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(71) Applicant (for all designated States except US): **ALMAC DIAGNOSTICS LIMITED** [GB/GB]; 20 Seagoe Industrial Estate, Almac House, Craigavon BT63 5QD (GB).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **HARKIN, Denis, Paul** [IE/GB]; 195 Ballygowan Road, Dromore, Co. Down BT25 IRQ (GB). **PROUTSKI, Vitali** [RU/GB]; 6 Kilwarlin Crescent, Hillsborough BT26 6QF (GB). **BLACK, Julie** [GB/GB]; 33 Primrose Way, Dromore, Co. Down, Northern Ireland BT25 1TL (GB). **KERR, Peter** [IE/GB];

26 Brooke Hall Heights, Belfast BT8 6WN (GB). **KENNEDY, Richard** [GB/GB]; 15 Edgumbe Gardens, Belfast BT4 2EG (GB). **WINTER, Andreas** [DE/DE]; Wallensteinstrasse 19, 86368 Gersthofen (DE). **DAVIS-ON, Timothy** [US/US]; 301 Washington Street, Apt. 2109, Conshohocken, PA 19428 (US). **BYLESJO, Max** [SE/GB]; 9 Locksley Lane, 110 Upper Lisburn Road, Belfast BT10 0BB (GB). **FARZTDINOV, Vadim** [RU/GB]; Apartment 62, 20 Wellwood Street, Belfast BT12 5GE (GB). **WILSON, Claire** [GB/GB]; The Coach House, Wimpstone, Stratford-upon-avon, Warwickshire CV37 8NS (GB). **HOLT, Robert, James** [GB/GB]; 33 Birchwood Drive, Lower Peover, Knutsford, Cheshire WA16 9QJ (GB).

(74) Agent: **GRISWOLD, Ian, James**; Johnson, Marcou & Isaacs, LLC, 317A East Liberty Street, Savannah, GA 31401 (US).

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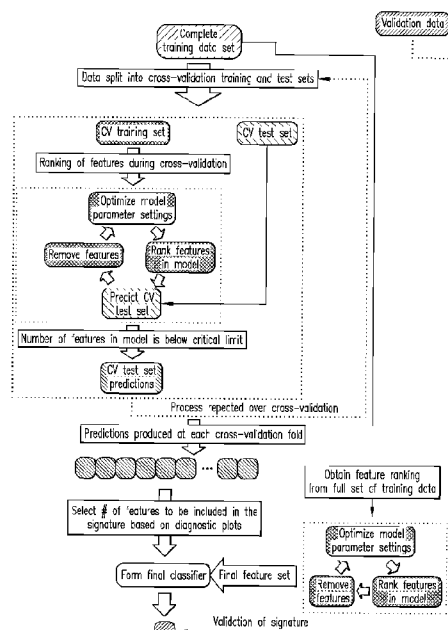


FIG. 1

(57) Abstract: A gene expression signature of colon cancer, microarrays including them and methods of using the colon gene expression signature are provided. The gene expression signature is especially useful for determining the prognosis of a patient diagnosed with colon cancer, such as stage II colon cancer. The gene signature described herein is also useful for determining effectiveness of surgical resection with or without adjuvant chemotherapy, and determining possibility of cancer recurrence in patients with colon cancer.



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## COLON CANCER GENE EXPRESSION SIGNATURES AND METHODS OF USE

### CROSS REFERENCE TO RELATED APPLICATIONS

- 5           This application claims the benefit of U.S. Provisional Application No. 61/435,922, filed on January 25, 2011, which is incorporated herein by reference in its entirety.

### FIELD OF THE INVENTION

- 10           The present disclosure relates to gene expression profiling in colon tissues, such as colon cancer tissues. In particular, the present disclosure concerns sensitive methods to measure mRNA levels in biopsied colon tumor tissues, including archived paraffin-embedded biopsy material. In addition, the disclosure provides sets of expressed transcripts forming gene expression signatures for the prognosis, diagnosis  
15           and treatment of colon cancer.

### BACKGROUND OF THE INVENTION

- Approximately 30% of all colon cancer patients are diagnosed with stage II disease. (Jemal *et al.*, *CA Cancer J. Clin.*, 2004). The 5-year survival for patients with  
20           stage II colon cancer treated by surgery is approximately 75-80%, demonstrating that the majority of patients are cured by surgery alone. (Benson, *The Oncologist*, 2006; Nauta *et al.*, *Arch. Surg.*, 1989.) Nevertheless, approximately 20-25% of these patients will develop recurrent disease within their lifetime. (Benson, *The Oncologist*, 2006; Gill *et al.*, *J. Clin. Oncol.*, 2004). In theory, these patients should benefit from  
25           adjuvant chemotherapy. However, only around 3-4% of patients have an absolute improvement in survival at 5-years with the use of adjuvant chemotherapy in stage II colon cancer. (Benson, *The Oncologist*, 2006; André *et al.*, *Annals of Surgical Oncology* 2006). As a consequence, the American Society of Clinical Oncology guidelines recommend that these patients should not be routinely treated with  
30           adjuvant chemotherapy. (Benson *et al.*, *J. Clin. Oncol.*, 2004). Despite this, it is clear that approximately 20% of stage II colon cancer patients, at higher risk of relapse, may be candidates for adjuvant treatment. (Benson, *The Oncologist*, 2006; Nauta *et al.*, *Arch. Surg.*, 1989; Gill *et al.*, *J. Clin. Oncol.*, 2004; André *et al.*, *Annals of Surgical Oncology* 2006.)

In diseases such as colon cancer, the first treatment is often the most important and offers the greatest chance of success, so there exists a need to use the treatment most effective for a patient's particular stage of colon cancer as the first treatment. This has traditionally been impossible because no method was available for predicting  
5 which drug treatment would be the most effective for a particular individual's physiology. Many times patients would needlessly undergo toxic drug therapy. For example, in Stage II tumor node metastasis (TNM) colon cancer, there has been no method of determining which patients will respond to adjuvant chemotherapy after surgery. Only one third of the 20% of stage II patients at risk for relapse after surgery  
10 derive any benefit from chemotherapy. This means that prescribing adjuvant chemotherapy exposes some patients to treatment that is unnecessary. Alternatively, a decision to withholding adjuvant chemotherapy at this stage will expose some patients to a higher risk of cancer relapse.

Currently, diagnostic tests used in clinical practice are based on a single  
15 analyte test, and therefore do not capture the potential value of knowing relationships between dozens of different markers. Moreover, diagnostic tests are frequently not quantitative, relying on immunohistochemistry. This method often yields different results in different laboratories, in part because the reagents are not standardized, and in part because the interpretations can be subjective and may not be easily quantified.  
20 RNA-based tests have not often been used because of the problem of RNA degradation over time and the fact that it is difficult to obtain fresh tissue samples from patients for analysis. Fixed paraffin-embedded tissue is more readily available and methods have been established to detect RNA in fixed tissue. However, these methods typically do not allow for the study of large numbers of genes (DNA or  
25 RNA) from small amounts of material. Thus, traditionally fixed tissue has been rarely used other than for immunohistochemical detection of proteins.

Recently, several groups have published studies concerning the classification of various cancer types by microarray gene expression analysis (see, *e.g.* Golub *et al.*, *Science* 286:531-537 (1999); Bhattacharjee *et al.*, *Proc. Natl. Acad. Sci. USA*  
30 98:13790-13795 (2001); Chen-Hsiang *et al.*, *Bioinformatics* 17 (Suppl. 1):S316-S322 (2001); Ramaswamy *et al.*, *Proc. Natl. Acad. Sci. USA* 98:15149-15154 (2001), Salazar *et al.*, *Journal of Clinical Oncology* 29: 17-24 (2010), O'Connell *et al.*, *Journal of Clinical Oncology* 28: 3937-3944 (2010) and Kerr *et al.*, *Journal of Clinical Oncology* 27 (suppl) 15s (2009)). However, these studies mostly focus on

improving and refining the already established classification of various types of cancer, and generally do not provide new insights into the relationships of the differentially expressed genes, and do not link the findings to treatment strategies in order to improve the clinical outcome of cancer therapy. In addition, cancer treatment and colon cancer clinical trials are still being pursued on the basis of the availability of new active compounds rather than the integrated approach of pharmacogenomics, which utilizes the genetic makeup of the tumor and the genotype of the patient to establish a personalized medication regime.

Although modern molecular biology and biochemistry have revealed more than 100 genes whose activities influence the behavior of tumor cells, state of their differentiation, and their sensitivity or resistance to certain therapeutic drugs, with a few exceptions, the status of these genes has not been exploited for the purpose of routinely making clinical decisions about drug treatments.

## SUMMARY OF THE INVENTION

There is a need to identify biomarkers useful for predicting prognosis of patients with colon cancer. The ability to classify patients as high risk (poor prognosis) or low risk (favorable prognosis) would enable selection of appropriate therapies for these patients. For example, high-risk patients are likely to benefit from aggressive therapy, whereas therapy may have no significant advantage for low risk patients. However, in spite of this need, a solution to this problem has not been available.

Therefore, microarray-based prognostic technologies are needed that provide a physician with information on the likelihood of recovery or relapse following administration of a particular treatment regimen, such as resection with or without chemotherapy. Technologies are also needed that can accurately diagnose a colon disease, particularly the diagnosis of a particular stage of colon cancer, or can predict a colon disease patient's response to a particular therapy. Specific knowledge regarding a tumor in a cancer patient would be extremely useful in prolonging remission, increasing the quality of patient life, and reducing healthcare costs. Such technologies may also be used to screen patient candidates for clinical trials for novel therapeutic compounds and methods to facilitate the regulatory approval process.

Disclosed are expression signatures from colon cancer that meet these needs. The disclosed signatures can be used for applications in prognosis of colon cancer,

diagnosis of colon cancer and classifying patient groups. In some embodiments, these results permit assessment of genomic evidence of the efficacy of surgery alone, or in combination with adjuvant chemotherapy for treatment of colon cancer. The signatures described herein may be significant in, and capable of, discriminating  
5 between two diagnoses or prognostic outcomes. An important aspect of the present disclosure is to use the measured expression of certain genes in colon cancer tissue to match patients to the most appropriate treatment, and to provide prognostic information. Thus, disclosed are methods of using such colon cancer signatures. The disclosed methods include detecting an expression level of at least 2 colon cancer-  
10 related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject and comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold. Depending of the prediction requested, the control threshold can be indicative of a diagnosis of colon cancer, indicative of known classification of colon  
15 cancer, indicative of a known response to treatment, indicative of having a history of long term survival, indicative of a history of recurrence and the like.

In various embodiments, RNA is isolated from a colon tissue sample, and used for preparing a gene expression profile. In certain embodiments involving prognosis of cancer, the sample is a colorectal tumor specimen, such as a colon cancer sample.  
20 In certain embodiments, the gene expression profile involves detecting the expression of at least 50 transcripts listed in Table 6, and which may also be listed in Table 1 and/or Table 2. The total number of transcripts detected in the gene expression profile can vary. For example, in some embodiments the total number of transcripts detected in the profile is from about 200 to about 1000, or from about 400 to about 800, or in  
25 other embodiments, the number of transcripts is from about 500 to about 700, or from about 550 to about 650. In various embodiments, at least about 50, at least about 100, at least about 200, at least about 300, at least about 400, at least about 500, at least about 600, or all transcripts, listed in Table 6 are detected as part of the total number of transcripts. Where additional transcripts are detected (in addition to those of Table  
30 6), they may be optionally selected from signal or expression level controls, and in some embodiments, are transcripts known to be expressed in colon cancer, such as those determined by *Colorectal Cancer DSA*<sup>TM</sup>. In certain embodiments, the additional transcripts may also be indicative of colon cancer prognosis.

The patient's expression profile is scored against an expression signature based on expression levels of the transcripts listed in Table 6 in high risk and low risk patient groups, such as patient with a high or low risk of clinical relapse, and the results may be used to determine a course of treatment. For example, a patient  
5 determined to be a high risk patient may be treated with adjuvant chemotherapy after surgery. For a patient deemed to be a low risk patient, adjuvant chemotherapy may be withheld after surgery. Accordingly, the invention provides, in certain aspects, a method for preparing a gene expression profile of a colon cancer tumor that is indicative of risk of recurrence.

10 The disclosure further provides a method for prognosing colon cancer. The method according to this aspect comprises preparing a gene expression profile of a colon cancer specimen (*e.g.*, as described herein). The gene expression profile is then classified or scored against a gene expression signature described herein. In various embodiments, the gene expression signature is based on the expression level of at  
15 least 50 transcripts listed in Table 6, and which may also be listed in Table 1 and/or Table 2. In some embodiments, the total number of transcripts on which the signature is based is less than about 800, less than about 700, less than about 600, less than about 500, less than about 400, less than about 300, less than about 200, or less than about 100 transcripts, and which includes transcripts from Table 6. For example, the  
20 signature may be based on the expression levels of at least about 400, at least about 500, or at least about 600 transcripts from Table 6. Optionally, the transcripts from Table 6 include the transcripts listed in Table 1.

Also disclosed are methods of preparing a personalized colon cancer genomics profile for a subject. The methods include detecting an expression level of at least 2  
25 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject and creating a report summarizing the data obtained by the gene expression analysis.

In some examples, of the disclosed methods, expression levels are determined from nucleic acids obtained from the subject that comprise RNA and/or cDNA  
30 transcribed from RNA extracted from a sample of colorectal tissue obtained from the subject, such as colon cancer sample.

Also disclosed are nucleic acid probes and primers (as well as sets of such probes and primers) for detecting a gene expression signature for colon cancer. In

some examples the probes are part of an array for use in the detection of a colon cancer signature.

The foregoing and other features and advantages of the disclosure will become more apparent from the following detailed description of several embodiments, which proceeds with reference to the accompanying figures.

### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 provides a flow chart showing an exemplary procedure used to derive a colon cancer transcript expression signature.

FIG. 2 provides a flow chart showing an exemplary outline of the stage II colon cancer prognostic signature generation and validation, using the *Colorectal Cancer DSA*<sup>TM</sup>.

FIG. 3A provides a graph of the receiver operating characteristic (ROC) curve of the 636 transcript prognostic signature in the training set.

FIG. 3B provides a Kaplan-Meier plot of recurrence from training data from the candidate model.

FIG. 4A provides a graph of the receiver operating characteristic (ROC) curve of the 636 transcript prognostic signature in the validation set.

FIG. 4B provides a Kaplan-Meier plot of recurrence from validation data from the candidate model.

FIG. 5 provides a Kaplan-Meier plot of overall survival from validation data from the candidate model.

FIG. 6 is Table 3 as described below.

FIG. 7 is Table 6 as described below.

### BRIEF DESCRIPTION OF THE TABLES

Table 1 provides a list of 10 candidate transcripts included in a core colon signature. These transcripts have been identified as having the highest impact on the classification of samples into poor and good prognosis groups

Table 2 provides a list 178 unique transcripts included in the colon signature. This table includes the weight rank of the transcript in the 636 transcript signature as well as the orientation of the transcript expressed in colon tissue.

Table 3 provides key patient and tumor characteristics in the study to identify the 636 transcript signature.

Table 4 provides performance metrics for the cross-validated training set and validation set used to identify the transcript signature.

5 Table 5 provides results of the statistical analysis showing Hazards Ratio for patient age, patient gender, pT-stage, tumor grade, tumor location and mucinous/non-mucinous subtype status.

Table 6 provides a list of the transcripts included in the 636-transcript colon signature.

10

### SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, as defined in 37 C.F.R. §1.822. Only one strand of each nucleic acid sequence is shown, but the  
15 complementary strand is understood as included by any reference to the displayed strand. In the accompanying sequence listing:

SEQ ID NOs: 1-636 are oligonucleotide transcripts from human colon cancer.

The Sequence Listing is submitted as an ASCII text file in the form of the file named ADL-0311\_Sequence\_Listing.txt, which was created on January 25, 2012, and  
20 is 232,154 bytes, which is incorporated by reference herein.

### DETAILED DESCRIPTION

#### ***I. Summary of Terms***

Unless defined otherwise, technical and scientific terms used herein have the  
25 same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. Definitions of common terms in molecular biology may be found in Benjamin Lewin, *Genes IX*, published by Jones and Bartlet, 2008 (ISBN 0763752223); Kendrew *et al.* (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Science Ltd., 1994 (ISBN 0632021829); Robert A. Meyers  
30 (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by VCH Publishers, Inc., 1995 (ISBN 9780471185710); Singleton *et al.*, *Dictionary of Microbiology and Molecular Biology* 2nd ed., J. Wiley & Sons (New York, N.Y. 1994), and March, *Advanced Organic Chemistry Reactions, Mechanisms and Structure* 4th ed., John Wiley & Sons (New York, N.Y. 1992).

The singular terms “a,” “an,” and “the” include plural referents unless context clearly indicates otherwise. Similarly, the word “or” is intended to include “and” unless the context clearly indicates otherwise. The term “comprises” means “includes.” In case of conflict, the present specification, including explanations of  
5 terms, will control.

To facilitate review of the various embodiments of this disclosure, the following explanations of terms are provided:

**Amplifying a nucleic acid molecule:** To increase the number of copies of a nucleic acid molecule, such as a gene or fragment of a gene, for example a transcript  
10 shown in Table 6. The resulting products are called amplification products.

An example of *in vitro* amplification is the polymerase chain reaction (PCR). Other examples of *in vitro* amplification techniques include quantitative real-time PCR, strand displacement amplification (see U.S. Patent No. 5,744,311); transcription-free isothermal amplification (see U.S. Patent No. 6,033,881); repair  
15 chain reaction amplification (see International Patent Publication No. WO 90/01069); ligase chain reaction amplification (see EP-A-320 308); gap filling ligase chain reaction amplification (see U.S. Patent No. 5,427,930); coupled ligase detection and PCR (see U.S. Patent No. 6,027,889); and NASBA™ RNA transcription-free amplification (see U.S. Patent No. 6,025,134).

**Array:** An arrangement of molecules, such as biological macromolecules (such nucleic acid molecules) or biological samples (such as tissue sections), in addressable locations on or in a substrate. In some examples an array is an array of polynucleotide probes (such as probes that hybridize to the nucleic acids sequences shown in Table 6, or the complement thereof), bound to a solid substrate so as not to  
20 be substantially dislodged during a hybridization procedure. A “microarray” is an array that is miniaturized so as to require or be aided by microscopic examination for evaluation or analysis. Arrays are sometimes called DNA chips or biochips.

The array of molecules (“features”) makes it possible to carry out a very large number of analyses on a sample at one time. In certain example arrays, one or more  
30 molecules (such as an oligonucleotide probe) will occur on the array a plurality of times (such as twice), for instance to provide internal controls.

In particular examples, an array includes nucleic acid molecules, such as oligonucleotide sequences. The polynucleotides used on an array may be cDNAs (“cDNA arrays”) that are typically about 500 to 5000 bases long, although shorter or

longer cDNAs can also be used. Alternatively, the polynucleotides can be oligonucleotides, which are typically about 20 to 80 bases long, although shorter and longer oligonucleotides are also suitable. In one example, the molecule includes oligonucleotides attached to the array via their 5'- or 3'-end.

5           Within an array, each arrayed sample is addressable, in that its location can be reliably and consistently determined within the at least two dimensions of the array. The number of addressable locations on the array can vary, for example from at least four, to at least 9, at least 10, at least 14, at least 15, at least 20, at least 30, at least 50, at least 75, at least 100, at least 150, at least 200, at least 300, at least 500, least 550, 10 at least 600, at least 800, at least 1000, at least 10,000, or more. The feature application location on an array can assume different shapes. For example, the array can be regular (such as arranged in uniform rows and columns) or irregular. Thus, in ordered arrays the location of each sample is assigned to the sample at the time when it is applied to the array, and a key may be provided in order to correlate each location 15 with the appropriate target or feature position. Often, ordered arrays are arranged in a symmetrical grid pattern, but samples could be arranged in other patterns (such as in radially distributed lines, spiral lines, or ordered clusters). Addressable arrays usually are computer readable, in that a computer can be programmed to correlate a particular address on the array with information about the sample at that position (such as 20 hybridization or binding data, including for instance signal intensity). In some examples of computer readable formats, the individual features in the array are arranged regularly, for instance in a Cartesian grid pattern, which can be correlated to address information by a computer.

**Binding or stable binding:** An association between two substances or 25 molecules, such as the association of a nucleic acid to another nucleic acid (such as the binding of a probe to a transcript shown in Table 6 or its complement), or the association of a protein with another protein or nucleic acid molecule. Binding can be detected by any procedure known to one skilled in the art, for example in the case of a nucleic acid, such as by physical or functional properties of the target:oligonucleotide 30 complex.

Physical methods of detecting the binding of complementary strands of nucleic acid molecules, include but are not limited to, such methods as DNase I or chemical footprinting, gel shift and affinity cleavage assays, Northern blotting, dot blotting and light absorption detection procedures. For example, one method involves

observing a change in light absorption of a solution containing an oligonucleotide (or an analog) and a target nucleic acid at 220 to 300 nm as the temperature is slowly increased. If the oligonucleotide or analog has bound to its target, there is a sudden increase in absorption at a characteristic temperature as the oligonucleotide (or  
5 analog) and target disassociate from each other, or melt. In another example, the method involves detecting a signal, such as a detectable label, present on one or both nucleic acid molecules (or antibody or protein as appropriate).

The binding between an oligomer and its target nucleic acid is frequently characterized by the temperature ( $T_m$ ) at which 50% of the oligomer is melted from its  
10 target. A higher ( $T_m$ ) means a stronger or more stable complex relative to a complex with a lower ( $T_m$ ).

**cDNA (complementary DNA):** A piece of DNA lacking internal, non-coding segments (introns) and regulatory sequences which determine transcription. cDNA can be synthesized by reverse transcription from messenger RNA (mRNA) extracted from  
15 cells and/or tissue samples, such a colon samples, including colon cancer samples.

**Clinical outcome:** Refers to the health status of a patient following treatment for a disease or disorder, or in the absence of treatment. Clinical outcomes include, but are not limited to, an increase in the length of time until death, a decrease in the length of time until death, an increase in the chance of survival, an increase in the risk  
20 of death, survival, disease-free survival, chronic disease, metastasis, advanced or aggressive disease, disease recurrence, death, and favorable or poor response to therapy.

**Colon cancer:** Cancer that forms in the tissues of the colon (the longest part of the large intestine). Most colon cancers are adenocarcinomas (cancers that begin in  
25 cells that make line internal organs and have gland-like properties). Cancer progression is characterized by stages, or the extent of cancer in the body. Staging is usually based on the size of the tumor, whether lymph nodes contain cancer, and whether the cancer has spread from the original site to other parts of the body. Stages of colon cancer include stage I, stage II, stage III and stage IV. Unless otherwise  
30 specified, the term colon cancer refers to colon cancer at Stage 0, Stage I, Stage II (including Stage IIA or IIB), Stage III (including Stage IIIA, IIIB or IIIC), or Stage IV. In some embodiments herein, the colon cancer is from any stage. In other embodiments, the colon cancer is a stage II colon cancer.

**Chemotherapeutic agents:** Any chemical agent with therapeutic usefulness in the treatment of diseases characterized by abnormal cell growth. Such diseases include tumors, neoplasms, and cancer as well as diseases characterized by hyperplastic growth such as psoriasis. In one embodiment, a chemotherapeutic agent is an agent of use in treating colon cancer. In one embodiment, a chemotherapeutic agent is a radioactive compound. One of skill in the art can readily identify a chemotherapeutic agent of use (see for example, Slapak and Kufe, *Principles of Cancer Therapy*, Chapter 86 in Harrison's *Principles of Internal Medicine*, 14th edition; Perry *et al.*, *Chemotherapy*, Ch. 17 in Abeloff, *Clinical Oncology 2nd ed.*, 2000 Churchill Livingstone, Inc; Baltzer and Berkery. (eds): *Oncology Pocket Guide to Chemotherapy*, 2nd ed. St. Louis, Mosby-Year Book, 1995; Fischer Knobf, and Durivage (eds): *The Cancer Chemotherapy Handbook*, 4th ed. St. Louis, Mosby-Year Book, 1993). Chemotherapeutic agents used for treating colon cancer include small molecules such as 5-fluorouracil, leucovorin, irinotecan, oxaliplatin, and capecitabine, and antibodies such bevacuzimab and cetuximab. Combination chemotherapy is the administration of more than one agent to treat cancer.

**Contacting:** Placement in direct physical association; includes both in solid and liquid form. Contacting includes contact between one molecule and another molecule, for example; contacting a sample with a nucleic acid probe, such as a probe for any of the sequences shown in Table 6.

**Control:** A "control" refers to a sample or standard used for comparison with an experimental sample, such as a tumor sample obtained from a patient with colon cancer. In some embodiments, the control is a sample obtained from a healthy patient or a non-cancerous tissue sample obtained from a patient diagnosed with colon cancer, such as a non-cancerous tissue sample from the same organ in which the tumor resides (*e.g.*, non-cancerous colon tissue can serve as a control for a colon cancer). In some embodiments, the control is a historical control or standard value (*i.e.*, a previously tested control sample or group of samples that represent baseline or normal values).

Controls or standards for comparison to a sample, for the determination of differential expression, include samples believed to be normal (in that they are not altered for the desired characteristic, for example a sample from a subject who does not have colon cancer) as well as laboratory values, even though possibly arbitrarily set. Laboratory standards and values may be set based on a known or determined

population value and can be supplied in the format of a graph or table that permits comparison of measured, experimentally determined values.

**Detecting expression:** Determining of a level expression in either a qualitative or quantitative manner can detect nucleic acid. Exemplary methods include microarray analysis, RT-PCR, and Northern blot. In some examples, detecting expression includes detecting the expression of one or more of the transcripts in Table 6.

**Differential expression or altered expression:** A difference, such as an increase or decrease, in the conversion of the information encoded in a gene (such as any of the genes from Table 1, 2, and/or nucleic acid transcripts in Table 6) into messenger RNA, the conversion of mRNA to a protein, or both. In some examples, the difference is relative to a control or reference value, such as an amount of expression of a nucleic acid transcript in tissue not affected by a disease, such as colon cancer, from the same subject, or an amount expected in a different subject who does not have colon cancer. The difference can also be in a non-cancerous tissue from a subject (that has the cancer in the same organ) as compared to tissue from a different subject not afflicted with colon cancer. Detecting differential expression can include measuring a change in gene or protein expression, such as a change in expression of one or more of the genes listed in Table 1, 2, and/or the expression one or more transcripts shown in Table 6.

**Downregulated or decreased:** When used in reference to the expression of a nucleic acid molecule, refers to any process that results in a decrease in production of the nucleic acid. A gene product can be RNA (such as mRNA, rRNA, tRNA, and structural RNA) or protein. Therefore, gene downregulation or deactivation includes processes that decrease transcription of a gene or translation of mRNA.

Gene downregulation includes any detectable decrease in the production of a gene product. In certain examples, production of a gene product decreases by at least 1.2 fold, such as at least 2-fold, at least 3-fold or at least 4-fold, as compared to a control (such an amount of gene expression, such as a normalized gene expression in a normal cell). In several examples, a control is a relative amount of gene expression or protein expression in one or more subjects who do not have colon cancer, such as the relative amount of gene expression or protein expression in "cancer-free" subjects who do not have any known cancer.

**Exon:** In theory, a segment of an interrupted gene that is represented in the messenger RNA product. In theory the term "intron" refers to any segment of DNA that is transcribed but removed from within the transcript by splicing together the exons on either side of it. Operationally, exon sequences occur in the mRNA  
5 sequence of a gene as defined by Ref. Seq ID numbers. Operationally, intron sequences are the intervening sequences within the genomic DNA of a gene, bracketed by exon sequences and having GT and AG splice consensus sequences at their 5' and 3' boundaries.

**Expression:** The process by which the coded information of a gene is  
10 converted into an operational, non-operational, or structural part of a cell, such as the synthesis of nucleic acid or a protein. Gene expression can be influenced by external signals. For instance, exposure of a cell to a hormone may stimulate expression of a hormone-induced gene. Different types of cells can respond differently to an identical signal. Expression of a gene also can be regulated anywhere in the pathway from  
15 DNA to RNA to protein. Regulation can include controls on transcription, translation, RNA transport and processing, degradation of intermediary molecules such as mRNA, or through activation, inactivation, compartmentalization or degradation of specific protein molecules after they are produced.

The expression of a nucleic acid molecule can be altered, for example relative  
20 to expression in a normal (*e.g.*, non-cancerous) sample. An alteration in gene expression, such as differential expression, includes but is not limited to: (1) overexpression; (2) underexpression; or (3) suppression of expression. Alternations in the expression of a nucleic acid molecule can be associated with, and in fact cause, a change in expression of the corresponding protein. **"Expression" and/or "relative  
25 expression"** can be considered the expression value after normalization of a specific transcript with respect to a threshold value, which is defined in the context of the expression of all other transcripts in an expression signature, such as a colon cancer expression signature. The overall expression data for a given sample is normalized using methods known to those skilled in the art in order to correct for differing  
30 amounts of starting material, varying efficiencies of the extraction and amplification reactions etc. Using a linear classifier on the normalized data to make a diagnostic or prognostic call (*e.g.* good or poor prognosis) effectively means to split the data space, *i.e.* all possible combinations of expression values for all genes in the signature, into two disjoint halves by means of a separating hyperplane. This split is empirically

derived on a large set of training examples, for example from patients with good and poor prognosis. Without loss of generality, one can assume a certain fixed set of values for all but one genes, which would automatically define a threshold value for this remaining gene where the decision would change from, for example, good to poor  
5 prognosis. Expression values above this dynamic threshold would then either indicate good (for a gene with a negative weight) or poor prognosis (for a gene with a positive weight). The precise value of this threshold depends on the actual measured expression profile of all other genes within the signature, but the general indication of certain genes remains fixed, *i.e.* high values or "relative over-expression" always  
10 contributes to either a poor prognosis decision (genes with a positive weight) or good prognosis decision (genes with a negative weights). Therefore, in the context of the overall gene expression signature relative expression can indicate if either up- or down-regulation of a certain transcript is indicative of good or poor prognosis.

**Gene amplification:** A process by which multiple copies of a gene or gene  
15 fragment are formed in a particular cell or cell line. The duplicated region (a stretch of amplified DNA) is often referred to as an "amplicon." Usually, the amount of the messenger RNA (mRNA) produced, *i.e.*, the level of gene expression, also increases in the proportion of the number of copies made of the particular gene expressed.

**Expression profile (or fingerprint or signature):** A pattern of gene  
20 expression, which is characteristic of, or correlated with, a specific disease stage or a specific prognostic outcome. The gene expression signature may be represented by a set of informative genes, or transcripts thereof, coding or non-coding or both. The expression levels of the transcripts within the signatures can be evaluated to make a prognostic determination with, but not limited to, the methods provided herein. Gene  
25 expression levels may be used to distinguish between two clinical conditions or outcomes such as normal and diseased tissue for diagnosis, or responsiveness compared to non-responsiveness for prognostic methods and recurring compared to non-recurring for predictive methods. Differential or altered gene expression can be detected by changes in the detectable amount of gene expression (such as cDNA or  
30 mRNA) or by changes in the detectable amount of proteins expressed by those genes. A distinct or identifiable pattern of gene expression, for instance a pattern of high and low expression of a defined set of genes or gene-indicative nucleic acids such as ESTs; in some examples, as few as one or two genes provides a profile, but more genes can be used in a profile, for example at least 2, at least 3, at least 4, at least 5, at

least 6, at least 7, at least 9, at least 10 or at least 11 and so on. In some embodiments, the profile comprises at least about 200 genes (or “transcripts”) and up to about 1000 transcripts, such as from about 400 transcripts to about 800 transcripts, or about 500 transcripts to about 700 transcripts. The profile comprises transcripts from Table 6  
5 (e.g., at least 100, at least 200, at least 300, at least 400, at least 500, or at least 600 transcripts from Table 6), including in some embodiments the 636 transcripts listed in Table 6. As used herein, the term “gene” refers to an expressed transcript, which may be a characterized gene, or may be an expressed transcript such as an EST. In some embodiments, the detection platform is a microarray, and each probe is considered as  
10 determining the expression of a separate “gene” or “transcript.”

A gene expression profile (also referred to as a **fingerprint** or **signature**) can be linked to a tissue or cell type (such as colon tissue), to a particular stage of normal tissue growth or disease progression (such as colon cancer), or to any other distinct or identifiable condition that influences gene expression in a predictable way. Gene  
15 expression profiles can include relative as well as absolute expression levels of specific genes, and can be viewed in the context of a test sample compared to a baseline or control sample profile (such as a sample from a subject who does not have colon cancer). In one example, a gene expression profile in a subject is read on an array (such as a nucleic acid array).

20 **Hybridization:** To form base pairs between complementary regions of two strands of DNA, RNA, or between DNA and RNA, thereby forming a duplex molecule, for example a duplex formed between a probe and any of the nucleic acid sequences shown in Table 6 or the complement thereof. Hybridization conditions resulting in particular degrees of stringency will vary depending upon the nature of  
25 the hybridization method and the composition and length of the hybridizing nucleic acid sequences. Generally, the temperature of hybridization and the ionic strength (such as the Na<sup>+</sup> concentration) of the hybridization buffer will determine the stringency of hybridization. Calculations regarding hybridization conditions for attaining particular degrees of stringency are discussed in Sambrook *et al.*, (1989)  
30 Molecular Cloning, second edition, Cold Spring Harbor Laboratory, Plainview, NY (chapters 9 and 11). The following is an exemplary set of hybridization conditions and is not limiting:

Very High Stringency (detects sequences that share at least 90% identity)

Hybridization: 5x SSC at 65°C for 16 hours

Wash twice: 2x SSC at room temperature (RT) for 15 minutes each

Wash twice: 0.5x SSC at 65°C for 20 minutes each

High Stringency (detects sequences that share at least 80% identity)

Hybridization: 5x-6x SSC at 65°C-70°C for 16-20 hours

5 Wash twice: 2x SSC at RT for 5-20 minutes each

Wash twice: 1x SSC at 55°C-70°C for 30 minutes each

Low Stringency (detects sequences that share at least 60% identity)

Hybridization: 6x SSC at RT to 55°C for 16-20 hours

Wash at least twice: 2x-3x SSC at RT to 55°C for 20-30 minutes each

10 **Isolated:** An “isolated” biological component (such as a nucleic acid molecule, protein, or cell) has been substantially separated or purified away from other biological components in the cell of the organism, or the organism itself, in which the component naturally occurs, such as other chromosomal and extra-chromosomal DNA and RNA, proteins and cells. The term also embraces nucleic acid  
15 molecules prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acid molecules. For example, an isolated cell, such as a colon cancer cell, is one that is substantially separated from other types of cells.

**Label:** An agent capable of detection, for example by ELISA, spectrophotometry, flow cytometry, or microscopy or other visual techniques. For  
20 example, a label can be attached to a nucleic acid molecule or protein, thereby permitting detection of the nucleic acid molecule or protein. For example a nucleic acid molecule or an antibody that specifically binds to a target molecule, such as a target nucleic acid molecule. Examples of labels include, but are not limited to, radioactive isotopes, enzyme substrates, co-factors, ligands, chemiluminescent agents,  
25 fluorophores, haptens, enzymes, and combinations thereof. Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed for example in Sambrook *et al.* (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989) and Ausubel *et al.* (In Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1998).

30 **Long term survival:** Disease-free survival for at least 3 years, more preferably for at least 5 years, even more preferably for at least 8 years following surgery or other treatment (*e.g.*, chemotherapy) for colon cancer.

**More aggressive:** As used herein, a “more aggressive” form of a colon cancer is a colon cancer with a relatively increased risk of metastasis or recurrence (such as

following surgical removal of the tumor). A “more aggressive” colon cancer can also refer to a colon cancer that confers an increased likelihood of death, or a decrease in the time until death, upon a subject with the colon cancer. A subject having a “more aggressive” form of a colon cancer is considered high risk (poor prognosis).

5           **Nucleic acid molecules representing genes:** Any nucleic acid, for example DNA (intron or exon or both), cDNA, or RNA (such as mRNA), of any length suitable for use as a probe or other indicator molecule, and that is informative about the corresponding gene, such as those listed in Tables 1, or 2, for example the transcripts listed in Table 6.

10           **Oligonucleotide:** A relatively short polynucleotide, including, without limitation, single-stranded deoxyribonucleotides, single- or double-stranded ribonucleotides, RNA:DNA hybrids and double-stranded DNAs. Oligonucleotides, such as single-stranded DNA probe oligonucleotides, are often synthesized by chemical methods, for example using automated oligonucleotide synthesizers that are  
15 commercially available. However, oligonucleotides can be made by a variety of other methods, including *in vitro* recombinant DNA-mediated techniques and by expression of DNAs in cells and organisms.

**Patient:** As used herein, the term “patient” includes human and non-human animals. The preferred patient for treatment is a human. “Patient” and “subject” are  
20 used interchangeably herein.

**Patient response:** can be assessed using any endpoint indicating a benefit to the patient, including, without limitation, (1) inhibition, to some extent, of tumor growth, including slowing down and complete growth arrest; (2) reduction in the number of tumor cells; (3) reduction in tumor size; (4) inhibition (*i.e.*, reduction,  
25 slowing down or complete stopping) of tumor cell infiltration into adjacent peripheral organs and/or tissues; (5) inhibition (*i.e.* reduction, slowing down or complete stopping) of metastasis; (6) enhancement of anti-tumor immune response, which may, but does not have to, result in the regression or rejection of the tumor; (7) relief, to some extent, of one or more symptoms associated with the tumor; (8) increase in the  
30 length of survival following treatment; and/or (9) decreased mortality at a given point of time following treatment.

**Polynucleotide:** When used in singular or plural, generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA, or even combinations thereof. Thus, for instance,

polynucleotides as defined herein include, without limitation, single- and double-stranded DNA, DNA including single- and double-stranded regions, single- and double-stranded RNA, and RNA including single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or include single- and double-stranded regions. The term "polynucleotide" also includes DNAs and RNAs that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritiated bases, are included within the term "polynucleotides" as defined herein. In general, the term "polynucleotide" embraces all chemically, enzymatically and/or metabolically modified forms of unmodified polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells.

**Probes and primers:** A probe comprises an isolated nucleic acid capable of hybridizing to a target nucleic acid (such one of the nucleic acid sequences shown in Table 6 or the complement thereof). A detectable label or reporter molecule can be attached to a probe. Typical labels include radioactive isotopes, enzyme substrates, co-factors, ligands, chemiluminescent or fluorescent agents, haptens, and enzymes. Methods for preparing and using nucleic acid probes and primers are described, for example, in Sambrook *et al.* (In *Molecular Cloning: A Laboratory Manual*, CSHL, New York, 1989), Ausubel *et al.* (ed.) (In *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1998), and Innis *et al.* (*PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc., San Diego, CA, 1990). Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed, for example in Sambrook *et al.* (In *Molecular Cloning: A Laboratory Manual*, CSHL, New York, 1989) and Ausubel *et al.* (In *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1998).

Probes are generally at least 12 nucleotides in length, such as at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, 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, at least 30, at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, at least 45, at least 50, or more contiguous nucleotides complementary to the target nucleic acid molecule, such as a primer of 15-

50 nucleotides, 20-50 nucleotides, or 15-30 nucleotides. In some examples, a probe is even longer, such as a cDNA probe, which can be from about 500 to more than 5000 nucleotides in length.

Primers are short nucleic acid molecules, for instance DNA oligonucleotides 10 nucleotides or more in length, which can be annealed to a complementary target nucleic acid molecule by nucleic acid hybridization to form a hybrid between the primer and the target nucleic acid strand. A primer can be extended along the target nucleic acid molecule by a polymerase enzyme. Therefore, primers can be used to amplify a target nucleic acid molecule (such as a nucleic acid sequence shown in Table 6).

10 The specificity of a primer and/or a probe increases with its length. Thus, for example, a primer that includes 30 consecutive nucleotides will anneal to a target sequence with a higher specificity than a corresponding primer of only 15 nucleotides. Thus, to obtain greater specificity, probes and primers can be selected that include at least 15, 20, 25, 30, 35, 40, 45, 50 or more consecutive nucleotides. In particular 15 examples, a primer is at least 15 nucleotides in length, such as at least 15 contiguous nucleotides complementary to a target nucleic acid molecule. Particular lengths of primers that can be used to practice the methods of the present disclosure include primers having 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 20 28, at least 29, at least 30, at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, at least 45, at least 50, or more contiguous nucleotides complementary to the target nucleic acid molecule to be amplified, such as a primer of 15-50 nucleotides, 20-50 nucleotides, or 15-30 nucleotides. One of most important factors considered in PCR primer design include 25 primer length, melting temperature ( $T_m$ ), and GC content, specificity, complementary primer sequences, and 3'-end sequence. In general, optimal PCR primers are generally 17-30 bases in length, and contain about 20-80%, such as, for example, about 50-60% G+C bases.  $T_m$ 's between 50°C and 80°C, e.g. about 50°C to 70° C are typically preferred.

30 Primer pairs can be used for amplification of a nucleic acid sequence, for example, by PCR, real-time PCR, or other nucleic-acid amplification methods known in the art. An "upstream" or "forward" primer is a primer 5' to a reference point on a nucleic acid sequence. A "downstream" or "reverse" primer is a primer 3' to a reference

point on a nucleic acid sequence. In general, at least one forward and one reverse primer are included in an amplification reaction.

Nucleic acid probes and primers can be readily prepared based on the nucleic acid molecules provided herein, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, © 1991, Whitehead Institute for Biomedical Research, Cambridge, MA) or PRIMER EXPRESS® Software (Applied Biosystems, AB, Foster City, CA).

Further guidelines for PCR primer and probe design may be found in Dieffenbach *et al.*, General Concepts for PCR Primer Design in: PCR Primer, A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York, 1995, pp. 133 155; Innis and Gelfand, Optimization of PCRs in: PCR Protocols, A Guide to Methods and Applications, CRC Press, London, 1994, pp. 5 11; and Plasterer, Primerselect: Primer and probe design. *Methods Mol. Biol.* 70:520 527, 1997.

**Prognosis:** The likelihood of the clinical outcome for a subject afflicted with a specific disease or disorder. With regard to cancer, the prognosis is a representation of the likelihood (probability) that the subject will survive (such as for one, two, three, four or five years) and/or the likelihood (probability) that the tumor will metastasize. The term "prediction" is used herein to refer to the likelihood that a patient will respond either favorably or unfavorably to a drug or set of drugs, and also the extent of those responses. The predictive methods of the present invention can be used clinically to make treatment decisions by choosing the most appropriate treatment modalities for any particular patient. The predictive methods of the present disclosure are valuable tools in predicting if a patient is likely to respond favorably to a treatment regimen, such as surgical intervention, chemotherapy with a given drug or drug combination, and/or radiation therapy.

**Purified:** The term "purified" does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified oligonucleotide preparation is one in which the oligonucleotide is more pure than in an environment including a complex mixture of oligonucleotides.

**Sample:** A biological specimen containing genomic DNA, RNA (including mRNA and microRNA), protein, or combinations thereof, obtained from a subject. Examples include, but are not limited to, peripheral blood, urine, saliva, tissue biopsy, aspirate, surgical specimen, and autopsy material, and includes fixed and/or paraffin embedded samples. In one example, a sample includes a biopsy of a colon (such as

colon cancer tumor), a sample of noncancerous tissue, or a sample of normal tissue (from a subject not afflicted with a known disease or disorder, such as a cancer-free subject).

**Sequence identity/similarity:** The identity/similarity between two or more nucleic acid sequences, or two or more amino acid sequences, is expressed in terms of the identity or similarity between the sequences. Sequence identity can be measured in terms of percentage identity; the higher the percentage, the more identical the sequences are. Sequence similarity can be measured in terms of percentage similarity (which takes into account conservative amino acid substitutions); the higher the percentage, the more similar the sequences are.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970; Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988; Higgins & Sharp, *Gene*, 73:237-44, 1988; Higgins & Sharp, *CABIOS* 5:151-3, 1989; Corpet *et al.*, *Nuc. Acids Res.* 16:10881-90, 1988; Huang *et al.* *Computer Appls. in the Biosciences* 8, 155-65, 1992; and Pearson *et al.*, *Meth. Mol. Bio.* 24:307-31, 1994. Altschul *et al.*, *J. Mol. Biol.* 215:403-10, 1990, presents a detailed consideration of sequence alignment methods and homology calculations.

The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul *et al.*, *J. Mol. Biol.* 215:403-10, 1990) is available from several sources, including the National Center for Biotechnology (NCBI, National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. Additional information can be found at the NCBI web site.

BLASTN is used to compare nucleic acid sequences, while BLASTP is used to compare amino acid sequences. If the two compared sequences share homology, then the designated output file will present those regions of homology as aligned sequences. If the two compared sequences do not share homology, then the designated output file will not present aligned sequences.

Once aligned, the number of matches is determined by counting the number of positions where an identical nucleotide or amino acid residue is presented in both sequences. The percent sequence identity is determined by dividing the number of matches either by the length of the sequence set forth in the identified sequence, or by

an articulated length (such as 100 consecutive nucleotides or amino acid residues from a sequence set forth in an identified sequence), followed by multiplying the resulting value by 100. For example, a nucleic acid sequence that has 1166 matches when aligned with a test sequence having 1554 nucleotides is 75.0 percent identical to the test sequence ( $1166 \div 1554 * 100 = 75.0$ ). The percent sequence identity value is rounded to the nearest tenth. For example, 75.11, 75.12, 75.13, and 75.14 are rounded down to 75.1, while 75.15, 75.16, 75.17, 75.18, and 75.19 are rounded up to 75.2. The length value will always be an integer. In another example, a target sequence containing a 20-nucleotide region that aligns with 20 consecutive nucleotides from an identified sequence as follows contains a region that shares 75 percent sequence identity to that identified sequence (that is,  $15 \div 20 * 100 = 75$ ).

One indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions, as described above. Nucleic acid sequences that do not show a high degree of identity may nevertheless encode identical or similar (conserved) amino acid sequences, due to the degeneracy of the genetic code. Changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid molecules that all encode substantially the same protein. Such homologous nucleic acid sequences can, for example, possess at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% sequence identity to a molecule listed in Table 6 determined by this method.

One of skill in the art will appreciate that the particular sequence identity ranges are provided for guidance only; it is possible that strongly significant homologs could be obtained that fall outside the ranges provided.

**Splicing or RNA splicing:** An RNA processing that removes introns and joins exons to produce mature mRNA with continuous coding sequence that moves into the cytoplasm of a eukaryotic cell.

**Transcript or gene product:** An RNA molecule that is generated or derived through the process of transcription from its corresponding DNA or a cDNA template. Transcripts include coding and non-coding RNA molecules such as, but not limited to, messenger RNAs (mRNA), alternatively spliced mRNAs, ribosomal RNA (rRNA), transfer RNAs (tRNAs) in addition to a large range of other transcripts, which are not translated into protein such as small nuclear RNAs (snRNAs), antisense molecules such as short interfering RNA (siRNA) and microRNA (miRNA) and other

RNA transcripts of unknown function. In some embodiments, a transcript is a nucleic acid sequence shown in Table 6.

**Therapeutic:** A generic term that includes both diagnosis and treatment.

**Treatment:** Includes both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. In tumor (e.g. cancer) treatment, a treatment such as surgery, chemotherapy or radiation may directly decrease the pathology of tumor cells, or render the tumor cells more susceptible to further treatment.

**Tumor, neoplasia, malignancy or cancer:** Neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues and the result of abnormal and uncontrolled growth of cells. The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Neoplasia, malignancy, cancer and tumor are often used interchangeably and refer to abnormal growth of a tissue or cells that results from excessive cell division. The amount of a tumor in an individual is the "**tumor burden**" which can be measured as the number, volume, or weight of the tumor. A tumor that does not metastasize is referred to as "**benign**." A tumor that invades the surrounding tissue and/or can metastasize is referred to as "**malignant**." A "**non-cancerous tissue**" is a tissue from the same organ wherein the malignant neoplasm formed, but does not have the characteristic pathology of the neoplasm. Generally, noncancerous tissue appears histologically normal. A "**normal tissue**" is tissue from an organ, wherein the organ is not affected by cancer or another disease or disorder of that organ. A "**cancer-free**" subject has not been diagnosed with a cancer of that organ and does not have detectable cancer.

The "pathology" of cancer includes all phenomena that compromise the well-being of the patient. This includes, without limitation, abnormal or uncontrollable cell growth, metastasis, interference with the normal functioning of neighboring cells, release of cytokines or other secretory products at abnormal levels, suppression or aggravation of inflammatory or immunological response, neoplasia, premalignancy, malignancy, invasion of surrounding or distant tissues or organs, such as lymph nodes, etc.

**Tumor-Node-Metastasis (TNM):** The TNM classification of malignant tumors is a cancer staging system for describing the extent of cancer in a patient's body. T describes the size of the primary tumor and whether it has invaded nearby tissue; N describes any lymph nodes that are involved; and M describes metastasis.

- 5 TNM is developed and maintained by the International Union Against Cancer to achieve consensus on one globally recognized standard for classifying the extent of spread of cancer.

**Upregulated or activation:** When used in reference to the expression of a nucleic acid molecule, refers to any process that results in an increase in production of  
10 a gene product. A gene product can be RNA (such as mRNA, rRNA, tRNA, and structural RNA) or protein. Therefore, gene upregulation or activation includes processes that increase transcription of a gene or translation of mRNA, such as an inflammatory gene.

Examples of processes that increase transcription include those that facilitate  
15 formation of a transcription initiation complex, those that increase transcription initiation rate, those that increase transcription elongation rate, those that increase processivity of transcription and those that relieve transcriptional repression (for example by blocking the binding of a transcriptional repressor). Gene upregulation can include inhibition of repression as well as stimulation of expression above an  
20 existing level. Examples of processes that increase translation include those that increase translational initiation, those that increase translational elongation and those that increase mRNA stability.

Gene upregulation includes any detectable increase in the production of a gene product, such as an inflammatory gene. In certain examples, production of a gene  
25 product increases by at least 1.2 fold, such as at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 8-fold, at least 10-fold, or at least 15-fold, as compared to a control (such an amount of gene expression and/or normalized gene expression in a normal cell).

**Weight:** With reference to the gene signatures disclosed herein, refers to the  
30 relative importance of an item in a statistical calculation, for example the relative importance of a Transcript in Table 6. The weight of each transcript in a gene expression signature may be determined on a data set of patient samples using analytical methods known in the art. Exemplary procedures are described below.

Suitable methods and materials for the practice or testing of this disclosure are described below. Such methods and materials are illustrative only and are not intended to be limiting. Other methods and materials similar or equivalent to those described herein can be used. For example, conventional methods well known in the art to which this disclosure pertains are described in various general and more specific references, including, for example, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory Press, 1989; Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 3d ed., Cold Spring Harbor Press, 2001; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates, 1992 (and Supplements to 2000); Ausubel *et al.*, Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology, 4th ed., Wiley & Sons, 1999; Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1990; Harlow and Lane, Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1999; Oligonucleotide Synthesis, (M. J. Gait, ed., 1984); Animal Cell Culture, Freshney, ed., 1987; Methods in Enzymology, Academic Press, Inc.); Handbook of Experimental Immunology, 4<sup>sup</sup>.th ed., D. M. Weir & C. C. Blackwell, eds., Blackwell Science Inc., 1987; Gene Transfer Vectors for Mammalian Cells, J. M. Miller & M. P. Calos, eds., 1987); and PCR: The Polymerase Chain Reaction, Mullis *et al.*, eds., 1994. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

## ***II. Description of Several Embodiments***

### ***A. Colon Cancer Expression Signature and Methods of Use***

Disclosed herein are expression signatures from colon cancer. The disclosed signatures can be used for applications in prognosis of colon cancer, diagnosis of colon cancer and classifying patient groups. In some embodiments, a sample obtained from a subject, such as a patient, is processed into a set of polynucleotide binding targets that represent transcripts expressed in the tissue sample. The polynucleotide binding targets are probed with complementary polynucleotide probes representing, or corresponding to the signatures described herein in order to obtain information on expression levels of the transcripts. A decision score is optionally calculated that represents the expression levels of the transcripts in the signature. The decision score is then compared to a control, such as a patient population, and genetically similar

samples are correlated with known patient response or clinical outcomes. For example, sensitive methods are also provided to predict patient response to, and prognosis after, treatment for colon cancer, such as surgical resection and/or chemotherapy. Generally, historical patient population data and tissue samples are analyzed to create genetic profiles for patients having a past history of colon cancer. In some embodiments, the genetic profile of a patient sample is converted to a decision score. The clinical outcomes of each patient are correlated to the genetic profile, or decision score derived mathematically from the genetic profile for each patient's individual cancer.

10 In some embodiments, a mathematical algorithm is generated using the known historical patient data and applied to the predictive methods for new patients with colon cancer. In some embodiment, the algorithm creates a threshold that separates two groups of patients depending on selection criteria, for example patient outcome, response to therapy and recurrence, and the like. In some examples, the mathematical algorithm or threshold is validated using further historical patient population data before being used in the predictive methods described herein. The mathematical algorithm or threshold may then be used as a reference, for example as a control, to compare decision scores derived from genetic profiling of patients desirous of predictive methods of colon cancer. In some embodiments, these results permit assessment of genomic evidence of the efficacy of surgery alone, or in combination with adjuvant chemotherapy for treatment of colon cancer.

25 The signatures described herein may be significant in, and capable of, discriminating between two diagnoses or prognostic outcomes. An important aspect of the present disclosure is to use the measured expression of certain genes in colon cancer tissue to match patients to the most appropriate treatment, and to provide prognostic information.

In some embodiments, the signatures are developed using a colorectal cancer-focused microarray research tool. In a specific embodiment, this research tool is a colorectal cancer transcriptome-focused research array developed by Almac Diagnostics, Ltd. (Almac Diagnostics, Ltd., N. Ireland) capable of delivering accurate expression data.

30 The *Colorectal Cancer DSA*<sup>TM</sup> research tool contains 61,528 probe sets and encodes 52,306 transcripts confirmed as being expressed in colon cancer and normal tissue. Comparing the *Colorectal Cancer DSA*<sup>TM</sup> research tool against the National

Center for Biotechnology Information (NCBI) human Reference Sequence (RefSeq) RNA database (available on the world wide web at [ncbi.nlm.nih.gov/RefSeq/](http://ncbi.nlm.nih.gov/RefSeq/)) using BLAST analysis, 21,968 (42%) transcripts are present and 26,676 (51%) of transcripts are absent from the human RefSeq database. Furthermore 7% of the content represents expressed antisense transcripts to annotated genes. (Johnston *et al.*, *J. Clin. Oncol.* 24: 3519, 2006; Pruitt *et al.*, *Nucleic Acids Research* 33: D501-D504, 2005). In addition, probe-level analysis of the *Colorectal Cancer DSA*<sup>TM</sup> compared with leading generic arrays, highlighted that approximately 20,000 (40%) transcripts are not contained on the leading generic microarray platform (Affymetrix) and are unique to the *Colorectal Cancer DSA*<sup>TM</sup>. Thus, the *Colorectal Cancer DSA*<sup>TM</sup> research tool includes transcripts that have not been available in hitherto performed gene expression studies.

In some embodiments, the expression of a transcript in a gene expression signature is considered informative if expression levels are increased or decreased between the conditions of interest. Increases or decreases in gene expression can be assessed by methods known to those skilled in the art that include, but are not limited to, using fold changes, t-tests, F-tests, Wilcoxon rank-sum tests, ANOVA (Cui *et al.*, *Genome Biology* 4:210, 2003)) or dedicated methods for detecting differential expression such as Significance Analysis of Microarrays (Tusher *et al.*, *Proc. Natl. Acad. Sci. USA* 98:5116-21, 2001)) or LIMMA (Smyth, *Stat. Appl. Genet. Mol. Biol.*, 3:Art.3, 2004)).

In some embodiments, the transcripts in the signature are used to form a weighted sum of their signals, where individual weights can be positive or negative. The resulting sum ("decisive function") is compared with a pre-determined reference point. The comparison with the reference point may be used to diagnose, or predict a clinical condition or outcome.

One of ordinary skill in the art will appreciate that the transcripts included in the signature provided in Table 1, 2, and/or 6 will carry unequal weights in a signature for diagnosis or prognosis of colon cancer. Therefore, while as few as 1 sequence may be used to diagnose or predict an outcome, the specificity and sensitivity or diagnosis or prediction accuracy may increase using more sequences. Table 6 ranks the transcripts in order of decreasing weight in the signature, defined as the rank of the average weight in the compound decision score function measured under cross-

validation. The weight rank also corresponds to the SEQ ID NO: in the accompanying sequence listing thus the transcript with the greatest weight is SEQ ID NO: 1.

In some embodiments, a signature includes at least 2, such as 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 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, at least 175, at least 200, at least 225, at least 250, at least 275, at least 300, at least 325, at least 350, at least 375, at least 400, at least 425, at least 450, at least 475, at least 500, at least 525, at least 550, at least 575, at least 600, at least 634, or even all 636 of the transcripts in Table 6 that carry the greatest weight, defined as the rank of the average weight in the compound decision score function measured under cross-validation, and still have prognostic value. In some embodiments, a signature includes the top 10 weighted transcripts, the second top 10 weighted transcripts, the third top 10 weighted transcripts, the fourth top 10 weighted transcripts, the fifth top 10 weighted transcripts, the sixth top 10 weighted transcripts, the seventh top 10 weighted transcripts, the eighth top 10 weighted transcripts, the ninth top 10 weighted transcripts, or the tenth top 10 weighted transcripts listed in Table 6. In yet further embodiments, a signature includes the 636, 634, 620, 610, 600, 590, 580, 570, 560, 550, 540, 530, 520, 510, 500, 490, 480, 470, 460, 450, 440, 430, 420, 410, 400, 390, 380, 370, 360, 350, 340, 330, 320, 310, 300, 290, 280, 270, 260, 250, 240, 230, 220, 210, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 transcripts having the greatest weight listed in Table 6. In some embodiments, the signature is based on expression levels of from about 200 to about 1000 transcripts, such as from about 400 to about 800 transcripts, such as from about 500 to about 700 transcripts, or in some embodiments, from about 550 to about 650 transcripts, including those from Table 6 (e.g., at least about 50, at least about 100, at least about 200, at least about 300, at least about 400, at least about 500, or at least about 600, or all transcripts from Table 6) as described above.

In one embodiment, a specific signature may be used for the methods disclosed herein that includes transcripts for MUM1 and SIGMAR1. In another embodiment, a signature may be used for the methods disclosed herein that includes transcripts for MUM1, SIGMAR1, ARSD, SULT1C2 and PPFIBP1. In yet another embodiment, a signature may be used for the methods disclosed herein that includes transcripts for

ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L and antisense sequences of MUC3A, OLFM4 and RNF39. This signature is represented by Table 1 below.

**Table 1: 10 candidate core transcripts within the 636 transcript signature**

| Gene Name             | Weight Rank in 636 transcript signature | DAUC (Univariate) | Orientation |
|-----------------------|-----------------------------------------|-------------------|-------------|
| ARSD                  | 3                                       | -0.0109           | Sense       |
| CXCL9                 | 24                                      | -0.0103           | Sense       |
| PCLO                  | 272                                     | -0.0095           | Sense       |
| SLC2A3                | 23                                      | -0.0087           | Sense       |
| FCGBP                 | 416                                     | -0.0062           | Sense       |
| SLC2A14 ///<br>SLC2A3 | 55                                      | -0.0061           | Sense       |
| BCL9L                 | 175                                     | -0.0059           | Sense       |
| MUC3A                 | 112                                     | -0.0084           | AntiSense   |
| OLFM4                 | 61                                      | -0.0083           | AntiSense   |
| RNF39                 | 14                                      | -0.0064           | AntiSense   |

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In some embodiments, a core set of gene transcripts in colon cancer signature is provided that is identified through a separate study to determine the contribution that each of the 636 probesets makes to the performance of the signature. In this embodiment, ten probesets from the 636 probeset signature were removed and a new signature was created based on 636 probesets, using the training dataset. The new signature was then used to predict the validation dataset (without threshold) and the AUC was measured. The difference in AUC from the 636 probeset signature was recorded. This process was repeated 0.5 million times and the average difference in AUC that occurred for signatures lacking said probeset was recorded. The probesets with the largest negative  $\Delta$ AUC are recorded in Table 1. In this embodiment, this set of 10 transcripts represents a candidate core set of genes whose absence from the signature significantly impairs the predictive performance of the signature. Thus in certain embodiments, the transcripts representing the genes in Table 1 are included in a colon cancer signature. In Table 1, the DAUC represents the drop in validation AUC if this transcript is omitted from the signature. The orientation describes the

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orientation of the transcript expressed in colon tissue. Three transcripts in this signature are expressed as antisense transcripts of MUC3A, OLFM4 and RNF39.

In some embodiments, the signature includes a combination of 626-636 transcripts from Table 6, that include ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L, MUC3A, OLFM4 and RNF39. In yet another embodiment, the signature includes transcripts 10-636, 10-50, 50-636, 100-636, listed in Table 6 which includes ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L, MUC3A, OLFM4 and RNF39 where the transcript orientation is noted in Table 6.

Notably, 176 transcripts have been identified as being unrepresented by the leading generic array by probe-level analysis (*i.e.* they are "unique" to the *Colorectal Cancer DSA*<sup>TM</sup> tool described above). This group of 176 transcripts listed in Table 2 are described herein as transcripts that are unique to the colon gene signatures and methods of use herein. Probe-sequence-level homology searches have identified these transcripts as not being contained on the leading generic array (Affymetrix) (*i.e.* they are "unique" to the *Colorectal Cancer DSA*<sup>TM</sup> research tool described above). A number of these transcripts are antisense transcripts not previously reported to be expressed. These 176 transcripts are presented in Table 2 below, where the weight rank corresponds to the numbers shown in Table 6. Thus the sequence of these unique transcripts can be found in Table 6.

**Table 2: Unique transcripts in 636 transcript signature**

| Weight Rank<br>in 636<br>Transcript<br>Signature | Gene Symbol                                  | Orientation | Gene Description                                                                                                         |
|--------------------------------------------------|----------------------------------------------|-------------|--------------------------------------------------------------------------------------------------------------------------|
| 424                                              | AC068491.1<br>(Clone_based<br>_vcga_gene)    | Sense       | non-protein coding RNA 152<br>(NCRNA00152), transcript variant 2,<br>non-coding RNA [Source:RefSeq<br>DNA;Acc:NR_024205] |
| 214                                              | AC004968.2<br>(Clone_based<br>_ensembl_gene) | Sense       | Known long non-coding RNA                                                                                                |

|     |                                                                                               |           |                                                                                                                                                                                                                                            |
|-----|-----------------------------------------------------------------------------------------------|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 50  | AC010522.1<br>(Clone-based<br>(Ensembl) ///<br>ZNF418 ///<br>ZNF814                           | AntiSense | cDNA FLJ52732, moderately similar<br>to Zinc finger protein 418<br>[Source:UniProtKB/TrEMBL;Acc:B<br>4DR41] /// zinc finger protein 418<br>[Source:HGNC Symbol;Acc:20647]<br>/// zinc finger protein 814<br>[Source:HGNC Symbol;Acc:33258] |
| 13  | AC018359.1<br>(Clone_based<br>_vega_gene)<br>///<br>AC123023.1<br>(Clone_based<br>_vega_gene) | AntiSense | Novel processed transcript ///<br>Putative processed transcript.                                                                                                                                                                           |
| 559 | AC069513.3<br>(Clone_based<br>_vega_gene)                                                     | AntiSense | Novel processed transcript.                                                                                                                                                                                                                |
| 242 | AC130352.2<br>(Clone_based<br>_ensembl_gen<br>e)                                              | AntiSense | Novel miRNA.                                                                                                                                                                                                                               |
| 593 | AC138128.1<br>(Clone_based<br>_ensembl_gen<br>e)                                              | Sense     | Novel long non-coding RNA.                                                                                                                                                                                                                 |
| 488 | AC138128.1<br>(Clone_based<br>_ensembl_gen<br>e)                                              | Sense     | Novel long non-coding RNA.                                                                                                                                                                                                                 |
| 177 | ACTN4                                                                                         | AntiSense | actinin, alpha 4 [Source:HGNC<br>Symbol;Acc:166]                                                                                                                                                                                           |
| 427 | AL354822.1<br>(Clone_based<br>_ensembl_gen                                                    | Sense     | Putative uncharacterized protein<br>ENSP00000383640<br>[Source:UniProtKB/TrEMBL;Acc:B                                                                                                                                                      |

|     |                                                                |           |                                                                                                                                        |
|-----|----------------------------------------------------------------|-----------|----------------------------------------------------------------------------------------------------------------------------------------|
|     | e) ///<br>AC145212.2<br>(Clone_based<br>_ensembl_gen<br>c)     |           | 7WNX9] /// Known protein coding.                                                                                                       |
| 290 | AL604028.2<br>(Clone_based<br>_ensembl_gen<br>e)               | Sense     | Known protein coding.                                                                                                                  |
| 498 | AMAC1L1                                                        | Sense     | acyl-malonyl condensing enzyme 1-<br>like 1 [Source:HGNC<br>Symbol;Acc:31043]                                                          |
| 93  | ANGPTL6                                                        | Sense     | angiopoietin-like 6 [Source:HGNC<br>Symbol;Acc:23140]                                                                                  |
| 73  | APBB2                                                          | AntiSense | amyloid beta (A4) precursor protein-<br>binding, family B, member 2<br>[Source:HGNC Symbol;Acc:582]                                    |
| 250 | ARHGAP26                                                       | AntiSense | Rho GTPase activating protein 26<br>[Source:HGNC Symbol;Acc:17073]                                                                     |
| 81  | ARHGEF1                                                        | AntiSense | Rho guanine nucleotide exchange<br>factor (GEF) 1 [Source:HGNC<br>Symbol;Acc:681]                                                      |
| 326 | ARHGEF2///<br>RP11-<br>336K24.6<br>(Clone_based<br>_vega_gene) | Sense     | Rho/Rac guanine nucleotide<br>exchange factor (GEF) 2<br>[Source:HGNC Symbol;Acc:682] ///<br>Known nncoding transcript with no<br>ORF. |
| 391 | ASPH                                                           | AntiSense | aspartate beta-hydroxylase<br>[Source:HGNC Symbol;Acc:757]                                                                             |
| 435 | ATP2B4                                                         | Sense     | ATPase, Ca <sup>++</sup> transporting, plasma<br>membrane 4 [Source:HGNC<br>Symbol;Acc:817]                                            |
| 108 | AXIN2                                                          | AntiSense | axin 2 [Source:HGNC                                                                                                                    |

|     |                                                              |           |                                                                                                                                     |
|-----|--------------------------------------------------------------|-----------|-------------------------------------------------------------------------------------------------------------------------------------|
|     |                                                              |           | Symbol;Acc:904]                                                                                                                     |
| 217 | BIRC6                                                        | Sense     | baculoviral IAP repeat-containing 6<br>[Source:HGNC Symbol;Acc:13516]                                                               |
| 224 | BLCAP ///<br>RP11-<br>425M5.5<br>(Clone_based<br>_vega_gene) | AntiSense | bladder cancer associated protein<br>[Source:HGNC Symbol;Acc:1055]<br>/// Putative processed transcript.                            |
| 373 | BMPR1A                                                       | AntiSense | bone morphogenetic protein receptor,<br>type IA [Source:HGNC<br>Symbol;Acc:1076]                                                    |
| 384 | BMPR1A                                                       | AntiSense | bone morphogenetic protein receptor,<br>type IA [Source:HGNC<br>Symbol;Acc:1076]                                                    |
| 552 | C2orf89                                                      | Sense     | UPF0632 protein C2orf89 Precursor<br>[Source:UniProtKB/Swiss-<br>Prot;Acc:Q86V40]                                                   |
| 486 | C6orf203                                                     | Sense     | Uncharacterized protein C6orf203<br>[Source:UniProtKB/Swiss-<br>Prot;Acc:Q9P0P8]                                                    |
| 436 | C8orf38                                                      | Sense     | UPF0551 protein C8orf38,<br>mitochondrial Precursor (Putative<br>phytoene synthase)<br>[Source:UniProtKB/Swiss-<br>Prot;Acc:Q330K2] |
| 256 | CAMK1D                                                       | Sense     | calcium/calmodulin-dependent<br>protein kinase ID [Source:HGNC<br>Symbol;Acc:19341]                                                 |
| 400 | CAPN12                                                       | Sense     | calpain 12 [Source:HGNC<br>Symbol;Acc:13249]                                                                                        |
| 87  | CCND2                                                        | AntiSense | cyclin D2 [Source:HGNC<br>Symbol;Acc:1583]                                                                                          |
| 82  | CCND2                                                        | AntiSense | cyclin D2 [Source:HGNC                                                                                                              |

|     |          |           |                                                                                               |
|-----|----------|-----------|-----------------------------------------------------------------------------------------------|
|     |          |           | Symbol;Acc:1583]                                                                              |
| 289 | CD200    | Sense     | CD200 molecule [Source:HGNC<br>Symbol;Acc:7203]                                               |
| 281 | CDC42SE2 | AntiSense | CDC42 small effector 2<br>[Source:HGNC Symbol;Acc:18547]                                      |
| 510 | CEACAM5  | AntiSense | carcinoembryonic antigen-related<br>cell adhesion molecule 5<br>[Source:HGNC Symbol;Acc:1817] |
| 159 | CHD2     | AntiSense | chromodomain helicase DNA<br>binding protein 2 [Source:HGNC<br>Symbol;Acc:1917]               |
| 309 | CHD2     | Sense     | chromodomain helicase DNA<br>binding protein 2 [Source:HGNC<br>Symbol;Acc:1917]               |
| 531 | COMMD10  | AntiSense | COMM domain containing 10<br>[Source:HGNC Symbol;Acc:30201]                                   |
| 429 | CPEB2    | Sense     | cytoplasmic polyadenylation element<br>binding protein 2 [Source:HGNC<br>Symbol;Acc:21745]    |
| 505 | CSNK1A1  | Sense     | casein kinase 1, alpha 1<br>[Source:HGNC Symbol;Acc:2451]                                     |
| 466 | CTBP2    | AntiSense | C-terminal binding protein 2<br>[Source:HGNC Symbol;Acc:2495]                                 |
| 522 | DDX17    | AntiSense | DEAD (Asp-Glu-Ala-Asp) box<br>polypeptide 17 [Source:HGNC<br>Symbol;Acc:2740]                 |
| 63  | DEDD     | Sense     | death effector domain containing<br>[Source:HGNC Symbol;Acc:2755]                             |
| 407 | DHRS11   | AntiSense | dehydrogenase/reductase (SDR<br>family) member 11 [Source:HGNC<br>Symbol;Acc:28639]           |
| 300 | DLG5     | Sense     | discs, large homolog 5 (Drosophila)<br>[Source:HGNC Symbol;Acc:2904]                          |

|     |                                              |           |                                                                                                                                                                                                                                                                 |
|-----|----------------------------------------------|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 344 | DSP                                          | AntiSense | desmoplakin [Source:HGNC Symbol;Acc:3052]                                                                                                                                                                                                                       |
| 378 | ECE1                                         | Sense     | endothelin converting enzyme 1 [Source:HGNC Symbol;Acc:3146]                                                                                                                                                                                                    |
| 151 | EEF2K                                        | AntiSense | eukaryotic elongation factor-2 kinase [Source:HGNC Symbol;Acc:24615]                                                                                                                                                                                            |
| 587 | EGFR                                         | AntiSense | epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) [Source:HGNC Symbol;Acc:3236]                                                                                                                                |
| 274 | EPHB4                                        | AntiSense | EPH receptor B4 [Source:HGNC Symbol;Acc:3395]                                                                                                                                                                                                                   |
| 588 | FAM190A ///<br>SEPP1 ///<br>UBTD1 ///<br>UTY | AntiSense | family with sequence similarity 190, member A [Source:HGNC Symbol;Acc:29349] /// selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:10751] /// ubiquitin domain containing 1 [Source:HGNC Symbol;Acc:25683] /// ubiquitously transcribed tetratricopeptide repe |
| 192 | FAM60A                                       | AntiSense | family with sequence similarity 60, member A [Source:HGNC Symbol;Acc:30702]                                                                                                                                                                                     |
| 229 | FANCD2                                       | Sense     | Fanconi anemia, complementation group D2 [Source:HGNC Symbol;Acc:3585]                                                                                                                                                                                          |
| 625 | FAT1                                         | AntiSense | FAT tumor suppressor homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:3595]                                                                                                                                                                                       |
| 12  | FNDC3B                                       | Sense     | fibronectin type III domain containing 3B [Source:HGNC Symbol;Acc:24670]                                                                                                                                                                                        |
| 446 | FNDC3B                                       | Sense     | fibronectin type III domain                                                                                                                                                                                                                                     |

|     |        |           |                                                                                                                                                                                           |
|-----|--------|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |        |           | containing 3B [Source:HGNC Symbol;Acc:24670]                                                                                                                                              |
| 183 | GCC2   | Sense     | GRIP and coiled-coil domain containing 2 [Source:HGNC Symbol;Acc:23218]                                                                                                                   |
| 395 | GFPT1  | AntiSense | glutamine--fructose-6-phosphate transaminase 1 [Source:HGNC Symbol;Acc:4241]                                                                                                              |
| 623 | GLB1   | AntiSense | galactosidase, beta 1 [Source:HGNC Symbol;Acc:4298]                                                                                                                                       |
| 332 | GMDS   | Sense     | GDP-mannose 4,6-dehydratase [Source:HGNC Symbol;Acc:4369]                                                                                                                                 |
| 363 | GNL1   | Sense     | guanine nucleotide binding protein-like 1 [Source:HGNC Symbol;Acc:4413] /// Guanine nucleotide-binding protein-like 1 (GTP-binding protein HSR1) [Source:UniProtKB/Swiss-Prot;Acc:P36915] |
| 512 | GPRC5A | AntiSense | G protein-coupled receptor, family C, group 5, member A [Source:HGNC Symbol;Acc:9836]                                                                                                     |
| 206 | GPT2   | AntiSense | glutamic pyruvate transaminase (alanine aminotransferase) 2 [Source:HGNC Symbol;Acc:18062]                                                                                                |
| 341 | GRB7   | Sense     | growth factor receptor-bound protein 7 [Source:HGNC Symbol;Acc:4567]                                                                                                                      |
| 62  | GRHL2  | Sense     | grainyhead-like 2 (Drosophila) [Source:HGNC Symbol;Acc:2799]                                                                                                                              |
| 49  | GSTO2  | Sense     | glutathione S-transferase omega 2 [Source:HGNC Symbol;Acc:23064]                                                                                                                          |
| 56  | GSTO2  | Sense     | glutathione S-transferase omega 2 [Source:HGNC Symbol;Acc:23064]                                                                                                                          |

|     |           |           |                                                                                            |
|-----|-----------|-----------|--------------------------------------------------------------------------------------------|
| 533 | HELZ      | Sense     | helicase with zinc finger<br>[Source:HGNC Symbol;Acc:16878]                                |
| 412 | HNRNPL    | AntiSense | heterogeneous nuclear<br>ribonucleoprotein L [Source:HGNC<br>Symbol;Acc:5045]              |
| 198 | HSPD1     | Sense     | heat shock 60kDa protein 1<br>(chaperonin) [Source:HGNC<br>Symbol;Acc:5261]                |
| 114 | IGLL5     | Sense     | immunoglobulin lambda-like<br>polypeptide 5 [Source:HGNC<br>Symbol;Acc:38476]              |
| 495 | IL32      | AntiSense | interleukin 32 [Source:HGNC<br>Symbol;Acc:16830]                                           |
| 394 | INPP4B    | Sense     | inositol polyphosphate-4-<br>phosphatase, type II, 105kDa<br>[Source:HGNC Symbol;Acc:6075] |
| 165 | ITGA6     | AntiSense | integrin, alpha 6 [Source:HGNC<br>Symbol;Acc:6142]                                         |
| 166 | ITGA6     | AntiSense | integrin, alpha 6 [Source:HGNC<br>Symbol;Acc:6142]                                         |
| 287 | KANK1     | AntiSense | KN motif and ankyrin repeat<br>domains 1 [Source:HGNC<br>Symbol;Acc:19309]                 |
| 226 | KANK1     | AntiSense | KN motif and ankyrin repeat<br>domains 1 [Source:HGNC<br>Symbol;Acc:19309]                 |
| 179 | KCNK1     | AntiSense | potassium channel, subfamily K,<br>member 1 [Source:HGNC<br>Symbol;Acc:6272]               |
| 513 | KIAA0319L | Sense     | KIAA0319-like [Source:HGNC<br>Symbol;Acc:30071]                                            |
| 126 | KIF24     | Sense     | kinesin family member 24<br>[Source:HGNC Symbol;Acc:19916]                                 |

|     |         |           |                                                                                           |
|-----|---------|-----------|-------------------------------------------------------------------------------------------|
| 278 | KLRAQ1  | AntiSense | KLRAQ motif containing 1<br>[Source:HGNC Symbol;Acc:30595]                                |
| 237 | LRRC37B | AntiSense | leucine rich repeat containing 37B<br>[Source:HGNC Symbol;Acc:29070]                      |
| 519 | MACC1   | Sense     | metastasis associated in colon cancer<br>1 [Source:HGNC<br>Symbol;Acc:30215]              |
| 301 | MACF1   | AntiSense | microtubule-actin crosslinking factor<br>1 [Source:HGNC<br>Symbol;Acc:13664]              |
| 238 | MAVS    | AntiSense | mitochondrial antiviral signaling<br>protein [Source:HGNC<br>Symbol;Acc:29233]            |
| 336 | MEF2A   | Sense     | myocyte enhancer factor 2A<br>[Source:HGNC Symbol;Acc:6993]                               |
| 567 | MIR612  | AntiSense | hsa-mir-612<br>[Source:miRBase;Acc:MI0003625]                                             |
| 431 | MMP1    | AntiSense | matrix metalloproteinase 1 (interstitial<br>collagenase) [Source:HGNC<br>Symbol;Acc:7155] |
| 397 | MMP25   | Sense     | matrix metalloproteinase 25<br>[Source:HGNC Symbol;Acc:14246]                             |
| 72  | MORC3   | Sense     | MORC family CW-type zinc finger 3<br>[Source:HGNC Symbol;Acc:23572]                       |
| 506 | MORC3   | Sense     | MORC family CW-type zinc finger 3<br>[Source:HGNC Symbol;Acc:23572]                       |
| 634 | MUC2    | AntiSense | mucin 2, oligomeric mucus/gel-<br>forming [Source:HGNC<br>Symbol;Acc:7512]                |
| 110 | MUC6    | Sense     | mucin 6, oligomeric mucus/gel-<br>forming [Source:HGNC<br>Symbol;Acc:7517]                |
| 133 | MUC6    | Sense     | mucin 6, oligomeric mucus/gel-                                                            |

|     |       |                     |                                                                                                                 |
|-----|-------|---------------------|-----------------------------------------------------------------------------------------------------------------|
|     |       |                     | forming [Source:HGNC Symbol;Acc:7517]                                                                           |
| 1   | MUM1  | Sense               | melanoma associated antigen (mutated) 1 [Source:HGNC Symbol;Acc:29641]                                          |
| 385 | MYO10 | Sense               | myosin X [Source:HGNC Symbol;Acc:7593]                                                                          |
| 599 | MYO1E | AntiSense           | myosin IE [Source:HGNC Symbol;Acc:7599]                                                                         |
| 448 | N/A   | No Transcript match | N/A                                                                                                             |
| 57  | N/A   | No Transcript match | N/A                                                                                                             |
| 628 | N/A   | No Transcript match | N/A                                                                                                             |
| 370 | N/A   | Sense               | non-protein coding RNA 152 (NCRNA00152), transcript variant 2, non-coding RNA [Source:RefSeq DNA;Acc:NR_024205] |
| 6   | N/A   | No Transcript match | N/A                                                                                                             |
| 66  | N/A   | No Genome match     | N/A                                                                                                             |
| 610 | N/A   | No Transcript match | N/A                                                                                                             |
| 308 | N/A   | No Transcript match | N/A                                                                                                             |
| 439 | N/A   | No Genome match     | N/A                                                                                                             |
| 131 | N/A   | No Genome match     | N/A                                                                                                             |
| 359 | NAA50 | AntiSense           | N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source:HGNC                                              |

|     |                    |                     |                                                                                                                                                              |
|-----|--------------------|---------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                    |                     | Symbol;Acc:29533]                                                                                                                                            |
| 333 | NAA50              | AntiSense           | N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source:HGNC Symbol;Acc:29533]                                                                         |
| 356 | NBN                | AntiSense           | nibrin [Source:HGNC Symbol;Acc:7652]                                                                                                                         |
| 137 | NCAPD2             | Sense               | non-SMC condensin I complex, subunit D2 [Source:HGNC Symbol;Acc:24305]                                                                                       |
| 348 | NCRNA00188         | AntiSense           | small nucleolar RNA, C/D box 65 [Source:HGNC Symbol;Acc:32726]                                                                                               |
| 297 | NCRNA00262         | No Transcript match | non-protein coding RNA 262[Source:HGNC Symbol;Acc:26785]                                                                                                     |
| 606 | NDUFA13 /// YJEFN3 | AntiSense           | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13 [Source:HGNC Symbol;Acc:17194] /// YjeF N-terminal domain containing 3 [Source:HGNC Symbol;Acc:24785] |
| 502 | NR6A1              | AntiSense           | nuclear receptor subfamily 6, group A, member 1 [Source:HGNC Symbol;Acc:7985]                                                                                |
| 420 | NR6A1              | AntiSense           | nuclear receptor subfamily 6, group A, member 1 [Source:HGNC Symbol;Acc:7985]                                                                                |
| 61  | OLFM4              | AntiSense           | olfactomedin 4 [Source:HGNC Symbol;Acc:17190]                                                                                                                |
| 129 | PARP14             | AntiSense           | poly (ADP-ribose) polymerase family, member 14 [Source:HGNC Symbol;Acc:29232]                                                                                |
| 515 | PML                | AntiSense           | promyelocytic leukemia [Source:HGNC Symbol;Acc:9113]                                                                                                         |

|     |         |           |                                                                                                                                 |
|-----|---------|-----------|---------------------------------------------------------------------------------------------------------------------------------|
| 323 | POSTN   | AntiSense | periostin, osteoblast specific factor<br>[Source:HGNC Symbol;Acc:16953]                                                         |
| 554 | PPDPF   | Sense     | pancreatic progenitor cell<br>differentiation and proliferation<br>factor homolog (zebrafish)<br>[Source:HGNC Symbol;Acc:16142] |
| 381 | PPFIBP1 | Sense     | PTPRF interacting protein, binding<br>protein 1 (liprin beta 1)<br>[Source:HGNC Symbol;Acc:9249]                                |
| 504 | PPP3CA  | Sense     | protein phosphatase 3, catalytic<br>subunit, alpha isozyme<br>[Source:HGNC Symbol;Acc:9314]                                     |
| 382 | PRKDC   | AntiSense | protein kinase, DNA-activated,<br>catalytic polypeptide [Source:HGNC<br>Symbol;Acc:9413]                                        |
| 450 | PRPF40A | AntiSense | PRP40 pre-mRNA processing factor<br>40 homolog A (S. cerevisiae)<br>[Source:HGNC Symbol;Acc:16463]                              |
| 525 | PTK2    | AntiSense | PTK2 protein tyrosine kinase 2<br>[Source:HGNC Symbol;Acc:9611]                                                                 |
| 215 | PTP4A1  | AntiSense | protein tyrosine phosphatase type<br>IVA, member 1 [Source:HGNC<br>Symbol;Acc:9634]                                             |
| 298 | RABGAP1 | AntiSense | RAB GTPase activating protein 1<br>[Source:HGNC Symbol;Acc:17155]                                                               |
| 194 | RBM47   | Sense     | RNA binding motif protein 47<br>[Source:HGNC Symbol;Acc:30358]                                                                  |
| 461 | RERE    | AntiSense | arginine-glutamic acid dipeptide<br>(RE) repeats [Source:HGNC<br>Symbol;Acc:9965]                                               |
| 355 | RHBDD1  | Sense     | rhomboid domain containing 1<br>[Source:HGNC Symbol;Acc:23081]                                                                  |
| 454 | RNF145  | AntiSense | ring finger protein 145                                                                                                         |

|     |                                          |           |                                                                                  |
|-----|------------------------------------------|-----------|----------------------------------------------------------------------------------|
|     |                                          |           | [Source:HGNC Symbol;Acc:20853]                                                   |
| 171 | RNF43                                    | Sense     | ring finger protein 43 [Source:HGNC Symbol;Acc:18505]                            |
| 496 | RP11-357H14.7<br>(Clone_based_vega_gene) | Sense     | Novel processed transcript.                                                      |
| 573 | RP11-460N11.2<br>(Clone_based_vega_gene) | AntiSense | Known pseudogene.                                                                |
| 172 | RP11-460N11.2<br>(Clone_based_vega_gene) | AntiSense | Known pseudogene.                                                                |
| 155 | RP11-460N11.2<br>(Clone_based_vega_gene) | AntiSense | Known pseudogene.                                                                |
| 247 | RP11-706O15.1<br>(Clone_based_vega_gene) | AntiSense | HCG1981372, isoform CRA_cNovel protein ;<br>[Source:UniProtKB/TrEMBL;Acc:B1B108] |
| 251 | RP11-761E20.1<br>(Clone_based_vega_gene) | Sense     | Novel processed transcript.                                                      |
| 307 | RP11-86H7.1<br>(Clone_based_vega_gene)   | Sense     | Novel processed transcript.                                                      |
| 575 | RP4-717I23.3<br>(Clone_based_vega_gene)  | AntiSense | Novel processed transcript.                                                      |

|     |         |           |                                                                                                                          |
|-----|---------|-----------|--------------------------------------------------------------------------------------------------------------------------|
| 209 | RUNX1   | AntiSense | runt-related transcription factor 1<br>[Source:HGNC Symbol;Acc:10471]                                                    |
| 95  | SAMD4B  | AntiSense | sterile alpha motif domain containing<br>4B [Source:HGNC<br>Symbol;Acc:25492]                                            |
| 17  | SATB2   | AntiSense | SATB homeobox 2 [Source:HGNC<br>Symbol;Acc:21637]                                                                        |
| 264 | SH3D19  | AntiSense | SH3 domain containing 19<br>[Source:HGNC Symbol;Acc:30418]                                                               |
| 235 | SH3GLB1 | AntiSense | SH3-domain GRB2-like endophilin<br>B1 [Source:HGNC<br>Symbol;Acc:10833]                                                  |
| 388 | SIPA1L3 | Sense     | signal-induced proliferation-<br>associated 1 like 3 [Source:HGNC<br>Symbol;Acc:23801]                                   |
| 157 | SLC6A6  | Sense     | solute carrier family 6<br>(neurotransmitter transporter,<br>taurine), member 6 [Source:HGNC<br>Symbol;Acc:11052]        |
| 259 | SLC6A6  | Sense     | solute carrier family 6<br>(neurotransmitter transporter,<br>taurine), member 6 [Source:HGNC<br>Symbol;Acc:11052]        |
| 462 | SMURF2  | Sense     | SMAD specific E3 ubiquitin protein<br>ligase 2 [Source:HGNC<br>Symbol;Acc:16809]                                         |
| 377 | SND1    | Sense     | staphylococcal nuclease and tudor<br>domain containing 1 [Source:HGNC<br>Symbol;Acc:30646]                               |
| 335 | SNTB2   | AntiSense | syntrophin, beta 2 (dystrophin-<br>associated protein A1, 59kDa, basic<br>component 2) [Source:HGNC<br>Symbol;Acc:11169] |

|     |         |           |                                                                                   |
|-----|---------|-----------|-----------------------------------------------------------------------------------|
| 329 | SOD2    | AntiSense | superoxide dismutase 2,<br>mitochondrial [Source:HGNC<br>Symbol;Acc:11180]        |
| 263 | SP100   | Sense     | SP100 nuclear antigen<br>[Source:HGNC Symbol;Acc:11206]                           |
| 243 | SPDYE2  | AntiSense | speedy homolog E2 (Xenopus laevis)<br>[Source:HGNC Symbol;Acc:33841]              |
| 594 | SPDYE2  | AntiSense | speedy homolog E2 (Xenopus laevis)<br>[Source:HGNC Symbol;Acc:33841]              |
| 636 | SRSF1   | AntiSense | serine/arginine-rich splicing factor 1<br>[Source: HGNC Symbol; Acc:10780]        |
| 561 | SSFA2   | Sense     | sperm specific antigen 2<br>[Source:HGNC Symbol;Acc:11319]                        |
| 369 | TBL1XR1 | AntiSense | transducin (beta)-like 1 X-linked<br>receptor 1 [Source:HGNC<br>Symbol;Acc:29529] |
| 605 | TEX10   | AntiSense | testis expressed 10 [Source:HGNC<br>Symbol;Acc:25988]                             |
| 453 | TFAM    | AntiSense | transcription factor A, mitochondrial<br>[Source:HGNC Symbol;Acc:11741]           |
| 629 | TLCD2   | Antisense | TLC domain containing 2 [Source:<br>HGNC Symbol; Acc:33522]                       |
| 470 | TLCD2   | Antisense | TLC domain containing 2 [Source:<br>HGNC Symbol; Acc:33522]                       |
| 35  | TMEM87A | Sense     | transmembrane protein 87A<br>[Source:HGNC Symbol;Acc:24522]                       |
| 624 | TMPRSS4 | AntiSense | transmembrane protease, serine 4<br>[Source:HGNC Symbol;Acc:11878]                |
| 102 | TRIM5   | Sense     | tripartite motif-containing 5<br>[Source:HGNC Symbol;Acc:16276]                   |
| 44  | TRPS1   | AntiSense | trichorhinophalangeal syndrome I<br>[Source:HGNC Symbol;Acc:12340]                |
| 221 | TSPAN1  | Sense     | tetraspanin 1 [Source:HGNC                                                        |

|     |           |           |                                                                           |
|-----|-----------|-----------|---------------------------------------------------------------------------|
|     |           |           | Symbol;Acc:20657]                                                         |
| 543 | TTC39B    | AntiSense | tetratricopeptide repeat domain 39B<br>[Source:HGNC Symbol;Acc:23704]     |
| 342 | U6 (RFAM) | Sense     | U6 spliceosomal RNA<br>[Source:RFAM;Acc:RF00026]                          |
| 288 | WSB1      | AntiSense | WD repeat and SOCS box-<br>containing 1 [Source:HGNC<br>Symbol;Acc:19221] |
| 523 | YLPM1     | AntiSense | YLP motif containing 1<br>[Source:HGNC Symbol;Acc:17798]                  |
| 386 | YPEL5     | AntiSense | yippee-like 5 (Drosophila)<br>[Source:HGNC Symbol;Acc:18329]              |
| 612 | ZFAND3    | Sense     | zinc finger, AN1-type domain 3<br>[Source:HGNC Symbol;Acc:18019]          |
| 76  | ZHX2      | AntiSense | zinc fingers and homeoboxes 2<br>[Source:HGNC Symbol;Acc:18513]           |
| 161 | ZNF75A    | AntiSense | zinc finger protein 75a<br>[Source:HGNC Symbol;Acc:13146]                 |
| 409 | ZXDC      | AntiSense | ZXD family zinc finger C<br>[Source:HGNC Symbol;Acc:28160]                |

In some embodiments, a signature includes at least 2, such as 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 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, or even all 176 of the transcripts listed in Table 2, for example those that carry the greatest weight, defined as the rank of the average weight in the compound decision score function measured under cross-validation, and still have prognostic value. In some embodiments, a signature includes the top 10 weighted transcripts, the second top 10 weighted transcripts, the third top 10 weighted transcripts, the fourth top 10 weighted transcripts, the fifth top 10 weighted transcripts, the sixth top 10 weighted transcripts, the seventh top 10 weighted transcripts, the eighth top 10 weighted transcripts, the ninth top 10 weighted transcripts, or the tenth top 10

weighted transcripts listed in Table 2. In yet further embodiments, a signature includes the 176, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 transcripts having the greatest weight listed in Table 2.

In some embodiments, the methods described herein include subjecting RNA isolated from a patient to gene expression profiling. Thus, the gene expression profile may be completed for a set of genes that includes at least two of the transcripts listed in Table 6, which in some examples are normalized as described below. In particular embodiments of the methods disclosed herein, the expression level of at least 2, such as 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 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, at least 175, at least 200, at least 225, at least 250, at least 275, at least 300, at least 325, at least 350, at least 375, at least 400, at least 425, at least 450, at least 474, at least 500, at least 525, at least 550, at least 575, at least 600, at least 634, or even all 636 of the transcripts in Table 6 or their expression products, and/or complement is determined, for example the transcripts in Table 6 that carry the greatest weight, defined as the rank of the average weight in the compound decision score function measured under cross-validation, and still have prognostic value. In some embodiments of this method, the expression level of at least at least 2, such as 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 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, or even all 176 of the transcripts in Table 2 or their expression products, and/or complement is determined, for example those that carry the greatest weight, defined as the rank of the average weight in the compound decision score function measured under cross-validation, and still have prognostic value. In the methods described herein, the combination of transcripts may be referred to as a signature or expression signature.

The relative expression levels of transcripts in a colon tissue are measured to form a gene expression profile. In one embodiment, the gene expression profile of a set of transcripts from a patient tissue sample is summarized in the form of a compound decision score and compared to a control threshold, such a threshold that is

mathematically derived from a training set of patient data. The threshold separates a patient group based on different characteristics such as, but not limited to, good/poor prognosis, responsiveness/non-responsiveness to treatment, cancer detection/diagnosis and cancer classification. The patient training set data is

5 preferably derived from colon tissue samples having been characterized by prognosis, likelihood of recurrence, or long term survival, diagnosis, cancer classification, personalized genomics profile, clinical outcome, treatment response. Expression profiles, and corresponding decision scores from patient samples may be correlated with the characteristics of patient samples in the training set that are on the same side

10 of the mathematically derived decision threshold. In this embodiment, the threshold of the linear classifier compound decision score was optimized to maximize the sum of sensitivity and specificity under cross-validation applied within the training dataset. These methods are also useful for determining prognosis of colon cancer and in a particular embodiment a patient with stage II colon cancer. In some examples, the

15 disclosed methods are predictive of poor clinical outcome, which can be measured, for example, in terms of shortened survival or increased risk of cancer recurrence, *e.g.* following surgical removal of the cancer, or following surgical removal of the cancer in combination with adjuvant chemotherapy.

Methods are provided for diagnosing colon cancer in a sample obtained from a

20 subject. Such methods include detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from the subject and comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of a diagnosis of colon cancer, wherein the expression

25 level, or a decision score derived therefrom, on the same side of the threshold indicates a diagnosis of colon cancer. In some examples, a control threshold is a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a known colon cancer sample (or samples).

Methods are provided for classifying a colon cancer sample. Such methods

30 include detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject and comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom, to a control threshold indicative of known classification, wherein the expression level, or a decision score

derived therefrom, on the same side of the threshold permits classification of the colon cancer sample. In some examples, a control threshold is a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) of known classification. In  
5 some examples, the colon cancer sample is classified as stage I, stage II, stage III and stage IV. In some examples the method further includes choosing a treatment plan that will be effective for the classified colon cancer, for example surgical resection, chemotherapy, radiation or any combination thereof.

Methods are provided for predicting a response to a treatment for colon  
10 cancer, such as a subject with stage II colon cancer. Such methods include detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject and comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom, to a control threshold indicative of a known  
15 response to treatment, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a similar response to treatment, thereby predicting response to treatment. In some examples, a control threshold is a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) having a  
20 known response to treatment. In some embodiments, the method is a method of predicting response from surgical resection, chemotherapy, radiation or any combination thereof.

Methods are provided for predicting long term survival of a subject with colon cancer, such as a subject diagnosed with stage II colon cancer. These methods include  
25 detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject and comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom, to a control threshold indicative of having a history of long term survival, wherein the expression level, or a decision  
30 score derived therefrom, on the same side of the threshold indicates long term survival of the subject, thereby predicting long term survival of a subject. In some examples, the control threshold is a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer

sample (or samples) obtained from a subject (or subjects) having a history of long term survival.

Also provided are methods for predicting of recurrence of colon cancer in a subject, such as subject diagnosed as having stage II colon cancer. These methods include detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject and comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of a history of recurrence, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a recurrence in the subject. In some examples, a control threshold is a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) having a history of recurrence.

Methods are provided for preparing a personalized colon cancer genomics profile for a subject. The methods include detecting an expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject and creating a report summarizing the data obtained by the gene expression analysis.

In particular embodiments of the methods disclosed herein, the expression levels for at least 2, such as 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 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, at least 175, at least 200, at least 225, at least 250, at least 275, at least 300, at least 325, at least 350, at least 375, at least 400, at least 425, at least 450, at least 474, at least 500, at least 525, at least 550, at least 575, at least 600, at least 634, or even all 636 of the transcripts in Table 6 or their expression products is determined and compared with a control threshold. In other embodiment of these methods the expression levels for MUM1 and SIGMAR1 or their expression products is determined and compared with a control threshold. In another embodiment, the expression levels for MUM1, SIGMAR1, ARSD, SULT1C2 and PPFIBP1 or their expression products is determined and compared with the control threshold. In additional embodiments, the expression levels for ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L and antisense

sequences of MUC3A, OLFM4 and RNF39 or their expression products is determined and compared with a control threshold. In still other embodiments, expression levels for substantially all the transcripts listed in one of Tables 1, 2, and/or 6 are determined in step and compared with a control threshold.

- 5           In some embodiments of the disclosed methods, the RNA levels are corrected for (normalize away) both differences in the amount of RNA assayed and variability in the quality of the RNA used. Control transcripts may be included in assays as positive or negative controls and to normalize readings and ensure reliable measurement data, but are preferably omitted for performing the actual prognosis.
- 10       The exact identity of the former is typically unimportant and a very broad variety of transcripts could be envisaged for all of the purposes disclosed herein. For the normalization controls, a broad variety of transcripts could be envisaged, although they have to fulfill the basic requirements of approximately constant and stable expression between a broad variety of subjects or conditions for the target tissue of
- 15       interest, in particular between the prognostic groups under consideration. Similarly the RNA degradation controls have to show intensity behavior, suitable for indicating (overly) degraded RNA. This may or may not include RNA controls, which show a stable intensity regardless of the overall RNA degradation of a sample as positive controls. In relation to these controls the intensity pattern for suitable other RNA
- 20       controls would be analyzed for which an intensity dependency on the RNA degradation stage is observed. This may or may not include specific analyses depending on varying positions of probe sequences with respect to the 3' end of a transcript.

- In some embodiments of the disclosed methods, where a microarray is used
- 25       for quantifying gene expression, one or more of the following controls can be used:
- (a)     Alignment controls, which are specific transcripts spiked in labeled form, which bind to specific positions on an array and ensure a proper grid alignment in the image processing of a scanned array.
- (b)     Amplification controls, which are specific unlabeled transcripts, *e.g.*
- 30       poly-A control transcripts, spiked in before any amplification is performed, so undergoing the same processing as the sample mRNA to ensure an appropriate performance of the cDNA synthesis and subsequent amplification reactions.

(c) Labeling and hybridization controls, which are specific controls spiked in before the labeling and hybridization to the chip for controlling the efficiency of these two steps separately from the prior amplification reaction.

(d) Background controls, which are probe sequences on the microarray for which no corresponding target sequences should be available in the sample. Thus, in principle no specific target binding should occur. These controls are used to establish background or cross-hybridization intensities. They would potentially be characterized by different GC-contents and a suitable spatial distribution over an entire microarray.

(e) Normalization controls, which are probe sequences detecting specifically chosen target sequences from the sample which are used to correct for varying input mRNA amounts, varying yield of amplification reactions and varying overall sensitivity of the measurement device. They are used to correct the measured intensity values and would thus ensure an increased analytical precision of the overall measurement device including the preparatory laboratory steps.

(f) RNA quality and degradation control, which are probe sequences from various positions with respect to the 3' position of their respective genes designed to indicate the RNA quality and detect RNA degradation. Corresponding probes or probe sets from multiple genes might represent differing RNA degradation behavior from different RNA species.

Whereas controls a) – d) can purely be derived based on sequence considerations and should not be naturally present in the tissue and condition of interest, controls e) and f) can be chosen by suitable analyses of prior patient data. This may or may not be the same training data on which the prognostic gene signature has been derived.

It should be understood that the above controls are only provided as example and that other embodiments of this disclosure could be envisaged (such as qPCR) in which different controls, with similar functionality would be used.

## **B. Probes, Primers and Arrays**

Disclosed are probes and primers specific for the disclosed colon cancer gene signatures. Also disclosed are arrays, which include probes for the disclosed colon cancer signatures. In some embodiments, a probe specific for the disclosed colon cancer gene signature includes a nucleic acid sequence that specifically hybridizes

one of SEQ ID NOs: 1-636 or the complement thereof. In some embodiments, a probe set for a disclosed colon cancer signature includes probes that specifically hybridize to at least 2, such as 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 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, at least 175, at least 200, at least 225, at least 250, at least 275, at least 300, at least 325, at least 350, at least 375, at least 400, at least 425, at least 450, at least 474, at least 500, at least 525, at least 550, at least 575, at least 600, at least 634, or even all 636 of the transcripts in Table 6, that carry the greatest weight, defined as the rank of the average weight in the compound decision score function measured under cross-validation, and still have prognostic value, such as a probe that specifically hybridizes to any one of SEQ ID NOs: 1-636 or the complement thereof. In some embodiments, a probe set for a disclosed colon cancer signature includes probes that specifically hybridize to the top 10 weighted transcripts, the second top 10 weighted transcripts, the third top 10 weighted transcripts, the fourth top 10 weighted transcripts, the fifth top 10 weighted transcripts, the sixth top 10 weighted transcripts, the seventh top 10 weighted transcripts, the eighth top 10 weighted transcripts, the ninth top 10 weighted transcripts, or the tenth top 10 weighted transcripts listed in Table 6. In yet further embodiments, a probe set for a disclosed colon cancer signature includes probes that specifically hybridize to 636, 634, 620, 610, 600, 590, 580, 570, 560, 550, 540, 530, 520, 510, 500, 490, 480, 470, 460, 450, 440, 430, 420, 410, 400, 390, 380, 370, 360, 350, 340, 330, 320, 310, 300, 290, 280, 270, 260, 250, 240, 230, 220, 210, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 transcripts having the greatest weight listed in Table 6 or the complement thereof. In some embodiments, a probe set for a disclosed cancer signature comprises about 200 to about 1000 probes, such as from about 400 to about 800 probes, such as from about 500 to about 700 probes, such as from about 550 to about 650 probes, where the probes detect transcripts from Table 6. The additional probes may be optionally selected from those that detect transcripts that are expressed in colon cancer, or which function as signal controls or expression level controls. Such optional probes can be selected from those included on the *Colorectal Cancer DSA<sup>TM</sup>* tool.

In some embodiments, a probe set for a disclosed colon cancer signature includes probes that specifically hybridize to transcripts for MUM1 and SIGMAR1. In other embodiments, a probe set for a disclosed colon cancer signature includes probes that specifically hybridize to transcripts for MUM1, SIGMAR1, ARSD, 5 SULT1C2 and PPFIBP1. In yet other embodiments, a probe set for a disclosed colon cancer signature includes probes that specifically hybridize to transcripts for ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L and antisense sequences of MUC3A, OLFM4 and RNF39. A set of probes or primers can be prepared that is substantially representative of the gene expression signature.

10 “Substantially representative of the gene expression signature” refers to probe sets that specifically hybridize to at least 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% of the coding or non-coding transcripts in the gene expression signature, for example at least 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% of the coding or non-coding transcripts in the gene expression signatures shown in Table 1, 2, or 6 or the 15 complement thereof.

It is advantageous to use probes which bind to the 3' regions of transcripts in the gene expression signature, specifically where the patient tissue to be analyzed for gene expression is RNA extracted from paraffin embedded tissue. Typically each probe will be capable of hybridizing to a complementary sequence in the respective 20 transcript, which occurs within 1kb, or 500bp, or 300bp, or 200bp, or 100bp of the 3' end of the transcript. In the case of mRNA, the “3' end of the transcript” is defined herein as the polyadenylation site, not including the poly(A) tail.

In one embodiment, a pool of probes making up 30% of the total absolute weight of the signature is used. In alternate embodiments, a pool of probes making up 25 40%, 60%, 70%, 80%, 90%, 95% or 100% of the total absolute weight of the signature is used in the methods described herein. The basis for inclusion of markers, as well as the clinical significance of mRNA level variations with respect to the reference set, is indicated below. In some embodiments, the disclosed probes are part of an array, for example the probes are bound to a solid substrate. Exemplary nucleic acid array and methods of making such arrays are discussed in Section D below. 30

In some embodiments, a probe specific for the disclosed colon cancer gene signature is part of a nucleic acid array, such as a microarray. In some examples, such arrays include a nucleic acid sequence that specifically hybridizes one of SEQ ID NOs: 1-636 or the complement thereof. In some embodiments, a nucleic acid array,

such as a microarray, includes probes that specifically hybridize to at least 2, such as 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 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, at least 175, at least 200, at least 225, at least 250, at least 275, at least 300, at least 325, at least 350, at least 375, at least 400, at least 425, at least 450, at least 474, at least 500, at least 525, at least 550, at least 575, at least 600, at least 634, or even all 636 of the transcripts in Table 6. In some embodiments, a nucleic acid array for a disclosed colon cancer signature includes probes that specifically hybridize to the top 10 weighted transcripts, the second top 10 weighted transcripts, the third top 10 weighted transcripts, the fourth top 10 weighted transcripts, the fifth top 10 weighted transcripts, the sixth top 10 weighted transcripts, the seventh top 10 weighted transcripts, the eighth top 10 weighted transcripts, the ninth top 10 weighted transcripts, or the tenth top 10 weighted transcripts listed in Table 6. In yet further embodiments, a nucleic acid array for a disclosed colon cancer signature includes probes that specifically hybridize to 636, 634, 620, 610, 600, 590, 580, 570, 560, 550, 540, 530, 520, 510, 500, 490, 480, 470, 460, 450, 440, 430, 420, 410, 400, 390, 380, 370, 360, 350, 340, 330, 320, 310, 300, 290, 280, 270, 260, 250, 240, 230, 220, 210, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 transcripts having the greatest weight listed in Table 6 or the complement thereof. In some embodiments, a nucleic acid array for a disclosed colon cancer signature comprises about 200 to about 1000 probes, such as from about 400 to about 800 probes, such as from about 500 to about 700 probes, such as from about 550 to about 650 probes, where the probes detect transcripts from Table 6. The additional probes may be optionally selected from those that detect transcripts that are expressed in colon cancer, or which function as signal controls or expression level controls. Such optional probes can be selected from those included on the *Colorectal Cancer DSA<sup>TM</sup>* tool. In some embodiments, a nucleic acid array for a disclosed colon cancer signature comprises more than about 1000 probes.

Also disclosed are primer pairs for the amplification of a gene expression signature for colon cancer nucleic acid. In some examples a primer pair includes a forward primer 15 to 40 nucleotides in length comprising a nucleic acid sequence that specifically hybridizes to any one of the nucleic acid sequences set forth as SEQ ID

NOs: 1-636 or its complement and a reverse primer 15 to 40 nucleotides in length comprising a nucleic acid sequence that specifically hybridizes to any one of the nucleic acid sequences set forth as SEQ ID NOs: 1-636 or its complement, wherein the set of primers is capable of directing the amplification of the nucleic acid.

5           Set of primer pairs for the amplification of a gene expression signature for colon cancer nucleic acids are also disclosed. In some embodiments, a primer set for a disclosed colon cancer signature includes primers that specifically hybridize to and are capable of amplifying at least 2, such as 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  
10   14, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, at least 175, at least 200, at least 225, at least 250, at least 275, at least 300, at least 325, at least 350, at least 375, at least 400, at least 425, at least 450, at least 474, at least 500, at least 525,  
15   at least 550, at least 575, at least 600, at least 634, or even all 636 of the transcripts in Table 6 that carry the greatest weight, defined as the rank of the average weight in the compound decision score function measured under cross-validation, and still have prognostic value such as primers that specifically hybridize to and are capable of amplifying any one of SEQ ID NOs: 1-636 or the complement thereof. In some  
20   embodiments, a primer set for a disclosed colon cancer signature includes primers that specifically hybridize to and are capable of amplifying the top 10 weighted transcripts, the second top 10 weighted transcripts, the third top 10 weighted transcripts, the fourth top 10 weighted transcripts, the fifth top 10 weighted transcripts, the sixth top 10 weighted transcripts, the seventh top 10 weighted  
25   transcripts, the eighth top 10 weighted transcripts, the ninth top 10 weighted transcripts, or the tenth top 10 weighted transcripts listed in Table 6. In yet further embodiments, a primer set for a disclosed colon cancer signature includes primers that specifically hybridize to and are capable of amplifying 636, 634, 620, 610, 600, 590, 580, 570, 560, 550, 540, 530, 520, 510, 500, 490, 480, 470, 460, 450, 440, 430, 420,  
30   410, 400, 390, 380, 370, 360, 350, 340, 330, 320, 310, 300, 290, 280, 270, 260, 250, 240, 230, 220, 210, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 transcripts having the greatest weight listed in Table 6 or the complement thereof.

In some embodiments, a primer set for a disclosed colon cancer signature includes primers that specifically hybridize to and are capable of amplifying transcripts for MUM1 and SIGMAR1. In another embodiment, a primer set for a disclosed colon cancer signature includes primers that specifically hybridize to and are capable of amplifying transcripts for MUM1, SIGMAR1, ARSD, SULT1C2 and PPFIBP1. In yet another embodiment, a probe set for a disclosed colon cancer signature includes probes that specifically hybridize to transcripts for ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L and antisense sequences of MUC3A, OLFM4 and RNF39. A set of probes or primers can be prepared that is substantially representative of the gene expression signature. “Substantially representative of the gene expression signature” refers to probe sets that specifically hybridize to at least 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% of the coding or non-coding transcripts in the gene expression signature, for example at least 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% of the coding or non-coding transcripts in the gene expression signatures shown in Table 1, 2, or 6 or the complement thereof.

### ***C. Statistical Determination of Colon Cancer Signatures***

The disclosed colon cancer signatures can be evaluated by statistical methods. In some embodiments, the gene expression profile of a patient tissue sample is evaluated by a linear classifier. As used herein, a linear classifier refers to a weighted sum of the individual gene intensities into a compound decision score (“decision function”). The decision score is then compared to a pre-defined cut-off threshold, corresponding to a certain set point in terms of sensitivity and specificity, which indicates if a sample, is above the threshold (decision function positive) or below (decision function negative).

Effectively, this means that the data space, *i.e.* the set of all possible combinations of gene expression values, is split into two mutually exclusive halves corresponding to different clinical classifications or predictions, *e.g.* one corresponding to good prognosis and the other to poor prognosis. In the context of the overall signature, relative over-expression of a certain gene can either increase the decision score (positive weight) or reduce it (negative weight) and thus contribute to an overall decision of, for example, either poor or good prognosis.

The interpretation of this quantity, *i.e.* the cut-off threshold for good versus poor prognosis, is derived in the development phase (“training”) from a set of patients

with known outcome. The corresponding weights and the good/poor prognosis cut-off threshold for the decision score are fixed *a priori* from training data by methods known to those of ordinary skill in the art. In a preferred embodiment of the present method, Partial Least Squares Discriminant Analysis (PLS-DA) is used for  
5 determining the weights. (Stähle, *J. Chemom.* 1 185-196, 1987; Nguyen and Rocke, *Bioinformatics* 18 39-50, 2002). Other methods for performing the classification, known to those skilled in the art, may also be with the methods described herein when applied to the transcripts of a colon cancer signature.

Different methods can be used to convert quantitative data measured on these  
10 genes or their products into a prognosis or other predictive use. These methods include, but not limited to pattern recognition (Duda *et al.* Pattern Classification, 2<sup>nd</sup> ed., John Wiley, New York 2001), machine learning (Schölkopf *et al.* Learning with Kernels, MIT Press, Cambridge 2002, Bishop, Neural Networks for Pattern Recognition, Clarendon Press, Oxford 1995), statistics (Hastie *et al.* The Elements of  
15 Statistical Learning, Springer, New York 2001), bioinformatics (Dudoit *et al.*, *J. Am. Statist. Assoc.* 97:77-87, 2002; Tibshirani *et al.*, *Proc. Natl. Acad. Sci. USA* 99:6567-6572, 2002) or chemometrics (Vandeginste, *et al.*, Handbook of Chemometrics and Qualimetrics, Part B, Elsevier, Amsterdam 1998).

In some embodiments, in a training step a set of patient samples for both good  
20 and poor prognosis cases are measured and the prediction method is optimised using the inherent information from this training data to optimally predict the training set or a future sample set. In this training step the used method is trained or parameterised to predict from a specific intensity pattern to a specific prognostic call. Suitable transformation or pre-processing steps might be performed with the measured data  
25 before it is subjected to the prognostic method or algorithm.

In some embodiments, a weighted sum of the pre-processed intensity values for each transcript is formed and compared with a threshold value optimised on the training set (Duda *et al.* Pattern Classification, 2<sup>nd</sup> ed., John Wiley, New York 2001). The weights can be derived by a multitude of linear classification methods, including  
30 but not limited to Partial Least Squares (PLS, (Nguyen *et al.*, 2002, *Bioinformatics* 18 (2002) 39-50)) or Support Vector Machines (SVM, (Schölkopf *et al.* Learning with Kernels, MIT Press, Cambridge 2002)).

In some embodiments, the data is transformed non-linearly before applying a weighted sum, for example as described above. This non-linear transformation might

include increasing the dimensionality of the data. The non-linear transformation and weighted summation might also be performed implicitly, *e.g.* through the use of a kernel function. (Schölkopf *et al.* Learning with Kernels, MIT Press, Cambridge 2002).

5           In some embodiments, a new data sample is compared with two or more class prototypes, being either real measured training samples or artificially created prototypes. This comparison is performed using suitable similarity measures for example but not limited to Euclidean distance (Duda *et al.* Pattern Classification, 2<sup>nd</sup> ed., John Wiley, New York 2001), correlation coefficient (van't Veer, *et al.*, *Nature* 10 415:530, 2002) etc. A new sample is then assigned to the prognostic group with the closest prototype or the highest number of prototypes in the vicinity.

          In some embodiments, decision trees (Hastie *et al.* The Elements of Statistical Learning, Springer, New York 2001) or random forests (Breiman, 2001 Random Forests, Machine Learning 45:5) are used to make a prognostic call from the 15 measured intensity data for the transcript set or their products.

          In some embodiments, neural networks (Bishop, Neural Networks for Pattern Recognition, Clarendon Press, Oxford 1995) are used to make a prognostic call from the measured intensity data for the transcript set or their products.

          In some embodiments, discriminant analysis (Duda *et al.* Pattern 20 Classification, 2<sup>nd</sup> ed., John Wiley, New York 2001), comprising but not limited to linear, diagonal linear, quadratic and logistic discriminant analysis, is used to make a prognostic call from the measured intensity data for the transcript set or their products.

          In some embodiments, Prediction Analysis for Microarrays (PAM, (Tibshirani 25 *et al.*, *Proc. Natl. Acad. Sci. USA* 99:6567-6572, 2002)) is used to make a prognostic call from the measured intensity data for the transcript set or their products.

          In some embodiments, Soft Independent Modelling of Class Analogy (SIMCA, (Wold, 1976, *Pattern Recogn.* 8:127-139)) is used to make a prognosis from the measured intensity data for the transcript set or their products.

30

#### **D.       Methods for detection of mRNA**

Gene expression can be evaluated by detecting mRNA encoding the gene of interest. Thus, the disclosed methods can include evaluating mRNA. RNA can be isolated from a sample of a tumor (for example, a colon cancer tumor) from a subject,

a sample of adjacent non-tumor tissue from the subject, a sample of tumor-free tissue from a normal (healthy) subject, or combinations thereof, using methods well known to one of ordinary skill in the art, including commercially available kits.

General methods for mRNA extraction are well known in the art and are disclosed in standard textbooks of molecular biology, including Ausubel *et al.*, Current Protocols of Molecular Biology, John Wiley and Sons (1997). Methods for RNA extraction from paraffin embedded tissues are disclosed, for example, in Rupp and Locker, *Biotechniques* 6:56-60, 1988, and De Andres *et al.*, *Biotechniques* 18:42-44, 1995. In one example, RNA isolation can be performed using purification kit, buffer set and protease from commercial manufacturers, such as QIAGEN® (Valencia, CA), according to the manufacturer's instructions. For example, total RNA from cells in culture (such as those obtained from a subject) can be isolated using QIAGEN® RNeasy® mini-columns. Other commercially available RNA isolation kits include MASTERPURE® Complete DNA and RNA Purification Kit (EPICENTRE® Madison, Wis.), and Paraffin Block RNA Isolation Kit (Ambion, Inc.). Total RNA from tissue samples can be isolated using RNA Stat-60 (Tel-Test). RNA prepared from tumor or other biological sample can be isolated, for example, by cesium chloride density gradient centrifugation.

The present signatures and methods described herein accommodate the use of archived paraffin-embedded biopsy material for assay of all markers in the set, and therefore are compatible with the most widely available type of biopsy material. The expression level of transcripts in a colon tissue sample may be determined using RNA obtained from a formalin-fixed, paraffin-embedded tissue sample, fresh frozen tissue or fresh tissue that has been stored in solutions such as RNAlater®. The isolation of RNA can, for example, be carried out following any of the procedures described above or throughout the application, or by any other method known in the art. While all techniques of gene expression profiling, as well as proteomics techniques, are suitable for use in performing the methods described herein, the gene expression levels are often determined by DNA microarray technology.

If the source of the tissue is a formalin-fixed, paraffin embedded tissue sample, the RNA may be fragmented, resulting in loss of information. The signatures provided herein are derived from pools of transcripts sequenced from their 3' end thereby providing an accurate representation of the transcriptome of the tissue. Thus

the signatures provided herein are useful for both fresh frozen and fixed paraffin-embedded tissues.

