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(57) Abstract: The present invention provides methods to determine the prognosis and appropriate treatment for patients diagnosed with cancer, based on the expression levels of one or more biomarkers. More particularly, the invention relates to the identification of genes, or sets of genes, able to distinguish breast cancer patients with a good clinical prognosis from those with a bad clinical prognosis. The invention further provides methods for providing a personalized genomics report for a cancer patient. The inventions also relates to computer systems and software for data analysis using the prognostic and statistical methods disclosed herein.



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METHODS TO PREDICT CLINICAL OUTCOME OF CANCER**CROSS REFERENCE**

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 61/263,763, filed November 23, 2009, which application is incorporated herein by reference in its entirety.

INTRODUCTION

[0002] Oncologists have a number of treatment options available to them, including different combinations of therapeutic regimens that are characterized as "standard of care." The absolute benefit from adjuvant treatment is larger for patients with poor prognostic features, and this has resulted in the policy to select only these so-called `high-risk` patients for adjuvant chemotherapy. See, e.g., S. Paik, et al., *J Clin Oncol.* 24(23):3726-34 (2006). Therefore, the best likelihood of good treatment outcome requires that patients be assigned to optimal available cancer treatment, and that this assignment be made as quickly as possible following diagnosis.

[0003] Today our healthcare system is riddled with inefficiency and wasteful spending – one example of this is that the efficacy rate of many oncology therapeutics working only about 25% of the time. Many of those cancer patients are experiencing toxic side effects for costly therapies that may not be working. This imbalance between high treatment costs and low therapeutic efficacy is often a result of treating a specific diagnosis one way across a diverse patient population. But with the advent of gene profiling tools, genomic testing, and advanced diagnostics, this is beginning to change.

[0004] In particular, once a patient is diagnosed with breast cancer there is a strong need for methods that allow the physician to predict the expected course of disease, including the likelihood of cancer recurrence, long-term survival of the patient, and the like, and select the most appropriate treatment option accordingly. Accepted prognostic and predictive factors in breast cancer include age, tumor size, axillary lymph node status, histological tumor type, pathological grade and hormone receptor status. Molecular diagnostics, however, have been demonstrated to identify more patients with a low risk of breast cancer than was possible with standard prognostic indicators. S. Paik, *The Oncologist* 12(6):631-635 (2007).

[0005] Despite recent advances, the challenge of breast cancer treatment remains to target specific treatment regimens to pathogenically distinct tumor types, and ultimately personalize tumor treatment in order to maximize outcome. Accurate prediction of prognosis

and clinical outcome would allow the oncologist to tailor the administration of adjuvant chemotherapy such that women with a higher risk of a recurrence or poor prognosis would receive more aggressive treatment. Furthermore, accurately stratifying patients based on risk would greatly advance the understanding of expected absolute benefit from treatment, thereby increasing success rates for clinical trials for new breast cancer therapies.

[0006] Currently, most diagnostic tests used in clinical practice are frequently not quantitative, relying on immunohistochemistry (IHC). This method often yields different results in different laboratories, in part because the reagents are not standardized, and in part because the interpretations are subjective and cannot be easily quantified. Other RNA-based molecular diagnostics require fresh-frozen tissues, which presents a myriad of challenges including incompatibilities with current clinical practices and sample transport regulations. 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 RNA) from small amounts of material. Thus, traditionally fixed tissue has been rarely used other than for IHC detection of proteins.

SUMMARY

[0007] The present invention provides a set of genes, the expression levels of which are associated with a particular clinical outcome in cancer. For example, the clinical outcome could be a good or bad prognosis assuming the patient receives the standard of care. The clinical outcome may be defined by clinical endpoints, such as disease or recurrence free survival, metastasis free survival, overall survival, etc.

[0008] The present invention accommodates the use of archived paraffin-embedded biopsy material for assay of all markers in the set, and therefore is compatible with the most widely available type of biopsy material. It is also compatible with several different methods of tumor tissue harvest, for example, via core biopsy or fine needle aspiration. The tissue sample may comprise cancer cells.

[0009] In one aspect, the present invention concerns a method of predicting a clinical outcome of a cancer patient, comprising (a) obtaining an expression level of an expression product (e.g., an RNA transcript) of at least one prognostic gene listed in Tables 1-12 from a tissue sample obtained from a tumor of the patient; (b) normalizing the expression level of the expression product of the at least one prognostic gene, to obtain a normalized expression level; and (c) calculating a risk score based on the normalized expression value, wherein increased expression of prognostic genes in Tables 1, 3, 5, and 7 are positively correlated

with good prognosis, and wherein increased expression of prognostic genes in Tables 2, 4, 6, and 8 are negatively associated with good prognosis. In some embodiments, the tumor is estrogen receptor-positive. In other embodiments, the tumor is estrogen receptor negative.

[0010] In one aspect, the present disclosure provides a method of predicting a clinical outcome of a cancer patient, comprising (a) obtaining an expression level of an expression product (e.g., an RNA transcript) of at least one prognostic gene from a tissue sample obtained from a tumor of the patient, where the at least one prognostic gene is selected from GSTM2, IL6ST, GSTM3, C8orf4, TNFRSF11B, NAT1, RUNX1, CSF1, ACTR2, LMNB1, TFRC, LAPTM4B, ENO1, CDC20, and IDH2; (b) normalizing the expression level of the expression product of the at least one prognostic gene, to obtain a normalized expression level; and (c) calculating a risk score based on the normalized expression value, wherein increased expression of a prognostic gene selected from GSTM2, IL6ST, GSTM3, C8orf4, TNFRSF11B, NAT1, RUNX1, and CSF1 is positively correlated with good prognosis, and wherein increased expression of a prognostic gene selected from ACTR2, LMNB1, TFRC, LAPTM4B, ENO1, CDC20, and IDH2 is negatively associated with good prognosis. In some embodiments, the tumor is estrogen receptor-positive. In other embodiments, the tumor is estrogen receptor negative.

[0010A] In one aspect, the present disclosure provides a method for predicting the clinical outcome of a human patient diagnosed with breast cancer comprising:

(a) quantitatively measuring a level of an RNA transcript of gp130/IL6ST in a tissue sample obtained from a tumor of the patient;

(b) normalizing the expression level of the RNA transcript of gp130/IL6ST to obtain a normalized expression level;

(c) comparing the normalized gp130/IL6ST expression level to a normalized gp130/IL6ST expression level obtained from a breast cancer reference set; and

(d) determining that the patient has an increased likelihood of good prognosis if the normalized gp130/IL6ST expression level is increased compared to the normalized gp130/IL6ST level obtained from the breast cancer reference set, wherein good prognosis is a reduced likelihood of recurrence or metastasis or increased likelihood of overall survival.

[0011] In various embodiments, the normalized expression level of at least 2, or at least 5, or at least 10, or at least 15, or at least 20, or at least 25 prognostic genes (as determined by assaying a level of an expression product of the gene) is determined. In alternative embodiments, the normalized expression levels of at least one of the genes that co-expresses with prognostic genes in Tables 16-18 is obtained.

[0012] In another embodiment, the risk score is determined using normalized expression levels of at least one a stromal or transferrin receptor group gene, or a gene that co-expresses with a stromal or transferrin receptor group gene.

[0013] In another embodiment, the cancer is breast cancer. In another embodiment, the patient is a human patient.

[0014] In yet another embodiment, the cancer is ER-positive breast cancer.

[0015] In yet another embodiment, the cancer is ER-negative breast cancer.

[0016] In a further embodiment, the expression product comprises RNA. For example, the RNA could be exonic RNA, intronic RNA, or short RNA (e.g., microRNA, siRNA, promoter-associated small RNA, shRNA, etc.). In various embodiments, the RNA is fragmented RNA.

[0017] In a different aspect, the invention concerns an array comprising polynucleotides hybridizing to an RNA transcription of at least one of the prognostic genes listed in Tables 1-12.

[0017A] In one aspect, the present disclosure provides a method for predicting the clinical outcome of a human patient diagnosed with breast cancer comprising:

extracting RNA from a fixed, paraffin-embedded tissue sample obtained from the patient;

reverse transcribing an RNA transcript of gp130/IL6ST to produce a cDNA of gp130/IL6ST;

amplifying the cDNA of gp130/IL6ST;

producing an amplicon of the RNA transcript of gp130/IL6ST;

quantitatively assaying a level of the amplicon of the RNA transcript of gp130/IL6ST;

normalizing the level of the amplicon of the RNA transcript of gp130/IL6ST to provide a normalized gp130/IL6ST amplicon level;

comparing the normalized IL6ST amplicon level to a normalized gp130/IL6ST amplicon level obtained from a breast cancer reference set; and

determining that the patient has an increased likelihood of good prognosis if the normalized gp130/IL6ST amplicon level is increased compared to the normalized gp130/IL6ST amplicon level obtained from the breast cancer reference set, wherein good prognosis is a reduced likelihood of recurrence or metastasis or increased likelihood of overall survival.

[0018] In a still further aspect, the invention concerns a method of preparing a personalized genomics profile for a patient, comprising (a) obtaining an expression level of an expression product (e.g., an RNA transcript) of at least one prognostic gene listed in Tables 1-12 from a tissue sample obtained from a tumor of the patient; (b) normalizing the expression level of the expression product of the at least one prognostic gene to obtain a normalized expression level; and (c) calculating a risk score based on the normalized expression value, wherein increased expression of prognostic genes in Tables 1, 3, 5, and 7 are positively correlated with good prognosis, and wherein increased expression of prognostic genes in Tables 2, 4, 6, and 8 are negatively associated with good prognosis. In some embodiments, the tumor is estrogen receptor-positive, and in other embodiments the tumor is estrogen receptor negative.

[0019] In various embodiments, a subject method can further include providing a report. The report may include prediction of the likelihood of risk that said patient will have a particular clinical outcome.

[0020] The invention further provides a computer-implemented method for classifying a cancer patient based on risk of cancer recurrence, comprising (a) classifying, on a computer, said patient as having a good prognosis or a poor prognosis based on an expression profile comprising measurements of expression levels of expression products of a plurality of prognostic genes in a tumor tissue sample taken from the patient, said plurality of genes comprising at least three different prognostic genes listed in any of Tables 1-12, wherein a good prognosis predicts no recurrence or metastasis within a predetermined period after initial diagnosis, and wherein a poor prognosis predicts recurrence or metastasis within said predetermined period after initial diagnosis; and (b) calculating a risk score based on said expression levels.

DETAILED DESCRIPTION

DEFINITIONS

[0021] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton *et al.*, Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, NY 1994), and March, Advanced Organic Chemistry

Reactions, Mechanisms and Structure 4th ed., John Wiley & Sons (New York, NY 1992), provide one skilled in the art with a general guide to many of the terms used in the present application.

[0022] One skilled in the art will recognize many methods and materials similar or equivalent to those described herein, which could be used in the practice of the present invention. Indeed, the present invention is in no way limited to the methods and materials described. For purposes of the present invention, the following terms are defined below.

[0022A] Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each claim of this application.

[0023] “Prognostic factors” are those variables related to the natural history of cancer, which influence the recurrence rates and outcome of patients once they have developed cancer. Clinical parameters that have been associated with a worse prognosis include, for example, lymph node involvement, and high grade tumors. Prognostic factors are frequently used to categorize patients into subgroups with different baseline relapse risks.

[0024] The term “prognosis” is used herein to refer to the prediction of the likelihood of cancer-attributable death or progression, including recurrence, metastatic spread, and drug resistance, of a neoplastic disease, such as breast cancer. The term “good prognosis” means a desired or “positive” clinical outcome. For example, in the context of breast cancer, a good prognosis may be an expectation of no recurrences or metastasis within two, three, four, five or more years of the initial diagnosis of breast cancer. The terms “bad prognosis” or “poor prognosis” are used herein interchangeably herein to mean an undesired clinical outcome. For example, in the context of breast cancer, a bad prognosis may be an expectation of a recurrence or metastasis within two, three, four, five or more years of the initial diagnosis of breast cancer.

[0025] The term “prognostic gene” is used herein to refer to a gene, the expression of which is correlated, positively or negatively, with a good prognosis for a cancer patient treated with the standard of care. A gene may be both a prognostic and predictive gene, depending on the correlation of the gene expression level with the corresponding endpoint. For example, using a Cox proportional hazards model, if a gene is only prognostic, its hazard ratio (HR) does not change when measured in patients treated with the standard of care or in patients treated with a new intervention.

[0026] The term “predictive gene” is used herein to refer to a gene, the expression of which is correlated, positively or negatively, with response to a beneficial response to treatment. For example, treatment could include chemotherapy.

[0027] The terms “risk score” or “risk classification” are used interchangeably herein to describe a level of risk (or likelihood) that a patient will experience a particular clinical

outcome. A patient may be classified into a risk group or classified at a level of risk based on the methods of the present disclosure, e.g. high, medium, or low risk. A “risk group” is a group of subjects or individuals with a similar level of risk for a particular clinical outcome.

[0028] A clinical outcome can be defined using different endpoints. The term “long-term” survival is used herein to refer to survival for a particular time period, e.g., for at least 3 years, more preferably for at least 5 years. The term “Recurrence-Free Survival” (RFS) is used herein to refer to survival for a time period (usually in years) from randomization to first cancer recurrence or death due to recurrence of cancer. The term “Overall Survival” (OS) is used herein to refer to the time (in years) from randomization to death from any cause. The term “Disease-Free Survival” (DFS) is used herein to refer to survival for a time period (usually in years) from randomization to first cancer recurrence or death from any cause.

[0029] The calculation of the measures listed above in practice may vary from study to study depending on the definition of events to be either censored or not considered.

[0030] The term “biomarker” as used herein refers to a gene, the expression level of which, as measured using a gene product.

[0031] The term “microarray” refers to an ordered arrangement of hybridizable array elements, preferably polynucleotide probes, on a substrate.

[0032] As used herein, the term “normalized expression level” as applied to a gene refers to the normalized level of a gene product, e.g. the normalized value determined for the RNA expression level of a gene or for the polypeptide expression level of a gene.

[0033] The term “C_t” as used herein refers to threshold cycle, the cycle number in quantitative polymerase chain reaction (qPCR) at which the fluorescence generated within a reaction well exceeds the defined threshold, i.e. the point during the reaction at which a sufficient number of amplicons have accumulated to meet the defined threshold.

[0034] The term “gene product” or “expression product” are used herein to refer to the RNA transcription products (transcripts) of the gene, including mRNA, and the polypeptide translation products of such RNA transcripts. A gene product can be, for example, an unspliced RNA, an mRNA, a splice variant mRNA, a microRNA, a fragmented RNA, a polypeptide, a post-translationally modified polypeptide, a splice variant polypeptide, etc.

[0035] The term “RNA transcript” as used herein refers to the RNA transcription products of a gene, including, for example, mRNA, an unspliced RNA, a splice variant mRNA, a microRNA, and a fragmented RNA. “Fragmented RNA” as used herein refers to

RNA a mixture of intact RNA and RNA that has been degraded as a result of the sample processing (e.g., fixation, slicing tissue blocks, etc.).

[0036] Unless indicated otherwise, each gene name used herein corresponds to the Official Symbol assigned to the gene and provided by Entrez Gene (URL: www.ncbi.nlm.nih.gov/sites/entrez) as of the filing date of this application.

[0036A] Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

[0037] The terms "correlated" and "associated" are used interchangeably herein to refer to a strength of association between two measurements (or measured entities). The disclosure provides genes and gene subsets, the expression levels of which are associated with a particular outcome measure. For example, the increased expression level of a gene may be positively correlated (positively associated) with an increased likelihood of good clinical outcome for the patient, such as an increased likelihood of long-term survival without recurrence of the cancer and/or metastasis-free survival. Such a positive correlation may be demonstrated statistically in various ways, e.g. by a low hazard ratio (e.g. $HR < 1.0$). In another example, the increased expression level of a gene may be negatively correlated (negatively associated) with an increased likelihood of good clinical outcome for the patient. In that case, for example, the patient may have a decreased likelihood of long-term survival without recurrence of the cancer and/or cancer metastasis, and the like. Such a negative correlation indicates that the patient likely has a poor prognosis, e.g., a high hazard ratio (e.g., $HR > 1.0$). "Correlated" is also used herein to refer to a strength of association between the expression levels of two different genes, such that expression level of a first gene can be substituted with an expression level of a second gene in a given algorithm in view of their correlation of expression. Such "correlated expression" of two genes that are substitutable in an algorithm usually gene expression levels that are positively correlated with one another, e.g., if increased expression of a first gene is positively correlated with an outcome (e.g., increased likelihood of good clinical outcome), then the second gene that is co-expressed and exhibits correlated expression with the first gene is also positively correlated with the same outcome

[0038] The term "recurrence," as used herein, refers to local or distant (metastasis) recurrence of cancer. For example, breast cancer can come back as a local recurrence (in the treated breast or near the tumor surgical site) or as a distant recurrence in the body. The

most common sites of breast cancer recurrence include the lymph nodes, bones, liver, or lungs.

[0039] The term "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. 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. In addition, the term "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. The term "polynucleotide" specifically includes cDNAs. The term includes DNAs (including cDNAs) 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.

[0040] The term "oligonucleotide" refers to 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 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.

[0041] The phrase "amplification" refers to a process by which multiple copies of a gene or RNA transcript are formed in a particular sample or cell line. The duplicated region (a stretch of amplified polynucleotide) is often referred to as "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.

[0042] The term "estrogen receptor (ER)" designates the estrogen receptor status of a cancer patient. A tumor is ER-positive if there is a significant number of estrogen receptors present in the cancer cells, while ER-negative indicates that the cells do not have a

significant number of receptors present. The definition of “significant” varies amongst testing sites and methods (e.g., immunohistochemistry, PCR). The ER status of a cancer patient can be evaluated by various known means. For example, the ER level of breast cancer is determined by measuring an expression level of a gene encoding the estrogen receptor in a breast tumor sample obtained from a patient.

[0043] The term "tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

[0044] The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, breast cancer, ovarian cancer, colon cancer, lung cancer, prostate cancer, hepatocellular cancer, gastric cancer, pancreatic cancer, cervical cancer, liver cancer, bladder cancer, cancer of the urinary tract, thyroid cancer, renal cancer, carcinoma, melanoma, and brain cancer.

[0045] The gene subset identified herein as the “stromal group” includes genes that are synthesized predominantly by stromal cells and are involved in stromal response and genes that co-express with stromal group genes. “Stromal cells” are defined herein as connective tissue cells that make up the support structure of biological tissues. Stromal cells include fibroblasts, immune cells, pericytes, endothelial cells, and inflammatory cells. “Stromal response” refers to a desmoplastic response of the host tissues at the site of a primary tumor or invasion. See, e.g., E. Rubin, J. Farber, Pathology, 985-986 (2nd Ed. 1994). The stromal group includes, for example, CDH11, TAGLN, ITGA4, INHBA, COLIA1, COLIA2, FN1, CXCL14, TNFRSF1, CXCL12, C10ORF116, RUNX1, GSTM2, TGFB3, CAV1, DLC1, TNFRSF10, F3, and DICER1, and co-expressed genes identified in Tables 16-18.

[0046] The gene subset identified herein as the “metabolic group” includes genes that are associated with cellular metabolism, including genes associated with carrying proteins for transferring iron, the cellular iron homeostasis pathway, and homeostatic biochemical metabolic pathways, and genes that co-express with metabolic group genes. The metabolic group includes, for example, TFRC, ENO1, IDH2, ARF1, CLDN4, PRDX1, and GBP1, and co-expressed genes identified in Tables 16-18.

[0047] The gene subset identified herein as the “immune group” includes genes that are involved in cellular immunoregulatory functions, such as T and B cell trafficking, lymphocyte-associated or lymphocyte markers, and interferon regulation genes, and genes

that co-express with immune group genes. The immune group includes, for example, CCL19 and IRF1, and co-expressed genes identified in Tables 16-18.

[0048] The gene subset identified herein as the “proliferation group” includes genes that are associated with cellular development and division, cell cycle and mitotic regulation, angiogenesis, cell replication, nuclear transport/stability, wnt signaling, apoptosis, and genes that co-express with proliferation group genes. The proliferation group includes, for example, PGF, SPC25, AURKA, BIRC5, BUB1, CCNB1, CENPA, KPNA, LMNB1, MCM2, MELK, NDC80, TPX2M, and WISP1, and co-expressed genes identified in Tables 16-18.

[0049] The term “co-expressed”, as used herein, refers to a statistical correlation between the expression level of one gene and the expression level of another gene. Pairwise co-expression may be calculated by various methods known in the art, e.g., by calculating Pearson correlation coefficients or Spearman correlation coefficients. Co-expressed gene cliques may also be identified using a graph theory.

[0050] As used herein, the terms “gene clique” and “clique” refer to a subgraph of a graph in which every vertex is connected by an edge to every other vertex of the subgraph.

[0051] As used herein, a “maximal clique” is a clique in which no other vertex can be added and still be a clique.

[0052] 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.

[0053] A “computer-based system” refers to a system of hardware, software, and data storage medium used to analyze information. The minimum hardware of a patient computer-based system comprises a central processing unit (CPU), and hardware for data input, data output (e.g., display), and data storage. An ordinarily skilled artisan can readily appreciate that any currently available computer-based systems and/or components thereof are suitable for use in connection with the methods of the present disclosure. The data storage medium may comprise any manufacture comprising a recording of the present information as described above, or a memory access device that can access such a manufacture.

[0054] To “record” data, programming or other information on a computer readable medium refers to a process for storing information, using any such methods as known in the art. Any convenient data storage structure may be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, e.g. word processing text file, database format, etc.

[0055] A “processor” or “computing means” references any hardware and/or software combination that will perform the functions required of it. For example, a suitable processor may be a programmable digital microprocessor such as available in the form of an electronic controller, mainframe, server or personal computer (desktop or portable). Where the processor is programmable, suitable programming can be communicated from a remote location to the processor, or previously saved in a computer program product (such as a portable or fixed computer readable storage medium, whether magnetic, optical or solid state device based). For example, a magnetic medium or optical disk may carry the programming, and can be read by a suitable reader communicating with each processor at its corresponding station.

[0056] As used herein, “graph theory” refers to a field of study in Computer Science and Mathematics in which situations are represented by a diagram containing a set of points and lines connecting some of those points. The diagram is referred to as a “graph”, and the points and lines referred to as “vertices” and “edges” of the graph. In terms of gene co-expression analysis, a gene (or its equivalent identifier, e.g. an array probe) may be represented as a node or vertex in the graph. If the measures of similarity (e.g., correlation coefficient, mutual information, and alternating conditional expectation) between two genes are higher than a significant threshold, the two genes are said to be co-expressed and an edge will be drawn in the graph. When co-expressed edges for all possible gene pairs for a given study have been drawn, all maximal cliques are computed. The resulting maximal clique is defined as a gene clique. A gene clique is a computed co-expressed gene group that meets predefined criteria.

[0057] “Stringency” of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the

higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

[0058] "Stringent conditions" or "high stringency conditions", as defined herein, typically: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

[0059] "Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0060] In the context of the present invention, reference to "at least one," "at least two," "at least five," etc. of the genes listed in any particular gene set means any one or any and all combinations of the genes listed.

[0061] The term "node negative" cancer, such as "node negative" breast cancer, is used herein to refer to cancer that has not spread to the lymph nodes.

[0062] The terms “splicing” and “RNA splicing” are used interchangeably and refer to 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.

[0063] In theory, the term “exon” refers to any segment of an interrupted gene that is represented in the mature RNA product (B. Lewin. *Genes IV* Cell Press, Cambridge Mass. 1990). 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 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.

GENE EXPRESSION ASSAY

[0064] The present disclosure provides methods that employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as, “Molecular Cloning: A Laboratory Manual”, 2nd edition (Sambrook et al., 1989); “Oligonucleotide Synthesis” (M.J. Gait, ed., 1984); “Animal Cell Culture” (R.I. Freshney, ed., 1987); “Methods in Enzymology” (Academic Press, Inc.); “Handbook of Experimental Immunology”, 4th edition (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); “Current Protocols in Molecular Biology” (F.M. Ausubel et al., eds., 1987); and “PCR: The Polymerase Chain Reaction”, (Mullis et al., eds., 1994).

1. Gene Expression Profiling

[0065] Methods of gene expression profiling include methods based on hybridization analysis of polynucleotides, methods based on sequencing of polynucleotides, and proteomics-based methods. The most commonly used methods known in the art for the quantification of mRNA expression in a sample include 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)); and PCR-based methods, such as reverse transcription polymerase chain reaction (RT-PCR) (Weis et al., *Trends in Genetics* 8:263-264 (1992)). Alternatively, antibodies may be employed that can recognize

specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes.

2. PCR-based Gene Expression Profiling Methods

a. Reverse Transcriptase PCR (RT-PCR)

[0066] Of the techniques listed above, the most sensitive and most flexible quantitative method is RT-PCR, which can be used to compare mRNA levels in different sample populations, in 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.

[0067] The first step is the isolation of mRNA from a target sample. The starting material is typically total RNA isolated from human tumors or tumor cell lines, and corresponding normal tissues or cell lines, respectively. Thus RNA can be isolated from a variety of primary tumors, including breast, lung, colon, prostate, brain, liver, kidney, pancreas, spleen, thymus, testis, ovary, uterus, etc., tumor, or tumor cell lines, with pooled DNA from healthy donors. If the source of mRNA is a primary tumor, mRNA can be extracted, for example, from frozen or archived paraffin-embedded and fixed (e.g. formalin-fixed) tissue samples.

[0068] 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, *Lab Invest.* 56:A67 (1987), and De Andrés *et al.*, *BioTechniques* 18:42044 (1995). In particular, RNA isolation can be performed using purification kit, buffer set and protease from commercial manufacturers, such as Qiagen, according to the manufacturer's instructions. For example, total RNA from cells in culture can be isolated using Qiagen RNeasy mini-columns. Other commercially available RNA isolation kits include MasterPure™ Complete DNA and RNA Purification Kit (EPICENTRE®, Madison, WI), 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 can be isolated, for example, by cesium chloride density gradient centrifugation.

[0069] In some cases, it may be appropriate to amplify RNA prior to initiating expression profiling. It is often the case that only very limited amounts of valuable clinical specimens are available for molecular analysis. This may be due to the fact that the tissues have already be used for other laboratory analyses or may be due to the fact that the original

specimen is very small as in the case of needle biopsy or very small primary tumors. When tissue is limiting in quantity it is generally also the case that only small amounts of total RNA can be recovered from the specimen and as a result only a limited number of genomic markers can be analyzed in the specimen. RNA amplification compensates for this limitation by faithfully reproducing the original RNA sample as a much larger amount of RNA of the same relative composition. Using this amplified copy of the original RNA specimen, unlimited genomic analysis can be done to discovery biomarkers associated with the clinical characteristics of the original biological sample. This effectively immortalizes clinical study specimens for the purposes of genomic analysis and biomarker discovery.

[0070] As RNA cannot serve as a template for PCR, the first step in gene expression profiling by real-time RT-PCR (RT-PCR) is the reverse transcription of the RNA template into cDNA, followed by its exponential amplification in a PCR reaction. The two most commonly used reverse transcriptases are avian myeloblastosis virus reverse transcriptase (AMV-RT) and Moloney murine leukemia virus reverse transcriptase (MMLV-RT). The reverse transcription step is typically primed using specific primers, random hexamers, or oligo-dT primers, depending on the circumstances and the goal of expression profiling. For example, extracted RNA can be reverse-transcribed using a GeneAmp RNA PCR kit (Perkin Elmer, CA, USA), following the manufacturer's instructions. The derived cDNA can then be used as a template in the subsequent PCR reaction. For further details see, e.g. Held *et al.*, *Genome Research* 6:986-994 (1996).

[0071] Although the PCR step can use a variety of thermostable DNA-dependent DNA polymerases, it typically employs the Taq DNA polymerase, which has a 5'-3' nuclease activity but lacks a 3'-5' proofreading endonuclease activity. Thus, TaqMan® PCR typically utilizes the 5'-nuclease activity of Taq or Tth polymerase to hydrolyze a hybridization probe bound to its target amplicon, but any enzyme with equivalent 5' nuclease activity can be used. Two oligonucleotide primers are used to generate an amplicon typical of a PCR reaction. A third oligonucleotide, or probe, is designed to detect nucleotide sequence located between the two PCR primers. The probe is non-extendible by Taq DNA polymerase enzyme, and is labeled with a reporter fluorescent dye and a quencher fluorescent dye. Any laser-induced emission from the reporter dye is quenched by the quenching dye when the two dyes are located close together as they are on the probe. During the amplification reaction, the Taq DNA polymerase enzyme cleaves the probe in a template-dependent manner. The resultant probe fragments disassociate in solution, and signal from the released reporter dye is free from the quenching effect of the second

fluorophore. One molecule of reporter dye is liberated for each new molecule synthesized, and detection of the unquenched reporter dye provides the basis for quantitative interpretation of the data.

[0072] TaqMan® RT-PCR can be performed using commercially available equipment, such as, for example, ABI PRISM 7900® Sequence Detection System™ (Perkin-Elmer-Applied Biosystems, Foster City, CA, USA), or LightCycler® 480 Real-Time PCR System (Roche Diagnostics, GmbH, Penzberg, Germany). In a preferred embodiment, the 5' nuclease procedure is run on a real-time quantitative PCR device such as the ABI PRISM 7900® Sequence Detection System™. The system consists of a thermocycler, laser, charge-coupled device (CCD), camera and computer. The system amplifies samples in a 384-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 384 wells, and detected at the CCD. The system includes software for running the instrument and for analyzing the data.

[0073] 5'-Nuclease assay data are initially expressed as Ct, or the threshold cycle. As discussed above, fluorescence values are recorded during every cycle and represent the amount of product amplified to that point in the amplification reaction. The point when the fluorescent signal is first recorded as statistically significant is the threshold cycle (C_t).

[0074] To minimize errors and the effect of sample-to-sample variation, RT-PCR is usually performed using an internal standard. The ideal internal standard is expressed at a constant level among different tissues, and is unaffected by the experimental treatment. RNAs most frequently used to normalize patterns of gene expression are mRNAs for the housekeeping genes glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) and β -actin.

[0075] The steps of a representative protocol for profiling gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA isolation, purification, primer extension and amplification are given in various published journal articles. M. Cronin, Am J Pathol 164(1):35-42 (2004). Briefly, a representative process starts with cutting about 10 μ m thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA are removed. After analysis of the RNA concentration, RNA repair and/or amplification steps may be included, if necessary, and RNA is reverse transcribed using gene specific primers followed by RT-PCR.

b. Design of Intron-Based PCR Primers and Probes

[0076] PCR primers and probes can be designed based upon exon or intron sequences present in the mRNA transcript of the gene of interest. Prior to carrying out primer/probe design, it is necessary to map the target gene sequence to the human genome

assembly in order to identify intron-exon boundaries and overall gene structure. This can be performed using publicly available software, such as Primer3 (Whitehead Inst.) and Primer Express® (Applied Biosystems).

[0077] Where necessary or desired, repetitive sequences of the target sequence can be masked to mitigate non-specific signals. Exemplary tools to accomplish this include the Repeat Masker program available on-line through the Baylor College of Medicine, which screens DNA sequences against a library of repetitive elements and returns a query sequence in which the repetitive elements are masked. The masked intron and exon sequences can then be used to design primer and probe sequences for the desired target sites using any commercially or otherwise publicly available primer/probe design packages, such as Primer Express (Applied Biosystems); MGB assay-by-design (Applied Biosystems); Primer3 (Steve Rozen and Helen J. Skaletsky (2000) Primer3 on the WWW for general users and for biologist programmers. In: Rrawetz S, Misener S (eds) Bioinformatics Methods and Protocols: Methods in Molecular Biology. Humana Press, Totowa, NJ, pp 365-386).

[0078] Other factors that can influence PCR primer design include primer length, melting temperature (T_m), and G/C 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, and exhibit T_m 's between 50 and 80 °C, e.g. about 50 to 70 °C.

[0079] For further guidelines for PCR primer and probe design see, e.g. Dieffenbach, CW. 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, T.N. Primerselect: Primer and probe design. Methods Mol. Biol. 70:520-527 (1997), the entire disclosures of which are hereby expressly incorporated by reference.

[0080] Table A provides further information concerning the primer, probe, and amplicon sequences associated with the Examples disclosed herein.

c. MassARRAY System

[0081] In the MassARRAY-based gene expression profiling method, developed by Sequenom, Inc. (San Diego, CA) following the isolation of RNA and reverse transcription, the obtained cDNA is spiked with a synthetic DNA molecule (competitor), which matches the targeted cDNA region in all positions, except a single base, and serves as an internal standard. The cDNA/competitor mixture is PCR amplified and is subjected to a post-PCR

shrimp alkaline phosphatase (SAP) enzyme treatment, which results in the dephosphorylation of the remaining nucleotides. After inactivation of the alkaline phosphatase, the PCR products from the competitor and cDNA are subjected to primer extension, which generates distinct mass signals for the competitor- and cDNA-derived PCR products. After purification, these products are dispensed on a chip array, which is pre-loaded with components needed for analysis with matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis. The cDNA present in the reaction is then quantified by analyzing the ratios of the peak areas in the mass spectrum generated. For further details see, e.g. Ding and Cantor, Proc. Natl. Acad. Sci. USA 100:3059-3064 (2003).

d. Other PCR-based Methods

[0082] 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)); BeadArray™ technology (Illumina, San Diego, CA; 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, TX) in a rapid assay for gene expression (Yang et al., Genome Res. 11:1888-1898 (2001)); and high coverage expression profiling (HiCEP) analysis (Fukumura et al., Nucl. Acids. Res. 31(16) e94 (2003)).

3. Microarrays

[0083] Differential gene expression can also be identified, or confirmed using the microarray technique. Thus, the expression profile of breast cancer-associated genes can be measured in either fresh or paraffin-embedded tumor tissue, using microarray technology. In this method, polynucleotide sequences of interest (including cDNAs and oligonucleotides) are plated, or arrayed, on a microchip substrate. The arrayed sequences are then hybridized with specific DNA probes 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 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 fixed (e.g. formalin-fixed) tissue samples, which are routinely prepared and preserved in everyday clinical practice.

[0084] In a specific embodiment of the microarray technique, PCR amplified inserts of cDNA clones are applied to a substrate in a dense array. Preferably at least 10,000 nucleotide sequences are applied to the substrate. The microarrayed genes, immobilized on the microchip at 10,000 elements each, are suitable for hybridization under stringent conditions. Fluorescently labeled cDNA probes may be generated through 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 determined simultaneously. 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 be performed by commercially available equipment, following manufacturer's protocols, such as by using the Affymetrix GenChip technology, or Agilent's microarray technology.

[0085] 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.

4. Gene Expression Analysis by Nucleic Acid Sequencing

[0086] Nucleic acid sequencing technologies are suitable methods for analysis of gene expression. The principle underlying these methods is that the number of times a cDNA sequence is detected in a sample is directly related to the relative expression of the mRNA corresponding to that sequence. These methods are sometimes referred to by the term Digital Gene Expression (DGE) to reflect the discrete numeric property of the resulting data. Early methods applying this principle were Serial Analysis of Gene Expression (SAGE) and Massively Parallel Signature Sequencing (MPSS). See, e.g., S. Brenner, et al., *Nature Biotechnology* 18(6):630-634 (2000). More recently, the advent of "next-generation" sequencing technologies has made DGE simpler, higher throughput, and more affordable.

As a result, more laboratories are able to utilize DGE to screen the expression of more genes in more individual patient samples than previously possible. See, e.g., J. Marioni, *Genome Research* 18(9):1509-1517 (2008); R. Morin, *Genome Research* 18(4):610-621 (2008); A. Mortazavi, *Nature Methods* 5(7):621-628 (2008); N. Cloonan, *Nature Methods* 5(7):613-619 (2008).

5. *Isolating RNA from Body Fluids*

[0087] Methods of isolating RNA for expression analysis from blood, plasma and serum (See for example, Tsui NB et al. (2002) 48,1647-53 and references cited therein) and from urine (See for example, Boom R et al. (1990) *J Clin Microbiol.* 28, 495-503 and reference cited therein) have been described.

6. *Immunohistochemistry*

[0088] Immunohistochemistry methods are also suitable for detecting the expression levels of the prognostic markers of the present invention. Thus, antibodies or antisera, preferably polyclonal antisera, and most preferably monoclonal antibodies specific for each marker are used to detect expression. The antibodies can be detected by direct labeling of the antibodies themselves, for example, with radioactive labels, fluorescent labels, hapten labels such as, biotin, or an enzyme such as horse radish peroxidase or alkaline phosphatase. Alternatively, unlabeled primary antibody is used in conjunction with a labeled secondary antibody, comprising antisera, polyclonal antisera or a monoclonal antibody specific for the primary antibody. Immunohistochemistry protocols and kits are well known in the art and are commercially available.

7. *Proteomics*

[0089] The term “proteome” is defined as the totality of the proteins present in a sample (e.g. tissue, organism, or cell culture) at a certain point of time. Proteomics includes, among other things, study of the global changes of protein expression in a sample (also referred to as “expression proteomics”). Proteomics typically includes the following steps: (1) separation of individual proteins in a sample by 2-D gel electrophoresis (2-D PAGE); (2) identification of the individual proteins recovered from the gel, e.g. by mass spectrometry or N-terminal sequencing, and (3) analysis of the data using bioinformatics. Proteomics methods are valuable supplements to other methods of gene expression profiling, and can be used, alone or in combination with other methods, to detect the products of the prognostic markers of the present invention.

8. General Description of the mRNA Isolation, Purification, and Amplification

[0090] The steps of a representative protocol for profiling gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA isolation, purification, primer extension and amplification are provided in various published journal articles (for example: T.E. Godfrey *et al.*, *J. Molec. Diagnostics* 2: 84-91 [2000]; K. Specht *et al.*, *Am. J. Pathol.* 158: 419-29 [2001]). Briefly, a representative process starts with cutting about 10 μ m thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA are removed. After analysis of the RNA concentration, RNA repair and/or amplification steps may be included, if necessary, and RNA is reverse transcribed using gene specific primers followed by RT-PCR. Finally, the data are analyzed to identify the best treatment option(s) available to the patient on the basis of the characteristic gene expression pattern identified in the tumor sample examined, dependent on the predicted likelihood of cancer recurrence.

9. Normalization

[0091] The expression data used in the methods disclosed herein can be normalized. Normalization refers to a process to correct for (normalize away), for example, differences in the amount of RNA assayed and variability in the quality of the RNA used, to remove unwanted sources of systematic variation in C_t measurements, and the like. With respect to RT-PCR experiments involving archived fixed paraffin embedded tissue samples, sources of systematic variation are known to include the degree of RNA degradation relative to the age of the patient sample and the type of fixative used to preserve the sample. Other sources of systematic variation are attributable to laboratory processing conditions.

[0092] Assays can provide for normalization by incorporating the expression of certain normalizing genes, which genes do not significantly differ in expression levels under the relevant conditions. Exemplary normalization genes include housekeeping genes such as PGK1 and UBB. (See, e.g., E. Eisenberg, *et al.*, *Trends in Genetics* 19(7):362-365 (2003).) Normalization can be based on the mean or median signal (C_T) of all of the assayed genes or a large subset thereof (global normalization approach). In general, the normalizing genes, also referred to as reference genes should be genes that are known not to exhibit significantly different expression in colorectal cancer as compared to non-cancerous colorectal tissue, and are not significantly affected by various sample and process conditions, thus provide for normalizing away extraneous effects.

[0093] Unless noted otherwise, normalized expression levels for each mRNA/tested tumor/patient will be expressed as a percentage of the expression level measured in the

reference set. A reference set of a sufficiently high number (e.g. 40) of tumors yields a distribution of normalized levels of each mRNA species. The level measured in a particular tumor sample to be analyzed falls at some percentile within this range, which can be determined by methods well known in the art.

[0094] In exemplary embodiments, one or more of the following genes are used as references by which the expression data is normalized: AAMP, ARF1, EEF1A1, ESD, GPS1, H3F3A, HNRPC, RPL13A, RPL41, RPS23, RPS27, SDHA, TCEA1, UBB, YWHAZ, B-actin, GUS, GAPDH, RPLPO, and TFRC. For example, the calibrated weighted average C_t measurements for each of the prognostic genes may be normalized relative to the mean of at least three reference genes, at least four reference genes, or at least five reference genes.

[0095] Those skilled in the art will recognize that normalization may be achieved in numerous ways, and the techniques described above are intended only to be exemplary, not exhaustive.

REPORTING RESULTS

[0096] The methods of the present disclosure are suited for the preparation of reports summarizing the expected or predicted clinical outcome resulting from the methods of the present disclosure. A “report,” as described herein, is an electronic or tangible document that includes report elements that provide information of interest relating to a likelihood assessment or a risk assessment and its results. A subject report includes at least a likelihood assessment or a risk assessment, e.g., an indication as to the risk of recurrence of breast cancer, including local recurrence and metastasis of breast cancer. A subject report can include an assessment or estimate of one or more of disease-free survival, recurrence-free survival, metastasis-free survival, and overall survival. A subject report can be completely or partially electronically generated, e.g., presented on an electronic display (e.g., computer monitor). A report can further include one or more of: 1) information regarding the testing facility; 2) service provider information; 3) patient data; 4) sample data; 5) an interpretive report, which can include various information including: a) indication; b) test data, where test data can include a normalized level of one or more genes of interest, and 6) other features.

[0097] The present disclosure thus provides for methods of creating reports and the reports resulting therefrom. The report may include a summary of the expression levels of the RNA transcripts, or the expression products of such RNA transcripts, for certain genes in the cells obtained from the patient’s tumor. The report can include information relating to

prognostic covariates of the patient. The report may include an estimate that the patient has an increased risk of recurrence. That estimate may be in the form of a score or patient stratifier scheme (e.g., low, intermediate, or high risk of recurrence). The report may include information relevant to assist with decisions about the appropriate surgery (e.g., partial or total mastectomy) or treatment for the patient.

[0098] Thus, in some embodiments, the methods of the present disclosure further include generating a report that includes information regarding the patient's likely clinical outcome, e.g. risk of recurrence. For example, the methods disclosed herein can further include a step of generating or outputting a report providing the results of a subject risk assessment, which report can be provided in the form of an electronic medium (e.g., an electronic display on a computer monitor), or in the form of a tangible medium (e.g., a report printed on paper or other tangible medium).

[0099] A report that includes information regarding the patient's likely prognosis (e.g., the likelihood that a patient having breast cancer will have a good prognosis or positive clinical outcome in response to surgery and/or treatment) is provided to a user. An assessment as to the likelihood is referred to below as a "risk report" or, simply, "risk score." A person or entity that prepares a report ("report generator") may also perform the likelihood assessment. The report generator may also perform one or more of sample gathering, sample processing, and data generation, e.g., the report generator may also perform one or more of: a) sample gathering; b) sample processing; c) measuring a level of a risk gene; d) measuring a level of a reference gene; and e) determining a normalized level of a risk gene. Alternatively, an entity other than the report generator can perform one or more sample gathering, sample processing, and data generation.

[00100] For clarity, it should be noted that the term "user," which is used interchangeably with "client," is meant to refer to a person or entity to whom a report is transmitted, and may be the same person or entity who does one or more of the following: a) collects a sample; b) processes a sample; c) provides a sample or a processed sample; and d) generates data (e.g., level of a risk gene; level of a reference gene product(s); normalized level of a risk gene ("prognosis gene")) for use in the likelihood assessment. In some cases, the person(s) or entity(ies) who provides sample collection and/or sample processing and/or data generation, and the person who receives the results and/or report may be different persons, but are both referred to as "users" or "clients" herein to avoid confusion. In certain embodiments, e.g., where the methods are completely executed on a single computer, the user or client provides for data input and review of data output. A "user" can be a health

professional (e.g., a clinician, a laboratory technician, a physician (e.g., an oncologist, surgeon, pathologist), etc.).

[00101] In embodiments where the user only executes a portion of the method, the individual who, after computerized data processing according to the methods of the present disclosure, reviews data output (e.g., results prior to release to provide a complete report, a complete, or reviews an "incomplete" report and provides for manual intervention and completion of an interpretive report) is referred to herein as a "reviewer." The reviewer may be located at a location remote to the user (e.g., at a service provided separate from a healthcare facility where a user may be located).

[00102] Where government regulations or other restrictions apply (e.g., requirements by health, malpractice, or liability insurance), all results, whether generated wholly or partially electronically, are subjected to a quality control routine prior to release to the user.

CLINICAL UTILITY

[00103] The gene expression assay and information provided by the practice of the methods disclosed herein facilitates physicians in making more well-informed treatment decisions, and to customize the treatment of cancer to the needs of individual patients, thereby maximizing the benefit of treatment and minimizing the exposure of patients to unnecessary treatments which may provide little or no significant benefits and often carry serious risks due to toxic side-effects.

[00104] Single or multi-analyte gene expression tests can be used measure the expression level of one or more genes involved in each of several relevant physiologic processes or component cellular characteristics. The expression level(s) may be used to calculate such a quantitative score, and such score may be arranged in subgroups (e.g., tertiles) wherein all patients in a given range are classified as belonging to a risk category (e.g., low, intermediate, or high). The grouping of genes may be performed at least in part based on knowledge of the contribution of the genes according to physiologic functions or component cellular characteristics, such as in the groups discussed above.

[00105] The utility of a gene marker in predicting cancer may not be unique to that marker. An alternative marker having an expression pattern that is parallel to that of a selected marker gene may be substituted for, or used in addition to, a test marker. Due to the co-expression of such genes, substitution of expression level values should have little impact on the overall prognostic utility of the test. The closely similar expression patterns of two genes may result from involvement of both genes in the same process and/or being under common regulatory control in colon tumor cells. The present disclosure thus contemplates

the use of such co-expressed genes or gene sets as substitutes for, or in addition to, prognostic methods of the present disclosure.

[00106] The molecular assay and associated information provided by the methods disclosed herein for predicting the clinical outcome in cancer, e.g. breast cancer, have utility in many areas, including in the development and appropriate use of drugs to treat cancer, to stratify cancer patients for inclusion in (or exclusion from) clinical studies, to assist patients and physicians in making treatment decisions, provide economic benefits by targeting treatment based on personalized genomic profile, and the like. For example, the recurrence score may be used on samples collected from patients in a clinical trial and the results of the test used in conjunction with patient outcomes in order to determine whether subgroups of patients are more or less likely to demonstrate an absolute benefit from a new drug than the whole group or other subgroups. Further, such methods can be used to identify from clinical data subsets of patients who are expected to benefit from adjuvant therapy. Additionally, a patient is more likely to be included in a clinical trial if the results of the test indicate a higher likelihood that the patient will have a poor clinical outcome if treated with surgery alone and a patient is less likely to be included in a clinical trial if the results of the test indicate a lower likelihood that the patient will have a poor clinical outcome if treated with surgery alone.

STATISTICAL ANALYSIS OF GENE EXPRESSION LEVELS

[00107] One skilled in the art will recognize that there are many statistical methods that may be used to determine whether there is a significant relationship between an outcome of interest (e.g., likelihood of survival, likelihood of response to chemotherapy) and expression levels of a marker gene as described here. This relationship can be presented as a continuous recurrence score (RS), or patients may stratified into risk groups (e.g., low, intermediate, high). For example, a Cox proportional hazards regression model may fit to a particular clinical endpoint (e.g., RFS, DFS, OS). One assumption of the Cox proportional hazards regression model is the proportional hazards assumption, i.e. the assumption that effect parameters multiply the underlying hazard.

