Innovation, Sciences et Développement économique Canada
Office de la Propriété Intellectuelle du Canada

Innovation, Science and Economic Development Canada
Canadian Intellectual Property Office

CA 2804626 C 2020/07/28

(11)(21) **2 804 626**

(12) **BREVET CANADIEN**
CANADIAN PATENT

(13) **C**

(86) **Date de dépôt PCT/PCT Filing Date:** 2011/07/25
(87) **Date publication PCT/PCT Publication Date:** 2012/02/02
(45) **Date de délivrance/Issue Date:** 2020/07/28
(85) **Entrée phase nationale/National Entry:** 2013/01/07
(86) **N° demande PCT/PCT Application No.:** US 2011/045253
(87) **N° publication PCT/PCT Publication No.:** 2012/015765
(30) **Priorités/Priorities:** 2010/07/27 (US61/368,217); 2010/11/16 (US61/414,310); 2011/05/12 (US61/485,536)

(51) **Cl.Int./Int.Cl.** ***C12Q 1/68*** (2018.01), ***C12Q 1/6809*** (2018.01), ***C40B 30/04*** (2006.01), *C12N 15/113* (2010.01)

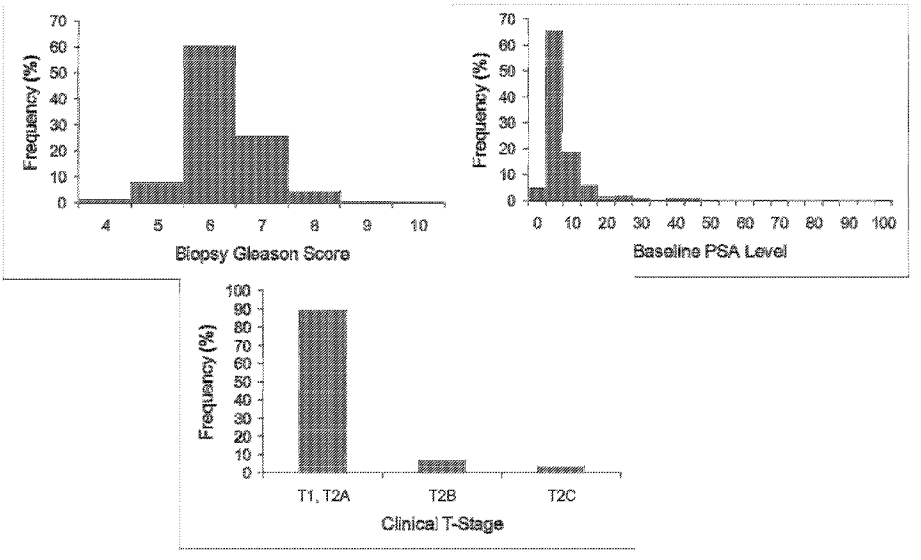
(72) **Inventeurs/Inventors:**
SHAK, STEVEN, US;
BAEHNER, FREDERICK L., US;
MADDALA, TARA, US;
LEE, MARK, US;
PELHAM, ROBERT J., US;
COWENS, WAYNE, US;
...

(73) **Propriétaire/Owner:**
GENOMIC HEALTH, INC., US

(74) **Agent:** SMART & BIGGAR LLP

(54) **Titre : PROCEDE D'UTILISATION DE L'EXPRESSION DE GLUTATHIONE-S-TRANFERASE MU 2 (GSTM2) POUR DETERMINER LE PRONOSTIC D'UN CANCER DE LA PROSTATE**

(54) **Title: METHOD FOR USING EXPRESSION OF GLUTATHIONE S-TRANSFERASE MU 2 (GSTM2) TO DETERMINE PROGNOSIS OF PROSTATE CANCER**



(57) **Abrégé/Abstract:**
Assays that involve measurement of expression levels of prognostic biomarkers, including Glutathionc S-Transferase Mu 2 (GSTM2) or co-expressed biomarkers, in a biological sample from a prostate cancer patient, and analysis of the measured

CA 2804626 C 2020/07/28

(11)(21) **2 804 626**

(13) **C**

(72) **Inventeurs(suite)/Inventors(continued):** CHERBAVAZ, DIANA, US; KIEFER, MICHAEL C., US; CRAGER, MICHAEL, US; GODDARD, AUDREY, US; BAKER, JOFFRE B., US

(57) **Abrégé(suite)/Abstract(continued):**
expression levels to provide information concerning the likely prognosis for said patient, and likelihood that said patient will have a recurrence of prostate cancer, or to classify the tumor by likelihood of clinical outcome or TMPRSS2 fusion status, are provided herein.

ABSTRACT

Assays that involve measurement of expression levels of prognostic biomarkers, including Glutathione S-Transferase Mu 2 (GSTM2) or co-expressed biomarkers, in a biological sample from a prostate cancer patient, and analysis of the measured expression levels to provide information concerning the likely prognosis for said patient, and likelihood that said patient will have a recurrence of prostate cancer, or to classify the tumor by likelihood of clinical outcome or TMPRSS2 fusion status, are provided herein.

METHOD FOR USING EXPRESSION OF GLUTATHIONE S-TRANSFERASE Mu 2 (GSTM2) TO DETERMINE PROGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD

[0001] The present disclosure relates to molecular diagnostic assays that provide information concerning methods to use gene expression profiles to determine prognostic information for cancer patients. Specifically, the present disclosure provides genes and microRNAs, the expression levels of which may be used to determine the likelihood that a prostate cancer patient will experience a local or distant cancer recurrence.

INTRODUCTION

[0002] Prostate cancer is the most common solid malignancy in men and the second most common cause of cancer-related death in men in North America and the European Union (EU). In 2008, over 180,000 patients will be diagnosed with prostate cancer in the United States alone and nearly 30,000 will die of this disease. Age is the single most important risk factor for the development of prostate cancer, and applies across all racial groups that have been studied. With the aging of the U.S. population, it is projected that the annual incidence of prostate cancer will double by 2025 to nearly 400,000 cases per year.

[0003] Since the introduction of pro state-specific antigen (PSA) screening in the 1990's, the proportion of patients presenting with clinically evident disease has fallen dramatically such that patients categorized as "low risk" now constitute half of new diagnoses today. PSA is used as a tumor marker to determine the presence of prostate cancer as high PSA levels are associated with prostate cancer. Despite a growing proportion of localized prostate cancer patients presenting with low-risk features such as low stage (T1) disease, greater than 90% of patients in the US still undergo definitive therapy, including prostatectomy or radiation. Only about 15% of these patients would develop metastatic disease and die from their prostate cancer, even in the absence of definitive therapy. A. Bill-Axelson, et al., J Nat'l Cancer Inst. 100(16): 1144-1154 (2008). Therefore, the majority of prostate cancer patients are being over-treated.

[0004] Estimates of recurrence risk and treatment decisions in prostate cancer are currently based primarily on PSA levels and/or tumor stage. Although tumor stage has been demonstrated to have significant association with outcome sufficient to be included in pathology reports, the College of American Pathologists Consensus Statement noted that variations in approach to the acquisition, interpretation, reporting, and analysis of this information exist. C. Compton, et al., Arch Pathol Lab Med 124:979-992 (2000). As a consequence, existing pathologic staging methods have been criticized as lacking reproducibility and therefore may provide imprecise estimates of individual patient risk.

SUMMARY

[0005] This application discloses molecular assays that involve measurement of expression level(s) of one or more genes, gene subsets, microRNAs, or one or more microRNAs in combination with one or more genes or gene subsets, from a biological sample obtained from a prostate cancer patient, and analysis of the measured expression levels to provide information concerning the likelihood of cancer recurrence. For example, the likelihood of cancer recurrence could be described in terms of a score based on clinical or biochemical recurrence-free interval.

[0006] In addition, this application discloses molecular assays that involve measurement of expression level(s) of one or more genes, gene subsets, microRNAs, or one or more microRNAs in combination with one or more genes or gene subsets, from a biological sample obtained to identify a risk classification for a prostate cancer patient. For example, patients may be stratified using expression level(s) of one or more genes or microRNAs associated, positively or negatively, with cancer recurrence or death from cancer, or with a prognostic factor. In an exemplary embodiment, the prognostic factor is Gleason pattern.

[0007] The biological sample may be obtained from standard methods, including surgery, biopsy, or bodily fluids. It may comprise tumor tissue or cancer cells, and, in some cases, histologically normal tissue, e.g., histologically normal tissue adjacent the tumor tissue. In exemplary embodiments, the biological sample is positive or negative for a TMPRSS2 fusion.

[0008] In exemplary embodiments, expression level(s) of one or more genes and/or microRNAs that are associated, positively or negatively, with a particular clinical outcome in prostate cancer are used to determine prognosis and appropriate therapy. The genes disclosed herein may be used alone or arranged in functional gene subsets, such as cell adhesion/migration, immediate-early stress response, and extracellular matrix-associated. Each gene subset comprises the genes disclosed herein, as well as genes that are co-expressed with one or more of the disclosed genes. The calculation may be performed on a computer, programmed to execute the gene expression analysis. The microRNAs disclosed herein may also be used alone or in combination with any one or more of the microRNAs and/or genes disclosed.

[0009] In exemplary embodiments, the molecular assay may involve expression levels for at least two genes. The genes, or gene subsets, may be weighted according to strength of association with prognosis or tumor microenvironment. In another exemplary embodiment, the molecular assay may involve expression levels of at least one gene and at least one microRNA. The gene-microRNA combination may be selected based on the likelihood that the gene-microRNA combination functionally interact.

[0010] The claimed invention pertains to a method for determining a likelihood of cancer recurrence in a human patient with prostate cancer, comprising: determining a level of an RNA transcript of Glutathione-S-Transferase Mu 2 (GSTM2) in a fixed, paraffin-embedded biological sample comprising prostate tumor tissue obtained from the patient; normalizing the level of the RNA transcript of GSTM2 against the level of either all assayed RNA transcripts in the sample or against the level of a reference set of RNA transcripts in the sample to obtain a normalized level of the RNA transcript of GSTM2; and predicting a likelihood of cancer recurrence for the patient, wherein increases in normalized level of the RNA transcript of GSTM2 are associated with decreases in risk of recurrence. Also disclosed and claimed is a method for determining a likelihood of upgrading or upstaging in a human patient with prostate cancer, comprising: determining a level of an RNA transcript of Glutathione-S-Transferase Mu 2 (GSTM2) in a fixed, paraffin-embedded biological sample comprising prostate tumor tissue obtained from the patient; normalizing the level of the RNA transcript of GSTM2 against the level of either all assayed RNA transcripts in the sample or against the level of a reference set of RNA transcripts in the sample to obtain a normalized level of the RNA transcript of GSTM2; wherein an increased expression level of GSTM2 is negatively associated with an increased risk of upgrading/upstaging.

BRIEF DESCRIPTION OF THE DRAWING

[0011] Figure 1 shows the distribution of clinical and pathology assessments of biopsy Gleason score, baseline PSA level, and clinical T-stage.

DEFINITIONS

[0012] 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.

[0013] 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 herein. For purposes of the invention, the following terms are defined below.

[0014] The terms "tumor" and "lesion" as used herein, refer to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. Those skilled in the art will realize that a tumor tissue sample may comprise multiple biological elements, such as one or more cancer cells, partial or fragmented cells, tumors in

various stages, surrounding histologically normal-appearing tissue, and/or macro or micro-dissected tissue.

[0015] 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 in the present disclosure include cancer of the urogenital tract, such as prostate cancer.

[0016] 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.

[0017] As used herein, the term "prostate cancer" is used interchangeably and in the broadest sense refers to all stages and all forms of cancer arising from the tissue of the prostate gland.

[0018] According to the tumor, node, metastasis (TNM) staging system of the American Joint Committee on Cancer (AJCC), AJCC Cancer Staging Manual (7th Ed., 2010), the various stages of prostate cancer are defined as follows: Tumor: Tl: clinically inapparent tumor not palpable or visible by imaging, T1a: tumor incidental histological finding in 5% or less of tissue resected, T1b: tumor incidental histological finding in more than 5% of tissue resected, T1c: tumor identified by needle biopsy; T2: tumor confined within prostate, T2a: tumor involves one half of one lobe or less, T2b: tumor involves more than half of one lobe, but not both lobes, T2c: tumor involves both lobes; T3: tumor extends through the prostatic capsule, T3a: extracapsular extension (unilateral or bilateral), T3b: tumor invades seminal vesicle(s); T4: tumor is fixed or invades adjacent structures other than seminal vesicles (bladder neck, external sphincter, rectum, levator muscles, or pelvic wall). Node: NO: no regional lymph node metastasis; Nl: metastasis in regional lymph nodes. Metastasis: M0: no distant metastasis; Ml: distant metastasis present.

[0019] The Gleason Grading system is used to help evaluate the prognosis of men with prostate cancer. Together with other parameters, it is incorporated into a strategy of prostate cancer staging, which predicts prognosis and helps guide therapy. A Gleason "score" or "grade" is given to prostate cancer based upon its microscopic appearance. Tumors with a low Gleason score typically grow slowly enough that they may not pose a significant threat to the patients in

their lifetimes. These patients are monitored ("watchful waiting" or "active surveillance") over time. Cancers with a higher Gleason score are more aggressive and have a worse prognosis, and these patients are generally treated with surgery (e.g., radical prostectomy) and, in some cases, therapy (e.g., radiation, hormone, ultrasound, chemotherapy). Gleason scores (or sums) comprise grades of the two most common tumor patterns. These patterns are referred to as Gleason patterns 1-5, with pattern 1 being the most well-differentiated. Most have a mixture of patterns. To obtain a Gleason score or grade, the dominant pattern is added to the second most prevalent pattern to obtain a number between 2 and10. The Gleason Grades include: G1: well differentiated (slight anaplasia) (Gleason 2-4); G2: moderately differentiated (moderate anaplasia) (Gleason 5-6); G3-4: poorly differentiated/undifferentiated (marked anaplasia) (Gleason 7-10).

[0020] Stage groupings: Stage I: Tla N0 M0 G1; Stage II: (T1a N0 M0 G2-4) or (T1b, c, T1, T2, N0 M0 Any G); Stage III: T3 N0 M0 Any G; Stage IV: (T4 N0 M0 Any G) or (Any T N1 M0 Any G) or (Any T Any N M1 Any G).

[0021] As used herein, the term "tumor tissue" refers to a biological sample containing one or more cancer cells, or a fraction of one or more cancer cells. Those skilled in the art will recognize that such biological sample may additionally comprise other biological components, such as histologically appearing normal cells (e.g., adjacent the tumor), depending upon the method used to obtain the tumor tissue, such as surgical resection, biopsy, or bodily fluids.

[0022] As used herein, the term "AUA risk group" refers to the 2007 updated American Urological Association (AUA) guidelines for management of clinically localized prostate cancer, which clinicians use to determine whether a patient is at low, intermediate, or high risk of biochemical (PSA) relapse after local therapy.

[0023] As used herein, the term "adjacent tissue (AT)" refers to histologically "normal" cells that are adjacent a tumor. For example, the AT expression profile may be associated with disease recurrence and survival.

[0024] As used herein "non-tumor prostate tissue" refers to histologically normal-appearing tissue adjacent a prostate tumor.

[0025] 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,

increased tumor stage, PSA level at presentation, and Gleason grade or pattern. Prognostic factors are frequently used to categorize patients into subgroups with different baseline relapse risks.

[0026] The term "prognosis" is used herein to refer to the likelihood that a cancer patient will have a cancer-attributable death or progression, including recurrence, metastatic spread, and drug resistance, of a neoplastic disease, such as prostate cancer. For example, a "good prognosis" would include long term survival without recurrence and a "bad prognosis" would include cancer recurrence.

[0027] As used herein, the term "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.

[0028] The term "gene product" or "expression product" are used herein to refer to the RNA (ribonucleic acid) 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.

[0029] 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.

[0030] The term "microRNA" is used herein to refer to a small, non-coding, single-stranded RNA of ~18 – 25 nucleotides that may regulate gene expression. For example, when associated with the RNA-induced silencing complex (RISC), the complex binds to specific mRNA targets and causes translation repression or cleavage of these mRNA sequences.

[0031] 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.

[0032] The terms "correlated" and "associated" are used interchangeably herein to refer to the association between two measurements (or measured entities). The disclosure provides genes,gene subsets, microRNAs, or microRNAs in combination with genes or gene subsets, the expression levels of which are associated with tumor stage. For example, the increased

expression level of a gene or microRNA may be positively correlated (positively associated) with a good or positive prognosis. Such a positive correlation may be demonstrated statistically in various ways, e.g. by a cancer recurrence hazard ratio less than one. In another example, the increased expression level of a gene or microRNA may be negatively correlated (negatively associated) with a good or positive prognosis. In that case, for example, the patient may experience a cancer recurrence.

[0033] The terms "good prognosis" or "positive prognosis" as used herein refer to a beneficial clinical outcome, such as long-term survival without recurrence. The terms "bad prognosis" or "negative prognosis" as used herein refer to a negative clinical outcome, such as cancer recurrence.

[0034] The term "risk classification" means a grouping of subjects by the level of risk (or likelihood) that the subject will experience a particular clinical outcome. A subject 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.

[0035] The term "long-term" survival is used herein to refer to survival for a particular time period, e.g., for at least 5 years, or for at least 10 years.

[0036] The term "recurrence" is used herein to refer to local or distant recurrence (i.e., metastasis) of cancer. For example, prostate cancer can recur locally in the tissue next to the prostate or in the seminal vesicles. The cancer may also affect the surrounding lymph nodes in the pelvis or lymph nodes outside this area. Prostate cancer can also spread to tissues next to the prostate, such as pelvic muscles, bones, or other organs. Recurrence can be determined by clinical recurrence detected by, for example, imaging study or biopsy, or biochemical recurrence detected by, for example, sustained follow-up prostate-specific antigen (PSA) levels $\geq$ 0.4 ng/mL or the initiation of salvage therapy as a result of a rising PSA level.

[0037] The term "clinical recurrence-free interval (cRFI)" is used herein as time (in months) from surgery to first clinical recurrence or death due to clinical recurrence of prostate cancer. Losses due to incomplete follow-up, other primary cancers or death prior to clinical recurrence are considered censoring events; when these occur, the only information known is that up through the censoring time, clinical recurrence has not occurred in this subject. Biochemical recurrences are ignored for the purposes of calculating cRFI.

[0038] The term "biochemical recurrence-free interval (bRFI)" is used herein to mean the time (in months) from surgery to first biochemical recurrence of prostate cancer. Clinical recurrences, losses due to incomplete follow-up, other primary cancers, or death prior to biochemical recurrence are considered censoring events.

[0039] The term "Overall Survival (OS)" is used herein to refer to the time (in months) from surgery to death from any cause. Losses due to incomplete follow-up are considered censoring events. Biochemical recurrence and clinical recurrence are ignored for the purposes of calculating OS.

[0040] The term "Prostate Cancer-Specific Survival (PCSS)" is used herein to describe the time (in years) from surgery to death from prostate cancer. Losses due to incomplete follow-up or deaths from other causes are considered censoring events. Clinical recurrence and biochemical recurrence are ignored for the purposes of calculating PCSS.

[0041] The term "upgrading" or "upstaging" as used herein refers to a change in Gleason grade from 3+3 at the time of biopsy to 3+4 or greater at the time of radical prostatectomy (RP), or Gleason grade 3+4 at the time of biopsy to 4+3 or greater at the time of RP, or seminal vessical involvement (SVI), or extracapsular involvement (ECE) at the time of RP.

[0042] In practice, the calculation of the measures listed above may vary from study to study depending on the definition of events to be considered censored.

[0043] The term "microarray" refers to an ordered arrangement of hybridizable array elements, e.g. oligonucleotide or polynucleotide probes, on a substrate.

[0044] The term "polynucleotide" 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.

[0045] The term "oligonucleotide" refers to a relatively short polynucleotide, including, without limitation, single-stranded deoxyribonucleotides, single- or double-stranded ribonucleotides, RNArDNA 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.

[0046] The term "Ct" 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.

[0047] The term "Cp" as used herein refers to "crossing point." The Cp value is calculated by determining the second derivatives of entire qPCR amplification curves and their maximum value. The Cp value represents the cycle at which the increase of fluorescence is highest and where the logarithmic phase of a PCR begins.

[0048] The terms "threshold" or "thresholding" refer to a procedure used to account for non-linear relationships between gene expression measurements and clinical response as well as to further reduce variation in reported patient scores. When thresholding is applied, all measurements below or above a threshold are set to that threshold value. Non-linear relationship between gene expression and outcome could be examined using smoothers or cubic splines to model gene expression in Cox PH regression on recurrence free interval or logistic regression on recurrence status. D. Cox, Journal of the Royal Statistical Society, Series B 34:187-220 (1972).

Variation in reported patient scores could be examined as a function of variability in gene expression at the limit of quantitation and/or detection for a particular gene.

[0049] As used herein, the term "amplicon," refers to pieces of DNA that have been synthesized using amplification techniques, such as polymerase chain reactions (PCR) and ligase chain reactions.

[0050] "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 re-anneal 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).

[0051] "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, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

[0052] "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 that 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 37-500C. 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.

[0053] 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 an eukaryotic cell.

[0054] The terms "co-express" and "co-expressed", as used herein, refer to a statistical correlation between the amounts of different transcript sequences across a population of different patients. 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 graph theory. An analysis of co-expression may be calculated using normalized expression data. A gene is said to be co-expressed with a particular disclosed gene when the expression level of the gene exhibits a Pearson correlation coefficient greater than or equal to 0.6.

[0055] 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.

[0056] 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.

[0057] 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.

[0058] As used herein, the terms "active surveillance" and "watchful waiting" mean closely monitoring a patient's condition without giving any treatment until symptoms appear or change. For example, in prostate cancer, watchful waiting is usually used in older men with other medical problems and early-stage disease.

[0059] As used herein, the term "surgery" applies to surgical methods undertaken for removal of cancerous tissue, including pelvic lymphadenectomy, radical prostatectomy, transurethral resection of the prostate (TURP), excision, dissection, and tumor biopsy/removal. The tumor tissue or sections used for gene expression analysis may have been obtained from any of these methods.

[0060] As used herein, the term "therapy" includes radiation, hormonal therapy, cryosurgery, chemotherapy, biologic therapy, and high-intensity focused ultrasound.

[0061] As used herein, the term "TMPRSS fusion" and "TMPRSS2 fusion" are used interchangeably and refer to a fusion of the androgen-driven TMPRSS2 gene with the ERG oncogene, which has been demonstrated to have a significant association with prostate cancer. S. Perner, et al., Urologe A. 46(7):754-760 (2007); S.A. Narod, et al., Br J Cancer 99(6):847-851 (2008). As used herein, positive TMPRSS fusion status indicates that the TMPRSS fusion is present in a tissue sample, whereas negative TMPRSS fusion status indicates that the TMPRSS fusion is not present in a tissue sample. Experts skilled in the art will recognize that there are numerous ways to determine TMPRSS fusion status, such as real-time, quantitative PCR or high-throughput sequencing. See, e.g., K. Mertz, et al., Neoplasis 9(3):200-206 (2007); C. Maher, Nature 458(7234):97-101 (2009).

GENE EXPRESSION METHODS USING GENES, GENE SUBSETS, AND MICRORNAS

[0062] The present disclosure provides molecular assays that involve measurement of expression level(s) of one or more genes, gene subsets, microRNAs, or one or more microRNAs in combination with one or more genes or gene subsets, from a biological sample obtained from a prostate cancer patient, and analysis of the measured expression levels to provide information concerning the likelihood of cancer recurrence.

[0063] The present disclosure further provides methods to classify a prostate tumor based on expression level(s) of one or more genes and/or microRNAs. The disclosure further provides genes and/or microRNAs that are associated, positively or negatively, with a particular prognostic outcome. In exemplary embodiments, the clinical outcomes include cRFI and bRFI. In another embodiment, patients may be classified in risk groups based on the expression level(s) of one or more genes and/or microRNAs that are associated, positively or negatively, with a prognostic factor. In an exemplary embodiment, that prognostic factor is Gleason pattern.

[0064] Various technological approaches for determination of expression levels of the disclosed genes and microRNAs are set forth in this specification, including, without limitation, RT-PCR, microarrays, high-throughput sequencing, serial analysis of gene expression (SAGE) and Digital Gene Expression (DGE), which will be discussed in detail below. In particular aspects, the expression level of each gene or microRNA may be determined in relation to various features of the expression products of the gene including exons, introns, protein epitopes and protein activity.

[0065] The expression level(s) of one or more genes and/or microRNAs may be measured in tumor tissue. For example, the tumor tissue may obtained upon surgical removal or resection of the tumor, or by tumor biopsy. The tumor tissue may be or include histologically "normal" tissue, for example histologically "normal" tissue adjacent to a tumor. The expression level of genes and/or microRNAs may also be measured in tumor cells recovered from sites distant from the tumor, for example circulating tumor cells, body fluid (e.g., urine, blood, blood fraction, etc.).

[0066] The expression product that is assayed can be, for example, RNA or a polypeptide. The expression product may be fragmented. For example, the assay may use primers that are complementary to target sequences of an expression product and could thus

measure full transcripts as well as those fragmented expression products containing the target sequence. Further information is provided in Table A (inserted in specification prior to claims).

[0067] The RNA expression product may be assayed directly or by detection of a cDNA product resulting from a PCR-based amplification method, e.g., quantitative reverse transcription polymerase chain reaction (qRT-PCR). (See e.g., U.S. Patent No. 7,587,279). Polypeptide expression product may be assayed using immunohistochemistry (IHC). Further, both RNA and polypeptide expression products may also be is assayed using microarrays.

CLINICAL UTILITY

[0068] Prostate cancer is currently diagnosed using a digital rectal exam (DRE) and Prostate-specific antigen (PSA) test. If PSA results are high, patients will generally undergo a prostate tissue biopsy. The pathologist will review the biopsy samples to check for cancer cells and determine a Gleason score. Based on the Gleason score, PSA, clinical stage, and other factors, the physician must make a decision whether to monitor the patient, or treat the patient with surgery and therapy.

[0069] At present, clinical decision-making in early stage prostate cancer is governed by certain histopathologic and clinical factors. These include: (1) tumor factors, such as clinical stage (e.g. T1, T2), PSA level at presentation, and Gleason grade, that are very strong prognostic factors in determining outcome; and (2) host factors, such as age at diagnosis and co-morbidity. Because of these factors, the most clinically useful means of stratifying patients with localized disease according to prognosis has been through multifactorial staging, using the clinical stage, the serum PSA level, and tumor grade (Gleason grade) together. In the 2007 updated American Urological Association (AUA) guidelines for management of clinically localized prostate cancer, these parameters have been grouped to determine whether a patient is at low, intermediate, or high risk of biochemical (PSA) relapse after local therapy. I. Thompson, et al., Guideline for the management of clinically localized prostate cancer, J Urol. 177(6):2106-31 (2007).

[0070] Although such classifications have proven to be helpful in distinguishing patients with localized disease who may need adjuvant therapy after surgery/radiation, they have less ability to discriminate between indolent cancers, which do not need to be treated with local therapy, and aggressive tumors, which require local therapy. In fact, these algorithms are of increasingly limited use for deciding between conservative management and definitive therapy

because the bulk of prostate cancers diagnosed in the PSA screening era now present with clinical stage T1c and PSA ≤10 ng/mL.

[0071] Patients with T1 prostate cancer have disease that is not clinically apparent but is discovered either at transurethral resection of the prostate (TURP, T1a, T1b) or at biopsy performed because of an elevated PSA (> 4 ng/mL, T1c). Approximately 80% of the cases presenting in 2007 are clinical T1 at diagnosis. In a Scandinavian trial, OS at 10 years was 85% for patients with early stage prostate cancer (T1/T2) and Gleason score ≤ 7, after radical prostatectomy.

[0072] Patients with T2 prostate cancer have disease that is clinically evident and is organ confined; patients with T3 tumors have disease that has penetrated the prostatic capsule and/or has invaded the seminal vesicles. It is known from surgical series that clinical staging underestimates pathological stage, so that about 20% of patients who are clinically T2 will be pT3 after prostatectomy. Most of patients with T2 or T3 prostate cancer are treated with local therapy, either prostatectomy or radiation. The data from the Scandinavian trial suggest that for T2 patients with Gleason grade ≤7, the effect of prostatectomy on survival is at most 5% at 10 years; the majority of patients do not benefit from surgical treatment at the time of diagnosis. For T2 patients with Gleason > 7 or for T3 patients, the treatment effect of prostatectomy is assumed to be significant but has not been determined in randomized trials. It is known that these patients have a significant risk (10-30%) of recurrence at 10 years after local treatment, however, there are no prospective randomized trials that define the optimal local treatment (radical prostatectomy, radiation) at diagnosis, which patients are likely to benefit from neo-adjuvant/adjuvant androgen deprivation therapy, and whether treatment (androgen deprivation, chemotherapy) at the time of biochemical failure (elevated PSA) has any clinical benefit.

[0073] Accurately determining Gleason scores from needle biopsies presents several technical challenges. First, interpreting histology that is "borderline" between Gleason pattern is highly subjective, even for urologic pathologists. Second, incomplete biopsy sampling is yet another reason why the "predicted" Gleason score on biopsy does not always correlate with the actual "observed" Gleason score of the prostate cancer in the gland itself. Hence, the accuracy of Gleason scoring is dependent upon not only the expertise of the pathologist reading the slides, but also on the completeness and adequacy of the prostate biopsy sampling strategy. T. Stamey, Urology 45:2-12 (1995). The gene/microRNA expression assay and associated information

provided by the practice of the methods disclosed herein provide a molecular assay method to facilitate optimal treatment decision-making in early stage prostate cancer. An exemplary embodiment provides genes and microRNAs, the expression levels of which are associated (positively or negatively) with prostate cancer recurrence. For example, such a clinical tool would enable physicians to identify T2/T3 patients who are likely to recur following definitive therapy and need adjuvant treatment.

