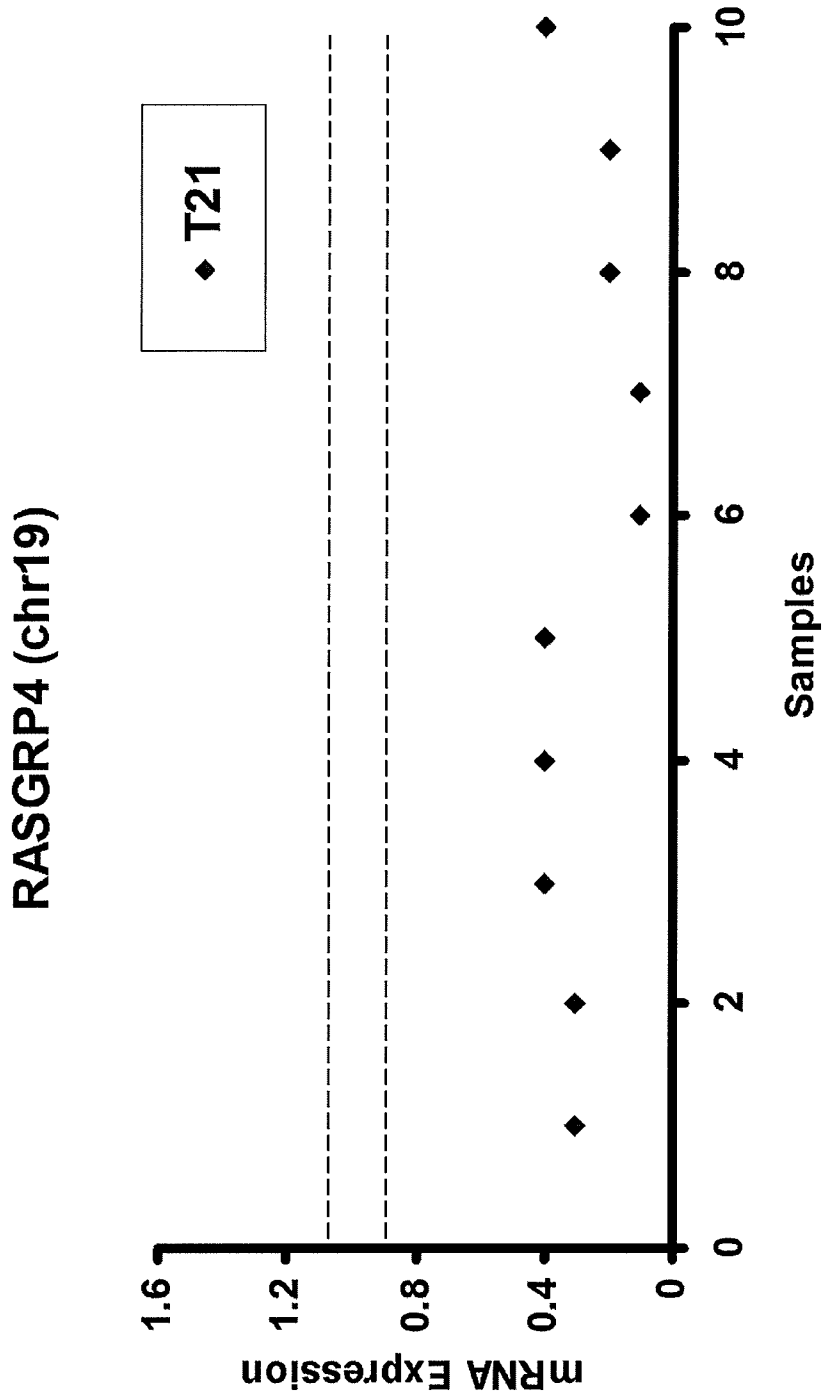

ERG(2nd Location)
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples


SORBS2(chr4)
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples


ABCC1 (chr16)
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples


NEK9 (chr14)
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples


FAM20A (chr17)
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples


RASGRP4 (chr19)
T21
mRNA Expression
1.6
1.2
0.8
0.4
0
0
2
4
6
8
10
Samples

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/067328

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal , BIOSIS, EMBASE, FSTA, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	AFFYMETRIX: "GeneChip exon array system for human, mouse, and rat" , INTERNET CITATION, 1 January 2006 (2006-01-01) , XP002480421 , Retrieved from the Internet: URL: http://www.affymetrix.com/products/arrays/exon_application.affx pages 1, 8	59-63