Coexpression Analysis

[00108] The present disclosure provides genes that co-express with particular prognostic and/or predictive gene that has been identified as having a significant correlation to recurrence and/or treatment benefit. To perform particular biological processes, genes often work together in a concerted way, i.e. they are co-expressed. Co-expressed gene

groups identified for a disease process like cancer can serve as biomarkers for disease progression and response to treatment. Such co-expressed genes can be assayed in lieu of, or in addition to, assaying of the prognostic and/or predictive gene with which they are co-expressed.

[00109] One skilled in the art will recognize that many co-expression analysis methods now known or later developed will fall within the scope and spirit of the present invention. These methods may incorporate, for example, correlation coefficients, co-expression network analysis, clique analysis, etc., and may be based on expression data from RT-PCR, microarrays, sequencing, and other similar technologies. For example, gene expression clusters can be identified using pair-wise analysis of correlation based on Pearson or Spearman correlation coefficients. (See, e.g., Pearson K. and Lee A., *Biometrika* 2, 357 (1902); C. Spearman, *Amer. J. Psychol* 15:72-101 (1904); J. Myers, A. Well, *Research Design and Statistical Analysis*, p. 508 (2nd Ed., 2003).) In general, a correlation coefficient of equal to or greater than 0.3 is considered to be statistically significant in a sample size of at least 20. (See, e.g., G. Norman, D. Streiner, *Biostatistics: The Bare Essentials*, 137-138 (3rd Ed. 2007).) In one embodiment disclosed herein, co-expressed genes were identified using a Spearman correlation value of at least 0.7.

Computer program

[00110] The values from the assays described above, such as expression data, recurrence score, treatment score and/or benefit score, can be calculated and stored manually. Alternatively, the above-described steps can be completely or partially performed by a computer program product. The present invention thus provides a computer program product including a computer readable storage medium having a computer program stored on it. The program can, when read by a computer, execute relevant calculations based on values obtained from analysis of one or more biological sample from an individual (e.g., gene expression levels, normalization, thresholding, and conversion of values from assays to a score and/or graphical depiction of likelihood of recurrence/response to chemotherapy, gene co-expression or clique analysis, and the like). The computer program product has stored therein a computer program for performing the calculation.

[00111] The present disclosure provides systems for executing the program described above, which system generally includes: a) a central computing environment; b) an input device, operatively connected to the computing environment, to receive patient data, wherein the patient data can include, for example, expression level or other value obtained from an assay using a biological sample from the patient, or microarray data, as described in detail

above; c) an output device, connected to the computing environment, to provide information to a user (e.g., medical personnel); and d) an algorithm executed by the central computing environment (e.g., a processor), where the algorithm is executed based on the data received by the input device, and wherein the algorithm calculates a, risk, risk score, or treatment group classification, gene co-expression analysis, thresholding, or other functions described herein. The methods provided by the present invention may also be automated in whole or in part.

Manual and Computer-Assisted Methods and Products

[00112] The methods and systems described herein can be implemented in numerous ways. In one embodiment of particular interest, the methods involve use of a communications infrastructure, for example the Internet. Several embodiments are discussed below. It is also to be understood that the present disclosure may be implemented in various forms of hardware, software, firmware, processors, or a combination thereof. The methods and systems described herein can be implemented as a combination of hardware and software. The software can be implemented as an application program tangibly embodied on a program storage device, or different portions of the software implemented in the user's computing environment (e.g., as an applet) and on the reviewer's computing environment, where the reviewer may be located at a remote site associated (e.g., at a service provider's facility).

[00113] For example, during or after data input by the user, portions of the data processing can be performed in the user-side computing environment. For example, the user-side computing environment can be programmed to provide for defined test codes to denote a likelihood "risk score," where the score is transmitted as processed or partially processed responses to the reviewer's computing environment in the form of test code for subsequent execution of one or more algorithms to provide a results and/or generate a report in the reviewer's computing environment. The risk score can be a numerical score (representative of a numerical value, e.g. likelihood of recurrence based on validation study population) or a non-numerical score representative of a numerical value or range of numerical values (e.g., low, intermediate, or high).

[00114] The application program for executing the algorithms described herein may be uploaded to, and executed by, a machine comprising any suitable architecture. In general, the machine involves a computer platform having hardware such as one or more central processing units (CPU), a random access memory (RAM), and input/output (I/O) interface(s). The computer platform also includes an operating system and microinstruction

code. The various processes and functions described herein may either be part of the microinstruction code or part of the application program (or a combination thereof) that is executed via the operating system. In addition, various other peripheral devices may be connected to the computer platform such as an additional data storage device and a printing device.

[00115] As a computer system, the system generally includes a processor unit. The processor unit operates to receive information, which can include test data (e.g., level of a risk gene, level of a reference gene product(s); normalized level of a gene; and may also include other data such as patient data. This information received can be stored at least temporarily in a database, and data analyzed to generate a report as described above.

[00116] Part or all of the input and output data can also be sent electronically; certain output data (e.g., reports) can be sent electronically or telephonically (e.g., by facsimile, e.g., using devices such as fax back). Exemplary output receiving devices can include a display element, a printer, a facsimile device and the like. Electronic forms of transmission and/or display can include email, interactive television, and the like. In an embodiment of particular interest, all or a portion of the input data and/or all or a portion of the output data (e.g., usually at least the final report) are maintained on a web server for access, preferably confidential access, with typical browsers. The data may be accessed or sent to health professionals as desired. The input and output data, including all or a portion of the final report, can be used to populate a patient's medical record which may exist in a confidential database at the healthcare facility.

[00117] A system for use in the methods described herein generally includes at least one computer processor (e.g., where the method is carried out in its entirety at a single site) or at least two networked computer processors (e.g., where data is to be input by a user (also referred to herein as a "client") and transmitted to a remote site to a second computer processor for analysis, where the first and second computer processors are connected by a network, e.g., via an intranet or internet). The system can also include a user component(s) for input; and a reviewer component(s) for review of data, generated reports, and manual intervention. Additional components of the system can include a server component(s); and a database(s) for storing data (e.g., as in a database of report elements, e.g., interpretive report elements, or a relational database (RDB) which can include data input by the user and data output. The computer processors can be processors that are typically found in personal desktop computers (e.g., IBM, Dell, Macintosh), portable computers, mainframes, minicomputers, or other computing devices.

[00118] The networked client/server architecture can be selected as desired, and can be, for example, a classic two or three tier client server model. A relational database management system (RDMS), either as part of an application server component or as a separate component (RDB machine) provides the interface to the database.

[00119] In one example, the architecture is provided as a database-centric client/server architecture, in which the client application generally requests services from the application server which makes requests to the database (or the database server) to populate the report with the various report elements as required, particularly the interpretive report elements, especially the interpretation text and alerts. The server(s) (e.g., either as part of the application server machine or a separate RDB/relational database machine) responds to the client's requests.

[00120] The input client components can be complete, stand-alone personal computers offering a full range of power and features to run applications. The client component usually operates under any desired operating system and includes a communication element (e.g., a modem or other hardware for connecting to a network), one or more input devices (e.g., a keyboard, mouse, keypad, or other device used to transfer information or commands), a storage element (e.g., a hard drive or other computer-readable, computer-writable storage medium), and a display element (e.g., a monitor, television, LCD, LED, or other display device that conveys information to the user). The user enters input commands into the computer processor through an input device. Generally, the user interface is a graphical user interface (GUI) written for web browser applications.

[00121] The server component(s) can be a personal computer, a minicomputer, or a mainframe and offers data management, information sharing between clients, network administration and security. The application and any databases used can be on the same or different servers.

[00122] Other computing arrangements for the client and server(s), including processing on a single machine such as a mainframe, a collection of machines, or other suitable configuration are contemplated. In general, the client and server machines work together to accomplish the processing of the present disclosure.

[00123] Where used, the database(s) is usually connected to the database server component and can be any device that will hold data. For example, the database can be a any magnetic or optical storing device for a computer (e.g., CDROM, internal hard drive, tape drive). The database can be located remote to the server component (with access via a network, modem, etc.) or locally to the server component.

[00124] Where used in the system and methods, the database can be a relational database that is organized and accessed according to relationships between data items. The relational database is generally composed of a plurality of tables (entities). The rows of a table represent records (collections of information about separate items) and the columns represent fields (particular attributes of a record). In its simplest conception, the relational database is a collection of data entries that "relate" to each other through at least one common field.

[00125] Additional workstations equipped with computers and printers may be used at point of service to enter data and, in some embodiments, generate appropriate reports, if desired. The computer(s) can have a shortcut (e.g., on the desktop) to launch the application to facilitate initiation of data entry, transmission, analysis, report receipt, etc. as desired.

Computer-readable storage media

[00126] The present disclosure also contemplates a computer-readable storage medium (e.g. CD-ROM, memory key, flash memory card, diskette, etc.) having stored thereon a program which, when executed in a computing environment, provides for implementation of algorithms to carry out all or a portion of the results of a response likelihood assessment as described herein. Where the computer-readable medium contains a complete program for carrying out the methods described herein, the program includes program instructions for collecting, analyzing and generating output, and generally includes computer readable code devices for interacting with a user as described herein, processing that data in conjunction with analytical information, and generating unique printed or electronic media for that user.

[00127] Where the storage medium provides a program that provides for implementation of a portion of the methods described herein (e.g., the user-side aspect of the methods (e.g., data input, report receipt capabilities, etc.)), the program provides for transmission of data input by the user (e.g., via the internet, via an intranet, etc.) to a computing environment at a remote site. Processing or completion of processing of the data is carried out at the remote site to generate a report. After review of the report, and completion of any needed manual intervention, to provide a complete report, the complete report is then transmitted back to the user as an electronic document or printed document (e.g., fax or mailed paper report). The storage medium containing a program according to the present disclosure can be packaged with instructions (e.g., for program installation, use, etc.) recorded on a suitable substrate or a web address where such instructions may be obtained. The computer-readable storage medium can also be provided in combination with one or

more reagents for carrying out response likelihood assessment (e.g., primers, probes, arrays, or other such kit components).

[00128] All aspects of the present invention may also be practiced such that a limited number of additional genes that are co-expressed with the disclosed genes, for example as evidenced by statistically meaningful Pearson and/or Spearman correlation coefficients, are included in a prognostic or predictive test in addition to and/or in place of disclosed genes.

[00129] Having described the invention, the same will be more readily understood through reference to the following Examples, which are provided by way of illustration, and are not intended to limit the invention in any way.

EXAMPLE 1:

[00130] The study included breast cancer tumor samples obtained from 136 patients diagnosed with breast cancer (“Providence study”). Biostatistical modeling studies of prototypical data sets demonstrated that amplified RNA is a useful substrate for biomarker identification studies. This was verified in this study by including known breast cancer biomarkers along with candidate prognostic genes in the tissues samples. The known biomarkers were shown to be associated with clinical outcome in amplified RNA based on the criteria outlined in this protocol.

Study design

[00131] Refer to the original Providence Phase II study protocol for biopsy specimen information. The study looked at the statistical association between clinical outcome and 384 candidate biomarkers tested in amplified samples derived from 25 ng of mRNA that was extracted from fixed, paraffin-embedded tissue samples obtained from 136 of the original Providence Phase II study samples. The expression level of the candidate genes was normalized using reference genes. Several reference genes were analyzed in this study: AAMP, ARF1, EEF1A1, ESD, GPS1, H3F3A, HNRPC, RPL13A, RPL41, RPS23, RPS27, SDHA, TCEA1, UBB, YWHAZ, B-actin, GUS, GAPDH, RPLPO, and TFRC.

[00132] The 136 samples were split into 3 automated RT plates each with 2X 48 samples and 40 samples and 3 RT positive and negative controls. Quantitative PCR assays were performed in 384 wells without replicate using the QuantiTect Probe PCR Master Mix® (Qiagen). Plates were analyzed on the Light Cycler® 480 and, after data quality control, all samples from the RT plate 3 were repeated and new RT-PCR data was generated. The data was normalized by subtracting the median crossing point (C_p) (point at which

detection rises above background signal) for five reference genes from the C_p value for each individual candidate gene. This normalization is performed on each sample resulting in final data that has been adjusted for differences in overall sample C_p . This data set was used for the final data analysis.

Data Analysis

[00133] For each gene, a standard z test was run.. (S. Darby, J. Reissland, Journal of the Royal Statistical Society 144(3):298-331 (1981)). This returns a z score (measure of distance in standard deviations of a sample from the mean), p value, and residuals along with other statistics and parameters from the model. If the z score is negative, expression is positively correlated with a good prognosis; if positive, expression is negatively correlated to a good prognosis. Using the p values, a q value was created using a library q value. The poorly correlated and weakly expressed genes were excluded from the calculation of the distribution used for the q values. For each gene, Cox Proportional Hazard Model test was run checking survival time matched with the event vector against gene expression. This returned a hazard ratio (HR) estimating the effect of expression of each gene (individually) on the risk of a cancer-related event. The resulting data is provided in Tables 1-6. A $HR < 1$ indicates that expression of that gene is positively associated with a good prognosis, while a $HR > 1$ indicates that expression of that gene is negatively associated with a good prognosis.

EXAMPLE 2:

Study design

[00134] Amplified samples were derived from 25 ng of mRNA that was extracted from fixed, paraffin-embedded tissue samples obtained from 78 evaluable cases from a Phase II breast cancer study conducted at Rush University Medical Center. Three of the samples failed to provide sufficient amplified RNA at 25 ng, so amplification was repeated a second time with 50 ng of RNA. The study also analyzed several reference genes for use in normalization: AAMP, ARF1, EEF1A1, ESD, GPS1, H3F3A, HNRPC, RPL13A, RPL41, RPS23, RPS27, SDHA, TCEA1, UBB, YWHAZ, Beta-actin, RPLPO, TFRC, GUS, and GAPDH.

[00135] Assays were performed in 384 wells without replicate using the QuantiTect Probe PCR Master Mix. Plates were analyzed on the Light Cycler 480 instruments. This data set was used for the final data analysis. The data was normalized by subtracting the median C_p for five reference genes from the C_p value for each individual candidate gene. This

normalization was performed on each sample resulting in final data that was adjusted for differences in overall sample C_p .

Data analysis

[00136] There were 34 samples with average C_p values above 35. However, none of the samples were excluded from analysis because they were deemed to have sufficient valuable information to remain in the study. Principal Component Analysis (PCA) was used to determine whether there was a plate effect causing variation across the different RT plates. The first principal component correlated well with the median expression values, indicating that expression level accounted for most of the variation between samples. Also, there were no unexpected variations between plates.

Data for Other Variables

[00137] Group – The patients were divided into two groups (cancer/non-cancer). There was little difference between the two in overall gene expression as the difference between median C_p value in each group was minimal (0.7).

[00138] Sample Age – The samples varied widely in their overall gene expression but there was a trend toward lower C_p values as they decreased in age.

[00139] Instrument – The overall sample gene expression from instrument to instrument was consistent. One instrument showed a slightly higher median C_p compared to the other three, but it was well within the acceptable variation.

[00140] RT Plate – The overall sample gene expression between RT plates was also very consistent. The median C_p for each of the 3 RT plates (2 automated RT plates and 1 manual plate containing repeated samples) were all within 1 C_p of each other.

Univariate Analyses for Genes Significantly Different Between Study Groups

[00141] The genes were analyzed using the z-test and Cox Proportional Hazard Model, as described in Example 1. The resulting data can be seen in Tables 7-12.

EXAMPLE 3:

[00142] The statistical correlations between clinical outcome and expression levels of the genes identified in Examples 1 and 2 were validated in breast cancer gene expression datasets maintained by the Swiss Institute of Bioinformatics (SIB). Further information concerning the SIB database, study datasets, and processing methods, is providing in P. Wirapati, et al., Breast Cancer Research 10(4):R65 (2008). Univariate Cox proportional hazards analyses were performed to confirm the relationship between clinical outcome (DFS, MFS, OS) of breast cancer patients and expression levels of the genes identified as

significant in the amplified RNA studies described above. The meta-analysis included both fixed-effect and random-effect models, which are further described in L. Hedges and J. Vevea, *Psychological Methods* 3 (4): 486-504 (1998) and K. Sidik and J. Jonkman, *Statistics in Medicine* 26:1964-1981 (2006) (the contents of which are incorporated herein by reference). The results of the validation for all genes identified as having a statistically significant association with breast cancer clinical outcome are described in Table 13. In those tables, "Est" designates an estimated coefficient of a covariate (gene expression); "SE" is standard error; "t" is the t-score for this estimate (i.e., Est/SE); and "fe" is the fixed estimate of effect from the meta analysis. Several of gene families with significant statistical association with clinical outcome (including metabolic, proliferation, immune, and stromal group genes) in breast cancer were confirmed using the SIB dataset. For example, Table 14 contains analysis of genes included in the metabolic group and Table 15 the stromal group.

EXAMPLE 4:

[00143] A co-expression analysis was conducted using microarray data from six (6) breast cancer data sets. The "processed" expression values are taken from the GEO website, however, further processing was necessary. If the expression values are RMA, they are median normalized on the sample level. If the expression values are MAS5.0, they are: (1) changed to 10 if they are <10; (2) log base e transformed; and (3) median normalized on the sample level.

[00144] Generating Correlation Pairs: A rank matrix was generated by arranging the expression values for each sample in decreasing order. Then a correlation matrix was created by calculating the Spearman correlation values for every pair of probe IDs. Pairs of probes which had a Spearman value ≥ 0.7 were considered co-expressed. Redundant or overlapping correlation pairs in multiple datasets were identified. For each correlation matrix generated from an array dataset, pairs of significant probes that occur in >1 dataset were identified. This served to filter "non-significant" pairs from the analysis as well as provide extra evidence for "significant" pairs with their presence in multiple datasets. Depending on the number of datasets included in each tissue specific analysis, only pairs which occur in a minimum # or % of datasets were included.

[00145] Co-expression cliques were generated using the Bron-Kerbosch algorithm for maximal clique finding in an undirected graph. The algorithm generates three sets of nodes: *compsub*, *candidates*, and *not*. *Compsub* contains the set of nodes to be extended or shrunk by one depending on its traversal direction on the tree search. *Candidates* consists of all the

nodes eligible to be added to *compsub*. *Not* contains the set of nodes that have been added to *compsub* and are now excluded from extension. The algorithm consists of five steps: selection of a candidate; adding the candidate node to *compsub*; creating new sets *candidates* and *not* from the old sets by removing all points not connected to the candidate node; recursively calling the extension operator on the **new** *candidates* and *not* sets; and upon return, remove the candidate node from *compsub* and place in the **old** *not* set.

[00146] There was a depth-first search with pruning, and the selection of candidate nodes had an effect on the run time of the algorithm. By selecting nodes in decreasing order of frequency in the pairs, the run time was optimized. Also, recursive algorithms generally cannot be implemented in a multi-threaded manner, but was multi-threaded the extension operator of the first recursive level. Since the data between the threads were independent because they were at the top-level of the recursive tree, they were run in parallel.

[00147] Clique Mapping and Normalization: Since the members of the co-expression pairs and cliques are at the probe level, one must map the probe IDs to genes (or Refseqs) before they can be analyzed. The Affymetrix gene map information was used to map every probe ID to a gene name. Probes may map to multiple genes, and genes may be represented by multiple probes. The data for each clique is validated by manually calculating the correlation values for each pair from a single clique.

[00148] The results of this co-expression analysis are set forth in Tables 16-18.

TABLE A

Gene	Sequence ID	Official Symbol	F Primer Seq	SEQ ID NO:	R Primer Seq	SEQ ID NO:	Probe Seq	SEQ ID NO:	Target Seq Length	Amplicon Sequence	SEQ ID NO:
A-Catenin	NM_001903.1	CTNNA1	CGTTCGGAT CCCTCTATAC TGCAAT	1	AGGTCCCTG TTGGCCCTTA TAGG	385	ATGCGCTACAGCACCCCTG ATGTGCGA	769	78	CGTTCGGATCTCTATACTGCAATCCAG GCATGCTACACACCTCTGATGTGCGA GCCTAATAGGCCAACAGGGACCT	1153
AAMP	NM_001087.3	AAMP	GTTGGCA GGTGGACA CTAA	2	CTCCATCCA CTCCAGGTC TC	386	CGCTTCAAAAGGACCAGA CCTCCTC	770	66	GTTGGCAGGTGGACACTAAGAGGAG GTTGGTCTTTGAAGCGGAGACCTG GAGTGGATGGAG	1154
ABCB1	NM_000927.2	ABCB1	AAACACCA CTGGAGCAT TGA	3	CAAGCCTGG AACTATAG CC	387	CTCGCCAATGATGCTGCT CAAGTT	771	77	AAACACCACTGGAGCATTTGACTACCAG GCTCGCAATGATGCTGCTAAGTTAA AGGGCTATAGGTTCCAGGCTTG	1155
ABCC10	NM_033450.2	ABCC10	ACCAGTGCC ACAATGCA G	4	ATAGCGCTG ACCACTGCC AG	388	CCATGAGCTGTAGCCGA ATGTCCA	772	68	ACCAGTGCCACAATGCAAGTGGTGGAC ATTGCGCTACAGCTCATGGGGCGGCA GTGGTCAGCGCTAT	1156
ABCC5	NM_005688.1	ABCC5	TGCAGACTG TACCATGCT GA	5	GGCCAGCAC CATAATCT AT	389	CTGCACACGGTCTTAGG CTCCG	773	76	TGCAGACTGTACCATGTGACCATTCG CCATCGCTGCACAGGTTCTAGGCTCC GATAGGATATGGTGTGGCC	1157
ABR	NM_001092.3	ABR	ACAGTCTG TCACCATGG AA	6	ACTAGGGTG CTCCGAGTG AC	390	TCTGCTCTACAAGCCCAT TGACCG	774	67	ACAGTCTGTACCATGGAAGCTCTGC TCTACAAGCCCATTGACCGGGTCACTC GGAGCACCTAGT	1158
ACTR2	NM_005722.2	ACTR2	ATCCGCATT GAAGACCC A	7	ATCCGCTAG AACTGCACC AC	391	CCCGCAGAAAACACATG GTATTCC	775	66	ATCCGATTGAAGACCCACCCGCGAGA AAGCACATGATATCTCTGGTGGTCCA GTCTAGCGGAT	1159
ACVR2B	NM_001106.2	ACVR2B	GACTGTCTC GTTTCCCTG GT	8	TGGGCTTAG ATGCTTGAC TC	392	CTCTGTACCAATGTGG ACCTGCC	776	74	GACTGTCTCTTCTCCCTGGTGACCTCTG TCACCAATGTGGACCTGCCCTTAAAG AGTCAAGCATCTAAGCCCA	1160
AD024	NM_020675.3	SPC25	TCAAAAGT ACGGACAC CTCCT	9	TGCAAAATGC TTTGATGGA AT	393	TGTAGGTATCTCTTAGTC CCGCCATCTGA	777	74	TCAAAAGTACGGACACCTCTCTGTCTAGA TGGCGGGAATAAGAGATACCTACAAGG ATTCCAATCAAAAGCATTTGCA	1161
ADAM12	NM_021641.2	ADAM12	GAGCATGC GTCATCTGC CT	10	CTGGTCAAG GTCTCCAATG T	394	CTGACACTCATCTGAGC CCTCCCA	778	66	GAGCATGCTCTACTGCTCTACCTGACA CTCATCTGAGCCCTCCCATGACATGGA GACCGTGACCCAG	1162
ADAM17	NM_003183.3	ADAM17	GAAGTGCC AGGAGGCG ATTA	11	CGGGCACTC ACTGCTATT ACC	395	TGCTACTTGCAAAAGGCG TGTCCTACTGC	779	73	GAAGTGCCAGGAGGCGATTAAATGTACT TTGCAAAAGGCGTCTCTACTGACACAGG TAATAGCAGTGAAGTCCCG	1163
ADAM23	NM_003812.1	ADAM23	CAAGGCC CATCTGAAT CA	12	ACCCAGAAT CCAACAGTG CAA	396	CTGCGCTGGATGGACAC CGC	780	62	CAAGGCCCATCTGAATCAGCTGCGCT GGATGGACACCGCTTGACACTGTTGGA TTCTGGGT	1164
ADAMTS8	NM_007037.2	ADAMTS8	GCGAGTTCA AAGTGTTCG AG	13	CACAGATGG CCAGTGTIT CT	397	CACACAGGTTGCCATCA ATCACCT	781	72	GCGAGTTCAAAAGTGTTCGAGGCCAAGG TGATTTGATGGCACCTCTGTGGGCCAG AAACACTGGCCATCTGTG	1165
ADM	NM_001124.1	ADM	TAAGCCAC AAGCACAC GG	14	TGGGCGCCT AAATCCCTAA	398	CGAGTGGAAAGTGTCTCC CACTTTC	782	75	TAAGCCACAAAGCACACGGGGTCTCAGC CCCCCGAGTGGAAAGTGTCTCCCACTTT CTTTAGGATTAGGCGGCCA	1166

TABLE A

AES	NM_001130.4	AES	ACGAGATG TCCTACGGC TTGA	15	GGGCACAAA TCCCGTTCA G	399	CGATCTCAGCCTGTTGT GCATCTCGAT	783	78	1167	ACGAGATGCTACGGCTTGAACATCG AGATGCACAAACAGGCTGAGATCTCA AAAGGCTGAACGGGATTTGGCC
AGR2	NM_006408.2	AGR2	AGCAACA TGTGACTAA TTGGA	16	TCTGATCTC CATCTGCCT CA	400	CAACACGTCACCAACCCT TTGCTCT	784	70	1168	AGCCAACTGTGACTAAATTGGAAGAAG AGCAAGGGTGGTGAAGCTTGTGATGAG GCAGATGGAGATCAGA
AK055699	NM_194317	LYPD6	CTGCATGTG ATTGAATAA GAAACAAG A	17	TGTGGACCT GATCCCTGT ACAC	401	TGACCACACCAAAAGCCT CCCTGG	785	78	1169	CTGCATGTGATTGAATAAGAAACAAGA AAGTGACACACCAAGCCTCCCTGGC TGGTGTACAGGGATCAGGTCACCA
AKR7A3	NM_012067.2	AKR7A3	GTGGAAAC GGAGCTCTT CC	18	CCAGAGGGT TGAAAGCAT AG	402	ACCTCAGTCCAAAAGTGC CTGAGGC	786	67	1170	GTGAAACCGAGCTCTTCCCTTGCCTC AGGCACCTTGGACTGAGGTTCTATGCCT TCAACCTCTGG
AKT3	NM_005465.1	AKT3	TTGTCTCTG CCTTGGACT ATCTACA	19	CCAGCATTA GATCTCCA ACTTGA	403	TCACGGTACACAATCTTT CCGGA	787	75	1171	TTGTCTCTGCTTGGACTATCTACATTC CGGAAAGATTGTGTACCGTGTCTCAA GTGGAGAATCTAATGCTGG
ALCAM	NM_001627.1	ALCAM	GAGGAATA TGGAAATCA AGGG	20	GTGGCGGAG ATCAAGAGG TC	404	CCAGTTCCTGCCGCTCTGC TCTTCT	788	66	1172	GAGGAATATGGAATCAAGGGGGGCA GTTCCTGCCGCTGCTCTTCTGCTCTT GATCTCCGCCAC
ALDH4	NM_003748.2	ALDH4A1	GGACAGGG TAAGACCGT GAT	21	AACCGGAAG AAGTCGATG AG	405	CTGCAGCGTCAATCTCC GCTTG	789	68	1173	GGACAGGTTAAGACCGGTGATCCAAAGCG GAGATTGACGTGACGCGGAACATCATC GACTCTCTCCGTT
ANGPT2	NM_001147.1	ANGPT2	CCGTGAAA GCTGCTCTG TAA	22	TTGCAGTGG GAAAGAACAG TC	406	AAAGCTGACACAGCCCTC CCAAAGTG	790	69	1174	CCGTGAAAGCTGCTCTGTAAAAGCTGA CACAGCCTCCCAAGTGAGCAGGACTG TTCTTCCCACTGCAA
ANXA2	NM_004039.1	ANXA2	CAAGACAC TAAGGGCG ACTACCA	23	CGTGTCCGG CTTCAGTCA T	407	CCACCACACAGGTACAG CAGCGCT	791	71	1175	CAAGACACTAAGGGCGACTACCAGAAA GCGTGTGTACTGTGTGTGGAGAT GACTGAAGCCCGACACG
AP-1 (JUN official)	NM_002228.2	JUN	GACTGCAA AGATGGAA ACGA	24	TAGCCATAA GGTCCGCTC TC	408	CTATGACGATGCCCTCA ACGCCTC	792	81	1176	GACTGCAAGATGGAAAGACCTTCTA TGACGATGCCCTCAACCGCTCTGCTCTC CCGTCCGAGAGCGGACCTTATGGCTA
APEX-1	NM_001641.2	APEX1	GATGAAAGC CTTTCGCAA GTT	25	AGGTCTCCA CACAGCACA AG	409	CTTTCGGGAAGCCAGGC CCTT	793	68	1177	GATGAAGCTTTTCGCAAGTCTCTGAAG GGCCTGGCTTCCGAAAGCCCTTGTG CTGTGTGGAGACCT
APOD	NM_001647.1	APOD	GTTTATGCC ATCGGCACC CAGTAGAG	26	GGAATACAC GAGGGCATA GTTTC	410	ACTGGATCTGGCCACC GACTATG	794	67	1178	GTTTATGCCATCGGCACCGTACTGGATC CTGGCCACCGACTATGAGAACTATGCC CTCGTGTATTC
ARF1	NM_001658.2	ARF1	ATCCCCGCA ACT	27	ACAAAGCACA TGGCTATGG AA	411	CTTGTCTTGGGTCAACC TGCA	795	64	1179	CAGTAGATATCCCGCAACTCGCTTGT CCTTGGGTACCTCTGCATTCCATAGCCA TGTGCTTGT
ARHI	NM_004675.1	DIRAS3	ATCAGAGA TTACCGCGT CGT	28	ACTTGTGCA GCACGCTAC TT	412	ACACCAGCGGTGCCGAC TACC	796	67	1180	ATCAGAGATTACCGGTCTGTGGTGTGTC GGCACCGCTGGTGTGGGAAAGATACG CTGCTGCACAAGT

TABLE A

ARNT2	NM_014862.3	ARNT2	GACTGGGTC AGTGATGG CA	29	GGAGTGACG CATGGACAG A	413	CTAGAGCCATCCTTGGC CATCTCG	797	68	GACTGGGTCAGTGATGGCAACAGGATG GCCAAGGATGGCTCTAGAACACTCTGT CCATGCGTCACTCC	1181
ARSD	NM_001669.1	ARSD	TCCTGAGA ACGAAACC ACT	30	TGGTGCAAT TTTCTCATG AG	414	CAAGAAATCTTGACGACG CATGGCT	798	79	TCCCTGAGAACGAAACCACTTTTGCAA GAATCTTGCAGCAGCATGGCTATGCAA CCGGCTCATAGGAAATGGCACCA	1182
AURKB	NM_004217.1	AURKB	AGCTGCAG AAGAGCTG CACAT	31	GCATCTGCC AACTCTCTC AT	415	TGACGAGCAGCGAACAG CCACG	799	67	AGCTGCAAGAGAGCTGCACATTTGACG AGCAGCGAACAGCCACGATCATGGAGG AGTTGCAGATGC	1183
B-actin	NM_001101.2	ACTB	CAGCAGAT GTGGATCA GCAAG	32	GCATTTGCG GTGGACGAT	416	AGGAGTATGACGAGTCC GGCCCC	800	66	CAGCAGATGTGGATCAGCAAGCAGGAG TATGACGAGTCCGGCCCCCTCCATCGTCC ACCGAAATGC	1184
B-Catenin	NM_001904.1	CTNNB1	GGCTCTTGT GCGTACTGT CCCT	33	TCAGATGAC GAAAGAGCAC AGATG	417	AGGCTCAGTGTGCTTC CCTGTCACCAG	801	80	GGCTCTTGTGCTACTGTCTTCGGGCT GGTGACAGGGAAGACATCACTGAGCCT GCCATCTGTCTTTCGTCATCTGA	1185
BAD	NM_032989.1	BAD	GGGTCAGG TGCTTCGAG AT	34	CTGTCTACT CGGCTCAAA CTC	418	TGGGCCACAGCATGTT CCAGATC	802	73	GGGTCAGGTGCTCGAGATCGGGCTTG GGCCAGAGCATGTTCAGATCCACAGA GTTTGAGCCGAGTGAGCAG	1186
BAG1	NM_004323.2	BAG1	CGTTGTCAG CACTTGGAA TACAA	35	GTTCAACTT CTTCTGTG GACTGT	419	CCCAATTAAACATGACCC GGCAACCAT	803	81	CGTTGTCAGCACTTGGAATACAAAGATG GTTGCCGGTCACTGTTAATTGGGAAAA AGAACAGTCCACAGGAAGAGGTTGAAC	1187
BAG4	NM_004874.2	BAG4	CCTACGGCC GCTACTACG	36	GGCGAAGA GGATATAAG GG	420	AGATGTGCCGGTACACC CACCTC	804	76	CCTACGCGCTACTACGGCTCTGGG GTGGAGATGTGCCGTACACCCACCTC CACCCCTATATCTCTCTCGCC	1188
BASE	NM_173859.1		GACTCCTCA GGCGAGAC TTTCTT	37	CGAAGGCAC TACTCAAATG GTTTC	421	CCAGCCTGCAGACAACT GGCCTC	805	72	GACTCCTCAGGGCAGACTTTCTTCCAG CCTGCAGACAACTGGCTCCAGAAACC ATTGAGTAGTGCCTTCG	1189
Bax	NM_004324.1	BAX	CCGCCGTGG ACACAGAC T	38	TGCCCCGTC GAAACATG TCA	422	TGCCACTCGGAAAAAGA CCTCTCG	806	70	CCGCCGTGGACACAGACTCCGCCCGAG AGGTCTTTTCCGAGTGGCAGCTGACAT GTTTCTGACGCCAA	1190
BBC3	NM_014417.1	BBC3	CCTGGAGG GTCTGTAC AAT	39	CTAAATGGG CTCCATCTC G	423	CATCATGGACTCCTGC CCTTACC	807	83	CCTGGAGGTCTGTACAAATCTCATCAT GGGACTCTGCCCCCTACCCAGGGGCCA CAGAGCCCCGAGATGGAGGCCAATTA G	1191
BCAR1	NM_014567.1	BCAR1	ACTGACAA GACCAGCA GCAT	40	TCCTGGGAG GTGAACTTA GG	424	AGTCACGACCCCTGCC TCAC	808	65	ACTGACAAGACCAGCAGCATCCAGTCA CGACCTTGCCCCCTACCCCTAAGTTCA CCTCCAGGA	1192
BCAR3	NM_003567.1	BCAR3	TGACTTCTCT AGTTCGTGA CTCTCTGT	41	TGAGCGAGG TTCTTCCACT GA	425	CAGCCCTGGGAACCTTG TCCTGACC	809	75	TGACTTCTAGTTCTGTGACTCTCTGTCC AGCCCTGGGAACCTTGTCTCTGACCTGTC AGTGGAAAGAACTCTGCTCA	1193
BCAS1	NM_003657.1	BCAS1	CCCCGAGA CAACGGAG ATAA	42	CTCGGGTTT GGCCTCTTT C	426	CTTTCCTTGGCATCCGC AACAG	810	73	CCCCGAGACACCGAGATAAAGTCTGT TGGGATGCCCAACGAAAGAAATCTTGG GAAAGAGGCCAAACCCGAG	1194

TABLE A

Bcl2	NM_000633.1	BCL2	CAGATGGA CCTAGTACC CACTGAGA	43	CCTATGATT TAAGGGCAT TTTTCC	427	TTCCACGCCGAAGGACA GCGAT	811	73	CAGATGGACCTAGTACCCACTGAGATT TCCACGCCGAAGGACAGCGATGGGAAA AATGCCCTTAATCATAGG	1195
BCL2L12	NM_138639.1	BCL2L12	AACCCACCC CTGTCTTGG	44	CTCAGCTGA CGGGAAAGG	428	TCCGGGTAGCTCTCAAAA CTCGAGG	812	73	AACCCACCCCTGTCTTGGAGTCCGGG TAGCTCTCAAACTCGAGGCTGCGCACC CCCTTCCCGTCACTGAG	1196
BGN	NM_001711.3	BGN	GAGCTCCGC AAGGATGA C	45	CTTGTGTTC ACCAGGACG A	429	CAAGGGTCTCCAGCACC TCTACGC	813	66	GAGCTCCGAAGGATGACTTCAAGGGT CTCCAGCACTCTACGCCCTCTCTCTGG TGAACAACAAG	1197
BIK	NM_001197.3	BIK	ATTCCTATG GCTCTGCAA TTGTCT	46	GGCAGGAGT GAATGGCTC TTC	430	CCGGTTAACTGTGGCCT GTGCC	814	70	ATTCTATGGCTCTGCAATTTGTACCCG TTAACTGTGGCTGTGTGCCAGGAAGAG CAATCTACTCTGTC	1198
BNIP3	NM_004052.2	BNIP3	CTGGACGG AGTAGCTCC AAG	47	GGTATCTTG TGGTGTCTG CG	431	CTCTCACTGTGACAGCCC ACCTCG	815	68	CTGGACGGAGTAGCTTCCAAAGAGCTCTC ACTGTGACAGCCCACTCTCGCTCGCAGA CACCACAAGATACC	1199
BSG	NM_001728.2	BSG	AATTTATG AGGGCCAC GG	48	GTGGCCAAG AGGTCAGAG TC	432	CTGTGTTCGACTCAGCCT CAGGGA	816	66	AATTTATGAGGGCCACGGGTCTGTGT CGACTCAGCCTCAGGGACGACTCTGAC CTCTTGCCAC	1200
BTRC	NM_033637.2	BTRC	GTGGGAC ACAGTTGGT CTG	49	TGAAGCAGT CAGTTGTGC TG	433	CAGTCGGCCAGGACGG TCTACT	817	63	GTTGGGACACAGTTGGTCTGCACTGCGG CCCAGGACGGTCTACTCAGCAAACTG ACTGCTTCA	1201
BUB1	NM_004336.1	BUB1	CCGAGGTTA ATCCAGCAC GTA	50	AAGACATGG CGCTCTCAG TTC	434	TGCTGGGAGCCTACACT TGCCCC	818	68	CCGAGGTTAATCCAGCACGATATGGGGC CAAGTGTAGGCTCCAGCAGGAACTGA GAGCGCCATGTCT	1202
BUB1B	NM_001211.3	BUB1B	TCAACAGA AGGCTGAA CCACTAGA	51	CAACAGAGT TGGCCGAGA CACT	435	TACAGTCCAGCACCGA CAATTCC	819	82	TCAACAGAGGCTGAACCACTAGAAAAG ACTACAGTCCCAAGCAGCAGCAATTTCA AGCTCGAGTGTCTCGGCAAACTCTGT G	1203
BUB3	NM_004725.1	BUB3	CTGAAGCA GATGGTTCA TCATT	52	GCTGATTC CAAGAGTCT AACC	436	CCTCGCTTTGTTTAAACAG CCCAGG	820	73	CTGAAGCAGATGGTTCATCATTTCTCTGG GCTGTAAACAAAGCAGGTTAAGGTT AGACTCTGGGAATCAGC	1204
c-kit	NM_000222.1	KIT	GAGGCAAC TGCTTATGG CTTAATTA	53	GGCACTCGG CTTGAGCAT AACC	437	TTACAGCGACAGTCATG GCCGCAT	821	75	GAGGCAACTGCTTATGGCTTAAATTAAG TCAGATCGGCCCATGACTGTCTGCTGTA AAGATGCTCAAGCCGAGTGCC	1205
C10orf16	NM_006829.2	C10orf16	CAAGAGCA GAGCCACC GT	54	TGAGACCGT TGGATTGGA TT	438	CCGGAGTCTAGCCTCC CAAAATC	822	67	CAAGAGCAGAGCCACCGTAGCCGGAGT CCTAGCTCCCAAAATTCGGAATTCAA TCCAACGGTCTCA	1206
C17orf37	NM_032339.3	C17orf37	GTGACTGCA CAGGACTCT GG	55	AGGACCAAA GGGAGACCA A	439	CCTGCTCTGTCTGGGGT CCAAAC	823	67	GTGACTGACAGGACTCTGGGTCTCTG CTCTGTCTGGGTCCAAACCTTGGTCT CCCTTTGGTCTCT	1207
C20orf1	NM_012112	TPX2	TCAGCTGTG AGCTGCGG ATA	56	ACGGTCTTA GGTTTGAGG TTAAGA	440	CAGGTCCCAATTGCCGGG CG	824	65	TCAGCTGTGAGCTGGGATACCGCCCG GCAATGGACCTCTCTCTTAAACCTCAA CCTAGGACCGT	1208

TABLE A

C6orf66	NM_014165.1	NDUFAF4	GCGGTATCA GGAATTCA ACCT	57	GCGACAGAG GGCTTCATC TT	441	TGATTTCCCGTTCCGCTC GGTTCT	825	70	GCGGTATCAGGAATTTCAACCTAGAGA ACCGAGCGGAACGGGAATATCAGCAAG ATGAAGCCCTCTGTCGC	1209
C8orf4	NM_020130.2	C8orf4	CTAGGAGTC AGCCCATCC AT	58	TGCCACGG CTTCTTAC CTTCTTAC	442	CATGGCTACCACTTTCGA CACAGCC	826	67	CTACGAGTCAGCCATCCATCCATGGC TACCACCTTCGACACAGCCCTCTCGTAAG AAAGCCGTGGGCA	1210
CACNA2D 2	NM_006030.1	CACNA2D 2	TGATGTCTGC AGAGAACT TCC	59	CACGATGTC TTCTCTCTTG A	443	AAAGCACACCGCTGGCA GGAC	827	67	TGATGTCGACAGAACTTCCAGAAAAGC ACACCGCTGGCAGGACAAATCAAGGA GGAAGACATCTGTG	1211
CAT	NM_001752.1	CAT	ATCCATTGC ATCTCACCA AGGT	60	TCCGGTTTA AGACCAAGTT TACCA	444	TGGCCTCACAAAGGACTA CCCTCTCATCC	828	78	ATCCATTCGATCTCACCAAGGTTTGGCC TCACAAAGGACTACCTCTCATCCAGTT GGTAACTGTCTTAAACCGGA	1212
CAV1	NM_001753.3	CAV1	GTGGCTCAA CATTGTGTT CC	61	CAATGGCCT CCATTTTAC AG	445	ATTTCAGCTGATCAGTG GGCTTCC	829	74	GTGGCTCAACATTTGTTTCCCATTTTCAG CTGATCAGTGGGCTCCAAAGGAGGGC TGTAATGTGAGGGCCATTG	1213
CBX5	NM_012117.1	CBX5	AGGGATG GTCCTGTGC ATT	62	AAAGGGGTG GGTAGAAAG GA	446	CATAATACATTCACCTCC CTGCCCTCCTC	830	78	AGGGATGGTCTCTGTCATTTCTTTG TACATAATACATTCACCTCCCTGCCCTCC TCTCCTTCTAGCCACCCCTTT	1214
CCL19	NM_006274.2	CCL19	GAACGCAT CATCCAGA GACTG	63	CCTCTGCAC GGTCATAGG TT	447	CGCTTCATCTTGGCTGAG GTCTC	831	78	GAACGCATCATCCAGAGACTGCAGAGG ACCTCAGCCAAAGATGAAGCGCCGACG AGTTAACTATGACCGTGCAGAGG	1215
CCL3	NM_002983.1	CCL3	AGCAGACA GTGGTCAGT CCTT	64	CTGCATGAT TCTGAGCAG GT	448	CTCTGCTGACACTCGAG CCACAT	832	77	AGCAGACAGTGGTCACTCTTCTTTG CTCTGCTGACACTCGAGCCACATTCGG TCACCTGCTAGAAATCATGCAG	1216
CCL5	NM_002985.2	CCL5	AGGTCTGA GCTCTGGCT TT	65	ATGCTGACT TCCTTCTTG GT	449	ACAGAGCCCTGGCAAAG CCAAAG	833	65	AGGTCTGAGCTCTGGCTTGGCTTGGC TTTGGCAGGGCTCTGTGACCAGGAAGG AAGTCAGCAT	1217
CCNB1	NM_031966.1	CCNB1	TTCAGGTG TTGCAGGA GAC	66	CATCTTCTTG GGCACACAA T	450	TGTCCTCAATTATTGATCG GTTCAATGCA	834	84	TTCAGGTGTTGTCAGGAGACCATGTAC ATGACGTCTCCATTATTGATCGGTCA TGCAGAAATAATTGTGTGCCAAAGA TG	1218
CCND3	NM_001760.2	CCND3	CTCTGTGC TACAGATTA TACCTTTGC	67	CACTGCAGC CCCAATGCT T	451	TACCCGCCATCCATGATC GCCA	835	76	CCTCTGTCTACAGATTATACCTTTGCC ATGTACCCGCCATCCATGATCGCCACG GGCAGCATTTGGGGCTGCAGTG	1219
CCNE2 variant 1	NM_057749var 1	CCNE2	GGTCAACA AGAAACAT CAGTATGA A	68	TTCAATGAT AATGCAAGG ACTGATC	452	CCCAGATAATACAGGTG GCCAACAAATTCCT	836	85	GGTCAACAAGAAACATCAGTATGAAT TAGGAATTGTGGCCACCTGTATTATCT GGGGGATCAGTCTCTGCAATTATCAT GAA	1220
CCR5	NM_000579.1	CCR5	CAGACTGA ATGGGGGT GG	69	CTGGTTTGT CTGGAGAAG GC	453	TGGAATAAGTACCTAAG GCGCCCC	837	67	CAGACTGAATGGGGTGGGGGGGGCG CCTTAGGTACTTATTCCAGATGCCCTTCT CCAGACAAACAG	1221
CCR7	NM_001838.2	CCR7	GGATGACA TGCACTCAG CTC	70	CCTGACATT TCCCTTTGTC T	454	CTCCCATCCCACTGGAG CCAA	838	64	GGATGACATGCACTCAGCTCTTGGCTC CACTGGGATGGAGGAGGACAAAGG GAAATGTCAGG	1222