[0074] In addition, the methods disclosed herein may allow physicians to classify tumors, at a molecular level, based on expression level(s) of one or more genes and/or microRNAs that are significantly associated with prognostic factors, such as Gleason pattern and TMPRSS fusion status. These methods would not be impacted by the technical difficulties of intra-patient variability, histologically determining Gleason pattern in biopsy samples, or inclusion of histologically normal appearing tissue adjacent to tumor tissue. Multi-analyte gene/microRNA expression tests can be used to measure the expression level of one or more genes and/or microRNAs involved in each of several relevant physiologic processes or component cellular characteristics. The methods disclosed herein may group the genes and/or microRNAs. The grouping of genes and microRNAs may be performed at least in part based on knowledge of the contribution of those genes and/or microRNAs according to physiologic functions or component cellular characteristics, such as in the groups discussed above. Furthermore, one or more microRNAs may be combined with one or moregenes. The gene-microRNA combination may be selected based on the likelihood that the gene-microRNA combination functionally interact. The formation of groups (or gene subsets), in addition, can facilitate the mathematical weighting of the contribution of various expression levels to cancer recurrence. The weighting of a gene/microRNA group representing a physiological process or component cellular characteristic can reflect the contribution of that process or characteristic to the pathology of the cancer and clinical outcome.

[0075] Optionally, the methods disclosed may be used to classify patients by risk, for example risk of recurrence. Patients can be partitioned into subgroups (e.g., tertiles or quartiles) and the values chosen will define subgroups of patients with respectively greater or lesser risk.

[0076] The utility of a disclosed gene marker in predicting prognosis may not be unique to that marker. An alternative marker having an expression pattern that is parallel to that of a disclosed gene may be substituted for, or used in addition to, that co-expressed gene or

microRNA. Due to the co-expression of such genes or microRNAs, substitution of expression level values should have little impact on the overall utility of the test. The closely similar expression patterns of two genes or microRNAs may result from involvement of both genes or microRNAs in the same process and/or being under common regulatory control in prostate tumor cells. The present disclosure thus contemplates the use of such co-expressed genes,gene subsets, or microRNAs as substitutes for, or in addition to, genes of the present disclosure.

METHODS OF ASSAYING EXPRESSION LEVELS OF A GENE PRODUCT

[0077] The methods and compositions of the present disclosure will 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. Exemplary 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).

[0078] Methods of gene expression profiling include methods based on hybridization analysis of polynucleotides, methods based on sequencing of polynucleotides, and proteomics-based methods. Exemplary methods known in the art for the quantification of RNA 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 PCT (RT-PCR) (Weis et al., Trends in Genetics 8:263-264 (1992)). Antibodies may be employed that can recognize sequence-specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. Representative methods for sequencing-based gene expression analysis include Serial Analysis of Gene Expression (SAGE), and gene expression analysis by massively parallel signature sequencing (MPSS).

Reverse Transcriptase PCR (RT-PCR)

[0079] Typically, mRNA or microRNA is isolated from a test sample. The starting material is typically total RNA isolated from a human tumor, usually from a primary tumor. Optionally, normal tissues from the same patient can be used as an internal control. Such normal tissue can be histologically-appearing normal tissue adjacent a tumor. mRNA or microRNA can be extracted from a tissue sample, e.g., from a sample that is fresh, frozen (e.g. fresh frozen), or paraffin-embedded and fixed (e.g. formalin-fixed).

[0080] General methods for mRNA and microRNA 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 a 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.

[0081] The sample containing the RNA is then subjected to reverse transcription to produce cDNA from the RNA template, followed by exponential amplification in a PCR reaction. The two most commonly used reverse transcriptases are avilo 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.

[0082] PCR-based methods use a thermostable DNA-dependent DNA polymerase, such as a Taq DNA polymerase. For example, 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 product. A third oligonucleotide, or probe, can be designed to facilitate detection of a nucleotide sequence of the amplicon located between the hybridization sites the two PCR primers. The probe can be detectably labeled, e.g., with a reporter dye, and can further be provided with both a fluorescent dye, and a quencher fluorescent dye, as in a Taqman® probe configuration. Where a Taqman® probe is used, 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.

[0083] TaqMan® RT-PCR can be performed using commercially available equipment, such as, for example, high-throughput platforms such as the ABI PRISM 7700 Sequence Detection System® (Perkin-Elmer-Applied Biosystems, Foster City, CA, USA), or Lightcycler (Roche Molecular Biochemicals, Mannheim, Germany). In a preferred embodiment, the procedure is run on a LightCycler® 480 (Roche Diagnostics) real-time PCR system, which is a microwell plate-based cycler platform.

[0084] 5'-Nuclease assay data are commonly initially expressed as a threshold cycle ("C_T"). Fluorescence values are recorded during every cycle and represent the amount of product amplified to that point in the amplification reaction. The threshold cycle (C_T) is generally described as the point when the fluorescent signal is first recorded as statistically significant. Alternatively, data may be expressed as a crossing point ("Cp"). The Cp value is calculated by determining the second derivatives of entire qPCR amplification curves and their maximum value. The Cp value represents the cycle at which the increase of fluorescence is highest and where the logarithmic phase of a PCR begins.

[0085] To minimize errors and the effect of sample-to-sample variation, RT-PCR is usually performed using an internal standard. The ideal internal standard gene (also referred to as a reference gene) is expressed at a quite constant level among cancerous and non-cancerous tissue of the same origin (i.e., a level that is not significantly different among normal and cancerous tissues), and is not significantly affected by the experimental treatment (i.e., does not

exhibit a significant difference in expression level in the relevant tissue as a result of exposure to chemotherapy), and expressed at a quite constant level among the same tissue taken from different patients. For example, reference genes useful in the methods disclosed herein should not exhibit significantly different expression levels in cancerous prostate as compared to normal prostate tissue. RNAs frequently used to normalize patterns of gene expression are mRNAs for the housekeeping genes glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) and β-actin. Exemplary reference genes used for normalization comprise one or more of the following genes: AAMP, ARF1, ATP5E, CLTC, GPS1, and PGK1. Gene expression measurements can be normalized relative to the mean of one or more (e.g., 2, 3, 4, 5, or more) reference genes. Reference-normalized expression measurements can range from 2 to 15, where a one unit increase generally reflects a 2-fold increase in RNA quantity.

[0086] Real time PCR is compatible both with quantitative competitive PCR, where internal competitor for each target sequence is used for normalization, and with quantitative comparative PCR using a normalization gene contained within the sample, or a housekeeping gene for RT-PCR. For further details see, e.g. Held et al., Genome Research 6:986-994 (1996).

[0087] The steps of a representative protocol for use in the methods of the present disclosure use fixed, paraffin-embedded tissues as the RNA source. For example, mRNA isolation, purification, primer extension and amplification can be performed according to methods available in the art. (see, e.g., Godfrey et al. J. Molec. Diagnostics 2: 84-91 (2000); Specht et al., Am. J. Pathol. 158: 419-29 (2001)). Briefly, a representative process starts with cutting about 10 μm thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA depleted from the RNA-containing sample. After analysis of the RNA concentration, RNA is reverse transcribed using gene specific primers followed by RT-PCR to provide for cDNA amplification products.

Design of Intron-Based PCR Primers and Probes

[0088] PCR primers and probes can be designed based upon exon or intron sequences present in the mRNA transcript of the gene of interest. Primer/probe design can be performed using publicly available software, such as the DNA BLAT software developed by Kent, W.J., Genome Res. 12(4):656-64 (2002), or by the BLAST software including its variations.

[0089] 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 sequences can then be used to design primer and probe sequences 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. See S. Rrawetz, S. Misener, Bioinformatics Methods and Protocols: Methods in Molecular Biology, pp. 365-386 (Humana Press).

[0090] Other factors that can influence PCR primer design include primer length, melting temperature (Tm), 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 Tm's between 50 and 80 0C, e.g. about 50 to 70 0C.

[0091] 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).

[0092] Table A provides further information concerning the primer, probe, and amplicon sequences associated with the Examples disclosed herein.

MassARRAY® System

[0093] In MassARRAY-based methods, such as the exemplary 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-derives 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).

Other PCR-based Methods

[0094] Further PCR-based techniques that can find use in the methods disclosed herein include, for example, 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 LuminexlOO 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).

Microarrays

[0095] Expression levels of a gene or microArray of interest can also be assessed using the microarray technique. In this method, polynucleotide sequences of interest (including cDNAs and oligonucleotides) are arrayed on a substrate. The arrayed sequences are then contacted under conditions suitable for specific hybridization with detectably labeled cDNA generated from RNA of a test sample. As in the RT-PCR method, the source of RNA typically is total RNA isolated from a tumor sample, and optionally from normal tissue of the same patient as an internal control or cell lines. RNA can be extracted, for example, from frozen or archived paraffin-embedded and fixed (e.g. formalin-fixed) tissue samples.

[0096] For example, PCR amplified inserts of cDNA clones of a gene to be assayed are applied to a substrate in a dense array. Usually at least 10,000 nucleotide sequences are applied to the substrate. For example, 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 washing under stringent

conditions 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 RNA abundance.

[0097] With dual color fluorescence, separately labeled cDNA probes generated from two sources of RNA are hybridized pair wise 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 at, Proc. Natl. Acad. ScL 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 Incyte's microarray technology.

Serial Analysis of Gene Expression (SAGE)

[0098] Serial analysis of gene expression (SAGE) is a method that allows the simultaneous and quantitative analysis of a large number of gene transcripts, without the need of providing an individual hybridization probe for each transcript. First, a short sequence tag (about 10-14 bp) is generated that contains sufficient information to uniquely identify a transcript, provided that the tag is obtained from a unique position within each transcript. Then, many transcripts are linked together to form long serial molecules, that can be sequenced, revealing the identity of the multiple tags simultaneously. The expression pattern of any population of transcripts can be quantitatively evaluated by determining the abundance of individual tags, and identifying the gene corresponding to each tag. For more details see, e.g. Velculescu et al., Science 270:484-487 (1995); and Velculescu et al., Cell 88:243-51 (1997).

Gene Expression Analysis by Nucleic Acid Sequencing

[0099] 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 RNA 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).

Isolating RNA from Body Fluids

[00100] Methods of isolating RNA for expression analysis from blood, plasma and serum (see, e.g., K. Enders, et al., Clin Chem 48,1647-53 (2002) (and references cited therein) and from urine (see, e.g., R. Boom, et al., J Clin Microbiol. 28, 495-503 (1990) and references cited therein) have been described.

Immunohistochemistry

[00101] Immunohistochemistry methods are also suitable for detecting the expression levels of genes and applied to the method disclosed herein. Antibodies (e.g., monoclonal antibodies) that specifically bind a gene product of a gene of interest can be used in such methods. 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 can be used in conjunction with a labeled secondary antibody specific for the primary antibody. Immunohistochemistry protocols and kits are well known in the art and are commercially available.

Proteomics

[00102] 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. my mass spectrometry or N- terminal sequencing, and (3) analysis of the data using bioinformatics.

General Description of the mRNA/microRNA Isolation, Purification and Amplification

[00103] The steps of a representative protocol for profiling gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA or microRNA isolation, purification, primer extension and amplification are provided in various published journal articles. (See, e.g., T.E. Godfrey, et al,. J. Molec. Diagnostics 2: 84-91 (2000); K. Specht et al., Am. J. Pathol. 158: 419-29 (2001), M. Cronin, et al., Am J Pathol 164:35-42 (2004)). Briefly, a representative process starts with cutting a tissue sample section (e.g.about 10 μm thick sections of a paraffin-embedded tumor tissue sample). The RNA is then extracted, and protein and DNA are removed. After analysis of the RNA concentration, RNA repair is performed if desired. The sample can then be subjected to analysis, e.g., by reverse transcribed using gene specific promoters followed by RT-PCR.

STATISTICAL ANALYSIS OF EXPRESSION LEVELS IN IDENTIFICATION OF GENES AND MICRORNAS

[00104] 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 a parameter of interest (e.g., recurrence) and expression levels of a marker gene/microRNA as described here. In an exemplary embodiment, the present invention provides a stratified cohort sampling design (a form of case-control sampling) using tissue and data from prostate cancer patients. Selection of specimens was stratified by T stage (T1, T2), year cohort (<1993, ≥1993), and prostatectomy Gleason Score (low/intermediate, high). All patients with clinical recurrence were selected and a sample of patients who did not experience a clinical recurrence was selected. For each patient, up to two enriched tumor specimens and one normal-appearing tissue sample was assayed.

[00105] All hypothesis tests were reported using two-sided p-values. To investigate if there is a significant relationship of outcomes (clinical recurrence-free interval (cRFI), biochemical recurrence-free interval (bRFI), prostate cancer-specific survival (PCSS), and overall survival (OS)) with individual genes and/or microRNAs, demographic or clinical covariates Cox Proportional Hazards (PH) models using maximum weighted pseudo partial-likelihood estimators were used and p-values from Wald tests of the null hypothesis that the hazard ratio (HR) is one are reported. To investigate if there is a significant relationship between individual genes and/or microRNAs and Gleason pattern of a particular sample, ordinal logistic

regression models using maximum weighted likelihood methods were used and p-values from Wald tests of the null hypothesis that the odds ratio (OR) is one are reported.

COEXPRESSION ANALYSIS

[00106] The present disclosure provides a method to determine tumor stage based on the expression of staging genes, or genes that co-express with particular staging genes. 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 tumor status and disease progression. Such co-expressed genes can be assayed in lieu of, or in addition to, assaying of the staging gene with which they are co-expressed.

[00107] In an exemplary embodiment, the joint correlation of gene expression levels among prostate cancer specimens under study may be assessed. For this purpose, the correlation structures among genes and specimens may be examined through hierarchical cluster methods. This information may be used to confirm that genes that are known to be highly correlated in prostate cancer specimens cluster together as expected. Only genes exhibiting a nominally significant (unadjusted $p < 0.05$) relationship with cRFI in the univariate Cox PH regression analysis will be included in these analyses.

[00108] 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).)

NORMALIZATION OF EXPRESSION LEVELS

[00109] 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 Ct or Cp 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 store the sample. Other sources of systematic variation are attributable to laboratory processing conditions.

[00110] Assays can provide for normalization by incorporating the expression of certain normalizing genes, which do not significantly differ in expression levels under the relevant conditions. Exemplary normalization genes disclosed herein include housekeeping genes. (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 (Ct or Cp) 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 prostate cancer as compared to non-cancerous prostate tissue, and are not significantly affected by various sample and process conditions, thus provide for normalizing away extraneous effects.

[00111] In exemplary embodiments, one or more of the following genes are used as references by which the mRNA or microRNA expression data is normalized: AAMP, ARF1, ATP5E, CLTC, GPS1, and PGK1. In another exemplary embodiment, one or more of the following microRNAs are used as references by which the expression data of microRNAs are normalized: hsa-miR-106a; hsa-miR-146b-5p; hsa-miR-191; hsa-miR-19b; and hsa-miR-92a. The calibrated weighted average C_T or Cp measurements for each of the prognostic and predictive genes or microRNAs may be normalized relative to the mean of five or more reference genes or microRNAs.

[00112] 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.

STANDARDIZATION OF EXPRESSION LEVELS

[00113] The expression data used in the methods disclosed herein can be standardized. Standardization refers to a process to effectively put all the genes or microRNAs on a comparable scale. This is performed because some genes or microRNAs will exhibit more variation (a broader range of expression) than others. Standardization is performed by dividing each expression value by its standard deviation across all samples for that gene or microRNA. Hazard ratios are then interpreted as the relative risk of recurrence per 1 standard deviation increase in expression.

KITS OF THE INVENTION

[00114] The materials for use in the methods of the present invention are suited for preparation of kits produced in accordance with well-known procedures. The present disclosure thus provides kits comprising agents, which may include gene (or microRNA)-specific or gene (or microRNA)-selective probes and/or primers, for quantifying the expression of the disclosed genes or microRNAs for predicting prognostic outcome or response to treatment. Such kits may optionally contain reagents for the extraction of RNA from tumor samples, in particular fixed paraffin-embedded tissue samples and/or reagents for RNA amplification. In addition, the kits may optionally comprise the reagent(s) with an identifying description or label or instructions relating to their use in the methods of the present invention. The kits may comprise containers (including microliter plates suitable for use in an automated implementation of the method), each with one or more of the various materials or reagents (typically in concentrated form) utilized in the methods, including, for example, chromatographic columns, pre-fabricated microarrays, buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP and dTTP; or rATP, rCTP, rGTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more probes and primers of the present invention (e.g., appropriate length poly(T) or random primers linked to a promoter reactive with the RNA polymerase). Mathematical algorithms used to estimate or quantify prognostic or predictive information are also properly potential components of kits.

REPORTS

[00115] The methods of this invention, when practiced for commercial diagnostic purposes, generally produce a report or summary of information obtained from the herein-described methods. For example, a report may include information concerning expression levels of one or more genes and /or microRNAs, classification of the tumor or the patient's risk of recurrence, the patient's likely prognosis or risk classification, clinical and pathologic factors, and/or other information. The methods and reports of this invention can further include storing the report in a database. The method can create a record in a database for the subject and populate the record with data. The report may be a paper report, an auditory report, or an electronic record. The report may be displayed and/or stored on a computing device (e.g., handheld device, desktop computer, smart device, website, etc.). It is contemplated that the report is provided to a physician and/or the patient. The receiving of the report can further

include establishing a network connection to a server computer that includes the data and report and requesting the data and report from the server computer.

COMPUTER PROGRAM

[00116] The values from the assays described above, such as expression data, 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, standardization, thresholding, and conversion of values from assays to a score and/or text or graphical depiction of tumor stage and related information). The computer program product has stored therein a computer program for performing the calculation.

[00117] 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 an expression score, thresholding, or other functions described herein. The methods provided by the present invention may also be automated in whole or in part.

[00118] All aspects of the present invention may also be practiced such that a limited number of additional genes and/or microRNAs that are co-expressed or functionally related with the disclosed genes, for example as evidenced by statistically meaningful Pearson and/or Spearman correlation coefficients, are included in a test in addition to and/or in place of disclosed genes.

[00119] 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.

EXAMPLES

EXAMPLE 1: RNA YIELD AND GENE EXPRESSION PROFILES IN PROSTATE CANCER BIOPSY CORES

[00120] Clinical tools based on prostate needle core biopsies are needed to guide treatment planning at diagnosis for men with localized prostate cancer. Limiting tissue in needle core biopsy specimens poses significant challenges to the development of molecular diagnostic tests. This study examined RNA extraction yields and gene expression profiles using an RT-PCR assay to characterize RNA from manually micro-dissected fixed paraffin embedded (FPE) prostate cancer needle biopsy cores. It also investigated the association of RNA yields and gene expression profiles with Gleason score in these specimens.

Patients and Samples

[00121] This study determined the feasibility of gene expression profile analysis in prostate cancer needle core biopsies by evaluating the quantity and quality of RNA extracted from fixed paraffin-embedded (FPE) prostate cancer needle core biopsy specimens. Forty-eight (48) formalin-fixed blocks from prostate needle core biopsy specimens were used for this study. Classification of specimens was based on interpretation of the Gleason score (2005 Int'l Society of Urological Pathology Consensus Conference) and percentage tumor (<33%, 33-66%, >66%) involvement as assessed by pathologists.

Table 1: Distribution of cases

Gleason score Category	~<33% Tumor	~33-66% Tumor	~>66% Tumor
Low (≤6)	5	5	6
Intermediate (7)	5	5	6
High (8, 9, 10)	5	5	6
Total	15	15	18

Assay Methods

[00122] Fourteen (14) serial 5 μm unstained sections from each FPE tissue block were included in the study. The first and last sections for each case were H&E stained and histologically reviewed to confirm the presence of tumor and for tumor enrichment by manual micro-dissection.

[00123] RNA from enriched tumor samples was extracted using a manual RNA extraction process. RNA was quantitated using the RiboGreen® assay and tested for the presence of genomic DNA contamination. Samples with sufficient RNA yield and free of genomic DNA tested for gene expression levels of a 24-gene panel of reference and cancer-related genes using quantitative RT-PCR. The expression was normalized to the average of 6 reference genes (AAMP, ARF1, ATP5E, CLTC, EEF1A1, and GPX1).

Statistical Methods

[00124] Descriptive statistics and graphical displays were used to summarize standard pathology metrics and gene expression, with stratification for Gleason Score category and percentage tumor involvement category. Ordinal logistic regression was used to evaluate the relationship between gene expression and Gleason Score category.

Results

[00125] The RNA yield per unit surface area ranged from 16 to 2406 ng/mm2. Higher RNA yield was observed in samples with higher percent tumor involvement ($p=0.02$) and higher Gleason score ($p=0.01$). RNA yield was sufficient (> 200ng) in 71% of cases to permit 96-well RT-PCR, with 87% of cases having >100ng RNA yield. The study confirmed that gene expression from prostate biopsies, as measured by qRT-PCR, was comparable to FPET samples used in commercial molecular assays for breast cancer. In addition, it was observed that greater biopsy RNA yields are found with higher Gleason score and higher percent tumor involvement. Nine genes were identified as significantly associated with Gleason score ($p < 0.05$) and there was a large dynamic range observed for many test genes.

EXAMPLE 2: GENE EXPRESSION ANALYSIS FOR GENES ASSOCIATED WITH PROGNOSIS IN PROSTATE CANCER

Patients and Samples

[00126] Approximately 2600 patients with clinical stage T1/T2 prostate cancer treated with radical prostatectomy (RP) at the Cleveland Clinic between 1987 and 2004 were identified. Patients were excluded from the study design if they received neo-adjuvant and/or adjuvant therapy, if pre-surgical PSA levels were missing, or if no tumor block was available from initial diagnosis. 127 patients with clinical recurrence and 374 patients without clinical recurrence after radical prostatectomy were randomly selected using a cohort sampling design. The specimens were stratified by T stage (T1, T2), year cohort (<1993, ≥1993), and prostatectomy Gleason

score (low/intermediate, high). Of the 501 sampled patients, 51 were excluded for insufficient tumor; 7 were excluded due to clinical ineligibility; 2 were excluded due to poor quality of gene expression data; and 10 were excluded because primary Gleason pattern was unavailable. Thus, this gene expression study included tissue and data from 111 patients with clinical recurrence and 330 patients without clinical recurrence after radical prostatectomies performed between 1987 and 2004 for treatment of early stage (T1, T2) prostate cancer.

[00127] Two fixed paraffin embedded (FPE) tissue specimens were obtained from prostate tumor specimens in each patient. The sampling method (sampling method A or B) depended on whether the highest Gleason pattern is also the primary Gleason pattern. For each specimen selected, the invasive cancer cells were at least 5.0 mm in dimension, except in the instances of pattern 5, where 2.2 mm was accepted. Specimens were spatially distinct where possible.

Table 2: Sampling Methods

Sampling Method A	Sampling Method B
For patients whose prostatectomy primary Gleason pattern is also the highest Gleason pattern	For patients whose prostatectomy primary Gleason pattern is not the highest Gleason pattern
Specimen 1 (A1) = primary Gleason pattern Select and mark largest focus (greatest cross-sectional area) of primary Gleason pattern tissue. Invasive cancer area ≥ 5.0 mm.	Specimen 1 (B1) = highest Gleason pattern Select highest Gleason pattern tissue from spatially distinct area from specimen B2, if possible. Invasive cancer area at least 5.0 mm if selecting secondary pattern, at least 2.2 mm if selecting Gleason pattern 5.
Specimen 2 (A2) = secondary Gleason pattern Select and mark secondary Gleason pattern tissue from spatially distinct area from specimen A1. Invasive cancer area ≥ 5.0 mm.	Specimen 2 (B2) = primary Gleason pattern Select largest focus (greatest cross-sectional area) of primary Gleason pattern tissue. Invasive cancer area ≥ 5.0 mm.

[00128] Histologically normal appearing tissue (NAT) adjacent to the tumor specimen (also referred to in these Examples as "non-tumor tissue") was also evaluated. Adjacent tissue was collected 3 mm from the tumor to 3 mm from the edge of the FPET block. NAT was preferentially sampled adjacent to the primary Gleason pattern. In cases where there was insufficient NAT adjacent to the primary Gleason pattern, then NAT was sampled adjacent to the secondary or highest Gleason pattern (A2 or B1) per the method set forth in Table 2. Six (6) 10 μm sections with beginning H&E at 5 μm and ending unstained slide at 5 μm were prepared

from each fixed paraffin-embedded tumor (FPET) block included in the study. All cases were histologically reviewed and manually micro-dissected to yield two enriched tumor samples and, where possible, one normal tissue sample adjacent to the tumor specimen.

Assay Method

[00129] In this study, RT-PCR analysis was used to determine RNA expression levels for 738 genes and chromosomal rearrangements (e.g., TMPRSS2-ERG fusion or other ETS family genes) in prostate cancer tissue and surrounding NAT in patients with early-stage prostate cancer treated with radical prostatectomy.

[00130] The samples were quantified using the RiboGreen assay and a subset tested for presence of genomic DNA contamination. Samples were taken into reverse transcription (RT) and quantitative polymerase chain reaction (qPCR). All analyses were conducted on reference-normalized gene expression levels using the average of the of replicate well crossing point (CP) values for the 6 reference genes (AAMP, ARF1, ATP5E, CLTC, GPS1, PGK1).

Statistical Analysis and Results

[00131] Primary statistical analyses involved 111 patients with clinical recurrence and 330 patients without clinical recurrence after radical prostatectomy for early-stage prostate cancer stratified by T–stage (T1, T2), year cohort (<1993, ≥1993), and prostatectomy Gleason score (low/intermediate, high). Gleason score categories are defined as follows: low (Gleason score ≤ 6), intermediate (Gleason score = 7), and high (Gleason score ≥ 8). A patient was included in a specified analysis if at least one sample for that patient was evaluable. Unless otherwise stated, all hypothesis tests were reported using two-sided p-values. The method of Storey was applied to the resulting set of p-values to control the false discovery rate (FDR) at 20%. J. Storey, R. Tibshirani, Estimating the Positive False Discovery Rate Under Dependence, with Applications to DNA Microarrays, Dept. of Statistics, Stanford Univ. (2001).

[00132] Analysis of gene expression and recurrence-free interval was based on univariate Cox Proportional Hazards (PH) models using maximum weighted pseudo-partial-likelihood estimators for each evaluable gene in the gene list (727 test genes and 5 reference genes). P-values were generated using Wald tests of the null hypothesis that the hazard ratio (HR) is one. Both unadjusted p-values and the q-value (smallest FDR at which the hypothesis test in question is rejected) were reported. Un-adjusted p-values <0.05 were considered statistically significant. Since two tumor specimens were selected for each patient, this analysis was performed using the

2 specimens from each patient as follows: (1) analysis using the primary Gleason pattern specimen from each patient (Specimens A1 and B2 as described in Table 2); (2) analysis using the highest Gleason pattern specimen from each patient (Specimens A1 and B1 as described in Table 2).

[00133] Analysis of gene expression and Gleason pattern (3, 4, 5) was based on univariate ordinal logistic regression models using weighted maximum likelihood estimators for each gene in the gene list (727 test genes and 5 reference genes). P-values were generated using a Wald test of the null hypothesis that the odds ratio (OR) is one. Both unadjusted p-values and the q-value (smallest FDR at which the hypothesis test in question is rejected) were reported. Un-adjusted p-values <0.05 were considered statistically significant. Since two tumor specimens were selected for each patient, this analysis was performed using the 2 specimens from each patient as follows: (1) analysis using the primary Gleason pattern specimen from each patient (Specimens A1 and B2 as described in Table 2); (2) analysis using the highest Gleason pattern specimen from each patient (Specimens A1 and B1 as described in Table 2).

[00134] It was determined whether there is a significant relationship between cRFI and selected demographic, clinical, and pathology variables, including age, race, clinical tumor stage, pathologic tumor stage, location of selected tumor specimens within the prostate (peripheral versus transitional zone), PSA at the time of surgery, overall Gleason score from the radical prostatectomy, year of surgery, and specimen Gleason pattern. Separately for each demographic or clinical variable, the relationship between the clinical covariate and cRFI was modeled using univariate Cox PH regression using weighted pseudo partial-likelihood estimators and a p-value was generated using Wald's test of the null hypothesis that the hazard ratio (HR) is one. Covariates with unadjusted p-values <0.2 may have been included in the covariate-adjusted analyses.

[00135] It was determined whether there was a significant relationship between each of the individual cancer-related genes and cRFI after controlling for important demographic and clinical covariates. Separately for each gene, the relationship between gene expression and cRFI was modeled using multivariate Cox PH regression using weighted pseudo partial-likelihood estimators including important demographic and clinical variables as covariates. The independent contribution of gene expression to the prediction of cRFI was tested by generating a p-value from a Wald test using a model that included clinical covariates for each nodule

(specimens as defined in Table 2). Un-adjusted p-values <0.05 were considered statistically significant.

[00136] Tables 3A and 3B provide genes significantly associated (p<0.05), positively or negatively, with Gleason pattern in the primary and/or highest Gleason pattern. Increased expression of genes in Table 3A is positively associated with higher Gleason score, while increased expression of genes in Table 3B are negatively associated with higher Gleason score.