In some embodiments, RNA samples used in the methods described herein may be prepared from a fixed, wax-embedded colon tissue specimen, by using one or more of the following steps, such as all of the following steps:

- (a) deparaffinizing using conventional methods and with multiple wash steps in organic solvent;
- (b) air drying and treating with protease to break inter- and intracellular bonds, resulting the release of RNA from the tissue;
- (c) removing contaminating genomic DNA;
- (d) washing in organic solvent; and eluting in a suitable RNase-free elution buffer.

The RNA-extraction methods may also include incubation of the tissue in a highly denaturing lysis buffer, which has the additional function of reversing much of the formalin crosslinking that occurs in tissues preserved this way to improve RNA yield and quality for performance in downstream assays.

Following RNA recovery, the RNA may optionally be further purified resulting in RNA that is substantially free from contaminating DNA or proteins. Further RNA purification may be accomplished by any of the aforementioned techniques for RNA recovery or with the use of commercially available RNA cleanup kits, such as RNeasy® MinElute® Cleanup Kit (QIAGEN®). The tissue specimen may, for example, be obtained from a tumor, and the RNA may be obtained from a microdissected portion of the tissue specimen enriched for tumor cells.

Methods of gene expression profiling include methods based on hybridization analysis of polynucleotides and methods based on sequencing of polynucleotides. In some examples, mRNA expression in a sample is quantified using Northern blotting or *in situ* hybridization (Parker & Barnes, *Methods in Molecular Biology* 106:247-283, 1999); RNase protection assays (Hod, *Biotechniques* 13:852-4, 1992); and PCR-based methods, such as reverse transcription polymerase chain reaction (RT-PCR) (Weis *et al.*, *Trends in Genetics* 8:263-4, 1992). Alternatively, antibodies can be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. Representative methods for sequencing-based gene expression analysis include Serial Analysis of Gene Expression (SAGE), and gene expression analysis by massively parallel

signature sequencing (MPSS). In one example, RT-PCR can be used to compare mRNA levels in different samples, to characterize patterns of gene expression, to discriminate between closely related mRNAs, and to analyze RNA structure. In specific examples, the disclosed colon cancer signatures are analyzed by nucleic acid  
5 microarray techniques, PCR techniques or combinations thereof.

### *1. Gene Expression Profiling With Microarray Methods*

In some embodiments, the expression profile of colon cancer-associated genes and/or transcripts, such as those shown in Table 6, can be measured in either fresh or  
10 paraffin-embedded tumor tissue, using microarray technology. In this method, polynucleotide sequences of interest, such as polynucleotide sequences that specifically hybridize to the nucleic acid sequences shown in Table 6 or a complement thereof, are plated, or arrayed, on a microchip substrate. The arrayed sequences are then hybridized with nucleic acids from cells or tissues of interest.

15 Just as in RT-PCR methods (see below), the source of mRNA typically is total RNA isolated from human tumors or tumor cell lines, and corresponding normal tissues or cell lines. Thus RNA can be isolated from a variety of primary tumors or tumor cell lines. If the source of mRNA is a primary tumor, mRNA can be extracted, for example, from frozen or archived paraffin-embedded and/or fixed (*e.g.* formalin-  
20 fixed) tissue samples, which are routinely prepared and preserved in everyday clinical practice.

In specific embodiments of the microarray technique, PCR amplified inserts of cDNA clones or oligonucleotides are applied to a substrate in a dense array. Short oligonucleotides may also be synthesized directly on a substrate using, for example, a  
25 combination of semiconductor-based photolithography and solid phase chemical synthesis technologies. (Affymetrix, Inc., Santa Clara, CA). In one embodiment, at least 10,000 nucleotide sequences are present on the substrate. The microarrayed transcripts, immobilized on the substrate are suitable for hybridization under stringent conditions. Fluorescently labeled nucleotide probes may be generated through  
30 incorporation of fluorescent nucleotides by reverse transcription of RNA extracted from tissues of interest. Labeled probes applied to the array hybridize with specificity to each nucleotide on the array. After washing to remove non-specifically bound probes, the array is scanned 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 transcript abundance.

With dual color fluorescence, separately labeled nucleotide probes generated from two sources may be hybridized pairwise to the array. The miniaturized scale of the hybridization affords a convenient and rapid evaluation of the expression pattern for large numbers of genes. Such methods have been shown to have the sensitivity required to detect rare transcripts, which are expressed at a few copies per cell, and to reproducibly detect at least approximately two-fold differences in the expression levels (Schena *et al.*, *Proc. Natl. Acad. Sci. USA* 93(2):106 149 (1996)). Microarray analysis can also be performed by commercially available equipment, following manufacturer's protocols, such as by using the Affymetrix GeneChip® technology (Affymetrix, Inc., Santa Clara, CA), or Agilent microarray technology (Agilent Technologies, Inc., Santa Clara, CA).

The development of microarray methods for large-scale analysis of gene expression makes it possible to search systematically for molecular markers of cancer classification and outcome prediction in a variety of tumor types, such as colon cancer tumors.

In particular embodiments provided herein, arrays can be used to evaluate a colon cancer gene expression profile, for example to prognose or diagnose a patient with colon cancer. When describing an array that consists essentially of probes or primers specific for the genes listed in Table 1, Table 2, and/or the transcripts listed in Table 6, such an array includes probes or primers specific for these colon cancer associated genes, and can further include control probes (for example to confirm the incubation conditions are sufficient). Exemplary control probes include GAPDH,  $\beta$ -actin, and 18S RNA.

#### *i. Array substrates*

The solid support of the array can be formed from inorganic material (such as glass) or an organic polymer. Suitable materials for the solid support include, but are not limited to: polypropylene, polyethylene, polybutylene, polyisobutylene, polybutadiene, polyisoprene, polyvinylpyrrolidone, polytetrafluoroethylene, polyvinylidene difluoride, polyfluoroethylene-propylene, polyethylenevinyl alcohol, polymethylpentene, polychlorotrifluoroethylene, polysulfones, hydroxylated biaxially oriented polypropylene, aminated biaxially oriented polypropylene, thiolated

biaxially oriented polypropylene, ethyleneacrylic acid, thylene methacrylic acid, and blends of copolymers thereof (see U.S. Patent No. 5,985,567).

In general, suitable characteristics of the material that can be used to form the solid support surface include: being amenable to surface activation such that upon  
5 activation, the surface of the support is capable of covalently attaching a biomolecule such as an oligonucleotide thereto; amenability to “*in situ*” synthesis of biomolecules; being chemically inert such that at the areas on the support not occupied by the oligonucleotides are not amenable to non-specific binding, or when non-specific binding occurs, such materials can be readily removed from the surface without  
10 removing the oligonucleotides.

In another example, a surface activated organic polymer is used as the solid support surface. One example of a surface activated organic polymer is a polypropylene material aminated via radio frequency plasma discharge. Other reactive groups can also be used, such as carboxylated, hydroxylated, thiolated, or  
15 active ester groups.

#### *ii. Array formats*

A wide variety of array formats can be employed in accordance with the present disclosure. One example includes a linear array of oligonucleotide bands,  
20 generally referred to in the art as a dipstick. Another suitable format includes a two-dimensional pattern of discrete cells (such as 4096 squares in a 64 by 64 array). As is appreciated by those skilled in the art, other array formats including, but not limited to slot (rectangular) and circular arrays are equally suitable for use (see U.S. Patent No. 5,981,185). In some examples, the array is a multi-well plate. In one example, the  
25 array is formed on a polymer medium, which is a thread, membrane or film. An example of an organic polymer medium is a polypropylene sheet having a thickness on the order of about 1 mil (0.001 inch) to about 20 mil, although the thickness of the film is not critical and can be varied over a fairly broad range. The array can include biaxially oriented polypropylene (BOPP) films, which in addition to their durability,  
30 exhibit low background fluorescence.

The array formats of the present disclosure can be included in a variety of different types of formats. A “format” includes any format to which the solid support can be affixed, such as microtiter plates (*e.g.*, multi-well plates), test tubes, inorganic sheets, dipsticks, and the like. For example, when the solid support is a polypropylene

thread, one or more polypropylene threads can be affixed to a plastic dipstick-type device; polypropylene membranes can be affixed to glass slides. The particular format is, in and of itself, unimportant. All that is necessary is that the solid support can be affixed thereto without affecting the functional behavior of the solid support or any  
5 biopolymer absorbed thereon, and that the format (such as the dipstick or slide) is stable to any materials into which the device is introduced (such as clinical samples and hybridization solutions).

The arrays of the present disclosure can be prepared by a variety of approaches. In one example, oligonucleotide or protein sequences are synthesized  
10 separately and then attached to a solid support (see U.S. Patent No. 6,013,789). In another example, sequences are synthesized directly onto the support to provide the desired array (see U.S. Patent No. 5,554,501). Suitable methods for covalently coupling oligonucleotides and proteins to a solid support and for directly synthesizing the oligonucleotides or proteins onto the support are known to those working in the  
15 field; a summary of suitable methods can be found in Matson *et al.*, *Anal. Biochem.* 217:306-10, 1994. In one example, the oligonucleotides are synthesized onto the support using conventional chemical techniques for preparing oligonucleotides on solid supports (such as PCT applications WO 85/01051 and WO 89/10977, or U.S. Patent No. 5,554,501).

20 A suitable array can be produced using automated means to synthesize oligonucleotides in the cells of the array by laying down the precursors for the four bases in a predetermined pattern. Briefly, a multiple-channel automated chemical delivery system is employed to create oligonucleotide probe populations in parallel rows (corresponding in number to the number of channels in the delivery system)  
25 across the substrate. Following completion of oligonucleotide synthesis in a first direction, the substrate can then be rotated by 90° to permit synthesis to proceed within a second set of rows that are now perpendicular to the first set. This process creates a multiple-channel array whose intersection generates a plurality of discrete cells.

30 The oligonucleotides can be bound to the polypropylene support by either the 3' end of the oligonucleotide or by the 5' end of the oligonucleotide. In one example, the oligonucleotides are bound to the solid support by the 3' end. However, one of skill in the art can determine whether the use of the 3' end or the 5' end of the oligonucleotide is suitable for bonding to the solid support. In general, the internal

complementarity of an oligonucleotide probe in the region of the 3' end and the 5' end determines binding to the support.

In particular examples, the oligonucleotide probes on the array include one or more labels that permit detection of oligonucleotide probe:target sequence  
5 hybridization complexes.

## 2. *Gene Expression Profiling With Microarray Methods*

One of the most sensitive and most flexible quantitative methods is RT-PCR, which can be used to compare mRNA levels in different sample populations, in  
10 normal and tumor tissues, with or without drug treatment, to characterize patterns of gene expression, to discriminate between closely related mRNAs, and to analyze RNA structure.

The first step is the isolation of RNA from a target sample such as human tumors or tumor cell lines, and corresponding normal tissues or cell lines,  
15 respectively. If the source of RNA is a primary tumor, RNA can be extracted, for example, from frozen or archived paraffin-embedded and/or fixed (*e.g.* formalin-fixed) tissue samples.

A variation of RT-PCR is real time quantitative RT-PCR, which measures PCR product accumulation through a dual-labeled fluorogenic probe (*e.g.*, TaqMan®  
20 probe). Real time PCR is compatible both with quantitative competitive PCR, where internal competitor for each target sequence is used for normalization, and with quantitative comparative PCR using a normalization gene contained within the sample, or a housekeeping gene for RT-PCR (see Heid *et al.*, *Genome Research* 6:986-994, 1996). Quantitative PCR is also described in U.S. Pat. No. 5,538,848.  
25 Related probes and quantitative amplification procedures are described in U.S. Pat. No. 5,716,784 and U.S. Pat. No. 5,723,591. Instruments for carrying out quantitative PCR in microtiter plates are available from PE Applied Biosystems (Foster City, CA).

In other examples, mRNA levels are measured using TaqMan® RT-PCR technology. TaqMan® RT-PCR can be performed using commercially available  
30 equipment. The system can include a thermocycler, laser, charge-coupled device (CCD) camera, and computer. In some examples, the system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and

detected at the CCD. The system includes software for running the instrument and for analyzing the data.

To minimize errors and the effect of sample-to-sample variation, RT-PCR can be performed using an internal standard. The ideal internal standard is expressed at a  
5 constant level among different tissues, and is unaffected by an experimental treatment. RNAs commonly used to normalize patterns of gene expression are mRNAs for the housekeeping genes GAPDH,  $\beta$ -actin, and 18S ribosomal RNA.

The steps of a representative protocol for quantitating gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA isolation,  
10 purification, primer extension and amplification are given in various published journal articles (see Godfrey *et al.*, *J. Mol. Diag.* 2:84 91, 2000; Specht *et al.*, *Am. J. Pathol.* 158:419-29, 2001). Briefly, a representative process starts with cutting about 10  $\mu$ m thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA are removed. Alternatively, RNA is isolated directly from a  
15 tumor sample or other tissue sample. After analysis of the RNA concentration, RNA repair and/or amplification steps can be included, if necessary, and RNA is reverse transcribed using gene specific promoters followed by RT-PCR and/or hybridization to a nucleic acid array.

In alternate embodiments, commonly used methods known in the art for the  
20 quantification of mRNA expression in a sample may be used with the colon signatures provided herein. Such methods include, but are not limited to, northern blotting and *in situ* hybridization (Parker & Barnes, *Methods in Molecular Biology* 106:247 283 (1999)); RNase protection assays (Hod, *Biotechniques* 13:852 854 (1992)). Alternatively, antibodies may be employed that can recognize specific  
25 duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes.

Further PCR-based techniques include, for example, differential display (Liang and Pardee, *Science* 257:967 971 (1992)); amplified fragment length polymorphism (iAFLP) (Kawamoto *et al.*, *Genome Res.* 12:1305 1312 (1999));  
30 BeadArray™ technology (Illumina, San Diego, Calif.; Oliphant *et al.*, *Discovery of Markers for Disease* (Supplement to *Biotechniques*), June 2002; Ferguson *et al.*, *Analytical Chemistry* 72:5618 (2000)); BeadsArray for Detection of Gene Expression (BADGE), using the commercially available Luminex100 LabMAP system and multiple color-coded microspheres (Luminex Corp., Austin, Tex.) in a rapid assay for

gene expression (Yang *et al.*, Genome Res. 11:1888 1898 (2001)); Competitive PCR and MassARRAY (Oeth *et al.*, 2004, SEQUONOME Application Note); and high coverage expression profiling (HiCEP) analysis (Fukumura *et al.*, Nucl. Acids. Res. 31(16) e94 (2003)).

5           The primers used for the amplification are selected so as to amplify a unique segment of the gene of interest (such as the genes listed in Table 1, Table and Table 6. Primers that can be used to these are commercially available or can be designed and synthesized according to well known methods using the sequences of these genes as available for example in GENBANK®.

10           An alternative quantitative nucleic acid amplification procedure is described in U.S. Pat. No. 5,219,727. In this procedure, the amount of a target sequence in a sample is determined by simultaneously amplifying the target sequence and an internal standard nucleic acid segment. The amount of amplified DNA from each segment is determined and compared to a standard curve to determine the amount of  
15           the target nucleic acid segment that was present in the sample prior to amplification.

          In some examples, gene expression is identified or confirmed using the microarray technique. Thus, the expression profile can be measured in either fresh or paraffin-embedded tumor tissue, using microarray technology. In this method, colon cancer signature nucleic acid sequences of interest (including cDNAs and  
20           oligonucleotides) are plated, or arrayed, on a microchip substrate. The arrayed sequences are then hybridized with isolated nucleic acids (such as cDNA or mRNA) from cells or tissues of interest. Just as in the RT-PCR method, the source of mRNA typically is total RNA isolated from human tumors, and optionally from corresponding noncancerous tissue and normal tissues or cell lines.

25           In a specific embodiment of the microarray technique, PCR amplified inserts of cDNA clones are applied to a substrate in a dense array. In some examples, the array includes probes specific to at least two of the colon cancer signature genes in Tables 1, 2, and 6. The microarrayed nucleic acids are suitable for hybridization under stringent conditions. Fluorescently labeled cDNA probes may be generated through  
30           incorporation of fluorescent nucleotides by reverse transcription of RNA extracted from tissues of interest. Labeled cDNA probes applied to the chip hybridize with specificity to each spot of DNA on the array. After stringent washing to remove non-specifically bound probes, the chip is scanned 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 mRNA abundance. With dual color fluorescence, separately labeled cDNA probes generated from two sources of RNA are hybridized pairwise to the array. The relative abundance of the transcripts from the two sources corresponding to each specified gene is thus  
5 determined simultaneously. The miniaturized scale of the hybridization affords a convenient and rapid evaluation of the expression pattern for colon cancer signature genes in Tables 1, 2, and 6. Microarray analysis can be performed by commercially available equipment, following manufacturer's protocols, such as are supplied with Affymetrix GeneChip® technology (Affymetrix, Santa Clara, CA), or Agilent's  
10 microarray technology (Agilent Technologies, Santa Clara, CA).

### 3. *Additional Methods of Gene Expression Analysis*

Serial analysis of gene expression (SAGE) is another method that allows the simultaneous and quantitative analysis of a large number of gene transcripts, without  
15 the need of providing an individual hybridization probe for each transcript. First, a short sequence tag (about 10-14 base pairs) is generated that contains sufficient information to uniquely identify a transcript, provided that the tag is obtained from a unique position within each transcript. Then, many transcripts are linked together to form long serial molecules that can be sequenced, revealing the identity of the  
20 multiple tags simultaneously. The expression pattern of any population of transcripts can be quantitatively evaluated by determining the abundance of individual tags, and identifying the gene corresponding to each tag (see, for example, Velculescu *et al.*, *Science* 270:484-7, 1995; and Velculescu *et al.*, *Cell* 88:243-51, 1997).

*In situ* hybridization (ISH) is another method for detecting and comparing  
25 expression of genes of interest. ISH applies and extrapolates the technology of nucleic acid hybridization to the single cell level, and, in combination with the art of cytochemistry, immunocytochemistry and immunohistochemistry, permits the maintenance of morphology and the identification of cellular markers to be maintained and identified, and allows the localization of sequences to specific cells  
30 within populations, such as tissues and blood samples. ISH is a type of hybridization that uses a complementary nucleic acid to localize one or more specific nucleic acid sequences in a portion or section of tissue (*in situ*), or, if the tissue is small enough, in the entire tissue (whole mount ISH). RNA ISH can be used to assay expression patterns in a tissue, such as the expression of cancer survival factor-associated genes.

Sample cells or tissues are treated to increase their permeability to allow a probe, such as a cancer survival factor-associated gene-specific probe, to enter the cells. The probe is added to the treated cells, allowed to hybridize at pertinent temperature, and excess probe is washed away. A complementary probe is labeled so that the probe's location and quantity in the tissue can be determined, for example, using autoradiography, fluorescence microscopy or immunoassay. The sample may be any sample as herein described, such as a non-tumor sample or a breast or lung tumor sample. Since the sequences of the cancer survival factor-associated genes of interest are known, probes can be designed accordingly such that the probes specifically bind the gene of interest.

*In situ* PCR is the PCR-based amplification of the target nucleic acid sequences prior to ISH. For detection of RNA, an intracellular reverse transcription step is introduced to generate complementary DNA from RNA templates prior to *in situ* PCR. This enables detection of low copy RNA sequences.

Prior to *in situ* PCR, cells or tissue samples are fixed and permeabilized to preserve morphology and permit access of the PCR reagents to the intracellular sequences to be amplified. PCR amplification of target sequences is next performed either in intact cells held in suspension or directly in cytocentrifuge preparations or tissue sections on glass slides. In the former approach, fixed cells suspended in the PCR reaction mixture are thermally cycled using conventional thermal cyclers. After PCR, the cells are cytocentrifuged onto glass slides with visualization of intracellular PCR products by ISH or immunohistochemistry. *In situ* PCR on glass slides is performed by overlaying the samples with the PCR mixture under a coverslip, which is then sealed to prevent evaporation of the reaction mixture. Thermal cycling is achieved by placing the glass slides either directly on top of the heating block of a conventional or specially designed thermal cycler or by using thermal cycling ovens.

Detection of intracellular PCR products is generally achieved by one of two different techniques, indirect *in situ* PCR by ISH with PCR-product specific probes, or direct *in situ* PCR without ISH through direct detection of labeled nucleotides (such as digoxigenin-11-dUTP, fluorescein-dUTP, <sup>3</sup>H-CTP or biotin-16-dUTP), which have been incorporated into the PCR products during thermal cycling.

In some embodiments of the detection methods, the expression of one or more "housekeeping" genes or "internal controls" can also be evaluated. These terms include any constitutively or globally expressed gene (or protein, as discussed below)

whose presence enables an assessment of cancer survival factor-associated gene (or protein) levels. Such an assessment includes a determination of the overall constitutive level of gene transcription and a control for variations in RNA (or protein) recovery.

5

The disclosure is further illustrated by the following non-limiting Examples.

## EXAMPLES

### Example 1

10 This example describes the generation and validation of an exemplary predictive tool for the categorization of colon cancer samples using the methods and reagents disclosed herein. This example includes materials published by inventors of the subject technology in Kennedy *et al*, *J. Clin. Oncol.*, 29(35) 4620-4626, 2011, which is specifically incorporated herein by reference in its entirety.

15 A colorectal cancer transcriptome focused research array was developed (*Colorectal Cancer DSA*<sup>TM</sup> (Almac Diagnostics, N. Ireland; which can be found on the world wide web at [almac-diagnostics.com](http://almac-diagnostics.com))) capable of delivering accurate expression data from FFPE derived RNA (Johnston *et al.*, *J Clin. Oncol.* 24: 3519, 2006).

20 The *Colorectal Cancer DSA*<sup>TM</sup> research tool contains 61,528 probe sets and encodes 52,306 transcripts confirmed as being expressed in colon cancer and normal tissue. Comparing the *Colorectal Cancer DSA*<sup>TM</sup> research tool against the National Center for Biotechnology Information (NCBI) human Reference Sequence (RefSeq) RNA database (which can be found on the world wide web at  
25 [ncbi.nlm.nih.gov/RefSeq/](http://ncbi.nlm.nih.gov/RefSeq/)) using BLAST analysis, 21,968 (42%) transcripts are present and 26,676 (51%) of transcripts are absent from the human RefSeq database. Furthermore 7% of the content represents expressed antisense transcripts to annotated genes. (Johnston *et al.*, *J Clin. Oncol.* 24: 3519, 2006; Pruitt *et al.*, *Nucleic Acids Research* 33: D501-D504, 2005). In addition, probe-level analysis of the *Colorectal Cancer DSA*<sup>TM</sup> compared with leading generic arrays, highlighted that approximately  
30 20,000 (40%) transcripts are not contained on the leading generic microarray platform (Affymetrix) and are unique to the *Colorectal Cancer DSA*<sup>TM</sup>. Thus, the *Colorectal Cancer DSA*<sup>TM</sup> research tool includes transcripts that have not been available in hitherto performed gene expression studies. Finally, because the transcript

information used to design the *Colorectal Cancer DSA*<sup>TM</sup> was generated in part by a high throughput sequencing approach, it has been possible to generate probes closer to the 3' end of the transcripts than are contained on other generic microarrays. The combination of relevant disease specific content and 3' based probe design has yielded a unique product capable of robust profiling from FFPE derived RNA.

The aim of this study was to assess the use of the *Colorectal Cancer DSA*<sup>TM</sup> research array, using FFPE derived tumor material to generate and independently validate a prognostic gene signature capable of accurately classifying stage II colon cancer patients as being at low or high risk of relapse, post surgery. Stage II colon cancer as used in this example is AJCC T3 or T4 node negative (NO) non metastatic (MO) colon cancer.

## METHODS

### *Sample Selection.*

Samples were collected retrospectively with the following eligibility criteria: stage II colon adenocarcinoma only, with no evidence of residual disease; patient age 45 years or older at time of primary surgery; six or more regional lymph nodes assessed; a minimum of 50% tumor cells present in the tissue section; no family history of colon cancer; no preoperative or postoperative cancer therapy within 1 year of surgery (although therapy given after recurrence was acceptable); and minimum patient follow-up of 5 years for low-risk patients. Low-risk patients were defined as those with no cancer recurrence within 5 years of primary surgery. High-risk patients were defined as those with metastatic cancer recurrence within 5 years of primary surgery. Patients with local disease recurrence were excluded because this recurrence may have been a result of local residual disease after surgery rather than metastatic tumor. Samples were collected from 12 centers. All samples underwent independent histopathologic review by a pathologist. The data set was compared with the Surveillance, Epidemiology, and End Results database to ensure it represented a general population with stage II colon cancer. Key patient and tumor characteristics are given in Table 3 (see FIG. 6).

### *Gene Expression Profiling From FFPE Tissue.*

Total RNA was extracted from FFPE tumor samples using the Roche High Pure RNA Paraffin Kit (Roche, Basel, Switzerland). Amplified cDNA targets were prepared using the Nugen WT-Ovation® FFPE System v2 in combination with the Nugen FL-Ovation® cDNA Biotin Module v2 and were performed in accordance

with manufacturer's instructions. Hybridization, washing, staining and scanning of fragmented, labelled cDNA was carried out according to standard Affymetrix protocols. Between 3.0 and 3.5µg fragmented, labelled cDNA was hybridized to the *Colorectal Cancer DSA*<sup>TM</sup> microarray (Almac, Craigavon, United Kingdom) on the  
5 Affymetrix 7G scanner (Affymetrix, Santa Clara, CA). A sample profile scheduling strategy was used that involved the stratification of samples into batches that were randomized against targeted clinical and sample property factors in addition to operators, reagent, and material lots. Quality control criteria were applied, and biologic and technical factors were balanced between low- and high-risk samples.  
10 This is performed in order to minimise systematic bias and diffuse any residual technical bias into technical variation.

***Classifier Model Identification.***

Model development started with 5,014 probe sets identified as stable and/or having comparable longitudinal stability under FFPE fixation to avoid the issue of  
15 differential degradation of probe sets. Signature generation was subsequently performed using the partial least squares classification method with selection of important features based on recursive feature elimination (RFE) during 10 repeats of five-fold cross validation. All aspects of the model development were appropriately nested within the cross validation, including an initial filtering to remove 50% of the  
20 probe sets with the lowest variance and intensity, reference-based robust multichip averaging (RefRMA) normalization and summarization, and RFE discarding the least important 10% of probe sets at each iteration. The total number of features to include in the final model was determined by the feature length with the highest average area under the receiver operating characteristics curve (AUC) under cross validation. The  
25 threshold for dichotomization of the predictions from each model was selected based on the maximum of the sum of sensitivity and specificity (minimum of the Youden J statistic (Youden, *Cancer* 3:32-35, 1950) from cross-validated training data. In the case of multiple thresholds with largely identical performance, the hazard ratio (HR) from Cox proportional hazards regression was used as a tiebreaker to favor higher HR  
30 values.

The precision of the predictions was evaluated by predicting technical replicates of a colorectal cancer cell line (HCT116) embedded in FFPE, which was profiled concurrently with the clinical samples. The repeated technical measurements of this sample were not included in model development but were predicted by all 50

cross-validation training subsets as an independent test set with a view to select models with high repeatability and reproducibility. Additionally, a permutation test was performed where the true class labels were reshuffled randomly 100 times followed by complete model development. This was done to assess what  
5 classification performance one can expect by chance from a data set with these characteristics and to reveal any bias in the signature generation procedure.

The independence of the final model in the context of known clinical factors was evaluated using univariate and multivariate Cox proportional hazards regression. The input used was the predicted dichotomized class labels together with tumor stage,  
10 patient tumor grade, tumor location, patient age, patient sex, mucinous/nonmucinous subtype, and number of lymph nodes retrieved. Microsatellite instability was not included as a factor because this information was not available for the majority of the samples. Gene Ontology annotation and enrichment of Gene Ontology biologic processes and molecular functions were performed using an internally developed tool  
15 based on the genes in the final signature. The hypergeometric distribution with false discovery rate multiple testing correction was used to determine functional classes of genes significantly enriched. The pathway analysis was generated through the use of Ingenuity Pathway Analysis (Ingenuity Systems, Redwood City, CA).

***Balancing, randomisation and Quality Control (QC) of samples.***

20 *Target population:* The population used to train the assay was matched to reflect the general population properties from the SEER and CRUK databases. The following properties were being considered:

- **Gender.** The gender prevalence amongst in the Stage II population is approximately between 50-60% male (56% in the UK and 57% in the US).
- 25 • **Tumour location** (distal/proximal). The prevalence in the Stage II population is approximately 55%-65% proximal and 35%-45% distal.
- **Patient age.** According to NCI's SEER Cancer Statistics Review Colon and Rectum Section, from 2001-2005, 0.1% of patients were diagnosed under age 20; 1.0% between 20 and 34; 3.7% between 35 and 44; 11.6% between 45 and  
30 54; 18.3% between 55 and 64; 25.1% between 65 and 74; 28.2% between 75 and 84 and 12.2% 85+ years of age.
- **Recurrence-free survival rate.** The rate of recurrence-free survival in the Stage II population is reported to be between 13%-22% (Gattaj *et al*, European Journal of Cancer, 2006) and ~30% from the SEER database.

*Pre-balancing:* Pre-balancing was performed so that the sample set put forward for hybridization was balanced with respect to selected clinical covariates whilst maintaining the general population statistics presented above. This excludes recurrence-free survival, which was intentionally enriched to increase the power of the biomarker discovery. The training set did not contain any samples with events after 5 years, whereas this was not a constraint in the validation set. The rationale for not using samples that recur after 5 years for signature generation (i.e. in the training set) is to avoid introducing additional heterogeneity in the sample population when performing the biomarker discovery.

The main aim of the balancing procedure was to reduce the association (if any) between the endpoint (high/low risk represented as a binary variable) and any of the factors listed below. Any association between these factors and the high/low risk endpoint would introduce a confounding that could limit the clinical utility of the assay. 603 colorectal samples were subjected to the pre-balancing in order to reduce strong associations between prognosis and any of the following factors: Gender; Tumor location within the bowel; Patient age; Contributing Centre; FFPE block age (date of surgery); Tumor content; and RNA quality.

Continuous parameters were tested using a Kolmogorov-Smirnoff test and categorical parameters were tested using a chi-squared test. A  $p$ -value  $\geq 0.4$  for all parameters was required to achieve balancing. 504 samples remained after balancing (335 low risk and 169 high risk) and were put forward to array profiling.

*Randomization of samples during array profiling:* Randomization of samples was performed to avoid confounding between known technical and biological factors, primarily the endpoint of interest (prognosis). In this study operator, hybridization-wash-stain (HWS) kit lot, array lot and array batch were considered together with the contributing center and the prognosis. Samples were first randomized into array batches such that each array batch had the same proportion of prognosis and contributing center. Operators were then assigned to each array batch according to availability. Each array batch was then assigned a HWS kit, ensuring that each operator used the same proportion of each kit. Array lots were allocated to each array batch, ensuring that they were evenly distributed amongst the array batches.

*Quality control of the training data:* QC procedures were applied on the resulting arrays, primarily based on values in the Affymetrix RPT files that contain various quality-related parameters. Limits were calculated based on visual inspection

of the distribution for each parameter for all samples: % present calls ( $\geq 20\%$  required); Image artefacts were identified to remove arrays with noticeable blotches ; Outliers were detected from principal component analysis (PCA) based on the Q residuals and Hotelling's  $T^2$ .

5           Assessment of gender genes was used to determine if observed expression levels matched the known gender in clinical information

The following Affymetrix quality parameters were also considered during the visual inspection of the distributions; broadly categorised as follows: RNA Quality; Signal Quality & Detection call; Background & Noise; and Background Homogeneity

10           A total of 319 colorectal samples passed the QC procedure. Due to preliminary results suggesting a heterogeneity introduced by the rectal samples, the rectal samples were removed to form a 249 colon-only set, which was put forward for final (post-QC) balancing.

15           *Final post-QC balancing:* The 249 colon samples passing QC were balanced using the same principles as the initial pre-balancing, with the addition of criteria for the % present call distribution to be similar in both low risk and high risk groups (this information is only available after hybridisation). A final set of 215 samples remained after QC and balancing.

20           The final colon set with 215 samples has the following properties compared to the known population distribution: Gender: 53% male (50-60% in population); Tumor location (distal/proximal): 62% proximal (55-65% proximal in population); Patient age: Closely follows the continuous distribution of the population; and Recurrence-free survival rate: 34% poor prognosis (high risk). Intentionally enriched compared to population around 15-20%.

25           *Quality control of the validation set and future sample sets:* Using a tailor-made QC procedure on the training set is an important step in order to facilitate the identification of biomarkers from a high-quality data set. However for prediction of future samples, QC has to be applied on a one-sample-at-a-time basis. Also, the QC procedure cannot be too specific to the data set and the system where the data has  
30           been generated. For this purpose a separate evaluation was performed using 40 samples replicated across two systems and scanners to identify QC parameters that are stable across systems. The AvgSigA parameter (average signal of the absent probe sets) was determined to be the most stable parameter across the different systems and hence the best candidate for a system-independent QC procedure. For this parameter,

higher values imply lower quality and lower values imply higher quality. The AvgSigA values are strongly negatively correlated to the % present call parameter which is a commonly used QC parameter and was the primary QC parameter used on the training set. The lower acceptance value of % present calls from the training set was set to 20%, which corresponds approximately to an upper acceptance value of 43 for the AvgSigA parameter for this data set. To accommodate younger FFPE samples, it was decided not to introduce a lower threshold on the AvgSigA (which will allow inclusion of higher-quality samples). The final inclusion range derived from this study was hence  $\text{AvgSigA} \leq 43$ , which was the QC metric applied to the independent validation set and is the QC that will be applied to future samples.

*Identifying probe sets that are stable over FFPE block age:* It was recognized that mRNA transcripts are likely to degrade at different rates and to different levels in FFPE samples, which could result in a signature generated from old material not performing as expected on fresh FFPE material. Therefore two independent longitudinal studies were performed to identify probe sets that are stable over FFPE block age. In the first study, 9 FFPE blocks were serially sectioned and analyzed by DNA microarray at seven time points in a 16-week timeframe following fixation. These samples were supplemented by a second longitudinal study at three 6 month intervals in a one year timeframe in which 8 FFPE blocks ranging from 6 months to 4 years of age which were serially sectioned and analyzed by DNA microarray resulting in 113 individual samples for analysis. 5014 transcripts were identified that either did not undergo further degradation with time or decayed at an equivalent rate following fixation. This list of probe sets was subsequently used for signature generation. A separate manuscript for presenting the details from this study is in preparation.

*Estimating the precision of the classifier during model development:* The ability of a classifier to consistently produce the same output from technical replicates is an important aspect of an assay when used in a test setting. For this purpose, a set of 39 reference samples, which are technical replicates of the same colorectal cancer cell line (HCT114), were hybridized together with the clinical samples. During model development, this set was predicted as an external test set during cross-validation in order to estimate the relative variance at each step in the model development process. No information was shared between the training set and the 39 sample reference set during cross-validation. The standard deviation from the predicted signature scores were calculated and visualized as the average with 95% confidence limits. The

variability is low for longer signatures, which then gradually increases over the feature selection procedure, which is also reflected in lower accuracy (AUC) for the shorter signatures. At the selected signature length (634 probe sets), the model shows both high precision and accuracy.

5        *Permutation analysis of the classification performance:* Permutation analysis was performed to evaluate what classification performance one can expect by chance from a data set with similar properties. This was performed by randomly reshuffling the true class labels (i.e. the true prognosis) and subsequently repeating the entire model development process (with filtering, normalization, feature selection and  
10        classification). The signature performance is significantly better than chance at longer signature lengths and specifically at the selected one where the number of probe sets is 634. Additionally, the permutation test reveals any underlying bias in the data set and/or the methodology used to develop the classifier. The median AUC over the random labels is 0.5, denoting chance, which confirms that there is no evident bias in  
15        the procedure used.

## RESULTS

### *Development of a Stage II Colon Cancer Prognostic Signature From FFPE*

*Tissues.* Disease-free survival at 5 years was used as the primary end point for this study. After balancing for clinical factors and applying quality control criteria to the  
20        initial data set, a training set of 215 patients (142 low-risk and 73 high-risk patients) was identified. Fifty percent variance-intensity filtering, RefRMA normalization, RFE feature selection, and partial least squares classification were performed under 10 repeats of five-fold cross validation for estimation of the classification performance. Cross validation indicated a 634-transcript signature to be optimal for prognostic  
25        classification. A receiver operating characteristic curve with an AUC of 0.68 ( $P < .001$ ) was generated, indicating a significant association between signature score and prognosis (FIG. 3A). The observed AUC was significantly higher than random in the permutation analysis and displayed a low variance in the evaluation of the precision from technical replicates. A threshold of 0.465 for dichotomization of the signature  
30        prediction scores was established from the Youden J statistics, yielding an HR of 2.62 ( $P < .001$ ; FIG. 3B). Table 4 contains a summary of the classification performance over the signature generation during cross validation.

**Table 4.** Classification Performance of the Training and Independent Validation Sets

| Data Set | AUC | Sensitivity | Specificity | NPV | PPV | HR |
|----------|-----|-------------|-------------|-----|-----|----|
|----------|-----|-------------|-------------|-----|-----|----|

|                   |                        |                        |                        |                        |                        |                        |
|-------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|
| Train(95<br>% CI) | 0.682(0.6<br>43-0.720) | 0.478(0.4<br>07-0.549) | 0.791(0.73<br>7-0.845) | 0.858(0.8<br>45-0.872) | 0.365(0.3<br>17-0.413) | 2.618(2.0<br>41-3.195) |
| Val.(95<br>% CI)  | 0.684(0.5<br>94-0.761) | 0.718(0.6<br>17-0.811) | 0.559(0.42<br>3-0.673) | 0.867(0.8<br>28-0.900) | 0.331(0.2<br>50-0.434) | 2.526(1.5<br>36-4.154) |

The 95% CIs are  $\pm 2$  standard deviations from cross validation (training set) or bootstrapping with 1,000 repeats (validation set); 80% and 20% priors have been used when calculating the NPVs and PPVs, respectively. The threshold  $t = 0.465$  was used for dichotomization of the signature score. Abbreviations: AUC, area under the receiver operating characteristics curve; HR, hazard ratio; NPV, negative predictive value (negative is low risk); PPV, positive predictive value (positive is high risk)

***Independent Validation of the Stage II Colon Cancer Prognostic Signature:***

The prognostic signature was applied to an independent validation set of 144 patients enriched for recurrence (85 low-risk and 59 high-risk patients) using the threshold score identified in the training set. The sample analysis was run separately and at a later time to the training set. The signature predicted disease recurrence with an HR of 2.53 ( $P < .001$ ) in the high-risk group (FIG. 4 and Table 4). The signature also predicted cancer-related death with an HR of 2.21 ( $P < .0084$ ) in the high-risk group (FIG. 5).

The fact that the signature described herein was developed from FFPE derived tumor material facilitates a large scale validation strategy based on retrospective analysis of existing FFPE tumor banks.

The hazard ratio is an expression of the hazard or chance of events occurring in the stage II colon cancer patients identified by the classifier as high risk as a ratio of the hazard of the events occurring in the patients identified by the classifier as low risk. There was a significantly lower probability of recurrence for the group predicted to have good prognosis compared to those predicted to have poor prognosis, within 5-years post surgery. The negative predictive value is the proportion of patients with negative test results who are correctly diagnosed (predicted negative). In a prognostic setting, the NPV is dependent on the prevalence of disease recurrence. The positive predictive value is the proportion of patients with positive test results who are correctly diagnosed (predictive positive). In a prognostic setting, the PPV is dependent on the prevalence of disease recurrence. Based on a population prevalence of 20% poor prognosis samples, this would imply that patients with a predicted poor

prognosis have a 33% probability of recurrence whereas patients with a predicted good prognosis have a 13% probability of recurrence within 5 years.

***Assessment of Signature Independence From Known Prognostic Factors:***

For a prognostic assay to be useful, it must perform independently from known prognostic factors used in the clinic. Therefore the independence of the assay was assessed in both a univariate and multivariate analysis (Table 5).

**Table 5.** Comparison of Transcript Signature to Standard Pathologic Parameters in the Independent Validation Set

|                                     |     | Univariate |             |         | Multivariate |             |         |
|-------------------------------------|-----|------------|-------------|---------|--------------|-------------|---------|
|                                     |     | HR         | CI          | p       | HR           | CI          | p       |
| Tumor Stage (T4 vs T3)              |     | 1.23       | 0.667-2.269 | 0.5067  | 1.617        | 0.84-3.110  | 0.1501  |
| Patient Age                         |     | 1.039      | 1.01-1.069  | 0.0086  | 1.046        | 1.014-1.078 | 0.0041  |
| Tumor Grade                         | II  | 0.815      | 0.456-1.456 | 0.4895  | 1.274        | 0.48-3.383  | 0.6265  |
|                                     | III | 1.326      | 0.654-2.689 | 0.434   | 2.161        | 0.636-7.339 | 0.2169  |
| Tumor Location (Proximal vs Distal) |     | 1.766      | 1.075-2.901 | 0.0248  | 2.158        | 1.224-3.804 | 0.0078  |
| Gender                              |     | 1.165      | 0.713-1.901 | 0.5426  | 0.971        | 0.549-1.720 | 0.9204  |
| Mucinous subtype                    |     | 0.825      | 0.418-1.627 | 0.5787  | 0.896        | 0.433-1.856 | 0.7682  |
| No. of Nodes Retrieved              |     | 1.007      | 0.983-1.032 | 0.5678  | 1.014        | 0.988-1.041 | 0.2824  |
| Prognostic Signature                |     | 2.526      | 1.536-4.154 | < 0.001 | 2.551        | 1.471-4.423 | < 0.001 |

Both the univariate and multivariate analyses have been performed using Cox

proportional hazards regression with *P* values coming from a log-likelihood test. For tumor grade, grade 1 has been used as the reference point for calculating the HR. Patient age and number of nodes retrieved are analyzed as continuous factors. The interpretation of the HR of patient age is the increased risk for a change in 1 year of age, and correspondingly, the interpretation of the HR of number of nodes retrieved is the increased risk for an increase of one retrieved node. Abbreviation: HR, hazard ratio.

The prediction of prognosis was significant in both the univariate ( $P < .001$ ) and multivariate ( $P < .001$ ) analysis, demonstrating that the signature provided prognostic information in addition to conventional risk factors. Furthermore, the independence of the signature was assessed with the addition of lymphovascular invasion in the samples where this had been recorded (100 of 144 samples in the validation set). The signature performed independently in the univariate ( $P < .001$ ) and multivariate analysis ( $P < .001$ ).

**Functional Analysis of the Genes in the Prognostic Signature:** Next it was asked if the assay detected biologic processes known to be relevant to colon cancer recurrence. The 634 probe sets were analyzed using Ingenuity Pathway Analysis, and a list of statistically significant pathways were identified, the most significant of which was *IGF-1* signaling.

## DISCUSSION

As disclosed herein a DNAmicroarray-based assay was developed that identifies patients at higher risk of recurrence after surgery for stage II colon cancer. Specifically, the signature identified a high-risk cohort with an HR of recurrence of 2.53 and an HR of cancer-related death of 2.21 in an independent validation set. Validation of a prognostic assay using a completely separate set is necessary to avoid overestimations of the performance of the signature from the training set. The HR of 2.53 for recurrence compares favorably with histologic factors currently used to make decisions in the clinic, which typically have anHR of approximately 1.5 or less. Moreover, the signature does not require individual interpretation and may offer a more standardized approach than conventional histopathologic factors. Importantly, the assay is performed on FFPE tissue and, therefore, is easily applied in current medical practice.

Although several DNAmicroarray-based prognostic tests in several cancer types have been published, only one has been introduced into clinical practice, and to date, none is used in colon cancer. This may be a result of two major factors. First, many of the signatures have been developed from fresh or frozen tissue. Second, inappropriate study methodology has resulted in a failure to validate the test in an independent data set.

Regarding the use of frozen tissue samples, although this tissue type provides excellent microarray data, a test generated from this tissue is unlikely to perform adequately in FFPE tissue. This can create difficulty in collecting enough samples to

develop and independently validate a prognostic test. In addition, implementation of fresh tissue– based assays requires a change in clinical practice, because samples need to be collected at the time of surgery.

FFPE is the standard for tumor archiving, and numerous tumor banks already exist for assay development. Importantly, no change in sample collection and processing is required for the development and clinical implementation of FFPE-based assays.

The disclosed methods were developed to work with FFPE tissue but using a DNA microarray platform, thereby vastly increasing the number of detectable mRNA transcripts and biologic processes relative to quantitative polymerase chain reaction technology. As a result of using FFPE material with a microarray platform, several methodologic issues needed to be considered. Formalin fixation results in the degradation of mRNA transcripts through the cross linking of RNA to protein. Most of this degradation occurs immediately, but some transcripts continue to degrade with time. The DNAmicroarray platform used for the study has probe sets designed to the 3' end of mRNA transcripts to enhance the ability to detect degraded transcripts. In addition, a separate set of colon cancer samples was analyzed over time to ensure we did not incorporate probe sets that detected unstable or differentially stable mRNA transcripts as part of the signature.

The predictive value of the signature is above and beyond known prognostic clinical covariates. This performance can largely be attributed to the initial balancing of prognosis against biologic and technical factors that was performed as part of establishing a suitable training set. Biologic factors considered include known prognostic factors such as pT stage and grade, as well as other nonprognostic factors that may have affected gene expression including tumor location, patient age, and sex. Technical factors such as FFPE block age and the contributing center were also balanced between high- and low-risk samples in the training set. In addition, randomization of operators and reagent kits was performed to avoid confounding between technical factors and known clinical factors. This minimized the risk that the assay was dependent on the operator or relied on the use of samples from specific centers or the use of specific batches of reagents. Because the assay was developed to be independent from known prognostic factors, we believe that it may be possible to develop a multiparametric test that incorporates several factors to give an even more accurate prognostic indicator.

Functional analysis of the gene signature revealed that *IGF-1* signaling, *TGF- $\beta$*  signaling, and *HMGB1* signaling were among the most significant pathways identified. All of these have been previously reported to confer a poor prognosis in colon cancer through promoting tumor growth, invasion, and metastasis and preventing apoptosis. In conclusion, disclosed herein is a validated and robust prognostic DNA microarray signature for stage II colon cancer from FFPE stored tumor tissue.

The disclosed signature can help physicians to make more informed clinical decisions regarding the risk of relapse and the potential to benefit from adjuvant chemotherapy. (Andre *et al.*, *Annals of Surgical Oncology* 13:887-898, 2006; Diaz-Rubio *et al.*, *Clin. Transl. Oncol.* 7: 3-11, 2005; Monga *et al.*, *Ann. Surg. Oncol.* 13: 1021-1134, 2006; Sobrero, *Lancet Oncol.* 7: 515-516, 2006). Furthermore, many patients want to know their likelihood of cure and the risks/benefits of treatment. (Gill *et al.*, *J. Clin. Oncol.* 22: 1797-1806, 2004; Kinney *et al.*, *Cancer* 91: 57-65, 2001; Carney *et al.*, *Ann. R. Coll. Surg. Engl.* 88: 447-449, 2006; Salkeld, *Health Expect* 7: 104-1014, 2004). Being able to predict the patient's prognosis provides the physician and the patient with a better assessment of the risks/benefits and the choice of therapy. The ability to offer individualized patient care will hopefully result in improved survival and quality of life for these patients.

In the past, many studies have implicated sample size as the primary reason for lack of convincing statistical evidence and point to larger trials being required to prove the benefit of adjuvant treatment. Using validated prognostic markers, such as the gene signature generated in this study, stage II patients can be stratified into high and low risk sub-populations. This approach may assist in improved clinical trial design by focusing on those patients at high risk of recurrence and therefore more likely to derive a benefit from adjuvant therapy. Thus, the *Colorectal Cancer DSA*<sup>TM</sup> may be a useful research tool for stratifying patients for inclusion in clinical trials, for decision-making regarding adjuvant and neo-adjuvant treatment, and for the identification of novel pathways or molecular targets for additional drug development

The prognostic signature reported in Table 6 accurately predicted for relapse for stage II colon cancer and is evaluated on an independent FFPE validation set. The overall accuracy for prediction of recurrence was substantial for this heterogeneous disease. Based on a population prevalence of 20% poor prognosis samples, this would imply that patients with a predicted poor prognosis have a 33% probability of

recurrence whereas patients with a predicted good prognosis have a 13% probability of recurrence within 5 years. One of the major advantages of the current approach is that it is based on expression profiling from FFPE tissue which is the preferred method of storage for the majority of available tissue banks. (Abramovitz *Proteome Sci.* 4:5, 2006). RNA extracted from FFPE tissue samples tends to have a shorter median length due to degradation and formalin-induced modification, which makes it difficult for generic arrays to detect. When defining the colon cancer transcriptome, a 3'-based sequencing approach was employed facilitating design of probesets to the 3' extremity of each transcript. This approach ensures much higher detection rate and is thus optimally designed to detect RNA transcripts from both fresh frozen and FFPE tissue samples. The results from the current study showed that the Almac Diagnostics *Colorectal Cancer DSA*<sup>TM</sup> research tool is capable of producing biologically meaningful and reproducible data from FFPE derived tissue.

### Example 2

#### Prognosis of Cancer

This example describes particular methods that can be used to prognose a subject diagnosed with colon cancer. However, one skilled in the art will appreciate that methods that deviate from these specific methods can also be used to successfully provide the prognosis of a subject with colon cancer.

A tumor sample and adjacent non-tumor sample is obtained from the subject. Approximately 1-100 µg of tissue is obtained for each sample type, for example using a fine needle aspirate. RNA and/or protein is isolated from the tumor and non-tumor tissues using routine methods (for example using a commercial kit).

In one example, the prognosis of a colon cancer tumor is determined by detecting expression levels of 2 or more of the transcript in Tables 1, 2, and/or 6 in a tumor sample obtained from a subject by microarray analysis or real-time quantitative PCR. For example, the disclosed gene signature can be utilized. The relative expression level of in the tumor sample is compared to the control (*e.g.*, RNA isolated from adjacent non-tumor tissue from the subject). In other cases, the control is a reference value, such as the relative amount of such molecules present in non-tumor samples obtained from a group of healthy subjects or cancer subjects.

In view of the many possible embodiments to which the principles of the disclosure may be applied, it should be recognized that the illustrated embodiments.

We claim:

1. A method for diagnosing colon cancer in a sample obtained from a subject, comprising:
  - 5 detecting an expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and
  - comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative
  - 10 of a diagnosis of colon cancer, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a diagnosis of colon cancer, thereby diagnosing colon cancer in the sample obtained from the subject.
2. The method of claim 1, wherein the control threshold comprises:
  - 15 a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a known colon cancer sample (or samples), wherein the expression level, or a decision score derived therefrom, on the same side of the threshold as a known colon cancer group indicates a diagnosis of colon cancer.
3. A method for classifying a colon cancer sample, comprising:
  - 20 detecting an expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and
  - comparing the expression level of the at least 2 colon cancer-related nucleic
  - 25 acid molecules, or a decision score derived therefrom to a control threshold indicative of known classification, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold permits classification of the colon cancer sample.
4. The method of claim 3, wherein the control threshold comprises:
  - 30 a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) of known classification, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold as a colon cancer sample (or samples) of

known classification permits classification of the colon cancer sample.

5. The method of any one of claims 3 or 4, wherein the colon cancer sample is classified as stage I, stage II, stage III and stage IV.

5

6. The method of any one of claims 3-5, further comprising choosing a treatment plan that will be effective for the classified colon cancer.

7. The method of claim 6, wherein the treatment is surgical resection, chemotherapy, radiation or any combination thereof.

10

8. A method for predicting a response to a treatment for colon cancer, comprising:

detecting an expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and

15

comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of a known response to treatment, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a similar response to treatment, thereby predicting response to treatment.

20

9. The method of claim 8, wherein the control threshold comprises:

a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) having a known response to treatment, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold as a colon cancer sample (or samples) having a known response to treatment indicates a similar response to treatment, thereby predicting response to treatment.

25

30

10. The method of any one of claims 8 or 9, wherein the treatment is surgical resection.

11. The method of any one of claims 8-10, wherein the treatment is

chemotherapy and/or radiation.

12. A method for predicting long term survival of a subject with colon cancer, comprising:

5 detecting an expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a subject; and

comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative  
10 of having a history of long term survival, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates long term survival of the subject, thereby predicting long term survival of a subject.

13. The method of claim 12, wherein the control threshold comprises:  
15 a threshold derived from corresponding transcripts from colon cancer-related nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) obtained from a subject (or subjects) having a history of long term survival, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold as a colon cancer sample (or samples) obtained from a subject (or subjects)  
20 having a history of long term survival indicates long term survival of the subject, thereby predicting long term survival of a subject.

14. The method of claim 13, wherein long term survival comprises at least  
25 5 year survival.

15. A method for predicting of recurrence of colon cancer in a subject, comprising:

detecting an expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 in a sample comprising nucleic acids obtained from a  
30 subject; and

comparing the expression level of the at least 2 colon cancer-related nucleic acid molecules, or a decision score derived therefrom to a control threshold indicative of a history of recurrence, wherein the expression level, or a decision score derived therefrom, on the same side of the threshold indicates a recurrence in the subject.

16. The method of claim 15, wherein the control threshold comprises:  
a threshold derived from corresponding transcripts from colon cancer-related  
nucleic acid molecules listed in Table 6 in a colon cancer sample (or samples) having  
5 a history of recurrence, wherein the expression level, or a decision score derived  
therefrom, on the same side of the threshold as a colon cancer sample (or samples) of  
known history of recurrence, indicates a recurrence in the subject.

17. A method of preparing a personalized colon cancer genomics profile  
10 for a subject, comprising:  
detecting an expression level of at least 2 colon cancer-related nucleic acid  
molecules listed in Table 6 in a sample comprising nucleic acids obtained from a  
subject; and  
creating a report summarizing the data obtained by the gene expression  
15 analysis.

18. The method of any one of claims 1-17, wherein the nucleic acids  
obtained from the subject comprise RNA and/or cDNA transcribed from RNA  
extracted from a sample of colorectal tissue obtained from the subject.

19. The method of claim 18, wherein the sample is a biopsy sample.

20. The method of any one of claims 18 or 19, wherein the sample is a  
fixed and/or paraffin embedded sample.

21. The method of any one of claims 1-20, wherein the expression level is  
normalized against a control gene or genes.

22. The method of any one of claims 1-21, wherein the level of expression  
30 is determined with PCR and/or or microarray-based methods.

23. The method of any one of claims 1-22, wherein detecting the  
expression level of at least 2 colon cancer-related nucleic acid molecules listed in  
Table 6 comprises detecting the expression levels for MUM1 and SIGMAR1

transcripts.

24. The method of any one of claims 1-23, wherein detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for MUM1, SIGMAR1, ARSD, SULT1C2 and PPFIBP1 transcripts.

25. The method of any one of claims 1-24, wherein detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for ARSD, CXCL9, PCLO, SLC2A3, FCGBP, SLC2A14, SLC2A3, BCL9L and antisense sequences of MUC3A, OLFM4 and RNF39 transcripts.

26. The method of any one of claims 1-25, wherein detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for the transcripts listed in Table 1.

27. The method of any one of claims 1-26, wherein detecting the expression level of at least 2 colon cancer-related nucleic acid molecules listed in Table 6 comprises detecting the expression levels for the transcripts listed in Table 2.

28. A nucleic acid probe for detecting a gene expression signature for colon cancer, comprising or consisting substantially of a nucleic acid molecule between 20 and 40 nucleotides in length, capable of specifically hybridizing to one of the nucleic acid sequences set forth as SEQ ID NOs: 1-636 or its complement.

29. The nucleic acid probe according to claim 28, wherein the probe is labeled.

30. The nucleic acid probe according to claim 29, wherein the probe is radiolabeled, fluorescently-labeled, biotin-labeled, enzymatically-labeled, or chemically-labeled.

31. A set of probes, for detecting a gene expression signature for colon

cancer, comprising 2 or more probes, wherein each probe comprises or consists substantially of a nucleic acid molecule between 20 and 40 nucleotides in length capable of specifically hybridizing to one of the nucleic acid sequences set forth as SEQ ID NOs: 1-636 or its complement.

5

32. The set of probes of claim 31, wherein the probes are labeled.

33. The set of probes of claim 32, wherein the probes are radiolabeled, fluorescently-labeled, biotin-labeled, enzymatically-labeled, or chemically-labeled.

10

34. The set of probes of any one of claims 31-33, wherein the set contains at least one probe complementary to each of the transcripts listed in Table 6.

35. The set of probes of claim 34, comprising at least one probe complementary to each transcript in a subset of the transcripts listed in Table 6, wherein the subset comprises at least 1%, 5%, 10%, 25%, 50%, 75% or 95% of the transcripts in Table 6.

36. A device for detecting a gene expression signature for colon cancer, comprising a nucleic acid array comprising the set of probes of any one of claims 31-35.

37. A pair of primers for the amplification of a gene expression signature for colon cancer nucleic acid, comprising:  
a forward primer 15 to 40 nucleotides in length comprising a nucleic acid sequence that specifically hybridizes to any one of the nucleic acid sequences set forth as SEQ ID NOs: 1-636 or its complement; and  
a reverse primer 15 to 40 nucleotides in length comprising a nucleic acid sequence that specifically hybridizes to any one of the nucleic acid sequences set forth as SEQ ID NOs: 1-636 or its complement, wherein the set of primers is capable of directing the amplification of the nucleic acid.

38. A set of primer pairs for the amplification of a gene expression signature for colon cancer nucleic acid, comprising at least 2 primer pairs suitable for

use in amplification of any one of the nucleic acid sequences set forth as SEQ ID NOs: 1-636.

39. The set of primer pairs of claim 38, wherein the set of primer pairs  
5 comprises primer pairs suitable for use in amplification of a subset of nucleic acid sequences set forth as SEQ ID NOs: 1-636 wherein the subset comprises at least 1%, 5%, 10%, 25%, 50%, 75% or 95% of the nucleic acid sequences set forth as SEQ ID NOs: 1-636.

10 40. A method for preparing a gene expression profile indicative of colon cancer prognosis, comprising:  
detecting the expression level of less than 1000 transcripts in a sample comprising RNA isolated from a colon cancer specimen, wherein at least 50 transcripts listed in Table 6 are detected.

15

41. The method of claim 40, wherein from 400 to 800 transcript expression levels are detected.

42. The method of claim 40 or 41, wherein from 500 to 700 transcript  
20 expression levels are detected.

43. The method of any one of claims 40-42, wherein at least 100 transcripts from Table 6 are detected.

25 44. The method of any one of claims 40-43, wherein at least 200 transcripts from Table 6 are detected.

45. The method of any one of claims 40-44, wherein at least 300 transcripts from Table 6 are detected.

30

46. The method of any one of claims 40-45, wherein at least 400 transcripts from Table 6 are detected.

47. The method of any one of claims 40-46, wherein at least 500

transcripts from Table 6 are detected.

48. The method of any one of claims 40-47, wherein at least 600 transcripts from Table 6 are detected.

5

49. The method of any one of claims 40-48, wherein all transcripts listed in Table 6 are detected.

50. The method of any one of claim 40-49, wherein the transcripts listed in Table 6 comprise the transcripts listed in Table 1.

10

51. The method of any one of claims 40-50, wherein the colon cancer specimen is a formalin fixed paraffin-embedded tissue sample.

52. The method of any one of claims 40-51, further comprising, scoring the expression level of the transcripts listed in Table 6, or a decision score derived therefrom, against corresponding levels or scores for high risk and low risk patient populations.

15

53. The method of claim 52, further comprising, selecting adjuvant chemotherapy where the patient is determined to be in the high risk group.

20

54. A method for prognosing colon cancer, comprising:  
preparing a gene expression profile for a colon cancer specimen comprising isolated RNA;  
and classifying the specimen based the expression levels of at least 50 transcripts listed in Table 6, or a decision score derived therefrom, in a low risk or high risk group.

25

55. The method of claim 54, wherein the level of less than 1000 transcripts are detected in the gene expression profile.

30

56. The method of claim 54 or 55, wherein the level of less than 800 transcripts are detected in the gene expression profile.

57. The method of any one of claims 54-56, wherein the level of less than 700 transcripts are detected in the gene expression profile.

5 58. The method of any one of claims 54-57, wherein the specimen is classified based on the expression level of at least 100 transcripts from Table 6.

59. The method of any one of claims 54-58, wherein the specimen is classified based on the expression level of at least 200 transcripts from Table 6.

10

60. The method of any one of claims 54-59, wherein the specimen is classified based on the expression level of at least 300 transcripts from Table 6.

15 61. The method of any one of claims 54-60, wherein the specimen is classified based on the expression level of at least 400 transcripts from Table 6.

62. The method of any one of claims 54-61, wherein the specimen is classified based on the expression level of at least 500 transcripts from Table 6.

20 63. The method of any one of claims 54-62, wherein the specimen is classified based on the expression level of at least 600 transcripts from Table 6.

64. The method of any one of claims 54-63, wherein the expression level of all transcripts listed in Table 6 are used to classify the specimen.

25

65. The method of any one of claims 54-64, wherein the transcripts listed in Table 6 comprise the transcripts listed in Table 1.

30 66. The method of any one of claims 54-65, wherein the colon cancer specimen is a formalin fixed paraffin-embedded tissue sample.

67. The method of any one of claims 54-66, further comprising, selecting adjuvant chemotherapy where the patient is determined to be in the high risk group.

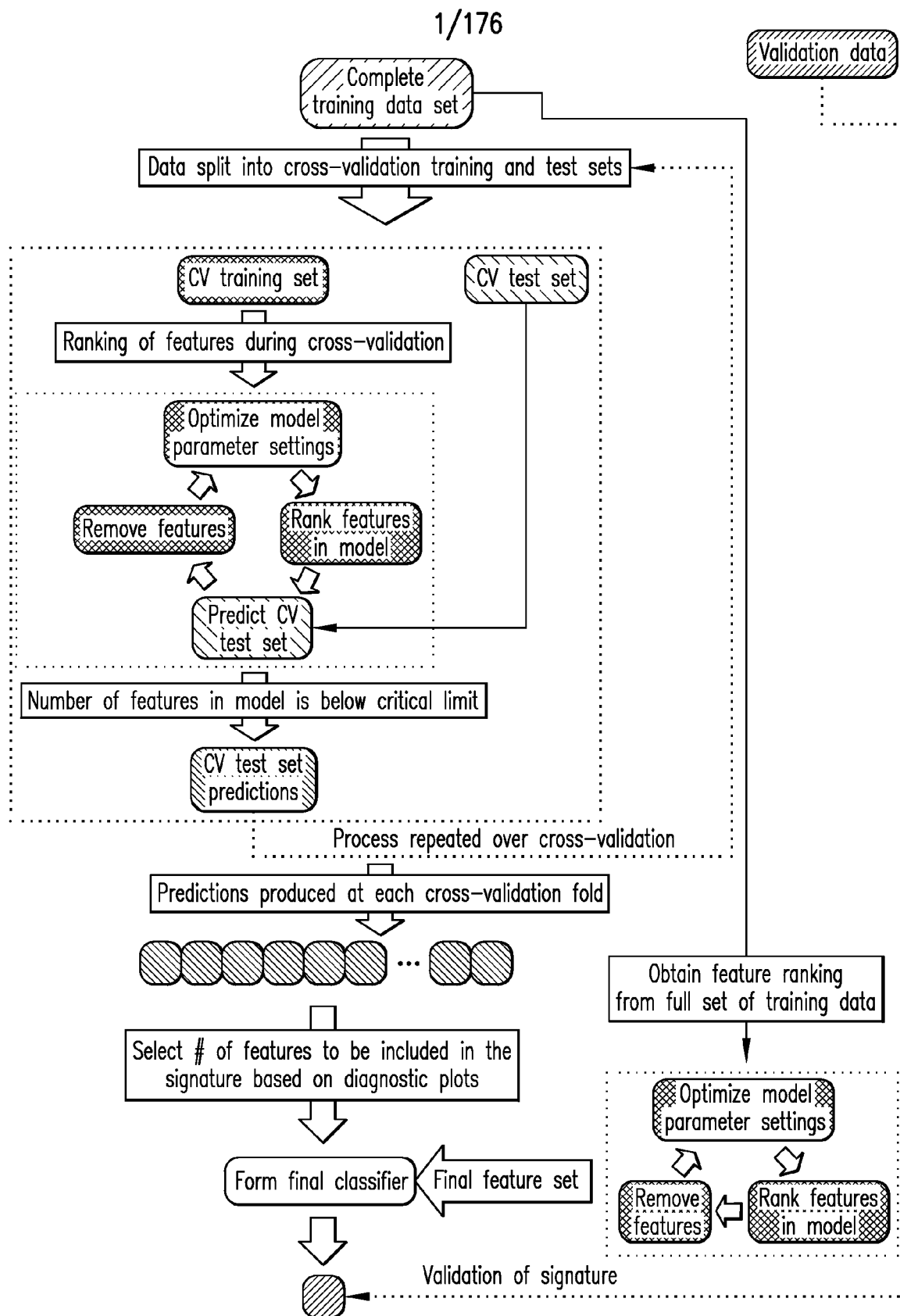


FIG. 1

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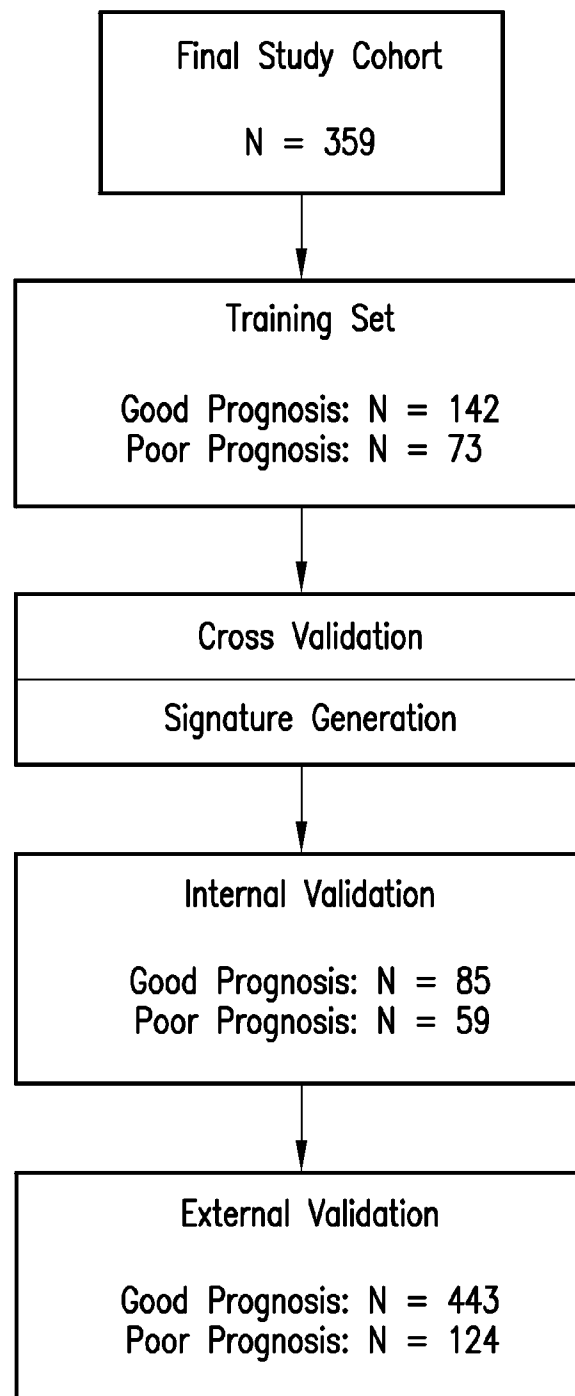


FIG.2

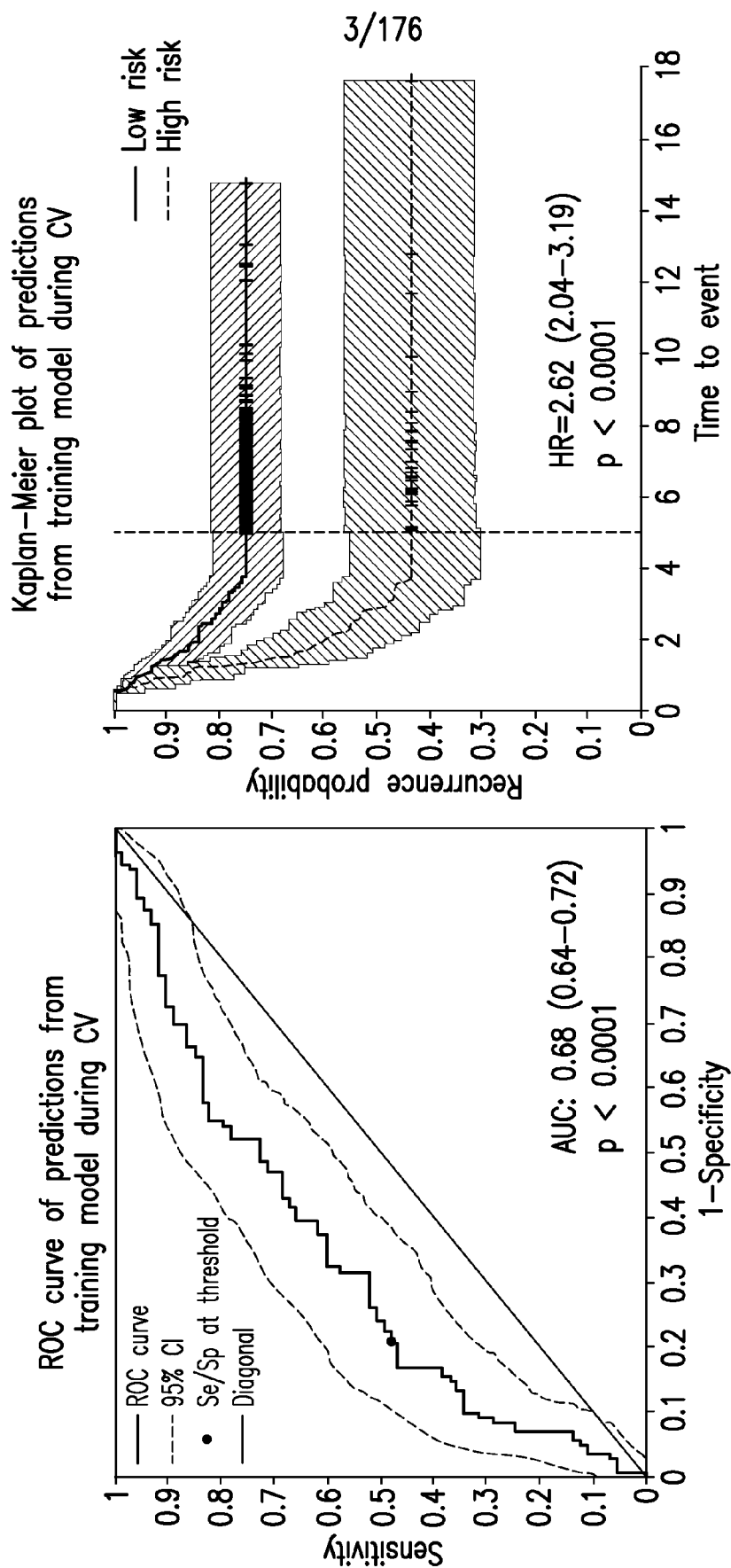


FIG.3B

FIG.3A

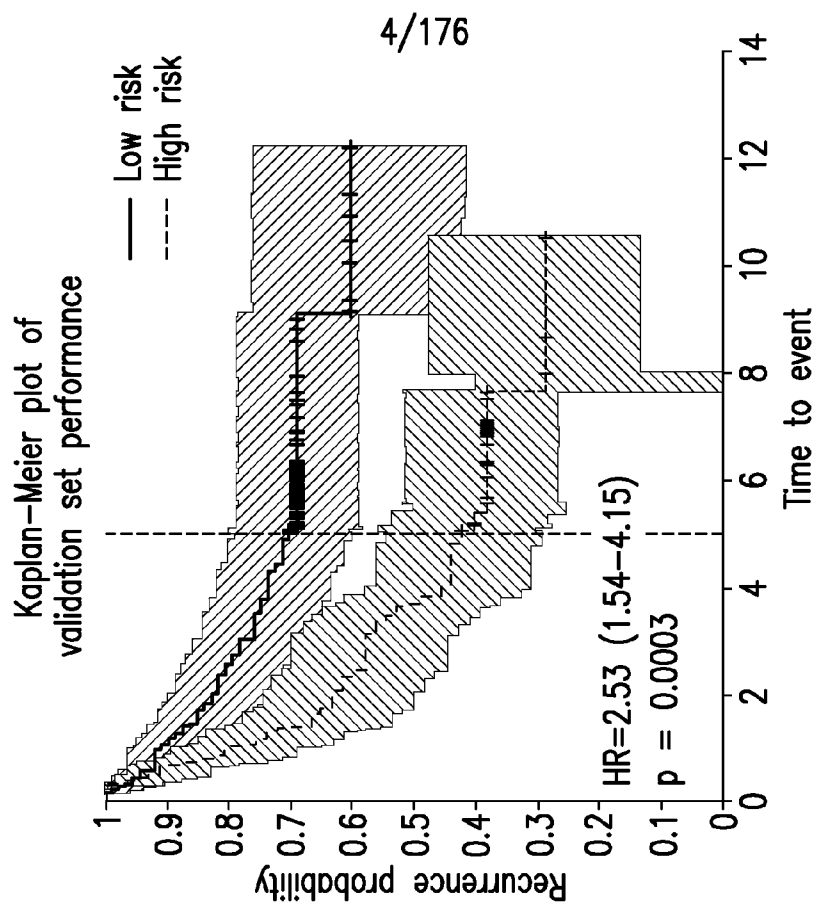


FIG.4B

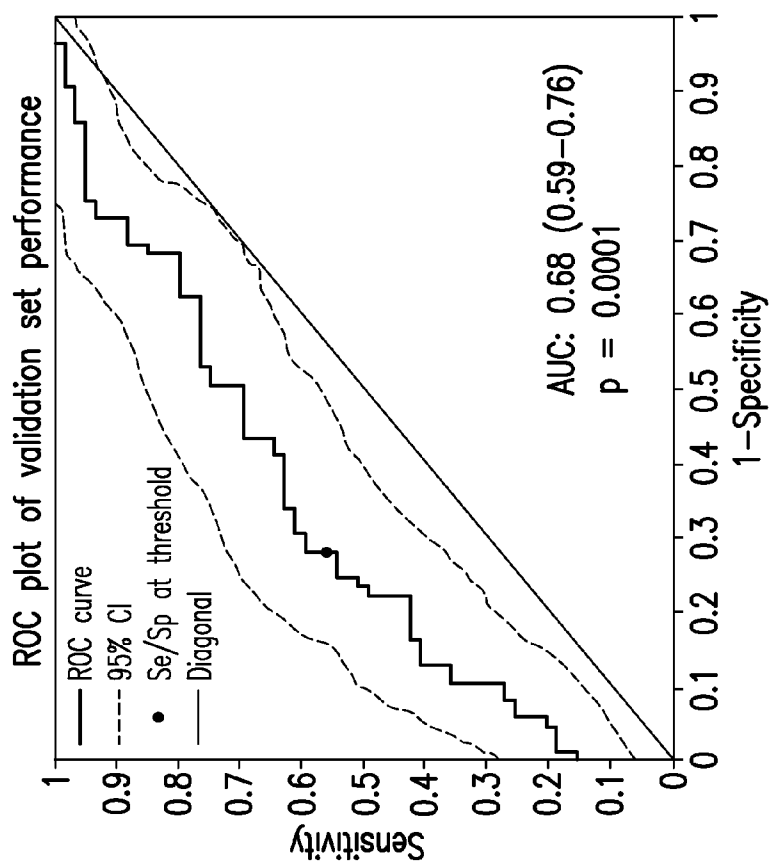


FIG.4A

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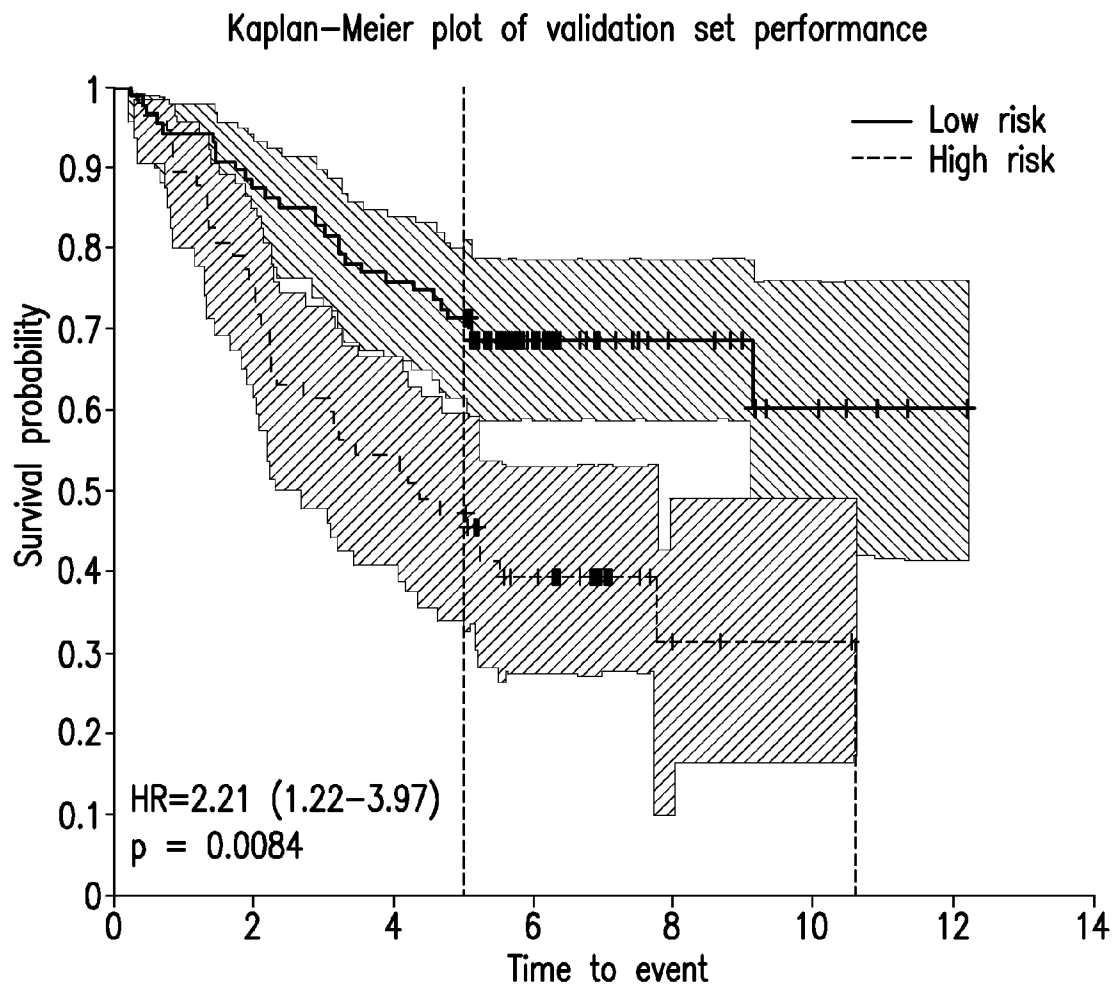


FIG.5

Table 3: Key Patient and Tumor Characteristics

|                          | TRAINING SET | % OF TOTAL (215) |
|--------------------------|--------------|------------------|
| Prognosis                |              |                  |
| Good                     | 142          | 66               |
| Poor                     | 73           | 34               |
| Age at Diagnosis (Years) |              |                  |
| Mean (SD)                | 71 (9.9)     |                  |
| Median                   | 72           |                  |
| Range                    | 45 to 95     |                  |
| FFPE Block 'Age' (Years) |              |                  |
| Mean (SD)                | 9.9 (3.2)    |                  |
| Median                   | 9.0          |                  |
| Range                    | 5.2 to 18.3  |                  |
| Contributing Centre      |              |                  |
| Alabama                  | 33           | 15               |
| Bethesda                 | 13           | 6                |
| Georgetown               | 0            | 0                |
| MGH                      | 12           | 6                |
| UPMC                     | 46           | 21               |
| Calgary                  | 34           | 16               |
| Karolinska               | 15           | 7                |
| NI240                    | 11           | 5                |
| St Vincents              | 51           | 24               |
| Asterand                 | 0            | 0                |
| BioServe                 | 0            | 0                |
| Cureline                 | 0            | 0                |
| Country of Origin        |              |                  |
| Europe                   | 77           | 36               |
| USA                      | 104          | 48               |
| Canada                   | 34           | 16               |
| Ethnicity                |              |                  |
| African American         | 20           | 9                |
| Asian                    | 5            | 2                |
| White                    | 190          | 89               |
| Unknown                  | 0            | 0                |
| Sex                      |              |                  |
| M                        | 106          | 49               |
| F                        | 109          | 51               |
| T Stage                  |              |                  |
| 3                        | 188          | 87               |
| 4                        | 27           | 13               |
| T Grade                  |              |                  |
| Well                     | 9            | 4                |
| Moderate                 | 174          | 81               |
| Poor                     | 31           | 14               |
| Undifferentiated         | 1            | 0.5              |
| Number of Nodes Assessed |              |                  |
| Mean (SD)                | 14 (7.5)     |                  |
| Median                   | 13           |                  |
| Range                    | 6 to 40      |                  |
| T Location               |              |                  |
| Caecum                   | 60           | 28               |
| Ascending Colon          | 46           | 21               |

|                          | VALIDATION SET | % OF TOTAL (144) |
|--------------------------|----------------|------------------|
| Prognosis                |                |                  |
| Good                     | 85             | 59               |
| Poor                     | 59             | 41               |
| Age at Diagnosis (Years) |                |                  |
| Mean (SD)                | 70 (10.1)      |                  |
| Median                   | 70             |                  |
| Range                    | 45 to 90       |                  |
| FFPE Block 'Age' (Years) |                |                  |
| Mean (SD)                | 7.48 (3.1)     |                  |
| Median                   | 8.2            |                  |
| Range                    | 1.38 to 15.8   |                  |
| Contributing Centre      |                |                  |
| Alabama                  | 9              | 6                |
| Bethesda                 | 2              | 1                |
| Georgetown               | 6              | 4                |
| MGH                      | 11             | 8                |
| UPMC                     | 11             | 8                |
| Calgary                  | 11             | 8                |
| Karolinska               | 29             | 20               |
| NI240                    | 2              | 1                |
| St Vincents              | 28             | 19               |
| Asterand                 | 5              | 3                |
| BioServe                 | 11             | 8                |
| Cureline                 | 19             | 13               |
| Country of Origin        |                |                  |
| Europe                   | 89             | 62               |
| USA                      | 44             | 31               |
| Canada                   | 11             | 8                |
| Ethnicity                |                |                  |
| African American         | 6              | 4                |
| Asian                    | 0              | 0                |
| White                    | 137            | 95               |
| Unknown                  | 1              | 1                |
| Sex                      |                |                  |
| M                        | 69             | 48               |
| F                        | 75             | 52               |
| T Stage                  |                |                  |
| 3                        | 119            | 83               |
| 4                        | 25             | 17               |
| T Grade                  |                |                  |
| Well                     | 12             | 8                |
| Moderate                 | 114            | 79               |
| Poor                     | 18             | 13               |
| Undifferentiated         | 0              | 0                |
| Number of Nodes Assessed |                |                  |
| Mean (SD)                | 13.1 (10.0)    |                  |
| Median                   | 10             |                  |
| Range                    | 6 to 98        |                  |
| T Location               |                |                  |
| Caecum                   | 33             | 23               |
| Ascending Colon          | 31             | 22               |

FIG.6

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| Signature rank | Probe Set ID                   | Gene Symbol | Orientation | Gene Description                                                                                 | SEQ ID NO: | Target sequence                                                                                                                                                                                                                             |
|----------------|--------------------------------|-------------|-------------|--------------------------------------------------------------------------------------------------|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1              | ADXCRA<br>D_5128.C1<br>_at     | MUM1        | Sense       | melanoma associated antigen (mutated) 1<br>[Source:HGNC<br>Symbol;Acc:29641]                     | 1          | CTGTTTTTCCCGGTAGATTCTGATACATTCAATCCCCT<br>ACTCCCCCAAAACAGTTGAAGCCCAGCCCACACTCTTA                                                                                                                                                            |
| 2              | ADXCRA<br>D_BG481<br>316_s_at  | SIGMAR1     | Sense       | sigma non-opioid intracellular receptor 1<br>[Source:HGNC<br>Symbol;Acc:8157]                    | 2          | CCGGTATACCAAGGGAGCCAGTTGTGTTCCAGACACACA<br>CATCACAGCTTGACTCACTAACTGAGGCCTTTCCATAGC<br>TCCACAGCTT                                                                                                                                            |
| 3              | ADXCRIH.<br>3975.C1_a<br>t     | ARSD        | Sense       | arylsulfatase D<br>[Source:HGNC<br>Symbol;Acc:717]                                               | 3          | TTGGCCAGTGTGTTTTCTAAGTCAATTCTAGTGTGTTTC<br>ATCCTCACCTCTTCCCTCTGTGGCTTTGATGATGGA                                                                                                                                                             |
| 4              | ADXCRA<br>D_NM_17<br>6825_s_at | SULT1C2     | Sense       | sulfotransferase family, cytosolic, 1C, member 2 [Source:HGNC<br>Symbol;Acc:11456]               | 4          | AGGCTGGTCTTAACTGACTGCTTTTTTATTATTACCATGC<br>ACTGGCAATTCCAAACAATGTCAGTGTTAAATGCTTCT<br>CCCTGAAAAAGAGAAAAAAGGAAAAAAGAAAAAGA<br>AAAGTGAAAAGAAAAACTCTTATTGGCCTAAGTTCTAAA<br>TAATAGCTAGGTTACCACTGAGTTTAACTATATGTATAT<br>GAGCTTCAAATAAGCACCTTTTAA |
| 5              | ADXCRA<br>G_AB0491<br>49_s_at  | PPFIBP1     | Sense       | PTPRF interacting protein, binding protein 1 (liprin beta 1)<br>[Source:HGNC<br>Symbol;Acc:9249] | 5          | AAATGCTGCAGCAGGTATGTCAGAGGCCAGAACCAAG<br>ATGGGATTTCCCTGCTGAACATATGTGAGATGCTGCATTT<br>CTATGTTGTGTTTGTCTGTGATGCAGCAGTAAGTTTTTGG<br>ATTCACCTTAGACCAGCACATTA                                                                                    |

FIG. 7-1

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|   |                              |       |                           |                                                                         |   |                                                                                                                                                                                                                                                                                                                         |
|---|------------------------------|-------|---------------------------|-------------------------------------------------------------------------|---|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 6 | ADXCRP<br>D.15673.C<br>1_at  | N/A   | No<br>Transcript<br>match | N/A                                                                     | 6 | GAAGGTCAGGACTTTGTGAACATATATAAACTGCAGATG<br>GCTATTAGATATCCAAGTAGAGATGCTGAAGAGATGAAT<br>GTATATAGAAGTCTGAATTTGGGAGAGAGATCTGGATAG<br>GAGATACTTACCTGGTGTAAACAGCTTACAGATTGTGT<br>AAAGTCATGAAACGGATAAGAACCTTAAAAAGAGAGAAAA<br>GGGAATAGAGGTTACCAAAATGAATTGCAGTTTCCAAATT<br>GCAGAG                                               |
| 7 | ADXCRP<br>D.7289.C1<br>_s_at | INO80 | Sense                     | INO80 homolog (S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:26956]   | 7 | CTCTGATTTGCACACCTGAAAAATCGCGGAATTGAGTTTC<br>GATAGATTGATTTTTAAACTTTTTGGAGTAGGGGTAT<br>AGGGAATCATTTAATTTAAATCATTAAAGATTCCCTGCT<br>CAAACCCAGATTCTGTGTACAGATGCTATTTAGAGGGA<br>ATCAGAAAAATGCCAAGCCTTTCTCTTTGAATGTGCTA<br>TTTTTATAACTGAACCTGTACATATGTATAAAGAGAGACA<br>CATCTTCCTTTTACTA                                        |
| 8 | ADXCRA<br>G_BC011<br>901_at  | KRT17 | Sense                     | keratin 17<br>[Source:HGNC<br>Symbol;Acc:6427]                          | 8 | GCTTCCTTGCCTGATGACAATAAAGCTTGTGACTCAGC<br>TAA                                                                                                                                                                                                                                                                           |
| 9 | ADXCRA<br>D_BE2959<br>38_at  | RBBP4 | Sense                     | retinoblastoma binding<br>protein 4<br>[Source:HGNC<br>Symbol;Acc:9887] | 9 | GGGTCAGAAAGATGCCTTCAGTTTTGGTCAGTGTCTAAA<br>AGTTAAGTCTGTTAGGCCAAGCATGGTGGCTCAGGCC<br>TGAATCCCAGCACTTGGGAGGCCGAGGCAAGTGGA<br>TCACAAGGTCAGGAGATGAGACCATCTTAGCCAACATG<br>GTGAAACCCCGTCTCTACTAAAAATACAAAAAATTAGCC<br>AGGCGTGGGGTGGTGCCTATAATCCAGCTACTTGG<br>GAGGCTGAGGCAGGGGAATCGCTTGAACNCGGAGGC<br>AGAGGTCACGCCCATGGACTCCAG |

FIG. 7-2

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|    |                                |                                                                                            |           |                                                                                                                                                                                                          |    |                                                                                                                                                                                                                                                                                                                                |
|----|--------------------------------|--------------------------------------------------------------------------------------------|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 10 | ADXCRA<br>D_NM_00<br>2260_s_at | KLRC1 ///<br>KLRC2                                                                         | Sense     | killer cell lectin-like<br>receptor subfamily C,<br>member 1<br>[Source:HGNC<br>Symbol;Acc:6374] ///<br>killer cell lectin-like<br>receptor subfamily C,<br>member 2<br>[Source:HGNC<br>Symbol;Acc:6375] | 10 | CTTCTAAAAGTTGCATGTTATGTGAGTCAGCTTATAGG<br>AAGTACCAAGAACAGTCAAACCCATGGAGACAGAAAGT<br>AGAAATAGTGGTTGCCAATGTCTCAGGGAGGTTGAAATA<br>GGAGATGACCACTAATTGATAGAACGTTTCTTTGTGTCG<br>TGATGAAAACTTTCTAAATTCAGTAATGGTGATGGTTGT<br>AACTTTGCGAATATACTAAACATCATTTGATTTTAATCAT<br>TTTAAGTGCATGAAATGTATGCTTTGTACATGACACTTCA<br>ATAAGCTATCCAGAAAA |
| 11 | ADXCRA<br>D_AF1438<br>66_s_at  | ZC3HAV1                                                                                    | Sense     | zinc finger CCH-type,<br>antiviral 1<br>[Source:HGNC<br>Symbol;Acc:23721]                                                                                                                                | 11 | AGCAAGCTTACTAAAACTGCACCTTCACACTTAGCTTAA<br>TGTTTGAGGGAATTAACCTTCATAAA                                                                                                                                                                                                                                                          |
| 12 | ADXCRP<br>D.14126.C<br>1_at    | FNDC3B                                                                                     | Sense     | fibronectin type III<br>domain containing 3B<br>[Source:HGNC<br>Symbol;Acc:24670]                                                                                                                        | 12 | ACCATGGCAACGAGGTAGTCTGTTCTATTTTGGAGTAT<br>GAAAGTAGTGCCCTTCTTAAATCTAATAATAAATGAGAGTT<br>CCAGAAAACCCAGTGTCTCAAAACAAATTTGATTTA                                                                                                                                                                                                    |
| 13 | ADXCRSS<br>.Hs#S192<br>6324_at | AC018359.1<br>(Clone_based_<br>vega_gene) ///<br>AC123023.1<br>(Clone_based_<br>vega_gene) | AntiSense | Novel processed<br>transcript /// Putative<br>processed transcript.                                                                                                                                      | 13 | TGGGCTTAAAACCTCAGCTCTGCCACTTACATTCCCTCATT<br>TCTTCTATCCTGGGTCTGCCAAAAATGTAAGAAAAATTT<br>TCACATTTTTTACCAGTTTTTCTCACCCTATGACACCCCT<br>GTCTCAAAATGATTATGCAACAGCCCCAGAGTCCCCCAT<br>CCAAAATTCCTTTGCAAAGAGCAAGATTTCCCTCGCTATT<br>TCTGAATTCATCCACACCTCTATTTCTCTCT                                                                     |

FIG. 7-3

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|    |                               |                                           |           |                                                                                     |    |                                                                                                                                                                                                                                                                                                          |
|----|-------------------------------|-------------------------------------------|-----------|-------------------------------------------------------------------------------------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 14 | ADXCRA<br>D_BX0911<br>64_s_at | RNF39                                     | AntiSense | RING finger protein 39<br>isoform 2<br>[Source:RefSeq<br>peptide;Acc:NP_73957<br>5] | 14 | ACTCCCCAAGGGTTCTCAATTCTCTTTTCCAGGCTCGT<br>CCATGACTGTTTCTTGTCCTCAGAGCCCTTGCCCTCCTT<br>GTCCTCCTCAGTCCCATCTCTGTCTCTTTTCAGCGG<br>CCCCATCCTTATCTACCTTCCCAAGTGCATCCCAGAAAA<br>ACATCTGTCCCTTCC                                                                                                                  |
| 15 | ADXCRA<br>D_BX6412<br>59_at   | NHLRC3                                    | Sense     | NHL repeat containing<br>3 [Source:HGNC<br>Symbol;Acc:33751]                        | 15 | CCTGAGCTTGGTGACTCAATTGTGTGCTAAGAAAAAAA<br>TCAAAATTCAGAAACATGCCGAGACCTCGACCCAGGTAAAT                                                                                                                                                                                                                      |
| 16 | ADXCRA<br>D_AA6012<br>08_x_at | AC004878.3<br>(Clone_based_<br>vega_gene) | AntiSense | Known pseudogene.                                                                   | 16 | GACTGGAGAAAAGAGAGGTGGCATAGGATTGACTAAGA<br>TGAAGGAAGGGGCCAGCGTGGTGGCTCACCCTGT<br>AACCCCAACACTTTGGAGGCTGAGCGGGCAGATCA<br>CCTGAGGTCAGGAATTCAGACCAGCCTGGCCAAACATG<br>GTGAAACCCCATCTCTACTAAAAGTACAAAAATTAGCCA<br>GGCGGTAGTGGTGTGCCTAT                                                                         |
| 17 | ADXCRA<br>D.10016.C<br>1_at   | SATB2                                     | AntiSense | SATB homeobox 2<br>[Source:HGNC<br>Symbol;Acc:21637]                                | 17 | ATCCTCAACAGCTAATCACTCTTTAACTCCTGAATTCTG<br>GCTCCTGTCCCCACTACTTTAATGAAATTATACTCTAAA<br>CTTCGCCAGTCTTCTCCCAACCACTGCCAAATCTCATG<br>ACATGTTTTAAGCCTCTCTCTCTTAACCTCTCAGCTTTC<br>CACAAGTAGACAAAGTCTTCTCTGGAAACTCTCCACGCA<br>TGTCCTCTATACTCTCACTACTGTCTCCCTCTTCTCCTT<br>CTCCACCTGCCCCCATCTCCTGGCATTTCTACTCTCTTT |

FIG. 7-4

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|    |                                |                                              |       |                                                                          |    |                                                                                                                                                                                                                                                                                                        |
|----|--------------------------------|----------------------------------------------|-------|--------------------------------------------------------------------------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 18 | ADXCRA<br>G_BC072<br>004_at    | CLCN2                                        | Sense | chloride channel 2<br>[Source:HGNC<br>Symbol;Acc:2020]                   | 18 | TTCTCCAGTTCATCCTACCTGGAATCTGACCCACTACC<br>CACCTGCAACAAAGTCTTCCAGAGGCAGGAAGATAGGCC<br>CTGCCCTGGCAGGATGGTTGGGTCACCTTGACCCCT<br>GCTCCCTTTGAGGGGAAAGGGTGGAACTAAGATG<br>GGTTTAACTGGAACCTCCAATGACCAGATGTATATAG<br>AGATTTACAAAGATTTTATATTAATTAATAAAACAAATT<br>CTTAAATAGAACAAAATAAACACCTAATGAGCCACTTAT<br>ATAT |
| 19 | ADXCRA<br>D_BF8807<br>25_at    | AC079781.1<br>(Clone_based_<br>ensembl_gene) | Sense | Known long non-coding<br>RNA                                             | 19 | ATGGTGGATAAATGGGACTTAGGACTAAAACTCATGCCT<br>TGGTGTGTTTTTGCAGTGATGTTTTGTTCTGGGGTGCAT<br>CACAA                                                                                                                                                                                                            |
| 20 | ADXCRA<br>G_NM_00<br>3234_s_at | TFRC                                         | Sense | transferrin receptor<br>(p90, CD71)<br>[Source:HGNC<br>Symbol;Acc:11763] | 20 | GCGTAGCTAAGTGAAAAGGTCATAGCTGAGATTCCTGG<br>TTCGGGTGTTACGCACACGTACTTAAATGAAAAGCATGTG<br>GCATGTTTCATCGTATAAC                                                                                                                                                                                              |
| 21 | ADXCRA<br>D_AL8320<br>68_at    | SIK3                                         | Sense | SIK family kinase 3<br>[Source:HGNC<br>Symbol;Acc:29165]                 | 21 | ACTCTCAAGAACAGTAGAGGGGAAAAAGAAAAAGAAAA<br>GAACAGTGGAGGTTGTGTAAGGACATTTGAGAAAGAG<br>ATTTCATGAAACAGGCCAAATGGTAGGTTTGCTAGTTCGC<br>AGGGGAGAACCAATGAATTAATTTAGAAAGAGCTTCTC<br>TGGGATTAGAATGAAAAATAAAATCACTGGCTGGGTGCAC<br>ACCTGTAATTCTAGCTATTTCAGGCAGGGAGGA                                                 |

FIG. 7-5

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|    |                                  |        |       |                                                                                                                |    |                                                                                                                                                                                                                                                       |
|----|----------------------------------|--------|-------|----------------------------------------------------------------------------------------------------------------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 22 | ADXCRA<br>D_NM_02<br>1777_at     | ADAM28 | Sense | ADAM<br>metallopeptidase<br>domain 28<br>[Source:HGNC<br>Symbol;Acc:206]                                       | 22 | TTGTCTCAGCATCAGTATATCCCATGCAATATTTGAGGT<br>GTGCTCATACTAAATATTGTTGATCTGAAATTCAAAT<br>TAACTGGGTGCTTTTTCTTTTCATCTGGCAACCCCTACT<br>AAGATCATAAACCCCTTGGA                                                                                                   |
| 23 | ADXCRA<br>D_BP3934<br>43_at      | SLC2A3 | Sense | solute carrier family 2<br>(facilitated glucose<br>transporter), member 3<br>[Source:HGNC<br>Symbol;Acc:11007] | 23 | ACTTGGGAGGAAATACACAGTAGTTAGAAAAAGCCTCCT<br>AGGTGATTTTGATGAATCCCAGTCTCAAATTTCTTCATTT<br>GGAATGATAATGTAGGCCACACGTATTACTGGAGAAAA<br>ATGTGCTCCCGAGACTTTCCAGAGCAGCAGAGCTGGGA<br>CTAGGCAGGTGAGGCAGCTACGTGCAAGTGTAGCCCT<br>GAGAATGAGCACCTCTTTAAAGAATGTACCTTG |
| 24 | ADXCRA<br>D_AA1315<br>06_at      | CXCL9  | Sense | chemokine (C-X-C<br>motif) ligand 9<br>[Source:HGNC<br>Symbol;Acc:7098]                                        | 24 | GAGAGGTTGTCTGTGGCCAGAAATTTAAACCTATACTCAC<br>TTTCCCAAATTGAATCACTGCTCACAC                                                                                                                                                                               |
| 25 | ADXCPRP<br>DRC.1543<br>2.C1_s_at | ZNF770 | Sense | zinc finger protein 770<br>[Source:HGNC<br>Symbol;Acc:26061]                                                   | 25 | TTGCATTAGGTATTAGTCTAGGGATAAAGTATACAGGCG<br>GATGTGCGTTGGTTATATACAAATATGTCATTTTATGTAA<br>GGGACTTGAGTATACCTTGATTTTGGT                                                                                                                                    |

FIG. 7-6

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|    |                               |         |       |                                                                                                               |    |                                                                                                                                                                                                                                                                                                   |
|----|-------------------------------|---------|-------|---------------------------------------------------------------------------------------------------------------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 26 | ADXCRA<br>G_BC004<br>542_s_at | PLXNB2  | Sense | plexin B2<br>[Source:HGNC<br>Symbol;Acc:9104]                                                                 | 26 | GAAAAAGCGGTACGATGCCTTCTGACCTCACCGGCCT<br>CCCCAAGGGTGCCGGCACCTCTGGTGGACTCACGGCT<br>GCTGGCCCCACGTCAAAGTCAAGTGAGACGTAGGT<br>CAAGTCCTACGTGGGGCCAGACATCCTGGGTCTCT<br>GGTCTGTCAGACAGGCTGCCCTAGAGCCCCACCCAGT<br>CCGGGGGACTGGAGCAGTTCCAGACCACCCACC<br>CCTTTTGTAAATCTTGTTCATTGTAAATCAAATACAGCG<br>TCTTTTTC |
| 27 | ADXCRA<br>D.4449.C1<br>_at    | ARHGAP8 | Sense | Rho GTPase activating<br>protein 8<br>[Source:HGNC<br>Symbol;Acc:677]                                         | 27 | TGCCTCTGGTCCTTGGACTCTTGTCCATGGTTCCTGAG<br>CTGTGG                                                                                                                                                                                                                                                  |
| 28 | ADXCRA<br>DRC.1402<br>9.C1_at | B4GALT5 | Sense | UDP-Gal:betaGlcNAc<br>beta 1,4-<br>galactosyltransferase,<br>polypeptide 5<br>[Source:HGNC<br>Symbol;Acc:928] | 28 | GCCCAGCCTTGAAGTCATGTTCTAAATTGTTGAATTT<br>GTGCCTCTTTGTTTTTCCCAACCAAGCCCTCAAATT<br>GTAGTCTCTGCGCTTCTGCAGAAATCTGGAAAATGCC<br>AGTTTCTCTCCCGCCCTTGTTCATATAAACATATTT<br>ATATATTGTGATGAGGAGTACTTTCTGAAGAGTACTTCG<br>TANNNNNNNAATTGCCTTGTTCCTTCAACTTCCTT<br>GATTTTCA                                      |
| 29 | ADXCRA<br>G_BC005<br>352_s_at | TNFAIP8 | Sense | tumor necrosis factor,<br>alpha-induced protein 8<br>[Source:HGNC<br>Symbol;Acc:17260]                        | 29 | AAAAGTCTAGATTGGTCTTGATATTGAGATAATAAAAAGT<br>AAGTAGCATTAAAGAAAGGTAACAATCTTCATTTCTACAGA<br>TGAACCTCATTGAAACAATTTAGGGGAATGAGGGGCAAA<br>AGGGAGAAATACTGCTAAAGAACATGAGCATATAAAAC<br>GCGTGCGTTTCAGTGTTTAAAGAGGCTTGATAAA                                                                                  |

FIG. 7-7

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|    |                               |       |       |                                                                                        |    |                                                                                                                                                                                                                                                                                                                          |
|----|-------------------------------|-------|-------|----------------------------------------------------------------------------------------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 30 | ADXCRA<br>D_BG619<br>847_at   | EWSR1 | Sense | Ewing sarcoma<br>breakpoint region 1<br>[Source:HGNC<br>Symbol;Acc:3508]               | 30 | ATAATTATGGGCTCAC TTC TACTGGAGATGTTGAAAGT<br>CTAAATCGGTTTGACCATTTTGATTGATGGCACAAATCTG<br>GTTAGAAAACCTTTGTTAGATCAATGACATAACCCCTGCT<br>GCCCTGCTGCCCTGCCCTCCCTCCCTTCTCCCATCCCT<br>TTTCCCTATCTGGTGCTGTACTTTGATGAAGGTGAGCT<br>ATAATATTGGTGGTTAATAATCCAGAAAGGCTTAGTTCT<br>GTGTGT                                                |
| 31 | ADXCRA<br>D_N86095<br>_at     | FLCN  | Sense | folliculin [Source:HGNC<br>Symbol;Acc:27310]                                           | 31 | GAGGAAGGCTGAAATGCTTTCTATTGGATACTATCTGG<br>GCATATTACTTCTCTGTGTTCACTGTCTGGGTGACAGGA<br>TTCATAGAAGCCCCAACTTTAGCACCCACGCAGCATACC<br>CTTGTAACAAAGCCGCACACGTACGCCCTCAAGCTAAA<br>ACAAAAGTGGACCGGGAGCCGAGGTGGGGGATCATGA<br>GGTCAAGAGTTTGAGACCAGCCTGGCAGATAACGGT<br>GAAACCCCGTCTCTACTAAATACCAAAAAAGGTTAGCC<br>GACATGGTGCAGGTCCCTT |
| 32 | ADXCRA<br>D_CX7857<br>94_s_at | GUF1  | Sense | GUF1 GTPase<br>homolog (S. cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:25799]            | 32 | CTTCTCTCTTACCTGCCATGCTTGAAGCCCCCGCCCC<br>TCTTCAAGTTGTCCTGCCCTTCAAGACCAATGTACA                                                                                                                                                                                                                                            |
| 33 | ADXCRIH.<br>2688.C1_s<br>_at  | ARSE  | Sense | arylsulfatase E<br>(chondrodysplasia<br>punctata 1)<br>[Source:HGNC<br>Symbol;Acc:719] | 33 | GAAAAAGTAGTCCACCACGATCCACCTTTGCTCTTTGAC<br>CTCTCAAGAGACCCCTTCTGAGACCCACATCCTCACACC<br>AGCCTCAGAGCCCGTGTCTATCAGGTGATGGAACGAG<br>TCCAGCAGGCGGTGTGGGAACACACGCGGACACTCAG<br>CCCAGTTCCTCTGCAGCTGGACAGGCTGGGCAATATCT<br>GGAGACCGTGGCTGCAGCCCTGCTGTGCCCCGTTCCC<br>CCTCTGCTGGTGCCTTAGGGAAGATGACCCACAAATAA<br>TGCTGTCAGTGAA       |

FIG. 7-8

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|    |                               |          |       |                                                                |    |                                                                                                                                                                                                                                                  |
|----|-------------------------------|----------|-------|----------------------------------------------------------------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 34 | ADXCRP<br>D.6725.C1<br>_s_at  | EFNA3    | Sense | ephrin-A3<br>[Source:HGNC<br>Symbol;Acc:3223]                  | 34 | TCTTCTGTGAAGACAGGACCTATGCAACGCACAGACAC<br>TTTTGGAGACCGTAAACAACAGCGCCCCCTCCCTTCC<br>AGTCTGAGCCGGGAACCATCTCCAGGACCTTGCCCT<br>GCTACCCCTATGTGGTCCCACCTATCCTCCTGGGCCTT<br>TTTCAAGTGCTTTGGCTGTGACTTTTCATACTCTGCTCTTA<br>GT                             |
| 35 | ADXCRP<br>D.16070.C<br>1_at   | TMEM87A  | Sense | transmembrane protein<br>87A [Source:HGNC<br>Symbol;Acc:24522] | 35 | GTCATGAGACGGGATTTGGTCACCAAGGAAGTGAGTAT<br>ATATAGAGAAGAGGTCCAAGGGCTGGGCCCTTGAATAT<br>TTAATATAATTTAGAAGTCTGTAAACGATGAAGTAGTAGC<br>AGAAAGAACTTGAGGAGAGACCAGTGAGGTGGGTAGCA<br>AAAC                                                                   |
| 36 | ADXCRP<br>D.2228.C2<br>_s_at  | KIAA0141 | Sense | KIAA0141<br>[Source:HGNC<br>Symbol;Acc:28969]                  | 36 | CCACTGGAAAGGAGTGTTGTAAGACTAGGTTTTGGCTA<br>AGAACTTCTCACCTCAGCCCTANAGAGGGAGCCTGTGG<br>GTTCTCAGAGAGATATCACAAATTTGAGTCCCCAAAGA<br>GGCAGATACCCACCCACCTTCCCCCAAATCTTAAAGCA<br>CCTGCGCCAGTACAGTCAAGAAGAGG                                               |
| 37 | ADXCRA<br>D_AW604<br>939_x_at | CD177    | Sense | CD177 molecule<br>[Source:HGNC<br>Symbol;Acc:30072]            | 37 | TTTGCCCTTCTGCTAACTCTATTACCCCCACGATTCTT<br>CACCGATGATGACCACCCACACTCAACCTCCCTCTGAC<br>CTCATAACCTAATGGCCTTGACACCAGATTCTTACCCA<br>TTCTGTCCATGAATCATCTTCCCCACACACAATCATTCA<br>TATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGG<br>AGCATCCGGACTTGCCCTATGGGAGAGGG |

FIG. 7-9

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|    |                               |                                             |       |                                                                                                                        |    |                                                                                                                                                                                                                                                                                                       |
|----|-------------------------------|---------------------------------------------|-------|------------------------------------------------------------------------------------------------------------------------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 38 | ADXCRA<br>D_AK0248<br>64_at   | RP11-294O2.2<br>(Clone_based_<br>vega_gene) | Sense | Novel processed<br>transcript.                                                                                         | 38 | GGAAGAGCTCGGTGAGCATGATCATGGCTCAGGTTCTC<br>CATCCACATGCCCTAAGACAGGGGTGAGTGTGAAGATGG<br>GAACTGACTCAGAATTAACCTGTGATCATGGGCAAGTT<br>GCCAAGTTAACCCCTCATATCTAAATTCAGGTATCCTTGA<br>ACAAACATAGACAGATACTGATGATCCGCCATGTTTACT<br>ATAACCATAAACTCTTTGTGAATTAATAATGGCCTCTCAA<br>CCTGGA                              |
| 39 | ADXCRA<br>D.10763.C<br>1_s_at | AC027612.6<br>(Clone_based_<br>vega_gene)   | Sense | lymphocyte-specific<br>protein 1 pseudogene<br>(LOC654342), non-<br>coding RNA<br>[Source:RefSeq<br>DNA;Acc:NR_027238] | 39 | CAGGGCCATACAGGGGTGTGTACATCACAGATAGGG                                                                                                                                                                                                                                                                  |
| 40 | ADXCRA<br>D_AL8320<br>68_x_at | SIK3                                        | Sense | SIK family kinase 3<br>[Source:HGNC<br>Symbol;Acc:29165]                                                               | 40 | GTA CTCTCAAGAACAGTAGAGGGGAAAAAGAAAA<br>AAGAACAGTGGAGGTGTGGTAAAGGACATTTGAGAAG<br>AGATTCTATGAACAGGCCAAATGGTAGGTTTGCTAGTTC<br>GCAGGGGAGAACCAATGAATTAATTTAGAAAGAGCTT<br>CTCTGGGATTAGAAATGAAATAAATCACTGGCTGGGTG<br>CACACCTGTAATTCTAGCTATTCAGGCAGGAGGATGGC<br>TCGAGCCTAGGAGTTGGAGGTCAGCATAGGCAACATAG<br>GGA |
| 41 | ADXCRA<br>G_BX6484<br>99_s_at | C4orf41                                     | Sense | UPF0636 protein<br>C4orf41<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q7Z392]                                             | 41 | CAAGACCGGCCCTTGGCTGTTGTACAGAGATGTTGGG<br>CAGAGCTATGCAGGTGTTTCATTGTGAACTCTAGCTTTG<br>ATCATGTATAAAAGTTAACCTTTTCTATTTTAAATGAT<br>GTTATACC                                                                                                                                                                |

FIG. 7-10

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|    |                               |        |           |                                                                                                  |    |                                                                                                                                                                                                                                                                           |
|----|-------------------------------|--------|-----------|--------------------------------------------------------------------------------------------------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 42 | ADXC RP<br>D.4415.C1<br>_s_at | TCOF1  | Sense     | Treacher Collins-<br>Franceschetti syndrome<br>1 [Source:HGNC<br>Symbol;Acc:11654]               | 42 | GAGAGACAAAGCAAGTGGTGTATGTCAAGGAGAAGAAAG<br>GGAAAGGGGTCTCTTTGGCTCCCAAGGGGCCAAGGACCGA<br>GCCA                                                                                                                                                                               |
| 43 | ADXCRA<br>D_CX7521<br>89_s_at | GTF2F1 | Sense     | general transcription<br>factor IIF, polypeptide<br>1, 74kDa<br>[Source:HGNC<br>Symbol;Acc:4652] | 43 | AGCGCGGCTCAAGGATCAGGACCAGGACGAGGATGA<br>GGAGGAGAAAGGAGAAACGTGGCCGACGAGGAGCGGAGC<br>GAGCTGCGCATCCACGACCTGGAGGACGACCTGGAGA<br>TGTCGTCCGATGCCAGTGTATGCCAGTGGTGAGGAGGG<br>GGCAGAGTCTCCGAGGCCAAGAAGAACGCCCGCTG<br>GCTCATGGCGGGGAGAGAAAGAAAGAAAGAGGAGGTT<br>CAGACGACGAGGCCCTCGA |
| 44 | ADXCRA<br>D_AW265<br>514_at   | TRPS1  | AntiSense | trichorhinophalangeal<br>syndrome I<br>[Source:HGNC<br>Symbol;Acc:12340]                         | 44 | GGAGTCCAGGATTAAGGTTTTGCAGGGTTTGGTTTCTA<br>GTGAGGGCTTTCTTCTCGCTTGCAGATGGCCATCTTC<br>TCTCCATAGGCTAACATGGCCCTCTACTTTGTGTGGGA<br>GAGTCAGAGATAGAGCAAGCCCTCTTGTGTCTCTTCATA<br>TAAGCCTACTAATCCCCATCAGACCAGGTCCTTATGAT<br>CTTAAAC                                                 |
| 45 | ADXC RP<br>D.2546.C1<br>_s_at | MED1   | Sense     | mediator complex<br>subunit 1<br>[Source:HGNC<br>Symbol;Acc:9234]                                | 45 | AGCAAGGTGTCTCAGAACCCCAATTCTTACCAGTTTGTG<br>CAAATCACAGGGAACGGGGGTCTACCATTGGCTCGAG<br>TCCAACCCCTCCTCATCACAACGCCACCTGTCTCTT<br>CGATGGCCGGC                                                                                                                                   |
| 46 | ADXCRA<br>D_CN427<br>849_at   | PLXNA3 | Sense     | plexin A3<br>[Source:HGNC<br>Symbol;Acc:9101]                                                    | 46 | CAGGTGTTGGACAGTCCACCCCTCCCTGCTATTTATAT<br>CCCTCTGCCTATTTATTGAATCGAACTTCGCCTCTGTCT<br>CCATCTGTAAATATGTG                                                                                                                                                                    |

FIG. 7-11

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|    |                              |        |       |                                                                                                            |    |                                                                                                                                                                                                                                                                                  |
|----|------------------------------|--------|-------|------------------------------------------------------------------------------------------------------------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 47 | ADXCRP<br>D.6189.C1<br>_s_at | CHD3   | Sense | chromodomain helicase<br>DNA binding protein 3<br>[Source:HGNC<br>Symbol;Acc:1918]                         | 47 | AGAGTGGCAGTTTGCATGGCGAACCCCCACCTTCCTCT<br>TTGCTGCCCCCTTCACTTTCTTGCTGCCCCCTTTCCAGTC<br>TCTCTTACACACCCACTCCTGGTGTCTGCTGATCCCCCTCT<br>TCTGTATCAGGTTTATTGGTTGTACATAT                                                                                                                 |
| 48 | ADXCRP<br>D.4446.C3<br>_at   | B3GNT3 | Sense | UDP-GlcNAc:betaGal<br>beta-1,3-N-<br>acetylglucosaminyltrans<br>ferase 3 [Source:HGNC<br>Symbol;Acc:13528] | 48 | GAATATTCTGGCTGGCGAACTCCTACACATCCTTCAAAA<br>CCCACCTGGTACTGTTCCAGCATCTTCCCTGGATGGCT<br>GGAGGAACCTCCAGAAAATATCCATCTTCTTTTGTGGCT<br>GCTAATGGCAGAAAGTGCCGTGTGCTAGAGTTCCAACGT<br>GGATGCATCCGTCGCCGTTTGAGTCAAAAGCTTACTTCCC<br>TGCTCTCACCTACTCACAGACGGGGATGCTAAGCCCGTG<br>CACCTGCTGTGGGT |
| 49 | ADXCRP<br>D.8017.C1<br>_at   | GSTO2  | Sense | glutathione S-<br>transferase omega 2<br>[Source:HGNC<br>Symbol;Acc:23064]                                 | 49 | TAAGACCTACTATCTGATAGCCCCACATGGTGACTATAG<br>TAAATAATAACTTAATTGCACATTTAAAAATAACTTAAAC<br>AGTGTAAATTGGGTGTTTGTAAATTGAAAGGATAAATGCT<br>TGGGGAGTGGATACCCCATTTCTCCATGATGTGCTTATT<br>GCATACTGCATGCCTGGACCAAAATATGTACCCCAT                                                               |