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CD1A	NM_001763.1	CD1A	GGAGTGGG AGGAACTG GAAA	71	TCATGGCG TATCTAGG AT	455	CGCACCATTCGGTCAATTT GAGG	839	78	GGAGTGGAAAGCACTGGAACATTAAT CCGTATAGCACCATTCGGTCAATTTGAG GGAATTCGTAGATACGCCCATGA	1223
CD24	NM_013230.1	CD24	TCCAACTAA TGCCACCAC CAA	72	GAGAGAGTG AGACCACGA AGAGACT	456	CTGTGACTGCAGGGCA CCACCA	840	77	TCCAACTAATGCCACCAAGAGGGGC TGGTGGTCCCTGCAGTCAACAGCCAG TCTCTCTGGTCTCACTCTCTC	1224
CD4	NM_000616.2	CD4	GTGCTGGA GTGCGGACT AAC	73	TCCCTGCAT TCAAGAGGC	457	CAGGTCCCTTGTCCAA GTCCAC	841	67	GTGCTGAGTCCGGACTAACCCAGGTC CCTTGCCCAAGTTCCACTGCTGCTCT TGAATGCAGGA	1225
CD4E	X55150		ATCACCGAC AGCACAGA CA	74	ACCTGTGTT TGGATTGC AG	458	CCCTGCTACCAATATGG ACTCCAGTCA	842	90	ATCACCGACGACAGACAGAAATCCCT GCTACCAATATGGACTCCAGTCATAGT ACAACGCTTACGCTACTGCAAAATCCA AACACAGGT	1226
CD4s	M59040.1		GACGAAGA CAGTCCCTG GAT	75	ACTGGGGTG GAATGTGTC TT	459	CACCGACAGCACAGACA GAATCCC	843	78	GACGAAGACAGTCCCTGGATCACCGAC AGCACAGACAGAAATCCCTGCTACCCAGA GACCAAGACACATTCACCCAGT	1227
CD4v6	AJ251595v6		CTCATACCA GCCATCCAA TG	76	TGCGGTTGA AGAAATCAG TCC	460	CACCAAGCCAGAGGAC AGTTCT	844	78	CTCATACGACCATCCAAATGCAAGGAA GGACAACACCAAGCCAGAGGACAGTT CCTGGACTGATTTCTTCAACCCAA	1228
CD68	NM_001251.1	CD68	TGGTTCCCA GCCCTGTGT	77	CTCCTCCAC CCTGGGTTG T	461	CTCCAAGCCAGATTCA GATTCAGTCA	845	74	TGGTCCCAGCCTGTGTCACCTCCAA GCCAGATTCAGATTCGAGTCAATGTAC ACAACCCAGGTGGAGAG	1229
CD82	NM_002231.2	CD82	GTGCAGGCT CAGGTGAA GTG	78	GACCTCAGG GCGATTCAI GA	462	TCAGCTTCTACAACTGG ACAGACAACGCTG	846	84	GTGCAGGCTCAGGTGAAAGTGTGCGGC TGGGTCAAGCTTCTACAACTGACACAGAC AACGCTGAGCTCATGAATCGCCCTGAG GTC	1230
CDC20	NM_001255.1	CDC20	TGGATTGGA GTCTGGA ATG	79	GCTTGCACT CCACAGGTA CACA	463	ACTGGCCGTGGCACTGG ACAACA	847	68	TGGATTGGAGTCTGGGAAATGTACTGG CCGTGGCACTGGACAACAGTGTGTACC TGTGGAGTGCAAGC	1231
cdc25A	NM_001789.1	CDC25A	TCTTGCTGG CTACGCCCTC TT	80	CTGCAITGT GGCACAGTT CTG	464	TGTCCCTGTAGACGTCC TCCGTCCATA	848	71	TCCTGTGGCTACGCCCTCTCTGTGCCCT GTTAGACGTCTCCGTCCATATCAGAA CTGTGCCACAATGCAG	1232
CDC25C	NM_001790.2	CDC25C	GGTGAGCA GAAGTGGC CTAT	81	CTTCAGTCTT GGCCTGTTC A	465	CTCCCCGTCTGATGCCAG AGAACT	849	67	GGTGAGCAAGTGGCTTATATCGCTC CCCGTCCGATGCCAGAGAACTTGAACAG GCCAAGACTGAAG	1233
CDC4	NM_018315.2	FBXW7	GCAGTCCGC TGTGTCTAA GAGCTGAA	82	GGATCCCA ACCTTTACC ATAA	466	TGCTCCACTAACAAACCTT CCTGCC	850	77	GCAGTCCGCTGTGTTCATATATGATGGC AGGAGGGTGTGTAGTGGAGCATATGAT TTTATGTAAAGGTGTGGATCC	1234
CDC42BP A	NM_003607.2	CDC42BPA	AGACGCAC ACTG	83	GCCGCTCAT TGATCTCCA	467	AATTCTGCATGGCCAG TTTCCTC	851	67	GAGCTGAAAGACGCACACTGTGCAGAGG AAACTGGCCATGCAGGAATTCATGGAG ATCAATGAGCGGC	1235
CDC42EP4	NM_012121.4	CDC42EP4	CGGAGAG GGCACCCAG TA	84	CCGTCAITG GCCTTCTTC	468	CTGCCCAAGAGCCTGTG ATCCAG	852	67	CGGAGAGGGCACCAAGTAAAGCTGCCCA AGAGCCTCTCATCCAGCCCTGTGAAGA AGGCCAATGACGG	1236

TABLE A

CDH11	NM_001797.2	CDH11	GTCGGCAG AAGCAGGA CT	85	CTACTCATG GCGCGATG	469	CCTTCTGCCCATAGTGAT CAGCGA	853	70	GTCGGCAGAAAGCAGGACTGTGTACCTTC TGCCCATAGTATCAGCGATGGCGGCA TCCGCCATGAGTAG	1237
CDH3	NM_001793.3	CDH3	ACCCATGTA CCGTCTCTG	86	CGGCTTCA GGTCTCAA T	470	CCAACCCAGATGAAATC GGCAACT	854	71	ACCCATGTACCGTCTCGGCCAGCCAA CCAGATGAAATCGCAACTTATAAT TGAGAACTGAAGCGG	1238
CDK4	NM_000075.2	CDK4	CCTTCCCA CAGCACAG TTC	87	TTGGGATGC TCAAAAGCC	471	CCAGTCGGCTCAGTAAA GCCACCT	855	66	CCTTCCCATCAGCACAGTCTGTGAGGT GGCTTACTAGGCGACTGGAGGCTTT TGAGCATCCCA	1239
CDK5	NM_004935.2	CDK5	AAGCCCTAT CCGATGTAC CC	88	CTGTGGCAT TGAGTTTGG G	472	CACAACATCCCTGGTGA ACGTCTGT	856	67	AAGCCCTATCCGATGTACCCGGCCACA ACATCCTGGTGAACTGTGTGCCCAA CTCAATGCCACAG	1240
CDKN3	NM_005192.2	CDKN3	TGGATCTCT ACCAAGCAA TGFG	89	ATGTACAGGA GTCCCTCCA TC	473	ATCACCCATCATCATCCA ATCGCA	857	70	TGGATCTTACAGCAATGTGGAATTA TCACCCATCATCATCAATCGCAGATG GAGGACTCTTGACAT	1241
CEACAM1	NM_001712.2	CEACAM1	ACTTGCCTG TTCAGAGCA CTCA	90	TGGCAAATC CGAAATTAGA GTGA	474	TCCTTCCACCCCGAGTC CTGTC	858	71	ACTTGCCTGTACAGCAGCTCATCTCT CCACCCCGAGTCTGTCTATCACTCT AATTCGATTTGCCA	1242
CEBPA	NM_004364.2	CEBPA	TTGGTTTGT CTCGGATAC TTG	91	GTCTCAGAC CCTTCCCTC AG	475	AAAATGAGACTCTCCGT CGCGAGC	859	66	TTGGTTTGTCTGGATACTTGGCAAAAT GAGACTCTCCGTCTCGCAGCTGGGGAA GGGTCTGAGAC	1243
CEBP1	NM_020974.1	SCUBE2	TGACAAATCA GCACACCTG CAT	92	TGTGACTAC AGCGTGAT CCTTA	476	CAGGCCCTCTTCCGAGC GGT	860	77	TGACAAATCAGCACACCTGCATTCACCG CTCGGAAGAGGGCTGAGCTGCATGAA TAAGGATCACGGCTGTAGTCA	1244
CENPA	NM_001809.2	CENPA	TAAATTAC TCGTGGTGT GGA	93	GCCTCTTGT AGGGCCAAT AG	477	CTTCAATTGGCAAGCCC AGGC	861	63	TAAATTACTCTGTGTGGACTTCAAT TGGCAAGCCAGGCCCTATTGGCCCTA CAAGAGGC	1245
CGA (CHGA official)	NM_001275.2	CHGA	CTGAAGGA GCTCCAAG ACCT	94	CAAAACCCG TGTGTTCTT C	478	TGCTGATGTGCCCTCTCC TTGG	862	76	CTGAAGGAGCTCCAAGACCTCGCTCTC CAAGGCCAAGGAGAGGGCACATCA GCAGAAGAAACACAGCGGTTTG	1246
CCalpha	NM_000735.2	CGA	CCAGAAATG CACGCTACA GGAA	95	GCCCATGCA CTGAAGTAT TGG	479	ACCCATTTCTTCTCCAGC CGGG	863	69	CCAGAAATGACGCTACAGGAAACCCA TCTTCTCCAGCCGGGTGCCCAATAC TTCAGTGCATGGGC	1247
CCB	NM_000737.2	CCB	CCACCATAG GCAGAGGC A	96	AGTCGTGGA GTGCTAGGG AC	480	ACACCCCTACTCCCTGTGC CTCCAG	864	80	CCACCATAGGCAGAGGCAGGCCCTTCTCT ACACCCCTACTCTGTGCTCCAGCCTC GACTAGTCCCTAGCACTCGACGACT	1248
CHAF1B	NM_005441.1	CHAF1B	GAGGCCAG TGGTGGAA ACAG	97	TCCGAGGCC ACAGCAAC	481	AGCTGATGATCTTGCCC TACCGCCTG	865	72	GAGGCCAGTGTGGAAACAGGTGTGGA GCTGATGATGTGCTCTACCGCCTGGT GTTTGTGTGGCTCCGA	1249
CHFR	NM_018223.1	CHFR	AAGGAAAT GGTCCCTCT GTG	98	GACGCAATC TTTCTGTCTG G	482	TGAAGTCTCCAGCTTTGC CTCAGC	866	76	AAGGAAATGTGCTCTGTGGCAAGTG ATGAAGTCTCCAGCTTTGCTCAGCTCT CCCAGACAGAAAGACTGCGTC	1250

TABLE A

CHI3L1	NM_001276.1	CHI3L1	AGAAATGGG TGTGAAGG CG	99	TGCAGAGCA GCACTGGAG	483	CACCAGGACCACAAAAGC CTGTTTG	867	66	AGAATGGGTGTGAAGCGTCTCAAAACA GGCTTTGTGGTCTGGTCTGCTCAGT GCTGCTTGA	1251
CKS2	NM_001827.1	CKS2	GGCTGGAC GTGGTTTG TCT	100	CGCTGCAGA AAATGAAAC GA	484		868	62	GGCTGGAGCTGGTTTGTCTGCTGCGCC CGTCTTCGCGCTCTCGTTTCAATTTCT GCAGCG	1252
Claudin 4	NM_001305.2	CLDN4	GGCTGCTTT GCTGCAACT G	101	CAGAGCGGG CAGCAGAAT A	485	CTGCGCCCGCTCTTCGCG CGCACAGACAAAGCCTTA CTCCGCC	869	72	GGCTGCTTGTGCAACTGTCTCACCCCG CACAGACAAAGCCTTACTCCGCCAAGTA TTTGTGCCCGCTCTG	1253
CLIC1	NM_001288.3	CLIC1	CGGTACTTG AGCAATGC CTA	102	TCGATCTCC TCATCATCT GG	486	CGGGAAGAAATTCGCTTC CACCTG	870	68	CGGTACTTGAGCAATGCCTACGCCCGG GAAGAAATTCCTTCCACCTGTCCAGAT GATGAGGAGATCGA	1254
CLU	NM_001831.1	CLU	CCCAGGAT ACCTACCAC TACCT	103	TGCGGGACT TGGGAAAGA	487	CCCTTCAGCCTGCCCCAC CG	871	76	CCCCAGGATACCTACCACTACCTGCCCC TCAGCCTGCCCAACCGAGGCCCTCACT TCCTTTTCCCAAGTCCCGCA	1255
CNOT2	NM_014515.3	CNOT2	AAATCGCA GCTTATCAC AAG	104	TGTTGGTAC CCCTGTGTG G	488	ACTCAGTTACCGAGCCA CGTCACG	872	67	AAATCGCAGCTTATCACAAAGGCACTCA GTTACCGAGCCACGTCACGCCAACCAAC AGGGTACCAACA	1256
COL1A1	NM_000088.2	COL1A1	GTGGCCATC CAGCTGACC CAGC'AAG	105	CAGTGGTAG GTGATGTTC TGGGA	489	TCCTGCGCTGATGTCCA CCG	873	68	GTGGCCATCAGCTGACCTTCTCTGGCC TGATGTCACCGAGGCCCTCCAGAACA TCACCTACCACTG	1257
COL1A2	NM_000089.2	COL1A2	AACTGGTAT AGGAGCT	106	AAACTGGCT GCCAGCAT G	490	TCTCCTAGCCAGACGTGT TCTTGTCTTGTG	874	80	CAGCCAAGAACTGGTATAGGAGCTCCA AGGACAAGAAACACGCTGGCTAGGAG AAACTATCAATGCTGCGAGCCAGTTT	1258
COMT	NM_000754.2	COMT	CCTATCGG CTGGAACG AGTT	107	CTCCTTGGT GTCAACCCAT GAG	491	CCTGCAGCCCATCCACA ACCT	875	67	CCTTATCGGCTGGAACGAGTTCATCTCTG CAGCCCATCCACAACTGCTCATGGGT GACACCAAGGAG	1259
Contig 51037	NM_198477	CXCL17	CGACAGTTG CGATGAAA GTCTAA	108	GGCTGCTAG AGACCATGG ACAT	492	CCTCCTCTGTTGCTGCC ACTAATGCT	876	81	CGACAGTTGCGATGAAAAGTTCTAATCT CTTCCCTCCTCTGTTGCTGCCACTAAT GCTGATGTCCATGGTCTTAGCAGCC	1260
COPS3	NM_003653.2	COPS3	ATGCCCAGT GTTCCTGAC TT	109	CTCCCATTT ACAAAGTGT GA	493	CGAAACGCTATTCTCAC AGGTTACG	877	72	ATGCCAGTGTCTGACTTCGAAACG CTATTCTCACAGGTTCAGCTTTCATCA GCCTTGTAAATGGGAG	1261
CRYAB	NM_001885.1	CRYAB	GATGTGATT GAGGTGA TGG	110	GAACTCCCT GGAGATGAA ACC	494	TGTTCACTCTGGCGCTCT TCATGT	878	69	GATGTGATTGAGGTGCATGGAAAAACAT GAAGAGCGCCAGGATGAACATGGTTTC ATCTCCAGGGAGTTC	1262
CRYZ	NM_001889.2	CRYZ	AAGTCTGA AATGCGAT CA	111	CACATGCAT GGACCTTGA TT	495	CCGATTCCAAAAGACCA TCAGGTTCT	879	78	AAGTCTGAAATTCGATCAGATATTG CAGTACCGATTCCAAAAGACCATCAGG TTCTAATCAAGGTCCATGCATGTG	1263
CSF1 isoC	NM_172211.1	CSF1	CAGCAAGA ACTGCAAC AACA	112	ATCCCTCGG ACTGCCCTCT	496	TTTGTGAATGCTCCAGC CAAGG	880	68	CAGCAAGAACTGCAACAAACAGCTTTGC TGAATGCTCCAGCCAAAGGCCATGAGAG GCAGTCCGAGGGAT	1264

TABLE A

CSF1	NM_000757.3	CSF1	TGCAGCGG CTGATTGAC A	113	CAACTGTTC CTGGTCTAC AAACTCA	497	TCAGATGGAGACCTCGT GCCAAATTACA	881	74	TGCAGCGCTGATTGACAGTCAAGTGG AGACCTGTGCCAAATTACATTTGAGTT TGTAGACCGAGAACAGTGG	1265
CSF1R	NM_005211.1	CSF1R	GAGCAAA CCAAACCTA CGA	114	CCTGCAGAG ATGGGTATG AA	498	AGCCACTCCCCACGCTG TTGT	882	80	GAGCAACCAACCTACGAGTGCAGG GCCACAAACGCTGGGAGTGGCTCC TGGGCTTCATACCCATCTCTGCAGG	1266
CSF2RA	NM_006140.3	CSF2RA	TACCACACC CAGCATTC TC	115	CTAGAGGCT GGTGCCACT GT	499	CGCAGATCCGATTCTCT GGGATC	883	67	TACCACCCAGCATTCCTCTGATCCC AGAGAAATCGGATCTCGGAACAGTGGC ACAGCCCTAG	1267
CSK (SRC)	NM_004383.1	CSK	CCTGAACAT GAAGGAGC TGA	116	CATCAGTTC TCCGAACCTC C	500	TCCCGATGGTCTGCAGC AGCT	884	64	CCTGAACATGAAGGAGCTGAAGCTGCT GCAGACCATCGGGAAGGGGAGTTTCGG AGACGTGATG	1268
CTGF	NM_001901.1	CTGF	GAGTTCAA GTGCCCTGA CG	117	AGTTGTAAAT GGCAGGCAC AG	501	AACATCATGTTCTTCTTC ATGACCTCGC	885	76	GAGTTCAAGTCCCTGACGGCGAGGTCT ATGAAGAAGAACATGATGTTTCATCAAG ACTGTGCTGCCATTACAACT	1269
CTHRC1	NM_138455.2	CTHRC1	GCTCACTTC GGCTAAAA TGC	118	TCAGTCCA TTGAATGTG AAA	502	ACCAACGCTGACAGCAT GCATTTC	886	67	GCTCACTTCGGCTAAAAATGCAGAAATG CATGTGTGCAGCGTTGGTATTTCACATT CAATGGAGCTGA	1270
CTSD	NM_001909.1	CTSD	GTACATGAT CCCTGTGA GAAGGT	119	GGGACAGCT TGTAGCCTT TGC	503	ACCCTGCCCGCGATCAC ACTGA	887	80	GTACATGATCCCTGTGAGAAAGGTGTC CACCTTCGCCGATCACACTGAAGCT GGGAGGAAAAGGTACAAGCTGTCC	1271
CTSL2	NM_001333.2	CTSL2	TGTCCTACT GAGCGAGC AGAA	120	ACCATGCA GCCCTGATT G	504	CTTGAGGACGCGAACAG TCCACCA	888	67	TGTCCTACTGAGCGAGCAATCTGCT GGACTGTTCGCTCTCAAGGCAATCA GGGCTGCAATGGT	1272
CTSL2m2	NM_001333.2m2		ACCAGGA ATAACCTAA CAGC	121	CTGTTCTTC AAGCCAAGA CA	505	AGGTGCAATATGGGCAT ATATCTCATTTG	889	79	ACCAGGCAATAACCTAACAGCACCCAT TATAGGTGCAATATGGGCATATATCTC CATTTGTCTTGGCTTGGAGAACAG	1273
CXCL10	NM_001565.1	CXCL10	GGAGCAAA ATCGATGCA GT	122	TAGGGAAGT GATGGGAGA GG	506	TCTGTGTGGTCCATCCTT GGAAGC	890	68	GGAGCAAAATCGATGCGTGTCTTCAA GGATGGACACACAGAGGCTGCCCTCTC CCATCACTTCCCTA	1274
CXCL12	NM_000609.3	CXCL12	GAGTACA GATGCCCAT GC	123	TTTGAGATG CTTGACGTT GG	507	TTCTTCGAAAAGCCATGTT GCCAGA	891	67	GAGTACAGATGCCCATGCCGATCTT CGAAAGCCATGTTGCCAGAGCCAACGT CAAGCATCTCAA	1275
CXCL14	NM_004887.3	CXCL14	TGCGCCCTT TCCTCTGTA	124	CAATGCGGC ATATACTGG G	508	TACCCTTAAGAACGCC CCTCCAC	892	74	TGCGCCCTTCTCTGTACATATACCCCT TAAGAAGCCCTCCACACACTGCC CCCAGTATGCCGCAATG	1276
CXCR4	NM_003467.1	CXCR4	TGACCGCTT CTACCCCAA TG	125	AGGATAAGG CCAACCATG ATGT	509	CTGAAACTGGAACACAA CCACCCACAAG	893	72	TGACCGCTTACCCCAATGACTTGTGG GTGTTGTGTTCCAGTTTCAGCACATCA TGGTTGGCCTTATCCT	1277
CYP17A1	NM_000102.2	CYP17A1	CCGAGTG ACTCTATCA CCA	126	GCCAGCATT GCCATTATC T	510	TGGACACACTGATGCAA GCCAAGA	894	76	CCGAGTGACTCTATCACCACACATGCT GGACACACTGATGCAAGCCCAAGATGAA CTCAGATAATGGCAATGCTGGC	1278

TABLE A

CYP19A1	NM_000103.2	CYP19A1	TCCATTATAG GTACTTTCA GCCATTGG	127	CACCATGGC GATGTACTT TCC	511	CACAGCCACGGGGCCCA AA	895	70	TCCATTATAGGTACTTTTCAGCCATTTGGC TTTGGGCCCCGTGGCTGTGAGGAAAAG TACATGCCCATGGTG	1279
CYP1B1	NM_000104.2	CYP1B1	CCAGCTTTTG TGCTGTGCA CTAT	128	GGGAATGIG GTAGCCCAA GA	512	CTCATGCCACCACTGCC AACACCTC	896	71	CCAGCTTTGTGCTGTCACTATTCTCTCA TGCCACCACTGCCAACACCTCTGTCTTG GGCTACCACATTCCC	1280
CYR61	NM_001554.3	CYR61	TGCTCATTC TTGAGGAG CAT	129	GTGGCTGCA TTAGTGTCC AT	513	CAGCACCCCTTGGCAGTTT CGAAAT	897	76	TGCTCATTTGTGAGGAGCAATTAAGGTAT TTCCAAACTGCCAAGGGTGTGGTGCG GATGGACATAATGAGCCAC	1281
DAB2	NM_001343.1	DAB2	TGGTGGGTC TAGGTGGTG TA	130	ACCAAAGAT GCTGTGTTC CA	514	CTGTACACTCCTCCTCAGG CAGGAC	898	67	TGGTGGGCTAGGTGGTGTAACTGTCA CACTCCCTCAGGCAGGACCATGGAACA CAGCATCTTTGGT	1282
DCC	NM_005215.1	DCC	AAATGTCTCT CCTCGACTG CT	131	TGAATGCCA TCTTTCTTCC A	515	ATCACTGGAACTCCTCG GTGCGAC	899	75	AAATGTCTCTCTGACTGTCTCCGCGGA GTCCGACCGAGGAGTTCCAGTGATCAA GTGGAAGAAAGATGGCATTC	1283
DCC_exons 18-23	X76132_18-23		GGTCACCGT TGGTGTTCAT CA	132	GAGCGTCCG GTGCAAAATC	516	CAGCCACGATGACCACCT ACCAGCACT	900	66	GGTCACCGTGGTGTATCATCACAGTGTCT GGTAGTGTTCATCGTGGCTGTGATTTCG ACCCGACGCTC	1284
DCC_exons 6-7	X76132_6-7		ATGGAGAT GTGTCATT CCTAGTG	133	CACCACCC AAGTATCCG TAAG	517	TGCTTCTCCCACTATCT GAAATAA	901	74	ATGGAGATGTGGTCAATTCCTAGTGATT ATTTTCAGATAGTGGGAGGAAGCAACT TACGGATACTTGGGTGGTG	1285
DCK	NM_000788.1	DCK	GCCGCCAC AAGACTAA GGAAT	134	CGATGTTC CTTCGATGG AG	518	AGCTGCCCGTCTTTCTCA GCCAGC	902	110	GCCGCCAAGACTAAGGAATAGCCAC CCGCCCAAGAGAAAGCTGCCCTCTTT CTCAGCAGCTCTGAGGGGACCCGCAT CAAGAAAATCTCCATCGAAGGGAACAT CG	1286
DICER1	NM_177438.1	DICER1	TCCAATTCC AGCATCACT GT	135	GGCAGTGAA GGCGATAAA GT	519	AGAAAAAGCTGTGTGTCT CCCCAGCA	903	68	TCCAATTCCAGCATCATCTGTGGAGAAA AGCTGTGTGTCTCCCCAGCATACTTTAT CGCTTCACTGCC	1287
DLC1	NM_006094.3	DLC1	GATTCAGAC GAGGATGA GCC	136	CACCTCTTG CTGTCCCTTT G	520	AAAGTCCATTGTGCCACT GATGGCA	904	68	GATTCAGACGAGGATGAGCCTTGTGCC ATCAGTGGCAATGGACTTTCCAAAGG GACAGCAAGAGGTG	1288
DLL4	NM_019074.2	DLL4	CACGGAGG TATAAGGC AGGAG	137	AGAAGGAAG GTCCAGCCG	521	CTACCTGGACATCCCTGC TCAGCC	905	67	CACGGAGGTATAAGGAGGAGCCTACC TGGACATCCCTGCTCAGCCCGCGGCT GGACCTTCTTCT	1289
DR5	NM_003842.2	TNFRSF10 B	CTCTGAGAC AGTGTCTCG ATGACT	138	CCATGAGGC CCAACTTCC T	522	CAGACTTGGTGCCCTTTG ACTCC	906	84	CTCTGAGACAGTGTCTCGATGACTTTGC AGACTTTGTGCCCCTTGTACTCTCTGGA GCCGCTCATGAGGAAGTTGGGCTCAT GG	1290
DSP	NM_004415.1	DSP	TGGCACTAC TGCATGATT GACA	139	CCTGCCGA TTGTTTTCAG T	523	CAGGGCCATGACAATCG CCAA	907	73	TGGCACTACTGCATGATTGACATAGAG AAGATCAGGCCATGACAATCGCCAAG CTGAAACAATGCGGAGG	1291
DTYMK	NM_012145.1	DTYMK	AAATCGCTG GGAACAAG TG	140	AATGCGTAT CTGTCCACG AC	524	CGCCCTGGCTCAACTTTT CCTTAA	908	78	AAATCGCTGGGAACAAGTGGCGGTAAAT TAAGGAAAAGTTGAGCAGGGCGTGAC CCTCTGCTGGACAGATACGCATT	1292

TABLE A

DUSP1	NM_004417.2	DUSP1	AGACATCA GCTCTGGT TCA	141	GACAAACAC CCTTCTCC AG	525	CGAGGCCATTGACTTCA TAGACTCCA	909	76	AGACATCAGCTCTCGTTCAACGAGGC CATTGACTTCATAGACTCCATCAAGAA TGCTGAGGAAGGGTGTGTGC	1293
DUSP4	NM_001394.4	DUSP4	TGGTGACG ATGGAGGA GC	142	CTCGTCCCG GTTTCATCAG GTTCATCAG	526	TTGAGCACACTGCAGTC CATCTCC	910	68	TGGTACGATGGAGGAGCTGGGGAGA TGACTCGCAGTGTGCTCAAAAGGCTGA TGAACCGGACGAG	1294
E2F1	NM_005225.1	E2F1	ACTCCCTCT ACCTTGAG CA	143	CAGGCCCTCA GTTCTCTCA GT	527	CAGAAGAACAGCTCAGG GACCCCT	911	75	ACTCCCTCTAGCCTTGACAAAGGGCAG GGGTCCCTGAGCTGTCTTCTGCCCAT ACTGAAGAACTGAGCCTG	1295
EBRP	AF243433.1		CTGCTGGAT GACTTTCCT C	144	CCAACAGTA CAGCCAGTT GC	528	CTCACAGAAAGCCCA CCTCAAC	912	76	CTGCTGGATGACCTTCTCCAGAGTGT GCTCACAGAAAGCCCAACCTCAACAC CAGCAACTGGCTGTACTGTGG	1296
EDN1 endothelin	NM_001955.1	EDN1	TGCCACCTG GACATCAAT TG	145	TGGACCTAG GGCTTCCAA GTC	529	CACTCCCGAGCACGTTG TTCCGT	913	73	TGCCACTGGACATCATTTGGGTCAAC ACTCCCGAGCACGTTGTCCGTATGGA CTTGAAGCCCTAGGTCCA	1297
EDN2	NM_001956.2	EDN2	CGACAAGG AGTGCCTCT ACTTCT	146	CAGGCCGTA AGGAGCTGT CT	530	CCACTTGGACATCATCTG GGTGAACACTC	914	79	CGACAAGGAGTGCCTACTTCTGCCA CTTGGACATCATCTGGGTGAACACTCCT GAACAGACAGCTCCTTACGGCCTG	1298
EDNRA	NM_001957.1	EDNRA	TTTCTCAA ATTGCCTC AAG	147	TTACACATC CAACACGTG CC	531	CCTTTCCTCAGGGCATC CTTTT	915	76	TTTCTCAAATTTGCCCTCAAGATGGAAA CCCTTTCCTCAGGGCATCCTTTTGGCT GGCACTGGTGGATGTGTAA	1299
EDNRB	NM_000115.1	EDNRB	ACTGTGAAC TGCTGGTG C	148	ACCACAGCA TGGGTGAGA G	532	TGCTACCTGCCCTTTGT CATGTG	916	72	ACTGTGAACCTGCTGGTGCAGTGTCCA CATGACAAAGGGGCAAGTAGACACCTC TCTCACCCATGCTGTGT	1300
EEF1A1	NM_001402.5	EEF1A1	CGAGTGGGA GACTGGTGT TCTC	149	CCGTTGTAA CGTTGACTG GA	533	CAAAGGTGACCACCAT CCGGGT	917	67	CGAGTGGAGACTGGTGTCTTCAAAACC GGTATGGTGGTCACTTTGTCTCCAGTCA ACGTTACACGG	1301
EEF1A2	NM_001958.2	EEF1A2	ATGGAATCC ACAGAGCC G	150	GGCGCTGAC TTCCITGAC TT	534	CTCGTCTAGCGCTTCTC GCTGTA	918	66	ATGGAATCCACAGAGCCGGCTTACAGC GAGAAGCGTACGACGAGATCGTCAAG GAACTCAGCGCC	1302
EFP	NM_005082.2	TRIM25	TTGAACAG AGCCTGACC AAG	151	TGTTGAGAT TCCTCGCAG TT	535	TGATGCTTCTCCAGAAA CTCGAACTCA	919	74	TTGAACAGAGCCTGACCAAGAGGGATG AGTTCAGATTTCTGGAGAAAAGCATCAA AACTGCGAGGAATCTCAACA	1303
EGR1	NM_001964.2	EGR1	GTCCCGCT GCAGATCTC T	152	CTCCAGCTT AGGTAGTT GTCCAT	536	CGGATCCTTCTCCTCACTC GCCCA	920	76	GTCCCGCTGCAGATCTCTGACCCCGTTC GGATCCTTCTCCTCACTCGCCCAACCATGG ACAACCTACCTTAAAGTGGAG	1304
EGR3	NM_004430.2	EGR3	CCATGTGGA TGAATGAG GTG	153	TGCCTGAGA AGAGGTGAG GT	537	ACCCAGTCTACCTTCTC CCCACC	921	78	CCATGTGATGAATGAGGTGTCTCTTT CCATACCCAGTCTACCTTCTCCCAACC CTACCTACCTCTCTCAGGCA	1305
EIF4EBP1	NM_004095.2	EIF4EBP1	GGCGGTGA AGAGTCAC AGT	154	TGGTAGTGT CTCCACACG AT	538	TGAGATGGACATTTAAA GCACCAAGCC	922	66	GGCGGTGAAGATGACAGTTTGGAGATG GACATTTAAAGCACACGCCATCGTGTG GAGCACTACCAA	1306

TABLE A

ESPL1	NM_012291.1	ESPL1	ACCCAG ACCGATC AG	169	TGTAGGCA GACTTCTC AAACA	553	CTGGCCCTCATGTCCTT TCACG	937	70	ACCCAGACCGGATCAGGCAAGCTGG CCCTCATGTCCCTTACGGGTGTTGAG GAAGTCTGCCCTACA	1321
ESRRG	NM_001438.1	ESRRG	CCAGCACC ATGTGTGAA GAT	170	AGTCTCTTG GGCATCGAG TT	554	CCCCAGACCAAGTGTGA ATACATGCT	938	67	CCAGCACATTGTGAAGATGCCCCAGA CCAAAGTGTGAATACATGCTCAACTCGA TGCCCAAGAGACT	1322
ESR1	NM_000125.1	ESR1	CGTGGTGCC CCCTCATGA C	171	GGCTAGTGG GGCATGTA G	555	CTGGAGATGCTGGACGC CC	939	68	CGTGTGCCCCCTCTATGACCTGCTGCTG GAGATGCTGGACGCCACCGCTACAT GCGCCCACTAGCC	1323
EIV5	NM_004454.1	EIV5	ACCATGTAT CGAGAGGG GC	172	TGACCAGGA ACTGCCACA G	556	TTACCAGAGGCGAGGTT CCCTTCA	940	67	ACCATGTATCGAGAGGGGCCCTTAC CAGAGGCGAGGTTCCCTTACGCTGGG CAGTTCCTGGTCA	1324
EZH2	NM_004456.3	EZH2	TGGAACA GCGAAGGA TACA	173	CACCGAACA CTCCCTAGT CC	557	TCCTGACTTCTGTGAGCT CAITGGC	941	78	TGGAACAACGGAAGGATACAGCCTGTG CACATCTGACTTCTGTGAGCTCATGTC GCGGACTAGGGAGGTTCGGTG	1325
F3	NM_001993.2	F3	GTGAAGGA TGTAAGC AGACGTA	174	AACCGGTGC TCTCCACAT TC	558	TGGCACGGGTCTTCTCT ACC	942	73	GTGAAGGATGTGAAGCAGACGTACTTG GCACGGGTCTTCTCTACCGGCGCAGGG AATGTGAGAGCACCGGT	1326
FAP	NM_004460.2	FAP	CTGACCAG AACCACGG CT	175	GGAAAGTGG TCATGTGGG TC	559	CGGCTGTCCACGAACC ACTTATA	943	66	CTGACCAGAACCGGCTTATCCGGCC TGTCACACGAACCACTTATACCCACA TGACCCACTTCC	1327
FASN	NM_004104.4	FASN	GCCTCTTCC TGTTGACG	176	GCTTTGGCC GGTAGCTCT	560	TGCCCCACTACGTACTG GCCTAC	944	66	GCCTCTCTCTGTGACGGCTCGCCAC CTACGTACTGGCTACACCCAGAGCTA CCGGGCAAGC	1328
FGFR2 isoform 1	NM_000141.2	FGFR2	GAGGACT GTGGCATG CA	177	GAGTGAGAA TTCGATCCA AGTCTTC	561	TCCAGAGACCAACGTT CAAGCAGTTG	945	80	GAGGACTGTGGCATGCAGTGGCCCTC CCAGAGACCAACGTTCAAGCAGTTGGT AGAAGACTTGGATCGAATTCACATC	1329
FGFR4	NM_002011.3	FGFR4	CTGGCTTAA GGATGGAC AGG	178	ACGAGACTC CAGTGTGA TG	562	CCTTTCATGGGGAGAAC CGCAAT	946	81	CTGGCTTAAAGGATGACAGGCTTTCA TGGGAGAACCCGATTTGGAGGCATCG GCTGCCCATCAGCACTGGAGTCTCGT	1330
FHIT	NM_002012.1	FHIT	CCAGTGA GCGCTTCCA T	179	CTCTCTGGG TCGTCTGAA ACAA	563	TCGGCCACTTCAATCAGG ACGCAG	947	67	CCAGTGGAGGCTTCCATGACCTGCCGT CCTGATGAAGTGGCCGATTGTTTCAG ACGACCCAGAGAG	1331
FLOT2	NM_004475.1	FLOT2	GACATCTGC GCTCCATCC	180	CAAACTGGT CCCGGTCT	564	AATCTGCTCCACTGTGAG GGTCCC	948	66	GACATCTGCTCCATCTCGGGACCCCT GACAGTGGAGCAGATTATCAGGACCG GGACCAAGTTG	1332
FN1	NM_002026.2	FN1	GGAAGTGA CAGACGTG AAGGT	181	ACACGGTAG CCGGTCACT	565	ACTTCAAGCGGTGTCC ACATGAT	949	69	GGAAGTGAACAGACGTGAAGGTCAACAT CATGTGGACACCGCTTGAGAGTGCAGT GACCGGTACCGGT	1333
FOS	NM_005252.2	FOS	CGAGCCCTT TGATGACTT CCT	182	GGAGCGGGC TGTTCTCAGA	566	TCCCAGCATCATCCAGG CCCAG	950	67	CGAGCCCTTTGATGACTTCTCTGTTCCTCA GCATCATCCAGGCCAGTGGCTCTGAG ACAGCCCCGTCC	1334

TABLE A

FOX2	NM_005251.1	FOX2	GAGAACAA GCAGGGCT GG	183	CTTGACGAA GCACCTGTT GA	567	AGAACAGCATCCGCCAC AACCTCT	951	66	GAGAACAGCAGGGCTGCGCAGAACAG CATCCGCCACAACTCTCGCTCAACGA GTCTTCGTCAAG	1335
FOX3A	NM_001455.1	FOX3	TGAAGTCCA GGACGATG ATG	184	ACGGCTTGC TTACTGAAG GT	568	CTCTACAGCAGCTCAGC CAGCCTG	952	83	TGAAGTCCAGGACGATGATGCGCTCT CTCGCCATGTCTCTACAGCAGCTCAGC CAGCCTGTCACTTCACTAGTAAGCAAGCC GT	1336
FOXP1	NM_032682.3	FOXP1	CGACAGAG CTTGTGCAC CT	185	GGTGTCCA TTGGAATCC T	569	CAGACCAAGCCTTTGCC CAGAAAT	953	70	CGACAGAGCTTGTGCACCTAAGTGCA GACCAAGCTTTGCCCAGAAATTAAGG ATTCCAATGGACGACC	1337
FOXP3	NM_014009.2	FOXP3	CTGTTTGGCT GTCCGGAG G	186	GTGGAGGAA CTCTGGGAA TG	570	TGTTTCCATGGCTACCCC ACAGGT	954	66	CTGTTTGTCTCGGAGGACCTGTGG GGTAGCCATGGAAACAGCACATTCCCA GAGTCTCCAC	1338
FSCN1	NM_003088.1	FSCN1	CCAGCTGCT ACTTTGACA TCGA	187	GGTCACAAA CTTGCCAT GGA	571	TGACCGGCGCATCACAC TGAGG	955	74	CCAGCTGCTACTTTGACATCGAGTGGC GTACCGGCGCATCACACTGAGGGCGT CCAATGGCAAGTTGTGACC	1339
FUS	NM_004960.1	FUS	GGATAATTTC AGACAACA ACACCATCT	188	TGAAGTAAT CAGCCACAG ACTCAAT	572	TCAAATTGTAACATTTCTCA CCCAGGCTTG	956	80	GGATAATTAGACAAACACACCATCTT TGTGCAAGGCTGGGTGAGAAATGTTAC AATTGAGTCTGTGGCTGATTACTTCA	1340
FYN	NM_002037.3	FYN	GAAGCGCA GATCATGA AGAA	189	CTCTCTAGA CACCACATG AT	573	CTGAAGCAGCACAAAGCT GGTCCAG	957	69	GAAGCGCAGATCATGAAGAAGCTGAA GCACGACAAGCTGTCTCAGCTATATGC AGTGGTGTCTGAGGAG	1341
G-Catenin	NM_002230.1	JUP	TCAGCAGC AAGGCGAT CAT	190	GGTGGTTTT CTTGAGCGT GTACT	574	CGCCCGCAGGCCCTCATC CT	958	68	TCAGCAGCAAGGGCATCATGAGGAGG ATGAGGCTGCGGGGCCAGTACACGC TCAAGAAAACACCC	1342
GAB2	NM_012296.2	GAB2	TGTTTGGAG GGAAGGGC T	191	GAAAGATAGC TGAGGGCTG TGAC	575	TGAGCCAGATTCCACAC CTCACGT	959	74	TGTTTGGAGGAAAGGCTGGGGCTCTG AGCCAGATTCCACACTCACGTTCACT CACAGCCCTCAGCTATCTTC	1343
GADD45	NM_001924.2	GADD45A	GTGCTGGTG ACGAATCC A	192	CCCGGCAAA AACAAATAA GT	576	TTCATCTCAATGGAAGG ATCCTGCC	960	73	GTGCTGTGACGAATCCACATTCATCTC AATGGAAGGATCTCGCTTAAGTCAAC TTATTTGTTTTGCCGGG	1344
GADD45B	NM_015675.1	GADD45B	ACCTTCGAC AAGACCAC ACT	193	TGGGAGTTC ATGGGTACA GA	577	AACTTCAGCCCCAGCTC CCAAAGTC	961	70	ACCTTCGACAAAGACACACACTTTGGGAC TTGGGAGCTGGGGCTGAAGTTGCTCTG TACCCATGAACCTCCCA	1345
GAPDH	NM_002046.2	GAPDH	ATCCACCC ATGGCAAA TTC	194	GATGGGATT TCCATTGAT GACA	578	CCGTTCTCAGCCTTGACG GTGC	962	74	ATCCACCATGGCAAAATTCATGGCA CCGTCAAGGCTGAGAACGGGAAGCTTG TCATCAATGGAATCCCAATC	1346
GATA3	NM_002051.1	GATA3	CAAAGGAG CTCACTGTG GTGTCT	195	GAGTCAGAA TGCCCTTAT CACAGATG	579	TGTTCCAACCACTGAATC TGGACC	963	75	CAAAGGAGCTCACTGTGGTGTGTGTGT TCCAAGCTGAATCTGGACCCCATCT GTGAATAAGCCATCTGACTC	1347
GBP1	NM_002053.1	GBP1	TTGGGAAAT ATTGGGCA TT	196	AGAAGCTAG GGTGGTTGT CC	580	TTGGGACATTGTAGACTT GGCCAGAC	964	73	TTGGGAAATATTGGGCAATTGGTCTGG CCAAGTCTACAATGTCCCAATATCAAG GACAACCACTCCTAGCTCT	1348

TABLE A

GBP2	NM_004120.2	GBP2	GCATGGGA ACCATCAAC CA	197	TGAGGAGTT TGCTTTGAT TCG	581	CCATGGACCAACTTCAC TATGTGACAGAGC	965	83	GCATGGGAACCAATCAACGACGAGGCCA TGGACCAACTTCACATATGTGACAGAGC TGACAGATCGAATCAAGGCAAACTCCT CA	1349
GCLM	NM_002061.1	GCLM	TGTAGAATC AACTCTTC ATCATCAAC TAG	198	CACAGAATC CAGCTGTGC AACT	582	TGCAGTTGACATGGCCT GTTGAGTCC	966	85	TGTAGAAATCAAACTCTTCATCATCAACT AGAAATGACATGAGCATGGCCTGTTC GTCTTGGAGTTGCACACAGCTGGATTCTG TG	1350
GDF15	NM_004864.1	GDF15	CGCTCCAGA CCATATGATG ACT	199	ACAGTGGAA GGACACAGGA CT	583	TGTTAGCCAAAGACTGC CACTGCA	967	72	CGTCCAGACCTATGATGACTTGTGTAGC CAAAGACTGCCACTGCATATGAGCAGT CTGGTCTTCCACTGT	1351
GHI	NM_000515.3	GHI	GATCCCAA GGCCCAACT C	200	AGCCATTGC AGCTAGGTG AG	584	TGTCCACAGGACCCTGA GTGGTTC	968	66	GATCCCAAGGCCAAACTCCCGAACCA CTCAGGTCTGTGGACAGCTCACCTA GCTGCAATGGCT	1352
GJA1	NM_000165.2	GJA1	GTTCACTGG GGGTGTATG G	201	AAATACCAA CATGCACCT CTCTT	585	ATCCCCCTCCCTCTCCACC CATCTA	969	68	GTTCACTGGGGGTGTATGGGGTATGATG GGTGAGAGGGAGGGGATAAGAGAGG TGCAATGTGTGTAATT	1353
GJB2	NM_004004.3	GJB2	TGTCATGTA CGACGGCTT CT	202	AGTCCACAG TGTTGGGAC AA	586	AGGCGTTGCACTTTCACC AGCC	970	74	TGTCATGTACGACGGCTCTCTCAATGCAG CGGTGGTGAAGTGCAACGCCCTGGCCT TGTCACCAACTGTGGACT	1354
GMNN	NM_015895.3	GMNN	GTTGCTAC GAGGATTG AGC	203	TGGTACCC ACTTCTGC AA	587	CCCTTTGCCCACTTACTG GGTGGA	971	67	GTTGCTACGAGGATTGAGCGTCTCCA CCCAGTAAGTGGGCAAGAGGGCGCAG GAAATGGGTACGCA	1355
GNAZ	NM_002073.2	GNAZ	TTCTGGACC TGGACCTT AG	204	AAAGAGCTG TGAGTGGCT GG	588	CCGGTGACAGCACTAA CCAGACC	972	68	TTCTGACCTGGGACCTTAGAGAGCCGG GTGACAGCACTAACAGACCTCCAGCC ACTCACAGCTCTT	1356
GPR30	NM_001505.1	GPER	CGTGCTCT ACACCATCT TC	205	ATGTTACCC ACCAGGATC AG	589	CTCTTCCCAATCGGCTTT GTGG	973	70	CGTGCTCTACCACTCTCTCTCTCC CATCGCTTTGTGGGCAACATCTTGATC CTGGTGGTGAACAT	1357
GPS1	NM_004127.4	GPS1	AGTACAAG CAGCTGCC AAG	206	GCAGCTCAG GGAAGTCAC A	590	CCTCTGCTGGCTTCTCT TGATCA	974	66	AGTACAAGCAGGCTGCCAAGTGCTCC TGCTGGCTCTCTTGATCCTGTGACTT CCTGAGCTGC	1358
GPX1	NM_000581.2	GPX1	GCTTATGAC CGACCCCA A	207	AAAGTTCCA GGCAACATC GT	591	CTCATCACTGGTCTCCG GTGTGT	975	67	GCTTATGACGACCCCAAGCTCATCAC CTGGTCTCCGCTGTGTCGCAACGATGT GCCTGGAACTTT	1359
GPX2	NM_002083.1	GPX2	CACACAGA TCTCTACT CCATCCA	208	GGTCCAGCA GTGTCTCT GAA	592	CATGCTGCATCTAAGG CTCTCAGG	976	75	CACACAGATCTCTACTCATCCAGTCC TGAGGAGCCTTAGGATGCAGCATGCCT TCAGGAGACTGCTGGACC	1360
GPX4	NM_002085.1	GPX4	CTGAGTGTG GTTTGCAGA T	209	TACTCCCTG GCTCTGCT T	593	CTGGCCTTCCCGTGTAAAC CAGTTC	977	66	CTGAGTGTGTTGCGGATCTCTGGCCTT CCCCTGTAAACAGTTTCGGGAAGCAGGA GCCAGGAGTA	1361
GRB7	NM_005310.1	GRB7	CCATCTGCA TCCATCTTG TT	210	GGCCACCAG GGTATTATC TG	594	CTCCCCACCTTGAAGAA GTGCCT	978	67	CCATCTGATCCATCTTGTGTTGGGCTCC CCACCTTGAGAAAGTGCCTCAGATAAT ACCTGTGTGGCC	1362