Table 3A

Gene significantly (p<0.05) associated with Gleason pattern for all specimens in the primary Gleason pattern or highest Gleason pattern odds ratio (OR) > 1.0 (Increased expression is positively associated with higher Gleason Score)

Table 3A	Primary Pattern		Highest Pattern	
Official Symbol	**OR**	**p-value**	**OR**	**p-value**
ALCAM	1.73	<.001	1.36	0.009
ANLN	1.35	0.027		
APOC1	1.47	0.005	1.61	<.001
APOE	1.87	<.001	2.15	<.001
ASAP2	1.53	0.005		
ASPN	2.62	<.001	2.13	<.001
ATP5E	1.35	0.035		
AURKA	1.44	0.010		
AURKB	1.59	<.001	1.56	<.001
BAX	1.43	0.006		
BGN	2.58	<.001	2.82	<.001
BIRC5	1.45	0.003	1.79	<.001
BMP6	2.37	<.001	1.68	<.001
BMPR1B	1.58	0.002		
BRCA2			1.45	0.013
BUB1	1.73	<.001	1.57	<.001
CACNA1D	1.31	0.045	1.31	0.033
CADPS			1.30	0.023
CCNB1	1.43	0.023		
CCNE2	1.52	0.003	1.32	0.035
CD276	2.20	<.001	1.83	<.001
CD68			1.36	0.022
CDC20	1.69	<.001	1.95	<.001
CDC6	1.38	0.024	1.46	<.001
CDH11			1.30	0.029
CDKN2B	1.55	0.001	1.33	0.023
CDKN2C	1.62	<.001	1.52	<.001
CDKN3	1.39	0.010	1.50	0.002
CENPF	1.96	<.001	1.71	<.001
CHRAC1			1.34	0.022
CLDN3			1.37	0.029

Table 3A	Primary Pattern		Highest Pattern	
Official Symbol	**OR**	**p-value**	**OR**	**p-value**
COL1A1	2.23	<.001	2.22	<.001
COL1A2			1.42	0.005
COL3A1	1.90	<.001	2.13	<.001
COL8A1	1.88	<.001	2.35	<.001
CRISP3	1.33	0.040	1.26	0.050
CTHRC1	2.01	<.001	1.61	<.001
CTNND2	1.48	0.007	1.37	0.011
DAPK1	1.44	0.014		
DIAPH1	1.34	0.032	1.79	<.001
DIO2			1.56	0.001
DLL4	1.38	0.026	1.53	<.001
ECE1	1.54	0.012	1.40	0.012
ENY2	1.35	0.046	1.35	0.012
EZH2	1.39	0.040		
F2R	2.37	<.001	2.60	<.001
FAM49B	1.57	0.002	1.33	0.025
FAP	2.36	<.001	1.89	<.001
FCGR3A	2.10	<.001	1.83	<.001
GNPTAB	1.78	<.001	1.54	<.001
GSK3B			1.39	0.018
HRAS	1.62	0.003		
HSD17B4	2.91	<.001	1.57	<.001
HSPA8	1.48	0.012	1.34	0.023
IFI30	1.64	<.001	1.45	0.013
IGFBP3			1.29	0.037
IL11	1.52	0.001	1.31	0.036
INHBA	2.55	<.001	2.30	<.001
ITGA4			1.35	0.028
JAG1	1.68	<.001	1.40	0.005
KCNN2	1.50	0.004		
KCTD12			1.38	0.012
KHDRBS3	1.85	<.001	1.72	<.001
KIF4A	1.50	0.010	1.50	<.001
KLK14	1.49	0.001	1.35	<.001
KPNA2	1.68	0.004	1.65	0.001
KRT2			1.33	0.022
KRT75			1.27	0.028
LAMC1	1.44	0.029		
LAPTM5	1.36	0.025	1.31	0.042
LTBP2	1.42	0.023	1.66	<.001
MANF			1.34	0.019
MAOA	1.55	0.003	1.50	<.001
MAP3K5	1.55	0.006	1.44	0.001
MDK	1.47	0.013	1.29	0.041

Table 3A	Primary Pattern		Highest Pattern	
Official Symbol	OR	p-value	OR	p-value
MDM2			1.31	0.026
MELK	1.64	<.001	1.64	<.001
MMP11	2.33	<.001	1.66	<.001
MYBL2	1.41	0.007	1.54	<.001
MYO6			1.32	0.017
NETO2			1.36	0.018
NOX4	1.84	<.001	1.73	<.001
NPM1	1.68	0.001		
NRIP3			1.36	0.009
NRP1	1.80	0.001	1.36	0.019
OSM	1.33	0.046		
PATE1	1.38	0.032		
PECAM1	1.38	0.021	1.31	0.035
PGD	1.56	0.010		
PLK1	1.51	0.004	1.49	0.002
PLOD2			1.29	0.027
POSTN	1.70	0.047	1.55	0.006
PPP3CA	1.38	0.037	1.37	0.006
PTK6	1.45	0.007	1.53	<.001
PTTG1			1.51	<.001
RAB31			1.31	0.030
RAD21	2.05	<.001	1.38	0.020
RAD51	1.46	0.002	1.26	0.035
RAF1	1.46	0.017		
RALBP1	1.37	0.043		
RHOC			1.33	0.021
ROBO2	1.52	0.003	1.41	0.006
RRM2	1.77	<.001	1.50	<.001
SAT1	1.67	0.002	1.61	<.001
SDC1	1.66	0.001	1.46	0.014
SEC14L1	1.53	0.003	1.62	<.001
SESN3	1.76	<.001	1.45	<.001
SFRP4	2.69	<.001	2.03	<.001
SHMT2	1.69	0.007	1.45	0.003
SKIL			1.46	0.005
SOX4	1.42	0.016	1.27	0.031
SPARC	1.40	0.024	1.55	<.001
SPINK1			1.29	0.002
SPP1	1.51	0.002	1.80	<.001
TFDP1	1.48	0.014		
THBS2	1.87	<.001	1.65	<.001
THY1	1.58	0.003	1.64	<.001
TK1	1.79	<.001	1.42	0.001
TOP2A	2.30	<.001	2.01	<.001

Table 3A	Primary Pattern		Highest Pattern	
Official Symbol	OR	p-value	OR	p-value
TPD52	1.95	<.001	1.30	0.037
TPX2	2.12	<.001	1.86	<.001
TYMP	1.36	0.020		
TYMS	1.39	0.012	1.31	0.036
UBE2C	1.66	<.001	1.65	<.001
UBE2T	1.59	<.001	1.33	0.017
UGDH			1.28	0.049
UGT2B15	1.46	0.001	1.25	0.045
UHRF1	1.95	<.001	1.62	<.001
VDR	1.43	0.010	1.39	0.018
WNT5A	1.54	0.001	1.44	0.013

Table 3B.

Gene significantly (p<0.05) associated with Gleason pattern for all specimens in the primary Gleason pattern or highest Gleason pattern odds ratio (OR) < 1.0 (Increased expression is negatively associated with higher Gleason score)

Table 3B	Primary Pattern		Highest Pattern	
Official Symbol	OR	p-value	OR	p-value
ABCA5	0.78	0.041		
ABCG2	0.65	0.001	0.72	0.012
ACOX2	0.44	<.001	0.53	<.001
ADH5	0.45	<.001	0.42	<.001
AFAP1			0.79	0.038
AIG1			0.77	0.024
AKAP1	0.63	0.002		
AKR1C1	0.66	0.003	0.63	<.001
AKT3	0.68	0.006	0.77	0.010
ALDH1A2	0.28	<.001	0.33	<.001
ALKBH3	0.77	0.040	0.77	0.029
AMPD3	0.67	0.007		
ANPEP	0.68	0.008	0.59	<.001
ANXA2	0.72	0.018		
APC			0.69	0.002
AXIN2	0.46	<.001	0.54	<.001
AZGP1	0.52	<.001	0.53	<.001
BIK	0.69	0.006	0.73	0.003
BIN1	0.43	<.001	0.61	<.001
BTG3			0.79	0.030
BTRC	0.48	<.001	0.62	<.001
C7	0.37	<.001	0.55	<.001
CADM1	0.56	<.001	0.69	0.001
CAV1	0.58	0.002	0.70	0.009
CAV2	0.65	0.029		

Table 3B	Primary Pattern		Highest Pattern	
Official Symbol	**OR**	**p-value**	**OR**	**p-value**
CCNH	0.67	0.006	0.77	0.048
CD164	0.59	0.003	0.57	<.001
CDC25B	0.77	0.035		
CDH1			0.66	<.001
CDK2			0.71	0.003
CDKN1C	0.58	<.001	0.57	<.001
CDS2			0.69	0.002
CHN1	0.66	0.002		
COL6A1	0.44	<.001	0.66	<.001
COL6A3	0.66	0.006		
CSRP1	0.42	0.006		
CTGF	0.74	0.043		
CTNNA1	0.70	<.001	0.83	0.018
CTNNB1	0.70	0.019		
CTNND1			0.75	0.028
CUL1			0.74	0.011
CXCL12	0.54	<.001	0.74	0.006
CYP3A5	0.52	<.001	0.66	0.003
CYR61	0.64	0.004	0.68	0.005
DDR2	0.57	0.002	0.73	0.004
DES	0.34	<.001	0.58	<.001
DLGAP1	0.54	<.001	0.62	<.001
DNM3	0.67	0.004		
DPP4	0.41	<.001	0.53	<.001
DPT	0.28	<.001	0.48	<.001
DUSP1	0.59	<.001	0.63	<.001
EDNRA	0.64	0.004	0.74	0.008
EGF			0.71	0.012
EGR1	0.59	<.001	0.67	0.009
EGR3	0.72	0.026	0.71	0.025
EIF5			0.76	0.025
ELK4	0.58	0.001	0.70	0.008
ENPP2	0.66	0.002	0.70	0.005
EPHA3	0.65	0.006		
EPHB2	0.60	<.001	0.78	0.023
EPHB4	0.75	0.046	0.73	0.006
ERBB3	0.76	0.040	0.75	0.013
ERBB4			0.74	0.023
ERCC1	0.63	<.001	0.77	0.016
FAAH	0.67	0.003	0.71	0.010
FAM107A	0.35	<.001	0.59	<.001
FAM13C	0.37	<.001	0.48	<.001
FAS	0.73	0.019	0.72	0.008
FGF10	0.53	<.001	0.58	<.001

Table 3B	Primary Pattern		Highest Pattern	
Official Symbol	OR	p-value	OR	p-value
FGF7	0.52	<.001	0.59	<.001
FGFR2	0.60	<.001	0.59	<.001
FKBP5	0.70	0.039	0.68	0.003
FLNA	0.39	<.001	0.56	<.001
FLNC	0.33	<.001	0.52	<.001
FOS	0.58	<.001	0.66	0.005
FOXO1	0.57	<.001	0.67	<.001
FOXQ1			0.74	0.023
GADD45B	0.62	0.002	0.71	0.010
GHR	0.62	0.002	0.72	0.009
GNRH1	0.74	0.049	0.75	0.026
GPM6B	0.48	<.001	0.68	<.001
GPS1			0.68	0.003
GSN	0.46	<.001	0.77	0.027
GSTM1	0.44	<.001	0.62	<.001
GSTM2	0.29	<.001	0.49	<.001
HGD			0.77	0.020
HIRIP3	0.75	0.034		
HK1	0.48	<.001	0.66	0.001
HLF	0.42	<.001	0.55	<.001
HNF1B	0.67	0.006	0.74	0.010
HPS1	0.66	0.001	0.65	<.001
HSP90AB1	0.75	0.042		
HSPA5	0.70	0.011		
HSPB2	0.52	<.001	0.70	0.004
IGF1	0.35	<.001	0.59	<.001
IGF2	0.48	<.001	0.70	0.005
IGFBP2	0.61	<.001	0.77	0.044
IGFBP5	0.63	<.001		
IGFBP6	0.45	<.001	0.64	<.001
IL6ST	0.55	0.004	0.63	<.001
ILK	0.40	<.001	0.57	<.001
ING5	0.56	<.001	0.78	0.033
ITGA1	0.56	0.004	0.61	<.001
ITGA3			0.78	0.035
ITGA5	0.71	0.019	0.75	0.017
ITGA7	0.37	<.001	0.52	<.001
ITGB3	0.63	0.003	0.70	0.005
ITPR1	0.46	<.001	0.64	<.001
ITPR3	0.70	0.013		
ITSN1	0.62	0.001		
JUN	0.48	<.001	0.60	<.001
JUNB	0.72	0.025		
KIT	0.51	<.001	0.68	0.007

Table 3B	Primary Pattern		Highest Pattern	
Official Symbol	OR	p-value	OR	p-value
KLC1	0.58	<.001		
KLK1	0.69	0.028	0.66	0.003
KLK2	0.60	<.001		
KLK3	0.63	<.001	0.69	0.012
KRT15	0.56	<.001	0.60	<.001
KRT18	0.74	0.034		
KRT5	0.64	<.001	0.62	<.001
LAMA4	0.47	<.001	0.73	0.010
LAMB3	0.73	0.018	0.69	0.003
LGALS3	0.59	0.003	0.54	<.001
LIG3	0.75	0.044		
MAP3K7	0.66	0.003	0.79	0.031
MCM3	0.73	0.013	0.80	0.034
MGMT	0.61	0.001	0.71	0.007
MGST1			0.75	0.017
MLXIP	0.70	0.013		
MMP2	0.57	<.001	0.72	0.010
MMP7	0.69	0.009		
MPPED2	0.70	0.009	0.59	<.001
MSH6	0.78	0.046		
MTA1	0.69	0.007		
MTSS1	0.55	<.001	0.54	<.001
MYBPC1	0.45	<.001	0.45	<.001
NCAM1	0.51	<.001	0.65	<.001
NCAPD3	0.42	<.001	0.53	<.001
NCOR2	0.68	0.002		
NDUFS5	0.66	0.001	0.70	0.013
NEXN	0.48	<.001	0.62	<.001
NFAT5	0.55	<.001	0.67	0.001
NFKBIA			0.79	0.048
NRG1	0.58	0.001	0.62	0.001
OLFML3	0.42	<.001	0.58	<.001
OMD	0.67	0.004	0.71	0.004
OR51E2	0.65	<.001	0.76	0.007
PAGE4	0.27	<.001	0.46	<.001
PCA3	0.68	0.004		
PCDHGB7	0.70	0.025	0.65	<.001
PGF	0.62	0.001		
PGR	0.63	0.028		
PHTF2	0.69	0.033		
PLP2	0.54	<.001	0.71	0.003
PPAP2B	0.41	<.001	0.54	<.001
PPP1R12A	0.48	<.001	0.60	<.001
PRIMA1	0.62	0.003	0.65	<.001

Table 3B	Primary Pattern		Highest Pattern	
Official Symbol	OR	p-value	OR	p-value
PRKAR1B	0.70	0.009		
PRKAR2B			0.79	0.038
PRKCA	0.37	<.001	0.55	<.001
PRKCB	0.47	<.001	0.56	<.001
PTCH1	0.70	0.021		
PTEN	0.66	0.010	0.64	<.001
PTGER3			0.76	0.015
PTGS2	0.70	0.013	0.68	0.005
PTH1R	0.48	<.001		
PTK2B	0.67	0.014	0.69	0.002
PYCARD	0.72	0.023		
RAB27A			0.76	0.017
RAGE	0.77	0.040	0.57	<.001
RARB	0.66	0.002	0.69	0.002
RECK	0.65	<.001		
RHOA	0.73	0.043		
RHOB	0.61	0.005	0.62	<.001
RND3	0.63	0.006	0.66	<.001
SDHC			0.69	0.002
SEC23A	0.61	<.001	0.74	0.010
SEMA3A	0.49	<.001	0.55	<.001
SERPINA3	0.70	0.034	0.75	0.020
SH3RF2	0.33	<.001	0.42	<.001
SLC22A3	0.23	<.001	0.37	<.001
SMAD4	0.33	<.001	0.39	<.001
SMARCC2	0.62	0.003	0.74	0.008
SMO	0.53	<.001	0.73	0.009
SORBS1	0.40	<.001	0.55	<.001
SPARCL1	0.42	<.001	0.63	<.001
SRD5A2	0.28	<.001	0.37	<.001
ST5	0.52	<.001	0.63	<.001
STAT5A	0.60	<.001	0.75	0.020
STAT5B	0.54	<.001	0.65	<.001
STS			0.78	0.035
SUMO1	0.75	0.017	0.71	0.002
SVIL	0.45	<.001	0.62	<.001
TARP	0.72	0.017		
TGFB1I1	0.37	<.001	0.53	<.001
TGFB2	0.61	0.025	0.59	<.001
TGFB3	0.46	<.001	0.60	<.001
TIMP2	0.62	0.001		
TIMP3	0.55	<.001	0.76	0.019
TMPRSS2	0.71	0.014		
TNF	0.65	0.010		

Table 3B	Primary Pattern		Highest Pattern	
Official Symbol	OR	p-value	OR	p-value
TNFRSF10A	0.71	0.014	0.74	0.010
TNFRSF10B	0.74	0.030	0.73	0.016
TNFSF10			0.69	0.004
TP53			0.73	0.011
TP63	0.62	<.001	0.68	0.003
TPM1	0.43	<.001	0.47	<.001
TPM2	0.30	<.001	0.47	<.001
TPP2	0.58	<.001	0.69	0.001
TRA2A	0.71	0.006		
TRAF3IP2	0.50	<.001	0.63	<.001
TRO	0.40	<.001	0.59	<.001
TRPC6	0.73	0.030		
TRPV6			0.80	0.047
VCL	0.44	<.001	0.55	<.001
VEGFB	0.73	0.029		
VIM	0.72	0.013		
VTI1B	0.78	0.046		
WDR19	0.65	<.001		
WFDC1	0.50	<.001	0.72	0.010
YY1	0.75	0.045		
ZFHX3	0.52	<.001	0.54	<.001
ZFP36	0.65	0.004	0.69	0.012
ZNF827	0.59	<.001	0.69	0.004

[00137] To identify genes associated with recurrence (cRFI, bRFI) in the primary and the highest Gleason pattern, each of 727 genes were analyzed in univariate models using specimens A1 and B2 (see Table 2, above). Tables 4A and 4B provide genes that were associated, positively or negatively, with cRFI and/or bRFI in the primary and/or highest Gleason pattern. Increased expression of genes in Table 4A is negatively associated with good prognosis, while increased expression of genes in Table 4B is positively associated with good prognosis.

Table 4A.

Genes significantly (p<0.05) associated with cRFI or bRFI in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) > 1.0 (increased expression is negatively associated with good prognosis)

Table 4A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
AKR1C3	1.304	0.022	1.312	0.013				
ANLN	1.379	0.002	1.579	<.001	1.465	<.001	1.623	<.001
AQP2	1.184	0.027	1.276	<.001				
ASAP2			1.442	0.006				

Table 4A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
ASPN	2.272	<.001	2.106	<.001	1.861	<.001	1.895	<.001
ATP5E	1.414	0.013	1.538	<.001				
BAG5			1.263	0.044				
BAX			1.332	0.026	1.327	0.012	1.438	0.002
BGN	1.947	<.001	2.061	<.001	1.339	0.017		
BIRC5	1.497	<.001	1.567	<.001	1.478	<.001	1.575	<.001
BMP6	1.705	<.001	2.016	<.001	1.418	0.004	1.541	<.001
BMPR1B	1.401	0.013			1.325	0.016		
BRCA2							1.259	0.007
BUB1	1.411	<.001	1.435	<.001	1.352	<.001	1.242	0.002
CADPS					1.387	0.009	1.294	0.027
CCNB1					1.296	0.016	1.376	0.002
CCNE2	1.468	<.001	1.649	<.001	1.729	<.001	1.563	<.001
CD276	1.678	<.001	1.832	<.001	1.581	<.001	1.385	0.002
CDC20	1.547	<.001	1.671	<.001	1.446	<.001	1.540	<.001
CDC6	1.400	0.003	1.290	0.030	1.403	0.002	1.276	0.019
CDH7	1.403	0.003	1.413	0.002				
CDKN2B	1.569	<.001	1.752	<.001	1.333	0.017	1.347	0.006
CDKN2C	1.612	<.001	1.780	<.001	1.323	0.005	1.335	0.004
CDKN3	1.384	<.001	1.255	0.024	1.285	0.003	1.216	0.028
CENPF	1.578	<.001	1.692	<.001	1.740	<.001	1.705	<.001
CKS2	1.390	0.007	1.418	0.005	1.291	0.018		
CLTC			1.368	0.045				
COL1A1	1.873	<.001	2.103	<.001	1.491	<.001	1.472	<.001
COL1A2			1.462	0.001				
COL3A1	1.827	<.001	2.005	<.001	1.302	0.012	1.298	0.018
COL4A1	1.490	0.002	1.613	<.001				
COL8A1	1.692	<.001	1.926	<.001	1.307	0.013	1.317	0.010
CRISP3	1.425	0.001	1.467	<.001	1.242	0.045		
CTHRC1	1.505	0.002	2.025	<.001	1.425	0.003	1.369	0.005
CTNND2					1.412	0.003		
CXCR4	1.312	0.023	1.355	0.008				
DDIT4	1.543	<.001	1.763	<.001				
DYNLL1	1.290	0.039					1.201	0.004
EIF3H					1.428	0.012		
ENY2	1.361	0.014			1.392	0.008	1.371	0.001
EZH2			1.311	0.010				
F2R	1.773	<.001	1.695	<.001	1.495	<.001	1.277	0.018
FADD			1.292	0.018				
FAM171B			1.285	0.036				
FAP	1.455	0.004	1.560	0.001	1.298	0.022	1.274	0.038
FASN	1.263	0.035						

Table 4A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
FCGR3A			1.654	<.001	1.253	0.033	1.350	0.007
FGF5	1.219	0.030						
GNPTAB	1.388	0.007	1.503	0.003	1.355	0.005	1.434	0.002
GPR68			1.361	0.008				
GREM1	1.470	0.003	1.716	<.001	1.421	0.003	1.316	0.017
HDAC1					1.290	0.025		
HDAC9			1.395	0.012				
HRAS	1.424	0.006	1.447	0.020				
HSD17B4	1.342	0.019	1.282	0.026	1.569	<.001	1.390	0.002
HSPA8	1.290	0.034						
IGFBP3	1.333	0.022	1.442	0.003	1.253	0.040	1.323	0.005
INHBA	2.368	<.001	2.765	<.001	1.466	0.002	1.671	<.001
JAG1	1.359	0.006	1.367	0.005	1.259	0.024		
KCNN2	1.361	0.011	1.413	0.005	1.312	0.017	1.281	0.030
KHDRBS3	1.387	0.006	1.601	<.001	1.573	<.001	1.353	0.006
KIAA0196							1.249	0.037
KIF4A	1.212	0.016			1.149	0.040	1.278	0.003
KLK14	1.167	0.023					1.180	0.007
KPNA2			1.425	0.009	1.353	0.005	1.305	0.019
KRT75							1.164	0.028
LAMA3					1.327	0.011		
LAMB1			1.347	0.019				
LAMC1	1.555	0.001	1.310	0.030			1.349	0.014
LIMS1							1.275	0.022
LOX					1.358	0.003	1.410	<.001
LTBP2	1.396	0.009	1.656	<.001	1.278	0.022		
LUM			1.315	0.021				
MANF					1.660	<.001	1.323	0.011
MCM2					1.345	0.011	1.387	0.014
MCM6	1.307	0.023	1.352	0.008			1.244	0.039
MELK	1.293	0.014	1.401	<.001	1.501	<.001	1.256	0.012
MMP11	1.680	<.001	1.474	<.001	1.489	<.001	1.257	0.030
MRPL13							1.260	0.025
MSH2			1.295	0.027				
MYBL2	1.664	<.001	1.670	<.001	1.399	<.001	1.431	<.001
MYO6			1.301	0.033				
NETO2	1.412	0.004	1.302	0.027	1.298	0.009		
NFKB1					1.236	0.050		
NOX4	1.492	<.001	1.507	0.001	1.555	<.001	1.262	0.019
NPM1					1.287	0.036		
NRIP3			1.219	0.031			1.218	0.018
NRP1			1.482	0.002			1.245	0.041

Table 4A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
OLFML2B			1.362	0.015				
OR51E1					1.531	<.001	1.488	0.003
PAK6			1.269	0.033				
PATE1	1.308	<.001	1.332	<.001	1.164	0.044		
PCNA							1.278	0.020
PEX10	1.436	0.005	1.393	0.009				
PGD	1.298	0.048			1.579	<.001		
PGK1			1.274	0.023			1.262	0.009
PLA2G7					1.315	0.011	1.346	0.005
PLAU					1.319	0.010		
PLK1	1.309	0.021	1.563	<.001	1.410	0.002	1.372	0.003
PLOD2			1.284	0.019	1.272	0.014	1.332	0.005
POSTN	1.599	<.001	1.514	0.002	1.391	0.005		
PPP3CA					1.402	0.007	1.316	0.018
PSMD13	1.278	0.040	1.297	0.033	1.279	0.017	1.373	0.004
PTK6	1.640	<.001	1.932	<.001	1.369	0.001	1.406	<.001
PTTG1	1.409	<.001	1.510	<.001	1.347	0.001	1.558	<.001
RAD21	1.315	0.035	1.402	0.004	1.589	<.001	1.439	<.001
RAF1					1.503	0.002		
RALA	1.521	0.004	1.403	0.007	1.563	<.001	1.229	0.040
RALBP1					1.277	0.033		
RGS7	1.154	0.015	1.266	0.010				
RRM1	1.570	0.001	1.602	<.001				
RRM2	1.368	<.001	1.289	0.004	1.396	<.001	1.230	0.015
SAT1	1.482	0.016	1.403	0.030				
SDC1					1.340	0.018	1.396	0.018
SEC14L1			1.260	0.048			1.360	0.002
SESN3	1.485	<.001	1.631	<.001	1.232	0.047	1.292	0.014
SFRP4	1.800	<.001	1.814	<.001	1.496	<.001	1.289	0.027
SHMT2	1.807	<.001	1.658	<.001	1.673	<.001	1.548	<.001
SKIL					1.327	0.008		
SLC25A21					1.398	0.001	1.285	0.018
SOX4					1.286	0.020	1.280	0.030
SPARC	1.539	<.001	1.842	<.001			1.269	0.026
SPP1			1.322	0.022				
SQLE			1.359	0.020	1.270	0.036		
STMN1	1.402	0.007	1.446	0.005	1.279	0.031		
SULF1			1.587	<.001				
TAF2							1.273	0.027
TFDP1			1.328	0.021	1.400	0.005	1.416	0.001
THBS2	1.812	<.001	1.960	<.001	1.320	0.012	1.256	0.038
THY1	1.362	0.020	1.662	<.001				

Table 4A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
TK1			1.251	0.011	1.377	<.001	1.401	<.001
TOP2A	1.670	<.001	1.920	<.001	1.869	<.001	1.927	<.001
TPD52	1.324	0.011			1.366	0.002	1.351	0.005
TPX2	1.884	<.001	2.154	<.001	1.874	<.001	1.794	<.001
UAP1					1.244	0.044		
UBE2C	1.403	<.001	1.541	<.001	1.306	0.002	1.323	<.001
UBE2T	1.667	<.001	1.282	0.023	1.502	<.001	1.298	0.005
UGT2B15			1.295	0.001			1.275	0.002
UGT2B17							1.294	0.025
UHRF1	1.454	<.001	1.531	<.001	1.257	0.029		
VCPIP1	1.390	0.009	1.414	0.004	1.294	0.021	1.283	0.021
WNT5A			1.274	0.038	1.298	0.020		
XIAP					1.464	0.006		
ZMYND8			1.277	0.048				
ZWINT	1.259	0.047						

Table 4B.
Genes significantly (p<0.05) associated with cRFI or bRFI in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) < 1.0 (increased expression is positively associated with good prognosis)

Table 4B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
AAMP	0.564	<.001	0.571	<.001	0.764	0.037	0.786	0.034
ABCA5	0.755	<.001	0.695	<.001			0.800	0.006
ABCB1	0.777	0.026						
ABCG2	0.788	0.033	0.784	0.040	0.803	0.018	0.750	0.004
ABHD2			0.734	0.011				
ACE			0.782	0.048				
ACOX2	0.639	<.001	0.631	<.001	0.713	<.001	0.716	0.002
ADH5	0.625	<.001	0.637	<.001	0.753	0.026		
AKAP1	0.764	0.006	0.800	0.005	0.837	0.046		
AKR1C1	0.773	0.033			0.802	0.032		
AKT1			0.714	0.005				
AKT3	0.811	0.015	0.809	0.021				
ALDH1A2	0.606	<.001	0.498	<.001	0.613	<.001	0.624	<.001
AMPD3					0.793	0.024		
ANPEP	0.584	<.001	0.493	<.001				
ANXA2	0.753	0.013	0.781	0.036	0.762	0.008	0.795	0.032
APRT			0.758	0.026	0.780	0.044	0.746	0.008
ATXN1	0.673	0.001	0.776	0.029	0.809	0.031	0.812	0.043
AXIN2	0.674	<.001	0.571	<.001	0.776	0.005	0.757	0.005
AZGP1	0.585	<.001	0.652	<.001	0.664	<.001	0.746	<.001
BAD			0.765	0.023				
BCL2	0.788	0.033	0.778	0.036				
BDKRB1	0.728	0.039						
BIK			0.712	0.005				
BIN1	0.607	<.001	0.724	0.002	0.726	<.001	0.834	0.034
BTG3					0.847	0.034		
BTRC	0.688	0.001	0.713	0.003				
C7	0.589	<.001	0.639	<.001	0.629	<.001	0.691	<.001
CADM1	0.546	<.001	0.529	<.001	0.743	0.008	0.769	0.015
CASP1	0.769	0.014	0.799	0.028	0.799	0.010	0.815	0.018
CAV1	0.736	0.011	0.711	0.005	0.675	<.001	0.743	0.006
CAV2			0.636	0.010	0.648	0.012	0.685	0.012
CCL2	0.759	0.029	0.764	0.024				
CCNH	0.689	<.001	0.700	<.001				
CD164	0.664	<.001	0.651	<.001				
CD1A					0.687	0.004		
CD44	0.545	<.001	0.600	<.001	0.788	0.018	0.799	0.023
CD82	0.771	0.009	0.748	0.004				

Table 4B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
CDC25B	0.755	0.006			0.817	0.025		
CDK14	0.845	0.043						
CDK2							0.819	0.032
CDK3	0.733	0.005			0.772	0.006	0.838	0.017
CDKN1A			0.766	0.041				
CDKN1C	0.662	<.001	0.712	0.002	0.693	<.001	0.761	0.009
CHN1	0.788	0.036						
COL6A1	0.608	<.001	0.767	0.013	0.706	<.001	0.775	0.007
CSF1	0.626	<.001	0.709	0.003				
CSK					0.837	0.029		
CSRP1	0.793	0.024	0.782	0.019				
CTNNB1	0.898	0.042			0.885	<.001		
CTSB	0.701	0.004	0.713	0.007	0.715	0.002	0.803	0.038
CTSK					0.815	0.042		
CXCL12	0.652	<.001	0.802	0.044	0.711	0.001		
CYP3A5	0.463	<.001	0.436	<.001	0.727	0.003		
CYR61	0.652	0.002	0.676	0.002				
DAP			0.761	0.026	0.775	0.025	0.802	0.048
DARC					0.725	0.005	0.792	0.032
DDR2					0.719	0.001	0.763	0.008
DES	0.619	<.001	0.737	0.005	0.638	<.001	0.793	0.017
DHRS9	0.642	0.003						
DHX9	0.888	<.001						
DLC1	0.710	0.007	0.715	0.009				
DLGAP1	0.613	<.001	0.551	<.001			0.779	0.049
DNM3	0.679	<.001			0.812	0.037		
DPP4	0.591	<.001	0.613	<.001	0.761	0.003		
DPT	0.613	<.001	0.576	<.001	0.647	<.001	0.677	<.001
DUSP1	0.662	0.001	0.665	0.001			0.785	0.024
DUSP6	0.713	0.005	0.668	0.002				
EDNRA	0.702	0.002	0.779	0.036				
EGF			0.738	0.028				
EGR1	0.569	<.001	0.577	<.001			0.782	0.022
EGR3	0.601	<.001	0.619	<.001			0.800	0.038
EIF2S3							0.756	0.015
EIF5	0.776	0.023	0.787	0.028				
ELK4	0.628	<.001	0.658	<.001				
EPHA2	0.720	0.011	0.663	0.004				
EPHA3	0.727	0.003			0.772	0.005		
ERBB2	0.786	0.019	0.738	0.003	0.815	0.041		
ERBB3	0.728	0.002	0.711	0.002	0.828	0.043	0.813	0.023
ERCC1	0.771	0.023	0.725	0.007	0.806	0.049	0.704	0.002