FIG. 7-12

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|    |                                |                                                                     |           |                                                                                                                                                                                                                                                        |    |                                                                                                                                                                                                                                           |
|----|--------------------------------|---------------------------------------------------------------------|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 50 | ADXCRRS<br>.Hs#S300<br>6539_at | AC010522.1<br>(Clone-based<br>(Ensembl) ///<br>ZNF418 ///<br>ZNF814 | AntiSense | cDNA FLJ52732,<br>moderately similar to<br>Zinc finger protein 418<br>[Source:UniProtKB/TrE<br>MBL;Acc:B4DR41] ///<br>zinc finger protein 418<br>[Source:HGNC<br>Symbol;Acc:20647] ///<br>zinc finger protein 814<br>[Source:HGNC<br>Symbol;Acc:33258] | 50 | ATTACTACCTTATTATGAAGTGTGCCCTCCAAAAT                                                                                                                                                                                                       |
| 51 | ADXCRA<br>G_NM_00<br>3890_at   | FCGBP                                                               | Sense     | Fc fragment of IgG<br>binding protein<br>[Source:HGNC<br>Symbol;Acc:13572]                                                                                                                                                                             | 51 | CTTTTCTGGGTCACAGAGGCCAAATGTGAGAGCATTGA<br>ATAAA                                                                                                                                                                                           |
| 52 | ADXCRRP<br>DRC.1112<br>6.C1_at | KDELR3                                                              | Sense     | KDEL (Lys-Asp-Glu-<br>Leu) endoplasmic<br>reticulum protein<br>retention receptor 3<br>[Source:HGNC<br>Symbol;Acc:6306]                                                                                                                                | 52 | GACCTTTTCATCAATAGATCGCCCTTAAAGACCCATTGT<br>AAGGTCATAAAAAACCTCGGCCAACTGCACAAAGATGG<br>TGCCTCACTGCAACAAGAAACCTTAAGGTGCTTACCGA<br>CGAAATAAAAAACATAAAATGATTGTTCTCCAAAGGCCTGA<br>GGGCAAGACTCATGATGGGCAAGTCAACCCCAATCTGG<br>AACAATGTCCTCCTCTTAG |
| 53 | ADXCRA<br>G_AL3899<br>51_s_at  | NUP50                                                               | Sense     | nucleoporin 50kDa<br>[Source:HGNC<br>Symbol;Acc:8065]                                                                                                                                                                                                  | 53 | GATTATGTTTTCCATGGAAGGACAAAGTCTGACTGTTTCAT<br>AGGCTGATTTTCTTTAAGAGGATTATTCTGTTTTACAATT<br>TCAATTCTAGATCACATTTTATATATGCTGTCATGCCAAAA<br>AAA                                                                                                 |

FIG. 7-13

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|    |                               |                                          |       |                                                                                                                                                                                                                                       |    |                                                                                                                                                                                                                                                    |
|----|-------------------------------|------------------------------------------|-------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 54 | ADXCRA<br>G_BC062<br>348_s_at | AL136419.1<br>(Clone_based_ensembl_gene) | Sense | Full-length cDNA clone<br>CS0DF029YN24 of<br>Fetal brain of Homo<br>sapiens (human)<br>Fragment<br>[Source:UniProtKB/TrE<br>MBL;Acc:Q86U40]                                                                                           | 54 | ACCTGTCCCTGTCCTACCTTAACTGATCAATCGACCTTG<br>TGACAGTCTTCTTCTGGACAATGGGTCTTATCATCTCCCC<br>CACCATGTACCTTGTGAC                                                                                                                                          |
| 55 | ADXCRA<br>D.2239.C1<br>_s_at  | SLC2A14 ///<br>SLC2A3                    | Sense | solute carrier family 2<br>(facilitated glucose<br>transporter), member<br>14 [Source:HGNC<br>Symbol;Acc:18301] ///<br>solute carrier family 2<br>(facilitated glucose<br>transporter), member 3<br>[Source:HGNC<br>Symbol;Acc:11007] | 55 | TAGACAGTATGAGTCAATGTGCAGTGTAGCCCCACACTT<br>GAGAGGATGAATGTATGTGCACCTGTCACTTTGCTCTGG<br>GTGGAAGTACGTTATTGTTGACTTATTTCTCTGTGTTTG<br>TTCTACAGCCCCCTTTTCATATGTTGCTCAGTCTCCCT<br>TTCCCTTCTTGGTGCTTACACATCTCAGACCCCTTAGCC<br>AAACCCCTTG                   |
| 56 | ADXCRA<br>D.8017.C1<br>_x_at  | GSTO2                                    | Sense | glutathione S-<br>transferase omega 2<br>[Source:HGNC<br>Symbol;Acc:23064]                                                                                                                                                            | 56 | AAGACCTACTATCTGATAGCCCCACATGGTGACTATAGT<br>AAATAATAACTTAAATTGCACATTTAAAAATAACTTAAACA<br>GTGTAATTGGGTGTTTGTAAATTGAAAGGATAAATGCTT<br>GGGGAGTGGATACCCCATCTCCATGATGTGCTTATT<br>GCATACTGCATGCCTGGACCAAAATATGTACCCCATAAA<br>TATATACACCTACTATGTGCCCCCGAAA |

FIG. 7-14

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|    |                               |          |                           |                                                                              |    |                                                                                                                                                                                                                                                                    |
|----|-------------------------------|----------|---------------------------|------------------------------------------------------------------------------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 57 | ADXCRA<br>D_BF1971<br>18_at   | N/A      | No<br>Transcript<br>match | N/A                                                                          | 57 | GAATTTGGTTTTGATCTCCCTATTGAGAGACTGGTGATC<br>AGTATTTGTCTATCCCTGCACAAATTTAAGCAAGTTT<br>TGCCATTCTGTTATCCTTCCTCATGAATATCTTGATTACT<br>TTTGGCCCTAACTCATCAAGTTCACAGAAATCCCAATT<br>GGAATCTTAGTTAAAAATTGTGTGTCTATGGACCAGTTG<br>AAGAAACTGACACATTTATAATACTGACTCTGTCCATA<br>AAG |
| 58 | ADXCRA<br>D_1045.C1<br>_s_at  | FBXO45   | Sense                     | F-box protein 45<br>[Source:HGNC<br>Symbol;Acc:29148]                        | 58 | CCAGCTTTAAAGGTGAGATTGTAGAGATGCTGTCAAAG<br>GGATAAGGAAATAGCAAGATTTTAAAGTAGTGTTTTGT<br>GAAGACTGATCCCCATTTTACAACCTGCCTGTTCTTCTC<br>CAGTCCNNNNNNNNNCAGCCAGCTTGACTATTAGAAAA<br>GTATGAAACTGGTTGGGTTTATTAAATATTTTAAATATA<br>TTGAGAAGCATGGTCTG                              |
| 59 | ADXCRA<br>D_BF9617<br>33_s_at | ST7L     | AntiSense                 | suppression of<br>tumorigenicity 7 like<br>[Source:HGNC<br>Symbol;Acc:18441] | 59 | AAATTCAAATATGGAACCTTGAGGCCAAAAAACAGAAGGT<br>TACTCTCAATGCCATCC                                                                                                                                                                                                      |
| 60 | ADXCRA<br>D_CX8721<br>71_at   | C12orf47 | Sense                     | N/A                                                                          | 60 | TATGTGCCAAATCTACTAGACATTGGAGAAACAGTAGGA<br>ACAACACATGGTACCGGCACATGGATCTTTTCAGG                                                                                                                                                                                     |

FIG. 7-15

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|    |                                |       |           |                                                                                 |    |                                                                                                                                                                                                                                                                                                                  |
|----|--------------------------------|-------|-----------|---------------------------------------------------------------------------------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 61 | ADXCRH.<br>283.C1_at           | OLFM4 | AntiSense | olfactomedin 4<br>[Source:HGNC<br>Symbol;Acc:17190]                             | 61 | AGTCTGGTTCTAATCTTCTGAGCTGCCCTTTGGAAGGAAG<br>TTATGAGGTAGAAGATTCTACTGACTTTTAGTAAGGTGG<br>ACAAATGAGAGAAAAAGAAAAAGCAGGTGCCCTCATCTACA<br>GATCCTTCTGGATTATTTGCCATGTACAAATTTAATGCA<br>TAAAAAGGCCCTCTCTCCATAAAACTCAGCACCTTTACAGA<br>TGTAATATATAAGCATGCCAAATTTACTTATCTGTGCAC<br>ATACAAAGCATCATCCAGGTGCTAGTGAGG            |
| 62 | ADXCRP<br>D.15298.C<br>1_at    | GRHL2 | Sense     | grainyhead-like 2<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:2799]           | 62 | GTAGGACAGTAGGACAGTACACAGTAGAAGACAGTCTAGG<br>ACAGTTCAGAGTACACAGTAGGACAGTTCACAGTAAGA<br>CAGTTCACGGTACCCAGTAGGACAGTACACAGTAGAAC<br>AGTTCACAGTGCAANNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>AGTTCACAGTAAGACAGT |
| 63 | ADXCRSS<br>.Hs#S191<br>8752_at | DEDD  | Sense     | death effector domain<br>containing<br>[Source:HGNC<br>Symbol;Acc:2755]         | 63 | GAAAGCTGCCAGAGGGTAATTGGTTTCCCAGAAAGTTCTT<br>AAATTTGGGAGCTGTCTTGCCGCAAGCCATTGAGACTG<br>GAAATTCCTTGGAGTTGGTATTGTTTTGTAAATTGACTAA<br>TAGAGAGTTAGGGAAGCCGAGGACCTTGTGGGGTGA<br>GTTCTCTAAATGGTTTAGGCTTGCTGTGTACTTTTGCA<br>ACGAGATTGTCTAATCTATGGGCCTCTGAGGT                                                             |
| 64 | ADXCRP<br>D_BC0356<br>61_at    | SMC5  | Sense     | structural maintenance<br>of chromosomes 5<br>[Source:HGNC<br>Symbol;Acc:20465] | 64 | TTCTTGTGCATTATTACATTTACTATACCTCCAGGACAA<br>TGTTGAAGAGAAATGATGTTATTAGTCCATTTTCACACTG<br>CTATAAAGAACTGCCGTGATTAGCCTAGCATGGTGGCG<br>GACACCTGTAATCCAGCTATGCAAGAGGCTGAGACGA<br>GAA                                                                                                                                    |

FIG. 7-16

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|    |                               |          |                    |                                                                                    |    |                                                                                                                                                                                                      |
|----|-------------------------------|----------|--------------------|------------------------------------------------------------------------------------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 65 | ADXCRA<br>D_BX0966<br>75_s_at | HKR1     | Sense              | HKR1, GLI-Kruppel<br>zinc finger family<br>member [Source:HGNC<br>Symbol;Acc:4928] | 65 | AACCCAACCTTAAAGCTGAAGACAGTCCCGGCTAAATC<br>CTCATACTGAATTGAGAACCTGTCTTCCCATTGGGTG<br>CTTCCCTCCGATTGATCCCAACCTTCACCTATTTTACG<br>TATACCTGCCCTTCCCTAAATTGGTTTTTACACTGCTGTG<br>CCCACTTTTGAGTGGTGCCCTTGCATA |
| 66 | ADXCRA<br>DRC.6154<br>.C1_at  | N/A      | No Genome<br>match | N/A                                                                                | 66 | TGGTGAAATTTGTACCCCGGATGCAGTTGGCACTTT                                                                                                                                                                 |
| 67 | ADXCRA<br>D_80.C1_s<br>_at    | PLK4     | Sense              | polo-like kinase 4<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:11397]            | 67 | AAAAATGTTGGTGGGCTACACAGTTAACTAGTGGAGCT<br>GTGTGGGTTTCAGTTTAAATGATGGGTCCCAGTTGGTTGT<br>GCAGGCAGGAGTGTCTTCTATCAGTTATACCTCACCAAA<br>TGGTCAAAACAACCTAGGTATGGA                                            |
| 68 | ADXCRA<br>G_BC027<br>959_at   | LOC80054 | Sense              | Homo sapiens<br>hypothetical LOC80054<br>(LOC80054), non-<br>coding RNA.           | 68 | TTGGAGATAAGGCTTTTAGGAAGTCATTAAAGTGAGATG                                                                                                                                                              |
| 69 | ADXCRA<br>D_BQ440<br>009_s_at | FBXO45   | Sense              | F-box protein 45<br>[Source:HGNC<br>Symbol;Acc:29148]                              | 69 | CAGGTGTTTTGTTCTAGTTCTAATTTCTTAAAAACCACT<br>ACATGTTACAAAAATTGGAATAACATTTGGGACAACCTG<br>GGTTAACTACAAAGAGGAGGATTTTAAGAGGAGATGTGT<br>TGTAATTGACTCATTTTGTATTATTTTGGCTTACAGTTCC<br>CATAGCTGTAGAGTCTGG      |

FIG. 7-17

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|    |                                |                                                        |           |                                                                                                              |    |                                                                                                                                                                                                                                                                                                                      |
|----|--------------------------------|--------------------------------------------------------|-----------|--------------------------------------------------------------------------------------------------------------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 70 | ADXCRA<br>D.14045.C<br>1_at    | AL031666.1<br>(Clone_based_ensembl_gene)<br>/// ZMYND8 | AntiSense | Known long non-coding<br>RNA /// zinc finger,<br>MYND-type containing<br>8 [Source:HGNC<br>Symbol;Acc:9397]  | 70 | GGCCAATGAGAACCCAGCCTTCAAATAAACAAAGCTTCT<br>CATTGTTAACACAGGTTCAAAGCAGGAGGTTGGAG<br>GTGTTTGCAGGGTATCCAGAAATCTGATCGCTGAATAC<br>TTTAGGCAAGAGTAAGATTCCACACACCTCCCCCTAA<br>ATCTTACAATTCCCTGATGAGGCAGGAACATGGGAAAAA<br>AAAGATACAGGTTAAATTACAAAGCAGAAAAATATGCCC<br>AGCTAGAAGCTAAAGACCTGGTCTCAAAAACACTGAACC<br>GAGGAGCACTGATT |
| 71 | ADXCRA<br>G_NM_00<br>2146_s_at | HOXB3                                                  | Sense     | homeobox B3<br>[Source:HGNC<br>Symbol;Acc:5114]                                                              | 71 | CCCTGGCCTGAGAGGTGCTTTTAAGTCTCCACCCCTT<br>GTTCCATCTGCCTGCCAACCCATCGGAAAGGAATCCAC<br>ATCATATTGGAGATGACCCCATCAACCCAGGGCTCCA<br>GCACTACCAAGTTGGAATCCACGCCCGGGAGTGGGT<br>AGAGGAAGACGAGACAGGACGAGGCAGAAAAAGCACAT<br>TTTAAAAACAGACAAAGATGGCTAGGCCCATCACCAACC<br>AACGGACTTACCTTACATCTTTGTAG                                  |
| 72 | ADXCRA<br>G_BC058<br>002_at    | MORC3                                                  | Sense     | MORC family CW-type<br>zinc finger 3<br>[Source:HGNC<br>Symbol;Acc:23572]                                    | 72 | TTTTTCTATCCCTGCCATTGAGTCTCCATTAGCACTCTA<br>TTCTCTCTCATTTATTCCACCCCGTCTTCC                                                                                                                                                                                                                                            |
| 73 | ADXCRA<br>D.14007.C<br>1_s_at  | APBB2                                                  | AntiSense | amyloid beta (A4)<br>precursor protein-<br>binding, family B,<br>member 2<br>[Source:HGNC<br>Symbol;Acc:582] | 73 | GAAACACGTGTATTATGGGAACAACAGAAAGGTCAGCC<br>TGAAGACTTTTGCCCTGTTGCTTCTGAGAGTGCTGGAT<br>ATGAGTCCCTGTCTCTGAAACTTCTAAAAATATGCACCC<br>TTAACAGCTTCCACGGAGGGATAAGCCCTTTGTCAATA<br>CAAAATGGTACAGTGAGCAGCAGA                                                                                                                    |

FIG. 7-18

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|    |                               |        |           |                                                                                                                 |    |                                                                                                                                                                                                                                                                                                                                 |
|----|-------------------------------|--------|-----------|-----------------------------------------------------------------------------------------------------------------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 74 | ADXCRA<br>G_BC012<br>165_s_at | RMND5A | Sense     | required for meiotic<br>nuclear division 5<br>homolog A (S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:25850] | 74 | AGTCTGGCCCCATAGTGACTTTTGGCCCCATGATTCTGCT<br>TCACTGTTGGAATCCTCTTTGAAGTTCCCCCTCTCTTTG<br>CTAAGCAGTGAAAGGAGAGACAGAGACAAACTCTTT<br>GGACTGTGAAAGAGAGAGTAGAGAAATCCAGGCAACAG<br>TCTGACCAAGGGTGTAAACCAG                                                                                                                                 |
| 75 | ADXCRA<br>G_AF1099<br>07_at   | NUMB   | AntiSense | numb homolog<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:8060]                                                | 75 | GGAGGGGAGATACACATATATAATTAATAAAAAATGT<br>CATCTTCCACAGAAAACACTGACTCTGCCTTCCAAAAGT<br>CACAAGTACAGATGGAGTCCAAGTTCAGGAGTGTGCC<br>CAAAACCAGATACTCAAAACCAAACTGCAGAAACATTGAG<br>GAAAAACAAGCCAAAGCCATTATTTTAGAAACACAACG<br>CAAAACAATAAGATAAAATTAAGTAAAAGGGAAGTAACA<br>GATGGAATAAAAACCAAGATATCACATTCCATAAAGGGC<br>AA                     |
| 76 | ADXCRA<br>D.9554.C1<br>_at    | ZHX2   | AntiSense | zinc fingers and<br>homeoboxes 2<br>[Source:HGNC<br>Symbol;Acc:18513]                                           | 76 | GTGGTGGTTATCGACAGGAATCTGTCAGAGAGCATACC<br>CATGGAGCATTTATAATTGGAGCCATTCCAGAATTCTG<br>GTTTGCATACAACCTTTTAAAAAGCCAGCTACCCGTAAA<br>TGTAACACTATCTGAGCTCTGCCCTTGCCTGTGATGAGTG<br>ATGTTGGTCCCTGCCCTTAGTTCTGCTCTCAGTCTCCAC<br>CATCGGCTTCTCAGATTTTCCCTCCAGGACCAGCAGGC<br>AGGTGGGTGTGGTGACTTTTGTGGCAGACACTGTGGCAG<br>ATTAAAGGTGGTTGCAAAAT |

FIG. 7-19

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|    |                                |        |       |                                                                                                                                                 |    |                                                                                                                                                                                                                                                                                                                          |
|----|--------------------------------|--------|-------|-------------------------------------------------------------------------------------------------------------------------------------------------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 77 | ADXCRA<br>DRC.1009<br>0.C1_at  | ELOVL5 | Sense | ELOVL family member<br>5, elongation of long<br>chain fatty acids<br>(FEN1/Elo2,<br>SUR4/Elo3-like, yeast)<br>[Source:HGNC<br>Symbol;Acc:21308] | 77 | ACCACCTGAAGGACCACACAGAATGGGTCCATGGTGCT<br>GTGAATGGACACACCAACAGCTTTTCACCCCTGGAAAA<br>CAATGTGAAGCCCAAGGAAGCTGCGGAAGGATGGAAGTC<br>AAAGAAATTGAAACCCCTCCAACACCGTCATCTGATTGTA<br>AGCACAATATGAGTTGTGCCCCAATGCTCGTTAACAGCT<br>GCTGTAACCTAGTCTGGCCTACAATAGTGTGATTCATGTA<br>GGACTTCTTTC                                            |
| 78 | ADXCRA<br>G_AF3502<br>51_s_at  | USP32  | Sense | ubiquitin specific<br>peptidase 32<br>[Source:HGNC<br>Symbol;Acc:19143]                                                                         | 78 | CTTGTAGCTGACATTTGGCAAAAAGCGTCACTGAAAAGGC<br>AAGCTAAATGTAGTTATTTTATCCTGTGGCCCTGAAAGCA<br>CAAAATAAAAAAT                                                                                                                                                                                                                    |
| 79 | ADXCRIH<br>RC.3651.<br>C1_s_at | TRIM31 | Sense | Tripartite motif-<br>containing 31<br>[Source:HGNC<br>Symbol;Acc:16289]                                                                         | 79 | GTTTACCGAAGGCACCAGTTCAGCCAGGAGTGAAATCC<br>GGAGAGGAGCAACGCCAGCCTGGGTCCAGTCCATCA<br>AACCCCATGAGCCCGACCACTCTCGCTCTTCCCTTACATT<br>CCCACGTCCCCCTTCTCTCCCAACCCCTCATATCAGCA<br>AGGGAAATTAATTAATGAGATTTGATAAATCAGTAGATA<br>GAATGAGGTCCCCCTTTTGAATAATTTAGCAGACTGGAA<br>CCCCCCCGCAAGCCTCTGTAGGGGGTGGATGGAGACA<br>CTTCTAACTTTAATAAA |

FIG. 7-20

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|    |                              |         |           |                                                                                                                                                                                                                                                                                                |    |                                                                                                                                                                                                                                                              |
|----|------------------------------|---------|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 80 | ADXCRIH.<br>1405.C1_s<br>_at | CFB     | Sense     | Complement factor B<br>Precursor (EC<br>3.4.21.47)(C3/C5<br>convertase)(Properdin<br>factor B)(Glycine-rich<br>beta<br>glycoprotein)(GBG)(PB<br>F2) [Contains<br>Complement factor B<br>Ba<br>fragment; Complement<br>factor B Bb fragment]<br>[Source: UniProtKB/Swi<br>ss-Prot; Acc: P00751] | 80 | CTGGAGGAGTGAGTCCCTATGCTGACCCCCAATACTTGC<br>AGAGGTGA                                                                                                                                                                                                          |
| 81 | ADXCRIH.<br>1405.C1_s<br>_at | ARHGEF1 | AntiSense | Rho guanine nucleotide<br>exchange factor (GEF)<br>1 [Source: HGNC<br>Symbol; Acc: 681]                                                                                                                                                                                                        | 81 | GCATTACACATGTGCATGCTCACACAGAGACGGTTCT<br>GGAGTTGTGGAGGAAAGCCTGCCCCGCCCTCCGGCCCC<br>CACTCCCTGAACCTACAGCTCTCTCCATGGCCCCCCTC<br>ACCTGCTCGGGCTGGGCCGGGGCTTAGGGCGAGAGGC<br>AGGGCAGGGACTTTCAGGGATCCGGCAGTCTCAGTG<br>ATGAGAGCACACCAGCTGGGAGAAAGGCCAAATCCCT<br>GGGCA |

FIG. 7-21

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|    |                              |       |           |                                                                                     |    |                                                                                                                                                                                                                                                                                                                        |
|----|------------------------------|-------|-----------|-------------------------------------------------------------------------------------|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 82 | ADXCRA<br>D.2812.C1<br>_x_at | CCND2 | AntiSense | cyclin D2<br>[Source:HGNC<br>Symbol;Acc:1583]                                       | 82 | AGGATTCCTTCTTGTTTAAGCAGGAGCAGCAGAAA<br>AGCCTAACACCCCGCTCTTTCCCATCGGCAGCCCCAC<br>GCCCATCATCACAAAGGCCCAAGGATGGGAAAGAGA<br>AAAGCTAGAAAGGACCCAGGGGCTCGGGACTACAGGA<br>AGAGTGGAAGTTACAGACTGTAAATAGAGTCGGGTAG<br>GCTTGCCCTTCTTATTGTCGGTCTTTTCATTGCT<br>GCTTCTGTTTAAGCTCAAGGTCAGTCACCATGAAATGA<br>ATTGCACCTCGGTTTCTCTTAGGCTCCA |
| 83 | ADXCRA<br>G_X56774<br>_x_at  | IGF1  | Sense     | insulin-like growth<br>factor 1 (somatomedin<br>C) [Source:HGNC<br>Symbol;Acc:5464] | 83 | CTCAGAGAAGAAAGGTTGCCAAAGACACATCCAGGA<br>GGGGAACAGAGGAGGGGACAGAGCAAGTCTGCAGA<br>TCAGAGGAAAGAAAGAGAGCAGAGGGGAGATTGG<br>AAGTAGAAATGCTGAATGCAGAGGCAAAAAAGGAAAT<br>GAAGGACAGGAGGATTAAACAGACAGAGGCAAGGATGA<br>TGAGAGGAGCAGACAGCAAGAATGAAAAGCAGAAAA<br>TACAATAGAGGAAATGAAGAAAAGTAGGCCTGCTGGAG<br>CTAGATGATGATGT               |
| 84 | ADXCRIH.<br>1727.C1_s<br>_at | FLNB  | Sense     | filamin B, beta<br>[Source:HGNC<br>Symbol;Acc:3755]                                 | 84 | GGCCCCATGGATTAAACGCCCTCATCCCAAGGTCCGTCC<br>CATGACATAACACTCCACACCCGCCCCAGCCAACTTCA<br>TGGGTCACCTTTTCTGGAAAATAATGATCTGTACAGACA<br>GGACAGAAATGAAACTCCTGGGCTCTTTGGCCTGAAAG<br>TTGGGAATGGTGGGAGAGAGGAGCAGCCTTATTGG<br>TGGTCTTTTCACCATTTGGCAGAAACAG                                                                          |

FIG. 7-22

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|    |                                |                      |           |                                                                                                                                                      |    |                                                                                                                                                                                                                                             |
|----|--------------------------------|----------------------|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 85 | ADXCRA<br>D_BC0178<br>96_x_at  | ARL17A ///<br>ARL17B | AntiSense | ADP-ribosylation factor-<br>like 17A [Source:HGNC<br>Symbol;Acc:24096] ///<br>ADP-ribosylation factor-<br>like 17B [Source:HGNC<br>Symbol;Acc:32387] | 85 | GGGAAACTCTGTCACTACTGAAATACAAAAAGTACAAAA<br>AAAAAAAATAATTAGCTGGGATGGTGGTCAAGCCT<br>ATACTCCAGCTACTCAGGAGGCTGAATTTGGAGGATC<br>CCTTGAGCCCCAGGGGGTTGAGGCTGCATTGAGGTATA<br>ATTTGCCACTGTATTTCAGCCTGGG                                              |
| 86 | ADXCRA<br>D_BP2959<br>13_s_at  | CTSD                 | Sense     | cathepsin D<br>[Source:HGNC<br>Symbol;Acc:2529]                                                                                                      | 86 | GGCTCTGCCACCCCTACCTGTTCAAGTGTCCTCCGGCCCCGT<br>TGAGGATGAGGCCCGCTAGAGGCCCTGAGGATGAGCTGG<br>AAGAGTGAGAGGGGACAAAACCCACCTTGTGGAGCC<br>TGCAGGTGTGTGCTGGGACTGAGCCAGTCCCAG                                                                          |
| 87 | ADXCRA<br>D_2812.C1<br>_at     | CCND2                | AntiSense | cyclin D2<br>[Source:HGNC<br>Symbol;Acc:1583]                                                                                                        | 87 | GGGCCTCGGGACTACAGGAAGAGTGGAAAGTTACAGA<br>CTGTAAATAGAGTCGGTAGGCTTGTGCCCTTCCTTATT<br>TGTCGGGTCTTTCATTTGCTGCTGCTGTTTAAAGCTCAA<br>GGTCAGTCACCATGAAATGAATTTGCACCTCGGTTTCT<br>CTTAGGCTCCA                                                         |
| 88 | ADXCRA<br>D_NM_01<br>4630_s_at | ZNF592               | Sense     | zinc finger protein 592<br>[Source:HGNC<br>Symbol;Acc:28986]                                                                                         | 88 | GAGAGCTCTGCCTAGTCTGGTTTGGCGAGGGCCCTTGA<br>TCACCTTGCCCCCTCCTCCCTGTCTCTCTGATTCTTTTC<br>CCTCAAAATAGTCCTGAGAACTAATTGTCACAGACATTG<br>GAATATTTGACTGCTCTCGTGCCATTTGAGAGGCTGCT<br>GCCCCAGGCAGGCCAGCCCCCTACTCTCTTGGCTACAC<br>TCATGTTGCTCAGACTATATTCA |

FIG. 7-23

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|    |                                |                                                          |           |                                                                                                               |    |                                                                                                                                                                                                                                        |
|----|--------------------------------|----------------------------------------------------------|-----------|---------------------------------------------------------------------------------------------------------------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 89 | ADXCRA<br>DRC.3108<br>.C1_s_at | APOE                                                     | Sense     | apolipoprotein E<br>[Source:HGNC<br>Symbol;Acc:613]                                                           | 89 | CTGGAACTGGCACTGGGTGCGCTTTGGGATTACCTGC<br>GCTGGTGCAGACACTGTCTGAGCAGGTGCAGGAGGA<br>GCTGCTCAGCTCCCAGGTCAACCAGGAAGTGAAGGCG<br>CTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAA<br>ATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAG<br>GAGACGGGGCACGGCTGTCCAAG |
| 90 | ADXCRA<br>G_BC062<br>632_s_at  | LRR37B2 ///<br>AC005562.3<br>(Clone_based_<br>vega_gene) | AntiSense | leucine rich repeat<br>containing 37, member<br>B2 [Source:HGNC<br>Symbol;Acc:25390] ///<br>Known pseudogene. | 90 | GATGAAGAGGGCTGATTGTATCTAAGTCTAGGCTCTTGC<br>TGCAGCTGGCACTTAATGCATTTTATTGACTGTTTTAGC<br>TAACATTCAATGGACA                                                                                                                                 |
| 91 | ADXCRA<br>G_BC016<br>467_s_at  | FKBP10                                                   | Sense     | FK506 binding protein<br>10, 65 kDa<br>[Source:HGNC<br>Symbol;Acc:18169]                                      | 91 | GCCAGACTGGGCTGTAGTTAGCTTTTCATCCCTAAAGAA<br>GGCTTTCCCTAAGGAACCATAGAGAGAGAGGAGAAAC<br>AAAGGCATGTGTGAGGGAAGCTGCTTGGGTGGTGTT<br>AGGGCTATGAAATCTTGGATTGGGGCTGAGGGGTGGG<br>AGGAGGGCAGAGCTCTGCACACTCAAAGGCTAAACTG<br>GTGTCA                   |
| 92 | ADXCRA<br>D.10820.C<br>1_at    | NOL8                                                     | Sense     | nucleolar protein 8<br>[Source:HGNC<br>Symbol;Acc:23387]                                                      | 92 | AAGCTGAGAAACTACCTGAGGTGTCTAAAGAAATGTATT                                                                                                                                                                                                |

FIG. 7-24

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|    |                               |         |           |                                                                                                        |    |                                                                                                                                                                                                                                                                                   |
|----|-------------------------------|---------|-----------|--------------------------------------------------------------------------------------------------------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 93 | ADXCRA<br>D_AI8625<br>59_x_at | ANGPTL6 | Sense     | angiopoietin-like 6<br>[Source:HGNC<br>Symbol;Acc:23140]                                               | 93 | GGAATTAAGGCTATTACTCTGAAGAAAGTTGGGGGCC<br>AGGGCTCCTATTTTTTCTGCTGAGGAGATGGAAGATCAG<br>GGCTTGATTCAATAAGAAATGGAGGGGCCAGGGGATG<br>CCTGGCAAAAGCCTTGCACTGTGAGGTGCAGGTAGAGG<br>CTTTTATTCTGGTGAGAGGACATGGACTCTCTCTCTCCC<br>CTCAGGTAACCTGTGCCCTGTA                                          |
| 94 | ADXCRA<br>D_3248.C1<br>_at    | SLCO4A1 | Sense     | solute carrier organic<br>anion transporter<br>family, member 4A1<br>[Source:HGNC<br>Symbol;Acc:10953] | 94 | ACTCCGCAGGGGCTGTGAATCCCACCTGGGAGGGGGGC<br>GGCCTGCAGCCCCGAGGAAGGCTTGTGTCTCCTCAGTT<br>AAACTGTGCATATCGAAATATATTTTGT                                                                                                                                                                  |
| 95 | ADXCRA<br>Hs#S300<br>2165_at  | SAMD4B  | AntiSense | sterile alpha motif<br>domain containing 4B<br>[Source:HGNC<br>Symbol;Acc:25492]                       | 95 | GGAGTTCTACGGGATCTGAGAGAAAAACCATGAGGAAA<br>GTTTTCAGGATCCTTAAACAAATTTTGGAGCGTGTGATG<br>TGGGGGACTGGAAAAAGATGTGGAGTATGTAAAAAGGAT<br>TTTGGAAAGAGCTTTTGAATATGATGCTGAGAGTCCTC<br>TGGAGATTTTCAGGCAATTGCTGGAGATTTTGAATGAG<br>TGGGGGTGGGGAAGGGGATCCCGGTGAAGATCACTGG<br>GCTACATGAGGTGATCTCTA |
| 96 | ADXCRA<br>D_CN408<br>490_x_at | CHAF1A  | Sense     | chromatin assembly<br>factor 1, subunit A<br>(p150) [Source:HGNC<br>Symbol;Acc:1910]                   | 96 | GGAGCGGCGCAAGGAGAGACAGGAAGCCCTGGAGGCT<br>AAACTTGAGGAAAAAAGGAAAAAGGAAGAAAGAGAAACG<br>GTTAAGAGAAGAAAGAGAGCGCATTAAGCAGAGAAGG<br>CCGAAATCACGAGGTTCTTCCAGAAAAACCAAGACTCCA<br>CAGG                                                                                                      |

FIG. 7-25

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|     |                                |          |       |                                                                                          |     |                                                                                                                                                                                                                                       |
|-----|--------------------------------|----------|-------|------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 97  | ADXCRA<br>D_CX8671<br>37_s_at  | TMEM97   | Sense | transmembrane protein<br>97 [Source:HGNC<br>Symbol;Acc:28106]                            | 97  | TTAATTTTCATGTTGGGAGCCCCCTACTACAAGTATGAA<br>GAGAAAAGAAAAAATGAAGGAAACAACCACTGGC<br>CCAGGGTAGAGATGCCACAGGGTGGTTGTTGGA<br>TACAATACAAGGAACACTGCTCAGAACCCACGCTTCA<br>GCAGCATTGAAACACTGGCAGCAATGCACAAGAGCAA<br>GATGTGTCAGGAACCATGTCAAACCCCTC |
| 98  | ADXCRA<br>D_CX7847<br>58_s_at  | PTK2     | Sense | PTK2 protein tyrosine<br>kinase 2<br>[Source:HGNC<br>Symbol;Acc:9611]                    | 98  | TAAGCTTTTAAGCATCATGAAGAACAATTTATGTTACAT<br>TAAGATACGTTCTAAAGGGGATGCCAAGGGGTGACA<br>TCTTAATTCCTAAACTACCTTAGCTGCATAGTGAAGAG<br>GA                                                                                                       |
| 99  | ADXCRA<br>D_6429.C1<br>_s_at   | SULT2B1  | Sense | sulfotransferase family,<br>cytosolic, 2B, member<br>1 [Source:HGNC<br>Symbol;Acc:11459] | 99  | GCCTGGAGCGTGAGCCAGACCCAACTCCAGCCCCAG<br>CCCCAGCCCCGGCCAGGCCTCTGAGACCCCCGACCCCA<br>CGACCTCATATAAACAACGTCGATTCTG                                                                                                                        |
| 100 | ADXCRA<br>D_CX8721<br>71_x_at  | C12orf47 | Sense | N/A                                                                                      | 100 | TATGTGCCAAATCTACTAGACATTGGAGAAACAGTAGGA<br>ACAACACATGTTACCGGCACATGGATCTTTCAGGAAAA<br>CGAAGTAGGTAAATAAACAGGAAAAAGCCCCGAGTCTGAT<br>GCTAAGA                                                                                              |
| 101 | ADXCRA<br>D_NM_02<br>2064_s_at | RNF123   | Sense | ring finger protein 123<br>[Source:HGNC<br>Symbol;Acc:21148]                             | 101 | CTGCCCTGTATCCTCATTGGTGGGAGCCCCAGCCATGGCC<br>CTAATTGTGCCCTGAGCTTGACTTTCAGTCAGGGCCACA<br>GTGAGCATTAATATT                                                                                                                                |
| 102 | ADXCRIH.<br>3995.C1_s<br>_at   | TRIM5    | Sense | tripartite motif-<br>containing 5<br>[Source:HGNC<br>Symbol;Acc:16276]                   | 102 | GGAGTTAAATGATAGTGCTTTCAGGATAGTTCCTTCCAT<br>ACTCCTTCTGTCTTCTTCATTGTGCCCTCT                                                                                                                                                             |

FIG. 7-26

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|     |                               |       |       |                                                                                    |     |                                                                                                                                                                                                                                                                                                                                |
|-----|-------------------------------|-------|-------|------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 103 | ADXCRA<br>G_U91543<br>_s_at   | CHD3  | Sense | chromodomain helicase<br>DNA binding protein 3<br>[Source:HGNC<br>Symbol;Acc:1918] | 103 | CAGCCGTTCCCTGCAGAAATCAGCTCTGTCTCATGTGG<br>AAGTGGAGAATCAGCCTTGCCCTTTAGGAACTTTT<br>GTGGGAAGAGAGCTTTGAAGAGAGGAGGGGACTTT<br>AGAGAGGATGAAAATGAGCCCTGGAGGGAGGAAGG<br>GACGAGGAGGGGTGGCTGCATGTTACCGTCCCCTACCT<br>CTCCCCACGTGGAGGGTGGAGCAGTTATGAGGGAGGA<br>AGTCAACTGCTG                                                                 |
| 104 | ADXCRA<br>D_4213.C1<br>_x_at  | APOL6 | Sense | apolipoprotein L, 6<br>[Source:HGNC<br>Symbol;Acc:14870]                           | 104 | CAGGCATTCCCTTCTATCGATAAATTACTCTTTCAACCAAT<br>TGCCAATCAGAAAAATTGTTATATCTACCTATAATCTAGAA<br>GCCCCACATCAAGTTGTTTGCCTTTCIGGACAGGAC<br>CAATGTATATCTTAAATGTATTTGATTGATCTCTCATGTC<br>TCCCTAAATGTATAAAACCACGCTGTTCCCGGACCACC<br>TGGAGCACATGTTCTCAGGGTCTCCTGAGGGCTGTGTC<br>ACAGGCCATGTTCACTTACATTTGGCTCAGAAATA                          |
| 105 | ADXCRA<br>D_BE2959<br>38_x_at | RBBP4 | Sense | retinoblastoma binding<br>protein 4<br>[Source:HGNC<br>Symbol;Acc:9887]            | 105 | GGGTCAGAAAGATGCCCTTCAGTTTTGGTCAGTGTCTAAA<br>AGTTAAGTCTGTTTAGGCCAAGCATGGTGGCTCACGCC<br>TGAAATCCCAGCACTTGGGAGGCCGAGGCAAGTGGA<br>TCACAAAGTCAGGAGATGAGACCATCTTAGCCCAACATG<br>GTGAACCCCGTCTCTACTAAAAATACAAAAAATTAGCC<br>AGGCGTGGGGTGGCTGCCTATAATCCCAGCTACTTGG<br>GAGGCTGAGGCAGGGGAATCGCTTGAACNCGGAGGC<br>AGAGGTCACGCCCATGGACTCCAGCC |

FIG. 7-27

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|     |                                 |       |           |                                                                                                              |     |                                                                                                                                                                                                                                                                                              |
|-----|---------------------------------|-------|-----------|--------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 106 | ADXCRA<br>D_NM_02<br>1651_at    | EIF3K | Sense     | eukaryotic translation<br>initiation factor 3,<br>subunit K<br>[Source:HGNC<br>Symbol;Acc:24656]             | 106 | CGCACCATTGCACTAGTGATAAGATCGAAACTCCAT                                                                                                                                                                                                                                                         |
| 107 | ADXCRA<br>G_AJ4205<br>36_at     | TPBG  | Sense     | trophoblast glycoprotein<br>[Source:HGNC<br>Symbol;Acc:12004]                                                | 107 | TTTGAATCACCATGTCTGATAAAACATGCAATTGCTTT<br>GGTGAATTTGTTGTTTATTGTTGTTGCTTTGAGTGAAT<br>GCTTCAGTTTGCTCTAGATTTTACTTTGTTGTAAAAAT<br>TACCATGTTTTAACCCCGAAAAACATTTAATGTTTTTGAA<br>ATGATTTTTTCATAACAATCTTATGAGTCTATTATAATA<br>GGAAGTATTTTGGAAATTTAATGGTGATATTCTTTGGAA<br>AA                           |
| 108 | ADXCRESS<br>.Hs#S191<br>8491_at | AXIN2 | AntiSense | axin 2 [Source:HGNC<br>Symbol;Acc:904]                                                                       | 108 | TGTGCACAGGAGACTCAGGACAGTGGGGGGAAAAAGTC<br>ACTTCTCCACATAAGAGGCTCAATCCCAACGCCACCC<br>TCCGTCAGACCCCTTTGGCCCCCAGCTCCGACCCCTCCA<br>GGGTTTACCAAGTTGGGCTTTTACAGCATGTCTGAGCA<br>AACACGCAGCGACCTTTTACATAATTGCAACCTCCTCCA<br>GAGAGGAGAGAGGCCACATTCTCTCGGCC                                             |
| 109 | ADXCRA<br>D_BM702<br>062_at     | TSKU  | Sense     | tsukushi small leucine<br>rich proteoglycan<br>homolog (Xenopus<br>laevis) [Source:HGNC<br>Symbol;Acc:28850] | 109 | TAACGGAGTGTCACTTTCAACCGGCCTCCCTACCCCT<br>GCTGGCCGGGGATGGAGACATGTCATTTGTAAAGCAG<br>AAAAAGTTGCATTTGTTCACTTTTGTAAATATTGTCCTGN<br>GCCTGTGTGGGGTGTGGGGGAAGCTGGGCATCAGT<br>GGCCACATGGGCATCAGGGGCTGCCCCCAGAGACC<br>CCACAGGGCAGTGAGCTCTGTCTTCCCCCACCCTGCCTA<br>GCCCATCATCTATCTAACCGGGTCTCTTGATTAAATA |

FIG. 7-28

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|     |                                |        |           |                                                                                  |     |                                                                                                                                                                                                                                                                                                                     |
|-----|--------------------------------|--------|-----------|----------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 110 | ADXCRRS<br>.Hs#S373<br>0315_at | MUC6   | Sense     | mucin 6, oligomeric<br>mucus/gel-forming<br>[Source:HGNC<br>Symbol;Acc:7517]     | 110 | CATGCACAGATGGCCACATTCTGCCTCCATCCACTCAAT<br>GCCAACAGGACGATTCTCCACCGACACACGCTCAAGG<br>CCACAGGGTCCACCCACACAGCGCCCAACAATGACGCT<br>GACCACAGCGGGACAGCCAGCCCTGAGCTCATTA<br>ACACAGCCAAAACCTCTACATCCCTACATTACACACTT<br>CCTCCACACACCATGCTGAAGCCACCTCAACTTCTACC<br>ACCAACATCACCCCAACCCACCAGTACAGGAACCCC<br>ACCAATGACAG         |
| 111 | ADXCRA<br>D_BM142<br>126_s_at  | SAMD4B | Sense     | sterile alpha motif<br>domain containing 4B<br>[Source:HGNC<br>Symbol;Acc:25492] | 111 | CCCCATTATGTCATGACCTCACTTAAGTGGAACTATA<br>TCATAACCCAGAGATTCTGTCGCCAGCCCCAGAGTCCGAC<br>AGACTGTCTGGTCCCTATTCTTAATGAGGG                                                                                                                                                                                                 |
| 112 | ADXCRRP<br>D.9207.C1<br>_s_at  | MUC3A  | AntiSense | mucin 3A, cell surface<br>associated<br>[Source:HGNC<br>Symbol;Acc:13384]        | 112 | CACATCTGGCCTGACGTTCTGTTGCATCAAGCCATCAT<br>CCACCGGGCGCCCTGGACGCGCGTNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNAATGCTGACCCACT<br>CAGTAGAGCAGGGGCCAGCCAGAGGGGACGAAGTCA<br>CCAATCCAGGCACCACCTTCCACATGTCCTGCAACT<br>TCTCTTTTCCAGTGTCTGAAGAAGGGAGGTGCCACC<br>CCTCCTCCAGATAAATGGCCCCAGAAAACGATCCAAA<br>AAATACCCAGGGAGCGATTCTTATGTA |
| 113 | ADXCRA<br>D_BM691<br>081_s_at  | ARRB2  | Sense     | arrestin, beta 2<br>[Source:HGNC<br>Symbol;Acc:712]                              | 113 | GATGATCAACTCTGCTAGGAAGCGGGTGGGAAGAAG<br>GGAGGGGATGGGTTGGAGAGGTGANGGCANGATTA<br>AGATCCCCCACTGTCAATGGGGATTGTCTCAGCCCCCTC<br>TTCCCTTCCCTCACCTGGAAGCTTCTTCAACCAATCCC<br>TTCACA                                                                                                                                          |

FIG. 7-29

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|     |                                  |         |       |                                                                                                                                                     |     |                                                                                                                                                                                                                                                                                                    |
|-----|----------------------------------|---------|-------|-----------------------------------------------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 114 | ADXCRRS<br>.Hs#S192<br>3930_s_at | IGLL5   | Sense | immunoglobulin<br>lambda-like polypeptide<br>5 [Source:HGNC<br>Symbol;Acc:38476]                                                                    | 114 | GCAGTCTCAGACACCAAGGAGGGGAGAGTGACTAGAAA<br>GAAAACCTTCTTCAGAGACATAGGGGATGGGGAAGAA<br>CTGCAGACTGAACTGGGCAAGGACTGTAGGACTTAA<br>CCAGAGAGATTTGAGGGAGAGATGAGGCTGAGAGCCA<br>GGGATCCTGCCATGTCCAGCATAAACACAGTACCTG<br>ACACAGATAGGTGCTTGGGAAGCTGTTGTCCGGATGAAT<br>GAGTGGACA                                   |
| 115 | ADXCRA<br>G_AF3957<br>51_s_at    | DCLRE1C | Sense | DNA cross-link repair<br>1C (PSO2 homolog, S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:17642]                                                   | 115 | AAGCTGGCAACTGGTGAGAGTATAGCAGTCAAAAAAAG<br>AAATGCTCACTCTTAGATACCTAAGAAATTCAAAGCGTT<br>TCAACCTAGAGCAACCCTAAACCTGACACAGAGAT<br>GACAGTCAATATTACAAATAGAG                                                                                                                                                |
| 116 | ADXCRA<br>G_AF0042<br>31_s_at    | LILRB2  | Sense | leukocyte<br>immunoglobulin-like<br>receptor, subfamily B<br>(with TM and ITIM<br>domains), member 2<br>[Source:HGNC<br>Symbol;Acc:6606]            | 116 | AGCCAGCAGATCCTACACACATTTTCACAACTAACCC<br>CAGAACAGGGCTGCAACCTATACCAA                                                                                                                                                                                                                                |
| 117 | ADXCRRP<br>DRC.1452<br>8.C1_s_at | GALNT4  | Sense | UDP-N-acetyl-alpha-D-<br>galactosamine:polypept<br>ide N-<br>acetyl/galactosaminyltra<br>nsferase 4 (GalNAc-T4)<br>[Source:HGNC<br>Symbol;Acc:4126] | 117 | TCACTTTCCTGGATTGTCACCTGTGAGTGTAATCCGGTT<br>GGCTGGAACCGCTTTTGGAAAGGATTGGGAGAGATGAA<br>ACAGCAGTTGTGTCTCTGTATAGACACAAATTGATTGG<br>AATACTTTGAATTCATATGCAGATAGGGAGGCCCATG<br>ATTGGTGGGTTTGACTGGCGTTTAGCATTTTCAGTGGCAT<br>TCTGTCCCCAACAGGAAAGGACAGGCGGATATCAAG<br>AATTGACCCCATCAGATCACCTACCATTGGCTGGAGGA |

FIG. 7-30

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|     |                               |                    |       |                                                                                                                                                    |     |                                                                                                                                                                                                                                                                                            |
|-----|-------------------------------|--------------------|-------|----------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 118 | ADXCRA<br>D_16974.C<br>1_s_at | WWC2               | Sense | WW and C2 domain<br>containing 2<br>[Source:HGNC<br>Symbol;Acc:24148]                                                                              | 118 | TAGTGTGTTTGGCCCTAAATCTAAGGATGGTGCCCTAGTGGT<br>GGCCCTGTGTTCTGAGGACAGAGAGAGCTGGAGGGGT<br>GGAGGGGAATGCATCGGCACTCATTGGTGTAACCAAG<br>AAGAGGGGGAAGATGCTTGTATAGAAATCAAAGTTGCC<br>AAAAACAAGAAAGAGTCTATCAAGCAGATTTCTAACATT<br>TAGCTAGAAACTACTTCATAGCTCTCATTTTITAG                                   |
| 119 | ADXCRA<br>D_AK0927<br>50_s_at | EHP1L1             | Sense | EH domain binding<br>protein 1-like 1<br>[Source:HGNC<br>Symbol;Acc:30682]                                                                         | 119 | CACTACCGCCCCCGCGCTGGCTTGCCCTCCTGTTCTCCA<br>GAGCAATAAAGTTGGACGAGACT                                                                                                                                                                                                                         |
| 120 | ADXCRA<br>D_CF2721<br>04_at   | HIST1H2AJ          | Sense | histone cluster 1, H2aj<br>[Source:HGNC<br>Symbol;Acc:4727]                                                                                        | 120 | GAGAGCCACCACACAAGACTAAGTAAAGACCCGAGTTGA                                                                                                                                                                                                                                                    |
| 121 | ADXCRA<br>D_1493.C1<br>_at    | TNPO1              | Sense | transportin 1<br>[Source:HGNC<br>Symbol;Acc:6401]                                                                                                  | 121 | GAATAAATGGGGTGGGCATATCAAACTAAAGATG                                                                                                                                                                                                                                                         |
| 122 | ADXCRA<br>D_BX1071<br>09_s_at | IGKJ3 ///<br>IGKJ4 | Sense | immunoglobulin kappa<br>joining 3<br>[Source:HGNC<br>Symbol;Acc:5721] ///<br>immunoglobulin kappa<br>joining 4<br>[Source:HGNC<br>Symbol;Acc:5722] | 122 | TTCTCTGCATCGGTCAGGTAGTGATATTAACAGCGAAA<br>AGAGATTTTGTGTTAGGGGAAAGTAATTAAGTTAACACT<br>GTGATCACCTTCGGCCAAAGGACACGACTGGAGATTA<br>AACGTAAGTAAATTTTTCACATATTGCTCTGAAATTTGGG<br>TCTGATGCCCAGTATTGACCTTTAGAGGCTTAAATAGGA<br>GTTTGGTAAAGATTGGTAAATGAGGGCATTAAAGATTTG<br>CCATGGGTTGCAAAAGTTAAACTCAG |

FIG. 7-31

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|     |                                |         |                           |                                                                                                             |     |                                                                                                                                                                                                                                                                                                                           |
|-----|--------------------------------|---------|---------------------------|-------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 123 | ADXCRA<br>D_AA7747<br>60_at    | EIF4G3  | Sense                     | eukaryotic translation<br>initiation factor 4<br>gamma, 3<br>[Source:HGNC<br>Symbol;Acc:3298]               | 123 | CAAAATACAAAATGCCCTCCAAGCTCAAAATAGCTATAAC<br>TGTAACCAAGACATGGAAGAAACCAAAAGATCGACCC<br>GAACCACTGAAGAGATGTTAGAGGCAGAAATTGGAGCTT<br>AAAGCTGAAGAGAGGCTTCCATTGACAAAAGTACTTGAA<br>TCTGAACAAGATAAAAATGAGCCAGGGTTTCATCCTGAA<br>AGAGACCCCTCTGACCTAAAAAAAGTGAAGCTGTGGA<br>AGAAAATGGAGAAAGAGCTGAGCCAGTACGTAATGGTG<br>CTGAGAGTGTCTCTGA |
| 124 | ADXCRA<br>G_BC010<br>540_at    | C11orf2 | Sense                     | Protein fat-free<br>homolog (Another new<br>gene 2 protein)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q9UID3] | 124 | CCGCAGGCAGGTGTCTCAGGACCGGCCCTAAATAACATGTG<br>T                                                                                                                                                                                                                                                                            |
| 125 | ADXCRESS<br>.Hs#S809<br>218_at | N/A     | No<br>Transcript<br>match | N/A                                                                                                         | 125 | AAATGTGACTGCTTTGTAAAACTCCAGAGTCAAGGACTC<br>ATAGGCAGGAGGATGTCATAAAATTAACAGGAAAGGATG<br>AGAAATCTCCACTCCACTCCCTCCCTCCCTCCCTTGATCA<br>CTCATTCCTCTCTCTCCATTTCATTAACCAACCCACTACAT<br>GCCATGCCCTAAGGAAGCAGCTATCTAAGAAAGTCCCTG<br>CCTGCAGGGGCTTTACAGACCAGGAGGAAGGCAACCC<br>ATAGAGCCAGGATCCTGTATAACCACTGCTGACTGCC                  |
| 126 | ADXCRA<br>D_AL0394<br>47_x_at  | KIF24   | Sense                     | kinesin family member<br>24 [Source:HGNC<br>Symbol;Acc:19916]                                               | 126 | AAACCTGGAGAATCTTTCACTTGAACCTCAACTTGACT<br>GGNGTTCAGTCAACCCANTCTCAGGGGAAGGGGGAAG<br>CACTATCTCCACANCANCACTNANTCTGGGCCTCCCGC<br>CCCATCTCCCCCAGCCCCCTCTCAGCAACTAGGCCAGGC<br>TTCAGCT                                                                                                                                           |

FIG. 7-32

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|     |                               |                      |           |                                                                                                               |     |                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------------|----------------------|-----------|---------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 127 | ADXCRP<br>D_8954.C1<br>_at    | CDK11A ///<br>CDC2L1 | Sense     | cyclin-dependent<br>kinase 11A<br>[Source:HGNC<br>Symbol;Acc:1729]                                            | 127 | GCAGGGCTGCCGGAGCGTCGAGGAGTTCAGTGCCTG<br>AACAGGATCGAGGAGGGCACCTATGGAGTGGTCTACAG<br>AGCAAAAGACAAAGAAACAGATGAAATTGTGGCTCTAAA<br>GCGGCTGAAGATGGAGAAGGAGAAGGAGGGCTTCCCG<br>ATCACGTCGCTGAGGGAGATCAACACCATCCTCAAGGC<br>CCAGCATCCCAACATCGTCACCGTTAGAGAGATTGTGG<br>TGGGCACACATTATGGAGGCGCAGTCGCCCTACGCA   |
| 128 | ADXCRSS<br>Hs#S301<br>0175_at | CDS2                 | Sense     | CDP-diacylglycerol<br>synthase<br>(phosphatidate<br>cytidyltransferase) 2<br>[Source:HGNC<br>Symbol;Acc:1801] | 128 | AGGAGTCAGGAGAACAAAGTCAGGGATTAGGAGACAGC<br>GGTTTGGTTTATTGTTATCCAG                                                                                                                                                                                                                                 |
| 129 | ADXCRA<br>D_AW297<br>731_at   | PARP14               | AntiSense | poly (ADP-ribose)<br>polymerase family,<br>member 14<br>[Source:HGNC<br>Symbol;Acc:29232]                     | 129 | AATAATTCTCAATTTCTTAGTCTCTTAATTTCTTAAATTTAA<br>AAAGGTTGTTTCTTACC TTTTAAATTTTAAAAATAATTA<br>TGTCAAAGTAATTTTGAATATAGTAACCTGATTCTACATT<br>TCTCATGGGATAAATTCTAAGGTAAAAAAATTGCAATA<br>AATCTTAAACTTTTATTAGTAGGTTTATTATTAGCAGCAG<br>ATGTCTAGCCAGGGTAGATTACTTTTATCAGACCAACCT<br>CTACCAACAAC TACTAGAGAGCTA |

FIG. 7-33

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|     |                                   |       |                    |                                                                                                                                   |     |                                                                                                                                                                                                                                                                                                                        |
|-----|-----------------------------------|-------|--------------------|-----------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 130 | ADXCRA<br>D_AU1464<br>90_at       | TAF15 | Sense              | TAF15 RNA<br>polymerase II, TATA<br>box binding protein<br>(TBP)-associated<br>factor, 68kDa<br>[Source:HGNC<br>Symbol;Acc:11547] | 130 | CTGGGAAATCCAGTGTTTGTATGTAAAAATAAAGGTAA<br>GTTAATTCTAGATTGAGGGCAGAGGCTATTTCTTAATC<br>TCCAATCTCCTTGGGAAGGAAAGTATTAGGAGGCAGT<br>AATGAGTAGAAA                                                                                                                                                                              |
| 131 | ADXCRESS<br>.Hs#S298<br>1341_at   | N/A   | No Genome<br>match | N/A                                                                                                                               | 131 | GGTACACTGGGCACGCAATCGCGTGTTAGTAGCCAAA<br>TAGTAAAAGGGCCGATTTCAACAGCGACTCCAAGACA<br>ACTGGCGTTGCCATTCTCAGTCTCCGGCCTATCCTAC<br>ACATCTAATACCCGGCTACAATAAAGCTATAGTAAAG<br>GTTACAGGGGCTCTTTTCGTCCCGTTGCGGGTAATCGGC<br>ATCTTACCGGATACATAATTTACCGAGCTCGCGGTTG<br>AGACAGTGCCCGAGATCGTTACACCATTCGTGTATGGAC<br>GGGCTCTG            |
| 132 | ADXCRA<br>G_NM_00<br>1988_at      | EVPL  | Sense              | envoplakin<br>[Source:HGNC<br>Symbol;Acc:3503]                                                                                    | 132 | GGACAGCAGCCACTCAGTTCTTCTCCACCTCCACCCA<br>GTGATCCCCAATAAACGGAATTCTGTCTCCCCCGTG                                                                                                                                                                                                                                          |
| 133 | ADXCRESS<br>.Hs#S373<br>0315_x_at | MUC6  | Sense              | mucin 6, oligomeric<br>mucus/gel-forming<br>[Source:HGNC<br>Symbol;Acc:7517]                                                      | 133 | ACAGATGGCCACATTCTGCCCTCCATCCACTCAATGCCA<br>ACAGGCACGATTCTCTCCACCGACAACGCTCAAGGCCAC<br>AGGTCACCCACACAGCGCCCAACAATGACGCTGACCA<br>CCAGCGGGACCAGCCAAAGCCCTGAGCTCATTAAACACA<br>GCCAAAACCTCTACATCCCTACATTACACACTTCTCTCC<br>ACACACCATGCTGAAGCCACCTCAACTTCTACCACCAA<br>CATCACCCCCAAACCCACCAAGTACAGGAACCCCAACCA<br>TGACAGTGACCA |

FIG. 7-34

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|     |                               |                                                       |       |                                                                                                             |     |                                                                                                                                                                                                                                                                                                                          |
|-----|-------------------------------|-------------------------------------------------------|-------|-------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 134 | ADXCRA<br>D_CN312<br>224_s_at | RPL32P3                                               | Sense | ribosomal protein L32<br>pseudogene 3<br>[Source:HGNC<br>Symbol;Acc:27024]                                  | 134 | TAGTACCTGCCTCATTAGCTAACGTGAGGATCTAGAG<br>CAGCATTTCATATAATGACGCGTGGGCACAGACAGAGA<br>CTCAACACAGAGAGCTTACGTTATGAGGCTTGGCAGG<br>CTGGAGCTCCTGTGGCCTCTCTCCTCAGCTCTGTGC<br>CCTGAGCTCGGCACAAAGGTTGGCCCATGACAGGT<br>GTTATTATGTGGAATAAATGAGAGGGACAAAGACATTT<br>GCTGATTTC                                                           |
| 135 | ADXCRA<br>D_CN312<br>224_s_at | AL031666.1<br>(Clone-based<br>(Ensembl) ///<br>ZMYND8 | Sense | Known long non-coding<br>RNA /// zinc finger,<br>MYND-type containing<br>8 [Source:HGNC<br>Symbol;Acc:9397] | 135 | GCCTCATCAGGGAATTGTAAGATTTAGGGGAGGTGTG<br>GGAAATCTTACTCTTTGCCCTAAAGTATTACGCGATCAG<br>AATCTGGATACCTGCAAAACACCTCCAACTCCCTGC<br>CTTGAAACCTGTGTTAACAAATGAGAAGCTTGTTTATTT<br>GAAGGCTGGGTCTC                                                                                                                                    |
| 136 | ADXCRIH.<br>2111.C1_a<br>t    | SNHG12                                                | Sense | small nucleolar RNA,<br>H/ACA box 44<br>[Source:HGNC<br>Symbol;Acc:32637]                                   | 136 | GGACAGATGAAGACTCTTAAGATGACAGAAGGTGATTTT<br>TCTGGTATCGAGGACTTCGGGGTAATGACAGTGATG<br>AAATGCAGGGGACCTGTTGCCCCCAAGTTTCTGGCA<br>GTGTGATACTGAGGAGTGAGCTTGTCTCTGGAGCT<br>GTGCTTTAAGATTATGTTACATGTAAAGCTGTCTCATT<br>TGTGACTATGGACCTATGGAGTTGGGACAATCTCTATG<br>GGAGCAGAAAGGCAAGGACCCCGGTCATTTTAGGTAGA<br>AACAAACAGCATGCTAATGCAAAA |
| 137 | ADXCRIH.<br>3648.C2_a<br>t    | NCAPD2                                                | Sense | non-SMC condensin I<br>complex, subunit D2<br>[Source:HGNC<br>Symbol;Acc:24305]                             | 137 | AAGAGAGAAGCTTCTGCACGCCAGAGGCCACCCAGTCC<br>CACAGGGCCTACCTGCCCGGATAAGAGGTTCCCTG<br>CCATTCTCTAGTCTCCCCCTTCAACAGCACACCAAAAT<br>AAGCCCAAGAAGATGACAGGAACCGTCCCCGCCAACTT<br>CACACGAGTGCTAAGGCGAAGACAGGCCATCTTGGGCCT<br>TCGGA                                                                                                    |

FIG. 7-35

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|     |                               |        |       |                                                                                                          |     |                                                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------------|--------|-------|----------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 138 | ADXCRA<br>G_BC015<br>816_s_at | MAST2  | Sense | microtubule associated<br>serine/threonine kinase<br>2 [Source:HGNC<br>Symbol;Acc:19035]                 | 138 | TGCCCTGATGCCCTCAGGTGACAGAAAGGCAGGACGTTCCA<br>TGCCGAGGCTGCCCCCTCACCCAGAAGTCTGAGCCCCA<br>GCCTCAGGAGGGGCCAAGAACCCAGGGGCCATCAAAA<br>GCATCGGATTTGGCATTGGTTCAGATGAGCTTTTAAA<br>GCAACATAGCAGTTGTTGCCATTTCTTGCACTCAGAC<br>CTGTGTAATATA                                                                                                   |
| 139 | ADXCRA<br>D_BP2850<br>69_x_at | IFIT3  | Sense | interferon-induced<br>protein with<br>tetratricopeptide<br>repeats 3<br>[Source:HGNC<br>Symbol;Acc:5411] | 139 | GCCCCAACCTGGGATTGCTGAGCAGGGGAAGCTTTGCAT<br>GTTGCTCTAAGGTACATTTTAAAGAGTTGTTTTTTGGCC<br>GGCGGCAG                                                                                                                                                                                                                                   |
| 140 | ADXCRA<br>G_AF2740<br>48_s_at | UHRF1  | Sense | ubiquitin-like with PHD<br>and ring finger domains<br>1 [Source:HGNC<br>Symbol;Acc:12556]                | 140 | ACCAAAGTTTGCAGCCTATACCTCAATAAAACAGGGATA<br>TTTTAAATCACATACCTGCAGACAAACTGGAGCAATGTT<br>ATTTTAAAGGGTTTTTTCACCTCCTTATTCTTAGATTAT<br>TAATGTATTAGGGAAGAAATGAGACAATTTTGTGTAGGCT<br>TTTTCTAAAGTCCAGTACTTTGTCCAGATTTTAGATTCTC<br>A                                                                                                       |
| 141 | ADXCRA<br>D_CN291<br>160_at   | SRGAP1 | Sense | SLIT-ROBO Rho<br>GTPase activating<br>protein 1<br>[Source:HGNC<br>Symbol;Acc:17382]                     | 141 | ATTGATTCTGACCATAGCAGTAGAGGGCCATTTTTGT<br>GCAGGAAATGTGCTTAGGACTCAGTCTGTTTTTCGATTA<br>TCCACCACAGAAACCCCTGAGACACAGAGCAGCTTAGAA<br>GTCTTACCCAGGGCGTAATAGAGTCCCTACTCCAGA<br>CCACTGCCACCCACCTCCCAAGTTGAGAACACAAGCT<br>CCAGCTGGGCTGGAGAGTCAGGCTTGGTGAGGGTGA<br>CTTTGGCGAAGTTTGTTCAGATCCATAAAGCAAACTGGA<br>ATTTGAGCTTTCACCTACCCTAGTATACG |

FIG. 7-36

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|     |                               |                                           |       |                                                                                                                                                   |     |                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------------|-------------------------------------------|-------|---------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 142 | ADXCRH.<br>1654.C3_s<br>_at   | CFTR                                      | Sense | cystic fibrosis<br>transmembrane<br>conductance regulator<br>(ATP-binding cassette<br>sub-family C, member<br>7) [Source:HGNC<br>Symbol;Acc:1884] | 142 | TTCTTCCACAGAAGCTCCAGGTAGAGGGTGTGTAAGT<br>AGATAGGCCATGGCAGCTGTGGGTAGACACACATGAAG<br>TCCAAGCATTTAGATGTATAGGTTGATGGTGGTA                                                                                                                                                                            |
| 143 | ADXCRP<br>D.10513.C<br>1_s_at | NR3C2                                     | Sense | nuclear receptor<br>subfamily 3, group C,<br>member 2<br>[Source:HGNC<br>Symbol;Acc:7979]                                                         | 143 | TGAGTTGTTTGTCCACAGTGCTATGTTATGCATTT<br>GTTTACATCTCATAACATGTGGTAAATATTTATGCAAGAT<br>GGCTAGCCAGACNNNNNNNNNNNNNNNNNNNNNNNC<br>ANCCGTGAAATAGAGAAATGCAGGGTGACCCATGTAAAC<br>AGGCTAGAGATACATTTGAAAAGATGAGGGTTAAAGA<br>GTGTGTACATGTTGGCAGGTAAAGAGATAGCATCCTCTA<br>GGGAGGATATTATCAGGAGTCAGAGTAATCTTGGTAAA |
| 144 | ADXCRH.<br>1055.C1_s<br>_at   | AC090937.2<br>(Clone_based_<br>vega_gene) | Sense | Novel processed<br>transcript.                                                                                                                    | 144 | AATCATTGATTGACTTGCTGTGAAC TTGCAGGAACTGT<br>TTCATAGTTTCATTACACAGAGTAAACTGTTTGCCATGC<br>AAGGTTATTTTGCACTCTGCATTTAAGTG                                                                                                                                                                              |
| 145 | ADXCRP<br>D.3033.C1<br>_x_at  | CTGF                                      | Sense | connective tissue<br>growth factor<br>[Source:HGNC<br>Symbol;Acc:2500]                                                                            | 145 | GACATTAACTCATTAGACTGGAAC TTGAAC TGATTCACA<br>TCTCATTTTCCGTAAAAATGATTTTCAGTAGCACAAAGTTA<br>TTTAAATCTGTTTTTCTAACTGGGGGAAAGATTCCCAC<br>CCAATTCAAAACATTTGCCCCATGTCAAACAAATAGTCTA<br>TCAACCCCGACACACTGGTTGAAGAAT                                                                                      |

FIG. 7-37

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|     |                                |          |       |                                                                             |     |                                                                                                                                                                                                                                                                                                            |
|-----|--------------------------------|----------|-------|-----------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 146 | ADXCRA<br>D_BI4946<br>81_at    | C11orf35 | Sense | collagen, type XXVII,<br>alpha 1 [Source:HGNC<br>Symbol;Acc:22986]          | 146 | GTATGTGAAAGTCTCTATTGTGTGATTTCTCTCCTAAAGT<br>TGTGTCTCTTTGGGAATTGGATTGATTTTATTTATTTAA<br>TACCTACATTTGGCCGTCCTCCCTCCCAACACTTCTGT<br>ATCCTGCCCCTGCCGCCAGCCTGGACGCTCTGCGT<br>GGAAGTCCGTGTTGTAGCAGCTCGGGCCTCATCTCAG<br>CGCTCGGATCCCTCCTGCTGCCAGAATCCACTGGCCTC<br>TGCTCATTTCTGGG                                  |
| 147 | ADXCRA<br>G_NM_17<br>3542_s_at | PLBD2    | Sense | phospholipase B<br>domain containing 2<br>[Source:HGNC<br>Symbol;Acc:27283] | 147 | TCCCTCAGGAAGCAGTCCCCTCGTCTCCCTTTCTGGGC<br>AGCTTCCTTGAGGACAGAAACTTGAAAACAACACAAAC<br>CAAAGTTTCTGGCCATCTGTGGCTGGAGGTTCTGAAT<br>GTCTCTCTCCATGTCAGGCAAGGGTCAGCCCCCATG<br>CTTCTGCCTCAGGCCCCACCCACCCACCCAGGCC<br>TGCCCTCACCTCAGGGCCATACCCACAGCGCCCTGAT<br>GGAGGAACCAAGACCGCAGGCTGTGCCACCATTAAACAA<br>GAGCGGCTGTG |
| 148 | ADXCRA<br>D_AW020<br>871_at    | SVIL     | Sense | supervillin<br>[Source:HGNC<br>Symbol;Acc:11480]                            | 148 | AAGGAGGCAGATGAGATTTTCATATCAAAAAAGA                                                                                                                                                                                                                                                                         |
| 149 | ADXCRA<br>G_AL1174<br>66_s_at  | LIMK2    | Sense | LIM domain kinase 2<br>[Source:HGNC<br>Symbol;Acc:6614]                     | 149 | TGACTTCTACCTCCCATGTTTGCTCTCCCAACTCATTAG<br>CTCCTGGGAGCATCCTCCTGAGCCACATGTGCAGGTA<br>CTGAAAACCTCCATCTTGGCTCCAGAGCTCTAGGAA<br>CTCTTCATCACAACTAGATTTGCCTCTTCTAAGTGTCTAT<br>GAGCTTGCAACCATATTTAA                                                                                                               |

FIG. 7-38

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|     |                               |                          |           |                                                                                                                              |     |                                                                                                                                                                                                                                                                               |
|-----|-------------------------------|--------------------------|-----------|------------------------------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 150 | ADXCRA<br>D_CN309<br>527_s_at | HIST1H4J ///<br>HIST1H4K | Sense     | histone cluster 1, H4j<br>[Source:HGNC<br>Symbol;Acc:4785] ///<br>histone cluster 1, H4k<br>[Source:HGNC<br>Symbol;Acc:4784] | 150 | CCACCGTAAAGTACTGCGCGACAATATCCAGGGCATC                                                                                                                                                                                                                                         |
| 151 | ADXCRA<br>D_W6818<br>0_at     | EEF2K                    | AntiSense | eukaryotic elongation<br>factor-2 kinase<br>[Source:HGNC<br>Symbol;Acc:24615]                                                | 151 | GTGGAATAAGTTCTCTAGCTCAGAAAGGATCTCAACCTC<br>TTGCAAGTTACTTTTCACTTTAAAGGGCCCTTAAAGAAG<br>CATTGCTTAGCTCTGTATCCAGGCCATCTCTCCCTCCC<br>CGAAGAGCAACAGACCAGCAACTGACATTAAGGTCACA<br>TGGGTGGGTGGGAGTAGAATTGCGGGGTGACAGTT<br>CCAGCCAATCCAGACACGAATCATGTTTGANGGACCCG<br>AGCCTCAAGGGTGATTCC |
| 152 | ADXCRA<br>D_BI7535<br>34_at   | KIAA0467                 | Sense     | KIAA0467<br>[Source:HGNC<br>Symbol;Acc:29040]                                                                                | 152 | AGACATATGACAATGTTTCAGCAGGTCATCTTTAATGCAG                                                                                                                                                                                                                                      |
| 153 | ADXCRA<br>G_NM_00<br>3376_at  | VEGFA                    | Sense     | vascular endothelial<br>growth factor A<br>[Source:HGNC<br>Symbol;Acc:12680]                                                 | 153 | ACGAAAGCGCAAGAAATCCCGGTATAAGTCCTGGAGCG<br>TTCCCTGTGGGCCTT                                                                                                                                                                                                                     |

FIG. 7-39

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|     |                                   |                                                  |           |                                                                                                                                                    |     |                                                                                                                                                                                                                                                                                                        |
|-----|-----------------------------------|--------------------------------------------------|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 154 | ADXCRA<br>D_BU5218<br>45_x_at     | SMARCA4                                          | Sense     | SWI/SNF related,<br>matrix associated, actin<br>dependent regulator of<br>chromatin, subfamily a,<br>member 4<br>[Source:HGNC<br>Symbol;Acc:11100] | 154 | CCTCGTGGATCATCAAGGACGACGCGGAGGTGGAGCG<br>GCTGACCTGTGAGGAGGAGGAGGAGAAAGATGTTCCGGC<br>CGTGGTCCCGCCACCGCAAGGAGGTGGACTACAGCG<br>ACTCACTGACGGAGAGCAGTGGCTCAAGGCCATCGAG<br>GAGGGCAGCTGGAGGAGATCGAAGAGGAGGTCCGGC<br>AGAAGAAATCATCACGGAAGCGCAAGCGA                                                             |
| 155 | ADXCRESS<br>.Hs#S301<br>7684_x_at | RP11-<br>460N11.2<br>(Clone_based_<br>vega_gene) | AntiSense | Known pseudogene.                                                                                                                                  | 155 | TAGGGTTTCTCTCCACTATGAATGATCTGATGTATAGTA<br>AGGTTGGAAGACCACTTAAAAATTTGCCACAATCTTTG<br>CATTGTAGGGTTTGTCTCCAGTATGAACATGTTATGTT<br>GAGTAAGGCCGAGGAAATAGTAAAAAGCTTTGCCACATT<br>CTTCACATTTATAGGGTTTCTCTCAAGTATGAATTCCTTT<br>ATGTTCTTTCAGTTTGGAGATTTCTAAAGGCTTTGCCA<br>CATTCAACATTTGTAGGGTTTCTCTCCCATATGAATAA |
| 156 | ADXCRA<br>G_XM_29<br>0516_x_at    | CDC42BPG                                         | Sense     | CDC42 binding protein<br>kinase gamma (DMPK-<br>like) [Source:HGNC<br>Symbol;Acc:29829]                                                            | 156 | ACTGGAGGGTCTCCGGGCACACTCTGGCCCTTCCCAGA<br>AAGGGGTCGTTTTTCTCGAATCTTCAACCAGTTGTGTA<br>TTGGAACACTAGGGCGCATTTTACTATTGATCACAGTCAT<br>TATATTGTT                                                                                                                                                              |
| 157 | ADXCRA<br>D.15527.C<br>1_at       | SLC6A6                                           | Sense     | solute carrier family 6<br>(neurotransmitter<br>transporter, taurine),<br>member 6<br>[Source:HGNC<br>Symbol;Acc:11052]                            | 157 | TTCGGAATAGGGAAGACTGTCTCTGAAGAAGGAGGAA<br>GTGTAGCTTATGGGAGGCTGAGGAGTTTGGAGTTTCTC<br>CTTGTGGGAAGGTGGAGCCATGAGGCTGAAGACAG<br>TTGTCCAACTCAGGGCATACAAATTGATGAGGAACTCA                                                                                                                                       |

FIG. 7-40

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|     |                               |        |           |                                                                                    |     |                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|--------|-----------|------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 158 | ADXCRIH.<br>895.C1_s_<br>at   | LRRC59 | Sense     | leucine rich repeat<br>containing 59<br>[Source:HGNC<br>Symbol;Acc:28817]          | 158 | AGGACCTCAGAGATGTAAGCATTTTAGCAGCCACACAAA<br>ATCTCTGGCTATGAAAGGGACTTCATGACCATCCAGTCC<br>AATATAACACTTCAGACAGAGAACTGAGGTCTTCCAT<br>GACTTGCCCTAGTCTCCAGCTAGTTTGAGGCAAACTG<br>GATCCCACTCTGGTATTCTTCTTCTTCTTACATCATTT<br>TCCCTCCTTTAAATGTCTGAGAGACCAGAACTCACA                                                    |
| 159 | ADXCRA<br>D_AA7091<br>48_s_at | CHD2   | AntiSense | chromodomain helicase<br>DNA binding protein 2<br>[Source:HGNC<br>Symbol;Acc:1917] | 159 | ACTAAAGACATTAAGCATTTGCACTTAATTGGGTACTTC<br>GGGAAAGAAGTGTAGGTTGGCATTAAAGGTACTTCTT<br>ACACTGCATGTTCTGTAAAGGACAGCAAAATACATCTATA<br>TAGGTTCACTGTAAATTCTCGAGGACTAATGGATCCGC<br>ATGTGAAAAGTAA                                                                                                                   |
| 160 | ADXCRA<br>D_15720.C<br>1_x_at | CHD1   | Sense     | chitinase domain<br>containing 1<br>[Source:HGNC<br>Symbol;Acc:28474]              | 160 | TGAGCCCCGTGCCCTGGCCTGGTCATTTCTCTTGCTGTG<br>CCCAACCTGCCATTAAATCCCATCCATCCTGAGCCCCGAC<br>GTGGTCATTTCTCTCACCACCCAGCATACCGCCCCAAG<br>TGGTCCTTT                                                                                                                                                                |
| 161 | ADXCRA<br>D_AA8296<br>35_at   | ZNF75A | AntiSense | zinc finger protein 75a<br>[Source:HGNC<br>Symbol;Acc:13146]                       | 161 | TAAGTACTTAAGTCCTGTCTCCTTGGCCCAAGCCAGACTA<br>GGCCCAACACCCCTCAATTACCCCTGGCTCCAAAGAGGG<br>CAAAAGCAACTCTCTTTCTCTAAGGCCAGGGAAGTATCT<br>ACCACAATCTCTGAAACCTGTGAACCTTTCTGTGGCCT<br>GTAGTTTCAAGTCCCACCTTAAGTGTCTTAAAAAAAAA<br>CCAAACAATGACCTACCTAATCCATCTAATTTCTCAACTA<br>ACTGCCACCATCTCTACTATATCCACCTGCATCCTATTT |
| 162 | ADXCRA<br>G_BC007<br>608_at   | HMGB3  | Sense     | high-mobility group box<br>3 [Source:HGNC<br>Symbol;Acc:5004]                      | 162 | TAGGCTTAGCTTGATTTCTGGGCCCACTGTCTGTGTCT<br>TAAGATGCCAACCT                                                                                                                                                                                                                                                  |

FIG. 7-41

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|     |                                 |        |           |                                                                                    |     |                                                                                                                                                                                                                                                                                                                   |
|-----|---------------------------------|--------|-----------|------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 163 | ADXCRP<br>DRC.1680<br>7.C1_s_at | LYPLA1 | Sense     | lysophospholipase I<br>[Source:HGNC<br>Symbol;Acc:6737]                            | 163 | TATGATGCACAGTTCGTGTCAACAGGAAATGATGGATGT<br>CAAGCAATTCATTGGTAACTCCTACCTCCAATTGATTG<br>ACGTCACTAAGAGGCCTTGTTGTAAGATACACCAGCAT<br>CATTGTAGTAGAGTGTAACACCTTTTCCCATGCCGAGTCT<br>TCAAATTTCTAATG                                                                                                                         |
| 164 | ADXCRP<br>D.5568.C1<br>_at      | DDX27  | Sense     | DEAD (Asp-Glu-Ala-<br>Asp) box polypeptide<br>27 [Source:HGNC<br>Symbol;Acc:15837] | 164 | CAGCTGGGCCCTGGCTGATGTCATGAGCCAACTCAAGA<br>AGAAGAGGGCAGCCACTACATTAGATGAGAAGATTGAG<br>AAAGTTCGAAAGAAAGGAAACAGAGGATAAAGAAAGC<br>CAAGTCTGGGAAGTTGGAAGGTTAGAAAGGAAAGCAAG<br>GAAGGCTCTGAACCAAGGAGCAGGAAGACCTTCAAGA<br>GAATGATGAGGAAGGCTCAGAAGATGAAGCCTCGGAGA<br>CTGACTACTCATCAGCTGATGAGAACATCCTC                        |
| 165 | ADXCRP<br>D.16185.C<br>1_at     | ITGA6  | AntiSense | integrin, alpha 6<br>[Source:HGNC<br>Symbol;Acc:6142]                              | 165 | AACCCACTCCAATTAGGCATTGCTCCCACCTCCTCCCAT<br>CAGTGCTCTCACAAAGGTCACCAGTGGCTTCTACATTGC<br>CAATCTAGCGATCAAAATCTCAGTAAAGTGTCATTTGATAT<br>AACTGATCTTTTCACTTCTCTCTTTGAAACCCCATCATGTG<br>GTTTCCAGGACCACACACTCCCTCCCTCTCCTCCTGCC<br>ATGGGTGTCAGTCTCCAGGGCTCTCCCTAACCTCCCATG<br>TGTAAGAA                                     |
| 166 | ADXCRSS<br>.Hs#S192<br>7899_at  | ITGA6  | AntiSense | integrin, alpha 6<br>[Source:HGNC<br>Symbol;Acc:6142]                              | 166 | TGCCCATTTCTCCAAAAGCACGTGCCAGCCCCCAATC<br>CCCTCTATATCTCAGCTGAAGCATCACCTCCATTAAATGA<br>AGCCTAGTCCTTTCTGCCTCGTGTGTTGCTTTGTTGCT<br>GCTCACACCTTTAGACAAGACTTGCTGCCACTGACTCC<br>CACCAGTCCCTGTTCCCTGGAAGAAATCAAGGAAGCCC<br>ACCTTGATCTCATTTGAGCTCCTAAATTTACAGAAATAG<br>GGACAAAGGTTCAAAGGGAGCCTCACAGGTCGCATGGT<br>GAACCAAGC |

FIG. 7-42

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|     |                               |         |       |                                                                                                       |     |                                                                                                                                                                                                                                                                                                                      |
|-----|-------------------------------|---------|-------|-------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 167 | ADXCRA<br>D.14605.C<br>1_s_at | NPIPL3  | Sense | nuclear pore complex<br>interacting protein-like 3<br>[Source:HGNC<br>Symbol;Acc:28989]               | 167 | AGCATCTGAAACTATATCCAGAAATGACACTGGATTTTCA<br>TAAAGTGTTGATCCTCACACCTCTTTATAGTCTTGCAC<br>CTAGCACAGTGGAGTGAACACCTTTAAATAGCACCTTGT<br>CCTTGAGTATATATGGAAGGAGTGAAGTATTGATAAGT<br>GCTCAGCTAATATGAGCAGCATCTCAGGAGTCTCCAAAT<br>CTTGAAATTACCAGGGAGTA                                                                           |
| 168 | ADXCRA<br>D_CA4403<br>61_at   | ROBO1   | Sense | roundabout, axon<br>guidance receptor,<br>homolog 1 (Drosophila)<br>[Source:HGNC<br>Symbol;Acc:10249] | 168 | GGAGTTGGAGCCCACTCTGGGGAAAAACATGTTGAGATC<br>TTGCCCTCTGCAAAAATAAGTAAATAAAATTTAAAAAAA<br>GTAAAAAATAAAATCAGCTGAGCATGGTGACATGCACC<br>TGTGGTACCAGCTACTTTGGAGGCTAAGTTGAGAGGCA<br>CTGATGGGAGGATCATTTGACGGCCAGAGGTTGAGGC                                                                                                      |
| 169 | ADXCRIH.<br>1552.C1_s<br>_at  | ATP2C2  | Sense | ATPase, Ca++<br>transporting, type 2C,<br>member 2<br>[Source:HGNC<br>Symbol;Acc:29103]               | 169 | GGCAGCTGGCGGTCAATTTACATCCCCCGCTGCAGAG<br>GGTCTTCCAGACGGAGAACCTGGAGCGCTTGATTTTGC<br>TGTTTTAACTGGATTGGCCTCATCCGCTTCATTTTGTG<br>AGAGCTCCTCAAACTATGTGAAAAATACTTTGCAGCCCC<br>CAAGAGAGTCCAGATGCACCTGAAGATGTGTAGTGA<br>CCGCACTCCGCGGCACCTTCCCTAATCATCTCGATCTG<br>GTTGTGACTG                                                 |
| 170 | ADXCRA<br>D_BM796<br>805_s_at | SLC39A7 | Sense | solute carrier family 39<br>(zinc transporter),<br>member 7<br>[Source:HGNC<br>Symbol;Acc:4927]       | 170 | ATAGTGTGGGCACTGTCTGACCAATGTTGCATTTGGAAG<br>GCTAAATGGGGCCATGAAGAAGGCTGGAAGGGACAGG<br>TGGTGATGGCAGCCTACCTGGTGTCCCTACCCACCT<br>GTTCTGGAGAACCAAGTTGCTACACAGGAAGTTCTCC<br>AAGTCCAGTTTCTTCTCCACCAAGTTGGTGGAGGC<br>TTCAGGGAAGACCCAGAGTCCCTGNACAGAGAGGGTAACA<br>GGAGGAGTCGGGGATAAACAATCAACATCAATCGTGTG<br>TCCTGATTTGGGAGTGAT |

FIG. 7-43

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|     |                               |                                                  |           |                                                                              |     |                                                                                                                                                                                                                                                                                        |
|-----|-------------------------------|--------------------------------------------------|-----------|------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 171 | ADXCRP<br>D.11457.C<br>1_at   | RNF43                                            | Sense     | ring finger protein 43<br>[Source:HGNC<br>Symbol;Acc:18505]                  | 171 | GGGCTTCCGTGCTGGCAGAACAAAGAAATGAATGGAT<br>GCATGGACAGATAGAGAGACTAATGCAGCTTGTGAGA<br>CAGGGCTACAGCTTCACTGATGTAAGAACAACTCCAC<br>CCTCATGCCCCAGCCTTTTCTTGGGGCAGGGGCACAT<br>GATAACCTTTCTCCACACTAAACC TTGCTCACTACCCAG<br>ACTAGTAGGCCTTAAACTCTGGGAGCAAGAATGGAAC<br>CTTCCCTATCTCAACA              |
| 172 | ADXCRP<br>.Hs#S301<br>7684_at | RP11-<br>460N11.2<br>(Clone_based_<br>vega_gene) | AntiSense | Known pseudogene.                                                            | 172 | CTCCACTATGAATGATCTGATGTATAGTAAGGTTGGAAG<br>ACCACCTTAAAAATTTGCCACAAATCTTTGCATTTGTAGG<br>GTTTGCTCCAGTATGAACATATGTTATGTTGAGTAAGGC<br>CTGAGGAATAGTAAAAAGCTTTGCC                                                                                                                            |
| 173 | ADXCRP<br>D.14252.C<br>1_s_at | LMTK2                                            | AntiSense | lemur tyrosine kinase 2<br>[Source:HGNC<br>Symbol;Acc:17880]                 | 173 | AACTAGTGGCTAGCATCGGCTTGACCTGCCTCATTCCC<br>CTCGAATAACTGAAGATCCTGTACAACAATGGAGACTCT<br>CGGAACATTTATCCACAGTGCAATTACAGAAAGCAGTTC<br>GTGATTTCTCTAGAAATAATAAATATGGCTCACTGGTGA<br>CCATTCCCTCAGGTGCTCTGTGGTGCCCCACACGTG<br>CGCCGGGATGTGCAGGCGTGGACGACGAGACGCCCCCT<br>GTGGAAGCACACATGCGGTGCACAC |
| 174 | ADXCRP<br>D.17881.C<br>1_s_at | C17orf88                                         | AntiSense | chromosome 17 open<br>reading frame 88<br>[Source:HGNC<br>Symbol;Acc: 17505] | 174 | TGGAGGTGCCACAAAAATCATCTGGTAAATGTTTAAAG<br>TAATCCCAAAATGCAACTCAAACTACAGAAATCCCAGGTG<br>AAGCTCAGTAATCTGTATTTT                                                                                                                                                                            |

FIG. 7-44

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|     |                                  |       |           |                                                                       |     |                                                                                                                                                                                                                                                                                                       |
|-----|----------------------------------|-------|-----------|-----------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 175 | ADXCRA<br>D_BM931<br>578_s_at    | BCL9L | Sense     | B-cell CLL/lymphoma 9-<br>like [Source:HGNC<br>Symbol;Acc:23688]      | 175 | TGCTCCTCGTGTCCGCATTGCTGGAGCTCCACCTCCC<br>TCTTGGTTTCTCCGACCCGCCCATTTTCTTCTGTCTT<br>TACCTGCTTCGTATCCTTTCCCTGCTGATGTGGCTGACC<br>CCTCTCCACCCCTCCCTGCAGGCGGCTGGCCAGGTG<br>GGCAGGTGCCAGCCGGAGCTGTAATAGAGCGCTGCG<br>CTTTGTGCTGGTTTGTGCGTGTGCTGATTTCTGTG                                                      |
| 176 | ADXCRA<br>D_BE2516<br>06_s_at    | ERF   | Sense     | Ets2 repressor factor<br>[Source:HGNC<br>Symbol;Acc:3444]             | 176 | CCATGGGCCACAAATCTCTACAAGTGCCCTGCTATCCCT<br>CTC                                                                                                                                                                                                                                                        |
| 177 | ADXCRESS<br>.Hs#S191<br>3861_at  | ACTN4 | AntiSense | actinin, alpha 4<br>[Source:HGNC<br>Symbol;Acc:166]                   | 177 | GTATCTGCTCAAGTAGAAGCTTCCGTCCTCTCTTGTAAACA<br>GGTCAGTGCTTCAGTTACCACCTGCCATTGAATTACCCAC<br>TCGCTATCAGTTGCCCTCTTATTTCCATAAAAAAGAAAC<br>GGAGGAAAAAACTGTTTAAGTTTACCTTGTTTAAAAGTA<br>ACACGAGTGCTTTTGTATTCTGTAACATAATACATAAA<br>TGAAGGCAAGGAAGGAACTGAGGGAAGGGAACAAAA<br>TGTGAGTGATGAAAAACACGGAGTTCATTAAATGAA |
| 178 | ADXCRCR<br>DRC.1045<br>0.C1_s_at | NCOR1 | Sense     | nuclear receptor<br>corepressor 1<br>[Source:HGNC<br>Symbol;Acc:7672] | 178 | GCAGGTCAAAAAACCTGCCCTCCTGTGACTTATTCCTG<br>AGACTTTTCAGGAGAGCCAGCCACACAGATGATGAAGAA<br>ATGATGGAAGTTCAATTTGGAGAGTCAAAATGGNNNNNN<br>NNNNNNNNNNNCTGCCCTTTGATACAGGCAATTGAGTG<br>GACTATAATAATAGTGGAGGGTTGAGATGTAGAGTTTTT                                                                                     |

FIG. 7-45

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|     |                               |                                              |           |                                                                                                                                    |     |                                                                                                                                                                                                                                                                                                                                |
|-----|-------------------------------|----------------------------------------------|-----------|------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 179 | ADXCRP<br>D.16001.C<br>1_x_at | KCNK1                                        | AntiSense | potassium channel,<br>subfamily K, member 1<br>[Source:HGNC<br>Symbol;Acc:6272]                                                    | 179 | GTGCTATGGGAACCAAGGTGCCAGGTGAGGCCAGGTGA<br>AGACAGGTGAGGCCAGGTGAAGATAGGTGAGGCCAGG<br>TGAAGACAGATGTTACGGGAACCAAGCAGGTAGAAAGCT<br>AAGTGCTGTGGAGAAAGAGCGGGAAGAAATGGAGGAG<br>GTGCTGGGACAACAGAACTTGAAAAGAACCTGCTTCT<br>CAGTAGCCCCAAGTCCTGTGTGTG                                                                                       |
| 180 | ADXCRA<br>D_BP3957<br>90_at   | CMIP (Entrez)                                | Sense     | C-Maf-inducing protein<br>(c-Mip)(Truncated c-<br>Maf-inducing<br>protein)(Tc-Mip)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q81Y22] | 180 | TGAAGAGCCTTCTGGGTACCTAGAGGTGCTGGGAAGGA<br>GTTTGGATTTAATCTTGGCTGTCTGTGACAGGGATTCTG<br>GAGGCCATGGGGAGGGTTGAGCAGGGGAGACAGGAGA<br>CAGGCAAGAGCGCTGTGAGAAAGCGTGGGCTGAGTGA<br>CCTGCTCCTTGGTGAGTGAGAGAGTCCTAGAACTGAGCA<br>CCATGGCATGCACCTG                                                                                             |
| 181 | ADXCRP<br>D.1872.C1<br>_at    | AL008582.1<br>(Clone_based_<br>ensembl_gene) | Sense     | Known long non-coding<br>RNA                                                                                                       | 181 | ATCCTTCCACAGTCTGCAAAACCAAGTTCTTCTGCAGTGT<br>TTTCTCTGGGAGTGTCTTGGGCTAAGCCACAGCGGTG<br>TCACCCACCAACACACACTGCCCTGCAAAAGGACTGCC<br>AATACCCCCAGCCCATTCGCCAGCCTCACATATAAATAA<br>GGACTTGCAGCCAGAAATCACATCCAGAGGGGAAGTTT<br>CACATGGCTTGGAAATCCTTTAAAAAAGGACAGCAAAACCA<br>AATNNNNNNNNNNNNCCCTCCCTACCCACACAACATCC<br>AGCCTGATCCCCGGGAATT |

FIG. 7-46

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|     |                                |         |       |                                                                                  |     |                                                                                                                                                                                                                                                                                                                             |
|-----|--------------------------------|---------|-------|----------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 182 | ADXCRP<br>D.6804.C1<br>_s_at   | SLC26A6 | Sense | solute carrier family 26,<br>member 6<br>[Source:HGNC<br>Symbol;Acc:14472]       | 182 | CGACAGCCCTGTTTCGGTCAACCAGACTCTGAACATGCT<br>ACATCCTGCCCAAGACTGCACCTCTGGAGGTGCAGGGC<br>ACCCTTGAGAAGCCCTCACCCCTAGGCCCTCCAGG<br>TGCTACCCAGGAGTCCCTCCATGTACACACACACAAC<br>TCAGGGAAGGAGTCTCTGGGACTCCAAGTTCAGCGCTC<br>CAGGCTGGGACAGGCCCTGCATGCAGTCAGGCTGGC<br>AGTGGCGGGTACAGGGGAGGAACTGGTGCTATTTTA<br>GCCTCAGGAATAAGATTTGTCTGCTCAA |
| 183 | ADXCRSS<br>.Hs#S191<br>7662_at | GCC2    | Sense | GRIP and coiled-coil<br>domain containing 2<br>[Source:HGNC<br>Symbol;Acc:23218] | 183 | ATGAGTACTGAGACCTGACCACTGCGTTAAGCAACATAG<br>AGGTCAGTGTCCTGACATGCTGGAACCAGAGCTTGATT<br>GCAGTTGGTTCTAGAAAAAATGGGGAGGCAATGTTT<br>GAGAGCATATATAGACAACCTCTTTTCAAGGGATTTGCTA<br>TAGGGAGAAAAAAGCGATGGGACAAAACCTAGAGGGAC                                                                                                             |
| 184 | ADXCRA<br>D_BC0179<br>75_x_at  | OSBP    | Sense | oxysterol binding<br>protein [Source:HGNC<br>Symbol;Acc:8503]                    | 184 | GACCAAGTTTAGGCAACATAGTGAACCCCTGTGTCTACAA<br>AAATAAAAAATTTAGCTGGCATTGTCATATGCCCTA<br>TAGTCCCAGCTACTTGGGAGGCTGAGGAGGGAGGATCA<br>CTTGAGCCCCAGGAGGTCAAGTTTGCAGTGAACCTACGATT<br>GCACCATTCGAT                                                                                                                                     |
| 185 | ADXCRP<br>D.13916.C<br>1_s_at  | DLG3    | Sense | discs, large homolog 3<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:2902]       | 185 | GGGCACTCGCATTGTCATTCTCTTGAGAGCTAGGAG<br>GGGTCAGCCTGAGGCCGGAGAGGAAGGGCTTTTGCT<br>GGGGTGAGAGGGTGAGAGACTTGACCTGAAAGCAGCTC<br>CTGCCCTGAGGTGCAANCCAGAGTCTCTGTGTCCGGAC<br>AGAGA                                                                                                                                                   |

FIG. 7-47

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|     |                               |         |       |                                                                                                                                                    |     |                                                                                                                                                                                                        |
|-----|-------------------------------|---------|-------|----------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 186 | ADXCRIH.<br>2384.C1_s<br>_at  | PHF3    | Sense | PHD finger protein 3<br>[Source:HGNC<br>Symbol;Acc:8921]                                                                                           | 186 | AATTTTACTATTGGTCATTTGCAGAACAGTAAATTCGT<br>GTGTTGGTACAGAGTGCTCTGTACCAGTGCTCATCATC<br>CCTTCTTCATACCAACGGTCCCTAGTTATAG                                                                                    |
| 187 | ADXCRA<br>D_BX3960<br>33_s_at | DNAJC16 | Sense | DnaJ (Hsp40) homolog,<br>subfamily C, member<br>16 [Source:HGNC<br>Symbol;Acc:29157]                                                               | 187 | TAGAGATGGGTTCTTCTGGTTGATACAGACTATGCATTG<br>CGCTAGCAGATGGGTAACCTGGCTAAACAAAGTCT<br>TTGCAGAAATACATGCCCAATTTCCAAAAA                                                                                       |
| 188 | ADXCRA<br>D_BI8560<br>32_s_at | SMARCD1 | Sense | SWI/SNF related,<br>matrix associated, actin<br>dependent regulator of<br>chromatin, subfamily d,<br>member 1<br>[Source:HGNC<br>Symbol;Acc:11106] | 188 | TCTCCCTGCCTCACAGGATTGTGACTCCCCAGCCCCTG<br>CCCTCAAAGCTTCAGACCCCTCAGGTAGCAGCAGGACC<br>TTGTGATCTTGGCCCTTGGATCTGAGATGTTTTGCAT<br>CTTCCAGGAGAGCCTCAGATTCTTCTCCAGGTTGTAT<br>CACCCCGAGTTAGCATATCCAGGCTCGCAGAC |
| 189 | ADXCRA<br>D_BQ016<br>677_x_at | POLR3A  | Sense | polymerase (RNA) III<br>(DNA directed)<br>polypeptide A, 155kDa<br>[Source:HGNC<br>Symbol;Acc:30074]                                               | 189 | GGTAGCCATTGGTCTTGGATCTGTGTAGAAATGAGTGC<br>TTTCCCTTCCTACTGATGTGATTGTGGATTAGGAATTCG<br>TGACCGAGTGATTTTGGCCAGTGGTTGGGTTTAAATTT<br>CTATTAAATTTGTAGTTTGGGCTGGGTGCT                                          |
| 190 | ADXCRA<br>D_BC0405<br>27_at   | CEP120  | Sense | centrosomal protein<br>120kDa [Source:HGNC<br>Symbol;Acc:26690]                                                                                    | 190 | GAAGGTTTGGACGATTATTGACTCGCCTGATAGAAGAA<br>AGGATACCTTTGATGAGAACGGGTGTGTATAATCACGA<br>GGATCGAATAAAGTGAACCTCGACCGACAGATCAGAG<br>AGATTTTGGCAAAAAGCAATGCCAGTAATTAATAACATTT<br>GGAAAGCTTTATAGAGACTCTAAGTCTA  |

FIG. 7-48

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|     |                               |        |           |                                                                                                |     |                                                                                                                                                                                                                                                                                              |
|-----|-------------------------------|--------|-----------|------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 191 | ADXCRA<br>D_CF1468<br>55_x_at | VPS53  | Sense     | vacuolar protein sorting<br>53 homolog (S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:25608] | 191 | TTGCCAGGCACGGCGCTCATGCCCTGTAGTCGCAACAC<br>TTTGGAGACCAAGGCAGGAGGATCATTGAGTCCAGG<br>AGTTTGAGACCAGCCTGGGCAACATACAGATGTCTACA<br>AAAAATAAAA                                                                                                                                                       |
| 192 | ADXCRA<br>D_1793.C1<br>_at    | FAM60A | AntiSense | family with sequence<br>similarity 60, member A<br>[Source:HGNC<br>Symbol;Acc:30702]           | 192 | TCATACAACAAATCCCATCTCTGTCCCCTGAAATTCCCC<br>TAGTTTCATTATTAGAAGGGGATTNNNNNNNNNNING<br>ACTTAAAGAGCACTTTACAGCAGCATTTCAGCTTTCCTAT<br>GAAATACTCAGCATCTTAAATATTATATACAACTCTTTTT<br>TTAGTAAGCTAGACACTGGCTTCAGAGTTCGTGGGAGT<br>GGGGAAATCAACCCATTCAAACTACTCTAGAAATTGT<br>CTTTGGCAGAATAGCAGGTATCCAAGTTA |
| 193 | ADXCRA<br>G_AL8320<br>08_at   | FNIP1  | Sense     | folliculin interacting<br>protein 1<br>[Source:HGNC<br>Symbol;Acc:29418]                       | 193 | AGTTCTAGGGGATATTTGTGCAATAAATACACATGTCAA<br>CTTGAA                                                                                                                                                                                                                                            |
| 194 | ADXCRA<br>D_10387.C<br>1_at   | RBM47  | Sense     | RNA binding motif<br>protein 47<br>[Source:HGNC<br>Symbol;Acc:30358]                           | 194 | AAAGCAGGTAGTTAGTTACCATTTGGAGAGGGGATTCCG<br>GAACCTAGAGAGAGATGAGGCTGAAGAGCGGGGAAGA<br>AACCAAGATGGCAAGGACTTTGTCTCATGCGCAAGCAT<br>ATAATTTATAGA                                                                                                                                                   |

FIG. 7-49

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|     |                                |        |       |                                                                                 |     |                                                                                                                                                                                                                                                                                                                         |
|-----|--------------------------------|--------|-------|---------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 195 | ADXCRA<br>D.10174.C<br>1_at    | PEA15  | Sense | phosphoprotein<br>enriched in astrocytes<br>15 [Source:HGNC<br>Symbol;Acc:8822] | 195 | AGAGGTAATATCCTTCCTATTCTTCCTTCACCTTCTGCCCC<br>TCCTCCACCTCTTCCAGCCTCCCTCACCTGACCTATT<br>TAGGGGTGATGGGATGAAAAGAGAGAGTGAAGGATA<br>TGTAATCAAGTGCAAAATACTGTGGTAAGTACAGAGAAT<br>GAATAAGGTGAAAGGAAAGTGAAAAGTGTGGGATGGT<br>TAGGGCTTTAAGGACTTCCAGGAAAATAGGATTCTGG                                                                 |
| 196 | ADXCRA<br>D_CF1267<br>72_s_at  | TTYH3  | Sense | tweety homolog 3<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:22222]           | 196 | GACCAAGGCTCTCCTGTGGGATCTTTGTTTTGTGTTTA<br>ACCATAATGGTTGTGTACTGAACCACTTCATATTTGTTAT<br>ATATAATATATATATATAATCTCCTTAAGACTCAGCCT<br>CCTGTTTACCCCCCGGCCTGNGCATCTGACCTCCCC<br>CACCCAGTGTGATTTAACATCCAGGAACTGAGGCCCTG<br>AA                                                                                                    |
| 197 | ADXCRA<br>D_CN272<br>025_at    | PABPN1 | Sense | poly(A) binding protein,<br>nuclear 1<br>[Source:HGNC<br>Symbol;Acc:8565]       | 197 | TAAGAGCTGTGGAGGACTGAAACTGGATAAAAAGGGG<br>GTCCTTTTCCCTTGCCCTGTCTCTCACTCAGATGCGCTT<br>CTTTTCGCCACTGTTTGGCAAAGTTTTCTGTTAAGCCC<br>CCCTCCCCCTGCCCCAGTTCTCCAGGTGCGTTACTATTT<br>CTGGGATCATGGGTCAGTTTTAGGACACTTGAACACTT<br>CTTTCCCCCTTCCCTTACAGTAACTGGGCGAGGGG<br>CCTACGGGGAGGGGCTTGTAAGTGAACATCTAGTGATC<br>ACGTTAACACCTAACTCTC |
| 198 | ADXCRIH<br>RC.2093.<br>C1_s_at | HSPD1  | Sense | heat shock 60kDa<br>protein 1 (chaperonin)<br>[Source:HGNC<br>Symbol;Acc:5261]  | 198 | GGACTGCAGCTAAGTGTCCTCACTCCCCAAAGCTTCCCTAT<br>TCCTAACTCCATGACAGCTCCTCAGTAGAGCTTTCCTCC<br>TCAGAAAGCAACTAGAACAATGCAGTTAACATTATTGGC<br>CCCAACGGCGTTTACTGTGTATTTTGGCTGAGATCTTTA<br>GAAGCCCCGAGGGCCTAAACAATTAAGTGAAGGAACATCTAA                                                                                                |

FIG. 7-50

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|     |                                |         |       |                                                                                       |     |                                                                                                                                                                                                                                                                                                                    |
|-----|--------------------------------|---------|-------|---------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 199 | RDCR243<br>_E10_s_at           | GOSR1   | Sense | golgi SNAP receptor<br>complex member 1<br>[Source:HGNC<br>Symbol;Acc:4430]           | 199 | TTACTGAACACAGCCTGGTTGTAGACTTCCTGTTTCT<br>ACACTGCTGCTCTTCACCATTTGGAATTCACCTGTGGTATT<br>TATATTACTGGCTTCAGTCGAGCCACAGGTAATAAAAG<br>GATATCATCTGTATTTCTCAACCATATCATGGTGTATAGA<br>TGCTGTTATTTCAGGCGAAGTTGCTCATGGTGGACTAA<br>CACCTGGTTGGTACAGA                                                                            |
| 200 | ADXCRA<br>D_AL8330<br>17_x_at  | MACROD1 | Sense | MACRO domain<br>containing 1<br>[Source:HGNC<br>Symbol;Acc:29598]                     | 200 | GAGCCATGATTGTGTTACTGCCTTCCAGCCTGGGCAAC<br>AGAGTGAGACTCCATCTCAAAAAAAGAGGCTGGCTCACT<br>AGAAAATCAGACTCTGAGGCTGCAGGCGGTGGCTCACT<br>CTTGTAATCCAGCACTTTGAGAGGCTGAGGCAGGAAG<br>ATTGCTTGAGCCCAAGGAGTTTGAGACCAACTTGAGCAA<br>CACAGTGGCACCCCTATCTCTACCTAAAAA                                                                  |
| 201 | ADXCRA<br>G_XM_04<br>0265_s_at | LARP4B  | Sense | La ribonucleoprotein<br>domain family, member<br>4B [Source:HGNC<br>Symbol;Acc:28987] | 201 | GGAGCCGCCACGGAATTGCGAAAGCCCAAGCTACGCAG<br>AGATTGTGTCAGAGAACGAGTAAAGAGCCTCCTTCTTCCC<br>CATTGCAACCCCAAAAAAGAACAAAGCCCAACACTGTTG<br>GTTGTGGGAAGGAGGAAAAGAGCTGGCAGAGCCCGC<br>AGAGAGATACCGGGAGCCCCCAGCCCTCAAGTCCACA<br>CCTGGAGCCCCCAGAGACCAAGAGCGCGCGCGGG<br>GGCCGGCCCTCGCCCTCGGCCATGGGGAAGCGGTCTCA<br>GCCGAGAGCAGAGCAC |

FIG. 7-51

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|     |                               |                                         |           |                                                                                                                                                                                                                                                         |     |                                                                                                                                                                                                                                               |
|-----|-------------------------------|-----------------------------------------|-----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 202 | RDCR489<br>_A06_x_at          | C17orf88 ///<br>LRRC37A ///<br>LRRC37A2 | AntiSense | chromosome 17 open<br>reading frame 88<br>[Source:HGNC Symbol;<br>Acc:17505] /// leucine<br>rich repeat containing<br>37A [Source:HGNC<br>Symbol;Acc:29069] ///<br>leucine rich repeat<br>containing 37, member<br>A2 [Source:HGNC<br>Symbol;Acc:32404] | 202 | CGTGCTACCATCACAGCTGAATGCAATGAAAGGCGGTC<br>CTCTGAGAGGAGCAGGGTGGAGATGCTAAAGTGGAGG<br>CCCCGTCCCATTTGCTGATAGATCCTCATCTGGCATGCG<br>CTCCACCCCTCCCATTTCTCTGCTCCACGTCATCGTAGC<br>CCCATCACAGAAAGATGCGACATGGAAAAACGCACTGTG<br>TCCACCCTA                 |
| 203 | ADXCRP<br>D.15720.C<br>1_s_at | CHID1                                   | Sense     | chitinase domain<br>containing 1<br>[Source:HGNC<br>Symbol;Acc:28474]                                                                                                                                                                                   | 203 | GCTGTGCCCCAACCTGCCATTAATCCCATCCATCCTGAG<br>CCCGACGTGGTC                                                                                                                                                                                       |
| 204 | ADXCRP<br>D.252.C5_<br>s_at   | WHSC1L1                                 | Sense     | Wolf-Hirschhorn<br>syndrome candidate 1-<br>like 1 [Source:HGNC<br>Symbol;Acc:12767]                                                                                                                                                                    | 204 | TTTTAGCAACCAGCCAGAGAGGGCGTGGTTTCATGAAA<br>AACGGGTACGAGAGTATAAAGGTCATAAACAGTATGAA<br>GAATTACTGGCTGAGGCAACCAACAAAGCCAGCAATCA<br>CTCTGAGAAACAAAAGATTTCGGAACCCCGACCTCAGA<br>GAGAACGTGCTCAGTGGGATATTGGCATTGCCCATGCA<br>GAGAAAGCATTGAAAATGACTCGAGAA |
| 205 | ADXCRA<br>G_BC026<br>694_s_at | TMEM184A                                | Sense     | transmembrane protein<br>184A [Source:HGNC<br>Symbol;Acc:28797]                                                                                                                                                                                         | 205 | CCTCGTGGGCACGTGGAGAGGGCCCCACGTGTCTCCA<br>CACGCCAGCCACAGGGAGCCCTGGCCAGGCGCCCA<br>GCCAGGGGAGCGTGTGCCTGGGATGGGTCACAGAACC<br>AGCGGGCACCTGTGAGGCTGGCCAGCACCGTGGGGCT<br>GTGGGAATCGCTCTTATTATTTAAA                                                   |

FIG. 7-52

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|     |                               |       |           |                                                                                                         |     |                                                                                                                                                                                                                                                                                            |
|-----|-------------------------------|-------|-----------|---------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 206 | ADXCRP<br>D.8832.C1<br>_at    | GPT2  | AntiSense | glutamic pyruvate<br>transaminase (alanine<br>amino transferase) 2<br>[Source:HGNC<br>Symbol;Acc:18062] | 206 | TTCCAAGTGGACCTCAAATGACAACTTTCTCAGGTGGT<br>GCCTGGATAGGAAAGGACCCGGAACAGAAATCTGTAGAA<br>AACCAAACTATCATGATCAGCATTCCTACCCGACGTTA<br>ACCTCTAGACTAGCTGACCTTATTTATTTTGAAGCAA<br>ATCAAGTGATACAGTCTCTTTTAAAAAACTGTGTAAAC<br>GTTGTAAGTTTTTAGGGGCTGTTTATAATCTGAAGATTT<br>ATAAAAAATTACTGGACTTGTAGGACTAT |
| 207 | ADXCRP<br>D.10116.C<br>1_s_at | OXSR1 | Sense     | oxidative-stress<br>responsive 1<br>[Source:HGNC<br>Symbol;Acc:8508]                                    | 207 | TGAGATGATCAGACACCCGGAGTTCAACGTCCCAGCAGT<br>CTTGGTAAAGGAGGGAGCCTACTGAGCCAGGAGGGA<br>GAAAAGAAGATTGACCAGCTTGCTAGAAAAATACTTAGC<br>NNNNNNNNNNNNNNNGTGGAGGGGGACGGAGA<br>GGAACAAGGATGGGAGGTAGGAATGAGGTATAGAAAA<br>GAGATAGCATCTCTTTGGCACAAAGACTAGTGGCT                                             |
| 208 | ADXCRA<br>D_BU1809<br>46_s_at | DOT1L | Sense     | DOT1-like, histone H3<br>methyltransferase (S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:24948]      | 208 | CCCAGGATGCGTCAGTCTGTTTCAGTGGTCAGCAGGCCCC<br>CCCACCCCCCGCCGACTGCCCTCGCCATCGTGGTCAG<br>ACCCCTCCCAACACAAACACGCTGCTGGTCTGTGTCA<br>GCCTTGTAAACGTGGGAGGCTCTGCCGTGCTTCCGGG<br>TGAACGTGATTTGGATTGCCGCCATTGTCACGGTCCG                                                                               |
| 209 | ADXCRP<br>D.11636.C<br>1_at   | RUNX1 | AntiSense | runt-related<br>transcription factor 1<br>[Source:HGNC<br>Symbol;Acc:10471]                             | 209 | ATAGGTAGCAAAGCTAAGGCCCAAGAAAGGTTAAGTAATT<br>TTCCCAAAGTCACACAGCTTTGATATACAGCAAAACTCA<br>TATCCCTGAGCTTCTACTCACTGTTCTTCCGGTTATTAT<br>CCCTGAGGTCAATAATCTCCACCCGCAAAACCCCAATAGC<br>ACCAGTACAAGAAATCTGGACTGGAGATACCTTTATCCAC<br>ACCTACCACTGCCCAAAAGTAAATCTGACTCTGTGA<br>TTCTAATGTACCAATGGTAC     |

FIG. 7-53

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|     |                               |                                             |       |                                                                                                                                                                                                                                                                   |     |                                                                                                                                                                                                                                                                                 |
|-----|-------------------------------|---------------------------------------------|-------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 210 | ADXCRA<br>D_AL5562<br>40_s_at | NMD3                                        | Sense | NMD3 homolog (S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:24250]                                                                                                                                                                                              | 210 | ATTTTATTGCAGTAGGAGGAAATATATTTAAATATTTG<br>TAGATTTATAGCAATAGAGACTCGTTATTTAAAGTTAA<br>ATAACAATTTGTTCTTTTGTGTTTGTGTTTCCAGTTAGGGC<br>AGTAGCTGCTTTTGTGCATAAATATCTTCCACCACATC                                                                                                         |
| 211 | ADXCRA<br>D_BX1129<br>07_s_at | TICAM2 ///<br>TMED7 ///<br>TMED7-<br>TICAM2 | Sense | toll-like receptor<br>adaptor molecule 2<br>[Source:HGNC<br>Symbol;Acc:21354] ///<br>transmembrane emp24<br>protein transport<br>domain containing 7<br>[Source:HGNC<br>Symbol;Acc:24253] ///<br>TMED7-TICAM2<br>readthrough<br>[Source:HGNC<br>Symbol;Acc:33945] | 211 | CTTGAGTAAAGACATTTTGCTTAATTTCTTTTCTTATTTC<br>CCCACTTGATATCCCTACCAGTACCGGGATCTGCAC<br>ACATCTTTTGCAGNTACCTCTTCATAGCCATGAACCAA<br>AACGTTCTATGAGGAGC                                                                                                                                 |
| 212 | ADXCRA<br>D_BQ670<br>114_s_at | IGF2R                                       | Sense | insulin-like growth<br>factor 2 receptor<br>[Source:HGNC<br>Symbol;Acc:5467]                                                                                                                                                                                      | 212 | CCTTCTGATTGTTTACAGTCATTGGAATAAGGCATGGC<br>TCAGATCGGCCACAGGCGGTACCTTGTGCCCAGGGTT<br>TTGCCCAAGTCCCTCATTTAAAGCATAAGGCCGGACG<br>CATCTCAAAACAGAGGGCTGCATTCGAAAGAAACCCCTTG<br>CTGCTTTAGTCCCGATAGGGTATTTGACCCCGATATATT<br>TTAGCATTTTAATTCCTCTCCCTTATTATTGACTTTTGAC<br>AATTACTCAGGTTTGA |

FIG. 7-54

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|     |                                  |                                              |           |                                                                                                                  |     |                                                                                                                                                                                                                                                                                             |
|-----|----------------------------------|----------------------------------------------|-----------|------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 213 | ADXCRA<br>D_CN264<br>940_at      | ID2                                          | Sense     | inhibitor of DNA binding<br>2, dominant negative<br>helix-loop-helix protein<br>[Source:HGNC<br>Symbol;Acc:5361] | 213 | TCCTGTCCTTGCAGGTAAGACCTGCTCCGGGGTCCCCG<br>CCCCGCCGCGCACACTCCCGCGGTGCTGGGCTGT<br>CACTAGGAGATCCGTAGCCCCAGACGGTGACTTTCGTAT<br>GAGCTATTTAACTTTATTTTCTTCAGAACTCTGCTGTAGAT<br>TGAGCTGTGCGTGAATTGCTAGTAAGTTCTGACATGTT<br>AATGCTCTGCTTTAAATCTGAATTGTTACCATAAACGT<br>GTTTAATGGAACCTGCTGGTCTGTGGA     |
| 214 | ADXCRSS<br>.Hs#S122<br>8858_x_at | AC004968.2<br>(Clone_based_<br>ensembl_gene) | Sense     | Known long non-coding<br>RNA                                                                                     | 214 | ACCTCATCCCCGAATAATAACTAAGCACTAGAGTGATGC<br>TGGGATGCTGGGGCTTGGTTAGGTGGCTGGGAAG<br>TTATCTTGGAGGTGAGACTCCAGTGGACTCTGCGGATG<br>GGTAAGGTCTCAGAGAGGTTGGGAAGTTATCTTGGAG<br>GTGAGACTCCAGTGGACTCTGCGGATTGGTAAGGTCTC<br>AGAGAGGTTGAGGTTAAGAAAGAGAGCATTCCAGACCAT<br>TCCAAAATCAGCACATAACACACATGGCTTGAAA |
| 215 | ADXCRP<br>D.6228.C1<br>_at       | PTP4A1                                       | AntiSense | protein tyrosine<br>phosphatase type IVA,<br>member 1<br>[Source:HGNC<br>Symbol;Acc:9634]                        | 215 | GTTTCTACAGTTCACCTTGTCTGCATAGAGGTCGTGCTGT<br>GCCTGGCAGTAATCTCCACTGCCCTTCAGAACTCCAT<br>AAATGTGTGACCAAGAACACACACAGAAATTGAGGAATATG<br>TTTACTCATTGAAGATTGTGGCCTAATCATACAGCCGGT<br>CCCGAG                                                                                                         |
| 216 | ADXCRA<br>D_AW963<br>267_s_at    | NFIX                                         | Sense     | nuclear factor I/X<br>(CCAAT-binding<br>transcription factor)<br>[Source:HGNC<br>Symbol;Acc:7788]                | 216 | ATGCAAGTAGGCAGCCAGCCCCGTCTGTCCCTCTCCGC<br>CCCCCCCCCCCCCGCCCGCTCACTGCGCTTCTGTTAT<br>ACCATCTTTGCCTGACTCTCTACGGCTTCTCCATTGAAT<br>GGCTAATGTGTATGTGAAAT                                                                                                                                          |