TABLE A

GREB1 variant a	NM_014668.2	GREB1	CAGATGAC AATGGCCA CAAT	211	GAAGCCTTT CTTCCACA GC	595	CACAATTCACAGAGAAA CCAAAGAGAGC	979	71	CAGATGACAATGGCCACAAATGCTCTTC TTGGTTCTCTGGGAAATGTGTGGCTG TGGAAAGAAAGGCTTC	1363
GREB1 variant b	NM_033090.1	GREB1	TGCTTAGGT GCGGTAAA ACCA	212	CAAGAGCCT GAAATGCGTC AGT	596	ACCACGCGAACGGTGCA TCG	980	73	TGCTTAGGTGCGGTAAAACACAGGCTT GTCCGATGCAACCGTTCGCGTGTAAAC TGACGCATTCAGGCTCTTG	1364
GREB1 variant c	NM_148903.1	GREB1	CCCAGGC ACCAGCTTT A	213	ACTTCGGCT GTGTGTAT ATGCA	597	TCCCCGAGCCCAGCAGG ACA	981	64	CCCAGGCACAGCTTACTCCCCGAG CCCAGAGGACATCTGCATATAACACA CAGCCGAAGT	1365
GRN	NM_002087.1	GRN	TGCCCCCAA GACACTGTG T	214	GAGTCCGT GGTAGCGTT CTC	598	TGACCTGATCCAGAGTA AGTGCCCTCCA	982	72	TGCCCCAAGACACATGTGTGTGACCTG ATCCAGATTAAGTCTCTCCAAAGGAG AACGCTACACGGACCTC	1366
GSTM1	NM_000561.1	GSTM1	AAGCTATG AGGAAAAG AAGTACAC GAT	215	GGCCCAGCT TGAATTTTC A	599	TCAGCCACTGGCTTCTGT CATAATCAGGAG	983	86	AAGCTATGAGGAAAAGAAATACACGAT GGGGACGCTCCTGATTATGACAGAAG CCAGTGGCTGAATGAAAAAATCAAGCT GGGC	1367
GSTM2 gene	NM_000848.gen e		CTGGGCTGT GAGGCTGA GA	216	GCGAATCTG CTCCTTTCT GA	600	CCCGCCTACCTCTCGTAA AGCAGATTCA	984	71	CTGGGCTGTAGGCTGAGAGTGAATCT GCTTTACGAGGGTAGCGGGGAATCAG AAAAGGACAGATTTCG	1368
GSTM2	NM_000848.2	GSTM2	CTGCAGGC ACTCCCTGA AAT	217	CCAAGAAAC CATGGCTGC TT	601	CTGAAGCTCTACTACA GTTCTGGG	985	68	CTGCAGGCACCTCTGAAATCTCTGAAG CTCTACTACAGTTTCTGGGGAAGCAG CCAATGGTTCTTGG	1369
GSTM3	NM_000849.3	GSTM3	CAATGCCAT CTTGCCTA CAT	218	GTCCACTCG AATCTTTCT TCTTCA	602	CTCGCAAGCACAAACATG TGTGGTGAGA	986	76	CAATGCCATTTGGCTACATCGCTCGC AAGCACAACATGTGTGTGAGACTGAA GAAGAAAAGATTTCGAGTGGAC	1370
GSTT1	NM_000853.1	GSTT1	CACCATCCC CACCTGTC T	219	GGCTCAGT GTGCATCAT TCT	603	CACAGCCGCTGAAAGC CACAAAT	987	66	CACCATCCCCCCTGCTTCCACAGCC GCCTGAAAGCCACAATGAGAAATGATGC ACACTGAGGCC	1371
GUS	NM_000181.1	GUSB	CCCCTCAG TAGCCAAGT CA	220	CAGCAGGT GGTATCAGT CT	604	TCAAAGTAAACGGGCTGT TTTCCAAACA	988	73	CCCCTCAGTAGCCAAGTCAACAATGTT TGGAAAACAGCCCGTTACTTGAGCAA GACTGATACCACTGGCTG	1372
H3F3A	NM_002107.3	H3F3A	CCAAACGT GTAACAATT ATGCC	221	TCTTAAAGCA CGTTCTCCA CG	605	AAAGACATCCAGTAGC ACGCCG	989	70	CCAAACGTGTAACAATATGCAAAAAG ACATCCAGTAGCACGCCGCATACGTG GAGAACGCTGCTTAAGA	1373
HDAC1	NM_004964.2	HDAC1	CAAGTACC ACAGCGAT GACTACATT AA	222	GCTTGCTGT ACTCCGACA TGTT	606	TCTTGCGCTCCATCCGT CCAGA	990	74	CAAGTACCACAGCGATGACTACATTA ATTCTTGGCTCCATCCGTCAGATAAC ATGTCGGAGTACAGCAAGC	1374
HDAC6	NM_006044.2	HDAC6	TCCTGTGCT CTGGAAGC C	223	CTCCAGGT CTCAGTTGA TCT	607	CAAGAACCTCCAGAGAAG GGCTCAA	991	66	TCTGTGCTCTGGAAGCCCTTGAGCCCT TCTGGAGGTCTTGTGAGATCAACTG AGACCCGTGAG	1375
HER2	NM_004448.1	ERBB2	CGGTGTGA GAAGTGCA GCAA	224	CCTCTCGCA AGTGTCTCA T	608	CCAGACCATAGCACACT CGGGCAC	992	70	CGGTGTGAGAAAGTGACGCAAGCCCTGT GCCCGAGTGTGCTATGGTCTGGCATG GAGCACTTGCAGAGG	1376

TABLE A

HES1	NM_005524.2	HES1	GAAAGATA GCTCGGGC A	225	GGAGGTGCT TCACTGTCA TTT	609	CAGAAATGTCGCTTCTC CAGCTT	993	68	GAAAGATAGCTCGGGCATTCAGAGCT GGAGAAGGGCGGACATTTCTGGAATGAC AGTGAAGCACCTCC	1377
HGFAC	NM_001528.2	HGFAC	CAGGACAC AAGTGCCA GATT	226	GCAGGGAGC TGGAGTAGC	610	CGCTACGTTCTCATCCA AGTGG	994	72	CAGGACACAAATGGCAGATTCGGGGT GGGGCCACTTGGATGAGAACGTCGAGCG GCTACTCCAGCTCCCTGC	1378
HLA-DPB1	NM_002121.4	HLA-DPB1	TCCATGATG GTTCGTCAG GTT	227	TGAGCAGCA CCATCAGTA ACG	611	CCCCGGACAGTGGCTCT GACG	995	73	TCCATGATGTTCTGCAGGTTTCTGCGG CCCCCGACAGTGGCTCTGACGGCGT TACTGATGGTGTGCTCA	1379
HMGB1	NM_002128.3	HMGB1	TGGCTGTC CATTTGGTGA T	228	GCTTGTCAT CTGCAGCAG TGTT	612	TTCCACATCTCTCCCAAGT TCTTTCGAA	996	71	TGGCTGTCCATTTGGTGAATGTTGCGAA GAAACTGGAGAGATGTGGAATAACAC TGCTGCAGATGACAAAC	1380
HNF3A	NM_004496.1	FOXA1	TCCAGGATG TTAGGAACT GTGAAG	229	GCGTGTCTG CGTAGTAGC TGTT	613	AGTCGGCTGGTTTCATGCC CTTCCA	997	73	TCCAGGATTTAGGAACTGTGAAGATG GAAAGGCATGAACACGACACTGGAA CAGCTACTACGCACACACG	1381
HNRPA	NM_004499.3	HNRNPAB	AGCAGGAG CGACCAACT GA	230	GTTTGCCAA GTTAAATTT GGTACATAA T	614	CTCCATATCCAAACAAA GCATGTGTGG	998	84	AGCAGGAGCGACCAACTGTATCGCACAC ATGCTTGTGGATATGGAGTGAACA CAATTATGTACCAAAATTTAACTTGCA AAC	1382
HNRPC	NM_004500.3	HNRNPC	GCAGCAGT CGGCTTCTC T	231	GGGAGGGAG AAGAGATT GAT	615	AGTCTCTACTCCCGGT TCTGGC	999	68	GCAGCAGTGGCTTCTCTACGCAGAAC CCGGAGTAGGAGACTCAGAAATCGAAT CTCTCTCCCTCCC	1383
HoxA1	NM_005522.3	HOXA1	AGTGACAG ATGGACAA TGC'AAGA	232	CCGAGTCGC CACTGTCTAA GT	616	TGAACTCCTTCTCTGGAAT ACCCCA	1000	69	AGTGACAGTGGACAAATGCAAGAATGA ACTCCTTCTCTGGAATACCCCATACTTAG CAGTGGCGACTCGG	1384
HoxA5	NM_019102.2	HOXA5	TCCCTTGTG TTCTTCTTG TGAA	233	GGCAATAAA CAGGCTCAT GATTAA	617	AGCCCTGTCTCTGTTGCC CTAAITCATC	1001	78	TCCCTGTGTCTCTCTGTGAAGAAGCC CTGTCTCGTTGCCCTTAATCATCTTTT AATCATGAGCCTGTTATTGCC	1385
HOXB13	NM_006361.2	HOXB13	CGTGCCCTTA TGGTTACTT TGG	234	CACAGGGTT TCAGCGAGC	618	ACACTCGGCGAGGAGTAG TACCCGC	1002	71	CGTGCCCTTATGGTTACTTTGGAGGCGG GTACTACTCTCTCGCGAGTGTCCCGGAG CTCGCTGAACCCCTGTG	1386
HOXB7	NM_004502.2	HOXB7	CAGCCTCAA GTTCGGTTT TC	235	GTTGGAAGC AAACGCACA	619	ACCGGAGCCTTCCCAGA ACAAACT	1003	68	CAGCCTCAAAGTTCGGTTTTCGCTACCGG AGCCTTCCAGAACAAACTTCTTGTGC GTTTGTCTCCAAC	1387
HSD17B1	NM_000413.1	HSD17B1	CTGGACCCG ACGGACAT C	236	CGCCTCGCG AAAGACTTG	620	ACCGCTTCTACCAATACC TCGCCCA	1004	78	CTGGACCCGACGGACATCCACACCTTC CACCGCTTCTACCAATACCTCGCCACA GCAAGCAAGTCTTTCGCGAGGCG	1388
HSD17B2	NM_002153.1	HSD17B2	GCTTCCAA GTGGGGAA TTA	237	TGCCTGCGA TATTGTGTA GG	621	AGTTGCTTCCATCCAACC TGGAGG	1005	68	GCTTCCAAAGTGGGAAATTAAGATTGC TTCCATCCAACTGGAGGCTTCTTAACA AATATCGCAGGCA	1389
HSHN1	NM_017493.3	OTUD4	CAGTCTCGC CATGTTGAA GT	238	ATAAACGCT TCAAAATT TCTCTG	622	CAGAAATGGCTGTATT ACTATCTTCGAGA	1006	77	CAGTCTCGCAATGTGAAGTCAAGATG GCCTGTATTCTATCTTCGAGAGAAC AGAGAGAAATTTGAAGCGTTTAT	1390

TABLE A

HSPA1A	NM_005345.4	HSPA1A	CTGCTGCGA CAGTCCACT A	239	CAGTTTCG TCTGGGAG	623	AGAGTGACTCCCCTGTGT CCCAAGG	1007	70	CTGCTGCGACAGTCCACTACCTTTTTCG AGAGTGACTCCCCTGTGTCCCAAGGCTT CCAGAGCGAACCTG	1391
HSPA1B	NM_005346.3	HSPA1B	GGTCCGCTT CGTCTTTCG A	240	GCACAGGTT CGCTCTGGA A	624	TGACTCCCGGGTCCCA AGG	1008	63	GGTCCGCTTTCGCTTTCGAGAGTGACTC CCGCGGTCCCAAGGCTTTCAGAGCGA ACCTGTGC	1392
HSPA4	NM_002154.3	HSPA4	TTCAGTGTG TCCAGTGCA TC	241	ATCTGTTTCC ATTGGCTCC T	625	CATTTCCTCAGACTTGT GAACCTCCACT	1009	72	TTCAGTGTGTCAGTGTCTTTTAGTGG AGGTTACAAAGTCTGAGGAAAATGAGG AGCCAATGGAAACAGAT	1393
HSPA5	NM_005347.2	HSPA5	GGCTAGTA GAACTGGA TCCCAACA	242	GGTCTGCC AAATGCTTT TC	626	TAATTAGACTAGGCCT CAGCTGCCTGCC	1010	84	GGCTAGTAACTGGATCCCAACACCA AACTCTTAATTAGACTAGGCTCTCAGCT GCACCTGCCGAAAAGCATTTTGGGCAGA CC	1394
HSPA8	NM_006597.3	HSPA8	CCCTCCCTCT GGTGGTGTCT T	243	GCTACATCT ACACTTGGT TGGCTTAA	627	CTCAGGGGCCACCAATTG AAGAGGTG	1011	73	CCTCCCTCTGGTGGTCTCTCAGGGC CCACCAATTGAAGAGGTGTGATTAAAGCCA ACCAAGTCTAGATGTAGC	1395
HSPB1	NM_001540.2	HSPB1	CCGACTGG AGGAGCAT AAA	244	ATGCTGGCT GACTCTGCT C	628	CGCACTTTTCTGAGCAG ACGTCCA	1012	84	CCGACTGGAGGAGCATAAAAGCGCAGC CGAGCCAGCGCCCGCACCTTTTCTGTA GCAGACGTCCAGAGCAGATCAGCCAG CAT	1396
IBSP	NM_004967.2	IBSP	GAATACCA CACTTTCTG CTACAACAC T	245	GGATTGACAG CTAACCCCTG TATACC	629	CCAGGCGTGGCGTCTC TCCATA	1013	83	GAATACCACTTTTCTGTACAAACACT GGGCTATGGAGAGGACGCCACGCTGG CACAGGGTATACAGGGTTAGCTGCAAT CC	1397
ICAM1	NM_000201.1	ICAM1	GCAGACAG TGACCAATCT ACAGCTT	246	CTCTGAGA CTCTTGGCT TCGT	630	CCGGCGCCCAACGTGAT TCT	1014	68	GCAGACAGTGACCACTCTACAGCTTTCC GGCGCCCAACGTGATTTCTGACGAAGCC AGAGTCTCAGAAAG	1398
ID1	NM_002165.1	ID1	AGAACCCG AAGGTGAG CAA	247	TCCAACTGA AGGTCCCTG ATG	631	TGGAGATTCTCCAGCAC GTCAATCGAC	1015	70	AGAACCCGAAAGGTGAGCAAGGTGGAG ATTCTCCAGCACGTATCGACTACATCA GGGACCTTCAGTTGGA	1399
ID4	NM_001546.2	ID4	TGGCTGGC TCTTAATT G	248	TGCAATCAT GCAAGACCA C	632	CTTTTGTTTTGCCCACTA TAGACTCGAAG	1016	83	TGGCTGGCTCTTAATTGCTTTTGTGTTT GCCCACTATAGACTCGGAAGTAACAGT TATAGTAGTGGTCTTGCATGATTGCA	1400
IDH2	NM_002168.2	IDH2	GGTGGAGA GTGGAGCC ATGA	249	GCTCGTTCA GCTTCACAT TGC	633	CCGTGAATGCAGCCCGC CAG	1017	74	GGTGGAGAGTGGAGCCATGACCAAGG ACCTGGCGGGCTGCATTCACGGCTCA GCAATGTGAAGTGAACGAGC	1401
IGF1R	NM_000875.2	IGF1R	GCATGGTA GCCGAAGA TTTCA	250	TTTCCGGTA ATAGTCTGT CTCATAGAT ATC	634	CCGTCAATACCAAAATC TCCGATTGTGA	1018	83	GCATGGTAGCCGAAGATTTCACAGTCA AAATCGAGATTTTGGTATGACGCGAG ATATCTATGAGACAGACTATTACCGGA AA	1402
IGF2	NM_000612.2	IGF2	CCGTGCTTC CGGACAAC TT	251	TGGACTGCT TCCAGGTGT CA	635	TACCCCGTGGGCAAGTT CTTCCAA	1019	72	CCGTGCTTCCGGACAACCTTCCCAGAT ACCCCTGGGCAAGTCTTCCAAATATG ACACCTGGAAAGCAGTCCA	1403

TABLE A

IGFBP6	NM_002178.1	IGFBP6	TGAACCGC AGAGACCA ACAG	252	GTCTTGGAC ACCCGCAGA AT	636	ATCCAGGCACCTCTACC ACGCCCTC	1020	77	TGAACCGCAGAGACCAACAGAGGAATC CAGGCACCTCTACCAGCCCTCCACAGC CCAAITCTCGGGGTGTCCAAGAC	1404
IGFBP7	NM_001553.1	IGFBP7	GGGTCACTA TGGAGTTCA AAGGA	253	GGGTCTGAA TGGCCAGGT T	637	CCCGGTACACAGGCAGG AGTTCT	1021	68	GGGTCACTATGGAGTTCAAAGACAGA ACTCTCTGCTGGTGACCGGACAACT GGCCATTCAAGACC	1405
IKBKE	NM_014002.2	IKBKE	GCCTCCCAT AGCTCCTTA CC	254	CAGAGCTCT TGCATGTGG AG	638	CAGCCCTACACGAAAGG ACCTGCT	1022	66	GCTCCCATAGCTCTTACCCAGCCCT ACACGAAAGGACCTGCTTCTCCACATG CAAGAGCTCTG	1406
IL-8	NM_000584.2	IL8	AAGGAACC ATCTCACTG TGTTAAAC	255	ATCAGGAAG GCTGCCAAG AG	639	TGACTTCCAAGCTGGCC GTGGC	1023	70	AAGGAACCATCTCACTGTGTGTAAACA TGACTTCCAAGCTGGCCGTGGCTCTCTT GGCAGCCTTCCGTAT	1407
IL10	NM_000572.1	IL10	GGCCTGTG ATCGATTTC TT	256	TGGAGCTTA TTAAAGGCA TCTTCA	640	CTGCTCCACGGCCTTGCT CTTG	1024	79	GGCGCTGTCACTGATTTCTTCCCTGTGA AAACAAGAGCAAGGCCGTGGAGCAGG TGAAGAATGCTTTTAAATAAGCTCCA	1408
IL11	NM_000641.2	IL11	TGGAAGGTT CCACAAGTC AC	257	TCTTGACCTT GCAGCTTTG T	641	CCTGTGATCAACAGTAC CCGTATGG	1025	66	TGGAAGGTCCACAAGTCACTCTGTGA TCAACAGTACCCGTATGGGACAAAGCT GCAAGGTCAAGA	1409
IL17RB	NM_018725.2	IL17RB	ACCTCTGG TGGTAAATG GA	258	GGCCCAAT GAAATAGAC TG	642	TCGGCTTCCCTGTGAGAGC TGAACA	1026	76	ACCTCTGGTGGTAAATGGACATTTTC TACATCGCTTCCCTGTAGAGCTGAAC ACAGTCTATTTCATTGGGGC	1410
IL6ST	NM_002184.2	IL6ST	GGCTAATG TTCCAGATC CT	259	AAAATGTG CCTTGGAGG AG	643	CATATTGCCCAGTGGTC ACCTCACA	1027	74	GGCTAATGTCCAGATCCTCTCAAAGA GTCATATGCCAGTGGTCACTCAACAC TCTCCAAGGCACAAATTT	1411
ING1	NM_005537.2	ING1	ACTTCTTG CGAGGTCA GTC	260	AACTCCGAG TGGTGATCC A	644	ATCAAAAACAGAGCCCC CAAAGCC	1028	66	ACTTCTCGGAGGTCACTCAAGGCTTT GGGGCTCTGTGTTTGAATGTGGATCAC CACTCGGAGTT	1412
INHBA	NM_002192.1	INHBA	GTGCCGA GCCATATAG CA	261	CGGTAGTGG TTGATGACT GTGA	645	ACGTCCGGGTCTCTACT GTCTTCC	1029	72	GTGCCCGAGCCATATAGCAGGCACGTC CGGTCTCTACGTCTCTTCCACTCAACA GTCAACAACCACTACCG	1413
IRF1	NM_002198.1	IRF1	AGTCCAGCC GAGATGCT AAG	262	AGAAGGTAT CAGGGCTGG AA	646	CCCACATGACTTCTCTT GGCCTT	1030	69	AGTCCAGCCGAGATGCTAAGAGCAAGG CCAAGAGAGAGTCACTGTGGGATTTCCA GCCCTGATACCTTCT	1414
IRS1	NM_005544.1	IRS1	CCACAGCTC ACCTCTGT CA	263	CCTCAGTGC CAGTCTCTT CC	647	TCCATCCAGCTCCAGCC AG	1031	74	CCACAGCTCACTTCTGTCAAGGTGTCCA TCCCAGCTCCAGCAGCTCCACAGAGAG GAAGAGACTGGCACTGAGG	1415
ITGA3	NM_002204.1	ITGA3	CCATGATCC TCACTCTGC TG	264	GAAGCTTTG TAGCCGGTG AT	648	CACTCCAGACCTCGTTA GCATGG	1032	77	CCATGATCTCACTCTGTGTGGACTA TACACTCCAGACCTCGCTTAGCATGGT AAATCACCGGCTACAAAGCTTC	1416
ITGA4	NM_000885.2	ITGA4	CAACGCTTC AGTGATCA ATCC	265	GTCTGGCCG GGATTCTTT	649	CGATCTCTCATCTGTA ATCGCC	1033	66	CAACGCTTCAGTGATCAATCCCGGGG GATTTACAGATGCAGGATCGGAAAGAA TCCCGCCAGAC	1417

TABLE A

ITGA5	NM_002205.1	ITGA5	AGGCCAGC CCTACATTA TCA	266	GTCCTCTC ACAGTCCAG CA	650	TCTGAGCCTTGCTCTA TCCGGC	1034	75	AGCCAGCCCTACATTATCAGAGCAAG AGCCGGATAGAGGACAAGGCTCAGATC TTGCTGGACTGTGGAGAAGAC	1418
ITGA6	NM_000210.1	ITGA6	CAGTGACA AACAGCCCT TCC	267	GTTTAGCT CATGGGCGT C	651	TCGCCATCTTTTGTGGGA TTCCCT	1035	69	CAGTGACAAAAGCCCTTCCAAACCCAA GGAATCCACAAAAGATGGCGATGACG CCCATGAGGCTAAAC	1419
ITGAV	NM_000210.2	ITGAV	ACTCGGACT GCACAAAGC TAAT	268	TGCATCAC CATTGAAT CT	652	CCGACAGCCACAGAATA ACCCAAA	1036	79	ACTCGGACTGCACAAAGCTATTTTGTGATG ACAGCTATTTGGGTATTTCTGTGGCTGT CGGAGATTTCAATGGTGTATGCA	1420
ITGB1	NM_000211.2	ITGB1	TCAGAAATG GATTGGCT CA	269	CCTGAGCTT AGCTGGTGT TG	653	TGCTAATGTAAAGGCATC ACAGTCTTTTCCA	1037	74	TCAGAAATGATTTGGCTCATTTGTGGA AAAGACTGTGATGCTTACATTTAGCAC AACACCAGCTAAGCTCAGG	1421
ITGB3	NM_000212.2	ITGB3	ACCGGGGA GCCCTACAT GA	270	CCTTAAAGT CTTTCACTG ACTCAAATCT	654	AAATACCTGCAACCGT ACTGCCGTGAC	1038	78	ACCGGGAGCCCTACATGACGAAATA CCTGCAACCGTTACTGCCGTGACGAGA TTGAGTACGTGAAAAGAGCTTAAAG	1422
ITGB4	NM_000213.2	ITGB4	CAAGGTGC CCTCAGTGG A	271	GGCACACC TTCATCTCAT	655	CACCAACCTGTACCCGT ATTGCGA	1039	66	CAAGGTGCCCTCAGTGGAGCTCACAA CCTGTACCCGTATTTGGACTATGAGAT GAAAGGTGTGCGC	1423
ITGB5	NM_000213.3	ITGB5	TCGTGAAA GATGACCA GGAG	272	GGTGAACAT CATGACGCA GT	656	TGCTATGTTTCTACAAAA CCGCCAAGG	1040	71	TCGTGAAAGATGACCAAGGAGGCTGTGC TATGTTTCTACAAAACCGCCAAAGACT GGCTCATGATGTTCAAC	1424
JAG1	NM_000214.1	JAG1	TGGCTTACA CTGGCAATG G	273	GCATAGCTG TGAGATGCG G	657	ACTCGATTTCACGCCA ACCACAG	1041	69	TGGCTTACACTGGCAATGTFAGTTTCTG TGTTGGCTGGGAAATCGAGTGCCTGCA TCTCACAGCTATGC	1425
JUNB	NM_000229.2	JUNB	CTGTACGCT GCTGCTTGG CGGACTTTG	274	AGGGGGTGT CCGTAAAGG TTACAACCTC	658	CAAGGGACACGCCCTTCT GAAGGT	1042	70	CTGTACGCTGCTGCTTGGGTTCAAGG ACACGCCCTTCTGAACGTCCCTTGCCCT TTACGGACACCCCT	1426
Ki-67	NM_0002417.1	MKI67	GGTGGACT T	275	TTCCACTGG GACGAT	659	CCACTTGTGCAACCACC GCTCGT	1043	80	CGGACTTTGGGTGCGACTTGACGAGCG GTGTTGACAAAGTGGCCTTGGGGCC GGATCGTCCCAGTGGAAAGATGTAA	1427
KIAA0555	NM_014790.3	JAKMIP2	AAGCCCGA GGCACTCAT T	276	TGTCGTGA GCTTGGTCC TG	660	CCCTTCAAGCTGCCAAT GAAGACC	1044	67	AAGCCGAGGCACTCATTTGTGCCCTTC AAGCTGCCAATGAAGACTCAGGACCA AGCTCACAGACA	1428
KIAA1199	NM_018689.1	KIAA1199	GCTGGGAG GCAGGACTT C	277	GAAAGCAGGT CAGAGTGAG CC	661	CTTCAAGGCCATGCTGA CCATCAG	1045	66	GCTGGAGGCGAGGACTTCTCTCTCAAG GCCATGCTGACCACAGCTGGCTCACT CTGACCTGCTTC	1429
KIF14	NM_014875.1	KIF14	GAGCTCCAT GGCTCATCC	278	TCACACCA CTGAATCT ACTG	662	TGCAATTCCTGTGACTCA CTGCTG	1046	69	GAGCTCATGGCTCATCCACAGCAGTG AGCTCAGAGGAATGCACACCCAGTAGG ATTCAGTGGGTGTA	1430
KIF20A	NM_005733.1	KIF20A	TCCTTTGCA GGAAGCCA GA	279	CCGTAGGGC CAATTCAGA C	663	AGTCAGTGGCCCATCAG CAATCAG	1047	67	TCTCTGCAAGGCCAGACAAACAGTC AGTGGCCCATCAGCAATCAGGCTCTGA ATTGGCCCTACCG	1431

TABLE A

KIF2C	NM_006845.2	KIF2C	AAITCTCTGC TCCAAAAG AAAGTCTT	280	CGTGATGCG AAGCTCTGA GA	664	AAGCCGCTCCACTCGCA TGTTCC	1048	73	AAITCTCTGCTCAAAAAGAAAGTCTCTCG AAGCCGCTCCACTCGCATGTCTCACTGTCTC TCAGAGCTTCGCATCACG	1432
KLK11	NM_006853.1	KLK11	CACCCCGGC TTCAACAAC	281	CATCTTCAC CAGCATGAT GTCA	665	CCTCCCAACAAGAGACC ACCGCA	1049	66	CACCCGCTTCAACAACAGCCTCCCC AACAAAGACCCACCCGCAATGACATCATG CTGGTGAAGATG	1433
KLK6	NM_002774.2	KLK6	GACGTGAG GGTCTCTGAT TCT	282	TCCTCACTC ATCACGTCC TC	666	TTACCCAGCTCCATCCT TGCAATC	1050	78	GACGTGAGGTCTCTGATTCCTCCTGGT TTACCCAGCTCATCTCTTGCACTACTG GGGAGACGTGATGATGAGGA	1434
KLRC1	NM_002259.3	KLRC1	CATCTCAT GGATTGGTG TG	283	GCCAAACCA TTCATTGTC AC	667	TTCGTAACAGCAGTCAAT CATCCATGG	1051	67	CATCTCATGGATTGGTGTGTTCTCGTAA CAGCAGTCAATCATCCATGGGTGACAAAT GAATGGTTTGGC	1435
KNSL2	BC000712.1		CCACCTCGC CATGATTTT TC	284	GCAATCTCT TCAAAACACT TCATCTT	668	TTTGACCCGGGTATTCCCA CCAGGAA	1052	77	CCACCTCGCCATGATTTTCTCTTTGACC GGGTATTTCCCAACCAGGAAGTGGACAGG ATGAAGTGTTTGAAGAGATTGC	1436
KNTC2	NM_006101.1	NDC80	ATGTGCCAG TGAGCTTGA GT	285	TGAGCCCT GGTTAACAG TA	669	CCTTGGAGAAACACAAG CACCTGC	1053	71	ATGTGCCAGTGGCTTGAGTCTCTTGGAA GAAACACAAAGCACCTGCTAGAAAGTAC TGTTAAACCAGGGGCTCA	1437
KPNA2	NM_002266.1	KPNA2	TGATGGTCC AAATGAAC GAA	286	AAGCTTCAC AAGTTGGGG C	670	ACTCTGTGTTTTCACCACC ATGCCA	1054	67	TGATGGTCCAAATGAACGAATTTGGCAT GGTGGTGAACACAGGAGTTGTGCCCCA ACTTGTGAAGCTT	1438
L1CAM	NM_000425.2	L1CAM	CTTGCTGGC CAATGCCTA	287	TGATTGTCC GCAGTCAGG	671	ATCTACGTTGTCCAGCTG CCAGCC	1055	66	CTTGCTGGCCAAATGCTACATCTACGTT GTCCAGCTGCCAGCCAAAGATCTGACT GCGGACAAATCA	1439
LAMA3	NM_000227.2	LAMA3	CAGATGAG GCACATGG AGAC	288	TGAAAATGG CAGAACGGT AG	672	CTGAJTCCTCAGGTCTCTT GGCTG	1056	73	CAGATGAGGCACATGGAGACCCAGGCC AAGGACCTTGAGGAATCAGTTGCTCAAC TACCGTCTGCCATTTCAA	1440
LAMA5	NM_005560.3	LAMA5	CTCCTGGCC AACAGCAC T	289	ACACAAAGGC CCAGCCCTCT	673	CTGTTCTGGAGCATGG CCTCTTC	1057	67	CTCCTGGCCAACAGCACTGCCTAGAA GAGGCCATGCTCCAGGAACAGCAGAGG CTGGGCCCTGTGT	1441
LAMB1	NM_002291.1	LAMB1	CAAGGAGA CTGGGAGG TGTC	290	CGGCAGAAC TGACAGTGT TC	674	CAAGTGCCCTGTACCACA CGGAAGG	1058	66	CAAGGAGACTGGGAGGTGTCTCAAGTG CCTGTACCCACACGGAAGGGGAACACTG TCAGTTCTGCCG	1442
LAMB3	NM_000228.1	LAMB3	ACTGACCA AGCTGAG ACCT	291	GTACACACTT GCAGCATTT CA	675	CCACTCGCCATACTGGG TGCACT	1059	67	ACTGACCAAGCCTGAGACCTACTGCAC CCAGTATGGCGAGTGGCAGATGAATG CTGCAAGTGTGAC	1443
LAMC2	NM_005562.1	LAMC2	ACTCAAGC GGAAATG AAGCA	292	ACTCCCTGA AGCCGAGAC ACT	676	AGGTCTTATCAGCACAG TCTCCGCTCC	1060	80	ACTCAAGCGGAAATTTGAAGCAGATAGG TCTTATCAGCACAGTCTCCGCCCTCTGG ATTCAGTGTCTCGGCTTCAGGGAGT	1444
LAPTM4B	NM_018407.4	LAPTM4B	AGCGATGA AGATGGTC GC	293	GACATGGCA GCACAAAGCA	677	CTGGACCGCGTTCTACTC CAACAG	1061	67	AGCGATGAAGATGGTCTCGGCCCTGGAC GCGGTCTACTCCAAACAGCTGCTGCTTG TGCTGCCATGTC	1445

TABLE A

LGALS3	NM_002306.1	LGALS3	AGCGAAA ATGGCAGA CAAT	294	CTTGAGGGT TTGGGTTTC CA	678	ACCCAGATAACGCATCA TGGAGCGA	1062	69	AGCGAAAAATGGCAGACAAATTTTCGC TCCATGATGCGTTATCTGGGTCTGGAA ACCCAAACCCCTCAAG	1446
LMK1	NM_016735.1		GCITCAGGT GTGTGACT GC	295	AAGAGCTGC CCATCCTTCT C	679	TGCTCCTCTGTGCACCA GFACTA	1063	67	GCTTCAGGTGTGTGACTGACAGTGCCTC CCTGTGCGACCACTACTATGAGAAAGGA TGGGCAGCTCTT	1447
LIMS1	NM_004987.3	LIMS1	TGAACAGT AATGGGA GCTG	296	TTCTGGGAA CTGCTGAA G	680	ACTGAGCGCACACGAAA CACTGCT	1064	71	TGAACAGTAATGGGAGCTGTACCATG AGCAGTGTTCGTGTGCGCTCAGTGTCTT CCAGCAGTTCACGAA	1448
LMNB1	NM_005573.1	LMNB1	TGCAAAAG CTGGGTGCA CA	297	CCCCACGAG TTCTGGTTCT TC	681	CAGCCCCCCTAACTGACC TCATC	1065	66	TGCAACGCTGGTGTGCACAGCAGGCC CCCAACTGACCTATCTGGAAGAACCA GAACTCGTGGG	1449
LOX	NM_002317.3	LOX	CCAAATGGG AGAACAAAC GG	298	CGCTGAGGC TGGTACTGT G	682	CAGGCTCAGCAAGCTGA ACACCTG	1066	66	CCAAATGGGAGAACACGCGCAGGTGT CAGCTTCTGAGCTTGGCTCAGCTGTA CCAGCTCAGCG	1450
LRIG1	NM_015541.1		CTGCAACAC CGAAGTGG AC	299	GTCTCTGGA CACAGGCTG G	683	TTACTCCAGGGGACAAG CCTTCCA	1067	67	CTGCAACACGAAAGTGGACTGTACTC CAGGGGACAAGCCTTCCACCCCCAGCC TGTGTCCAGAGAC	1451
LSM1	NM_014462.1	LSM1	AGACCAAG CTGGAAGC AGAG	300	GAGGAATGG AAAGACCTC GG	684	CCTTCAGGGCCTGCACCT TCAACT	1068	66	AGACCAAGCTGGAAGCAGAGAAAGTTG AAAGTGCAGGCCCTGAAGGACCCAGGT CTTTCATTCTC	1452
LTBP1	NM_206943.1	LTBP1	ACATCCAG GGCTCTGTG G	301	GCAGACACA ATGGAAAGA ACC	685	CTGTGTTTAGGCACCTCC CTTGCG	1069	67	ACATCCAGGGCTGTGTGTCGCAAGG GGAGTGCTAAACACAGAGGGTCTTT CCATTGTGTCTG	1453
LYRIC	NM_178812.2	MTDH	GACCTGGCC TTGCTGAAG AGAACTG	302	CGACAGTT TCTTCCGGTT T	686	TTCTCTCTCTGTCTCTCG CTCCGG	1070	67	GACCTGGCTTGTCTGAAGAAATCTCCGG AGCGAGGAACAGAGAGAAAGAACCCG GAAGAACTGTCCG	1454
MAD1L1	NM_003550.1	MAD1L1	TCCTGCAA GAG	303	AGCCGTACC AGCTCAGAC TT	687	CATGTTCTTCAACAATCGC TGCAATC	1071	67	AGAAAGCTTCCCTGCAAGAGCAGGATG CAGCGATTGTGAAGAACATGAAGTCTG AGCTGTACGGCT	1455
MCM2	NM_004526.1	MCM2	GACTTTTGC CCGCTACCT TTC	304	GCCACTAAC TGCTTCAGT ATGAAGAG	688	ACAGCTCATTTGTGTAC GCCGGA	1072	75	GACTTTGCCCGTACCTTTCATTCGGG CGTGACAAACATAGCTGTGTCTTTC ATACTGAAGCAGTTAGTGGC	1456
MELK	NM_014791.1	MELK	AGGATCGC CTGTGAGAA GAG	305	TGCACATAA GCAACAGCA GA	689	CCCGGGTTGTCTTCCGTC AGATAG	1073	70	AGGATCGCTGTCAAGAGAGGAGACCC GGGTGTCTTCCGTCAAGATAGTATCTGC TGTGTCTATGTGCA	1457
MGMT	NM_002412.1	MGMT	GTGAAATG AAACGCAC CACA	306	GACCTGTCT CACAAACCAG AC	690	CAGCCCTTTGGGGAAAGC TGG	1074	69	GTGAAATGAACGCACACACATGGACA GCCCTTTGGGGAAGCTGGAGCTGTCTG GTTGTGAGCAGGGTC	1458
mGSTI	NM_020300.2	MGST1	ACGGATCTA CCACACCAT TGC	307	TCCATATCC AACAAAAA ACTCAAAG	691	TTTGACACCCCTTCCCCA GCCA	1075	79	ACGGATCTACCAACATTCATATTTG ACACCCCTCCACGCCAAATAGAGCT TTGAGTTTTTTGTGGATATGGA	1459

TABLE A

MMP1	NM_002421.2	MMP1	GGGAGATC ATCGGGAC AACTC	308	GGGCTGGT TGAAAAGCA T	692	AGCAAGATTCTCTCCAG GTCCATCAAAAGG	1076	72	GGGAGATCATCGGGACAACTCTCCCTT TGATGGACTGGAGAAATCTTGCTCA TGCTTTCAACAGAGCC	1460
MMP12	NM_002426.1	MMP12	CCAAGCTT GCCAAATCC T	309	ACGGTAGTG ACAGCATCA AAACTC	693	AACAGCTCTCTGTGAC CCCAAAT	1077	78	CCAACGTTGCCAAATCTGACAAATTC AGAACCAGCTCTGTGACCCAAATTT GAGTTTGTGCTGTCACTACCGT	1461
MMP2	NM_004530.1	MMP2	CCATGATGG AGAGGCAG ACA	310	GGAGTCCGT CCTTACCGT CAA	694	CTGGGAGCATGGCGATG GATAACC	1078	86	CCATGATGAGGAGACATCATATGAT CAACTTTGGCCGCTGGGAGCATGGCGA TGGATACCCCTTTGACGGTAAGGACGG ACTCC	1462
MMP7	NM_002423.2	MMP7	GGATGGTA GCAGTCTAG GGATTAACT	311	GGAATGTCC CATACCCAA AGAA	695	CCTGTATGCTGCAACTCA TGAACCTTGGC	1079	79	GGATGGTAGCAGCTAGGGATTAACTT CCTGTATGCTGCAACTCATGAACTTGGC CATTCCTTGGGTATGGGACATTC	1463
MMP8	NM_002424.1	MMP8	TCACCTCTC ATCTTACC AGGAT	312	TGTCACCGT GATCTCTTT GGTAA	696	AAGCAATGTTGATATCT GCCTCTCCCTGTG	1080	79	TCACCTCTCATCTTACCAGGATCTCAC AGGGAGAGGCAGATATCAACAATTTGCTT TTTACCAAGAGATCACGGTGACA	1464
MMTV-like env	AF346816.1		CCATACGTG CTGCTACCT GT	313	CCTAAAAGGT TTGAATGGC AGA	697	TCATCAAAACCATGGTTC ATCACCAATATC	1081	72	CCATACGTGCTGCTACCTGTAGATATTTG GTGATGAACCATGGTTTGATGATCTGTC CATTCAAAACCTTTAGG	1465
MNAT1	NM_002431.1	MNAT1	CGAGAGTCT GTAGGAGG GAAACC	314	GGTTCCGAT ATTGGTGG TCTTAC	698	CGAGGGCAACCTGTATC GTCCA	1082	75	CGAGAGTCTGTAGGAGGAAACCGCCA TGGACGATCAGGGTTGCCCTCGGTGTA AGACCACCAATATCGAAACC	1466
MRP1	NM_004996.2	ABCC1	TCATGGTGC CCGTCAATG	315	CGATTGTCT TTGCTCTTCA TGTG	699	ACCTGATACGTCTTTGGTC TTCATCGCCAT	1083	79	TCATGGTCCCGTCAATGCTGTGATGG CGATGAAGACCAAGACGTATACAGGTGG CCCACATGAAGAGCAAAAGACAATCG	1467
MRP3	NM_003786.2	ABCC3	TCATCTCTG CGATCTACT TCCT	316	CCGTTGAGT GGAATCAGC AA	700	TCTGTCTGGCTGGAGTC GCTTTTCAT	1084	91	TCATCTGGCGATCTACTTCTCTGGCA GAACTAGGTCCCTCTGCTCTGGCTGG AGTCGCTTTCATGGTCTTGTGATTCCA CTCAACGG	1468
MS4A1	NM_021950.2	MS4A1	TGAGAAAC AACTGCA CCCA	317	CAAGGCCCTC AAATCTCAA GG	701	TGAACTCCGACGTAGC ATCCAAA	1085	70	TGAGAAACAAACTGCACCCACTGAACT CCGCAGCTAGCATCCAAATCAGCCCTT GAGATTGAGGCCCTTG	1469
MSH2	NM_000251.1	MSH2	GATGCAGA ATTGAGGC AGAC	318	TCTTGGCAA GTCTGGTTAA GA	702	CAAGAAAGATTACTTCG TCGATTCCAGA	1086	73	GATGCAGAAATTGAGCAGACTTTACAA GAAGATTACTTCTCGTCGATTCCAGATC TTAACCGACTTGCCAAGA	1470
MTA3	XM_038567		GCTCGTGGT TCTGTAGTC CA	319	ACAAAAGGA GAGCGTGAA GT	703	TCAGTCAACATCACCCCTC CTAGGATGA	1087	69	GCTCGTGGTCTGTAGTCCAGTCACTCT AGGAGGGTGATGTTGACTGAGACTTCA CGTCTCCCTTTGT	1471
MX1	NM_002462.2	MX1	GAAGGAAT GGGAATCA GTCAATGA	320	GTCATTATAG AGTCAGATC CGGGACAT	704	TCACCTGGAGATCAGC TCCCGA	1088	78	GAAGGAATGGGAATCAGTCATGAGCTA ATCACCTGGAGATCAGTCCCGAGAT GTCCCGATCTGACTAATAGAC	1472
MYBL2	NM_002466.1	MYBL2	GCCGAGAT CGCCAAGA TG	321	CTTTTGTATG GTAGAGGTTC CAGTGATTTC	705	CAGCAITGTCTGTCTCC CTGGCA	1089	74	GCCGAGATCGCCAAGATGTTGCCAGGG AGGACAGACAATGCTGTGAAGAATCAC TGGAACTCTACCATCAAAAAG	1473

TABLE A

NAT1	NM_000662.4	NAT1	TGGTTTGA GACCAGA TGT	322	TGAATCATG CCAGTGCTG TA	706	TGGAGTGTGTAAACAT ACCCCTCCA	1090	75	TGGTTTGAGACCACGATGTTGGGAGG GTATGTTACAGCACTCCAGCCAAAA ATACAGCACTGGCATGATCA	1474
NAT2	NM_000015.1	NAT2	TAACTGACA TTCCTGAGC ACCAGAT	323	ATGGCTTGC CCACAATGC	707	CGGGCTGTTCCTTTGAG AACCCTAACA	1091	73	TAACTGACATCTTGAGCACCAGATCC GGGCTGTCCCTTTGAGAACCTTAACAT GCATTGTGGCAAGCCAT	1475
NRG1	NM_013957.1	NRG1	CGAGACTCT CCCTCATAGT GAAAAGGTA T	324	CTTGGCGTG TGGAAATCT ACAG	708	ATGACCACCCGGGCTCG TATGTCA	1092	83	CGAGACTCTCTCATAGTGAAAAAGGTAT GTGTACGCCATGACCACCCGGCTCGT ATGTACCTGTAGATTTCCACACGCCA AG	1476
OPN, osteopontin	NM_000582.1	SPP1	CAACCCGAA GTTTTCACCT CCAGTT	325	CCTCAGTCC ATAAACCCAC ACTATCA	709	TCCCCACAGTAGACACA TATGATGGCCG	1093	80	CAACCCGAAATTTTCACTCCAGTTGTCCC CACAGTAGACACATATGATGGCCGAGG TGATAGTGTGTTTATGGACTGAGG	1477
p16-INK4	L27211.1		GGGAAAGG TCCCTCAGA CA	326	TGATGATCT AAGTTTCCC GAGGTT	710	CTCAGAGCCTCTCTGGTT CTTCAATCGG	1094	76	GCGGAAGTCCCTCAGACATCCCGAT TGAAAGAACCCAGAGAGGCTCTGAGAA ACCTCGGAAACTTAGATCATCA	1478
PAI1	NM_000602.1	SERPINE1	CCGCAACGT GGTTTCTC A	327	TGCTGGGTT TCTCCTCCTG TT	711	CTCGGTGTGGCCATGCT CCAG	1095	81	CCGCAACGTGGTTTCTCACCCCTATGGG GTGGCCTCGGTGTGGCCATGCTCCAG CTGACAAAGGAGGAGAAACCCAGCA	1479
PGF	NM_002632.4	PGF	GTGGTTTTC CCTCGGAGC	328	AGCAAGGGA ACAGCCTCA T	712	ATCTTCTCAGACGTCCCG AGCCAG	1096	71	GTGGTTTCTCCCTGGAGCCCTGCTC GGGACGCTGAGAAAGATGCCGGTCAATG AGGCTGTCCCTTGTCT	1480
PR	NM_000926.2	PGR	GCATCAGG CTGTCAATTA TGG	329	AGTAGTTGT GCTGCCCTT CC	713	TGTCCCTTACCTGTGGGAG CTGTAAGGTC	1097	85	GCATCAGCTGTCAATATGGTGTCTTAA CCTGTGGAGCTGTAAAGGTCTTCTTAA GAGGGCAATGGAAGGGCAGCAACAAT ACT	1481
PRDX1	NM_002574.2	PRDX1	AGGACTGG GACCCATG AAC	330	CCCATAATC CTGAGCAAT GG	714	TCCTTTGGTATCAGACCC GAAGCG	1098	67	AGGACTGGGACCCATGAACATTCCTTT GGTATCAGACCCGAAAGCGCACCAATGC TCAGGATTATGGG	1482
PTEN	NM_000314.1	PTEN	TGGCTAAGT GAAGATGA CAATCATG	331	TGCACATAT CATTACACC AGTTCGT	715	CCTTCCAGCTTTACAGT GAATTGCTCA	1099	81	TGGCTAAGTGAAGATGACAAATCATGTT GCAGCAATTCACGTAAAGCTGGAAAG GGACGAACTGGTGAATGATATGTGCA	1483
PTP4A3	NM_007079.2	PTP4A3	AATATTGT GCGGGGTA TGG	332	AACGAGATC CCTGTGCTT GT	716	CCAAGAGAAAACGAGATT TAAAAACCCACC	1100	70	AATATTGTGCGGGGTATGGGGTGGG TTTTTAAATCTCGTTTCTCTTGGACAAG CACAGGATCTCGTT	1484
RhoB	NM_004040.2	RHOB	AAGCATGA ACAGGACTT GACC	333	CCTCCCAA GTACGTTGC	717	CTTTCACACCCCTGGGG AAGACAT	1101	67	AAGCATGAACAGGACTTGACCAATCTTT CCAACCCCTGGGAAAGACATTTGCAAC TGACTTGGGGAGG	1485
RPL13A	NM_012423.2	RPL13A	GCAAGGAA AGGGTCTTA GTCAC	334	ACACCTGCA CAATTCTCC G	718	CCTCCGAAAGTTGCTTGA AAGCAC	1102	68	GCAAGGAAAGGGTCTTAGTCACTGCCT CCCAGAGTTGCTTGAAGACACTCGGAG AATTGTGCAGGTGT	1486
RPL41	NM_021104.1	RPL41	GAAACCTCT GCGCCATG A	335	TTCCTTTGCG CTTCAGCC	719	CATTGCTTCTTCTCTCA CTTGGC	1103	66	GAAACCTCTGCGCATGAGAGCAAGT GGAGGAAGACGAATGCGCAGGCTG AAGCGCAAAAGAA	1487