Table 4B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
EREG					0.754	0.016	0.777	0.034
ESR2			0.731	0.026				
FAAH	0.708	0.004	0.758	0.012	0.784	0.031	0.774	0.007
FAM107A	0.517	<.001	0.576	<.001	0.642	<.001	0.656	<.001
FAM13C	0.568	<.001	0.526	<.001	0.739	0.002	0.639	<.001
FAS	0.755	0.014						
FASLG			0.706	0.021				
FGF10	0.653	<.001			0.685	<.001	0.766	0.022
FGF17			0.746	0.023	0.781	0.015	0.805	0.028
FGF7	0.794	0.030			0.820	0.037	0.811	0.040
FGFR2	0.683	<.001	0.686	<.001	0.674	<.001	0.703	<.001
FKBP5			0.676	0.001				
FLNA	0.653	<.001	0.741	0.010	0.682	<.001	0.771	0.016
FLNC	0.751	0.029	0.779	0.047	0.663	<.001	0.725	<.001
FLT1			0.799	0.044				
FOS	0.566	<.001	0.543	<.001			0.757	0.006
FOXO1					0.816	0.039	0.798	0.023
FOXQ1	0.753	0.017	0.757	0.024	0.804	0.018		
FYN	0.779	0.031						
GADD45B	0.590	<.001	0.619	<.001				
GDF15	0.759	0.019	0.794	0.048				
GHR	0.702	0.005	0.630	<.001	0.673	<.001	0.590	<.001
GNRH1					0.742	0.014		
GPM6B	0.653	<.001	0.633	<.001	0.696	<.001	0.768	0.007
GSN	0.570	<.001	0.697	0.001	0.697	<.001	0.758	0.005
GSTM1	0.612	<.001	0.588	<.001	0.718	<.001	0.801	0.020
GSTM2	0.540	<.001	0.630	<.001	0.602	<.001	0.706	<.001
HGD	0.796	0.020	0.736	0.002				
HIRIP3	0.753	0.011			0.824	0.050		
HK1	0.684	<.001	0.683	<.001	0.799	0.011	0.804	0.014
HLA-G			0.726	0.022				
HLF	0.555	<.001	0.582	<.001	0.703	<.001	0.702	<.001
HNF1B	0.690	<.001	0.585	<.001				
HPS1	0.744	0.003	0.784	0.020	0.836	0.047		
HSD3B2							0.733	0.016
HSP90AB1	0.801	0.036						
HSPA5			0.776	0.034				
HSPB1	0.813	0.020						
HSPB2	0.762	0.037			0.699	0.002	0.783	0.034
HSPG2					0.794	0.044		
ICAM1	0.743	0.024	0.768	0.040				
IER3	0.686	0.002	0.663	<.001				

Table 4B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
IFIT1	0.649	<.001	0.761	0.026				
IGF1	0.634	<.001	0.537	<.001	0.696	<.001	0.688	<.001
IGF2					0.732	0.004		
IGFBP2	0.548	<.001	0.620	<.001				
IGFBP5	0.681	<.001						
IGFBP6	0.577	<.001			0.675	<.001		
IL1B	0.712	0.005	0.742	0.009				
IL6	0.763	0.028						
IL6R			0.791	0.039				
IL6ST	0.585	<.001	0.639	<.001	0.730	0.002	0.768	0.006
IL8	0.624	<.001	0.662	0.001				
ILK	0.712	0.009	0.728	0.012	0.790	0.047	0.790	0.042
ING5	0.625	<.001	0.658	<.001	0.728	0.002		
ITGA5	0.728	0.006	0.803	0.039				
ITGA6	0.779	0.007	0.775	0.006				
ITGA7	0.584	<.001	0.700	0.001	0.656	<.001	0.786	0.014
ITGAD			0.657	0.020				
ITGB4	0.718	0.007	0.689	<.001	0.818	0.041		
ITGB5			0.801	0.050				
ITPR1	0.707	0.001						
JUN	0.556	<.001	0.574	<.001			0.754	0.008
JUNB	0.730	0.017	0.715	0.010				
KIT	0.644	0.004	0.705	0.019	0.605	<.001	0.659	0.001
KLC1	0.692	0.003	0.774	0.024	0.747	0.008		
KLF6	0.770	0.032	0.776	0.039				
KLK1	0.646	<.001	0.652	0.001	0.784	0.037		
KLK10			0.716	0.006				
KLK2	0.647	<.001	0.628	<.001			0.786	0.009
KLK3	0.706	<.001	0.748	<.001			0.845	0.018
KRT1							0.734	0.024
KRT15	0.627	<.001	0.526	<.001	0.704	<.001	0.782	0.029
KRT18	0.624	<.001	0.617	<.001	0.738	0.005	0.760	0.005
KRT5	0.640	<.001	0.550	<.001	0.740	<.001	0.798	0.023
KRT8	0.716	0.006	0.744	0.008				
L1CAM	0.738	0.021	0.692	0.009			0.761	0.036
LAG3	0.741	0.013	0.729	0.011				
LAMA4	0.686	0.011			0.592	0.003		
LAMA5							0.786	0.025
LAMB3	0.661	<.001	0.617	<.001	0.734	<.001		
LGALS3	0.618	<.001	0.702	0.001	0.734	0.001	0.793	0.012
LIG3	0.705	0.008	0.615	<.001				
LRP1	0.786	0.050			0.795	0.023	0.770	0.009

Table 4B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
MAP3K7					0.789	0.003		
MGMT	0.632	<.001	0.693	<.001				
MICA	0.781	0.014	0.653	<.001			0.833	0.043
MPPED2	0.655	<.001	0.597	<.001	0.719	<.001	0.759	0.006
MSH6					0.793	0.015		
MTSS1	0.613	<.001			0.746	0.008		
MVP	0.792	0.028	0.795	0.045	0.819	0.023		
MYBPC1	0.648	<.001	0.496	<.001	0.701	<.001	0.629	<.001
NCAM1					0.773	0.015		
NCAPD3	0.574	<.001	0.463	<.001	0.679	<.001	0.640	<.001
NEXN	0.701	0.002	0.791	0.035	0.725	0.002	0.781	0.016
NFAT5	0.515	<.001	0.586	<.001	0.785	0.017		
NFATC2	0.753	0.023						
NFKBIA	0.778	0.037						
NRG1	0.644	0.004	0.696	0.017	0.698	0.012		
OAZ1	0.777	0.034	0.775	0.022				
OLFML3	0.621	<.001	0.720	0.001	0.600	<.001	0.626	<.001
OMD	0.706	0.003						
OR51E2	0.820	0.037	0.798	0.027				
PAGE4	0.549	<.001	0.613	<.001	0.542	<.001	0.628	<.001
PCA3	0.684	<.001	0.635	<.001				
PCDHGB7	0.790	0.045			0.725	0.002	0.664	<.001
PGF	0.753	0.017						
PGR	0.740	0.021	0.728	0.018				
PIK3CG	0.803	0.024						
PLAUR	0.778	0.035						
PLG							0.728	0.028
PPAP2B	0.575	<.001	0.629	<.001	0.643	<.001	0.699	<.001
PPP1R12A	0.647	<.001	0.683	0.002	0.782	0.023	0.784	0.030
PRIMA1	0.626	<.001	0.658	<.001	0.703	0.002	0.724	0.003
PRKCA	0.642	<.001	0.799	0.029	0.677	0.001	0.776	0.006
PRKCB	0.675	0.001			0.648	<.001	0.747	0.006
PROM1	0.603	0.018			0.659	0.014	0.493	0.008
PTCH1	0.680	0.001			0.753	0.010	0.789	0.018
PTEN	0.732	0.002	0.747	0.005	0.744	<.001	0.765	0.002
PTGS2	0.596	<.001	0.610	<.001				
PTH1R	0.767	0.042			0.775	0.028	0.788	0.047
PTHLH	0.617	0.002	0.726	0.025	0.668	0.002	0.718	0.007
PTK2B	0.744	0.003	0.679	<.001	0.766	0.002	0.726	<.001
PTPN1	0.760	0.020	0.780	0.042				
PYCARD			0.748	0.012				
RAB27A			0.708	0.004				

Table 4B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
RAB30	0.755	0.008						
RAGE			0.817	0.048				
RAP1B					0.818	0.050		
RARB	0.757	0.007	0.677	<.001	0.789	0.007	0.746	0.003
RASSF1	0.816	0.035						
RHOB	0.725	0.009	0.676	0.001			0.793	0.039
RLN1			0.742	0.033			0.762	0.040
RND3	0.636	<.001	0.647	<.001				
RNF114			0.749	0.011				
SDC2					0.721	0.004		
SDHC	0.725	0.003	0.727	0.006				
SEMA3A	0.757	0.024	0.721	0.010				
SERPINA3	0.716	0.008	0.660	0.001				
SERPINB5	0.747	0.031	0.616	0.002				
SH3RF2	0.577	<.001	0.458	<.001	0.702	<.001	0.640	<.001
SLC22A3	0.565	<.001	0.540	<.001	0.747	0.004	0.756	0.007
SMAD4	0.546	<.001	0.573	<.001	0.636	<.001	0.627	<.001
SMARCD1	0.718	<.001	0.775	0.017				
SMO	0.793	0.029	0.754	0.021			0.718	0.003
SOD1	0.757	0.049	0.707	0.006				
SORBS1	0.645	<.001	0.716	0.003	0.693	<.001	0.784	0.025
SPARCL1	0.821	0.028			0.829	0.014	0.781	0.030
SPDEF	0.778	<.001						
SPINT1	0.732	0.009	0.842	0.026				
SRC	0.647	<.001	0.632	<.001				
SRD5A1					0.813	0.040		
SRD5A2	0.489	<.001	0.533	<.001	0.544	<.001	0.611	<.001
ST5	0.713	0.002	0.783	0.011	0.725	<.001	0.827	0.025
STAT3	0.773	0.037	0.759	0.035				
STAT5A	0.695	<.001	0.719	0.002	0.806	0.020	0.783	0.008
STAT5B	0.633	<.001	0.655	<.001			0.814	0.028
SUMO1	0.790	0.015						
SVIL	0.659	<.001	0.713	0.002	0.711	0.002	0.779	0.010
TARP							0.800	0.040
TBP	0.761	0.010						
TFF3	0.734	0.010	0.659	<.001				
TGFB1I1	0.618	<.001	0.693	0.002	0.637	<.001	0.719	0.004
TGFB2	0.679	<.001	0.747	0.005	0.805	0.030		
TGFB3					0.791	0.037		
TGFBR2					0.778	0.035		
TIMP3					0.751	0.011		
TMPRSS2	0.745	0.003	0.708	<.001				

Table 4B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
TNF			0.670	0.013			0.697	0.015
TNFRSF10A	0.780	0.018	0.752	0.006	0.817	0.032		
TNFRSF10B	0.576	<.001	0.655	<.001	0.766	0.004	0.778	0.002
TNFRSF18	0.648	0.016			0.759	0.034		
TNFSF10	0.653	<.001	0.667	0.004				
TP53			0.729	0.003				
TP63	0.759	0.016	0.636	<.001	0.698	<.001	0.712	0.001
TPM1	0.778	0.048	0.743	0.012	0.783	0.032	0.811	0.046
TPM2	0.578	<.001	0.634	<.001	0.611	<.001	0.710	0.001
TPP2			0.775	0.037				
TRAF3IP2	0.722	0.002	0.690	<.001	0.792	0.021	0.823	0.049
TRO	0.744	0.003	0.725	0.003	0.765	0.002	0.821	0.041
TUBB2A	0.639	<.001	0.625	<.001				
TYMP	0.786	0.039						
VCL	0.594	<.001	0.657	0.001	0.682	<.001		
VEGFA			0.762	0.024				
VEGFB	0.795	0.037						
VIM	0.739	0.009			0.791	0.021		
WDR19							0.776	0.015
WFDC1					0.746	<.001		
YY1	0.683	0.001			0.728	0.002		
ZFHX3	0.684	<.001	0.661	<.001	0.801	0.010	0.762	0.001
ZFP36	0.605	<.001	0.579	<.001			0.815	0.043
ZNF827	0.624	<.001	0.730	0.007	0.738	0.004		

[00138] Tables 5A and 5B provide genes that were significantly associated ($p<0.05$), positively or negatively, with recurrence (cRFI, bRFI) after adjusting for AUA risk group in the primary and/or highest Gleason pattern. Increased expression of genes in Table 5A is negatively associated with good prognosis, while increased expression of genes in Table 5B is positively associated with good prognosis.

Table 5A.
Gene significantly ($p<0.05$) associated with cRFI or bRFI after adjustment for AUA risk group in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) > 1.0 (increased expression negatively associated with good prognosis)

Table 5A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
AKR1C3	1.315	0.018	1.283	0.024				
ALOX12							1.198	0.024

Table 5A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
ANLN	1.406	<.001	1.519	<.001	1.485	<.001	1.632	<.001
AQP2	1.209	<.001	1.302	<.001				
ASAP2			1.582	<.001	1.333	0.011	1.307	0.019
ASPN	1.872	<.001	1.741	<.001	1.638	<.001	1.691	<.001
ATP5E	1.309	0.042	1.369	0.012				
BAG5			1.291	0.044				
BAX					1.298	0.025	1.420	0.004
BGN	1.746	<.001	1.755	<.001				
BIRC5	1.480	<.001	1.470	<.001	1.419	<.001	1.503	<.001
BMP6	1.536	<.001	1.815	<.001	1.294	0.033	1.429	0.001
BRCA2							1.184	0.037
BUB1	1.288	0.001	1.391	<.001	1.254	<.001	1.189	0.018
CACNA1D			1.313	0.029				
CADPS					1.358	0.007	1.267	0.022
CASP3					1.251	0.037		
CCNB1					1.261	0.033	1.318	0.005
CCNE2	1.345	0.005	1.438	<.001	1.606	<.001	1.426	<.001
CD276	1.482	0.002	1.668	<.001	1.451	<.001	1.302	0.011
CDC20	1.417	<.001	1.547	<.001	1.355	<.001	1.446	<.001
CDC6	1.340	0.011	1.265	0.046	1.367	0.002	1.272	0.025
CDH7	1.402	0.003	1.409	0.002				
CDKN2B	1.553	<.001	1.746	<.001	1.340	0.014	1.369	0.006
CDKN2C	1.411	<.001	1.604	<.001	1.220	0.033		
CDKN3	1.296	0.004			1.226	0.015		
CENPF	1.434	0.002	1.570	<.001	1.633	<.001	1.610	<.001
CKS2	1.419	0.008	1.374	0.022	1.380	0.004		
COL1A1	1.677	<.001	1.809	<.001	1.401	<.001	1.352	0.003
COL1A2			1.373	0.010				
COL3A1	1.669	<.001	1.781	<.001	1.249	0.024	1.234	0.047
COL4A1	1.475	0.002	1.513	0.002				
COL8A1	1.506	0.001	1.691	<.001				
CRISP3	1.406	0.004	1.471	<.001				
CTHRC1	1.426	0.009	1.793	<.001	1.311	0.019		
CTNND2					1.462	<.001		
DDIT4	1.478	0.003	1.783	<.001			1.236	0.039
DYNLL1	1.431	0.002					1.193	0.004
EIF3H					1.372	0.027		
ENY2					1.325	0.023	1.270	0.017
ERG	1.303	0.041						
EZH2			1.254	0.049				
F2R	1.540	0.002	1.448	0.006	1.286	0.023		
FADD	1.235	0.041	1.404	<.001				

Table 5A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
FAP	1.386	0.015	1.440	0.008	1.253	0.048		
FASN	1.303	0.028						
FCGR3A			1.439	0.011			1.262	0.045
FGF5	1.289	0.006						
GNPTAB	1.290	0.033	1.369	0.022	1.285	0.018	1.355	0.008
GPR68			1.396	0.005				
GREM1	1.341	0.022	1.502	0.003	1.366	0.006		
HDAC1					1.329	0.016		
HDAC9			1.378	0.012				
HRAS	1.465	0.006						
HSD17B4					1.442	<.001	1.245	0.028
IGFBP3			1.366	0.019			1.302	0.011
INHBA	2.000	<.001	2.336	<.001			1.486	0.002
JAG1	1.251	0.039						
KCNN2	1.347	0.020	1.524	<.001	1.312	0.023	1.346	0.011
KHDRBS3			1.500	0.001	1.426	0.001	1.267	0.032
KIAA0196							1.272	0.028
KIF4A	1.199	0.022					1.262	0.004
KPNA2					1.252	0.016		
LAMA3					1.332	0.004	1.356	0.010
LAMB1			1.317	0.028				
LAMC1	1.516	0.003	1.302	0.040			1.397	0.007
LIMS1							1.261	0.027
LOX					1.265	0.016	1.372	0.001
LTBP2			1.477	0.002				
LUM			1.321	0.020				
MANF					1.647	<.001	1.284	0.027
MCM2					1.372	0.003	1.302	0.032
MCM3			1.269	0.047				
MCM6			1.276	0.033			1.245	0.037
MELK			1.294	0.005	1.394	<.001		
MKI67	1.253	0.028	1.246	0.029				
MMP11	1.557	<.001	1.290	0.035	1.357	0.005		
MRPL13							1.275	0.003
MSH2			1.355	0.009				
MYBL2	1.497	<.001	1.509	<.001	1.304	0.003	1.292	0.007
MYO6			1.367	0.010				
NDRG1	1.270	0.042					1.314	0.025
NEK2			1.338	0.020			1.269	0.026
NETO2	1.434	0.004	1.303	0.033	1.283	0.012		
NOX4	1.413	0.006	1.308	0.037	1.444	<.001		
NRIP3							1.171	0.026

Table 5A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
NRP1			1.372	0.020				
ODC1					1.450	<.001		
OR51E1					1.559	<.001	1.413	0.008
PAK6							1.233	0.047
PATE1	1.262	<.001	1.375	<.001	1.143	0.034	1.191	0.036
PCNA					1.227	0.033	1.318	0.003
PEX10	1.517	<.001	1.500	0.001				
PGD	1.363	0.028	1.316	0.039	1.652	<.001		
PGK1			1.224	0.034			1.206	0.024
PIM1					1.205	0.042		
PLA2G7					1.298	0.018	1.358	0.005
PLAU					1.242	0.032		
PLK1			1.464	0.001	1.299	0.018	1.275	0.031
PLOD2					1.206	0.039	1.261	0.025
POSTN	1.558	0.001	1.356	0.022	1.363	0.009		
PPP3CA					1.445	0.002		
PSMD13					1.301	0.017	1.411	0.003
PTK2			1.318	0.031				
PTK6	1.582	<.001	1.894	<.001	1.290	0.011	1.354	0.003
PTTG1	1.319	0.004	1.430	<.001	1.271	0.006	1.492	<.001
RAD21			1.278	0.028	1.435	0.004	1.326	0.008
RAF1					1.504	<.001		
RALA	1.374	0.028			1.459	0.001		
RGS7			1.203	0.031				
RRM1	1.535	0.001	1.525	<.001				
RRM2	1.302	0.003	1.197	0.047	1.342	<.001		
SAT1	1.374	0.043						
SDC1					1.344	0.011	1.473	0.008
SEC14L1							1.297	0.006
SESN3	1.337	0.002	1.495	<.001			1.223	0.038
SFRP4	1.610	<.001	1.542	0.002	1.370	0.009		
SHMT2	1.567	0.001	1.522	<.001	1.485	0.001	1.370	<.001
SKIL					1.303	0.008		
SLC25A21					1.287	0.020	1.306	0.017
SLC44A1			1.308	0.045				
SNRPB2	1.304	0.018						
SOX4					1.252	0.031		
SPARC	1.445	0.004	1.706	<.001			1.269	0.026
SPP1			1.376	0.016				
SQLE			1.417	0.007	1.262	0.035		
STAT1							1.209	0.029
STMN1	1.315	0.029						

Table 5A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
SULF1			1.504	0.001				
TAF2					1.252	0.048	1.301	0.019
TFDP1					1.395	0.010	1.424	0.002
THBS2	1.716	<.001	1.719	<.001				
THY1	1.343	0.035	1.575	0.001				
TK1					1.320	<.001	1.304	<.001
TOP2A	1.464	0.001	1.688	<.001	1.715	<.001	1.761	<.001
TPD52					1.286	0.006	1.258	0.023
TPX2	1.644	<.001	1.964	<.001	1.699	<.001	1.754	<.001
TYMS							1.315	0.014
UBE2C	1.270	0.019	1.558	<.001	1.205	0.027	1.333	<.001
UBE2G1	1.302	0.041						
UBE2T	1.451	<.001			1.309	0.003		
UGT2B15			1.222	0.025				
UHRF1	1.370	0.003	1.520	<.001	1.247	0.020		
VCPIP1			1.332	0.015				
VTI1B					1.237	0.036		
XIAP					1.486	0.008		
ZMYND8			1.408	0.007				
ZNF3							1.284	0.018
ZWINT	1.289	0.028						

Table 5B.

Genes significantly (p<0.05) associated with cRFI or bRFI after adjustment for AUA risk group in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) < 1.0 (increased expression is positively associated with good prognosis)

Table 5B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
AAMP	0.535	<.001	0.581	<.001	0.700	0.002	0.759	0.006
ABCA5	0.798	0.007	0.745	0.002			0.841	0.037
ABCC1			0.800	0.044				
ABCC4			0.787	0.022				
ABHD2			0.768	0.023				
ACOX2	0.678	0.002	0.749	0.027	0.759	0.004		
ADH5	0.645	<.001	0.672	0.001				
AGTR1	0.780	0.030						
AKAP1	0.815	0.045	0.758	<.001				
AKT1			0.732	0.010				
ALDH1A2	0.646	<.001	0.548	<.001	0.671	<.001	0.713	0.001
ANPEP	0.641	<.001	0.535	<.001				

Table 5B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
ANXA2	0.772	0.035			0.804	0.046		
ATXN1	0.654	<.001	0.754	0.020	0.797	0.017		
AURKA			0.788	0.030				
AXIN2	0.744	0.005	0.655	<.001				
AZGP1	0.656	<.001	0.676	<.001	0.754	0.001	0.791	0.004
BAD			0.700	0.004				
BIN1	0.650	<.001	0.764	0.013	0.803	0.015		
BTG3					0.836	0.025		
BTRC	0.730	0.005						
C7	0.617	<.001	0.680	<.001	0.667	<.001	0.755	0.005
CADM1	0.559	<.001	0.566	<.001	0.772	0.020	0.802	0.046
CASP1	0.781	0.030	0.779	0.021	0.818	0.027	0.828	0.036
CAV1					0.775	0.034		
CAV2			0.677	0.019				
CCL2			0.752	0.023				
CCNH	0.679	<.001	0.682	<.001				
CD164	0.721	0.002	0.724	0.005				
CD1A					0.710	0.014		
CD44	0.591	<.001	0.642	<.001				
CD82	0.779	0.021	0.771	0.024				
CDC25B	0.778	0.035			0.818	0.023		
CDK14	0.788	0.011						
CDK3	0.752	0.012			0.779	0.005	0.841	0.020
CDKN1A	0.770	0.049	0.712	0.014				
CDKN1C	0.684	<.001			0.697	<.001		
CHN1	0.772	0.031						
COL6A1	0.648	<.001	0.807	0.046	0.768	0.004		
CSF1	0.621	<.001	0.671	0.001				
CTNNB1					0.905	0.008		
CTSB	0.754	0.030	0.716	0.011	0.756	0.014		
CXCL12	0.641	<.001	0.796	0.038	0.708	<.001		
CYP3A5	0.503	<.001	0.528	<.001	0.791	0.028		
CYR61	0.639	0.001	0.659	0.001			0.797	0.048
DARC					0.707	0.004		
DDR2					0.750	0.011		
DES	0.657	<.001	0.758	0.022	0.699	<.001		
DHRS9	0.625	0.002						
DHX9	0.846	<.001						
DIAPH1	0.682	0.007	0.723	0.008	0.780	0.026		
DLC1	0.703	0.005	0.702	0.008				
DLGAP1	0.703	0.008	0.636	<.001				
DNM3	0.701	0.001			0.817	0.042		

Table 5B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
DPP4	0.686	<.001	0.716	0.001				
DPT	0.636	<.001	0.633	<.001	0.709	0.006	0.773	0.024
DUSP1	0.683	0.006	0.679	0.003				
DUSP6	0.694	0.003	0.605	<.001				
EDN1					0.773	0.031		
EDNRA	0.716	0.007						
EGR1	0.575	<.001	0.575	<.001			0.771	0.014
EGR3	0.633	0.002	0.643	<.001			0.792	0.025
EIF4E	0.722	0.002						
ELK4	0.710	0.009	0.759	0.027				
ENPP2	0.786	0.039						
EPHA2			0.593	0.001				
EPHA3	0.739	0.006			0.802	0.020		
ERBB2			0.753	0.007				
ERBB3	0.753	0.009	0.753	0.015				
ERCC1							0.727	0.001
EREG					0.722	0.012	0.769	0.040
ESR1			0.742	0.015				
FABP5	0.756	0.032						
FAM107A	0.524	<.001	0.579	<.001	0.688	<.001	0.699	0.001
FAM13C	0.639	<.001	0.601	<.001	0.810	0.019	0.709	<.001
FAS	0.770	0.033						
FASLG	0.716	0.028	0.683	0.017				
FGF10					0.798	0.045		
FGF17			0.718	0.018	0.793	0.024	0.790	0.024
FGFR2	0.739	0.007	0.783	0.038	0.740	0.004		
FGFR4			0.746	0.050				
FKBP5			0.689	0.003				
FLNA	0.701	0.006	0.766	0.029	0.768	0.037		
FLNC					0.755	<.001	0.820	0.022
FLT1			0.729	0.008				
FOS	0.572	<.001	0.536	<.001			0.750	0.005
FOXQ1	0.778	0.033			0.820	0.018		
FYN	0.708	0.006						
GADD45B	0.577	<.001	0.589	<.001				
GDF15	0.757	0.013	0.743	0.006				
GHR			0.712	0.004			0.679	0.001
GNRH1					0.791	0.048		
GPM6B	0.675	<.001	0.660	<.001	0.735	<.001	0.823	0.049
GSK3B	0.783	0.042						
GSN	0.587	<.001	0.705	0.002	0.745	0.004	0.796	0.021
GSTM1	0.686	0.001	0.631	<.001	0.807	0.018		

Table 5B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
GSTM2	0.607	<.001	0.683	<.001	0.679	<.001	0.800	0.027
HIRIP3	0.692	<.001			0.782	0.007		
HK1	0.724	0.002	0.718	0.002				
HLF	0.580	<.001	0.571	<.001	0.759	0.008	0.750	0.004
HNF1B			0.669	<.001				
HPS1	0.764	0.008						
HSD17B10	0.802	0.045						
HSD17B2					0.723	0.048		
HSD3B2							0.709	0.010
HSP90AB1	0.780	0.034			0.809	0.041		
HSPA5			0.738	0.017				
HSPB1	0.770	0.006	0.801	0.032				
HSPB2					0.788	0.035		
ICAM1	0.728	0.015	0.716	0.010				
IER3	0.735	0.016	0.637	<.001			0.802	0.035
IFIT1	0.647	<.001	0.755	0.029				
IGF1	0.675	<.001	0.603	<.001	0.762	0.006	0.770	0.030
IGF2					0.761	0.011		
IGFBP2	0.601	<.001	0.605	<.001				
IGFBP5	0.702	<.001						
IGFBP6	0.628	<.001			0.726	0.003		
IL1B	0.676	0.002	0.716	0.004				
IL6	0.688	0.005	0.766	0.044				
IL6R			0.786	0.036				
IL6ST	0.618	<.001	0.639	<.001	0.785	0.027	0.813	0.042
IL8	0.635	<.001	0.628	<.001				
ILK	0.734	0.018	0.753	0.026				
ING5	0.684	<.001	0.681	<.001	0.756	0.006		
ITGA4	0.778	0.040						
ITGA5	0.762	0.026						
ITGA6			0.811	0.038				
ITGA7	0.592	<.001	0.715	0.006	0.710	0.002		
ITGAD			0.576	0.006				
ITGB4			0.693	0.003				
ITPR1	0.789	0.029						
JUN	0.572	<.001	0.581	<.001			0.777	0.019
JUNB	0.732	0.030	0.707	0.016				
KCTD12	0.758	0.036						
KIT					0.691	0.009	0.738	0.028
KLC1	0.741	0.024			0.781	0.024		
KLF6	0.733	0.018	0.727	0.014				
KLK1			0.744	0.028				