FIG. 7-55

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|     |                               |        |       |                                                                              |     |                                                                                                                                                                                                                                                                                                                     |
|-----|-------------------------------|--------|-------|------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 217 | ADXCRA<br>D.17288.C<br>1_at   | BIRC6  | Sense | baculoviral IAP repeat-<br>containing 6<br>[Source:HGNC<br>Symbol;Acc:13516] | 217 | TACACAACTTTATTACAGGCACAAAATTATCAAAAATAC<br>GGTATAAAATTACCTTAAGGCTATGTATATAAGGGATGT<br>GTGTATGTGTGTATACACACAAAATAAATTTTGTGTTTC<br>CACTTGGATCCCCCTCCCTAAGATAACTCATTGTGTACAT<br>GCAAAATTAGAAAAATGCNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>TATTAA |
| 218 | ADXCRA<br>D.10737.C<br>1_s_at | ABR    | Sense | active BCR-related<br>gene [Source:HGNC<br>Symbol;Acc:81]                    | 218 | AACTGCATGATGCACCTGCTCCGCTCCCTGCCCGACCC<br>CAACCTCATCACCTTCCTCTTCCTGCTGGAACACTTGAA<br>AAGGTTGCCGAGAGGAGGCCCATCAACAAAATGTCAC<br>TTCACAACTGGCTACCGTGTGTTGGACCCACGTAACGTG<br>AGACCCTCAGAAAGTGGAGAGCAAGCAACACTCACCTC<br>GGCTCGGACATCTGGCCCCATGACGTCATGGCGCAG<br>GTCCAGGTCCTCCT                                           |
| 219 | ADXCRA<br>G_BC015<br>928_s_at | ARRDC3 | Sense | arrestin domain<br>containing 3<br>[Source:HGNC<br>Symbol;Acc:29263]         | 219 | GCTCATAACAAAATATACCAGCATTTCATGATAGCATTTCA<br>GCATTTTCCAAGGTACCAAGTGACTTATTTTGTGTTGT<br>TGTTGTTGTTGATTTTAGAAGGAATTCAGCTCTGATGTT<br>TTTAAAGAAAACCAAGCATCTCTGATGTTGCAACATACGT<br>GTAAAATGGGTGTTACATCTATCCTGCCATTTAACCCCA<br>CAGTTAAT                                                                                   |
| 220 | ADXCRA<br>G_AF1366<br>31_at   | NRN1   | Sense | neurtin 1<br>[Source:HGNC<br>Symbol;Acc:17972]                               | 220 | TATCCAACGGTATAGATCACAAAGGGGGGATGTTAAAT<br>GTTAATCTAAATATAGCTAAAAAAGATTTTGACATAAA<br>AGAGCCCTGATTTTAA                                                                                                                                                                                                                |

FIG. 7-56

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|     |                               |        |       |                                                              |     |                                                                                                                                                                                                                                                                                                                    |
|-----|-------------------------------|--------|-------|--------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 221 | ADXCRP<br>D.8313.C1<br>_at    | TSPAN1 | Sense | tetraspanin 1<br>[Source:HGNC<br>Symbol;Acc:20657]           | 221 | GACAAAGCTCTAGGATGATGGCTGAGGGGTAGAAGAAG<br>GGCAAGGGAGACAGAGGTCTTGGAGATGACGCCCAT<br>ATCTCTGGCATGAGCAACCCAGATGGCAGGGGTGGG<br>GCCTGGTTTGTGGAAGGGGTGCCACTAGCAGATGT<br>GTACCCAGTGGAGTGCAGCTCAGATTGGAGCTGGCC<br>ATGGTATTTGAAAATCATGTGCGCACAGGTAGCCACT<br>GAAGCCATGGGAGTGAAAGAGAACACACTTGGAAAGTGAA<br>CTCTGGGAAA           |
| 222 | ADXCRP<br>D.8891.C1<br>_at    | RNF213 | Sense | ring finger protein 213<br>[Source:HGNC<br>Symbol;Acc:14539] | 222 | TGGACCGTCCAAGAAGGAGCTACATCAGAGGTTTTGGT<br>AGATGCTGCTGTAGACCTCATATCCGATGAATGGGAAG<br>CTGCTAATGCCATACCCAGCAGAGAGAGAAGGAGCAGGA<br>TGCAGCCCCGCTTGAGGCCGCCAGCGTGCCTTCTGCA<br>GACTGTGAGCAGAGCAA                                                                                                                          |
| 223 | ADXCRA<br>D_BG709<br>217_s_at | FRYL   | Sense | FRY-like<br>[Source:HGNC<br>Symbol;Acc:29127]                | 223 | AGCTTTGCAGTTATAGGCTCTAACCTGGACATGTCAGAA<br>GCCAACTACAAACTGATGGAACTTAATCTGGAAATAAGA<br>GAGTCTCTACGCATGGTGCAATCATACCAACTTCTAGCA<br>CAGGCCAAACCAATGGGAAATATGGTGAGCACTGGATT<br>CTGAGACACTTCAGGCCCTTTAGGAAAGAACTAAACTG<br>AAGATGATGAAGAAATATTAACCAAGCACCTTTTAATGGA<br>CCCTTGCTTCACTGATAACTTTTCTGGCAGCATCTACTTT<br>TTAGT |

FIG. 7-57

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|     |                             |                                                          |           |                                                                                                                   |     |                                                                                                                                                                                                                                                                                                                        |
|-----|-----------------------------|----------------------------------------------------------|-----------|-------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 224 | ADXCRP<br>D.17672.C<br>1_at | BLCAP ///<br>RP11-425M5.5<br>(Clone_based_<br>vega_gene) | AntiSense | bladder cancer<br>associated protein<br>[Source:HGNC<br>Symbol;Acc:1055] ///<br>Putative processed<br>transcript. | 224 | AGGCTAGGAGATGCCTGAGCCTCCACTGACCTCTGTG<br>CATGTGGCCACCAGTGGCCACTCTGTCCCTTTTGAAA<br>CTGTCTCTGGCTTTCTAGGAACCCCATGTTTTGGTCT<br>TCTCCTCTGGCCCTCCTTCTCAGTCTCCTCAGCAGGA<br>CTCTATTCTGTACCCATTCTCTAAATGTCACGAATCG<br>TTTCTGGCCTTGCTCTTCTTTGAGTGCATCTCTGTTCT<br>TCATCTATCCCTGTTGAGATGCTCACCCCTTCTTTGGTGA<br>GTCCTCAACCGGTACAGTA |
| 225 | ADXCRP<br>D.14904.C<br>1_at | RBM19                                                    | Sense     | RNA binding motif<br>protein 19<br>[Source:HGNC<br>Symbol;Acc:29098]                                              | 225 | AATTGTGCCTACCTCAGATAGACAGTGCCAGAAATTAAGT<br>GAGTCAAGCCCAAGTAAAGCCCCAGAGAAGA                                                                                                                                                                                                                                            |
| 226 | ADXCRP<br>D.12875.C<br>1_at | KANK1                                                    | AntiSense | KN motif and ankyrin<br>repeat domains 1<br>[Source:HGNC<br>Symbol;Acc:19309]                                     | 226 | TCTTCACACAGACAAATTCGATCAGTCCTCAGGCTTTAA<br>GTCACCTTCTCAAGAATGCCGTACTTGCCTAGGCTAGATT<br>AGATCCTACTGTTACATGCTCCCTTTTA                                                                                                                                                                                                    |
| 227 | ADXCRH.<br>157.C4_s_<br>at  | HMB1                                                     | Sense     | high-mobility group box<br>1 [Source:HGNC<br>Symbol;Acc:4983]                                                     | 227 | TTTAGTAGTACGTGATGACAACATACCATTTTTTAAGAT<br>GTTGAGAAATGGGAACAGTTTTTTTAGGGTTTATTCTTGA<br>CCACAGATCTTAAGAAAAAT                                                                                                                                                                                                            |
| 228 | ADXCRH.<br>278.C1_s_<br>at  | MRPL23                                                   | Sense     | mitochondrial ribosomal<br>protein L23<br>[Source:HGNC<br>Symbol;Acc:10322]                                       | 228 | GGCGGCTCCCCAGCTGGTTCGGGCTGTGACGGGGTG<br>GCCAGCAGGGACGCGCCCCCAGGTGGCAGCTGTGGCA<br>GAGCAGCAGCCCGCGGGCGGGCATCCCCAGCTG<br>GTTCCGGCCGTGACGGGGCGGCCAGCAGGGACGCGC<br>CCCAGGTGGCAGCTGTGGCAGAGCAGTCCCCGACACC<br>TAAATAAAAGTCTTGCTGCAGGA                                                                                         |

FIG. 7-58

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|     |                               |                                             |           |                                                                                          |     |                                                                                                                                                                                                                                                                                                     |
|-----|-------------------------------|---------------------------------------------|-----------|------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 229 | ADXCRP<br>D.14739.C<br>1_s_at | FANCD2                                      | Sense     | Fanconi anemia,<br>complementation group<br>D2 [Source:HGNC<br>Symbol;Acc:3585]          | 229 | AGATAAATTGTTGCCCTGCTTCTGTGCTCTGCCAGCCTG<br>TGATCATATTGGGTTAGAGTTAGAAATCCGCTGTTTGCC<br>TTTCTTACTGGTAGGATCCTT                                                                                                                                                                                         |
| 230 | ADXCRH.<br>481.CB1_<br>at     | RP11-122C9.1<br>(Clone_based_<br>vega_gene) | AntiSense | Known pseudogene.                                                                        | 230 | ATCTCGCCATTGGAATTTTCAGTTCTGTACATCTGCCTA<br>TATTCCTTGATAGTAGTCTTTGCTTTTCATAGATAAGCT<br>TCCTCCTTGCCCTTCGAAGCATCTTTTGGGCAAACTTCT<br>TTCTCAGGCGCTTGATCTTCAGCTCTGCG                                                                                                                                      |
| 231 | ADXCRP<br>D.5372.C1<br>_at    | MGEA5                                       | Sense     | meningioma expressed<br>antigen 5<br>(hyaluronidase)<br>[Source:HGNC<br>Symbol;Acc:7056] | 231 | AAACGAACTGTAAAAGACCATGCAAGAGAGGCAAAATAAAA<br>CTTGAAGTGAATGCTTAA                                                                                                                                                                                                                                     |
| 232 | ADXCRP<br>D.14347.C<br>1_x_at | TYRO3                                       | Sense     | TYRO3 protein tyrosine<br>kinase [Source:HGNC<br>Symbol;Acc:12446]                       | 232 | AGCAGCTACCAAATCTCAAAATATCCTAAGACTAACAC<br>AAGGCAGCTGTGTCTGAGCCCAACCCCTTCTAAACGGTG<br>ACCTTAGTGCCAACTTCCCTCTAACTGGACAGCCTCT<br>TCTGTCCACAGTCTCCACGAGAGAAATCAGGCCCTGAT<br>GAGGGGAATTCCTGGAACCTGGACCCAGCCTTGGT<br>GGGGAGCCCTCTGGAATGCATGGGGGGGCTCCTAGC<br>TGTTAGGGACATTTCCAAGCTGTAGTTGCTGTTTAAAA<br>TA |

FIG. 7-59

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|     |                                 |         |           |                                                                                      |     |                                                                                                                                                                                                                                                                                                                          |
|-----|---------------------------------|---------|-----------|--------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 233 | ADXCRA<br>D_BX5094<br>55_s_at   | DECR1   | Sense     | 2,4-dienoyl CoA<br>reductase 1,<br>mitochondrial<br>[Source:HGNC<br>Symbol;Acc:2753] | 233 | CATCATGTTTTGTGGGCAATACAAGTTGTTATAATTAA<br>AACCCCTAATTTGAATATTTTGTACCAAGAACCAAGG<br>CAATGTTTAAATTTGTTATAAAACCTGTTTGTGAAGTGCT<br>GTGTTAAATTTGTGCTGCTGGCTAATAGGCCCTCATTTCAA<br>TTTAATAAATATTTATTGAGGACTGGCTTTATGTCCTGGCC<br>CTGTGC                                                                                          |
| 234 | ADXCPRP<br>D.15787.C<br>1_s_at  | SAPS2   | Sense     | SAPS domain family,<br>member 2<br>[Source:HGNC<br>Symbol;Acc:19253]                 | 234 | AGTATCTGATATGTGTGGAGGAGCCATCTTTTCCTG<br>AAAGTCCTTTTAGGAATCATTATTTCTGGTCCCTCTGAAGT<br>TTGCCGTACCACTCATAAATATCTATCCACACCCCTTA<br>CAAGAAGAAAGGAAGATCTTAAGACCTAGAAGGAA                                                                                                                                                       |
| 235 | ADXCRRSS<br>.Hs#S298<br>4711_at | SH3GLB1 | AntiSense | SH3-domain GRB2-like<br>endophilin B1<br>[Source:HGNC<br>Symbol;Acc:10833]           | 235 | ACTTGACCTAGGCAGTGACCATTTCTCTCCCACCTTTCACA<br>CATGTTCACTTGACTTCCAGGCCATACTCTTAGTTTCCA<br>TTTTACCTCACTGCCCTCACTCGTTATCATCTTCCCTTGCCCT<br>CGTCCCTCAACTCTCTATGCTAGAGTACTTCAGGGATCA<br>GTCCCTTGATCCTCTCCTTTTCTCTATAGTACTCCTTTGA<br>GGTTTATCTAGTCTCACAGATTTAAATATCTTTGATATG<br>CTGACAACTCTCTAATTATCTAATTCACCCCTGCCC            |
| 236 | ADXCPRP<br>D.9852.C1<br>_at     | DNAJC10 | AntiSense | DnaJ (Hsp40) homolog,<br>subfamily C, member<br>10 [Source:HGNC<br>Symbol;Acc:24637] | 236 | AAAAATTTCTCTTTTGCTCTTTTCGTAGAAATAAACTTAACA<br>GTTGGATAGGCCCTGATCCAGCTTTCTGGCATGTCTG<br>AGCATAAGCCTGACAGTCTACTTTTCCAGCTTTCACCTTT<br>TCCTTTAATCATCTAGCCAAAGAGCTCAAAATTCCTGGAGC<br>AAAATTTCTGGCAAGGTCCACACCAAGGAGCATAGAAAT<br>CAATCACCCCAATGATTTTCCCTTGAGAACCTTTTTCACCT<br>GAAAGTCTGAGGTGTTAGATCTGTGGATACCTTGATCCC<br>GGGAA |

FIG. 7-60



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|     |                               |                                              |           |                                                                                                                                                                      |     |                                                                                                                                                                                                                                                                                                                                    |
|-----|-------------------------------|----------------------------------------------|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 240 | ADXCRA<br>D_AL8322<br>50_s_at | SNRPN ///<br>SNURF                           | Sense     | small nuclear<br>ribonucleoprotein<br>polypeptide N<br>[Source:HGNC<br>Symbol;Acc:11164] ///<br>SNRPN upstream<br>reading frame<br>[Source:HGNC<br>Symbol;Acc:11171] | 240 | ACTTGAACCCCGAAGGCAGTGTGTTGTGTGAGCAGAAA<br>TTGCTTCATTGCA                                                                                                                                                                                                                                                                            |
| 241 | ADXCRA<br>D_BQ187<br>449_s_at | SLC37A1                                      | Sense     | solute carrier family 37<br>(glycerol-3-phosphate<br>transporter), member 1<br>[Source:HGNC<br>Symbol;Acc:11024]                                                     | 241 | GGCCATGGCACTGCTGTTCAGCTCAGGCACAGGGGC<br>ACAGCAGAGGTTTGGGAAGCGGTCTCCCCACCGGCAC<br>TGGATTGGCGGTCCAAAGCCAGCAACCGGCTTCGC<br>TCCACAACACACACACACCTGGGACTGTTTTTAATACA<br>TAGCAACAGACTGGGTATTTATTTAAGATGIGTATTGT<br>GTCATATGAAGTTNAAGAGACATAAATGGCATTTTGTTA<br>TTTATTAAAGACAAACTCCAATTGTTCTCTGGCTGTTTTT<br>TCAGTTGTGCTAGCAAATACTTATCTGCCCT |
| 242 | ADXCRA<br>D_12485.C<br>1_at   | AC130352.2<br>(Clone_based_<br>ensembl_gene) | AntiSense | Novel miRNA.                                                                                                                                                         | 242 | AGACTGACTGCTAACTGTATGAATGATGAGGGGATTG<br>CACGTATAATCTTAAGTGTACATCAATGTTAATTTTTTA<br>TTTTATCCACTGCTCTTTGAAAACCTAACTCTTGACTAAGA<br>ACTGACTTTCCCTGTACTTGTGTTGACTCTAAGTAACTT<br>CCAAATCCACATAGTCCAAAGATGATGTGCTGAGAAATC<br>TCTCAAAAGGAAAAATGCTAAGAAATACAGGCAGAGTTATG<br>CGGCAAAATTTGCAGAAATTAACACAATTGCACCTGTGAG<br>TATGAAGCAC         |

FIG. 7-62

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|     |                               |                                                  |                    |                                                                                                                                        |     |                                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|--------------------------------------------------|--------------------|----------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 243 | ADXCRP<br>D.15952.C<br>1_s_at | SPDYE2                                           | AntiSense          | speedy homolog E2<br>(Xenopus laevis)<br>[Source:HGNC<br>Symbol;Acc:33841]                                                             | 243 | ATGGACAGAACGGAGACTAGGTTCCGTAAGAGGGGACA<br>GATTACGGGAAAGATCACGACCAGCCGTC AACCCACC<br>CCCAGAATGAGCAGAGTCCCCAGCGGAGCACCT                                                                                                                                                                                                     |
| 244 | ADXCRP<br>D.3305.C1<br>_at    | SMURF1                                           | Sense              | SMAD specific E3<br>ubiquitin protein ligase<br>1 [Source:HGNC<br>Symbol;Acc:16807]                                                    | 244 | TTTGTACATATGCAATAAACTCACGACTTTACATTT                                                                                                                                                                                                                                                                                      |
| 245 | ADXCRP<br>D.5066.C1<br>_at    | N/A                                              | No Genome<br>match | N/A                                                                                                                                    | 245 | GGAA GTGGACGCAAAAGTGGATGCGGCGAGCAGAAA                                                                                                                                                                                                                                                                                     |
| 246 | ADXCRA<br>D_AL8331<br>74_x_at | C1orf21                                          | Sense              | Uncharacterized protein<br>C1orf21 (Cell<br>proliferation-inducing<br>gene 13 protein)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q9H246] | 246 | TGCCCATGCATGATGGCTTACACCTGTAAATCCAACACT<br>TTGGGAGTCTGAGGTGGAGGATTGCTTGGGTCCAGGA<br>GTTTAAGACCAGCCTGGCCAAACATGGTGAACCCCTGCC<br>TCTACAAAAATACAAAAATTAGGCAGGCATGATGGTGT<br>GCACCTGTGGTCCCAGCTACTCAGGATGCTGAGGTGG<br>GAGGATCACTTGAGCCTGGGAGATGGAGGTGCAGTGA<br>GCCGTGATCATGCCATTGCACTCCAGCCTGGGTGACAG<br>GGTAAGAAACTGTCTCAAAA |
| 247 | ADXCRP<br>D.11335.C<br>1_at   | RP11-<br>706O15.1<br>(Clone_based_<br>vega_gene) | AntiSense          | HCG1981372, isoform<br>CRA_cNovel protein ;<br>[Source:UniProtKB/TrE<br>MBL;Acc:B1B108]                                                | 247 | TGGAGTGCATAGGTAGCAGTGCTTCTCCCCAAGGCTG<br>GGGCGATGGAATCAGTTAGACTATTGAGGGCATCTGGA<br>AGGCATCTGTGTCAAGGTTAGTCCTCAGGGTATGGTG<br>GCCAATGGGTTCTTTTGGTTGACTGTTGACAATGCGTT<br>TGTGAATGGCAGCCTGCAGTGGTGACGCTGAAGCCCA<br>CAGAA                                                                                                      |

FIG. 7-63

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|     |                               |                                                  |           |                                                                                                           |     |                                                                                                                                                                                                                                                                                                                      |
|-----|-------------------------------|--------------------------------------------------|-----------|-----------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 248 | ADXCRA<br>D_DN602<br>385_s_at | MAPK1IP1L                                        | Sense     | mitogen-activated<br>protein kinase 1<br>interacting protein 1-<br>like [Source:HGNC<br>Symbol;Acc:19840] | 248 | TTCATTCCACAAAAACCTGAGGCAGCTCTTTTGCCC<br>AGAGCGTTCCTGTAGCCACCCACCCCACTTGCC<br>CTTGTTCTTTAGAGGAGCACACATCCCTTGATTC<br>CTCCCTGATGTGGTAACTGGCACACTCCAGGGGTCT<br>AAAAACATAAAACAGTTGTGTTTAGGGAACCTTAAGTCA<br>TGC                                                                                                            |
| 249 | ADXCRA<br>G_BC033<br>465_at   | VDR                                              | Sense     | vitamin D (1,25-<br>dihydroxyvitamin D3)<br>receptor<br>[Source:HGNC<br>Symbol;Acc:12679]                 | 249 | ACAGAGGCTTCTTCAGATCAGTGCTTGAGTTTGGG                                                                                                                                                                                                                                                                                  |
| 250 | ADXCRA<br>D.11659.<br>C1_at   | ARHGAP26                                         | AntiSense | Rho GTPase activating<br>protein 26<br>[Source:HGNC<br>Symbol;Acc:17073]                                  | 250 | ATTCTGCATGATTCACGGACTAGGAGTCCCTGGTCAA<br>AACTTCAAAAACTAAGTGATGGGTCCCAAGTTACTCA<br>GTGCAGAAACTTGATTGAGTAACATGTCAGCTTGTG<br>GGCTTGAAAAGTCTTAAGTGCTCTACTTCTTCTATCC<br>TTGTGCTTTCCCGGGACTTTACACAATCCCACCTCCC<br>ACTGGACAATTGTCAAATCCCAGAGAGATGGGAAGT<br>CTGTTCACTCTGTATCACCATAA                                          |
| 251 | ADXCRA<br>D_AA601<br>031_at   | RP11-<br>761E20.1<br>(Clone_based<br>_vega_gene) | Sense     | Novel processed<br>transcript.                                                                            | 251 | GACGGTCCGCCGTGCCCCAAGAGGAACGGGATGACAT<br>TCAACTGGGACTTGCCCTCACCTTGGCTTGGGGACCT<br>CGAGAGCGGTCCCGTGGGGCAGTGTTACTCGTGGT<br>GGTAGAAGTGGAGGGCGTGTCGGGTACTTGAGTTC<br>ATGGGCATCTCTCCCGCCGCTCTCAGCCTATCTGCA<br>CCATGTCTCACACGTTCAAGTTGACGCTCTTACCGTTT<br>GAAGGCGCACGTGGGCAAGAAGTCCTGGGCAGCACA<br>AGAAAGTCAATCACGTTGAGACAGAG |

FIG. 7-64

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|     |                                 |          |       |                                                                                                                       |     |                                                                                                                                                                                                                                                                                                           |
|-----|---------------------------------|----------|-------|-----------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 252 | ADXCRA<br>G_BC015<br>773_s_at   | PPP1R14C | Sense | protein phosphatase 1,<br>regulatory (inhibitor)<br>subunit 14C<br>[Source:HGNC<br>Symbol;Acc:14952]                  | 252 | GACTCTAGCCACAGCCTAACCAAGGATTATCAAAGGAG<br>GTGGACACTCAAGGAAGGGCCACGCCAGGCTGCGTTT<br>CCTGCAAGGACTCAGATGTTCAAGTACCTTATGATACAGG<br>GAAGATAGTTTTCTTACAAGTAGTTGGTAATATTTTTT<br>TCTTAAGTTGTACATTTGACTCAGCTGTCAAATTTCTCAC<br>ACTTGATATATCTACACACAACCTAAGTTAAA                                                     |
| 253 | RDCR178<br>_E08_s_at            | INSR     | Sense | insulin receptor<br>[Source:HGNC<br>Symbol;Acc:6091]                                                                  | 253 | GGGAACAGGGAATGCCGATTTTATATACATGGTACACA<br>GAGAGGGGTGTCACTTCACAAAATCTTCCAGCATGTTCT<br>TCAGAAATATTAATTTATATCGAGGTGAGGTGGGAATG<br>AAAAGAACAGGTCAGCACNNNNNNNNNNCCCTATAACAT<br>ACAAAAGAACATGGTGGACTTTCAGGGAGTGCAA                                                                                              |
| 254 | ADXCPR<br>DRC.1444<br>4.C1_s_at | PRKDC    | Sense | protein kinase, DNA-<br>activated, catalytic<br>polypeptide<br>[Source:HGNC<br>Symbol;Acc:9413]                       | 254 | GAGATTTTGTGGTGGTGTATTCGAGAATTCCTTAAAT<br>GGTCCATTAAAGCAAATAACACCACAGCAGCAGGAGAAG<br>AGTCCAGTAACACCAAATCGCTTTTCAAGCGACTTTAT<br>AGCCTTGGCTTCAACCCCAATGCTTTCAAGAGGCTGGG<br>AGCATCACTTGCCTTTAAATAATATCTACAGGGAATTCAG<br>GGAAAGAAGAGTCTCTGGTGGAAACAGTTTGTGTTGAAG<br>CCTTGGTGATATACATGGAGAGTCTGGCCTTAGCACAT     |
| 255 | ADXCPR<br>D.1547.C1<br>_x_at    | HCN3     | Sense | hyperpolarization<br>activated cyclic<br>nucleotide-gated<br>potassium channel 3<br>[Source:HGNC<br>Symbol;Acc:19183] | 255 | TTCCCTCTGAGTTTGCTGTTGGTGCAGGAATAAGGAAA<br>GGCCCAAGGTATCCAAGCCTGGGAAGGGCAGGCCAG<br>CCAGCACCTCTGCCCTTCTCAGGGACAAGAGTAGTCCTT<br>TACCACCTCACTCTGCCTGTCCCTCTCCTACTCTACA<br>GCATTAAAGACTGTGGGACCAGGACCCTAAGTCTCCTT<br>TCCTTCTGGGTGGGAGTTCTGGGTTCTTGGTGTGTG<br>GGAGAAGTTTATAATTGCTTCCAAACACAGCTGGGTTTAA<br>ATATA |

FIG. 7-65

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|     |                                |                                         |           |                                                                                                                                                                                                                                                           |     |                                                                                                                                                                                                                                                                                                                     |
|-----|--------------------------------|-----------------------------------------|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 256 | ADXCRSS<br>.Hs#S297<br>8040_at | CAMK1D                                  | Sense     | calcium/calmodulin-<br>dependent protein<br>kinase ID<br>[Source:HGNC<br>Symbol;Acc:19341]                                                                                                                                                                | 256 | TTCTGGATGTATCTTCAGGAGCATTAGCATTCCCTGGTA<br>GGTTGAAGATGGGCCAGTAAGGAAACAGAAAGGGTCAA<br>AGGTGATGCCAAGATTTTGGCCAAAGCACCTGAAAGAT<br>GGAGTTGCCCCATGACTAAGATGGGGAAGCACGGGGTC<br>AGCACCGATTTGGGGGAAGATCAGGATTTTCATCTTG<br>GATGTGCTGAGTTTGAACATCTGAGTCATATCCCAAGTG<br>AAGAGTTTGAA TAGGCCGTTGGATATATTTAGGATAAAA<br>GCCTGGGCTA |
| 257 | ADXCRA<br>D_CX8722<br>80_s_at  | P4HB                                    | Sense     | prolyl 4-hydroxylase,<br>beta polypeptide<br>[Source:HGNC<br>Symbol;Acc:8548]                                                                                                                                                                             | 257 | ACCAGCGCATCCTCGAGTTCCTTTGGCCTGAAGAAGGAA<br>GAGTGCCCGGCCGTGCGCCTCATCACCCCTGGAGGAGG<br>AGATGACCAAGTACAAGCCCCGAATCGGAGGAGCTGACG<br>GCAGAGAGGATCACAGAGTTCTGCCACCCGCTTCCTGGA<br>GGCAAAATCAAGCCCCACCTGA                                                                                                                   |
| 258 | RDCR489<br>_A06_at             | C17orf88 ///<br>LRRC37A ///<br>LRRC37A2 | AntiSense | chromosome 17 open<br>reading frame 88<br>[Source:HGNC<br>Symbol;Acc:17505] ///<br>leucine rich repeat<br>containing 37A<br>[Source:HGNC<br>Symbol;Acc:29069] ///<br>leucine rich repeat<br>containing 37, member<br>A2 [Source:HGNC<br>Symbol;Acc:32404] | 258 | CGTGCTACCATCACAGCTGAATGCAATGAAAGCGGGTC<br>CTCTGAGAGGAGCAGGGTGGAGATGCTAAAGTGGAGG<br>CCCCGTCCCATTGCTGATAGATCCTCATCTGTGGCA                                                                                                                                                                                             |

FIG. 7-66

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|     |                                |         |       |                                                                                                                         |     |                                                                                                                                                                                                                   |
|-----|--------------------------------|---------|-------|-------------------------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 259 | ADXCRA<br>D_15527.C<br>1_x_at  | SLC6A6  | Sense | solute carrier family 6<br>(neurotransmitter<br>transporter, taurine),<br>member 6<br>[Source:HGNC<br>Symbol;Acc:11052] | 259 | TGATCTAGAGGTCCCCCTTCGGAAATAGGGAAGACTGT<br>CTCTGAAGAGGAGGAAGTGTAGCTTATGGGAGGCTGA<br>GGAGTTTGGAGTTTCTCCTTGTGGGAAGTGGAGCCA<br>TGGAGGCTGAAGACAGTTGTCCAACCTCAGGGCATACAA<br>ATTGATGAGGAACTC                             |
| 260 | ADXCRA<br>DRC.2992<br>.C1_s_at | TAPBP   | Sense | TAP binding protein<br>(tapasin)<br>[Source:HGNC<br>Symbol;Acc:11566]                                                   | 260 | CTGCCCCGAGTGAGACTGGGACAAGATGCTCTGCTG<br>GACTTGAGCTTTGCCCTACATGCCCCACCTCCGAGGC<br>CGCCTCATCTCTGGCTCCGGTCCCCCTCCCTTTGGGC<br>TAGAGTGGCGACGCCAGCACCTGGGTAAGGGACATCT<br>GCTC                                           |
| 261 | ADXCRA<br>D_AB0331<br>02_s_at  | FAM184B | Sense | family with sequence<br>similarity 184, member<br>B [Source:HGNC<br>Symbol;Acc:29235]                                   | 261 | GTGAGCCAAGTTCGAACCTCCTGCATTCACACCAGCCT                                                                                                                                                                            |
| 262 | ADXCRA<br>D_BM264<br>147_s_at  | CDK12   | Sense | cyclin-dependent<br>kinase 12<br>[Source:HGNC<br>Symbol;Acc:24224]                                                      | 262 | GATGGGATAATTTGGGAGGCTTCTCATTTCTGGCTTCTAT<br>TTCTATGTGAGTACCAGCATATAGAGTGTTTTAAAAACA<br>GATACATGTCATATAATTTATCTGCACAGACT                                                                                           |
| 263 | ADXCRA<br>G_AK1603<br>79_at    | SP100   | Sense | SP100 nuclear antigen<br>[Source:HGNC<br>Symbol;Acc:11206]                                                              | 263 | ACCAATACCACAGGTTCTCAGTTGTGAGTGGGAGCTA<br>AATGATGAGAACTCATGAACACAAATGAAGGGAACAGAC<br>ACTAGGCTCTACTTGAGGGTGGGAAGATGGGAAGAGGGA<br>GAGGAGCAGAAAAAGTACCTATTGGTGATGAAGTACTC<br>TGTACAAACAAACCCGTGACAAAGAGTTTCCCTATATAAC |

FIG. 7-67

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|     |                                 |         |           |                                                                             |     |                                                                                                                                                                                                                                                                                                                       |
|-----|---------------------------------|---------|-----------|-----------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 264 | ADXCRH.<br>3937.C1_a<br>t       | SH3D19  | AntiSense | SH3 domain containing<br>19 [Source:HGNC<br>Symbol;Acc:30418]               | 264 | AACAGCTGCTTTTGGTATCAATACCCTGTTGGTTATTAG<br>TTTAAATTTTAGTCAATGATGCTTTTGGTGGGTGTGA<br>AGGGGAAGAAATCTTGAGCATGTAATGACTTAAATTG<br>TTCCCAATCAAATTAATTTCTGGGCCAGTATAAGACC<br>TACACACTCACATTTACAAGTGAGGGCATGGATGGGG<br>GTAGGGCAGGCGAGGAAAGGAGAAAAGAGACAATC<br>AGCACCCCTGAGGGGCTGAACATAGGGGGCATCCAAA<br>ACGTGCTTGCTGTGGGAAGAAT |
| 265 | ADXCRP<br>DRC.1366<br>3.C1_s_at | DYNC1H1 | Sense     | dynein, cytoplasmic 1,<br>heavy chain 1<br>[Source:HGNC<br>Symbol;Acc:2961] | 265 | CATTTGGATGACGACACGATCATAAACCACCTCTGGAGAA<br>CCTGAAGAGAGAGGGCTGCAGAGTCAACAGGAAAGTT<br>GAGGACCGACATTGTCTATGCAGAGGTGGAGACCG<br>TGTCACAGCAGTACCTCCCGCTCTCCACCCCTGCAGC<br>AGCATCTACTTACCCTGAGTCCCTCAAGCAGATACA<br>CTTCTGTACCAGTACTCCCTCCAGTTTCTCCTGGACAT<br>TTATCACAACGTCTCTATACGAGAACCCGAAACCTGA                          |
| 266 | ADXCRP<br>D.15326.C<br>1_s_at   | ZNF69   | Sense     | zinc finger protein 69<br>[Source:HGNC<br>Symbol;Acc:13138]                 | 266 | ATGACATACAGTGCATGGCTCACAATCCCAGGAGATGA<br>GGCAGCACAGCTGCAGAGCAACACAGAGTGGGAGA<br>ACATCCAGGATGCACATTCAACCAGCAGGTGGGAGCA<br>AGACAGACAGGGACCTGTGGGCCAAAGCGTT                                                                                                                                                             |
| 267 | ADXCRA<br>G_BC007<br>608_x_at   | HMGB3   | Sense     | high-mobility group box<br>3 [Source:HGNC<br>Symbol;Acc:5004]               | 267 | TAGGCTTAGCTTGATTTCTGGGCCCTGTCTGTGTTCT<br>TAAGATGCCAACCTGTTGCTTTTCTTTTCTTTTCTCCCC<br>ATTTAAAGGATAGTACCTACTCCCTCTAACCCACCTCAC<br>CCCATCTTGAATGACATTTTATCCTTCGAAAGAACAA<br>GGCTGTGATGTAGTACTATTGTCTGTCTCCTGTGTG<br>TGCTGTCTTGTACAAATGATTTGGGGACGTTGGAT<br>GCATTCAATTTCT                                                  |

FIG. 7-68

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|     |                               |                                                                                                                                                      |       |                                                                                                    |     |                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|-------|----------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 268 | ADXCRA<br>D_CR747<br>486_s_at | PPPDE2                                                                                                                                               | Sense | PPPDE peptidase<br>domain containing 2<br>[Source:HGNC<br>Symbol;Acc:24577]                        | 268 | GCCCCACTGTCACTAACTGTAAACTCAGGCTCAGGCTT<br>CAACTGC                                                                                                                                                                                                                                                |
| 269 | ADXCRA<br>D_BE8322<br>79_s_at | PARP6                                                                                                                                                | Sense | poly (ADP-ribose)<br>polymerase family,<br>member 6<br>[Source:HGNC<br>Symbol;Acc:26921]           | 269 | AAGATTCTTCTTTGTATATGAGGATGGTCAGGTGGGCGA<br>TGCCAACATTAACTACTCAGGACCCCAAGATACAGAAGG<br>AAATCATGCGTGTGATCGGAACCTCAGGTTTACACAACT<br>GAGGGGCCCCAGCCCTCGTACCACCCCTGTTACCCC<br>AGGATCCATCTGCCCTCATAAAAGTGTTCAGGTACAGCA<br>GCTGAGGCTGCCCTGAGGAATCAAGGGGCCATTACCAA<br>GGGCAGGAAAAGGATATGTAAGAGGTGGCCTTCA |
| 270 | ADXCRA<br>D_CV5731<br>77_s_at | AC138866.2<br>(Clone_based_<br>ensembl_gene)<br>/// AC146949.1<br>(Clone_based_<br>ensembl_gene)<br>/// AC146944.2<br>(Clone_based_<br>ensembl_gene) | Sense | Novel long non-coding<br>RNA /// Known non-<br>coding long RNA ///<br>Novel long non-coding<br>RNA | 270 | TTGCAGCGAGTCAGGATCGCAGCACTACACTCC                                                                                                                                                                                                                                                                |

FIG. 7-69

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|     |                               |       |           |                                                                                  |     |                                                                                                                                                                                                                                                                                                                              |
|-----|-------------------------------|-------|-----------|----------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 271 | ADXCRA<br>D_BX0983<br>87_at   | EFR3A | Sense     | EFR3 homolog A (S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:28970]           | 271 | TTCACAGGAAGTAGGTAACACCGAAATTTAGTCAGTGT<br>CATTATTAGAGTTGTGCTTTCATAAAAAAGATCTCTCAAG<br>TGTGACAAAGGCTAAATTAGAAAGAAGAGACTGGAGGTA<br>GAGCCAGTTAGGAGATCCTTGTAATAATCCACAGTTGA<br>TGGAAATGAGGATCTATAGTAGCCAGGCTGGAGGTAACA<br>AAGAGGGACAGGAGGCGCAGGAGTACTCTACTTTAAAGT<br>AG                                                          |
| 272 | ADXCRA<br>D_XM_37<br>4484_at  | PCLO  | Sense     | piccolo (presynaptic<br>cytomatrix protein)<br>[Source:HGNC<br>Symbol;Acc:13406] | 272 | AGTTGTTAAGTGTATCAGATGTGTTGGGCATGTGAATCT<br>CCAAGTGCCTGTGTAATAAATA                                                                                                                                                                                                                                                            |
| 273 | ADXCRA<br>D_AW957<br>273_s_at | APOL1 | Sense     | apolipoprotein L, 1<br>[Source:HGNC<br>Symbol;Acc:618]                           | 273 | GTGGTTGTCATGTGATGGGTCCCCTCCAGGTTACTAAA<br>GGTGTCATGTCCCCTGCTTGAACACTGAAGGCGAGGTG<br>GTGGGCCATGGCCATGTTCCCAGCTGAGGAGCAGGT<br>GTCCCTGAGAACCCCAAACTTCCCAGAGAGTATGTGAGA<br>ACCAAC                                                                                                                                                |
| 274 | ADXCRP<br>D.15551.C<br>1_at   | EPHB4 | AntiSense | EPH receptor B4<br>[Source:HGNC<br>Symbol;Acc:3395]                              | 274 | GGAGACATCGATCTCTTTGCAAATTCCTCAGCCTC<br>ATTAGGCTCTTCATAAGTGAAGGGTCGATGTAGACCTT<br>AGTACCATGTCCGATGAGATACTGTCCGTGTTTGTCCGA<br>ATATTGCTTCTCTCCCATTTGCTCTGCTTCCTGAGGCA<br>GAGAACTGCGACCACAATGACCACCAAGGACCAAGACC<br>ACACCCACGACTGCCGTGCCCGCAATCAGGGCCAGCT<br>GTCGCCCGCAGCCCTCGCTCTCATCCAGTTGGGTCCG<br>GCTGTGATGTTCTTGGCCGAAGGGCC |

FIG. 7-70

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|     |                               |        |           |                                                                                                                                |     |                                                                                                                                                                                                                                                                                                                                     |
|-----|-------------------------------|--------|-----------|--------------------------------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 275 | ADXCRPD<br>_BX11171<br>_9_at  | TAF15  | Sense     | TAF15 RNA<br>polymerase II, TATA<br>box binding protein<br>(TBP)-associated factor,<br>68kDa [Source:HGNC<br>Symbol;Acc:11547] | 275 | GGAGTTTGTGACTAGATGGGCAATATAGTAAGATGTCAT<br>CTTTAAAAATGAAAAATAGCTGGCCACTGTGGCACA<br>CGCCTGTAGTCCAGCTACTTGGGAAGCTGAGGTAGGA<br>GGATTGCTTGAGCCAGGAGTTCAAGGCTGCAGTGAGC<br>TATGATTGTGCTTATGAATAGCCACTGCACCTCCAGTCTG<br>GGCAATAGTGAGTCGGTCAAAATTCATTCCCCCTCCGC<br>CCCATACCTCTTCAAAATGTTT                                                   |
| 276 | ADXCRPD<br>_14035.C1<br>_s_at | KCNE3  | Sense     | potassium voltage-<br>gated channel, Isk-<br>related family, member<br>3 [Source:HGNC<br>Symbol;Acc:6243]                      | 276 | ACTGCATCAGGTCTCAGTGTCCTATCTGTAAAGATCAAC<br>AAGAAACACGGTTAAGGGAGGTCTGCTCACTGGGTGGGA<br>GAAGAGGGGCTGGTAGACCGAAGCCTTGTGCATAAGGA<br>TTTTTCCCAGGAAAGATAGACTTTTATAAACAGTGGGA<br>GCCCATGAACAAACATATAAAAGTAGCAACAGATAATGA<br>CC                                                                                                             |
| 277 | ADXCRPD<br>_8986.C1_<br>_at   | HOXB8  | AntiSense | homeobox B8<br>[Source:HGNC<br>Symbol;Acc:5119]                                                                                | 277 | TATTGTAACCTTCCGCCCTTTTCAGGCGCAGACAACAG<br>AACAAAGTATAGAGGAACAACAAATATATAATTAGCCC<br>TCCCTCCCCCCCATAAAGCAATTCACGGATACAGAATAC<br>ATTCTCTCACAGTAAACCTAAGAACACTTGTAAACAATTG<br>CCACAGCGCGCATGCTAACTAAAGTAACCTCTTTTGA                                                                                                                    |
| 278 | ADXCRPD<br>_10916.C1<br>_at   | KLRAQ1 | AntiSense | KLRAQ motif containing<br>1 [Source:HGNC<br>Symbol;Acc:30595]                                                                  | 278 | TACTGCTTGCATATCCTTTCCCTCAGCTAACCGTCCCTCCT<br>GGGCCCTTCTGCTTCTGACCCCTCAGGACCTTAGGAC<br>ATAATCAGTCCCTGCTTCTATCTTCAGTATCTCCTCATTA<br>CAATAAAGCATTTGCTGCAGCTCATTTAACTCTTGTGTC<br>CACAGTGAGTCTCTTCCATTACTTAATCACACTTAATCT<br>CTGTCCCTGACTCCTGTCCCCAGCCTTTCTTTACACTTG<br>CCCGTCTGCAGGCTCTCATGCTTCTCCATTTGGCAACT<br>TCAGGAAGGTACGCGAGCTCCC |

FIG. 7-71

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|     |                               |          |           |                                                                                                 |     |                                                                                                                                                                                                                                                                                   |
|-----|-------------------------------|----------|-----------|-------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 279 | ADXCRA<br>G_AY2067<br>18_s_at | PPARA    | Sense     | peroxisome proliferator-<br>activated receptor alpha<br>[Source:HGNC<br>Symbol;Acc:9232]        | 279 | GCCAGTCACCCCTCGGATCGAGAGAGGGGTAGAGTC<br>TTCTTCAATGGCAGTTTACTTCAAATGGCAGATTTTCAC<br>AAGAGTTGGTTATTTTACAAATGGTTAGTTGTTAAGT<br>CTCCTTTGTATGTAAGGTAGTTTTTCAACATCTAAAATT<br>TTTGTTTAGCCTTCAAAACCAACTTACCAACCTCAGTC<br>CAGCTGGGAAGGCAGCGTTGATTATGGTAGTTTGTCAA<br>GAATATATGGACCTGGAAACAC |
| 280 | ADXCRA<br>D.9565.C1<br>_at    | PKM2     | Sense     | pyruvate kinase,<br>muscle [Source:HGNC<br>Symbol;Acc:9021]                                     | 280 | CACTGCTCAGGGTTGGAGGCTCAGTCCCTTTGCCCTGT<br>CTGTTCCAGCTCTGGAGCTAACTCAGGGATCCCTGATC<br>AGGTTACATAGGTTTGGTAAATGAGTGCTGGAAATTA<br>ACTTCTCCAGTAGTCTTAGGTCATGCTCAGTGAACCTT<br>AACTTTATCCAGATATGTTTTCTTCAGCCTTTCTATT<br>CCCTTTCTAGCCAGTGAAAGACCCGCTGC                                     |
| 281 | ADXCRA<br>D.12822.C<br>1_x_at | CDC42SE2 | AntiSense | CDC42 small effector 2<br>[Source:HGNC<br>Symbol;Acc:18547]                                     | 281 | CGAGAGTATATCAGTTAAAGGGTAAGAAATGTAGACCC<br>CATATTTAATTTCAGTAGCACCAAGTTCAAATCCAGTTATT<br>CAGAAATTAACAAAGCAACTGTTGCTCAAAAAAATGCCAA<br>TAAACTCCCGAGCCAACTGAGAT                                                                                                                        |
| 282 | ADXCRA<br>D.4113.C1<br>_s_at  | FA2H     | Sense     | fatty acid 2-hydroxylase<br>[Source:HGNC<br>Symbol;Acc:21197]                                   | 282 | ACCAAGGAGCTGGTCAGACGGCCCTTTCTAATCCCTACA<br>TGTTGAGCTTATGTAAAAAATGTTGTTCCCTCCTGTTTTT<br>GGTTCCCTTCTTACCCACAAACCATTACTACTTG                                                                                                                                                         |
| 283 | ADXCRA<br>G_BC000<br>004_x_at | HSCB     | Sense     | HscB iron-sulfur cluster<br>co-chaperone homolog<br>(E. coli) [Source:HGNC<br>Symbol;Acc:28913] | 283 | CAACAGAGTGAGACTTAATCTTGAAAAAATAAATA                                                                                                                                                                                                                                               |

FIG. 7-72

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|     |                             |        |           |                                                                                                             |     |                                                                                                                                                                                                                                                                                                                              |
|-----|-----------------------------|--------|-----------|-------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 284 | ADXCRP<br>D.7428.C1<br>_at  | EIF2S2 | Sense     | eukaryotic translation<br>initiation factor 2,<br>subunit 2 beta, 38kDa<br>[Source:HGNC<br>Symbol;Acc:3266] | 284 | AGTAGAGGGCCCTCAACCCACACACTGGCTGAAACTGC<br>CACCAACTGCCACGATGAACCCCACTGCTGTTTATGCC<br>CCCATTTTCCTTTTTTTGTATCTACACCCACACGATTCCC<br>AATGTTGGATATTTCTACATGAATAAAGCAAGGATCAGT<br>GCCTCTTATGT                                                                                                                                       |
| 285 | ADXCRP<br>D.240.C1_<br>s_at | TCEAL4 | Sense     | transcription elongation<br>factor A (SII)-like 4<br>[Source:HGNC<br>Symbol;Acc:26121]                      | 285 | AGGCCAAACAGGAGATGAGGAAATGTTAAAGGATAAA<br>GGAAAGCCAGAGAGTGAGGGAGAGGCAAAAGAAAGGAA<br>AGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNTGAAGGAGAGCCAGGGAGTGAACACAAGGG<br>CTGCAGGAAAGCGCCAGCTGAGGATGATGTACCCAG<br>GAAAGCCAAAAGAAAACCTAATAAGGGCTGGCTCATT<br>ACCTCAAGGAGTATAAAGAGGCCATAC |
| 286 | ADXCRH.<br>3436.C1_s<br>_at | USP12  | Sense     | ubiquitin specific<br>peptidase 12<br>[Source:HGNC<br>Symbol;Acc:20485]                                     | 286 | TGTGGGTGACAGTTTTACATTTTCTTCTTCTTAATG<br>CAGCTGGATCTAAGTAAATGTTTTGAAGTTTATCAGAA<br>ACTAAATGTACTTTTAAACGTATAGGGTCAGGGTTGGG<br>GGAAAATACAGGTATAGTAAGTAAGAAAAGTGACCCAT<br>GAAGAAAGCATCGTGAGGTTGTATGTTGGTTGACTGTG<br>ATTAAATGCGGGGCTGGTGAAGTTGTAAGTGGTGGC<br>TGATTGCCGTGTACTATGTACATGATTGTTGGATGGCT<br>GTCC                       |
| 287 | ADXCRP<br>D.10809.C<br>1_at | KANK1  | AntiSense | KN motif and ankyrin<br>repeat domains 1<br>[Source:HGNC<br>Symbol;Acc:19309]                               | 287 | GAAAACCTATAACATGATGAGTAAGAGTTCTATGGTAGA<br>GAGTAGGAGAGGAAAGGTGAAAACCTGCCACAAGCCAA<br>ATGAGACTGCAGCAAAGTATGTAAGGAGCCCTGTTCTCA<br>GGTCCACCCACATCCAGCTATCACCCCTCTCTGACCCGCC<br>TTTTCCCATGAGCCCTGAAAAGGTCACAGAC                                                                                                                  |

FIG. 7-73

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|     |                               |                                              |           |                                                                             |     |                                                                                                                                                                                                                                                                                                                                       |
|-----|-------------------------------|----------------------------------------------|-----------|-----------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 288 | ADXCRP<br>D.8357.C1<br>_at    | WSB1                                         | AntiSense | WD repeat and SOCS<br>box-containing 1<br>[Source:HGNC<br>Symbol;Acc:19221] | 288 | GAGGCACAACCTTCAACACTAATTGCCCTTTACTAAGCC<br>GACCAGGGCTAGACACTAAGCCAGAAAAGCCTTTTCCA<br>GAGTTTCCTCTTCCGCACAAAAGCTTTCCTTCTGTCACT<br>CCACCAACCAACCCAGCTCCTCCCTTAAGTGTGTTGAAA<br>GATAATTCTAAAAGTCTCCTCCCCCGAACCGCTGCGTTT<br>CTTAAGGCCACACCAATTTTAAAAATACTGTATTGCTTTTG<br>CCAGGCTGTTGGGACCTCTTCCATCTCATTTCTATCTAA<br>GAGTGGTTGGTACACACGAGGAC |
| 289 | ADXCRSS<br>.Hs#S833<br>047_at | CD200                                        | Sense     | CD200 molecule<br>[Source:HGNC<br>Symbol;Acc:7203]                          | 289 | AAAGCAGATGGGTGTGTTTCAGACAAGATCTGGAAGCTG<br>TGGCATGGCAGACAAAGGGAGATGGGACCCCTTTGGC<br>ACTGGAGGAAGAGGCTTGAATCTTCTTGAGCACATAA<br>AGTTCCAAAAGACCTAAGCAGAAAATGCTTCCGAAGAG<br>GAGGATCTGTATGGCAAGATGACTGTAATCAGGCTCAT<br>AAAAGTAAGACCTTACATAAATACAAAGTGAGGGGAAG<br>ACATTTTCATGTAGGAGGAATGGCTCAAGCAAAAATACCA<br>AGCGGGAAATTGCGTGGT             |
| 290 | ADXCRA<br>D_AW134<br>504_at   | AL604028.2<br>(Clone_based_<br>ensembl_gene) | Sense     | Known protein coding.                                                       | 290 | AGAAGTTTTGAGAAAGCAGTTTTGTTGGGTCAAGGGGTA<br>CTTTCAAATTACACTTATGAGTCAGTATCTATAAAAAGTT<br>TCAGAAGTACCTACAATTTAGCCCTCTACATCCAAGCAG<br>TAGCTTTGCAG                                                                                                                                                                                         |
| 291 | ADXCRA<br>D_BC0332<br>51_at   | RHOQ                                         | Sense     | ras homolog gene<br>family, member Q<br>[Source:HGNC<br>Symbol;Acc:17736]   | 291 | CAGTGAGCTATAATACAAGGCTTCATTGCACCTCCAGCCT<br>AGGCATTAGAGCGGAGACCGGTGTTTATTTAAA                                                                                                                                                                                                                                                         |

FIG. 7-74

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|     |                               |        |           |                                                                                                               |     |                                                                                                                                                                                           |
|-----|-------------------------------|--------|-----------|---------------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 292 | ADXCRA<br>D_CN297<br>218_at   | CUL9   | Sense     | cullin 9 [Source:HGNC<br>Symbol;Acc:15982]                                                                    | 292 | GCAGATGCAGGAACACCTAGAGCAGCCCCAGAGTCA<br>CGGGCTGAGGGGGGGAGCTGCCCCGTGCATAGGG<br>AGGGGATTCCAGCGTCTGTAGTCTTCTGTTTGCT<br>GAATAAAGGTCTCTTTCTCACAC                                               |
| 293 | ADXCRA<br>D.9433.C1<br>_s_at  | PAG1   | Sense     | phosphoprotein<br>associated with<br>glycosphingolipid<br>microdomains 1<br>[Source:HGNC<br>Symbol;Acc:30043] | 293 | CAGAAATGTTAGTGCCGTGCTCTAACCAAGTAAGCTTAG<br>TGTTCCCCACAGTGATCTGTATCTGGCCTGAGTCTCCTC<br>AAGCAGCAACCCCCACTGTCCAGCATGTGGAAGGTAGA<br>TCCTTATGACAACACACAGACCCCATAGTTACCAGGAAAGA<br>A            |
| 294 | ADXCRA<br>D_BE0438<br>58_x_at | QPR1   | AntiSense | quinolinate<br>phosphoribosyltransfera<br>se [Source:HGNC<br>Symbol;Acc:9755]                                 | 294 | GTGTTTAAGGGCATTTACAGATGGGAAATAAGGTGCA<br>GAGGGCTAGAGAGATGGGCTCAAGGCTGTGGTGCCAG<br>TGACACTGGCTTCCCCTGTGTGTCTTCTTCTTGAAC<br>ATCAGGCCACGCAGCAGCAGAACAAAGATAAAGAACCA<br>ATCCAAAACACGCGTGGTGGC |
| 295 | ADXCRA<br>D_CN423<br>589_s_at | VPS26B | Sense     | vacuolar protein sorting<br>26 homolog B (S.<br>pombe) [Source:HGNC<br>Symbol;Acc:28119]                      | 295 | GGCCGAGAAAGATGCTGGGCACCCACCCAGCACCCCCA<br>TCTACCAACACACGCGCTGGGGCGGGGGGACCT<br>TGTGAGGCTCAGTTGACCCGTTACTTGCAACCTGAAAA                                                                     |
| 296 | ADXCRA<br>D.17323.C<br>1_at   | ANKS4B | Sense     | ankyrin repeat and<br>sterile alpha motif<br>domain containing 4B<br>[Source:HGNC<br>Symbol;Acc:26795]        | 296 | CAAGAATCTGGCATTTCTCTTCAGTTATCTTATATGTACA<br>TATAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNGAGATGAAGGTCTCAGTCTCTTACCCAC<br>TGCACTCTAGCCCCAGGGGGTAAGAGAGACTCCAT                         |

FIG. 7-75

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|     |                               |            |                           |                                                                                   |     |                                                                                                                                                                                                                                                                                                                    |
|-----|-------------------------------|------------|---------------------------|-----------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 297 | ADXCRP<br>D.8537.C1<br>_at    | NCRNA00262 | No<br>Transcript<br>match | non-protein coding RNA<br>262[Source:HGNC<br>Symbol;Acc: 26785]                   | 297 | CCTCTACGCCAGAGAAGGGAATGGAGAGGTCAGGCTG<br>GCTAGAGAGTGGGGTTGAGTCGTCCATGCCCTTGAATG<br>CCAGGATGAGGGCTAAGAGTCAAAATGGAATGGGTGAC<br>TTCATATGCAGAAGTTTTTACAAGAGAGAGAAGAACTCAGT<br>TGGCCCAAGAGAAGTGGGGTCGTATGTGGGTAATCAC<br>GTAACAGTGATCGTTTCAGTCATCGGGAATGCTTTCAAG<br>GTGTTGGACAC                                          |
| 298 | ADXRSS<br>.Hs#S298<br>6790_at | RABGAP1    | AntiSense                 | RAB GTPase activating<br>protein 1<br>[Source:HGNC<br>Symbol;Acc:17155]           | 298 | CCTCTACGAGGTGTGCTATTCTCATCTCATCTTATAGG<br>CAAGTTAACTGAGGTATAAGGAGGTTGGTTATGTAACTT<br>GACCAAAGTCACACAATAAGGACTGGGAGATCTGGGA<br>TTTGAGCCCTGGCAGATGGACTCCATCCAAAGTCCTCA<br>CTATCCTAGCACCTCTCTATCCCCCTCCCTTCCCTCTCTC<br>CTACCTTCTTCTGTGCTGCTTTCAAACAGACAGTTATCT<br>CTACCCCTTAAAAACACAGCTGTGCTGACTACTCTGCTTA<br>GATGCCC |
| 299 | ADXCRIH.<br>2921.C1_s<br>_at  | CALM3      | Sense                     | calmodulin 3<br>(phosphorylase kinase,<br>delta) [Source:HGNC<br>Symbol;Acc:1449] | 299 | CCTCTGGGACAAAGTAAGTCAATGTGGCAGTTCAGTGG<br>TCTGGGTTTTTCCCCCTTTCTGTTCATTTTCATCTGGCTC<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGC<br>TTCCCCCTCACTGCCCCAGGTCGATCAAGTGG                                                                                                                                                     |
| 300 | ADXCRP<br>D.15035.C<br>1_at   | DLG5       | Sense                     | discs, large homolog 5<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:2904]        | 300 | TGGTCAAGAAGGACTATGACGCCCTTCGGGAAGAGGTAC<br>AGTG                                                                                                                                                                                                                                                                    |

FIG. 7-76

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|     |                               |        |           |                                                                                   |     |                                                                                                                                                                                                                                                                                                             |
|-----|-------------------------------|--------|-----------|-----------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 301 | ADXCRA<br>D_15234.C<br>1_at   | MACF1  | AntiSense | microtubule-actin<br>crosslinking factor 1<br>[Source:HGNC<br>Symbol;Acc:13664]   | 301 | AGAATAGCAACTGGCTCAGTCCCTTATAGGTGTCTACACTA<br>ATATCAAGGAACAGGCCAGGCCCAAGGAGAGAGAGG<br>GAATATGTTTCTGTGCTGATCCTTTCTCTAGATTTTATC<br>TCAGTTGTATGACATTGAAGCACCTGACTGAGCAATTGA<br>GCATGATGTGTTCTCCTGACCATCCTTCTAAAACCATTT<br>TCCACCAGTTTCTACCTTCTGATGGCGCTTAGTCACCT<br>GCACTTACAAACAGGTGCCCAA                      |
| 302 | ADXCRA<br>D_CN337<br>685_s_at | ZNF609 | Sense     | zinc finger protein 609<br>[Source:HGNC<br>Symbol;Acc:29003]                      | 302 | GGCTCTGATGATGGACCCTCAGTGATGGATGAAACAAG<br>CAATGATGCCCTTTGATTCCTTTAGAAAGGAAGTGATGGA<br>AAAAGAAAAATGTAAAAAACCTCTAGTTTAAACCTGA<br>AAAGATTCTTCCAAAGAGCCTAAAGTCAGCCCGTCCCA<br>TTGCCCTGCCATCCCCCACAGCAAATCTACACCTTC<br>CAGACAGCCACCTTCACAGCAGCGAGCCAGGCTCTTC<br>CTCAGGCTTGACCGCCACAGTGGCACAAAGCCATGCCCA<br>ACAGTC |
| 303 | ADXCRA<br>D_AV7068<br>78_s_at | DDX17  | Sense     | DEAD (Asp-Glu-Ala-<br>Asp) box polypeptide<br>17 [Source:HGNC<br>Symbol;Acc:2740] | 303 | TTTTCATGCAGATTAGTTAGAATTCAGTGCCAGGTTTCTT<br>CTGCCCCACCAAAATGATCCAGTCTGGAAATACATTTTG                                                                                                                                                                                                                         |

FIG. 7-77

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|     |                                |               |       |                                                                                                                                                                    |     |                                                                                                                                                                                                                                                                                        |
|-----|--------------------------------|---------------|-------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 304 | ADXCRA<br>D_BQ325<br>790_s_at  | MICA /// HCP5 | Sense | MHC class I<br>polypeptide-related<br>sequence A<br>[Source:HGNC<br>Symbol;Acc:7090] ///<br>HLA complex P5<br>(HCP5), mRNA<br>[Source:RefSeq<br>DNA;Acc:NM_006674] | 304 | GTAGGCTAGGATCATGGGGGAA TAGTTAGTAATGACA<br>GGGATAGTTGAAC TTA AAAAAAAGTTTGTGAGGCTGAC<br>AAAGATGAACGGACACATTTCTGATCTTGGAGGGTTC<br>ATAGGTTAGAA GATGGTAGAT                                                                                                                                  |
| 305 | ADXCRIH.<br>1351.C1_s<br>_at   | SDC4          | Sense | syndecan 4<br>[Source:HGNC<br>Symbol;Acc:10661]                                                                                                                    | 305 | GATGGTGGGATATTTGTGTCTGTGTTCTTATAATATTA<br>TTATTCTTCC TTGGTTCTAGAAAAATAGATAAATATATTT<br>TTTCAGGAAATAGTGTGGTGTTTCCAGTTTGATGTTGCT<br>GGGTGGTTGAGTGAGTGAGTGAATTTTCATGTGGCTGGGTGG<br>GTT                                                                                                    |
| 306 | ADXCRP<br>DRC.3995<br>.C1_s_at | IQSEC1        | Sense | IQ motif and Sec7<br>domain 1<br>[Source:HGNC<br>Symbol;Acc:29112]                                                                                                 | 306 | GAAACAGCATGGGACCCGTGTGATTGGGTCCAGGCTGG<br>GCTGTCAGGGAAGCGCCCTGGTGTCTCCGACTCATCAA<br>TTCTCGGGTCTTTTTTAAAGCCAGGCTCCCCAAAGCA<br>CTCTTTGTCTCGCAATTTT GAGGAGGTTGTTCCGACCTG<br>GAAGCGTTAAACTGCTGCATGTCATCTGGCGTCAGCTG<br>TGAGGCTCGGCTCTGCGTGTGTGCGTTTGCAAAATGT<br>ATTGGCGTGACTGTAAACACATCGTT |

FIG. 7-78

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|     |                                |                                            |                           |                                                                                    |     |                                                                                                                                                                                                                                                                                                               |
|-----|--------------------------------|--------------------------------------------|---------------------------|------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 307 | ADXCRP<br>D.10961.C<br>1_at    | RP11-86H7.1<br>(Clone_based_<br>vega_gene) | Sense                     | Novel processed<br>transcript.                                                     | 307 | GTCAGCTCAGTTGAGGGTTAATGATGAGGCAGGCTGA<br>TGCGGGTCTTTGCCAGTCCAGGGTTCCAAGAGCC<br>TTCCTGGGAGAGGGGCTGAGTTGAATGGTGCAAGAT<br>GAACAAGAAATGCCAAGATAGAGAAAGGTGGGAGGG<br>CTTCCAGGCAGAGAGAGAGCATGGCTAAAGGGCTAG<br>GGCATGAAGCAGCAGGGGACCCAGCCATGTAGTA<br>TCACTGGAGGATGAGAAATAAGGGGAGAGAGGGAG<br>GGAGAGAGGTATACCTCTGAGGGCA |
| 308 | ADXCRSS<br>.Hs#S192<br>3995_at | N/A                                        | No<br>Transcript<br>match | N/A                                                                                | 308 | AGTTCAGGGCTATAGTCGGCTATGTTGATCTGGTGTCA<br>TGCTAAGTTCCGCATCAATATGGTGACTTCTAGGGAGTG<br>GGGACCACCAAGTTGCCTAAGGAGGGGTGAACCTGC<br>CTACGTTGGAAATAGAGCTGGTCAAAACTCCTGTGCTCA<br>TCAGTAGTAATAGCACCTGTGAATA                                                                                                             |
| 309 | ADXCRSS<br>.Hs#S374<br>4180_at | CHD2                                       | Sense                     | chromodomain helicase<br>DNA binding protein 2<br>[Source:HGNC<br>Symbol;Acc:1917] | 309 | GACAGCTTGGAGGAAGGATTGACCATGGGTGATTCC<br>ATGGAGGTAGAGAAGCAAGAGAGACCTGATGATTACAA<br>TGATGGCTAAGTGTAGTAGTATGCCCATTAGGATTGAATTGA<br>ATTAGGGGAAATTGTGTGAAGTGTGGAAAGGAAGCAAT<br>ATTGTGTGATTAGCTCCAAAGCTGGCCACTGGTAGAAG<br>TTGTTCAATGGAAGAACCAAGGATGGAATTGAGTGGGC<br>CAGAGAGCCCTAGATTATGGGT                          |
| 310 | ADXCRP<br>D.1981.C1<br>_s_at   | MRPS10                                     | Sense                     | mitochondrial ribosomal<br>protein S10<br>[Source:HGNC<br>Symbol;Acc:14502]        | 310 | TATTCAGCGAAACTTACCTGAAGGGTTGCCATGGAAG<br>TAACAAAGACACAAATTAGAACAGTTACCAGAACACATCA<br>AGGAGCCCAATCTGGGAAAACACTATCAGAAGAAAAAGA<br>AGAAAGCTAGTCATAAAGCCCTCAGGGAGGCCATTTTTC<br>CCTAAA                                                                                                                             |

FIG. 7-79

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|     |                               |        |       |                                                                                |     |                                                                                                                                                                                                                                                                                                             |
|-----|-------------------------------|--------|-------|--------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 311 | ADXCRA<br>D_10195.C<br>1_at   | SLK    | Sense | STE20-like kinase<br>(yeast) [Source:HGNC<br>Symbol;Acc:11088]                 | 311 | CAATGCGAGATCTTCAGTTGCAAGTGTGAAAGCCCAATGT<br>CCGCGAACTGCATCAGCTGCAGAAATGAAAAATGCCACT<br>TGTTGGTTGAGCATGAGACTCAGAACTGAAGGAGTTA<br>GATGAGGAACATAGCCAAGAAATTAAGGAGTGGAGAGA<br>GAAATTGAGACCTAGGAGAAAGGCACTGGAAGAAGAGT<br>TTGCCAGGAAACTACAGGAACAGGAAGTATTATATAAAA<br>TGACTGGGGAGTCTGAATGCCTTAACACATCAACCCCG<br>GA |
| 312 | ADXCRA<br>G_AF1321<br>97_x_at | CYFIP2 | Sense | cytoplasmic FMR1<br>interacting protein 2<br>[Source:HGNC<br>Symbol;Acc:13760] | 312 | TTTCAGAACTGTCAAAATGTACCATATTTGTATTAAGAGT<br>TGTTGGGAATTTTGTACAATGAATTTACATTTATTTATG<br>GTGACATATTTACGCTTGATGATCAAAATAATGATGTTAAAT<br>TCCTAAATCATATTTGCTATGCAGCTGAAGATGATATTTT<br>GATTTGATTTTGGGGGTACCTGTGTTGAGTTGATAAAC<br>ATTTCCATCTTCATTAATAAAGTCTTCCAAACTAAA                                             |
| 313 | ADXCRA<br>D_CR749<br>083_at   | SSR1   | Sense | signal sequence<br>receptor, alpha<br>[Source:HGNC<br>Symbol;Acc:11323]        | 313 | TAAAGCATGGATCTCGCTTTGGTTGTAAAAAA                                                                                                                                                                                                                                                                            |
| 314 | ADXCRA<br>G_BC051<br>650_s_at | TOM1L2 | Sense | target of myb1-like 2<br>(chicken)<br>[Source:HGNC<br>Symbol;Acc:11984]        | 314 | ATGGTGGGGGTCTCTCACCTTCTTGACCCCTCTCTCCATC<br>ATTCAGCTGCCAGCCCCAGGCTTCACACCCCAAGCTGGCT<br>CAGCAGCCGAGCCTGGCACCAGGGTCCCTGCAGGCT<br>CCCTGGGCAGGGAGAGGGGCCAAGGACAATTGGGAGGG<br>CAGCAGGCAGCCCCGAGATGGTGGCCATGTGGCACGC<br>TGCTGAGACGACACTACCAATAAACCAAACTGC                                                        |

FIG. 7-80

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|     |                                |                                           |       |                                                                                          |     |                                                                                                                                                                                                                                                                             |
|-----|--------------------------------|-------------------------------------------|-------|------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 315 | ADXCRA<br>D_CN256<br>682_s_at  | TRAPPC6A                                  | Sense | trafficking protein<br>particle complex 6A<br>[Source:HGNC<br>Symbol;Acc:23069]          | 315 | CTGCCCCGTCTGTAAAGTTCAGGTGGTGATTCCGAAATC<br>CTAAGCCTGCCCTCGACCTGCTGAGCCGCACTGCTGCC<br>CCTGGCCTCACCGGCCCTCAGGAGACGGTGGGGCCGCT<br>GCATTCGGGGTGGTCTTTGGGAATCCCAGGCCCTAGG<br>GGTCACATTTGCTCAGGAAAGTGGGTATCAAAATTGAGGT<br>GGGGGTGTCAGAGGAGGCAAAAGGGGTCCCAGCTGCGG<br>TCAGGACTGTGGT |
| 316 | ADXCRA<br>D_BC0406<br>47_x_at  | OAF                                       | Sense | OAF homolog<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:28752]                         | 316 | CCTGGGTGACGGGAATAAGACTCGGTCTCCAAAAGAA                                                                                                                                                                                                                                       |
| 317 | ADXCRA<br>D_BX4213<br>36_s_at  | PPIF                                      | Sense | peptidylprolyl<br>isomerase F<br>[Source:HGNC<br>Symbol;Acc:9259]                        | 317 | AAGGCTGCTAGGGATGTTAGACCTCGGCCAGGACCCAC<br>CACATTGCTTCCTAATACCCACCCCTTCCTCACGACCTCA<br>TTTCTGGGCA                                                                                                                                                                            |
| 318 | ADXCRA<br>D_NM_14<br>5809_x_at | AC107983.1<br>(Clone_based_<br>vega_gene) | Sense | TL132 protein<br>(LOC220594), non-<br>coding RNA<br>[Source:RefSeq<br>DNA;Acc:NR_003554] | 318 | TACCTGTTTATCTGTAACGTGTTATCCAAACAAATTAAATA<br>CTGTGGATGCCCTTTAAAAA                                                                                                                                                                                                           |

FIG. 7-81

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|     |                             |        |       |                                                                                                                                                     |     |                                                                                                                                                                                                                                                                                                                                       |
|-----|-----------------------------|--------|-------|-----------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 319 | ADXC<br>D.11050.C<br>1_at   | GALNT5 | Sense | UDP-N-acetyl-alpha-D-<br>galactosamine;polypept<br>ide N-<br>acetyl/galactosaminyltra<br>nsferase 5 (GalNAc-T5)<br>[Source:HGNC<br>Symbol;Acc:4127] | 319 | GACAGTGGATAAATTTCAAAGAGGCATCTTTGTGTGGC<br>CCATGAACCTTTGGTTGGAGAACAAATTCCTCCAGATGTCA<br>CTGCAAAAAACAGAAATTAAGAAACTGATACAAATAAGG<br>TGCCCTGTGCATGGCTGGTGGATTGTTTCTACTGACAAA<br>AGTTACTTTTTTGAACCTTGAACATACGACCCCTGGCCTT<br>GATGTTGGGTGGGAAATATGAGCTCTCATTCAA<br>GGTGTGGATGTGTGGTGGTGAATTTGAGATCATCCCT<br>GTCCTCGAGTGGGCCATATATTCAAGAAAT |
| 320 | ADXC<br>D.15212.C<br>1_s_at | CHD3   | Sense | chromodomain helicase<br>DNA binding protein 3<br>[Source:HGNC<br>Symbol;Acc:1918]                                                                  | 320 | ATGAGTATCTCAGCTCCTTCAAGGTGGCACAGTACGTC<br>GTGCGGGAAGAGACAAAGATTGAGGAAATTTGAGCGAGA<br>GATCATCAAGCAGGAGGAGAAATGTGACCCTGACTACT<br>GGGAGAAGCTGCTGAGGCATCACTATGAGCAACAGCAG<br>GAAGACCTAGCCCGGAATCTAGGCAAGGGCAAGCGGG<br>TTCGCAAGCAAGTTAACTACAATGATGCTGCTCAGGAAG<br>ACCAAGACAACCAGTCAGAGTACTCGGTGGGT                                         |
| 321 | ADXC<br>G_AF1722<br>69_s_at | TNIIK  | Sense | TRAF2 and NCK<br>interacting kinase<br>[Source:HGNC<br>Symbol;Acc:30765]                                                                            | 321 | CTATGCCCGGATAACTAAGGATGTGGTCTCCAATGGG<br>GAGAAATGCCCCACGCTGTGGCCTACATTTCATCCAAATC<br>AGATAATGGCTGGGGCGAGAAAGCTATTGAGATCCGG<br>TCAGTGGAAACAGGAC                                                                                                                                                                                        |
| 322 | ADXC<br>D.17448.C<br>1_at   | CAPS   | Sense | calcyphosine<br>[Source:HGNC<br>Symbol;Acc:1487]                                                                                                    | 322 | CCACCATTCGGGGTCCCCCAGGAAGCCAGGTGACCCC<br>AGGTGGGAGGCTGTGTGTGGAGGCCATCCTGGAAGGA<br>AGTTTAGACCTGCCCAGGTGTGGAGCGGAGGGGCACAG<br>GGCATCCTAACCTCAGAAACTGAAA                                                                                                                                                                                 |

FIG. 7-82

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|     |                               |       |           |                                                                                    |     |                                                                                                                                                                                                                                                                                                            |
|-----|-------------------------------|-------|-----------|------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 323 | ADXCRP<br>D.12030.C<br>1_at   | POSTN | AntiSense | periostin, osteoblast<br>specific factor<br>[Source:HGNC<br>Symbol;Acc:16953]      | 323 | AGCAAAGTGATTCTCCATCTGGCCTCAGAGCAGATGC<br>CAAGCCTAATTGGGCCACCAGATCCGTGAAGGTGTTT<br>GCTGTTTTCCAGCCAGCTCAATACTTGTGGCAGAAT<br>CAGGAATTAGGACCTGATCAATCAAAATGGATCACACCAT<br>TAGTTGGTCACAATATCCTTTGTTGTTACCATTTTGATT<br>CCATTTACTGTTATACTGTACCCGTCAATCCTATCTCA<br>ATTGTATTTCTTCCAGCGTCTCAAGACTGCTACTCCCA<br>TAATA |
| 324 | ADXCRA<br>G.AF1769<br>12_at   | CLCF1 | Sense     | cardiotrophin-like<br>cytokine factor 1<br>[Source:HGNC<br>Symbol;Acc:17412]       | 324 | GCTTGCCCCAGAACTTAGTCTCTTTGCCACGCCTCACC<br>CCTCCTGGTGCTCATCAGACTCTTGCCACCCCTGGCTC<br>CCACTCCCTGCTTGCCCTCTGGTGGAGCTGCACAGAGCT<br>CTGGAAGAGGCCCTCTTCTCCCGCACTGGGGCGA<br>TGGGCGCACCTCAGACTTACCCACTGCTGCTGCCACCA<br>CCAAACCCCTTGATCCCTCAGTCTCCACACAGCTTCT<br>GTCCACCCAGGTTTCCCTCACCCACCTTTGCTAAGT<br>CTTCCT     |
| 325 | ADXCRP<br>DRC.1274<br>6.C1_at | FAT1  | Sense     | FAT tumor suppressor<br>homolog 1 (Drosophila)<br>[Source:HGNC<br>Symbol;Acc:3595] | 325 | GCCCTGCTGCGAAGTGGAGTCGGAGGTGATGAGT<br>GACTATGAGAGCGGGGACGACGTCACCTCGAAGAGG<br>TGACGATCCCGCCCTGGATTCCAGCAGCACACGGAA<br>GTCTGACTCTCAACTCCCCCCTAAAGTGCCTGACTTTAGT<br>GAACCTAGAGGTGATGTGGCTCATCCGCGCTGTTCTTT<br>GCAGCAGTGCTTCCAAGCTTTTGGGTGAGCCGAA                                                             |

FIG. 7-83

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|     |                               |                                                            |       |                                                                                                                                                                                             |     |                                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|------------------------------------------------------------|-------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 326 | ADXCRP<br>D_3213.C1<br>_at    | ARHGEF2///R<br>P11-336K24.6<br>(Clone_based_<br>vega_gene) | Sense | Rho/Rac guanine<br>nucleotide exchange<br>factor (GEF) 2<br>[Source:HGNC<br>Symbol;Acc:682] ///<br>Known nncoding<br>transcript with no ORF.                                                | 326 | AGAAGCAACACGATGATGGGCCCCCAGTTTGAATTC<br>AGACAGTGGAGGAGGAATATTGCTAGGAG                                                                                                                                                                                                                                                     |
| 327 | ADXCRIH.<br>2217.C1_s<br>_at  | ADIPO2                                                     | Sense | adiponectin receptor 2<br>[Source:HGNC<br>Symbol;Acc:24041]                                                                                                                                 | 327 | TACTCTCAGCAGTCAGAGGCTTGCTGTGCAG<br>TTTTTAATTTCTTTTGGCCCTAGGCTGGTGGACCT<br>CTACAGCTTCATTCTTTCACCATTAATAGTGGCCTTTT<br>CAGTATTTCCCTCTTCCCTTTTATAAATTATGCTAAAGC<br>CACAAAGCACATTTTGGGATCATAGAAGTTGGGT<br>TCCAGAAAGGCATCTGTGTGATGGTCCATTGATGTGG<br>GATTTCCCTACTTGCTGTATTCTCAGTTTCTAATAAAA                                      |
| 328 | ADXCRA<br>D_CN390<br>037_s_at | C15orf42                                                   | Sense | Treslin (TopBP1-<br>interacting, replication-<br>stimulating<br>protein)(TopBP1-<br>interacting checkpoint<br>and replication<br>regulator)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q7Z2Z1] | 328 | AAGGACTGTCCAAGAGCCAGCCAGTTTCAGGGCTCAGG<br>CCTCACCCATTGCCCACTCCTGGGGAGACCATCACCTG<br>GCTCATCGTTTCCACCAAGAGTGCCCCACAGGAGTGCC<br>CCACAGACCCGCTGGACCAGCCTGCTGCGGGTCCCTGG<br>CCAGGGGCTGGCTAACGGTGAGGGCTGACTCTGAACT<br>GTCTCTCAGTCTCCAGAAAGTTTCAAGCCTGTTGTGT<br>CCCAAATCTGATTCCCTCTATTGTCTTGTAAATCAAACTC<br>TAAGTGAAAACCTTCCCAT |

FIG. 7-84

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|     |                                 |         |           |                                                                               |     |                                                                                                                                                                                                                                                                                                                  |
|-----|---------------------------------|---------|-----------|-------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 329 | ADXCRSS<br>.Hs#S192<br>3663_at  | SOD2    | AntiSense | superoxide dismutase<br>2, mitochondrial<br>[Source:HGNC<br>Symbol;Acc:11180] | 329 | GAAGGTCTAACAGTTTCAAACAATAGCCAGGGGAAGTTA<br>GAGTCACCTAGAGACATCCTTAACACGTGCCCTGAGC<br>TACTTTTCAGAAACCCAGACCCCCACCAAAATGGATTAC<br>ACAGACGTCAGATAAGGGGGAACACCCAGGGACTAACT<br>CTGACCTCCATTCTTTGCTCTCAGTTTCTTCCTGAGGG<br>CCTGGCCAGACCTTAATGTTCCCTTCTGCGGACCCCAA                                                        |
| 330 | ADXCRP<br>DRC.1111<br>8.C1_s_at | TNS1    | Sense     | tensin 1 [Source:HGNC<br>Symbol;Acc:11973]                                    | 330 | CACCTGCACTCTAGTGACCCCTGGTGCCGCCAGACCCCT<br>TCTCTTCTACAAAGACCCCCAGCAGGAGTGGGAGGGTCT<br>GCAATGGCATCGCCCTGTCCTGCCCTTGGCCAGAAGCCT<br>GGAGCTTTGGTTTGAGGAGGTAGAGATATGTGTATCCAT<br>AGGAAGAGATCTGTCAGAACAGGCAGCTGTTGAGCTCG<br>GGGTGCTTCCCTCAAGGCATGTGGCTCAGCAGCAAGAA<br>AGGCAAGTTGCTCCTGCTGGGGCCCTGGACTCTGCCTT<br>AGCTCC |
| 331 | ADXCRH.<br>3717.C1_s<br>_at     | GABARAP | Sense     | GABA(A) receptor-<br>associated protein<br>[Source:HGNC<br>Symbol;Acc:4067]   | 331 | TCTCTCCAGCCTCTCTTAGGAGGGGTAATGGTGGAGTT<br>GGCATCTTGTAACCTCTCCTTTCTCCTTTCTCCCTTTCT<br>CTGCCCGCCTTCCCATCCTGCTGTAGACTTCTTGATTG<br>TCAGTCTGTGTCACAT                                                                                                                                                                  |

FIG. 7-85

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|     |                               |                                              |           |                                                                                                                               |     |                                                                                                                                                                                                                                                                                                                    |
|-----|-------------------------------|----------------------------------------------|-----------|-------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 332 | ADXCRA<br>D_9610.C1<br>_x_at  | GMDS                                         | Sense     | GDP-mannose 4,6-<br>dehydratase<br>[Source:HGNC<br>Symbol;Acc:4369]                                                           | 332 | ATCCACGGCCGCGTTAGAAAGAGGGTGCACGCTGCC<br>GCCGAGGTAGAGGGTCCCGAGTCCTGGGCGCTCGC<br>ACCCACAGCCCGAGTCCCTCCCGCGGAAGGACT<br>CGTGCTGTGGTAGAGACGCGCGCTTGCGCGGCCA<br>GCCCTGCAGGCAGGAGCTGAGCGGCGCAGGACACG<br>GGCAGCTGGAGGGCGCGCTGGTATTACTCACTTCC<br>CTCCTAGCCAGAGAAGTGCAGCAATTCCAAACAGTTCT<br>CATAGGAGCGTCCCTGACAACTTCATGTTATA |
| 333 | ADXCRA<br>D_11405.C<br>1_x_at | NAA50                                        | AntiSense | N(alpha)-<br>acetyltransferase 50,<br>NatE catalytic subunit<br>[Source:HGNC<br>Symbol;Acc:29533]                             | 333 | GTACCACAAACACACTCAACTTGTCTATGAATTAGAGAA<br>CAAGATACTGCTGCTGCTCTTTTGTACTTTTGAATATA<br>CAATGTTTGTAGGCTCTGCCCTTCAATGTGAAAGCAGG<br>ACATTAAATTTGAAATTTATTTGACAATTAATGTTTAGGA<br>CCATCTAACTTCAACTGCAAAACTAAACAGATCTACCTT<br>GTCCCTTCCTTCAAA                                                                              |
| 334 | ADXCRA<br>G_AF1388<br>61_s_at | AL138478.1<br>(Clone_based_<br>ensembl_gene) | Sense     | Known long non-coding<br>RNA.                                                                                                 | 334 | GGTTCATTTTAGTTTCAGATAGATGGCTTACCACAAAGAA<br>CTCTTGAAAGAATACTGATTAGGAGGGCAGGGAAGT<br>AGGAGCTTATGGTATATTATAAGGCTGGGAAAAATCTAT<br>GATGCAAAACCCCTTCCACATAGTACT                                                                                                                                                         |
| 335 | ADXCRA<br>D_R42604<br>_at     | SNTB2                                        | AntiSense | syntrophin, beta 2<br>(dystrophin-associated<br>protein A1, 59kDa,<br>basic component 2)<br>[Source:HGNC<br>Symbol;Acc:11169] | 335 | ACTCATTCCTTAACCTAATCACCTAAAAATAATCTTATCAT<br>CTATTCTTCTTCAGGNAAAAATGGNGCCCTGGGTGTTAT<br>TTTAAACGACTTGCCATCCTTCCTGTTTGTAGAGTNTCTTT<br>GTTAACTGGGGGCATACCTTCGNGACCCCGGTCCTACCT<br>TCCTCATTCAGACCTGTGCTGTTCAATTGCTGTATTCCCA<br>GTCCCTTAAAAA                                                                           |

FIG. 7-86

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|     |                                |        |       |                                                                                                 |     |                                                                                                                                                                                                                                                                 |
|-----|--------------------------------|--------|-------|-------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 336 | ADXCRRS<br>.Hs#S273<br>2484_at | MEF2A  | Sense | myocyte enhancer<br>factor 2A<br>[Source:HGNC<br>Symbol;Acc:6993]                               | 336 | ATATCTGACAGATGTGTAAACCAAGTTACCAGCATGGTG<br>TGGAAATCGTAGTTCCAAAGTCATATAATACCAGACATTCA<br>AGAAAACCTAGTGCCCTGTTAACTGGGGGAAGCAAAATTTA<br>TATCCTTTTGAAGAAAGTCACCTTATTCTGTGTATCAG<br>AAATCTCTTTCAAATAACCTTTTCAGAACTATAGAGCATCA<br>TACAAAGATGACCAAGCATACAAAGAAAACAA    |
| 337 | ADXCRRP<br>D.2240.C1<br>_s_at  | RSRC1  | Sense | arginine/serine-rich<br>coiled-coil 1<br>[Source:HGNC<br>Symbol;Acc:24152]                      | 337 | AACATCAAAGCTGGATTAGAACATCTGCCACCAGCTGA<br>ACAGGCCAAAGGCAGACTACAGCTGGTTCTTGAAAGCTG<br>CTGCAAAAGCTGATGAAGCATTGAA                                                                                                                                                  |
| 338 | ADXCRRP<br>D.8064.C1<br>_s_at  | CYP3A5 | Sense | cytochrome P450,<br>family 3, subfamily A,<br>polypeptide 5<br>[Source:HGNC<br>Symbol;Acc:2638] | 338 | AGCCTTAGCAAAAAATGCCTCCTCACCACCTCCCCAGGAG<br>AATTTTATAAAAAGCATAATCACTGATTCTTCACTGAC<br>ATAATGTAGGAAGCCTCTGAGGAGAAAAACAAGGGGAG<br>AAACATAGAGAACGGTTGCTACTGGCAGGAAGCATAAGA<br>TCCTTGACAAATATTGCTGGCCCTGGTTCACCTGTTTAC<br>TGTTATCACAAATAATGCTA                      |
| 339 | ADXCRA<br>D_CB1624<br>48_s_at  | CREBL2 | Sense | cAMP responsive<br>element binding<br>protein-like 2<br>[Source:HGNC<br>Symbol;Acc:2350]        | 339 | ACAGAGTCATTTGAGCTTTCTCCCCTCCCCTAGTATCT<br>TTACAGGAGCAGGGAAGAGCAGTAGAGGATGTATAATT<br>TTGGCGGAAGTTAAATTACAATTTATTGAGGTTATTCCT<br>AAACCTATTTATTGGTGTTTGGAGGAGATCACACACT<br>AAGAGAACGTTGATTGCCCTCGGCTATTGTGCTGGCTGG<br>ACACTTTGGTCACTTTTGAAGCATGTTAATAAATGTCAC<br>G |

FIG. 7-87

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|     |                              |           |       |                                                                                            |     |                                                                                                                                                                                                                                                                                                 |
|-----|------------------------------|-----------|-------|--------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 340 | ADXCRP<br>1113.C1_x<br>_at   | IGFBP2    | Sense | insulin-like growth<br>factor binding protein 2,<br>36kDa [Source:HGNC<br>Symbol;Acc:5471] | 340 | TCCAAACACCGGCAGAAAACGGAGAGTGCTTGGGTGGT<br>GGGTGCTGGAGGATTTCCAGTTCTGACACACGTATTTA<br>TATTTGAAAGAGACACACCGAGCTCGGCACCTCCC<br>CGGCTCTCTCTCCAGCTGCAGATGCCACACCTGCT<br>CCTTCTTGCTTTCCCGGGGAGGAAAGGGGTTGTGGT<br>CGGGAGCTGGGTACAGTTTGGGAGGGGGAAGAG<br>AAATTTTATTTTGAACCCCTGTGTCCTTTTGCATAAG<br>ATT     |
| 341 | ADXCRP<br>D.6986.C1<br>_x_at | GRB7      | Sense | growth factor receptor-<br>bound protein 7<br>[Source:HGNC<br>Symbol;Acc:4567]             | 341 | TGAGAGCGGAGGGTCCGCCACTCCAGTTTTCCTCT<br>CTGCTTCTTTGCCTCCCTCAGATAGAAAACAGCCCCCA<br>CTCAGTCCACTCTGACCCCTCTCCTCAAGGGAAGGC<br>CTTGGTGGCCCCCTCTCCTTCTCCTAGCTCTGGAGGT<br>GCTGCTTAGGGCAGGGAATTATGGGAGAAGTGGGG<br>CAGCCAGGCGGTTTACGCCCCACACTTTGTACAGAC<br>CGAGAGGCCAGTTGATCTGCTCTGTTTATACTAGTGAC<br>AATA |
| 342 | ADXCRP<br>D.17978.C<br>1_at  | U6 (RFAM) | Sense | U6 spliceosomal RNA<br>[Source:RFAM;Acc:RF<br>00026]                                       | 342 | AAAGACTCATATAAGGGTCCCTCTCTTTTCATCCTC<br>CCTCCATATTCAGTTGCTAAGTCTCACTACTTTGCTCC<br>CATCAAGATTCTCTTTACTATTCTTCTATCCAGACCTTC<br>CTCTTATTCCTATTGTCATTGCTTATTTTAGGTTCTCAT<br>CATCTTCACTAAGATAAATAACAACAGCTTCGTGACCCAG<br>CGTAGGCAA                                                                   |

FIG. 7-88

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|     |                               |           |           |                                                                                               |     |                                                                                                                                                                                                                                                                                                                                 |
|-----|-------------------------------|-----------|-----------|-----------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 343 | ADXCRA<br>D_AA7747<br>60_s_at | EIF4G3    | Sense     | eukaryotic translation<br>initiation factor 4<br>gamma, 3<br>[Source:HGNC<br>Symbol;Acc:3298] | 343 | GCTCAATAGCTATAACTGTACCAAGACATGGAAGAAA<br>CCAAAAGATCGGACCCGAACCACTGAAGAGATGTTAGA<br>GGCAGAAATTGGAGCTTAAAGCTGAAGAGGAGCTTTCCA<br>TTGACAAAGTACTTGAATCTGAACAAGATAAAATGAGCC<br>AGGGTTTCATCCTGAAAGAGAGACCCCTCTGACCTA                                                                                                                   |
| 344 | ADXCRA<br>D.12198.C<br>1_at   | DSP       | AntiSense | desmoplakin<br>[Source:HGNC<br>Symbol;Acc:3052]                                               | 344 | TGCGAATCTTCTGCAGCTCCATCAGCATCCATGTATCTT<br>GCTTGTCATTTTCTCTGTGTTACAAATTACTTTATTATG<br>GTTGACATCTTGGCAGGTTCCATGATGAGTGATTTTCAGT<br>AGTGGTCACTGTCTGGTGTCTGGGATAGCCAGGGAGCT<br>GAATGACCAGGGTCTGGTAATGCTTCTGGGCATCGGTG<br>AACTGAGACTGTATTTCCGCTTGTGTCATCATCTCCAAC<br>ATCTTAAGCCTTGGCTATTTCTGATGAACCTCTTGGCAC<br>TGTAACCAAGGTCGGATAT |
| 345 | ADXCRA<br>D_CF2721<br>04_x_at | HIST1H2AJ | Sense     | histone cluster 1, H2aj<br>[Source:HGNC<br>Symbol;Acc:4727]                                   | 345 | CAACTATGCGGAGCGGGTCTGGTGGAGCGCCGGTG<br>TACCTGGCGGCGGTGCTGGAGTACCTGACCGCCGAGA<br>TCCTGGAGCTGGCTGGCAACGCGGCCCGGACAAACAA<br>GAAGACTCGCATCATCCCGCGTCACTCCAGCTGGCCA<br>TCCGCAACGATGAGGAGCTCAACAAGCTTCTGGGCAAA<br>GTCACCATCGCACAGGGTGGGTCTTCCCAACATCCA<br>GGCCGTGCTGCTGCCAAAGAAAACCTGAGAGCCACCACA<br>AGACTAAGTAAAGACCGGAGTTGA         |

FIG. 7-89

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|     |                               |                    |           |                                                                                                                         |     |                                                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------------|--------------------|-----------|-------------------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 346 | ADXCRP<br>D.15112.C<br>1_s_at | KIF21A             | Sense     | kinesin family member<br>21A [Source:HGNC<br>Symbol;Acc:19349]                                                          | 346 | CATATTTCAGCGGATCATCAACTTTTTCTCCTACCATCT<br>ATCCTCAGACAAAGAAACCATTTGAAATTTATAGACCTAGC<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>AGACACTGACCAAGAGAGAAAGAAAGAAAGGGTGT<br>CGGAAAGAGAAACAAATGAATTAGAAAGTGAAGAAAGT<br>CAAGAAAGTGAGTGATCA        |
| 347 | ADXCRP<br>D.1233.C1<br>_s_at  | MRPL52             | Sense     | mitochondrial ribosomal<br>protein L52<br>[Source:HGNC<br>Symbol;Acc:16655]                                             | 347 | TGCTCTTAAACCCAAAGGGGCTTCACTGAAGAGCCCAC<br>TTCCAAGTCAATAAAAA                                                                                                                                                                                                                                                                      |
| 348 | ADXCRP<br>DRC.462.<br>C7_at   | NCRNA00188         | AntiSense | small nucleolar RNA,<br>C/D box 65<br>[Source:HGNC<br>Symbol;Acc:32726]                                                 | 348 | CTTCTCTTGGGCTGAGATGCTGCTGCCAGCTCTAAAC<br>AGCACTCTGTTCTCAAAACCTCATGGCAGGCTCCTGGC<br>TCCAATACTCAGCTGCCAAACATGATGCTGATTCTTCAC<br>GAATTTGCAACCCAGTTCTCTCGGGTTTGACACACCCC<br>ACTGTGGCCGGGAAACCGGTCGCCCTCCGCTTCGCAGA<br>CTCCAGGCTCTGGCAGATGTGGCCCTCCATAAACAACGG<br>GAATGAAAAGGTCACACCTTATGTGCGCCAGGCCCTTA<br>AGGAGTCGGAATATCCCAATCCTCC |
| 349 | ADXCRA<br>G_AB0825<br>33_at   | SGK269<br>(Entrez) | Sense     | Tyrosine-protein kinase<br>Sgk269 (EC<br>2.7.10.2)(Sugen kinase<br>269)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q9H792] | 349 | TGCTGTGGTACTTTGCTGTGTACTCCGTGGCATCATGTT<br>ACTGTGTA                                                                                                                                                                                                                                                                              |

FIG. 7-90

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|     |                               |        |       |                                                                                                                                   |     |                                                                                                                                                                                                                                                                                      |
|-----|-------------------------------|--------|-------|-----------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 350 | ADXCRA<br>D_BX1117<br>19_x_at | TAF15  | Sense | TAF15 RNA<br>polymerase II, TATA<br>box binding protein<br>(TBP)-associated<br>factor, 68kDa<br>[Source:HGNC<br>Symbol;Acc:11547] | 350 | GGAGTTTGTGACTAGATGGGCAATATAGTAGATGTCAT<br>CTTTTAAAAATGAAAAAATTAGCTGGCCACTGTGGCACA<br>CGCTGTAGTCCAGCTACTTGGGAAGCTGAGGTAGGA<br>GGATTGCTTGAGCCAGGAGTTCAAGGCTGCAGTGAGC<br>TATGATTGTGCTTATGAATAGCCACTGCACCTCCAGTCTG<br>GGCAATAGTGAGTCGGTCAAAATCCATTCCCCCTCCG<br>CCCCATACCTCTTCAAAATGTTTAA |
| 351 | ADXCRA<br>D_BU1925<br>98_s_at | ICAM1  | Sense | intercellular adhesion<br>molecule 1<br>[Source:HGNC<br>Symbol;Acc:5344]                                                          | 351 | CACCTCCTGACGGATGCCAGCTTGGGCACTGCTGTCTA<br>CTGACCCCAACCCCTTGATGATATGATTTATTTCATTTGTT<br>ATTTTACCAGCTATTTATTGAGTGCTCTTTTATGTAGGCTA<br>AATGAACATAGGTCTCTGGCCTCACGG                                                                                                                      |
| 352 | ADXCRA<br>G_BX6471<br>67_s_at | ANXA4  | Sense | annexin A4<br>[Source:HGNC<br>Symbol;Acc:542]                                                                                     | 352 | AGCCTAGGCAATGCAGCGAGGCCCTTGCTAGAAAATTT<br>AAAAAAAATAAAAAAATTAGCTGGCGTGGTGGCAGC<br>TACCTGTAGTCCAGCTACTCGGGAGGCTGAGGCGGCA<br>GGATCTCTTGAGCTAAGTAGTTCGAGGCTGAAAGTGA                                                                                                                     |
| 353 | ADXCRA<br>D_AK0927<br>50_x_at | EHP1L1 | Sense | EH domain binding<br>protein 1-like 1<br>[Source:HGNC<br>Symbol;Acc:30682]                                                        | 353 | TTAGCCAAAGTATGGTGGCAGCGCCCTGTAATCCCAGCA<br>ACTTGGAAGGCTGAGGCAGGAGAAATCGCTTGAACCTGG<br>GAGGCAGAGGTTGCAGTGAGCCAAAGATCAGACCACTAC<br>CGCCCCGCGCTGGCTTGGCCCTCCTGTTCTCCAGAGCAA<br>TAAAGTTGGACGAGACTACCC                                                                                    |
| 354 | ADXCRIH.<br>1053.C1_a<br>t    | PIGR   | Sense | polymeric<br>immunoglobulin<br>receptor [Source:HGNC<br>Symbol;Acc:8968]                                                          | 354 | CACAGCTCTTCTTGGCGTATTATACCTCAGTCTTA<br>ACTTTTACACAGGGGTGCTCACCTCTGCCCTATTGGG<br>AGAGGTCATAAAATGCTCGAGTCCTAAGGCCCTTAGGG<br>GTCATGTATGATGAGCATACACACAGGTAATTATAAACC<br>CACATTCTTACCATTTCACACATA                                                                                        |

FIG. 7-91

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|     |                                 |        |           |                                                                      |     |                                                                                                                                                                                                                                                                                                                                      |
|-----|---------------------------------|--------|-----------|----------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 355 | ADXCRIH.<br>D.16386.C<br>1_x_at | RHBDD1 | Sense     | rhomboid domain<br>containing 1<br>[Source:HGNC<br>Symbol;Acc:23081] | 355 | GGATGGCACCATGTTTGAGAGGCTACAGAGGAGACCCCA<br>GAGCCAGTAAGCAAGACATAGAGTTTATAGAGAGGACT<br>TACAGCATAGTCCAGTGGCAGCGGGCTAGACAGGAGAA<br>CCGCAATGGCTTGAAAAGCACGAAGTATAAAGCGTTG<br>AGCTCAACGGTTTATACCTTCAGAGAACTCAACAATCAA<br>CTGAAGGCACCTAACTGAGAAAACAAAGAACTTGAAATG<br>GCTCAGGATCGCAATATGGCCATTTCAGAGCCCAATTACA<br>AGACCAAAGGAAGCATCAGAAGCTGA |
| 356 | ADXCRIH.<br>2179.C1_a<br>t      | NBN    | AntiSense | nibrin [Source:HGNC<br>Symbol;Acc:7652]                              | 356 | ATTTCTTTAGCTGACCATAGTGAGCTTCCTTGAGTTCA<br>CGTTTCTTCCCAATTCATTTTCTTGAGATATTTTGCTAC<br>TTTCTGGTACTGCTTCATCACTGAAAGTGTCATTTGTTTC<br>TATATCCATCCTTGGCCTTTTCTAACATTGACATCTTCC<br>TCCTGTTTTTGAACTTTCACATCAATTTCTAAGTCTGGTT<br>TTGTGCTCTTGAATAACTGTTCCAATACTTCATCTTCTAT<br>GGCCACATCATCCATT                                                 |
| 357 | ADXCRA<br>D_CN311<br>761_s_at   | ZNF655 | Sense     | zinc finger protein 655<br>[Source:HGNC<br>Symbol;Acc:30899]         | 357 | GTATCAAATTCACGCCCATGCAAAAAGATTATAAATGTAAT<br>AAGCATGTATGTGTGTGAGGAGATTTCAGTCATAACCCAA<br>CGCTCATTCAACATCAAAGAAATTTATACCTAAGAGAACT<br>TATTTGGGTGTAGTAAATGGCAGATCTTTCAATAGGAGT<br>TTAACTAGTCTTTGTCATATCAGAAATATCCATAGTAGACA<br>AGAAATTTGATGTACGCAAAATGGAAAAAAGTCGACACCAC<br>ATTCAGGCTTTACCCCAACATCGAAATAAT                             |

FIG. 7-92

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|     |                               |                                                   |                    |                                                                                                              |     |                                                                                                                                                                                                                                                                                               |
|-----|-------------------------------|---------------------------------------------------|--------------------|--------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 358 | ADXCRA<br>D_BE4676<br>88_s_at | CCND2                                             | Sense              | cyclin D2<br>[Source:HGNC<br>Symbol;Acc:1583]                                                                | 358 | CGTTCAGTACAAACATTTATGCGGTAGGCTCAGATGTTG<br>TAATTTGCACCTTAGGTACAGGTGTCAGGAACAGACTA<br>AAAAGAATCCACCAGGCTGTTTGAGATCCTCATCTTG<br>GAGCTTTTCAAAGCGGNGCTTCATCTGCAAAGGCC<br>CTTCATCTTGAAGTTTTCCCTCCGCTTTTCCCTCC<br>CCTGGCATGGACACCTTGTGTTAGGATCATCTCTGCAA<br>GTTTCCTAGGCTCTGAATCTCGGAGTAGATGAACCTGCA |
| 359 | ADXCRA<br>D_11405.C<br>1_at   | NAA50                                             | AntiSense          | N(alpha)-<br>acetyltransferase 50,<br>NatE catalytic subunit<br>[Source:HGNC<br>Symbol;Acc:29533]            | 359 | GTACCACAAACACACTCAACTTGTCTATGAATTAGAGAA<br>CAAGATACTGCTGCTCTCTTTTGTACCTTTTGAATATA<br>CAATGTTTGTAGGCTCTGCCCTTCAATGTGAAAGCAGG<br>ACATTAAATTTGAAATTTATTTGACAAATTAATGTTTAGGA<br>CCATCTAACTTCAACTGCAAAACTAAACAGATCTACCTT<br>GTCCTTC                                                                |
| 360 | ADXCRA<br>Hs#S812<br>597_at   | RP11-<br>1415C14.3<br>(Clone_based_<br>vega_gene) | AntiSense          | glucuronidase, beta<br>pseudogene<br>(LOC653391), non-<br>coding RNA<br>[Source:RefSeq<br>DNA;Acc:NR_029426] | 360 | ATTACAGTTATAGCTCTCTCAAGCAAAAAACAGCAGAG<br>AAAAACTTAGTTTACCTTAGGGCTATTTATTTACTTAGG<br>GATTTGTTAAAGGTCGAATGGGGTCACACAGAACTACTA<br>AGAAAGCTGTTCAACCCAGGCCTCACTAAGAACTCTTC<br>TTCATTTCAGTAGCTGTATAGTAACATGAC                                                                                      |
| 361 | ADXCRIH.<br>949.C1_at         | N/A                                               | No Genome<br>match | N/A                                                                                                          | 361 | CTTTAGTAGTTTCTCGTCAGTCCCGCAGCCACCGCAGC<br>CGGGTCCCCCTCGTG                                                                                                                                                                                                                                     |

FIG. 7-93

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|     |                               |        |       |                                                                                                                                                                                                                        |     |                                                                                                                                                                                                                                                                                     |
|-----|-------------------------------|--------|-------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 362 | ADXCRP<br>D.4532.C1<br>_at    | DUOXA2 | Sense | dual oxidase maturation<br>factor 2 [Source:HGNC<br>Symbol;Acc:32698]                                                                                                                                                  | 362 | AGAGAGGGGGCTACCTCTTATCCTCGGCGACCCACTG<br>CACAAAGCAGGCCGCTCTCCAGACTTAAATGTATCAC<br>CACTAACCTGTAGGGGGACCCAACTCTGGACTCCTTCC<br>CCGCTTGGACATCGCAGGCCGGGAAGCAGTGCCCG<br>CCAGGCCTGGCCAGGAGAGCTCCAGGAAGGGCACTG<br>AGCGTGTGCGCGAGGCCCTCGGACATCCGCAGGCA<br>CCAGGAAAGTCTCCTGGGCGATCTGTAATAAAC |
| 363 | ADXCRP<br>D.13185.C<br>1_s_at | GNL1   | Sense | guanine nucleotide<br>binding protein-like 1<br>[Source:HGNC<br>Symbol;Acc:4413] ///<br>Guanine nucleotide-<br>binding protein-like 1<br>(GTP-binding protein<br>HSR1)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:P36915] | 363 | CTGAATGGGCAGAGCTGGATTTTACAGGGTTGGGATTT<br>TGCCAGGTGAGTAAGATAGAGGGGAGAAGTGGGACCA<br>GGAAGTTCAGGTCTGTGAACGGGCTGGCTGAGGAG<br>CTGGATCATGAAATCTCGAGTCAAGTAAGAAAGGAAATTG<br>AGGACACGAGTTGGGTATTGCATAGTGTACTGTGTTAA<br>GGTCAGGGGTCAAAGACTTACTGGCATGGAGTAACCCAG<br>AGTAAGTG                 |
| 364 | ADXCRA<br>D_CN481<br>679_s_at | MARS   | Sense | methionyl-tRNA<br>synthetase<br>[Source:HGNC<br>Symbol;Acc:6898]                                                                                                                                                       | 364 | CAGGCAAAAACGTCCCCGAAGCCAGCAGTTGTAGAGAC<br>TGTTACAACAGCCCAAGCCACAGCAGATACAAGCGCTGA<br>TGGATGAAGTGACAAAACAAGGAAACATTGTCCGAAAA<br>CTGAAAGCACAAAAGGCAGACAAAGAACGAGTTGCTGC<br>GGAGGTGGCGAAACTCTTGGATCTAAA                                                                                |

FIG. 7-94

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|     |                               |          |           |                                                                                       |     |                                                                                                                                                                                                                                                                                                                        |
|-----|-------------------------------|----------|-----------|---------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 365 | ADXCRA<br>D_BX1168<br>94_x_at | EIF2C2   | Sense     | eukaryotic translation<br>initiation factor 2C, 2<br>[Source:HGNC<br>Symbol;Acc:3263] | 365 | CAGAGTCCCGTGTGTCTCTAAAAATCTCTAAACCAGTC<br>TATGAACCTCAGGGCTTTAAACATTTTAAATTTATTTGGT<br>CATTCAATTTACTTGTGTTTTAATACATGATTCTCTATGAAA<br>TTGATGGGCTCAAACTAGCTGTGAATCTTCTGAGAGTGA<br>AAGCAACA                                                                                                                                |
| 366 | ADXCRIH.<br>179.C1_at         | NET1     | AntiSense | neuroepithelial cell<br>transforming 1<br>[Source:HGNC<br>Symbol;Acc:14592]           | 366 | TATAAGTAACCCCTATGATGCTCCCCCTTACGAGAAAAACA<br>AAACTGTACACATTTATAAACAAACAGTCTCTCCCATCA<br>GTTAACACACAGAGCCCTCTCTACACCAAAGTCTCTTTC<br>CGTTTGCCACCAGAAAGGCTTTGCTCCCTCGCTCTTCG<br>GATGCCGGGCTGTGTCTGTGTGTCTTTAAGCTCTTGC<br>TGTCCCTCTGCCATCTGCATGCCAGAGCCACATCTGTAA<br>GCGTTTTCATCAACTTCTACCTGAGTAACACTGGAAACT<br>GTCCTCGTGC |
| 367 | ADXCRA<br>D_BG772<br>667_s_at | C11orf35 | AntiSense | Uncharacterized protein<br>C11orf35<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q8IXW0]   | 367 | ACAGCTCCTTTGACCTCAGTGACAGGCACTCACCTACC<br>TGACCCCCAAACTGAAGCCTCACTTTTCCAGCCGTGT<br>CCACACCTCTGGGCTACCCCATACCATGACAAGTATT<br>CCCTCTGCTCCAGGAGAAAAGCCAGGTCCCAGACCTGA<br>CCCATTAACCCCAATCATTTCCA                                                                                                                          |
| 368 | ADXCRA<br>D_BE1385<br>16_at   | ATL2     | AntiSense | atlastin GTPase 2<br>[Source:HGNC<br>Symbol;Acc:24047]                                | 368 | GACCAGGAAGTCCTATAAAGAATTATATTTCTATAGAATT<br>AAAAATGCAGTTCTGTCAGCCTGGACAAC                                                                                                                                                                                                                                              |

FIG. 7-95

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|     |                               |         |           |                                                                                                                                |     |                                                                                                                                                                                                                           |
|-----|-------------------------------|---------|-----------|--------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 369 | ADXCRA<br>D_14668.C<br>1_s_at | TBL1XR1 | AntiSense | transducin (beta)-like 1<br>X-linked receptor 1<br>[Source:HGNC<br>Symbol;Acc:29529]                                           | 369 | ATAAGAACTTATGGATTTCCTACACGGAGACAAAAAA<br>GATATCCCTTTATGTNGTTTAAAGTGGCAGCTGCTCTT<br>TCTTATTCCCATTTAATCAATGAGTATTGATTCAAGTTTT<br>CCTTTCTATTTTCCCTTATGATAAGTTTCTTACAGTAGCT<br>TATACAACAACAAATAGCATAGAAAAAACTACTGGATTCA<br>AT |
| 370 | ADXCRA<br>D_11100.C<br>1_x_at | N/A     | Sense     | non-protein coding RNA<br>152 (NCRNA00152),<br>transcript variant 2,<br>non-coding RNA<br>[Source:RefSeq<br>DNA;Acc:NR_024205] | 370 | ACAGGTAACCTTCTCACTAAGTGGGGGTGTCTGAGGCC<br>AGGAGAGCTCTACTCATTCCTCTGTGTGATCCCAGCA<br>GTGAGCATAGAGCAGGTGCCCTGCAATGTTAAGC                                                                                                     |
| 371 | ADXCRA<br>D_CB0552<br>15_at   | BMP2    | Sense     | bone morphogenetic<br>protein 2<br>[Source:HGNC<br>Symbol;Acc:1069]                                                            | 371 | AGAAAGAATAAAGCAGGATCCATAGAAAATAATTAGGAAA<br>ACGATGAACCTGCAGGAAAGTGAATGATGGTTTGTGTT<br>CTTCTTCCCTAAATTAGTATCCCTTCAAAGGGGCTGAT<br>CTGGCCAAAGTATTCAATAAAACGTAAGATTTCTTCATT                                                   |
| 372 | ADXCRA<br>D_BP2850<br>69_at   | IFIT3   | Sense     | interferon-induced<br>protein with<br>tetra-trico-peptide<br>repeats 3<br>[Source:HGNC<br>Symbol;Acc:5411]                     | 372 | GATTGCTGAGCAGGGAAGCTTTGCATGTTGCTCTAAGG<br>TACATTTTTTAAA                                                                                                                                                                   |

FIG. 7-96

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|     |                               |        |           |                                                                                                                           |     |                                                                                                                                                                                                                                                                                                                                       |
|-----|-------------------------------|--------|-----------|---------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 373 | ADXCRA<br>D_BE6446<br>66_at   | BMPR1A | AntiSense | bone morphogenetic<br>protein receptor, type IA<br>[Source:HGNC<br>Symbol;Acc:1076]                                       | 373 | CACCCCATGCACTGTACAAATACTGCAAAACACTATAGTT<br>GCATTATAGGACCATTAAAAAAA                                                                                                                                                                                                                                                                   |
| 374 | ADXCRA<br>D_AW979<br>272_s_at | BICD1  | Sense     | bicaudal D homolog 1<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:1049]                                                  | 374 | TTCTGAGGGACTGCTTCTGGAGCCGGCCCTCTTGTGTG<br>ATTGAATTAGTCAGTGATGGTTCTCAGGACTAGATTAGA<br>TTGTTACTCTTAAAAATAA                                                                                                                                                                                                                              |
| 375 | ADXCRA<br>D_2443.C1<br>_s_at  | TCEB3  | Sense     | transcription elongation<br>factor B (SIII),<br>polypeptide 3 (110kDa,<br>elongin A)<br>[Source:HGNC<br>Symbol;Acc:11620] | 375 | GGCCGCTTCAGACAACCACCTGAAAAAGCCAAAAGCACA<br>GAGACCCAGAGAAAGCCAAATTGGACAAAAGCAAGCAA<br>GGTCTGGACAGCTTTGACACAGGAAAAAGGAGCAGGAGA<br>CCTGTTGCCCCAAGGTAAAGAGAGAGGGTTCTAACAAACC<br>TAAAGACTCCAGAAAGGAAAGTCAAAACTAAATTTGGATA<br>GAAAGTCACTGGGCTCCCTCCCTAAAGTTGAGGAGACA<br>GATATGGAGGATGAATTCGAGCAGCCCAACCATGTCTTTT<br>GAATCCTACCTCAGCTATGACCA |
| 376 | ADXCRA<br>D_AL1575<br>11_at   | SNAPC3 | Sense     | small nuclear RNA<br>activating complex,<br>polypeptide 3, 50kDa<br>[Source:HGNC<br>Symbol;Acc:11136]                     | 376 | ACAAC TGGAA TTAGGATTTTCTCCTGATGAAGGAAAAA<br>AGACATTAAGTCTGCATTATATTTTAAACCCCATGAAAAG<br>ACTGAAACCAACCAACAAACAAAGAAAACTTGACTTGTTA<br>TTAGAACAGTCATTATATTTTCTTCTTCAAAACTGT<br>TATTTTACCATGTTGTATCTTCTCCCAAAGTAATATGCA<br>GATGAAGCAAAATAACTCAGCAAAAGTGTATGGACCAA<br>GCCCTTCCCATCATTTCTAGCATTAAGTGAA                                      |

FIG. 7-97

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|     |                                |         |       |                                                                                                        |     |                                                                                                                                                                                                                                                                                                                               |
|-----|--------------------------------|---------|-------|--------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 377 | ADXCRP<br>.Hs#S186<br>2874_at  | SND1    | Sense | staphylococcal<br>nuclease and tudor<br>domain containing 1<br>[Source:HGNC<br>Symbol;Acc:30646]       | 377 | TGGATGTGTTGCTGTTGGCCAAAGAAGAAATGAGAAGGAG<br>CGAATTTGGGCAGTGGGACCTCCAGGCAGCCTTACAGT<br>TTTCAGTTGGGAGTGAGATGAGACCTGGAATTTAGGG<br>GTCTGTGTAGTTAAACCATCGGTTGACAAAGATTGCCC<br>AGATTGAGTATGTGAAGGTGTGATGGGGAGGAGAGAG<br>AGTGTAGGAAGTCTGGGTCCTGCCATCTGAGAACAA<br>GGAGCCCAGAGGCAGCATATGCAGCCCCGAAAGGAGAG<br>AATCCATGCTGAGGGTCGTGAATAC |
| 378 | ADXCRP<br>DRC.7243<br>.C1_x_at | ECE1    | Sense | endothelin converting<br>enzyme 1<br>[Source:HGNC<br>Symbol;Acc:3146]                                  | 378 | GAGAAACAGCTGTCACCTCCCGCAGACCCCTAATCCTCT<br>CTCGC                                                                                                                                                                                                                                                                              |
| 379 | ADXCRA<br>G_BC039<br>833_at    | RNF44   | Sense | ring finger protein 44<br>[Source:HGNC<br>Symbol;Acc:19180]                                            | 379 | AATATTGTTGCTGATTTCAGAGGGATATTCACTAATAAAT<br>GTAT                                                                                                                                                                                                                                                                              |
| 380 | ADXCRP<br>D.12441.C<br>1_s_at  | CCDC55  | Sense | coiled-coil domain<br>containing 55<br>[Source:HGNC<br>Symbol;Acc:25305]                               | 380 | ATTCTGAATCATCACTGGGAGCAAAACACAGACTCACAA<br>GAGGAAGGCAAGAGAAGGGTAAAGAACAAAGAGAGAC<br>CACCTGAGGCAGTGAGCAAGTTTGCAAAGCGGAACAAT<br>GAAGAACTGTAATGTCAGCTAGAGACAGGTACTTGGC<br>CAGGCAGATGGCGGGTTAATGCAAAGACCTATA                                                                                                                      |
| 381 | ADXCRP<br>DRC.1049<br>3.C1_at  | PPFIBP1 | Sense | PTPRF interacting<br>protein, binding protein<br>1 (liprin beta 1)<br>[Source:HGNC<br>Symbol;Acc:9249] | 381 | ATTGCTTGAACCTGGGTAACCTGATTGATGTAATGCCAA<br>AGGAGAAGGAGTAAAGGAAAATGACATAGAGTCTGAG<br>CTAGAGTAACAGGGACAGTATTAATTAATTAATTAACCAA<br>TATCAATAAGAACATTTAAGAGACGAGCCACCATG                                                                                                                                                           |