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RPLPO	NM_001002.2	RPLP0	CCATTCTAT CATCAACG GGTACAA	336	TCAGCAAGT GGGAAGGTG TAAATC	720	TCTCCACAGACAAAGGCC AGGACTCG	1104	75	CCATTCTATCATCAACGGGTACAAACG AGTCTGGCCTTGTCTGTGGAGACGGA TTACACCTTCCACTTGTCTGA	1488
RPS23	NM_001025.1	RPS23	GTCTGGTT GCTGGATT GG	337	CCTTAAAGC GGACTCCAG G	721	ATCACCAACAGCATGAC CTTTGGG	1105	67	GTCTGGTTGCTGGATTGTGTCGCAAG GTCAATGCTGTGGTGATATTCTGGAGT CCGCTTAAAG	1489
RPS27	NM_001030.3	RPS27	TCACCAACGG TCTTTAGCC A	338	TCCTCTCTGT AGGCTGGCA	722	AGGACAGTGGAGCAGCC AACACAC	1106	80	TCACCAACGGTCTTTAGCCATGCACAAA CGGTAGTTTGTGTGTGGCTGCTCCAC TGTCTCTGCCAGCTACAGAGGA	1490
RRM1	NM_001033.1	RRM1	GGGCTACTG GCAGCTAC ATT	339	CTCTCAGCA TCGGTACAA GG	723	CATTGGAAATTGCCATTGA GTCCAGC	1107	66	GGGCTACTGGCAGCTACATTGTCTGGGA CTAATGGCAATTCCCAATGGCTTGTACC GATGCTGAGAG	1491
RRM2	NM_001034.1	RRM2	CAGCGGGA TTAAACAGT CCT	340	ATCTGCGTT GAAAGCAGTG AG	724	CCAGCACAGCCAGTTAA AAGATGCA	1108	71	CAGCGGGAATTAACACAGTCTCTTTAAACCA GCACAGCCAGTTAAAGATGCAGCCTC ACTGCTTCAACGCAGAT	1492
RUNX1	NM_001754.2	RUNX1	AACAGAGA CATTGCCAA CCA	341	GTGATTGTC CCAGGAAAG TTT	725	TTGGATCTGCTTGTGCTGC CAAAACC	1109	69	AACAGAGACATTGCCAACCATATTGGA TCTGCTGTGCTGCCAAACCAAGCAACTT CTGGCAAAATCAC	1493
S100A10	NM_002966.1	S100A10	ACACCAAA ATGCCATCT CAA	342	TTTATCCCT AGCGAATTT GT	726	CAGCCATCGAAACCAT GATGTTT	1110	77	ACACCAAAATGCCATCTTCAAAATGGAAC ACGCCATGGAACCAATGATGTTTACAT TTCACAAATTCGTGGGATAAA	1494
S100A2	NM_005978.2	S100A2	TGGCTGTGC TGGTCACTA CCT	343	TCCCCCTTA CTCAGCTTG AACT	727	CACAAGTACTTCTGCCA AGAGGGGAC	1111	73	TGGCTGTGCTGCTACTCTTCCACAA GTACTCTGCCAAGAGGGCGCAAGTT CAAGCTGAGTAAGGGGA	1495
S100A4	NM_002961.2	S100A4	GACTGCTGT CATGGCGTG CCT	344	CGAGTACTT GTGGAAGGT GGAC	728	ATCACATCCAGGGCCTT CTCCAGA	1112	70	GACTGCTGCTATGGGTGCCCTCTGGA GAAGCCCTGGATGTGATGGTGTCCAC CTTCCACAAGTACTCG	1496
S100A7	NM_002963.2	S100A7	CCTGCTGAC GATGATGA AGGA	345	GCGAGGTAA TTTGTGCCCT TT	729	TTCCCAACTTCTCTTAGT GCCTGTGACA	1113	75	CCTGCTGACGATGATGAAGGAGAACTT CCCCAACTTCTTAGTGTGACAAA AAGGGCACAAATTAACCTGC	1497
S100A8	NM_002964.3	S100A8	ACTCCCTGA TAAAGGGG AATTT	346	TGAGGACAC TCGGTCTCT AGC	730	CATGCCGTCTACAGGGA TGACCTG	1114	76	ACTCCCTGATAAAGGGGAATTTCCATG CCGTCTACAGGGATGACCTGAAGAAAT TGCTAGAGACCGAGTGTCTCTCA	1498
S100A9	NM_002965.3	S100A9	CACCTGCC TCTACCCAA C	347	CTAGCCCCA CAGCCAAGA	731	CCCGGGGCTTGTATGTC AAACT	1115	67	CACCTGCTCTTACCCAACCAAGGGGCC CGGGGCTGTATTGTCAAACTGTCTTGG CTGTGGGCTAG	1499
S100B	NM_006272.1	S100B	CATGGCCGT GTAGACCCCT AA	348	AGTTTTAAG GGTGCCCG GAGACTTTG	732	CCGGAGGGAACCCCTGAC TACAGAA	1116	70	CATGGCCGTGTAGACCCCTAACCCGGAG GGAACCCCTGACTACAGAAATTAACCCCG GGGCACCTTAAACT	1500
S100G	NM_004057.2	S100G	ACCTGAGC ACTGGAGG AA	349	GAGACTTTG GGGATTCC A	733	AGGATAAGACCACAGCA CAGGCGC	1117	67	ACCTGAGCAGTGGAGGAAAGCGCCT GTGCTGTGGTCTTATCTCTATGTGGAATC CCCCAAAGTCTC	1501

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S100P	NM_005980.2	S100P	AGACAAGG ATGCCGTGG ATAA	350	GAAGTCCAC CTGGGCATC TC	734	TTGTCAAGGACCTGGA CGCCAA	1118	67	AGACAAGGATGCCGTGGATAAATTTGCT CAAGGACCTGGACGCCAATGGAGATGC CCAGGTGGACTTC	1502
SDHA	NM_004168.1	SDHA	GCAGAACT GAAGATGG GAAGAT	351	CCCTTTCCA AACTTGAGG C	735	CTGTCCACCAAAATGCAC GCTGATA	1119	67	GCAGAACTGAAGATGGGAAGATTATC AGCGTGCATTTGGTGGACAGAGCCTCA AGTTTGGAAAGG	1503
SEMA3F	NM_004186.1	SEMA3F	CGCGAGGC CCCTCAITAT ACA	352	CACTCGCCG TTGACATCC T	736	CTCCCCACAGCGCATCG AGGAA	1120	86	CGGAGCCCTCAITATACACTGGGCA GCCTCCCCACAGCATCGAGGAATGC GTGCTCTCAGGCAAGGATGTCAACGGC GAGTG	1504
SFRP2	NM_003013.2	SFRP2	CAAGCTGA ACGGTGTGT CC	353	TGCAAGCTG TCTTTGAGC C	737	CAGCACCGATTCTCTCAG GTCCCT	1121	66	CAAGCTGAACGGTGTCTCCGAAAGGGA CCTGAAGAAATCGGTGCTGTGGCTCAA AGACAGCTGCA	1505
SIR2	NM_012238.3	SIRT1	AGCTGGGG TGTCGTGTT CAT	354	ACAGCAAGG CGAGCATAA AT	738	CCTGACTTCAGGTCAAG GGATGG	1122	72	AGCTGGGGTGTCTGTTTCATGTGGAAAT ACCTGACTTCAGGTCAAGGGATGGTAT TTATGCTCGCTGTGCTGT	1506
SKIL	NM_005414.2	SKIL	AGAGGCTG AATATGCA GGACA	355	CTATCGGCC TCAGCATGG TC	739	CCAAATCTCTGCCTCAGTT CTGCCA	1123	66	AGAGGCTGAATATGACGGACACAGTTGGC AGAAGTGAAGCAGAGATTGGACCATGC TGAGGCCGATAG	1507
SKP2	NM_005983.2	SKP2	AGTTGCAG AATCTAAGC CTGGAA	356	TGAGTTTITT GCGAGAGTA TTGACA	740	CCTGGGCTTTTCGGATCC CA	1124	71	AGTTGCAGAACTAAGCTGGAAGGCC TGCGGCTTTCGGATCCCATTTGTCAATAC TCTGCCAAAAACTCA	1508
SLPI	NM_003064.2	SLPI	ATGGCCAAAT GTTTGATGC T	357	ACACTTCAA GTACACGCTT GC	741	TGGCCATCCATCTCACA GAAATTGG	1125	74	ATGGCCAAATGTTTGATGCTTTAACCCCCC CAATTTCTGTGAGATGGATGGCCAGTG CAAGCGTACTTGAAGTGT	1509
SNAIL	NM_005985.2	SNAIL	CCCAATCGG AAGCTAA CTA	358	GTAGGGCTG CTGGAAGGT AA	742	TCTGGATTAGAGTCTGTC AGCTCGC	1126	69	CCCAATCGGAAGCCTAACTACAGCGAG CTGCAGGACTCTAATCCAGAGTTTACCT TCCAGCAGCCCTAC	1510
STK15	NM_003600.1	AURKA	CATCTTCCA GGAGGACC ACT	359	TCCGACCTT CAATCAITTT CA	743	CTCTGTGGCACCCCTGGA CTACCTG	1127	69	CATCTCCAGGAGGACACACTCTCTGTG GCACCCCTGGACTACTGCCCCCTGAAA TGATTGAAGGTCGGA	1511
STMN1	NM_005563.2	STMN1	AATACCCA ACGCACAA ATGA	360	GGAGACAAT GCAAAACCAC AC	744	CAGTTCTCTGCCCCGTT TCTTG	1128	71	AATACCCAACGCACAAATGACCGCACG TTCTCTGCCCGTTTCTTGCCCCAGTGT GGTTTGCATTGTCTCC	1512
STMY3	NM_005940.2	MMP11	CCTGGAGG CTGCAACAT ACC	361	TACAAATGGC TTTGAGGA TAGCA	745	ATCCTCTGAAAGCCCTTT TCGCAGC	1129	90	CCTGGAGCTGCAACATACCTCAATCC TGTCCCAGGCCGATCTCTCTGAAGCC CTTTTCGCAGCACTGCTATCTCCAAAG CCATTGTA	1513
SURV	NM_001168.1	BIRC5	TGTTTTGAT TCCCGGGCT TA	362	CAAAAGCTGT CAGCTCTAG CAAAAG	746	TGCCTTCTTCTCCCTCA CTTCTCACT	1130	80	TGTTTGTATTTCCGGGCTTACCAGGTGA GAAAGTGTGTGATGTGGGAAGCATTTCT CCCTTTGTAGAGCTGACAGCTTTG	1514
SYK	NM_003177.1	SYK	TCCTCAGCA AAAGCGAT GTCT	363	TTCAATCCCTC GATATGGCT TCT	747	CCATAGGAGAATGCTTC CCACATCAACT	1131	85	TCTCCAGCAAAAGCGATGTCTGGAGCT TTGGAGTGTGTGATGTGGGAAGCATTTCT CCTATGGCAGAAAGCATATATCAGGGA TGAA	1515

TABLE A

TAGLN	NM_003186.2	TAGLN	GATGGAGC AGGTGGCTC AGT	748	CCCATAGTCTCAGCCG CCTTCAG	1132	73	GATGGAGCAGTGGCTCAGTTCCTGAA GGCGGCTGAGGACTCTGGGGTTCATCAA GACTGACATGTTCCAGACT	1516
TCEAI	NM_201437.1	TCEAI	CAGCCCTGA GGCAAGAG A	749	CTTCCAGCGCAATGTGA AGCAACA	1133	72	CAGCCCTGAGGCAAGAGAAAAGTA CTTCCAGCGCAATGTAAAGCAACAGAA AGGATGAGACAAATGCTCG	1517
TFRC	NM_003234.1	TFRC	GCCAACTGC TTTCAATTG TG	750	AGGGATCTGAACCAATA CAGAGCAGACA	1134	68	GCCAACTGCTTTTCATTTCTGTGAGGGATCT GAACCAATACAGAGACACATAAAGG AAATGGGCTGAGT	1518
TGFB2	NM_003238.1	TGFB2	ACCAGTCCC CCAGAAAGA CTA	751	TCCTGAGCCCGAGGAAG TCCC	1135	75	ACCAGTCCCCAGAGAGACTATCTGTAG CCCGAGGAAGTCCCCCGGAGGTGATT TCCATCTACAACAGCACAGG	1519
TGFB3	NM_003239.1	TGFB3	GGATCGAG CTCTCCAG ATCCT	752	CGGCCAGATGAGCACAT TGCC	1136	65	GGATCGAGCTCTTCCAGATCTTTCGGCC AGATGAGCACATTGCCAAACAGCGCTA TATCGGTGGC	1520
TGFB2	NM_003242.2	TGFB2	AACACCAA TGGGTTCCT TCT	753	TTCTGGGCTCCTGATTGC TCAAGC	1137	66	AACACCAATGGGTTCATCTTCTGGGC TCCTGATTGCTCAAGCACAGTTTGGCCT GATGAAGAG	1521
TIMP3	NM_000362.2	TIMP3	CTACCTGCC TTGCTTTGT GA	754	CCAAGAACGAGTGTCTC TGGACCG	1138	67	CTACCTGCCCTTGGTTTGTGACTTCCAAG AACGAGTGTCTCTGGACCGACATGCTC TCCAATTTCGGT	1522
TNFRSF1 A	NM_003839.2	TNFRSF1 A	CCAGCCAC AGACAGTT A	755	TGTTCTCTACTGAGCCTG GAAGCA	1139	67	CCAGCCACAGACCAGTACTGTCTCTC ACTGAGCCTGGAAGCAATCCACACCT CCTTCTCTGAA	1523
TNFRSF1 B	NM_002546.2	TNFRSF1 B	TGGCGACC AAGACACC TT	756	AGGGCCTAATGCACGCA CTAAAGC	1140	67	TGGCGACAAGACACACTTGAAGGGCCT AATGCACGCACATAAGCACCTCAAAGAC GTACCACCTTCCC	1524
TNFSF1	NM_003701.2	TNFSF1	CATATCGTT GGATCACA GCAC	757	TCCACCATCGCTTTCTCT GCTCTG	1141	71	CATATCGTTGGATCAGACACATCAGA GCAGAGAAAGGATGGTGGATGGCTCA TGGTAGATCTGGCCAA	1525
TWIST1	NM_000474.2	TWIST1	GCCTGCG GAAGATCA TC	758	CCACGCTGCCCTCGGAC AAGC	1142	64	GCCTGCGGAAGATCATCCCCAGGCTG CCCTCGACAAGCTGAGCAAGATTGAG ACCTCAAGC	1526

TABLE A

UBB	NM_018955.1	UBB	GAGTCGAC CCTGCACCT G	375		759	1143	522	1527
VCAM1	NM_001078.2	VCAM1	TGGCTTCAG GAGCTGAA TACC	376	GCGAATGCC ATGACTGAA	760	1144	89	1528
VIM	NM_003380.1	VIM	TGCCCTTAA AGGAACCA ATGA	377	TGCTGTCTGT GATGAGAAA ATAGTG	761	1145	72	1529
VTN	NM_000638.2	VTN	AGTCAA1CT TCGCACAG G	378	GC1TCAACG GCAAGTTC TCTT	762	1146	67	1530
WAVE3	NM_006646.4	WASF3	CTCTCCAGT GTGGGCAC C	379	GCGGTGTAG CTCCACAG T	763	1147	68	1531
WISPI	NM_003882.2	WISPI	AGAGGCAT CCATGAACT TCACA	380	CAAACTCCA CAGTACTTG GGTTGA	764	1148	75	1532
Wnt-5a	NM_003392.2	WNT5A	GTATCAGG ACCACATGC AGTACATC	381	TGTCGGAAT TGATACTGG CA1T	765	1149	75	1533
Wnt-5b	NM_032642.2	WNT5B	TGTCTTCAG GGTCTTGTC CA	382	GTGCACGTG GATGAAAGA GT	766	1150	79	1534
WWOX	NM_016373.1	WWOX	ATCGCAGCT GGTGGGTGT AC	383	AGCTCCCTG TTGCATGGA CTT	767	1151	74	1535

TABLE A

YWHAZ	NM_003406.2	YWHAZ	GTGGACATC GGATACCC AAG	384	GCAGACAAA AGTTGGAAG GC	768	CCCCTCCTTCTCCTGCTT CAGCTT	1152	81	GTGGACATCGGATACCCAAGGAGACGA AGCTGAAGCAGGAGAAAGGAGGGGAAA ATTAAACCGGCCTTCCAACTTTTGTCTGC	1536

Table 1: Cox proportional hazards for Prognostic Genes that are positively associated with good prognosis for breast cancer (Providence study)

Table 1			
Gene_all	z (Coef)	HR	p (Wald)
GSTM2	-4.306	0.525	0.000
IL6ST	-3.730	0.522	0.000
CEGP1	-3.712	0.756	0.000
Bcl2	-3.664	0.555	0.000
GSTM1	-3.573	0.679	0.000
ERBB4	-3.504	0.767	0.000
GADD45	-3.495	0.601	0.000
PR	-3.474	0.759	0.001
GPR30	-3.348	0.660	0.001
CAV1	-3.344	0.649	0.001
C10orf116	-3.194	0.681	0.001
DR5	-3.102	0.543	0.002
DICER1	-3.097	0.296	0.002
EstR1	-2.983	0.825	0.003
BTRC	-2.976	0.639	0.003
GSTM3	-2.931	0.722	0.003
GATA3	-2.874	0.745	0.004
DLC1	-2.858	0.564	0.004
CXCL14	-2.804	0.693	0.005
IL17RB	-2.796	0.744	0.005
C8orf4	-2.786	0.699	0.005
FOXO3A	-2.786	0.617	0.005
TNFRSF11B	-2.690	0.739	0.007
BAG1	-2.675	0.451	0.008
SNAI1	-2.632	0.692	0.009
TGFB3	-2.617	0.623	0.009
NAT1	-2.576	0.820	0.010
FUS	-2.543	0.376	0.011
F3	-2.527	0.705	0.012
GSTM2 gene	-2.461	0.668	0.014
EPHB2	-2.451	0.708	0.014
LAMA3	-2.448	0.778	0.014
BAD	-2.425	0.506	0.015
IGF1R	-2.378	0.712	0.017
RUNX1	-2.356	0.511	0.018
ESRRG	-2.289	0.825	0.022
HSHN1	-2.275	0.371	0.023
CXCL12	-2.151	0.623	0.031
IGFBP7	-2.137	0.489	0.033
SKIL	-2.121	0.593	0.034
PTEN	-2.110	0.449	0.035
AKT3	-2.104	0.665	0.035
MGMT	-2.060	0.571	0.039
LRIG1	-2.054	0.649	0.040
S100B	-2.024	0.798	0.043
GREB1 variant a	-1.996	0.833	0.046
CSF1	-1.976	0.624	0.048
ABR	-1.973	0.575	0.048
AK055699	-1.972	0.790	0.049

Table 2: Cox proportional hazards for Prognostic Genes that are negatively associated with good prognosis for breast cancer (Providence study)

Table 2			
Gene_all	z (Coef)	HR	p (Wald)
S100A7	1.965	1.100	0.049
MCM2	1.999	1.424	0.046
Contig 51037	2.063	1.185	0.039
S100P	2.066	1.170	0.039
ACTR2	2.119	2.553	0.034
MYBL2	2.158	1.295	0.031
DUSP1	2.166	1.330	0.030
HOXB13	2.192	1.206	0.028
SURV	2.216	1.329	0.027
MELK	2.234	1.336	0.026
HSPA8	2.240	2.651	0.025
cdc25A	2.314	1.478	0.021
C20_orf1	2.336	1.497	0.019
LMNB1	2.387	1.682	0.017
S100A9	2.412	1.185	0.016
CENPA	2.419	1.366	0.016
CDC25C	2.437	1.384	0.015
GAPDH	2.498	1.936	0.012
KNTC2	2.512	1.450	0.012
PRDX1	2.540	2.131	0.011
RRM2	2.547	1.439	0.011
ADM	2.590	1.445	0.010
ARF1	2.634	2.973	0.008
E2F1	2.716	1.486	0.007
TFRC	2.720	1.915	0.007
STK15	2.870	1.860	0.004
LAPTM4B	2.880	1.538	0.004
EpCAM	2.909	1.919	0.004
ENO1	2.958	2.232	0.003
CCNB1	3.003	1.738	0.003
BUB1	3.018	1.590	0.003
Claudin 4	3.034	2.151	0.002
CDC20	3.056	1.555	0.002
Ki-67	3.329	1.717	0.001
KPNA2	3.523	1.722	0.000
IDH2	3.994	1.638	0.000

Table 3: Cox proportional hazards for Prognostic Genes that are positively associated with good prognosis for ER-negative (ER0) breast cancer (Providence study)

Gene_ER0	HR	z (Coef)	p (Wald)
SYK	0.185	-2.991	0.003
Wnt-5a	0.443	-2.842	0.005
WISP1	0.455	-2.659	0.008
CYR61	0.405	-2.484	0.013
GADD45	0.520	-2.474	0.013
TAGLN	0.364	-2.376	0.018
TGFB3	0.465	-2.356	0.018
INHBA	0.610	-2.255	0.024
CDH11	0.584	-2.253	0.024
CHAF1B	0.551	-2.113	0.035
ITGAV	0.192	-2.101	0.036
SNAI1	0.655	-2.077	0.038
IL11	0.624	-2.026	0.043
KIAA1199	0.692	-2.005	0.045
TNFRSF11B	0.659	-1.989	0.047

Table 4: Cox proportional hazards for Prognostic Genes that are negatively associated with good prognosis for ER-negative (ER0) breast cancer (Providence study)

Gene_ER0	HR	z (Coef)	p (Wald)
RPL41	3.547	2.062	0.039
Claudin 4	2.883	2.117	0.034
LYRIC	4.029	2.364	0.018
TFRC	3.223	2.596	0.009
VTN	2.484	3.205	0.001

Table 5: Cox proportional hazards for Prognostic Genes that are positively associated with good prognosis for ER-positive (ER1) breast cancer (Providence study)

Gene_ER1	HR	z (Coef)	p (Wald)
DR5	0.428	-3.478	0.001
GSTM2	0.526	-3.173	0.002
HSHIN1	0.175	-3.031	0.002
ESRRG	0.736	-3.028	0.003
VTN	0.622	-2.935	0.003
Bcl2	0.469	-2.833	0.005
ERBB4	0.705	-2.802	0.005
GPR30	0.625	-2.794	0.005
BAG1	0.339	-2.733	0.006
CAV1	0.635	-2.644	0.008
IL6ST	0.503	-2.551	0.011
C10orf116	0.679	-2.497	0.013
FOXO3A	0.607	-2.473	0.013
DICER1	0.311	-2.354	0.019
GADD45	0.645	-2.338	0.019
CSF1	0.500	-2.312	0.021
F3	0.677	-2.300	0.021
GBP2	0.604	-2.294	0.022
APEX-1	0.234	-2.253	0.024
FUS	0.322	-2.252	0.024
BBC3	0.581	-2.248	0.025
GSTM3	0.737	-2.203	0.028
ITGA4	0.620	-2.161	0.031
EPHB2	0.685	-2.128	0.033
IRF1	0.708	-2.105	0.035
CRYZ	0.593	-2.103	0.035
CCL19	0.773	-2.076	0.038
SKIL	0.540	-2.019	0.043
MRP1	0.515	-1.964	0.050

Table 6: Cox proportional hazards for Prognostic Genes that are negatively associated with good prognosis for ER-positive (ER1) breast cancer (Providence study)

Gene_ER1	HR	z (Coef)	p (Wald)
CTHRC1	2.083	1.958	0.050
RRM2	1.450	1.978	0.048
BUB1	1.467	1.988	0.047
LMNB1	1.764	2.009	0.045
SURV	1.380	2.013	0.044
EpCAM	1.966	2.076	0.038
CDC20	1.504	2.081	0.037
GAPDH	2.405	2.126	0.033
STK15	1.796	2.178	0.029
HSPA8	3.095	2.215	0.027
LAPTM4B	1.503	2.278	0.023
MCM2	1.872	2.370	0.018
CDC25C	1.485	2.423	0.015
ADM	1.695	2.486	0.013
MMP1	1.365	2.522	0.012
CCNB1	1.893	2.646	0.008
Ki-67	1.697	2.649	0.008
E2F1	1.662	2.689	0.007
KPNA2	1.683	2.701	0.007
DUSP1	1.573	2.824	0.005
GDF15	1.440	2.896	0.004

Table 7: Cox proportional hazards for Prognostic Genes that are positively associated with good prognosis for breast cancer (Rush study)

Gene_all	z (Coef)	HR	p (Wald)
GSTM2	-3.275	0.752	0.001
GSTM1	-2.946	0.772	0.003
C8orf4	-2.639	0.793	0.008
ELF3	-2.478	0.769	0.013
RUNX1	-2.388	0.609	0.017
IL6ST	-2.350	0.738	0.019
AAMP	-2.325	0.715	0.020
PR	-2.266	0.887	0.023
FHIT	-2.193	0.790	0.028
CD44v6	-2.191	0.754	0.028
GREB1 variant c	-2.120	0.874	0.034
ADAM17	-2.101	0.686	0.036
EstR1	-2.084	0.919	0.037
NAT1	-2.081	0.878	0.037
TNFRSF11B	-2.074	0.843	0.038
ITGB4	-2.006	0.740	0.045
CSF1	-1.963	0.750	0.050

Table 8: Cox proportional hazards for Prognostic Genes that are negatively associated with good prognosis for breast cancer (Rush study)

Gene_all	z (Coef)	HR	p (Wald)
STK15	1.968	1.298	0.049
TFRC	2.049	1.399	0.040
ITGB1	2.071	1.812	0.038
ITGAV	2.081	1.922	0.037
MYBL2	2.089	1.205	0.037
MRP3	2.092	1.165	0.036
SKP2	2.143	1.379	0.032
LMNB1	2.155	1.357	0.031
ALCAM	2.234	1.282	0.025
COMT	2.271	1.412	0.023
CDC20	2.300	1.253	0.021
GAPDH	2.307	1.572	0.021
GRB7	2.340	1.205	0.019
S100A9	2.374	1.120	0.018
S100A7	2.374	1.092	0.018
HER2	2.425	1.210	0.015
ACTR2	2.499	1.788	0.012
S100A8	2.745	1.144	0.006
ENO1	2.752	1.687	0.006
MMP1	2.758	1.212	0.006
LAPTM4B	2.775	1.375	0.006
FGFR4	3.005	1.215	0.003
C17orf37	3.260	1.387	0.001

Table 9: Cox proportional hazards for Prognostic Genes that are positively associated with good prognosis for ER-negative (ER0) breast cancer (Rush study)

Gene_ER0	z (Coef)	HR	p (Wald)
SEMA3F	-2.465	0.503	0.014
LAMA3	-2.461	0.519	0.014
CD44E	-2.418	0.719	0.016
AD024	-2.256	0.617	0.024
LAMB3	-2.237	0.690	0.025
Ki-67	-2.209	0.650	0.027
MMP7	-2.208	0.768	0.027
GREB1 variant c	-2.019	0.693	0.044
ITGB4	-1.996	0.657	0.046
CRYZ	-1.976	0.662	0.048
CD44s	-1.967	0.650	0.049

Table 10: Cox proportional hazards for Prognostic Genes that are negatively associated with good prognosis for ER-negative (ER0) breast cancer (Rush study)

Gene_ER0	z (Coef)	HR	p (Wald)
S100A8	1.972	1.212	0.049
EEF1A2	2.031	1.195	0.042
TAGLN	2.072	2.027	0.038
GRB7	2.086	1.231	0.037
HER2	2.124	1.232	0.034
ITGAV	2.217	3.258	0.027
CDH11	2.237	2.728	0.025
COL1A1	2.279	2.141	0.023
C17orf37	2.319	1.329	0.020
COL1A2	2.336	2.577	0.020
ITGB5	2.375	3.236	0.018
ITGA5	2.422	2.680	0.015
RPL41	2.428	6.665	0.015
ALCAM	2.470	1.414	0.013
CTHRC1	2.687	3.454	0.007
PTEN	2.692	8.706	0.007
FN1	2.833	2.206	0.005

Table 11: Cox proportional hazards for Prognostic Genes that are positively associated with good prognosis for ER-positive (ER1) breast cancer (Rush study)

Gene_ER1	z (Coef)	HR	p (Wald)
GSTM1	-3.938	0.628	0.000
HNF3A	-3.220	0.500	0.001
EstR1	-3.165	0.643	0.002
Bcl2	-2.964	0.583	0.003
GATA3	-2.641	0.624	0.008
ELF3	-2.579	0.741	0.010
C8orf4	-2.451	0.730	0.014
GSTM2	-2.416	0.774	0.016
PR	-2.416	0.833	0.016
RUNX1	-2.355	0.537	0.019
CSF1	-2.261	0.662	0.024
IL6ST	-2.239	0.627	0.025
AAMP	-2.046	0.704	0.041
TNFRSF11B	-2.028	0.806	0.043
NAT1	-2.025	0.833	0.043
ADAM17	-1.981	0.642	0.048

Table 12: Cox proportional hazards for Prognostic Genes that are negatively associated with good prognosis for ER-positive (ER1) breast cancer (Rush study)

Gene_ER1	z (Coef)	HR	p (Wald)
HSPA1B	1.966	1.382	0.049
AD024	1.967	1.266	0.049
FGFR4	1.991	1.175	0.047
CDK4	2.014	1.576	0.044
ITGB1	2.021	2.163	0.043
EPHB2	2.121	1.342	0.034
LYRIC	2.139	1.583	0.032
MYBL2	2.174	1.273	0.030
PGF	2.176	1.439	0.030
EZH2	2.199	1.390	0.028
HSPA1A	2.209	1.452	0.027
RPLPO	2.273	2.824	0.023
LMNB1	2.322	1.529	0.020
IL-8	2.404	1.166	0.016
C6orf66	2.468	1.803	0.014
GAPDH	2.489	1.950	0.013
P16-INK4	2.490	1.541	0.013
CLIC1	2.557	2.745	0.011
ENO1	2.719	2.455	0.007
ACTR2	2.878	2.543	0.004
CDC20	2.931	1.452	0.003
SKP2	2.952	1.916	0.003
LAPTM4B	3.124	1.558	0.002

Table 13: Validation of Prognostic Genes in SIB data sets.

Table 13 Official Symbol	EMC2 -Est	EMC2-SE	EMC2-t	JRH1-SE	JRH1-t	JRH2-SE	JRH2-t	MGH-SE	MGH-t	NCH-SE	NCH-t	NKI-SE	NKI-t	NKI-SE	NKI-t
AAMP	NA	NA	NA	-0.05212	-0.10291	0.105615	1.01216	0.620209	-0.43441	0.088826	0.283082	0.312939	0.228446	1.36986	
ABCC1	NA	NA	NA	NA	NA	2.36153	0.76485	0.284341	0.891591	0.213191	0.154486	0.380002	0.094607	0.258279	0.366298
ABCC3	NA	NA	NA	0.386945	0.767255	0.305901	0.544322	0.221759	0.572162	-0.00756	0.167393	-0.04517	0.06613	0.096544	0.684974
ABR	NA	NA	NA	0.431151	0.817818	0.758422	1.0123	NA	NA	NA	NA	-0.06114	0.095839	-0.63795	
ACTR2	NA	NA	NA	NA	NA	-0.26297	0.4774	0.205648	0.349398	0.131215	0.267434	0.490644	0.539449	0.254409	2.120401
ADAM17	NA	NA	NA	0.078212	0.564555	-0.20948	1.06045	0.435924	0.681266	-0.18523	0.407965	-0.45402	0.068689	0.12741	0.539115
ADM	NA	NA	NA	NA	NA	0.320052	0.201407	0.142364	1.582732	0.314064	0.201161	1.561257	0.264131	0.06376	4.142582
LYPD6	NA	NA	NA	NA	NA	NA	NA	0.120883	-3.17855	-0.23802	0.209786	-1.1346	-0.4485	0.106865	-4.19691
AKT3	NA	NA	NA	NA	NA	-2.10931	1.58606	0.576851	-2.48154	0.181912	0.147743	0.149731	0.140716	1.064065	
ALCAM	NA	NA	NA	-0.17112	0.224449	-0.7624	0.120168	0.239833	-1.51888	0.002712	0.084499	0.032094	-0.3019	0.094459	-3.19609
APEX1	NA	NA	NA	0.068917	0.410873	0.167732	-0.02247	0.181782	-0.42215	-0.00097	0.268651	-0.00361	-0.13398	0.232019	-0.57746
ARF1	NA	NA	NA	0.839013	0.346692	0.369609	0.40789	0.804729	2.534493	-0.15337	0.204529	-0.74984	0.944168	0.204641	4.613777
AURKA	NA	NA	NA	0.488329	0.248241	1.967157	0.285095	0.169472	1.593732	-0.07663	0.213247	-0.35934	0.643963	0.101097	6.369754
BAD	NA	NA	NA	0.027049	0.547028	0.049446	0.121904	0.587599	0.207461	0.38364	0.389915	0.983907	0.149641	0.221188	0.676533
BAG1	NA	NA	NA	0.505074	0.709869	0.711503	-0.13983	0.36181	-0.38648	-0.36295	0.282963	-1.28267	-0.58733	-0.41603	0.138093
BBC3	NA	NA	NA	NA	NA	0.182425	0.78708	NA	NA	0.056993	0.249671	0.228274	-0.5633	0.158825	-3.54669
BCAR3	NA	NA	NA	NA	NA	-0.29238	0.522706	0.216837	-1.91825	0.072246	0.304443	-0.26067	0.114992	-2.26685	
BCL2	NA	NA	NA	-1.10678	0.544697	-2.03192	0.124104	1.23296	-2.00629	NA	NA	NA	0.30738	0.079518	-3.86557
BIRC5	NA	NA	NA	-0.40529	0.608667	0.319899	0.242736	NA	NA	0.268836	0.122325	2.197719	0.390779	0.069127	5.6531
BTRC	NA	NA	NA	NA	NA	0.017988	0.648834	NA	NA	-0.63958	0.485936	-1.31618	-0.52394	0.139699	-3.75051
BUB1	NA	NA	NA	0.84036	0.319874	2.627159	0.565139	0.268687	0.769133	0.104644	0.142318	0.735283	0.426611	0.094852	4.49763
C10orf116	NA	NA	NA	-0.1418	0.261554	-0.54216	0.036378	NA	NA	0.064337	0.14087	0.456713	-0.22589	0.082836	-2.72696
C17orf37	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.1532	0.294177	0.520775	NA	NA	NA
TPX2	NA	NA	NA	NA	NA	0.311175	0.271756	NA	NA	-0.01014	0.317222	-0.03198	0.336914	0.116472	4.609812
C8orf4	NA	NA	NA	NA	NA	-0.06402	0.197663	0.106335	-0.66236	-0.03221	0.189009	-0.1704	-0.3396	0.083273	-4.07813
CAV1	NA	NA	NA	-0.20701	0.254401	-0.81372	-0.19588	0.2269	-0.30391	0.078825	0.340843	0.231265	-0.30885	0.133788	-2.30848
CCL19	NA	NA	NA	0.101779	0.483649	0.21044	-0.45509	0.246585	1.606752	0.024132	0.130045	0.185564	-0.08897	0.087102	-1.02143
CCNB1	NA	NA	NA	0.14169	0.276165	0.513063	0.587021	NA	NA	-0.02016	0.230327	-0.08751	0.495483	0.10424	4.75329
CDC20	NA	NA	NA	-0.82502	0.360648	-2.2876	0.075789	0.198727	0.478159	0.482934	0.216025	2.235547	0.35587	0.125008	2.846778
CDC25A	NA	NA	NA	-0.15046	0.724766	-0.2076	0.358589	0.227966	1.12773	0.078265	0.111013	0.705008	0.48387	0.105238	4.597864
CDC25C	NA	NA	NA	0.047781	0.511454	0.093422	1.07486	0.240266	1.418769	-0.22371	0.269481	-0.83013	0.287063	0.136568	2.101979
CDH11	NA	NA	NA	-0.55211	0.469473	-1.17601	0.072308	0.190053	0.141931	-0.0883	0.124418	-0.70971	-0.13223	0.097541	-1.35564
CDK4	NA	NA	NA	NA	NA	0.759572	0.757398	0.129757	1.423276	0.304045	0.17456	1.741779	0.267465	0.148641	1.799403

Table 13 Official Symbol	EMC2 -Est	EMC2-SE	EMC2-t	JRH1-Est	JRH1-SE	JRH1-t	JRH2-Est	JRH2-SE	JRH2-t	MGH-Est	MGH-SE	MGH-t	NCH-Est	NCH-SE	NCH-t	NKI-Est	NKI-SE	NKI-t
SCUBF2	NA	NA	NA	NA	NA	NA	-0.0454	0.120869	-0.37564	NA	NA	NA	-0.01783	0.063429	-0.28108	-0.24635	0.048622	-5.0667
CENPA	NA	NA	NA	NA	NA	NA	0.296857	0.253493	1.171066	NA	NA	NA	0.225878	0.249928	0.903772	0.467131	0.081581	5.726013
CHAF1B	NA	NA	NA	0.591417	0.58528	1.010486	0.284056	0.637446	0.445616	0.47534	0.323193	1.470762	0.233081	0.291389	0.799896	0.519868	0.125204	4.152168
CLDN4	NA	NA	NA	-0.54144	0.470758	-1.15014	0.33033	0.351865	0.938798	0.185116	0.314723	0.588187	-0.23129	0.426627	-0.54213	0.564756	0.210595	2.681716
CLIC1	NA	NA	NA	0.678131	0.359483	1.886406	0.764626	0.767633	0.996083	0.171995	0.821392	0.209395	-0.05548	0.414451	-0.13385	0.383134	0.165674	2.312578
COL1A1	NA	NA	NA	NA	NA	NA	0.273073	0.249247	1.095592	NA	NA	NA	0.004033	0.146511	0.027527	NA	NA	NA
COL1A2	NA	NA	NA	NA	NA	NA	0.216939	0.367138	0.590892	0.157848	0.123812	1.274901	0.057815	0.163831	0.352894	-0.00235	0.064353	-0.03653
COMT	NA	NA	NA	0.749278	0.356566	2.101373	-0.05068	0.448567	-0.11298	-2.45771	1.02805	-2.39065	0.526063	0.226489	2.322687	-0.00764	0.129967	-0.05878
CRYZ	NA	NA	NA	NA	NA	NA	-0.31201	0.303615	-1.02766	-0.53751	0.214408	-2.50696	-0.32472	0.253244	-1.28224	-0.25514	0.124909	-2.04264
CSFI	NA	NA	NA	NA	NA	NA	-1.40833	1.21432	-1.15977	NA	NA	NA	-0.14894	0.352724	-0.42226	-0.11194	0.240555	-0.46532
CTHRC1	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.574897	0.535382	1.073807	-0.08389	0.137325	-0.6109	0.024002	0.097692	0.245691
CXCL12	NA	NA	NA	-0.36476	0.372499	-0.97921	-0.4566	0.219587	-2.07935	NA	NA	NA	-0.08863	0.138097	-0.64183	-0.36944	0.138735	-2.66293
CXCL14	NA	NA	NA	-0.23692	0.333761	-0.70985	0.361375	0.159544	2.265049	NA	NA	NA	-0.06592	0.093353	-0.70609	-0.16877	0.054117	-3.11866
CYR61	NA	NA	NA	0.310818	0.515557	0.602878	-0.24435	0.252867	-0.9663	0.571476	0.323144	1.768487	-0.11281	0.164296	-0.68663	0.087147	0.082372	1.057965
DICER1	NA	NA	NA	NA	NA	NA	-0.33943	0.39364	-0.8623	0.038811	0.409835	0.0947	0.086141	0.143687	0.599504	-0.46887	0.150367	-3.11814
DLC1	NA	NA	NA	0.13581	0.37927	0.358083	-0.4102	0.387258	-1.05923	-0.09793	0.247069	-0.39638	-0.03473	0.238947	-0.14533	-0.35001	0.130472	-2.68262
TNFRSF10B	NA	NA	NA	-0.09001	0.619057	-0.1454	0.80742	0.544479	-1.482922	0.159018	0.456205	0.348567	-0.19927	0.160381	-1.24248	0.053214	0.164091	0.324294
DUSP1	NA	NA	NA	-0.20229	0.200782	-1.00753	-0.02736	0.224043	-0.12212	NA	NA	NA	-0.03006	0.152909	-0.19657	-0.0472	0.09086	-0.51952
E2F1	NA	NA	NA	NA	NA	NA	0.845576	0.685556	1.233416	-1.06849	0.824212	-1.29638	0.356102	0.38254	0.930888	0.617258	0.121385	5.085126
EEF1A2	0.26278	0.091435	2.873951	NA	NA	NA	0.362569	0.17103	2.119915	NA	NA	NA	-0.0028	0.233293	-0.01199	-0.01585	0.06608	-0.23987
ELF3	NA	NA	NA	1.34589	0.628064	2.142919	0.569231	0.430739	1.321522	0.209853	0.239225	0.87722	0.026264	0.109569	0.2397	0.165848	0.143091	1.159039
ENO1	NA	NA	NA	NA	NA	NA	0.179739	0.312848	0.574525	NA	NA	NA	-0.01727	0.097939	-0.17629	0.3682	0.094778	3.884888
EPHB2	NA	NA	NA	0.155831	0.717587	0.21716	-0.19469	0.90381	-0.21541	1.38257	0.444196	3.112522	-0.46953	0.395102	-1.18837	0.318437	0.123672	2.574851
ERBB2	NA	NA	NA	-0.32795	0.215691	-1.52044	0.065275	0.189094	0.3452	0.314084	0.126321	2.486396	0.23616	0.121533	1.943176	0.08469	0.056744	1.492504
ERBB4	NA	NA	NA	NA	NA	NA	-0.12516	0.182846	-0.68451	-0.13567	0.114364	-1.18626	0.191218	0.114326	1.672568	-0.28508	0.066294	-4.30028
ESRRG	NA	NA	NA	NA	NA	NA	0.122595	0.204322	0.600009	0.356845	0.216506	1.648199	0.023341	0.078378	0.297795	-0.16542	0.093598	-1.76733
ESR1	NA	NA	NA	-0.14448	0.127214	-1.13569	0.009283	0.107091	0.086687	-0.12127	0.111184	-1.09075	0.127143	0.109672	1.159302	-0.16933	0.044665	-3.79121
EZH2	NA	NA	NA	NA	NA	NA	0.36213	0.244107	1.483489	NA	NA	NA	0.008861	0.200897	0.044106	0.478266	0.107424	4.452134
F3	NA	NA	NA	0.719395	0.524742	1.37095	-0.21237	0.363632	-0.58402	-0.00167	0.448211	-0.00372	-0.13187	0.134218	-0.98248	-0.29217	0.093753	-3.11637
FGFR4	NA	NA	NA	0.864262	0.479596	1.802063	0.451249	0.296065	1.524155	0.230309	0.229234	1.00469	-0.15142	0.109674	-1.3806	-0.04922	0.146198	-0.33666
FHIT	NA	NA	NA	1.00058	0.938809	1.065797	-1.58314	0.766553	-2.06527	0.087228	0.322399	0.270559	-0.08366	0.344886	-0.24256	-0.1378	0.121745	-1.13183
FN1	NA	NA	NA	0.056943	0.154068	0.369595	0.282152	0.407361	0.692634	0.417442	0.859619	0.485613	-0.05187	0.111777	-0.46402	0.112875	0.066759	1.690796
FOXA1	NA	NA	NA	NA	NA	NA	0.054619	0.1941	0.281398	NA	NA	NA	-0.04211	0.103534	-0.40677	-0.08953	0.043624	-2.05225
FUS	NA	NA	NA	NA	NA	NA	2.73816	1.95693	1.399212	-0.18397	0.269637	-0.88227	0.119801	0.199389	0.600841	0.115971	0.188545	0.615084