Table 5B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
KLK2	0.697	0.002	0.679	<.001				
KLK3	0.725	<.001	0.715	<.001			0.841	0.023
KRT15	0.660	<.001	0.577	<.001	0.750	0.002		
KRT18	0.623	<.001	0.642	<.001	0.702	<.001	0.760	0.006
KRT2					0.740	0.044		
KRT5	0.674	<.001	0.588	<.001	0.769	0.005		
KRT8	0.768	0.034						
L1CAM	0.737	0.036						
LAG3	0.711	0.013	0.748	0.029				
LAMA4					0.649	0.009		
LAMB3	0.709	0.002	0.684	0.006	0.768	0.006		
LGALS3	0.652	<.001	0.752	0.015	0.805	0.028		
LIG3	0.728	0.016	0.667	<.001				
LRP1							0.811	0.043
MDM2			0.788	0.033				
MGMT	0.645	<.001	0.766	0.015				
MICA	0.796	0.043	0.676	<.001				
MPPED2	0.675	<.001	0.616	<.001	0.750	0.006		
MRC1							0.788	0.028
MTSS1	0.654	<.001			0.793	0.036		
MYBPC1	0.706	<.001	0.534	<.001	0.773	0.004	0.692	<.001
NCAPD3	0.658	<.001	0.566	<.001	0.753	0.011	0.733	0.009
NCOR1			0.838	0.045				
NEXN	0.748	0.025			0.785	0.020		
NFAT5	0.531	<.001	0.626	<.001				
NFATC2			0.759	0.024				
OAZ1			0.766	0.024				
OLFML3	0.648	<.001	0.748	0.005	0.639	<.001	0.675	<.001
OR51E2	0.823	0.034						
PAGE4	0.599	<.001	0.698	0.002	0.606	<.001	0.726	<.001
PCA3	0.705	<.001	0.647	<.001				
PCDHGB7							0.712	<.001
PGF	0.790	0.039						
PLG							0.764	0.048
PLP2			0.766	0.037				
PPAP2B	0.589	<.001	0.647	<.001	0.691	<.001	0.765	0.013
PPP1R12A	0.673	0.001	0.677	0.001			0.807	0.045
PRIMA1	0.622	<.001	0.712	0.008	0.740	0.013		
PRKCA	0.637	<.001			0.694	<.001		
PRKCB	0.741	0.020			0.664	<.001		
PROM1	0.599	0.017	0.527	0.042	0.610	0.006	0.420	0.002
PTCH1	0.752	0.027			0.762	0.011		

Table 5B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
PTEN	0.779	0.011	0.802	0.030	0.788	0.009		
PTGS2	0.639	<.001	0.606	<.001				
PTHLH	0.632	0.007	0.739	0.043	0.654	0.002	0.740	0.015
PTK2B			0.775	0.019	0.831	0.028	0.810	0.017
PTPN1	0.721	0.012	0.737	0.024				
PYCARD			0.702	0.005				
RAB27A RAB30	0.761	0.011	0.736	0.008				
RARB			0.746	0.010				
RASSF1	0.805	0.043						
RHOB	0.755	0.029	0.672	0.001				
RLN1	0.742	0.036	0.740	0.036				
RND3	0.607	<.001	0.633	<.001				
RNF114	0.782	0.041	0.747	0.013				
SDC2					0.714	0.002		
SDHC	0.698	<.001	0.762	0.029				
SERPINA3			0.752	0.030				
SERPINB5			0.669	0.014				
SH3RF2	0.705	0.012	0.568	<.001			0.755	0.016
SLC22A3	0.650	<.001	0.582	<.001				
SMAD4	0.636	<.001	0.684	0.002	0.741	0.007	0.738	0.007
SMARCD1	0.757	0.001						
SMO	0.790	0.049					0.766	0.013
SOD1	0.741	0.037	0.713	0.007				
SORBS1	0.684	0.003	0.732	0.008	0.788	0.049		
SPDEF	0.840	0.012						
SPINT1			0.837	0.048				
SRC	0.674	<.001	0.671	<.001				
SRD5A2	0.553	<.001	0.588	<.001	0.618	<.001	0.701	<.001
ST5	0.747	0.012	0.761	0.010	0.780	0.016	0.832	0.041
STAT3			0.735	0.020				
STAT5A	0.731	0.005	0.743	0.009			0.817	0.027
STAT5B	0.708	<.001	0.696	0.001				
SUMO1	0.815	0.037						
SVIL	0.689	0.003	0.739	0.008	0.761	0.011		
TBP	0.792	0.037						
TFF3	0.719	0.007	0.664	0.001				
TGFB1I1	0.676	0.003	0.707	0.007	0.709	0.005	0.777	0.035
TGFB2	0.741	0.010	0.785	0.017				
TGFBR2					0.759	0.022		
TIMP3					0.785	0.037		
TMPRSS2	0.780	0.012	0.742	<.001				

Table 5B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
TNF			0.654	0.007			0.682	0.006
TNFRSF10B	0.623	<.001	0.681	<.001	0.801	0.018	0.815	0.019
TNFSF10	0.721	0.004						
TP53			0.759	0.011				
TP63			0.737	0.020	0.754	0.007		
TPM2	0.609	<.001	0.671	<.001	0.673	<.001	0.789	0.031
TRAF3IP2	0.795	0.041	0.727	0.005				
TRO	0.793	0.033	0.768	0.027	0.814	0.023		
TUBB2A	0.626	<.001	0.590	<.001				
VCL	0.613	<.001	0.701	0.011				
VIM	0.716	0.005			0.792	0.025		
WFDC1					0.824	0.029		
YY1	0.668	<.001	0.787	0.014	0.716	0.001	0.819	0.011
ZFHX3	0.732	<.001	0.709	<.001				
ZFP36	0.656	0.001	0.609	<.001			0.818	0.045
ZNF827	0.750	0.022						

[00139] Tables 6A and 6B provide genes that were significantly associated ($p<0.05$), positively or negatively, with recurrence (cRFI, bRFI) after adjusting for Gleason pattern in the primary and/or highest Gleason pattern. Increased expression of genes in Table 6A is negatively associated with good prognosis, while increased expression of gene in Table 6B is positively associated with good prognosis.

Table 6A.

Genes significantly ($p<0.05$) associated with cRFI or bRFI after adjustment for Gleason pattern in the primary Gleason pattern or highest Gleason pattern with a hazard ratio (HR) > 1.0 (increased expression is negatively associated with good prognosis)

Table 6A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
AKR1C3	1.258	0.039						
ANLN	1.292	0.023			1.449	<.001	1.420	0.001
AQP2	1.178	0.008	1.287	<.001				
ASAP2			1.396	0.015				
ASPN	1.809	<.001	1.508	0.009	1.506	0.002	1.438	0.002
BAG5			1.367	0.012				
BAX							1.234	0.044
BGN	1.465	0.009	1.342	0.046				
BIRC5	1.338	0.008			1.364	0.004	1.279	0.006

Table 6A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
BMP6	1.369	0.015	1.518	0.002				
BUB1	1.239	0.024	1.227	0.001	1.236	0.004		
CACNA1D			1.337	0.025				
CADPS					1.280	0.029		
CCNE2			1.256	0.043	1.577	<.001	1.324	0.001
CD276	1.320	0.029	1.396	0.007	1.279	0.033		
CDC20	1.298	0.016	1.334	0.002	1.257	0.032	1.279	0.003
CDH7	1.258	0.047	1.338	0.013				
CDKN2B	1.342	0.032	1.488	0.009				
CDKN2C	1.344	0.010	1.450	<.001				
CDKN3	1.284	0.012						
CENPF	1.289	0.048			1.498	0.001	1.344	0.010
COL1A1	1.481	0.003	1.506	0.002				
COL3A1	1.459	0.004	1.430	0.013				
COL4A1	1.396	0.015						
COL8A1	1.413	0.008						
CRISP3	1.346	0.012	1.310	0.025				
CTHRC1			1.588	0.002				
DDIT4	1.363	0.020	1.379	0.028				
DICER1							1.294	0.008
ENY2					1.269	0.024		
FADD			1.307	0.010				
FAS							1.243	0.025
FGF5	1.328	0.002						
GNPTAB							1.246	0.037
GREM1	1.332	0.024	1.377	0.013	1.373	0.011		
HDAC1					1.301	0.018	1.237	0.021
HSD17B4							1.277	0.011
IFN-γ					1.219	0.048		
IMMT					1.230	0.049		
INHBA	1.866	<.001	1.944	<.001				
JAG1			1.298	0.030				
KCNN2			1.378	0.020			1.282	0.017
KHDRBS3			1.353	0.029	1.305	0.014		
LAMA3					1.344	<.001	1.232	0.048
LAMC1	1.396	0.015						
LIMS1							1.337	0.004
LOX					1.355	0.001	1.341	0.002
LTBP2			1.304	0.045				
MAGEA4	1.215	0.024						
MANF					1.460	<.001		
MCM6			1.287	0.042			1.214	0.046

Table 6A	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
MELK					1.329	0.002		
MMP11	1.281	0.050						
MRPL13							1.266	0.021
MYBL2	1.453	<.001			1.274	0.019		
MYC					1.265	0.037		
MYO6			1.278	0.047				
NETO2	1.322	0.022						
NFKB1							1.255	0.032
NOX4					1.266	0.041		
OR51E1					1.566	<.001	1.428	0.003
PATE1	1.242	<.001	1.347	<.001			1.177	0.011
PCNA							1.251	0.025
PEX10			1.302	0.028				
PGD			1.335	0.045	1.379	0.014	1.274	0.025
PIM1					1.254	0.019		
PLA2G7					1.289	0.025	1.250	0.031
PLAU					1.267	0.031		
PSMD13							1.333	0.005
PTK6	1.432	<.001	1.577	<.001	1.223	0.040		
PTTG1					1.279	0.013	1.308	0.006
RAGE							1.329	0.011
RALA	1.363	0.044			1.471	0.003		
RGS7	1.120	0.040	1.173	0.031				
RRM1	1.490	0.004	1.527	<.001				
SESN3			1.353	0.017				
SFRP4	1.370	0.025						
SHMT2	1.460	0.008	1.410	0.006	1.407	0.008	1.345	<.001
SKIL					1.307	0.025		
SLC25A21					1.414	0.002	1.330	0.004
SMARCC2					1.219	0.049		
SPARC			1.431	0.005				
TFDP1					1.283	0.046	1.345	0.003
THBS2	1.456	0.005	1.431	0.012				
TK1					1.214	0.015	1.222	0.006
TOP2A			1.367	0.018	1.518	0.001	1.480	<.001
TPX2	1.513	0.001	1.607	<.001	1.588	<.001	1.481	<.001
UBE2T	1.409	0.002			1.285	0.018		
UGT2B15			1.216	0.009			1.182	0.021
XIAP					1.336	0.037	1.194	0.043

Table 6B.
Genes significantly (p<0.05) associated with cRFI or bRFI after adjustment for Gleason pattern in the primary Gleason pattern or highest Gleason pattern with hazard ration (HR) < 1.0 (increased expression is positively associated with good prognosis)

Table 6B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
AAMP	0.660	0.001	0.675	<.001			0.836	0.045
ABCA5	0.807	0.014	0.737	<.001			0.845	0.030
ABCC1	0.780	0.038	0.794	0.015				
ABCG2							0.807	0.035
ABHD2			0.720	0.002				
ADH5	0.750	0.034						
AKAP1			0.721	<.001				
ALDH1A2	0.735	0.009	0.592	<.001	0.756	0.007	0.781	0.021
ANGPT2					0.741	0.036		
ANPEP	0.637	<.001	0.536	<.001				
ANXA2			0.762	0.044				
APOE			0.707	0.013				
APRT			0.727	0.004			0.771	0.006
ATXN1	0.725	0.013						
AURKA	0.784	0.037	0.735	0.003				
AXIN2	0.744	0.004	0.630	<.001				
AZGP1	0.672	<.001	0.720	<.001	0.764	0.001		
BAD			0.687	<.001				
BAK1			0.783	0.014				
BCL2	0.777	0.033	0.772	0.036				
BIK			0.768	0.040				
BIN1	0.691	<.001						
BTRC			0.776	0.029				
C7	0.707	0.004			0.791	0.024		
CADM1	0.587	<.001	0.593	<.001				
CASP1	0.773	0.023			0.820	0.025		
CAV1					0.753	0.014		
CAV2			0.627	0.009			0.682	0.003
CCL2			0.740	0.019				
CCNH	0.736	0.003						
CCR1			0.755	0.022				
CD1A					0.740	0.025		
CD44	0.590	<.001	0.637	<.001				
CD68	0.757	0.026						
CD82	0.778	0.012	0.759	0.016				
CDC25B	0.760	0.021						
CDK3	0.762	0.024			0.774	0.007		
CDKN1A			0.714	0.015				

Table 6B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
CDKN1C	0.738	0.014			0.768	0.021		
COL6A1	0.690	<.001	0.805	0.048				
CSF1	0.675	0.002	0.779	0.036				
CSK					0.825	0.004		
CTNNB1	0.884	0.045			0.888	0.027		
CTSB	0.740	0.017	0.676	0.003	0.755	0.010		
CTSD	0.673	0.031	0.722	0.009				
CTSK					0.804	0.034		
CTSL2			0.748	0.019				
CXCL12	0.731	0.017						
CYP3A5	0.523	<.001	0.518	<.001				
CYR61	0.744	0.041						
DAP					0.755	0.011		
DARC					0.763	0.029		
DDR2							0.813	0.041
DES	0.743	0.020						
DHRS9	0.606	0.001						
DHX9	0.916	0.021						
DIAPH1	0.749	0.036	0.688	0.003				
DLGAP1	0.758	0.042	0.676	0.002				
DLL4							0.779	0.010
DNM3	0.732	0.007						
DPP4	0.732	0.004	0.750	0.014				
DPT			0.704	0.014				
DUSP6	0.662	<.001	0.665	0.001				
EBNA1BP2							0.828	0.019
EDNRA	0.782	0.048						
EGF			0.712	0.023				
EGR1	0.678	0.004	0.725	0.028				
EGR3	0.680	0.006	0.738	0.027				
EIF2C2			0.789	0.032				
EIF2S3							0.759	0.012
ELK4	0.745	0.024						
EPHA2			0.661	0.007				
EPHA3	0.781	0.026					0.828	0.037
ERBB2	0.791	0.022	0.760	0.014	0.789	0.006		
ERBB3			0.757	0.009				
ERCC1							0.760	0.008
ESR1			0.742	0.014				
ESR2			0.711	0.038				
ETV4			0.714	0.035				
FAM107A	0.619	<.001	0.710	0.011			0.781	0.019

Table 6B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
FAM13C	0.664	<.001	0.686	<.001			0.813	0.014
FAM49B	0.670	<.001	0.793	0.014	0.815	0.044	0.843	0.047
FASLG			0.616	0.004			0.813	0.038
FGF10	0.751	0.028			0.766	0.019		
FGF17			0.718	0.031	0.765	0.019		
FGFR2	0.740	0.009			0.738	0.002		
FKBP5			0.749	0.031				
FLNC					0.826	0.029		
FLT1	0.779	0.045	0.729	0.006				
FLT4							0.815	0.024
FOS	0.657	0.003	0.656	0.004				
FSD1							0.763	0.017
FYN	0.716	0.004			0.792	0.024		
GADD45B	0.692	0.009	0.697	0.010				
GDF15			0.767	0.016				
GHR			0.701	0.002	0.704	0.002	0.640	<.001
GNRH1					0.778	0.039		
GPM6B	0.749	0.010	0.750	0.010	0.827	0.037		
GRB7			0.696	0.005				
GSK3B	0.726	0.005						
GSN	0.660	<.001	0.752	0.019				
GSTM1	0.710	0.004	0.676	<.001				
GSTM2	0.643	<.001			0.767	0.015		
HK1	0.798	0.035						
HLA-G			0.660	0.013				
HLF	0.644	<.001	0.727	0.011				
HNF1B			0.755	0.013				
HPS1	0.756	0.006	0.791	0.043				
HSD17B10	0.737	0.006						
HSD3B2							0.674	0.003
HSP90AB1			0.763	0.015				
HSPB1	0.787	0.020	0.778	0.015				
HSPE1			0.794	0.039				
ICAM1			0.664	0.003				
IER3	0.699	0.003	0.693	0.010				
IFIT1	0.621	<.001	0.733	0.027				
IGF1	0.751	0.017	0.655	<.001				
IGFBP2	0.599	<.001	0.605	<.001				
IGFBP5	0.745	0.007	0.775	0.035				
IGFBP6	0.671	0.005						
IL1B	0.732	0.016	0.717	0.005				
IL6	0.763	0.040						

Table 6B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
IL6R			0.764	0.022				
IL6ST	0.647	<.001	0.739	0.012				
IL8	0.711	0.015	0.694	0.006				
ING5	0.729	0.007	0.727	0.003				
ITGA4			0.755	0.009				
ITGA5	0.743	0.018	0.770	0.034				
ITGA6	0.816	0.044	0.772	0.006				
ITGA7	0.680	0.004						
ITGAD			0.590	0.009				
ITGB4	0.663	<.001	0.658	<.001	0.759	0.004		
JUN	0.656	0.004	0.639	0.003				
KIAA0196	0.737	0.011						
KIT					0.730	0.021	0.724	0.008
KLC1	0.755	0.035						
KLK1	0.706	0.008						
KLK2	0.740	0.016	0.723	0.001				
KLK3	0.765	0.006	0.740	0.002				
KRT1							0.774	0.042
KRT15	0.658	<.001	0.632	<.001	0.764	0.008		
KRT18	0.703	0.004	0.672	<.001	0.779	0.015	0.811	0.032
KRT5	0.686	<.001	0.629	<.001	0.802	0.023		
KRT8	0.763	0.034	0.771	0.022				
L1CAM	0.748	0.041						
LAG3	0.693	0.008	0.724	0.020				
LAMA4					0.689	0.039		
LAMB3	0.667	<.001	0.645	<.001	0.773	0.006		
LGALS3	0.666	<.001			0.822	0.047		
LIG3			0.723	0.008				
LRP1	0.777	0.041					0.769	0.007
MDM2			0.688	<.001				
MET	0.709	0.010	0.736	0.028	0.715	0.003		
MGMT	0.751	0.031						
MICA			0.705	0.002				
MPPED2	0.690	0.001	0.657	<.001	0.708	<.001		
MRC1							0.812	0.049
MSH6							0.860	0.049
MTSS1	0.686	0.001						
MVP	0.798	0.034	0.761	0.033				
MYBPC1	0.754	0.009	0.615	<.001				
NCAPD3	0.739	0.021	0.664	0.005				
NEXN			0.798	0.037				
NFAT5	0.596	<.001	0.732	0.005				

Table 6B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
NFATC2	0.743	0.016	0.792	0.047				
NOS3	0.730	0.012	0.757	0.032				
OAZ1	0.732	0.020	0.705	0.002				
OCLN					0.746	0.043	0.784	0.025
OLFML3	0.711	0.002			0.709	<.001	0.720	0.001
OMD	0.729	0.011	0.762	0.033				
OSM							0.813	0.028
PAGE4	0.668	0.003	0.725	0.004	0.688	<.001	0.766	0.005
PCA3	0.736	0.001	0.691	<.001				
PCDHGB7					0.769	0.019	0.789	0.022
PIK3CA			0.768	0.010				
PIK3CG	0.792	0.019	0.758	0.009				
PLG							0.682	0.009
PPAP2B	0.688	0.005			0.815	0.046		
PPP1R12A	0.731	0.026	0.775	0.042				
PRIMA1	0.697	0.004	0.757	0.032				
PRKCA	0.743	0.019						
PRKCB	0.756	0.036			0.767	0.029		
PROM1	0.640	0.027			0.699	0.034	0.503	0.013
PTCH1	0.730	0.018						
PTEN	0.779	0.015			0.789	0.007		
PTGS2	0.644	<.001	0.703	0.007				
PTHLH	0.655	0.012	0.706	0.038	0.634	0.001	0.665	0.003
PTK2B	0.779	0.023	0.702	0.002	0.806	0.015	0.806	0.024
PYCARD			0.659	0.001				
RAB30	0.779	0.033	0.754	0.014				
RARB	0.787	0.043	0.742	0.009				
RASSF1	0.754	0.005						
RHOA			0.796	0.041			0.819	0.048
RND3	0.721	0.011	0.743	0.028				
SDC1			0.707	0.011				
SDC2					0.745	0.002		
SDHC	0.750	0.013						
SERPINA3			0.730	0.016				
SERPINB5			0.715	0.041				
SH3RF2			0.698	0.025				
SIPA1L1			0.796	0.014			0.820	0.004
SLC22A3	0.724	0.014	0.700	0.008				
SMAD4	0.668	0.002			0.771	0.016		
SMARCD1	0.726	<.001	0.700	0.001			0.812	0.028
SMO							0.785	0.027
SOD1			0.735	0.012				

Table 6B	cRFI		cRFI		bRFI		bRFI	
	Primary Pattern		Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value	HR	p-value
SORBS1			0.785	0.039				
SPDEF	0.818	0.002						
SPINT1	0.761	0.024	0.773	0.006				
SRC	0.709	<.001	0.690	<.001				
SRD5A1	0.746	0.010	0.767	0.024	0.745	0.003		
SRD5A2	0.575	<.001	0.669	0.001	0.674	<.001	0.781	0.018
ST5	0.774	0.027						
STAT1	0.694	0.004						
STAT5A	0.719	0.004	0.765	0.006			0.834	0.049
STAT5B	0.704	0.001	0.744	0.012				
SUMO1	0.777	0.014						
SVIL			0.771	0.026				
TBP	0.774	0.031						
TFF3	0.742	0.015	0.719	0.024				
TGFB1I1	0.763	0.048						
TGFB2	0.729	0.011	0.758	0.002				
TMPRSS2	0.810	0.034	0.692	<.001				
TNF							0.727	0.022
TNFRSF10A			0.805	0.025				
TNFRSF10B	0.581	<.001	0.738	0.014	0.809	0.034		
TNFSF10	0.751	0.015	0.700	<.001				
TP63			0.723	0.018	0.736	0.003		
TPM2	0.708	0.010	0.734	0.014				
TRAF3IP2			0.718	0.004				
TRO			0.742	0.012				
TSTA3			0.774	0.028				
TUBB2A	0.659	<.001	0.650	<.001				
TYMP	0.695	0.002						
VCL	0.683	0.008						
VIM	0.778	0.040						
WDR19							0.775	0.014
XRCC5	0.793	0.042						
YY1	0.751	0.025					0.810	0.008
ZFHX3	0.760	0.005	0.726	0.001				
ZFP36	0.707	0.008	0.672	0.003				
ZNF827	0.667	0.002			0.792	0.039		

[00140] Tables 7A and 7B provide genes significantly associated ($p<0.05$), positively or negatively, with clinical recurrence (cRFI) in negative TMPRSS fusion specimens in the primary or highest Gleason pattern specimen. Increased expression of genes in Table 7A is negatively

associated with good prognosis, while increased expression of genes in Table 7B is positively associated with good prognosis.

Table 7A.
Genes significantly (p<0.05) associated with cRFI for TMPRSS2-ERG fusion negative in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) > 1.0 (increased expression is negatively associated with good prognosis)

Table 7A	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
ANLN	1.42	0.012	1.36	0.004
AQP2	1.25	0.033		
ASPN	2.48	<.001	1.65	<.001
BGN	2.04	<.001	1.45	0.007
BIRC5	1.59	<.001	1.37	0.005
BMP6	1.95	<.001	1.43	0.012
BMPR1B	1.93	0.002		
BUB1	1.51	<.001	1.35	<.001
CCNE2	1.48	0.007		
CD276	1.93	<.001	1.79	<.001
CDC20	1.49	0.004	1.47	<.001
CDC6	1.52	0.009	1.34	0.022
CDKN2B	1.54	0.008	1.55	0.003
CDKN2C	1.55	0.003	1.57	<.001
CDKN3	1.34	0.026		
CENPF	1.63	0.002	1.33	0.018
CKS2	1.50	0.026	1.43	0.009
CLTC			1.46	0.014
COL1A1	1.98	<.001	1.50	0.002
COL3A1	2.03	<.001	1.42	0.007
COL4A1	1.81	0.002		
COL8A1	1.63	0.004	1.60	0.001
CRISP3			1.31	0.016
CTHRC1	1.67	0.006	1.48	0.005
DDIT4	1.49	0.037		
ENY2			1.29	0.039
EZH2			1.35	0.016
F2R	1.46	0.034	1.46	0.007
FAP	1.66	0.006	1.38	0.012
FGF5			1.46	0.001
GNPTAB	1.49	0.013		
HSD17B4	1.34	0.039	1.44	0.002
INHBA	2.92	<.001	2.19	<.001
JAG1	1.38	0.042		
KCNN2	1.71	0.002	1.73	<.001
KHDRBS3			1.46	0.015
KLK14	1.28	0.034		

Table 7A	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
KPNA2	1.63	0.016		
LAMC1	1.41	0.044		
LOX			1.29	0.036
LTBP2	1.57	0.017		
MELK	1.38	0.029		
MMP11	1.69	0.002	1.42	0.004
MYBL2	1.78	<.001	1.49	<.001
NETO2	2.01	<.001	1.43	0.007
NME1			1.38	0.017
PATE1	1.43	<.001	1.24	0.005
PEX10	1.46	0.030		
PGD	1.77	0.002		
POSTN	1.49	0.037	1.34	0.026
PPFIA3	1.51	0.012		
PPP3CA	1.46	0.033	1.34	0.020
PTK6	1.69	<.001	1.56	<.001
PTTG1	1.35	0.028		
RAD51	1.32	0.048		
RALBP1			1.29	0.042
RGS7	1.18	0.012	1.32	0.009
RRM1	1.57	0.016	1.32	0.041
RRM2	1.30	0.039		
SAT1	1.61	0.007		
SESN3	1.76	<.001	1.36	0.020
SFRP4	1.55	0.016	1.48	0.002
SHMT2	2.23	<.001	1.59	<.001
SPARC	1.54	0.014		
SQLE	1.86	0.003		
STMN1	2.14	<.001		
THBS2	1.79	<.001	1.43	0.009
TK1	1.30	0.026		
TOP2A	2.03	<.001	1.47	0.003
TPD52	1.63	0.003		
TPX2	2.11	<.001	1.63	<.001
TRAP1	1.46	0.023		
UBE2C	1.57	<.001	1.58	<.001
UBE2G1	1.56	0.008		
UBE2T	1.75	<.001		
UGT2B15	1.31	0.036	1.33	0.004
UHRF1	1.46	0.007		
UTP23	1.52	0.017		

Table 7B.
Genes significantly (p<0.05) associated with cRFI for TMPRSS2-ERG fusion negative in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) < 1.0 (increased expression is positively associated with good prognosis)

Table 7B	Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value
AAMP	0.56	<.001	0.65	0.001
ABCA5	0.64	<.001	0.71	<.001
ABCB1	0.62	0.004		
ABCC3			0.74	0.031
ABCG2			0.78	0.050
ABHD2	0.71	0.035		
ACOX2	0.54	<.001	0.71	0.007
ADH5	0.49	<.001	0.61	<.001
AKAP1	0.77	0.031	0.76	0.013
AKR1C1	0.65	0.006	0.78	0.044
AKT1			0.72	0.020
AKT3	0.75	<.001		
ALDH1A2	0.53	<.001	0.60	<.001
AMPD3	0.62	<.001	0.78	0.028
ANPEP	0.54	<.001	0.61	<.001
ANXA2	0.63	0.008	0.74	0.016
ARHGAP29	0.67	0.005	0.77	0.016
ARHGDIB	0.64	0.013		
ATP5J	0.57	0.050		
ATXN1	0.61	0.004	0.77	0.043
AXIN2	0.51	<.001	0.62	<.001
AZGP1	0.61	<.001	0.64	<.001
BCL2	0.64	0.004	0.75	0.029
BIN1	0.52	<.001	0.74	0.010
BTG3	0.75	0.032	0.75	0.010
BTRC	0.69	0.011		
C7	0.51	<.001	0.67	<.001
CADM1	0.49	<.001	0.76	0.034
CASP1	0.71	0.010	0.74	0.007
CAV1			0.73	0.015
CCL5	0.67	0.018	0.67	0.003
CCNH	0.63	<.001	0.75	0.004
CCR1			0.77	0.032
CD164	0.52	<.001	0.63	<.001
CD44	0.53	<.001	0.74	0.014
CDH10	0.69	0.040		
CDH18	0.40	0.011		
CDK14	0.75	0.013		
CDK2			0.81	0.031
CDK3	0.73	0.022		

Table 7B	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
CDKN1A	0.68	0.038		
CDKN1C	0.62	0.003	0.72	0.005
COL6A1	0.54	<.001	0.70	0.004
COL6A3	0.64	0.004		
CSF1	0.56	<.001	0.78	0.047
CSRP1	0.40	<.001	0.66	0.002
CTGF	0.66	0.015	0.74	0.027
CTNNB1	0.69	0.043		
CTSB	0.60	0.002	0.71	0.011
CTSS	0.67	0.013		
CXCL12	0.56	<.001	0.77	0.026
CYP3A5	0.43	<.001	0.63	<.001
CYR61	0.43	<.001	0.58	<.001
DAG1			0.72	0.012
DARC	0.66	0.016		
DDR2	0.65	0.007		
DES	0.52	<.001	0.74	0.018
DHRS9	0.54	0.007		
DICER1	0.70	0.044		
DLC1			0.75	0.021
DLGAP1	0.55	<.001	0.72	0.005
DNM3	0.61	0.001		
DPP4	0.55	<.001	0.77	0.024
DPT	0.48	<.001	0.61	<.001
DUSP1	0.47	<.001	0.59	<.001
DUSP6	0.65	0.009	0.65	0.002
DYNLL1			0.74	0.045
EDNRA	0.61	0.002	0.75	0.038
EFNB2	0.71	0.043		
EGR1	0.43	<.001	0.58	<.001
EGR3	0.47	<.001	0.66	<.001
EIF5			0.77	0.028
ELK4	0.49	<.001	0.72	0.012
EPHA2			0.70	0.007
EPHA3	0.62	<.001	0.72	0.009
EPHB2	0.68	0.009		
ERBB2	0.64	<.001	0.63	<.001
ERBB3	0.69	0.018		
ERCC1	0.69	0.019	0.77	0.021
ESR2	0.61	0.020		
FAAH	0.57	<.001	0.77	0.035
FABP5	0.67	0.035		
FAM107A	0.42	<.001	0.59	<.001
FAM13C	0.53	<.001	0.59	<.001