FIG. 7-98

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|     |                                 |        |           |                                                                                                 |     |                                                                                                                                                                                                                                                                                                                 |
|-----|---------------------------------|--------|-----------|-------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 382 | ADXCRPD<br>.14444.C1<br>_at     | PRKDC  | AntiSense | protein kinase, DNA-<br>activated, catalytic<br>polypeptide<br>[Source:HGNC<br>Symbol;Acc:9413] | 382 | CTGCTGGTGTATTGCTTAATGGACCATTTAAGGAA<br>TTCTCGAATACACCGACCAAAAATCTCTTAAAGTACT<br>GTCAACAGGGTCCACAATCCATCCAAATAGCTTCTAG<br>TAAGGCAACAGTATCCTGACTTTCAAATTTCTTGTGTTA<br>GTGAACCCAGTGAATCAGCTGCATAACTAGTGGCTCATAC<br>AGTTGCCCTTGTCACCTGATCAACATCACACGCCAAGTCGA<br>AGCAGCACAGGAAACGTCGCTTATAGAGCTGGTACA               |
| 383 | ADXCRA<br>G_NM_1944<br>28_at    | DHX34  | Sense     | DEAH (Asp-Glu-Ala-<br>His) box polypeptide 34<br>[Source:HGNC<br>Symbol;Acc:16719]              | 383 | CTGAATTTGCCCCATCCACCTGGGTCACCTTTGAGAGTTGT<br>GCAGGGGGCTGGAGCACCTGGTGTTCACGTGGGACC<br>ACAGGCTGCACCATAGACCCACTCACAAATAAAAAAATA<br>AAAGGCCGAGCCGGGCATGGTGTCTCACTCCCGTAATA<br>AAAAATAAAGAACACAGGCTGAGCCGGGAAA                                                                                                       |
| 384 | ADXCRA<br>D_BE64466<br>6_x_at   | BMPR1A | AntiSense | bone morphogenetic<br>protein receptor, type IA<br>[Source:HGNC<br>Symbol;Acc:1076]             | 384 | CCAGAAAAAGCACCCCCATGCACGTACAAATACTGCAAA<br>CACTATAGTTGCATTCATAGGACCATTAAAAAAAAGAG<br>CCAAATTACAAAAACAATCTATATTTTACAAACATTTCACT<br>TGGGTTCTTAAGCTAAAGATATTACTGTTTACTTTGGTAC<br>GATAACTAGAAAAACACAAACATTATGCTCCAGA                                                                                                |
| 385 | ADXCRA<br>SS_Hs#S3018<br>206_at | MYO10  | Sense     | myosin X<br>[Source:HGNC<br>Symbol;Acc:7593]                                                    | 385 | TCCTTTGTCCCTGGTCGCTTGGTAAATGTGTAGTCGCGTA<br>TCTGAGACATAGATTGTGCTTTATTCGGTGTGTGGAGA<br>GTAGAACTAGCAGCAGTACCTGGAAAGGGGCCCTGAT<br>CTCGGGGTGTGGATGAGTAGAGACTCTTCAGTTGAGAT<br>TTAGCTCTAGTGAGGGTTGGGTGCAACAATGTAGGAAA<br>GAGTGAAGAGATGAGCAGCTCATGTCTGAGTTTATTCTG<br>TTTCTGTTACTGTGTACAGACAGCCCTCAGATCATAGT<br>TCATGAT |

FIG. 7-99

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|     |                                |         |           |                                                                                                   |     |                                                                                                                                                                                                                                                                                                                        |
|-----|--------------------------------|---------|-----------|---------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 386 | ADXCRA<br>D_BF5155<br>92_x_at  | YPEL5   | AntiSense | yippe-like 5<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:18329]                                 | 386 | GCTCATTGCTGACTGTTTTCCCTTAAAAGCTGGGAAGGCT<br>GTGGGTCAATTACGCTCGCCACCTGTTTCTGTACTGCC<br>CACAAAGCTGAGAAATGAAATTTGTACTTTTAAATGGTTGG<br>GGGAGGGGAGAAATATTTCTGACACACAAGATATATGAC<br>ATCACACTTGAGTGTCAAAGTTTTTAGGAACACAGCCA<br>CGCCCATTTGTTACACTTTACTCCTTCCACTTTACAATG<br>AAGAGGTATGAGGAGCTGCTACAGAAACCTTCTGGCTT<br>GCAAGTTTA |
| 387 | ADXCRA<br>G_BC015<br>944_s_at  | TIA1    | Sense     | TIA1 cytotoxic granule-<br>associated RNA<br>binding protein<br>[Source:HGNC<br>Symbol;Acc:11802] | 387 | ATTTGGAGAAAAATACGCTAGATTTTAAATGTTAGAGCT<br>GTTCCCGGAGACTTATTGCAGAAATAGATGAGAAGCAA<br>ATCAAGACTACTATTTC                                                                                                                                                                                                                 |
| 388 | ADXCRSS<br>.Hs#S218<br>3619_at | SIPA1L3 | Sense     | signal-induced<br>proliferation-associated<br>1 like 3 [Source:HGNC<br>Symbol;Acc:23801]          | 388 | GCTGACAGTGAGTACTGATGGCCTGGATGTAGGGTGA<br>GAGAAAGAGAGGGGCTAGGATGACCCCTGAGGTTTGG<br>GCCTGGACACACAGCTGAGGGTGAAGATACTGCATTGA<br>GGGACCCAGGGTCGGGGTTTGCAGGGAGTGGCCAGA<br>AGGCTTGTGAAGAATCAGAGACGTGGCTGAGTCTGTT<br>CGGTGCTGGTGCCCGTCAGACAGCTGCGTGAGATGG<br>CAAGGAGACAGTTGGATACGCATACCTGAAGTTGAGAG<br>AG                      |

FIG. 7-100

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|     |                               |         |           |                                                                                                                                                    |     |                                                                                                                                                                                                                                                                                                         |
|-----|-------------------------------|---------|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 389 | ADXCRP<br>D.2761.C1<br>_s_at  | SMARCC1 | Sense     | SWI/SNF related,<br>matrix associated, actin<br>dependent regulator of<br>chromatin, subfamily c,<br>member 1<br>[Source:HGNC<br>Symbol;Acc:11104] | 389 | ACTGCCTGGCAGAACATACCACTGAACCTAGTATGTGCTA<br>GAGAGGGCACAAACATCCGCTCCTCCCTAGGCCTGC<br>TGGCTCTGGTTTCTATGCAGATGATTCATTGGATTGGG<br>GGTGAGTGTTTTGTTTTCTGGGGCAGTGTGAGCTTTG<br>AGGTTGGAATATTGGAGGCATTCCCTAGTTTCCCTCAA<br>CTAGCCTGGAAGTTAGGAGTCTAGGGTAATTACCCCC<br>CAATGAGTCTAGCCTACTATTCACTGCTT                 |
| 390 | ADXCRA<br>D_BX1040<br>39_s_at | CYP1B1  | Sense     | cytochrome P450,<br>family 1, subfamily B,<br>polypeptide 1<br>[Source:HGNC<br>Symbol;Acc:2597]                                                    | 390 | AAAGCTGTGTTTATATGAAGAAAGTAAGGTGCTTGGAG<br>TTTACCTGGCTTATTTAATATGCTTATAACCTAGTTAAAG<br>AAAGGAAAAGAAAAACAAAAACGAATGAAAACTGAA<br>TTTGGAGGCTGGAGTATCAGATTACTGCTTTAATCAGA<br>AACCTCATTGTGTTTCTACCGGAGAGAGAAATGTATT                                                                                           |
| 391 | ADXCRP<br>D.12476.C<br>1_x_at | ASPH    | AntiSense | aspartate beta-<br>hydroxylase<br>[Source:HGNC<br>Symbol;Acc:757]                                                                                  | 391 | AAAGAACTTCTATCCAGAATGCATAAAGAAATTACCGCTC<br>AGCAACAAAAACAATAAAATTAGAAATGGGCAAAAAAG<br>AAACTTCACTAAAGATAATGGGTGTAGCCAATAAGCACA<br>AGAAAAAGTGCTTGACATCATATTTCATCAGGGAATTGC<br>AAATGTAACCTACAGTAAGAAAGCCACGGCATACCCACC<br>AGAATGGCTAAATTAATAAGAGACTGACACCCACCAATGT<br>TGGTACATATGTAGAACCAACCAATTCCACACATAG |

FIG. 7-101

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|     |                               |          |           |                                                                                               |     |                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------------|----------|-----------|-----------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 392 | ADXCRA<br>D_AL8335<br>13_at   | EEA1     | Sense     | early endosome antigen<br>1 [Source:HGNC<br>Symbol;Acc:3185]                                  | 392 | TTTTATAGCGTGTAGTTGACCCCTTGAACAATTTGAGTGC<br>CAACCTCCTGTGCAGCTGAAATTCATGTATAACTTTTGA<br>CTCCCCAAAAATTTAACTACTAATAGCCTATTGTTGACC<br>AGAAAGCCTTACCTATAATATAAACAGTTGATTCACACAT<br>ATTTGCATGTTATATATATATATATACAGTATTCCTTTT<br>TCTTTGCACATTAATAAAAAAGACATTTATTCTGCATCATGA<br>TCAGACTTACATTTAGCAATCAACA |
| 393 | ADXCRA<br>G_BC017<br>424_s_at | KIAA1217 | Sense     | KIAA1217<br>[Source:HGNC<br>Symbol;Acc:25428]                                                 | 393 | GAGTGCATGATATTGTTAGCCAAAAGGAGAGACAT<br>ACAGACGGTTAATATCGATGCCAGAAAAGAGATGACCC<br>CCCGACAAGAAAGGACTGACAATGAGGATCCAGTCGTG<br>TGCTGGACAAGAAACCAGTGATCATCATTTTCGATGAG<br>CCCATGGACATCCGGTCTGCCTATAAGAGACTTTCAACT<br>ATCTTTGAGGA                                                                      |
| 394 | ADXCRA<br>D.6743.C1<br>_at    | INPP4B   | Sense     | inositol polyphosphate-<br>4-phosphatase, type II,<br>105kDa [Source:HGNC<br>Symbol;Acc:6075] | 394 | GAGGAGTCGAACATGATCTTGAGGACTCTACTCTTGGGA<br>GGCTTAAAGGAATGTGTTGTCTGTAAATGTCACAGGGAA<br>TCAGGAAGGAAGAGCCAGTTAGGTCAAGCGTTAGAAT<br>ATGTTAAGCTTAATAGGCTTTGACACTCAGATGTGCCCA<br>TCAAGCAGTTAGGAATTGGATTATTTGTTTGGAAAGG<br>TCAGAACTAGTCAAGAGATTTCATAGTCCTTGGTAAA                                         |
| 395 | RDCR342<br>_D10_x_at          | GFPT1    | AntiSense | glutamine--fructose-6-<br>phosphate<br>transaminase 1<br>[Source:HGNC<br>Symbol;Acc:4241]     | 395 | CAGAAATTCATGCTTCTCTGGCAACAACAATAACTATTA<br>GAAAACTTTAACCTCACCCAGAAAGTTNNNNNNNNNN<br>NNNNNNNNNNNNNNNNNNNNNNCAGCTTACTTAAATAAT<br>TGTGCTAAATAGCTTATCTTCACAAATTTAAAGTAAAAAC<br>CTTTGAAAAAGAGGACTTCACCAAAAAACAACACACTC<br>TCCCTATAGCCCTGAAGATCTGGCCAGAAAAAGCTCCAT<br>TAA                              |

FIG.7-102

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|     |                              |                                             |       |                                                                                             |     |                                                                                                                                                                                                                                                                                                                        |
|-----|------------------------------|---------------------------------------------|-------|---------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 396 | ADXCRA<br>D.8154.C1<br>_s_at | RP11-294O2.2<br>(Clone_based_<br>vega_gene) | Sense | Novel processed<br>transcript.                                                              | 396 | GATAATAACCTTTAATGAACCTCAATACTCGGGAAAGGCT<br>TCACATTTCTGGGACTCAGCATTTATCCAAAAATCTATTA<br>AGAGCCATACACCATTTAGCTGCAATTGATTATACAAA<br>AAAAANGACCAAAAGTGTACATAATAATAAATAGAACAC<br>AGAGAAAGAAAGAAACTACATGTGTTACAAATTTGGTAAG<br>ATAACAAACAAACAAACAAAAATTAATCACTTTTTTTGGT<br>CCTGTGACACACATGATAATTTTGTCTTAATTCCTCTAA<br>CAATGA |
| 397 | ADXCRA<br>D_A18200<br>50_at  | MMP25                                       | Sense | matrix metalloproteinase<br>25 [Source:HGNC<br>Symbol;Acc:14246]                            | 397 | CGGCAGGTCCTGGATCACCAAGGACCTTGAAAGCATG<br>TGGAAGACTTTGATCAATGGGGAATCATTAAAGGGTTT<br>TGCATTCCGGAACATATCATCAGCTTCAGCGGGGGCAG<br>GGGTAGGATAGAGGCAGGGAGGCAGGAAGTTCTCGC<br>AGGTCCAGGCAAGAGATGGTGAGTGTGTCCTGGG<br>GAAGGGGCAGTGGACGGATCTGAGGGAGGTTCAATT<br>AGGATGGGCAAGGATTGAGATCTGGCTGGATCC                                   |
| 398 | ADXCRA<br>D_CD672<br>976_at  | ARHGEF2                                     | Sense | Rho/Rac guanine<br>nucleotide exchange<br>factor (GEF) 2<br>[Source:HGNC<br>Symbol;Acc:682] | 398 | GGGACATCCGAAAGCTACACCACAGATGCCAGTGTTC<br>ATGCCTTCTTCCCGCAACTTTAGGAAAAATTTATTTATTA<br>TTGTTATTAGTTATGGGGGAGAGGGGAGATTTAAAG<br>GACCAGGGACATGGGAACCAAGCCATAGGGATCAGAG<br>GGCCTTGTCCTTGAACACTACTGGGGTATATTCAGGCT<br>CATCCACGCAG                                                                                            |

FIG. 7-103

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|     |                                 |        |       |                                                                              |     |                                                                                                                                                                                                                                                                                       |
|-----|---------------------------------|--------|-------|------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 399 | ADXCRA<br>D_BX0928<br>82_at     | MSX1   | Sense | msh homeobox 1<br>[Source:HGNC<br>Symbol;Acc:7391]                           | 399 | CAGCAAGAAAAGCGCAGAGAAATCGGTGTCTGACGAT<br>TTTGAAATGAGAAACAATCTCAAAAAAAAAAAAAAAAAA<br>AAAAAAAAAANGAAAAGAGAAAAAAAAAGACTAGCCAG<br>CCAGGAAGATGAATCCTAGCTTCTTCCATTGAAAAATTT<br>AAGACAAGNTCAACAACAACAACATTTGCTCTGGGGGC<br>AGGAAAACACAGATGTGTGCAAAGGTAGGTTGAAGG<br>GACCTCTCTCTTACCAGTACCAGAAA |
| 400 | ADXCRIH.<br>2218.C1_a<br>t      | CAPN12 | Sense | calpain 12<br>[Source:HGNC<br>Symbol;Acc:13249]                              | 400 | AGAGCAGGAGAGACGGCAGAGATATGTTGCTAGGTGAA<br>TATATATTTATATAATAATAATCCGTAAGTTAATAAAGTAAAT<br>AGTAATTCCTG                                                                                                                                                                                  |
| 401 | ADXCRA<br>G_NM_02<br>5168_s_at  | LRRC1  | Sense | leucine rich repeat<br>containing 1<br>[Source:HGNC<br>Symbol;Acc:14307]     | 401 | GTATGGACTGAGAGGCATTTAAATTCGGCAAGGAGG<br>TGGAAATGCTGACAATGAGGAGGAAGCTTATAGTGGGT<br>CAAACAAGGAGGTGCTAGTGTGTGTTTAAAAAGAAGG<br>CTTACAATTAGCCAGGC                                                                                                                                          |
| 402 | ADXCRP<br>DRC.1038<br>0.C1_s_at | WHSC1  | Sense | Wolf-Hirschhorn<br>syndrome candidate 1<br>[Source:HGNC<br>Symbol;Acc:12766] | 402 | TCCCAAGGTCGCTAGAAACTCGTCTTCGCGTTGCCCC<br>CTTTCTGGCTCTCAGCGCCGTCGCCACTCGGGAGAGG<br>CTGGGTGAGGCCCGGTGTGAGGACTGACCCCTGGATTCCT<br>CGAAACTGCCATTGTGATCATTAATCTGCTCTTTTGAAA<br>TGGCTG                                                                                                       |

FIG. 7-104

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|     |                               |        |       |                                                                                     |     |                                                                                                                                                                                                                                                                                                          |
|-----|-------------------------------|--------|-------|-------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 403 | ADXCRA<br>G_BC015<br>714_s_at | PHF21A | Sense | PHD finger protein 21A<br>[Source:HGNC<br>Symbol;Acc:24156]                         | 403 | GTTACATGAAATAGTGCCAGCTGGAGGTTCTTTGCCAG<br>CACCATGCCAAGTGAAATAATATATTTACTCTCTCTATTA<br>TACACCAGTGTGCTCGCCTGCAGCAGCCTCCACAGCCACG<br>ATGGTTTGTCTCTGTTTTCTTGGGTGGGAGCAGGGA<br>CGGCGGAGGAGGAGAGCAGGTTTCAGATCCTTACTT<br>GCCGAGCCGTTTGTAGGTAGAGAAAGACAAGTCCAAA<br>GAGTGTGTGGGCTTTCCTGTTTCTAAACTTTCGCTACTA<br>TA |
| 404 | ADXCRA<br>DRC.1379<br>6.C1_at | SH3D19 | Sense | SH3 domain containing<br>19 [Source:HGNC<br>Symbol;Acc:30418]                       | 404 | TGTCTGTGCCTCATGGAATTGCCAATGAAGATATTGTCT<br>CTCAAAACCCCGGAGAACTCTCTTTGTAAGCGTGGGAT                                                                                                                                                                                                                        |
| 405 | ADXCRA<br>G_BC064<br>577_at   | CPNE7  | Sense | copine VII<br>[Source:HGNC<br>Symbol;Acc:2320]                                      | 405 | CCCTGTGCTTTTGGCGTGGGCCTCTGCACCTGGGTC<br>CATGGGTCTGCGGGGTCTGCGGGTCTGCCTGGCCT<br>GTGGTTCTGCCGTGGGCTTCAGGAGTAATAAAGTG<br>TCACCCTATCCTTGTA                                                                                                                                                                   |
| 406 | ADXCRA<br>D.14989.C<br>1_s_at | IGF2   | Sense | insulin-like growth<br>factor 2 (somatomedin<br>A) [Source:HGNC<br>Symbol;Acc:5466] | 406 | GGCCATCCGAAATAGCAACAACCCAGACTGGCTCCTC<br>ACTCCCTTTTCCATCATAAAATCACAGAGCAGTCAGA<br>GGGACCCAGTAAGACCAAGAGGGGAGGACAGAGCA<br>TGAAAACCAAAATCCATGCAAAATGAAATGTAATTGGCAC<br>GACCCTCACCCCAATCTTACATCTCAATCCCACCTCT<br>AAAAGCACTCATCTTATGTCATCCCCCGCAGCT                                                          |

FIG. 7-105

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|     |                             |        |           |                                                                                        |     |                                                                                                                                                                                                                                                                                                                                     |
|-----|-----------------------------|--------|-----------|----------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 407 | ADXCRA<br>D_14930.C<br>1_at | DHRS11 | AntiSense | dehydrogenase/reductase (SDR family)<br>member 11<br>[Source:HGNC<br>Symbol;Acc:28639] | 407 | GATATTTGTCTATGAACAGTAGACAGACCCCTCTAATTC<br>CATAGGGAATCATTTCCATGACTTCCCCCAATACCCCTA<br>CTCTTCTCTATCTCTGTGACAGTCTCTGGCCCTGCTCCC<br>TCCTAAACTGCTCAAAATCCTTACCAAAATGGCTTACAA<br>ATCTCTCTCCTCCGG                                                                                                                                         |
| 408 | ADXCRA<br>G_AK0914<br>65_at | LARP1  | Sense     | La ribonucleoprotein<br>domain family, member<br>1 [Source:HGNC<br>Symbol;Acc:29531]   | 408 | CCCTGTGGATCCCAACCAGGAAGTTCTCTCTGGGCCAC<br>CTCGGTTCCAGCAAGTTCTACGGATGCCCTGGCCCAAC<br>AAGTTGTTGGTGCTCTCTGAGCCCTCCACCATCGCCCG<br>CTCTTACCAACCACCTGTCCAGAGTCACCAAACTACC<br>GCAACACCAGGACCCCTCGCACTCCCCGGACACCCACA<br>GCTCAAAGACTCAAGCCAGACATCACGGTTTTACCCAG<br>TGGTGAAAGAGGACGGACACTGGATGCCAAGATGCCT<br>C                               |
| 409 | ADXCRA<br>D_AA7021<br>87_at | ZXDC   | AntiSense | ZXD family zinc finger<br>C [Source:HGNC<br>Symbol;Acc:28160]                          | 409 | TATAGTTCTGTTGTAGGCTACACATGAACAGCAACCAAA<br>AAGAGGAAAAATCTTCTTTGTCCCCATGCTTTTCCCTTG<br>AATTCTGCACCTTTTCATATTAACATTAGCCCTTGCTTTGT<br>GATTGCTTTGCTTTATTTTACCCCTGCTTAATCTTAAC<br>CTTCCCAAATATTTCCATACAGGGTGACCTCTCCTAGA<br>CAACACACAGCGGAGAGTGCTTCCCATGTATTCAAT<br>CTTCGCTCTTTGAAAGGAGAGTGCCCTCATTACACTTC<br>ACTGTGACACAGGATACCCCTTGTTT |

FIG. 7-106

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|     |                               |                        |           |                                                                                                                                                                 |     |                                                                                                                                                                                                                                                                                                               |
|-----|-------------------------------|------------------------|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 410 | ADXCRA<br>D_8783.C1<br>_at    | NOTCH2 ///<br>NOTCH2NL | Sense     | Notch homolog 2<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:7882] ///<br>Notch homolog 2<br>(Drosophila) N-terminal<br>like [Source:HGNC<br>Symbol;Acc:31862] | 410 | ATGGAAAAGAACACCGATGAGAAATTAGACACTGGAAAATA<br>TGTATGTGTGGTTAATAAAGTGCTTTAA                                                                                                                                                                                                                                     |
| 411 | ADXCRA<br>D_CR740<br>197_s_at | BBS4                   | Sense     | Bardet-Biedl syndrome<br>4 [Source:HGNC<br>Symbol;Acc:969]                                                                                                      | 411 | TCAGGTTGTGAGGTTTATTAGTCCCCAAGGCAACACAA<br>ATATTAGATTAAATAATCCAACCTTTAATAGTATACATTTAAA<br>AGAAAAAAACAAAGCCCTGGAAAGTTGAGGCCAAGCC<br>TGCTGAGTATTGCAGCTGCATTTGCCCAAAGGGAATCC<br>AGAACAAAGTCCCTCCCTGTATTTTGTCTTGAGAGGGGT<br>CAGCTAGAAGCTAGATCCTATCAGGATGAGGAGCAGC<br>AGCCCAGGGCTTGCTGTGATCAGCACCAACGATTTTAA<br>AGA |
| 412 | ADXCRA<br>D_AL0440<br>78_at   | HNRNPL                 | AntiSense | heterogeneous nuclear<br>ribonucleoprotein L<br>[Source:HGNC<br>Symbol;Acc:5045]                                                                                | 412 | GTGGTGTCTTGATGTAGTGAGCTCAAGTCTGCGGCTG<br>TTTCTGGGGACGTGGTGGAGGCTGCATGTTCTGTTCTC<br>TCCAGGAAGAGCTAGTGTTTCTACCCCTGTGTGTTGGT<br>GAGCAATGTGCAGAGGCAGAGCCGCTGAAGTATGGTTC<br>CTGAGGGGTGGCGAAGCACCCGCCCTCACTCCAGGTCA<br>CCTCATCAGCCCCTCGTTTTTTTTTGGCCCCACCTTGGG<br>GCTTGCCAAACTGAGAGGCATTCAAAAACCATGGCAC             |

FIG.7-107

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|     |                                |         |       |                                                                                    |     |                                                                                                                                                                                                                                                                                                                    |
|-----|--------------------------------|---------|-------|------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 413 | ADXCRA<br>D_CF1274<br>03_at    | TMEM53  | Sense | transmembrane protein<br>53 [Source:HGNC<br>Symbol;Acc:26186]                      | 413 | AGGACGCGGGCTCTCGCTGGCCCGAGCTCTACCTCTA<br>CTCGAGGGCTGACGAAGTAGTCTCGCCAGACATAG<br>AACGCATGGTGGAGGCACGCCTGGCACGCCGGGTCTT<br>GGCGCGTT                                                                                                                                                                                  |
| 414 | ADXCRIH.<br>766.C1_s_<br>at    | CLPTM1L | Sense | CLPTM1-like<br>[Source:HGNC<br>Symbol;Acc:24308]                                   | 414 | GAAGCATTTGGAGGAATTCCTAGACATTGCGTTTTCTGT<br>GTTGCCAAAATCCCTTCCGACATTTCTCAGACATCTCCC<br>AAGTTCCCATCACGTCAGATTTGG                                                                                                                                                                                                     |
| 415 | ADXCRA<br>G_NM_19<br>4428_x_at | DHX34   | Sense | DEAH (Asp-Glu-Ala-<br>His) box polypeptide 34<br>[Source:HGNC<br>Symbol;Acc:16719] | 415 | ATGTCTCCAGATTCCAGGTGCAGGTTCTTAGCACCTCC<br>GCAGCCGCTCTCTCTTTGAGTCCATCCTCAGTCTCTCCTA<br>CCCCTTGAAGTAGGGGACCCTGAATTTGCCCATCCAC<br>CTGGGTCACTTTGAGAGTTGTGCAGGGGGGCTGGGAG<br>CACTGGTGTTCACGTGGGACCACAGGCTGCACCATAG<br>ACCCACTCACAATAAAAAAATAAAAGGCCGAGCCGGGC<br>ATGGTTGCTCACTCCCGTAATAAAAAATAAAGAACAG<br>GCTGAGCCCGGAAA |
| 416 | ADXCRA<br>D_BG696<br>656_s_at  | FCGBP   | Sense | Fc fragment of IgG<br>binding protein<br>[Source:HGNC<br>Symbol;Acc:13572]         | 416 | TGTGATTGTCAGCAATGACCATGCTGGGAAACTGTGTG<br>GGCCTGTGGAAACTTTGACGGGACCAGACCAATGAT<br>TGGCATGACTCCAGGAGAAGCCAGCGATGGAGAAATG<br>GAGAGCGCAGGACTTCTCCCCATGTTATGGCTGATCAG<br>TCATCCACCAGGAACGAAGATTTCTGAAGAAGACCTG<br>GTCCCTCTGGAGGTTGCGGTGGCTGAAGGATGCATCAT<br>GTGCTCCTACCCCTGCTCTACCGCTTTTCTGGGTACA                      |

FIG.7-108

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|     |                        |         |       |                                                                                                                                                                   |     |                                                                                                                                                                                                                                                                                                    |
|-----|------------------------|---------|-------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 417 | RDCR333_A08_s_at       | C1orf27 | Sense | Protein odr-4 homolog (hODR-4)(Transactivated by transforming growth factor beta protein 1)(LAG1-interacting protein)<br>[Source:UniProtKB/Swiss-Prot;Acc:Q5SWX8] | 417 | ACATTGGAAGTTAAGAGAGTTCGAGGGAAGAAATTATAA<br>AGACTAGGAGTCCTAGAAAAGAGAAAATTTAGAGAAATAAA<br>AGGAGAGGCAGTACTTGAAAGATAACACAATTTTTTACAA<br>ATTTGTTGGA AAAACATGAATTCATAAAATTCAGGAAGCA<br>CAATATATACCCCAACATATATTTAAATAAAATCCAGGCCCT<br>AGACTCA                                                             |
| 418 | ADXCR1H.2331.C1_x_at   | G3BP2   | Sense | GTPase activating protein (SH3 domain) binding protein 2<br>[Source:HGNC Symbol;Acc:30291]                                                                        | 418 | TTCCCCCTTTGAATGAGGTCTTCCATGTTTGAGGGAAAG<br>TCTTGCACTATTGCATATATTTGGGACACAGATTTTCA<br>TAGTTCCCATTTTGGGGGCTTAAGGANNNNNNNN<br>NCTGTTGAAACAGTTTATACITTTCTGATATAGTACTTG<br>AAATTCCTTACCAGAAAATTACTTTGGAGTTTGAAGCCCTT<br>TATTAATACTACTTTTAAAGAAGCAGTTGTTTTATTGTCA<br>ATGTTTTTTTCCCCCAGCATATTTTCTTGATTTTC |
| 419 | ADXCRA_D_AL583362_s_at | BUB3    | Sense | budding uninhibited by benzimidazoles 3 homolog (yeast)<br>[Source:HGNC Symbol;Acc:1151]                                                                          | 419 | TGAGATGGTTTGATGGTTTGCTGCATTAAAGGTATTTGG<br>GCAACAAAATTGGAGGGCAAGTGACTGCAGT                                                                                                                                                                                                                         |

FIG. 7-109

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|     |                                |                                           |           |                                                                                                                                |     |                                                                                                                                                                                                                                                                                                  |
|-----|--------------------------------|-------------------------------------------|-----------|--------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 420 | ADXCRRS<br>.Hs#S775<br>346_at  | NR6A1                                     | AntiSense | nuclear receptor<br>subfamily 6, group A,<br>member 1<br>[Source:HGNC<br>Symbol;Acc:7985]                                      | 420 | TACTAACTTTCTGCACTAAACCACCAAGTCTGTCTCCT<br>CTGCAATGIGTAGTTCTGATGGCTCCGGTTTTTCCCCC<br>CACCTTTTATTTGAAGCCTGACTTGCAGGAGATACCC<br>CTCTAACTGTATAGCTTCTACTCCATTAAAGATTAGTCA<br>GAGATGGTAATCAACCCACCTGAGCTCTTTCACCTACCTG<br>CTGCTGCAACTATGTCAGGATAAGGGGAGCACACTCA<br>CACTTCAGGCCCTTCACGTCTGTCCAGTTACTTTT |
| 421 | ADXCRA<br>G_NM_00<br>2526_at   | NT5E                                      | Sense     | 5'-nucleotidase, ecto<br>(CD73) [Source:HGNC<br>Symbol;Acc:8021]                                                               | 421 | CTTTGAACCACCTTTGCCAATTGTAGATTCCCAACAATAAA<br>ATTGAAGA                                                                                                                                                                                                                                            |
| 422 | ADXCRA<br>G_NM_14<br>5754_s_at | KIFC2                                     | Sense     | kinesin family member<br>C2 [Source:HGNC<br>Symbol;Acc:29530]                                                                  | 422 | GGACTAGGAAGGGCTATTCCAGGCTCAGCCCCTGCTCCT<br>GCAGCTTTGCCGCTGAGTGTAGGAAACAGGCATGAC<br>AGACCAGGTGAGGGTTGTGCCAGCTGGGCCACGGC<br>CATGCGTGGGTGGCCCAATAACACCCGTGGACTCC                                                                                                                                    |
| 423 | ADXCRRP<br>D.7912.C1<br>_x_at  | MTA2                                      | Sense     | metastasis associated<br>1 family, member 2<br>[Source:HGNC<br>Symbol;Acc:7411]                                                | 423 | TTTCTCTTTCTGTCCGGTGTCCGGACTTTCCTAATTGGA<br>GTTTGAGGCCCCCTAAGCTGGCATCAACCCCAGGCCACG<br>CTCGCTCTTCTCCCTCCCTCCCTCCCTCTGCGCTTTTG<br>TACGCCAGTTCTCAGAAATAAAGATCTTTTGTCCGTTTTT<br>TTAACCTCGGATTCTGTAATTGGTTCTTA                                                                                        |
| 424 | ADXCRRP<br>D.11100.C<br>1_at   | AC068491.1<br>(Clone_based_<br>vega_gene) | Sense     | non-protein coding RNA<br>152 (NCRNA00152),<br>transcript variant 2,<br>non-coding RNA<br>[Source:RefSeq<br>DNA;Acc:NR_024205] | 424 | CCACAGGTAACCTTCTCACTAAGTGGGGGTGTCTGAGG<br>CCAGGGAGAGCTCTACTCATTCCTCCCTGTGTGATCCCAG<br>CAGTGAGCATAGAGCAGGTGCCCTGCAAT                                                                                                                                                                              |

FIG. 7-110

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|     |                              |                                                                                          |       |                                                                                                                                 |     |                                                                                                                                                                                                                                                                                    |
|-----|------------------------------|------------------------------------------------------------------------------------------|-------|---------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 425 | RDCR269<br>_G02_at           | PPP2R2D                                                                                  | Sense | protein phosphatase 2,<br>regulatory subunit B,<br>delta isoform<br>[Source:HGNC<br>Symbol;Acc:23732]                           | 425 | CCCCATGCCCTGTGGAGATGGAGGTGTGTGCTGATCC<br>CTCGTCCCCCTGTGGAGATAGAGGTGTGTACTGATCCC<br>CTGTTCCCTATCTAGATGAAGGTGTGTACTGCTGATCC<br>CCCGTCC                                                                                                                                               |
| 426 | ADXCRP<br>D.15397.C<br>1_at  | THBD                                                                                     | Sense | thrombomodulin<br>[Source:HGNC<br>Symbol;Acc:11784]                                                                             | 426 | TTTTGACAGTGTGAAAATGTTCAGAAAGTTGCTCTAG<br>ATTGAGAGAGAGACAAACACCTCCAGGAGACAGTTC<br>AAGAAAGCTTCAAACTGCATGATTCATGCCAATTAGCAA<br>TTGACTGTCACTGTTCCCTTGTCACCTGGTAGACCAAATA<br>AAACCACTCTACTGGTCTTGTGGAATTGGAGCTTGG<br>GAATGGATCCTGGAGGATGCCCAATTAGGGCCTAGCCT<br>TAATCAGTCCTCAGAGATTTCTTC |
| 427 | ADXCRP<br>D.7988.C1<br>_s_at | AL354822.1<br>(Clone_based_ensembl_gene)<br>/// AC145212.2<br>(Clone_based_ensembl_gene) | Sense | Putative<br>uncharacterized protein<br>ENSP00000383640<br>[Source:UniProtKB/TrE<br>MBL;Acc:B7WNX9] ///<br>Known protein coding. | 427 | CCCACCTGTGTAGTCTTAACCTATTCTTCTAAACTCAC<br>CATTAAACCTAAATAATAGTCAAATTTAGGGGGCTGTAT<br>TTGTCTTACTCGAGTCTTCTACCATAGTTGAAACTGTCTG<br>TACCCAAACGAGTTACAGAGAAATGCCACACTTTGAGA<br>CGAATTCAGGAGTCCCTTTATTAGCTGGTGACTGAGAGA<br>CGGCTAACACAGGAAATACTCTCGGCCCTAAAGAAATGG<br>GCTA              |

FIG.7-1111

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|     |                              |       |       |                                                                                                  |     |                                                                                                                                                                                                                                                                                                            |
|-----|------------------------------|-------|-------|--------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 428 | ADXCRA<br>G_X81197<br>_at    | ARCN1 | Sense | archain 1<br>[Source:HGNC<br>Symbol;Acc:649]                                                     | 428 | GAAGACGCCAATGATGGCTGAAGAGTTTTTCCCAGATTT<br>ACAAGCCACTGGAGACCCCTTTTTCTGATACAATGCAC<br>GATTCTGCGCGCAAGGACCCTCGACTCACCCTCATG<br>TTTCAGTGTACAGAGACATTCTTTGATAAGGAAATGGC<br>ACAAACATAAAGGGAAGGCTGCTAATTTCTTTGGCAG<br>ATTGATTGCCAGCAGGAAAGCAAGCTCTCCAGAGAA<br>TGCCCCCAGTTAAATACCTCCTCTACCTTTACCTAAGTT<br>GCTC    |
| 429 | ADXCRIH.<br>2554.C1_s<br>_at | CPEB2 | Sense | cytoplasmic<br>polyadenylation<br>element binding protein<br>2 [Source:HGNC<br>Symbol;Acc:21745] | 429 | TGATCTGGTCAGTAGTGGAAATTCGATTTTATGCAGACTG<br>GATGTAATATTTGTAATCCCTGTGCAATTTTGTGACGTG<br>CGTTCTAATTCATGTGCAGTGATATAGTATAGATAAAA<br>GAATGAGTAAAAAGAAAATACAAGAATTCTAAAGAAAAGTT<br>GGTTTAGCCCCCTTTGATAGTCCATGGTTAAGACATCCT<br>TTATAACCAAGATGCCAGCACACTG                                                         |
| 430 | ADXCRRP<br>D.5.C1_at         | WBP11 | Sense | WW domain binding<br>protein 11<br>[Source:HGNC<br>Symbol;Acc:16461]                             | 430 | CAGAAAGAGGGCTCAACTTAGCCCAATATTTTATGCTGTC<br>AAGAAATGCTCAGCATGTGGAAGTGGAGAGTATTCCCTTT<br>GCCAGATATGCCACATGCTCCTTCCAACATTTTGATCCA<br>GGACATTCCTCCTGGGTGCCAGCCACCCCTCTATC<br>CTAAAGAAAACCTCAGCCTATGGACCTCCCAACTCGGG<br>CCAGTTTCTATCCTCCCTCCTCCTTGGACATGGGGGT<br>TTCCACCGTTTGCCCCCCTGGCAGAAAACCTCCCTGG<br>GCCT |

FIG.7-112

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|     |                               |        |           |                                                                                                      |     |                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|--------|-----------|------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 431 | ADXCRA<br>D_11028.C<br>1_at   | MMP1   | AntiSense | matrix metalloproteinase<br>1 (interstitial<br>collagenase)<br>[Source:HGNC<br>Symbol;Acc:7155]      | 431 | GAGTCCAAGAGAATGGCCGAGTTCATGAGCTGCACACG<br>ATGTAAGTTGTACTCTCTGAAATTGTTGGTCCACCTTTC<br>ATCTTCATCAAATGAGCATCCCCCTCCAATACCTGG                                                                                                                                                                 |
| 432 | ADXCRA<br>D_BG258<br>265_at   | DOK3   | Sense     | docking protein 3<br>[Source:HGNC<br>Symbol;Acc:24583]                                               | 432 | GAGTCACGAACCTTATTCTCCAAACAAAGCAACAAGG<br>ACTTTGACTTCTCAGCAGCACTCAGCTCTGGTTCTTGAA<br>ACACCCCCGTTACTTGCTATTCCTCCTACCTCATACAA<br>TCTCCTCCAGCCTCTACTGCTGCCCTTCTCTGAGTTCT<br>TCCAGGGTCCCTAGGCTCAGATGTAGTGTAGCTCAACC<br>CTGCTACACAAAGAATCTTCTGAAGCCTGTAAAAATGT<br>CCATGCATGTTCTGTGAGTGATCTACCAA |
| 433 | ADXCRA<br>D_BQ016<br>677_at   | POLR3A | Sense     | polymerase (RNA) III<br>(DNA directed)<br>polypeptide A, 155kDa<br>[Source:HGNC<br>Symbol;Acc:30074] | 433 | CCGGGGTAGCCATTGGTTCTTGGATCTGTGTTAGAATG<br>AGTGCTTTCCTTCCCTACTGATGTGATTGTGGATTAGGA<br>ATTCGTGACCGAGTGATTTTGGCCAGTGGTTGGGTTTA<br>AAATTCTATTAAATTTGTAGTTTGGGCTGGGTGCT                                                                                                                        |
| 434 | ADXCRA<br>D_BP3766<br>05_s_at | GLUL   | Sense     | glutamate-ammonia<br>ligase [Source:HGNC<br>Symbol;Acc:4341]                                         | 434 | GTGGAGGCCCATACCGGGCCTGCTTGTATGCTGGAGT<br>CAAGATTGGGGAGTAATGCCGAGGTGATGCCTGCCCC<br>AGTGGGAATTCAGATTGGACCT                                                                                                                                                                                  |

FIG.7-113

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|     |                               |                    |       |                                                                                                                                        |     |                                                                                                                                                                                                                                                                   |
|-----|-------------------------------|--------------------|-------|----------------------------------------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 435 | ADXCRP<br>D.11491.C<br>1_at   | ATP2B4             | Sense | ATPase, Ca++<br>transporting, plasma<br>membrane 4<br>[Source:HGNC<br>Symbol;Acc:817]                                                  | 435 | TTCAATTTTCTTCCCCTCTGCTAGTTTGGAAAGTTATATTA<br>TACCAAGTTTTTTAGTATTAGCCTAGAAATCTTAACATAA<br>AGACTTCTAATAAGCAATATCTTTAAATTTTTTTTNCCTAC<br>CCAATACTAGATCATGAGCATTTTCCCACATCATAAAGA<br>ATTGGTCACAAGTCAGCCCCCAACATAGTCCAGTGGAA<br>TCCAATGATA                             |
| 436 | ADXCRP<br>D.11413.C<br>1_s_at | C8orf38            | Sense | UPF0551 protein<br>C8orf38, mitochondrial<br>Precursor (Putative<br>phytoene synthase)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q330K2] | 436 | AAGGCAACACTTCTGTCTAGTAGAATTGCTTTGGATTGTA<br>AATATGTTTACTTTCAGAGGAAATCAGTCAGAGTGGATGG<br>CTCAGCAAAACCCATCACAACTGCGGAAAAAGGAAAGTG<br>ACTGGCTAGAGTAAGGAAATAGATTTTCTCTAAGTTAA<br>CTGGCCTACGTGTGAATCGAACCCCTGCACCCTGGCCTC<br>ATTAGCAACCAACACTGTGAAGAACACAGCTGTGGCAGAGA |
| 437 | ADXCRA<br>G_AB0825<br>33_x_at | SGK269<br>(Entrez) | Sense | Tyrosine-protein kinase<br>Sgk269 (EC<br>2.7.10.2)(Sugen kinase<br>269)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q9H792]                | 437 | TTCACCCCTCTACTTACATATTGTAAAGTTGTATAAATCT<br>ATCATTGAAAGGTCCCCTCTGCCAGCAGTGGTGCCACC<br>CTTTGGTTTGTGTGGTACTTTTGTGTGTACTCCGTGGC<br>ATCATGTTACTGTGTA                                                                                                                  |
| 438 | ADXCRP<br>D.7912.C1<br>_at    | MTA2               | Sense | metastasis associated<br>1 family, member 2<br>[Source:HGNC<br>Symbol;Acc:7411]                                                        | 438 | TTTCTCTTTTCTGTCCGGGTGCCGGACTTTCCTAATTGGA<br>GTTTGAGGCCCCCTAAGCTGGCATCAAC                                                                                                                                                                                          |

FIG.7-114

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|     |                               |      |                    |                                                                      |     |                                                                                                                                                                                                                                                                                                             |
|-----|-------------------------------|------|--------------------|----------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 439 | ADXCRP<br>.Hs#S192<br>4022_at | N/A  | No Genome<br>match | N/A                                                                  | 439 | TACAAAGAGTACCACGAGACACGAGAAACCTTGTGGGA<br>ACACAGGGGACCACCCCTAAGGCTAAATACTACTTG<br>GTGACCGATAGCGAACAAAGTACCGTGAGGGAAGGTGA<br>AAAGAACCCCGAGAGGGGAGTGAAGAAAGAAATCTGAAAC<br>CTAGTGTTTACAAGCAGCGGAAATGGCACAAAGCCATGA<br>ATCGTGACTTTTGTAGAACGGGCCAGCGAGTTATGAC<br>AAAA                                            |
| 440 | ADXCRP<br>D.11083.C<br>1_at   | DSP  | Sense              | desmoplakin<br>[Source:HGNC<br>Symbol;Acc:3052]                      | 440 | TCTCTCCGAGGTCGAGGGCCCTGAGGGGCAGTTACTC<br>CAGGAACAGGAAAGTGTCAACAAGCTCAGTTGAGGAA<br>TGAGCATTTCCAGAAAGGCGATAGAAGATAAAAGCAGAA<br>GCTTAAGTGAAGCAAAATACGAAATTGAGAGGCTGCA<br>GTCTCTCACAGAGAACCTGACCAAGGAGCACTTGATGT<br>TAGAAGAAGAACTGCGGAACCTGAGGCTGGAGTACGAT<br>GACCTGAGGAGAGACGAAACGAGCCCCACAGC                  |
| 441 | ADXCRP<br>DRC.1676<br>1.C1_at | PER1 | Sense              | period homolog 1<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:8845] | 441 | CATAGCCAAAGGCTTCAAGCTCTCAGGACTTGGCTATGG<br>AGGAGGACGAAGAAGGCAGGAGCTCATCCAGTCCAGC<br>CTTACCCTACAGCAGGAAACTGCACCAGCTAGACTCCAT<br>TCTGGGACCATCTCCAGGAGTCCATGAGAGGCTTTCTT<br>CTCCTATGTCCCAATTCTCAGAACTCAGATGTGGCTAGA<br>CCAAACCCCTGGGAAACTGCCCCAGCTTCTCCCACCATA<br>GGGCCGGACCCCATCACCAGCCTAGATCCAGGGCT<br>GCCTC |

FIG.7-115

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|     |                                |          |       |                                                                                                                                               |     |                                                                                                                                                                             |
|-----|--------------------------------|----------|-------|-----------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 442 | ADXCRP<br>DRC.3805<br>.C1_s_at | JUN      | Sense | jun oncogene<br>[Source:HGNC<br>Symbol;Acc:6204]                                                                                              | 442 | AAC TTGTGCGCGCAGCCCAAACTAACCTCACGTGAAGT<br>GACGGACTGTTCTATGACTGCAAGATGGAACGACCT<br>TCTATGACGATGCCCTCAACGCCCTCGTTCTCCCGTCC<br>GAGAGCGGACCTTATGGCTACAGTAACCCCAAGATCCT<br>GAAA |
| 443 | ADXCRA<br>D_BQ673<br>982_s_at  | C9orf3   | Sense | Aminopeptidase O (AP-<br>O)(EC 3.4.11.-)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q8N6M6]                                                      | 443 | GTTTGTGATCATACACTGTTACAGAGAAAGAGAGGAG<br>GCATATTATNAACGTGTGGACTTCAGTGTATTCCCTTCT<br>CTTCAAAATGATGTTCCAGGTGTCTA                                                              |
| 444 | ADXCRP<br>D.9576.C1<br>_x_at   | PICK1    | Sense | protein interacting with<br>PRKCA 1<br>[Source:HGNC<br>Symbol;Acc:9394]                                                                       | 444 | CTCGGCGGCCCTTTATTATTCTGTTCCTCCAGCTCGGC<br>CACTTCTCTGAAGGAGGGCTGGGTTCTGGGCCCTGTATC<br>GAATAAACACAAACCTGGATGGCGC                                                              |
| 445 | ADXCRP<br>D.18146.C<br>1_s_at  | SERPINE1 | Sense | serpin peptidase<br>inhibitor, clade E (nexin,<br>plasminogen activator<br>inhibitor type 1),<br>member 1<br>[Source:HGNC<br>Symbol;Acc:8583] | 445 | GGAGGATGGTCAGGCGTCACCAACAACCCCATCACCCA<br>GTAACAAGAACCCTTGACTCTCGTCAGTCCCCTCTGCATCA<br>AGACACTTACCCATTCCACCTCATGCCTGCTAACTTG<br>AATGAAACAATCGCTGGGAAAGCATTAA                |

FIG. 7-116

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|     |                                 |        |                           |                                                                                                      |     |                                                                                                                                                                                                                                                                                                               |
|-----|---------------------------------|--------|---------------------------|------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 446 | ADXCRESS<br>.Hs#S297<br>8758_at | FNDC3B | Sense                     | fibronectin type III<br>domain containing 3B<br>[Source:HGNC<br>Symbol;Acc:24670]                    | 446 | ATGTGAGAGTGCTTTGCAGTTGGAAAGTGCTGTAGGAA<br>CCCTGAATTCATCTGAAACTGTAGCTTAGTGTAAATG<br>ATGCTGTTATTACTTTTTGAATAGTCTGGAGTCTTGTT<br>TAAAGAAAAAATTATTCTGTGATATTTGTTGAATGAAGCA<br>CAGTGAGGAAGACTTTACTCAGGGCCCTTGTAATAGCT<br>ATAGGGACCACCTGCAATAGGGTCTTGCAGTGGGGAGA<br>GAGAAATAGGCTCAATTCTGAATACATCATCATGGGCAAG<br>TGGG |
| 447 | ADXCRA<br>D_BX0942<br>82_at     | GGCX   | Sense                     | gamma-glutamyl<br>carboxylase<br>[Source:HGNC<br>Symbol;Acc:4247]                                    | 447 | TCTAAAGCTGTTTTTAACCTCCGAGATTACAACCTTAGAGG<br>AACCAAGGA                                                                                                                                                                                                                                                        |
| 448 | ADXCRA<br>D_AA1795<br>10_at     | N/A    | No<br>Transcript<br>match | N/A                                                                                                  | 448 | AAATTGAAGGATTTGCTGTTATTCTACCTGCATTGGAC<br>TTGACCTGGGTGTTGGGTGAGTAGCAATCTGTTACTGTT<br>TCTCTATGTGGACGATGAGGAAAGGTTGAGAAATCCA<br>GCGAAAGGACACTTCTGTTAATAGCTCAATCTGCTGCC<br>ATGGTTGGGAAAA                                                                                                                         |
| 449 | ADXCRA<br>G_AJ2707<br>78_s_at   | TCF7L2 | Sense                     | transcription factor 7-<br>like 2 (T-cell specific,<br>HMG-box)<br>[Source:HGNC<br>Symbol;Acc:11641] | 449 | TTTTCTGTATGAAACCCAGATGTCACCAAATGGACATT<br>AATAGTTGCATTAAGGATCAGTAGCATTAAACAAAAGTTG<br>CTTAAAGCCATTATGTAATCAAGACTTGAAAATGAGT<br>GAGGGAAATTTAGCGACACTGTCTGAGCA                                                                                                                                                  |

FIG. 7-117

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|     |                               |         |           |                                                                                                             |     |                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|---------|-----------|-------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 450 | ADXCRA<br>D_AW771<br>618_at   | PRPF40A | AntiSense | PRP40 pre-mRNA<br>processing factor 40<br>homolog A (S.<br>cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:16463] | 450 | TGAATTCCCAACTTCCGAGATGTTGTTTAAATGAGACTC<br>ACCCATTATTTTCAATCTTCCCTTCAATCTCCTCCCTCTTA<br>ACTGGTTTCCTCTTACCCAAGAAAAGCCCTTCTCTTAAC<br>TGCAAGCTTATTTGAATTTTACCTTATTGAATATCTTTCA<br>ACTATTTGGCAGACCTTTAACTTTCCCTACCATGCCAAT<br>GGTCACTAAACACCTTAAATGCCACTCTTAACACCTTAA<br>ATGCCACCCCTTAACAGTATTCTTTCAGTCTCATTC |
| 451 | ADXCRA<br>D_BQ898<br>896_s_at | ARHGAP4 | Sense     | Rho GTPase activating<br>protein 4<br>[Source:HGNC<br>Symbol;Acc:674]                                       | 451 | TGTCCAGCAAGTGCAGGGTGCCTGCACCTCACCCCTGTG<br>CAGAGAGGTGGATGGGGCCGTGCACACAGGGATGCC<br>CGCTCCACATCCTGCCTGCCCTCAGCCCTGGCCCGAG<br>GCCCTTTTGAGGCAGCTGAGGAAGGATGCTGGGA<br>AAGCCCTCTTCTGCAGCTTTGTGGAAGGCTGATCAGTG<br>GCTGCTGGGTGGCGGTACCCCTTGCTCAGATGCCTGG<br>CAGGGCTGGTGGCGATTTCATAAAGACCTCGTGTGAT<br>TCCCC       |
| 452 | ADXCRA<br>D_9582.C1<br>_s_at  | SESN2   | Sense     | sestrin 2<br>[Source:HGNC<br>Symbol;Acc:20746]                                                              | 452 | CAGGAGAGAAGAGGCCCGGCATGGGATCTGGGTTTC<br>TAGAGGGCATGTGATGACTGTAAATGTTCACTGGGTGG<br>GTAGGGAGTGGTATCCAGTGTTCAAGTGCAGAAATCTTT<br>GGCTTTGCTACCAAGTTCATATGA                                                                                                                                                     |
| 453 | ADXCRA<br>D_AW661<br>890_at   | TFAM    | AntiSense | transcription factor A,<br>mitochondrial<br>[Source:HGNC<br>Symbol;Acc:11741]                               | 453 | GGTTAATCTTTGTTACTAGCCCTCACTACTCAGAAATTGG<br>TGAGACCTCTCCATTTCTGCTTCACTCAGCTTACGTGGT<br>TTGCTCACACTGACACCAACAACACCTGTCAATCCCTA<br>TGTCCCTCCTGCTCTTCCAAAAATACCTAGAAAATTGCTGC<br>TCTATTGACGGTAGTATTC                                                                                                         |

FIG. 7-118

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|     |                               |                                            |           |                                                                                                                                                             |     |                                                                                                                                                                                                                                                                                              |
|-----|-------------------------------|--------------------------------------------|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 454 | ADXCRA<br>D_AA8308<br>54_s_at | RNF145                                     | AntiSense | ring finger protein 145<br>[Source:HGNC<br>Symbol;Acc:20853]                                                                                                | 454 | GCTCTAAAAGTTATGAACCTGACATTCTTGGTCTTACAC<br>AATCTGGACCCAGTCTACTCTTCTATAACCATCTTCCAC<br>TTAATTTACAAATCTTTATTAAAGGCACAGGTACTCCTACT<br>TATCCCCTATTGCCCTCTCTCATGCTGAATCAATCATGCC<br>AAAAGCTAAGAAAACATGAGCATGCTTGGGACTAAAGAA<br>ACAGAACTGAGGATTTCCCTACACATCCTAACTGCAAGGA<br>CAGTCCATCAAAAAGCCAGAGA |
| 455 | ADXCRA<br>D_CB9973<br>64_s_at | FLT1                                       | Sense     | fms-related tyrosine<br>kinase 1 (vascular<br>endothelial growth<br>factor/vascular<br>permeability factor<br>receptor)<br>[Source:HGNC<br>Symbol;Acc:3763] | 455 | GGAAGCTTTAGCTACCAATCCAGTACCCCTCCTAACTAGA<br>ATGTATACACATCAGCCAGGACTGACTGACTACTTTCATT<br>AGAGATATACTGTACTCATTGGG                                                                                                                                                                              |
| 456 | ADXCRA<br>D_CX1658<br>54_s_at | Z83843.1<br>(Clone_based_<br>ensembl_gene) | Sense     | Novel long non coding<br>RNA.                                                                                                                               | 456 | TACCTGTGGTTCAGGTACCTGGAGGGCTGACGTAGGA<br>GGATTGCCTGAGCCCAGCAGGCCAAAGCTACAGTGAG<br>CTGTGATTGTGCCACTGCACCTCCAGCCTGGCGGAGGAG<br>AGCAAGACTCTGTCTCANAAATAAATACATAAAATACAG<br>CGTCCAAAAGTGTGTCATCTTCTTTCTTTCACAAATTTTA<br>TAATAAGGGGTAAATGCCGTGTGAGTCTATTTCATTAT                                   |
| 457 | ADXCRA<br>D_BM128<br>089_at   | APOL2                                      | Sense     | apolipoprotein L, 2<br>[Source:HGNC<br>Symbol;Acc:619]                                                                                                      | 457 | CTTTGGACTAAAGAAATATATTGGGCGGAAGAA TAGAGGG                                                                                                                                                                                                                                                    |

FIG. 7-119

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|     |                                |         |           |                                                                                                                                                 |     |                                                                                                                                                                                                                                                                                                        |
|-----|--------------------------------|---------|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 458 | ADXCRA<br>D.BX1061<br>90_at    | ZFAND3  | Sense     | zinc finger, AN1-type<br>domain 3<br>[Source:HGNC<br>Symbol;Acc:18019]                                                                          | 458 | TTCTGCTTTTCCCTGTTCCCTATCCTTACGCAGGATTGTTT<br>TACTGTTAGCCAGGTTAAGTTTAAGCTTCTTGAGGACTT<br>TAGTACTGAAAGACAAATGGCTCACTTGTAAAGACCTAGTT<br>GAAGAGTACAGATTTAGATTGTTTCAGTGTGCTGTG                                                                                                                              |
| 459 | ADXCPRP<br>D.2974.C1<br>_s_at  | LRRFIP2 | Sense     | leucine rich repeat (in<br>FLI) interacting protein<br>2 [Source:HGNC<br>Symbol;Acc:6703]                                                       | 459 | AACATATGTGTAGTGTGCTGCAGCATAAGATGGAAGAA<br>CTTAAAGAAGCCCTGCGGCAAAAGAGATGAGCTTATTGA<br>GAAACATGGCTTAGTTATAATCCCCGATGGCACTCCCAA<br>TGGTGATGTCAGTCATGAACCAAGTGGCTGGAGGCCATCA<br>CTG                                                                                                                        |
| 460 | ADXCRIH.<br>638.C2_at          | CEACAM6 | AntiSense | carcinoembryonic<br>antigen-related cell<br>adhesion molecule 6<br>(non-specific cross<br>reacting antigen)<br>[Source:HGNC<br>Symbol;Acc:1818] | 460 | AAGCTTTTAGAGAATACACTACACCAGGGAGTATGACTA<br>CTAGTATGACTATTAGGAGGGTAATACCAAGAGTTGGAC<br>TACGCACCTTAGGCAAGATACAAACCAACTAAAATAGAA<br>TAAAGAAATGAGTCAGATGAGTGTAGCCATTTTAACCAAG<br>CAGCACATTTGTTAATTTCTACAACCTTAGTCTCAGCGATA<br>CCCATTGTATTTAGCCATGTTCAACAACAAGTGTGAGAA<br>ACTGCACAGACTCCTCCCTGTTTCAGCTGGTAG |
| 461 | ADXCPRP<br>D.14645.C<br>1_s_at | RERE    | AntiSense | arginine-glutamic acid<br>dipeptide (RE) repeats<br>[Source:HGNC<br>Symbol;Acc:9965]                                                            | 461 | CTTTGTCCGCTGTCATGATTCGCCACGTCCTTCTTCTG<br>TCCTCTCACGGCTAGGCCCTCCAGTGAAAGGTAGACAGT<br>AAGCCTGGCATTCAAGTCTTCTGAAATTTCTCACATCAAT<br>TCCAGGGGAAAATCCAACCACTCCAACA                                                                                                                                          |

FIG. 7-120

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|     |                               |         |       |                                                                                     |     |                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|---------|-------|-------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 462 | ADXCRP<br>D.12819.C<br>1_at   | SMURF2  | Sense | SMAD specific E3<br>ubiquitin protein ligase<br>2 [Source:HGNC<br>Symbol;Acc:16809] | 462 | ATCCAGCAAGGAATAGTGCAGCACCTAGGGACTAGCAA<br>TGATAGGAAGTTGCACCATATTTGGCCCAGCAAGGGCA<br>AAGGAGAGAGTAGTTGTGGAGTCCAGAGAGACCCCT<br>GGTTGTTGCTTCTCATTTATTGAACCCGATTAAAGCCA<br>GAGAACAAAGAGCCCAGTTTATGTAGTACATGACGCAG<br>CCTCTAGGCACAGGGTAAAGGATGGAGAATAGATCTG<br>GAGGATTAAATAGTAAACAACAACGCCGCGAGATCCTCTAA<br>GTC |
| 463 | ADXCRP<br>D.1255.C1<br>_s_at  | CCDC90A | Sense | coiled-coil domain<br>containing 90A<br>[Source:HGNC<br>Symbol;Acc:21097]           | 463 | TTGAGAACAGAAATAGTGGCATTGCATGCCCAGCAAGA<br>TCGGGCCCTTACCCAGACAGACAGAGAAAGATCGAAACTG<br>AGGTTGCTGGCC                                                                                                                                                                                                        |
| 464 | ADXCRP<br>D.18183.C<br>1_at   | RAB11A  | Sense | RAB11A, member RAS<br>oncogene family<br>[Source:HGNC<br>Symbol;Acc:9760]           | 464 | TATTTCTTATGCTGTCAGATTACATTTTTCCTTTGAGTGC<br>TTTGGGTGCAGCCGTGGAATCCTGATGTAAAAGCATAG<br>GTTCTTGCATTACTGAGTAAACAT                                                                                                                                                                                            |
| 465 | ADXCRA<br>D_BM128<br>089_x_at | APOL2   | Sense | apolipoprotein L, 2<br>[Source:HGNC<br>Symbol;Acc:619]                              | 465 | GCAGATGGCAAGTGCACCAAGGAGAAAGGCAGGAACAC<br>TGGAGCCTGCAATAAGGGAGGAGAGGGGACTGGAGAG<br>TGTGGGAATGGGAAGAAGTAGTTTACTTTGGACTAAA<br>GAATATATTGGCGGAAGAATAGAGGGGAGCTTGCAGG<br>AACCAGCAATGAGAAGGCCAGGAAAAGAAAGAGCTGAA<br>AATGGAGAAAACACAGATTAGAACTGTTGGATA                                                          |

FIG.7-121

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|     |                                  |       |           |                                                                                                     |     |                                                                                                                                                                                                                                                                                                                          |
|-----|----------------------------------|-------|-----------|-----------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 466 | ADXCRRS<br>.Hs#S300<br>7624_x_at | CTBP2 | AntiSense | C-terminal binding<br>protein 2<br>[Source:HGNC<br>Symbol;Acc:2495]                                 | 466 | CACCCCTTCTTGACCACAAAAAGGTGGCCATCCTGACTG<br>GTCTCTACCTTCAGGAAAAACAATGGGGACCTGAGGGC<br>GCTCAACCACCCAGACCACCCAGAAAGTCACAGGAGCA<br>CGGAACAGGAAGCAGGGAGACAGCACACAGTAAGCAC<br>ATGGCAAGCACACAGTAACACACACGGCAAGTACATGGC<br>AAATACACAGCAGGTACACAGCGAGCACACAGTAAGCA<br>CACGGTAAACACTCAGCAAGTACATGGCAAAATGCACAG<br>CAGGTACACAGCGAGC |
| 467 | ADXCRA<br>D_AK0243<br>15_x_at    | WDR45 | Sense     | WD repeat domain 45<br>[Source:HGNC<br>Symbol;Acc:28912]                                            | 467 | CCCGGGCCAGGCAAGGTGGTGCACACCTGTAAATCCCA<br>GCACTTTGGGGAACAAGGTGGGAGAATCACTTGAGTCC<br>GGCAGTTTGAGACCAGCCTGGCCAACATAATGAGACCG<br>CATCTTCACAAAAAATATGT                                                                                                                                                                       |
| 468 | ADXCRRP<br>D.9576.C1<br>_at      | PICK1 | Sense     | protein interacting with<br>PRKCA 1<br>[Source:HGNC<br>Symbol;Acc:9394]                             | 468 | AGCTCGGCCACTTCTCTGAAGGAGGGCTGGTTCTGG<br>GCCTGTATCGAATAAACACACAAACCT                                                                                                                                                                                                                                                      |
| 469 | ADXCRRP<br>D.4701.C2<br>_s_at    | GBP1  | Sense     | guanylate binding<br>protein 1, interferon-<br>inducible, 67kDa<br>[Source:HGNC<br>Symbol;Acc:4182] | 469 | ACTTCAGGAACAGGAGCAACTACTAAAAGAGGGATTTC<br>AAAAAGAAAGCAGAAATAATGAAAAATGAGATACAGGATC<br>TCCAGACGAAAATGAGACGACGAAAGGCATGTACCATA<br>AGCTAAAGACCAGAGCCTTCCTGTCAACCCCTAACCAAG<br>GCATAATTGAAACAATTTAGAAATTTGGAACAAGCGTCA<br>CTACATTTGATAATAATTAGATCTTGCATCATACACCAA<br>AAGTTTATAAAGGCATGTGTACAAATGATCAAAA                      |

FIG.7-122

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|     |                               |        |           |                                                                                   |     |                                                                                                                                                                                                                                                                     |
|-----|-------------------------------|--------|-----------|-----------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 470 | ADXCRA<br>D_BF7268<br>49_x_at | TLCD2  | Antisense | TLC domain containing<br>2 [Source: HGNC<br>Symbol; Acc:33522]                    | 470 | GCCAGCCTGGATATTTAAATTGTTCTGTGCTCTCCTCC<br>TTTTTTTCTCTCTGTGATTCCTCTTTGTGAGCTCCCTTGC<br>CTATATTGCATCTCAGTTGACACCCCTGATTCTGACTT<br>GTCCATTATCTTCTACCAAGTCTCTGCCGA                                                                                                      |
| 471 | ADXCRP<br>D.13978.C<br>1_s_at | PEX5   | Sense     | peroxisomal biogenesis<br>factor 5 [Source:HGNC<br>Symbol;Acc:9719]               | 471 | GTAGGAGTGCTCATGGTTCTGTCAATCTTGGACCTCTCC<br>TGGCTGAGCTCTGATTCCTGTGAGCACGATGCTGATG<br>CAATAGTCCCTGTGTCATCACTGCAGCGGTCCTCAGGAG<br>CTGCCAGGGCCAAATTGCTACAGAGTGTCTGGGTGTG<br>GCATAGGAGGAAGGTTTGTCTTGAAATGAGGCT                                                           |
| 472 | ADXCRIH.<br>928.C1_s_<br>at   | SORD   | Sense     | sorbitol dehydrogenase<br>[Source:HGNC<br>Symbol;Acc:11184]                       | 472 | ATCTAGGCCACTCGCTCTGGTGGGACCCCTCGTGCTTGT<br>GGGGCTGGGCTCTGAGATGACCACCGTACCCCTACTG<br>CATGCAGCCATCCGGGAGGTGGATATCAAGGGCGTGTT<br>TCGATACTGCAACACGTGGCCAGTGGCGATTTCGATGC<br>TTGCGTCCAAGTCTGTGAATGTAAACCCCTCGTCACC<br>CATAGGTTTCTCTTGAGAAAGCTCTGGAGGCCCTTTGA<br>AACATTTA |
| 473 | ADXCRP<br>D.1593.C1<br>_s_at  | LCP1   | Sense     | lymphocyte cytosolic<br>protein 1 (L-plastin)<br>[Source:HGNC<br>Symbol;Acc:6528] | 473 | GAAGTAAGCCTCATCATCAGAGCCTTTCCTCAAAACTGG<br>AGTCCCAAATGTATCAGGNNNNNNNNNNNNNNCAGCCA<br>CTAAGAACCCCTCTGCTTTTAACTCTAGAAATTTGGGCTT<br>GGACCAGATCTAACATCTTGAATACTCTGCCCTCTAGAG<br>CCTTCAGCCTTAATGGAAGGTT                                                                  |
| 474 | ADXCRP<br>D.9621.C1<br>_at    | C9orf7 | Sense     | Calcium channel flower<br>homolog<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q9UGQ2] | 474 | TAAAGCGTGGCCGTGGCTCGCGTGCCTGCCATCT                                                                                                                                                                                                                                  |

FIG.7-123

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|     |                                 |       |       |                                                                                                                     |     |                                                                                                                                                                                                                                                                                                   |
|-----|---------------------------------|-------|-------|---------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 475 | ADXCRA<br>G_NM_02<br>0384_at    | CLDN2 | Sense | claudin 2<br>[Source:HGNC<br>Symbol;Acc:2041]                                                                       | 475 | AAGTCCTCCTCAGGCTTGGAGAACTTCCTCAGCGTCAC<br>CTCCTTCATTGAGCCTTCTCTGATCACTCCATCCCTCTC<br>CTACCCCTCCCTCCCCAACCCCTCAATGTATAAATTGCT<br>TCTTGATGCTTAGCATTACAAATTTTGGATTGATCGTTAT<br>TTGTGTGTGTGTGCCGATCTCACAAAGTATATTGTAAC<br>CCTTCGGTGGTGGGGCCATATCCTAGACCTCTCTGT<br>ATCCCCCAGACTATCTGTACAGTGCCAGGCCACAC |
| 476 | ADXCRA<br>D_BP3323<br>15_x_at   | SSR3  | Sense | signal sequence<br>receptor, gamma<br>(translocon-associated<br>protein gamma)<br>[Source:HGNC<br>Symbol;Acc:11325] | 476 | TCACTGTAAGGTACAGTTAGGGTAACACTTTAGAGGTTT<br>ATTATTTTAAAAAACTTTTCTTGAACCTCCTGGCCAGCAT<br>GGTGAACCCCGTCTCTACTAAAAATACCAAAATTAGCC<br>AGGCGTATGTTGGTGCCTGTGATCTCAGCTACTTGG<br>GAGGCTGAAGCAGGAGAACTGCCTGAACCCAGGAGGC<br>GGAGGTTGCAGTGAGTCGAGATCGTGTACTACTGCCT<br>GGGTGGCAAGGGT                          |
| 477 | ADXCRA<br>D.9270.C1<br>_at      | TRIM2 | Sense | tripartite motif-<br>containing 2<br>[Source:HGNC<br>Symbol;Acc:15974]                                              | 477 | TGCCATTTTCCAAGAAATGACGGTGGTGGCTTTTAGTCAG<br>AAAATGGCCTTCTGTGCT                                                                                                                                                                                                                                    |
| 478 | ADXCRA<br>DRC.1555<br>1.C1_s_at | EPHB4 | Sense | EPH receptor B4<br>[Source:HGNC<br>Symbol;Acc:3395]                                                                 | 478 | GGAGAGAAAGCAGAAATATTCGGACAAACACGGACAGTAT<br>CTCATCGGACATGGTACTAAGGTCTACATCGACCCCTT<br>CACTTATGAAGACCCCTAATGAGGCTGTGAGGGAATTTG<br>CAAAAGAGATCGATGTCTCTCTACGTCAAGATTGAAGAG<br>G                                                                                                                     |

FIG.7-124

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|     |                               |        |       |                                                                                                                                                      |     |                                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|--------|-------|------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 479 | ADXCRIH.<br>1483.C1_s<br>_at  | AES    | Sense | amino-terminal<br>enhancer of split<br>[Source:HGNC<br>Symbol;Acc:307]                                                                               | 479 | AGCTGCCCCCTTTCCCGTCCCTGGGCACCCCCGAGTCTCCC<br>CCGACCCCGGGTCCCAGGTATGCTCCCACCTCCACCT<br>GCCCACTCACACCTCTGCTAGTTCCAGACACCTCCA<br>CGCCACCTGGTCTCTCCCATCGCCACAAAAAGGGG<br>GGCACGAGGGACGAGCTTAGCTGAGCTGGGAGGAGC<br>AGGTGAGGGTGGCGACCCAGGATTCCCCCTCCCCT<br>TCCCAAATAAGATGAGGGTACT                                                |
| 480 | ADXCRA<br>D_BG179<br>551_x_at | IL17RC | Sense | cysteine-rich with EGF-<br>like domains 1<br>[Source:HGNC<br>Symbol;Acc:14630] ///<br>interleukin 17 receptor<br>C [Source:HGNC<br>Symbol;Acc:18358] | 480 | AGCGGAGCAAGTGTCCTCCGGGGCCTTCAGCCAGCCCCCTGG<br>ATAGCTACTTCCATCCCCCGGGACTCCCGCGCCGGG<br>ACGCGGGGTGGACCAAGGTGCGGGACCTGGGGCGGG<br>CGACGGGACTTAAATAAAGGCAGACGCTGTTTTCTACC<br>CAAAAA                                                                                                                                            |
| 481 | ADXCRC<br>D.8757.C1<br>_at    | FAM83G | Sense | family with sequence<br>similarity 83, member G<br>[Source:HGNC<br>Symbol;Acc:32554]                                                                 | 481 | AGATGTGCACAAACAGAGCCCCCGGTACAGGTCCAG<br>CTCGGAGGGAGAGAGCCTTGTTGGGCTGTTATTCC<br>CAGGGCTCCAGCAAGCCACTCCCTGGGTGACCTCCGG<br>CAAGGCCCTCTCTGGGCTCGGTGGCCTGTGGATAAG<br>GAGGGAGACCCCACTCGCCTGCCTGCCTGCATCAC<br>GGGGCCATTGTGAGGTTGGGGGAAGACCTGGCCGTGG<br>AGCTACAAGCTTGTCGGATGTCAAGGGGACATTACTGT<br>TGCTAATAAAGTCCAAAGTGGCCAATGCCTT |

FIG. 7-125

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|     |                                |         |       |                                                                                                       |     |                                                                                                                                                                                                                                                                                                       |
|-----|--------------------------------|---------|-------|-------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 482 | ADXCRA<br>G_NM_00<br>0937_s_at | POLR2A  | Sense | polymerase (RNA) II<br>(DNA directed)<br>polypeptide A, 220kDa<br>[Source:HGNC<br>Symbol;Acc:9187]    | 482 | CGGTGAACCTTCTGGATCCCGTTTCTGATGCAGATTCTTG<br>TCTTGTTCTCCACTTGTGCTGTTAGAACTCACTGGCCCA<br>GTGGTGTCTACCTCCTACCCACCCACCCCTGCCTG<br>TCCCCAAATTGAAGATCCTTCCCTGCTGTGGCTTGATG<br>CGGGCGGGTAAAGGGTATTTAACTTAGGGGTAGTTC<br>CTGCTGTGAGTGGTTACAGCTGATCCTCGGGAAGAACA<br>AAGCTAAAGCTGCCTTT                           |
| 483 | ADXCRA<br>D_8320.C1<br>_at     | GRIN2D  | Sense | glutamate receptor,<br>ionotropic, N-methyl D-<br>aspartate 2D<br>[Source:HGNC<br>Symbol;Acc:4588]    | 483 | GCGATGAACCCCAACCTCCCTGAAGCCAAAACCTCCCAC<br>CCTGCCGCACACTCCGGACCCCACTTGCCACCAAG<br>CACATCCTCTCCAAATCCAACCCCTTATTTCGACCCCTTC<br>AGTATGACCCAGCAGACCTCCAAAAGCCTCCTCTGC<br>CCAGATCTCCAGCCGGTCTGGGCTGGGTTGCGGAG<br>GGGAGGGTCTGGGAGTCCACACTTCTCCACCAACTCC<br>CTCCCACTCTCTTATTCCACATTGCAGTGTGTTGGAATA<br>AACC |
| 484 | ADXCRA<br>D_AK0218<br>12_s_at  | RASA1   | Sense | RAS p21 protein<br>activator (GTPase<br>activating protein) 1<br>[Source:HGNC<br>Symbol;Acc:9871]     | 484 | TGTCCTGGGCACCGTAGCGAGACTCTGCTTTCTACAA                                                                                                                                                                                                                                                                 |
| 485 | ADXCRA<br>D_AU1339<br>80_at    | SLC20A2 | Sense | solute carrier family 20<br>(phosphate<br>transporter), member 2<br>[Source:HGNC<br>Symbol;Acc:10947] | 485 | GCAGGCAGTAAGAAGCAGGGATTTCTTCAAATGCTAGT<br>AAGCACAAAGAGAGGGAGAAGTTTTGTAAAGTAACGAA<br>CAGGGCCGGGCATGGTGGCGTGAAGAGGCCGAGGT                                                                                                                                                                               |

FIG. 7-126

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|     |                               |                                          |       |                                                                                  |     |                                                                                                                                                                                                                                                                                                       |
|-----|-------------------------------|------------------------------------------|-------|----------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 486 | ADXCRP<br>.Hs#S300<br>3228_at | C6orf203                                 | Sense | Uncharacterized protein<br>C6orf203<br>[Source:UniProtKB/Swiss-Prot;Acc:Q9P0P8]  | 486 | GAGCACCAGATCCTATAGAGCCCTTAGACCATCGTAGA<br>GACTTTGCTTTCTCTGAGTGCCTTGGTAGGATTTGAG<br>GAAAGGAGTGACATCGTATGAATGACTTTATTATGTGCC<br>CACGTGGAGGTGCAATAGGCAGCTATTGTGTGCAG<br>GTCCCAGGTTCAATTGATTCACTAAGAGGACTCAAAAGA<br>CTCAGCACGTAGTCCTACTCACAGCTGTGATTTATTATC<br>GCACAA                                     |
| 487 | ADXCRP<br>D.7046.C1<br>_at    | MED28                                    | Sense | mediator complex<br>subunit 28<br>[Source:HGNC<br>Symbol;Acc:24628]              | 487 | CAGATTCTTTTTTATGGTGGCTTTGCTTGTITTAATTTTT<br>GCATGACTTTTCATCTTTTATGTGTGTTCCCTGTAGTTT<br>GATCCGAAGGAAAAGAGTATAGTAGCCTGAGAATCAGG<br>AGATGGAGTTTATGTCGTAGGCCTTATGATAATTACCC<br>CGCGTGGTGTGTAGAAAAGTATGTAATTTGCTCTGTT<br>TTAAGACTTTGAACACCTCAAGAAAGAGG                                                     |
| 488 | ADXCRP<br>D.12748.C<br>1_x_at | AC138128.1<br>(Clone_based_ensembl_gene) | Sense | Novel long non-coding<br>RNA.                                                    | 488 | GTGGAGAAAGTTGGCGTCTAGGCTGGGATTGGTCG<br>GGGGACCTTAAAGAAAAAGGCCAGGGCTGAGGGTCCT<br>GAGGAGAGAGAGAGAGGCCACGTGGATGGAGGACTGT<br>CACCCCTTCTCGGTTCTGTCAACCCCTTGAGTCTAACT<br>CACTGTTGAGGGGAGGAAGAGGGGGATGGACGGAAG<br>GGAGACCGAGGAAAGGCTTTCGGAGTGGGACATTAT<br>CCACCCAGAGGTGTGCTACCCACAAACCCGCCGAGATC<br>CTTAGAGT |
| 489 | ADXCRP<br>G_AB0133<br>84_s_at | HIP1R                                    | Sense | huntingtin interacting<br>protein 1 related<br>[Source:HGNC<br>Symbol;Acc:18415] | 489 | CTGTGCTCTGGAAAGGCTACCAAATACTGGCCAAGGTC<br>AGGAGGAGCAAAAATGAGCCAGCACCCAGCGCCTTGGC<br>TTTGTGTAGCATTTCTCCTCTCTGAAGTGTCTGTT                                                                                                                                                                               |

FIG.7-127

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|     |                                |         |       |                                                                                                                             |     |                                                                                                                                                                                                                                                                            |
|-----|--------------------------------|---------|-------|-----------------------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 490 | ADXCRA<br>D_B12234<br>41_s_at  | PRPF8   | Sense | PRP8 pre-mRNA<br>processing factor 8<br>homolog (S. cerevisiae)<br>[Source:HGNC<br>Symbol;Acc:17340]                        | 490 | GCTACAGCTGGCGAACCCCAAGAGTTCTACACGAGG<br>TGCACAGGCCCTCTCATTCTCACTTTGCTCTCCTGC<br>AGGAGGGGAGGTTTACTCTCGGATCGGGAGGACCT<br>GTATGCCTGACCGTTTCCCT                                                                                                                                |
| 491 | ADXCRA<br>D_6.C2_s_<br>at      | OS9     | Sense | osteosarcoma amplified<br>9, endoplasmic<br>reticulum lectin<br>[Source:HGNC<br>Symbol;Acc:16994]                           | 491 | GGGAAGCCAAATATAGCCAAAGAGCAGCCTGTGGATGA<br>TGCTGCAGAAAGTCCCTCAGAGGGAAACCAGAGAAGGA                                                                                                                                                                                           |
| 492 | ADXCRA<br>DRC.3178<br>.C1_s_at | POLR2A  | Sense | polymerase (RNA) II<br>(DNA directed)<br>polypeptide A, 220kDa<br>[Source:HGNC<br>Symbol;Acc:9187]                          | 492 | TACATCCCTTCACCAGGTGGTGCCATGTCTCCCAGCTA<br>CTCGCCAAACGTACCTGCCTACGAGCCCCGCTCTCCTG<br>GGGCTACACACCCACAGAGTCCCTCTTATTTCCCCACT<br>TCACCTCTCTACTCCCCCTACCTCTCCATCCTATTCTCCA<br>ACCACTCCCAACTATAGTCCCAATCACCACAGCTATTCTCG<br>CCAACGTCA                                           |
| 493 | ADXCRA<br>D_BM675<br>236_at    | PLEKHG3 | Sense | pleckstrin homology<br>domain containing,<br>family G (with RhoGef<br>domain) member 3<br>[Source:HGNC<br>Symbol;Acc:20364] | 493 | GAAGAGGATTCAGGGTCAGCCTAGGGGACCCTGGCTC<br>CCTCCGATAGGCAGGAAGGAGGAGGATGCGGAGGAG<br>AGGCTGAGCCTTCCACGGGCTCCTGTTAGGGGTGTG<br>GTGAGGCCAGGTTGGGAGGGAAGCCTAAGGACCTT<br>CCACACCTCCACAGCCAGAGTCAGTTGAGGCTGGGA<br>CAAAGGGGAAGGAGAGGGAAGGAGGACCGCCTGAC<br>CTTGCCCAAGGAGCTTCTCTAAACTGC |

FIG. 7-128

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|     |                              |                                                  |           |                                                                                     |     |                                                                                                                                                                                                                                                                                               |
|-----|------------------------------|--------------------------------------------------|-----------|-------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 494 | ADXCRA<br>D.9019.C1<br>_at   | BMPR1A                                           | AntiSense | bone morphogenetic<br>protein receptor, type IA<br>[Source:HGNC<br>Symbol;Acc:1076] | 494 | GTAAGGAGTGGTGATTGCAAAATAAGCACATTATAC<br>ACAA                                                                                                                                                                                                                                                  |
| 495 | ADXCRIH.<br>2173.C1_a<br>t   | IL32                                             | AntiSense | interleukin 32<br>[Source:HGNC<br>Symbol;Acc:16830]                                 | 495 | TGCTGCTCCTCATAATAAGCCGCCACTGTCTCCAGGTA<br>GCCCTCTTTGAAGTCGTCCTCCAGCTCTGCCAGGCTCG<br>ACATCACCTGTCCACGTCCTGATTCTGCATTTTGCAATTT<br>TATCATAAAATCTTTCTATGGCCTGGTGCAATTCGGGCCT<br>TCAGCTTCTTCATGTTCATCAGAGAGGACCTTCGGGAAG<br>CACATGGCGGCCAAAGTTCAAGGAGGCCAAGGCCTGA<br>GATGACCCAGCTCCAAAGGA          |
| 496 | ADXCRA<br>D_AA5273<br>40_at  | RP11-<br>357H14.7<br>(Clone_based_<br>vega_gene) | Sense     | Novel processed<br>transcript.                                                      | 496 | TCCCCAACACACACACGCGTCCTGTTCACCTACGTAG<br>GATCTGTGAACACAGGCTCAGTGCCCTTTGAGGGAGGAGG<br>GAACGTTTAGATTGAGACCACCCCACTCCCGGGTGATT<br>AAATAAATATGTCTCTCCCCACCCACGCAGGATTGG<br>AAAAAGTTAATTGTGGTTTCAGAAAAAGTTAACCCCTGCG<br>TTGCTTCGACCCCTTCTCTCCAGGGAAGGTTGGGTAA<br>ATGTCTACGAATCGCCTTGAGAGAGAACTAAAG |
| 497 | ADXCRA<br>D_NM_01<br>4985_at | CEP152                                           | Sense     | centrosomal protein<br>152kDa [Source:HGNC<br>Symbol;Acc:29298]                     | 497 | TACACAGTTTCCAAATTAAGTAGGCAGACTGAGCATGCC<br>CATCAGTTTCTATTGCTGCTTCCATCCCTCGAAATGAT<br>AGAAAAAGATTTAAACAGCAAAATAAAGAATGAGAAAAAG<br>AAGAAATTATAAGTGGGTTTTAAAAAGTTGCAGTGGGCC<br>AGGCATCATGGCTC                                                                                                    |

FIG.7-129

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|     |                               |         |       |                                                                                                        |     |                                                                                                                                                                                                                                                                                                   |
|-----|-------------------------------|---------|-------|--------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 498 | ADXCRP<br>D.10945.C<br>1_at   | AMAC1L1 | Sense | acyl-malonyl<br>condensing enzyme 1-<br>like 1 [Source:HGNC<br>Symbol;Acc:31043]                       | 498 | TGCCCGATCACACAGGAGTATGCCCAAACTCTCTCAGG<br>CCTCTAGCAGCTGACAACCACTGCTTTAAATCCCTATTA<br>CATTATTATGA                                                                                                                                                                                                  |
| 499 | ADXCRA<br>D_BU0730<br>65_s_at | PNMA2   | Sense | paraneoplastic antigen<br>MA2 [Source:HGNC<br>Symbol;Acc:9159]                                         | 499 | CCTGGGGCAGGACCCACAGCCAGTGGGGTAAGACCT<br>TTAAAAATTTTTCTTTAATGTATGGGACTGAAATCAA<br>ACCATGAAAGCCCAATTATTGACCTTCCTTCCTCCCTCC<br>TTCCCTCCCTTCCTCCTCTCTCTCTCTCTCTCTCTCTCT<br>CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT<br>CTTTTCTCTTTCTCTTTATTTCTTGGTCTCACTCTCAT<br>CACCC                                 |
| 500 | ADXCRA<br>D_BC0332<br>51_x_at | RHOQ    | Sense | ras homolog gene<br>family, member Q<br>[Source:HGNC<br>Symbol;Acc:17736]                              | 500 | TCAAGACGAGCCTGGACAACACAAGACCCCAATT<br>CTACTAAATTTTTTTTTTAAATTAGCCAGATGTGTAATG<br>CATGCCTCTGTAGTCCCAGCTACTCAGGAGGCTGAGGT<br>GGGAGGATCACCTTGAGTGCAGGAATTCAAAAGCTGCAGT<br>GAGCTATAATACAAGGCTTCATTGCACTCCAGCCTAGG<br>CATTAGAGCGAGACCCGTGTTATTTAAA                                                     |
| 501 | ADXCRH.<br>1424.C1_s<br>_at   | TAX1BP1 | Sense | Tax1 (human T-cell<br>leukemia virus type I)<br>binding protein 1<br>[Source:HGNC<br>Symbol;Acc:11575] | 501 | TTAAGGACAAACTCAAGAGGCCACAACATGAAAGAGA<br>ACAACTTGAATGTCAGTTGAAGACAGAGAGGATGAAAA<br>GGAACTTTATAAGGTACATTTGAAGAATACAGAAATAG<br>AAAATACCAAGCTTATGTAGAGGTCCAGACTTTAAAAA<br>ATTAGATGGGAACAAGAAAGCGTGATTACTCATTTCA<br>AAAAGAGATTGGCAGGCTGCAGTTATGTTTGGCTGAAA<br>GGAAATCTGCAAGACITTCCTGCTTACAACCTCAAGTAA |

FIG. 7-130

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|     |                               |         |           |                                                                                                |     |                                                                                                                                                                                                                                                                                                                                       |
|-----|-------------------------------|---------|-----------|------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 502 | ADXCRP<br>D.11691.C<br>1_s_at | NR6A1   | AntiSense | nuclear receptor<br>subfamily 6, group A,<br>member 1<br>[Source:HGNC<br>Symbol;Acc:7985]      | 502 | CAACATGGACATTTATACTAATAAGGAGGGCAGAGGCG<br>AATATGTGAGAAGGTCCACCACCTCAGAGCTTGAATCA<br>GCTTACGATGATGAAAGGTAAGCTTTATCACTGATCT<br>CAACAGCAGACTGGTGGC                                                                                                                                                                                       |
| 503 | ADXCRH.<br>3022.C1_s<br>_at   | XPC     | Sense     | xeroderma<br>pigmentosum,<br>complementation group<br>C [Source:HGNC<br>Symbol;Acc:12816]      | 503 | GAGTCAGGCTTACTAATGCTGCCCTCACTGCCTCTTTGC<br>AGTAGGGGAGAGAGCAGAGAAGTACAGGTCATCTGCTG<br>GGATCTAGTTTTCCAAAGTAACATTTTGTGGTGACAGAAG<br>CCT                                                                                                                                                                                                  |
| 504 | ADXCRP<br>DRC.2277<br>.C1_at  | PPP3CA  | Sense     | protein phosphatase 3,<br>catalytic subunit, alpha<br>isozyme [Source:HGNC<br>Symbol;Acc:9314] | 504 | GATCAATCAAGTCTTGGTTGTGGCTTGCTGAATTAAAT<br>ATTTATGAGTGGTGCAATTTTAAAGTATCGTGACCAAGAC<br>ACCATATTA                                                                                                                                                                                                                                       |
| 505 | ADXCRP<br>D.12620.C<br>1_at   | CSNK1A1 | Sense     | casein kinase 1, alpha<br>1 [Source:HGNC<br>Symbol;Acc:2451]                                   | 505 | AATACAGAACTGAGCCTAGGCCAGGGAAGTGGATTGG<br>GGTTAGATCTAAGCAAGATCAGCATGTAAGTGATAGTG<br>GAGAAAGTAAATGGAGAGGTGAGGACTCATCCCCTTGG<br>TGGAAATTCGGAATTAATAAAGCAGGAGGAGAGTCAGG<br>ATAATGGGCTGTTGAATAAAGAAAGTAAGTGACAAGGAA<br>GAGGTAATGTGTATCCAAAGAAAGTAGGAAAGAAATGAGA<br>CTTAAAGCGTAGGGGTAGGCTGTGTAAGAGCTCAGT<br>ACCCACAGGTGCTCAGTCAAGTAACCTTGAC |

FIG.7-131

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|     |                               |          |       |                                                                                               |     |                                                                                                                                                                                                                                                                                                                               |
|-----|-------------------------------|----------|-------|-----------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 506 | ADXCRA<br>G_BC058<br>002_x_at | MORC3    | Sense | MORC family CW-type<br>zinc finger 3<br>[Source:HGNC<br>Symbol;Acc:23572]                     | 506 | TGGGATTGCAGTCGCCTGCCACCCGTGCCCCGGTAAC TT<br>TTGTATTTTGGTTGAGACAGGGTTTCGCCGTGTTGGCCA<br>GGCTGGTCTAGAACTCCTGACCTCAGGTGATCCACCCG<br>CCTTGGCCTCCCAAAGTGCTGGGATTACAGCGGTGAGC<br>CACACACCCCGGCCAAAAAATTTTTTCTATCCC<br>TGCCATTTCAGTCTCCATTAGCACTCTATTCTCTCATTT<br>ATTCACCCCGTCTT                                                     |
| 507 | ADXCRP<br>D.3154.C1<br>_s_at  | ATP6V0A1 | Sense | ATPase, H+<br>transporting, lysosomal<br>V0 subunit a1<br>[Source:HGNC<br>Symbol;Acc:865]     | 507 | ACCACCCCTAGCTTTGTGTGTAGTGTAGTATTTCTGG<br>CTGTCACTCATCTCACTGGCACCCAGCCTTGCCCTCT<br>TAGCCTCCATCCATCCAGACAGCCCTTCCACCTCCTG<br>GTGTGAGCCAGTCTGCATTCACGACGCCATCCCAAAGC<br>CCTTTCATCTTACCCGTGCATTGTAGATGGAAGGAGCAC<br>CCATGCCATTCA                                                                                                  |
| 508 | ADXCRIH.<br>2039.C1_s<br>_at  | PVR      | Sense | poliovirus receptor<br>[Source:HGNC<br>Symbol;Acc:9705]                                       | 508 | AAAAAGTCTATGATCTTGAGGGCAGACAGCAGAAATTC<br>CTCTTATAAGAAAACTGTTTGGGAAAAATACGTTGAGGG<br>AGAGAAGACCTTGGGCCAAGATGCTAAATGGGAATGCA<br>AAGCTTGAGCTGCTCTGCAAGAAAAAATAAGCAGGACA<br>GAGGATTTGCTCTGGACAGAGATGGA                                                                                                                           |
| 509 | ADXCRP<br>D.2058.C2<br>_s_at  | PHLDA1   | Sense | pleckstrin homology-like<br>domain, family A,<br>member 1<br>[Source:HGNC<br>Symbol;Acc:8933] | 509 | TGGTGAATTTTCTAGGAGCGATGATGTACTGTAAATTGN<br>NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN<br>NNNNNNAATGCTTGTCTAAGACATTTCTGAATGTAGA<br>CCATTTTCCAAAAAGGAACTTTATTTTCAAAAACCTAAT<br>CCGTAGTAATTCCTAATCTTGGAGAATAAAAAAGGCGGG<br>TGGAGGGGAAACATTAAAGAAATTTATTCATTATTTCTCG<br>AGTACTTTTCAGAAAAGTCTGACACTTTCATTGTTGTGCCA<br>GCTGTTGAAATTAACACT |

FIG.7-132

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|     |                                |         |           |                                                                                                     |     |                                                                                                                                                                                                                                                                                                                                   |
|-----|--------------------------------|---------|-----------|-----------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 510 | ADXCRRS<br>.Hs#S176<br>4949_at | CEACAM5 | AntiSense | carcinoembryonic<br>antigen-related cell<br>adhesion molecule 5<br>[Source:HGNC<br>Symbol;Acc:1817] | 510 | GATAGTGATGGGTCTTCCCAATTGTCCTTAAACCCTGTAC<br>ATATTGTGCAGCCTGGCTGGACTGGATGTTTCAGTA<br>GAAATAACACAGGGGACACACAGAGCAAGCCTGGAGG<br>TCAGCTCAGTCGTTAGGCAGTGGAGGCACAAGGTGGG<br>GCAGTTTTTCCCAGGTGTTTGATGATGACTGACTTGAGC<br>CAGAGACCCCTAAAGATAGAGTGGAGTCCAGGGAATGA<br>TCTAGAACTTCAGGTGACAGGCAGGAGCTGCCCGGATT<br>TAACAGCAGAACCATA             |
| 511 | ADXCRIH.<br>50.C1_at           | GPRC5A  | Sense     | G protein-coupled<br>receptor, family C,<br>group 5, member A<br>[Source:HGNC<br>Symbol;Acc:9836]   | 511 | CTAACTCTGTCCTGAAGAGTGGGACAAATGCAGCCGGG<br>CGGCAGATCTAGCGGGAGCTCAAAGGGATGTGGGCGA<br>AATCTTGAGTCTTCTGAGAAAAGTGTACAAGACACTACG<br>GGAACAGTTTGCCTCTCTCCAGCCTCAACCCACAATTCT<br>TCCATGCTGGG                                                                                                                                              |
| 512 | ADXCRRP<br>D.11875.C<br>1_at   | GPRC5A  | AntiSense | G protein-coupled<br>receptor, family C,<br>group 5, member A<br>[Source:HGNC<br>Symbol;Acc:9836]   | 512 | GATGGACAGGGTTCTGAAAAAACTGAAAAATGAATTCTAG<br>AAAGCAGCATTTGAGAGGGAAAAAGAGAAGTATCAGCA<br>TTTAGGAATATGAAGTGTCTGGAGCTAGAGAAACAGCCT<br>GGGAAAAGAGCAAAGGGCTAGAGCAGGAAAGAGAAAA<br>GAGAAATGAGACTAGCGGTGGTTGGATATTATTTGTAAC<br>CAAAGTCAAAGGACGGGAGATCTAGAGTCCAGCCACA<br>AAGAACTTGCTCCTATAAAAAACCAATGGACCCCAACCT<br>TCACTTGACGTAGAGGTCTTTCCT |

FIG. 7-133

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|     |                               |           |           |                                                                                 |     |                                                                                                                                                                                                                                                                                                                                |
|-----|-------------------------------|-----------|-----------|---------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 513 | ADXCRA<br>.Hs#S299<br>0374_at | KIAA0319L | Sense     | KIAA0319-like<br>[Source:HGNC<br>Symbol;Acc:30071]                              | 513 | AACATGGTCCTGGAGGTTACAGTGTAGTGAGGGGCAAA<br>GACATGGAGCCAATGGTTGAGCTGAAACCTCATGTGAG<br>GAGTTAACTGGATGGAGAAAGGAGTCAAGAGAGTTCTA<br>GGTAGAGGAGGCAGCATGTCAAAGGCACAGTAAAGGG<br>AGGATGAATGGTCCATTTTCAGGGATGGAAGAAGGCTGC<br>TAGATTGGAACATAGGGAAGGAGGGAATGTGTGATACA<br>AGCTGGAGCTAGAAAGGTAGGTGGTCAGAACATAG                                |
| 514 | ADXCRA<br>G_BC001<br>557_s_at | SMC4      | Sense     | structural maintenance<br>of chromosomes 4<br>[Source:HGNC<br>Symbol;Acc:14013] | 514 | GAAAAATTTACACAGCTAGATTTGGAAGATGTTCAAGTT<br>AGAGAAAAGTTAAACATGCCACGAGTAAAGCCCAAAAA<br>CTG                                                                                                                                                                                                                                       |
| 515 | ADXCRA<br>D_AW291<br>023_at   | PML       | AntiSense | promyelocytic leukemia<br>[Source:HGNC<br>Symbol;Acc:9113]                      | 515 | TTAAAGGTCCTGCTCTATCGTTCTGTGTCTGGCTCTGC<br>AAACTGCTGGTATGTAAAGACCCCTCTTCCAGACAGGC<br>CACGAATCCCCGAAGGCCGGCTGGCCTCTTCTCTG<br>CCTCTGTCCCAACCTCCCTGACACACCCCTCCATCCACG<br>TTAATAAACACAGGGAACACACACAGAGGGCTCAGTAGAG<br>AAAAACACATCATAATGACTGATTTATAATTTTATAGCT<br>TTAAATAATAAATTTATTTTTCCTTAAAGTATTATAA<br>CACGATTACAAAAAGCCCTCGTGC |

FIG.7-134

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|     |                               |       |           |                                                                                      |     |                                                                                                                                                                                                                                                                                                                 |
|-----|-------------------------------|-------|-----------|--------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 516 | ADXCRA<br>D_13012.C<br>1_at   | TRIO  | AntiSense | triple functional domain<br>(PTPRF interacting)<br>[Source:HGNC<br>Symbol;Acc:12303] | 516 | TAGATGCCGTCATCTTCCGTGGTGACGCCCAATCTT<br>CAGCGTGGCCTCTCCAGGTCACTGTAGGAGATGCTGT<br>AGTGACCATCGTTGTTCAAGGTGTTGTTCAGGGCCC<br>TTCAGGTAATTGAGGCTTTGGGGCGCCACAGACTCG<br>ACATCTAGGAACAACGGTCTCCCTGTCTCACACGTGA<br>CCTCACTCAATGGAATGACGAATTCTGGGGAACGTCA<br>TAAATGTAGTTGGATTGAGAAAGCTTGTGCTGAGTCCT<br>TCCCGTGACTTCCGATAA |
| 517 | ADXCRA<br>D_BC0257<br>70_s_at | RHOJ  | Sense     | ras homolog gene<br>family, member J<br>[Source:HGNC<br>Symbol;Acc:688]              | 517 | CACTATGCAGTTACTGTGACTGTGGAGGCAAGCAACA<br>CTTGCTCGGACTGTATGACACCGCGGGACAGAGGACT<br>ACAACCAGCTGAGGCCACTCTCCTACCCCAACACGGAT<br>GTGTTTTGATCTGCTTCTCTGTCTGTAACCCCTG                                                                                                                                                  |
| 518 | ADXCRA<br>D_BE1385<br>16_x_at | ATL2  | AntiSense | atlastin GTPase 2<br>[Source:HGNC<br>Symbol;Acc:24047]                               | 518 | GACCAGGAAGTCCTATAAAGAAATTATTTCTATAGAATT<br>AAAAATGCAGTTCTGTGAGCCTGGACAACAAAGTGAGA<br>CCCCCATAGCTACAAAAAANAANAAGTTTTTTTAAAG<br>AGTTGGCATGTTGGCACACGCCCTGTAGTCCTAGCTTC<br>TCGGGAGGCTGAGGTGGGAGGATTGCTTGAGATTGGG<br>AGGTTGAGGCTGCAGTGAGCCGTGATCACACCACCTGCA<br>CTCCATCCTGGTTAACAGAGTGAGACCACCTTAAATTAA             |
| 519 | ADXCRA<br>G_AJ3135<br>24_s_at | MACC1 | Sense     | metastasis associated<br>in colon cancer 1<br>[Source:HGNC<br>Symbol;Acc:30215]      | 519 | CAAAGCAACAAATGGAGGCATATGAAATTCCTCATCGAG<br>GAAACACTGGAGATGTTGCTGTTGAGATGATGTGGAA<br>CCTGCCATGATTTTCTGTATACCTGGAGTGTCACTAT<br>GGAAATAACTACAGAGATGTGTTACAAGACCTTCAGTCA<br>GCTTTGGACAGAAATGAAAAACCCCTGTGACTAAACACTG<br>GAGAGAAATTAAGTGGAGTTTTAATACTAGTAAATTCCTTG<br>GAGGTTTTGAGAGTAAGTGAATTCCTCCACT                |

FIG. 7-135

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|     |                                |        |           |                                                                                                                                |     |                                                                                                                                                                                                                                                                                                                              |
|-----|--------------------------------|--------|-----------|--------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 520 | ADXCRA<br>D_AL5986<br>28_at    | SCD    | Sense     | stearoyl-CoA<br>desaturase (delta-9-<br>desaturase)<br>[Source:HGNC<br>Symbol;Acc:10571]                                       | 520 | TGTTAACCCATTCCAGTACAGTATTCTTTTAAATTCAAA<br>AGTATTGAAAGCCAACTCTGCCCTTATGATGCTAAG<br>CTGATATTATTCTCTTATCCTCTCTCTCTCTCTAGGC<br>CCATTGTCCTCCTTTTCACTTTATTGCTATCGCCCTCCTT<br>TCCCTTATTGCCTCCCAGGCAAG                                                                                                                              |
| 521 | ADXCRIH.<br>3160.C1_s<br>_at   | ATP5G1 | Sense     | ATP synthase, H+<br>transporting,<br>mitochondrial Fo<br>complex, subunit C1<br>(subunit 9)<br>[Source:HGNC<br>Symbol;Acc:841] | 521 | AGCCACAGTTGGTGTGGCTGGTTCAGGGGCTGGCATTG<br>GAACCGTGTTGGCAGCTTGATCATGGCTATGCCAGG<br>AACCCGTCTCTCAAGCAGCAGCTCTTCTCTATGCCATT<br>CTTGGCTTTGCCCTCTCTGAGGCCATGGGGCTTTTCTG<br>TTTGATGGTCGCCCTTCCCTCATCCTCTTCGCCATGTGAGG<br>CTCCATGGGGGTCACCGGCCCTGTTGCTACTGCAACTC<br>CACACCATTCCTGGTGTGGTGGGTGTGTTAAGCTTTACCA<br>TTAAACA             |
| 522 | ADXCRRS<br>.Hs#S373<br>2256_at | DDX17  | AntiSense | DEAD (Asp-Glu-Ala-<br>Asp) box polypeptide<br>17 [Source:HGNC<br>Symbol;Acc:2740]                                              | 522 | GGCTTAACCAGCTAGACATTCTCTCTAAATACATACGTAA<br>CAAAAATTGATGGCAGGAGATTTTATTGGGATCACTGGA<br>TACCTACACTCAACAGGCAGAACTTGGCTAATTCCATTT<br>ATACCACTACTGAGACAGTGAAGACAAATTAAGAATCAG<br>AACAGGAAGCACATAGCATAGGATACCCGTGTCAGCG<br>ACATATTTAATATGCCCTTCAGCTTAAGACTCAATACTG<br>AACAGACCAAAAGGCCACCTCAATTGCCGCTCCCGCCA<br>CACTTGCTATTGAAACT |

FIG. 7-136

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|     |                             |        |                    |                                                                                  |     |                                                                                                                                                                                                                                                                                                                     |
|-----|-----------------------------|--------|--------------------|----------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 523 | ADXCRA<br>D_AI7031<br>62_at | YLP M1 | AntiSense          | YLP motif containing 1<br>[Source:HGNC<br>Symbol;Acc:17798]                      | 523 | CCAAGGCATTGCTAATCTCTGTACTTCAGTAAACACTGA<br>AAAGTCAACGTAACTCTATAGGTGCGCATATCTTGAATG<br>ACAGGGAAAGGCAACATCTCTACAGAGGTGTGATCGA<br>AAGCATTTTACATTAGGTACACAGAAACTTTAAACTCAC<br>ACTATGTAAGCCTCTAATCAGCCTGAGCAAAATCCATTG<br>CCTACACAGTCATTTA                                                                               |
| 524 | ADXCRA<br>D_CB8529<br>16_at | IREB2  | Sense              | iron-responsive element<br>binding protein 2<br>[Source:HGNC<br>Symbol;Acc:6115] | 524 | GGTTGAAAGATGAAATGCCTGTATGTGCTCTGAAGAAAT<br>GGTAATTCCAGATTG                                                                                                                                                                                                                                                          |
| 525 | ADXCRA<br>D_AI8057<br>00_at | PTK2   | AntiSense          | PTK2 protein tyrosine<br>kinase 2<br>[Source:HGNC<br>Symbol;Acc:9611]            | 525 | TCCACCTGCCGAGAGCTGAGATTATAGTCACGTGTGCC<br>TGGCTGGAATATAGCCTTTTGACTCCATGTCATTACCCG<br>CACTCTTCGCTCTTCCCTGGAATGTATTTCCTGAGCCTGT<br>CTGCCCTAAAAATCCAAATTTCTCCTTTAAGCTTTGGCT<br>CAAATGCTATCTATACTCTGCTGCCCTCCCCCAAGTCCCC<br>CTAGTGACACACAGGGTCTCTTCTGCTCTTCCCTTATGT<br>TCTTCTTTGTCAGAGCAACATCACAGCAGTACCCCAACA<br>TTTGG |
| 526 | ADXCRA<br>D_AF1724<br>50_at | N/A    | No Genome<br>match | N/A                                                                              | 526 | GCGGCGGGCAGGGCTTGCCTTTCTTAGTCTGATGCCAA<br>G                                                                                                                                                                                                                                                                         |

FIG.7-137

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|     |                                 |       |       |                                                                          |     |                                                                                                                                                                                                                                                                     |
|-----|---------------------------------|-------|-------|--------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 527 | ADXCRA<br>D_BM711<br>746_s_at   | DNAH2 | Sense | dynein, axonemal,<br>heavy chain 2<br>[Source:HGNC<br>Symbol;Acc:2948]   | 527 | GGCCATGACACCTGATCATTTGGATCAAGAGGGGCACT<br>GCTCTACTCATGAGCCTGGACAGCTGAGACCTCCTCCT<br>CTTCTCCGCTTGAGAGAGAGGGTCAGGGACTCCAGGA<br>GCTAAGACAGATGTTGCACCTAGGACTGAGGCCGGACC<br>TCACTCAGACTTTGACCTTGCCGAAATTTGTGATGTG<br>GCCCTGGAGATACCTAGTTGTGTAGCCATAAA                    |
| 528 | ADXCRA<br>D_BE7927<br>95_s_at   | SCRN2 | Sense | secernin 2<br>[Source:HGNC<br>Symbol;Acc:30381]                          | 528 | CAGGAAGGCCTCGAGGCCACACAGGGGCTGCTGGCCG<br>GCGAGTGGGCCCCACCCCTCTGGAGCTGGGCAGCCT<br>CTTCCAGGCCCTTGTGAAGAGGGAGAGCCAGGCTTATG<br>CGTAAGCTTCATAGCTTCTGCTGGCCTGGGTGGACCC<br>AGGACCCCTGGGGCCTGGGTGCCCTGAGTGGTGTA<br>AGTGGAGCAATCCCTTCACGCTCCTTGCCCATGTTCTG<br>AGCGGCCAGCTTGG |
| 529 | ADXCRP<br>DRC.1364<br>7.C1_s_at | CDHR1 | Sense | cadherin-related family<br>member 1<br>[Source:HGNC<br>Symbol;Acc:14550] | 529 | CTGGTGGACTATTCCATCACCCTGCAGAGCCCCGCCAA<br>CGTGTTCGACATCAATCCACACAGGGGGAGATCTGGC<br>TCAAGAATTCATCCGCTCCCTGGATGCCCTGCACAAC<br>ATCACACCTGGAAAGGACTGCCTATGTCCTCCTAGAGGT<br>GCAGGCCAAGGACCGGGGCTCCACACATCACTTCAGCA<br>CCACAGCCTTACTCAAGATTGA                             |

FIG. 7-138

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|     |                                |           |           |                                                                                                   |     |                                                                                                                                                                                                                                                                                         |
|-----|--------------------------------|-----------|-----------|---------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 530 | ADXCRA<br>G_NM_19<br>8389_s_at | PDPN      | Sense     | podoplanin<br>[Source:HGNC<br>Symbol;Acc:29602]                                                   | 530 | TGCGCCTCAGATTCCATATTTGAACACCAGCTGATTGAG<br>AGAAGGGGAATGAGAAGAGCTGGATGAGTTTAAATAAC<br>TCATTGTTCAAGATTCCTGAACAGGAGTTGGGATAATGGC<br>CATCTTTTCTTCCCTATCCTTTCTTCCCCCTCACTGTGA<br>AAATAACAGTCCACCCCAAGTCATACACTGGACCCAG<br>TGCCTGCGGGGACAGGACTGTGGGTTTCTTGGTCACAC<br>CTGTGTTGGTGCTCAATGCAGTGT |
| 531 | ADXCRSS<br>.Hs#S273<br>3081_at | COMMD10   | AntiSense | COMM domain<br>containing 10<br>[Source:HGNC<br>Symbol;Acc:30201]                                 | 531 | TAGTTTCATTACTCTTTAGGCAGAAAAATAGGTTCAAGG<br>GTCTAGTAAAGGAGGCAAAATGGGCAGAAAAACAACCTCT<br>TGTTTGCTATCCCACTGCACCTTGAATGGACCTCTATAA<br>TTCACACCATTTATAAGTGTCTCGCATATCAACATCACA<br>TTAGGTAATTTACTGCCCTCCAATTCCTGTGCCATAACTAT<br>TCCATCCTGAAAAGTCATAATACAATGTTATTGGAACAAT<br>CTATTCATATGGTA    |
| 532 | ADXCRA<br>G_BC012<br>866_at    | TNFRSF10A | Sense     | tumor necrosis factor<br>receptor superfamily,<br>member 10a<br>[Source:HGNC<br>Symbol;Acc:11904] | 532 | ATGTATACAAAGTAAATTCTTAGCCAGGTGTAGTGGCTC<br>ATGCCGTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGG<br>TGGATCACTTGAGGTCAGAAAGTTCAAGACCAGCCTGAC<br>CAACATCGTGAAATGCCCGTCTTTACAAA                                                                                                                          |

FIG. 7-139

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|     |                                   |         |       |                                                                                                       |     |                                                                                                                                                                                                                                                                                                           |
|-----|-----------------------------------|---------|-------|-------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 533 | ADXCRESS<br>.Hs#S300<br>8397_s_at | HELZ    | Sense | helicase with zinc finger<br>[Source:HGNC<br>Symbol;Acc:16878]                                        | 533 | AGTGGCTTCCTTGGAGTAGTGGGTGAAAGTCTGCTTAA<br>AAAGAGGGCTTAGGAGAGAAATGGGGAAGGAATTGAA<br>ATACATCAACATAGACAACTCTTGAGGAGTTTGCCATG<br>AAGAGACACTTTGCATCCAGAGGACACTTTCATCCAG<br>AGAGTGGCTTCCTTGGAGTAGTGGGTGAAAGTCTGCTT<br>AAAAAGAGGGCTTAGGAGAGAAATGGGGGAAGGAATTG<br>AAATACATCAACATAGACAACTCTTGAGGAGTTTGCCA<br>TGAAG |
| 534 | ADXCRA<br>G_AB0807<br>47_s_at     | FOXP4   | Sense | forkhead box P4<br>[Source:HGNC<br>Symbol;Acc:20842]                                                  | 534 | GAGCTGGAAAAAAGTCAGACTCTCCACAGACCCCTAT<br>GGGGACCCCCAACTCAAGGCCAAGGACTGGGCGTAT<br>CGGATGCTCATACACCCCTGGCCTGGCCCTTTACTG<br>AGAAGACTCCTTGATATTTCCCAAGAACCCTCCACATA<br>CACCCCTCACAAGCCACCCTCCTGAGAGGCGAGGGG<br>CCCTCGCCCCCTCCCATGTATTTCCCAACCTGTGTTT<br>CGTTTGACCAGCACAGAAATAT                                |
| 535 | ADXCRRP<br>D.9899.C1<br>_s_at     | TAOK2   | Sense | TAO kinase 2<br>[Source:HGNC<br>Symbol;Acc:16835]                                                     | 535 | GGAGCACACAGTCACCTCTCACAGCTCCATTATCCAG<br>CGGCTGCCGGGCTCTGACAACCTATATGATGACCCCTA<br>CCAGCCAGAGATAAC                                                                                                                                                                                                        |
| 536 | ADXCRA<br>D_BE3865<br>16_s_at     | PRKAR2A | Sense | protein kinase, cAMP-<br>dependent, regulatory,<br>type II, alpha<br>[Source:HGNC<br>Symbol;Acc:9391] | 536 | GCTGCCATTGCTGTGGTTATGGGCATTTAGAAAATTGA<br>AAGTCAGCACTAAAGGATGGGCAGAGGTTCAACCCACA<br>CCTCCACTTTGCTTCTGAAGGCCCATTCATTAGACCAC<br>TGTAAGATTACTCCAACCCAGTTTATATCTTTGGTTC<br>AAAACGGCATGTCTCTCCAACAATTTAAGTGCCTGATAC<br>AAAGTCCAAAGTATAAACATGCTCCTTTACTCTCTTGCT<br>GCTACTCTTGCTTTTG                             |

FIG. 7-140

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|     |                                   |                                      |       |                                                                                                 |     |                                                                                                                                                                                                                                                                                                                                   |
|-----|-----------------------------------|--------------------------------------|-------|-------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 537 | ADXCRA<br>G_AB04<br>5118_at       | FRAT2                                | Sense | frequently rearranged<br>in advanced T-cell<br>lymphomas 2<br>[Source:HGNC<br>Symbol;Acc:16048] | 537 | GTAGCTATTGATGTACACTTCGCAACGGAGTGCTCTGAA<br>ATTGTGGTGGTCTGATTTATAGGAT                                                                                                                                                                                                                                                              |
| 538 | ADXCRA<br>D.17448.<br>C1_x_at     | CAPS                                 | Sense | calcyphosine<br>[Source:HGNC<br>Symbol;Acc:1487]                                                | 538 | CAGAGGTCTTGCAGCCCCCTGTGGATGCCCCCCGCCGA<br>GGTCCCCGATCCCGCACCCGGACTGCTGCTCCCT<br>GCCCCACCATTCGGGGTCCCCCAGGAAGCCAGGTGA<br>CCCCAGTGGAGGCTGTGTGGAGGCCATCCTGG<br>AAGGAAGTTTAGACCTGCCCAGGTGTGGAGCGAGGG<br>GCACAGGGGCATCCTAACCTCAGAACTGAAATAAAG<br>CCTTTGNNNNNNNTCTGTAAACATCAACCCCAAT<br>CAGAAGATGGCAATGGGGATAAAAAATAGCAGGTAA<br>CACGTCA |
| 539 | ADXCRA<br>D_CX16<br>4907_s_<br>at | RALBP1                               | Sense | ralA binding protein 1<br>[Source:HGNC<br>Symbol;Acc:9841]                                      | 539 | TGACAGCAGCTGATGTTGTTAAACAGTGGAAGGAAAA<br>GAAGAAAAAGAAAAGCCAATTCAGGAGCCAGAGGTG<br>CCTCAGATTGATGTTCCAAATCTCAAACCCATTTTGG<br>AATTCCTTTGGCTGATGCAGTAGAGAGGACCATGATGT<br>ATGATGGCATTCCGCTGCCAGCCGTTTCCGTGAATG<br>TATAGATT                                                                                                              |
| 540 | ADXCRA<br>D.12155.<br>C1_at       | AC058791.1<br>(Clone-based<br>(Vega) | Sense | Novel processed<br>transcript.                                                                  | 540 | AAATAGAACATCCTGAGTTACAGAAATTCAGCCCTAG<br>TGATCCTGGCCTAAAAATACAGAACAAATCAAGTTGAG<br>TGGTTGAAATGAGAGGCTAGGCAGGGTTGGAACAT<br>GCTAATGTTTACTGAGTGAATCTTTTCCTTCTCAGTAG<br>AGTTGCCCTTGCAGCTGAAA                                                                                                                                          |

FIG. 7-141

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|     |                                 |          |           |                                                                                                                                                                                    |     |                                                                                                                                                                                                                                                                                |
|-----|---------------------------------|----------|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 541 | ADXCRA<br>D_CN479<br>989_at     | SLC39A14 | Sense     | solute carrier family 39<br>(zinc transporter),<br>member 14<br>[Source:HGNC<br>Symbol;Acc:20858]                                                                                  | 541 | TCTCTGGCTGATATGTTCCCTGAGATGAATGAGGTCTGT<br>CAAGA                                                                                                                                                                                                                               |
| 542 | ADXCRA<br>D_CN298<br>065_x_at   | CHP      | Sense     | Calcium-binding protein<br>p22 (Calcium-binding<br>protein<br>CHP)(Calcineurin<br>homologous<br>protein)(Calcineurin B<br>homolog)<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q99653] | 542 | GTTACAGGTGCTACGCATGATGGTCGGAGTAAATATCT<br>CAGATGAGCAGCTGGGCAGCATCGCAGACAGGACCATT<br>CAGGAGGCTGATCAGGATGGGACAGTGCCATATCTTT<br>CACAGAATTTGTTAAGTTTTGGAGAAGGTGGATGTAGA<br>ACAGAAATGAGCATCCGATTTCTTCACTAAAGGAGACC<br>AAACTGTTCCCTTGGGCTCTAGTATTTAAGAACTGGAAC<br>TGAAAGTCCTCCTTCTAC |
| 543 | ADXCRESS<br>.Hs#S162<br>3594_at | TTC39B   | AntiSense | tetratricopeptide repeat<br>domain 39B<br>[Source:HGNC<br>Symbol;Acc:23704]                                                                                                        | 543 | GAATCCATTATCAATGTTGCTAGTGTAATACACAAGAAA<br>ACCCAATGAGAGAAATTCAAATATTAAAGAAACAAGCTTT<br>TGTTGATTGAGCTTTAAATGCCACACACCATTAATATAT<br>CTAAGATGCTTGCTGCTCCCAATAACCAATTTTTCCTC<br>CAATGAGGATGCAAGTCCTAACTTCTATGCTCCCGAATT<br>TATCATACTAGCACCTA                                       |