Table 13 Official Symbol	EMC2 -Est	EMC2-SE	EMC2-t	JRH1-Est	JRH1-SE	JRH1-t	JRH2-Est	JRH2-SE	JRH2-t	MGH-Est	MGH-SE	MGH-t	NCH-Est	NCH-SE	NCH-t	NKI-Est	NKI-SE	NKI-t
GADD45A	NA	NA	NA	NA	NA	NA	0.28352	0.324263	-0.28352	0.33447	0.236846	-1.41219	-0.43753	0.333292	-1.31276	-0.15889	0.115794	-1.37217
GAPDH	-0.00386	0.125637	-0.03075	0.869317	0.274798	3.163476	0.728889	0.497848	1.464079	NA	NA	NA	0.396067	0.169944	2.330574	0.286211	0.073946	3.870541
GATA3	NA	NA	NA	-0.33431	0.127225	-2.62767	-0.00759	0.145072	-0.05233	0.190453	0.170135	1.119423	0.058244	0.115942	0.502355	-0.13285	0.054984	-2.41625
GBP2	NA	NA	NA	0.120416	0.247997	0.485554	-0.49134	0.289525	-1.69704	0.517501	0.299148	1.729916	0.082647	0.173301	0.4769	-0.19825	0.1358	-1.45985
GDF15	NA	NA	NA	0.219861	0.231613	0.94926	0.317951	0.183188	1.735654	NA	NA	NA	0.200247	0.14325	1.397885	0.052347	0.063101	0.829563
GRB7	NA	NA	NA	-0.46505	0.485227	-0.95842	0.143585	0.218034	0.658544	NA	NA	NA	0.027699	0.459937	0.060224	0.126284	0.054856	2.302117
GSTM1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.18141	0.14912	-1.21652
GSTM2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.15655	0.118111	-1.32547
GSTM3	NA	NA	NA	-1.19919	0.478486	-2.50622	-0.08173	0.176832	-0.46219	NA	NA	NA	-0.09058	0.129247	-0.70086	-0.336	0.086817	-3.87028
HOXB13	NA	NA	NA	NA	NA	NA	0.780988	0.524959	1.487712	0.461343	0.122399	3.769173	0.453876	0.324863	1.39713	0.161713	0.053047	3.048485
OTUD4	NA	NA	NA	NA	NA	NA	-0.54088	1.59038	-0.34009	0.154269	0.633438	0.243542	0.150174	0.149267	1.006076	-0.08847	0.130112	-0.67992
HSPA1A	NA	NA	NA	0.199478	0.304533	0.655029	0.56215	0.592113	0.949396	NA	NA	NA	0.187486	0.231047	0.811463	0.174571	0.117296	1.488295
HSPA1B	NA	NA	NA	NA	NA	NA	0.60089	0.32867	1.828247	NA	NA	NA	NA	NA	NA	0.249602	0.129038	1.934329
HSPA8	NA	NA	NA	0.88406	0.420719	2.101308	1.13504	0.667937	1.699322	0.647034	0.346081	1.869603	0.208652	0.225656	0.924646	0.054243	0.178314	0.304198
IDH2	NA	NA	NA	-0.0525	0.232201	-0.22611	0.151299	0.327466	0.46203	NA	NA	NA	0.265828	0.105592	2.517501	0.284862	0.089145	3.195498
IGF1R	NA	NA	NA	-0.62963	0.509985	-1.23461	-0.05773	0.176259	-0.32753	-0.11077	0.162941	-0.67982	-0.37931	0.371019	-1.02236	-0.13655	0.08362	-1.63299
IGFBP7	NA	NA	NA	NA	NA	NA	0.047112	0.479943	0.098162	NA	NA	NA	0.163138	0.200674	0.81295	0.06541	0.10077	0.649097
IL11	NA	NA	NA	NA	NA	NA	1.19114	1.41017	0.844678	NA	NA	NA	-0.17423	0.144228	-1.20804	-0.048	0.126254	-0.38015
IL17RB	NA	NA	NA	NA	NA	NA	0.143131	0.294647	0.485771	-0.44343	0.132744	-3.3405	NA	NA	NA	-0.01632	0.122679	-0.13305
IL6ST	NA	NA	NA	-0.08851	0.151324	-0.58488	-0.00958	0.287723	-0.03329	-0.76052	0.386504	-1.96769	-0.4336	0.319875	-1.35553	-0.41477	0.111102	-3.73322
IL8	NA	NA	NA	0.222258	0.235694	0.942994	0.262285	0.346572	0.756798	-0.12567	0.154036	-0.81583	-1.28729	0.493461	-2.6087	0.171912	0.07248	2.371858
INHBA	NA	NA	NA	0.095254	0.476446	0.199927	0.342597	0.27142	1.262239	NA	NA	NA	-0.12767	0.132531	-0.96331	0.133895	0.111083	1.20536
IRF1	NA	NA	NA	0.87337	0.941443	0.927693	-0.39282	0.392589	-1.00059	0.474132	0.503423	0.941816	-0.2456	0.294202	-0.8348	-0.08017	0.171067	-0.46864
ITGA4	NA	NA	NA	NA	NA	NA	-0.91318	0.542311	-1.68388	NA	NA	NA	0.034844	0.074049	0.470549	-0.05101	0.133497	-0.38211
ITGA5	NA	NA	NA	1.44044	0.636806	2.261976	0.97846	0.67341	1.452993	0.206218	0.263291	0.783232	0.367111	0.333768	1.099899	0.500604	0.163986	3.052724
ITGAV	NA	NA	NA	0.14845	0.345246	0.429983	0.383127	0.60722	0.630953	-0.23212	0.278464	-0.83358	-0.14166	0.222286	-0.6373	-0.21993	0.158945	-1.38371
ITGB1	NA	NA	NA	1.22836	0.683544	1.797046	-0.0587	1.73799	-0.03378	-0.13651	0.121624	-1.12236	-0.52799	0.346298	-1.52468	0.150333	0.133426	1.126714
ITGB4	NA	NA	NA	0.548277	0.334628	1.638467	0.252015	0.365768	0.689002	-0.12971	0.168517	-0.76973	0.189568	0.163609	1.158665	0.166748	0.175308	0.951172
ITGB5	NA	NA	NA	-0.17231	0.250618	-0.68752	0.037961	0.401861	0.094464	0.682674	0.74847	0.912093	-0.04952	0.16668	-0.29707	0.010302	0.104545	0.098544
MKI67	NA	NA	NA	-0.43304	0.708832	-0.61092	0.482583	0.321739	1.499921	NA	NA	NA	0.128582	0.129422	0.99351	0.397232	0.176102	2.255693
KIAA1199	NA	NA	NA	NA	NA	NA	-0.02195	0.382802	-0.05735	0.081394	0.121221	0.671448	NA	NA	NA	0.238809	0.113748	2.099457
KPNA2	0.301662	0.171052	1.763569	-0.5507	0.55364	-0.99468	0.21269	0.266724	0.828477	-1.6447	1.00101	-1.64304	0.213725	0.196767	1.086183	0.422135	0.089135	4.735922
LAMA3	NA	NA	NA	-0.74591	0.563373	-1.32401	-0.21092	0.29604	-0.71245	NA	NA	NA	-0.03143	0.133752	-0.23497	-0.30023	0.122124	-2.45838
LAMB3	NA	NA	NA	NA	NA	NA	0.345497	0.263827	1.309559	0.03108	0.139904	0.222154	0.106874	0.139587	0.765644	-0.03167	0.069644	-0.45477

Table 13 Official Symbol	EMC2 -Est	EMC2-SE	EMC2-t	JRH1-Est	JRH1-SE	JRH1-t	JRH2-Est	JRH2-SE	JRH2-t	MGH-Est	MGH-SE	MGH-t	NCH-Est	NCH-SE	NCH-t	NKI-Est	NKI-SE	NKI-t
LAPTM4B	NA	NA	NA	NA	NA	NA	-0.04029	0.234986	-0.17148	0.352765	0.40304	0.875261	0.156358	0.140366	1.113931	0.334588	0.083358	4.013853
LMNB1	NA	NA	NA	0.648703	0.285233	2.274292	0.621431	0.389912	-0.1593772	NA	NA	NA	-0.1517	0.242463	-0.62567	0.461325	0.098382	4.689115
LRIG1	NA	NA	NA	NA	NA	NA	-0.00217	0.260339	-0.00832	-0.61468	0.216033	-2.84532	-0.24368	0.172969	-1.40878	-0.50209	0.1119	-4.48694
MTDH	NA	NA	NA	NA	NA	NA	-0.10827	0.493025	-0.21961	0.084824	0.292285	0.290209	0.039288	0.233351	0.168365	0.430557	0.145357	2.962066
MCM2	NA	NA	NA	0.875004	0.492588	1.77634	0.77667	0.376275	0.264102	0.118904	0.288369	0.412333	0.586577	0.252123	2.236551	0.504911	0.154078	3.276983
MELK	NA	NA	NA	0.850914	0.313784	2.711783	0.16347	0.256575	0.637124	NA	NA	NA	0.216763	0.1352	1.603277	0.471343	0.103644	4.547711
MGMT	NA	NA	NA	NA	NA	NA	0.151967	0.583459	0.260459	0.267185	0.295678	0.903635	-0.37332	0.507157	-0.73611	-0.14716	0.165874	-0.88716
MMP1	NA	NA	NA	0.43277	0.16023	2.70093	-0.02427	0.158939	-0.15272	0.180359	0.078781	2.289386	0.559716	0.331212	1.689903	0.167053	0.064595	2.586172
MMP7	NA	NA	NA	0.198055	0.143	1.385	0.106475	0.193338	0.550719	-1.06791	1.30502	-0.81831	0.012294	0.101346	0.121311	NA	NA	NA
MYBL2	NA	NA	NA	0.731162	0.267911	2.729123	0.098974	0.600361	0.164857	0.612646	0.509356	1.202785	0.396938	0.171503	2.314467	0.751827	0.151477	4.963308
NAT1	NA	NA	NA	-0.57746	15.1186	-0.0382	-0.01397	0.117033	-0.11939	-0.05035	0.105736	-0.47614	-0.15619	0.139368	-1.12073	-0.20435	0.058054	-3.52
PGF	NA	NA	NA	0.901309	0.501058	1.798812	1.43389	1.27617	1.123589	NA	NA	NA	0.05255	0.14245	0.368898	0.055127	0.36118	0.152631
PGR	NA	NA	NA	NA	NA	NA	-0.33243	0.276025	-1.20435	-0.95852	0.593621	-1.61469	-0.01033	0.08386	-0.12312	-0.30421	0.073055	-4.16405
PRDX1	NA	NA	NA	NA	NA	NA	-0.41082	0.47383	-0.86703	NA	NA	NA	0.253047	0.182621	1.38564	0.231612	0.161791	1.431551
PTEN	NA	NA	NA	-0.17429	0.629039	-0.27708	-0.15599	0.541475	-0.28808	-0.10814	0.287261	-0.37645	0.113229	0.228164	0.496261	-0.3204	0.149745	-2.13962
RPL41	NA	NA	NA	NA	NA	NA	1.02038	1.83528	0.555981	0.213155	0.288282	0.739398	0.030854	0.188269	0.163881	-0.08602	0.122667	-0.70126
RPLP0	NA	NA	NA	0.398754	0.282913	1.409458	0.246775	1.2163	0.20289	0.488909	0.174981	2.794069	0.004595	0.198497	0.023148	0.008104	0.079365	0.102105
RRM2	NA	NA	NA	NA	NA	NA	0.196643	0.262745	0.748418	NA	NA	NA	0.229458	0.11665	1.967064	0.434693	0.152104	2.857867
RUNX1	NA	NA	NA	-0.22834	0.318666	-0.71656	0.302803	0.420043	0.720886	0.277566	0.267511	1.037587	0.124568	0.088457	1.408231	-0.18878	0.138365	-1.36435
S100A8	NA	NA	NA	NA	NA	NA	0.066629	0.11857	0.561939	NA	NA	NA	0.142073	0.080349	1.768194	0.094631	0.041656	2.271738
S100A9	NA	NA	NA	NA	NA	NA	0.111103	0.13176	0.843223	NA	NA	NA	0.090314	0.058415	1.546083	0.111093	0.045472	2.443086
S100B	NA	NA	NA	0.097319	0.589664	0.165041	-0.2365	0.349444	-0.67678	NA	NA	NA	0.239753	0.145105	1.652272	0.195383	0.295751	0.660633
S100P	NA	NA	NA	0.378047	0.120687	3.132458	0.302607	0.133752	2.262448	NA	NA	NA	0.202856	0.092114	2.202218	0.103276	0.04811	2.146677
SEMA3F	NA	NA	NA	-0.27556	0.615782	-0.4475	0.498631	0.616195	0.80921	0.107802	0.274191	0.393164	-0.17978	0.185166	-0.97092	NA	NA	NA
SKIL	NA	NA	NA	NA	NA	NA	0.026279	0.587743	0.044712	NA	NA	NA	0.143484	0.103564	1.385462	0.124124	0.120741	1.028019
SKP2	NA	NA	NA	NA	NA	NA	0.2502	0.469372	0.533053	0.470759	0.2802	1.680082	-0.71691	0.354699	-2.02117	0.056728	0.128585	0.441174
SNAIL	NA	NA	NA	NA	NA	NA	0.165897	1.09586	0.151385	0.163855	0.228308	0.717693	-0.04601	0.259767	-0.17711	0.057651	0.124454	0.463235
SYK	NA	NA	NA	-0.26425	0.588491	-0.44903	-0.22515	0.492582	-0.45707	NA	NA	NA	-1.30716	0.591071	-2.21151	0.178238	0.168423	1.058276
TAGLN	NA	NA	NA	NA	NA	NA	0.042223	0.251268	0.168039	0.010727	0.098919	0.108442	0.194543	0.115463	1.684895	0.077881	0.119491	0.651776
TFR3	NA	NA	NA	-0.91825	0.636275	-1.44317	0.162921	0.352486	0.462206	0.029015	0.193689	0.149803	0.056174	0.166875	0.336622	0.157216	0.10845	1.449663
TGFB3	NA	NA	NA	-1.0219	0.358953	-2.84689	-0.39774	0.470041	-0.84619	0.046498	0.2296	0.202518	-0.30473	0.247338	-1.23202	-0.36531	0.09592	-3.80851
TNFRSF11B	NA	NA	NA	NA	NA	NA	-0.10399	0.440721	-0.23595	-1.15976	0.400921	-2.89274	-0.2492	0.289075	-0.86207	-0.22072	0.10171	-2.17005
VTN	NA	NA	NA	-0.18721	0.475541	-0.39367	-2.39601	1.83129	-1.30837	NA	NA	NA	0.048066	0.34143	0.140779	-0.05675	0.116352	-0.48774
WISP1	NA	NA	NA	NA	NA	NA	0.437936	0.592058	0.739684	-0.03674	0.212861	-0.1726	NA	NA	NA	-0.36317	0.153002	-2.3736

Table 13 Official Symbol	EMC2 ~Est	EMC2~SE	EMC2~t	JRH1~Est	JRH1~SE	JRH1~t	JRH2~Est	JRH2~SE	JRH2~t	MGH~Est	MGH~SE	MGH~t	NCH~Est	NCH~SE	NCH~t	NKI~Est	NKI~SE	NKI~t
WNT5A	NA	NA	NA	NA	NA	NA	0.180255	0.286462	0.629246	0.06984	0.223411	0.312605	-0.14987	0.146576	-1.02248	-0.29433	0.084559	-3.48081
C6orf66	NA	NA	NA	NA	NA	NA	0.35565	0.504627	0.704778	0.179742	0.364806	0.492706	-0.53606	0.448343	-1.19564	0.296686	0.199046	1.49054
FOXO3A	NA	NA	NA	NA	NA	NA	-0.04428	0.39855	-0.1111	0.176454	0.221502	0.796625	0.059822	0.171485	0.348846	-0.2855	0.194121	-1.47074
GPR30	NA	NA	NA	0.01829	0.925976	0.019752	-0.298	0.747388	-0.39872	-0.03208	0.1214	-0.26427	0.157898	0.174583	0.904429	0.080079	0.104254	0.768115
KNTC2	NA	NA	NA	NA	NA	NA	-0.02315	0.289403	-0.07999	-0.14241	0.246904	-0.57677	0.274706	0.14532	1.890352	0.432186	0.120356	3.590897

Table 13 Official Symbol	STNO -Est	STNO -SE	STNO-t	STOCK -Est	STOCK -SE	STOCK -t	TRANS BIG-Est	TRANS BIG-SE	TRANS BIG-t	UCSF -Est	UCSF -SE	UCSF-t	UPP-Est	UPP-SE	UPP-t	fe	sefe
AAMP	0.189376	0.309087	0.612695	0.836415	0.549695	1.521598	0.051406	0.111586	0.460681	0.770516	0.762039	1.011124	1.25423	0.577991	2.169982	0.146929	0.085151
ABCC1	NA	NA	NA	0.640672	0.375725	1.705162	NA	NA	NA	NA	NA	NA	0.274551	0.271361	1.011756	0.281451	0.104466
ABCC3	0.311364	0.100031	3.112675	0.166453	0.159249	1.045237	NA	NA	NA	0.381707	0.250896	1.521375	0.178451	0.097237	1.835219	0.172778	0.048133
ABR	0.095087	0.266216	0.357181	0.08129	0.196104	0.414525	NA	NA	NA	-0.17319	0.728313	-0.23779	-0.16409	0.120793	-1.35847	-0.06034	0.067134
ACTR2	NA	NA	NA	0.302753	0.39656	0.763448	NA	NA	NA	NA	NA	NA	0.21463	0.335554	0.607064	0.199885	0.117995
ADAM17	NA	NA	NA	0.437069	0.276977	1.577997	NA	NA	NA	0.35888	0.433785	0.827322	0.131246	0.194946	0.673243	0.129961	0.090699
ADM	NA	NA	NA	0.555634	0.242705	2.289339	0.025583	0.038218	0.669405	NA	NA	NA	0.361033	0.203349	1.775435	0.119028	0.030564
LYPD6	NA	NA	NA	-0.42358	0.145799	-2.90525	-0.06178	0.031054	-1.98944	NA	NA	NA	-0.1544	0.073668	-2.09587	-0.12675	0.026288
AKT3	NA	NA	NA	0.12232	0.182253	0.671155	NA	NA	NA	NA	NA	NA	-0.06832	0.125172	-0.5458	0.05204	0.071861
ALCAM	-0.14634	0.126842	-1.15369	-0.41301	0.190485	-2.16822	NA	NA	NA	-0.25661	0.251874	-1.01879	-0.1468	0.143998	-1.01942	-0.15502	0.046361
APEX1	0.005151	0.257871	0.019976	0.739037	0.539346	1.370247	NA	NA	NA	-0.96465	0.704753	-1.36878	1.23743	0.466987	2.649817	0.019915	0.10244
ARF1	0	0.107397	0	0.862387	0.279535	3.085077	NA	NA	NA	0.304097	0.58718	0.517894	0.751279	0.361093	2.080569	0.281544	0.07587
AURKA	0.38795	0.127032	3.053955	0.688845	0.210275	3.275924	0.020041	0.064473	0.310835	-0.0146	0.28312	-0.05156	0.427382	0.126638	3.374832	0.262652	0.041246
BAD	-0.30035	0.250277	-1.20006	0.228387	0.543493	0.420221	NA	NA	NA	-0.43933	0.659711	-0.66594	0.351434	0.360157	0.97578	0.059151	0.126378
BAG1	NA	NA	NA	-0.39593	0.380547	-1.04043	NA	NA	NA	0.516764	0.524112	0.98598	0.380154	0.211079	1.801003	-0.16426	0.087173
BBC3	NA	NA	NA	-0.26155	0.219839	-1.18974	-0.04709	0.086372	-0.5452	0.263477	0.606256	0.434597	-0.13039	0.141473	-0.92165	-0.14598	0.061462
BCAR3	NA	NA	NA	-0.49692	0.265837	-1.86927	NA	NA	NA	NA	NA	NA	-0.29435	0.182614	-1.61186	-0.28755	0.080198
BCL2	-0.38181	0.112494	-3.39408	-0.73699	0.228055	-3.23162	NA	NA	NA	-0.3453	0.410691	-0.84078	-0.11988	0.174734	-0.68605	-0.32009	0.056047
BIRC5	0.190534	0.126151	1.510365	0.582957	0.159354	3.658251	0.007906	0.045316	0.174454	0.357332	0.286621	1.246706	0.43455	0.110681	3.926148	0.186649	0.031964
BTRC	NA	NA	NA	-0.92763	0.307218	-3.01944	NA	NA	NA	NA	NA	NA	-0.0225	0.1807	-0.12451	-0.40405	0.100468
BUB1	0.357653	0.101235	3.532899	1.09451	0.258044	4.241563	0.014276	0.040135	0.355694	0.376719	0.340175	1.107427	0.469009	0.162539	2.885517	0.154368	0.032048
Cl0orf11 6	-0.09621	0.085948	-1.11936	-0.34745	0.112777	-3.08087	NA	NA	NA	0.013111	156.117	8.40E-05	-0.00923	0.100902	-0.09148	-0.13	0.042521
C17orf37	NA	NA	NA	0.382862	0.185356	2.06555	NA	NA	NA	NA	NA	NA	0.385651	0.113625	3.394068	0.362223	0.092012
TPX2	NA	NA	NA	0.800822	0.195737	4.091316	NA	NA	NA	0.213479	0.284008	0.751665	0.44053	0.139377	3.160708	0.480408	0.073094
C8orf4	NA	NA	NA	-0.36113	0.130038	-2.77713	NA	NA	NA	NA	NA	NA	0.0037	0.109064	0.033921	-0.18346	0.048256
CAV1	0.135002	0.093948	1.436991	-0.65852	0.275751	-2.38811	NA	NA	NA	-0.54391	0.428883	-1.2682	-0.31503	0.150431	-2.09415	-0.11726	0.058989
CCL19	-0.0546	2531.93	05	-0.15743	0.154207	-1.02087	NA	NA	NA	0	0.434462	0	-0.1048	0.106112	-0.98765	-0.05608	0.050769
CCNB1	0.37726	0.156356	2.412827	0.828029	0.223403	3.706436	NA	NA	NA	-0.35808	0.431863	-0.82915	0.611916	0.142007	4.309055	0.456916	0.062513
CDC20	0.059565	1057.7	5.63E-05	0.642601	0.178622	3.597547	NA	NA	NA	-0.65381	0.404188	-1.61759	0.490188	0.130676	3.751171	0.319134	0.064899
CDC25A	0.288245	0.213701	1.348824	0.168571	0.225272	0.7483	NA	NA	NA	-0.31967	0.397525	-0.80414	0.330359	0.191096	1.728759	0.267201	0.060819

Table 13 Official Symbol	STNO -Est	STNO ~SE	STNO-t	STOCK -Est	STOCK ~SE	STOCK -t	TRANS BIG-Est	TRANS BIG-SE	TRANS BIG-t	UCSF -Est	UCSF ~SE	UCSF-t	UPP-Est	UPP-SE	UPP-t	fe	sefe
CDC25C	0.420797	0.155926	2.698697	1.02036	0.337803	3.020577	NA	NA	NA	-0.33774	0.477196	-0.70776	0.8277213	0.232669	3.555321	0.382935	0.077595
CDH11	-0.05652	0.1231	-0.45913	-0.21142	0.211537	-0.99942	NA	NA	NA	-0.20567	0.246195	-0.83541	-0.22621	0.164541	-1.37482	-0.11417	0.053045
CDK4	0.279447	0.142472	1.961417	1.40458	0.463254	3.031987	NA	NA	NA	-0.37577	0.674081	-0.55746	0.814832	0.297251	2.741225	0.305255	0.069562
SCUBE2	-0.21559	0.074112	-2.90896	-0.24679	0.122745	-2.01059	0.016505	0.023486	0.702739	NA	NA	NA	-0.14287	0.077009	-1.8552	-0.05439	0.018349
CENPA	NA	NA	NA	0.724539	0.195614	3.703922	0.002888	0.04791	0.060269	0.679912	0.275146	2.471095	0.536476	0.157029	3.416414	0.185486	0.037867
CHAF1B	0.259119	0.162074	1.59877	0.281358	0.148493	1.894756	NA	NA	NA	-0.03447	0.352745	-0.09773	0.209129	0.093425	2.238469	0.300765	0.05807
CLDN4	0.40922	0.128817	3.176755	1.20235	0.33711	3.56664	0.03236	0.053171	0.608591	0	1.8541	0	0.08503	0.258939	0.328378	0.125868	0.045235
CLIC1	0.238723	0.209629	1.138788	2.00024	0.600443	3.331274	-0.26608	0.160756	-1.65519	0.377361	0.552842	0.682584	0.999191	0.414232	2.412153	0.222753	0.088912
COL1A1	0.127256	0.081743	1.556791	0.05098	0.156488	0.325773	0.087944	0.034256	2.567237	NA	NA	NA	-0.05544	0.13355	-0.41509	0.083989	0.029343
COL1A2	-0.01925	0.078156	-0.24625	-0.17504	0.228915	-0.76466	NA	NA	NA	-0.1405	0.184661	-0.76085	-0.15924	0.220113	-0.72346	-0.00069	0.041375
COMT	NA	NA	NA	0.643165	0.360056	1.786292	NA	NA	NA	0.356582	0.628139	0.56768	0.404183	0.257299	1.570869	0.212925	0.092124
CRYZ	-0.38719	0.143353	-2.70092	0.122949	0.340718	0.360853	NA	NA	NA	-0.52792	0.412283	-1.28048	-0.37265	0.225119	-1.65534	-0.33167	0.071579
CSF1	NA	NA	NA	-0.11449	0.197258	-0.58042	-0.09782	0.196881	-0.49684	NA	NA	NA	0.120517	0.148659	0.810694	-0.0334	0.090261
CTHRC1	NA	NA	NA	0.263783	0.247606	1.065334	NA	NA	NA	NA	NA	NA	-0.14789	0.176843	-0.83626	-0.00169	0.069075
CXCL12	0.066487	0.189775	0.350348	-0.65036	0.168426	-3.86137	NA	NA	NA	-0.05795	0.270065	-0.21456	-0.35344	0.150278	-2.35189	-0.28998	0.062826
CXCL14	-0.20969	0.073458	-2.8546	-0.14079	0.096118	-1.46476	NA	NA	NA	NA	NA	NA	-0.1861	0.08384	-2.21976	-0.14219	0.032611
CYR61	NA	NA	NA	-0.38308	0.231645	-1.65372	NA	NA	NA	-0.22327	0.263371	-0.84773	-0.41188	0.174362	-2.36221	-0.04446	0.059831
DICER1	NA	NA	NA	-1.06544	0.322204	-3.30672	NA	NA	NA	0	0.311799	0	0.208326	0.307144	0.678268	-0.19602	0.085879
DLC1	0.519601	0.221066	2.350434	-0.66099	0.298518	-2.21425	NA	NA	NA	-0.31503	0.345828	-0.91094	-0.404	0.200673	-2.01324	-0.19876	0.076441
TNFRSF1 OB	-0.03773	0.174479	-0.21623	-0.03558	0.198203	-0.1795	NA	NA	NA	0.932141	0.524911	1.775808	0.127348	0.157658	0.807748	0.02034	0.072745
DUSP1	0.095682	0.223995	0.42716	-0.14883	0.12682	-1.17351	NA	NA	NA	0.008053	0.779738	0.010327	-0.41475	0.153012	-2.71055	-0.11225	0.054628
E2F1	0.171825	0.110793	1.550865	0.699408	0.207377	3.37264	NA	NA	NA	NA	NA	NA	0.570954	0.172882	3.302565	0.433836	0.067966
EEF1A2	NA	NA	NA	-0.01256	0.130353	-0.09633	NA	NA	NA	0.433528	0.267338	1.621648	-0.04242	0.091692	-0.46259	0.068177	0.041066
ELF3	0.406692	0.148275	2.742822	0.233332	0.357735	0.652248	NA	NA	NA	0.841389	0.55748	1.509272	0.096421	0.256911	0.375307	0.196003	0.066053
ENO1	NA	NA	NA	0.428884	0.194952	2.199947	NA	NA	NA	0.899319	0.369574	2.433394	0.288434	0.179833	1.603899	0.233559	0.058687
EPHB2	NA	NA	NA	0.192999	0.451341	0.427612	NA	NA	NA	0.355634	0.604801	0.588018	0.211632	0.199057	1.063173	0.284709	0.094113
ERBB2	0.268938	0.074504	3.609693	0.092164	0.188964	0.487734	NA	NA	NA	0.301674	0.170749	1.766769	0.349689	0.107646	3.248509	0.181046	0.034939
ERBB4	-0.10396	0.068988	-1.50697	-0.73759	0.209821	-3.51532	NA	NA	NA	NA	NA	NA	-0.1859	0.117619	-1.58055	-0.16266	0.037384
ESRRG	NA	NA	NA	-0.32843	0.127583	-2.57425	NA	NA	NA	NA	NA	NA	-0.04663	0.091723	-0.50839	-0.0602	0.044609
ESR1	-0.14983	0.057346	-2.61275	-0.2159	0.120078	-1.798	-0.0019	0.019747	-0.0963	-0.30054	0.138369	-2.17201	-0.05086	0.082082	-0.6196	-0.04576	0.015905
FZHZ	0.293772	0.156133	1.88155	0.79436	0.243012	3.26881	-0.03007	0.04916	-0.61166	0.123884	0.404373	0.306361	0.615257	0.155425	3.958546	0.134411	0.0393
F3	NA	NA	NA	-0.3284	0.132658	-2.47552	NA	NA	NA	-0.08026	0.491948	-0.16315	-0.20405	0.109227	-1.86809	-0.22911	0.055029

Table 13 Official Symbol	STNO ~Est	STNO ~SE	STNO-t	STOCK ~Est	STOCK ~SE	STOCK ~t	TRANS BIG-Est	TRANS BIG-SE	TRANS BIG-t	UCSF ~Est	UCSF ~SE	UCSF-t	UPP-Est	UPP-SE	UPP-t	fe	sefe
FGFR4	0.201581	0.15216	1.324796	-0.06118	0.174787	-0.35001	NA	NA	NA	0.149034	0.333338	0.447096	0.204299	0.102078	2.001401	0.075374	0.053791
FHIT	-0.16819	0.17858	-0.94184	-0.27141	0.367689	-0.73815	NA	NA	NA	0.225378	0.678656	0.332095	0.053025	0.245338	0.216132	-0.11401	0.082797
FN1	0.049279	0.11577	0.425659	0.185381	0.202933	0.913508	NA	NA	NA	0.13258	0.244458	0.542343	-0.15952	0.26761	-0.59607	0.070337	0.045477
FOXA1	NA	NA	NA	-0.18849	0.161048	-1.17039	NA	NA	NA	NA	NA	NA	0.139273	0.160139	0.869701	-0.07105	0.037194
FUS	NA	NA	NA	0.368833	0.437273	0.843485	NA	NA	NA	NA	NA	NA	-0.15247	0.345172	-0.44173	0.063142	0.111165
GADD45 A	0.390085	0.342821	1.137868	-0.24644	0.303688	-0.81148	NA	NA	NA	0.153778	0.296649	0.518384	-0.4297	0.20668	-2.07904	-0.18353	0.077839
GAPDH	NA	NA	NA	0.907441	0.296513	3.060375	NA	NA	NA	NA	NA	NA	0.493907	0.232859	2.121056	0.303991	0.05522
GATA3	-0.20281	0.068842	-2.94607	-0.25592	0.122639	-2.08677	NA	NA	NA	-0.2038	0.135112	-1.50836	0.052882	0.108852	0.485817	-0.12484	0.03218
GBP2	0.104968	0.124764	0.841332	-0.17667	0.338601	-0.52176	NA	NA	NA	0.161775	0.235299	0.687529	0.215873	0.198252	1.088882	0.030811	0.064103
GDF15	-0.02683	0.097032	-0.27646	0.251857	0.169158	1.488886	NA	NA	NA	0.462744	0.465751	0.993544	0.139286	0.128201	1.086466	0.095577	0.04245
GRB7	0.28938	0.08099	3.573025	0.464983	0.21274	2.185687	NA	NA	NA	0.492397	0.361768	1.361085	0.39613	0.142688	2.776197	0.203411	0.041043
GSTM1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.18141	0.14912
GSTM2	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.12675	0.336406	-0.37676	NA	NA	NA	-0.15328	0.111442
GSTM3	-0.38478	0.15382	-2.50148	-0.43469	0.17404	-2.49766	0.035771	0.038412	0.931246	0.11963	0.323329	0.369995	-0.05308	0.123135	-0.43107	-0.06296	0.030752
HOXB13	NA	NA	NA	0.193	0.369898	0.521765	NA	NA	NA	0.540678	0.49567	1.090802	0.342881	0.212428	1.614105	0.227421	0.046188
OTUD4	0.372577	0.253393	1.470352	-0.19372	0.251083	-0.77155	NA	NA	NA	-0.97971	0.713147	-1.37378	0.231981	0.294286	0.788284	0.034041	0.081167
HSPA1A	NA	NA	NA	0.765501	0.440826	1.736515	NA	NA	NA	NA	NA	NA	0.722677	0.40563	1.781616	0.243271	0.092738
HSPA1B	0.033372	0.19398	0.172039	0.069621	0.248436	0.280237	NA	NA	NA	NA	NA	NA	0.187302	0.176407	1.061761	0.198207	0.083268
HSPA8	0.22166	0.199205	1.112723	0.32649	0.265007	1.232005	NA	NA	NA	-0.30224	0.477926	-0.63239	0.126525	0.166299	0.760828	0.218804	0.082393
IDH2	0.127942	0.255302	0.50114	0.574289	0.193387	2.969636	NA	NA	NA	-0.009	0.554612	-0.01623	0.659908	0.186426	3.539785	0.303626	0.056121
IGF1R	-0.16723	0.112062	-1.49233	-0.35887	0.141569	-2.53498	NA	NA	NA	0.277384	0.391147	0.709155	-0.04996	0.122321	-0.40843	-0.14872	0.0484
IGFBP7	0.121056	0.164973	0.733793	-0.55896	0.34775	-1.60736	NA	NA	NA	-0.50275	0.332753	-1.51087	-0.16594	0.185086	-0.89655	0.005398	0.068861
IL11	NA	NA	NA	0.086327	0.225669	0.38254	NA	NA	NA	NA	NA	NA	0.000507	0.151608	0.003346	-0.05199	0.075711
IL17RB	NA	NA	NA	-0.01403	0.212781	-0.06594	NA	NA	NA	NA	NA	NA	-0.1861	0.139748	-1.33168	-0.16557	0.069337
IL6ST	NA	NA	NA	-0.65682	0.195937	-3.35217	NA	NA	NA	-0.11749	0.19789	-0.5937	-0.26213	0.150485	-1.74192	-0.31568	0.063376
IL8	0.548269	0.238841	2.29554	0.382317	0.203112	1.882296	NA	NA	NA	-0.3673	0.460322	-0.79791	0.076262	0.135635	0.562257	0.136391	0.05243
INHBA	-0.12998	0.113709	-1.14313	0.249729	0.184419	1.354139	NA	NA	NA	0.094476	0.303634	0.311152	0.036575	0.162207	0.225485	0.026824	0.056655
IRF1	0.307333	0.166134	1.84991	0.248132	0.447433	0.554568	NA	NA	NA	0.380822	0.370842	1.026912	-0.01044	0.283877	-0.03676	0.082446	0.091982
ITGA4	0.02688	2341.09	1.15E-05	0.198854	0.302824	0.656665	NA	NA	NA	-0.54938	0.583992	-0.94073	-0.01192	0.18086	-0.0659	0.002027	0.059101
ITGA5	NA	NA	NA	0.025981	0.423908	0.061288	NA	NA	NA	NA	NA	NA	0.406364	0.36399	1.116415	0.431369	0.112958
ITGAV	0	0.216251	0	-0.403	0.45413	-0.88742	NA	NA	NA	-0.59197	0.499066	-1.18615	-0.24399	0.30418	-0.80213	-0.15415	0.089488
ITGB1	0.131284	0.165432	0.793583	0.195878	0.3192	0.613653	NA	NA	NA	0.430257	0.540622	0.795856	-0.18009	0.530248	-0.33962	0.026471	0.072949

Table 13 Official Symbol	STNO ~Est	STNO ~SE	STNO-t	STOCK ~Est	STOCK ~SE	STOCK ~t	TRANS BIG-Est	TRANS BIG-SE	TRANS BIG-t	UCSF ~Est	UCSF ~SE	UCSF-t	UPP-Est	UPP-SE	UPP-t	fe	sefe
ITCB4	0.100533	0.106548	0.943547	0.035914	0.241068	0.14898	NA	NA	NA	0.754519	0.285307	2.644586	0.075057	0.181963	0.412483	0.132678	0.060938
ITCB5	-0.19722	0.165947	-1.18843	-0.29946	0.281956	-1.06207	NA	NA	NA	-0.19391	0.378906	-0.51177	-0.21379	0.157719	-1.35549	-0.09296	0.063571
MKI67	-0.07823	0.088982	-0.87915	0.96424	0.257398	3.746105	NA	NA	NA	-0.19193	0.462712	-0.4148	0.597931	0.152281	3.926498	0.183915	0.058442
KIAA119 9	NA	NA	NA	0.293164	0.194272	1.509039	NA	NA	NA	NA	NA	NA	0.070065	0.141965	0.493538	0.153718	0.066186
KPN2	0.328818	0.112579	2.920776	0.857218	0.267225	3.207851	NA	NA	NA	0.32028	0.315031	1.016662	0.615022	0.206117	2.983849	0.374909	0.054897
LAMA3	-0.28334	0.120229	-2.3567	-0.42291	0.12869	-3.28625	NA	NA	NA	-0.14266	0.366741	-0.38899	-0.27285	0.091038	-2.99711	-0.26764	0.050305
LAMB3	NA	NA	NA	-0.15767	0.230936	-0.68274	NA	NA	NA	NA	NA	NA	-0.1353	0.168256	-0.8041	-0.00591	0.051501
LAPTM4 B	0.405684	0.113287	3.581029	0.28652	0.19422	1.475234	NA	NA	NA	NA	NA	NA	0.095487	0.136338	0.700367	0.270104	0.051492
LMNB1	NA	NA	NA	0.755925	0.25541	2.959653	NA	NA	NA	0.121429	0.384263	0.316005	0.805734	0.199208	4.044687	0.481816	0.073226
LRIG1	-0.31422	0.128149	-2.45197	-0.95351	0.258142	-3.69375	NA	NA	NA	NA	NA	NA	-0.05954	0.178366	-0.33383	-0.37679	0.062403
MTDH	0.242242	0.285145	0.84954	0.472647	0.340076	1.389828	0.052038	0.077589	0.670683	NA	NA	NA	0.45556	0.239663	1.900836	0.158361	0.059133
MCM2	0.008185	0.084857	0.096455	0.732134	0.216462	3.382275	NA	NA	NA	0.138969	0.340074	0.408643	0.602555	0.182898	3.294487	0.275153	0.05978
MELK	NA	NA	NA	0.749617	0.195032	3.843559	0.022669	0.036962	0.613293	NA	NA	NA	0.46629	0.128065	3.641042	0.132605	0.031744
MGMT	NA	NA	NA	0.377527	0.48364	0.780595	NA	NA	NA	0.368174	0.453282	0.812241	0.725329	0.346508	2.093253	0.085317	0.117786
MMP1	0.083945	0.055744	1.505895	0.28871	0.081435	3.545299	NA	NA	NA	0.150509	0.33411	0.450477	0.11015	0.051829	2.12525	0.151235	0.027295
MMP7	0.102783	0.072986	1.408258	-0.00343	0.153901	-0.0223	NA	NA	NA	0.166646	0.143301	1.162909	0.059637	0.10332	0.57721	0.08418	0.042799
MYBL2	0.399355	0.118084	3.381957	0.579872	0.192026	3.019758	NA	NA	NA	0.030169	0.282699	0.106717	0.445705	0.102011	4.369186	0.479924	0.057205
NAT1	-0.14333	0.060602	-2.36509	-0.26529	0.117131	-2.26487	NA	NA	NA	-0.1696	0.138069	-1.22836	-0.05668	0.076583	-0.7401	-0.14009	0.030446
PGF	-0.17016	0.153912	-1.10557	-0.08334	0.183966	-0.45304	0.095422	0.145828	0.654349	-1.00442	0.630097	-1.59407	0.038005	0.124883	0.304328	0.009034	0.063633
PGR	NA	NA	NA	-0.18022	0.108941	-1.65427	NA	NA	NA	0.451216	0.527475	0.855426	-0.01652	0.065638	-0.25164	-0.12464	0.038764
PRDX1	NA	NA	NA	1.52553	0.420489	3.62799	NA	NA	NA	0.358079	0.32938	1.08713	0.706059	0.303105	2.32942	0.347764	0.10081
PTEN	0	226.764	0	-0.26976	0.225651	-1.19546	NA	NA	NA	NA	NA	NA	0.110294	0.254356	0.433621	-0.15381	0.092467
RPL41	NA	NA	NA	-0.40807	0.786496	-0.51884	NA	NA	NA	NA	NA	NA	0.24408	0.604521	0.403758	-0.01769	0.094765
RPLP0	NA	NA	NA	0.018324	0.458438	0.039971	NA	NA	NA	NA	NA	NA	0.964584	0.554848	1.738465	0.108162	0.064823
RRM2	0.305217	0.104337	2.9253	0.926244	0.22125	4.186414	0.038487	0.042471	0.906208	-0.03281	0.279791	-0.11727	0.674794	0.149386	4.517117	0.159696	0.03419
RUNX1	-0.17832	0.165636	-1.07657	-0.39722	0.244634	-1.62372	NA	NA	NA	-0.58909	0.385997	-1.52616	-0.2142	0.105479	-2.03071	-0.07498	0.052758
S100A8	0.093477	0.04547	2.055818	0.164366	0.096581	1.701846	NA	NA	NA	0.123771	0.178963	0.691601	0.125784	0.065874	1.909478	0.106936	0.024582
S100A9	NA	NA	NA	0.15514	0.10905	1.42265	NA	NA	NA	NA	NA	NA	0.135096	0.074987	1.801592	0.112811	0.030203
S100B	0.136825	0.163838	0.835124	-0.11862	0.158461	-0.74859	-0.01591	0.034049	-0.46712	-0.05362	0.218098	-0.24584	-0.13315	0.115177	-1.15608	-0.01134	0.030069
S100P	0.19922	0.078236	2.546395	0.201435	0.097583	2.064251	NA	NA	NA	0.416003	0.200351	2.076371	0.174292	0.063687	2.736705	0.179884	0.028697
SEMA3F	0.023257	0.162267	0.143327	0.472655	0.292764	1.614457	NA	NA	NA	NA	NA	NA	0.545294	0.227357	2.398404	0.117569	0.092557

Table 13 Official Symbol	STNO ~Est	STNO ~SE	STNO-t	STOCK ~Est	STOCK ~SE	STOCK ~t	TRANS BIG-Est	TRANS BIG-SE	TRANS BIG-t	UCSF ~Est	UCSF ~SE	UCSF-t	UPP-Est	UPP-SE	UPP-t	fe	sefe
SKIL	NA	NA	NA	0.015831	0.262101	0.060402	NA	NA	NA	0.141704	0.348326	0.406814	0.179419	0.152532	1.176271	0.134826	0.065866
SKP2	NA	NA	NA	0.312141	0.339582	0.919192	NA	NA	NA	NA	NA	NA	0.482145	0.194873	2.47415	0.167902	0.091018
SNAIL	NA	NA	NA	0.152799	0.210056	0.72742	NA	NA	NA	NA	NA	NA	0.329059	0.159704	2.060431	0.140674	0.078745
SVK	0.21812	0.150626	1.44809	-0.06882	0.155403	-0.44285	NA	NA	NA	0.159029	0.431388	0.368645	0.066162	0.136668	0.484107	0.063381	0.072639
TAGLN	-0.00434	0.108525	-0.04003	-0.2578	0.197826	-1.30316	NA	NA	NA	NA	NA	NA	-0.06802	0.191196	-0.35574	0.032416	0.049944
TFR	0.406546	0.131339	3.095394	0.178145	0.153331	1.161833	-0.03263	0.051129	-0.63826	-0.22576	0.249301	-0.90558	0.545839	0.208978	2.611945	0.062825	0.038345
TGFB3	-0.07166	0.134442	-0.53298	-1.08462	0.322799	-3.36005	0.013681	0.046103	0.296755	-0.25719	0.253264	-1.01551	-0.49773	0.225603	-2.20621	-0.10353	0.03709
TNFRSF1 1B	0	0.08306	0	-0.10987	0.128194	-0.85708	NA	NA	NA	NA	NA	NA	-0.03866	0.087545	-0.44163	-0.09599	0.046815
VTN	-0.01674	0.109545	-0.15278	0.100648	0.186529	0.539584	0.226938	0.091337	2.484623	-0.22804	0.193542	-1.17822	0.167418	0.152274	1.099452	0.063022	0.050706
WISP1	0.03435	0.194412	0.176685	0.236658	0.340736	0.694549	-0.00282	0.068308	-0.04121	NA	NA	NA	-0.29716	0.212939	-1.39552	-0.05687	0.054306
WNT5A	0.121343	0.108022	1.123317	-0.01524	0.172902	-0.08815	NA	NA	NA	-0.96994	0.719267	-1.34851	-0.23507	0.152819	-1.5382	-0.12181	0.051129
C6orf66	NA	NA	NA	0.530409	0.355488	1.492059	NA	NA	NA	NA	NA	NA	-0.04983	0.251179	-0.19837	0.167784	0.123636
FOXO3A	NA	NA	NA	0.087341	0.128833	0.67794	NA	NA	NA	-0.03591	0.49687	-0.07227	-0.00291	0.074227	-0.03914	0.007101	0.054798
GPR30	NA	NA	NA	-0.36866	0.173755	-2.12169	NA	NA	NA	NA	NA	NA	-0.07779	0.125956	-0.61763	-0.02487	0.058543
KNTC2	NA	NA	NA	0.442783	0.170315	2.599789	-0.00276	0.041235	-0.06696	-0.02041	0.366566	-0.05558	0.347484	0.117596	2.954896	0.093083	0.034359

Table 14: Validation of Transferrin Receptor Group genes in SIB data sets.

	Genes						
Study data set	TFRC	ENO1	IDH2	ARF1	CLDN4	PRDX1	GBP1
EMC2~Est	NA	NA	NA	NA	NA	NA	NA
EMC2~SE	NA	NA	NA	NA	NA	NA	NA
EMC2~t	NA	NA	NA	NA	NA	NA	NA
JRH1~Est	-0.91825	NA	-0.0525	0.839013	-0.54144	NA	0.137268
JRH1~SE	0.636275	NA	0.232201	0.346692	0.470758	NA	0.159849
JRH1~t	-1.44317	NA	-0.22611	2.420053	-1.15014	NA	0.858735
JRH2~Est	0.162921	0.179739	0.151299	0.369609	0.33033	-0.41082	-0.07418
JRH2~SE	0.352486	0.312848	0.327466	0.40789	0.351865	0.47383	0.198642
JRH2~t	0.462206	0.574525	0.46203	0.906149	0.938798	-0.86703	-0.37345
MGH~Est	0.029015	NA	NA	2.03958	0.185116	NA	0.15434
MGH~SE	0.193689	NA	NA	0.804729	0.314723	NA	0.188083
MGH~t	0.149803	NA	NA	2.534493	0.588187	NA	0.820595
NCH~Est	0.056174	-0.01727	0.265828	-0.15337	-0.23129	0.253047	0.095457
NCH~SE	0.166875	0.097939	0.105592	0.204529	0.426627	0.182621	0.1323
NCH~t	0.336622	-0.17629	2.517501	-0.74984	-0.54213	1.38564	0.721522
NKI~Est	0.157216	0.3682	0.284862	0.944168	0.564756	0.231612	0.13712
NKI~SE	0.10845	0.094778	0.089145	0.204641	0.210595	0.161791	0.075391
NKI~t	1.449663	3.884888	3.195498	4.613777	2.681716	1.431551	1.818777
STNO~Est	0.406546	NA	0.127942	0	0.40922	NA	0.298139
STNO~SE	0.131339	NA	0.255302	0.107397	0.128817	NA	0.113901
STNO~t	3.095394	NA	0.50114	0	3.176755	NA	2.617528
STOCK~Est	0.178145	0.428884	0.574289	0.862387	1.20235	1.52553	0.068821
STOCK~SE	0.153331	0.194952	0.193387	0.279535	0.33711	0.420489	0.183692
STOCK~t	1.161833	2.199947	2.969636	3.085077	3.56664	3.62799	0.374652
TRANSBIG~Est	-0.03263	NA	NA	NA	0.03236	NA	NA
TRANSBIG~SE	0.051129	NA	NA	NA	0.053171	NA	NA
TRANSBIG~t	-0.63826	NA	NA	NA	0.608591	NA	NA
UCSF~Est	-0.22576	0.899319	-0.009	0.304097	0	0.358079	-0.43879
UCSF~SE	0.249301	0.369574	0.554612	0.58718	1.8541	0.32938	0.874728
UCSF~t	-0.90558	2.433394	-0.01623	0.517894	0	1.08713	-0.50163
UPP~Est	0.545839	0.288434	0.659908	0.751279	0.08503	0.706059	0.119778
UPP~SE	0.208978	0.179833	0.186426	0.361093	0.258939	0.303105	0.117879
UPP~t	2.611945	1.603899	3.539785	2.080569	0.328378	2.32942	1.01611
Fe	0.062825	0.233559	0.303626	0.281544	0.125868	0.347764	0.139381
Sefe	0.038345	0.058687	0.056121	0.07587	0.045235	0.10081	0.044464

Table 15: Validation of Stromal Group genes in SIB data sets.