Table 7B	Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value
FAS	0.71	0.035		
FASLG	0.56	0.017	0.67	0.014
FGF10	0.57	0.002		
FGF17	0.70	0.039	0.70	0.010
FGF7	0.63	0.005	0.70	0.004
FGFR2	0.63	0.003	0.71	0.003
FKBP5			0.72	0.020
FLNA	0.48	<.001	0.74	0.022
FOS	0.45	<.001	0.56	<.001
FOXO1	0.59	<.001		
FOXQ1	0.57	<.001	0.69	0.008
FYN	0.62	0.001	0.74	0.013
G6PD			0.77	0.014
GADD45A	0.73	0.045		
GADD45B	0.45	<.001	0.64	0.001
GDF15	0.58	<.001		
GHR	0.62	0.008	0.68	0.002
GPM6B	0.60	<.001	0.70	0.003
GSK3B	0.71	0.016	0.71	0.006
GSN	0.46	<.001	0.66	<.001
GSTM1	0.56	<.001	0.62	<.001
GSTM2	0.47	<.001	0.67	<.001
HGD			0.72	0.002
HIRIP3	0.69	0.021	0.69	0.002
HK1	0.68	0.005	0.73	0.005
HLA-G	0.54	0.024	0.65	0.013
HLF	0.41	<.001	0.68	0.001
HNF1B	0.55	<.001	0.59	<.001
HPS1	0.74	0.015	0.76	0.025
HSD17B3	0.65	0.031		
HSPB2	0.62	0.004	0.76	0.027
ICAM1	0.61	0.010		
IER3	0.55	<.001	0.67	0.003
IFIT1	0.57	<.001	0.70	0.008
IFNG			0.69	0.040
IGF1	0.63	<.001	0.59	<.001
IGF2	0.67	0.019	0.70	0.005
IGFBP2	0.53	<.001	0.63	<.001
IGFBP5	0.57	<.001	0.71	0.006
IGFBP6	0.41	<.001	0.71	0.012
IL10	0.59	0.020		
IL1B	0.53	<.001	0.70	0.005
IL6	0.55	0.001		
IL6ST	0.45	<.001	0.68	<.001

Table 7B	Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value
IL8	0.60	0.005	0.70	0.008
ILK	0.68	0.029	0.76	0.036
ING5	0.54	<.001	0.82	0.033
ITGA1	0.66	0.017		
ITGA3	0.70	0.020		
ITGA5	0.64	0.011		
ITGA6	0.66	0.003	0.74	0.006
ITGA7	0.50	<.001	0.71	0.010
ITGB4	0.63	0.014	0.73	0.010
ITPR1	0.55	<.001		
ITPR3			0.76	0.007
JUN	0.37	<.001	0.54	<.001
JUNB	0.58	0.002	0.71	0.016
KCTD12	0.68	0.017		
KIT	0.49	0.002	0.76	0.043
KLC1	0.61	0.005	0.77	0.045
KLF6	0.65	0.009		
KLK1	0.68	0.036		
KLK10			0.76	0.037
KLK2	0.64	<.001	0.73	0.006
KLK3	0.65	<.001	0.76	0.021
KLRK1	0.63	0.005		
KRT15	0.52	<.001	0.58	<.001
KRT18	0.46	<.001		
KRT5	0.51	<.001	0.58	<.001
KRT8	0.53	<.001		
L1CAM	0.65	0.031		
LAG3	0.58	0.002	0.76	0.033
LAMA4	0.52	0.018		
LAMB3	0.60	0.002	0.65	0.003
LGALS3	0.52	<.001	0.71	0.002
LIG3	0.65	0.011		
LRP1	0.61	0.001	0.75	0.040
MGMT	0.66	0.003		
MICA	0.59	0.001	0.68	0.001
MLXIP	0.70	0.020		
MMP2	0.68	0.022		
MMP9	0.67	0.036		
MPPED2	0.57	<.001	0.66	<.001
MRC1	0.69	0.028		
MTSS1	0.63	0.005	0.79	0.037
MVP	0.62	<.001		
MYBPC1	0.53	<.001	0.70	0.011
NCAM1	0.70	0.039	0.77	0.042

Table 7B	Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value
NCAPD3	0.52	<.001	0.59	<.001
NDRG1			0.69	0.008
NEXN	0.62	0.002		
NFAT5	0.45	<.001	0.59	<.001
NFATC2	0.68	0.035	0.75	0.036
NFKBIA	0.70	0.030		
NRG1	0.59	0.022	0.71	0.018
OAZ1	0.69	0.018	0.62	<.001
OLFML3	0.59	<.001	0.72	0.003
OR51E2	0.73	0.013		
PAGE4	0.42	<.001	0.62	<.001
PCA3	0.53	<.001		
PCDHGB7	0.70	0.032		
PGF	0.68	0.027	0.71	0.013
PGR			0.76	0.041
PIK3C2A			0.80	<.001
PIK3CA	0.61	<.001	0.80	0.036
PIK3CG	0.67	0.001	0.76	0.018
PLP2	0.65	0.015	0.72	0.010
PPAP2B	0.45	<.001	0.69	0.003
PPP1R12A	0.61	0.007	0.73	0.017
PRIMA1	0.51	<.001	0.68	0.004
PRKCA	0.55	<.001	0.74	0.009
PRKCB	0.55	<.001		
PROM1			0.67	0.042
PROS1	0.73	0.036		
PTCH1	0.69	0.024	0.72	0.010
PTEN	0.54	<.001	0.64	<.001
PTGS2	0.48	<.001	0.55	<.001
PTH1R	0.57	0.003	0.77	0.050
PTHLH	0.55	0.010		
PTK2B	0.56	<.001	0.70	0.001
PYCARD			0.73	0.009
RAB27A	0.65	0.009	0.71	0.014
RAB30	0.59	0.003	0.72	0.010
RAGE			0.76	0.011
RARB	0.59	<.001	0.63	<.001
RASSF1	0.67	0.003		
RB1	0.67	0.006		
RFX1	0.71	0.040	0.70	0.003
RHOA	0.71	0.038	0.65	<.001
RHOB	0.58	0.001	0.71	0.006
RND3	0.54	<.001	0.69	0.003
RNF114	0.59	0.004	0.68	0.003

Table 7B	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
SCUBE2			0.77	0.046
SDHC	0.72	0.028	0.76	0.025
SEC23A			0.75	0.029
SEMA3A	0.61	0.004	0.72	0.011
SEPT9	0.66	0.013	0.76	0.036
SERPINB5			0.75	0.039
SH3RF2	0.44	<.001	0.48	<.001
SHH			0.74	0.049
SLC22A3	0.42	<.001	0.61	<.001
SMAD4	0.45	<.001	0.66	<.001
SMARCD1	0.69	0.016		
SOD1	0.68	0.042		
SORBS1	0.51	<.001	0.73	0.012
SPARCL1	0.58	<.001	0.77	0.040
SPDEF	0.77	<.001		
SPINT1	0.65	0.004	0.79	0.038
SRC	0.61	<.001	0.69	0.001
SRD5A2	0.39	<.001	0.55	<.001
ST5	0.61	<.001	0.73	0.012
STAT1	0.64	0.006		
STAT3	0.63	0.010		
STAT5A	0.62	0.001	0.70	0.003
STAT5B	0.58	<.001	0.73	0.009
SUMO1	0.66	<.001		
SVIL	0.57	0.001	0.74	0.022
TBP	0.65	0.002		
TFF1	0.65	0.021		
TFF3	0.58	<.001		
TGFB1I1	0.51	<.001	0.75	0.026
TGFB2	0.48	<.001	0.62	<.001
TGFBR2	0.61	0.003		
TIAM1	0.68	0.019		
TIMP2	0.69	0.020		
TIMP3	0.58	0.002		
TNFRSF10A	0.73	0.047		
TNFRSF10B	0.47	<.001	0.70	0.003
TNFSF10	0.56	0.001		
TP63			0.67	0.001
TPM1	0.58	0.004	0.73	0.017
TPM2	0.46	<.001	0.70	0.005
TRA2A	0.68	0.013		
TRAF3IP2	0.73	0.041	0.71	0.004
TRO	0.72	0.016	0.71	0.004
TUBB2A	0.53	<.001	0.73	0.021

Table 7B	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
TYMP	0.70	0.011		
VCAM1	0.69	0.041		
VCL	0.46	<.001		
VEGFA			0.77	0.039
VEGFB	0.71	0.035		
VIM	0.60	0.001		
XRCC5			0.75	0.026
YY1	0.62	0.008	0.77	0.039
ZFHX3	0.53	<.001	0.58	<.001
ZFP36	0.43	<.001	0.54	<.001
ZNF827	0.55	0.001		

[00141] Tables 8A and 8B provide genes that were significantly associated ($p<0.05$), positively or negatively, with clinical recurrence (cRFI) in positive TMPRSS fusion specimens in the primary or highest Gleason pattern specimen. Increased expression of genes in Table 8A is negatively associated with good prognosis, while increased expression of genes in Table 8B is positively associated with good prognosis.

Table 8A.

Genes significantly ($p<0.05$) associated with cRFI for TMPRSS2-ERG fusion positive in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) > 1.0 (increased expression is negatively associated with good prognosis)

Table 8A	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
ACTR2	1.78	0.017		
AKR1C3	1.44	0.013		
ALCAM			1.44	0.022
ANLN	1.37	0.046	1.81	<.001
APOE	1.49	0.023	1.66	0.005
AQP2			1.30	0.013
ARHGDIB	1.55	0.021		
ASPN	2.13	<.001	2.43	<.001
ATP5E	1.69	0.013	1.58	0.014
BGN	1.92	<.001	2.55	<.001
BIRC5	1.48	0.006	1.89	<.001
BMP6	1.51	0.010	1.96	<.001
BRCA2			1.41	0.007
BUB1	1.36	0.007	1.52	<.001
CCNE2	1.55	0.004	1.59	<.001
CD276			1.65	<.001
CDC20	1.68	<.001	1.74	<.001
CDH11			1.50	0.017
CDH18	1.36	<.001		

Table 8A	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
CDH7	1.54	0.009	1.46	0.026
CDKN2B	1.68	0.008	1.93	0.001
CDKN2C	2.01	<.001	1.77	<.001
CDKN3	1.51	0.002	1.33	0.049
CENPF	1.51	0.007	2.04	<.001
CKS2	1.43	0.034	1.56	0.007
COL1A1	2.23	<.001	3.04	<.001
COL1A2	1.79	0.001	2.22	<.001
COL3A1	1.96	<.001	2.81	<.001
COL4A1			1.52	0.020
COL5A1			1.50	0.020
COL5A2	1.64	0.017	1.55	0.010
COL8A1	1.96	<.001	2.38	<.001
CRISP3	1.68	0.002	1.67	0.002
CTHRC1			2.06	<.001
CTNND2	1.42	0.046	1.50	0.025
CTSK			1.43	0.049
CXCR4	1.82	0.001	1.64	0.007
DDIT4	1.54	0.016	1.58	0.009
DLL4			1.51	0.007
DYNLL1	1.50	0.021	1.22	0.002
F2R	2.27	<.001	2.02	<.001
FAP			2.12	<.001
FCGR3A			1.94	0.002
FGF5	1.23	0.047		
FOXP3	1.52	0.006	1.48	0.018
GNPTAB			1.44	0.042
GPR68			1.51	0.011
GREM1	1.91	<.001	2.38	<.001
HDAC1			1.43	0.048
HDAC9	1.65	<.001	1.67	0.004
HRAS	1.65	0.005	1.58	0.021
IGFBP3	1.94	<.001	1.85	<.001
INHBA	2.03	<.001	2.64	<.001
JAG1	1.41	0.027	1.50	0.008
KCTD12			1.51	0.017
KHDRBS3	1.48	0.029	1.54	0.014
KPNA2			1.46	0.050
LAMA3	1.35	0.040		
LAMC1	1.77	0.012		
LTBP2			1.82	<.001
LUM	1.51	0.021	1.53	0.009
MELK	1.38	0.020	1.49	0.001
MKI67			1.37	0.014

Table 8A	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
MMP11	1.73	<.001	1.69	<.001
MRPL13			1.30	0.046
MYBL2	1.56	<.001	1.72	<.001
MYLK3			1.17	0.007
NOX4	1.58	0.005	1.96	<.001
NRIP3			1.30	0.040
NRP1			1.53	0.021
OLFML2B			1.54	0.024
OSM	1.43	0.018		
PATE1	1.20	<.001	1.33	<.001
PCNA			1.64	0.003
PEX10	1.41	0.041	1.64	0.003
PIK3CA	1.38	0.037		
PLK1	1.52	0.009	1.67	0.002
PLOD2			1.65	0.002
POSTN	1.79	<.001	2.06	<.001
PTK6	1.67	0.002	2.38	<.001
PTTG1	1.56	0.002	1.54	0.003
RAD21	1.61	0.036	1.53	0.005
RAD51			1.33	0.009
RALA	1.95	0.004	1.60	0.007
REG4			1.43	0.042
ROBO2	1.46	0.024		
RRM1			1.44	0.033
RRM2	1.50	0.003	1.48	<.001
SAT1	1.42	0.009	1.43	0.012
SEC14L1			1.64	0.002
SFRP4	2.07	<.001	2.40	<.001
SHMT2	1.52	0.030	1.60	0.001
SLC44A1			1.42	0.039
SPARC	1.93	<.001	2.21	<.001
SULF1	1.63	0.006	2.04	<.001
THBS2	1.95	<.001	2.26	<.001
THY1	1.69	0.016	1.95	0.002
TK1			1.43	0.003
TOP2A	1.57	0.002	2.11	<.001
TPX2	1.84	<.001	2.27	<.001
UBE2C	1.41	0.011	1.44	0.006
UBE2T	1.63	0.001		
UHRF1	1.51	0.007	1.69	<.001
WISP1	1.47	0.045		
WNT5A	1.35	0.027	1.63	0.001
ZWINT	1.36	0.045		

Table 8B.

Genes significantly (p<0.05) associated with cRFI for TMPRSS2-ERG fusion positive in the primary Gleason pattern or highest Gleason pattern with hazard ratio (HR) < 1.0 (increased expression is positively associated with good prognosis)

Table 8B	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
AAMP	0.57	0.007	0.58	<.001
ABCA5			0.80	0.044
ACE	0.65	0.023	0.55	<.001
ACOX2			0.55	<.001
ADH5			0.68	0.022
AKAP1			0.81	0.043
ALDH1A2	0.72	0.036	0.43	<.001
ANPEP	0.66	0.022	0.46	<.001
APRT			0.73	0.040
AXIN2			0.60	<.001
AZGP1	0.57	<.001	0.65	<.001
BCL2			0.69	0.035
BIK	0.71	0.045		
BIN1	0.71	0.004	0.71	0.009
BTRC	0.66	0.003	0.58	<.001
C7			0.64	0.006
CADM1	0.61	<.001	0.47	<.001
CCL2			0.73	0.042
CCNH	0.69	0.022		
CD44	0.56	<.001	0.58	<.001
CD82			0.72	0.033
CDC25B	0.74	0.028		
CDH1	0.75	0.030	0.72	0.010
CDH19			0.56	0.015
CDK3			0.78	0.045
CDKN1C	0.74	0.045	0.70	0.014
CSF1			0.72	0.037
CTSB			0.69	0.048
CTSL2			0.58	0.005
CYP3A5	0.51	<.001	0.30	<.001
DHX9	0.89	0.006	0.87	0.012
DLC1			0.64	0.023
DLGAP1	0.69	0.010	0.49	<.001
DPP4	0.64	<.001	0.56	<.001
DPT			0.63	0.003
EGR1			0.69	0.035
EGR3			0.68	0.025
EIF2S3			0.70	0.021
EIF5	0.71	0.030		
ELK4	0.71	0.041	0.60	0.003

Table 8B	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
EPHA2	0.72	0.036	0.66	0.011
EPHB4			0.65	0.007
ERCC1			0.68	0.023
ESR2			0.64	0.027
FAM107A	0.64	0.003	0.61	0.003
FAM13C	0.68	0.006	0.55	<.001
FGFR2	0.73	0.033	0.59	<.001
FKBP5			0.60	0.006
FLNC	0.68	0.024	0.65	0.012
FLT1			0.71	0.027
FOS			0.62	0.006
FOXO1			0.75	0.010
GADD45B			0.68	0.020
GHR			0.62	0.006
GPM6B			0.57	<.001
GSTM1	0.68	0.015	0.58	<.001
GSTM2	0.65	0.005	0.47	<.001
HGD	0.63	0.001	0.71	0.020
HK1	0.67	0.003	0.62	0.002
HLF			0.59	<.001
HNF1B	0.66	0.004	0.61	0.001
IER3			0.70	0.026
IGF1	0.63	0.005	0.55	<.001
IGF1R			0.76	0.049
IGFBP2	0.59	0.007	0.64	0.003
IL6ST			0.65	0.005
IL8	0.61	0.005	0.66	0.019
ILK			0.64	0.015
ING5	0.73	0.033	0.70	0.009
ITGA7	0.72	0.045	0.69	0.019
ITGB4			0.63	0.002
KLC1			0.74	0.045
KLK1	0.56	0.002	0.49	<.001
KLK10			0.68	0.013
KLK11			0.66	0.003
KLK2	0.66	0.045	0.65	0.011
KLK3	0.75	0.048	0.77	0.014
KRT15	0.71	0.017	0.50	<.001
KRT5	0.73	0.031	0.54	<.001
LAMA5			0.70	0.044
LAMB3	0.70	0.005	0.58	<.001
LGALS3			0.69	0.025
LIG3			0.68	0.022
MDK	0.69	0.035		

Table 8B	Primary Pattern		Highest Pattern	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
MGMT	0.59	0.017	0.60	<.001
MGST1			0.73	0.042
MICA			0.70	0.009
MPPED2	0.72	0.031	0.54	<.001
MTSS1	0.62	0.003		
MYBPC1			0.50	<.001
NCAPD3	0.62	0.007	0.38	<.001
NCOR1			0.82	0.048
NFAT5	0.60	0.001	0.62	<.001
NRG1	0.66	0.040	0.61	0.029
NUP62	0.75	0.037		
OMD	0.54	<.001		
PAGE4			0.64	0.005
PCA3			0.66	0.012
PCDHGB7			0.68	0.018
PGR			0.60	0.012
PPAP2B			0.62	0.010
PPP1R12A	0.73	0.031	0.58	0.003
PRIMA1			0.65	0.013
PROM1	0.41	0.013		
PTCH1	0.64	0.006		
PTEN			0.75	0.047
PTGS2			0.67	0.011
PTK2B			0.66	0.005
PTPN1			0.71	0.026
RAGE	0.70	0.012		
RARB			0.68	0.016
RGS10			0.84	0.034
RHOB			0.66	0.016
RND3			0.63	0.004
SDHC	0.73	0.044	0.69	0.016
SERPINA3	0.67	0.011	0.51	<.001
SERPINB5			0.42	<.001
SH3RF2	0.66	0.012	0.51	<.001
SLC22A3	0.59	0.003	0.48	<.001
SMAD4	0.64	0.004	0.49	<.001
SMARCC2			0.73	0.042
SMARCD1	0.73	<.001	0.76	0.035
SMO			0.64	0.006
SNAI1			0.53	0.008
SOD1			0.60	0.003
SRC	0.64	<.001	0.61	<.001
SRD5A2	0.63	0.004	0.59	<.001
STAT3			0.64	0.014

Table 8B	Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value
STAT5A			0.70	0.032
STAT5B	0.74	0.034	0.63	0.003
SVIL			0.71	0.028
TGFB1I1			0.68	0.036
TMPRSS2	0.72	0.015	0.67	<.001
TNFRSF10A			0.69	0.010
TNFRSF10B	0.67	0.007	0.64	0.001
TNFRSF18	0.38	0.003		
TNFSF10			0.71	0.025
TP53	0.68	0.004	0.57	<.001
TP63	0.75	0.049	0.52	<.001
TPM2			0.62	0.007
TRAF3IP2	0.71	0.017	0.68	0.005
TRO			0.72	0.033
TUBB2A			0.69	0.038
VCL			0.62	<.001
VEGFA			0.71	0.037
WWOX			0.65	0.004
ZFHX3	0.77	0.011	0.73	0.012
ZFP36			0.69	0.018
ZNF827	0.68	0.013	0.49	<.001

[00142] Tables 9A and 9B provide genes significantly associated ($p<0.05$), positively or negatively, with TMPRSS fusion status in the primary Gleason pattern. Increased expression of genes in Table 9A are positively associated with TMPRSS fusion positivity, while increased expression of genes in Table 10A are negatively associated with TMPRSS fusion positivity.

Table 9A.
Genes significantly ($p<0.05$) associated with TMPRSS fusion status in the primary Gleason pattern with odds ratio (OR) > 1.0 (increased expression is positively associated with TMPRSS fusion positivity

Table 9A Official Symbol	p-value	Odds Ratio	Official Symbol	p-value	Odds Ratio
ABCC8	<.001	1.86	MAP3K5	<.001	2.06
ALDH18A1	0.005	1.49	MAP7	<.001	2.74
ALKBH3	0.043	1.30	MSH2	0.005	1.59
ALOX5	<.001	1.66	MSH3	0.006	1.45
AMPD3	<.001	3.92	MUC1	0.012	1.42
APEX1	<.001	2.00	MYO6	<.001	3.79
ARHGDIB	<.001	1.87	NCOR2	0.001	1.62
ASAP2	0.019	1.48	NDRG1	<.001	6.77
ATXN1	0.013	1.41	NETO2	<.001	2.63
BMPR1B	<.001	2.37	ODC1	<.001	1.98
CACNA1D	<.001	9.01	OR51E1	<.001	2.24

Table 9A Official Symbol	p-value	Odds Ratio	Official Symbol	p-value	Odds Ratio
CADPS	0.015	1.39	PDE9A	<.001	2.21
CD276	0.003	2.25	PEX10	<.001	3.41
CDH1	0.016	1.37	PGK1	0.022	1.33
CDH7	<.001	2.22	PLA2G7	<.001	5.51
CDK7	0.025	1.43	PPP3CA	0.047	1.38
COL9A2	<.001	2.58	PSCA	0.013	1.43
CRISP3	<.001	2.60	PSMD13	0.004	1.51
CTNND1	0.033	1.48	PTCH1	0.022	1.38
ECE1	<.001	2.22	PTK2	0.014	1.38
EIF5	0.023	1.34	PTK6	<.001	2.29
EPHB4	0.005	1.51	PTK7	<.001	2.45
ERG	<.001	14.5	PTPRK	<.001	1.80
FAM171B	0.047	1.32	RAB30	0.001	1.60
FAM73A	0.008	1.45	REG4	0.018	1.58
FASN	0.004	1.50	RELA	0.001	1.62
GNPTAB	<.001	1.60	RFX1	0.020	1.43
GPS1	0.006	1.45	RGS10	<.001	1.71
GRB7	0.023	1.38	SCUBE2	0.009	1.48
HDAC1	<.001	4.95	SEPT9	<.001	3.91
HGD	<.001	1.64	SH3RF2	0.004	1.48
HIP1	<.001	1.90	SH3YL1	<.001	1.87
HNF1B	<.001	3.55	SHH	<.001	2.45
HSPA8	0.041	1.32	SIM2	<.001	1.74
IGF1R	0.001	1.73	SIPA1L1	0.021	1.35
ILF3	<.001	1.91	SLC22A3	<.001	1.63
IMMT	0.025	1.36	SLC44A1	<.001	1.65
ITPR1	<.001	2.72	SPINT1	0.017	1.39
ITPR3	<.001	5.91	TFDP1	0.005	1.75
JAG1	0.007	1.42	TMPRSS2ERGA	0.002	14E5
KCNN2	<.001	2.80	TMPRSS2ERGB	<.001	1.97
KHDRBS3	<.001	2.63	TRIM14	<.001	1.65
KIAA0247	0.019	1.38	TSTA3	0.018	1.38
KLK11	<.001	1.98	UAP1	0.046	1.39
LAMC1	0.008	1.56	UBE2G1	0.001	1.66
LAMC2	<.001	3.30	UGDH	<.001	2.22
LOX	0.009	1.41	XRCC5	<.001	1.66
LRP1	0.044	1.30	ZMYND8	<.001	2.19

Table 9B.

Genes significantly (p<0.05) associated with TMPRSS fusion status in the primary Gleason pattern with odds ratio (OR) < 1.0 (increased expression is negatively associated with TMPRSS fusion positivity)

Table 9B Official Symbol	p-value	Odds Ratio
ABCC4	0.045	0.77
ABHD2	<.001	0.38
ACTR2	0.027	0.73
ADAMTS1	0.024	0.58
ADH5	<.001	0.58
AGTR2	0.016	0.64
AKAP1	0.013	0.70
AKT2	0.015	0.71
ALCAM	<.001	0.45
ALDH1A2	0.004	0.70
ANPEP	<.001	0.43
ANXA2	0.010	0.71
APC	0.036	0.73
APOC1	0.002	0.56
APOE	<.001	0.44
ARF1	0.041	0.77
ATM	0.036	0.74
AURKB	<.001	0.62
AZGP1	<.001	0.54
BBC3	0.030	0.74
BCL2	0.012	0.70
BIN1	0.021	0.74
BTG1	0.004	0.67
BTG3	0.003	0.63
C7	0.023	0.74
CADM1	0.007	0.69
CASP1	0.011	0.70
CAV1	0.011	0.71
CCND1	0.019	0.72
CCR1	0.022	0.73
CD44	<.001	0.57
CD68	<.001	0.54
CD82	0.002	0.66
CDH5	0.007	0.66
CDKN1A	<.001	0.60
CDKN2B	<.001	0.54
CDKN2C	0.012	0.72
CDKN3	0.037	0.77
CHN1	0.038	0.75
CKS2	<.001	0.48

Table 9B Official Symbol	p-value	Odds Ratio
COL11A1	0.017	0.72
COL1A1	<.001	0.59
COL1A2	0.001	0.62
COL3A1	0.027	0.73
COL4A1	0.043	0.76
COL5A1	0.039	0.74
COL5A2	0.026	0.73
COL6A1	0.008	0.66
COL6A3	<.001	0.59
COL8A1	0.022	0.74
CSF1	0.011	0.70
CTNNB1	0.021	0.69
CTSB	<.001	0.62
CTSD	0.036	0.68
CTSK	0.007	0.70
CTSS	0.002	0.64
CXCL12	<.001	0.48
CXCR4	0.005	0.68
CXCR7	0.046	0.76
CYR61	0.004	0.65
DAP	0.002	0.64
DARC	0.021	0.73
DDR2	0.021	0.73
DHRS9	<.001	0.52
DIAPH1	<.001	0.56
DICER1	0.029	0.75
DLC1	0.013	0.72
DLGAP1	<.001	0.60
DLL4	<.001	0.57
DPT	0.006	0.68
DUSP1	0.012	0.68
DUSP6	0.001	0.62
DVL1	0.037	0.75
EFNB2	<.001	0.32
EGR1	0.003	0.65
ELK4	<.001	0.60
ERBB2	<.001	0.61
ERBB3	0.045	0.76
ESR2	0.010	0.70
ETV1	0.042	0.74
FABP5	<.001	0.21
FAM13C	0.006	0.67
FCGR3A	0.018	0.72
FGF17	0.009	0.71

Table 9B Official Symbol	p-value	Odds Ratio
FGF6	0.011	0.70
FGF7	0.003	0.63
FN1	0.006	0.69
FOS	0.035	0.74
FOXP3	0.010	0.71
GABRG2	0.029	0.74
GADD45B	0.003	0.63
GDF15	<.001	0.54
GPM6B	0.004	0.67
GPNMB	0.001	0.62
GSN	0.009	0.69
HLA-G	0.050	0.74
HLF	0.018	0.74
HPS1	<.001	0.48
HSD17B3	0.003	0.60
HSD17B4	<.001	0.56
HSPB1	<.001	0.38
HSPB2	0.002	0.62
IFI30	0.049	0.75
IFNG	0.006	0.64
IGF1	0.016	0.73
IGF2	0.001	0.57
IGFBP2	<.001	0.51
IGFBP3	<.001	0.59
IGFBP6	<.001	0.57
IL10	<.001	0.62
IL17A	0.012	0.63
IL1A	0.011	0.59
IL2	0.001	0.63
IL6ST	<.001	0.52
INSL4	0.014	0.71
ITGA1	0.009	0.69
ITGA4	0.007	0.68
JUN	<.001	0.59
KIT	<.001	0.64
KRT76	0.016	0.70
LAG3	0.002	0.63
LAPTM5	<.001	0.58
LGALS3	<.001	0.53
LTBP2	0.011	0.71
LUM	0.012	0.70
MAOA	0.020	0.73
MAP4K4	0.007	0.68
MGST1	<.001	0.54

Table 9B Official Symbol	p-value	Odds Ratio
MMP2	<.001	0.61
MPPED2	<.001	0.45
MRC1	0.005	0.67
MTPN	0.002	0.56
MTSS1	<.001	0.53
MVP	0.009	0.72
MYBPC1	<.001	0.51
MYLK3	0.001	0.58
NCAM1	<.001	0.59
NCAPD3	<.001	0.40
NCOR1	0.004	0.69
NFKBIA	<.001	0.63
NNMT	0.006	0.66
NPBWR1	0.027	0.67
OAZ1	0.049	0.64
OLFML3	<.001	0.56
OSM	<.001	0.64
PAGE1	0.012	0.52
PDGFRB	0.016	0.73
PECAM1	<.001	0.55
PGR	0.048	0.77
PIK3CA	<.001	0.55
PIK3CG	0.008	0.71
PLAU	0.044	0.76
PLK1	0.006	0.68
PLOD2	0.013	0.71
PLP2	0.024	0.73
PNLIPRP2	0.009	0.70
PPAP2B	<.001	0.62
PRKAR2B	<.001	0.61
PRKCB	0.044	0.76
PROS1	0.005	0.67
PTEN	<.001	0.47
PTGER3	0.007	0.69
PTH1R	0.011	0.70
PTK2B	<.001	0.61
PTPN1	0.028	0.73
RAB27A	<.001	0.21
RAD51	<.001	0.51
RAD9A	0.030	0.75
RARB	<.001	0.62
RASSF1	0.038	0.76
RECK	0.009	0.62
RHOB	0.004	0.64

Table 9B Official Symbol	p-value	Odds Ratio
RHOC	<.001	0.56
RLN1	<.001	0.30
RND3	0.014	0.72
S100P	0.002	0.66
SDC2	<.001	0.61
SEMA3A	0.001	0.64
SMAD4	<.001	0.64
SPARC	<.001	0.59
SPARCL1	<.001	0.56
SPINK1	<.001	0.26
SRD5A1	0.039	0.76
STAT1	0.026	0.74
STS	0.006	0.64
SULF1	<.001	0.53
TFF3	<.001	0.19
TGFA	0.002	0.65
TGFB1I1	0.040	0.77
TGFB2	0.003	0.66
TGFB3	<.001	0.54
TGFBR2	<.001	0.61
THY1	<.001	0.63
TIMP2	0.004	0.66
TIMP3	<.001	0.60
TMPRSS2	<.001	0.40
TNFSF11	0.026	0.63
TPD52	0.002	0.64
TRAM1	<.001	0.45
TRPC6	0.002	0.64
TUBB2A	<.001	0.49
VCL	<.001	0.57
VEGFB	0.033	0.73
VEGFC	<.001	0.61
VIM	0.012	0.69
WISP1	0.030	0.75
WNT5A	<.001	0.50

[00143] A molecular field effect was investigated, and determined that the expression levels of histologically normal-appearing cells adjacent to the tumor exhibited a molecular signature of prostate cancer. Tables 10A and 10B provide genes significantly associated ($p<0.05$), positively or negatively, with cRFI or bRFI in non-tumor samples. Table 10A is negatively associated with good prognosis, while increased expression of genes in Table 10B is positively associated with good prognosis.