FIG.7-142

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|     |                               |                                                              |       |                                                                                                                       |     |                                                                                                                                                                                                                                                                          |
|-----|-------------------------------|--------------------------------------------------------------|-------|-----------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 544 | ADXCRA<br>D_D81713<br>_at     | LRCH1                                                        | Sense | leucine-rich repeats and<br>calponin homology<br>(CH) domain containing<br>1 [Source:HGNC<br>Symbol;Acc:20309]        | 544 | TAATAAGTGTAGCATCGTGTCTTGAAGTATACTTTTG<br>CACTGTAACCTGGTTACGTTAAGAGAGCCTTAGCACCA<br>AAGGTAGATAATGAAGAAATGGCATAGGAAAGTGGAGA<br>TGATAAAAAGTTGATTGTTGAACCAAAAAGGGTTTGAAG<br>GGAAGCTTCGACTGAGTATCAGAAATTACTTAAGGCACA<br>TAGGACCTGAATCAGGRAACCAGCACCTTCTTACAACCTG<br>CCAGTTTTA |
| 545 | ADXCRA<br>D_BX1018<br>33_s_at | RP11-<br>125K10.4<br>(Clone_based_<br>vega_gene) ///<br>RCL1 | Sense | Putative processed<br>transcript /// RNA<br>terminal phosphate<br>cyclase-like 1<br>[Source:HGNC<br>Symbol;Acc:17687] | 545 | TGCAAGGACTCACCTCCTTGAGCCTTGGTTTTTGTGTA<br>GGGATTAAATGAGATAATATGAGTGGCAGCTCTTCATGA<br>GTCCGTCAGTGCTAAGCAAAATGTCAGAAATTGGTGATT<br>AGACTATTTATCTTTGATCTTCTGAATGGATTGCTGTCAT<br>GGACACGGACACGGATCTTCATCTGGTTCATTGTATTTA<br>TATGTAGGGGATGGATGGC                               |
| 546 | ADXCRIH.<br>2931.C3_s<br>_at  | STAT1                                                        | Sense | signal transducer and<br>activator of transcription<br>1, 91kDa<br>[Source:HGNC<br>Symbol;Acc:11362]                  | 546 | GGAGAAGTTAAGCAACATCTAGCAAATGTTATGCATAAA<br>GTCAGTGCCCAACTGTTATAGGTTGTTGGATAAATCAGT<br>GGTTATTAGGGAACCTGCTGACGTAGGAACGGTAAATT<br>TCTGTGGGAGAAATCTTACATGTTTCTTTGCTTTAAGTG<br>TAACTGGCAGTTTCCATTGGTTACCTGTGAAATAGTT<br>CAAAGCCTAGTTTATATACAAATTATATCAGTCCTCTTTCA<br>A       |

FIG. 7-143

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|     |                               |         |           |                                                                                                                                   |     |                                                                                                                                                                                                                                                                                    |
|-----|-------------------------------|---------|-----------|-----------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 547 | ADXCRP<br>D.13803.C<br>1_at   | SLC11A2 | AntiSense | solute carrier family 11<br>(proton-coupled<br>divalent metal ion<br>transporters), member<br>2 [Source:HGNC<br>Symbol;Acc:10908] | 547 | GAATTGTCATTCACTCTGTGCTATATTACTTGAGGG<br>GCTAAGAAAAATGTATGGTCAGTGAACACACAGTAGTGA<br>CCCTTAATGCCCTTATAAAGACCATCCATCCAGTCTGC<br>GCTTTGACTGTGTCAAGTATCAGTAATAATGCTTTTG<br>GGGCTCAGATGAACAGCGAACACCAATCAGCCAGGA<br>CTCTGGAAGGAAAGCTCCAAAAATGANGAAGTCCTTTCA<br>ACACCATTTTCCATTACTGTTCTCA |
| 548 | ADXCRP<br>D.9382.C1<br>_at    | SETMAR  | Sense     | SET domain and<br>mariner transposase<br>fusion gene<br>[Source:HGNC<br>Symbol;Acc:10762]                                         | 548 | TTTGATTAAATAAAAAATGCGTTGAGCCTAGTTATA                                                                                                                                                                                                                                               |
| 549 | RDCR448<br>_D01_s_at          | FOXO3   | Sense     | forkhead box O3<br>[Source:HGNC<br>Symbol;Acc:3821]                                                                               | 549 | GTTGCTTCCCCACCCTGAGGAGAGACACCATGGCTTA<br>CTACTCAGGACAAAGTATGCCCGCTCAGGGTGTGATTT<br>CAGGTGGCTTCCAAACTTGACGCAGTTTAAAGATGGT<br>GGGACAGACTTTGCCCTCTACCTAGTGAACCCCACTTA<br>AAGAAATAGGAGGCATTTGAATCTCTTGGAAAAAGGCCATG<br>AAG                                                             |
| 550 | ADXCRA<br>D_CX7558<br>99_s_at | GTSE1   | Sense     | G-2 and S-phase<br>expressed 1<br>[Source:HGNC<br>Symbol;Acc:13698]                                                               | 550 | TGGGAATATAGTGAAACTCCTGTCCCTACAAAAATAC<br>AAAAATTAGCCGGGTGTGGTAGTGCATGCCTGTAGTCC<br>CAGCTACTTGGAGGCTGAAGTGGAGGATGGCCTGA<br>GCTCAAGGAGATGCAGGCTGCAGTGGGCTGTGATTGTG<br>CCACTGCACTCCAGCCTGGGCACCAATGTGAGAACCTG<br>TCCTGGAA                                                             |

FIG. 7-144

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|     |                               |         |                    |                                                                                      |     |                                                                                                                                                                                                                                                                                                                       |
|-----|-------------------------------|---------|--------------------|--------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 551 | ADXCRA<br>D_18410.C<br>1_x_at | N/A     | No Genome<br>match | N/A                                                                                  | 551 | TTGAAAGACACCAGTGCACACCCAAACTCCTGGCCTTC<br>TGTGGTTCCCTTTGCTCCAGAACACAGATGTGCTANN<br>GAAAAACAACGAAACCCGAGCCNAAACNACCAACCCC<br>CAGGGGGGGCGCTCTAAAGAATCCCTCGAGGGGCC<br>CAAGCTTACGCGTACCCAGCTTTTCTTGACAAAGGGG<br>CCCCTAAAGGGGAGTCGGAATAAAAACTAAAGGCCCT<br>TGGCCGTCCTTTTACAACGCCCGGAACTGGGAAA<br>ACATGCCAACCTTGGGGGATCTTTTG |
| 552 | ADXCRA<br>G_BC049<br>209_at   | C2orf89 | Sense              | UPF0632 protein<br>C2orf89 Precursor<br>[Source:UniProtKB/Swi<br>ss-Prot;Acc:Q86V40] | 552 | GATGCTCTTCAGTTCACACTATATCCCTATCTGATAATTC<br>CAGAACTCTATCATGTCTGAGTCTGGGTCTGATGCTTT<br>CATTGTTCTTCAGATTGTGATTTTCTTGCTCCCCAGTG<br>TGACTTGTAATTTTAAATTGAAAGCTGGATATGATGTATT<br>TGGCAATGGGAAGTGAGGGAATATGTTTTTAGTGTGA<br>GGTTTATGTTAATCTTTCTCAGAGTTGGCTGTTTAAT<br>GTTTGTCTGTGGTCTGAATGTTCCTTAAAACT                        |
| 553 | ADXCRA<br>D_BX3865<br>35_s_at | FKBP8   | Sense              | FK506 binding protein<br>8, 38kDa<br>[Source:HGNC<br>Symbol;Acc:3724]                | 553 | AAGGATTGGGGTCTGTCAGCCCCAGCCAGCAGGAGGG<br>ACTGAGGCCCTCTAGGAGGAAAGCCAGAGGAGGGG<br>GCCCTCATTCTTCAGACCCAGTTTTCCCCACCCCTCCT<br>TACCCGCTGGGCTAGGTCTCCGCCAGGGCTGGCCTC<br>AGTTTCTCTCAACAGGCCTGGGGCAGCCCTTCCCT<br>GCCTAGTCCCCGCTGAGTGCCAGCSCCCACCCCGC<br>CTGCCGCCCCCTGTTTCAGGTTCCCTCCCGCCACAGTG<br>AAATAA                      |

FIG. 7-145

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|     |                                   |          |       |                                                                                                                                             |     |                                                                                                                                                                                                                                                                                                                                            |
|-----|-----------------------------------|----------|-------|---------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 554 | ADXCR<br>AD_BX4<br>42668_x<br>_at | PPDPF    | Sense | pancreatic<br>progenitor cell<br>differentiation and<br>proliferation factor<br>homolog<br>(zebrafish)<br>[Source:HGNC<br>Symbol;Acc:16142] | 554 | TGCGGAGGCGCTAGTCCACCAGAGCBCCCTCC<br>CCGCCCTCTTCCCANATCCGNATCCCTCGCC<br>CCCTCCCCACCTCCACCCCCACCCCTGTA<br>AACTAGGCGGCTGCAGCAAGCAGACCTTCGC<br>ATCAACMCMSCASACACCAAACACAGTGAG<br>ASCCCGCTCTCTACCGCCCGGCGCCAGCAC<br>TCGCTAGCTTTCCTGACACCTGGAACGTGC<br>ACCTGGCACCAAGCGGAAATAAACTCCAAG<br>CAGCCAGTAGCCCCGATGGTGTGCTGCCTGAC<br>CTGTGTGGCCGGAGGTTTC |
| 555 | ADXCR<br>PD.9655<br>.C1_at        | C17orf63 | Sense | Uncharacterized<br>protein C17orf63<br>[Source:UniProtKB/<br>Swiss-<br>Prot;Acc:Q8WU58]                                                     | 555 | TTAGGTAGGTAAGGAATGATCACATTGGAGTT<br>TGG                                                                                                                                                                                                                                                                                                    |
| 556 | ADXCR<br>AD_AI75<br>0956_s_<br>at | COL12A1  | Sense | collagen, type XII,<br>alpha 1<br>[Source:HGNC<br>Symbol;Acc:2188]                                                                          | 556 | ACGTGCTTATTAGGAAATGAGTCTGTATGGAA<br>ATCTACCACAGATAATGGTTAACGAACCGG<br>GTCGACATCACAAAGGAGGGTGGAGACTCTT<br>TTTACTAACTTGAATGAGACAAAAGCAGTGGT<br>GTCAGTTTATAATCCTGATGCATTTTCAGTAAT<br>AATGTAGAAAAACATTAATTTAAAAAGTTCCA<br>ACACACAGCCATGAGGAGCCTCAGTTTTTGAA<br>AGAGGTGCATAATAAAACTACTAACCCAGAGGA<br>GTCATATGCCATTTTAAGAA                        |

FIG. 7-146

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|     |                               |                                           |           |                                                                                                       |     |                                                                                                                                                                                                                                                                                        |
|-----|-------------------------------|-------------------------------------------|-----------|-------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 557 | ADXCRA<br>D_CA4403<br>61_x_at | ROBO1                                     | Sense     | roundabout, axon<br>guidance receptor,<br>homolog 1 (Drosophila)<br>[Source:HGNC<br>Symbol;Acc:10249] | 557 | GCCAGGAGTTGGAGGCCCACTCTGGGGAACACATGTTGA<br>GATCTTGCCTCTGCAAAATAAAGTAAATAAAATTTAAA<br>AAAAGTAAAAATAAAATCAAGCTGAGCATGGTGACATG<br>CACCTGTGGTACCAGCTACTTTGGAGGCTAAGTTGAGA<br>GGCACTGATGGGAGGATCATTTGACGGCCACAGAGGTTG<br>AGGCTGCAGTGAGCTGTGTTTGTGTCATTGCACTCCAG<br>CCTGCGTAACAGAGTAAACCTTCT |
| 558 | ADXCRA<br>D_BU5851<br>82_s_at | IGLV2-14                                  | AntiSense | immunoglobulin lambda<br>variable 2-14<br>[Source:HGNC<br>Symbol;Acc:5888]                            | 558 | CTTGAGCCAGAGAAGCGATTAGAAACCCCTGAGGGCC<br>GATTACTGACATCATAAATCATGAGTTTGGGGCTTTGC<br>CTGGTGATGTTGGTACCAGGAGACATAGTTATAACCA<br>CCAACGTCACCTGCTGGTCCAGTGCAGGAGATGGTGAT<br>CGACTGTCCAGGAGACCCAGACACGGAGGCAG                                                                                 |
| 559 | ADXCRA<br>D_AA6825<br>39_at   | AC069513.3<br>(Clone_based_<br>vega_gene) | AntiSense | Novel processed<br>transcript.                                                                        | 559 | GTCTGAATATCTTACTCACAGCTCACCTTTTGGTGCCT<br>TTGATCCGTATTAGAAATTATCCACATCTTCTCTCTGGG<br>CAATATTCTACTTTTATATTGACCCCAATTATTTACTGCT<br>TTGGTGTGCTCTTCTCCTAACACATATGGGTTCACTTT<br>GAAACCTGAAACCCACATTTACAAAAACATTTTCAATAT<br>GAAACATTGTTCCATGACTCATTTACTGGAGTACCATCAA<br>CATTACAT             |

FIG. 7-147

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|     |                              |       |       |                                                                                                               |     |                                                                                                                                                                                                                                                                                                                    |
|-----|------------------------------|-------|-------|---------------------------------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 560 | ADXCRP<br>D.8173.C1<br>_s_at | CD93  | Sense | CD93 molecule<br>[Source:HGNC<br>Symbol;Acc:15855]                                                            | 560 | GCAGGATTTTCTACGGGTGTTTGATGTTCTCCTGAAGTGG<br>AAGCTGTGTGTTGGCGTGCCACGGTGGGATTTTCGTGA<br>CTCTATAATGATTGTTACTCCCCCTCCCTTTTCAAATCC<br>AATGTACCAATCCGGATCAGGGTGTGAGGAGGCTGG<br>GGCTAAGGGGCTCCCCCTGAATATCTTCTCTGCTCAGTTC<br>CACCATCTAAGAGAGAAAGGTGAGTTGCTCATGCTGATT<br>AGGATTGAA                                          |
| 561 | ADXCRP<br>D.12400.C<br>1_at  | SSFA2 | Sense | sperm specific antigen<br>2 [Source:HGNC<br>Symbol;Acc:11319]                                                 | 561 | TCCTCTGTCAATGTTTCGATTATCTCCAGGAAAAGAGACC<br>AGATGCAGCCACCTTCTTACCTATAAGTACACACCT<br>GAAGAGGAGCAGGAATTGGAAAAGCGGGTGATGGAAC<br>ATGATGTCAGTCTTTAGTTAAATCGACCATTTTCATCTC<br>TCCATCATCTGTGAAGAAAGAAAGAGCCGCCAGAGTG<br>AGGCGCCGCGGTGGAGGAATGCCATCATGGAAGGAC<br>TCCTACCTGTTACGGCTTGCTCCACCACCAATGTCTCA<br>GTCTACCTGTCCCTT |
| 562 | ADXCRP<br>D.1899.C1<br>_at   | RAPH1 | Sense | Ras association<br>(RalGDS/AF-6) and<br>pleckstrin homology<br>domains 1<br>[Source:HGNC<br>Symbol;Acc:14436] | 562 | GGTAATGAGCTCAATGCCTCCATTTAATCACTTTTATAA<br>GGCTCTCTCCAATAAGGCTGCTGTGCTGCTCCTGCC<br>AGTGTGGAGTAATAACATTTTACTGCACACACCTTA<br>TGGGAAAGTGTTTATACTGAGTGTAGTTTGGAGGGGT<br>AAATGAAGATTATTTCCACAAATTAAGATTGCACCTAGTA<br>CAGCCCTTACACACTCTGATGGTATTTACCAAAACAT<br>GGCATGTCTTTTCACGTATATTCTGTAAACACCCAA                      |

FIG. 7-148

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|     |                               |         |       |                                                                                             |     |                                                                                                                                                                                                                                                                                                          |
|-----|-------------------------------|---------|-------|---------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 563 | ADXCRA<br>D_CN341<br>871_at   | IRF6    | Sense | interferon regulatory<br>factor 6 [Source:HGNC<br>Symbol;Acc:6121]                          | 563 | AGCTTTAAGAGGAAAGAGCTCTATTTTTCTTGTTTCTTC<br>TCTGAGCTAGACTGAGCTGGGATCTAAGATGTACTTCT<br>CTGACTACAAAGGACAGATATCATTTAGATTTTTTGCA<br>GTTGAAGAAATGGTTGTTGAGTGTGTTAAGGCTGGG<br>ATGAAGAAGGCTGGCAGTACTCTTCTGGAAAGGCTC<br>ACCTAGCACGAACTGC                                                                          |
| 564 | ADXCRA<br>G_BC021<br>570_x_at | ZNRF3   | Sense | zinc and ring finger 3<br>[Source:HGNC<br>Symbol;Acc:18126]                                 | 564 | GGTAATAAGAGAGCCCTCCTTGTCAACCCCAAAATGTGA<br>GCCCCCTGTGGCAAAACACCCCTACCCCAATTACAA<br>ATCAACAGACAAAATCTCCGAGTCCTTTGCCTCTTTTG<br>ATAACATGTTGTTCTGTTTGTAAAGTGTGTGCTTGG<br>GGTCCGAGGTGTGGATTGAGTTCTCTGCTTTGTTTTT<br>TTTTAAGATATTGTATGTAATGTAAAAAGTTATTAAATA<br>TATATTTTAAAGAACCCCTAACTGCCAACTTTTTGCTGAAAA<br>A |
| 565 | ADXCRP<br>D.4759.C1<br>_s_at  | FOXRED2 | Sense | FAD-dependent<br>oxidoreductase domain<br>containing 2<br>[Source:HGNC<br>Symbol;Acc:26264] | 565 | GAGTCACCTTTAGTCACCTGGTCCGTAACCATCTTTCCT<br>GTCTAAACTTCTCACCCACCACCTCTGGCTTATACCCCT<br>GCTCTCTTTAAATAGCCAGTCAGAAATTAGCTTAGATTG<br>TGCGGTCCAACCCTAGCCCATAGGGGAACAACACAGCA<br>GTAGGGGTACCTGCATCAGGGATAAGAACCATTCCC<br>CTCCCTTGTCCGGTGTGCTCTCGCCATTGCACCATCC<br>ATGAGACGCACCTCTTGATAGAAGTA                   |

FIG. 7-149

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|     |                                |                       |           |                                                                                                                                                                                                    |     |                                                                                                                                                                                                                                                         |
|-----|--------------------------------|-----------------------|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 566 | ADXCRIH.<br>2824.C1_s<br>_at   | TBK1                  | Sense     | TANK-binding kinase 1<br>[Source:HGNC<br>Symbol;Acc:11584]                                                                                                                                         | 566 | GGGAACCTCTGAATACCATAGGATTAATATATGAAAAA<br>TTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG<br>GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTG<br>TGTTATGCCTGCAGAAATGCCAGTACCTTACTGCTTTAT<br>CAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGA<br>ATTAA                                |
| 567 | ADXCRA<br>D_AW449<br>577_s_at  | MIR612                | AntiSense | hsa-mir-612<br>[Source:miRBase;Acc:<br>MI0003625]                                                                                                                                                  | 567 | TAAAGAAACACCTGCGGGGCTCCGGCCCTCCCTCCC<br>TCCCTCCCAGGCTCACCTCCTACCTTCCTTACTTCCCTT<br>GTAAAGGCATAGCCAGGGGACATTGCCCCCAGCTTCA<br>CATCCACATGTCTCCTAGCATGGCACATGCATATCCTGC<br>CCAAGGAGCATGAAGTCAGACCAGCAAACCTGAACACGA<br>GGCACAGTCCCTGCATGCTCTGGGACCGAGCACTGAG |
| 568 | ADXCRIH<br>RC.2845.<br>C1_s_at | RTEL1 ///<br>TNFRSF6B | Sense     | regulator of telomere<br>elongation helicase 1<br>[Source:HGNC<br>Symbol;Acc:15888] ///<br>tumor necrosis factor<br>receptor superfamily,<br>member 6b, decoy<br>[Source:HGNC<br>Symbol;Acc:11921] | 568 | AGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGG<br>GGCGCAGGACGGGGCGCTGCTGGTGGCGCTGCTGCA<br>GGCGCTGCGCGTGCCAGGATCCCCGGGCTGGAGCG<br>GAGCGTCCGTGAGCGCTTCCCTCCCTGTGCACCTGATCCT<br>GGCCCCCTCTATTATTATTCTACATCCTTGGCACCCCACT<br>TGCACTGAAAGAGGC                         |

FIG. 7-150

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|     |                                |         |       |                                                                                                  |     |                                                                                                                                                                                                                                                                               |
|-----|--------------------------------|---------|-------|--------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 569 | ADXCRA<br>D_CN341<br>871_x_at  | IRF6    | Sense | interferon regulatory<br>factor 6 [Source:HGNC<br>Symbol;Acc:6121]                               | 569 | AGCTTTAAGAGGAAAGAGCTCTATTTTCTTGTGTTCTTC<br>TCTGAGCTAGACTGAGCTGGGATCTAAGATGTACTTCT<br>CTGACTACAAAGGACAGTATCATTTAGATTTTGTGCA<br>GTTGGAAGAAATGGTGTGTTGAGTGTGTTAAGGCTGGG<br>ATGAAGAAGGCTGGGCAGTACTCTTCTGGAAAGGCTC<br>ACCTAGCACGAACCTGC                                            |
| 570 | ADXCRIH<br>RC.1844.<br>C1_s_at | NDRG2   | Sense | NDRG family member 2<br>[Source:HGNC<br>Symbol;Acc:14460]                                        | 570 | GGAATGGGAGTTGGCGGCAGTGAACGAGTGTGGGA<br>AGGATTGGTGGTGGGCAACAGGAAGGGCCTGGGGC<br>CGTTTGGGTGCCCTAATTTGGTAGCTCAGTGTGCATT<br>AGAGTGGGACTGGGAGGGAGGTAAAGCTTGGGTGGG<br>CTGCTTGGGGCTTGGCATAGGGTGAAAGGGCTACCCCT<br>GGGGCTTTGACCCCCCTGTAGTATGTGTGGAGGGTGCC<br>CTCCCGT                    |
| 571 | ADXCRA<br>G_BX6406<br>30_s_at  | SLC30A7 | Sense | solute carrier family 30<br>(zinc transporter),<br>member 7<br>[Source:HGNC<br>Symbol;Acc:19306] | 571 | AAACTGCTATTTCTAACTCTTCATGAAAGCATTACCTTTG<br>GAAAGTTAACTTTTTTTTCCCTTCATCACCGTCTTTGA<br>AACAAATTATTTCCAAATTCATAAGAACTTTGGTAAAAA<br>AAAAATAAAGGAAATTATATGTTTTCTTTGGACATTCA<br>TTGGAAGGCTTGTGAAGACATGATCCCCCAGAAGCCT<br>TAGTGACCCAGATCTCAACCAGAGACTCAAGATAGCCT<br>CAAATACAGTGAAAG |

FIG.7-151

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|     |                              |                                                  |           |                                                                                                                                                                                                                                                                                                        |     |                                                                                                                                                                                                                                                                               |
|-----|------------------------------|--------------------------------------------------|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 572 | ADXCR1H.<br>2819.C2_x<br>_at | RGPD3 ///<br>RGPD4 ///<br>RGPD5 ///<br>RGPD6     | AntiSense | RANBP2-like and GRIP<br>domain containing 3<br>[Source:HGNC<br>Symbol;Acc:32416] ///<br>RANBP2-like and GRIP<br>domain containing 4<br>[Source:HGNC<br>Symbol;Acc:32417] ///<br>RANBP2-like and GRIP<br>domain containing 5<br>[Source:HGNC<br>Symbol;Acc:32418] ///<br>RANBP2-like and GRIP<br>domain | 572 | AACGTGATTTTAACTTAGCACAATTAACCTGCAGCATATTT<br>ACTTCATAGCCCCCTTAACATGTCACCTTTTACCAACAAAG<br>CTTTTCCTTCATATTCTAATCACAATAATTTCTCAACAA<br>TTTATAACAATCTGTAATCTGACCTTGCAATAAATAGTC<br>ATAAAACGTTATTTTATTACTATTATTATTTTAGAGACA<br>AGGTCTCCTCGTGCCGAA                                 |
| 573 | ADXCR1H.<br>3580.C1_a<br>t   | RP11-<br>460N11.2<br>(Clone_based_<br>vega_gene) | AntiSense | Known pseudogene.                                                                                                                                                                                                                                                                                      | 573 | TCCACACCAAAATAGATTCACCAATAGATATTACAAGT<br>AGGAGAAATTTTATGACTACTCAGATAAAACGACCATTG<br>ATCATTACAAACATACAGTCAATAAACATACAGAAATA<br>ATATGTGTATACAAAAACACAGAAATTATTATTGGGAA<br>TAGACATATGACTGATTCATATGTAACTTTGTCTCCACG<br>CTGTCTTAAAGTGTACAGAGTTGAATATTGTCATTCACA<br>ATTGTCACACAAAA |

FIG.7-152

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|     |                                |                                             |           |                                                                                                                                                                                                   |     |                                                                                                                                                                                                                                                                             |
|-----|--------------------------------|---------------------------------------------|-----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 574 | ADXCRIH.<br>1401.C1_s<br>_at   | KRT18                                       | Sense     | Keratin, type I<br>cytoskeletal 18<br>(Cytokeratin-18)(CK-<br>18)(Keratin-<br>18)(K18)(Cell<br>proliferation-inducing<br>gene 46 protein)<br>[Source:U+E67niProtK<br>B/Swiss-<br>Prot;Acc:P05783] | 574 | CACCAAAGTTCTGAGGCATTAAGCCAGCAGAA                                                                                                                                                                                                                                            |
| 575 | ADXCRA<br>D_AA6209<br>26_at    | RP4-717123.3<br>(Clone_based_<br>vega_gene) | AntiSense | Novel processed<br>transcript.                                                                                                                                                                    | 575 | TAAACTCTCTGAGACTGTTTTCCCCCATGTCAAAACA<br>CCTATTTGCATGGCTATATGGAAATTAAATGAAATAGC<br>AAATATGAAAAACTTTTGGCCCGAGTGATAATTCATATCA<br>GGCACTGATCTGTTTTCTTTTGGCCCTAACCTACTTTTCC<br>TGCATCATATACCACCTACACCTCTTTACAAACCTTATTAA<br>TAGAGCCACTCTAGACTACTTTATTTCCCCAAGCCATAC<br>AATGTACT |
| 576 | ADXCRA<br>G_NM_00<br>1909_x_at | CTSD                                        | Sense     | cathepsin D<br>[Source:HGNC<br>Symbol;Acc:2529]                                                                                                                                                   | 576 | AAACCCACCTTGTTGGAGCCTGCAGGGTGGTGGTGGG<br>ACTGAGCCAGTCCCAGGGGCATGTATTGGCCCTGGAGGT<br>GGGGTTGGGATTGGGGGCTGGTGCAGCCCTCCCTCTG<br>CAGCTGACCTCTGTTGTCTCCTCCCTTGGGCGGCTGAGA<br>GCCCCAGCTGACATGGAAATACAGTTGTTGGCCTCCGG<br>CCT                                                       |

FIG.7-153

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|     |                                |       |           |                                                                                               |     |                                                                                                                                                                                                                                                                                                       |
|-----|--------------------------------|-------|-----------|-----------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 577 | ADXCRA<br>D_AV6969<br>77_at    | LCN12 | Sense     | lipocalin 12<br>[Source:HGNC<br>Symbol;Acc:28733]                                             | 577 | CTAGACCCACTGCTGGTCCCTTTCTCCCTCCTGCTTCT<br>CACCTGAAGCCACCTGCCCTCCTTTGTGCCCTCCCTT<br>GCTTCTCCTGGCTCTGTCCCTGCTCCCTTTTGTG<br>CTCCATCCCGACTCCATCTCCCCACCAAGGCTGGTCAC<br>CCAGGCCAGCGTCTGTTGAAGGATGAAGCAGCTCCTG<br>TCCGGCCAGCCCTGCCTCACAGCTGTGCGAGCTCTG<br>CCCTTCTCAGCTCTCAAACCTGAATAAATGCACCAAGCC<br>CA     |
| 578 | ADXCRA<br>G_NM_00<br>1918_s_at | DBT   | Sense     | dihydrolipoamide<br>branched chain<br>transacylase E2<br>[Source:HGNC<br>Symbol;Acc:2698]     | 578 | TGGCAGAGCAACACTTCGTCTCAGAAAAA<br>CCAAAAACCAAAAGCCAAAGTGTGGTGTGCACCTA<br>TAGTCCAGCTACTCAGGAAGCTGAGACAAGAGATCA<br>ATTGAGCCAGGAGTTCAAGCTGTAGTGAGCTGTGAT<br>TGTGCCACTATCCTCCAGT                                                                                                                           |
| 579 | ADXCRA<br>D_8253.C1<br>_x_at   | TEAD3 | AntiSense | TEA domain family<br>member 3<br>[Source:HGNC<br>Symbol;Acc:11716]                            | 579 | GGAGCAGTCCCCACCAAGGTTTGTGAGATTCAAGCCT<br>CAGGCAAGAGAAAAATCAAAAGCCTTCTGCTACTCTCTC<br>CCTCTGGGCTCTGGTCTGCCCAGAGGCTGGACTCCT<br>TCCTCTACCTTGCTCTCAATCTGGAGGGTGTGGGGG<br>TGCTCCATCTTACTGGGCCCCCTGGCTGGCTTGTGGGC<br>TGAGGTGCTAATGGGCTCTAGTAGCTGCTGTGCTCCCT<br>TCTTCATGCCCCAGTCTGAAACAGGTGCTCCCCTAACCC<br>AG |
| 580 | ADXCRA<br>D_5008.C1<br>_s_at   | DGAT1 | Sense     | diacylglycerol O-<br>acyltransferase<br>homolog 1 (mouse)<br>[Source:HGNC<br>Symbol;Acc:2843] | 580 | CAGGGAGGCTCTCTGCCCTATGGGGCTCTGCTCCTGC<br>ACCCCTCAGGGATGGCGACAGCAGGCCACACACAGTC<br>TGATGCCAGCTGGAGTCTTGTGCTGACCTGCCCGGGT<br>CCGAGGGGTGTCATAAAGTGCTGTCCAGTGA                                                                                                                                            |

FIG. 7-154

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|     |                               |         |       |                                                                                                  |     |                                                                                                                                                                                                                                                                     |
|-----|-------------------------------|---------|-------|--------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 581 | ADXCRP<br>D.13135.C<br>1_x_at | MLPH    | Sense | melanophilin<br>[Source:HGNC<br>Symbol;Acc:29643]                                                | 581 | AGGATCCGAGTGGTAGTGTTTCTGAGAGTCAGGGTCTA<br>GGTCTGGAGTGCACACGGAGGCCGATGTAGAGGAGG<br>AGGCCCTGAGGAGGAAGCTGGAGGAGCTGACCAGCAA<br>CGTCAGTGACCAAGGAGACCTCGTCCGAGGAGGAGGAG<br>GCCAAGGACGAAAAGGCAGAGCCCAACAGGGACAAAT<br>CAGTTGGGCCCTCTAGCGT                                   |
| 582 | ADXCRA<br>D_BM726<br>905_s_at | FAM118B | Sense | family with sequence<br>similarity 118, member<br>B [Source:HGNC<br>Symbol;Acc:26110]            | 582 | AGTAACAATAGCCAGAGGTTGAAGGGCGGGGTAGAAAG<br>GGGGGAATGTTGCAGCGTAATCCTTCATACCACCTGG<br>TTCTTGATATTCTCCGCTGTTCAAGTTCAGAATAAA<br>AGCGACAGCAGGACCCCAAATGCAGTCCCAACCCACTC<br>CCCAGGCTAGACATGCTTGTGTCCACACAGCACACCAA<br>TGTGATACTTCCACTGACCCGCT                              |
| 583 | RDCR301<br>_B05_at            | EME2    | Sense | essential meiotic<br>endonuclease 1<br>homolog 2 (S. pombe)<br>[Source:HGNC<br>Symbol;Acc:27289] | 583 | ATGCAGTGTGTTCTGAGGTCTGTCACCCCTGAGGCTG<br>TGTGTGTCCTTTGCCAAATTAAGAGTCTTACTGAATGC<br>GGTGCATCCAGGAGACAG                                                                                                                                                               |
| 584 | ADXCRP<br>D.3751.C1<br>_s_at  | YIPF2   | Sense | Yip1 domain family,<br>member 2<br>[Source:HGNC<br>Symbol;Acc:28476]                             | 584 | ACTTTTATTTTCTATGCAAAGGTGATTCAGAGAATTTATA<br>TAAAGCGGGCGAGGGGCAGCCGAGCAGGGAGCTTTG<br>GGACAGGGCTGGGGCCCCCATATCCCCCGGGCCAC<br>CTGCTTCCCTCCTATGGCTCCCTGGAACAGGAGGA<br>GAGCCAAGGGGGGGCCAGCCTGGACAGCGCCCCGC<br>TCCTGCCTGGTGCACACACGGCGGGCCTGAGCTCCA<br>GCATCTGAGTTTGGGGTA |

FIG. 7-155

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|     |                                |       |           |                                                                                                                                                 |     |                                                                                                                                                                                                                                                                      |
|-----|--------------------------------|-------|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 585 | ADXCRA<br>D_AA4204<br>97_at    | BTBD3 | Sense     | BTB (POZ) domain<br>containing 3<br>[Source:HGNC<br>Symbol;Acc:15854]                                                                           | 585 | TGCACATTGTGACATGTACACTAAACTTAAAGTATAATA<br>ATAATAAATAAAAAAGAAAGAACCTAGTGTGTTA<br>AACCTTAAATGCCCTTAGAAATAACCTAGACCAGTGT<br>CTTAAACTGTGGTCATGAGATCAGTTGAATGGATTATGA<br>CCAACATTGAAA                                                                                    |
| 586 | ADXCRA<br>DRC.8779<br>.C1_s_at | RBM4B | Sense     | RNA binding motif<br>protein 4B<br>[Source:HGNC<br>Symbol;Acc:28842]                                                                            | 586 | CTTGCTTTCCCTAGGAGTTGAATCCTTCTCCCTGCCCTAC<br>CTGCAGCATCTCCTTCCCTTTAAATGACCATGTAGTG<br>GCAAGCAGCCCTTTACTCTTCTGTAGCTCTGGACTCTT<br>AACACTTAAGTTACTCTTCTGAAATTGCTAGGACCATTG<br>GGNNNNNNNNNNNNNNNNNNNNNNNNNNNNATGTCCGACC<br>TGTGATCGTGGGTACAGCATTAGCTGAAATTTACCCCTTGT<br>T |
| 587 | ADXCRA<br>D_AU1478<br>61_at    | EGFR  | AntiSense | epidermal growth factor<br>receptor (erythroblastic<br>leukemia viral (v-erb-b)<br>oncogene homolog,<br>avian) [Source:HGNC<br>Symbol;Acc:3236] | 587 | AAGGACCCTGAAAAATGACTTCTCATTTCTGCCCTGCAG<br>AAAAGAGAAATATTAGGATAGTGTGTGCAAAAAAAT<br>GCAAGCTTGCAATGAGAGATGCAGAGTGTGAGGGAGAG<br>AGGCACGAAGGGGTGGAGAAAAAGACAGAGAAATTG<br>AGGTTACTCAGGGCTTTGAAGGGAAAAACAGGAAGANG<br>AAGAAAGTCTGTCTNCCATGGGTGCGGCAACCCACACTT<br>TACACATTTT |

FIG. 7-156

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|     |                               |                                           |           |                                                                                                                                                                                                                                                                                                         |     |                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|-------------------------------------------|-----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 588 | RDCR108<br>_G11_at            | FAM190A ///<br>SEPP1 ///<br>UBTD1 /// UTY | AntiSense | family with sequence<br>similarity 190, member<br>A [Source:HGNC<br>Symbol;Acc:29349] ///<br>selenoprotein P,<br>plasma, 1<br>[Source:HGNC<br>Symbol;Acc:10751] ///<br>ubiquitin domain<br>containing 1<br>[Source:HGNC<br>Symbol;Acc:25683] ///<br>ubiquitously transcribed<br>tetra tricopeptide repe | 588 | ATAAGTGTAACGAGGACTCTAAAAGAACTTGTGTATA<br>ATGCTATCCAAGGTATGTAGCCCGAGGGAATAACCAACC<br>TGATGTGTGTTATGACCCATTTTAAAGCCTCCCGTGATCA<br>CAGTTTTTAAATAAATTAAGGACTGGTCCTATTTCTAG<br>GTGACACAAGTAAGGTAATAGCTAGAACGGGAAAAAAG<br>AGGGCCCCCAAAATGTAAACCTTAAATTTGGTGCTTG<br>TGCCGCTATTGATAGTAAGCAGCATGGAATAGGATGTG<br>GT |
| 589 | ADXCR1H.<br>1549.C1_a<br>t    | ELOVL5                                    | AntiSense | ELOVL family member<br>5, elongation of long<br>chain fatty acids<br>(FEN1/Elo2,<br>SUR4/Elo3-like, yeast)<br>[Source:HGNC<br>Symbol;Acc:21308]                                                                                                                                                         | 589 | TACAGTGCATAAATCAATCCAAATTTAGACCCTGGCAA<br>CCAGTTCCCATTTGCTCATCTACGGGACTCTGTCAACG<br>GTAATAGGCAATCATCTCTCTTGAAAAGTATACATCCT<br>CTCTCGCACTGGTGGAAAGCAAATTGACTTTTGTGTGTC<br>TGATAAAACCCCTTAGCACTTCAA                                                                                                         |
| 590 | ADXCRA<br>D_BU5409<br>35_s_at | FZR1                                      | Sense     | fizzy/cell division cycle<br>20 related 1<br>(Drosophila)<br>[Source:HGNC<br>Symbol;Acc:24824]                                                                                                                                                                                                          | 590 | GGCAGGACCGTGCCACACCAGCTGTCCAGAGTCGGAG<br>GACCCAGCTCCTCAGCTTGCAATGGACTCTGCCCTTCCC<br>AGCGCTTGTCCTCCCGAGGAAAGCGGCTGGCGGGCGG<br>GGAGCTGGGCCTGGAGGATCCTGGAGTCTCATTAAATG<br>CCTGATTTGTGACCATGTCCACCAGTATCTGGGGTG                                                                                               |

FIG. 7-157

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|     |                               |                                              |           |                                                                                            |     |                                                                                                                                                                                                                                                                                               |
|-----|-------------------------------|----------------------------------------------|-----------|--------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 591 | ADXCRP<br>D.4167.C1<br>_at    | POLR2F                                       | AntiSense | polymerase (RNA) II<br>(DNA directed)<br>polypeptide F<br>[Source:HGNC<br>Symbol;Acc:9193] | 591 | TTGGCATTCTCCAAGTCATCTAGCCCTTCATCCTCCTC<br>CACATCATCAAAAGTCGTGCGCATCAAAAATTGTCCTCGTT<br>GTCTGACATGACACCCCTCGCTCAGCGACCCCGCTGC<br>GCCCGGTCCCGCGGAGACCCGCAACAGCGACAC<br>TACGACTCGCGGCTCCTAGCTTATCTTGGCCCTCGT<br>GCCGAATTCCGCCACCCAGGCTCGCTACAATTACGGAC<br>CGTTATAGTA                             |
| 592 | ADXCRA<br>D_BX4062<br>09_s_at | RAB1F                                        | Sense     | RAB interacting factor<br>[Source:HGNC<br>Symbol;Acc:9797]                                 | 592 | CAACCTTTTAGCTATGATGACACATAACAAAAGATGTTTA<br>TGTAATAATAGTTGAAATCTGCCCTTTTCTCATTTCAAGAA<br>GGCATACAAAATATCTGAGAGTGACITTTGTTGTATGGCTA<br>CCCTTGATCTACAGTAATTTATTCTTT                                                                                                                             |
| 593 | ADXCRP<br>D.12748.C<br>1_at   | AC138128.1<br>(Clone_based_<br>ensembl_gene) | Sense     | Novel long non-coding<br>RNA.                                                              | 593 | GTGGAGAAAGTTGGCGTCTAGGCTGGGGATTGGTCG<br>GGGACCTTAAAGAAAAGCCAGGCTGAGGGTCCT<br>GAGGAGAGAGAGAGAGGCCACGTGGATGGAGGACTGT<br>CACCCCTTCTCGGTTCTGTACCCCTTGAGTCTAACT<br>CACTGTTAGGGAGGAAGAGGGGATGGACGGAAG<br>GGAGACCGAGGAAGGCTTTCGGGAGTGGGACATTAT<br>CCACCCAGAGGTGTGCTACCCACAAACCACCGGAGATC<br>CTTAGAGT |
| 594 | ADXCRP<br>D.2825.C4<br>_x_at  | SPDYE2                                       | AntiSense | speedy homolog E2<br>(Xenopus laevis)<br>[Source:HGNC<br>Symbol;Acc:33841]                 | 594 | GAACTGATTTCAAGGAATGGGTCTTCCCTTCAGAGCC<br>ACATGTGTGCGGGACACCCAGACAGAAAACACAAACAC<br>AAAGTCGAGTGGAGGCAATTTGGAAGGAGCAGTGAAGC<br>CGAGCCAGGAATACCAAGATGGCGAGCCAGTGTGCTT<br>GTAGAGATTGTAGAGAGGTTAGAAATTGACACTGTGGAC<br>CCTGGCCTCGATAGAGAAAGGCATCAGCTAAGGAAGTT<br>GTTCA                              |

FIG.7-158

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|     |                               |        |       |                                                                                                                                      |     |                                                                                                                                                                                                                                                                                                                  |
|-----|-------------------------------|--------|-------|--------------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 595 | ADXCRA<br>D.2994.C1<br>_s_at  | CORO1C | Sense | coronin, actin binding<br>protein, 1C<br>[Source:HGNC<br>Symbol;Acc:2254]                                                            | 595 | GAACATTCTGGATAGCAAGCCCACCTGCAAAACAAGAAGT<br>GCGACCTGATCAGCATCCCCAAGAAACCCACAGACACG<br>GCCAGTGTGCAAAATGAAGCCCAAGTTGGATGAGATTTTA<br>AAAGAGATCAAATCTATAAAAGACACAAATCTGCAATCAA<br>GATGAGCCGTATTTCCAAGTTAGAACAAGCAGATGGCA<br>AAGATAGCAGCCTGAAGGTCCCACC                                                                |
| 596 | ADXCRA<br>G_BX6473<br>58_x_at | NPIPL2 | Sense | nuclear pore complex<br>interacting protein-like 2<br>[Source:HGNC<br>Symbol;Acc:34409]                                              | 596 | TGATAATCTCAAGACTCCTCCCTTAGCTACTCAGGAGGC<br>CGAGGCGGAAAAACCCACCCAAACCCAAAGAGGTGGAGG<br>GTGGATGAGGTGGAACAATCACCGAAACCCAAAGAGGC<br>GGAGGGCGGATGAGGTGGAACAATCGCCCAAGCCCAA<br>GAGCAGAGGGAGGCCGAGGCACACAATTACCCCAA<br>CCCAAGAGGCGGAGGTTGAGTAAGCTGAGAACACGCC<br>ATTGCACTCAAGCCTGGGCAATAAGAAATAATCCGTGG<br>GTCGA         |
| 597 | ADXCRA<br>D_BX1176<br>13_at   | HIF1A  | Sense | hypoxia inducible factor<br>1, alpha subunit (basic<br>helix-loop-helix<br>transcription factor)<br>[Source:HGNC<br>Symbol;Acc:4910] | 597 | AATTTACCAAGCCACATATTGGGAATGGTACCCCGGC<br>AGAAAGGAGTAGAGTAAGCAAGCCAGAAAGGAAATACTA<br>TGGTGCCTTTGAGTAACTGCAGTGTGGCTGAAGAATGT<br>GGAAAATGATGAGGATAAAGAGGTGGACAGGGAACTAG<br>GTAAGGGAGGGCCTTCCTTTTAAATAATTAGACCTTGTC<br>CTGTGTACATTTAATGGGATTTTAAATCAGGCCATAATGC<br>CAAAATTTCTTACTTCGGAAGGATCTTTATGGTGATGGT<br>TTCAGA |

FIG.7-159

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|     |                                 |                                                         |           |                                                                                                                                   |     |                                                                                                                                                                                                                                                                       |
|-----|---------------------------------|---------------------------------------------------------|-----------|-----------------------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 598 | ADXCRA<br>D_CK3002<br>13_at     | TIMM22                                                  | Sense     | translocase of inner<br>mitochondrial<br>membrane 22 homolog<br>(yeast) [Source:HGNC<br>Symbol;Acc:17317]                         | 598 | ATTTTCTTGGCCTAGTTGTGTGCCATGGATATTT                                                                                                                                                                                                                                    |
| 599 | ADXCRA<br>D.15724.C<br>1_at     | MYO1E                                                   | AntiSense | myosin IE<br>[Source:HGNC<br>Symbol;Acc:7599]                                                                                     | 599 | GAGGGATATTATTTCCATAGCCATTACCATGATACATAT<br>GATACTGCCCTAGGTAGAGCTGGGACTGTAGGGTGGGG<br>AACCAATGCTGTCTGCACACTGAAACTATGAATGCCAA<br>GATATCACTGCCAGATCCTTCTGTGGATAGCTGGCGGC<br>AT                                                                                           |
| 600 | ADXCRA<br>D_NM_00<br>6932_x_at  | RP3-412A9.10<br>(Clone_based_<br>vega_gene) ///<br>SMTN | Sense     | Putative processed<br>transcript /// smoothelin<br>[Source:HGNC<br>Symbol;Acc:11126]                                              | 600 | GAAGCCTGACCCCAAGTGTGTCTTACCTATGTGCAGT<br>CGCTCTACAACCACTGCGACGCCACGAACTGCGCCTG<br>CGCGGAAGAATGTCTAGCCTGCCGCCCGCATGGCC<br>AGCCAGTGGCAAGCTGCCGCCGCCACTCTCCGGGCAC<br>CGTCTCCTGCCCTGTGCGTCCGCCACCGCTGCCCTGTC<br>TGTTCGACACCCCTCCCCCCACATACACACGCGCGT<br>TTTGATAAATTATTGGT |
| 601 | ADXCRA<br>DRC.1380<br>3.C1_s_at | SLC11A2                                                 | Sense     | solute carrier family 11<br>(proton-coupled<br>divalent metal ion<br>transporters), member<br>2 [Source:HGNC<br>Symbol;Acc:10908] | 601 | GCATTATTACTGATCTTGACACAGTCAAAAGCGCAGA<br>CTGGATGGATGGTCTTTTATAAGGCATTTAAGGGTACAC<br>TACTGTGTTTCACTGACCATACATTTTCTTAGCCCCCTCA<br>AGTAATATAGCACAGAGTTATGAATGACAATCCCCCTAA<br>CCATTCTCTTCATATCTGCCTCTTCCCCCTTACCATCGT<br>AATTCTCCAACTGGTCATAAAGGCACTCTGTG                |

FIG. 7-160

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|     |                                |       |           |                                                                                                          |     |                                                                                                                                                                                                                                                                                                       |
|-----|--------------------------------|-------|-----------|----------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 602 | ADXCRP<br>DRC.8133<br>.C1_at   | SLA   | Sense     | Src-like-adaptor<br>[Source:HGNC<br>Symbol;Acc:10902]                                                    | 602 | CATTAAGTCCTCTGTAAAGGTGTGAGGCAAGCCNNNNNN<br>NNNNNNNNNTGGGTAAAGTCCTAACCCCCACAAAGGT<br>GTCCCAGTGACTACCT                                                                                                                                                                                                  |
| 603 | ADXCRP<br>D.13304.C<br>1_at    | GREM1 | AntiSense | gremlin 1, cysteine knot<br>superfamily, homolog<br>(Xenopus laevis)<br>[Source:HGNC<br>Symbol;Acc:2001] | 603 | TTGGCTGGTTCTGAATGTCATTTTCTCCCTGGTGTGG<br>TTTTACATTTTCAGCTTCTTCCCTTTTCTCTCTCCAC<br>CCTCAAAATTCGCCTTAGCATTTGTGCTTAATAAT<br>CCACTCTGTGCTTATAGTTGGAGAAATGGGACAATACA<br>AAGATTTGGGTGGGTCATACAGTGTATACAAAACAC<br>AGACACTATGTGTTGGACAAATTCGCCTAGCGTGAGAA<br>TCATCAGTAGTGAGTTAAACGTTTGAAATCAGAGCCAA           |
| 604 | ADXCRP<br>D.11084.C<br>1_at    | TJP2  | Sense     | tight junction protein 2<br>(zona occludens 2)<br>[Source:HGNC<br>Symbol;Acc:11828]                      | 604 | TAATTATTGCTGTGGATTCTCTCTAGCATTTTAGCTCAT<br>TCCAGTAAATGATTTTCTTTATGAAATAGAACTACCN<br>NNNNNNNNNNNNNNNGTTCAACAACAACAACTGA<br>AGGGGAGAAAAATACACCATTACCACAGCAACAAATT<br>AGTTTATG                                                                                                                           |
| 605 | ADXCRSS<br>.Hs#S373<br>9317_at | TEX10 | AntiSense | testis expressed 10<br>[Source:HGNC<br>Symbol;Acc:25988]                                                 | 605 | TTCTCCCAGTACCTCATTTGCACAAGCCTTCTGCCATT<br>CTTCAAAATATCGAAGCCTGTTCTCACCTCAAGCCATT<br>GTACTTGCTGTTTCTTATGCCCTGAATGTTCTTCCACAG<br>ATGTTGACAAGACTTGCTCCTTCACTTCAATGACATTCA<br>GATATCTTATTCAGAGAGCATTTGACAACCTATCTAAA<br>ATAGCTCCCCCTCACTGTTCTGCCCCATGCTCTTTATAC<br>CCCATTTACTTTCATCTTCTTCTCTAGTAGTACATTAT |

FIG.7-161

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|     |                               |                       |           |                                                                                                                                                                                      |     |                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|-----------------------|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 606 | ADXRSS<br>.Hs#S298<br>5244_at | NDUFA13 ///<br>YJEFN3 | AntiSense | NADH dehydrogenase<br>(ubiquinone) 1 alpha<br>subcomplex, 13<br>[Source:HGNC<br>Symbol;Acc:17194] ///<br>YjeF N-terminal domain<br>containing 3<br>[Source:HGNC<br>Symbol;Acc:24785] | 606 | AGAACTAGCAAAAGCCAAAGGCCCTGGGGCGGGAGGA<br>GCCTGGTATGTTCAAGGGGCAGAAAGGGAGGCTGAAGC<br>AGAGTGATCAAGCGGACAGGGCAGGCAGAGCCTCAAA<br>TCCAGACTGAGGAACATGGTGAACGAGGACACTTCGG<br>GGTCCACACATAAAGACGGAGACAGAGACTCAGGGC<br>AGGAAAGTCACATGCCCTGGGACACCCAGTAAACAGA<br>GCCAAACTCAAACCTCAGCCTGTCTGCAGCTGACATAG<br>GATGAAGTT |
| 607 | ADXRCP<br>D.13218.C<br>1_s_at | THRA                  | Sense     | thyroid hormone<br>receptor, alpha<br>(erythroblastic leukemia<br>viral (v-erb-a) oncogene<br>homolog, avian)<br>[Source:HGNC<br>Symbol;Acc:11796]                                   | 607 | TAAGTTATTAAGTGGGCTGACCCAGAGGGGAGGACCCC<br>CCCTTTACCACCCCATGCACTTTGCAGAGCTGCCCCCTC<br>TTCCCCCACAATCAGAGAGAAATGCCCCCACACCCAGAGC<br>CCCAAGGGTAGGGCTGCCGATCAGAGCTGTGAGTTAAC<br>ACAACAGG                                                                                                                       |
| 608 | ADXRCP<br>D.7267.C1<br>_s_at  | MED12                 | Sense     | mediator complex<br>subunit 12<br>[Source:HGNC<br>Symbol;Acc:11957]                                                                                                                  | 608 | AGCACCCAGTAGTGGTTGGGGCCCTCCCTCAGGCTCCA<br>TTTTTAATAAGTTTTTAGTATTTTGTAAATGTGAGGCATT<br>GAGCTGTTGGGTTTGTATATTTATATATAGAGACCCC<br>AGAGCTGTTGCACCCAATACACAGAGCTTCTTTGCAA                                                                                                                                      |

FIG. 7-162

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|     |                                 |       |                           |                                                                                                      |     |                                                                                                                                                                                                                                                                                                                         |
|-----|---------------------------------|-------|---------------------------|------------------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 609 | ADXCRA<br>D_BP3971<br>77_s_at   | KLF6  | Sense                     | Kruppel-like factor 6<br>[Source:HGNC<br>Symbol;Acc:2235]                                            | 609 | TACACACATGTGAGTCTGGCTGGGCTGGTATTTTGTG<br>ATCTTCCTGGAAATGAGCAGTGACTAACGCTCACATAAC<br>TGGTTTTTTTTTATCTGGGCTGATGAATACATTACCT<br>AAGAAACTCATTCGTTTACTTAAGAGGGGAAGTGCAG<br>TTTTCTTTGGCAGTTCAGAAATCCAAGCATTGATTGCT<br>GGGTTTGGAAAACTCCTTTTTTGGCCTTCTATGTGCTTA<br>GCCATAACAAATCCAT                                             |
| 610 | ADXCRESS<br>.Hs#S191<br>8301_at | N/A   | No<br>Transcript<br>match | N/A                                                                                                  | 610 | AGAGGGGTCACCATACTTTTCTTCAGTTCATGTAACT<br>GAACAATCTTTTCTTGCTAATCTGAACACCCCTGTGCAA<br>TAGAGTCTGACTCCATTTTTTGTGTTGACTGCAGACA<br>TCTTTTCAGCCTAACCCCTTCCATCTTCTTTCTGTCCAA<br>CACTGGGGCAAGCTGACAAAAATCCTCAGGTGCTCCTC<br>TTCTGTAACCCAGCAGTAAGTTCGAATCATACACTGCCAC<br>CCTCACCCCAACCCCTGTCCCTTAACCACATTAAACCCCA<br>AAGCCAGTCTCCT |
| 611 | ADXCRIH<br>RC:2931.<br>C2_s_at  | STAT1 | Sense                     | signal transducer and<br>activator of transcription<br>1, 91kDa<br>[Source:HGNC<br>Symbol;Acc:11362] | 611 | GGCCCTGTTGAAGATGCTTGTAATTTTACTTTTCCCTTGT<br>AAATGCTATTCCCATCACAGCTGAACCTTGTGAGATCCC<br>CG                                                                                                                                                                                                                               |

FIG. 7-163

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|     |                                 |        |       |                                                                                          |     |                                                                                                                                                                                                                                                                                                                               |
|-----|---------------------------------|--------|-------|------------------------------------------------------------------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 612 | ADXCRP<br>.Hs#S191<br>8097_at   | ZFAND3 | Sense | zinc finger, AN1-type<br>domain 3<br>[Source:HGNC<br>Symbol;Acc:18019]                   | 612 | GAGGAGATAAACTAACAGAGGTCAAGAAGATGAAGAGT<br>TGTTCAAACATGGTACAGTTGAGATTCCCTAGCAATTATT<br>CTAGTCAGACGTGTCTGTCAAGTAGGCCATTGGATATC<br>GGATTGGGATTTGAGGGGAATCCATAGATGGAATAT<br>AAGTTCAAGAGGCATCAGCATGGATACCTATTTGGATC<br>TGGATGAAATTACCTAAAGGAGAAAAATGCAGGAGGACG<br>TGATGCTGGGTGATTTTAGAGGAGAAACCATGAAGGATT<br>CCAAGGAGCAGCAGTTGGTCA |
| 613 | ADXCRP<br>DRC.1321<br>0.C1_s_at | ROD1   | Sense | ROD1 regulator of<br>differentiation 1 (S.<br>pombe) [Source:HGNC<br>Symbol;Acc:10253]   | 613 | AAAAATTCATCCCATATCCAGAAAGTACCAGTTATAAG<br>ATTGCTGACCAAGCAAAGTTTTCATCAAAGTGTACCT<br>CATTGCTCTGACCAAAGACTGACTGTTGTGGTTTTAACT                                                                                                                                                                                                    |
| 614 | ADXCRP<br>D.5524.C1<br>_s_at    | EML2   | Sense | echinoderm microtubule<br>associated protein like<br>2 [Source:HGNC<br>Symbol;Acc:18035] | 614 | ACACCAGTGTGCTACAGTGGCGGGTGGTCTGATGCGG<br>CCAGGGAAGAGTCAGGTGTCAGGCAGGAATTCATTTT<br>TCGGGAGATGTCTATTGCCGAGTAGAGTAATATATACCC<br>AGAGTATGTCTATAGCAGAGGGGGTTATGGGGCGGG<br>AGGGTAGACTGACATACAGAAGTCTCTATTATCCGGGT<br>GGGAAGAGGGGAGTCACATCGCTTT                                                                                      |

FIG. 7-164

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|     |                               |                   |           |                                                                                                                                                                                                                                                     |     |                                                                                                                                                                                                                                                                                                                           |
|-----|-------------------------------|-------------------|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 615 | ADXCRA<br>D_CA3134<br>35_s_at | HIST2H2AA4        | AntiSense | histone cluster 2,<br>H2aa4 [Source:HGNC<br>Symbol;Acc:29668]                                                                                                                                                                                       | 615 | CCAGCTGGAGGTGACGAGGGATGATGCGCGTCTTCTTG<br>TTGTCCCGAGCCGCGTTGCCCGCAGCTCCAGGATCTC<br>GGCGGTCAAGATACTCGAGGACCGCAGCCATGTAGACG<br>GGCGCGCCGGCCCGCCACTCGCTCCGCGTAGTTGCCTT<br>TGCGCAGCAAGCGATGCACTCGCCCTACCGGGAACGTG<br>AAGCCAGCGCGGACGAGCGCGACTTGGCCCTTGGCG<br>CGGGCCTTGCCTCCTTGTGCTTGCACGACGACACATGAC<br>AGCGATAGTAGTCACCGAGAG |
| 616 | ADXCRA<br>D_CX8704<br>01_x_at | BAT1<br>//SNORD84 | Sense     | small nucleolar RNA,<br>C/D box 84<br>[Source:HGNC<br>Symbol;Acc:32743] ///<br>HLA-B associated<br>transcript 1 Fragment<br>[Source:UniProtKB/TrE<br>MBL;Acc:B0V2L0] ///<br>small nucleolar RNA,<br>C/D box 84<br>[Source:HGNC<br>Symbol;Acc:32743] | 616 | GAACTATGATTGCACACTACTGTGCTCCAGCTTGGGCAAC<br>AGAGTGAGATCTTGTCTCCAAAAGTCTTGAAGGATTTT<br>AGGAAGTTGTTAAAAGTCTTGAACGATGTTTGGGGCA<br>TGTTAGGGTCTTGAATGTTTAAATTCCTCTAATAACTGCT<br>TATTCAGAGAGAGCAATTTCTGACTGGGTGCAGGGCA                                                                                                          |
| 617 | ADXCRA<br>D.6719.C1<br>_s_at  | FGFBP1            | Sense     | fibroblast growth factor<br>binding protein 1<br>[Source:HGNC<br>Symbol;Acc:19695]                                                                                                                                                                  | 617 | ATGAACTTTTGTGCTTAGTGAGTGCAACGAAATATTTAA<br>ACAAAGTTTTGTATTTTTGTCTTTGTGTTTTGGAATTTGC<br>CTTATTTTCTTGATGCGATGTTTCAGAGGCTGTTTCCT<br>GCAGCATGTATTTCCATGGCCACACAGCTATGTGTTTG<br>AGCAGCGAAGAGTCTTTGAGCTGAATGAGCCAGAGTGA<br>TAATTTCAAGTGCACGAACTTTCTGCTGAATTAATGGTA                                                              |

FIG. 7-165

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|     |                               |                                              |       |                                                                                                             |     |                                                                                                                                                                                                                                                                                              |
|-----|-------------------------------|----------------------------------------------|-------|-------------------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 618 | ADXCRA<br>D_AL5471<br>57_x_at | ANP32A                                       | Sense | acidic (leucine-rich)<br>nuclear phosphoprotein<br>32 family, member A<br>[Source:HGNC<br>Symbol;Acc:13233] | 618 | GGAGGATGAAGAAGGTTATACGATGGAGAGGTAGATG<br>ACGAGGAAGATGAAGAAAGCTTGGTGAAGAAAGG<br>GGTCAGAAGCGAAACGAGAACCCTGAAGATGAGGGAG<br>AAGATGATGACTAAGTGGATAACCTATTTTGAA                                                                                                                                    |
| 619 | ADXCRA<br>D_AK0219<br>81_at   | AL157877.1<br>(Clone_based_<br>ensembl_gene) | Sense | Known long non-coding<br>RNA.                                                                               | 619 | GTGAGCTGTGATGTTGCCGCTACACTCCAGGTGACAGA<br>GCAAGACCCTAAGACCTTATCTCTT                                                                                                                                                                                                                          |
| 620 | ADXCRIH.<br>311.C1_s_<br>at   | ARHGAP12                                     | Sense | Rho GTPase activating<br>protein 12<br>[Source:HGNC<br>Symbol;Acc:16348]                                    | 620 | ATCAACTGAATCCAATAATTTCTCTGTGGCAAATAACACTTT<br>CCTCATTTTCATACCTTTTCTCCTCTCTCCATGCCAACAT<br>TTCTCCACCCACAAACGTACACTTTTATTTCTCCATCAAT<br>ATTTGAAAGCGAGTGATTTGTGACCAGGA                                                                                                                          |
| 621 | ADXCRA<br>D_BP2098<br>40_s_at | GOLGA2                                       | Sense | golgin A2<br>[Source:HGNC<br>Symbol;Acc:4425]                                                               | 621 | CAGCAACCCCTGCATTCTTTTTTTTACCGGGCTGACGA<br>GAATGATGAGGTGAAGATCACTGTCTATCTAAAAGCCGG<br>CTACTGTGAGCAAAAGCCTGAAGAAGTGGGGCTGGATAC<br>CCTGCCCCCACCATATCCCTACCATCCCTTCTCAGT                                                                                                                         |
| 622 | ADXCRA<br>D_15297.C<br>1_s_at | IGF2R                                        | Sense | insulin-like growth<br>factor 2 receptor<br>[Source:HGNC<br>Symbol;Acc:5467]                                | 622 | ACAAGCAGACATGCACCTCTCTTCTTCTCTGACACACG<br>CCGCTGGCCTGCGAGCAAGCGACCGAATGTTCCGTGA<br>GGAATGGAAGCTCTATTGTTGACTTGCTCTCCCTTATTC<br>ATCGCACTGGTGGTTATGAGGCTTATGGTAAGAGTGAG<br>GATGATGCCTCCGATACCAACCCCTGATTTCTACATCAAT<br>ATTTGTGAGCCACTAAATCCCATGCACGGAGTGCCCTG<br>TCCTGCCGGAGCCGCTGTGTGCAAAAGTTC |

FIG. 7-166

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|     |                                |         |           |                                                                                    |     |                                                                                                                                                                                                                                                                                                                                |
|-----|--------------------------------|---------|-----------|------------------------------------------------------------------------------------|-----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 623 | ADXCRP<br>D.16372.C<br>1_x_at  | GLB1    | AntiSense | galactosidase, beta 1<br>[Source:HGNC<br>Symbol;Acc:4298]                          | 623 | TCCTCTTCTCAGTCTTCATCATGTTTTGTCCCTCAAACA<br>TCAGCCTTACGTCTCTCTTTCTCCCTCTGCATCCTCTC<br>TCCTTGAGAGACCTCATCCAGCCCATGTTTTCAACAATC<br>ATCTATACAACAATGATCTTCTACATACATTCTCTGGCCC<br>AGATCCCTGCCCTGAATCCCAAGCCTATAGATCCAACAA<br>CCCTCCTCCAATACTGTCTTTCCAGGCCATTCTCCAGGC<br>CTCTGCTATGGTCTGAATGTTGTGTCCAAAACATGAT<br>GAAG                |
| 624 | ADXCRSS<br>.Hs#S159<br>1474_at | TMPRSS4 | AntiSense | transmembrane<br>protease, serine 4<br>[Source:HGNC<br>Symbol;Acc:11878]           | 624 | AAGACAGTCCTCAGAAAACCCCAAGCTTTTCATACAGATGC<br>CAAAAAGTCCATGGGTTTAATCTTTGACCATTTTGA<br>GTGCAGGGACTTATTCATGCTTACATCCTCACAACCTCAG<br>CTTGGGACTGCCCTCACACCTGGCAGCTGATCCTTTTT<br>GTTTTTAAATGTAAGAAGCCACACTGAGGGCTCTCCAG<br>GCGGAAAAGTTAGGACACAGGACCAGCATTTCTTTCC<br>AGCCACTTGTGGATCCCTGATTGAATGTCAACCCTTGACT<br>GCCTAACTCATCTCTTTCC  |
| 625 | ADXCRP<br>D.8597.C2<br>_at     | FAT1    | AntiSense | FAT tumor suppressor<br>homolog 1 (Drosophila)<br>[Source:HGNC<br>Symbol;Acc:3595] | 625 | CGACTAATCATCTTACGGCAGAGAACAACACCCACCAC<br>CAAGTAAAAATATCCCTGCAACAACACACACGGATTCCA<br>ATTCTTCGGGCCAACCCAATGTTCCACGGCGTGGACA<br>CATACTGGTTGGCGCAGGCATCCTCGCAGTGACGTCC<br>CCTGTACTCGTGGCTGCAGTTGCAGTGATAGGAGCCGT<br>GCGTGTCTCACAGAGGGCCCCCGTGCAGGCAAGGGTT<br>TCCAGAGCACTCGTCGATATCACTCTGACACCTTTCTCC<br>CCTAAAACCCGAATCACACTGACAA |

FIG. 7-167

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|     |                                |                                              |                           |                                                                                                  |     |                                                                                                                                                                                                                                                                                              |
|-----|--------------------------------|----------------------------------------------|---------------------------|--------------------------------------------------------------------------------------------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 626 | ADXCRA<br>D_CD721<br>975_s_at  | ETNK1                                        | Sense                     | ethanolamine kinase 1<br>[Source:HGNC<br>Symbol;Acc:24649]                                       | 626 | ACTATCCAGGAAAGGAAATTTACAGTATATCTCATTTTG<br>GGGTTTGGGAAGGATGTGTACAAAATAGTGAATTGAAAA<br>TTGATAAAAATAAAAAATCTTATATACTTATATTGGGTAAA<br>GGAAGATAGGAGAAGTGACAGAGCGAGAGAGAGAGAGAG<br>AGTGTATTATGTGTGAAGGAAATAAGAAAGCTCAGTCTTA<br>TAAGAAGTCTCAGATAATGTGTAGACTTTACAGAAAAAGC<br>AGTTTAAGAATGGTAT       |
| 627 | ADXCRA<br>G_XM_37<br>4317_s_at | AC011043.1<br>(Clone_based_<br>ensembl_gene) | Sense                     | Putative<br>uncharacterized protein<br>DKFZp667B1610<br>[Source:UniProtKB/TrE<br>MBL;Acc:Q69YS9] | 627 | GTATCCAAGTCCATTGTTACTAGGTTGGAGGCTGGAGA<br>TTCTAAATGGCTTCCAGACCATCTCTGATTCTCTTTTG<br>GGAGATGGGCTCTGAAAAGACAATGTCAGTAGTTTGGG<br>AAATTCTAGAAAAGTGCTTGGAAACGTGGGAAGAGCT<br>CTTGCCTAGTGCCCTAAATGCTCCATTTCAGCTCTAGCC<br>AAGTAGATACTTGGTAGGTATAGAGCCGGGTTTGCGTTT<br>ATATTAGCAAAACCTATGTCAGAGTTGAAGA |
| 628 | ADXCRIH.<br>3322.C1_a<br>t     | N/A                                          | No<br>Transcript<br>match | N/A                                                                                              | 628 | TTCTTTATGGTGGTGGGATGATTATTGTAATCATACTTG<br>GGAACAGAAAGTGATGAAAAAGGTATGTTACTTGAGATAT<br>GGAAACGCTATTTTCCATGTTTAGTTATGGGTATTCA<br>AGTCTAACTAGTGGAAAGTATGGATACATT                                                                                                                               |
| 629 | ADXCRA<br>D_BF7268<br>49_at    | TLCD2                                        | Antisense                 | TLC domain containing<br>2 [Source: HGNC<br>Symbol; Acc:33522]                                   | 629 | TCTGTGATTCTCTTTGTCAGCTCCTTTGCCTATATTGCA<br>TCTCAGTTGACACCCCTGATTCTGACTTGTCCTTATCTT<br>CCTACCAGTCTCTGCCGA                                                                                                                                                                                     |

FIG. 7-168

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|     |                                  |        |       |                                                                                      |     |                                                                                                                                                                                                                                                                              |
|-----|----------------------------------|--------|-------|--------------------------------------------------------------------------------------|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 630 | ADXCRA<br>G_D50419<br>_s_at      | ZNF175 | Sense | zinc finger protein 175<br>[Source:HGNC<br>Symbol;Acc:12964]                         | 630 | GTTGTATCAACAATGATTAACTCCTTTATTATACATACAC<br>ATGAATGTGCATTTTGGTAAATGCATAAATGAGATTCTA<br>TAATGTTTACTGATCTTTATATTACAGATTTTCTCTCTTT<br>TAGGATTAGCTCAGCTTGCCCCCTTTCCATCTCCACC<br>ATCTATAGTGAGCCTCTCCATAATTAGTGCCAACCATTA<br>GTCTCGTTCATATTTTACACCAGGAGTCAACAAA                    |
| 631 | ADXCRA<br>G_BC028<br>135_s_at    | P2RY2  | Sense | purinergic receptor<br>P2Y, G-protein coupled,<br>2 [Source:HGNC<br>Symbol;Acc:8541] | 631 | CCCCAGCCCCAAGAGATGAACATCTGGGGACTAATATCA<br>TAGACCCATCTGGAGGCTCCCCATGGGCTAGGAGCCAGT<br>GTGAGGCTGTAACTTATACTAAAGTTGTGTGCTGCT                                                                                                                                                   |
| 632 | ADXCRP<br>D.3982.C2<br>_at       | TNPO3  | Sense | transportin 3<br>[Source:HGNC<br>Symbol;Acc:17103]                                   | 632 | GAAGACTAAACAGAAACCAGAACTGAAACATTACACCTG<br>GTAGCAAATGACACTTTG                                                                                                                                                                                                                |
| 633 | ADXCRSS<br>.Hs#S548<br>4315_s_at | MEX3A  | Sense | mex-3 homolog A (C.<br>elegans)<br>[Source:HGNC<br>Symbol;Acc:33482]                 | 633 | TTCTCGCCCCACCTAGGGACAGATTCCCCCTGCTCTTTT<br>TGTCCTAGAAACCCCGCTAGTTTGGGATGGTAGCGTCT<br>GGGTGGGAGGGGCTTCCCTTCCCCACTCGAGGGTG<br>CGGGTGGGAAGGGGGGTGGGTGGGACAGCCCTG<br>GGCAGGGAGGATGCTCTCTCCACTGTAGAAAGTAGAG<br>TAGGATTGTGTCAGACTTAATTTGAGGCATCTAGTGAA<br>GACACGTACAAATCCACCAAGGAA |

FIG. 7-169

176/176

[illegible]

FIG. 7-170

ADL\_0311WP\_Sequence\_Listing.txt  
SEQUENCE LISTING

<110> Almac Diagnostics Limited  
Harkin, Denis Paul  
Proutski, Vitali  
Black, Julie  
Kerr, Peter  
Kennedy, Richard  
Winter, Andreas  
Davison, Timothy  
Bylesjo, Max  
Farztdinov, Vadi m  
Wilson, Claire  
Holt, Robert James

<120> Colon Cancer Gene Expression Signatures and Methods of Use

<130> ADL-0311WP

<150> US 61/435,922  
<151> 2011-01-25

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aaaaattagc caggcgtggg ggtgcgtgcc tat aatccca gctacttggg aggctgaggc 240

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&lt;210&gt; 10

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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tgaccactaa ttgatagaac gtttctttgt gtcgtgatga aaactttcta aatttcagta 180

atggtgatgg ttgt aacttt gcgaatat ac taaacatcat tgatttttaa tcattttaag 240

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;211&gt; 113

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

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&lt;211&gt; 227

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

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cct t t gaggg gaaaggggt g gaact aagat ggggt t t at aa ct ggaacct c caat gaccag 180

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gagaaccaat gaat t aat t t agaaagagct t ct ct gggat t agaat gaaa at aaat cact 180  
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gt gct cccga gact t t ccag agcagcagag ct gggact ag gcaggt gagg cagct acgt g 180

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 aaaccaaagc cct caaat t g t agt ct ct gt cggct t ct gc agaat t ct gg aaaat gccag 120  
 t t t t cct ccc ccgccct t gt t t t ccat aaa acat at t t at at at t gt gat gaggagt act 180

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t t c t g a a g a g t a c t t c g t a n n n n n n n n n a a t t g c c t t g t t t g c c t t c a a c t t c c t t g a t t 240  
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gttaaccctc atatctaat tcaggtatcc ttgaacaaac atagacagat actgatgatc 180  
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agttggaggt cagcataggc aacataggga 270

<210> 41  
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gccggc 126

<210> 46  
<211> 95  
<212> DNA  
<213> Homo sapi ens

<400> 46  
caggt gt t gg gacagt ccca ccct ccct gc t at t t at at c cct ct gcct a t t t att gaat 60  
cgaact t cgc ct ct gt ct cc at ct gt aaat at gt g 95

<210> 47  
<211> 145  
<212> DNA  
<213> Homo sapi ens

<400> 47

ADL\_0311WP\_Sequence\_Listing.txt

agagtggcag tttgcatggc gaacccccca ctccctcttt gctgccctt cactttcttg 60  
ctgcccttt cccagtctct ctccacaccc actcctggtc tgtcctgatc ccctctctg 120  
tatcaggttt attggttga catat 145

<210> 48  
<211> 245  
<212> DNA  
<213> Homo sapiens

<400> 48  
gaatattctg gctggcgaac tcctacacat ccttcaaac ccacctgga ctgttccagc 60  
atcttccctg gatggctgga ggaactccag aaaatatcca tcttctttt gtggctgcta 120  
atggcagaag tgcctgtgct agagtccaa ctgtggatgc atccgtcccg tttgagtcaa 180  
agtcttactt ccctgctctc acctactcac agacggggat gctaacccgt gcacctgctg 240  
tgggt 245

<210> 49  
<211> 193  
<212> DNA  
<213> Homo sapiens

<400> 49  
taagacctac tatctgatag cccacatgg tgactatagt aaataataac ttaattgcac 60  
atttaaaaat aacttaaca gtgtaatgg gtgtttgtg attgaaagga taaatgcttg 120  
ggggagtggg taccctatc tccatgatgt gcttattgca tactgcatgc ctggaccaa 180  
atatgtacc cat 193

<210> 50  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 50  
atttactacc ttattatgaa gtgtgccctc caaat 36

<210> 51  
<211> 43  
<212> DNA  
<213> Homo sapiens

<400> 51  
cttttctggg tcacagaggc caaatgtgag agcatagaat aaa 43

<210> 52  
<211> 213  
<212> DNA  
<213> Homo sapiens

<400> 52  
gaccttttca tcaatagatc gcccttaag acctattga aggtcataaa aaacctcggc 60  
caactgcaca aagatggtgc ctactgcaa caagaaacct taagggtgtct taccgacgaa 120  
ataaaaaaca taaatgattg ttctccaagg cctgagggca agactcatga tgggcaagt c 180

ADL\_0311WP\_Sequence\_Listing.txt

aaccccaatc t ggaacaatg t ccctcctct tag 213

<210> 53  
<211> 122  
<212> DNA  
<213> Homo sapiens

<400> 53  
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attattctgt tttaacaattt caattctaga tcacatttta tatatgctgc atgccaaaaa 120  
aa 122

<210> 54  
<211> 96  
<212> DNA  
<213> Homo sapiens

<400> 54  
acctgtccct gtccctacctt aactgatcaa tgcacctgt gacagtcttc ttctggacaa 60  
tgggtcttat catctcccca ccatgtacct tgtgac 96

<210> 55  
<211> 203  
<212> DNA  
<213> Homo sapiens

<400> 55  
tagacagtat gagtcaatgt gcagtgtagc ccacacttga gaggatgaat gtatgtgcac 60  
tgtcactttg ctctgggtgg aagtacgtta ttgttgactt attttctctg tgtttgttcc 120  
tacagcccct ttttcatatg ttgctcagtc tccctttccc ttcttgggtgc ttacacatct 180  
cagacccttt agccaaaccc ttg 203

<210> 56  
<211> 223  
<212> DNA  
<213> Homo sapiens

<400> 56  
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tttaaaaata acttaaacag tgtaatggg ttgtttgtaa ttgaaaggat aaatgcttgg 120  
gggagtggat accccattct ccatgatgtg ctatattgcat actgcatgcc tggaccaaaa 180  
tatgtacccc ataatatat acacctacta tgtgcccccg aaa 223

<210> 57  
<211> 240  
<212> DNA  
<213> Homo sapiens

<400> 57  
gaatttgggtt ttgatctccc tattgagaga ctgggtgtaca gtatttgtct atccctgcac 60  
aaattattaa agcaagtttt gccattctgt tatccttccct catgaatatc ttgattactt 120

ADL\_0311WP\_Sequence\_Listing.txt

t t g g c c c t a a c t c a t c a a g t t c c a c a g a a a t c c c a a t t g g a a t c t t a g t t a a a a t t g t g t 180  
t g t c t a t g g a c c a g t t g a a g a a a a c t g a c a c a t t t a t a a t a c t g a c t c t g t t c c a t a a a g 240

<210> 58  
<211> 211  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc \_ f e a t u r e  
<222> ( 1 2 3 ) . . ( 1 3 1 )  
<223> n i s a , c , g , o r t

<400> 58  
c c a g c t t t a a a g g t g a g a t t g t a g a g a t g c t g t c a a a g g g a t a a g g a a a t a g c a a g a t t t 60  
t t a a g t a g t g t g t t t g t g a a g a c t g a t c c c c a t t t t a c a a c t g c c t g t t c t t t c t c c a g t 120  
c c n n n n n n n n n c a g c c a g c t t g a c t a t t a g a a a a g t a t g a a a c t g g t t g g g g t t t a t t t a 180  
a t a t t t t t a a t a t a t t g a g a a g c a t g g t c t g 211

<210> 59  
<211> 56  
<212> DNA  
<213> Homo sapiens

<400> 59  
a a a t t c a a t a t g g a a c t t g a g g c c a a a a a a c a g a a g g t t a c t c t c a a t g c c a t c c 56

<210> 60  
<211> 73  
<212> DNA  
<213> Homo sapiens

<400> 60  
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t g g a t c t t t c a g g 73

<210> 61  
<211> 266  
<212> DNA  
<213> Homo sapiens

<400> 61  
a g t c t g g t t c t a a t c t t c t g a g c t g c c t t t g g a a g g a a g t t a t g a g g t a g a a g a t t c t a c 60  
t g a c t t t t a g t a a g g t g g a c a a t g a g a g a a a a g a a a a g c a g g t g c c t c a t c t a c a g a t c 120  
c t t c t g g g a t t t a t t t g c c a t g t a c a a t t t a a t g c a t a a a a a g g c c t c t c t c c a t a a a a c 180  
t c a g c a c t t t a c a g a t g t a g a a t a t a t a a g c a t g c c a a a t t t a c t t a t c t g t c a c a t a c a 240  
a a g c a t c a t t c c a g g t g c t a g t g a g g 266

<210> 62  
<211> 243  
<212> DNA  
<213> Homo sapiens

# ADL\_0311WP\_Sequence\_Listing.txt

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<220>
<221> misc_feature
<222> (128)..(218)
<223> n i s a, c, g, o r t

<400> 62
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acagt t caca gt aagacagt t cacggt acc cagt aggaca gt acacagt a gaacagt t ca      120
cagt gcannn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnat aggacagt t c acagt aagac      240
agt      243

<210> 63
<211> 228
<212> DNA
<213> Homo sapiens

<400> 63
gaagct gcca gagggtaatt ggttttccca gaagttctta aatttgggag ctgtcttgcc      60
gcaagccatt gagactggaa attcttggag ttggtattgt ttttgtaaat tgactaatag      120
agagttaggg aagcctggag acttgttggg ggtgagttct ctaaatggtt ttaggcttgt      180
ctgtgtactt ttgcaacgag attgtctaat tctatgggcc tctgaggt      228

<210> 64
<211> 158
<212> DNA
<213> Homo sapiens

<400> 64
ttcttgtgca ttattacatt tactcatacc tccaggacaa tgttgaagag aaatgatgta      60
ttagtccatt ttcacactgc tataaagaac tgcctgtatt agcctagcat ggtggcggac      120
acctgtaatc ccagctatgc aagaggctga gacgagaa      158

<210> 65
<211> 183
<212> DNA
<213> Homo sapiens

<400> 65
aaccacaacct taaagctgaa gacagtcccg gctaaatcct catactgaat tgagaacctg      60
tcttcccat tgggtgtgct tccctccgatt gatcccaacc cttcacctat tttagctata      120
cctgcccttt cctaattggt ttttacctg ctgtgccac cttttgagt ggtgcctttgc      180
ata      183

<210> 66
<211> 37
<212> DNA
<213> Homo sapiens

<400> 66
tggtgaaatt ttgtaccccg gatgcagttg gcacttt      37

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ADL\_0311WP\_Sequence\_Listing.txt

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<210> 67
<211> 138
<212> DNA
<213> Homo sapiens

<400> 67
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gggtcccagttggttgtgcaggcaggagtgcttctatcagttatacctcaccaaatggt120
caaacaactaggatgga138

<210> 68
<211> 39
<212> DNA
<213> Homo sapiens

<400> 68
ttggagataaggcttttaggaagtcattaaagtgagatg39

<210> 69
<211> 177
<212> DNA
<213> Homo sapiens

<400> 69
caggttgttttgttctagttctaatcttcttaaaaaccactacatggttacaaaattggaa60
taacatttggggacaactgggttaactacaagaggaggaTTTTAAGAGGagatgtgttg120
tattgactcattttgtattatttttgcttaccttcccatagctgttagagctctgg177

<210> 70
<211> 284
<212> DNA
<213> Homo sapiens

<400> 70
ggccaatgagaaccagccttcaaataaacagcttctcattgttaacacagggttcaaa60
ggcaggagggttggaggtgttttgcagggtatccagaattctgatcgctgaatactttag120
ggcaaagagt aagatttcccacacctccccctaaatcttacaattccctgatgaggcagg180
aacatgggaaaaaaagatacaggttaaattacaagcagaaaaatatgccagctagaa240
gctaaagacc tggctctcaaacactgaaccgaggagcactgatt284

<210> 71
<211> 254
<212> DNA
<213> Homo sapiens

<400> 71
ccctggcctgagaggttgcttttaagcttccacccttgttccatctgcctgccaaacc60
atcggaaggaaatccacatcatattggagatgaccccatcaacccagggtccagcact120
accaagttgg aattccacgccggggagtggtagaggaa gacgagacag gacgaggcag180
aaaagcacat tttaaaaaccagacaagatggctaggccatcaccaaccaa cggacttacc240

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ttacatcttt gt ag

<210> 72  
 <211> 70  
 <212> DNA  
 <213> Homo sapiens

<400> 72  
 ttttttctat ccctgccatt cagtctccat tagcactcta ttctctctca tttattccac 60  
 cccgtcttcc 70

<210> 73  
 <211> 178  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
 gaaacacgtg tattatggga acaactgaaa ggcagcctg aagacttttg ccctgttgct 60  
 ttctgagagt gctggatag agtccctgtc tctgaaactt ctaaaaat at gcacccttaa 120  
 ccagctttcc acggagggat aagcctttgt caatacaaat ggtacagtga gcagcaga 178

<210> 74  
 <211> 176  
 <212> DNA  
 <213> Homo sapiens

<400> 74  
 agtctggccc catagt gact tttgccccat gat tctgctt cactgttgga atcctctttg 60  
 aagt tcccc tctctttgct aaagcagtga aggaagagaa cagagacaaa ctctttggac 120  
 tgtgaaagag aaggt agaga attccaggca acagtctgac caagggtgt a aaccag 176

<210> 75  
 <211> 274  
 <212> DNA  
 <213> Homo sapiens

<400> 75  
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 actctgcctt ccaaaagtca caagtacaga tggagctcaa gttcaggagt ggtgcccaaa 120  
 cccagat act caaaccaaac tgcagaaaca ttcaggaaaa aacaagccaa agccattatt 180  
 tt agaaacac aacgcaaaac aat aagat aa aatt aagt aa aagggaagt a acagat ggaa 240  
 taaaaaccaa gat atcacat tccat aaagg gcaa 274

<210> 76  
 <211> 290  
 <212> DNA  
 <213> Homo sapiens

<400> 76  
 gt ggt ggtta tgcacaggaa tctgtcagag agcat accca tggagcat tt ataat tggga 60  
 gccattccag aattctggtt tgcatacaac tctttaaaaa gccagctacc ctgaaat gta 120  
 cactatctga gctctgcctt tgcctgtgat gagt gatgtt ggtcctgcct cttagt tctg 180

ADL\_0311WP\_Sequence\_Listing.txt

ct ct cagt ct ccaccat cgg ct t ct cagat t t t cct t cca ggaccagcag gcaggt gggt 240  
gt ggt gact t t gt ggcagac act gt ggcag at t aaaggt g gt t gcaa t t 290

<210> 77  
<211> 242  
<212> DNA  
<213> Homo sapiens

<400> 77  
accacct gaa ggaccaccag aat ggg t cca t ggct gct gt gaat ggacac accaacagct 60  
t t t caccct ggaaaacaat gt gaagccaa ggaagct gcg gaaggat gga agt caaagaa 120  
t t gaaaccct ccaaaccag t cat ct gat t gt aagcacia t at gagt t gt gcccacat gc 180  
t cgt t aacag ct gct gt aac t agt ct ggcc t acaat agt g t gat t cat gt aggact t ct t 240  
t c 242

<210> 78  
<211> 89  
<212> DNA  
<213> Homo sapiens

<400> 78  
ct t gt agct g acat t t ggca aaagcgt cac t gaaaggcaa gct aaat gt a gt t at t t t at 60  
cct gt ggccc t gaagcacia aat aaaaat 89

<210> 79  
<211> 284  
<212> DNA  
<213> Homo sapiens

<400> 79  
gt t t accgaa ggcaccagt t cagccaggag t gaaat ccgg agaggagcaa cgccagcct g 60  
ggc cacagt c cat caaacc cat gagcccg accact ct cg ct ct t cct t a cat t cccacg 120  
t cccct t ct ct cccaacc ct cat at cag caagggaaat t aat t aat ga gat t t gat aa 180  
at cagt agat agaat gaggt cccct t t t g aaat at t t ag cagact ggaa cccccccgca 240  
agcct ct gt a ggggt ggat ggagacact t ct aact t t aa t aaa 284

<210> 80  
<211> 46  
<212> DNA  
<213> Homo sapiens

<400> 80  
ct ggaggagt gagt ccct at gct gaccca at act t gcag aggt ga 46

<210> 81  
<211> 230  
<212> DNA  
<213> Homo sapiens

<400> 81  
gcat t cacac at gt gcat gc t cacacagag acggt t ct gg agt t gt ggag ggaagcct gc 60

ADL\_0311WP\_Sequence\_Listing.txt

cccgcccttcc ggccccactc cctgaacct a cagctctctc catggcccc ctcacctgct 120  
 cgggctgggc cggggcttag ggcgagaggc aggggcaggg actttcaggg atccggcagt 180  
 ct cagt gat g agagcacacc agctggggag aaaggccaaa tccctgggca 230

<210> 82  
 <211> 298  
 <212> DNA  
 <213> Homo sapiens

<400> 82  
 aggattcctt cttgtgttta agcaggagca ggcagaaaag cctaacacc cccgtctttc 60  
 ccatcggcag cccacgccc atcatcacac aaggcccca ggatgggaaa gagaaaagct 120  
 agaaggaccc aggggcctcg ggactacagg aagagtggaa agttacagac tgtaataga 180  
 gtcgggtagg cttgtgccct tccttatttg tccggttctt tcat ttgctg cttctgttta 240  
 agctcaagggt cagtcacca tgaaatgaat ttgcacctcg gtttctcttt aggctcca 298

<210> 83  
 <211> 278  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 aagcaagtct gcagatcaga ggaaagaaga aagagcagag gagggagatt ggaagt agaa 120  
 atgctgaatg cagaggcaaa aaaggaaaat gaaggacagg aggattaaac agacagaggc 180  
 aaggatgatg agagaggagc agacagcaag aatgaaaagc agaaaataca atagaggaaa 240  
 tgaagaaaag taggcctgct ggagctagat gatgatgt 278

<210> 84  
 <211> 218  
 <212> DNA  
 <213> Homo sapiens

<400> 84  
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 gcccagcca acttcatggg tca tttttc tggaaaataa tgatctgtac agacaggaca 120  
 gaatgaaact cctgcggctc tttggcctga aagttgggaa tggttgggga gagaaggcag 180  
 cagcttattg gtggtctttt caccattggc agaaacag 218

<210> 85  
 <211> 179  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 catggtggtg caagcctata ctcccagcta ctcaggaggc tgaatttgga ggatcccttg 120  
 agcccagggg ggttgaggct gcattgaggt ataat ttgc cactgtattt cagcctggg 179

ADL\_0311WP\_Sequence\_Listing.txt

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<210> 86
<211> 146
<212> DNA
<213> Homo sapiens

<400> 86
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ct gaggat ga gct ggaagga gt gagagggg acaaaaccca cct t gt t gga gcct gcaggg 120
t ggt gct ggg act gagccag t cccag 146

<210> 87
<211> 166
<212> DNA
<213> Homo sapiens

<400> 87
gggcct cggg act acaggaa gagt ggaaag tt acagact g t aaat agagt cgggt aggct 60
t gt gccct t c ctt att t gt c cggt t ctt t c att t gct gct t ct gt t t aag ct caagggt c 120
agt caccat g aaat gaat t t gcacct cggt t t ct ctt t ag gct cca 166

<210> 88
<211> 217
<212> DNA
<213> Homo sapiens

<400> 88
gagagct ct g cct agt ct gg ttt ggcgagg gccct t gat c acct t gcccc t cct ccct gt 60
ct t ct ct gat t ctt t t cctt caaaat agt c ct gagaact a att gt cacag acat t ggaat 120
att t gt act g ct ct cgt gcc att t gagagg ct gct gcccc aggcaggcca gccct act c 180
ct ct t ggct a cact cat gt t gct cagact a t att t ca 217

<210> 89
<211> 211
<212> DNA
<213> Homo sapiens

<400> 89
ct gggaact g gcact ggg t c gct ttt ggga tt acct gcgc t ggg t gcaga cact gt ct ga 60
gcaggt gcag gaggagct gc t cagct ccca ggt caccag gaact gaggg cgct gat gga 120
cgagaccat g aaggagt t ga aggcct acaa at cggaact g gaggaacaac t gaccccgggt 180
ggcggaggag acgcgggcac ggct gt ccaa g 211

<210> 90
<211> 94
<212> DNA
<213> Homo sapiens

<400> 90
gat gaagagg gct gat t gt a t ctaact t ag ggt ct t gcat gcagct ggca ct t aat gcat 60
ttt att gact gt ttt agct a acat t caat g gaca 94

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ADL\_0311WP\_Sequence\_Listing.txt

<210> 91  
 <211> 197  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
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 gaagagagga agaaaacaaa gggcatgtgt gagggagct gcttgggtgg gtgttagggc 120  
 tatgaaatct tggatttggg gctgaggggt gggagggagg gcagagctct gcacactcaa 180  
 aggctaaact ggtgtca 197

<210> 92  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens

<400> 92  
 aagctgagaa actacctgag gtgtctaaag aaatgtatt 39

<210> 93  
 <211> 212  
 <212> DNA  
 <213> Homo sapiens

<400> 93  
 ggaattaaagg ctattactct gaagaaagt tggggggccag ggctcctatt tttttgctga 60  
 ggagatggaa gatcagggct tgtattcaat aagaatggga gggggccaggg gatgcctggc 120  
 aaaagccttg cactgtgagg tgcaggtaga ggcttttatt ctggtgagag gacatggact 180  
 ctctctctcc cctcaggtaa ctgtgccctg ta 212

<210> 94  
 <211> 104  
 <212> DNA  
 <213> Homo sapiens

<400> 94  
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 tgtgtgtcct cagttaaaac tgtgcatatc gaaatatatt ttgt 104

<210> 95  
 <211> 251  
 <212> DNA  
 <213> Homo sapiens

<400> 95  
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 ttttggagcg tgtgatgtgg gggactggaa aagatgtgga gtatgtaaaa gggattttgg 120  
 aagaagcttt tggaaataga tgctgagagt cctctggaga tttcaggcaa ttgctggaga 180  
 tttttagaat gagtgggggt ggggaagggg atcccgtga agatcactgg gctacatgag 240  
 ggtgatctct a 251

<210> 96

## ADL\_0311WP\_Sequence\_Listing.txt

<211> 155  
 <212> DNA  
 <213> Homo sapiens

<400> 96  
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 ggaagaagag aaacggttaa gagaagaaga gaagcgcat t aaagcagaga aggccgaaat 120  
 cacgaggttc ttccagaaac caaagactcc acagg 155

<210> 97  
 <211> 220  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
 tt aatttt ca t gttgcggag cccctactac aagtatgaag agaaaagaaa aaaaaaatga 60  
 aggaaacaac cactggccca gggtagagat gcctacaggg tggttgcttg ttggat acaa 120  
 tacaaggaa actgctcaga acccacgtct tcagcagcat ttgaaacact ggcagcaatg 180  
 cacaagagca agatgggtgtc aggaaccatg tcaaaccctc 220

<210> 98  
 <211> 119  
 <212> DNA  
 <213> Homo sapiens

<400> 98  
 taagctttta agcatcatga agaacaattt atgttcacat taagat acgt tctaaagggg 60  
 gatggccaag gggtagacatc tt aattccta aactacctta gctgcat agt ggaagagga 119

<210> 99  
 <211> 103  
 <212> DNA  
 <213> Homo sapiens

<400> 99  
 gcctggagcg tgagcccaga cccaactcca gccccagccc cagccccggc caggcctctg 60  
 agacccccgca cccacgacct tcat aat aaa cacgtcgatt ctg 103

<210> 100  
 <211> 122  
 <212> DNA  
 <213> Homo sapiens

<400> 100  
 tatgtgccaa atctactaga cattggagaa acagtaggaa caacacatgg taccggcaca 60  
 tggatctttc aggaaaacga agtaggt aat aaacaggaaa aagcccagat ctgatgctaa 120  
 ga 122

<210> 101  
 <211> 93  
 <212> DNA  
 <213> Homo sapiens

<400> 101

ADL\_0311WP\_Sequence\_Listing.txt

ct gcct gt at cct cat t ggt gggagcccag ccat ggccct aat t gt gcct gagct t gact 60  
t t cagt cagg gccacagt ga gcatt aaat t at t 93

<210> 102  
<211> 70  
<212> DNA  
<213> Homo sapi ens

<400> 102  
ggagt t aaat gt agt gct t t ccaggat agt t cct t ccat a ct cct t ct gt t cct t t cat t 60  
gt gcccct ct 70

<210> 103  
<211> 238  
<212> DNA  
<213> Homo sapi ens

<400> 103  
cagccgt t t c cct gcagaat cagct ct gt c t cat gt ggaa gt ggagaat c agcct t gcct 60  
ggcct t t agg aact t t t gt g ggaagagag ct t t gaagag aggaggggga ct t t agagag 120  
ggat gaaaat gagccct ggg agggaggaag ggacgaggag gggg ggct gc at gt t accgt 180  
cccct acct c t cccacgt g gagggg ggag cagt t at gag ggaggaagt c aact gct g 238

<210> 104  
<211> 269  
<212> DNA  
<213> Homo sapi ens

<400> 104  
caggcat t cc t t t ct at cga t aat t act ct t t caaccaat t gccaat cag aaaat t gt t a 60  
t at ct acct a t aat ct agaa gccccacat caagt t gt t t t gcct t t ct g gacaggacca 120  
at gt at at ct t aaat gt at t t gat t gat ct ct cat gt ct c cct aaaat gt at aaaaccac 180  
gct gt t cccc gaccacct gg agcacat gt t ct cagggt ct cct gagggct gt gt cacagg 240  
ccat gt t cac t t acat t t gg ct cagaat a 269

<210> 105  
<211> 291  
<212> DNA  
<213> Homo sapi ens

<220>  
<221> m i s c \_ f e a t u r e  
<222> ( 258) . . ( 258)  
<223> n i s a , c , g , o r t

<400> 105  
gggt cagaaa gat gcct t ca gt t t t ggt ca gt gt ct aaaa gt t aagt ct g t t t aggccaa 60  
gcatt ggt ggc t cagcct ga aat cccagca ct t ggggagg ccgaggcaag t ggat cacia 120  
ggc caggaga t gagacct c t t agccaaca t ggt gaaacc ccgt ct ct ac t aaaat acaa 180  
aaaaat t agc caggcgt ggg ggt gcgt gcc t at aat ccca gct act t ggg aggct gaggc 240

aggggaatcg cttgaacnccg ggaggcagag gtcacgccat ggactccagc c 291

<210> 106  
 <211> 36  
 <212> DNA  
 <213> Homo sapiens

<400> 106  
 cgcaccattg cactagt gat aagatcgaaa ctccat 36

<210> 107  
 <211> 243  
 <212> DNA  
 <213> Homo sapiens

<400> 107  
 tttgaaatca ccatgtctga taaaaacatg caattgcttt ggtgaatttg ttgttttat 60  
 tgttgttgct ttgagtgaat gcttcagttt gctctagatt ttactttgtt tgttaaaaat 120  
 taccatgttt taacccccga aaacatttaa tgtttttgaa atgatttttt cataacaatc 180  
 ttatgagtct attatataat aggaagtatt ttggaaattt aatggtgata ttctttgga 240  
 aaa 243

<210> 108  
 <211> 220  
 <212> DNA  
 <213> Homo sapiens

<400> 108  
 tgtgcacagg agactcagga cagtgggggg aaaagt cact tctccacata agaggctcaa 60  
 atccaacgc caccctccgt cagaccctt tggccccagc tccgaccct ccagggttta 120  
 ccaagt tggg ctttcacagc atgtctgagc aaacacgcag cgaccttta cataattgca 180  
 acctctcca gagaggagag aggccacatt ctctcgcccc 220

<210> 109  
 <211> 263  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (116)..(116)  
 <223> nisa, c, g, or t

<400> 109  
 taacggagtgt tcactttcaa ccggcctccc ctaccctgc tggccgggga tggagacatg 60  
 tcat ttgtaa aagcagaaaa aggttgcatt tgttcacttt tgtaatattg tcctgngcct 120  
 gtgttggggt gttgggggaa gctgggcac agtggccaca tgggcatcag gggctggccc 180  
 cacagagacc ccacagggca gtgagctctg tcttccccca cctgcctagc ccatcatcta 240  
 tctaaccggt ccttgattta ata 263

<210> 110

ADL\_0311WP\_Sequence\_Listing.txt

<211> 278  
 <212> DNA  
 <213> Homo sapiens

<400> 110  
 catgcacaga tggccacatt ctgcctccat ccactcaatg ccaacaggca cgattcctcc 60  
 accgacaacg ctcaaggcca cagggtccac ccacacagcg ccaacaatga cgctgaccac 120  
 cagcggggacc agccaagccc tgagctcatt aaacacagcc aaaacctcta catccctaca 180  
 ttcacacact tcctccacac accatgctga agccacctca acttctacca ccaacatcac 240  
 ccccaaacc accagtacag gaaccccacc aatgacag 278

<210> 111  
 <211> 107  
 <212> DNA  
 <213> Homo sapiens

<400> 111  
 ccccatatatg tcatgacctc acttaagtgg aacactatat cataacccag agattcgtcc 60  
 cagccccaga gtccgacaga ctgtctggtc cctattccta atgaggg 107

<210> 112  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (65)..(99)  
 <223> nisa, c, g, or t

<400> 112  
 cacatctggc ctgacgttct cgttgcatac agccatcatc caccggggcgc ccctggacgc 60  
 gcgtnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnna atgctgaccc actcagtaga 120  
 gcagggggcca gccagagggg gacgaagtca ccaatccagg caccaccttc ccacatgtcc 180  
 ctgcaacttc tctctttcca gtgtgctgaa gaaggagggt gccaccctc ctccagataa 240  
 atggccccag aaaacgatcc aaaaaaatac ccagggagcg attccttatg ta 292

<210> 113  
 <211> 157  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (64)..(64)  
 <223> nisa, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (69)..(69)  
 <223> nisa, c, g, or t

<400> 113  
 gatgatcaac tctgctagga agcgggggtgg gaagaaggga ggggatgggg ttgggagagg 60

ADL\_0311WP\_Sequence\_Listing.txt

t ganggcang attaagatcc ccactgtcaa tgggggattg tctcagcccc tcttcccttc 120  
ccctcacctg gaagcttctt caaccaatcc cttcaca 157

<210> 114  
<211> 236  
<212> DNA  
<213> Homo sapiens

<400> 114  
gcagtctcag acaccaagga ggggagagt g act agaaaga aaaccttctt gcagagacat 60  
aggggatggg gaagaactgc agactgaact ggggcaaagg actgtaggac tt aaccagag 120  
agatttgagg gagagatgag gctgagagcc aggggatcct gccatgtccc agcataaaaa 180  
cagtacctga cacagatagg t gcttgggaa gctgttgtcg gatgaatgag tggaca 236

<210> 115  
<211> 137  
<212> DNA  
<213> Homo sapiens

<400> 115  
aagctggcaa ctggtgagag tatagcagtc aaaaaaagaa aatgctcact cttagatacc 60  
taagaattca aagcgtttca acctagagca accactaaaa aacctgcaca gagatgacag 120  
tcaatattac aatagag 137

<210> 116  
<211> 65  
<212> DNA  
<213> Homo sapiens

<400> 116  
agcccagcag atcctacaca cattttcaca aactaaccctc agaacaggct gcaaacctat 60  
accaa 65

<210> 117  
<211> 269  
<212> DNA  
<213> Homo sapiens

<400> 117  
tcactttcct ggattgtcac tgtgagtgt a attccggttg gctggaaccg cttttggaaa 60  
ggattgggag agatgaaaca gcagttgtgt gt cctgttat agacacaatt gattggaata 120  
cttttgaatt ctat atgcag ataggggagc ccatgattgg tgggtttgac tggcgtttag 180  
catttcagt gcat tctgtc cccaaacagg aaagggacag gcggat atca agaattgacc 240  
ccatcagatc acctacctg gctggagga 269

<210> 118  
<211> 225  
<212> DNA  
<213> Homo sapiens

<400> 118

ADL\_0311WP\_Sequence\_Listing.txt

t agt gt t t t g ccct aaat ct aaggat ggt g cct agt ggt g gccct gt gt t ct gaggacag 60  
agagagct gg aggggt ggag gggaaat gcat cggcact cat t t ggt gt aac caagaagagg 120  
gggaaagat g t c t t gat aga at caaagt t g ccaaaaacaa agaagagt ct at caagcaga 180  
t t t ct aacat t t agct agaa act act t cat agct ct cat t t t t ag 225

<210> 119  
<211> 61  
<212> DNA  
<213> Homo sapi ens

<400> 119  
cact accgcc ccgcgct ggc t t gccct cct gt t ct ccaga gcaat aaagt t ggacgagac 60  
t 61

<210> 120  
<211> 36  
<212> DNA  
<213> Homo sapi ens

<400> 120  
gagagccacc acaagact aa gt aaagaccg agt t ga 36

<210> 121  
<211> 35  
<212> DNA  
<213> Homo sapi ens

<400> 121  
gaat aaat gg ggt t gggcat at caaact aa agat g 35

<210> 122  
<211> 260  
<212> DNA  
<213> Homo sapi ens

<400> 122  
t t ct ct gcat cggcaggt t agt gat at t a acagcgaaaa gagat t t t t g t t t aggggaa 60  
agt aat t aag t t aacact gt ggat cacct t cggccaaggg acacgact gg agat t aaacg 120  
t aagt aat t t t t cact at t g t ct t ct gaaa t t t ggggt ct g at ggccagt a t t gact t t t a 180  
gaggct t aaa t aggagt t t g gt aaagatt g gt aaat gagg gcatt t t aaga t t t gccat gg 240  
gt t gcaaaaag t t aaact cag 260

<210> 123  
<211> 285  
<212> DNA  
<213> Homo sapi ens

<400> 123  
caaat at aca aaat gcct cc aagct caaat agct at aact gt accaaaga cat ggaagaa 60  
acaaaaagat cggacccgaa ccact gaaga gat gt t agag gcagaat t gg agct t aaagc 120  
t gaagaggag ct t t ccat t g acaaagt act t gaat ct gaa caagat aaaa t gagccaggg 180  
gt t t cat cct gaaagagacc cct ct gacct aaaaaaagt g aaagct gt gg aagaaaat gg 240

agaagaagct gagccagt ac gt aat ggt gc t gagagt gt t t ct ga 285

<210> 124  
 <211> 39  
 <212> DNA  
 <213> Homo sapi ens

<400> 124  
 ccgcaggcag gt gt caggac cggcct aat a aacat gt gt 39

<210> 125  
 <211> 266  
 <212> DNA  
 <213> Homo sapi ens

<400> 125  
 aaat gt gact gct t t gt aaa act ccagagt caaggact ca t aggcaggag gat gt cat aa 60  
 at t aacagga aaggat gaga aat ct ccact ccact ccct c ct ccct ccct t gat cact ca 120  
 t t ccct ct ct t ccatt cat t aaccacccac t acat gccat gccct aagga agcagct at c 180  
 t aagaagt cc ct gcct gcag gggct t t aca gaccaggagg aaggcaaccc at agagccag 240  
 gat cct gat a accact gct g act gcc 266

<210> 126  
 <211> 159  
 <212> DNA  
 <213> Homo sapi ens

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 42 ) . . ( 42 )  
 <223> n i s a , c , g , o r t

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 56 ) . . ( 56 )  
 <223> n i s a , c , g , o r t

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 90 ) . . ( 90 )  
 <223> n i s a , c , g , o r t

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 93 ) . . ( 93 )  
 <223> n i s a , c , g , o r t

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 98 ) . . ( 98 )  
 <223> n i s a , c , g , o r t

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 100 ) . . ( 100 )  
 <223> n i s a , c , g , o r t

<400> 126  
 aaaccct gga agaat ctt t c act t gaact c aact t gact g gngt t cagt c aaccant ct c 60

ADL\_0311WP\_Sequence\_Listing.txt

aggggaaggg gggaagcact atctccacan cancactnan tctgggcctc ccgccccatc 120  
tccccagcc cctctcagca actaggccag gcttcagct 159

<210> 127  
<211> 262  
<212> DNA  
<213> Homo sapiens

<400> 127  
gcagggtgc cggagcgtcg aggagttcca gtgcctgaac aggatcgagg agggcaccta 60  
tggagtggtc tacagagcaa aagacaagaa aacagatgaa attgtggctc taaagcggct 120  
gaagatggag aaggagaagg agggcttccc gatcacgtcg ctgagggaga tcaacacat 180  
cctcaaggcc cagcatccca acatcgtcac cgttagagag attgtggtgg gcacacatta 240  
tggaggcgca gtgcctacg ca 262

<210> 128  
<211> 59  
<212> DNA  
<213> Homo sapiens

<400> 128  
aggagtcagg agaacaagtc agggattagg agacagcggc ttggtttatt gttatccag 59

<210> 129  
<211> 267  
<212> DNA  
<213> Homo sapiens

<400> 129  
aat aattctc aatttcttag tctcttaatt cttaaat tta aaaaggttgt ttcttacctt 60  
t taaaat ttt taaaaaat aat tatgtcaagt aatttttgaa tatagt aacc tgattctaca 120  
tttctcatgg gat aattct aaggtaaaaa aaattgcaaa taaatcttaa actttattta 180  
gtaggtttat tattagcagc agatgtctag ccagggtaga ttacttttat cagaccaacc 240  
tctaccaaac aactactaga agagcta 267

<210> 130  
<211> 129  
<212> DNA  
<213> Homo sapiens

<400> 130  
ctgggaaatc cagtgttgt atgtaaaaat aaaaggt aag tt aattctag attgaggggc 60  
agaggctatt tcttaattctc caatctcctt gggaagggaag agtattagga ggcagtaatg 120  
gagt agaaa 129

<210> 131  
<211> 276  
<212> DNA  
<213> Homo sapiens

<400> 131

ADL\_0311WP\_Sequence\_Listing.txt

ggt acaact gg gcacgcaat g cgcgt gtt ag tagccaaat a gt aaaagggc cgt att t caa 60  
cagcgact cc aagacaact g gcgt t gcca t t ct cagt ct ccggcct at c ct acacat ct 120  
aat acccggc t acaat at aa agct at agt a aaggt t cacg gggt ct t t t c gt cccgt t gc 180  
gggt aat cgg cat ct t cacc gat act acaa t t t caccgag ct cgcgggt t g agacagt gcc 240  
cagat cgt t a caccat t cgt gt at ggacgg gct ct g 276

<210> 132  
<211> 71  
<212> DNA  
<213> Homo sapi ens

<400> 132  
ggacagcagc cact cagt t c t t cct ccacc t ccaccaggt gat cccaat a aacgaat t ct 60  
gt ct ccccgt g 71

<210> 133  
<211> 279  
<212> DNA  
<213> Homo sapi ens

<400> 133  
acagat ggcc acat t ct gcc t ccat ccact caat gccaac aggcacgat t cct ccaccga 60  
caacgct caa ggccacaggg t ccaccaca cagcgccaac aat gacgct g accaccagcg 120  
ggaccagcca agccct gagg t cat t aaaca cagccaaaac ct ct acat cc ct acat t cac 180  
acact t cct c cacacacat gct gaagcca cct caact t c t accaccaac at caccacca 240  
aaccaccag t acaggaacc ccaccaat ga cagt gacca 279

<210> 134  
<211> 237  
<212> DNA  
<213> Homo sapi ens

<400> 134  
t agt acct gc ct cat t cagc t aacgt gagg at ct agagca gcat t t gcat aaat gacgcg 60  
t ggggcacag agcagact ca acacagagca gct t acgt t a t gaggct t gg caggct ggga 120  
gct cct gt cg gcct ct ct cc t cagct ct gt gccact gag ct cggcaca ggggt t ggccc 180  
at gacaggt g t t t at t at gt ggaaat aaat gagagggaca agacat t t gc t gat t t c 237

<210> 135  
<211> 170  
<212> DNA  
<213> Homo sapi ens

<400> 135  
gcct cat cag ggaat t gt aa gat t t agggg gaggt gt ggg aaat ct t act ct t t gccct a 60  
aagt at t cag cgat cagaat t ct ggat acc ct gcaaaaca cct ccaacct ccct gcct t t 120  
gaaccct gt g t t aacaat ga gaagct t gt t t at t t gaagg ct ggggt t ct c 170

<210> 136

## ADL\_0311WP\_Sequence\_Listing.txt

<211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 ggacagatga agactcttaa gatgacagaa ggtgatTTTT ctggtgatcg aggacttccg 60  
 gggtaatgac agtgatgaaa tgcaggggac ctggttgccc ccaagtttcc tggcagtgtg 120  
 tgatactgag gaggtgagct tgtttctgga gctgtgcttt aagattcatg ttacatgtaa 180  
 agctgtcctc atttgtgact atggacctat ggagttggga caatctctat gggaagcaga 240  
 aggcaaggac cccggtcatt tttaggtagaa acaacagcat gctaatgcaa aa 292

<210> 137  
 <211> 194  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
 aagagagaag cttctgcacg ccagaggcac ccagtccac aggcgcctac ctgccccgga 60  
 taagaggttc cctgccattt ctctagtctc ccccttcaa cagcacacca aatagccca 120  
 agaagatgac aggaaccgtc cccgccaaact tcacacgagt gct aaggcga agacagccat 180  
 cttgggcctt cgga 194

<210> 138  
 <211> 202  
 <212> DNA  
 <213> Homo sapiens

<400> 138  
 tgcctgatgc ctcaggtgac agaaggcagg acgttccatg ccgaggctgc cccctcacc 60  
 agaagtctga gccagcctc aggaggggcc aagaaccagg gggccatcaa aagcatcg 120  
 atttggcatt ggttccagat gagcttttaa agcaaacaat a gcagttgttt gccatttctt 180  
 gcaactcagac ctgtgtaat a ta 202

<210> 139  
 <211> 86  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
 gcccacaacct gggattgctg agcaggggaag ctttgcattg tgctctaagg tacattttta 60  
 aagagttgtt ttttggccgg gcgcag 86

<210> 140  
 <211> 199  
 <212> DNA  
 <213> Homo sapiens

<400> 140  
 accaaagttt gcagcctata cctcaataaa acagggatat tttaaatcac atacctgcag 60  
 acaaactgga gcaatgttat ttttaaagg tttttttcac ctcttattc tt agattatt 120  
 aatgtattag ggaagaatga gacaattttg tgtaggcttt ttctaaagtc cagtactttg 180

tccagatttt agattctca 199

<210> 141  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 attgattcct gaccatagca gtgagaggcc atttttgtg caggaaatgt gcttaggact 60  
 cagcttgtt ttcgattatc caccacagaa accctgagac acagagcagc ttagaagtct 120  
 ctacccaggc gtaaatagag ctccctactc cagaccacct gccaccacc tccaagttg 180  
 agaacacaag ctccagctgg gctggagagt caggcttgg gcagggtgac tttggcgaag 240  
 ttttgtcaga tccataaagc aaactggaat ttgagctttc acttacccta gtat acg 297

<210> 142  
 <211> 110  
 <212> DNA  
 <213> Homo sapiens

<400> 142  
 ttctttccac agaagctcca ggtagagggt gtgt aagt ag ataggccatg ggcactgtgg 60  
 gt agacacac atgaagtcca agcat ttaga tgt at aggt t gat ggt ggt a 110

<210> 143  
 <211> 269  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (92)..(115)  
 <223> n i s a, c, g, o r t

<220>  
 <221> misc\_feature  
 <222> (118)..(118)  
 <223> n i s a, c, g, o r t

<400> 143  
 tgagttgttt gttcaccagt gatgctatgt tatgcatttg tttacatctc ataacatgtg 60  
 gtaaatatt atgcaagatg gctagccaga cnnnnnnnnnn nnnnnnnnnn nnnnncancc 120  
 gtgaaataga gaatgcaggg tgacccatgt aaacaggcta gagat acatt t gaaaaagat 180  
 gagggttaaa gagtgtgtac atgttggcag gt aaagagat agcat cct ct agggaggat a 240  
 ttatcaggag tcagagtaat cttggtaaa 269

<210> 144  
 <211> 106  
 <212> DNA  
 <213> Homo sapiens

<400> 144  
 aatcattgat tgacttgtct gtgaacttgc aggaactgtt tcat agtttc attacacaga 60

gt aaact gtt t gccat gcaa ggt tat ttt g cat ct gcatt t aagt g 106

<210> 145  
 <211> 184  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
 gacatt aact catt agact g gaact tgaac tgatt cacat ct catt ttt c cgt aaaaat g 60  
 att t cagt ag cacaagt tat ttaaat ctgt ttt tctaact gggggaaaag att cccaccc 120  
 aatt caaaac att gt gccat gt caaacaaa tagt ct at ca accccagaca ct ggt t t gaa 180  
 gaat 184

<210> 146  
 <211> 247  
 <212> DNA  
 <213> Homo sapiens

<400> 146  
 gt at gt gaaa gt ct ct att t gt gt att t ct ct cct aaagt t gt gt ct ct t t gggaatt gg 60  
 att t gat ttt t att att t aa t acct cact t tggcccg t cc cccct cccaa cact t ct gt a 120  
 t cct cgccct gccgccccag cct ggacgt ct gcgt ggaa gt gcgt gt t t gt agcagct c 180  
 gggcct cat c t cagcgt cg gat cct cct gct gccagaa t cact ggcc t ct gt ct cat 240  
 t ct t ggg 247

<210> 147  
 <211> 277  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 t ccct cagga agcagt cccc t cgt ct cct t t ct gggcag ct t cct t gag gacagaaact 60  
 t gaaaacaaa cacaaccaa agt t t ct ggc cat ct gt ggc t ggagggt t c t gaat gt cct 120  
 ct ct ccat gt caggcagagg gt cagcccc at gct t ct gc ct caggcccc accccacccc 180  
 accccaggcc t gccct cac ct cagggcc t acccacagc gccct gat gg aggaaccaga 240  
 ccgcaggct g t gccaccat t aaacaagagc ggct gt g 277

<210> 148  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<400> 148  
 aaggaggcag at gagat t t c at at caaaaa ga 32