Gene	CXCL14	TNFRSF11B	CXCL12	C10orf116	RUNX1	GSTM2	TGFB3	BCAR3	CAV1	DLC1	TNFRSF10B	F3	DICER1
EMC2-Est	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EMC2-SE	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EMC2-t	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
JRH1-Est	-0.23692	NA	-0.36476	-0.1418	-0.22834	NA	-1.0219	NA	-0.20701	0.13581	-0.09001	0.719395	NA
JRH1-SE	0.333761	NA	0.372499	0.261554	0.318666	NA	0.358953	NA	0.254401	0.37927	0.619057	0.524742	NA
JRH1-t	-0.70985	NA	-0.97921	-0.54216	-0.71656	NA	-2.84689	NA	-0.81372	0.358083	-0.1454	1.37095	NA
JRH2-Est	0.361375	-0.10399	-0.4566	0.036378	0.302803	NA	-0.39774	-0.29238	-0.19588	-0.4102	0.80742	-0.21237	-0.33943
JRH2-SE	0.159544	0.440721	0.219587	0.182183	0.420043	NA	0.470041	0.522706	0.289251	0.387258	0.544479	0.363632	0.39364
JRH2-t	2.265049	-0.23595	-2.07935	0.19968	0.720886	NA	-0.84619	-0.55935	-0.67721	-1.05923	1.482922	-0.58402	-0.8623
MGH-Est	NA	-1.15976	NA	NA	0.277566	NA	0.046498	-0.41595	-0.06896	-0.09793	0.159018	-0.00167	0.038811
MGH-SE	NA	0.400921	NA	NA	0.267511	NA	0.2296	0.216837	0.2269	0.247069	0.456205	0.448211	0.409835
MGH-t	NA	-2.89274	NA	NA	1.037587	NA	0.202518	-1.91825	-0.30391	-0.39638	0.348567	-0.00372	0.0947
NCH-Est	-0.06592	-0.2492	-0.08863	0.064337	0.124568	NA	-0.30473	0.072246	0.078825	-0.03473	-0.19927	-0.13187	0.086141
NCH-SE	0.093353	0.289075	0.138097	0.14087	0.088457	NA	0.247338	0.304443	0.340843	0.238947	0.160381	0.134218	0.143687
NCH-t	-0.70609	-0.86207	-0.64183	0.456713	1.408231	NA	-1.23202	0.237306	0.231265	-0.14533	-1.24248	-0.98248	0.599504
NKI-Est	-0.16877	-0.22072	-0.36944	-0.22589	-0.18878	-0.15655	-0.36531	-0.26067	-0.30885	-0.35001	0.053214	-0.29217	-0.46887
NKI-SE	0.054117	0.10171	0.138735	0.082836	0.138365	0.118111	0.09592	0.114992	0.133788	0.130472	0.164091	0.093753	0.150367
NKI-t	-3.11866	-2.17005	-2.66293	-2.72696	-1.36435	-1.32547	-3.80851	-2.26685	-2.30848	-2.68262	0.324294	-3.11637	-3.11814
STNO-Est	-0.20969	0	0.066487	-0.09621	-0.17832	NA	-0.07166	NA	0.135002	0.519601	-0.03773	NA	NA
STNO-SE	0.073458	0.08306	0.189775	0.085948	0.165636	NA	0.134442	NA	0.093948	0.221066	0.174479	NA	NA
STNO-t	-2.8546	0	0.350348	-1.11936	-1.07657	NA	-0.53298	NA	1.436991	2.350434	-0.21623	NA	NA
STOCK-Est	-0.14079	-0.10987	-0.65036	-0.34745	-0.39722	NA	-1.08462	-0.49692	-0.65852	-0.66099	-0.03558	-0.3284	-1.06544
STOCK-SE	0.096118	0.128194	0.168426	0.112777	0.244634	NA	0.322799	0.265837	0.275751	0.298518	0.198203	0.132658	0.322204
STOCK-t	-1.46476	-0.85708	-3.86137	-3.08087	-1.62372	NA	-3.36005	-1.86927	-2.38811	-2.21425	-0.1795	-2.47552	-3.30672

Gene	CXXL14	TNFRSF11B	CXCL12	C10orf116	RUNX1	GSTM2	TGFB3	BCAR3	CAV1	DLC1	TNFRSF10B	F3	DICER1
TRANSBIG-Est	NA	NA	NA	NA	NA	NA	0.013681	NA	NA	NA	NA	NA	N/A
TRANSBIG-SE	NA	NA	NA	NA	NA	NA	0.046103	NA	NA	NA	NA	NA	N/A
TRANSBIG-t	NA	NA	NA	NA	NA	NA	0.296755	NA	NA	NA	NA	NA	N/A
UCSF-Est	NA	NA	-0.05795	0.013111	-0.58909	-0.12675	-0.25719	NA	-0.54391	-0.31503	0.932141	-0.08026	0
UCSF-SE	NA	NA	0.270065	156.117	0.385997	0.336406	0.253264	NA	0.428883	0.345828	0.524911	0.491948	0.311799
UCSF-t	NA	NA	-0.21456	8.40E-05	-1.52616	-0.37676	-1.01551	NA	-1.2682	-0.91094	1.775808	-0.16315	0
UPP-Est	-0.1861	-0.03866	-0.35344	-0.00923	-0.2142	NA	-0.49773	-0.29435	-0.31503	-0.404	0.127348	-0.20405	0.208326
UPP-SE	0.08384	0.087545	0.150278	0.100902	0.105479	NA	0.225603	0.182614	0.150431	0.200673	0.157658	0.109227	0.307144
UPP-t	-2.21976	-0.44163	-2.35189	-0.09148	-2.03071	NA	-2.20621	-1.61186	-2.09415	-2.01324	0.807748	-1.86809	0.678268
Fe	-0.14219	-0.09599	-0.28998	-0.13	-0.07498	-0.15328	-0.10353	-0.28755	-0.11726	-0.19876	0.02034	-0.22911	-0.19602
Seft	0.032611	0.046815	0.062826	0.042521	0.052758	0.111442	0.03709	0.080198	0.058989	0.076441	0.072745	0.055029	0.085879

Table 16: Genes that co-express with Prognostic genes in ER+ breast cancer tumors (Spearman corr. coef. ≥ 0.7)

Prognostic Gene	Table 16 Co-expressed Genes				
INHBA	AEBP1	CDH11	COL10A1	COL11A1	COL1A2
	COL5A1	COL5A2	COL8A2	ENTPD4	LOXL2
	LRRC15	MMP11	NOX4	PLAU	THBS2
	THY1	VCAN			
CAV1	ANK2	ANXA1	AQP1	C10orf56	CAV2
	CFH	COL14A1	CRYAB	CXCL12	DAB2
	DCN	ECM2	FHL1	FLRT2	GNG11
	GSN	IGF1	JAM2	LDB2	NDN
	NRN1	PCSK5	PLSCR4	PROS1	TGFB2
NAT1	PSD3				
GSTM1	GSTM2				
GSTM2	GSTM1				
ITGA4	ARHGAP15	ARHGAP25	CCL5	CD3D	CD48
	CD53	CORO1A	EVI2B	FGL2	GIMAP4
	IRF8	LCK	PTPRC	TFEC	TRAC
	TRAF3IP3	TRBC1	EVI2A	FLI1	GPR65
	IL2RB	LCP2	LOC100133233	MNDA	PLAC8
	PLEK	TNFAIP8			
CCL19	ARHGAP15	ARHGAP25	CCL5	CCR2	CCR7
	CD2	CD247	CD3D	CD3E	CD48
	CD53	FLJ78302	GPR171	IL10RA	IL7R
	IRF8	LAMP3	LCK	LTB	PLAC8
	PRKCB1	PTPRC	PTPRCAP	SASH3	SPOCK2
	TRA@	TRBC1	TRD@	PPP1R16B	TRAC
CDH11	TAGLN	ADAM12	AEBP1	ANGPTL2	ASPN
	BGN	BICC1	C10orf56	C1R	C1S
	C20orf39	CALD1	COL10A1	COL11A1	COL1A1
	COL1A2	COL3A1	COL5A1	COL5A2	COL6A1
	COL6A2	COL6A3	COL8A2	COMP	COPZ2
	CRISPLD2	CTSK	DACT1	DCN	DPYSL3
	ECM2	EFEMP2	ENTPD4	FAP	FBLN1
	FBLN2	FBN1	FERMT2	FLRT2	FN1
	FSTL1	GAS1	GLT8D2	HEPH	HTRA1

Prognostic Gene	Table 16 Co-expressed Genes				
	ISLR	ITGBL1	JAM3	KDELC1	LAMA4
	LAMB1	LOC100133502	LOX	LOXL2	LRRC15
	LRRC17	LUM	MFAP2	MFAP5	MMP2
	MRC2	MXRA5	MXRA8	MYL9	NDN
	NID1	NID2	NINJ2	NOX4	OLFML2B
	OMD	PALLD	PCOLCE	PDGFRA	PDGFRB
	PDGFRL	POSTN	PRKCDBP	PRKD1	PTRF
	RARRES2	RCN3	SERPINF1	SERPINH1	SFRP4
	SNAI2	SPARC	SPOCK1	SPON1	SRPX2
	SSPN	TCF4	THBS2	THY1	TNFAIP6
	VCAN	WWTR1	ZEB1	ZFPM2	INHBA
	PLS3	SEC23A	WISP1		
TAGLN	CDH11	ADAM12	AEBP1	ANGPTL2	ASPN
	BGN	BICC1	C10orf56	C1R	C1S
	C20orf39	CALD1	COL10A1	COL11A1	COL1A1
	COL1A2	COL3A1	COL5A1	COL5A2	COL6A1
	COL6A2	COL6A3	COL8A2	COMP	COPZ2
	CRISPLD2	CTSK	DACT1	DCN	DPYSL3
	ECM2	EFEMP2	ENTPD4	FAP	FBLN1
	FBLN2	FBN1	FERMT2	FLRT2	FN1
	FSTL1	GAS1	GLT8D2	HEPH	HTRA1
	ISLR	ITGBL1	JAM3	KDELC1	LAMA4
	LAMB1	LOC100133502	LOX	LOXL2	LRRC15
	LRRC17	LUM	MFAP2	MFAP5	MMP2
	MRC2	MXRA5	MXRA8	MYL9	NDN
	NID1	NID2	NINJ2	NOX4	OLFML2B
	OMD	PALLD	PCOLCE	PDGFRA	PDGFRB
	PDGFRL	POSTN	PRKCDBP	PRKD1	PTRF
	RARRES2	RCN3	SERPINF1	SERPINH1	SFRP4
	SNAI2	SPARC	SPOCK1	SPON1	SRPX2
	SSPN	TCF4	THBS2	THY1	TNFAIP6
	VCAN	WWTR1	ZEB1	ZFPM2	ACTA2
	CNN1	DZIP1	EMILIN1		
ENO1	ATP5J2	C10orf10	CLDN15	CNGB1	DET1
	EIF3CL	HS2ST1	IGHG4	KIAA0195	KIR2DS5
	PARP6	PRH1	RAD1	RIN3	RPL10
	SGCG	SLC16A2	SLC9A3R1	SYNPO2L	THBS1

Prognostic Gene	Table 16				
	Co-expressed Genes				
	ZNF230				
IDH2	AEBP1	HIST1H2BN	PCDHAC1		
ARF1	CRIM1				
DICER1	ADM	LOC100133583			
AKT3	AKAP12	ECM2	FERMT2	FLRT2	JAM3
	LOC100133502	PROS1	TCF4	WWTR1	ZEB1
CXCL12	ANXA1	C1R	C1S	CAV1	DCN
	FLRT2	SRPX			
CYR61	CTGF				
IGFBP7	VIM				
KIAA1199	COL11A1	PLAU			
SPC25	ASPM	BUB1	BUB1B	CCNA2	CCNE2
	CDC2	CDC25C	CENPA	CEP55	FANCI
	GINS1	HJURP	KIAA0101	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF4A	MAD2L1
	MELK	NCAPG	NEK2	NUSAP1	PRC1
	STIL	ZWINT			
WISP1	CDH11	COL5A2			

Table 17: Genes that co-express with Prognostic Genes in ER- breast cancer tumors (Spearman corr. coef. ≥ 0.7)

Prognostic Gene	Table 17 Co-expressed Genes				
IRF1	APOL6	CXCL10	GABBR1	GBP1	HCP5
	HLA-E	HLA-F	HLA-G	HLA-J	INDO
	PSMB8	PSMB9	STAT1	TAP1	UBD
	UBE2L6	WARS	APOBEC3F	APOBEC3G	APOL1
	APOL3	ARHGAP25	BTN3A1	BTN3A2	BTN3A3
	C1QB	CCL5	CD2	CD38	CD40
	CD53	CD74	CD86	CSF2RB	CTSS
	CYBB	FGL2	GIMAP5	GZMA	hCG_1998957
	HCLS1	HLA-C	HLA-DMA	HLA-DMB	HLA-DPA1
	HLA-DQB1	HLA-DQB2	HLA-DRA	HLA-DRB1	HLA-DRB2
	HLA-DRB3	HLA-DRB4	HLA-DRB5	HLA-DRB6	IL10RA
	IL2RB	LAP3	LAPTM5	LOC100133484	LOC100133583
	LOC100133661	LOC100133811	LOC730415	NKG7	PLEK
	PSMB10	PTPRC	RNASE2	SLAMF8	TFEC
	TNFRSF1B	TRA@	TRAC	TRAJ17	TRAV20
	ZNF749				
CDH11	ADAM12	AEBP1	ANGPTL2	ASPN	CFH
	CFHR1	COL10A1	COL11A1	COL1A1	COL1A2
	COL3A1	COL5A1	COL5A2	COL6A3	CRISPLD2
	CTSK	DACT1	DCN	FAP	FBN1
	FN1	HTRA1	LOX	LRRC15	LUM
	NID2	PCOLCE	PDGFRB	POSTN	SERPINF1
	SPARC	THBS2	THY1	VCAN	DAB2
	GLT8D2	ITGB5	JAM3	LOC100133502	MMP2
	PRSS23	TIMP3	ZEB1		
CCL19	ITGA4	ADAM28	AIF1	APOBEC3F	APOBEC3G
	APOL3	ARHGAP15	ARHGAP25	CASP1	CCDC69
	CCR2	CCR7	CD2	CD247	CD27
	CD37	CD3D	CD3G	CD48	CD52
	CD53	CD74	CD86	CD8A	CLEC4A
	CORO1A	CTSS	CXCL13	DOCK10	EVI2A
	EVI2B	FGL2	FLJ78302 (CCR2)	FYB	GIMAP4
	GIMAP5	GIMAP6	GMFG	GPR171	GPR18
	GPR65	GZMA	GZMB	GZMK	hCG_1998957

Prognostic Gene	Table 17				
	Co-expressed Genes				
	HCLS1	HLA-DMA	HLA-DMB	HLA-DPA1	HLA-DQA1
	HLA-DQA2	HLA-DQB1	HLA-DQB2	HLA-DRB1	HLA-DRB2
	HLA-DRB3	HLA-DRB4	HLA-DRB5	HLA-E	IGHM
	IGSF6	IL10RA	IL2RG	IL7R	IRF8
	KLRB1	KLRK1	LAPTM5	LAT2	LCK
	LCP2	LOC100133484	LOC100133583	LOC100133661	LOC100133811
	LOC730415	LPXN	LRMP	LST1	LTB
	LY96	LYZ	MFNG	MNDA	MS4A4A
	NCKAP1L	PLAC8	PLEK	PRKCB1	PSCDBP
	PTPRC	PTPRCAP	RAC2	RNASE2	RNASE6
	SAMHD1	SAMSN1	SASH3	SELL	SELPLG
	SLA	SLAMF1	SLC7A7	SP140	SRGN
	TCL1A	TFEC	TNFAIP8	TNFRSF1B	TRA@
	TRAC	TRAJ17	TRAT1	TRAV20	TRBC1
	TYROBP	ZNF749	ITM2A	LTB	P2RY13
	PRKCB1	PTPRCAP	SELL	TRBC1	
ITGA4	CCL19	ADAM28	AIF1	APOBEC3F	APOBEC3G
	APOL3	ARHGAP15	ARHGAP25	CASP1	CCDC69
	CCR2	CCR7	CD2	CD247	CD27
	CD37	CD3D	CD3G	CD48	CD52
	CD53	CD74	CD86	CD8A	CLEC4A
	CORO1A	CTSS	CXCL13	DOCK10	EVI2A
	EVI2B	FGL2	FLJ78302 (CCR2)	FYB	GIMAP4
	GIMAP5	GIMAP6	GMFG	GPR171	GPR18
	GPR65	GZMA	GZMB	GZMK	hCG_1998957
	HCLS1	HLA-DMA	HLA-DMB	HLA-DPA1	HLA-DQA1
	HLA-DQA2	HLA-DQB1	HLA-DQB2	HLA-DRB1	HLA-DRB2
	HLA-DRB3	HLA-DRB4	HLA-DRB5	HLA-E	IGHM
	IGSF6	IL10RA	IL2RG	IL7R	IRF8
	KLRB1	KLRK1	LAPTM5	LAT2	LCK
	LCP2	LOC100133484	LOC100133583	LOC100133661	LOC100133811
	LOC730415	LPXN	LRMP	LST1	LTB
	LY96	LYZ	MFNG	MNDA	MS4A4A
	NCKAP1L	PLAC8	PLEK	PRKCB1	PSCDBP
	PTPRC	PTPRCAP	RAC2	RNASE2	RNASE6
	SAMHD1	SAMSN1	SASH3	SELL	SELPLG
	SLA	SLAMF1	SLC7A7	SP140	SRGN

Prognostic Gene	Table 17 Co-expressed Genes				
	TCL1A	TFEC	TNFAIP8	TNFRSF1B	TRA@
	TRAC	TRAJ17	TRAT1	TRAV20	TRBC1
	TYROBP	ZNF749	MARCH1	C17orf60	CSF1R
	FLI1	FLJ78302	FYN	IKZF1	INPP5D
	NCF4	NR3C1	P2RY13	PLXNC1	PSCD4
	PTPN22	SERPINB9	SLCO2B1	VAMP3	WIPF1
IDH2	AEBP1	DSG3	HIST1H2BN	PCDHAC1	
ARF1	FABP5L2	FLNB	IL1RN	PAX6	
DICER1	ARS2	IGHA1	VDAC3		
TFRC	RGS20				
ADAM17	TFDP3	GPR107			
CAV1	CAV2	CXCL12	IGF1		
CYR61	CTGF				
ESR1	CBLN1	SLC45A2			
GSTM1	GSTM2				
GSTM2	GSTM1				
IL11	FAM135A				
IL6ST	P2RY5				
IGFBP7	SPARCL1	TMEM204			
INHBA	COL10A1	FN1	SULF1		
SPC25	KIF4A	KIF20A	NCAPG		
TAGLN	ACTA2	MYL9	NNMT	PTRF	
TGFB3	GALNT10	HTRA1	LIMA1		
TNFRSF10B	BIN3				
FOXA1	CLCA2	TFAP2B	AGR2	MLPH	SPDEF
CXCL12	DCN	CAV1	IGF1	CFH	
GBP2	APOL1	APOL3	CD2	CTSS	CXCL9
	CXCR6	GBP1	GZMA	HLA-DMA	HLA-DMB
	IL2RB	PTPRC	TRBC1		

Table 18: Genes that co-express with Prognostic Genes in all breast cancer tumors (Spearman corr. coef. ≥ 0.7)

Prognostic Gene	Table 18 Co-expressed Genes				
S100A8	S100A9				
S100A9	S100A8				
MKI67	BIRC5	KIF20A	MCM10		
MTDH	ARMC1	AZIN1	ENY2	MTERFD1	POLR2K
	PTDSS1	RAD54B	SLC25A32	TMEM70	UBE2V2
GSTM1	GSTM2				
GSTM2	GSTM1				
CXCL12	AKAP12	DCN	F13A1		
TGFB3	C10orf56	JAM3			
TAGLN	ACTA2	CALD1	COPZ2	FERMT2	HEPH
	MYL9	NNMT	PTRF	TPM2	
PGF	ALMS1	ATP8B1	CEP27	DBT	FAM128B
	FBXW12	FGFR1	FLJ12151	FLJ42627	GTF2H3
	HCG2P7	KIAA0894	KLHL24	LOC152719	PDE4C
	PODNL1	POLR1B	PRDX2	PRR11	RIOK3
	RP5-886K2.1	SLC35E1	SPN	USP34	ZC3H7B
	ZNF160	ZNF611			
CCL19	ARHGAP15	ARHGAP25	CCL5	CCR2	CCR7
	CD2	CD37	CD3D	CD48	CD52
	CSF2RB	FLJ78302	GIMAP5	GIMAP6	GPR171
	GZMK	IGHM	IRF8	LCK	LTB
	PLAC8	PRKCB1	PTGDS	PTPRC	PTPRCAP
	SASH3	TNFRSF1B	TRA@	TRAC	TRAJ17
	TRAV20	TRBC1			
IRF1	ITGA4	MARCH1	AIF1	APOBEC3F	APOBEC3G
	APOL1	APOL3	ARHGAP15	ARHGAP25	BTN3A2
	BTN3A3	CASP1	CCL4	CCL5	CD2
	CD37	CD3D	CD48	CD53	CD69
	CD8A	CORO1A	CSF2RB	CST7	CYBB
	EVI2A	EVI2B	FGL2	FLI1	GBP1
	GIMAP4	GIMAP5	GIMAP6	GMFG	GPR65
	GZMA	GZMK	hCG_1998957	HCLS1	HLA-DMA
	HLA-DMB	HLA-DPA1	HLA-DQB1	HLA-DQB2	HLA-DRA
	HLA-DRB1	HLA-DRB2	HLA-DRB3	HLA-DRB4	HLA-DRB5
	HLA-E	HLA-F	IGSF6	IL10RA	IL2RB

Prognostic Gene	Table 18 Co-expressed Genes				
	IRF8	KLRK1	LCK	LCP2	LOC100133583
	LOC100133661	LOC100133811	LST1	LTB	LY86
	MFNG	MNDA	NKG7	PLEK	PRKCB1
	PSCDBP	PSMB10	PSMB8	PSMB9	PTPRC
	PTPRCAP	RAC2	RNASE2	RNASE6	SAMSN1
	SLA	SRGN	TAP1	TFEC	TNFAIP3
	TNFRSF1B	TRA@	TRAC	TRAJ17	TRAV20
	TRBC1	TRIM22	ZNF749		
ITGA4	IRF1	MARCH1	AIF1	APOBEC3F	APOBEC3G
	APOL1	APOL3	ARHGAP15	ARHGAP25	BTN3A2
	BTN3A3	CASP1	CCL4	CCL5	CD2
	CD37	CD3D	CD48	CD53	CD69
	CD8A	CORO1A	CSF2RB	CST7	CYBB
	EVI2A	EVI2B	FGL2	FLI1	GBP1
	GIMAP4	GIMAP5	GIMAP6	GMFG	GPR65
	GZMA	GZMK	hCG_1998957	HCLS1	HLA-DMA
	HLA-DMB	HLA-DPA1	HLA-DQB1	HLA-DQB2	HLA-DRA
	HLA-DRB1	HLA-DRB2	HLA-DRB3	HLA-DRB4	HLA-DRB5
	HLA-E	HLA-F	IGSF6	IL10RA	IL2RB
	IRF8	KLRK1	LCK	LCP2	LOC100133583
	LOC100133661	LOC100133811	LST1	LTB	LY86
	MFNG	MNDA	NKG7	PLEK	PRKCB1
	PSCDBP	PSMB10	PSMB8	PSMB9	PTPRC
	PTPRCAP	RAC2	RNASE2	RNASE6	SAMSN1
	SLA	SRGN	TAP1	TFEC	TNFAIP3
	TNFRSF1B	TRA@	TRAC	TRAJ17	TRAV20
	TRBC1	TRIM22	ZNF749	CTSS	
SPC25	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXO1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6

Prognostic Gene	Table 18				
	Co-expressed Genes				
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	CENPA	KPNA2	LMNB1	MCM2	MELK
	NDC80	TPX2			
AURKA	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GIN51	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	SPC25	BIRC5	BUB1	CCNB1
	CENPA	KPNA2	LMNB1	MCM2	MELK
	NDC80	TPX2	PSMA7	CSE1L	
BIRC5	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GIN51	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3

Prognostic Gene	Table 18				
	Co-expressed Genes				
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	SPC25	BUB1	CCNB1
	CENPA	KPNA2	LMNB1	MCM2	MELK
	NDC80	TPX2	MKI67		
BUB1	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	SPC25	CCNB1
	CENPA	KPNA2	LMNB1	MCM2	MELK
	NDC80	TPX2			
CCNB1	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	SPC25
	CENPA	KPNA2	LMNB1	MCM2	MELK

Prognostic Gene	Table 18 Co-expressed Genes				
	NDC80	TPX2			
CENPA	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXMI	GINSI	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	SPC25	KPNA2	LMNB1	MCM2	MELK
	NDC80	TPX2			
KPNA2	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXMI	GINSI	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	CENPA	SPC25	LMNB1	MCM2	MELK
	NDC80	TPX2	NOL11	PSMD12	
LMNB1	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L

Prognostic Gene	Table 18 Co-expressed Genes				
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	CENPA	KPNA2	SPC25	MCM2	MELK
	NDC80	TPX2			
MCM2	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	CENPA	KPNA2	LMNB1	SPC25	MELK
	NDC80	TPX2			
MELK	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9

Prognostic Gene	Table 18 Co-expressed Genes				
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	CENPA	KPNA2	LMNB1	MCM2	SPC25
	NDC80	TPX2			
NDC80	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	CENPA	KPNA2	LMNB1	MCM2	MELK
	SPC25	TPX2			
TPX2	ASPM	ATAD2	AURKB	BUB1B	C12orf48
	CCNA2	CCNE1	CCNE2	CDC2	CDC45L
	CDC6	CDCA3	CDCA8	CDKN3	CENPE
	CENPF	CENPN	CEP55	CHEK1	CKS1B
	CKS2	DBF4	DEPDC1	DLG7	DNAJC9
	DONSON	E2F8	ECT2	ERCC6L	FAM64A
	FBXO5	FEN1	FOXM1	GINS1	GTSE1
	H2AFZ	HJURP	HMMR	KIF11	KIF14

Prognostic Gene	Table 18 Co-expressed Genes				
	KIF15	KIF18A	KIF20A	KIF23	KIF2C
	KIF4A	KIFC1	MAD2L1	MCM10	MCM6
	NCAPG	NEK2	NUSAP1	OIP5	PBK
	PLK4	PRC1	PTTG1	RACGAP1	RAD51AP1
	RFC4	SMC2	STIL	STMN1	TACC3
	TOP2A	TRIP13	TTK	TYMS	UBE2C
	UBE2S	AURKA	BIRC5	BUB1	CCNB1
	CENPA	KPNA2	LMNB1	MCM2	MELK
	NDC80	SPC25			
CDH11	INHBA	WISP1	COL1A1	COL1A2	FN1
	ADAM12	AEBP1	ANGPTL2	ASPN	BGN
	BNC2	C1QTNF3	COL10A1	COL11A1	COL3A1
	COL5A1	COL5A2	COL5A3	COL6A3	COMP
	CRISPLD2	CTSK	DACT1	DCN	DKK3
	DPYSL3	EFEMP2	EMILIN1	FAP	FBN1
	FSTL1	GLT8D2	HEG1	HTRA1	ITGBL1
	JAM3	KIAA1462	LAMA4	LOX	LOXL1
	LRP1	LRRC15	LRRC17	LRRC32	LUM
	MFAP5	MICAL2	MMP11	MMP2	MXRA5
	MXRA8	NID2	NOX4	OLFML2B	PCOLCE
	PDGFRB	PLAU	POSTN	SERPINF1	SPARC
	SPOCK1	SPON1	SRPX2	SULF1	TCF4
	THBS2	THY1	VCAN	ZEB1	
INHBA	CDH11	WISP1	COL1A1	COL1A2	FN1
	ADAM12	AEBP1	ANGPTL2	ASPN	BGN
	BNC2	C1QTNF3	COL10A1	COL11A1	COL3A1
	COL5A1	COL5A2	COL5A3	COL6A3	COMP
	CRISPLD2	CTSK	DACT1	DCN	DKK3
	DPYSL3	EFEMP2	EMILIN1	FAP	FBN1
	FSTL1	GLT8D2	HEG1	HTRA1	ITGBL1
	JAM3	KIAA1462	LAMA4	LOX	LOXL1
	LRP1	LRRC15	LRRC17	LRRC32	LUM
	MFAP5	MICAL2	MMP11	MMP2	MXRA5
	MXRA8	NID2	NOX4	OLFML2B	PCOLCE
	PDGFRB	PLAU	POSTN	SERPINF1	SPARC
	SPOCK1	SPON1	SRPX2	SULF1	TCF4
	THBS2	THY1	VCAN	ZEB1	

Prognostic Gene	Table 18 Co-expressed Genes				
	INHBA	CDH11	COL1A1	COL1A2	FN1
WISP1	ADAM12	AEBP1	ANGPTL2	ASPN	BGN
	BNC2	C1QTNF3	COL10A1	COL11A1	COL3A1
	COL5A1	COL5A2	COL5A3	COL6A3	COMP
	CRISPLD2	CTSK	DACT1	DCN	DDIT3
	DPYSL3	EFEMP2	EMILIN1	FAP	FBN1
	FSTL1	GLT8D2	HEG1	HTRA1	ITGBL1
	JAM3	KIAA1462	LAMA4	LOX	LOXL1
	LRP1	LRRC15	LRRC17	LRRC32	LUM
	MFAP5	MICAL2	MMP11	MMP2	MXRA5
	MXRA8	NID2	NOX4	OLFML2B	PCOLCE
	PDGFRB	PLAU	POSTN	SERPINF1	SPARC
	SPOCK1	SPON1	SRPX2	SULF1	TCF4
	THBS2	THY1	VCAN	ZEB1	
COL1A1	INHBA	WISP1	CDH11	COL1A2	FN1
	ADAM12	AEBP1	ANGPTL2	ASPN	BGN
	BNC2	C1QTNF3	COL10A1	COL11A1	COL3A1
	COL5A1	COL5A2	COL5A3	COL6A3	COMP
	CRISPLD2	CTSK	DACT1	DCN	DDIT3
	DPYSL3	EFEMP2	EMILIN1	FAP	FBN1
	FSTL1	GLT8D2	HEG1	HTRA1	ITGBL1
	JAM3	KIAA1462	LAMA4	LOX	LOXL1
	LRP1	LRRC15	LRRC17	LRRC32	LUM
	MFAP5	MICAL2	MMP11	MMP2	MXRA5
	MXRA8	NID2	NOX4	OLFML2B	PCOLCE
	PDGFRB	PLAU	POSTN	SERPINF1	SPARC
	SPOCK1	SPON1	SRPX2	SULF1	TCF4
	THBS2	THY1	VCAN	ZEB1	
COL1A2	INHBA	WISP1	COL1A1	CDH11	FN1
	ADAM12	AEBP1	ANGPTL2	ASPN	BGN
	BNC2	C1QTNF3	COL10A1	COL11A1	COL3A1
	COL5A1	COL5A2	COL5A3	COL6A3	COMP
	CRISPLD2	CTSK	DACT1	DCN	DDIT3
	DPYSL3	EFEMP2	EMILIN1	FAP	FBN1
	FSTL1	GLT8D2	HEG1	HTRA1	ITGBL1
	JAM3	KIAA1462	LAMA4	LOX	LOXL1
	LRP1	LRRC15	LRRC17	LRRC32	LUM

Prognostic Gene	Table 18				
	Co-expressed Genes				
	MFAP5	MICAL2	MMP11	MMP2	MXRA5
	MXRA8	NID2	NOX4	OLFML2B	PCOLCE
	PDGFRB	PLAU	POSTN	SERPINF1	SPARC
	SPOCK1	SPON1	SRPX2	SULF1	TCF4
	THBS2	THY1	VCAN	ZEB1	
FN1	INHBA	WISP1	COL1A1	COL1A2	CDH11
	ADAM12	AEBP1	ANGPTL2	ASPN	BGN
	BNC2	C1QTNF3	COL10A1	COL11A1	COL3A1
	COL5A1	COL5A2	COL5A3	COL6A3	COMP
	CRISPLD2	CTSK	DACT1	DCN	DDIT3
	DPYSL3	EFEMP2	EMILIN1	FAP	FBN1
	FSTL1	GLT8D2	HEG1	HTRA1	ITGBL1
	JAM3	KIAA1462	LAMA4	LOX	LOXL1
	LRP1	LRRC15	LRRC17	LRRC32	LUM
	MFAP5	MICAL2	MMP11	MMP2	MXRA5
	MXRA8	NID2	NOX4	OLFML2B	PCOLCE
	PDGFRB	PLAU	POSTN	SERPINF1	SPARC
	SPOCK1	SPON1	SRPX2	SULF1	TCF4
	THBS2	THY1	VCAN	ZEB1	

The claims defining the invention are as follows:

1. A method for predicting the clinical outcome of a human patient diagnosed with breast cancer comprising:
 - (a) quantitatively measuring a level of an RNA transcript of gp130/IL6ST in a tissue sample obtained from a tumor of the patient;
 - (b) normalizing the expression level of the RNA transcript of gp130/IL6ST to obtain a normalized expression level;
 - (c) comparing the normalized gp130/IL6ST expression level to a normalized gp130/IL6ST expression level obtained from a breast cancer reference set; and
 - (d) determining that the patient has an increased likelihood of good prognosis if the normalized gp130/IL6ST expression level is increased compared to the normalized gp130/IL6ST level obtained from the breast cancer reference set, wherein good prognosis is a reduced likelihood of recurrence or metastasis or increased likelihood of overall survival.
2. The method of claim 1, further comprising generating a report based on the normalized gp130/IL6ST expression level.
3. The method of claim 1 or 2, wherein the tissue sample is a fixed paraffin-embedded tissue.
4. The method of any one of claims 1 to 3, wherein the level of the RNA transcript of gp130/IL6ST is obtained using a PCR-based method.
5. The method of any one of claims 1 to 4, further comprising measuring a level of an RNA transcript of P2RY5.
6. The method of any one of claims 1 to 5, wherein the tissue sample is obtained by core biopsy or fine needle aspiration.
7. The method of any one of claims 1 to 6, wherein the breast cancer is estrogen receptor (ER) positive breast cancer.

8. The method of any one of claims 1 to 7, wherein the level of the RNA transcript of gp130/IL6ST is a crossing point (C_p) value and the normalized gp130/IL6ST expression level is a normalized C_p value.

9. The method of any one of claims 1 to 7, wherein the level of the RNA transcript of gp130/IL6ST is a threshold cycle (C_t) value and the normalized gp130/IL6ST expression level is a normalized C_t value.

10. The method of any one of claims 1 to 9, wherein good prognosis is a reduced likelihood of recurrence or metastasis.

11. A method for predicting the clinical outcome of a human patient diagnosed with breast cancer comprising:

- extracting RNA from a fixed, paraffin-embedded tissue sample obtained from the patient;

- reverse transcribing an RNA transcript of gp130/IL6ST to produce a cDNA of gp130/IL6ST;

- amplifying the cDNA of gp130/IL6ST;

- producing an amplicon of the RNA transcript of gp130/IL6ST;

- quantitatively assaying a level of the amplicon of the RNA transcript of gp130/IL6ST;

- normalizing the level of the amplicon of the RNA transcript of gp130/IL6ST to provide a normalized gp130/IL6ST amplicon level;

- comparing the normalized IL6ST amplicon level to a normalized gp130/IL6ST amplicon level obtained from a breast cancer reference set; and

- determining that the patient has an increased likelihood of good prognosis if the normalized gp130/IL6ST amplicon level is increased compared to the normalized gp130/IL6ST amplicon level obtained from the breast cancer reference set, wherein good prognosis is a reduced likelihood of recurrence or metastasis or increased likelihood of overall survival.

12. The method of claim 11, further comprising: generating a report based on the normalized gp130/IL6ST amplicon level.

13. The method of claim 11 or 12, wherein the cDNA of gp130/IL6ST is amplified using a PCR-based method.
14. The method of any one of claims 11 to 13, further comprising amplifying an RNA transcript of P2RY5 from the fixed, paraffin-embedded tissue sample obtained from the patient.
15. The method of any one of claims 11 to 14, wherein the breast cancer is estrogen receptor (ER) positive breast cancer.
16. The method of any one of claims 11 to 15, wherein the level of the amplicon of the RNA transcript of gp130/IL6ST is a crossing point (C_p) value and the normalized gp130/IL6ST amplicon level is a normalized C_p value.
17. The method of any one of claims 11 to 15, wherein the level of the amplicon of the RNA transcript of gp130/IL6ST is a threshold cycle (C_t) value and the normalized gp130/IL6ST amplicon level is a normalized C_t value.
18. The method of any one of claims 11 to 17, wherein good prognosis is a reduced likelihood of recurrence or metastasis.
19. The method of claim 1 or claim 11, substantially as herein described with reference to the Tables and/or Examples, excluding comparative Examples.

SEQUENCE LISTING

<110> Genomic Health, Inc.
 BAKER, JOFFRE B.
 Cronin, Maureen T.
 Collin, Francois
 Liu, Mei-Lan

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aatgc 66

<210> 1185
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1185
ggctcttgtg cgtactgtcc ttcgggctgg tgacagggaa gacatcactg agcctgccat 60
ctgtgctctt cgtcatctga 80

<210> 1186
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1186
 gggtcaggtg cctcgagatc gggcttgggc ccagagcatg ttccagatcc cagagtttga 60
 gccgagtga cag 73

 <210> 1187
 <211> 81
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1187
 cgttgtcagc acttgggaata caagatgggt gccgggtcat gttaattggg aaaaagaaca 60
 gtccacagga agaggttgaa c 81

 <210> 1188
 <211> 76
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1188
 cctacggcgc ctactacggg cctgggggtg gagatgtgcc ggtacacca cctccaccct 60
 tatatcctct tcgcc 76

 <210> 1189
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1189
 gactcctcag ggcagacttt cttcccagcc tgcagacaac tggcctccag aaaccattga 60
 gtagtgcctt cg 72

 <210> 1190
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1190
 ccgccgtgga cacagactcc ccccagaggg tctttttccg agtggcagct gacatgtttt 60
 ctgacggcaa 70

 <210> 1191

<211> 83
 <212> DNA
 <213> Artificial Sequence

 <220>

 <223> Synthetic oligonucleotide

 <400> 1191
 cctggagggt cctgtacaat ctcatcatgg gactcctgcc cttacccagg ggccacagag 60
 ccccgagat ggagcccaat tag 83

 <210> 1192
 <211> 65
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1192
 actgacaaga ccagcagcat ccagtcacga cccctgccct caccacctaa gttcacctcc 60
 cagga 65

 <210> 1193
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1193
 tgacttccta gtctgtgact ctctgtccag ccctgggaac tttgtcctga cctgtcagtg 60
 gaagaacctc gctca 75

 <210> 1194
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1194
 ccccgagaca acggagataa gtgctgttgc ggatgccaac ggaaagaatc ttgggaaaga 60
 ggccaaacct gag 73

 <210> 1195
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1195
 cagatggacc tagtaccac tgagatttcc acgccgaagg acagcgatgg gaaaaatgcc 60
 cttaaatcat agg 73

 <210> 1196
 <211> 73

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1196
 aaccaccccc tgtcttggag ctccgggtag ctctcaaact cgaggctgcg caccaccttt 60
 cccgtcagct gag 73

 <210> 1197
 <211> 66
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide

 <400> 1197
 gagctccgca aggatgactt caaggggtctc cagcacctct acgccctcgt cctgggtgaac 60
 aacaag 66

 <210> 1198
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1198
 attcctatgg ctctgcaatt gtcaccggtt aactgtggcc tgtgcccagg aagagccatt 60
 cactcctgcc 70

 <210> 1199
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1199
 ctggacggag tagctccaag agctctcact gtgacagccc acctcgctcg cagacaccac 60
 aagatacc 68

 <210> 1200
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1200
 aattttatga gggccacggg tctgtgttcg actcagcctc agggacgact ctgacctott 60
 ggccac 66

 <210> 1201
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

 <400> 1201
 gttgggacac agttggtctg cagtcggccc aggacggtct actcagcaca actgactgct 60
 tca 63

 <210> 1202
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1202
 ccgaggttaa tccagcacgt atggggccaa gtgtaggctc ccagcaggaa ctgagagcgc 60
 catgtctt 68

 <210> 1203
 <211> 82
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1203
 tcaacagaag gctgaaccac tagaaagact acagtcccag caccgacaat tccaagctcg 60
 agtgtctcgg caaactctgt tg 82

 <210> 1204
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1204
 ctgaagcaga tggttcatca tttcctgggc tgtaaacaag agcgagggtta aggttagact 60
 cttgggaatc agc 73

 <210> 1205
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1205
 gaggcaactg cttatggctt aattaagtca gatgcggcca tgactgtcgc tgtaaagatg 60
 ctcaagccga gtgcc 75

 <210> 1206
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 1206

caagagcaga gccaccgtag ccggagtcct agcctcccaa attcggaaat ccaatccaac 60
ggtctca 67

<210> 1207

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1207

gtgactgcac aggactctgg gttcctgctc tgttctgggg tccaaacctt ggtctccctt 60
tggtcct 67

<210> 1208

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1208

tcagctgtga gctgcggata ccgcccggca atgggacctg ctcttaacct caaacctagg 60
accgt 65

<210> 1209

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1209

gcggtatcag gaatttcaac ctagagaacc gagcgggaacg ggaaatcagc aagatgaagc 60
cctctgtcgc 70

<210> 1210

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1210

ctacgagtca gcccatccat ccattggctac cacttcgaca cagcctctcg taagaaagcc 60
gtgggca 67

<210> 1211

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1211
tgatgctgca gagaacttcc agaaagcaca ccgctggcag gacaacatca aggaggaaga 60
catcgtg 67

<210> 1212
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1212
atccattcga tctcaccaag gtttggcctc acaaggacta ccctctcatc ccagttggta 60
aactggtctt aaaccgga 78

<210> 1213
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1213
gtggctcaac attgtgttcc catttcagct gatcagtggg cctccaagga ggggctgtaa 60
aatggaggcc attg 74

<210> 1214
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1214
aggggatggg ctctgtcatt tctcttttga cataatacat tcacctccct gcctcctctc 60
ctttctaccc accccttt 78

<210> 1215
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1215
gaacgcatca tccagagact gcagaggacc tcagccaaga tgaagcgccg cagcagttaa 60
cctatgaccg tgcagagg 78

<210> 1216
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1216
agcagacagt ggtcagtcct ttcttggtc tgctgacact cgagcccaca ttccgtcacc 60
tgctcagaat catgcag 77

<210> 1217
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1217
aggttctgag ctctggcttt gccttggtt tgccagggct ctgtgaccag gaaggaagtc 60
agcat 65

<210> 1218
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1218
ttcaggttgt tgcaggagac catgtacatg actgtctcca ttattgatcg gttcatgcag 60
aataattgtg tgcccaagaa gatg 84

<210> 1219
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1219
cctctgtgct acagattata cctttgccat gtaccgcga tccatgatcg ccacgggcag 60
cattggggct gcagtg 76

<210> 1220
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1220
ggtcaccaag aaacatcagt atgaaattag gaattgttgg ccacctgtat tatctggggg 60
gatcagtcct tgcattatca ttgaa 85

<210> 1221
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1221
cagactgaat gggggtgggg ggggcgcctt aggtacttat tccagatgcc ttctccagac 60

aaaccag 67

<210> 1222
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1222
 ggatgacatg cactcagctc ttggctccac tgggatggga ggagaggaca agggaaatgt 60
 cagg 64

<210> 1223
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1223
 ggagtggaag gaactggaaa cattattccg tatacgcacc attcggtcat ttgagggaat 60
 tcgtagatac gcccatga 78

<210> 1224
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1224
 tccaactaat gccaccacca aggcggctgg tgggtgccctg cagtcaacag ccagtctctt 60
 cgtggtctca ctctctc 77

<210> 1225
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1225
 gtgctggagt cgggactaac ccaggctcct tgtcccaagt tccactgctg cctcttgaat 60
 gcaggga 67

<210> 1226
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1226
 atcaccgaca gcacagacag aatccctgct accaatatgg actccagtca tagtacaacg 60
 cttcagccta ctgcaaatcc aaacacaggt 90

<210> 1227
 <211> 78
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1227
 gacgaagaca gtccctggat caccgacagc acagacagaa tccctgctac cagagaccaa 60
 gacacattcc accccagt 78

 <210> 1228
 <211> 78
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1228
 ctcataccag ccattcaatg caaggaagga caacaccaag cccagaggac agttcctgga 60
 ctgatttctt caacccaa 78

 <210> 1229
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1229
 tggttcccag ccctgtgtcc acctccaagc ccagattcag attcgagtca tgtacacaac 60
 ccagggtgga ggag 74

 <210> 1230
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1230
 gtgcaggctc aggtgaagtg ctgcggctgg gtcagcttct acaactggac agacaacgct 60
 gagctcatga atcgccctga ggtc 84

 <210> 1231
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1231
 tggattggag ttctgggaat gtactggcgc tggcaactgga caacagtgtg tacctgtgga 60
 gtgcaagc 68

 <210> 1232
 <211> 71

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1232
 tcttgctggc tacgcctctt ctgtccctgt tagacgtcct ccgtccatat cagaactgtg 60
 ccacaatgca g 71

 <210> 1233
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1233
 ggtgagcaga agtggcctat atcgctcccc gtcgatgccg gagaacttga acaggccaag 60
 actgaag 67

 <210> 1234
 <211> 77
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1234
 gcagtcgct gtgttcaata tgatggcagg agggttgtta gtggagcata tgattttatg 60
 gtaaaggtgt gggatcc 77

 <210> 1235
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1235
 gagctgaaag acgcacactg tcagaggaaa ctggccatgc aggaattcat ggagatcaat 60
 gagcggc 67

 <210> 1236
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1236
 cggagaaggg caccagtaag ctgccaaga gcctgtcatc cagccccgtg aagaaggcca 60
 atgacgg 67

 <210> 1237
 <211> 70
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

 <400> 1237
 gtcggcagaa gcaggacttg tacctttctgc ccatagtgat cagcgatggc ggcattccgc 60
 ccatgagtag 70

 <210> 1238
 <211> 71
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1238
 acccatgtac cgtcctcggc cagccaaccc agatgaaatc ggcaacttta taattgagaa 60
 cctgaaggcg g 71

 <210> 1239
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1239
 ccttcccatc agcacagttc gtgaggtggc tttactgagg cgactggagg cttttgagca 60
 tcccaa 66

 <210> 1240
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1240
 aagccctatc cgatgtaccc ggccacaaca tccctgggtga acgtcgtgcc caaactcaat 60
 gccacag 67

 <210> 1241
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1241
 tggatctcta ccagcaatgt ggaattatca cccatcatca tccaatcgca gatggaggga 60
 ctctgacat 70

 <210> 1242
 <211> 71
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 1242

acttgccctgt tcagagcact cattccttcc cccccccagt cctgtcctat cactctaatt 60
cggatttgcc a 71

<210> 1243

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1243

ttggttttgc tcggatactt gccaaaatga gactctccgt cggcagctgg gggaaggggc 60
tgagac 66

<210> 1244

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1244

tgacaatcag cacacctgca ttcaccgctc ggaagagggc ctgagctgca tgaataagga 60
tcacggctgt agtcaca 77

<210> 1245

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1245

taaattcact cgtgggtgtgg acttcaattg gcaagcccag gccctattgg ccctacaaga 60
ggc 63

<210> 1246

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1246

ctgaaggagc tccaagacct cgctctccaa ggcgccaagg agagggcaca tcagcagaag 60
aaacacagcg gttttg 76

<210> 1247

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1247
ccagaatgca cgctacagga aaacccattc ttctcccagc cgggtgcccc aatacttcag 60
tgcattgggc 69

<210> 1248
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1248
ccaccatagg cagaggcagg ccttctctaca cctactccc tgtgcctcca gcctcgacta 60
gtccctagca ctgcagact 80

<210> 1249
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1249
gaggccagtg gtggaaacag gtgtggagct gatgagtctg ccctaccgcc tgggtgtttgc 60
tgtggcctcg ga 72

<210> 1250
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1250
aaggaagtgg tccctctgtg gcaagtgatg aagtctccag ctttgcctca gctctcccag 60
acagaaagac tgcgtc 76