Table 10A
Genes significantly (p<0.05) associated with cRFI or bRFI in Non-Tumor Samples with hazard ratio (HR) > 1.0 (increased expression is negatively associated with good prognosis)

Table 10A	cRFI		bRFI	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
ALCAM			1.278	0.036
ASPN	1.309	0.032		
BAG5	1.458	0.004		
BRCA2	1.385	<.001		
CACNA1D			1.329	0.035
CD164			1.339	0.020
CDKN2B	1.398	0.014		
COL3A1	1.300	0.035		
COL4A1	1.358	0.019		
CTNND2			1.370	0.001
DARC	1.451	0.003		
DICER1			1.345	<.001
DPP4			1.358	0.008
EFNB2			1.323	0.007
FASN			1.327	0.035
GHR			1.332	0.048
HSPA5			1.260	0.048
INHBA	1.558	<.001		
KCNN2			1.264	0.045
KRT76			1.115	<.001
LAMC1	1.390	0.014		
LAMC2			1.216	0.042
LIG3			1.313	0.030
MAOA			1.405	0.013
MCM6	1.307	0.036		
MKI67	1.271	0.008		
NEK2			1.312	0.016
NPBWR1	1.278	0.035		
ODC1			1.320	0.010
PEX10			1.361	0.014
PGK1	1.488	0.004		
PLA2G7			1.337	0.025
POSTN	1.306	0.043		
PTK6			1.344	0.005
REG4			1.348	0.009
RGS7			1.144	0.047
SFRP4	1.394	0.009		
TARP			1.412	0.011
TFF1			1.346	0.010
TGFBR2	1.310	0.035		

Table 10A	cRFI		bRFI	
Official Symbol	HR	p-value	HR	p-value
THY1	1.300	0.038		
TMPRSS2ERGA			1.333	<.001
TPD52			1.374	0.015
TRPC6	1.272	0.046		
UBE2C	1.323	0.007		
UHRF1	1.325	0.021		

Table 10B

Genes significantly (p<0.05) associated with cRFI or bRFI in Non-Tumor Samples with hazard ratio (HR) < 1.0 (increased expression is positively associated with good prognosis)

Table 10B	cRFI		bRFI	
Official Symbol	HR	p-value	HR	p-value
ABCA5	0.807	0.028		
ABCC3	0.760	0.019	0.750	0.003
ABHD2	0.781	0.028		
ADAM15	0.718	0.005		
AKAP1	0.740	0.009		
AMPD3			0.793	0.013
ANGPT2			0.752	0.027
ANXA2			0.776	0.035
APC	0.755	0.014		
APRT	0.762	0.025		
AR	0.752	0.015		
ARHGDIB			0.753	<.001
BIN1	0.738	0.016		
CADM1	0.711	0.004		
CCNH	0.820	0.041		
CCR1			0.749	0.007
CDK14			0.772	0.014
CDK3	0.819	0.044		
CDKN1C	0.808	0.038		
CHAF1A	0.634	0.002	0.779	0.045
CHN1			0.803	0.034
CHRAC1	0.751	0.014	0.779	0.021
COL5A1			0.736	0.012
COL5A2			0.762	0.013
COL6A1			0.757	0.032
COL6A3			0.757	0.019
CSK	0.663	<.001	0.698	<.001
CTSK			0.782	0.029
CXCL12			0.771	0.037
CXCR7			0.753	0.008

Table 10B	cRFI		bRFI	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
CYP3A5	0.790	0.035		
DDIT4			0.725	0.017
DIAPH1			0.771	0.015
DLC1	0.744	0.004	0.807	0.015
DLGAP1	0.708	0.004		
DUSP1	0.740	0.034		
EDN1			0.742	0.010
EGR1	0.731	0.028		
EIF3H	0.761	0.024		
EIF4E	0.786	0.041		
ERBB2	0.664	0.001		
ERBB4	0.764	0.036		
ERCC1	0.804	0.041		
ESR2			0.757	0.025
EZH2			0.798	0.048
FAAH	0.798	0.042		
FAM13C	0.764	0.012		
FAM171B			0.755	0.005
FAM49B			0.811	0.043
FAM73A	0.778	0.015		
FASLG			0.757	0.041
FGFR2	0.735	0.016		
FOS	0.690	0.008		
FYN	0.788	0.035	0.777	0.011
GPNMB			0.762	0.011
GSK3B	0.792	0.038		
HGD	0.774	0.017		
HIRIP3	0.802	0.033		
HSP90AB1	0.753	0.013		
HSPB1	0.764	0.021		
HSPE1	0.668	0.001		
IFI30			0.732	0.002
IGF2			0.747	0.006
IGFBP5			0.691	0.006
IL6ST			0.748	0.010
IL8			0.785	0.028
IMMT			0.708	<.001
ITGA6	0.747	0.008		
ITGAV			0.792	0.016
ITGB3			0.814	0.034
ITPR3	0.769	0.009		
JUN	0.655	0.005		
KHDRBS3			0.764	0.012
KLF6	0.714	<.001		

Table 10B	cRFI		bRFI	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
KLK2	0.813	0.048		
LAMA4			0.702	0.009
LAMA5	0.744	0.011		
LAPTM5			0.740	0.009
LGALS3	0.773	0.036	0.788	0.024
LIMS1			0.807	0.012
MAP3K5			0.815	0.034
MAP3K7			0.809	0.032
MAP4K4	0.735	0.018	0.761	0.010
MAPKAPK3	0.754	0.014		
MICA	0.785	0.019		
MTA1			0.808	0.043
MVP			0.691	0.001
MYLK3			0.730	0.039
MYO6	0.780	0.037		
NCOA1			0.787	0.040
NCOR1			0.876	0.020
NDRG1	0.761	<.001		
NFAT5	0.770	0.032		
NFKBIA			0.799	0.018
NME2			0.753	0.005
NUP62			0.842	0.032
OAZ1			0.803	0.043
OLFML2B			0.745	0.023
OLFML3			0.743	0.009
OSM			0.726	0.018
PCA3	0.714	0.019		
PECAM1			0.774	0.023
PIK3C2A			0.768	0.001
PIM1	0.725	0.011		
PLOD2			0.713	0.008
PPP3CA	0.768	0.040		
PROM1			0.482	<.001
PTEN			0.807	0.012
PTGS2	0.726	0.011		
PTTG1			0.729	0.006
PYCARD			0.783	0.012
RAB30			0.730	0.002
RAGE	0.792	0.012		
RFX1	0.789	0.016	0.792	0.010
RGS10	0.781	0.017		
RUNX1			0.747	0.007
SDHC			0.827	0.036
SEC23A			0.752	0.010

Table 10B	cRFI		bRFI	
Official Symbol	**HR**	**p-value**	**HR**	**p-value**
SEPT9			0.889	0.006
SERPINA3			0.738	0.013
SLC25A21			0.788	0.045
SMARCD1	0.788	0.010	0.733	0.007
SMO	0.813	0.035		
SRC	0.758	0.026		
SRD5A2			0.738	0.005
ST5			0.767	0.022
STAT5A			0.784	0.039
TGFB2	0.771	0.027		
TGFB3			0.752	0.036
THBS2			0.751	0.015
TNFRSF10B	0.739	0.010		
TPX2			0.754	0.023
TRAF3IP2			0.774	0.015
TRAM1	0.868	<.001	0.880	<.001
TRIM14	0.785	0.047		
TUBB2A	0.705	0.010		
TYMP			0.778	0.024
UAP1	0.721	0.013		
UTP23	0.763	0.007	0.826	0.018
VCL			0.837	0.040
VEGFA	0.755	0.009		
WDR19	0.724	0.005		
YBX1			0.786	0.027
ZFP36	0.744	0.032		
ZNF827	0.770	0.043		

[00144] Table 11 provides genes that are significantly associated ($p<0.05$) with cRFI or bRFI after adjustment for Gleason pattern or highest Gleason pattern.

Table 11
Genes significantly ($p<0.05$) associated with cRFI or bRFI after adjustment for Gleason pattern in the primary Gleason pattern or highest Gleason pattern Some HR <= 1.0 and some HR > 1.0

Table 11	cRFI		bRFI		bRFI	
	Highest Pattern		Primary Pattern		Highest Pattern	
Official Symbol	HR	p-value	HR	p-value	HR	p-value
HSPA5	0.710	0.009	1.288	0.030		
ODC1	0.741	0.026	1.343	0.004	1.261	0.046

[00145] Tables 12A and 12B provide genes that are significantly associated ($p<0.05$) with prostate cancer specific survival (PCSS) in the primary Gleason pattern. Increased expression of

genes in Table 12A is negatively associated with good prognosis, while increased expression of genes in Table 12B is positively associated with good prognosis.

Table 12A

Genes significantly (p<0.05) associated with prostate cancer specific survival (PCSS) in the Primary Gleason Pattern HR > 1.0 (Increased expression is negatively associated with good prognosis)

Table 12A Official Symbol	HR	p-value	Official Symbol	HR	p-value
AKR1C3	1.476	0.016	GREM1	1.942	<.001
ANLN	1.517	0.006	IFI30	1.482	0.048
APOC1	1.285	0.016	IGFBP3	1.513	0.027
APOE	1.490	0.024	INHBA	3.060	<.001
ASPN	3.055	<.001	KIF4A	1.355	0.001
ATP5E	1.788	0.012	KLK14	1.187	0.004
AURKB	1.439	0.008	LAPTM5	1.613	0.006
BGN	2.640	<.001	LTBP2	2.018	<.001
BIRC5	1.611	<.001	MMP11	1.869	<.001
BMP6	1.490	0.021	MYBL2	1.737	0.013
BRCA1	1.418	0.036	NEK2	1.445	0.028
CCNB1	1.497	0.021	NOX4	2.049	<.001
CD276	1.668	0.005	OLFML2B	1.497	0.023
CDC20	1.730	<.001	PLK1	1.603	0.006
CDH11	1.565	0.017	POSTN	2.585	<.001
CDH7	1.553	0.007	PPFIA3	1.502	0.012
CDKN2B	1.751	0.003	PTK6	1.527	0.009
CDKN2C	1.993	0.013	PTTG1	1.382	0.029
CDKN3	1.404	0.008	RAD51	1.304	0.031
CENPF	2.031	<.001	RGS7	1.251	<.001
CHAF1A	1.376	0.011	RRM2	1.515	<.001
CKS2	1.499	0.031	SAT1	1.607	0.004
COL1A1	2.574	<.001	SDC1	1.710	0.007
COL1A2	1.607	0.011	SESN3	1.399	0.045
COL3A1	2.382	<.001	SFRP4	2.384	<.001
COL4A1	1.970	<.001	SHMT2	1.949	0.003
COL5A2	1.938	0.002	SPARC	2.249	<.001
COL8A1	2.245	<.001	STMN1	1.748	0.021
CTHRC1	2.085	<.001	SULF1	1.803	0.004
CXCR4	1.783	0.007	THBS2	2.576	<.001
DDIT4	1.535	0.030	THY1	1.908	0.001
DYNLL1	1.719	0.001	TK1	1.394	0.004
F2R	2.169	<.001	TOP2A	2.119	<.001
FAM171B	1.430	0.044	TPX2	2.074	0.042
FAP	1.993	0.002	UBE2C	1.598	<.001

Table 12A Official Symbol	HR	p-value	Official Symbol	HR	p-value
FCGR3A	2.099	<.001	UGT2B15	1.363	0.016
FN1	1.537	0.024	UHRF1	1.642	0.001
GPR68	1.520	0.018	ZWINT	1.570	0.010

Table 12B

Genes significantly (p<0.05) associated with prostate cancer specific survival (PCSS) in the Primary Gleason Pattern HR < 1.0 (Increased expression is positively associated with good prognosis)

Table 12B Official Symbol	HR	p-value	Official Symbol	HR	p-value
AAMP	0.649	0.040	IGFBP6	0.578	0.003
ABCA5	0.777	0.015	IL2	0.528	0.010
ABCG2	0.715	0.037	IL6ST	0.574	<.001
ACOX2	0.673	0.016	IL8	0.540	0.001
ADH5	0.522	<.001	ING5	0.688	0.015
ALDH1A2	0.561	<.001	ITGA6	0.710	0.005
AMACR	0.693	0.029	ITGA7	0.676	0.033
AMPD3	0.750	0.049	JUN	0.506	0.001
ANPEP	0.531	<.001	KIT	0.628	0.047
ATXN1	0.640	0.011	KLK1	0.523	0.002
AXIN2	0.657	0.002	KLK2	0.581	<.001
AZGP1	0.617	<.001	KLK3	0.676	<.001
BDKRB1	0.553	0.032	KRT15	0.684	0.005
BIN1	0.658	<.001	KRT18	0.536	<.001
BTRC	0.716	0.011	KRT5	0.673	0.004
C7	0.531	<.001	KRT8	0.613	0.006
CADM1	0.646	0.015	LAMB3	0.740	0.027
CASP7	0.538	0.029	LGALS3	0.678	0.007
CCNH	0.674	0.001	MGST1	0.640	0.002
CD164	0.606	<.001	MPPED2	0.629	<.001
CD44	0.687	0.016	MTSS1	0.705	0.041
CDK3	0.733	0.039	MYBPC1	0.534	<.001
CHN1	0.653	0.014	NCAPD3	0.519	<.001
COL6A1	0.681	0.015	NFAT5	0.536	<.001
CSF1	0.675	0.019	NRG1	0.467	0.007
CSRP1	0.711	0.007	OLFML3	0.646	0.001
CXCL12	0.650	0.015	OMD	0.630	0.006
CYP3A5	0.507	<.001	OR51E2	0.762	0.017
CYR61	0.569	0.007	PAGE4	0.518	<.001
DLGAP1	0.654	0.004	PCA3	0.581	<.001
DNM3	0.692	0.010	PGF	0.705	0.038
DPP4	0.544	<.001	PPAP2B	0.568	<.001
DPT	0.543	<.001	PPP1R12A	0.694	0.017
DUSP1	0.660	0.050	PRIMA1	0.678	0.014

Table 12B Official Symbol	HR	p-value	Official Symbol	HR	p-value
DUSP6	0.699	0.033	PRKCA	0.632	0.001
EGR1	0.490	<.001	PRKCB	0.692	0.028
EGR3	0.561	<.001	PROM1	0.393	0.017
EIF5	0.720	0.035	PTEN	0.689	0.002
ERBB3	0.739	0.042	PTGS2	0.611	0.004
FAAH	0.636	0.010	PTH1R	0.629	0.031
FAM107A	0.541	<.001	RAB27A	0.721	0.046
FAM13C	0.526	<.001	RND3	0.678	0.029
FAS	0.689	0.030	RNF114	0.714	0.035
FGF10	0.657	0.024	SDHC	0.590	<.001
FKBP5	0.699	0.040	SERPINA3	0.710	0.050
FLNC	0.742	0.036	SH3RF2	0.570	0.005
FOS	0.556	0.005	SLC22A3	0.517	<.001
FOXQ1	0.666	0.007	SMAD4	0.528	<.001
GADD45B	0.554	0.002	SMO	0.751	0.026
GDF15	0.659	0.009	SRC	0.667	0.004
GHR	0.683	0.027	SRD5A2	0.488	<.001
GPM6B	0.666	0.005	STAT5B	0.700	0.040
GSN	0.646	0.006	SVIL	0.694	0.024
GSTM1	0.672	0.006	TFF3	0.701	0.045
GSTM2	0.514	<.001	TGFB1I1	0.670	0.029
HGD	0.771	0.039	TGFB2	0.646	0.010
HIRIP3	0.730	0.013	TNFRSF10B	0.685	0.014
HK1	0.778	0.048	TNFSF10	0.532	<.001
HLF	0.581	<.001	TPM2	0.623	0.005
HNF1B	0.643	0.013	TRO	0.767	0.049
HSD17B10	0.742	0.029	TUBB2A	0.613	0.003
IER3	0.717	0.049	VEGFB	0.780	0.034
IGF1	0.612	<.001	ZFP36	0.576	0.001
			ZNF827	0.644	0.014

[00146] Analysis of gene expression and upgrading/upstaging was based on univariate ordinal logistic regression models using weighted maximum likelihood estimators for each gene in the gene list (727 test genes and 5 reference genes). P-values were generated using a Wald test of the null hypothesis that the odds ratio (OR) is one. Both unadjusted p-values and the q-value (smallest FDR at which the hypothesis test in question is rejected) were reported. Un-adjusted p-values <0.05 were considered statistically significant. Since two tumor specimens were selected for each patient, this analysis was performed using the 2 specimens from each patient as follows: (1) analysis using the primary Gleason pattern specimen from each patient

(Specimens A1 and B2 as described in Table 2); and (2) analysis using the highest Gleason pattern specimen from each patient (Specimens A1 and B1 as described in Table 2). 200 genes were found to be significantly associated ($p<0.05$) with upgrading/upstaging in the primary Gleason pattern sample (PGP) and 203 genes were found to be significantly associated ($p<0.05$) with upgrading/upstaging in the highest Gleason pattern sample (HGP).

[00147] Tables 13A and 13B provide genes significantly associated ($p<0.05$), positively or negatively, with upgrading/upstaging in the primary and/or highest Gleason pattern. Increased expression of genes in Table 13A is positively associated with higher risk of upgrading/upstaging (poor prognosis), while increased expression of genes in Table 13B is negatively associated with risk of upgrading/upstaging (good prognosis).

TABLE 13A

Genes significantly ($p<0.05$) associated with upgrading/upstaging in the Primary Gleason Pattern (PGP) and Highest Gleason Pattern (HGP) OR > 1.0 (Increased expression is positively associated with higher risk of upgrading/upstaging (poor prognosis))

Table 13A	PGP		HGP	
Gene	OR	p-value	OR	p-value
ALCAM	1.52	0.0179	1.50	0.0184
ANLN	1.36	0.0451	.	.
APOE	1.42	0.0278	1.50	0.0140
ASPN	1.60	0.0027	2.06	0.0001
AURKA	1.47	0.0108	.	.
AURKB	.	.	1.52	0.0070
BAX	.	.	1.48	0.0095
BGN	1.58	0.0095	1.73	0.0034
BIRC5	1.38	0.0415	.	.
BMP6	1.51	0.0091	1.59	0.0071
BUB1	1.38	0.0471	1.59	0.0068
CACNA1D	1.36	0.0474	1.52	0.0078
CASP7	.	.	1.32	0.0450
CCNE2	1.54	0.0042	.	.
CD276	.	.	1.44	0.0265
CDC20	1.35	0.0445	1.39	0.0225
CDKN2B	.	.	1.36	0.0415
CENPF	1.43	0.0172	1.48	0.0102
CLTC	1.59	0.0031	1.57	0.0038

Table 13A	PGP		HGP	
Gene	OR	p-value	OR	p-value
COL1A1	1.58	0.0045	1.75	0.0008
COL3A1	1.45	0.0143	1.47	0.0131
COL8A1	1.40	0.0292	1.43	0.0258
CRISP3	.	.	1.40	0.0256
CTHRC1	.	.	1.56	0.0092
DBN1	1.43	0.0323	1.45	0.0163
DIAPH1	1.51	0.0088	1.58	0.0025
DICER1	.	.	1.40	0.0293
DIO2	.	.	1.49	0.0097
DVL1	.	.	1.53	0.0160
F2R	1.46	0.0346	1.63	0.0024
FAP	1.47	0.0136	1.74	0.0005
FCGR3A	.	.	1.42	0.0221
HPN	.	.	1.36	0.0468
HSD17B4	.	.	1.47	0.0151
HSPA8	1.65	0.0060	1.58	0.0074
IL11	1.50	0.0100	1.48	0.0113
IL1B	1.41	0.0359	.	.
INHBA	1.56	0.0064	1.71	0.0042
KHDRBS3	1.43	0.0219	1.59	0.0045
KIF4A	.	.	1.50	0.0209
KPNA2	1.40	0.0366	.	.
KRT2	.	.	1.37	0.0456
KRT75	.	.	1.44	0.0389
MANF	.	.	1.39	0.0429
MELK	1.74	0.0016	.	.
MKI67	1.35	0.0408	.	.
MMP11	.	.	1.56	0.0057
NOX4	1.49	0.0105	1.49	0.0138
PLAUR	1.44	0.0185	.	.
PLK1	.	.	1.41	0.0246
PTK6	.	.	1.36	0.0391
RAD51	.	.	1.39	0.0300
RAF1	.	.	1.58	0.0036
RRM2	1.57	0.0080	.	.
SESN3	1.33	0.0465	.	.
SFRP4	2.33	<0.0001	2.51	0.0015
SKIL	1.44	0.0288	1.40	0.0368
SOX4	1.50	0.0087	1.59	0.0022

Table 13A	PGP		HGP	
Gene	OR	p-value	OR	p-value
SPINK1	1.52	0.0058	.	.
SPP1	.	.	1.42	0.0224
THBS2	.	.	1.36	0.0461
TK1	.	.	1.38	0.0283
TOP2A	1.85	0.0001	1.66	0.0011
TPD52	1.78	0.0003	1.64	0.0041
TPX2	1.70	0.0010	.	.
UBE2G1	1.38	0.0491	.	.
UBE2T	1.37	0.0425	1.46	0.0162
UHRF1	.	.	1.43	0.0164
VCPIP1	.	.	1.37	0.0458

TABLE 13B

Genes significantly (p<0.05) associated with upgrading/upstaging in the Primary Gleason Pattern (PGP) and Highest Gleason Pattern (HGP) OR < 1.0 (Increased expression is negatively associated with higher risk of upgrading/upstaging (good prognosis))

Table 13B	PGP		HGP	
Gene	OR	p-value	OR	p-value
ABCC3	.	.	0.70	0.0216
ABCC8	0.66	0.0121	.	.
ABCG2	0.67	0.0208	0.61	0.0071
ACE	.	.	0.73	0.0442
ACOX2	0.46	0.0000	0.49	0.0001
ADH5	0.69	0.0284	0.59	0.0047
AIG1	.	.	0.60	0.0045
AKR1C1	.	.	0.66	0.0095
ALDH1A2	0.36	<0.0001	0.36	<0.0001
ALKBH3	0.70	0.0281	0.61	0.0056
ANPEP	.	.	0.68	0.0109
ANXA2	0.73	0.0411	0.66	0.0080
APC	.	.	0.68	0.0223
ATXN1	.	.	0.70	0.0188
AXIN2	0.60	0.0072	0.68	0.0204
AZGP1	0.66	0.0089	0.57	0.0028
BCL2	.	.	0.71	0.0182
BIN1	0.55	0.0005	.	.
BTRC	0.69	0.0397	0.70	0.0251
C7	0.53	0.0002	0.51	<0.0001

Table 13B	PGP		HGP	
Gene	OR	p-value	OR	p-value
CADM1	0.57	0.0012	0.60	0.0032
CASP1	0.64	0.0035	0.72	0.0210
CAV1	0.64	0.0097	0.59	0.0032
CAV2	.	.	0.58	0.0107
CD164	.	.	0.69	0.0260
CD82	0.67	0.0157	0.69	0.0167
CDH1	0.61	0.0012	0.70	0.0210
CDK14	0.70	0.0354	.	.
CDK3	.	.	0.72	0.0267
CDKN1C	0.61	0.0036	0.56	0.0003
CHN1	0.71	0.0214	.	.
COL6A1	0.62	0.0125	0.60	0.0050
COL6A3	0.65	0.0080	0.68	0.0181
CSRP1	0.43	0.0001	0.40	0.0002
CTSB	0.66	0.0042	0.67	0.0051
CTSD	0.64	0.0355	.	.
CTSK	0.69	0.0171	.	.
CTSL1	0.72	0.0402	.	.
CUL1	0.61	0.0024	0.70	0.0120
CXCL12	0.69	0.0287	0.63	0.0053
CYP3A5	0.68	0.0099	0.62	0.0026
DDR2	0.68	0.0324	0.62	0.0050
DES	0.54	0.0013	0.46	0.0002
DHX9	0.67	0.0164	.	.
DLGAP1	.	.	0.66	0.0086
DPP4	0.69	0.0438	0.69	0.0132
DPT	0.59	0.0034	0.51	0.0005
DUSP1	.	.	0.67	0.0214
EDN1	.	.	0.66	0.0073
EDNRA	0.66	0.0148	0.54	0.0005
EIF2C2	.	.	0.65	0.0087
ELK4	0.55	0.0003	0.58	0.0013
ENPP2	0.65	0.0128	0.59	0.0007
EPHA3	0.71	0.0397	0.73	0.0455
EPHB2	0.60	0.0014	.	.
EPHB4	0.73	0.0418	.	.
EPHX3	.	.	0.71	0.0419
ERCC1	0.71	0.0325	.	.
FAM107A	0.56	0.0008	0.55	0.0011

Table 13B	PGP		HGP	
Gene	OR	p-value	OR	p-value
FAM13C	0.68	0.0276	0.55	0.0001
FAS	0.72	0.0404	.	.
FBN1	0.72	0.0395	.	.
FBXW7	0.69	0.0417	.	.
FGF10	0.59	0.0024	0.51	0.0001
FGF7	0.51	0.0002	0.56	0.0007
FGFR2	0.54	0.0004	0.47	<0.0001
FLNA	0.58	0.0036	0.50	0.0002
FLNC	0.45	0.0001	0.40	<0.0001
FLT4	0.61	0.0045	.	.
FOXO1	0.55	0.0005	0.53	0.0005
FOXP3	0.71	0.0275	0.72	0.0354
GHR	0.59	0.0074	0.53	0.0001
GNRH1	0.72	0.0386	.	.
GPM6B	0.59	0.0024	0.52	0.0002
GSN	0.65	0.0107	0.65	0.0098
GSTM1	0.44	<0.0001	0.43	<0.0001
GSTM2	0.42	<0.0001	0.39	<0.0001
HLF	0.46	<0.0001	0.47	0.0001
HPS1	0.64	0.0069	0.69	0.0134
HSPA5	0.68	0.0113	.	.
HSPB2	0.61	0.0061	0.55	0.0004
HSPG2	0.70	0.0359	.	.
ID3	.	.	0.70	0.0245
IGF1	0.45	<0.0001	0.50	0.0005
IGF2	0.67	0.0200	0.68	0.0152
IGFBP2	0.59	0.0017	0.69	0.0250
IGFBP6	0.49	<0.0001	0.64	0.0092
IL6ST	0.56	0.0009	0.60	0.0012
ILK	0.51	0.0010	0.49	0.0004
ITGA1	0.58	0.0020	0.58	0.0016
ITGA3	0.71	0.0286	0.70	0.0221
ITGA5	.	.	0.69	0.0183
ITGA7	0.56	0.0035	0.42	<0.0001
ITGB1	0.63	0.0095	0.68	0.0267
ITGB3	0.62	0.0043	0.62	0.0040
ITPR1	0.62	0.0032	.	.
JUN	0.73	0.0490	0.68	0.0152
KIT	0.55	0.0003	0.57	0.0005

Table 13B	PGP		HGP	
Gene	OR	p-value	OR	p-value
KLC1	.	.	0.70	0.0248
KLK1	.	.	0.60	0.0059
KRT15	0.58	0.0009	0.45	<0.0001
KRT5	0.70	0.0262	0.59	0.0008
LAMA4	0.56	0.0359	0.68	0.0498
LAMB3	.	.	0.60	0.0017
LGALS3	0.58	0.0007	0.56	0.0012
LRP1	0.69	0.0176	.	.
MAP3K7	0.70	0.0233	0.73	0.0392
MCM3	0.72	0.0320	.	.
MMP2	0.66	0.0045	0.60	0.0009
MMP7	0.61	0.0015	0.65	0.0032
MMP9	0.64	0.0057	0.72	0.0399
MPPED2	0.72	0.0392	0.63	0.0042
MTA1	.	.	0.68	0.0095
MTSS1	0.58	0.0007	0.71	0.0442
MVP	0.57	0.0003	0.70	0.0152
MYBPC1	.	.	0.70	0.0359
NCAM1	0.63	0.0104	0.64	0.0080
NCAPD3	0.67	0.0145	0.64	0.0128
NEXN	0.54	0.0004	0.55	0.0003
NFAT5	0.72	0.0320	0.70	0.0177
NUDT6	0.66	0.0102	.	.
OLFML3	0.56	0.0035	0.51	0.0011
OMD	0.61	0.0011	0.73	0.0357
PAGE4	0.42	<0.0001	0.36	<0.0001
PAK6	0.72	0.0335	.	.
PCDHGB7	0.70	0.0262	0.55	0.0004
PGF	0.72	0.0358	0.71	0.0270
PLP2	0.66	0.0088	0.63	0.0041
PPAP2B	0.44	<0.0001	0.50	0.0001
PPP1R12A	0.45	0.0001	0.40	<0.0001
PRIMA1	.	.	0.63	0.0102
PRKAR2B	0.71	0.0226	.	.
PRKCA	0.34	<0.0001	0.42	<0.0001
PRKCB	0.66	0.0120	0.49	<0.0001
PROM1	0.61	0.0030	.	.
PTEN	0.59	0.0008	0.55	0.0001
PTGER3	0.67	0.0293	.	.