<210> 149  
 <211> 174  
 <212> DNA  
 <213> Homo sapiens

<400> 149  
 t gact t ct ac ct cccat gtt t gct ct ccca act catt agc t cct gggcag cat cct cct g 60

ADL\_0311WP\_Sequence\_Listing.txt

agccacat gt gcaggt act g gaaaacct cc at ct t ggct c ccagagct ct aggaact ct t 120  
cat cacaact agat t t gcct ct t ct aagt g t ct at gagct t gcacat at t t aa 174

<210> 150  
<211> 37  
<212> DNA  
<213> Homo sapi ens

<400> 150  
ccaccgt aaa gt act gcgcg acaat at cca gggcat c 37

<210> 151  
<211> 248  
<212> DNA  
<213> Homo sapi ens

<220>  
<221> mi sc\_f eat ur e  
<222> (223) .. (223)  
<223> n i s a, c, g, or t

<400> 151  
gt ggaat aag t t ct cct agc t cagaaggat ct caacct ct t gcaagtt ac t t t t cact t t 60  
t aagggccct t aaagaagca t t t gct t agc t ct gt at cca ggccat ct ct ccct ccccg a 120  
agagcaacag accagcaact gacat t aagg t cacat ggg t ggg t ggggag t agaat t gcg 180  
ggggt gacag t t ccagccaa t ccagacacg aat cat gt t t ganggacccg agcct caagg 240  
gt gat t cc 248

<210> 152  
<211> 39  
<212> DNA  
<213> Homo sapi ens

<400> 152  
agacat at ga caat gt t cag caggt cat ct t t aat gcag 39

<210> 153  
<211> 53  
<212> DNA  
<213> Homo sapi ens

<400> 153  
acgaaagcgc aagaaat ccc ggt at aagt c ct ggagcgt t ccct gt gggc ct t 53

<210> 154  
<211> 215  
<212> DNA  
<213> Homo sapi ens

<400> 154  
cct cgt ggat cat caaggac gacgcggagg t ggagcggct gacct gt gag gaggaggagg 60  
agaagat gt t cggccgt ggc t cccgccacc gcaaggaggt ggact acagc gact cact ga 120  
cggagaagca gt ggct caag gccat cgagg agggcacgct ggaggagat c gaagaggagg 180

t ccggcagaa gaaat cat ca cggaagcgca agcga 215

<210> 155  
 <211> 277  
 <212> DNA  
 <213> Homo sapiens

<400> 155  
 tagggtttct ctccactatg aatgatctga tgtatagt aa ggttcgaaga ccacttaaaa 60  
 attttgccac aatctttgca tttgtagggt ttgtctccag tatgaactat gttatgttga 120  
 gtaaggcctg aggaatagta aaaagctttg ccacattctt cacatttata gggtttctct 180  
 caagtatgaa tttctttatg tttctttcagt tttaggatt ttctaaaggc ttggccacat 240  
 tcatcacatt tgtagggttt ctctccata tgaataa 277

<210> 156  
 <211> 125  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 actggagggt ctccgggcac actctggccc ttcccagaaa gggggtcgtt tttctcgaat 60  
 cttcaaccag ttgtgtattg gaaactagg cgcattttac tattgatcac agtcattata 120  
 ttgtt 125

<210> 157  
 <211> 151  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 ttcggaataa gggaagactg tctctgaaga aggaggaagt gt agcttatg ggaggctgag 60  
 gagtttggag tttctccttg tgggaagggt ggagccatgg aggctgaaga cagttgtcca 120  
 actcagggca taaaattga tgaggaactc a 151

<210> 158  
 <211> 233  
 <212> DNA  
 <213> Homo sapiens

<400> 158  
 aggacctcag agatgt aagc attttagcag ccacacaaaa tctctggcta tgaaagggac 60  
 ttcatgacca tccagctcaa tataacactt gcagacagag aaactgaggt cttccatgac 120  
 ttgcctagt c tcccagctag tttgaggcaa aactggattc ccactctggt attctttctt 180  
 ccttttacct cattttccct cctttaaaat gt cctgagag accagaactc aca 233

<210> 159  
 <211> 169  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
 actaaagaca ttaagcattt gcacttaatt gggtaacttcg ggaaagaagt gtgt aggttg 60

ADL\_0311WP\_Sequence\_Listing.txt

gcattaaagg tacttcttac actgcatgtt ctgt aaggac agcaaat ac atct at at ag 120  
gtt cactgtt aaattctcga ggactaatgg atccgcatgt gaaaagt aa 169

<210> 160  
<211> 123  
<212> DNA  
<213> Homo sapiens

<400> 160  
tgagccccgt gcctggcctg gtcat t t c t t gctgtgcc caacctgcc a t t aatcccat 60  
ccatcctgag cccgacgtgg tcat t t c t c caccaccag cat accgccc aacgt ggt cc 120  
ttt 123

<210> 161  
<211> 274  
<212> DNA  
<213> Homo sapiens

<400> 161  
taagtactta agtcctgtct ccttggccaa gccagactag gcccaacacc ctcaat t cac 60  
cctggctcca aagagggcaa aagcaactct ct t t c t c t aa ggccagggaa gt at ct acca 120  
caatctctga aacctgtgaa ct t t t c t g t ggcctgtagt t t caagtccc acct t aact g 180  
t cct t aaaaa aaaaaccaa caatgacct a cctaatccat ct aat t t c t c aact aact gc 240  
caccatctct act at at cca cctgcatcct at t t 274

<210> 162  
<211> 53  
<212> DNA  
<213> Homo sapiens

<400> 162  
taggcttagc ttgat t t c t g ggcccactgt ctgtgt t c t t aagatgccaa cct 53

<210> 163  
<211> 169  
<212> DNA  
<213> Homo sapiens

<400> 163  
tatgatgcac agt t cgtgtc aacaggaaat gatggatgtc aagcaat t ca t t ggt aaact 60  
cctacctcca attgat t gac gt cact aaga ggcct t g t g agaagtacac cagcatcat t 120  
gtagt agagt gtaaacct t t t cccatgcc agtct t caaa t t t c t aat g 169

<210> 164  
<211> 260  
<212> DNA  
<213> Homo sapiens

<400> 164  
cagctgggcc ctggctgatg tcatgagcca actcaagaag aagagggcag ccaactacat t 60  
agatgagaag attgagaaag t t c gaaagaa aaggaaaaca gaggat aaag aagccaagt c 120

ADL\_0311WP\_Sequence\_Listing.txt

t gggaagt t g gaaaaggt ag aaagaagcaa aggaaggct c t gaaccaaag gaggaggaag 180  
acct t caaga gaat gat gag gaaggct cag aagat gaagc ct cggagact gact act cat 240  
cagct gat ga gaacat cct c 260

<210> 165  
<211> 239  
<212> DNA  
<213> Homo sapiens

<400> 165  
aaccact cc aat taggcat t gct cccact cct ccccat c agt gct ct ca caaggt cacc 60  
agt ggct t ct acat t gccaa t ct agcgat c aaat ct cagt aagt gt cat t t gat at aact 120  
gat ct t t cac t t cct ct t t g aaaccccat c at gt ggt t t c caggaccaca cact ccct cc 180  
ct ct cct cct gccat ggg t g t cagt ct cca gggct ct ccc t aacct ccat gt gt aagaa 239

<210> 166  
<211> 278  
<212> DNA  
<213> Homo sapiens

<400> 166  
t gccat t ct ccaaaaagca cgt gccagc cccaat ccc ct ct at at ct cagct gaagc 60  
at cacct cca t t aat gaagc ct agt cct t t cct gcct cgt gt gt t gct t t gt t gct gct c 120  
acacct t t ag acaagact t g ct gccact ga ct cccaccag t ccct gt t cc ct ggaagaaa 180  
t caaggaagc ccacct t gat ct cat t t gag ct cct aat t t t acagaaat a gggacaaagg 240  
t t caaaggga gcct cacagg t cgc at ggt g aaccaagc 278

<210> 167  
<211> 214  
<212> DNA  
<213> Homo sapiens

<400> 167  
agcat ct gaa act at at cca gaat gacact ggat t t t cat aaaagt gt t g at cct cacac 60  
ct ct t t at ag t ct t gcacct agcacagt gg agt gaaacac t t t aaat agc act t gt t cct 120  
t gagt at at a t ggaaaaaag t gaagt at t g at aagt gct c agct aat at g agcagcat ct 180  
caggagt ct c caat t ct t ga at t accagg agt a 214

<210> 168  
<211> 193  
<212> DNA  
<213> Homo sapiens

<400> 168  
ggagt t ggag cccact ct gg ggaaaacat g t t gagat ct t gcct ct gcaa aaat aaagt a 60  
aaat aaaat t t aaaaaaagt aaaaaaat aa aat cagct ga gcat ggt gac at gcacct gt 120  
ggt accagct act t t ggagg ct aagt t gag aggcact gat gggaggat ca t t t gacggcc 180  
cagaggt t ga ggc 193

ADL\_0311WP\_Sequence\_Listing.txt

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<210> 169
<211> 240
<212> DNA
<213> Homo sapiens

<400> 169
ggcagctggc ggtcatttac atcccccgctgcagagggt cttccagacg gagaacctgg      60
gagcgcttga tttgctgttt ttaactggat tggcctcatc cgtcttcatt ttgtcagagc      120
tcctcaaaact atgtgaaaaa tactgttgca gcccgaagag agtccagatg caccctgaag      180
atgtgtagtg gaccgcactc cgcggcacct tcctaatca tctcgatctg gttgtgactg      240

<210> 170
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (213)..(213)
<223> nisa, c, g, or t

<400> 170
atagtgttgg gcactgtctg accatgttgc atttggaagg ctaaatgggg ccatgaagaa      60
ggctggaagg gacaggtggt gatggcagcc tacctggtgt cccctacccc acctgttctc      120
ggagaaccaa gttgctacac aggaagttct ccaaggtcca gtttcttttc tcccaccagt      180
tggaggaggc ttcaggaag accagagtcc tgnacagaga gggtaacagg aggagtcggg      240
gataaacatc aaacatcaat cgtgtgtcct gat ttgggag t gat      284

<210> 171
<211> 245
<212> DNA
<213> Homo sapiens

<400> 171
gggccttccg tgcctggcaga acaaagaaat gaatggatgc atggacagat agagagacta      60
atgcagcttg ttgagacagg ggctacagct tcaactgatgt aagaacaact ccaccctcat      120
gccccagcct ttttcttggg gcagggggcac atgataacct tttctcccaca ctaaaccttg      180
ctcactacca gactagtagg ccttaaaactc tgggagcaag aatggaactc cttctatct      240
caaca      245

<210> 172
<211> 142
<212> DNA
<213> Homo sapiens

<400> 172
ctccactatg aatgatctga tgtatagt aa ggttcgaaga ccacttaaaa attttccac      60
aatctttgca tttgtagggt ttgtctccag tatgaactat gttatgttga gt aaggcctg      120
aggaatagta aaaagctttg cc      142

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ADL\_0311WP\_Sequence\_Listing.txt

<210> 173  
<211> 256  
<212> DNA  
<213> Homo sapiens

<400> 173  
aact agt ggc tagcat cggc ttgacct gcc tcat tcccct cgaat aact g aagat cct gt 60  
acaacaat gg agact ct cgg aacat t t at c cacagt gcaa t t acagaaag cagt t cgt ga 120  
t t t ct ct aga aat aat aaat at ggct cact ggt gaccat t cccct cacgt gt cct ct gt g 180  
gt gccacac gt gcgccggg at gt gcaggc gt ggacgcag agacgccct gt ggaaagca 240  
cacat gcggt gcacac 256

<210> 174  
<211> 99  
<212> DNA  
<213> Homo sapiens

<400> 174  
t ggaggt gcc acaaaaat ca t ct ggt aaat t gt t t aaagt aat cccaaat gcaact caaa 60  
t ct acagaat cccaggt gaa gct cagt aat ct gt at t t t 99

<210> 175  
<211> 227  
<212> DNA  
<213> Homo sapiens

<400> 175  
t gt ct cct cg t gt ccgcatt gct ggagct c cacct ccct c t t ggt t t ct c cgcacccgcc 60  
cat t t t cct t ct gt ct t t ac ct gct t cgt a t cct t t ccct gct gat gt gg ct gaccct c 120  
t cccaccct ccct gcaggc ggct ggccag gt gggcaggt gccagccgga gct gt aaat a 180  
gagcgct gcg ct t t t gt gct ggt t t gt gcg t gt gct gt at t t ct gt g 227

<210> 176  
<211> 41  
<212> DNA  
<213> Homo sapiens

<400> 176  
ccat ggcca caaat ct ct a caagt gcct g ct at ccct ct c 41

<210> 177  
<211> 270  
<212> DNA  
<213> Homo sapiens

<400> 177  
gt at ct gct c aagt agaagc t t ccgt ct ct ct t gt aacag gt cagt gct t cagt t accac 60  
t gccatt gaa t t acccact c gct at cact t gcct ct t at t t ccat aaaaa aagaaacgga 120  
ggaaaaaact gt t t aagt t t t acct t gtt t aaaagt aaca cgagt gct t t t gt t at t ct g 180  
t aaact aaat acat aaat ga aggcaaagga aggaaact ga gggaagggaa caaaat gt ga 240  
gt gat gaaaa cacggagt t c at t aaat gaa 270

ADL\_0311WP\_Sequence\_Listing.txt

<210> 178  
 <211> 191  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (109)..(126)  
 <223> n i s a, c, g, o r t

<400> 178  
 gcagggt caaa aacct gccct cctgt gactt attccct gag actttt cagg agagccagcc 60  
 cacagat gat gaagaaat ga t ggaagt t ca ttt ggagagt caaat gggnn nnnnnnnnnn 120  
 nnnnnnct gc cttt gat aca ggcaatt cag t ggact at aa t aat agt gga ggggt t gagat 180  
 gt agagt ttt t 191

<210> 179  
 <211> 211  
 <212> DNA  
 <213> Homo sapiens

<400> 179  
 gt gct at ggg aaccagggt gc cagggt gaggc cagggt gaaga cagggt gaggc cagggt gaaga 60  
 taggt gaggc cagggt gaaga cagat gt t ac gggaaccagc aggt agaaag ct aagt gct g 120  
 t ggagaaaga gcgggaagaa at ggaggagg t gt ct gggac aacagaact t gaaaagaacc 180  
 t gct t ct cag tagccccaag t cct gt gt gt g 211

<210> 180  
 <211> 205  
 <212> DNA  
 <213> Homo sapiens

<400> 180  
 t gaagagcct t ct ggggt acc tagaggt gct gggaaggagt t t ggatt t aa t ct t ggct gt 60  
 cct gt gacag ggat t cggag gccat ggggg aggggt t gac agggagacag gagacaggca 120  
 agaggcgct g t gagaagcgt gggct gagt g acct gct cct t ggt gagt ga gaagt cct ag 180  
 aact gagcac cat ggcat gc acct g 205

<210> 181  
 <211> 287  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (235)..(248)  
 <223> n i s a, c, g, o r t

<400> 181  
 at cct t ccac agt ct gcaaa ccagt t cct t ct gcagt gt t t t cct ct ggg agt gt ct t gg 60  
 gct aagccac agcgggt gt ca ccccaccaca cacact gcc t gcaaaaagga ct gccaat ac 120

ADL\_0311WP\_Sequence\_Listing.txt

ccccagccca t tccccagcc t cacaat aa at aaggact t gcgacccaga at cacaat cca 180  
gaagggaagt t t cacaat ggc t t ggaat cct t t aaaaaagg acagcaaacc aaat nnnnnn 240  
nnnnnnnncc ct ccct accc acaacat cca gcct gat ccc gggaat t 287

<210> 182  
<211> 294  
<212> DNA  
<213> Homo sapiens

<400> 182  
cgacagccct gt t t cggt ca ccagact ct g aacat gct ac at cct gccca agact gcacc 60  
t ct ggaggt g cagggcaccc t t gagaagcc cct caccct aggccgct c caggt gct ac 120  
ccaggagt cc cct ccat gt a cacacacaca act cagggaa ggaggt cct g ggact ccaag 180  
t t cagcgct c caggt ct ggg acagggcct g cat gcagt ca ggct ggcagt ggcgcggt ac 240  
agggagggaa ct ggt gcata t t t t agcct c aggaat aaag at t t gt ct gc t caa 294

<210> 183  
<211> 193  
<212> DNA  
<213> Homo sapiens

<400> 183  
at gagt act g agacct gacc act gcgt t aa gcaacat aga ggt cagt gt c cat gacat gc 60  
t ggaaccaga gct t gat t gc agt t ggt t ct agaaaaaat gggggaggca at gt t t gaga 120  
gcat at at ag acaact ct t t t caagggat t t gct at aggg agaaaaaaag cgat gggaca 180  
aaact agagg gac 193

<210> 184  
<211> 168  
<212> DNA  
<213> Homo sapiens

<400> 184  
gaccagt t t a ggcaacat ag t ggaaccct g t gt ct acaaa aaat aaaaaa at t t agct gg 60  
gcat t t t ggc at at gcct at agt cccagct act t gggagg ct gaggagg aggat cact t 120  
gagcccagga ggt caagt t t gcagt gaact acgat t gcac cat t gcat 168

<210> 185  
<211> 156  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mi sc\_feat ure  
<222> (131)..(131)  
<223> n i s a, c, g, or t

<400> 185  
gggcact cgc at t t ggt cat t ct ct t gaga gct aggaggg gt cagcct ga ggccggagag 60  
gaagggct t t t t gcct ggggt gagaggggt ga gagact t gac ct gaaagcag ct cct gcccc 120

ADL\_0311WP\_Sequence\_Listing.txt

t gaggt gcaa nccagagt cc t gt gt gcgga cagaga 156

<210> 186  
<211> 109  
<212> DNA  
<213> Homo sapiens

<400> 186  
aat t t t t act att ggt cat t t gcagaacag t aaat t ct gt gt gt t ggt ac agagt gct ct 60  
gt accagt gc t cat cat ccc t t ct t cat ac caacggg ccc t agt t at ag 109

<210> 187  
<211> 106  
<212> DNA  
<213> Homo sapiens

<400> 187  
t agagat ggg t t ct t ct ggt t gat acagac t at gcatt gc gt ct agcaga t ggggt aaac 60  
t ggcct aaaa caagt ct t t g cagaat acat gccaat t t cc aaaaaa 106

<210> 188  
<211> 188  
<212> DNA  
<213> Homo sapiens

<400> 188  
t ct ccct gcc t cacaggat t gt gact cccc agcccct gcc ct caaagct t cagaccct c 60  
aggat agcagc aggacct t gt gat ct t ggcc cct t ggat ct gagat ggt t t t gcat ct t t c 120  
caggagagcc t cacatt t ct t ct t ccagggt t gt at cacccc cgagt t agca t at cccaggc 180  
t cgcagac 188

<210> 189  
<211> 148  
<212> DNA  
<213> Homo sapiens

<400> 189  
ggtagccatt t ggt t ct t gga t ct gt gt t ag aat gagt gct t t ccct t cct act gat gt ga 60  
t t gt ggatt a ggaat t cgt g accgagt gat t t t t ggccag t ggt t ggggt t t aaaat t ct a 120  
t t aaaat t t g t agt t t gggc t ggggt gct 148

<210> 190  
<211> 184  
<212> DNA  
<213> Homo sapiens

<400> 190  
gaagggt t t gg acgatt at t t gact cgcct g at agaagaaa gggat act t t gat gagaacg 60  
gggt gt gt at a at cacgagga t cgaat aat a agt gaact cg accgacagat cagagagat t 120  
t t ggcaaaaa gcaat gccag t aat t aat aa cat t t ggaaa agct t t at ag agact ct aag 180  
t ct a 184

ADL\_0311WP\_Sequence\_Listing.txt

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<210> 191
<211> 123
<212> DNA
<213> Homo sapiens

<400> 191
ttgccaggca cggcggctca tgcctgtagt cgcaacactt tgggagacca aggcaggagg      60
atcacttgag tccaggagtt tgagaccagc ctgggcaaca tacagatgtc taaaaaat a      120
aaa                                          123

<210> 192
<211> 263
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (65)..(76)
<223> n i s a, c, g, o r t

<400> 192
tcatacaaca aatcccatct ctgtccctg aaattccct agtttcattc attagaaggg      60
gattnnnnnn nnnnnngact taaagagcac ttacagcag cattcagctt tcctatgaaa      120
tactcagcat cttaaataat atatacaact ctttttttag taagctagac actggcttca      180
gagttcgtgg gagggggga aatcaacca ttcaaaacta ctctagaaat tgtcttttgg      240
cagaatagca ggtatccaag tta                                          263

<210> 193
<211> 45
<212> DNA
<213> Homo sapiens

<400> 193
agttctaggg gatatttgtg caataaat acacatgtcaac ttgaa      45

<210> 194
<211> 125
<212> DNA
<213> Homo sapiens

<400> 194
aaagcaggta gttagttacc atttggagag ggattccgga acctagagag agatgaggct      60
gaagaggcgg gaagaaacca gatggcaagg actttgtctc atgcgcaaag catataattt      120
ataga                                          125

<210> 195
<211> 233
<212> DNA
<213> Homo sapiens

<400> 195
agaggtaata tccttcctat tcttccttca ctctgccccc tcctcccacc tcttcccagc      60
ctccctcacc tgacctattt aggggggtgat gggatgaaaa gaagagagt g aaggatatgt      120

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ADL\_0311WP\_Sequence\_Listing.txt

aat caagt gc aaaat act gt ggt aagt aca gagaat gaat aaggt ggaaa ggaaagt gaa 180  
aagt gt ggga t ggt tagggg ct ttaaggac ttcccaggaa aat aggat t c t gg 233

<210> 196  
<211> 197  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (142)..(142)  
<223> nisa, c, g, or t

<400> 196  
gaccagggcc tctcctgtgg gatctttgtt ttgtgtttaa ccat aat ggt t gt gt act ga 60  
accacttcat atttgttata tataat at at at at at aa tctccttaag actcagcctc 120  
ctgggtttacc cccccggcct gngcatctga cctccccac cccagtgtga ttt aacatcc 180  
aggaactgag gcctgaa 197

<210> 197  
<211> 289  
<212> DNA  
<213> Homo sapiens

<400> 197  
taagagctgt ggaggactga aaactggat aaaaagggggt ccttttctt gccctgtct 60  
ctcactcaga tgcgttctt ttctgccact gtttggcaaa gttttctgtt aagccccct 120  
ccccctgcc cagtctcca ggtgcgttac ttttctggg atcatggggt cagt tttagg 180  
acacttgaac acttctttc ccccttccc ttcacagt aa ctggggcagg ggcctacggg 240  
gaggggcttg tactgaacta tctagt gatc acgttaacac ct aactctc 289

<210> 198  
<211> 195  
<212> DNA  
<213> Homo sapiens

<400> 198  
ggactgcagc taagtgtcca ctccccaaag tcttctatt cctaactcca tgacagctcc 60  
tcagt agagc tttcctctc agaagcaact agaacaatgc agttaacatt atttggcccc 120  
aacggcgttt actgtgtatt ttggctgaga tctttagaag cccgaggcct aaacaattaa 180  
ctgaggaaca tctaa 195

<210> 199  
<211> 213  
<212> DNA  
<213> Homo sapiens

<400> 199  
ttactgaact acagcctggt ttgt agactt cctgtttcta cactgctgct cttcaccatt 60  
ggaattcact gtggtattta tattactggc tt cagtccga gccacaggt a ataaaaggat 120

ADL\_0311WP\_Sequence\_Listing.txt

at cat ct gt a t t t ct caacc at at cat ggt gt at agat gc t g t t at t cag gcgaact t gc 180  
t cat ggggt gg act aacacct ggt t t ggt ac aga 213

<210> 200  
<211> 221  
<212> DNA  
<213> Homo sapi ens

<400> 200  
gagccat gat t gt gt t act g cct t ccagcc t gggcaacag agt gagact c cat ct caaaa 60  
aaaaaaaaa gaaagaaaga aaat cagact ct gaggt gc aggcggg ggc t cact ct t gt 120  
aat cccagca ct t t gagagg ct gaggcagg aagat t gct t gagcccagga gt t t gagacc 180  
aact t gagca acacagt ggc accct at ct c t acct aaaaa a 221

<210> 201  
<211> 278  
<212> DNA  
<213> Homo sapi ens

<400> 201  
ggagccgcca cggaat t gcg aaagcccagc t acgcagaga t t t gt cagag aacgagt aaa 60  
gagcct cct t ct t ccccat t gcaaccccaa aaagaacaaa agccaaacac t gt t ggt t gt 120  
gggaaggagg aaaagaagct ggcagagccc gcagagagat accgggagcc cccagccct c 180  
aagt ccacac ct ggagcccc cagagaccag aggcggccgg cggggggccg gccct cgccc 240  
t cgcccat gg ggaagcgt ct cagccgagag cagagcac 278

<210> 202  
<211> 198  
<212> DNA  
<213> Homo sapi ens

<400> 202  
cgt gct acca t cacagct ga at gcaat gaa aggcggg cct ct gagaggag cagggt ggag 60  
at gct aaagt ggaggccccg t cccat t gct gat agat cct cat ct ggcat gcgct ccacc 120  
ct ccccat t c t ct gct ccca cgt at cgt ag ccccat caca gaagat gcga cat ggaaaaa 180  
cgcact gt gt ccaccct a 198

<210> 203  
<211> 50  
<212> DNA  
<213> Homo sapi ens

<400> 203  
gct gt gcca acct gccat t aat cccat cc at cct gagcc cgacgt ggt c 50

<210> 204  
<211> 217  
<212> DNA  
<213> Homo sapi ens

<400> 204

ADL\_0311WP\_Sequence\_Listing.txt

t t t t a g c a a c c a g c c a g a g a g g g c g t g g g t t c a t g a a a a c g g g t a c g a g a g t a t a a a g g 60  
t c a t a a a c a g t a t g a a g a a t t a c t g g c t g a g g c a a c c a a a c a a g c c a g c a a t c a c t c t g a 120  
g a a a c a a a a g a t t c g g a a a c c c c g a c c t c a g a g a a a c g t g c t c a g t g g g a t a t t g g c a t 180  
t g c c c a t g c a g a g a a a g c a t t g a a a t g a c t c g a g a a 217

<210> 205  
<211> 175  
<212> DNA  
<213> Homo sapiens

<400> 205  
c c t c g t g g g c a c g t g g a g a a g g g c c c a c g t g t c t c c a c a c g c c a g c c a c a g g g g a g c c c t 60  
g g c c a g g c g c c c a g c c a g g g g a g c g t g t g c c t g g g a t g g g t c a c a g a a c c a g c g g g c a c c 120  
t g t g a g g c t g g c c a g c a c c g t g g g g c t g t g g g a a t c g c t c t t a t t t a t a t t t a a a 175

<210> 206  
<211> 265  
<212> DNA  
<213> Homo sapiens

<400> 206  
t t c c a a g t g c g a c c t c a a a t g a c a a c t t t c t c a g g t g g t g c c t g g a t a g g a a a g g c a c c g 60  
g a a c a g a a t c t g t a g a a a c c a a a c c t a t c a t g a t c a g c a t t c c t a c c c g a c g t t a a c c t 120  
c c t a g a c t a g c t g a c c t t a t t t a t t t t g a a g c a a a t c a a g t g t a t a c a g t c t c t t t t t a 180  
a a a a a c t g t g t a a a c g t t g t a a a g t t t t t a g g g g c t g t t t a a t a a t c t g a a g a t t t a t a a a 240  
a a a t t a c t g g a c t t g t t a g g a c t a t 265

<210> 207  
<211> 223  
<212> DNA  
<213> Homo sapiens

<220>  
<221> m i s c \_ f e a t u r e  
<222> ( 1 1 5 ) . . ( 1 3 2 )  
<223> n i s a , c , g , o r t

<400> 207  
t g a g a t g a t c a g a c a c c g g a g t t c a a c g t c c c a g c a g t c t t g g t a a a a g g a g g g a g c c t a 60  
c t g a g c c a g g a g g g a g a a a a g a a g a t t g a c c a g c t t g c t a g a a a a t a c t t a g c n n n n n n 120  
n n n n n n n n n n n n g t g g a g g g g g g a c g g a g a g g a a c a a g g a t g g g g a g g t a g g a a t g a g g t 180  
a t a g a a a a g a g a t a g c a t c t t c t t t g g c a c a a g a c t a g t g g c t 223

<210> 208  
<211> 188  
<212> DNA  
<213> Homo sapiens

<400> 208  
c c c a g g a t g c g t c a g t c t g t t c a g t g g t c a g c a g g c c c c c c a c c c c c c g c c g a c t g c c c t 60

ADL\_0311WP\_Sequence\_Listing.txt

cgccatcgtggtcagacccc cctcccaaca caacacgctgctggctctgtgtcagcctttg 120  
 taacgtggga ggctctgccg tgtcttccgg gtgaactgta tttggattgc gcgcattgtc 180  
 acggtccg 188

<210> 209  
 <211> 254  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
 ataggtagca aagctaaggc ccagaaaggt taagtaattt tcccaaagtc acacagcttt 60  
 gatatacagc aaaactcata tccctgagct ttctactcac tgttcttccg gttattatcc 120  
 ctgaggtcat aaatctccac ccgcaaacc aatagcacca gtacaagaaa tctggactgg 180  
 agatacttta tccacacct a ccaactgcccc aaaaagtaaa atctgactct gtgattctaa 240  
 tgtaccaatg gtac 254

<210> 210  
 <211> 158  
 <212> DNA  
 <213> Homo sapiens

<400> 210  
 atttttattg cagtaggagg aaatatattt aaaatatgt tagatttat gcaaatagag 60  
 actcgttatt taagggttaa ataacaattt gttcttttgt tgtttttgcc agtttagggc 120  
 agtagctgct tttgtcataa atatcttctt accacatc 158

<210> 211  
 <211> 135  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (94)..(94)  
 <223> nisa, c, g, or t

<400> 211  
 ctfgagtaaa gacattttgc ttaatttctt ttttcttatt cccacttgt atatccctca 60  
 ccagtaccgg gatctgcaca catctttttg cagntacctc ttcatagcca tgaacaaaa 120  
 cgttctatga ggagc 135

<210> 212  
 <211> 248  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ccttcctgat tgtttacagt cattggaata aggcatggct cagatcggcc acagggcggt 60  
 accttgtgcc cagggttttg cccaagtcc tcatttaaaa gcataggcc ggacgcatct 120  
 caaacagag ggctgcattc gaagaaacc ttgctgcttt agtccgatagggtatttga 180

ccccgatata ttttagcatt ttaattctct cccctattt attgactttg acaattactc 240  
aggtttga 248

<210> 213  
<211> 259  
<212> DNA  
<213> Homo sapiens

<400> 213  
tcctgtcctt gcaggt aaga cctgctccgg ggtccccgcc ccgccgccgc aactcccgc 60  
ggtcgtctgg gctgtcacta ggagatccgt agcccagacg gtgactttcg tatgagctat 120  
ttaactttat tttcttcaga atctgctgta gattgagctg tgcgtgaaat tgcgtagt aag 180  
ttctgacatg ttaatgcgtc tgtctttaaa tctgaattgt taccataaac gtgtttaatg 240  
gaacttgctg gtctgtgga 259

<210> 214  
<211> 262  
<212> DNA  
<213> Homo sapiens

<400> 214  
acctcatccc cgaataataa ct aagcacta gaggatgct ggggatgctg gggcttggtt 60  
taggtggctg gggaagttat ct tggaggtg agactccagt ggactctgcg gatgggt aag 120  
gtctcagaga ggttggggaa gttatcttgg aggtgagact ccagtggact ctgcggattg 180  
gt aaggtctc agagaggttg aggttaagaa gagagcatct cagaccattc caaaatcagc 240  
acataacaca catggcttga aa 262

<210> 215  
<211> 161  
<212> DNA  
<213> Homo sapiens

<400> 215  
gtttctacag ttcacttgtc tgcatagagg tcgtgctgtg cctggcagta atctccactg 60  
cccttcagaa actccataaa tgtgtgacca agaaccacac agaattgagg aat atgttta 120  
ctcattgaag attgtggcct aatcatacag ccggtccga g 161

<210> 216  
<211> 135  
<212> DNA  
<213> Homo sapiens

<400> 216  
atgcaagt aggcagccagcc cgtctgttcc ctctccgcc ccgccgccgc cgcgcccgctc 60  
actgcgcttc tgttatacca tctttgcctg actctctacg gcttctccat tgaatggcta 120  
atgtgtatgt gaaat 135

<210> 217  
<211> 278  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (177)..(247)

<223> n i s a, c, g, o r t

<400> 217

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tacacaaact ttattacagg cacaaaattt tcaaaaat ac ggtataaaat taccttaagg      60
ctatgtatat aagggatgtg tgtatgtgtg tatacacaca aaaataaat t t t g t g t t c c      120
acttggatcc cctccctaag ataactcatt gtgtacatgc aaatataga aaatgcnnnn      180
nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn      240
nnnnnnnnctat ttttatcacc attttcatgc tgtattaa      278
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<210> 218

<211> 242

<212> DNA

<213> Homo sapiens

<400> 218

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aactgcatga tgcacctgct ccgctccctg cccgacccca acctcatcac cttcctcttc      60
ctgctggaac acttgaaaag ggttgccgag aaggagccca tcaacaaaat gtcacttcac      120
aacctggcta ccgtgtttgg acccacgt aa ctgagaccct cagaagt gga gagcaaagca      180
caactcacct cggtgcgga catctggccc catgacgtca tggcgcaggt ccaggtcctc      240
ct      242
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<210> 219

<211> 205

<212> DNA

<213> Homo sapiens

<400> 219

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gctcataaca aatataccag cattcatgat agcatttcag cattttccaa ggtaccaagt      60
gtacttat t t t t g t t g t t g t t t t a g a a g g a a t t c a g c t c t g a t g t t t      120
ttaaagaaaa ccagcatctc t gatgttgca acat acgtgt aaaatgggtg t t a c a t c t a t      180
cctgccattt aacccacag ttaat      205
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<210> 220

<211> 94

<212> DNA

<213> Homo sapiens

<400> 220

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tatccaacgg tatagatcac aaggggggga tgttaaatgt t a a t c t a a a a t a t a g c t a a a      60
aaaagatttt gacataaaaag agccttgatt ttaa      94
```

<210> 221

<211> 273

<212> DNA

<213> Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 221  
gacaaagct c t aggat gat g gct gaggggt agaagaaggg gcaagggaga cagaggt ct t 60  
ggagat gacg cccat at ct c t ggcat gacg aaccagat g gcagggggg g gggcct ggt t 120  
t gt gggaagg ggt gt cccac t agcagat gt gt acccagt g gaggt gcagc t cagat t gga 180  
gct ggccat g ggt at t t gaa aat cat gt gc gcacaggt ag ccact gaagc cat gggagt g 240  
aaagagaaca ct t ggaaagt gaact ct ggg aaa 273

<210> 222  
<211> 168  
<212> DNA  
<213> Homo sapi ens

<400> 222  
t ggaccgt cc aagaaggagc t acat cagag gt t t t ggt ag at gct gct gt agacct cat a 60  
t cccgat gaat gggaagct gc t aat gccat a cccagcagag agaaggaagc aggat gcagc 120  
cccgt t t gag gccgccagcg t gcct t ct gc agact gt gag cagagcaa 168

<210> 223  
<211> 277  
<212> DNA  
<213> Homo sapi ens

<400> 223  
agct t t gcag t t at aggct c t aacct ggac at gt cagaag ccaact acaa act gat ggaa 60  
ct t aat ct gg aaat aagaga gt ct ct acgc at ggt gcaat cat accaact t ct agcacag 120  
gccaaaccaa t gggaaat at ggt gagcact ggat t ct gag acact t cagg cct t t t agga 180  
aagaaact aa act gaagat g at gaagaat a t t aaccaagc acct t t t aat ggaccct t gc 240  
t t cact gat a act t t ct ggc agcat ct act t t t t agt 277

<210> 224  
<211> 290  
<212> DNA  
<213> Homo sapi ens

<400> 224  
agggt ct agga gat gcct gag cct ccact ga cct ct gt gca t gt ggcccac cagt ggccac 60  
t ct gt cct t t t ggaaact gt cct ct ggct t t ct aggaacc ccat gt t t t t ggt ct t ct cc 120  
t ct ggcccct cct t ct cagt ct cct cagca ggact ct at t cct gt accca t t cct aaaat 180  
gt cacgaact cgt t t ct ggc ct t gt cct t c t t t gagt gca t ct ct ggt t c t t cat ct at c 240  
cct gt t gaga t gct caccct t ct t t ggt ga gct cccaacc ggt acaggt a 290

<210> 225  
<211> 68  
<212> DNA  
<213> Homo sapi ens

<400> 225  
aat t gt gcct acct cagat a gacagt gcca gaat t aagt g agt caagcca agt aaagccc 60  
agagaaga 68

ADL\_0311WP\_Sequence\_Listing.txt

<210> 226  
<211> 105  
<212> DNA  
<213> Homo sapiens

<400> 226  
tcttcacaca gacaattcga tcagtccttc aggtcttaag tcacttctca agaagccgt 60  
acttgcctag gctagattag atcctactgt tacatgctcc cttta 105

<210> 227  
<211> 98  
<212> DNA  
<213> Homo sapiens

<400> 227  
tttagtaggt acgtcatgac aactaccatt tttttaagat gttgagaatg ggaacagttt 60  
ttttagggtt tattcttgac cacagatctt aagaaaat 98

<210> 228  
<211> 206  
<212> DNA  
<213> Homo sapiens

<400> 228  
ggcggcgtcc ccagctggtt cgggctgtga cgggggtggcc agcagggacg cgccccaggt 60  
gggcagctgt ggcagagcag cgacccgcgg cggggcggca tccccagctg gttcgggccg 120  
tgacggggcg gccagcaggg acgcgccccca ggtgggcagc tgtggcagag cagtcgagac 180  
acctaaataa aagctctgct gcagga 206

<210> 229  
<211> 99  
<212> DNA  
<213> Homo sapiens

<400> 229  
agataaattg ttgcctgctt ctgtgtctct gccagcctgt gatcatattg ggttagagtt 60  
agaaatccgc tgtttgcctt tcttactggt aggatcctt 99

<210> 230  
<211> 147  
<212> DNA  
<213> Homo sapiens

<400> 230  
atcctcgcca ttcgaaattc agttctgtac atctgcctat attccttgtg atagtgttt 60  
gtttttcat agataagctt cctccttgcc tttcgaagca tcttttgggc aaacttcttt 120  
ctcaggcgct tgatcttcag ctctgcg 147

<210> 231  
<211> 57  
<212> DNA  
<213> Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 231  
aaacgaactg taaaagacca tgcaagaggc aaaataaaac ttgaagt gaa tgc ttaa 57

<210> 232  
<211> 269  
<212> DNA  
<213> Homo sapiens

<400> 232  
agcagctac caaatctcaa aat atcctaa gactaacaca aggcagctgt gtctgagccc 60  
aaccccttcta aacggtgacc tttagtgcca acttcccctc taactggaca gcctcttctg 120  
tcccacagtct tccacgagag aaatcaggcc tgatgagggg gaattcctgg aacctggacc 180  
ccagccttgg tgggggagcc ctctggaatg catggggcgg gtctagctg ttaggacat 240  
ttccaagctg ttagtgtctg tttaaaata 269

<210> 233  
<211> 204  
<212> DNA  
<213> Homo sapiens

<400> 233  
catcatgttt ttgtgggcaa atacaagttg ttataattaa aaccctaat ttgaatattt 60  
ttgttacc aa gaaccaaggc aaatgtttaa ttgttat aa aacctgttg tgaagtgtg 120  
tgttaaat t g t gctgctggc taataggcct cat t t caat t taataaat at ttatt gagga 180  
ctggctttat gtctggccct gtgc 204

<210> 234  
<211> 155  
<212> DNA  
<213> Homo sapiens

<400> 234  
agt atctgat atgtgtgtgg aggcagccat cttttcctga aagtcctttt aggaatcat t 60  
atttctggtc ctctgaagt t gccgctacc actcat aaat atctatccac accccttaca 120  
agaagaat aa ggaagatctt aagacctaga aggaa 155

<210> 235  
<211> 272  
<212> DNA  
<213> Homo sapiens

<400> 235  
acttgacct a ggcagt gacc attctctccc actttcacac atgttcactt gacttccagg 60  
ccat actctt agtttccatt ttacctcact gcctcactcg ttatcatctt ccttgcctcg 120  
ttcctcaact ctctatgcta gagtacttca gggatcagtc cttgatcctc tcttttctc 180  
tatacttact cctttgaggg ttatctagt ctcacagatt taaat atctt tgat atgctg 240  
acaactctct aattatctaa ttaccctgc cc 272

<210> 236  
<211> 277

## ADL\_0311WP\_Sequence\_Listing.txt

<212> DNA  
<213> Homo sapiens

<400> 236  
 aaaattttctc tttgctcttt cgt agaaat a aaacttaaca gttggatagg ccctgatccc 60  
 agctttctgg catgtctgag cataagcctg acagtctact tttccagctt tcaactttcc 120  
 tttaatcatc ctagccaaga gctcaaattc tggagcaaaa ttctggcaag gtccacacca 180  
 aggagcatag aaatcaatca cccaatgatt tttcccttgt agaacttttt cactgaaagt 240  
 ctgaggtgtt agatctgtgg atacttgatc ccgggaa 277

<210> 237  
 <211> 272  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (106)..(189)  
 <223> n i s a, c, g, o r t

<400> 237  
 ggcacaacat ttttgaggac aattaaaatt ttatatctac atagcttca cccaactct 60  
 tccattttcta gatatctatg ctacaggaat acttgccac taagcnnnnn nnnnnnnnnn 120  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180  
 nnnnnnnnnnt ggggtgacct tctaagtcct aggaaggaaa gaaattatga agtgaaagaa 240  
 tatcatataa gtgataccat gaagtgaag aa 272

<210> 238  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (36)..(213)  
 <223> n i s a, c, g, o r t

<400> 238  
 ggagt agcca agactcctgt ttctctgcat ttttcnnnnn nnnnnnnnnn nnnnnnnnnn 60  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnntggggtc cctgttgccc agcatgcctg 240  
 gaccctcaac acttaatagt gatataaca tatatccaac ccttggtaaa tgcaggact 300

<210> 239  
 <211> 229  
 <212> DNA  
 <213> Homo sapiens

<400> 239  
 ggcctttagt taacatccga gtgacgaagc cgggttcccc agtacagctg tcttttgggt 60

ADL\_0311WP\_Sequence\_Listing.txt

gcggt catt g t gaggaaggg gat gaggat gag tgt ggggt gt g gct ggaggag gagct agat g 120  
ccggt ggaca gt gggcaggt ggat t t gggg aggagaggat cagcagcagc agaagt act c 180  
agt gat aggg ggct ggct gg gt caggaat g gt gagat gaa cat gcaagt 229

<210> 240  
<211> 51  
<212> DNA  
<213> Homo sapiens

<400> 240  
act tgaacc cgaaggcagt gtt tgt ggt g agcagaaat t gct t catt tgc a 51

<210> 241  
<211> 300  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (203)..(203)  
<223> n i s a, c, g, o r t

<400> 241  
gggccat ggc act gct gtt c agct caggca caggggcaca gcagaggt t t gggaagcggg 60  
ct cccaccg gcaact gggat t ggcgggt cc aagcccagca accggct t cg ct ccacaaca 120  
cacaccacac ct gggact gt t t t t aat aca t agcaacaga ct ggggt t at t t at t t aagat 180  
gt gt at t gt g t cat at gaag t t naagagac at aaat ggca t t t t gt t at t t at t aagaca 240  
aact ccaat t gt t ct ct ggc t g t t t t t t c agt t gt gt ct agcaaat act t at ct gccct 300

<210> 242  
<211> 286  
<212> DNA  
<213> Homo sapiens

<400> 242  
agact gact g ct aaact gt a t gaat gat ga ggggat t t gc acgt at aat c t t aact gt ac 60  
at caaat gt t aat t t t t at t t t at ccact gt ct t t gaaa acct aact ct t gact aagaa 120  
ct gact t t cc t gt act t gt t gt t gact ct a agt aaact t c caat t ccaca t agt ccaaag 180  
at gat gt gct gagaaat ct c t caaaggaaa aat gct aaga at acaggcag agt t at gcgg 240  
caaat t t t gc agaat t aaca caat t gcact t gt gact at g aagcac 286

<210> 243  
<211> 109  
<212> DNA  
<213> Homo sapiens

<400> 243  
at ggacagaa cggagact ag gt t ccgt aag aggggacaga t t acgggaaa gat cacgacc 60  
agccgt caac cccacccccca gaat gagcag agt cccagc ggagcacct 109

ADL\_0311WP\_Sequence\_Listing.txt

<210> 244  
 <211> 37  
 <212> DNA  
 <213> Homo sapiens

<400> 244  
 t t t g t t a c a t a t g c a a t a a a c t c a c g a c t t t a c a t t t 37

<210> 245  
 <211> 34  
 <212> DNA  
 <213> Homo sapiens

<400> 245  
 g g a a g t g g a c g c a a a g t g g a t g c g g c a g c a g a a a 34

<210> 246  
 <211> 287  
 <212> DNA  
 <213> Homo sapiens

<400> 246  
 t g g c c a t g c a t g a t g g c t t a c a c c t g t a a t t c c a a c a c t t t g g g a g t c t g a g g t g g g a g g 60  
 a t t g c t t g g g t c c a g g a g t t t a a g a c c a g c c t g g c c a a c a t g g t g a a a c c c t g c c t c t a c 120  
 a a a a a t a c a a a a t t a g g c a g g c a t g a t g g t g t g c a c c t g t g g t c c c a g c t a c t c a g g a 180  
 t g c t g a g g t g g g a g g a t c a c t t g a g c c t g g g a g a t g g a g g t t g c a g t g a g c c g t g a t c a t 240  
 g c c a t t g c a c t c c a g c c t g g g t g a c a g g g t a a g a a a c t g t c t c a a a a 287

<210> 247  
 <211> 196  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
 t g g a g t g c a t a g g t a g c a g t g c t t c t c c c c a a g g c t g g g g c g a t g g a a t c a g t t a g a c t 60  
 a t t g a g g g c a t c t g g a a g g g c a t c t g t g t c a g g g t t a g t c c t c a g g g t a t g g t g g c c a a t 120  
 g g g t t t c t t t t g g t t g a c t g t t g a c a a t g c g t t t g t t g a a t g g c a g c c t g c a c t a g g t g a 180  
 c g c t g a a g c c a c a g a a 196

<210> 248  
 <211> 189  
 <212> DNA  
 <213> Homo sapiens

<400> 248  
 t t c a t t c c c c a c a a a a c c t g a g g c a g c t c t t t t g c c c a g a g c g t t c c c t g t a g c c a c c c c 60  
 c a c c c c a c t t g c c c t t g g t t c t t t a g a a g g a g c a c a c a c a t c c c t t g a t t c c t c c c t g a t 120  
 g t g g t a a a c t g g c a c a c t c c a g g g g t c t a a a a c a t a a a a c a g t t g t g t t t a g g g a a c c t t 180  
 a a g t c a t g c 189

<210> 249  
 <211> 35  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 249

acagaggctt cttcagatca gtgcttgagt ttggg

35

&lt;210&gt; 250

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

attctgcatg attcacggac taggagtcct tggcAAAA cttAAAAac taagt gatgg

60

gtcccaagt t actcagtggc agaaacttga tt cagtaaca tgtcagcttg tgggcttgaa

120

aagctttaag tgtctctact tcttctatcc ttgtgctttc ccgggacttt acacaatccc

180

acctcccact ggacaattgt caaatcccag agagtatggg aagctgttc atctctgatc

240

accataa

247

&lt;210&gt; 251

&lt;211&gt; 282

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 251

gacggtccgc cgtgcccaag aggaacggga tgacattcaa ctgggacttg cctcaccttg

60

gcttggggga cctcgagagc ggtcccgtgg gggcagtggt actcgtggtg gtagaagtgg

120

agggcgtgtc cgggtacttg agttcatggg catctctccc gccgcctctc agcctatctg

180

caccatgtct cacacgttca gttgcagctc ttaccgtttt gaaggcgcac gtgggcaaga

240

agtcctgggc agcacaagaa agtcaatcac gttgagacag ag

282

&lt;210&gt; 252

&lt;211&gt; 226

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

gactctagcc acagcctaac caaggattat caaaggaggt ggacactcaa ggaagggcca

60

cgccaggctg cgtttcctgc aaggactcag atgttcagta ccttatgata cagggaagat

120

agttttctta caagtgttt ggtaatattt tttttcttaa gttgtacatt tgactcagct

180

gtcaaatttc tcacacttgt atatatctac acacaactaa gttaaa

226

&lt;210&gt; 253

&lt;211&gt; 188

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (135)..(144)

&lt;223&gt; n i s a, c, g, o r t

&lt;400&gt; 253

gggaacaggg aatgccgatt ttatatacat ggtacacaga gaggggtgtc acttcacaaa

60

ADL\_0311WP\_Sequence\_Listing.txt

at ctt ccagc at gtt ctt ca gaat at t aat t t at at gcga ggt gaggt t g ggaat gaaaa 120  
 gaacaggt ca gcacnnnnnn nnnncct at a acat acaaaa gaacat ggt g gact t t cagg 180  
 gagt gcaa 188

<210> 254  
 <211> 269  
 <212> DNA  
 <213> Homo sapi ens

<400> 254  
 gagat t t t t g t ggt cggt gt at t cgagaat t cct t aat g gt ccat t aag caaat aacac 60  
 cacagcagca ggagaagagt ccagt aaaca ccaaat cgct t t t caagcga c t t t at agcc 120  
 t t gcgct t ca ccccaat gct t t caagaggc t gggagcat c act t gcct t t aat aat at ct 180  
 acagggaaat t caggggaagaa gagt ct ct gg t ggaacagt t t gt gt t t gaa gcct t ggt ga 240  
 t at acat gga gagt ct ggcc t t agcacat 269

<210> 255  
 <211> 273  
 <212> DNA  
 <213> Homo sapi ens

<400> 255  
 t t cct t ct ga gt t t gct gt t ggt gcaggaa t aagggaaag gcccaaggt a t ccaagcct g 60  
 gggaagggca ggccagccag cacct ct gcc t t ct cagga caagagt agt cct t t accac 120  
 cct cact ct g cct gt cccct ct cct act ct acagcat t aa agact gt ggg accaggaccc 180  
 t aagt ct cct t t cct t ct gg gt ggggagt t ct ggggt t ct t ggt gt gt gg gagaagt t t t 240  
 at aat t gct t ccaaacagct ggg t t t aat at a 273

<210> 256  
 <211> 279  
 <212> DNA  
 <213> Homo sapi ens

<400> 256  
 t t ct ggat gt at ctt cagga gcatt agcat t ccct ggt ag gt t gaagat g ggccagt aag 60  
 ggaaacagaa ggg t caaagg t gat gccaag at t t t t gcc aaagcacct g aaagat ggag 120  
 t t gcccat ga ct aagat ggg gaagcacggg gt cagcaccg at t t gggggg aagat cagga 180  
 t t t cat t ct t ggat gt gct g agt t t gaaac at ct gagt ca t at ccaagt g aagagt t t ga 240  
 at aggccgt t ggat at at t t aggat aaaag cct gggct a 279

<210> 257  
 <211> 174  
 <212> DNA  
 <213> Homo sapi ens

<400> 257  
 accagcgcat cct cgagt t c t t t ggct ga agaaggaaga gt gcccggcc gt gcgcct ca 60  
 t caccct gga ggaggagat g accaagt aca agcccgaat c ggaggagct g acggcagaga 120

ADL\_0311WP\_Sequence\_Listing.txt

ggat cacaga gttctgccac cgcttcctgg agggcaaaat caagccccac ctga 174

<210> 258  
<211> 109  
<212> DNA  
<213> Homo sapiens

<400> 258  
cgtgctacca t cacagctga atgcaatgaa aggcggctct ctgagaggag cagggtggag 60  
atgctaaagt ggaggccccg tcccatctgct gatagatcct catctggca 109

<210> 259  
<211> 167  
<212> DNA  
<213> Homo sapiens

<400> 259  
tgatctagag gtcccccttc ggaaatagg aagactgtct ctgaagaagg aggaagtgt a 60  
gcttatggga ggctgaggag tttggagttt ctcttctgg gaagggtggga gccatggagg 120  
ctgaagacag tttgtccaact caggggcat ac aaattgatga ggaactc 167

<210> 260  
<211> 155  
<212> DNA  
<213> Homo sapiens

<400> 260  
ctgccctc agtgagactg ggacaagatg ctctgctgga cttgagcttt gcctacatgc 60  
ccccacctc cgaggccgcc tcatctctgg ctccgggtcc ccctcccttt gggctagagt 120  
ggcgacgcca gcacctgggt aaggggacatc tgcctc 155

<210> 261  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 261  
gtgagccaag ttcgaactcc tgcattccaa ccagcct 37

<210> 262  
<211> 110  
<212> DNA  
<213> Homo sapiens

<400> 262  
gatgggat aa tttgggaggc tttctcattct ggcttctatt tctatgtgag taccagcat a 60  
tagagtgttt taaaaacaga tacatgtcat ataatttatc tgcacagact 110

<210> 263  
<211> 190  
<212> DNA  
<213> Homo sapiens

<400> 263  
accaaatacc acagggttctc agttgtgagt gggagctaaa tgatgagaac tcatgaacac 60

ADL\_0311WP\_Sequence\_Listing.txt

aat gaagga acagacact a ggggt ct act t gaggggt ggaa gat gggaaga gggagaggag 120  
cagaaaaagt acct at t ggt gat gaagt ac t ct gt acaac aaaccct ga caagagt t t c 180  
cct at at aac 190

<210> 264  
<211> 291  
<212> DNA  
<213> Homo sapi ens

<400> 264  
aacagct gct t t t ggt at ca at accct gt t ggt t at t agt t t aaaat t t t agt caat gat 60  
gct t t t t ggg t ggggt gt gaa gggggaagaa aat ct t gac at gt aat gac t t aaat t gt t 120  
t cccaaat ca aat t aaat t c t gggccagt a t aagacct ac aact cacat t t cacaagt g 180  
agggcat gga t ggggggt agg ggcaggcagg gaaaggagaa aagaggacaa t cagcacccc 240  
t gaggggct g aacat agggg gcat ccaaaa cgt gct t gct gt gggaagaa t 291

<210> 265  
<211> 263  
<212> DNA  
<213> Homo sapi ens

<400> 265  
cat t t t g gat gacgacacga t cat aaccac t ct ggagaac ct gaagagag aggct gcaga 60  
ggc caccagg aaagt t gagg agacggacat t gt cat gcag gaggt ggaga ccgt gt ccca 120  
gcagt acct c ccgt ct cca ccgcct gcag cagcat ct ac t t caccat gg agt ccct caa 180  
gcagat acac t t ct t gt acc agt act ccct ccagt t t t t c ct ggacat t t at cacaacgt 240  
cct at acgag aaccgaacc t ga 263

<210> 266  
<211> 144  
<212> DNA  
<213> Homo sapi ens

<400> 266  
at gacat aca gt gcat ggct cacaat ccca ggagat gagg gcagcacagc t gcagagcaa 60  
cacagagt gg ggagaacat c caggat gcac at t caaccag caggt gggga gcaagacaga 120  
cagggacct g t gggccaaag cgt t 144

<210> 267  
<211> 248  
<212> DNA  
<213> Homo sapi ens

<400> 267  
t aggct t agc t t gat t t ct g ggccact gt ct gt gt t ct t aagat gccaa cct gt t gct t 60  
t t t t t t t t t t t t ccccca t t t aaaagga t agt acct ac t ccct ct aac cacct caccc 120  
cat t ct t gaa t gacat t t t a t cct t cgga agaacaaggc t gt gat gt ag t gact at t gt 180  
ct gt gt ct cc t gt gt gt gt c t gt t ct t gt c acaaat gt at t t ggggacgt t ggat gcat t 240

cattttct 248

<210> 268  
 <211> 45  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
 gccccactgt cactaactgt aaactcaggc tcaggcttca actgc 45

<210> 269  
 <211> 265  
 <212> DNA  
 <213> Homo sapiens

<400> 269  
 aagattcttc ttgtat atg aggatggcag ggtgggcgat gccaacatt a atactcagga 60  
 cccaagata cagaaggaaa tcatgcgtgt gatcggaact caggtttaca caaactgagg 120  
 gggccccagc cctcgtacca cccctgttac cccaggatcc atctgccctc ataaaagtgt 180  
 tcaggtagag cagctgaggc tgcctgagg aatcaagggg ccattaccaa ggggcaggaa 240  
 aaggatatgt aagaggtggc cttca 265

<210> 270  
 <211> 33  
 <212> DNA  
 <213> Homo sapiens

<400> 270  
 ttgcagcgag tcaggatcgc agcactacac tcc 33

<210> 271  
 <211> 234  
 <212> DNA  
 <213> Homo sapiens

<400> 271  
 ttcacaggaa gt aggt aaac accgaaattt agtcagtgtc attattagag ttgtgctttc 60  
 ataaaaagaa tctctcaagt gtgacaaggc taaattagaa agaagagact ggaggt agag 120  
 gccagttagg agatccttgt aataatccac agttgatgga atgaggatct atagt agcca 180  
 ggctggaggt aacaaagagg gacaggaggg caggagtact ctactttaaa gt ag 234

<210> 272  
 <211> 61  
 <212> DNA  
 <213> Homo sapiens

<400> 272  
 agttgttaag tgtatcagat gtgttgggca tgtgaatctc caagtgcctg tgtaataaat 60  
 a 61

<210> 273  
 <211> 157  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 273

gt ggt t gt ca t gt gat ggggt cccct ccagg t t act aaagg gt gcat gt cc cct gct t gaa 60

cact gaaggg caggt ggt gg gccat ggcca t ggt cccag ct gaggagca ggt gt ccct g 120

agaacccaaa ct t cccagag agt at gt gag aaccaac 157

&lt;210&gt; 274

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 274

ggagacat cg at ct ct t t t g caaat t ccct cacagcct ca t t aggggt ct t cat aagt gaa 60

gggggt cgat g t agacct t ag t accat gt cc gat gagat ac t gt ccgt gt t t gt ccgaat a 120

t t ct gct t ct ct cccat t gc t ct gct t cct gaggcagaga act gcgacca caat gaccac 180

caggaccagg accacacca cgact gccgt gcccgcaat c agggccagct gct cccgcca 240

gccct cgct c t cat ccagt t ggggt ccggct gt gat gt t cc t ggccgaagg gcc 293

&lt;210&gt; 275

&lt;211&gt; 253

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 275

ggagt t t gt g act agat ggg caat at agt a agat gt cat c t t t t aaaaat gaaaaaat t a 60

gct ggccact gt ggcacacg cct gt agt cc cagct act t g ggaagct gag gt aggaggat 120

t gct t gagcc caggagt t ca aggct gcagt gagct at gat t gt gct t at g aat agccact 180

gcact ccagt ct gggcaat a gt gagt cggt caaat t ccat t t cccct cc gcccct acc 240

t ct t caaat g t t t 253

&lt;210&gt; 276

&lt;211&gt; 195

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 276

act gcat cag gt ct cagt gt ccct at ct gt aagat caaca agaaacacgg t t aagggagg 60

t cgt cact gg ggt gggagaa gaggggct gg t agaccgaag cct t gt gcat aaggat t t t t 120

t cccaggaaa agat agact t t at aaacagt gggagcccat gaacaaacat at aaaagt ag 180

caacagat aa t gacc 195

&lt;210&gt; 277

&lt;211&gt; 195

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 277

t at t gt aact ct t ccgccct t t t caggcgc agacaacaga acaaagt at a gaggaacaac 60

aaaat at at a at t agccct c cct cccccc at aaagcaat t cacggat ac agaat acat t 120

ADL\_0311WP\_Sequence\_Listing.txt

ctcttcacag taaacct aag aacacttgt aacaattgcc acagcgcgca t gct aact aa 180  
agtaacctct tttga 195

<210> 278  
<211> 297  
<212> DNA  
<213> Homo sapiens

<400> 278  
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cctcaggacc ttaggacata atcactccct gcttctatct tcagtatctc ctcat t acaa 120  
ataaagcatt t gctgcagct cat ttaactc ttgtgtccac agtgagtctc ttccattact 180  
taatcacact taattctctg tcctgactcc tgtccccagc cttttctttc actttgcccg 240  
tctgtcaggc tctcatgctt ctccatttgg caacttcagg aaggtacgcg agctccc 297

<210> 279  
<211> 256  
<212> DNA  
<213> Homo sapiens

<400> 279  
gccagtcacc ctgcggatcg agagaggggg tagagcttct t tcaaatggc agttttactt 60  
caaatggcag atttcacaag agttggttat tttttacaat ggtttagggt gttaagtctc 120  
ctttgtatgt aaggtagttt tttcaacatc taaaattttt gttttagcct tcaaaaccaa 180  
cttaccaacc tcagtcagc tgggaaggca gcgttgattat tggtagtttg tcaagaatat 240  
atggacctgg aaacac 256

<210> 280  
<211> 223  
<212> DNA  
<213> Homo sapiens

<400> 280  
cactgctcag ggttggaggc tcagtcacct t gccctgtct gttccagctc tggagctaac 60  
tcagggatcc ctgatcaggg ttacataggt ttggtaaaat gagtgtgga aattaaacttt 120  
ctcccagt ag tcttaggtca tgctcagtga acttaaaact t atccagat a tggttttcct 180  
tcagcctttc tattcccttt ctagccagt g aaagaccgc tgc 223

<210> 281  
<211> 140  
<212> DNA  
<213> Homo sapiens

<400> 281  
cgagagtata tcagttaag ggt aagaaat gt agacccca t attttaatt cagt agcacc 60  
agttcaaatc cagttattca gaatt aacaa agcaactgtt gctcaaaaaa atgccaat aa 120  
actcccagc caactgagat 140

## ADL\_0311WP\_Sequence\_Listing.txt

<210> 282  
 <211> 112  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 282  
 accaaggagc t ggtcagacg gccctttcta atcctacatg ttgagcttat gtaaaaaatg 60  
 ttgtttcctc ctgtttttgg ttcctttctt acccaciaaac cattactact tg 112  
  
 <210> 283  
 <211> 34  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 283  
 caacagagt g agacttaatc ttgaaaaat a aata 34  
  
 <210> 284  
 <211> 166  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 284  
 agtagagggc cctcaaccca cacactggct gaaactgcc ccaactgcc cgatgaaccc 60  
 aactgctgtt tatgccccca ttttcttttt ttgtatcta caccacacg attccaatg 120  
 ttggatattt ctacatgaat aaagcaagga tcagtgcctc ttatgt 166  
  
 <210> 285  
 <211> 288  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (78)..(157)  
 <223> nisa, c, g, or t  
  
 <400> 285  
 aggcaaaac aggagatgag gaaatgttaa aggataaagg aaagccagag agtgagggag 60  
 aggcaaaaga aggaaagnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnntga aggagagcca gggagt gaaa 180  
 caagggtgc aggaaagcgc ccagctgagg atgatgtacc caggaaagcc aaaagaaaaa 240  
 ct aat aagg gctggctcat tacctcaagg agtat aaga ggccat ac 288  
  
 <210> 286  
 <211> 276  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 286  
 tgtgggtga cagttttaca tttacttttt ctcttaatg cagctggatc taagt aaat 60  
 gt ttt gaagt ttatcagaaa ct aat gt ac tttt aaacg tat aggg ca ggggt tggggg 120  
 aaaaat acag gtat agt aag taagaaaagt gacccat gaa gaaagcat cg tgaggt tgt a 180

ADL\_0311WP\_Sequence\_Listing.txt

tgttggttga ctgtgattaa aatgcggggc tgggtgaagt tgt aagt ggt ggctgattgc 240  
cgtgtactat gtacatgatt gt tgggatgg ctgtcc 276

<210> 287  
<211> 183  
<212> DNA  
<213> Homo sapiens

<400> 287  
gaaaacctat aacatgatga gt aagagttc t at ggt agag aggt aggaga ggaaaggt ga 60  
aaactgccac aagccaaatg agactgcagc aaagt at gta aggagcctgt tctcaggtcc 120  
acccacatcc agctatcacc ctctctgacc gccttttccc atgagcctga aagggtcaca 180  
gac 183

<210> 288  
<211> 295  
<212> DNA  
<213> Homo sapiens

<400> 288  
gacgcacaac ct tcaacact aattgccctt tactaagccg accagggcta gacactaagc 60  
cagaaaagcc ttttccagag tttcctcttc cgcacaaaag ctttcttct gt cactccac 120  
ccaaccaccc agctcctccc ttaagtgttt gaaagataat tctaaaagtc tctcccccg 180  
aaccgctgcg tttcttaagg ccacaccatt ttaaaaat ac tgtattgctt ttgccaggct 240  
gttgggacct ct tccatctc atttctatct aagagt ggtt ggtacacacg aggac 295

<210> 289  
<211> 285  
<212> DNA  
<213> Homo sapiens

<400> 289  
aaagcagatg ggtgtgttca gacaagatct ggaagctgtg gcatggcaga caaagggaga 60  
tgggacctt ttggcactgg aggaagaggc ttgaatcttc ttggagcact aaaagttcca 120  
aaagacctaa gcagaaaatg ct tccgaaga ggaggatctg tatggcaaga tgactgtaat 180  
caggctcata aaagt aagac ct t acat aaa tacaagt gag ggggaagaca tttcatgtag 240  
gaggaatggc tcaagcaaaa ataccaaggc gggaaattgc gtggt 285

<210> 290  
<211> 129  
<212> DNA  
<213> Homo sapiens

<400> 290  
agaagttttg agaagcagtt ttgtttgggt caaggggtac tttcaaatt a cacttatgag 60  
tcagtatcta taaaaagttt cagaagtacc tacaatttag ccctctacat ccaagcagta 120  
gctttgcag 129

<210> 291

## ADL\_0311WP\_Sequence\_Listing.txt

<211> 70  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 291  
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 tttattt aaa 70  
  
 <210> 292  
 <211> 135  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 292  
 gcagat gcag gaaacacct a gagcagcccc agagt cacgg ggct gagggg gcgggagct g 60  
 cccct gt cat agggaggggg attcccagcg tctgt agtgc tt cct gttt g ct gaataaag 120  
 gtctctttct cacac 135  
  
 <210> 293  
 <211> 156  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 293  
 cagaaat gtt agt gccgt gc tctaaccaag taagcttagt gttccccaca gt gatctgt a 60  
 tctggcctga gtctctcaa gcagcaaccc ccaactgtcca gcatgtggaa ggt agatcct 120  
 tatgacaaca ccagacccat agttaccagg aaagaa 156  
  
 <210> 294  
 <211> 175  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 294  
 gtgttt aagg gcat t t caca gatgggaaat aaggtgcaga gggct agaga gatgggct ca 60  
 aggctgt ggt gccagt gaca ctggct tccc ctgtgt tgtc cttt gctctt gaacatcacg 120  
 ccacgcagca gcagaacaaa gat aaagaac caattccaaa accaggcgt g gtggc 175  
  
 <210> 295  
 <211> 112  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 295  
 ggccgagaag atgctgggca cccaccagc acccccatct accaacacca gcggctgggg 60  
 gcggggggcgg accttgtgag gctcagttga cccgttactt gcaacctgaa aa 112  
  
 <210> 296  
 <211> 149  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> mi sc\_feat ure

ADL\_0311WP\_Sequence\_Listing.txt

<222> (46)..(86)

<223> n i s a, c, g, or t

<400> 296

caagaat ct g gcat t t ct ct t cagt t at ct t at at gt aca t at aannnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnnnnnnn nnnnnnggag at gaaggt ct cagt ct ct t a cccact gcac 120

t ct agcccag gcggt aagag agact ccat 149

<210> 297

<211> 239

<212> DNA

<213> Homo sapi ens

<400> 297

cct ct acgcc agagaagga at ggagaggt caggct ggct agagagt ggg gt t gagt cgt 60

ccat gccct t gaat gccagg at gagggct a aagagt caaa t ggaat ggg gact t cat at 120

gcagaagt t t t tacaagaga agagaact ca gt t gggccaa gagaagt ggg gt cgt cat gt 180

gggt aat cac gt aacagt ga t cgt t cagt c at gcggaat g ct t t caaggt gt t ggacac 239

<210> 298

<211> 278

<212> DNA

<213> Homo sapi ens

<400> 298

cct ct acgag gt gt gct at t ct cat cct ca t ct t at aggc aagt t aact g aggt at aagg 60

aggt t ggt t a t gt aact t ga ccaaagt cac acaat aaggg act gggagat ct gggat t t g 120

agccct ggca gat ggact cc at ccaaagt c ct cact at cc t agcacct ct ct at cccct c 180

cct t t cct ct ct cct acct t ct t ct gt gct gct t t caaac agacagt t at ct ct accct t 240

aaaaacacag ct gt gct gac t act ct gct t agat gccc 278

<210> 299

<211> 145

<212> DNA

<213> Homo sapi ens

<220>

<221> mi sc\_feat ure

<222> (79)..(112)

<223> n i s a, c, g, or t

<400> 299

cct ct gggac aagt aagt ca at gt gggcag t t cagt cgt c t ggg t t t t t cccct t t t ct 60

gt t cat t t ca t ct ggct cnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnt gct t ccc 120

ct cact gccc aggt cgat ca agt gg 145

<210> 300

<211> 42

<212> DNA

<213> Homo sapi ens

<400> 300

t ggt caagaa ggact at gac gccct t c gga agaggt acag t g 42

<210> 301  
 <211> 256  
 <212> DNA  
 <213> Homo sapi ens

<400> 301  
 agaat agcaa ct ggct cagt cct t t aggt g t ct acact aa t at caaagga acaggccagg 60  
 cccaaggaga gagagggaat at gt t t ct gt gcct gat cct t t ct ct agat t t t at ct cag 120  
 t t gt at gaca t t gaagcacc t gact gagca at t gagcat g at gt gt t ct c ct gaccat cc 180  
 t t ct aaaacc at t t t ccacc agt t t ct acc t t ct gat ggc gct t t agt ca cct gcact t a 240  
 caaacaggt g cccaaa 256

<210> 302  
 <211> 274  
 <212> DNA  
 <213> Homo sapi ens

<400> 302  
 ggct ct gat g at ggaccct c agt gat ggat gaaacaagca at gat gcct t t gat t ct t t a 60  
 gaaaggaagt gt at ggaaaa agaaaaat gt aaaaaaccct ct agt t t aaa acct gaaaag 120  
 at t cct t cca agagcct aaa gt cagcccgt cccat t gccc ct gccat ccc cccacagcaa 180  
 at ct acacct t ccagacagc cacct t caca gcagcgagcc caggct ct t c ct caggct t g 240  
 accgccacag t ggcaacaagc cat gcccaac agt c 274

<210> 303  
 <211> 78  
 <212> DNA  
 <213> Homo sapi ens

<400> 303  
 t t t t cat gca gat t agt t ag aat t cact gc cagggt t t ct t ct gccaccca aaat gat cca 60  
 gt ct ggaat a acat t t t g 78

<210> 304  
 <211> 137  
 <212> DNA  
 <213> Homo sapi ens

<400> 304  
 gt aggct agg gat cat gggg gaat agt t ag t aat gacagg gat agt t gaa ct t aaaaaaa 60  
 aagt t t gt ga ggct gacaaa gat gaaacgg acacat t t cc t gat ct t gga gggt t cat ag 120  
 ggt agaagat ggt agat 137

<210> 305  
 <211> 161  
 <212> DNA  
 <213> Homo sapi ens

<400> 305  
 gat ggt ggga t at t t gt gt c t gt gt t ct t a t aat at att a t t at t ct t cc t t ggt t ct ag 60

## ADL\_0311WP\_Sequence\_Listing.txt

aaaaat agat aaat at at t t t t t caggaa at agt gt ggt g t t t ccagt t t gat gt t gct 120  
gggt ggt t ga gt gagt gaat t t t cat gt gg ct gggt gggt t 161

<210> 306  
<211> 255  
<212> DNA  
<213> Homo sapi ens

<400> 306  
gaaacagcat gggaccgt gt gat t ggggt cc aggct gggct gt caggggaag cgccct ggt g 60  
t ct ccgact c at caat t ct c ggggt ct t t t t t aaaagcca ggct ccccaa agcact ct t t 120  
gt ct cgcaat t t t gaggagg t t gt t ccgac ct ggaagcgt t aaact gct g cat gt cat ct 180  
ggcgt cagct gt gaggct gc gct ct gcgt g t t gt gcgt t t gcaaaat gt a t t ggcgt gac 240  
t gt aaacaca t cgt t 255

<210> 307  
<211> 289  
<212> DNA  
<213> Homo sapi ens

<400> 307  
gt caagct ca gt t gagggt t aat gat gagg caggct gat g cgggt t ct t t gcccagt ccc 60  
aggggt t ccaa gaagcct t cc t gggagaggg ggcct gagt t gaat ggt gca agat gaacaa 120  
gaaat ggcaa gat agagaaa ggt ggggagg gct t cccagg cagaagagag agcat ggct a 180  
aagggct agg ggcat gaagc agcaggggac cccagccat gt agt at cac t ggaggat ga 240  
gaat aagggg gagaaggagg gagggagaga aggt at act t ct gagggca 289

<210> 308  
<211> 181  
<212> DNA  
<213> Homo sapi ens

<400> 308  
agt t cagggc t at agt gcgc t at gt t gat c t ggt gt t cat gct aagt t cc gcat caat at 60  
ggg gact t ct agggagt ggg ggaccaccag gt t gcct aag gaggggt gaa cct gcct acg 120  
t t ggaaat ag agct ggt caa aact cct gt g ct cat cagt a gt agaat agc acct gt gaat 180  
a 181

<210> 309  
<211> 253  
<212> DNA  
<213> Homo sapi ens

<400> 309  
gacagct t gg aaggaaggat t gaccat ggg t t gat t ccat ggaggt agag aagcaagaga 60  
gacct gat ga t t acaat gat ggct aagt gt agt at gccca t t aggat t ga at t gaat t ag 120  
gggaaat t gt gt gaagt gt t t ggaaggaag caat at t gt g t gat t agct c caaagct ggc 180  
cact ggt aga agt t gt t t ca at ggaagaac aaggat ggaa t t gagt gggc cagagagccc 240

t agat t aat g ggt 253

<210> 310  
 <211> 159  
 <212> DNA  
 <213> Homo sapiens

<400> 310  
 t a t t c a g c g a a a c t t a c c t g a a g g g g t t g c c a t g g a a g t a a c a a g a c a c a a t t a g a a c a 60  
 g t t a c c a g a a c a c a t c a a g g a g c c a a t c t g g g a a a c a c t a t c a g a a g a a a a g a a g a a a 120  
 g c t a g t c a t a a a g c c t c a g g g a g g c c a t t t t t g c c t a a a 159

<210> 311  
 <211> 269  
 <212> DNA  
 <213> Homo sapiens

<400> 311  
 c a a a t g c g a g a t c t t c a g t t g c a g t g t g a a g c c a a t g t c c g c g a a c t g c a t c a g c t g c a g 60  
 a a t g a a a a a t g c c a c t t g t t g g t t g a g c a t g a g a c t c a g a a a c t g a a g g a g t t a g a t g a g 120  
 g a a c a t a g c c a a g a a t t a a a g g a g t g g a g a g a g a a a t t g a g a c c t a g g a g a a a g g c a c t g 180  
 g a a g a a g a g t t t g c c a g g a a a c t a c a g g a a c a g g a a g t a t t a t a t a a a a t g a c t g g g g a g 240  
 t c t g a a t g c c t t a a c a c a t c a a c c c c g g a 269

<210> 312  
 <211> 234  
 <212> DNA  
 <213> Homo sapiens

<400> 312  
 t t t c a g a a a c t g t c a a a t g t a c c a t a t t t g t a t t a a g a g t t g t t g g g a a t t t t t g t a c a a 60  
 t g a a t t t a c a t t t a t t t a t g g t g a c a t a t t t a c g c t t g t g a t c a a a t a a t g a t g t t a a a t 120  
 t c t t a a a t c a t a t t t g c t a t g c a g c t g a a g a t g a t a t t t t g a t t t g t a t t t t g g g g g t a c 180  
 c t g t g t t g a g t t g a t a a a c a t t t c c a t c t t c a t t a a a a c t g c t t c c a a a c t a a a 234

<210> 313  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 t a a a g c a t g g a t c t c g c t t t g g t t g t a a a a a a 32

<210> 314  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<400> 314  
 a t g g t g g g g g t c t c t c a c c t t c t t g a c c c t c t c t c c a t c a t t c a g c t g c c a g c c c a g g c t 60  
 t c a c a c c c a a g c t g g c t c a g c a g c c g a g c c t g g c a c c g a g g g t c c c t g c a g g c t c c c t g g 120

ADL\_0311WP\_Sequence\_Listing.txt

gcaggagag ggccaaggac aat tgggagg gcagcaggca gcccgcagat ggt ggccat g 180  
t ggcacgct g ct gagacgac act accaat a aaccaaact g c 221

<210> 315  
<211> 238  
<212> DNA  
<213> Homo sapi ens

<400> 315  
ct gcccgt ct gt aagt t cca ggt ggt gat t ccgaaat cct aagcct gcct cgcacct gct 60  
gagccgcact gct gcccct g gcct caccgg cct caggaga cggt ggggcc gct gcat t t c 120  
ggggt ggt ct t gggaat ccc aggccct agg ggt cacat t t gct caggaag t ggggt at caa 180  
at t gaggt gg ggggt gt caga ggaggcaaag ggggt cccagc t gcggt cagg act gt ggt 238

<210> 316  
<211> 36  
<212> DNA  
<213> Homo sapi ens

<400> 316  
cct ggggt gac ggaat aagac t cggt ct cca aaagaa 36

<210> 317  
<211> 87  
<212> DNA  
<213> Homo sapi ens

<400> 317  
aaggct gct a gggat gt tag acct cggcca ggaccaccca cat t gct t cc t aat acccac 60  
cct t cct cac gacct cat t t ct gggca 87

<210> 318  
<211> 59  
<212> DNA  
<213> Homo sapi ens

<400> 318  
t acct gt t t a t ct gt aact g t t at ccaaac aaat t aaat a ct gt ggat gc ct t t aaaaa 59

<210> 319  
<211> 299  
<212> DNA  
<213> Homo sapi ens

<400> 319  
gacagt ggat aact t t caaa gaggcac t t t gt gt ggccc at gaact t t g gt t ggagaac 60  
aat t cct cca gat gt cact g caaaaaaaca gaat t aaaga aact gat aca at aaggt gcc 120  
ct gt cat ggc t ggt ggat t g t t t t ct act g acaaaagt t a ct t t t t gaa ct t ggaacat 180  
acgaccct gg cct t gat gt t t ggggt gggg aaaat at gga gct ct cat t c aaggt gt gga 240  
t gt gt ggt gg t gaaat t gag at cat t ccct gct cccgagt gggccat at a t t cagaaat 299

<210> 320  
<211> 260

ADL\_0311WP\_Sequence\_Listing.txt

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<212> DNA
<213> Homo sapiens

<400> 320
at gagt at ct cagct cct t c aaggt ggcac agt acgt cgt gcggaagaa gacaagat t g 60
aggaaat t ga gcgagagat c at caagcagg aggagaat gt ggaccct gac t act gggaga 120
agct gct gag gcat cact at gagcaacagc aggaagacct agcccggaat ct aggcaagg 180
gcaagcgggt t cgcaagcaa gt t aact aca at gat gct gc t caggaagac caagacaacc 240
agt cagagt a ct cggg gggt 260

<210> 321
<211> 131
<212> DNA
<213> Homo sapiens

<400> 321
ct at ggccgg at aact aagg at gt ggt gct ccaat gggga gaaat gcca cgt ct gt ggc 60
ct acat t cat t ccaat caga t aat gggct g gggcgagaaa gct at t gaga t ccggt cagt 120
ggaaacagga c 131

<210> 322
<211> 137
<212> DNA
<213> Homo sapiens

<400> 322
ccaccat t gc gggg ccccca ggaagccagg t gaccccagg t gggaggct g t gt gt ggagg 60
ccat cct gga aggaagt t t a gacct gcca ggt gt ggagc gaggggcaca ggggcat cct 120
aacct cagaa act gaaa 137

<210> 323
<211> 277
<212> DNA
<213> Homo sapiens

<400> 323
agcaaagt gt at t ct ccat c t ggcct caga gcagat gcca agcct aat t g ggccaccaga 60
t ccgt gaagg t ggt t t gct g t t t t ccagcc agct caat aa ct t gt t t ggc agaat cagga 120
at t aggacct gat caat caa at ggat caca ccat t agt t g gt cacaat at cct t t gt t gt 180
t caccat t t t gat t ccat t t act gt t at ac t gt caccgt c acat cct at c t caat t gt at 240
t t cct t ccag cgt ct caaga ct gct act cc cat aat a 277

<210> 324
<211> 271
<212> DNA
<213> Homo sapiens

<400> 324
gct t gcccc gaact tagt c t c t t t gcccc gcct caccct t cct ggt gct cat cagact c 60
t t gccacccc t ggct cccac t ccct gct t g cct ct ggt gg agct gcacag agct ct ggga 120

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ADL\_0311WP\_Sequence\_Listing.txt

agaggccctc tt cctccccg cactggggcg atgggcgcac ct cagactta cccactgctg 180  
ctgccaccac caacccttg atccctcagt cctccacac agcttctgtc caccacaggt 240  
ttccctcacc ccacctttgc taagtcttcc t 271

<210> 325  
<211> 225  
<212> DNA  
<213> Homo sapiens

<400> 325  
gccctgctgc gaagtggagt ccgaggtcat gatgagt gac tatgagagcg gggacgacgg 60  
tcacttcgaa gaggtgacga tcccggccct ggattccag cagcacacgg aagtctgact 120  
ctcaactccc cccaaagtgc ctgactttag tgaacctaga ggtgatgtgc gtcacccgcg 180  
ctgttctttg cagcagtgct tccaagcttt ttgggtgag ccgaa 225

<210> 326  
<211> 68  
<212> DNA  
<213> Homo sapiens

<400> 326  
agaagcaaca cgatgatggg cccccagtt tgaatttcag acagtggagg agggaatatt 60  
gctaggag 68

<210> 327  
<211> 272  
<212> DNA  
<213> Homo sapiens

<400> 327  
tactctcagc agtcagaggc ttgcttgctc tgtgcagatt tttaattttc tttttggcc 60  
ctaggctggt tgggacctct acagcttcat tctttcacca ttaaatagt ggccttttca 120  
gtattttccc tcttcccctt tataaattat gctaaagcca caaagcacat ttttgggat 180  
catagaaggt tggggttcca gaaaggcatc tgtgtgatgg ttccattgat gtgggatttc 240  
cctacttgct gtattctcag tttctaat aa aa 272

<210> 328  
<211> 285  
<212> DNA  
<213> Homo sapiens

<400> 328  
aaggactgtc caagagccag ccagttcagg gctcaggcct caccattgc ccactcctgg 60  
ggagaccatc acctggctca tcgtttccac caagagt gcc ccacaggagt gccccacaga 120  
cccgtggac cagcctgctg cgggtcctgg ccaggggtct ggctaaccgt gagggctgac 180  
tctgaactgt ctctcagctc ccagaaagtg ttcaagcctg ttgtgttccc aaatctgatt 240  
cctcctattg tcttgtaat caaactctaa gtgaaaactt cccat 285

<210> 329

## ADL\_0311WP\_Sequence\_Listing.txt

<211> 231  
 <212> DNA  
 <213> Homo sapiens

<400> 329  
 gaagggt cat a acagt t t caa acaat agcca gggaaggt t ag agt cacct ag agacat cct t 60  
 aacacgt gcc cct gagct ac t t t t cagaaa cccagacccc caccaa at gg at t cacacag 120  
 acgt cagat a aggggggaaca ccagggact a aact ct gacc t ccat t ct t t gct ct cagt t 180  
 t ct t cct gag gggcct ggcc agacct t aat gt t cct t t ct gcggacccca a 231

<210> 330  
 <211> 273  
 <212> DNA  
 <213> Homo sapiens

<400> 330  
 cacct gcact ct agt gaccc t ggggt gccgc cagaccct t c t ct t ct acaa agaccccagc 60  
 aggagt ggga ggggt ct gcaa t ggcat cgcc ct gt cct gcc t t ggccagaa gcct ggagct 120  
 t t ggt t t gag gaggt agaga t at gt gt at c cat aggaaga gat ct gt cag aacaggcagc 180  
 t gt t gagct c ggggt gt ct t cct caaggca t gt ggct cag cagcaagaaa ggcaagt t gc 240  
 t cct gct ggg gccct ggact ct gcct t agc t cc 273

<210> 331  
 <211> 133  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 t ct ct ccagc ct ct ct t agg aggggt aat g gt ggagt t gg cat ct t gt aa ct ct cct t t c 60  
 t cct t t ct t c ccct t t ct ct gcccgcct t t cccat cct gc t gt agact t c t t gat t gt ca 120  
 gt ct gt gt ca cat 133

<210> 332  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 332  
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 t cct ggggcc t cgcacccca cagcccagat ccct t ccccg cggaagggac t cgt ggct gt 120  
 ggggt agagac gcgcgct t gg cgcggccagc cct gcaggca ggagct gage ggcgcagggga 180  
 cacgggcagc t gggaggggc gcct ggt gat t t act cact t ccct cct agc cagagaagt g 240  
 cagcaat t cc aaacagt t ct cat aggagcg t ccct gacaa ct t cat gt t a t a 292

<210> 333  
 <211> 211  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 gt accacaaa cacact caac t t gt ct at ga at t agagaac aagat act gc t gct gct t ct 60

ADL\_0311WP\_Sequence\_Listing.txt

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ttttgacttt t gaaatatac aatgttttgt aggctctgcc cttcaatgtg aaagcaggac | 120 |
| attaaatttg aaattatttg acaattaaat gttaggacc atctaacttc aactgcaaaa   | 180 |
| ctaaacagat ctaccttgct cttccttcaa a                                 | 211 |

<210> 334  
 <211> 142  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 334                                                          |     |
| ggttcatttt agtttcagat agatggcttc accaaagaac tcttgaaaga atactgatt a | 60  |
| gggaggggca gggaagtagg agcttatggg atattataag gctgggaaaa atctatgat g | 120 |
| caaacccttt ccacatagta ct                                           | 142 |

<210> 335  
 <211> 208  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (56)..(56)  
 <223> n i s a, c, g, o r t

<220>  
 <221> misc\_feature  
 <222> (65)..(65)  
 <223> n i s a, c, g, o r t

<220>  
 <221> misc\_feature  
 <222> (114)..(114)  
 <223> n i s a, c, g, o r t

<220>  
 <221> misc\_feature  
 <222> (142)..(142)  
 <223> n i s a, c, g, o r t

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 335                                                         |     |
| actcattctt aacctaatca cctaaaataa ttcttatcat ctattcttct tcaggnaaaa | 60  |
| atggngccct gggtgtatt ttaacgactt gccatccttc ctgttttgag agtntcttg   | 120 |
| ttaactgggg gcataccttc gngacccggg cctaccttcc tcattcagac ctgtgctgtt | 180 |
| cattgctgta ttccagtc cttaaaaa                                      | 208 |

<210> 336  
 <211> 227  
 <212> DNA  
 <213> Homo sapiens

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 336                                                          |     |
| atctctgaca gatgtgtaaa ccaagttacc agcatgggtg ggaatcgtag ttccaagtca  | 60  |
| tataatacca gacattcaag aaaactagt g ccctgttaac tgggggaagc aaatttatat | 120 |
| cccttttgga gaaagtcacc ttattctgtg tatcagaaat ctctttcaaa taacctttca  | 180 |

ADL\_0311WP\_Sequence\_Listing.txt

gaact at aga gcat cat aca aagat gacca agcat acaag aaaacaa 227

<210> 337  
<211> 101  
<212> DNA  
<213> Homo sapiens

<400> 337  
aacat caaag ct ggat t aga acat ct gcc a ccagct gaac aggccaaagg cagact acag 60  
ct ggt t ct t g aagct gct gc aaaagct gat gaagcat t ga a 101

<210> 338  
<211> 212  
<212> DNA  
<213> Homo sapiens

<400> 338  
agcct t agca aaaat gcct c ct caccact c cccaggagaa t t t t t at aaa aagcat aat c 60  
act gat t cct t cact gacat aat gt aggaa gcct ct gagg agaaaaacaa agggagaaac 120  
at agagaacg gt t gct act g gcagaagcat aagat c t t g t acaat at t g ct ggccct gg 180  
t t cacct gt t t act gt t at c acaat aat gc t a 212

<210> 339  
<211> 235  
<212> DNA  
<213> Homo sapiens

<400> 339  
acagagt cat t t gagct t t c t cccct cccg ct agt at ct t t acaggagca gggaagagca 60  
gt agaggat g t at aat t t t g ggcgaagt t a aat t acaat t t at t t gaggt t at t cct aaa 120  
cct at t t at t t ggt gt t t t g gaggagat ca cact aaga gaacgt t gat t gcct cggct 180  
at t gt gct gg ct ggacact t t ggt cact t t t gaagcat gt t aat aaat gt cact g 235

<210> 340  
<211> 271  
<212> DNA  
<213> Homo sapiens

<400> 340  
t ccaaacacc ggcagaaaac ggagagt gct t ggggt ggt gg gt gct ggagg at t t t ccagt 60  
t ct gacacac gt at t t at at t t ggaaagag accagcaccg agct cggcac ct ccccggcc 120  
t ct ct ct t cc cagct gcaga t gccacacct gct cct t ct t gct t t ccccg ggggaggaag 180  
ggggt t gt gg t cggggagct ggggt acagg t t t ggggagg gggaagagaa at t t t t at t t 240  
t t gaaccct gt gt ccct t t t gcat aagat t 271

<210> 341  
<211> 270  
<212> DNA  
<213> Homo sapiens

<400> 341

ADL\_0311WP\_Sequence\_Listing.txt

t gaggagcgg gaggggttccg ccactccagt ttctcctct gcttctttgc ctccctcaga 60  
 tagaaaacag cccccactcc agtccactcc tgaccctct cctcaaggga aggccttggg 120  
 tggccccctc tcttctcct agctctggag gtgctgctct agggcaggga attatggag 180  
 aagtgggggc agcccaggcg gt t t c a c g c c c c a c a c t t t g t a c a g a c c g a g a g g c c a g t t 240  
 gatctgctct gt t t t a t a c t a g t g a c a a t a 270

<210> 342  
 <211> 207  
 <212> DNA  
 <213> Homo sapiens

<400> 342  
 aaagactcat cataagggtc ct t c c t c t t t t c t a t c c t c c c t c c a t a t t c a g t t g c t a a g 60  
 t c t c a a c t a c t t t g c t c c c a t c a a g a t t c t c t t a c t a t t t c t t c t a t c c a g a c c t t c c t 120  
 c t t t a t t c c t a t t g t c a t t g t c t t a t t t t a g g t t c t c a t c a t c t t t c a c t a a g a t a a c t a 180  
 c a a c a g c t t c g t g a c c a g c g t a g g c a a 207

<210> 343  
 <211> 189  
 <212> DNA  
 <213> Homo sapiens

<400> 343  
 gctcaaatag ctataactgt accaaagaca t g g a a g a a a c c a a a a g a t c g g a c c c g a a c c 60  
 a c t g a a g a g a t g t t a g a g g c a g a a t t g g a g c t t a a a g c t g a a g a g g a g c t t t c c a t t g a c 120  
 a a a g t a c t t g a a t c t g a a c a a g a t a a a a t g a g c c a g g g g t t t c a t c c t g a a a g a g a c c c c 180  
 t c t g a c c t a 189

<210> 344  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 344  
 tgcgaatctt ctgcagctcc atcagcatcc atgtatcttg cttgtcatttt tctctgttgg 60  
 t t a c a a t t a c t t t a t t a t g g t t g a c a t c t t g g c a g g t t c c a t g a t g a g t g a t t t c a g t a g 120  
 t g g t c a c t g t c t g g t g c t g g g g a t a g c c a g g g a g c t g a a t g a c c a g g g t c t g g t a a t g c t 180  
 t c t g g g c a t c g g t g a a c t g a g a c t g t a t t t t c c g c t t g t c a t c a t c t c c a a a c a t c t c t a 240  
 a g c c t t g g c t a t t t c t g a t g a a c t c t t g g c a c t g t a a c t c a a g g t c g g a t a t 292

<210> 345  
 <211> 286  
 <212> DNA  
 <213> Homo sapiens

<400> 345  
 caactatgcg gagcgggtcg gtgctggagc gccgggtgtac ctggcggcgg t g c t g g a g t a 60  
 c c t g a c c g c c g a g a t c c t g g a g c t g g c t g g c a a c g c g g c c c g c g a c a a c a a g a a g a c t c g 120

ADL\_0311WP\_Sequence\_Listing.txt

cat cat cccg cgt cacct cc agct ggccat ccgcaacgat gaggagct ca acaagct t ct 180  
 gggcaaagt c accat cgcac aggggt ggcgt cct gcccaac at ccaggccg t gct gct gcc 240  
 aaagaaaact gagagccacc acaagact aa gt aaagaccg agt t ga 286

<210> 346  
 <211> 247  
 <212> DNA  
 <213> Homo sapi ens

<220>  
 <221> mi sc\_f eat ur e  
 <222> ( 80) .. ( 131)  
 <223> n i s a, c, g, or t

<400> 346  
 cat at t t cag cggat cat ca act t t t t c t c ct accat act at cct cagac aaagaaacca 60  
 t t gaaat t at agacct agcn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 120  
 nnnnnnnnnnn ngt ggct ggt aaagaggat a at acagacac t gaccaagag aagaaagaag 180  
 aaaagggt gt t t cggaaga gaaaacaat g aat t agaagt ggaagaaagt caagaagt ga 240  
 gt gat ca 247

<210> 347  
 <211> 55  
 <212> DNA  
 <213> Homo sapi ens

<400> 347  
 t gct ct t aaa cccaaagggg ct t cact gaa gagccact t ccaagt caat aaaaa 55

<210> 348  
 <211> 291  
 <212> DNA  
 <213> Homo sapi ens

<400> 348  
 ct t ct ct t gg gct gagat gc t gct gccagc t ct aaaacag cact ct gt t c t caaaacct c 60  
 at ggcaggct cct ggct cca at act cagct gccaaacat g at gct gat t c t t cacgaat t 120  
 t gcaaccag t t ct ct cggg t t t gcacacc cccact gt gg gccggggaac cgggt cccgg 180  
 cct t cgcaga ct ccaggct c t ggcagat gt ggccct ccat aacaacggga at gaaaaggt 240  
 cacacct t at gt gcgccagg ccct t aagga gt cggaat at cccaat cct c c 291

<210> 349  
 <211> 47  
 <212> DNA  
 <213> Homo sapi ens

<400> 349  
 t gct gt ggt a ct t t gct gt g t act ccgt gg cat cat gt t a ct gt gt a 47

<210> 350  
 <211> 255  
 <212> DNA

&lt;213&gt; Homo sapiens

<400> 350  
 ggagt t t g t g act agat ggg caat at agt a agat gt cat c t t t t aaaaat gaaaaaat t a 60  
 gct ggccact gt ggcacacg cct gt agt cc cagct act t g ggaagct gag gt aggaggat 120  
 t gct t gagcc caggagt t ca aggct gcagt gagct at gat t gt gct t at g aat agccact 180  
 gcact ccagt ct gggcaat a gt gagt cggg caaat t ccat t t cccct cc gcccat acc 240  
 t ct t caaat g t t t aa 255

<210> 351  
 <211> 145  
 <212> DNA  
 <213> Homo sapiens

<400> 351  
 cact t cct ga cggat gccag ct t gggcact gct gt ct act gacccaacc ct t gat gat a 60  
 t gt at t t at t cat t t gt t at t t t accagct at t t at t gag t gt ct t t t at gt aggct aaa 120  
 t gaacat agg t ct ct ggcct cacgg 145

<210> 352  
 <211> 150  
 <212> DNA  
 <213> Homo sapiens

<400> 352  
 agcct aggca at gcagcgag gcct t gt ct a gaaaat t t aa aaaaaaaaaa aaaaat t agc 60  
 t gggcgt ggt ggcacgt acc t gt agt t cca gct act cggg aggct gaggc ggcaggat ct 120  
 ct t gagct aa gt agt t cgag gct gaagt ga 150

<210> 353  
 <211> 173  
 <212> DNA  
 <213> Homo sapiens

<400> 353  
 t t agccaagt at ggt ggcac ggcct gt aa t cccagcaac t t ggaaggct gaggcaggag 60  
 aat cgct t ga acct gggagg cagaggt t gc agt gagccaa gat cagacca ct accgcccc 120  
 gcgct ggct t gccct cct gt t ct ccagagc aat aaagt t g gacgagact a ccc 173

<210> 354  
 <211> 178  
 <212> DNA  
 <213> Homo sapiens

<400> 354  
 cacagct ct t ct t ggcgt at t t at act cac t gagt ct t aa ct t t t cacca ggggt gct ca 60  
 cct ct gcccc t at t gggaga ggt cat aaaa t gt ct cgagt cct aaggcct t aggggt cat 120  
 gt at gat gag cat acacaca ggt aat t at a aaccacat t ct t accat t t cacacat a 178

<210> 355  
 <211> 295

## ADL\_0311WP\_Sequence\_Listing.txt

<212> DNA  
 <213> Homo sapiens

<400> 355  
 ggatggcacc atgtttgaga ggctacagag gagaccaga gccagt aagc aagacat aga 60  
 gt t t at agag aggact taca gcat agt cca gt ggcagcgg gct agacagg agaaccgcaa 120  
 tggcttgaaa aagcacgaag tataaagcgt tgagctcaac ggt t t at act t cagagaaac 180  
 tcaacaat ca actgaaggca ct aact gaga aaaacaaaga act t gaaat g gct caggat c 240  
 gcaat at ggc cat t cagagc caat t t acaa gaccaaagga agcat cagaa gct ga 295

<210> 356  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<400> 356  
 atttcttt ag ctgaccat ag tgagcttcc ttgagttcac gtttcttccc aatttcat t t 60  
 tcttgagat a ttttgctact ttctggact gcttcatcac tgaaagtgtc atttgttct 120  
 atatccatcc ttggcctttt tctaaccattg acatcttcc tctgtttttg aactttcaca 180  
 tcaatttcta actctggttt tgtgtccttg aataactgtt ccaat acttc atcttctatg 240  
 gccacatcat ccat t 255

<210> 357  
 <211> 266  
 <212> DNA  
 <213> Homo sapiens

<400> 357  
 gtatcaaatt cagccatgc aaaaagatt a taaatgtaat aagcatgtat gtgtgtgagg 60  
 agattcagtc ataaccaaac gctcat tcaa catcaaagaa tttatacct a agagaact t a 120  
 tttgggtgt a gtaaatggca gatctttcaa taggagttta actagtcttt gtcatatcag 180  
 aat atccat a gt agacaaga atttgatgt a acgcaaatgg aaaaactcga caccacatt t 240  
 caggctttac ccaacatcga aat aat 266

<210> 358  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (136)..(136)  
 <223> n i s a, c, g, or t

<400> 358  
 cgttcagtac aaacatttat gcggtaggct cagatgttgt aatttgcact taggtaccag 60  
 gtgtcaggaa acagactaaa aagaattcca ccaggctgtt tgagatcct catcttggag 120  
 ctttttcaaa agcggngctt catctgcaaa gggccctttc atcttgaagt ttttccctc 180  
 cgtctttccc ctccctggc atggacacct tgtgtttagg atcatctctg caagtttct 240

ADL\_0311WP\_Sequence\_Listing.txt

aggt ct gaat ct gcgagt ag at gaacct gc a 271

<210> 359  
<211> 204  
<212> DNA  
<213> Homo sapiens

<400> 359  
gt accacaaa cacact caac ttgtctatga attagagaac aagat actgc t gct gct t ct 60  
ttttgacttt tgaaat at ac aatgttttgt aggct ct gcc ct t caat gt g aaagcaggac 120  
attaaatttg aaatt at ttg acaattaaat gt ttaggacc at ct aact t c aact gcaaaa 180  
ctaaacagat ctacctt gtc ct t c 204

<210> 360  
<211> 185  
<212> DNA  
<213> Homo sapiens

<400> 360  
attacagtta tagctctctc aagcaaaaaa acagcagaga aaaactt agt ttacctt agg 60  
ggctatttat ttacttaggg atttgtt aaa aggtcgaat g gggtcacaca gaat act aag 120  
aagagctgtt caccaggcc t cactaagaa ctcttcttca tt cagt agct gt at agt aac 180  
at gac 185

<210> 361  
<211> 54  
<212> DNA  
<213> Homo sapiens

<400> 361  
cttt agt agt ttctcgtcag tcccgcagcc accgcagccg ggtccccct cgt g 54

<210> 362  
<211> 261  
<212> DNA  
<213> Homo sapiens

<400> 362  
agagaggggg ctcacctctt atcctcggcg acccactgca caagcaggcc gctctcccag 60  
actt aaaat g tatcaccact aacctgtgag ggggacccaa tctggactcc ttccccgctt 120  
tgggacatcg caggccggga agcagt gccc gccaggcct g ggccaggaga gctccaggaa 180  
gggcactgag cgctgctggc gcgaggcctc ggacatccgc aggcaccagg gaaagtctcc 240  
tggggcgatc tgt aaat aaa c 261

<210> 363  
<211> 236  
<212> DNA  
<213> Homo sapiens

<400> 363  
ctgaatgggc agagctggat tttaacagggt tgggat tttg ccagggtgagt aagat agagg 60

ADL\_0311WP\_Sequence\_Listing.txt

ggagaagt gg gaccaggaag t t ccaggt ct gt gaacgggc ct ggct gagg agct ggat ca 120  
t gaaat ct cg agt caagt aa gaaggaaat t gaggacacga gt t gggat at t gcat agt gt t 180  
act gt gt t aa ggt caggggt caaagact t a ct ggcat gga gt aaccagag t aagt g 236

<210> 364  
<211> 179  
<212> DNA  
<213> Homo sapi ens

<400> 364  
caggcaaaaa cgt ccccgaa gccagcagt t gt agagact g t t acaacagc caagccacag 60  
cagat acaag cgct gat gga t gaagt gaca aaacaaggaa acat t gt ccg aaaact gaaa 120  
gcacaaaagg cagacaagaa cgaggt t gct gcggaggt gg cgaaact ct t ggat ct aaa 179

<210> 365  
<211> 167  
<212> DNA  
<213> Homo sapi ens

<400> 365  
cagagt cccg t gt gt cct aa aaat ct cct a aaaccagt ct at gaact cag ggct t t aaaa 60  
cat t t t t aat t t at t t ggt c att caat t t a ct t gt t t t t a at acat gat t ct ct at gaaa 120  
t t gat gggct caaact agct gt gaat ct t c t gagagt gaa agcaaca 167

<210> 366  
<211> 280  
<212> DNA  
<213> Homo sapi ens

<400> 366  
t at aaagt aa ccct at gat g ct cccct t ac gagaaaacaa aact gt acac at t t at aaac 60  
aaacagt ct c t cccat cagt t aacacacag agcct t ct ct acaccaaagt ct ct t t ccgt 120  
t t gccaccag aaagggt t t gt ccct cgct ct t cggat gc cgggct gt gt ct ggt gt gt c 180  
t t t aagct ct t gct gt cct c t gccat ct gc at gccagagc cacat ct gt a agcgt t t t ca 240  
t caact t ct a cct gagt aac act ggaaact gt cct cgt gc 280

<210> 367  
<211> 176  
<212> DNA  
<213> Homo sapi ens

<400> 367  
acagct cct t t gacct cagt gacaggcact cacct acct g acccccaaac t gaagcct ca 60  
ct t t t cccag ccgt gt ccac accct ct ggg ct accccat t accat gacaa gt at t ccct c 120  
t gct ccagga gaaaagccag gt cccagacc t gacccat t a aaaccaat c at t cca 176

<210> 368  
<211> 69  
<212> DNA  
<213> Homo sapi ens

## ADL\_0311WP\_Sequence\_Listing.txt

<400> 368  
gaccaggaag t cct at aaag aat t at at t t ct at agaatt aaaaat gcag t t ct gt cagc 60  
ct ggacaac 69

<210> 369  
<211> 200  
<212> DNA  
<213> Homo sapi ens

<220>  
<221> mi sc\_ fea t ur e  
<222> (55)..(55)  
<223> n i s a, c, g, or t

<400> 369  
at aagaactt at gggatt t c ct acacggag acaaaaaaag at att cct t t at gt ng t t t a 60  
aaagt ggcag ct gct c t t t c t t t at t ccat t t t aat caat gagt att gat t caagt t t t c 120  
ct t t ct at t t t t c c t t at ga t aagt t t c t t acagt agct t at acaacaac aaat agcat a 180  
gaaaaaact ac t ggatt t caat 200

<210> 370  
<211> 110  
<212> DNA  
<213> Homo sapi ens

<400> 370  
acaggt aacc t t ct cact aa gt ggggggt gt ct gaggccag ggagagct ct act cat t ccc 60  
ct gt gt gat c ccagcagt ga gcat agagca ggt gccct gc aat gt t aagc 110

<210> 371  
<211> 156  
<212> DNA  
<213> Homo sapi ens

<400> 371  
agaaagaat a aagcaggat c cat agaaat a at taggaaaa cgat gaacct gcaggaaagt 60  
gaat gat ggt t t gt t gt t ct t c t t t cct aa at tagt gat c cct t caaagg ggct gat ct g 120  
gccaaagt at t caat aaaac gt aagatt t c t t catt 156

<210> 372  
<211> 50  
<212> DNA  
<213> Homo sapi ens

<400> 372  
gatt gct gag cagggaagct t t gcat g t t g ct c t aaggt a cat t t t t aaa 50

<210> 373  
<211> 64  
<212> DNA  
<213> Homo sapi ens

<400> 373  
caccat gc act gt acaaa t act gcaaac act at agt t g cat t cat agg accat t aaaa 60

aaaa

64

<210> 374  
 <211> 95  
 <212> DNA  
 <213> Homo sapiens

<400> 374  
 ttctgagga ctgcttctgg agccggccct ctgtgtgat tgaattagtc agtgatggtt 60  
 ct caggacta gattagattg ttactcttaa aataa 95

<210> 375  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 375  
 ggccgcttca gacaaccacc tgaaaaagcc aaagcacaga gaccagaga aagccaaatt 60  
 ggacaaaagc aagcaaggtc tggacagctt tgacacagga aaaggagcag gagacctgtt 120  
 gcccaaggt a aaagagaagg gtcttaacaa cctaaagact ccagaaggga aagtcaaac 180  
 taatttggat agaaagtcac tgggctccct ccctaaagtt gaggagacag atatggagga 240  
 tgaattcgag cagccaacca tgtcttttga atcctacctc agctatgacc a 291

<210> 376  
 <211> 269  
 <212> DNA  
 <213> Homo sapiens

<400> 376  
 acaactggaa ttaggatttt ctctgatga aggaaaaaaa gacattagtc ctgcattata 60  
 tttttaaac catgaaaaga ctgaaaccaa ccaaacaaaa gaaaaacttg acttgttatt 120  
 agaacagtcattattttt tttcttctt caaaactgtt attttaccat gttgtatctt 180  
 ctccccaaag taat atgcag atgaagcaaa ataaactcagc aaagtgtcat ggaccaagcc 240  
 ctttccatca tttctagcat taaagt gaa 269

<210> 377  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 377  
 tggatgtgtt gctgttggcc aagaagaatg agaaggagcg aatttgggca gtgggacctc 60  
 caggcagcct tacagttttc agttggggag tgagatgaga cctggaattt aggggtctgt 120  
 gt agttaaaa ccatgcggtg tacaagattg cccagattga gtatgtggaa ggtgtgatgg 180  
 ggaggagaga gagtgttagg aagtgtggg gtctgccat ctgagaacag gagcccagag 240  
 gcagcatatg cagcccgaaa ggagagaatc catgctgagg gt cgtgaata c 291

<210> 378  
 <211> 43  
 <212> DNA

<213> Homo sapiens

<400> 378  
gagaaacagc tgtcacctcc cgcagaccct aatcctctct cgc 43

<210> 379  
<211> 44  
<212> DNA  
<213> Homo sapiens

<400> 379  
aatattgttg ctgatttcag agggatattc actaataaat gtat 44

<210> 380  
<211> 187  
<212> DNA  
<213> Homo sapiens

<400> 380  
attctgaatc atcactggga gcaaacaca gactcacaag aggaagggca agagaagggt 60  
aaagaacaag agagaccacc tgaggcagt g agcaagtttg caaagcggaa caatgaagaa 120  
actgtaatgt cagctagaga caggtacttg gccaggcaga tggcgcggt t aatgcaaag 180  
acctata 187

<210> 381  
<211> 152  
<212> DNA  
<213> Homo sapiens

<400> 381  
attgcttgaa ctgggt aact gat t t gat gt aaatgccaaa ggagaaggag taaaaggaaa 60  
atgacataga gtctgagcta gagt aacagg gacagtatt a attaatatta accaaatatc 120  
aaatagaac atttaagaga cgagccacca tg 152

<210> 382  
<211> 272  
<212> DNA  
<213> Homo sapiens

<400> 382  
ctgctgtggt gttatttgct t aatggacca t t t aaggaat tctcgaat ac accgaccaca 60  
aaaatctctt aaagtactgt caacagggtc cacaattcca tccaat at ag ct t ct agt aa 120  
ggcaacagta tcctgacttt caaat t t ct t gttgttagt g aaccagt gaa t cagct gcat 180  
aact agtggc tcat acagtt gcct t gt cac ct gat caaca t cacacgcaa gt cgaagcag 240  
cacaggaaac gtccgcttat agagctggt a ca 272

<210> 383  
<211> 184  
<212> DNA  
<213> Homo sapiens

<400> 383  
ctgaatttgc ccatccacct gggtcacttt gagagt t gt g caggggggct gggagcact g 60

ADL\_0311WP\_Sequence\_Listing.txt

gtgttcacgt gggaccacag gctgcacat aagaccact cacaat aaaa aaat aaaagg 120  
ccgagccggg cat ggttgct cactcccgta at aaaaaaat aaaagaacag gct gagccgg 180  
gaaa 184

<210> 384  
<211> 191  
<212> DNA  
<213> Homo sapiens

<400> 384  
ccagaaaaag caccatgc actgtacaaa tactgcaaac actatagttg cattcatagg 60  
accattaaaa aaaaagagcc aaattacaaa acaatctata ttttacaac atttcagttg 120  
ggttcttaag ct aaagatat tactgtttac tttggtacga taactagaaa acacaaacat 180  
tatgctccag a 191

<210> 385  
<211> 278  
<212> DNA  
<213> Homo sapiens

<400> 385  
tctttgtcct ggtcgtcttg gt aaatgtgt agt cgcgtat ctgagacata gat tgtgctt 60  
tattcggtgc tgtggagagt agaaactagc agcagtacct ggaaaggggc cctgatctgc 120  
gggtgtggat gagt agagac tcttcagttg agat tt agct ct agt gaggg t tgggt gcaa 180  
caaatgtagg aaagagt gaa gagat gagca gctcatgtct gagt tt attc tgtttctgtt 240  
actgtgtcac agaccagcct cagatcatag ttcatgat 278

<210> 386  
<211> 281  
<212> DNA  
<213> Homo sapiens

<400> 386  
gctcattgct gactgttttc cttaaaagct gggaaggctg tgggtcaatt cagctcgcca 60  
cctgtttctg tactgccac aagctgagaa tgaattttgt acttttaaat ggttgggggg 120  
aggggagaaat attttctgac acaagatat t gacattcac acttgagtgt caaagt tttt 180  
aggaacacag ccacgcccatt tgtttacac tttactcctt ccactttaca atgaagaggt 240  
atgaggagct gctacagaaa ccttctggct tgcaaagttt a 281

<210> 387  
<211> 94  
<212> DNA  
<213> Homo sapiens

<400> 387  
attttggaga aaaat acgct agat tttaaa tgttagagct gttcccggag acttattgca 60  
gaaat agatg agaagcaaat caagactact attc 94

<210> 388

## ADL\_0311WP\_Sequence\_Listing.txt

<211> 265  
 <212> DNA  
 <213> Homo sapiens

<400> 388  
 gct gacagt g agt act gat g gcct ggat gt aggggt gaga gaaagagagg gggct aggat 60  
 gaccct gagg ttt gggcct g gacaccagct gaggggt gaa gat act gcat t gagggaccc 120  
 cagggt cggg gt ttt gcaggg agt ggccaga aggcct t gt g aagaat caga gacgt ggct g 180  
 agt ct gt t cg gt gct gggg g cccgt cagac agct gcgt ga gat ggcaagg agacagt t gg 240  
 at acgcat ac ct gaagt t ga gagag 265

<210> 389  
 <211> 261  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
 act gcct ggc agaacat acc act gaact ag t at gt gct ag aggagggcac aaacat ccgc 60  
 t cct t ccct a ggcct gct gg ct ct ggt t t t ct at gcagat gat t cat t gg at t gggggg t g 120  
 agt gt t t t gt t t t t ct gggg gcagt gt gag ct t t gaggggt t ggaat at t g ggaggcat t c 180  
 ct t agt t t cc t caact agcc t ggaaagt t a ggagt ct agg gt aat t accc cccaat gagt 240  
 ct agcct act at t cact gct t 261

<210> 390  
 <211> 194  
 <212> DNA  
 <213> Homo sapiens

<400> 390  
 aaagct gt gt t t at at ggaa gaaagt aagg t gct t ggagt t t acct ggct t at t t aat at 60  
 gct t at aacc t agt t aaaga aaggaaaaga aaacaaaaaa cgaat gaaaa t aact gaat t 120  
 t ggaggct gg agt aat caga t t act gct t t aat cagaaac cct cat t gt g t t t ct accgg 180  
 agagagaat g t at t 194

<210> 391  
 <211> 268  
 <212> DNA  
 <213> Homo sapiens

<400> 391  
 aaagaact t c t at ccagaat gcat aaagaa t t accgct ca gcaacaaaaa acaat aaaat 60  
 t agaaat ggg caaaaaagaa act t cact aa agat aat ggg t gt agccaat aagcacaaga 120  
 aaaagt gct t gacat cat t a t t cat caggg aat t gcaaat gt aaact aca gt aagaagcc 180  
 acggcat acc caccagaat g gct aaaat t a aaaagact ga caccaccaa t gt t ggt aca 240  
 t at gt agaac aaccaat t cc acacat ag 268

<210> 392  
 <211> 262  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 392

```

t t t t a t a g c g   t g t a g t t g a c   c c t t g a a c a a   t t t g a g t g c c   a a c c t c c t g t   g c a g c t g a a a           60
t t c a t g t a t a   a c t t t t g a c t   c c c c a a a a a t   t t a a c t a c t a   a t a g c c t a t t   g t t g a c c a g a           120
a g c c t t a c c t   a t a a t a t a a a   c a g t t g a t t c   a c a c a t a t t t   t g c a t g t t a t   a t a t a t a t t a           180
t a t a c a g t a t   t c t t t t t t c t   t t g c a c a t t a   a a a a a g a c a   t t t a t t c t g c   a t c a t g a t c a           240
g a c t t a c a t t   t a g c a a t c a a   c a                                     262

```

&lt;210&gt; 393

&lt;211&gt; 203

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 393

```

g a g g t g c a t g   a t a t t g t t a g   c c a a a a g g g a   g a a g a c a t a c   a g a c g g t t a a   t a t c g a t g c c           60
a g a a a g a g a   t g a c c c c c c g   a c a a g a a g g g   a c t g a c a a t g   a g g a t c c a g t   c g t g t g c c t g           120
g a c a a g a a a c   c a g t g a t c a t   c a t t t t c g a t   g a g c c c a t g g   a c a t c c g g t c   t g c c t a t a a g           180
a g a c t t t c a a   c t a t c t t t g a   g g a                                     203

```

&lt;210&gt; 394

&lt;211&gt; 230

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 394

```

g a g g a g t c g a   a c a t g a t c t t   g a g g a c t c t a   c t c t t g g a g g   c t t a a a g g a a   t g t g t t g t c t           60
g t a a t t g t c a   c a g g g a a t c a   g g a a g g a a g a   g c c a g t t a g g   g t c a a g c g t t   a g a a t a t g t t           120
a a g c t t a a t a   g g c t t t g a c a   c t c a g a t g t g   c c c a t c a a g c   a g t t a g g a a t   t g g a t t a t t t           180
t g t t t g g a a g   a g g t c a g a a c   t a g t c a a g a g   a t t t c a t a g t   c c t t g g t a a a           230

```

&lt;210&gt; 395

&lt;211&gt; 235

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; m i s c \_ f e a t u r e

&lt;222&gt; (66)..(98)

&lt;223&gt; n i s a , c , g , o r t

&lt;400&gt; 395

```

c a g a a t t c t a   t g c t t c t c t g   g c a a c a a c a a   t a a c t a t t a g   a a a a t c t t a a   c c t c a c c c a g           60
a a g t t n n n n n   n n n n n n n n n n   n n n n n n n n n n   n n n n n n n n c a   g c t t a c t t a a   a t a a t t g t g c           120
t a a a t a g c t t   a t c t t c a c a a   t t t a a a a g t a   a a a a c c t t t g   a a a a a g a a g g   a c t t c a c c a a           180
a a a c a a a c a c   a c t c t c c c t a   t a g c c c t g a a   g a t c t g g c c a   g a a a a g c t c c   a t t a a           235

```

&lt;210&gt; 396

&lt;211&gt; 283

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (124)..(124)

<223> n i s a, c, g, o r t

<400> 396

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gat aat aacc t t t aat gaac t caat act cg ggaaaggct t cacat t t ct g ggact cagca      60
t t at ccaaaa t at ct att aa gagccat aca ccat t ct agc t gcaat t gat t at acaaaaa      120
aaangaccaa agt ggt t aca ataat aaaat agaacacaga gaaagaagaa aact acat gt      180
gt t acaat t t ggt aagat aa acaaacaaac aacaaaaat t aat cact t t t t t t ggt cct g      240
t gacacacat gataat t t t t gt ctt aatt c t cct aacaaa t ga      283