-/- ·

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" documentwhich may throw doubts on priority claim(s) orwhich is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 February 2013	02/05/2013

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Ripaud, Leslie

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Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ELENA PICCHIASSI ET AL: "Identi fi cati on of uni versal mRNA markers for noni nvasi ve prenatal screeni ng of tri somi es", PRENATAL DIAGNOSIS, vol . 30, no. 8, 30 June 2010 (2010-06-30) , pages 764-770, XP055051550, ISSN: 0197-3851 , D0I: 10.1002/pd .2541 abstract page 766, l eft-hand col umn, paragraph 6th-8th page 767, l eft-hand col umn, l ast paragraph - r i ght-hand col umn, paragraph 2nd	1-3 , 5-22 , 24-42 , 44-58
X	N. B. Y. TSUI ET AL: "Synergy of Total PLAC4 RNA Concentrati on and Measurement of the RNA Si ngl e-Nucl eoti de Polymorphi sm Al l el i c Rati o for the Noni nvasi ve Prenatal Detecti on of Tri somy 21", CLINICAL CHEMISTRY, vol . 56, no. 1, 1 January 2010 (2010-01-01) , pages 73-81 , XP055050064, ISSN: 0009-9147 , D0I: 10. 1373/cl i nchem. 2009 . 132662 abstract tabl e 1 page 78, r i ght-hand col umn, l ast paragraph	1-3 , 5-22 , 24-42 , 44-58
X	W0 2005/021793 Al (PANTARHEI BIOSCI ENCE BV [NL] ; 0UDEJANS C0RNELIS BARTH0L0MEUS [NL] ; VIS) 10 March 2005 (2005-03-10) exampl es 2, 3	1-3 , 5-22 , 24-42 , 44-58
A	A. T. J. I. GO ET AL: "Non-i nvasi ve aneupl oi dy detecti on usi ng free fetal DNA and RNA i n maternal pl asma: recent progress and future possi bi l i ti es", HUMAN REPRODUCTION UPDATE, vol . 17, no. 3, 12 November 2010 (2010-11-12) , pages 372-382 , XP055052831 , ISSN: 1355-4786, D0I: 10. 1093/humupd/dmq054 the whol e document	1-3 , 5-22 , 24-42 , 44-63

-/--

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	GOATTIET J J ET AL: "A novel method to identify syncytiotrophoblast-derived RNA products representative of trisomy 21 placental RNA in maternal plasma", METHODS IN MOLECULAR BIOLOGY, HUMANA PRESS INC, NJ, US, vol. 444, 1 January 2008 (2008-01-01), pages 291-302, XP009132506, ISSN: 1064-3745 the whole document --- SJAKSTE N ET AL: "Nuclear matrix proteins and hereditary diseases", RUSSIAN JOURNAL OF GENETICS, NAUKA/INTERPERIODICA, M0, vol. 41, no. 3, 1 March 2005 (2005-03-01), pages 221-226, XP019301467, ISSN: 1608-3369 abstract page 223, left-hand column ---	1-3, 5-22, 24-42, 44-63
A		1-3, 5-22, 24-42, 44-63

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/067328

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-3, 5-22, 24-42, 44-63 (all partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-3, 5-22, 24-42, 44-63 (all partially)

concerns a method for screening a fetus for trisomy 21 comprising measuring the expression level of at least one first polynucleotide (claims 20, 39), or at least one first and one second polynucleotides (claim 1) in a sample from a pregnant female; as well as an article (claim 59) and a kit (claim 62), both comprising a support and at least said first and second polynucleotides, wherein invention 1 is characterised by said first polynucleotide being SEQ ID N° 8 and said second polynucleotide being selected among SEQ ID N° 9 - 3248.

2-3143. claims: 1-63 (partially)

idem invention 1, wherein inventions 2-3143 are characterised by said first marker being SEQ ID N° 9 - 3150, respectively. Said second marker is a different marker selected among SEQ ID N° 8-3248. The claims are broken down to the respective inventions according to the chromosomal location of the genes.

3144. claims: 1-63 (partially)

idem invention 1, wherein said first marker is selected among SEQ ID N° 3151 - 3248. Said second marker is a different marker selected among SEQ ID N° 8-3248. The claims are broken down to the respective inventions according to the chromosomal location of the genes.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2012/067328

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2005021793 A1	10-03-2005	AU 2003263660 A1	16-03-2005
		WO 2005021793 A1	10-03-2005