<210> 1251
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1251
agaatgggtg tgaaggcgtc tcaaacaggc tttgtgggtc tgggtgctgt ccagtgtgtc 60
tctgca 66

<210> 1252
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1252
ggctggacgt ggttttgtct gctgcgcccg ctcttcgcgc tctcgtttca tttctgtcag 60

<210> 1253

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1253

ggctgctttg ctgcaactgt ccaccccgca cagacaagcc ttactccgcc aagtattctg 60
ctgcccgctc tg 72

<210> 1254

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1254

cgggtacttga gcaatgccta cgcccgggaa gaattcgctt ccacctgtcc agatgatgag 60
gagatcga 68

<210> 1255

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1255

ccccaggata cctaccacta cctgcccttc agcctgcccc accggaggcc tcaattcttc 60
tttcccaagt cccgca 76

<210> 1256

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1256

aaatcgcagc ttatcacaag gcaactcagtt accgagccac gtcacgcca caacaggggt 60
accaaca 67

<210> 1257

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1257

gtggccatcc agctgacctt cctgcgcctg atgtccaccg aggctccca gaacatcacc 60
taccactg 68

<210> 1258
 <211> 80
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1258
 cagccaagaa ctggtatagg agctccaagg acaagaaaca cgtctggcta ggagaaacta 60
 tcaatgctgg cagccagttt 80

 <210> 1259
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1259
 ccttatcggc tggaacgagt tcatcctgca gcccatccac aacctgctca tgggtgacac 60
 caaggag 67

 <210> 1260
 <211> 81
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1260
 cgacagttgc gatgaaagtt ctaatctctt cctcctcct gttgctgcca ctaatgctga 60
 tgtccatggt ctctagcagc c 81

 <210> 1261
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1261
 atgccagtg ttctgactt cgaaacgcta ttctcacagg ttcagctctt catcagcact 60
 tgtaatgggg ag 72

 <210> 1262
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1262
 gatgtgattg aggtgcatgg aaaacatgaa gagcgccagg atgaacatgg tttcatctcc 60
 agggagttc 69

 <210> 1263
 <211> 78

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1263
 aagtcctgaa attgcatca gatattgcag taccgattcc aaaagaccat caggttctaa 60
 tcaaggtcca tgcattgtg 78

 <210> 1264
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1264
 cagcaagaac tgcaacaaca gctttgctga atgctccagc caaggccatg agaggcagtc 60
 cgagggat 68

 <210> 1265
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1265
 tgcagcggct gattgacagt cagatggaga cctcgtgcc aattacattt gagtttgtag 60
 accaggaaca gttg 74

 <210> 1266
 <211> 80
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1266
 gagcacaacc aaacctacga gtgcagggcc cacaacagcg tggggagtgg ctctggggcc 60
 ttcataccca tctctgcagg 80

 <210> 1267
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1267
 taccacaccc agcattcctc ctgatcccag agaaatcgga tctgcgaaca gtggcaccag 60
 cctctag 67

 <210> 1268
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

 <400> 1268
 cctgaacatg aaggagctga agctgctgca gaccatcggg aagggggagt tcggagacgt 60
 gatg 64

 <210> 1269
 <211> 76
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1269
 gagttcaagt gccctgacgg cgagggtcatg aagaagaaca tgatgttcat caagacctgt 60
 gcctgccatt acaact 76

 <210> 1270
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1270
 gctcacttcg gctaaaatgc agaaatgcat gctgtcagcg ttggtatttc acattcaatg 60
 gagctga 67

 <210> 1271
 <211> 80
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1271
 gtacatgac cctgtgaga aggtgtccac cctgcccgcg atcacactga agctgggagg 60
 caaaggctac aagctgtccc 80

 <210> 1272
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1272
 tgtctcactg agcgagcaga atctggtgga ctgttcgcgt cctcaaggca atcagggctg 60
 caatggt 67

 <210> 1273
 <211> 79
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 1273
accaggcaat aacctaacag cacccattat aggtgcaata tgggcatata tctccattgt 60
gtcttggett ggagaacag 79

<210> 1274
<211> 68
<212> DNA
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<220>
<223> Synthetic oligonucleotide

<400> 1274
ggagcaaat cgatgcagtg cttccaagga tggaccacac agaggctgcc tctcccatca 60
cttccta 68

<210> 1275
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1275
gagctacaga tgcccatgcc gattcttcga aagccatggt gccagagcca acgtcaagca 60
tctcaaa 67

<210> 1276
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1276
tgcgcccttt cctctgtaca tataccetta agaacgcccc ctccacacac tgccccccag 60
tatatgccgc attg 74

<210> 1277
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1277
tgaccgcttc taccccaatg acttgtgggt ggttgtgttc cagtttcagc acatcatggt 60
tggccttacc ct 72

<210> 1278
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1278
ccggagtgac tctatcacca acatgctgga cacactgatg caagccaaga tgaactcaga 60
taatggcaat gctggc 76

<210> 1279
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1279
tccttatagg tactttcagc catttggctt tgggccccgt ggctgtgcag gaaagtacat 60
cgccatgggtg 70

<210> 1280
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1280
ccagctttgt gcctgtcact attcctcatg ccaccactgc caacacctct gtcttgggct 60
accacattcc c 71

<210> 1281
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1281
tgctcattct tgaggagcat taaggatatt cgaaactgcc aagggtgctg gtgcggatgg 60
acactaatgc agccac 76

<210> 1282
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1282
tgggtgggtct aggtgggtgta actgtcacac tccctcaggc aggaccatgg aacacagcat 60
ctttggt 67

<210> 1283
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1283

aaatgtcctc ctcgactgct ccgcggagtc cgaccgagga gttccagtga tcaagtggaa 60
gaaagatggc attca 75

<210> 1284
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1284
ggtcaccgtt ggtgtcatca cagtgtctgggt agtgggtcatc gtggctgtga tttgcacccg 60
acgtc 66

<210> 1285
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1285
atggagatgt ggtcattcct agtgattatt ttcagatagt gggaggaagc aacttacgga 60
tacttgggggt ggtg 74

<210> 1286
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1286
gccgccacaa gactaaggaa tggccacccc gcccaagaga agctgcccgt ctttctcagc 60
cagctctgag gggacccgca tcaagaaaat ctccatcgaa gggaacatcg 110

<210> 1287
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1287
tccaattcca gcatactgt ggagaaaagc tgtttgtctc ccagcatac tttatcgct 60
tactgcc 68

<210> 1288
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1288
gattcagacg aggatgagcc ttgtgccatc agtggcaaataa ggactttcca aagggacagc 60

aagaggtg 68

<210> 1289
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1289
 cacggaggta taaggcagga gcctacctgg acatccctgc tcagccccgc ggctggacct 60
 tccttct 67

<210> 1290
 <211> 84
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1290
 ctctgagaca gtgcttcgat gactttgcag acttggtgcc ctttgactcc tgggagccgc 60
 tcatgaggaa gttgggcctc atgg 84

<210> 1291
 <211> 73
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1291
 tggcactact gcatgattga catagagaag atcagggcca tgacaatcgc caagctgaaa 60
 acaatgcggc agg 73

<210> 1292
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1292
 aaatcgctgg gaacaagtgc cgtaattaa ggaaaagttg agccagggcg tgaccctcgt 60
 cgtggacaga tacgcatt 78

<210> 1293
 <211> 76
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1293
 agacatcagc tcctggttca acgaggccat tgacttcata gactccatca agaatgctgg 60
 aggaagggtg ttgtc 76

<210> 1294
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1294
 tggtagcatg ggaggagctg cgggagatgg actgcagtgt gctcaaaagg ctgatgaacc 60
 gggacgag 68

 <210> 1295

 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1295
 actccctcta cccttgagca agggcagggg tccctgagct gttcttctgc ccataactga 60
 aggaactgag gcctg 75

 <210> 1296
 <211> 76
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1296
 ctgctggatg accttctctc cagagtggct caccagaagc cccaacctca acaccagcaa 60
 ctggctgtac tgttgg 76

 <210> 1297
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1297
 tgccacctgg acatcatttg ggtcaacact ccgagcacg ttgttccgta tggacttgga 60
 agccctaggt cca 73

 <210> 1298
 <211> 79
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1298
 cgacaaggag tgcgtctact tctgccactt ggacatcatc tgggtgaaca ctctgaaca 60
 gacagctcct tacggcctg 79

<210> 1299
 <211> 76
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1299
 tttcctcaaa tttgcctcaa gatggaaacc ctttgctca gggcatcctt ttggctggca 60
 ctggttgat gtgtaa 76

 <210> 1300
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1300
 actgtgaact gctggtgca gtgtccacat gacaaagggg caggtagcac cctctctcac 60
 ccatgctgtg gt 72

 <210> 1301
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1301
 cgagtggaga ctggtgttct caaaccggg atggtgggtca cctttgctcc agtcaacgtt 60
 acaacgg 67

 <210> 1302
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1302
 atggactcca cagagccggc ctacagcgag aagcgctacg acgagatcgt caaggaagtc 60
 agcgcc 66

 <210> 1303
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1303
 ttgaacagag cctgaccaag agggatgagt tcgagtttct ggagaaagca tcaaaaactgc 60
 gaggaatctc aaca 74

 <210> 1304
 <211> 76

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1304
 gtccccgctg cagatctctg acccggttcgg atcctttcct cactcgccca ccatggacaa 60
 ctaccctaag ctggag 76

 <210> 1305
 <211> 78
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1305
 ccatgtggat gaatgaggtg tctcctttcc ataccagtc tcaccttctc cccaccctac 60
 ctcacctctt ctcaggca 78

 <210> 1306
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1306
 ggcggtgaag agtcacagtt tgagatggac atttaaagca ccagccatcg tgtggagcac 60
 taccaa 66

 <210> 1307
 <211> 71
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1307
 tcgagggcaa gaagagcaag cacgcgcca gaggcacca cctgtgggag ttcacccggg 60
 acatcctcat c 71

 <210> 1308
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1308
 gctagtactt tgatgctccc ttgatggggg ccagagagcc tccctgcagc caccagactt 60
 ggctccagc tgttc 75

 <210> 1309
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

 <400> 1309
 caaggccgtg aacgagaagt cctgcaactg cctcctgctc aaagtcaacc agattggctc 60
 cgtgaccg 68

 <210> 1310
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1310
 agccccagca actacagtct gggatgccaa ggccagccat gatgtcagtg gccagcatg 60
 gtcaaccttt gaaca 75

 <210> 1311
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1311
 gggccctcca gaacaatgat gggctttatg atcctgactg cgatgagagc gggctcttta 60
 aggccaaagca gtgca 75

 <210> 1312
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1312
 cgctgttca ccaagattga caccattgag cccgatgaga tcaccgtcag cagcgacttc 60
 gaggcacgcc ac 72

 <210> 1313
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1313
 caaccaggca gctccatcgg cagtgtccat catgcatcag gtgagccgca ccgtggacag 60
 cattac 66

 <210> 1314
 <211> 77
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 1314
tgaacggggt atcctcctta gccacggggc ccgtcccatt tgagcctgtc aatgtcacca 60
ctgaccgaga ggtacct 77

<210> 1315
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1315
tgggtccatcg ccagttatca catctgtatg cggaacctca aaagagtccc tgggtgtgaag 60
caagatcgct agaaca 76

<210> 1316
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1316
tggctcttaa tcagtttcgt tacctgcctc tggagaattt acgcattatt cgtgggacaa 60
aactttatga ggatcgatat gccttg 86

<210> 1317
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1317
gtccaggtgg atgtgaaaga tccccagcag gccctcaagg agctggctaa gatgtgtatc 60
ctggcgg 67

<210> 1318
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1318
ccaacactag gctccccacc agccatatgc cttctcatct gggcacttac tactaaagac 60
ctggcggagg 70

<210> 1319
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1319
 ggcattgagc ctctctacat caaggcagag ccggccagcc ctgacagtcc aaaggggttc 60
 tcggaga 67

<210> 1320
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1320
 gtcactccgc caccgtagaa tcgcctacca tttgggtgcaa gcaaaaagca atcagcaatt 60
 ggacag 66

<210> 1321
 <211> 70
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1321
 acccccagac cggatcaggc aagctggccc tcatgtcccc ttcacggtgt ttgaggaagt 60
 ctgccctaca 70

<210> 1322
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1322
 ccagcaccat tggtgaagat ccccagacca agtgtgaata catgctcaac tcgatgccca 60
 agagact 67

<210> 1323
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1323
 cgtgggtgcc ctctatgacc tgctgctgga gatgctggac gccaccgcc tacatgcgcc 60
 cactagcc 68

<210> 1324
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1324

accatgtatc gagagggggcc cccttaccag aggcgagggtt cccttcagct gtggcagttc 60
ctgggtca 67

<210> 1325

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1325

tggaacagc gaaggataca gcctgtgcac atcctgactt ctgtgagctc attgcgcggg 60
actagggagt gttcgggtg 78

<210> 1326

<211> 73

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1326

gtgaaggatg tgaagcagac gtacttggca cgggtcttct cctacccggc agggaatgtg 60
gagagcaccg gtt 73

<210> 1327

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1327

ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc cacatgaccc 60
acttcc 66

<210> 1328

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1328

gcctcttctt gttcgacggc tcgcccacct acgtactggc ctacacccag agctaccggg 60
caaagc 66

<210> 1329

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1329

gagggactgt tggcatgcag tgccctccca gagaccaacg ttcaagcagt tggtagaaga 60
cttgatcga attctcactc 80

<210> 1330
 <211> 81
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1330
 ctggcttaag gatggacagg cctttcatgg ggagaaccgc attggaggca ttcggctgcg 60
 ccatcagcac tggagtctcg t 81

 <210> 1331
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1331
 ccagtggagc gcttccatga cctgcgtcct gatgaagtgg ccgatttggt tcagacgacc 60
 cagagag 67

 <210> 1332
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1332
 gacatctgcg ctccatcctc gggaccctga cagtggagca gatttatcag gaccgggacc 60
 agtttg 66

 <210> 1333
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1333
 ggaagtgaca gacgtgaagg tcaccatcat gtggacaccg cctgagagtg cagtgaccgg 60
 ctaccgtgt 69

 <210> 1334
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1334
 cgagcccttt gatgacttcc tgttcccagc atcatccagg ccagtggtct ctgagacagc 60
 ccgctcc 67

 <210> 1335

<211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1335
 gagaacaagc agggctggca gaacagcatc cgccacaacc tctcgctcaa cgagtgcctc 60
 gtcaag 66

 <210> 1336
 <211> 83
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1336
 tgaagtccag gacgatgatg cgctctctc gcccatgctc tacagcagct cagccagcct 60
 gtcaccttca gtaagcaagc cgt 83

 <210> 1337
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1337
 cgacagagct tgtgcaccta agctgcagac caagcctttg cccagaattt aaggattcca 60
 atggacgacc 70

 <210> 1338
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1338
 ctgtttgctg tccggaggca cctgtggggg agccatggaa acagcacatt cccagagttc 60
 ctccac 66

 <210> 1339
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1339
 ccagctgcta ctttgacatc gagtggcgtg accggcgcat cacactgagg gcgtccaatg 60
 gcaagtttgt gacc 74

 <210> 1340
 <211> 80
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1340

ggataattca gacaacaaca ccattcttgt gcaaggcctg ggtgagaatg ttacaattga 60
gtctgtggct gattacttca 80

<210> 1341

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1341

gaagcgaga tcatgaagaa gctgaagcac gacaagctgg tccagctcta tgcagtgggtg 60
tctgaggag 69

<210> 1342

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1342

tcagcagcaa gggcatcatg gaggaggatg aggctgcgg gcgccagtac acgctcaaga 60
aaaccacc 68

<210> 1343

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1343

tgtttggagg gaagggctgg ggctctgagc cagattccac acctcacgtt cagtcacagc 60
cctcagctat ctcc 74

<210> 1344

<211> 73

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1344

gtgctgggtga cgaatccaca ttcatctcaa tggaaggatc ctgccttaag tcaacttatt 60
tgtttttgcc ggg 73

<210> 1345

<211> 70

<212> DNA

<213> Artificial Sequence

<220>
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 <400> 1345
 accctcgaca agaccacact ttgggacttg ggagctgggg ctgaagttgc tctgtacca 60
 tgaactcca 70

 <210> 1346
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1346
 attccacca tggcaaattc catggcaccg tcaaggctga gaacgggaag cttgtcatca 60
 atggaaatcc catc 74

 <210> 1347
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1347
 caaaggagct cactgtggtg tctgtgttcc aaccactgaa tctggacccc atctgtgaat 60
 aagccattct gactc 75

 <210> 1348
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1348
 ttgggaaata tttgggcatt ggtctggcca agtctacaat gtcccaatat caaggacaac 60
 caccctagct tct 73

 <210> 1349
 <211> 83
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1349
 gcatgggaac catcaaccag caggccatgg accaacttca ctatgtgaca gagctgacag 60
 atcgaatcaa ggcaaactcc tca 83

 <210> 1350
 <211> 85
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 1350

tgtagaatca aactcttcat catcaactag aagtgcagtt gacatggcct gttcagtcct 60
tggagttgca cagctggatt ctgtg 85

<210> 1351

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1351

cgctccagac ctatgatgac ttgttagcca aagactgcca ctgcatatga gcagtcctgg 60
tccttcact gt 72

<210> 1352

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1352

gatcccaagg cccaactccc cgaaccactc agggctcctgt ggacagctca cctagctgca 60
atggct 66

<210> 1353

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1353

gttcactggg ggtgtatggg gtagatgggt ggagagggag gggataagag aggtgcatgt 60
tggatatt 68

<210> 1354

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1354

tgtcatgtac gacggcttct ccatgcagcg gctgggtgaag tgcaacgcct ggccttgctc 60
caacactgtg gact 74

<210> 1355

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1355
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 gtacgca 67

<210> 1356
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1356
 ttctggacct gggaccttag gagccgggtg acagcactaa ccagacctcc agccactcac 60
 agctcttt 68

<210> 1357
 <211> 70
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1357
 cgtgcctcta caccatcttc ctcttcccca tcggctttgt gggcaacatc ctgatcctgg 60
 tggagaacat 70

<210> 1358
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1358
 agtacaagca ggctgccaaag tgccctcctgc tggcttcctt tgatcactgt gacttccctg 60
 agctgc 66

<210> 1359
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1359
 gcttatgacc gaccccaagc tcatcacctg gtctccgggtg tgtcgcaacg atgttgctg 60
 gaacttt 67

<210> 1360
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1360

cacacagatc tctactcca tccagtcctg aggagcctta ggatgcagca tgccttcagg 60
agacactgct ggacc 75

<210> 1361
<211> 66
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1361
ctgagtgtgg ttgcggtatc ctggccttcc cgtgtaacca gttcgggaag caggagccag 60
ggagta 66

<210> 1362
<211> 67
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1362
ccatctgcat ccatcttggt tgggctcccc acccttgaga agtgctcag ataataccct 60
ggtggcc 67

<210> 1363
<211> 71
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1363
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agaaaggctt c 71

<210> 1364
<211> 73
<212> DNA
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<220>

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<400> 1364
tgcttaggtg cggtaaaacc agcgcttgct cgatgcaccg ttgcggtggt aaactgacgc 60
attcaggctc ttg 73

<210> 1365
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<212> DNA
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aagt 64

<210> 1366
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<220>
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<400> 1366
 tgccccaag acactgtgtg tgacctgac cagagtaagt gcctctccaa ggagaacgct 60
 accacggacc tc 72

<210> 1367
 <211> 86
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1367
 aagctatgag gaaaagaagt acacgatggg ggacgctcct gattatgaca gaagccagtg 60
 gctgaatgaa aaattcaagc tgggcc 86

<210> 1368
 <211> 71
 <212> DNA
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<220>
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<400> 1368
 ctgggctgtg aggctgagag tgaatctgct ttacgagggt aggcggggaa tcagaaaagg 60
 agcagattcg c 71

<210> 1369
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1369
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 tttcttgg 68

<210> 1370
 <211> 76
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1370
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 aaagattcga gtggac 76

<210> 1371
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1371
 caccatcccc accctgtctt ccacagccgc ctgaaagcca caatgagaat gatgcacact 60
 gaggcc 66

 <210> 1372
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1372
 cccactcagt agccaagtca caatgttttg aaaacagccc gtttacttga gcaagactga 60
 taccacctgc gtg 73

 <210> 1373
 <211> 70
 <212> DNA
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 <220>
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 <400> 1373
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 gtgcttaaga 70

 <210> 1374
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
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 ggagtacagc aagc 74

 <210> 1375
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 <220>
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 <400> 1375
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 gtggag 66

 <210> 1376
 <211> 70

<212> DNA
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 <220>
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 <400> 1376
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 ttgcgagagg 70

 <210> 1377
 <211> 68

 <212> DNA
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 <220>
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 <400> 1377
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 gcacctcc 68

 <210> 1378
 <211> 72
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 <220>
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 <400> 1378
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 ccagctccct gc 72

 <210> 1379
 <211> 73
 <212> DNA
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 <220>
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 <400> 1379
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 atggtgctgc tca 73

 <210> 1380
 <211> 71
 <212> DNA
 <213> Artificial Sequence

 <220>
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 agatgacaag c 71

 <210> 1381
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<213> Artificial Sequence

<220>

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<400> 1381

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tacgcagaca cgc 73

<210> 1382

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1382

agcaggagcg accaactgat cgcacacatg ctttgtttgg atatggagtg aacacaatta 60
tgtaccaaatt ttaacttggc aaac 84

<210> 1383

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

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<400> 1383

gcagcagtcg gcttctctac gcagaaccgg ggagtaggag actcagaatc gaatctcttc 60
tccctccc 68

<210> 1384

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

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<400> 1384

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gcgactcgg 69

<210> 1385

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1385

tcccttgtgt tccttctgtg aagaagccct gttctcggtg ccctaattca tcttttaatc 60
atgagcctgt ttattgcc 78

<210> 1386

<211> 71

<212> DNA

<213> Artificial Sequence

<220>
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 <400> 1386
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 gaaaccctgt g 71

 <210> 1387
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1387
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 cttccaac 68

 <210> 1388
 <211> 78
 <212> DNA
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 <220>
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 <400> 1388
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 caagtctttc gcgaggcg 78

 <210> 1389
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1389
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 cgcaggca 68

 <210> 1390
 <211> 77
 <212> DNA
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 <220>
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 <400> 1390
 cagtctcgcc atgttgaagt cagaatggcc tgtattcact atcttcgaga gaacagagag 60
 aaatttgaag cgtttat 77

 <210> 1391
 <211> 70
 <212> DNA
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 <220>

<223> Synthetic oligonucleotide

<400> 1391
ctgctgcgac agtccactac ctttttcgag agtgactccc gttgtcccaa ggcttcccag 60
agcgaacctg 70

<210> 1392
<211> 63
<212> DNA
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<220>
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<400> 1392
ggctccgcttc gtcttttcgag agtgactccc gcgggtcccaa ggctttccag agcgaacctg 60
tgc 63

<210> 1393
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1393
ttcagtgtgt ccagtgcac tttagtggag gttcacaagt ctgaggaaaa tgaggagcca 60
atggaaacag at 72

<210> 1394
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1394
ggctagtaga actggatccc aacaccaaac tottaattag acctaggcct cagctgcact 60
gcccgaagaaag catttgggca gacc 84

<210> 1395
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1395
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gtgtagatgt agc 73

<210> 1396
<211> 84
<212> DNA
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<220>
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<400> 1396
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gtccagagca gagtcagcca gcat 84

<210> 1397
<211> 83
<212> DNA
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<220>
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<400> 1397
gaataccaca ctttctgcta caaacactggg ctatggagag gacgccacgc ctggcacagg 60
gtatacaggg ttagctgcaa tcc 83

<210> 1398
<211> 68
<212> DNA
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<220>
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<400> 1398
gcagacagtg accatctaca gctttccggc gcccaacgtg attctgacga agccagaggt 60
ctcagaag 68

<210> 1399
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1399
agaaccgcaa ggtgagcaag gtggagattc tccagcacgt catcgactac atcagggacc 60
ttcagttgga 70

<210> 1400
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1400
tggcctggct cttaatttgc ttttgTTTTG cccagtatag actcggaagt aacagttata 60
gctagtggtc ttgcatgatt gca 83

<210> 1401
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1401
ggtggagagt ggagccatga ccaaggacct ggcgggctgc attcacggcc tcagcaatgt 60

gaagctgaac gagc

74

<210> 1402

<211> 83

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1402

gcatggtagc cgaagatttc acagtcaaaa tcggagattt tggatatgacg cgagatatct 60
atgagacaga ctattaccgg aaa 83

<210> 1403

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1403

ccgtgcttcc ggacaacttc cccagatacc ccgtgggcaa gttcttccaa tatgacacct 60
ggaagcagtc ca 72

<210> 1404

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1404

tgaaccgcag agaccaacag aggaatccag gcacctctac cacgccctcc cagcccaatt 60
ctgcgggtgt ccaagac 77

<210> 1405

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1405

gggtcactat ggagttcaaa ggacagaact cctgcctggt gaccgggaca acctggccat 60
tcagaccc 68

<210> 1406

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1406

gcctcccata gctccttacc ccagccctac acgaaaggac ctgcttctcc acatgcaaga 60
gctctg 66

<210> 1407
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1407
 aaggaaccat ctactgtgt gtaaacaatga cttccaagct ggccgtggct ctcttggcag 60
 ccttcctgat 70

 <210> 1408
 <211> 79
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1408
 ggcgctgtca tcgatttctt ccctgtgaaa acaagagcaa ggccgtggag caggtgaaga 60
 atgcctttaa taagctcca 79

 <210> 1409
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1409
 tggaaggttc cacaagtcac cctgtgatca acagtaccgc tatgggacaa agctgcaagg 60
 tcaaga 66

 <210> 1410
 <211> 76
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1410
 accctctggg ggtaaatgga cattttccta catcggttc cctgtagagc tgaacacagt 60
 ctatttcatt ggggcc 76

 <210> 1411
 <211> 74
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide

 <400> 1411
 ggcctaagt tccagatcct tcaaagagtc atattgccca gtggtcacct cacactcctc 60
 caaggcaciaa tttt 74

 <210> 1412
 <211> 66

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1412
 actttcctgc gaggtcagtc aaggctttgg gggctctggt ttgaatgtgg atcaccactc 60
 ggagtt 66

 <210> 1413
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1413
 gtgcccgcgc catatagcag gcacgtccgg gtcctcactg tccttccact caacagtcac 60
 caaccactac cg 72

 <210> 1414
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1414
 agtccagccg agatgctaag agcaaggcca agaggaagtc atgtggggat tccagccctg 60
 ataccttct 69

 <210> 1415
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1415
 ccacagctca cttctgtca ggtgtccatc ccagctccag ccagctccca gagaggaaga 60
 gactggcact gagg 74

 <210> 1416
 <211> 77
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1416
 ccatgatcct cactctgctg gtggactata cactccagac ctcgcttagc atggtaaadc 60
 accggctaca aagcttc 77

 <210> 1417
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

 <400> 1417
 caacgcttca gtgatcaatc ccggggcgat ttacagatgc aggatcggaa agaatcccgg 60
 ccagac 66

 <210> 1418
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1418
 aggccagccc tacattatca gagcaagagc cggatagagg acaaggctca gatcttgctg 60
 gactgtggag aagac 75

 <210> 1419
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1419
 cagtgacaaa cagcccttcc aacccaagga atcccacaaa agatggcgat gacgcccattg 60
 aggctaaac 69

 <210> 1420
 <211> 79
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1420
 actcggactg cacaagctat ttttgatgac agctatttgg gttattctgt ggctgtcgga 60
 gatttcaatg gtgatggca 79

 <210> 1421
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1421
 tcagaattgg atttggctca tttgtggaaa agactgtgat gccttacatt agcacaacac 60
 cagctaagct cagg 74

 <210> 1422
 <211> 78
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 1422
accgggggagc cctacatgac gaaaataacct gcaaccgtta ctgccgtgac gagattgagt 60
cagtgaaaga gcttaagg 78

<210> 1423
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1423
caaggtgccc tcagtggagc tcaccaacct gtacccgatat tgcgactatg agatgaaggt 60
gtgcgc 66

<210> 1424
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1424
tcgtgaaaga tgaccaggag gctgtgctat gtttctacaa aaccgccaag gactgcgtca 60
tgatgttcac c 71

<210> 1425
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1425
tggcttacac tggcaatggt agtttctgtg gttggctggg aaatcgagtg ccgcatctca 60
cagctatgc 69

<210> 1426
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1426
ctgtcagctg ctgcttgggg tcaagggaca cgccttctga acgtccoctg cccctttacg 60
gacacccct 70

<210> 1427
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1427
cggactttgg gtgcgacttg acgagcgggtg gttcgacaag tggccttgcg ggccggatcg 60
tcccagtga agagttgtaa 80

<210> 1428
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1428
aagcccgagg cactcattgt tgccttcaa gctgccaatg aagacctcag gaccaagctc 60
acagaca 67

<210> 1429
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1429
gctgggaggc aggacttctt ctcaaggcc atgctgacca tcagctggct cactctgacc 60
tgcttc 66

<210> 1430
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1430
gagctccatg gctcatcccc agcagtgagc tcagaggaat gcacaccacag taggattcag 60
tgggtgtga 69

<210> 1431
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1431
tctcttgacg gaagccagac aacagtcagt ggcccatcag caatcagggt ctgaattggc 60
cctacgg 67

<210> 1432
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1432
aattcctgct caaaagaaa gtcttcgaag ccgctccact cgcattgtcca ctgtctcaga 60

gcttcgcac acg

73

<210> 1433

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1433

caccccggt tcaacaacag cctccccaac aaagaccacc gcaatgacat catgctgggtg 60
aagatg 66

<210> 1434

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1434

gacgtgaggg tcttgattct ccttggtttt accccagctc catccttgca tcaactgggga 60
ggacgtgatg agtgagga 78

<210> 1435

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1435

catcctcatg gattgggtgtg tttcgtaaca gcagtcacat tccatgggtg acaatgaatg 60
gtttggc 67

<210> 1436

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1436

ccacctcgcc atgatttttc ctttgaccgg gtattccac caggaagtgg acaggatgaa 60
gtgtttgaag agattgc 77

<210> 1437

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1437

atgtgccagt gagcttgagt ccttggagaa acacaagcac ctgctagaaa gtactgttaa 60
ccaggggctc a 71

<210> 1438
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1438
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 gaagctt 67

 <210> 1439
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1439
 cttgctggcc aatgcctaca tctacgttgt ccagctgccca gccaaagatcc tgactgcgga 60
 caatca 66

 <210> 1440
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1440
 cagatgaggc acatggagac ccaggccaag gacctgagga atcagttgct caactaccgt 60
 tctgccattt caa 73

 <210> 1441
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1441
 ctcttgcca acagcactgc actagaagag gccatgctcc aggaacagca gaggctgggc 60
 cttgtgt 67

 <210> 1442
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1442
 caaggagact gggaggtgtc tcaagtgcct gtaccacacg gaagggaac actgtcagtt 60
 ctgccg 66

 <210> 1443
 <211> 67

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1443
 actgaccaag cctgagacct actgcaccca gtatggcgag tggcagatga aatgctgcaa 60
 gtgtgac 67

 <210> 1444
 <211> 80
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1444
 actcaagcgg aaattgaagc agataggtct taccagcaca gtctccgcct cctggattca 60
 gtgtctcggc ttcagggagt 80

 <210> 1445
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1445
 agcgatgaag atggtcgcgc cctggacgag gttctactcc aacagctgct gcttgtgctg 60
 ccatgtc 67

 <210> 1446
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1446
 agcggaaaat ggcagacaat ttttcgctcc atgatgcgtt atctgggtct ggaaacccaa 60
 accctcaag 69

 <210> 1447
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1447
 gcttcaggtg ttgtgactgc agtgccctcc tgctgcacca gtactatgag aaggatgggc 60
 agctctt 67

 <210> 1448
 <211> 71
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

 <400> 1448
 tgaacagtaa tggggagctg taccatgagc agtgtttcgt gtgcgctcag tgcttccagc 60
 agttccaga a 71

 <210> 1449
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1449
 tgcaaacgct ggtgtcacag ccagccccc aactgacctc atctggaaga accagaactc 60
 gtgggg 66

 <210> 1450
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1450
 ccaatgggag aacaacgggc aggtgttcag cttgctgagc ctggggtcac agtaccagcc 60
 tcagcg 66

 <210> 1451
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1451
 ctgcaacacc gaagtggact gttactccag gggacaagcc ttccaccccc agcctgtgtc 60
 cagagac 67

 <210> 1452
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1452
 agaccaagct ggaagcagag aagttgaaag tgcaggccct gaaggaccga ggtctttcca 60
 ttcctc 66

 <210> 1453
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 <212> DNA
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<220>
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<400> 1453
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 tgtctgc 67

<210> 1454
 <211> 67
 <212> DNA
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<220>
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<400> 1454
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 ctgtccg 67

<210> 1455
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1455
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 tacggct 67

<210> 1456
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1456
 gacttttgcc cgctaccttt cattccggcg tgacaacaat gagctgttgc tottcatact 60
 gaagcagtta gtggc 75

<210> 1457
 <211> 70
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1457
 aggatcgctt gtcagaagag gagaccggg ttgtcttccg tcagatagta tctgctgttg 60
 cttatgtgca 70

<210> 1458
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1458
 gtgaaatgaa acgcaccaca ctggacagcc ctttggggaa gctggagctg tctggttggtg 60
 agcagggtc 69

<210> 1459
 <211> 79
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1459
 acggatctac cacaccattg catatttgac accccttccc cagccaaata gagctttgag 60
 tttttttggtt ggatatgga 79

<210> 1460
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1460
 gggagatcat cgggacaact ctcccttttga tggacctgga ggaaatcttg ctcatgcttt 60
 tcaaccaggc cc 72

<210> 1461
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1461
 ccaacgcttg ccaaattcctg acaattcaga accagctctc tgtgacccca atttgagttt 60
 tgatgctgtc actaccgt 78

<210> 1462
 <211> 86
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide

<400> 1462
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 cccctttgac ggtaaggacg gactcc 86

<210> 1463
 <211> 79
 <212> DNA
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<220>
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<400> 1463

ggatggtagc agtctagga ttaacttcct gtatgctgca actcatgaac ttggccattc 60
tttgggtatg ggacattcc 79

<210> 1464
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1464
tcacctctca tcttcaccag gatctcacag ggagaggcag atatcaacat tgctttttac 60
caaagagatc acggtgaca 79

<210> 1465
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1465
ccatacgtgc tgctacctgt agatattggt gatgaaccat ggtttgatga ttctgccatt 60
caaaccttta gg 72

<210> 1466
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1466
cgagagtctg taggagggaa accgccatgg acgatcaggg ttgccctcgg tgtaagacca 60
ccaaatatcg gaacc 75

<210> 1467
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1467
tcatggtgcc cgtcaatgct gtgatggcga tgaagaccaa gacgtatcag gtggcccaca 60
tgaagagcaa agacaatcg 79

<210> 1468
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1468
tcatcctggc gatctacttc ctctggcaga acctaggtcc ctctgtcctg gctggagtcg 60
ctttcatggt cttgctgatt ccaactcaacg g 91

<210> 1469
 <211> 70
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide

 <400> 1469
 tgagaaacaa actgcaccca ctgaactccg cagctagcat ccaaatacagc ccttgagatt 60
 tgaggccttg 70

 <210> 1470
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1470
 gatgcagaat tgaggcagac tttaacaagaa gattttacttc gtcgattccc agatcttaac 60
 cgacttgcca aga 73

 <210> 1471
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1471
 gctcgtgggt ctgtagtcca gtcatacctag gagggatgatg ttgactgaga cttcacgctc 60
 tccctttgt 69

 <210> 1472
 <211> 78
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1472
 gaaggaatgg gaatcagtca tgagctaatac accctggaga tcagctcccc agatgtcccc 60
 gatctgactc taatagac 78

 <210> 1473
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1473
 gccgagatcg ccaagatggt gccagggagg acagacaatg ctgtgaagaa tcaactggaac 60
 tctaccatca aaag 74

 <210> 1474

<211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1474
 tggttttgag accacgatgt tgggagggta tgtttacagc actccagcca aaaaatacag 60
 cactggcatg attca 75

 <210> 1475
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1475
 taactgacat tcttgagcac cagatccggg ctgttccctt tgagaacctt aacatgcatt 60
 gtgggcaagc cat 73

 <210> 1476
 <211> 83
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1476
 cgagactctc ctcatagtga aaggtatgtg tcagccatga ccaccccggc tcgtatgtca 60
 cctgtagatt tccacacgcc aag 83

 <210> 1477
 <211> 80
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1477
 caaccgaagt ttctactcca gttgtcccca cagtagacac atatgatggc cgagggtgata 60
 gtgtggttta tggactgagg 80

 <210> 1478
 <211> 76
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1478
 gcggaaggtc cctcagacat ccccgattga aagaaccaga gaggctctga gaaacctcgg 60
 gaaacttaga tcatca 76

 <210> 1479
 <211> 81
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1479

ccgcaacgtg gttttctcac cctatggggt ggcctcggtg ttggccatgc tccagctgac 60
aacaggagga gaaacccagc a 81

<210> 1480

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1480

gtggttttcc ctcgagccc cctggctcgg gacgtctgag aagatgccgg tcatgaggct 60
gttccttgcc t 71

<210> 1481

<211> 85

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1481

gcatcaggct gtcattatgg tgccttacc tgtgggagct gtaaggtctt ctttaagagg 60
gcaatggaag ggcagcaca ctact 85

<210> 1482

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1482

aggactggga cccatgaaca ttcctttggt atcagacccg aagcgcacca ttgctcagga 60
ttatggg 67

<210> 1483

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1483

tggctaagtg aagatgacaa tcatgttgca gcaattcact gtaaagctgg aaagggacga 60
actggtgtaa tgatatgtgc a 81

<210> 1484

<211> 70

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1484
 aatatttgtg cggggtatgg ggggtgggttt ttaaattctcg tttctcttgg acaagcacag 60
 ggatctcggt 70

<210> 1485
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1485
 aagcatgaac aggacttgac catctttcca acccctgggg aagacatttg caactgactt 60
 ggggagg 67

<210> 1486
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1486
 gcaaggaaag ggtcttagtc actgcctccc gaagttgctt gaaagcactc ggagaattgt 60
 gcaggtgt 68

<210> 1487
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1487
 gaaacctctg cgccatgaga gccaaagtga ggaagaagcg aatgcgcagg ctgaagcgca 60
 aaagaa 66

<210> 1488
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1488
 ccattctatc atcaacgggt acaaacgagt cctggccttg tctgtggaga cggattacac 60
 cttcccactt gctga 75

<210> 1489
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1489
 gttctggttg ctggatttgg tcgcaaaggt catgctgttg gtgatattcc tggagtcgc 60
 ttttaagg 67

<210> 1490
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1490
 tcaccacggt ctttagccat gcacaaacgg tagttttgtg tgttggctgc tccactgtcc 60
 tctgccagcc tacaggagga 80

<210> 1491
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1491
 gggctactgg cagctacatt gctgggacta atggcaattc caatggcctt gtaccgatgc 60
 tgagag 66

<210> 1492
 <211> 71
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1492
 cagcgggatt aaacagtcct ttaaccagca cagccagtta aaagatgcag cctcaactgct 60
 tcaacgcaga t 71

<210> 1493
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1493
 aacagagaca ttgccaaacca tattggatct gcttgctgtc caaaccagca aacttcctgg 60
 gcaaatcac 69

<210> 1494
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1494

acacaaaaat gccatctcaa atggaacacg ccatggaaac catgatgttt acatttcaca 60
aattcgctgg ggataaa 77

<210> 1495
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1495
tggctgtgct ggctactacc ttccacaagt actcctgcc aagagggcgac aagttcaagc 60
tgagtaaggg gga 73

<210> 1496
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1496
gactgctgtc atggcgtgcc ctctggagaa ggccctggat gtgatgggtg ccaccttcca 60
caagtactcg 70

<210> 1497
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1497
cctgctgacg atgatgaagg agaacttccc caacttcctt agtgccctgtg acaaaaaggg 60
cacaaattac ctgcg 75

<210> 1498
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1498
actccctgat aaaggggaat ttccatgccg totacagga tgacctgaag aaattgctag 60
agaccgagtg tctca 76

<210> 1499
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1499
caccctgcct ctaccaacc agggccccgg ggccctgttat gtcaaactgt cttggctgtg 60
gggctag 67

<210> 1500
 <211> 70
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1500
 catggccgtg tagaccctaa cccggaggga accctgacta cagaaattac cccggggcac 60
 ccttaaaact 70

 <210> 1501
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1501
 accctgagca ctggaggaag agcgccctgtg ctgtggtctt atcctatgtg gaatccccca 60
 aagtctc 67

 <210> 1502
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1502
 agacaaggat gccgtggata aattgctcaa ggacctggac gccaatggag atgcccaggt 60
 ggacttc 67

 <210> 1503
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1503
 gcagaactga agatgggaag atttatcagc gtgcatttgg tggacagagc ctcaagtttg 60
 gaaaggg 67

 <210> 1504
 <211> 86
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1504
 cgcgagcccc tcattataca ctgggcagcc tccccacagc gcatcgagga atgcgtgctc 60
 tcaggcaagg atgtcaacgg cgagtg 86

 <210> 1505

<211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1505
 caagctgaac ggtgtgtccg aaagggacct gaagaaatcg gtgctgtggc tcaaagacag 60
 cttgca 66

 <210> 1506
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1506
 agctggggtg tctgtttcat gtggaatacc tgacttcagg tcaagggatg gtatttatgc 60
 tcgccttgct gt 72

 <210> 1507
 <211> 66
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1507
 agaggctgaa tatgcaggac agttggcaga actgaggcag agattggacc atgctgaggc 60
 cgatag 66

 <210> 1508
 <211> 71
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1508
 agttgcagaa tctaagcctg gaaggcctgc ggctttcgga tcccattgtc aatactctcg 60
 caaaaaactc a 71

 <210> 1509
 <211> 74
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1509
 atggccaatg tttgatgctt aaccccccca atttctgtga gatggatggc cagtgcgaagc 60
 gtgacttgaa gtgt 74

 <210> 1510
 <211> 69
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1510

cccaatcgga agcctaacta cagcgagctg caggactcta atccagagtt taccttccag 60
cagccctac 69

<210> 1511

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1511

catcttccag gaggaccact ctctgtggca ccctggacta cctgccccct gaaatgattg 60
aaggtcgga 69

<210> 1512

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1512

aatacccaac gcacaaatga ccgcacgttc tctgccccgt ttcttgcccc agtgtgggtt 60
gcattgtctc c 71

<210> 1513

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1513

cctggaggct gcaacatacc tcaatcctgt ccaggccgg atcctcctga agcccttttc 60
gcagcactgc tatectccaa agccattgta 90

<210> 1514

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1514

tgttttgatt cccgggctta ccagggtgaga agtgagggag gaagaaggca gtgtcccttt 60
tgctagagct gacagctttg 80

<210> 1515

<211> 85

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

 <400> 1515
 tctccagcaa aagcgatgtc tggagctttg gagtgttgat gtgggaagca ttctcctatg 60
 ggcagaagcc atatcgaggg atgaa 85

 <210> 1516
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1516

 gatggagcag gtggctcagt tcctgaaggc ggctgaggac tctgggggtca tcaagactga 60
 catgttccag act 73

 <210> 1517
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1517
 cagccctgag gcaagagaag aaagtacttc cagcggcaat gtaagcaaca gaaaggatga 60
 gacaaatgct cg 72

 <210> 1518
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1518
 gccaaactgct ttcatttgtg agggatctga accaatacag agcagacata aaggaaatgg 60
 gcctgagt 68

 <210> 1519
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1519
 accagtcccc cagaagacta tcctgagccc gaggaagtcc ccccggaggt gatttccatc 60
 tacaacagca ccagg 75

 <210> 1520
 <211> 65
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 1520

ggatcgagct cttccagatc cttcggccag atgagcacat tgccaaacag cgctatatcg 60
gtggc 65

<210> 1521

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1521

aacaccaatg ggttccatct ttctgggctc ctgattgctc aagcacagtt tggcctgatg 60
aagagg 66

<210> 1522

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1522

ctacctgcct tgctttgtga cttccaagaa cgagtgtctc tggaccgaca tgctctccaa 60
tttcggt 67

<210> 1523

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1523

ccagcccaca gaccagttac tgttctctac tgagcctgga agcaaataca cacctccttt 60
ctctgaa 67

<210> 1524

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1524

tggcgaccaa gacaccttga agggcctaata gcacgcacta aagcactcaa agacgtacca 60
ctttccc 67

<210> 1525

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1525
 catatcggttg gatcacagca catcagagca gagaaagcga tggatggatgg ctcatgggta 60
 gatctggcca a 71

<210> 1526
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1526
 gcgctgcgga agatcatccc cacgctgccc tcggacaagc tgagcaagat tcagaccctc 60
 aagc 64

<210> 1527
 <211> 522
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1527
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 ctgaccggca agaccatcac cctggaagtg gagcccagtg acaccatcga aaatgtgaag 120
 gccaagatcc aggataaaga aggcattcct cccgaccagc agagggtcat ctttgcaggc 180
 aagcagctgg aagatggccg cactctttct gactacaaca tccagaagga gtcgaccctg 240
 cacctgggtc tgcgtctgag aggtgggtatg cagatcttcg tgaagaccct gaccggcaag 300
 accatcactc tggaagtgga gccagtgac accatcgaaa atgtgaaggc caagatccaa 360
 gataaagaag gcatccctcc cgaccagcag aggtcatct ttgcaggcaa gcagctggaa 420
 gatggccgca ctctttctga ctacaacatc cagaaggagt cgaccctgca cctggtcctg 480
 cgcttgaggg gtggctgtta attcttcagt catggcattc gc 522

<210> 1528
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1528
 tggcttcagg agctgaatac cctcccaggc acacacaggt gggacacaaa taagggtttt 60
 ggaaccacta ttttctcatc acgacagca 89

<210> 1529
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1529
 tgcccttaaa ggaaccaatg agtccctgga acgccagatg cgtgaaatgg aagagaactt 60
 tgccgttgaa gc 72

<210> 1530
 <211> 67

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1530
 agtcaatctt cgcacacggc gagtggacac tgtggaccct ccctaccac gctccatcgc 60
 tcagtac 67

 <210> 1531
 <211> 68
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1531
 ctctccagtg tgggcaccag ccggccagaa cagatgcgag cagtccatga ctctgggagc 60
 tacaccgc 68

 <210> 1532
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1532
 agaggcatcc atgaacttca cacttgcggg ctgcatcagc acacgctcct atcaacccaa 60
 gtactgtgga gtttg 75

 <210> 1533
 <211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1533
 gtatcaggac cacatgcagt acatcggaga aggcgcgaag acaggcatca aagaatgcca 60
 gtatcaattc cgaca 75

 <210> 1534
 <211> 79
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 1534
 tgtcttcagg gtcttgcca gaatgtagat gggttccgta agaggcctgg tgctctctta 60
 ctctttcatc cacgtgcac 79

 <210> 1535
 <211> 74
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1535

atcgacgtg gtgggtgtac aactgtgt ttacctggc gaggccttc accaagtcca 60
tgcaacaggg agct 74

<210> 1536

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 1536

gtgacatcg gatacccaag gagacgaagc tgaagcagga gaaggagggg aaaattaacc 60
ggccttcaa ctttgtctg c 81