```

<210> 397

<211> 259

<212> DNA

<213> Homo sapiens

<400> 397

```

cggcagggt c ct ggat cacc aaggacct t g aaagcat gt g gaagact t t g at caat gggg      60
gaat catt aa ggggt t t t gc att ccggaac t at cat cagc t t cagcgggg ggcaggggggt      120
aggat agagg cagggaggca ggaagt t ct c gcagggt cca ggcaagagat ggt ggagt gt      180
ggt cct gggg aaggggggcag t ggacggat c t gagggaggt t cagt t agga t gggcaagga      240
t t gagat ct g gct ggat cc      259

```

<210> 398

<211> 202

<212> DNA

<213> Homo sapiens

<400> 398

```

gggacat ccg aaagct acac cacagat gcc agt ggt t cat gcct t ct t cc cgcaact t t a      60
ggaaaat t t a t t t att t att g t t t att agt t at gggggga gaggggagat t t aaaggacc      120
agggacat gg gaaccaagcc at agggat ca gagggcct t g t cct t gaaca ct act ggggt      180
at att caggc t cat ccacgc ag      202

```

<210> 399

<211> 257

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (90)..(90)

<223> n i s a, c, g, o r t

<220>

<221> misc\_feature

<222> (164)..(164)

<223> n i s a, c, g, o r t

ADL\_0311WP\_Sequence\_Listing.txt

<400> 399  
caggcaagaa aagcgcagag aaatcgggtgt ctgacgattt tggaaatgag aacaatctca 60  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaan gaaaagagaa aaaaaagact agccagccag 120  
gaagatgaat cctagcttct tccattggaa aatttaagac aagntcaaca acaaaacatt 180  
tgctctgggg ggcagggaaa acacagatgt gttgcaaagg taggttgaag ggacctctct 240  
cttaccagta ccagaaa 257

<210> 400  
<211> 91  
<212> DNA  
<213> Homo sapiens

<400> 400  
agagcaggag agacggcaga gat atgttgc taggtgaata tatatttat taaataatcc 60  
gt aagttaat aaagtaata gt aattctct g 91

<210> 401  
<211> 132  
<212> DNA  
<213> Homo sapiens

<400> 401  
gt atggactg agaggcat t aaattctggc aaggagggtg gaaatgctga caatgaggag 60  
gaagcttat a gtgggtcaaa caaggagggtg tctagtgtgt tgtttaaaaa gaaggcttac 120  
aattagccag gc 132

<210> 402  
<211> 158  
<212> DNA  
<213> Homo sapiens

<400> 402  
tcccaagggc cgctagaaac tctgtcttcgc gttgccccct tctctggctct cagcgccgtc 60  
gccactcggg agaggctggg tgaggcccggt gtgaggactg accctggatt cctcgaaact 120  
gccattgtga tcat t actct gctctttgga aatggctg 158

<210> 403  
<211> 271  
<212> DNA  
<213> Homo sapiens

<400> 403  
gt tacatgaa atagtccag ctggaggttc tttgccagca ccatgccaag tgaaataata 60  
tatttactct ctctattata caccagtgtg tgcctgcagc agcctccaca gccacgatgg 120  
gtttgtttct gt t t t c t t g g g t g g g g a g c a g g g g a g g a g a g c a g g t t t c 180  
agatccttac ttgccgagcc gtttgtttag gt agagaaga caagtccaaa gagtgtgtgg 240  
gctttcctgt ttctaaactt tctgctactat a 271

<210> 404  
<211> 77

## ADL\_0311WP\_Sequence\_Listing.txt

<212> DNA  
 <213> Homo sapiens  
  
 <400> 404  
 t gt ct gt gcc t cat ggaat t gccaat gaag at at t gt ct c t caaaacccc ggagaact ct 60  
 ct t gt aagcg t ggggat 77  
  
 <210> 405  
 <211> 131  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 405  
 ccct gt gct t t t t gccgt cg ggcct ct gca cct ggggt cca t ggggt ct gc ggggt ct gcg 60  
 ggggt ct gcct ggcct gt ggg t t ct gccggt ggggct t cag gagt aat aaa gt gt caccct 120  
 at cct t gt aa a 131  
  
 <210> 406  
 <211> 226  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 406  
 ggccat ccga aaat agcaac aaccagact ggct cct cac t ccct t t t cc at cact aaaa 60  
 at cacagagc agt cagaggg acccagt aag accaaaggag gggaggacag agcat gaaaa 120  
 ccaaaat cca t gcaa at gaa at gt aat t gg cagcaccct c acccccaa at ct t acat ct c 180  
 aat t cccat c ct aaaaagca ct cat act t t at gcat cccc gcagct 226  
  
 <210> 407  
 <211> 171  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 407  
 gat at t t gt c t at gaacagt agcacagacc ct ct aat t cc at agggaat c at t t ccat ga 60  
 ct t ccccaa at accct act ct t ct ct at c t ct gt gacag t ct ct ggccc t gct ccct cc 120  
 t aaact gct c aaaat cct t a ccaaaat ggc t t acaaat ct ct ct cct ccg g 171  
  
 <210> 408  
 <211> 266  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 408  
 ccct gt ggat cccaaccagg aagt t cct cc t gggccacct cgggt t ccagc aagt t cct ac 60  
 ggat gccct g gccacaagt t gt t t ggt gc t cct gagccc t ccaccat cg cccgct ct ct 120  
 accaaccact gt cccagagt caccaaact a ccgcaacacc aggaccct c gcact ccccg 180  
 gacaccacag ct caaagact caagccagac at caggt t t t acccagt gg t gaaagaagg 240  
 acggacact g gat gccaaga t gcct c 266  
  
 <210> 409

## ADL\_0311WP\_Sequence\_Listing.txt

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<211> 300
<212> DNA
<213> Homo sapiens

<400> 409
t at agt t ct g t t gt aggct a cacat gaaca gcaaccaaaa agaggaaaaa t ct t ct t t gt      60
ccccat gct t t t t cct t gaa t t ct gcact t t t cat att aa catt agccct t gct t t gt ga    120
t t t gcct t t g ct t t at t t t a ccct gt ct t a at ct t aacct t cccaaat at t t ccat acag   180
ggg gcacct c t cct agacaa cacacagcgg agagt gt gct t cccat gt at t caat ct t cg          240
t ct ct t gaaa ggagaggt gc cct cat t aca ct t cact gt g acacaggat a ccct t ggt t t        300

<210> 410
<211> 67
<212> DNA
<213> Homo sapiens

<400> 410
at ggaaaaga acacgat gag aat t agacac t ggaaaat at gt at gt gt gg t t aat aaagt      60
gct t t aa                                         67

<210> 411
<211> 274
<212> DNA
<213> Homo sapiens

<400> 411
t caggt t gt g aggt t t at t a gt ccccaagg caaacacaaa t at t agat t a at aat ccaac      60
t t t aat agt a t acat t t aaa agaaaaaaaaa caaaagccct ggaagt t gag gccaaagcct g        120
ct gagt at t g cagct gcatt t gcccaaagg gaat ccagaa caagt ccct c cct gt at t t t          180
gt t ct t gaga ggggt cagt c t agaagct ag at cct at cag gat gaggagc agcagcccag          240
ggct t gt ct g gat cagcacc aacgat t t t a aaga                                         274

<210> 412
<211> 265
<212> DNA
<213> Homo sapiens

<400> 412
gt ggt gt t ct t gat gt agt g agct caagt c t gcggct gt t t ct ggggacg t ggt ggaggc      60
t gcat gt t ct gt t ct ct cca ggaagagct a gt ggt t t t ct accct gt gt g t t ggt gagca    120
at gt gcagag gcagagccgc t gaagt at gg t t cct gaggg gt ggcgaagc accgccct ca          180
ct ccaggt ca cct cat cagc cct cgt t t t t t t t t t gggccc cacct t gggg ct t gccaaac    240
t gagaggcat t caaaacat ggcac                                                         265

<210> 413
<211> 120
<212> DNA
<213> Homo sapiens

<400> 413
aggacgcggg ct ct cgct gg cccgagct ct acct ct act c gagggct gac gaagt agt cc      60

```

ADL\_0311WP\_Sequence\_Listing.txt

tggccagaga catagaacgc atggtggagg cagcctggc acgccgggtc ctggcgcgtt 120

<210> 414  
<211> 102  
<212> DNA  
<213> Homo sapiens

<400> 414  
gaagcatttg gaggaattcc tagacattgc gttttctgtg ttgccaaaat cccttccgac 60  
atttctcaga catctcccaa gttcccatca cgtcagattt gg 102

<210> 415  
<211> 281  
<212> DNA  
<213> Homo sapiens

<400> 415  
atgtctccag attccaggtg caggttctta gcacctccgc agccgctctc tcttgagtcc 60  
atcctcagtc tctcctaccc cttegaagt ag ggggaccctg aatttgccca tccacctggg 120  
tcactttgag agttgtgcag gggggctggg agcactggtg ttcacgtggg accacaggct 180  
gcaccataag acccactcac aataaaaaaa taaaaggccg agccgggcat ggttgctcac 240  
tcccgtaata aaaaaataaa agaacaggct gagccgggaa a 281

<210> 416  
<211> 265  
<212> DNA  
<213> Homo sapiens

<400> 416  
tgtgattgtc agcaatgacc atgctgggaa actgtgtggg gcctgtggaa actttgacgg 60  
ggaccagacc aatgattggc atgactccca ggagaagcca gcgatggaga aatggagagc 120  
gcaggacttc tccccatgtt atggctgatc agtcatccac caggaacgaa gatttcctga 180  
agaagacctg gtccctctgg aggttgcggt ggctgaagga tgcatacatgt gctcctaccc 240  
tgctctaccg cttttctggg tcaca 265

<210> 417  
<211> 203  
<212> DNA  
<213> Homo sapiens

<400> 417  
acattggaaa gtttaagagag ttcgagggaa gaattataaa gactaggagt cctagaaaga 60  
gaaaatttag agaataaaag gagaggcagt acttgaaaga taacacaatt tttacaaatt 120  
tgttggaaaa acatgaattc ataaattcag gaagcacaat atatacccaa catatattta 180  
aataaaatcc aggcctagac tca 203

<210> 418  
<211> 274  
<212> DNA  
<213> Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

```

<220>
<221>  mi sc_ fe at ure
<222>  (108)..(118)
<223>  n i s a, c, g, or t

<400>  418
ttcccccttt gaatgaggtc ttccatgttt gagggaaagt cttgcactat tgcataat 60
ttggggacac agattttcat agtttccatt tttggggggc ttaaggannn nnnnnnnct 120
gtttgaaaca gttttatact ttctgatata gtacttgaaa ttcttaccag aaaattactt 180
tggagttttg aagcctttat taatactact tttaaagaag cagttgtttt attgtcaatg 240
ttttttttcc cccacgcata ttttcttgta tttc 274

<210>  419
<211>  71
<212>  DNA
<213>  Homo sapi ens

<400>  419
tgagatggtt tgatggtttg ctgcattaaa ggtatttggg caaacaaaat tggagggcaa 60
gtgactgcag t 71

<210>  420
<211>  269
<212>  DNA
<213>  Homo sapi ens

<400>  420
tactaacttt cctgcactaa accaccaagt ctgtctctc tgaatgtgt agttcctgat 60
ggctccggtt tttcccccca cttttttatt ttgaagcctg acttgcagga gataccctc 120
taactgtata gcttctact ccattaaaga ttagt cagag atggtaatca acccacctga 180
gctctttcac tacctgctgc tgaactatg gt caggat aa ggggagcaca ctcacacttc 240
aggccttcac gtctgttcca gttactttt 269

<210>  421
<211>  47
<212>  DNA
<213>  Homo sapi ens

<400>  421
ctttgaacca ctttgcaatt gtagattccc aacaataaaa ttgaaga 47

<210>  422
<211>  149
<212>  DNA
<213>  Homo sapi ens

<400>  422
ggactaggaa gggctattcc aggctcagcc ctgctcctgc agctttgccg ctgagtgtag 60
gaaaaacagg catgacagac cagggtgagg gttgtgccca gctgggccac ggccatgcgt 120
ggggtggccc aataaacacc gtggactcc 149

```

ADL\_0311WP\_Sequence\_Listing.txt

<210> 423  
 <211> 185  
 <212> DNA  
 <213> Homo sapiens

<400> 423  
 t t t c t c t t t c t g t c c g g t g t c c g g a c t t t c c t a a t t g g a g t t t g a g g c c c c t a a g c t g g c 60  
 a t c a a c c c c a g g c c a c g t c g c t c t t t c c t t c c c t c c c c t c c c c t c t g c c t t t t g t a c g 120  
 c c a g t t c t c a g a a t a a a g a t c t t t t t g t c c g t t t t t t a a c c t c g g a t t c t g t a a t t g g t 180  
 t c t t a 185

<210> 424  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<400> 424  
 c c a c a g g t a a c c t t c t c a c t a a g t g g g g t g t c t g a g g c c a g g g a g a g c t c t a c t c a t t c 60  
 c c c t g t g t g a t c c c a g c a g t g a g c a t a g a g c a g g t g c c c t g c a a t 105

<210> 425  
 <211> 122  
 <212> DNA  
 <213> Homo sapiens

<400> 425  
 c c c c c a t g c c c t g t g g a g a t g g a g g t g t g t g c t g a t c c c t c g t g c c c c t g t g g a g a t a g a 60  
 g g t g t g t a c t g a t c c c c t g t t c c c c t a t c t a g a t g a a g g t g t g t a c t g c t g a t c c c c c g t 120  
 c c 122

<210> 426  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<400> 426  
 t t t t t g a c a g t g t t g a a a a t g t t c a g a a g g t t g c t c t a g a t t g a g a g a a g a g a c a a a c a c 60  
 c t c c c a g g a g a c a g t t c a a g a a g c t t c a a a c t g c a t g a t t c a t g c c a a t t a g c a a t t g a 120  
 c t g t c a c t g t t c c t t g t c a c t g g t a g a c c a a a t a a a a c c a g c t c t a c t g g t c t t g t g g a 180  
 a t t g g g a g c t t g g g a a t g g a t c c t g g a g g a t g c c c a a t t a g g g c c t a g c c t t a a t c a g t c 240  
 c t c a g a g a t t t c t t c 255

<210> 427  
 <211> 236  
 <212> DNA  
 <213> Homo sapiens

<400> 427  
 c c c a c t c t g t g t a g t c t t a a c t t a t t t c t t c t a a a c t c a c c a t t a a c c t a a a t a a t a g t c 60  
 a a a t t t a g g g g g g c t g t a t t t g t c t t a c t c g a g t c t t c t a c c a t a g t t g a a a c t g t c g t a 120  
 c c c a a a c g a g t t a c a g a g a a a t g c c a c a c t t t g a g a c g a a t t c a g g a g t c c t t t a t t a g c 180

ADL\_0311WP\_Sequence\_Listing.txt

t ggt gact ga gagacggct a acacaggaaa t act ct cggc cct aaagaat gggct a 236

<210> 428  
<211> 275  
<212> DNA  
<213> Homo sapi ens

<400> 428  
gaagacgcca at gat ggct g aagagt t t t t cccagatt t a caagccact g gagaccct t 60  
t t t t ct gat a caat gcacga t t ct ct ggc gcaaggaccc t cgact cacc cccat gt t t c 120  
agt gt cacag agacatt t ct t t gat aaggaa at ggcacaaa cat aaaggga aaggct gct a 180  
att t t ct t t g gcagatt t g t a t t ggccagca ggaaagcaag ct ct ccagag aat gccccca 240  
gt t aaat acc t cct ct acct t t acct aagt t gct c 275

<210> 429  
<211> 223  
<212> DNA  
<213> Homo sapi ens

<400> 429  
t gat ct ggt c agt agt ggaa t t cgatt t t a t gcagact gg at gt aat at t t gt aat ccct 60  
gt gcaatt t t t gt gacgt ggc gt t ct aat t c at gt gcagt g at at agt at a gat aaaagaa 120  
t gagt aaaag aaaat acaag aat t ct aaag aaagt t ggt t t t agcccct t t gat agt cca 180  
t ggt t aagac at cct t t at a aaccaaagat ggccagcaca ct g 223

<210> 430  
<211> 273  
<212> DNA  
<213> Homo sapi ens

<400> 430  
cagaagaggg ct caact t ag ccaat at t t t gat gct gt ca agaat gct ca gcat gt ggaa 60  
gt ggagagt a t t cct t t gcc agat at gcca cat gct cct t ccaacatt t t gat ccaggac 120  
att ccaact t c ct ggg t gcc agccaccct c t at cct aaag aaaacct cag cct at ggacc 180  
t cccaact cg ggccagtt t c t at cct t ccc t cct t cct t g gacat ggggg t t t ccaccgt 240  
t t gccccct ggcagaaaaa cct ccct ggg cct 273

<210> 431  
<211> 112  
<212> DNA  
<213> Homo sapi ens

<400> 431  
gagt ccaaga gaat ggccga gt t cat gacg t gcacacgat gt aagt t gt a ct ct ct gaaa 60  
t t gtt ggt cc acct t t cat c t t cat caaat gagcat cccc t ccaat acct gg 112

<210> 432  
<211> 262  
<212> DNA  
<213> Homo sapi ens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 432  
gagt cagcaa ccttattctc caaaacaaaa gcaacaagga ctttgacttc tcagcagcac 60  
tcagctctgg ttcttgaaac acccccgtta cttgctattc ctctacctc ataacaatct 120  
ccttcccagc ctctactgct gccttctctg agttcttccc agggctctag gctcagatgt 180  
agtgtagctc aaccctgcta cacaaagaat ctctgaaag cctgtaaaaa tgtccatgca 240  
tgttctgtga gtgatctacc aa 262

<210> 433  
<211> 152  
<212> DNA  
<213> Homo sapiens

<400> 433  
ccggggtagc cattgggtct tggatctgtg ttagaatgag tgccttccct tcctactgat 60  
gtgattgtgg attaggaatt cgtgaccgag tgatttttgg ccagtggttg ggtttaaaat 120  
tctattaaaa tttgtagttt gggctgggtg ct 152

<210> 434  
<211> 99  
<212> DNA  
<213> Homo sapiens

<400> 434  
gtggaggccc attaccgggc ctgcttgtat gctggagtc aagattgcggg gactaatgcc 60  
gaggtcatgc ctgccagtg ggaatttcag attggacct 99

<210> 435  
<211> 207  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (115)..(115)  
<223> nisa, c, g, or t

<400> 435  
ttcatttttc ttcccctctg ctagtttggga agttatatta taccaagtgt tttagtatta 60  
gcctagaaat cttaacataa agacttctaa taagcaatat ctttaatttt ttttncctac 120  
ccaatactag atcatgagca ttttcccaca tcataaagaa ttggtcacia gtgagcccca 180  
aacatagtcc agtggaatcc aatgata 207

<210> 436  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 436  
aaggcaacac ttctgtcagt agaattgctt tggattgtaa atatgtttac ttcagaggaa 60  
atcagtcaga gtggatggct cagcaaaacc catcacaact gcggaaaaag gaagtgactg 120

gct agaggt a aggaaat aga t t t t c t c t a a g t t a a c t g g c c t a c g t g t g a a t c g a a c c c t 180  
g c a c c c t g g c c t c a t t a g c a c c a a c a c t g t g a a g a a c a g c t g t g g c a g a g a 231

<210> 437  
<211> 133  
<212> DNA  
<213> Homo sapi ens

<400> 437  
t t c a c c c c t c t a c t t a c a t a t t g t a a a g t t g t a t a a a t c t a t c a t t g a a a g g t c c c c t c t 60  
g c c a g c a g t g g t g c c a c c c t t t g g t t t g c t g t g g t a c t t t g c t g t g t a c t c c g t g g c a t c 120  
a t g t t a c t g t g t a 133

<210> 438  
<211> 66  
<212> DNA  
<213> Homo sapi ens

<400> 438  
t t t c t c t t t c t g t c c g g t g t c c g g a c t t t c c t a a t t g g a g t t t g a g g c c c c t a a g c t g g c 60  
a t c a a c 66

<210> 439  
<211> 233  
<212> DNA  
<213> Homo sapi ens

<400> 439  
t a c a a a g a g t a c c a c g a g a c a c g a g a a a c c t t g t g g g a a c a c a g g g g g a c c a c c c c t a a 60  
g g c t a a a t a c t a c t t g g t g a c c g a t a g c g a a c a a g t a c c g t g a g g g a a a g g t g a a a a g a a 120  
c c c c g a g a g g g g a g t g a a a a a g a a t c t g a a a c c t a g t g t t t a c a a g c a g c g a a a a t g g c a 180  
c a a g c c a t g a a t c g t g t a c t t t t t g t a g a a c g g g c c a g c g a g t t a t g a c a a a a 233

<210> 440  
<211> 260  
<212> DNA  
<213> Homo sapi ens

<400> 440  
t c t c t t c c g a g g t c g a g g c c c t g a g g c g g c a g t t a c t c c a g g a a c a g g a a g t g t c a a a c 60  
a a g c t c a c t t g a g g a a t g a g c a t t t c c a g a a g g c g a t a g a a g a t a a a a g c a g a a g c t t a a 120  
g t g a a a g c a a a a t a c g a a a t t g a g a g g c t g c a g t c t c t c a c a g a g a a c c t g a c c a a g g a g 180  
c a c t t g a t g t t a g a a g a a g a a c t g c g g a a c c t g a g g c t g g a g t a c g a t g a c c t g a g g a g a 240  
g a c g a a a c g a g c c c c a c a g c 260

<210> 441  
<211> 270  
<212> DNA  
<213> Homo sapi ens

<400> 441  
c a t a g c c a a g g c t t c a a g c t c t c a g g a c t t g g c t a t g g a g g a g g a c g a a g a a g g c a g g a g 60

ADL\_0311WP\_Sequence\_Listing.txt

ct cat ccagt ccagcct tac ct acagcagg aaact gcacc agct agact c cat t ct ggga 120  
ccat ct ccag gagt ccat ga gaggc t t t ct t ct cct at gt cccaat t ct c agaact caga 180  
t gt ggct aga ccaacccct g ggaaact gcc ccagct t ct c ccacat agg ggccggaccc 240  
ccat caccag cct agat cca gggct gcct c 270

<210> 442  
<211> 156  
<212> DNA  
<213> Homo sapiens

<400> 442  
aact t gt gcg cgagcccaa act aacct ca cgt gaagt ga cggact gt t c t at gact gca 60  
aagat ggaaa cgacct t ct a t gacgat gcc ct caacgcct cgt t cct ccc gt ccgagagc 120  
ggacct t at g gct acagt aa cccaagat c ct gaaa 156

<210> 443  
<211> 103  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (48)..(48)  
<223> n i s a, c, g, o r t

<400> 443  
gt t t t gagat cat aact gt t acagagaaa gagaggaggc at at t at naa cgt gt ggact 60  
t cagt gt t at t cct t ct ct t caaaat gat g t t ccaggt gt ct a 103

<210> 444  
<211> 101  
<212> DNA  
<213> Homo sapiens

<400> 444  
ct cggcggcc t t t at t t at t ct gt t ccccc agct cggcca ct t ct ct gaa ggagggct gg 60  
gt t ct gggcc t gt at cgaat aaacacaaac ct ggat ggcg c 101

<210> 445  
<211> 144  
<212> DNA  
<213> Homo sapiens

<400> 445  
ggaggat ggt caggcgt cac caacaacccc at caccagat aacaagaacc t t gact ct cg 60  
t cagt ccct c t gcat caaga cact t accca t t t cccacct cat gcct gct aact t gaat g 120  
aaacaat cgc t gggaaagca t t aa 144

<210> 446  
<211> 276  
<212> DNA  
<213> Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 446  
atgtgagagt gctttgcagt tggaaagtgc tgtaggaacc ctgaattcat ctgaaactgt 60  
agcttagtgt ttaaatgatg tctgttatta cttttttgaa tagtctggag tcttgttaa 120  
agaaaaaatt attctgtgat atttgttgaa tgaagcacag tgaggaagac tttactcagg 180  
gcccttgtaa tagctatagg gaccactgca atagggtctt gcagtggggg agagagaat a 240  
ggctcaattc tgaatacatc atcatgggca agtggg 276

<210> 447  
<211> 48  
<212> DNA  
<213> Homo sapiens

<400> 447  
tctaaagctg tttttaactc cgagattaca acttagagga accaagga 48

<210> 448  
<211> 168  
<212> DNA  
<213> Homo sapiens

<400> 448  
aaattgaagg atttgctgtt attcctacct gcattggact tgacctgggt gttgggtgag 60  
tagcaatctg tttactgtttc tctatgtgga cgatgaggaa agggttgaga aatccagcga 120  
aaggacactt ctgttaatag ctcaatctgc tggccatggt tgggaaaa 168

<210> 449  
<211> 147  
<212> DNA  
<213> Homo sapiens

<400> 449  
tttttctgta tgaaaccag atgtcaccaa atggacatta atagttgcat taaggatcag 60  
tagcattaac aaaagttgct ttaaaagcca ttatgtaat caagacttga aaatgagtga 120  
gggaatttta gcgacactgt ctgagca 147

<210> 450  
<211> 272  
<212> DNA  
<213> Homo sapiens

<400> 450  
tgaattccca actttccgag atgttgttta atgagactca cccttathtt tcaattcttc 60  
cttcattctc tccctcttaa ctgggtttcct cttaaccaag aaaagccttt ctcttaactg 120  
caagcttatt tgaattttac cttaattgaat atctttcaac tatttggcag accttaact 180  
ttccctacca tgccaatggt cactaaacac cttaaatgcc actcttaaca ccttaaatgc 240  
cacccttaac agtatcttt cagtcctcat tc 272

<210> 451  
<211> 267  
<212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 451

```

t g t c c a g c a a   g t g c a g g g t g   c c t g c a c t t c   a c c c t g t g c a   g a g a g g t g g g   a t g g g g c c g t           60
g c a c a c a g g g   a t g c c c g c t c   c a c a t c c t g c   c t g c c c c t c a   g c c c t g g c c c   a g g c c c c t t t           120
t g g a g g c a g c   t g a g g a a g g a   t g c t g g g g a a   a g c c c t c t t c   t g c a g c t t t g   t g g a a g g c t g           180
a t c a g t g g c t   g c t g g g t g g c   g g g t a c c c t t   g c t c a g a t g c   c t g g c a g g g c   t g g g t g g c g a           240
t t c a t a a a g a   c c t c g t g t t g   a t t c c c c                                     267

```

&lt;210&gt; 452

&lt;211&gt; 138

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 452

```

c a g g a g a g a a   g a g g c c c c g g   c a t g g g g a t c   t g g g t t c t a g   a g g g c a t g t g   a t g a c t g t a a           60
a t g t t c a c t g   g g t g g g t a g g   g a g t g g t a t c   c a g t g t t c a a   g t g c a g a a a t   c t t t g g c t t t           120
g c t a c c a g t t   c c a t a t g a                                     138

```

&lt;210&gt; 453

&lt;211&gt; 176

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 453

```

g g t t a a t c t t   t g t t a c t a g c   c c t c a c t a c t   c a g a a t t g g t   g a g a c c t c t c   c a t t t t c t g c t           60
t c a c t c a g c t   t a c g t g g t t t   g c t c a c a c t g   a c a c c a a c a a   a c a c c t g t c a   a t c c c t a t g t           120
c c c t c c t g t c   t t c c a a a a a t   a c c t a g a a a t   t g c t g c t c t a   t t g a c g g t a g   t a t t t c           176

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&lt;210&gt; 454

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 454

```

g c t c t a a a a g   t t a t g a a c c t   g a c a t t c t t g   g t c t t a c a c a   a t c t g g a c c c   a g t c t a c t c t           60
t c t a t a a c c a   t c t t c c a c t t   a a t t t a c a a a   t c t t t a t t a a   g g c a c a g g t a   c t c c t a c t t a           120
t c c c c t a t t g   c c t c t c t c a t   g c t g a a t c a a   t c a t g c c a a a   a g c t a a g a a a   a c a t g a g c a t           180
g c t t g g g a c t   a a a g a a a c a g   a a c t g a g g a t   t t c c t a c a c a   t c c t a a c t g c   a a g g a c a g t c           240
c a t c a a a a g c   c a g a g a                                     256

```

&lt;210&gt; 455

&lt;211&gt; 101

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 455

```

g g a a g c t t t a   g c t a c c a a t c   c a g t a c c c t c   c t a a c t a g a a   t g t a t a c a c a   t c a g c c a g g a           60
c t g a c t g a c t   a c t t c a t t a g   a g a t a t a c t g   t a c t c a t t g g   g                                     101

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ADL\_0311WP\_Sequence\_Listing.txt

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<210> 456
<211> 230
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (131)..(131)
<223> nisa, c, g, or t

<400> 456
tacctgtggt tccaggtacc tggagggtg acgtaggagg attgcctgag cccagcaggc      60
caaagctaca gtgagctgtg attgtgccac tgcactccag cctgggcgag gagagcaaga      120
ctctgtctca naaataaat a cataaaat ac agcgtccaaa agtgtgtcat cttctttctc      180
ttcacaattt tataataagg gggtaaaat g cctgtgagtc tattcattat      230

<210> 457
<211> 38
<212> DNA
<213> Homo sapiens

<400> 457
ctttggacta aagaatatat tgggcgaaga atagaggg      38

<210> 458
<211> 154
<212> DNA
<213> Homo sapiens

<400> 458
ttctgctttt cctgttccct atccttacgc aggattgttt tactgttagc caggttaagt      60
ttaagcttct tgaggacttt agtactgaaa gacaatggct cacttgt aag acctagtga      120
agagtacaga tttagatttg ttcagtgtgc tgtg      154

<210> 459
<211> 156
<212> DNA
<213> Homo sapiens

<400> 459
aacatatgtg tagtgtgctg cagcat aaga t ggaagaact taaagaaggc ctgcggcaaa      60
gagatgagct tattgagaaa catggcttag ttataatccc cgatggcact cccaatggg      120
atgtcagtc tgaaccagt g gctggagcca t cactg      156

<210> 460
<211> 267
<212> DNA
<213> Homo sapiens

<400> 460
aagcttttag agaatacact acaccaggga gtatgactac tagtatgact attaggaggg      60
taataccaag agttggacta cgcaccttag gcaagataca aaccaactaa aatagaataa      120
agaatgagtc agatgagtg agccatttta accaagcagc acatttgtta atttctacaa      180

```

ctt agt ct ca gcgat accca ttgtatttag ccatgttcaa caacaagtgt cagaaactgc 240  
acagactcct ccctgttcag ctggt ag 267

<210> 461  
<211> 143  
<212> DNA  
<213> Homo sapiens

<400> 461  
ctttgtccgc tgtcatgatt cgccacgtgc cttcttctgt cctctcacgg ctaggcctcc 60  
agt gaaaggt agacagt aag cctgggcat t cagtcttctg aatttctcac atcaattcca 120  
gggaaaatcc aaccactcca aca 143

<210> 462  
<211> 270  
<212> DNA  
<213> Homo sapiens

<400> 462  
atccagcaag gaat agt gca gcacct aggg act agcaat g at aggaagt t gcaccat at t 60  
tggcccagca agggcaaagg gagagagt ag ttgtgggagt ccagagagac cctggttgtt 120  
gcttctcat t t at t gaaccc gat t t aaagc cagagaacaa agagcccagt ttatgt agt a 180  
cat gacgcag cctcct aggc acagggt aaa ggat ggagaa tagat ct gga ggat t aaat a 240  
gt aacaacaa cgcgcgagat cctct aagt c 270

<210> 463  
<211> 88  
<212> DNA  
<213> Homo sapiens

<400> 463  
ttgagaacag aaat agt ggc at t gcat gcc cagcaagat c gggccct t ac ccagacagac 60  
aggaagat cg aaact gaggt t gct ggcc 88

<210> 464  
<211> 102  
<212> DNA  
<213> Homo sapiens

<400> 464  
tatttcttat gctgtcagat tacatttttc ctttgagtgc tttgggt gca gccgt ggaat 60  
cct gat gt aa aagcat aggt tcttgcatt a ctgagt aaac at 102

<210> 465  
<211> 221  
<212> DNA  
<213> Homo sapiens

<400> 465  
gcagat ggca agt gcaccaa ggagaaggca ggaacact gg agcct gcaat aagggaggag 60  
aggggact gg agagt gt ggg gaat gggaag aagt agt t t a ctttggact a aagaat at at 120  
tgggcgaaga at agaggggg agct t gcagg aaccagcaat gagaaggcca ggaaaagaaa 180

ADL\_0311WP\_Sequence\_Listing.txt

gagct gaaaa tggagaaaac cagagt taga actgttggat a 221

<210> 466  
<211> 281  
<212> DNA  
<213> Homo sapiens

<400> 466  
cacccttctt gaccacaaaa aggtggccat cctgactggt ctctaccttc aggaaaacaa 60  
atggggacct gagggcgctc aaccacccca gaccaccag aagt cacagg agcacggaac 120  
aggaagcagg gagacagcac acagt aagca catggcaagc acacagt aaa cacacggcaa 180  
gtacatggca aat acacagc aggt acacag cgagcacaca gt aagcacac ggt aacact 240  
cagcaagt ac atggcaaatg cacagcaggt acacagcgag c 281

<210> 467  
<211> 133  
<212> DNA  
<213> Homo sapiens

<400> 467  
cccgggccag gcaaggtggg tcacacctgt aatcccagca ctttggggaa caaggtggga 60  
gaatcacttg agtccggcag tttgagacca gcctggccaa cat aatgaga ccgcatcttc 120  
acaaaaaat a tgt 133

<210> 468  
<211> 62  
<212> DNA  
<213> Homo sapiens

<400> 468  
agctcggcca ctctctctgaa ggagggctgg gtctctgggcc tgtatcgaat aaacacaaac 60  
ct 62

<210> 469  
<211> 266  
<212> DNA  
<213> Homo sapiens

<400> 469  
acttcaggaa caggagcaac tactaaaaga gggatttcaa aaagaaagca gaat aatgaa 60  
aaatgagat a caggatctcc agacgaaaat gagacgacga aaggcatgta ccat aagcta 120  
aagaccagag ccttcctgtc acccctaacc aaggcat aat tgaaacaatt ttagaatttg 180  
gaacaagcgt cactacattt gat aat aat agatcttgca tcat aacacc aaaagtttat 240  
aaaggcatgt ggtacaatga tcaaaa 266

<210> 470  
<211> 147  
<212> DNA  
<213> Homo sapiens

<400> 470

ADL\_0311WP\_Sequence\_Listing.txt

gccagcctg gatatttaa ttgttctgtg ctctcctcct tttttttctc tctgtgattc 60  
tctttgtcag ctcttttgcc tatatttgca tctcagttga caccctgat tctgacttgt 120  
ccttatcttc ctaccagtct ctgccga 147

<210> 471  
<211> 187  
<212> DNA  
<213> Homo sapiens

<400> 471  
gtaggagtgc tcatggttct gtcat tcttg gacctctcct ggctgagctc t gattccctg 60  
tgagcacgat gctgatgcaa tagtctgtg tcatcactgc agcggctcctc aggagctgcc 120  
agggccaat t gctacagagt gtctgggtgt gtggcatagg aggaaggttt gcttgtgaaa 180  
tgaggct 187

<210> 472  
<211> 235  
<212> DNA  
<213> Homo sapiens

<400> 472  
atctacgcca ctcgctctgg tgggacctc gtgcttgtgg ggctgggctc t gatatgacc 60  
accgtacccc tactgcatgc agccatccgg gaggtggat a tcaagggcgt gt ttcgat ac 120  
tgcaacacgt ggccagtggc gat ttcgat g ct tgcgtcca agtctgtgaa tgtaaaaccc 180  
ctcgtcacc atagggtttcc tctggagaaa gctctggagg cctttgaaac attta 235

<210> 473  
<211> 177  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (59)..(71)  
<223> n i s a, c, g, o r t

<400> 473  
gaagt aagcc tcatcatcag agcctttcct caaaactgga gtcccaaatg tcatcaggnn 60  
nnnnnnnnnn ncagccacta agaaccctc tgc ttttaac tctagaattt gggcttggac 120  
cagatctaac atcttgaata ctctgccctc tagagccttc agccttaatg gaaggtt 177

<210> 474  
<211> 34  
<212> DNA  
<213> Homo sapiens

<400> 474  
taaagcgtgg ccgtggctcg cgtgcctgcc atct 34

<210> 475  
<211> 268  
<212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 475

```

aagt cct cct caggct t gga gaact t cct c agcgt cacct cct t cat t ga gcct t ct ct g      60
at cact ccat ccct ct cct a cccct ccct c ccccaaccct caat gt at aa att gct t ct t      120
gat gct t agc att cacaat t ttt gat t gat cgt t at t t gt gt gt gt gt ccgat ct cac      180
aagt at att g taaaccct t c ggt ggg t ggg ggccat at cc t agacct ct c t gt at ccccc      240
agact at ct g t aacagt gcc aggcacac                                              268

```

&lt;210&gt; 476

&lt;211&gt; 244

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 476

```

t cact gt aag gt acagt t ag ggt aacact t t agagg t t t a t t at t t t t aa aaaact t t t c      60
t t gaact cct ggccagcat g gt gaaacccc gt ct ct act a aaaat accaa aat t agccag      120
gcgt gat ggt ggg t gcct gt gat ct cagct act t gggagg ct gaagcagg agaact gcct      180
gaaccaggga ggcggagg t gcagt gagt c gagat cgt gc t act act gcc t ggg t ggcaa      240
gggt                                              244

```

&lt;210&gt; 477

&lt;211&gt; 57

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 477

```

t gccat t t t c caagaat gac ggt ggt ggct t t t agt caga aaat ggcct t ct gt gct      57

```

&lt;210&gt; 478

&lt;211&gt; 153

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 478

```

ggagagaagc agaat at t cg gacaaacacg gacagt at ct cat cggacat ggt act aagg      60
t ct acat cga cccct t cact t at gaagacc ct aat gaggc t gt gagggaa t t t gcaaaag      120
agat cgat gt ct cct acgt c aagat t gaag agg                                              153

```

&lt;210&gt; 479

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 479

```

agct gcccct t t cccgt cct gggcacccc agt ct ccccc gaccccggt cccaggt at g      60
ct cccacct c cacct gcccc act caccacc t ct gct agt t ccagacacct ccacgcccac      120
ct ggt cct ct cccat cgccc acaaaagggg gggcacgagg gacgagct t a gct gagct gg      180
gaggagcagg gt gaggg t gg gcgaccagg at t cccct c ccct t cccaa at aaagat ga      240
gggt act                                              247

```

ADL\_0311WP\_Sequence\_Listing.txt

<210> 480  
 <211> 154  
 <212> DNA  
 <213> Homo sapiens

<400> 480  
 agcggagcaa gtgtcccggg ccttcagcca gccctggat a gctacttcca tccccgggg 60  
 actcccgcgc cgggacgcgg ggtgggacca ggtgcgggac ctggggcggg cgacgggact 120  
 taaat aaagg cagacgctgt ttctacca aaaa 154

<210> 481  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 481  
 agatgtgcac aaacagagcc cccgcgtaca ggtccagctg cggagggaga gaggcttgtg 60  
 tggggctgtt attcccaggg ctccagcaag ccaactccctg ggtgacctcc ggcaaggccc 120  
 tctctgggcc tcggtggcct gtggataagg aggggagacc ccaactcgcc tgcctgcctg 180  
 catcacgggg ccattgtgag gttgggggaa gacctggccg tggagctaca agcttgtgcg 240  
 gatgtcaggg gacattactg ttgctaat aa agtccaaagt ggccaatgcc tt 292

<210> 482  
 <211> 248  
 <212> DNA  
 <213> Homo sapiens

<400> 482  
 cgggtaactt ctggatcccg ttctgatgc agattcttgt ctgttctcc acttgtgctg 60  
 ttagaactca ctggcccagt ggtgttctac ctctacccc acccaccccc tgcctgtccc 120  
 caaat tgaag atccttcctt gcctgtggct tgatgcgggg cgggt aaagg gtatttt aac 180  
 ttaggggtag ttctctgctgt gagggttac agctgacct cggaagaac aaagctaaag 240  
 ctgccttt 248

<210> 483  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<400> 483  
 gcgatgaacc caacctccct gaagccaaaa ctcccaccc tgcgcacac tccggaccac 60  
 ccaacttgcc accaagcaca tcctctccaa atccaacct tatttgcgac ccttcagtga 120  
 tgaccagca gacctccaaa aagcctcctc tggccagatc tccagccggg tctggggctg 180  
 ggttgcgggag gggagggctc gggagtcac acttctccac caacttccct tccactctc 240  
 ttattccaca ttgcagtgtt tggaaataac c 271

<210> 484  
 <211> 37

## ADL\_0311WP\_Sequence\_Listing.txt

<212> DNA  
 <213> Homo sapiens  
 <400> 484  
 tgtcctgggc accgtagcga gactctgctt tctacaa 37

<210> 485  
 <211> 110  
 <212> DNA  
 <213> Homo sapiens  
 <400> 485  
 gcaggcagta agaagcaggg atttcttcaa atgctagt aa gcacaaagag agggagaagt 60  
 tttt gtaagt aacgaacagg gccgggcatg gtggcgtgag aggccgaggt 110

<210> 486  
 <211> 238  
 <212> DNA  
 <213> Homo sapiens  
 <400> 486  
 gaccaccaga tcctatagag cctttagacc atcgtagaga ctttgctttt ctctgagtgc 60  
 tttggtaggg atttgaggaa aggagt gaca tcgtatgaat gactttatta tgtgccacg 120  
 tggaggtgtc aaataggcag ctattgtgtt gcagggtcccc aggttcattg attcactaag 180  
 aggactcaaa agactcagca cgtagtccta ctcacagctg tgatttatta tcgcacaa 238

<210> 487  
 <211> 226  
 <212> DNA  
 <213> Homo sapiens  
 <400> 487  
 cagattcttt tttatggtgg ctttgcttgt tttaaatttt tgcatactt ttcatctttt 60  
 tatgtgtgtt tcctgtagt t gatccgaag gaaaagagta tagtagcctg agaatcagga 120  
 gatgggagtt ttagtcgtag gccttatgat aattaccccg cggtggtgtg tagaaaagta 180  
 tgtaaatttg ctctgtttta agactttgaa ctacctcaag aagagg 226

<210> 488  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens  
 <400> 488  
 gtgggagaag ttggcgtcct aggctgggga ttggcgggg gaccttaaag aaaaaggcca 60  
 gggctgaggg tcctgaggag agagagagag gccacgtgga tggaggactg tccccctt 120  
 ctcggttctg tccccctt gagtctaact cactgttgag gggaggaaga agggggatgg 180  
 acggaaggga gaccgaggaa aggctttcg gagggggac attatccacc cagaggtgtg 240  
 ctaccacaaa ccaccgcgag atccttagag t 271

<210> 489  
 <211> 109  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 489

ctgtgctctg gaaaggctac caaatactgg ccaaggtcag gaggagcaaa aatgagccag 60

caccagcgcct ttggctttgt gttagcat t t cctcctgaag t g t t c t g t t 109

&lt;210&gt; 490

&lt;211&gt; 134

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 490

gctacagctg gcgaacccca aagagttcta ccacgaggtg cacaggccct ct cactt cct 60

caactttgct ct cctgcagg agggggaggt t t actctgcg gatcgaggagg acctgtatgc 120

ctgaccgttt ccct 134

&lt;210&gt; 491

&lt;211&gt; 74

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 491

gggaagccaa atataggcca agagcagcct gtggatgatg ctgcagaagt ccctcagagg 60

gaaccagaga agga 74

&lt;210&gt; 492

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 492

t acatccctt caccaggtgg t gccatgtct cccagctact cgccaacgtc acctgcctac 60

gagccccgct ct cctggggg ctacacaccc cagagtcctt ct t at t cccc cactt cacct 120

t cctactccc ctacctctcc atcctattct ccaaccagtc ccaactatag tcccacatca 180

cccagctatt cgccaacgtc a 201

&lt;210&gt; 493

&lt;211&gt; 253

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 493

gaagaggatt cagggtcagc ct aggggacc ctggctccct ccgataggca ggaaggagga 60

gggatgcgga ggagaggctg agccttccac gggcctcctg t t aggggtgt t ggtggagggc 120

caggttgggg agggaagcct aaggaccctc cacacctccc acagccagag t cagt t gagg 180

ctgggacaaa ggggaaggag agagggaagg aggaccgcct gacctt gccc agaaggagct 240

t cctctaaac tgc 253

&lt;210&gt; 494

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 494  
gt aaaggagt gggt gat t t g caaat aaagc acat t at aca caa 43

<210> 495  
<211> 250  
<212> DNA  
<213> Homo sapi ens

<400> 495  
t gct gct cct cat aat aagc cgccact gt c t ccaggt agc cct ct t t gaa gt cgt cct cc 60  
agct ct gcca ggct cgacat cacct gt cca cgt cct gat t ct gcatt t t t g catt t t t at ca 120  
t aaaaat ct t t ct at ggcct g gt gcatt t cgg gcct t cagct t ct t cat gt c at cagagagg 180  
acct t cgga agcacat ggc ggccaaaagt t caaggagcc aaggcct gag at gaccagc 240  
t ccaaaggga 250

<210> 496  
<211> 262  
<212> DNA  
<213> Homo sapi ens

<400> 496  
t cccaacaa cacaacgct cct gt t ccac ct acgt agga t ct gt gaaac aggct cagt g 60  
cct t t gaggg aggaggaac gt t t agatt g agaccacccc act cccgggt gat t aaat aa 120  
at at gt ct ct cccccacccc acgcaggat t ggaaaaagt t aat t gt ggt t t cagaaaagt 180  
t aaccct gc gt t gct t cga cccct t ct ct ccagggaagg gt t gggt aaa t gt ct acgaa 240  
t cgcct t gag agagaact aa ag 262

<210> 497  
<211> 170  
<212> DNA  
<213> Homo sapi ens

<400> 497  
t acacagt t t ccaat t t aag taggcagact gagcat gcc at cagt t t cc t att gct gct 60  
t ccat ccct c gaaat gat ag aaaagat t t t aaacagcaaa t aaagaat ga gaaaaagaag 120  
aaat t at aag t ggggt t t t aa aaagt t gcag t gggccaggc at cat ggct c 170

<210> 498  
<211> 89  
<212> DNA  
<213> Homo sapi ens

<400> 498  
t gcccgat ca cacaggagt a t gccc aaact ct ct caggcc t ct agcagct gacaaccact 60  
gct t t aaat c cct att acat t t att at ga 89

<210> 499  
<211> 242  
<212> DNA  
<213> Homo sapi ens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 499  
cctgggggca ggacccacag ccagtgggct aagaccttta aaaaattttt ttctttaatg 60  
tatgggactg aaatcaaacc atgaaagcca attattgacc ttcttctctt ccttccttcc 120  
ctcccttctt ccttctctcc ttctctctc ctctctctc tcctctctc tctttcttc 180  
cttccttctt ttttttctt ttctcttct tctttattc ttgggtctca ctctcatcac 240  
cc 242

<210> 500  
<211> 220  
<212> DNA  
<213> Homo sapiens

<400> 500  
tcaagacgag cctggacaac acaacaagac cccaattct actaaatttt ttttttaat 60  
tagccagatg tggtaatgca tgcctctgt a gtcccagct a ctcaggaggc tgaggtggga 120  
ggatcacttg agtgcaggaa ttcaaagctg cagtgcagct a taatacaagg ctctattgca 180  
ctccagccta ggcattagag cgagaccgtg ttattttaa 220

<210> 501  
<211> 271  
<212> DNA  
<213> Homo sapiens

<400> 501  
ttaaggaca aactcaagaa ggcacaacat gaaagagaac aacttgaatg tcagttgaag 60  
acagagaagg atgaaaagga actttatag ggtacatttg aagaatcacg aaatagaaaa 120  
taccaagctt atgtcagagg tcagacttt aaaaaattta gatgggaaca aagaaagcgt 180  
gattactcat ttcaaaaaga gattggcagg ctgcagttat gt ttggctga aaggaaatct 240  
gcaagacttt cctgcttaca acctcaagta a 271

<210> 502  
<211> 133  
<212> DNA  
<213> Homo sapiens

<400> 502  
caacatggac atttatacta ataggaggg cagaggcgaa tatgtgagaa ggtccaccac 60  
ctcagagctt gaatcagctt cacgatgat gaaaggtaag ctttatcact gatctcaaca 120  
gcagactggg ggc 133

<210> 503  
<211> 119  
<212> DNA  
<213> Homo sapiens

<400> 503  
gagt caggct tactaatgct gccctcactg cctctttgca gt aggggaga gagcagagaa 60  
gtacaggtca tctgctggga tctagttttc caagtacat tttgtggtga cagaagcct 119

## ADL\_0311WP\_Sequence\_Listing.txt

<210> 504  
 <211> 87  
 <212> DNA  
 <213> Homo sapiens

<400> 504  
 gat caaat ca agt ct t ggt t gt ggct t gct gaatt aaat a ttt at gagt g gt gcat t t t t 60  
 aagt at cgt g accaagacac cat at t a 87

<210> 505  
 <211> 298  
 <212> DNA  
 <213> Homo sapiens

<400> 505  
 aat acagaac t gaggcct agg ccagggaact gggat t gggg t t agat ct aa gcaagat cag 60  
 cat gt aagt g at agt ggaga aagt aaat gg agaggt gagg act cat cccc t t ggt ggaaa 120  
 t t cggaat t a at aaagcagg aggagagt ca ggat aat ggg ct gt t gaat a aagaaagt aa 180  
 gt gacaagga agaggt aat g t gt at ccaag aagt aggaaa gaaat gagac t t aaagcgt a 240  
 ggggggt t agg ct gt gt aaga gct cagt acc caacaggt gc t cagt caagt aact t gac 298

<210> 506  
 <211> 247  
 <212> DNA  
 <213> Homo sapiens

<400> 506  
 t gggat t gca gt cgcct gcc accgt gcccg gct aact t t t gt at t t t ggt t gagacaggg 60  
 t t t cgccgt g t t ggccaggc t ggt ct agaa ct cct gacct caggt gat cc acccgcc t t g 120  
 gcct cccaaa gt gct gggat t acaggcgt g agccaccaca cccggccaaa aaaaaaat t t 180  
 t t t t t ct at c cct gccat t c agt ct ccat t agcact ct at t ct ct ct cat t t at t ccacc 240  
 ccgt ct t 247

<210> 507  
 <211> 204  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
 accaccct a gct t t gt gt g t agt gt agt g at t t t ct ggc t gt cact cat act cact ggg 60  
 caccagcct t gccct ct tag cct ccat cca t ccagacagc cct t cccacc t cct ggt ggt 120  
 gagccagt ct gcat t cccac gccat cccaa agccct t t ca t ct t acccgt gcat t gt aga 180  
 t ggaaggagc acccat gcca t t ca 204

<210> 508  
 <211> 179  
 <212> DNA  
 <213> Homo sapiens

<400> 508  
 aaaaaggt ct at gat ct t ga gggcagacag cagaat t cct ct t at aaaga aaact gt t t g 60

## ADL\_0311WP\_Sequence\_Listing.txt

ggaaaat acg t t gagggaga gaagacctt g ggccaagat g ct aaat ggga at gcaaagct 120  
t gagct gct c t gcaagaaaa aat aagcagg acagaggatt t gct ct ggac agagat gga 179

<210> 509  
<211> 291  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (39)..(83)  
<223> n i s a, c, g, o r t

<400> 509  
t ggt gaatt t t ct aggagcg at gat gt act gt aat t gt nn nnnnnnnnnn nnnnnnnnnn 60  
nnnnnnnnnn nnnnnnnnnn nnaat gct t gt t ct aagac att t ct gaat gt agaccatt 120  
t t ccaaaaag gaaact t t at t t t caaaaac ct aat ccgt a gt aat t cct a at ct t ggaga 180  
at aaaaaagg gcggt ggagg ggaaaacatt aagaatt t at t catt t att t c t cgagt act t 240  
t cagaaagt c t gacact t t c att gt t gt gc cagct ggt t g aaatt aaaac t 291

<210> 510  
<211> 282  
<212> DNA  
<213> Homo sapiens

<400> 510  
gat agt gat g ggt ct t ccca t t gt cct t aa accct gt aca t att gt gcag cct ggcct gg 60  
gact ggat gt t t cagt agaa at aacacagg ggacaccaga ggcaagcct g gaggt cagct 120  
cagt cg t t ag gcagt ggagg cacaaggt gg ggcagt t t t t cccaggt gt t t gat gat gac 180  
t gact t gagc cagagacccc t aaagat aga gt ggagt cca gggaat gat c t agaact t ca 240  
ggg gacaggc aggagct gcc cggat t t aac agcagaacca t a 282

<210> 511  
<211> 164  
<212> DNA  
<213> Homo sapiens

<400> 511  
ct aact ct gt cct gaagagt gggacaaat g cagccgggcg gcagat ct ag cgggagct ca 60  
aagggat gt g ggcgaaat ct t gagt ct t ct gagaaaact g t acaagacac t acgggaaca 120  
gt t t gcct ct ct cccagcct caaccacaat t ct t ccat gc t ggg 164

<210> 512  
<211> 294  
<212> DNA  
<213> Homo sapiens

<400> 512  
gat ggacagg gt t ct gaaaa aact gaaaat gaat t ct aga aagcagcat t t gagagggaa 60  
aagagaagt g at cagcat t t aggaat at ga act gt ct gga gct agagaaa cagcct ggga 120

ADL\_0311WP\_Sequence\_Listing.txt

aaagagcaaa gggct agagc aggaaagaga aaagagaat g agact agcgg t ggt t t ggat 180  
at t at t t gt a accaaagt ca aaggacggga gat ct agagt ccagccaaca aagaact t gc 240  
t cct at aaaa accaaat gga cccaccct t cact t gacgt agaggt cct t t cct 294

<210> 513  
<211> 262  
<212> DNA  
<213> Homo sapi ens

<400> 513  
aacat ggt cc t ggaggt t ac agt gt agt ga ggggcaaaga cat ggagcca at ggt t gacg 60  
t gaaacct ca t gt gaggagt t aact ggat g gagaaaggag t caagagagt t ct aggt aga 120  
ggaggcagca t gt caaaggc acagt aaagg gaggat gaat ggt ccat t t c agggat ggaa 180  
gaaggct gct agat t ggaac at agggaagg agggaat gt g t gat acaagc t ggagct aga 240  
aaggt aggt g gt cagaacat ag 262

<210> 514  
<211> 81  
<212> DNA  
<213> Homo sapi ens

<400> 514  
gaaaaat t t a cacagct aga t t t ggaagat gt t caagt t a gagaaaagt t aaaacat gcc 60  
acgagt aaag ccaaaaaact g 81

<210> 515  
<211> 296  
<212> DNA  
<213> Homo sapi ens

<400> 515  
t t aaaaggt c ct gct ct at c gt t ct gt gt c t ggct ct gca aact gct ggt at gt aaaaga 60  
ccct ct t t cc agacaggcca cgaact cccc gaaggccggg ct ggcct ct t ct ct gcct ct 120  
gt cccaacct ccct gacaca ccct ccat cc acgt t aat aa aacaggggaac acaccagagg 180  
gct cagt aga gaaaaacaca t cat aat gac t gat t t at aa t t t t at agc t t t aaaat aa 240  
t aaat t t at t t t t t ccat t aaagt at t at aacacgatt a caaaaagccc t cgt gc 296

<210> 516  
<211> 285  
<212> DNA  
<213> Homo sapi ens

<400> 516  
t agat gccgt cat ct t ccgt ggt cagccc acaat ct t ca gcgt ggcct c t cccaggt ca 60  
ct gt aggaga t gct gt agt g accat cgt t g t t caaggt gt t gt gt t cagg gccct t ccag 120  
gt aat t gagg ct t t gggg cg gccacagact cgacat ct ag gaacaacggt ct cccct gt c 180  
t cacacgt ga cct cact caa t ggaat gacg aat t ct gggg gaacgt cat a aat gt agt t g 240  
ggat t gagaa gct t gt t gct gagt cct t cc cgt gact t cc gat aa 285

ADL\_0311WP\_Sequence\_Listing.txt

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<210> 517
<211> 148
<212> DNA
<213> Homo sapiens

<400> 517
cact at gcag t t act gt gac t gt gggaggc aagcaacact t gct cggact gt at gacacc 60
gcgggacagg aggact acaa ccagct gagg ccact ct cct accccaacac ggat gt gt t t 120
t t gat ct gct t ct ct gt cgt aaaccct g 148

<210> 518
<211> 269
<212> DNA
<213> Homo sapiens

<400> 518
gaccaggaag t cct at aaag aat t at at t t ct at agaat t aaaaat gcag t t ct gt cagc 60
ct ggacaaca aagt gagacc cccat agct a caaaaaaaaaa aaaaaaagt t t t t t aagag 120
t t gggcat gg t ggcacacgc ct gt agt cct agct t ct cgg gaggct gagg t gggaggat t 180
gct t gagat t gggaggt t ga ggct gcagt g agccgt gat c acaccact gc act ccat cct 240
gggt aacaga gt gagaccac t t aaat t aa 269

<210> 519
<211> 263
<212> DNA
<213> Homo sapiens

<400> 519
caaagcaaca aat ggaggca t at gaaat t c ct cat cgagg aaacact gga gat gt t gct g 60
t t gagat gat gt ggaaacct gcct at gat t t t ct gt at ac ct ggagt gct cact at ggaa 120
at aact acag agat gt gt t a caagacct t c agt cagct t t ggacagaat g aaaaacct g 180
t gact aaaca ct ggagagaa t t aact ggag t t t t aat act agt aaat t ct t t ggaggt t t 240
t gagagt aac t gcat t ct cc act 263

<210> 520
<211> 182
<212> DNA
<213> Homo sapiens

<400> 520
t g t t aaccca t t ccagt aca gt at t c t t t aaaat t caaa agt at t gaaa gccacaact 60
ct gcct t t at gat gct aagc t gat at t at t t c t t c t t a t cct ct ct ct ct t t ct aggcc 120
cat t gt cct c ct t t t cact t t at t gct at c gccct cct t t ccct t at t gc ct cccaggca 180
ag 182

<210> 521
<211> 276
<212> DNA
<213> Homo sapiens

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ADL\_0311WP\_Sequence\_Listing.txt

<400> 521  
agccacagt t ggt gt ggct g gt t caggggc t ggcat t gga accgt gt t t g gcagct t gat 60  
cat t ggct at gccaggaacc cgt ct ct caa gcagcagct c t t ct cct at g ccat t ct t gg 120  
ct t t gccct c t ct gaggcca t ggggct t t t ct gt t t gat g gt cgcct t cc t cat cct ct t 180  
cgccat gt ga ggct ccat gg ggggt caccg gcct gt t gct act gcaact c cacaccat t c 240  
t t ggt gct gg ggt gt gt t aa gct t t accat t aaaca 276

<210> 522  
<211> 288  
<212> DNA  
<213> Homo sapi ens

<400> 522  
ggct t aacca gct agacat t cct ct aaat a cat acgt aac aaaaat t gat ggcaggagat 60  
t t t at t ggga t cact ggat a cct acact ca acaggcagaa ct t ggct aat t ccat t t at a 120  
ccact act ga gacagt gaag acaaat t aag aat cagaaca ggaagcacat agcat aggga 180  
t acccgt gt c agcgacat at t t aat at gcc cct cagct t a agact caat a ct gaacagac 240  
caaaaggcca cct caat t gc cgct cccgcc acact t gct a t t gaaact 288

<210> 523  
<211> 210  
<212> DNA  
<213> Homo sapi ens

<400> 523  
ccaaggcat t gct aat ct ct gt act t cagt aaacact gaa aagt caacgt aact ct at ag 60  
gt cgcat at t ct t gaat gac agggaaaggc aaacat ct ct acagaggt gt gat cgaaagc 120  
at t t t acat t aggt acacag aaact t t aaa ct cacact at gt aagcct ct aat cagcct g 180  
agcaaaaat cc at t gcct aca cagt cat t t a 210

<210> 524  
<211> 54  
<212> DNA  
<213> Homo sapi ens

<400> 524  
ggt t gaaaga t gaaat gcct gt at gt gct c t gaagaaat g gt aat t ccag at t g 54

<210> 525  
<211> 277  
<212> DNA  
<213> Homo sapi ens

<400> 525  
t ccacct gcc gagaagct ga gat t at agt c act gt gcct g gct ggaat at agcct t t t ga 60  
ct ccat gt ca t t acccgca c t ct t cgct ct t cct ggaat g t at t t cct ga gcct gt ct gc 120  
cct aaaaat t ccaat t t ct c ct t t aagct t t ggct caaat gct at ct at a ct ct gct gcc 180  
t cccccaagt cccct agt g acacacaggg t cct ct t ct g ct ct t cct t a t gt t ct t ct t 240  
t gt cagagca acat cacagc agt accccaa cat t t gg 277

# ADL\_0311WP\_Sequence\_Listing.txt

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<210> 526
<211> 39
<212> DNA
<213> Homo sapiens

<400> 526
gcggcgggca gggcttgcct ttcttagtct gatgccaaag          39

<210> 527
<211> 223
<212> DNA
<213> Homo sapiens

<400> 527
gggccaatgac acctgatcat tggatcaaga ggggcactgc tctactcatg agcctggaca          60
gctgagacct cctcctcttc tccgcttgag agagaggggtc agggactcca ggagctaaga          120
cagatgttgc acctaggact gaggccggac ctactcaga ctttgacctt ggccgaattt          180
gtgtgatgtg gccctggaga tacctagt tgtagccat aaa          223

<210> 528
<211> 239
<212> DNA
<213> Homo sapiens

<400> 528
caggaaggcc tcgaggccac acaggggctg ctggccggcg agtgggcccc acccctctgg          60
gagctgggca gcctcttcca ggccttcgtg aagagggaga gccaggctta tgcgt aagct          120
tcatagcttc tgcctggcctg ggggtggacc aggaccctg gggcctgggt gccctgagt g          180
gtggtaaagt ggagcaatcc cttcacgctc cttggccatg ttctgagcgg ccagcttgg          239

<210> 529
<211> 211
<212> DNA
<213> Homo sapiens

<400> 529
ctggtggact attccatcac ccatgcagag cccgccaacg tgttcgacat caattcccac          60
acggggggaga tctggctcaa gaattccatc cgctccctgg atgccctgca caacatcaca          120
cctggaaggg actgcctatg gtccctagag gtgcaggcca aggaccgggg ctcccacatc          180
acttcagcac cacagcctta ctcaagattg a          211

<210> 530
<211> 256
<212> DNA
<213> Homo sapiens

<400> 530
tcggcctcag attccatatt tgaacaccag ctgattgaga gaaggggaat gagaagagct          60
ggatgagttt aaataactca ttgttcagat tcctgaacag gagtgggat aatggccatc          120
ttttctttcc tatcctttct tccccctca ctgtgaaaaa taacagtcca cccaagtca          180

```

t acaact ggac ccagt gcct g cggggacagg act gt ggggt t t ct t ggt cac acct gt gt t g 240  
gt gct caat g cagt gt 256

<210> 531  
<211> 250  
<212> DNA  
<213> Homo sapi ens

<400> 531  
t agt t t cat t t act ct t t ag gcagaaaat a ggt t caaggg t ct agt aaag gaggcaaat g 60  
ggcagaaaac aacct ct t gt t t gct at ccc act gcact t g aaat ggacct ct at aat t ca 120  
ct accat t t a t aagt gt ct c gcat at caac at cacat t ag gt aat t t act gcct ccaat t 180  
cct ggt ccat aact at t cca t cct gaaaag t cat aat aca at gt t at t gg aacaat ct at 240  
t cat at ggt a 250

<210> 532  
<211> 143  
<212> DNA  
<213> Homo sapi ens

<400> 532  
at gt at acaa agt aaat t ct t agccaggt g t agt ggct ca t gcct gt aat cccagcact t 60  
t gggaggct g aggcgggt gg at cact t gag gt cagaagt t caagaccagc ct gaccaaca 120  
t cgt gaaat g ccgt ct t t ac aaa 143

<210> 533  
<211> 273  
<212> DNA  
<213> Homo sapi ens

<400> 533  
agt ggct t cc t t ggagt agt ggggt gaaagt ct gct t aaaa agagggct t a ggagagaat t 60  
gggggaagga at t gaaat ac at caacat ag acaact ct t g aggagt t t t g ccat gaagag 120  
acact t t gca t ccagaggac act t t gcat c cagagagt gg ct t cct t gga gt agt ggggt g 180  
aaagt ct gct t aaaaagagg gct t aggaga gaat t ggggg aaggaat t ga aat acat caa 240  
cat agacaac t ct t gaggag t t t t gccat g aag 273

<210> 534  
<211> 250  
<212> DNA  
<213> Homo sapi ens

<400> 534  
gagct ggaaa aaagt cagac t ct ccacaga cccct at gg gggaccccca act caaggcc 60  
aaggact ggg cgt at cggat gct cat aaca cccct ggcct ggccct t t a ct gagaagac 120  
t cct t ggat a t t t cccaaga accccccaca t acaccct c acaagccacc cct cct gaga 180  
ggcagggggc cct ccgcccc ct ccccat gt at t ccccacc t gt gt t ccgt t t gaccagca 240  
cagaaat at t 250

ADL\_0311WP\_Sequence\_Listing.txt

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<210> 535
<211> 91
<212> DNA
<213> Homo sapiens

<400> 535
gggagcacac agt cacct ct cacagct cca t t at ccagcg gct gccgggc t ct gacaacc 60
t at at gat ga cccct accag ccagagat aa c 91

<210> 536
<211> 250
<212> DNA
<213> Homo sapiens

<400> 536
gct gccatt g ct gt ggt t at gggcat t t ag aaaact t gaa agt cagcact aaaggat ggg 60
cagagg t t ca acccacacct ccact t t gct t ct gaaggcc cat t cat t ag accact t gt a 120
aagatt act c caaccagtt t t t at at ct t t ggt t caaaa cggcatt gt ct ct ccaacaat 180
t t aagt gcct gat acaaagt ccaaagt at a aacat gct cc t t t act ct ct t gct gct act 240
ct t gct t t t g 250

<210> 537
<211> 64
<212> DNA
<213> Homo sapiens

<400> 537
gt agct at t g at gt aact t cgcaacggag t gt ct gaaat t gt ggt ggt c ct gat t t at a 60
ggat 64

<210> 538
<211> 299
<212> DNA
<213> Homo sapiens

<220>
<221> mi sc_feat ure
<222> ( 224) . . ( 232)
<223> n i s a, c, g, or t

<400> 538
cagagg t ct t gcagcccct g t ggat gcccc cgccgaggt c ccccgat ccc cgcacccgga 60
ct gct gct cc ct gccccacc at t gcgggt c cccaggaag ccaggt gacc ccaggt ggga 120
ggct gt gt gt ggaggccat c ct ggaaggaa gt t t agacct gccaggt gt ggagcgaggg 180
gcacaggggc at cct aacct cagaaact ga aat aaagcct t t gnnnnnnn nnt ct gt aaa 240
acat caacc ccaat cagaa gat ggcaaat ggggaat aaa aat agcaggt aacacgt ca 299

<210> 539
<211> 195
<212> DNA
<213> Homo sapiens

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ADL\_0311WP\_Sequence\_Listing.txt

<400> 539  
t gacagcagc t gat g t t g t t aaacagt gga aggaaaagaa gaaaaagaaa aagccaat t c 60  
aggagccaga ggt gcct cag at t gat g t t c caaat ct caa acccat t t t t ggaat t cct t 120  
t ggct gat gc agt agagagg accat gat gt at gat ggcat t cggct gcca gccgt t t t cc 180  
gt gaat gt at agat t 195

<210> 540  
<211> 171  
<212> DNA  
<213> Homo sapi ens

<400> 540  
aaaat agaac at cct gagt t acagaaat t c agccct agt g t at cct ggcc t aaaaat aca 60  
gaacaat caa gt t gagt ggt t ggaaat gag aggct aggca ggg t t ggaaa cat gct aat g 120  
t t t act gagt gaaat ct t t c ct t ct cagt a gagt t gccct t gcagct gaa a 171

<210> 541  
<211> 44  
<212> DNA  
<213> Homo sapi ens

<400> 541  
t ct ct ggct g at at gt t ccc t gagat gaat gaggt ct gt c aaga 44

<210> 542  
<211> 249  
<212> DNA  
<213> Homo sapi ens

<400> 542  
gt t acaggt g ct acgcat ga t ggt cggagt aaat at ct ca gat gagcagc t gggcagcat 60  
cgcagacagg accat t cagg aggct gat ca ggat ggggac agt gccat at ct t t cacaga 120  
at t t gt t aag gt t t t ggaga aggt ggat gt agaacagaaa at gagcat cc gat t t ct t ca 180  
ct aaaggaga ccaaact gt t cct t gcggt c t agt at t t aa gaact ggaac t t gaaagt cc 240  
t cct t ct ac 249

<210> 543  
<211> 213  
<212> DNA  
<213> Homo sapi ens

<400> 543  
gaat ccat t a t caat gt t gc t agt gt aat a cacaagaaaa cccaat gaga gaaat t caaa 60  
t att aagaaa caagct t t t g t t gat t gaggc t t t aaat ggc cacacacat t at aat at ct 120  
aagat gct t g t gct ccccaa t aaccaat t t t t gcct ccaa t gaggat gca agt cct aact 180  
t ct at gct cc cgaat t t at c at act agcac ct a 213

<210> 544  
<211> 242  
<212> DNA  
<213> Homo sapi ens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 544  
t aat aag t g t a g c a t c g t g t g t c t t g a a g t a t a c t t t t g c a c t g t a a c t t g g g t t a c g t 60  
t a a a g a g a g c t t a g c a c c a a a g g t a g a t a a t g a a g a a t g g c a t a g g a a a g t g g a g a t g a 120  
t a a a a a g t t g a t t g t t g a a c c a a a a g g g t t t g a a g g g a a g c t t c g a c t g a g t a t c a g a a 180  
a t t a c t t a a g g c a c a t a g g a c c t g a a t c a g g r a a c c a g c a c t t c t t a c a a c t g c c a g t t t 240  
t a 242

<210> 545  
<211> 215  
<212> DNA  
<213> Homo sapiens

<400> 545  
t g c a a g g a c t c a c c t c c t t g a g c c t t g g t t t t t g t t g t a g g g a t t a a a t g a g a t a a t a t g 60  
a g t g g c a g c t c t t c a t g a g t c c t g c a g t g c t a a g c a a a t g t c a g a a a t t g g t g t a t t a g a 120  
c t a t t t a t c t t t g a t c t t c t g a a t g g a t t g c t g t c a t g g a c a c g g a c a c g g a t c t t c a t c 180  
t g g t t c a t t g t a t t t a t a t g t g a g g g a t g g a t g g c 215

<210> 546  
<211> 237  
<212> DNA  
<213> Homo sapiens

<400> 546  
g g a g a a g t t a a g c a a c a t c t a g c a a a t g t t a t g c a t a a a g t c a g t g c c c a a c t g t t a t a g 60  
g t t g t t g g a t a a a t c a g t g g t t a t t t a g g g a a c t g c t t g a c g t a g g a a c g g t a a a t t t c t 120  
g t g g g a g a a t t c t t a c a t g t t t t c t t t g c t t t a a g t g t a a c t g g c a g t t t t c c a t t g g t t 180  
t a c c t g t g a a a t a g t t c a a a g c c t a g t t t a t a t a c a a t t a t a t c a g t c c t c t t t c a a 237

<210> 547  
<211> 257  
<212> DNA  
<213> Homo sapiens

<220>  
<221> m i s c \_ f e a t u r e  
<222> ( 2 2 0 ) . . ( 2 2 0 )  
<223> n i s a , c , g , o r t

<400> 547  
g a a t t g t c a t t c a t a a c t c t g t g c t a t a t t a c t t g a g g g g c t a a g a a a a a t g t a t g g t c a 60  
g t g a a a c a c a g t a g t g t a c c c t t a a a t g c c t t a t a a a a g a c c a t c c a t c c a g t c t g c g c t 120  
t t t g a c t g t g t g c a a g t a t c a g t a a t a a t g c t t t t g g g g g c t c a g a t g a a c a g c g a a c a c 180  
c a a t c a g c c a g g a c t c t g g a a g g a a a g c t c c a a a a t g a n g a a g t c c t t t c a a c a c c a t t 240  
t t c c a t t a c t g t t c t c a 257

<210> 548  
<211> 34

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<212> DNA
<213> Homo sapiens

<400> 548
tttgattaat aaaaatgcgt tgagcctagt t at a 34

<210> 549
<211> 194
<212> DNA
<213> Homo sapiens

<400> 549
gttgcttccc caccctgagg agaggacacc atggcttact actcaggaca agt at gcccc 60
gctcagggtg tgatttcagg tggcttccaa acttgtacgc agttt aaaga tgg tggggac 120
agactttgcc tctacctagt gaacccact taaagaat aa ggagcat ttg aat ct ct tgg 180
aaaaggccat gaag 194

<210> 550
<211> 198
<212> DNA
<213> Homo sapiens

<400> 550
tgggaaat at agt gaaact c ctgtccct ac aaaaaat aca aaaat tagcc ggggtgt ggt a 60
gtgcatgcct gt agtcccag ctacttggga ggctgaagt g ggaggatggc ctgagct caa 120
ggagatgcag gctgcagtgg gctgtgat t g tggcact gca ctccagcct g ggcaccaat g 180
tgagaacctg tcttggaa 198

<210> 551
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (76)..(77)
<223> n i s a, c, g, or t

<220>
<221> misc_feature
<222> (101)..(101)
<223> n i s a, c, g, or t

<220>
<221> misc_feature
<222> (106)..(106)
<223> n i s a, c, g, or t

<400> 551
ttgaaagaca ccagtgacac cccaaactcc tggccttctg tgggttccct ttgctccaga 60
acacagatgt gtctanngaa aaacaaacga aaaccgagcc naaacnacca aacccaggg 120
gggggccgct ctaaagaat c cctcgagggg cccaagctta cgcgtacca gcttttcttg 180
taciaaagggg cccctaaagg ggagtcggaa taaaaaact a aaggcccttg gcccgctctt 240
tttacaacgc cccggaactg gggaaaacat gccaaccttg ggggatcttt tg 292

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ADL\_0311WP\_Sequence\_Listing.txt

<210> 552  
 <211> 268  
 <212> DNA  
 <213> Homo sapiens

<400> 552  
 gat gct ctt c agt t caact a t att ccct at ct gat aat t c cagaat ct ct at cat gt ct g 60  
 agt ct ggg t c t gat gct t t c att gt t t c t t cagatt gt ga t t t t t c t t gc ct cccagt gt 120  
 gact t gt aat t t t t aat t ga aagct ggat a t gat gt at t t ggcaat ggga agt gagggaa 180  
 at at gt t t t t agt gt gaggg t t t at gt t aa t c t t t c t cag agt t gggct g t t t aat gt t t 240  
 t gct gt ggt c t gaat gt t cc t t aaaact 268

<210> 553  
 <211> 269  
 <212> DNA  
 <213> Homo sapiens

<400> 553  
 aaggatt ggg ggt cgt gcag cccagccagc aggagggact gaggccct ct aggaggaaag 60  
 cccagagggga gggggccct c att cct t cag acccagtt t t ccccccacct cct t accccg 120  
 ct gggct agg t ct ccgccag ggct ggcct c agt t t c t cct caacaggcct gggggcagcc 180  
 ct t cccct gc ct agt ccccg cct gagt gcc agcsccccac cccgcct gcc gccccct gt t 240  
 caggt t ccct ccccgccaca gt gaaat aa 269

<210> 554  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 47 ) . . ( 47 )  
 <223> n i s a , c , g , o r t

<220>  
 <221> m i s c \_ f e a t u r e  
 <222> ( 52 ) . . ( 52 )  
 <223> n i s a , c , g , o r t

<400> 554  
 t gcggaggcg ct agt ccacc agagcbct c cccgcccct c t t cccant cc gnat ccct cg 60  
 cccccctccc cacct cccac ccccccacct gt aaact agg cggct gcagc aagcagacct 120  
 t cgcat caac m m s c a s a c a c c a m a a a c c a gt gagasccc cgct ct ct ac cgccccgggcc 180  
 cagcact cgc tagct t t cct gacacct gga act gt gcacc t ggcaccaag cggaaaat aa 240  
 act ccaagca gccagt agcc ccgat ggt gt gt gcct gacc t gt gt ggccg gaggt t c 297

<210> 555  
 <211> 35  
 <212> DNA  
 <213> Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 555  
t t aggt aggt aaggaat gat cacatt ggag ttt gg 35

<210> 556  
<211> 273  
<212> DNA  
<213> Homo sapiens

<400> 556  
acgt gctt at t aggaaat ga gt ct gt at gg aaat ct cacc acagat aat g gtt aacgaac 60  
cgggt cgaca t cacaaagga ggggt ggagac t cttttt act aact t gaat g agacaaaagc 120  
agt ggt gt ca gttt at aat c ct gat gcat t t cagt aat aa t gt agaaaaa catt at ttt a 180  
aaaaagt t cc aacacacagc cat gaggagc ct cagt ttt g aaagaggt gc at aat aaaac 240  
t act aaccag aggagt ct at gccat ttt aa gaa 273

<210> 557  
<211> 256  
<212> DNA  
<213> Homo sapiens

<400> 557  
gccaggagt t ggagcccact ct ggggaaaa cat gtt gaga t ctt gcct ct gcaaaaat aa 60  
agt aaaat aa aat t t aaaaa aagt aaaaaa at aaaat cag ct gagcat gg t gacat gcac 120  
ct gt ggt acc agct act ttt g gaggct aagt t gagaggcac t gat gggagg at cat ttt gac 180  
ggcccagagg ttt gaggct gc agt gagct gt gttt gt gt ca ttt gcact cca gcct gcgt aa 240  
cagagt aaaa cct t ct 256

<210> 558  
<211> 185  
<212> DNA  
<213> Homo sapiens

<400> 558  
ctt ggagcca gagaagcgt t agaaacccc t gagggccga t t act gacat cat aaat cat 60  
gagttt gggg gcttt gcct g ggt gat gtt g gt accaggag acat agt t at aaccaccaac 120  
gt cact gct g gtt ccagt gc aggagat ggt gat cgact gt ccaggagacc cagacacgga 180  
ggcag 185

<210> 559  
<211> 246  
<212> DNA  
<213> Homo sapiens

<400> 559  
gt ct gaat at ctt act caca gct caccttt ttt ggt gcct t t gat ccgt at t agaaat t at 60  
ccacat ctt c t ct ct gggca at at t ct act tttt at at t g acccaatt at ttt act gct t 120  
t ggt gt gt cc ttt ct cct aa cacat at ggg ttt cact ttt ga aaccct gaaa cccacat tta 180  
caaaaacat t t t caat at ga aacat t gtt c cat gact cat t act ggagt a ccat caacat 240

ttacat

246

<210> 560  
 <211> 242  
 <212> DNA  
 <213> Homo sapiens

<400> 560  
 gcaggatattt tctacgggtg tttagatgttc ctgaagt gga agctgtgtgt tggcgtgcc 60  
 cggtggggat ttctgtactc tataatgatt gttactcccc ctcccttttc aaattccaat 120  
 gtgaccaatt ccggatcagg gtgtgaggag gctggggct a aggggctccc ctgaat atct 180  
 tctctgctca cttccaccat ct aagaggaa aagggtgagt t gctcatgctg attaggattg 240  
 aa 242

<210> 561  
 <211> 285  
 <212> DNA  
 <213> Homo sapiens

<400> 561  
 tcctctgtca atgttctgatt atctccagga aaagagacca gatgcagccc accttccttc 60  
 acctataagt acacacctga agaggagcag gaattggaaa agcgggtgat ggaacatgat 120  
 ggtcagctctt tagttaaatc gaccattttc atctctccat catctgtgaa gaaagaagaa 180  
 gccccccaga gtgaggcgcc gcgggtggag gaatgccatc atggaaggac tcctacctgt 240  
 tcacggcttg ctccaccacc aatgtctcag tctacctgtt ccctt 285

<210> 562  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<400> 562  
 ggtaatgagc tcaatgcctc catttaatca cttttataag gctctctcca ataaggctgc 60  
 tgtgctgtgc tcctgccagt gttggagt aa tataacattt ttactgcaca caccttatgg 120  
 gaaagtgttt atactgagt gtagttttagg aggggtaat gaagattatt tcacaaatt 180  
 aagattgcac tttagtacacg cttttacaca actctgatgg tatttacc aaacatggcat 240  
 gtcttttcac gtatatctcct gaaaacacca a 271

<210> 563  
 <211> 211  
 <212> DNA  
 <213> Homo sapiens

<400> 563  
 agctttaaga ggaaagagct ctatttttct tgttttcttc tctgagctag actgagctgg 60  
 ggatctaaga tgtacttctc tgactacaaa agggacagta tcatttagat tttttgcagt 120  
 t ggaagaaat ggggtgttga gtgtgttaag gctgggatga agaagggtg ggcagtactc 180  
 ttctggaaag gctcacctag cacgaacctg c 211

ADL\_0311WP\_Sequence\_Listing.txt

<210> 564  
<211> 276  
<212> DNA  
<213> Homo sapiens

<400> 564  
ggtaaataag agagccctcc ttgtcaaccc aaaatgtgag cccctgtgg caaaaccacc 60  
ccctacccca ttaacaaatc aacagacaaa attctccgag tctttgcct cttttgat aa 120  
catgttgttc tgttttgt aa agtgtgtgtg cttgggggttc cgaggtgtgg gat t gaggttc 180  
tctgctttgt ttttttttaa gatattgtat gtaaatgt aa aaagtattt aaat at at at 240  
tttaaagaac cctaactgcc aacttttgct gaaaaa 276

<210> 565  
<211> 257  
<212> DNA  
<213> Homo sapiens

<400> 565  
gagtcacctt tagtcacctg gtccgt aacc atctttcctg tctaaacttc tccccacc 60  
actctggctt ataccctgc tctctttaaa atagccagtc agaattagct tagattgtgc 120  
gggccaaccc tagcccatag gggaacaaca cagcagtagg gggtacctgc atcagggat a 180  
agaacccatt cccctccctt gttccgggtgt gctctcgcca ttgcaccatc catgagacgc 240  
actcttgtat agaagta 257

<210> 566  
<211> 198  
<212> DNA  
<213> Homo sapiens

<400> 566  
gggaacctct gaataccata ggattaat at gaaaaaat ttccctccct aaagtacatc 60  
cacgttatga tttagacggg gatgctagca tggct aaggc aataacaggg gtgtgtgtt 120  
atgcctgcag aattgccagt accttactgc tttatcagga attaatgcga aaggggat ac 180  
gatggctgat tgaattaa 198

<210> 567  
<211> 228  
<212> DNA  
<213> Homo sapiens

<400> 567  
taaaagaaac acctgcggcg gctccgcgcc tccctccctc cctcccaggc tcaacctct a 60  
ccttctttac tttcccttgt a aaggcatagc caggggacat tgtccccag cttcacatcc 120  
acatgtctcc tagcatggca catgcatatc ctgcccaagg agcatgaagt cagaccagca 180  
aactgaacac gaggcacagt cctgcatgct ctgggaccga gcactgag 228

<210> 568  
<211> 201  
<212> DNA

## ADL\_0311WP\_Sequence\_Listing.txt

&lt;213&gt; Homo sapiens

&lt;400&gt; 568

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agct gaagct gcgt cggcgg ct cacggagc t cct gggggc gcaggacggg gcgct gct gg      60
t gcggct gct gcaggcgt g cgcgt ggcca ggat gcccg gct ggagcgg agcgt ccgt g      120
agcgt t cct ccct gt gcac t gat cct ggc ccct ct t at t t at t ct aca t cct t ggcac      180
cccact t gca ct gaaagagg c                                                    201

```

&lt;210&gt; 569

&lt;211&gt; 211

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 569

```

agct t t aaga ggaaagagct ct at t t t t ct t g t t t t c t t c t ct gagct ag act gagct gg      60
ggat ct aaga t gt act t ct c t gact acaaa agggacagt a t cat t t agat t t t t t gcagt      120
t ggaagaaat gggt t gt t ga gt gt gt t aag gct gggat ga agaagggct g ggcagt act c      180
t t ct ggaaag gct cacct ag cacgaacct g c                                                    211

```

&lt;210&gt; 570

&lt;211&gt; 233

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 570

```

ggaat gggag t t ggcgggca gt gaacgagt gt ggggaagg at t ggt ggt g gggcaacagg      60
aaggggcct g gggccgt t t g ggt gccct aa ct t t ggt agc t cagt gt gca t t t agagt gg      120
gact ggggag ggaggt aagc t t ggggt ggg ct gct t gggg ct t ggcat ag ggt ggaaagg      180
gct accct gg ggct t t gacc ccct gt agt at gt gt ggag ggt gccct cc cgt                233

```

&lt;210&gt; 571

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 571

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aaact gct at t t ct aact ct t cat gaaagc att acct t t g gaaagtt aaa c t t t t t t t t      60
cct t t cat ca ccgt ct t t ga aacaaatt at t t t ccaatt c at aagaact t t ggt aaaaaa      120
aaaaat aaaa ggaaatt ata t g t t t t t c t t t ggacatt ca t t ggaaggct t g t t gaagac      180
at gat ccccc agaagcct t a gt gaccaga t ct caaccag agact caaga t agcct caaa          240
t acagt gaaa g                                                    251

```

&lt;210&gt; 572

&lt;211&gt; 218

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 572

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aact gt at t t t aact tagca caattaact g cagcat at t t act t cat agc ccct t aacat      60
gt cact t t t a ccaacaaagc t t t t t c t t c at at t ct aat cacaaaaatt t ct caacaat      120

```

## ADL\_0311WP\_Sequence\_Listing.txt

t t a t a a c a a t c t g t a a a t c t g a c c t t g c a a t a a a t a g t c a t a a a c g t t a t t t t t a t t a c 180  
t a t t a t t a t t t t t a g a g a c a a g g t c t c c t c g t g c c g a a 218

<210> 573  
<211> 250  
<212> DNA  
<213> Homo sapiens

<400> 573  
t c c c a c a c c a a a a t a g a t t c c c a a a t a g a t a t t a c a a g t a g g a g a a t t t t t a t g a c t a c t 60  
c a g a t a a a a c g a c c a t t g a t c a c t t a c a a a c a t a c a a g t c a t a a c a a t a c a g a a a t a a t 120  
a t g t g t a t a c a a a a c a c a g a a a t t a t t a t a t t g g g a a t a g a c a t a t g a c t g a t t c a t a t 180  
g t a a c t t t g t c t c c a c g c t g t c t t a a a g t g t a c a g a g t t g a a t a t t g t c a t t c a c a a t t g 240  
t c a c a c a a a a 250

<210> 574  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 574  
c a c c a a a g t t c t g a g g c a t t a a g c c a g c a g a a 32

<210> 575  
<211> 245  
<212> DNA  
<213> Homo sapiens

<400> 575  
t a a a a c t c t c t g a g a c t g t t t t c c c c c c a t g t c a a a c a c c t a t t t t g c a t g g c t a t a t g 60  
g a a a t t a a a t g a a a t a g c a a a t a t g a a a a c t t t t g g c c c a g t g t a a t t c a t a t c a g g 120  
c a c t g a t c t g t t t t c t t t t t g c c c t a a c c t a c t t t t c c t g c a t c a t a t a c c a c t a c a c c t 180  
c t t t a c a a a c c t t a t t a a t a g a g c c a c t c t a g a c t a c t t t a t t t c c c c a a g c c a t a c a a t 240  
g t a c t 245

<210> 576  
<211> 192  
<212> DNA  
<213> Homo sapiens

<400> 576  
a a a a c c c a c c t t g t t g g a g c c t g c a g g g t g g t g c t g g g a c t g a g c c a g t c c a g g g g c a t 60  
g t a t t g g c c t g g a g g t g g g g t t g g g a t t g g g g g c t g g t g c c a g c c t t c c t c t g c a g c t g a 120  
c c t c t g t t g t c c t c c c c t t g g g c g g c t g a g a g c c c a g c t g a c a t g g a a a t a c a g t t g t t 180  
g g c c t c c g g c c t 192

<210> 577  
<211> 269  
<212> DNA  
<213> Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 577  
ct agaccac t gct ggt ccc ct t t ct ccct cct gct t ct c acct gaagcc acct gccct 60  
cct t t gt gcc ct ccct t gct t cct cct ggg ct ct gt cccc t gct cccct t t gt cct cca 120  
t cccgact cc at ct ccccca ccaggct ggt caccacaggc cagcgt ct gt t gaaggat ga 180  
agcagct cct gt ccggccca gccct gcct c acagct gt gc gagct ct gcc ct t ct cagct 240  
ct caaacct g aat aat gca ccaagccca 269

<210> 578  
<211> 172  
<212> DNA  
<213> Homo sapi ens

<400> 578  
t ggcagagca acact t cgt c t cagaaaaa aaaaaaaac caaaaaccaa aaagccaagt 60  
gt ggt ggt gt gcacct at ag t cccagct ac t caggaagct gagacaagag gat caat t ga 120  
gcccaggagt t caaagct gt agt gagct gt cat t gt gcca ct at cct cca gt 172

<210> 579  
<211> 269  
<212> DNA  
<213> Homo sapi ens

<400> 579  
ggagcagt gc ccaccaaggg t t t gt cagat t caagcct ca ggcaagagaa aaat caaaag 60  
cct t ct gct a ct ct ct ccct ct gggcct ct ggt ct gccca gaggt gggga ct cct t cct c 120  
t acct t gct c t caat ct gga ggggt gct ggg ggggt gcct cc at ct t act gg gccct ggct 180  
ggct t gt ggg ct gaggt gct aat ggggt ct agt agct gct gt gct ccct t ct t cat gcc 240  
agt ct gaaac aggt gct ccc ct aaccag 269

<210> 580  
<211> 144  
<212> DNA  
<213> Homo sapi ens

<400> 580  
cagggaggcc t ct ct gccc t at ggggt c t gt cct gcac ccct cagggga t ggcgacagc 60  
aggccagaca cagt ct gat g ccagct gggga gt ct t gct ga ccct gccccg ggt ccgaggg 120  
t gt caat aaa gt gct gt cca gt ga 144

<210> 581  
<211> 204  
<212> DNA  
<213> Homo sapi ens

<400> 581  
aggat ccgag t ggt agt gt t t ct gagagt c aggggt ct agg t gct ggagt g cgcacggagg 60  
ccgat gt aga ggaggaggcc ct gaggagga agct ggagga gct gaccagc aacgt cagt g 120  
accaggagac ct cgt ccgag gaggaggagg ccaaggacga aaaggcagag cccaacaggg 180

acaaatcagt tgggcctcta gcgt 204

<210> 582  
 <211> 214  
 <212> DNA  
 <213> Homo sapiens

<400> 582  
 agt aacaat a gccagaggt t gaagggcggg gt agaagagg ggggaat gt t gcagcgt aat 60  
 cct t cat acc acct ggt t ct t gat at t ct g ccgcct gt t c aagt t caaga at aaaagcga 120  
 cagcaggacc caaat gcagc t cccaacca ct cccaggc t agacat gct t gt gt ccaca 180  
 cagcacacca at gt gat act t ccact gacc ggct 214

<210> 583  
 <211> 95  
 <212> DNA  
 <213> Homo sapiens

<400> 583  
 at gcagt gt g t t ct gaggt c ct gt caccct t gaggt gt g t gt gt cct t t gccaaat t aa 60  
 agagt ct t ac t gaat gcggt gcat ccagga gacag 95

<210> 584  
 <211> 244  
 <212> DNA  
 <213> Homo sapiens

<400> 584  
 act t t t at t t t t ct at gcaa ggt gat t cag agaat t t at a t aaaggcggg cgaggggcag 60  
 ccgagcaggg agct t t ggga cagggt ggg gccccat at ccccccggg ccacct gct t 120  
 t ccct cct at ggct cccct g gaacaggagg gagagccaag ggggcggccc agcct ggaca 180  
 gcgcccgt c ct gcct gggg gcacacacgg cgggcct gag ct ccagcat c t gagt t t ggg 240  
 ggt a 244

<210> 585  
 <211> 170  
 <212> DNA  
 <213> Homo sapiens

<400> 585  
 t gcacat t gt gacat gt aca ct aaaact t a aagt at aat a at aat aaaat aaaaaaaaaa 60  
 gaaaagaacc t agt gt gt t a aacct t aaat gccct t agaa at aacct aga ccagt gt t t c 120  
 t t aaact gt g gt cat gagat cagt t gaat g gat t at gacc aacat t gaaa 170

<210> 586  
 <211> 233  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> mi sc\_f eat ur e  
 <222> (160)..(183)

<223> n i s a, c, g, or t

<400> 586  
 cttgctttcc ctaggagt t g aatccttctc cctgcctacc tgcagcatct cctttccctt 60  
 taaaatgacc atgtagtggc aagcagcctt ttactcttct gttagctctg gactcttaac 120  
 acttaagtta ctcttctgaa attgctagga ccat tggggn nnnnnnnnnn nnnnnnnnnn 180  
 nnnatgtccg acctgtgatc gtggtagcgc attagctgaa atttaccctt gtt 233

<210> 587  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (191)..(191)  
 <223> n i s a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (207)..(207)  
 <223> n i s a, c, g, or t

<400> 587  
 aaggaccctg aaaaatgact tctcatttcc tgcctgcaga aaagagaaat attaggatag 60  
 tgttgtgtgc aaaaaaatgc aagcttgcaa tgagagatgc agagtgtgag ggagagaggc 120  
 acgaaggggg tggagaaaaa agacagagaa tttgaggttg actcacggct ttgaagggaa 180  
 aacaggaaga ngaagaaagt ctgtctncca tgggtcggca acccacactt tacacatttt 240

<210> 588  
 <211> 273  
 <212> DNA  
 <213> Homo sapiens

<400> 588  
 at aagtgtac caggactcta aaagaaactt gtttgtat aa t gctatccaa ggtatgtagc 60  
 ccagggaata accaacctga tgttgtttat gaccattttt aagcctcccg tgatcacagt 120  
 ttttaaaata aaattaaagga ctggtcctat tttctaggtga cacaagt aag gtaatagcta 180  
 gaacgggaaa aaagaggggc ccccaaaaat gt aaccttaa aatttggtgc ttgtgccgct 240  
 attgatagta agcagcatgg aataggatgt ggt 273

<210> 589  
 <211> 179  
 <212> DNA  
 <213> Homo sapiens

<400> 589  
 taacagt gca taaatcaatc caaat t t aga ccctggcaac cagttcccca ttgctcatct 60  
 acgggactct gtcaacggt a aataggcaat catctctctt gaaaagtata catcctctct 120  
 cgcactggtg gaaagcaaat tgactttttg tttgctgtat aaaaccctta gcacttcaa 179

## ADL\_0311WP\_Sequence\_Listing.txt

<210> 590  
 <211> 186  
 <212> DNA  
 <213> Homo sapiens

<400> 590  
 ggcaggaccg t gccacacca gct gt ccaga gt cggaggac cccagct cct cagct t gcat 60  
 ggact ct gcc tt cccagcgc tt gt cccccg aggaaagcgg ct gggcgggc ggggagct gg 120  
 gcct ggagga t cct ggagt c t cat t aaat g cct gat t t gt gaccat gt cc accagt at ct 180  
 ggggt g 186

<210> 591  
 <211> 238  
 <212> DNA  
 <213> Homo sapiens

<400> 591  
 tt cggcatt c t ccaagt cat ct agccct t c at cct cct cc acat cat caa agt cgt cgcc 60  
 at caaaat t g t cct cgt t gt ct gacat gac accct cgcct cagcgacccc gct gcgcccc 120  
 ggt cccgcgc ggagaccgc aaacagcgac act acgact c gcgcggct cc t agct t at ct 180  
 t gcgcct cgt gccgaat t cg ccaccaggc ct cgct acaa tt acggaccg tt at agt a 238

<210> 592  
 <211> 148  
 <212> DNA  
 <213> Homo sapiens

<400> 592  
 caacct t t t a gct at gat ga cacat aacaa aagat gt t t a t gt act aat a gt t gaaat ct 60  
 gcct t t t t ct cat t caagaa ggcat acaaa t at ct gagag t gact t t gt t gt at ggct ac 120  
 cct t gt gat c t acagt aat t t at t c t t t 148

<210> 593  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<400> 593  
 gt gggagaag tt ggcgt cct aggct gggga tt ggt cgggg gacct t aaag aaaaaggcca 60  
 gggct gaggg t cct gaggag agagagagag gccacgt gga t ggaggact g t caccacct t 120  
 ct cggt t ct g t caccacct t gagt ct aact cact gt t gag gggaggaaga agggggat gg 180  
 acggaaggga gaccgaggaa aggct t t cgg gagt ggggac at t at ccacc cagaggt gt g 240  
 ct acccaciaa ccaccgcgag at cct t agag t 271

<210> 594  
 <211> 233  
 <212> DNA  
 <213> Homo sapiens

<400> 594  
 gaact gat t t caaggaat gg gt cct t ccct t cagagccac at gt gt gcgg gacaccaga 60

ADL\_0311WP\_Sequence\_Listing.txt

cagaaaacac aaacacaaag t cgagt ggag ggcatt t t gga aggagcagt g aagccgagcc 120  
aggaaat acc aagat ggca gccagt gt gc t t gt agagat t gt agagagg gt agaatt ga 180  
cact gt ggac cct ggcct cg at agagaaag gcat cagct a aggaagt t gt t ca 233

<210> 595  
<211> 217  
<212> DNA  
<213> Homo sapi ens

<400> 595  
gaacatt ct g gat agcaagc ccact gcaaa caagaagt gc gacct gat ca gcat ccccaa 60  
gaaaaccaca gacacggcca gt gt gcaaaa t gaagccaag t t ggat gaga t t t t aaaaga 120  
gat caaat ct at aaaagaca caat ct gcaa t caagat gag ccgt at t t cc aagt t agaac 180  
aagcagat gg caaagat agc agcct gaagg t cccacc 217

<210> 596  
<211> 267  
<212> DNA  
<213> Homo sapi ens

<400> 596  
t gat aat ct c aagact cct c cct t agct ac t caggaggcc gaggcggaaa aaccacccaa 60  
accaagagg t ggagggt gg at gaggt gga acaat caccg aaaccaaga ggcggagggc 120  
ggat gaggt g gaacaat cgc ccaagcccaa gaggcagagg gaggccgagg cacaacaat t 180  
acccaaaccc aagaggcgga ggt t gagt aa gct gagaaca cgccat t gca ct caagcct g 240  
ggcaat aaga at aaat ccgt ggg t cga 267

<210> 597  
<211> 275  
<212> DNA  
<213> Homo sapi ens

<400> 597  
aat t t accaa gccacat at t gggaat ggt a cccaggcag aaggagt aga gt aagcaagc 60  
cagaaaggaa at act at ggt gct t t t gagt aact gcagt g t ggct gaaga at gt ggaaaa 120  
t gat gaggat aaagagggt gg acagggaact aggt aaggga gggcct t cct t t t aaat aat 180  
t agacct t gt cct gt gt aca t t t aat ggga t t t t aat cag gccat aat gc caaat t t ct t 240  
t act t cgga g gat ct t t at ggt gat ggt t t caga 275

<210> 598  
<211> 35  
<212> DNA  
<213> Homo sapi ens

<400> 598  
at t t t t ct t g gcct agt t gt gt gccat gga t at t t 35

<210> 599  
<211> 156  
<212> DNA

<213> Homo sapiens

<400> 599  
gagggat att attttccat a gccattacca t gat acat at gat act gcct aggt agagct 60  
gggact gt ag ggt gggaac caat gct gt c ct gcacact g aaact at gaa t gccagat a 120  
t cact gccag at cct t ct gt ggat agct gg cggcat 156

<210> 600  
<211> 243  
<212> DNA  
<213> Homo sapiens

<400> 600  
gaagcct gac cccaagt gt g t c t t c a c c t a t g t g c a g t c g c t c t a c a a c c a c c t g c g a c g 60  
ccacgaact g cgcct gcgcg gcaagaat gt ct agcct gcc cgcccgcat g gccagccagt 120  
ggcaagct gc cgccccact ct ccgggcac cgt ct cct gc ct gt gcgt cc gccaccgct 180  
gccct gt ct g t t g c g a c a c c c t c c c c c c c c a c a t a c a c a c g c a g c g t t t t g a t a a a t t a t t 240  
ggt 243

<210> 601  
<211> 229  
<212> DNA  
<213> Homo sapiens

<400> 601  
gcatt att ac t gat act t gc acacagt caa aagcgcagac t ggat ggat g gt c t t t t a t a 60  
aggcatt t aa gggta cact a ct gt g t t t c a ct gaccat ac at t t t t c t t a g c c c t c a a g 120  
t aat at agca cagagt t at g aat gacaat t c c c c t a a c c a t t c c t c t t c a t a t c t g c c t c 180  
t t c c c t t a c c a t c g t a a t t c t c c a a a c t g g t c a t a a a g g c a c t c t g t g 229

<210> 602  
<211> 93  
<212> DNA  
<213> Homo sapiens

<220>  
<221> m i s c \_ f e a t u r e  
<222> ( 33 ) . . ( 48 )  
<223> n i s a , c , g , o r t

<400> 602  
catt aagt cc t ct gt aaggt gt caggcaag c n n n n n n n n n n n n n n n n n t g g g t a a g t c c t 60  
a a c c c c c c a c a a a g g t g t t c c c a g t g a c t a c c t 93

<210> 603  
<211> 273  
<212> DNA  
<213> Homo sapiens

<400> 603  
t t c g c t g g t t c t g a a t g t c a t t t t t c c t c c c t g g t g t g g t t t t a c a t t t t c a g c t t c t t t 60  
c c c t t t t c t t c t c t c c c a c c c t c a a a a t t c t g c c t t a g c a t t t g t g t g c t t a a t t a a a t c 120

ADL\_0311WP\_Sequence\_Listing.txt

cactctgtgc tttatagttg gagaatgtgg acaatacaaa gatttggggt ggggtcatac 180  
 agtgtataca aaacacagac actatgtgtt tggacaaat t cgcctagcgt gagaatcatc 240  
 agtagtgagt taaacgtttg aaatcagagc caa 273

<210> 604  
 <211> 164  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (80)..(98)  
 <223> nisa, c, g, or t

<400> 604  
 taattattgc tgtggatttc tctctagcat tttagctcat tccagtaaat gatttttttc 60  
 tttatgaaat agaactacn nnnnnnnnnn nnnnnnnngt tcaacaacaa caaactgaag 120  
 ggggagaaaa atacaccatt accacagcaa caaattagtt tatg 164

<210> 605  
 <211> 275  
 <212> DNA  
 <213> Homo sapiens

<400> 605  
 tttctcccagt acctcatttg cacaagcctt cctgccattc ttcaaatatg cgaagcctgt 60  
 tctcacctca aagccattgt acttgctgtt tctatgcct gaatgttctt cccacagatg 120  
 ttgacaagac ttgctccttc acttcaatga cattcagata tcttattctc agagagcatt 180  
 tgacaacctat tctaaaatag ctccccctca ctgttctgc ccatgctctt tatacccat 240  
 tttactttca tctttcttcc tagtactgac attat 275

<210> 606  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<400> 606  
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 agggaggctg aagcagagt g atcaagcgga cagggcaggc agagcctcaa atcccagact 120  
 gaggaacatg gtgaacgagg aacttcggg ggtccacaca taaagacgga gacagagact 180  
 cagggcagga aagtcacatg ccctgggaca cccagtaaa cagagccaaa ctcaaacctc 240  
 agcctgtctg cagctgacat aggatgaagt t 271

<210> 607  
 <211> 160  
 <212> DNA  
 <213> Homo sapiens

<400> 607  
 taagttatta actgaggctg accagagggg aggaccccc ctttaccacc ccatgcactt 60

ADL\_0311WP\_Sequence\_Listing.txt

tgcgagctgc cccttcttcc cccacatcag agagaaatgc cccacacca gagccccaag 120  
 ggt agggctg ccgatcagag ctgtgagtta acacaacagg 160

<210> 608  
 <211> 155  
 <212> DNA  
 <213> Homo sapiens

<400> 608  
 agcaccagta gtggttgggg ccctcccctc aggctccatt tttaataagt ttttagtatt 60  
 tttgttaatg tgaggcattg agctgttggg ttttgtatat tatttatata gagaccccag 120  
 agctgttgca cccaatacac agagcttctt tgcga 155

<210> 609  
 <211> 252  
 <212> DNA  
 <213> Homo sapiens

<400> 609  
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 gactaacgct cacataactg gttttttttt ttatctgggc tgatgaatac atttacctaa 120  
 gaaactcatt ttcgttttact taagagggga agtgcagttt tcttttggca gttcagaatc 180  
 caagcacttg atttgctggg tttggaaaac tcttttttg gccttctatg tgcttagcca 240  
 taacaattcc at 252

<210> 610  
 <211> 286  
 <212> DNA  
 <213> Homo sapiens

<400> 610  
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 tctgaacacc ctgtgcaata gagtctgact ccattttttg atgtttgact gcagacatct 120  
 tttcagccta acccttccat ctctctttc tgtccaacac tggggcaagc tgacaaaaat 180  
 cctcaggtgc tctcttctg taaccagcag taagttcgaa tcatacactg ccaccctcac 240  
 cccaaccctg tcccttaacc acattaaaac ccaaagccag tctcct 286

<210> 611  
 <211> 80  
 <212> DNA  
 <213> Homo sapiens

<400> 611  
 gggcctgttg aagatgcttg tattttactt ttcccttgta aatgctattc ccatcacagc 60  
 tgaacttgtt gagatccccg 80

<210> 612  
 <211> 290  
 <212> DNA  
 <213> Homo sapiens

ADL\_0311WP\_Sequence\_Listing.txt

<400> 612  
gaggagat aa actaacagag gtcaagaaga tgaagagttg tttcaaacat ggtacagttg 60  
agattcctag cattattcta gtacagcgtg tctgtcaagt aggccattgg atatcgggat 120  
tgggatttga ggggaatcca tagatggaaa tat aagttca agaggcatca gcatggat ac 180  
cctatttggg tctggatgaa attacctaaa ggagaaaatg caggaggacg t gat gct ggg 240  
tgattttaga ggagaaacca tgaaggattc caaggagcag cagttggtca 290

<210> 613  
<211> 117  
<212> DNA  
<213> Homo sapiens

<400> 613  
aaaaattcat cccat atcca gaaagtacca gttat aaaga ttgctgacca agcaaagttt 60  
tgcataaag tgtcacctca ttgctctgac caaagactga ctgttgtggt ttt aact 117

<210> 614  
<211> 214  
<212> DNA  
<213> Homo sapiens

<400> 614  
acaccagtgt gctacagtgg cgggtggtct gatgcggcca gggaagagtc aggtgtcagg 60  
gcaggaattc tat ttttcggg agatgtctat tgcagagt ag agt aat at at acccagagt a 120  
tgtctat agc agaggggggtt atggggggcgg gagggtagac tgacat acag aagt ct ct at 180  
ttatccgggt gggaagaggg agtcacatcg cttt 214

<210> 615  
<211> 283  
<212> DNA  
<213> Homo sapiens

<400> 615  
ccagctggag gtgacgaggg atgatgcgcg tcttcttgtt gtcccgagcc gcgttgccccg 60  
ccagctccag gatctcggcg gtacagat act cgaggaccgc agccatgt ag acgggcgcgc 120  
cgccccccac tcgctccgcg tagttgcctt tgcgcagcaa gcatgact cgccct accg 180  
ggaactgaag gccagcgcgg gacgagcgcg acttggcctt ggcgcggggc t tgcct cct t 240  
gcttgccacg accagacatg acagcgat ag tagt caccga gag 283

<210> 616  
<211> 192  
<212> DNA  
<213> Homo sapiens

<400> 616  
gaactatgat tgcactactg t gctccagct tgggcaacag agtgagatct t gct ccaaa 60  
agt cct t gaa ggattttagg aagttgttaa aagtccttgaa acgatgtttg ggggcatgtt 120  
agggttcttg aatgtttaat tcctctaat a actgcttat t caagagaagc atttctgact 180

gggtgcaggg ca

192

<210> 617  
 <211> 234  
 <212> DNA  
 <213> Homo sapiens

<400> 617  
 atgaactttt gtgcttagtg agtgcaacga aatatttaa caagttttgt atttttt gct 60  
 tttgtgtttt ggaatttgcc ttatttttct tggatgcat gttcagaggc tgtttcctgc 120  
 agcatgtatt tccatggccc acacagctat gtgtttgagc agcgaagagt ctttgagctg 180  
 aatgagccag agtgataatt tcagtgaac gaactttctg ctgaattaat ggt a 234

<210> 618  
 <211> 146  
 <212> DNA  
 <213> Homo sapiens

<400> 618  
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 tggagaagaa gaaaggggtc agaagcgaaa acgagaacct gaagatgagg gagaagatga 120  
 tgactaagtg gataacctat tttgaa 146

<210> 619  
 <211> 63  
 <212> DNA  
 <213> Homo sapiens

<400> 619  
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 ctt 63

<210> 620  
 <211> 149  
 <212> DNA  
 <213> Homo sapiens

<400> 620  
 atcaactgaa tccaatat ttcctgtggcaa ataacacttt cctcatttca taccttttct 60  
 cctctcttcc atgccaacat ttctccaccc acaacgtaca ctttttattt ctccatcaat 120  
 atttgaaagc gaggat tttg tgaccagga 149

<210> 621  
 <211> 151  
 <212> DNA  
 <213> Homo sapiens

<400> 621  
 cagcaacccc tgcattcctt ttttttaccg ggctgacgag aatgatgagg tgaagatcac 60  
 tgtcatctaa aagccggcta ctgtcagcaa agcctgaaga agtggggctg gat accctgc 120  
 cccaccata tcctaccat cccttctcag t 151

## ADL\_0311WP\_Sequence\_Listing.txt

<210> 622  
 <211> 258  
 <212> DNA  
 <213> Homo sapiens

<400> 622  
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 ccgaatgttc cgtgaggaat ggaagctcta ttgttgactt gtctcccctt attcatcgca 120  
 ctgggtggtta tgaggcttat ggt aagagt g aggat gat gc ctccgat acc aaccct gat t 180  
 tctacatcaa tattt gt cag ccactaaatc ccatgcacgg agt gccct gt cct gccggag 240  
 ccgctgtgtg caaagttc 258

<210> 623  
 <211> 278  
 <212> DNA  
 <213> Homo sapiens

<400> 623  
 tctcctcttc agtcttcatc atgtttttgt ccctcaaaca tcagccttac gt cctctttt 60  
 ct tccctctg catcctctct ccttgagaga cctcatccag cccatgtttt caacaatcat 120  
 ctatacaaca atgatcttct acat acattc ctggcccaga tccctgccct gaattcccag 180  
 cctatagatc caacaaccct cctccaat ac tgtctttccc agccattctc caggcctctg 240  
 ctatggctctg aatgtttgtg tccaaaaaca t gat gaag 278

<210> 624  
 <211> 290  
 <212> DNA  
 <213> Homo sapiens

<400> 624  
 aagacagtcc tcagaaaacc caagctttca tacagatgcc aaaaaagtcc atggggttta 60  
 attctttgac cattttgagt gcagggactt attcatgctt acatcctcac aactcagctt 120  
 ggggactgcc tcacacctgg cagctgatcc tttttgtttt ttaaatgt aa gaagccacac 180  
 tgagggtctt ccaggcggaa aaagttagga cacaggacca gcatttcttt ccagccactt 240  
 gtggatccct gattgaatgt cacccttgac tgcctaactc atctctttcc 290

<210> 625  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 625  
 cgactaatca tcttacggca gagaacaaac accaccacca agt aaaaat a tccctgcaac 60  
 aaacacaacg gattccaatt ccttccggcc aaccaatgt tcacggcgt ggacacat ac 120  
 tggttgggcg caggcatcct cgcagt gacg tcccctgt ac t cgtggctgc agt tgcagt g 180  
 ataggagccg tgcgtgttct cacagagggc cccgtgcagg caagggtttc cagagcactc 240  
 gtcgat atca ctctgacacc tttctcccct aaaacccgaa tcacactgac aa 292

## ADL\_0311WP\_Sequence\_Listing.txt

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<210> 626
<211> 249
<212> DNA
<213> Homo sapiens

<400> 626
act at ccagg aaaggaaat t t acagt at at ct cat t t t gg ggt t t ggaag gat gt gt aca 60
aaat agt gt a at t gaaaat t gat aaaat aa aaaat ct t at at act t at at t gggg aaagg 120
aagat aggag aagt gacaga gcgagagaga gagagagt gt t t at gt gt ga aggaaat aag 180
aaagct cagt ct t at aagaa gt ct cagat a at gt gt agac t t t acagaaa agcagt t t aa 240
gaat ggt at 249

<210> 627
<211> 262
<212> DNA
<213> Homo sapiens

<400> 627
gt at ccaagt ccat t gt t ac t aggt t ggag gct ggagat t ct aaat ggct t ccagacat 60
ct ct ct gat t ct ct t t ggga gat ggggt ct gaaagacaat gt cagt agt t t t gggaaat t 120
ct agaaaagt g t gct t ggaaa cgt gggaaga gct ct t gcct agt gcct aaa t gct ccat t t 180
gcagct ct ag ccaagt agat act t ggt agg t at agagccg ggt t t gcgt t t at at t agca 240
aaacct at gt cagagt t gaa ga 262

<210> 628
<211> 147
<212> DNA
<213> Homo sapiens

<400> 628
t t ct t t at gg t ggt gggat g at t at t gt aa t cat act t gg gaacagaagt gat gaaaaag 60
gt at gt t act t gagat at gg gaaacgct at t t t ccat gt t t agt t at ggg gt at t caagt 120
ct aact agt g gaaagt at gg at acat t 147

<210> 629
<211> 97
<212> DNA
<213> Homo sapiens

<400> 629
t ct gt gat t c t ct t t gt cag ct cct t t gcc t at at t t gca t ct cagt t ga caccct gat 60
t ct gact t gt cct t at ct t c ct accagt ct ct gccga 97

<210> 630
<211> 234
<212> DNA
<213> Homo sapiens

<400> 630
gt t gt at caa caat gat t aa ct cct t t at t at acat acac at gaat gt gc at t t t t ggt a 60
aat gcat aaa t gagat t ct a t aat gt t t ac t gat ct t t at at t acagat t t t ct ct t ct t 120

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ADL\_0311WP\_Sequence\_Listing.txt

t taggatt ag ct cagct tgc cccccct ttc cat ct ccacc at ct at agt g agcct ct cca 180  
t aat t agt gc caaccatt ag tct cgt tcat at tttt acac caggagt caa caaa 234

<210> 631  
<211> 115  
<212> DNA  
<213> Homo sapi ens

<400> 631  
ccccagccca agagat gaac at ct ggggac t aat at cat a gacccat ct g gaggct ccca 60  
t gggct agga gccagt gt ga ggct gt aact t at act aaag gt t gt gt t gc ct gct 115

<210> 632  
<211> 56  
<212> DNA  
<213> Homo sapi ens

<400> 632  
gaagact aaa cagaaaccag aact gaaaca t t cacct ggt agcaa at gac act t t g 56

<210> 633  
<211> 251  
<212> DNA  
<213> Homo sapi ens

<400> 633  
t t ct cgcccc acct agggac agat t ccccc t gct ct t t t t gt cct agaaa ccccgct agt 60  
t t gggat ggt agcgt ct ggg gt ggggaggg ct t cccct t c cccact cgag ggt gcggggt g 120  
gggaaggggg ggt ggggt gga gacagccct g gggcagggag gat ggt ct ct cccact gt aga 180  
aagt agagt a ggat t gt ggt cagact t aat t t gaggcat c t agt gaagac acgt acaaat 240  
ccaccaagga a 251

<210> 634  
<211> 294  
<212> DNA  
<213> Homo sapi ens

<400> 634  
gct ggt cat c t caat ggcag gt ggt aggggt act cagaagg gt ggt t gact ccgt gagagg 60  
ggaagaggt g gaccgagagg t ct gaggggt t gaggact ca ggcggaggat t ggat gt ggt 120  
caact cagca at cggt gct g t gct t gt gt g ggt gggggggc cccgt gct t c cagt ggt ggg 180  
t gt t ggggt t ggggt caccg t agt ggt ggt gct gat ggggt at cat ggt t g ggggt ct gt gt 240  
gccggt ggggt gt t ggggt t g cggt caccga t agt t gt ggt ggt gat ggggt gt ca 294

<210> 635  
<211> 221  
<212> DNA  
<213> Homo sapi ens

<400> 635  
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caacaaacca at aaaaagac t aacaat t ca gt agaaaaat ggacaaagaa caaat at gga 120

ADL\_0311WP\_Sequence\_Listing.txt

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gattcataga aatgagagat aaatgtcatg atgagaaggt gaggtgctca cttgatttat | 180 |
| aagagaaatg aaaattaaaa ctacaccaga tgccattttt t                     | 221 |

<210> 636  
 <211> 279  
 <212> DNA  
 <213> Homo sapiens

|                                                                                 |     |
|---------------------------------------------------------------------------------|-----|
| <400> 636<br>cgcggcgatt cttgaggtcg atgtcgcgga tagcgccgtat tttgtagaac acgtcctcaa | 60  |
| tgtccttggg tcggatgtct ggaggt aagt taccacgtat gatgcggcaa tcgttgttcc              | 120 |
| ctgcggggcc acgaatcaca ccacctcccg acatggcggg gacgaaaagc gcggactcga               | 180 |
| gaacaggcct tcccaccaag cctagcgcac ggcagagcga gcccgcagcg gcaccacgtc               | 240 |
| tcccgcggcc cctccaaaat ggcgcttta tcagctcgg                                       | 279 |