Table 13B	PGP		HGP	
Gene	OR	p-value	OR	p-value
PTH1R	0.69	0.0259	0.71	0.0327
PTK2	0.75	0.0461	.	.
PTK2B	0.70	0.0244	0.74	0.0388
PYCARD	0.73	0.0339	0.67	0.0100
RAD9A	0.64	0.0124	.	.
RARB	0.67	0.0088	0.65	0.0116
RGS10	0.70	0.0219	.	.
RHOB	.	.	0.72	0.0475
RND3	.	.	0.67	0.0231
SDHC	0.72	0.0443	.	.
SEC23A	0.66	0.0101	0.53	0.0003
SEMA3A	0.51	0.0001	0.69	0.0222
SH3RF2	0.55	0.0002	0.54	0.0002
SLC22A3	0.48	0.0001	0.50	0.0058
SMAD4	0.49	0.0001	0.50	0.0003
SMARCC2	0.59	0.0028	0.65	0.0052
SMO	0.60	0.0048	0.52	<0.0001
SORBS1	0.56	0.0024	0.48	0.0002
SPARCL1	0.43	0.0001	0.50	0.0001
SRD5A2	0.26	<0.0001	0.31	<0.0001
ST5	0.63	0.0103	0.52	0.0006
STAT5A	0.60	0.0015	0.61	0.0037
STAT5B	0.54	0.0005	0.57	0.0008
SUMO1	0.65	0.0066	0.66	0.0320
SVIL	0.52	0.0067	0.46	0.0003
TGFB1I1	0.44	0.0001	0.43	0.0000
TGFB2	0.55	0.0007	0.58	0.0016
TGFB3	0.57	0.0010	0.53	0.0005
TIMP1	0.72	0.0224	.	.
TIMP2	0.68	0.0198	0.69	0.0206
TIMP3	0.67	0.0105	0.64	0.0065
TMPRSS2	.	.	0.72	0.0366
TNFRSF10A	0.71	0.0181	.	.
TNFSF10	0.71	0.0284	.	.
TOP2B	0.73	0.0432	.	.
TP63	0.62	0.0014	0.50	<0.0001
TPM1	0.54	0.0007	0.52	0.0002
TPM2	0.41	<0.0001	0.40	<0.0001
TPP2	0.65	0.0122	.	.

Table 13B	PGP		HGP	
Gene	OR	p-value	OR	p-value
TRA2A	0.72	0.0318	.	.
TRAF3IP2	0.62	0.0064	0.59	0.0053
TRO	0.57	0.0003	0.51	0.0001
VCL	0.52	0.0005	0.52	0.0004
VIM	0.65	0.0072	0.65	0.0045
WDR19	0.66	0.0097	.	.
WFDC1	0.58	0.0023	0.60	0.0026
ZFHX3	0.69	0.0144	0.62	0.0046
ZNF827	0.62	0.0030	0.53	0.0001

EXAMPLE 3: IDENTIFICATION OF MICRORNAS ASSOCIATED WITH CLINICAL RECURRENCE AND DEATH DUE TO PROSTATE CANCER

[00148] MicroRNAs function by binding to portions of messenger RNA (mRNA) and changing how frequently the mRNA is translated into protein. They can also influence the turnover of mRNA and thus how long the mRNA remains intact in the cell. Since microRNAs function primarily as an adjunct to mRNA, this study evaluated the joint prognostic value of microRNA expression and gene (mRNA) expression. Since the expression of certain microRNAs may be a surrogate for expression of genes that are not in the assessed panel, we also evaluated the prognostic value of microRNA expression by itself.

Patients and Samples

[00149] Samples from the 127 patients with clinical recurrence and 374 patients without clinical recurrence after radical prostatectomy described in Example 2 were used in this study. The final analysis set comprised 416 samples from patients in which both gene expression and microRNA expression were successfully assayed. Of these, 106 patients exhibited clinical recurrence and 310 did not have clinical recurrence. Tissue samples were taken from each prostate sample representing (1) the primary Gleason pattern in the sample, and (2) the highest Gleason pattern in the sample. In addition, a sample of histologically normal-appearing tissue adjacent to the tumor (NAT) was taken. The number of patients in the analysis set for each tissue type and the number of them who experienced clinical recurrence or death due to prostate cancer are shown in Table 14.

Table 14. Number of Patients and Events in Analysis Set

	Patients	Clinical Recurrences	Deaths Due to Prostate Cancer
Primary Gleason Pattern Tumor Tissue	416	106	36
Highest Gleason Pattern Tumor Tissue	405	102	36
Normal Adjacent Tissue	364	81	29

Assay Method

[00150] Expression of 76 test microRNAs and 5 reference microRNAs were determined from RNA extracted from fixed paraffin-embedded (FPE) tissue. MicroRNA expression in all three tissue type was quantified by reverse transcriptase polymerase chain reaction (RT-PCR) using the crossing point (C_p) obtained from the Taqman® MicroRNA Assay kit (Applied Biosystems, Inc., Carlsbad, CA).

Statistical Analysis

[00151] Using univariate proportional hazards regression (Cox DR, Journal of the Royal Statistical Society, Series B 34:187-220, 1972), applying the sampling weights from the cohort sampling design, and using variance estimation based on the Lin and Wei method (Lin and Wei, Journal of the American Statistical Association 84:1074-1078, 1989), microRNA expression, normalized by the average expression for the 5 reference microRNAs hsa-miR-106a, hsa-miR-146b-5p, hsa-miR-191, hsa-miR-19b, and hsa-miR-92a, and reference-normalized gene expression of the 733 genes (including the reference genes) discussed above, were assessed for association with clinical recurrence and death due to prostate cancer. Standardized hazard ratios (the proportional change in the hazard associated with a change of one standard deviation in the covariate value) were calculated.

[00152] This analysis included the following classes of predictors:

[00153] 1. MicroRNAs alone

[00154] 2. MicroRNA-gene pairs Tier 1

[00155] 3. MicroRNA-gene pairs Tier 2

[00156] 4. MicroRNA-gene pairs Tier 3

[00157] 5. All other microRNA-gene pairs Tier 4

[00158] The four tiers were pre-determined based on the likelihood (Tier 1 representing the highest likelihood) that the gene-microRNA pair functionally interacted or that the microRNA was related to prostate cancer based on a review of the literature and existing microarray data sets.

[00159] False discovery rates (FDR) (Benjamini and Hochberg, Journal of the Royal Statistical Society, Series B 57:289-300, 1995) were assessed using Efron's separate class methodology (Efron, Annals of Applied Statistics 2:197-223., 2008). The false discovery rate is the expected proportion of the rejected null hypotheses that are rejected incorrectly (and thus are false discoveries). Efron's methodology allows separate FDR assessment (q-values) (Storey, Journal of the Royal Statistical Society, Series B 64:479-498, 2002) within each class while utilizing the data from all the classes to improve the accuracy of the calculation. In this analysis, the q-value for a microRNA or microRNA-gene pair can be interpreted as the empirical Bayes probability that the microRNA or microRNA-gene pair identified as being associated with clinical outcome is in fact a false discovery given the data. The separate class approach was applied to a true discovery rate degree of association (TDRDA) analysis (Crager, Statistics in Medicine 29:33-45, 2010) to determine sets of microRNAs or microRNA-gene pairs that have standardized hazard ratio for clinical recurrence or prostate cancer-specific death of at least a specified amount while controlling the FDR at 10%. For each microRNA or microRNA-gene pair, a maximum lower bound (MLB) standardized hazard ratio was computed, showing the highest lower bound for which the microRNA or microRNA-gene pair was included in a TDRDA set with 10% FDR. Also calculated was an estimate of the true standardized hazard ratio corrected for regression to the mean (RM) that occurs in subsequent studies when the best predictors are selected from a long list (Crager, 2010 above). The RM-corrected estimate of the standardized hazard ratio is a reasonable estimate of what could be expected if the selected microRNA or microRNA-gene pair were studied in a separate, subsequent study.

[00160] These analyses were repeated adjusting for clinical and pathology covariates available at the time of patient biopsy: biopsy Gleason score, baseline PSA level, and clinical T-

stage (T1–T2A *vs.* T2B or T2C) to assess whether the microRNAs or microRNA-gene pairs have predictive value independent of these clinical and pathology covariates.

Results

[00161] The analysis identified 21 microRNAs assayed from primary Gleason pattern tumor tissue that were associated with clinical recurrence of prostate cancer after radical prostatectomy, allowing a false discovery rate of 10% (Table 15). Results were similar for microRNAs assessed from highest Gleason pattern tumor tissue (Table 16), suggesting that the association of microRNA expression with clinical recurrence does not change markedly depending on the location within a tumor tissue sample. No microRNA assayed from normal adjacent tissue was associated with the risk of clinical recurrence at a false discovery rate of 10%. The sequences of the microRNAs listed in Tables 15-21 are shown in Table B.

Table 15. MicroRNAs Associated with Clinical Recurrence of Prostate Cancer Primary Gleason Pattern Tumor Tissue

				Absolute Standardized Hazard Ratio			
MicroRNA	*p*-value	*q*-value[a] (FDR)	Direction of Association[b]	Uncorrected Estimate	95% Confidence Interval	Max. Lower Bound @10% FDR	RM-Corrected Estimate[c]
hsa-miR-93	<0.0001	0.0%	(+)	1.79	(1.38, 2.32)	1.19	1.51
hsa-miR-106b	<0.0001	0.1%	(+)	1.80	(1.38, 2.34)	1.19	1.51
hsa-miR-30e-5p	<0.0001	0.1%	(-)	1.63	(1.30, 2.04)	1.18	1.46
hsa-miR-21	<0.0001	0.1%	(+)	1.66	(1.31, 2.09)	1.18	1.46
hsa-miR-133a	<0.0001	0.1%	(-)	1.72	(1.33, 2.21)	1.18	1.48
hsa-miR-449a	<0.0001	0.1%	(+)	1.56	(1.26, 1.92)	1.17	1.42
hsa-miR-30a	0.0001	0.1%	(-)	1.56	(1.25, 1.94)	1.16	1.41
hsa-miR-182	0.0001	0.2%	(+)	1.74	(1.31, 2.31)	1.17	1.45
hsa-miR-27a	0.0002	0.2%	(+)	1.65	(1.27, 2.14)	1.16	1.43
hsa-miR-222	0.0006	0.5%	(-)	1.47	(1.18, 1.84)	1.12	1.35
hsa-miR-103	0.0036	2.1%	(+)	1.77	(1.21, 2.61)	1.12	1.36
hsa-miR-1	0.0037	2.2%	(-)	1.32	(1.10, 1.60)	1.07	1.26
hsa-miR-145	0.0053	2.9%	(-)	1.34	(1.09, 1.65)	1.07	1.27
hsa-miR-141	0.0060	3.2%	(+)	1.43	(1.11, 1.84)	1.07	1.29
hsa-miR-92a	0.0104	4.8%	(+)	1.32	(1.07, 1.64)	1.05	1.25
hsa-miR-22	0.0204	7.7%	(+)	1.31	(1.03, 1.64)	1.03	1.23
hsa-miR-29b	0.0212	7.9%	(+)	1.36	(1.03, 1.76)	1.03	1.24
hsa-miR-210	0.0223	8.2%	(+)	1.33	(1.03, 1.70)	1.00	1.23
hsa-miR-486-5p	0.0267	9.4%	(-)	1.25	(1.00, 1.53)	1.00	1.20
hsa-miR-19b	0.0280	9.7%	(-)	1.24	(1.00, 1.50)	1.00	1.19
hsa-miR-205	0.0289	10.0%	(-)	1.25	(1.00, 1.53)	1.00	1.20

[a]The *q*-value is the empirical Bayes probability that the microRNA's association with clinical recurrence is a false discovery, given the data.
[b]Direction of association indicates where higher microRNA expression is associated with higher (+) or lower (-) risk of clinical recurrence.
[c]RM: regression to the mean.

Table 16. MicroRNAs Associated with Clinical Recurrence of Prostate Cancer Highest Gleason Pattern Tumor Tissue

				Absolute Standardized Hazard Ratio			
MicroRNA	*p*-value	*q*-value[a] (FDR)	Direction of Association[b]	Uncorrected Estimate	95% Confidence Interval	Max. Lower Bound @10% FDR	RM-Corrected Estimate[c]
hsa-miR-93	<0.0001	0.0%	(+)	1.91	(1.48, 2.47)	1.24	1.59
hsa-miR-449a	<0.0001	0.0%	(+)	1.75	(1.40, 2.18)	1.23	1.54
hsa-miR-205	<0.0001	0.0%	(-)	1.53	(1.29, 1.81)	1.20	1.43
hsa-miR-19b	<0.0001	0.0%	(-)	1.37	(1.19, 1.57)	1.15	1.32
hsa-miR-106b	<0.0001	0.0%	(+)	1.84	(1.39, 2.42)	1.22	1.51
hsa-miR-21	<0.0001	0.0%	(+)	1.68	(1.32, 2.15)	1.19	1.46
hsa-miR-30a	0.0005	0.4%	(-)	1.44	(1.17, 1.76)	1.13	1.33
hsa-miR-30e-5p	0.0010	0.6%	(-)	1.37	(1.14, 1.66)	1.11	1.30
hsa-miR-133a	0.0015	0.8%	(-)	1.57	(1.19, 2.07)	1.13	1.36
hsa-miR-1	0.0016	0.8%	(-)	1.42	(1.14, 1.77)	1.11	1.31
hsa-miR-103	0.0021	1.1%	(+)	1.69	(1.21, 2.37)	1.13	1.37
hsa-miR-210	0.0024	1.2%	(+)	1.43	(1.13, 1.79)	1.11	1.31
hsa-miR-182	0.0040	1.7%	(+)	1.48	(1.13, 1.93)	1.11	1.31
hsa-miR-27a	0.0055	2.1%	(+)	1.46	(1.12, 1.91)	1.09	1.30
hsa-miR-222	0.0093	3.2%	(-)	1.38	(1.08, 1.77)	1.08	1.27
hsa-miR-331	0.0126	3.9%	(+)	1.38	(1.07, 1.77)	1.07	1.26
hsa-miR-191*	0.0143	4.3%	(+)	1.38	(1.06, 1.78)	1.07	1.26
hsa-miR-425	0.0151	4.5%	(+)	1.40	(1.06, 1.83)	1.07	1.26
hsa-miR-31	0.0176	5.1%	(-)	1.29	(1.04, 1.60)	1.05	1.22
hsa-miR-92a	0.0202	5.6%	(+)	1.31	(1.03, 1.65)	1.05	1.23
hsa-miR-155	0.0302	7.6%	(-)	1.32	(1.00, 1.69)	1.03	1.22
hsa-miR-22	0.0437	9.9%	(+)	1.30	(1.00, 1.67)	1.00	1.21

[a]The *q*-value is the empirical Bayes probability that the microRNA's association with death due to prostate cancer is a false discovery, given the data.
[b]Direction of association indicates where higher microRNA expression is associated with higher (+) or lower (-) risk of clinical recurrence.
[c]RM: regression to the mean.

[00162] Table 17 shows microRNAs assayed from primary Gleason pattern tissue that were identified as being associated with the risk of prostate-cancer-specific death, with a false discovery rate of 10%. Table 18 shows the corresponding analysis for microRNAs assayed from highest Gleason pattern tissue. No microRNA assayed from normal adjacent tissue was associated with the risk of prostate-cancer-specific death at a false discovery rate of 10%.

Table 17. MicroRNAs Associated with Death Due to Prostate Cancer Primary Gleason Pattern Tumor Tissue

				Absolute Standardized Hazard Ratio			
MicroRNA	*p*-value	*q*-value[a] (FDR)	Direction of Association[b]	Uncorrected Estimate	95% Confidence Interval	Max. Lower Bound @10% FDR	RM-Corrected Estimate[c]
hsa-miR-30e-5p	0.0001	0.6%	(-)	1.88	(1.37, 2.58)	1.15	1.46
hsa-miR-30a	0.0001	0.7%	(-)	1.78	(1.33, 2.40)	1.14	1.44
hsa-miR-133a	0.0005	1.2%	(-)	1.85	(1.31, 2.62)	1.13	1.41
hsa-miR-222	0.0006	1.4%	(-)	1.65	(1.24, 2.20)	1.12	1.38
hsa-miR-106b	0.0024	2.7%	(+)	1.85	(1.24, 2.75)	1.11	1.35
hsa-miR-1	0.0028	3.0%	(-)	1.43	(1.13, 1.81)	1.08	1.30
hsa-miR-21	0.0034	3.3%	(+)	1.63	(1.17, 2.25)	1.09	1.33
hsa-miR-93	0.0044	3.9%	(+)	1.87	(1.21, 2.87)	1.09	1.32
hsa-miR-26a	0.0072	5.3%	(-)	1.47	(1.11, 1.94)	1.07	1.29
hsa-miR-152	0.0090	6.0%	(-)	1.46	(1.10, 1.95)	1.06	1.28
hsa-miR-331	0.0105	6.5%	(+)	1.46	(1.09, 1.96)	1.05	1.27
hsa-miR-150	0.0159	8.3%	(+)	1.51	(1.07, 2.10)	1.03	1.27
hsa-miR-27b	0.0160	8.3%	(+)	1.97	(1.12, 3.42)	1.05	1.25

[a]The *q*-value is the empirical Bayes probability that the microRNA's association with death due to prostate cancer endpoint is a false discovery, given the data.
[b]Direction of association indicates where higher microRNA expression is associated with higher (+) or lower (-) risk of death due to prostate cancer.
[c]RM: regression to the mean.

Table 18. MicroRNAs Associated with Death Due to Prostate Cancer Highest Gleason Pattern Tumor Tissue

				Absolute Standardized Hazard Ratio			
MicroRNA	*p*-value	*q*-value[a] (FDR)	Direction of Association[b]	Uncorrected Estimate	95% Confidence Interval	Max. Lower Bound @10% FDR	RM-Corrected Estimate[c]
hsa-miR-27b	0.0016	6.1%	(+)	2.66	(1.45, 4.88)	1.07	1.32
hsa-miR-21	0.0020	6.4%	(+)	1.66	(1.21, 2.30)	1.05	1.34
hsa-miR-10a	0.0024	6.7%	(+)	1.78	(1.23, 2.59)	1.05	1.34
hsa-miR-93	0.0024	6.7%	(+)	1.83	(1.24, 2.71)	1.05	1.34
hsa-miR-106b	0.0028	6.8%	(+)	1.79	(1.22, 2.63)	1.05	1.33
hsa-miR-150	0.0035	7.1%	(+)	1.61	(1.17, 2.22)	1.05	1.32
hsa-miR-1	0.0104	9.0%	(-)	1.52	(1.10, 2.09)	1.00	1.28

[a]The *q*-value is the empirical Bayes probability that the microRNA's association with clinical endpoint is a false discovery, given the data.
[b]Direction of association indicates where higher microRNA expression is associated with higher (+) or lower (-) risk of death due to prostate cancer.
[c]RM: regression to the mean.

[00163] Table 19 and Table 20 shows the microRNAs that can be identified as being associated with the risk of clinical recurrence while adjusting for the clinical and pathology covariates of biopsy Gleason score, baseline PSA level, and clinical T-stage. The distributions of these covariates are shown in Figure 1. Fifteen (15) of the microRNAs identified in Table 15 are also present in Table 19, indicating that these microRNAs have predictive value for clinical recurrence that is independent of the Gleason score, baseline PSA, and clinical T-stage.

[00164] Two microRNAs assayed from primary Gleason pattern tumor tissue were found that had predictive value for death due to prostate cancer independent of Gleason score, baseline PSA, and clinical T-stage (Table 21).

Table 19. MicroRNAs Associated with Clinical Recurrence of Prostate Cancer Adjusting for Biopsy Gleason Score, Baseline PSA Level, and Clinical T-Stage Primary Gleason Pattern Tumor Tissue

				Absolute Standardized Hazard Ratio			
MicroRNA	*p*-value	*q*-value[a] (FDR)	Direction of Association[b]	Uncorrected Estimate	95% Confidence Interval	Max. Lower Bound @10% FDR	RM-Corrected Estimate[c]
hsa-miR-30e-5p	<0.0001	0.0%	(-)	1.80	(1.42, 2.27)	1.23	1.53
hsa-miR-30a	<0.0001	0.0%	(-)	1.75	(1.40, 2.19)	1.22	1.51
hsa-miR-93	<0.0001	0.1%	(+)	1.70	(1.32, 2.20)	1.19	1.44
hsa-miR-449a	0.0001	0.1%	(+)	1.54	(1.25, 1.91)	1.17	1.39
hsa-miR-133a	0.0001	0.1%	(-)	1.58	(1.25, 2.00)	1.17	1.39
hsa-miR-27a	0.0002	0.1%	(+)	1.66	(1.28, 2.16)	1.17	1.41
hsa-miR-21	0.0003	0.2%	(+)	1.58	(1.23, 2.02)	1.16	1.38
hsa-miR-182	0.0005	0.3%	(+)	1.56	(1.22, 1.99)	1.15	1.37
hsa-miR-106b	0.0008	0.5%	(+)	1.57	(1.21, 2.05)	1.15	1.36
hsa-miR-222	0.0028	1.1%	(-)	1.39	(1.12, 1.73)	1.11	1.28
hsa-miR-103	0.0048	1.7%	(+)	1.69	(1.17, 2.43)	1.13	1.32
hsa-miR-486-5p	0.0059	2.0%	(-)	1.34	(1.09, 1.65)	1.09	1.25
hsa-miR-1	0.0083	2.7%	(-)	1.29	(1.07, 1.57)	1.07	1.23
hsa-miR-141	0.0088	2.8%	(+)	1.43	(1.09, 1.87)	1.09	1.27
hsa-miR-200c	0.0116	3.4%	(+)	1.39	(1.07, 1.79)	1.07	1.25
hsa-miR-145	0.0201	5.1%	(-)	1.27	(1.03, 1.55)	1.05	1.20
hsa-miR-206	0.0329	7.2%	(-)	1.40	(1.00, 1.91)	1.05	1.23
hsa-miR-29b	0.0476	9.4%	(+)	1.30	(1.00, 1.69)	1.00	1.20

[a]The *q*-value is the empirical Bayes probability that the microRNA's association with clinical recurrence is a false discovery, given the data.
[b]Direction of association indicates where higher microRNA expression is associated with higher (+) or lower (-) risk of clinical recurrence.
[c]RM: regression to the mean.

Table 20. MicroRNAs Associated with Clinical Recurrence of Prostate Cancer Adjusting for Biopsy Gleason Score, Baseline PSA Level, and Clinical T-Stage Highest Gleason Pattern Tumor Tissue

				Absolute Standardized Hazard Ratio			
MicroRNA	*p*-value	*q*-value[a] (FDR)	Direction of Association[b]	Uncorrected Estimate	95% Confidence Interval	Max. Lower Bound @10% FDR	RM-Corrected Estimate[c]
hsa-miR-30a	<0.0001	0.0%	(-)	1.62	(1.32, 1.99)	1.20	1.43
hsa-miR-30e-5p	<0.0001	0.0%	(-)	1.53	(1.27, 1.85)	1.19	1.39
hsa-miR-93	<0.0001	0.0%	(+)	1.76	(1.37, 2.26)	1.20	1.45
hsa-miR-205	<0.0001	0.0%	(-)	1.47	(1.23, 1.74)	1.18	1.36
hsa-miR-449a	0.0001	0.1%	(+)	1.62	(1.27, 2.07)	1.18	1.38
hsa-miR-106b	0.0003	0.2%	(+)	1.65	(1.26, 2.16)	1.17	1.36
hsa-miR-133a	0.0005	0.2%	(-)	1.51	(1.20, 1.90)	1.16	1.33
hsa-miR-1	0.0007	0.3%	(-)	1.38	(1.15, 1.67)	1.13	1.28
hsa-miR-210	0.0045	1.2%	(+)	1.35	(1.10, 1.67)	1.11	1.25
hsa-miR-182	0.0052	1.3%	(+)	1.40	(1.10, 1.77)	1.11	1.26
hsa-miR-425	0.0066	1.6%	(+)	1.48	(1.12, 1.96)	1.12	1.26
hsa-miR-155	0.0073	1.8%	(-)	1.36	(1.09, 1.70)	1.10	1.24
hsa-miR-21	0.0091	2.1%	(+)	1.42	(1.09, 1.84)	1.10	1.25
hsa-miR-222	0.0125	2.7%	(-)	1.34	(1.06, 1.69)	1.09	1.23
hsa-miR-27a	0.0132	2.8%	(+)	1.40	(1.07, 1.84)	1.09	1.23
hsa-miR-191*	0.0150	3.0%	(+)	1.37	(1.06, 1.76)	1.09	1.23
hsa-miR-103	0.0180	3.4%	(+)	1.45	(1.06, 1.98)	1.09	1.23
hsa-miR-31	0.0252	4.3%	(-)	1.27	(1.00, 1.57)	1.07	1.19
hsa-miR-19b	0.0266	4.5%	(-)	1.29	(1.00, 1.63)	1.07	1.20
hsa-miR-99a	0.0310	5.0%	(-)	1.26	(1.00, 1.56)	1.06	1.18
hsa-miR-92a	0.0348	5.4%	(+)	1.31	(1.00, 1.69)	1.06	1.19
hsa-miR-146b-5p	0.0386	5.8%	(-)	1.29	(1.00, 1.65)	1.06	1.19
hsa-miR-145	0.0787	9.7%	(-)	1.23	(1.00, 1.55)	1.00	1.15

[a]The *q*-value is the empirical Bayes probability that the microRNA's association with clinical clinical recurrence is a false discovery, given the data.
[b]Direction of association indicates where higher microRNA expression is associated with higher (+) or lower (-) risk of clinical recurrence. [c]RM: regression to the mean.

Table 21. MicroRNAs Associated with Death Due to Prostate Cancer Adjusting for Biopsy Gleason Score, Baseline PSA Level, and Clinical T-Stage Primary Gleason Pattern Tumor Tissue

				Absolute Standardized Hazard Ratio			
MicroRNA	*p*-value	*q*-value[a] (FDR)	Direction of Association[b]	Uncorrected Estimate	95% Confidence Interval	Max. Lower Bound @10% FDR	RM-Corrected Estimate[c]
hsa-miR-30e-5p	0.0001	2.9%	(-)	1.97	(1.40, 2.78)	1.09	1.39
hsa-miR-30a	0.0002	3.3%	(-)	1.90	(1.36, 2.65)	1.08	1.38

[a]The *q*-value is the empirical Bayes probability that the microRNA's association with clinical recurrence is a false discovery, given the data.
[b]Direction of association indicates where higher microRNA expression is associated with higher (+) or lower (-) risk of clinical recurrence.
[c]RM: regression to the mean.

[00165] Accordingly, the normalized expression levels of hsa-miR-93; hsa-miR-106b; hsa-miR-21; hsa-miR-449a; hsa-miR-182; hsa-miR-27a; hsa-miR-103; hsa-miR-141; hsa-miR-92a; hsa-miR-22; hsa-miR-29b; hsa-miR-210; hsa-miR-331; hsa-miR-191; hsa-miR-425; and hsa-miR-200c are positively associated with an increased risk of recurrence; and hsa-miR-30e-5p; hsa-miR-133a; hsa-miR-30a; hsa-miR-222; hsa-miR-1; hsa-miR-145; hsa-miR-486-5p; hsa-miR-19b; hsa-miR-205; hsa-miR-31; hsa-miR-155; hsa-miR-206; hsa-miR-99a; and hsa-miR-146b-5p are negatively associated with an increased risk of recurrence.

[00166] Furthermore, the normalized expression levels of hsa-miR-106b; hsa-miR-21; hsa-miR-93; hsa-miR-331; hsa-miR-150; hsa-miR-27b; and hsa-miR-10a are positively associated with an increased risk of prostate cancer specific death; and the normalized expression levels of hsa-miR-30e-5p; hsa-miR-30a; hsa-miR-133a; hsa-miR-222; hsa-miR-1; hsa-miR-26a; and hsa-miR-152 are negatively associated with an increased risk of prostate cancer specific death.

[00167] Table 22 shows the number of microRNA-gene pairs that were grouped in each tier (Tiers 1-4) and the number and percentage of those that were predictive of clinical recurrence at a false discovery rate of 10%.

Table 22.

Tier	Total Number of MicroRNA-Gene Pairs	Number of Pairs Predictive of Clinical Recurrence at False Discovery Rate 10% (%)
Tier 1	80	46 (57.5%)
Tier 2	719	591 (82.2%)
Tier 3	3,850	2,792 (72.5%)
Tier 4	54,724	38,264 (69.9%)

[00168] This description contains a sequence listing in electronic form in ASCII text format. A copy of the sequence listing in electronic form is available from the Canadian Intellectual Property Office.

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
AAMP	NM_001087	1	GTGTGGCAGGTGG ACACTAA	2	CTCCATCCACTCCAG GTCTC	3	CGCTTCAAAGGACCAGACCT CCTC	4	GTGTGGCAGGTGGACACTAAGGAGGAGGTCTGGTCC TTTGAAGCGGGAGACCTGGAGTGGAG
ABCA5	NM_172232	5	GGTATGGATCCCCA AAGCCA	6	CAGCCCGCTTTCTGTT TTTA	7	CACATGTGGCGAGCAATTCG AACT	8	GGTATGGATCCCCAAAGCCAAACACAGCACATGTGGCGA GCAATTCGAACTGCATTTAAAAACAGAAAGCGGGCT
ABCB1	NM_000927	9	AAACACCACTGGA GCATTGA	10	CAAGCCTGGAACCTA TAGCC	11	CAAGCCTGGAGCATTGACTACCAGGCTCGCCAA	12	AAACACCACTGGAGCATTGACTACCAGGCTCGCCAA TGATGCTGCTCAAGTTAAAGGGGCTATAGGTTCCAG
ABCC1	NM_004996	13	TCATGGTGCCCGT CAATG	14	CGATTGTCTTTGCTCT TCATGTG	15	ACCTGATACGTCTTGGTCTT CATCGCCAT	16	TCATGGTGCCCGTCAATGCTGTGATGGCGATGAAGA CCAAGACGTATCAGGTGGCCCACATGAAGAGCAAAG
ABCC3	NM_003786	17	TCATCCTGGCGAT CTACTTCCT	18	CCGTTGAGTGGAATC AGCAA	19	TCTGTCCTGGCTGGAGTCGC TTTCAT	20	TCATCCTGGCGATCTACTTCCTCTGGCAGAACCTAGG TCCCTCTGTCCTGGCTGGAGTCGCTTTCATGGTCTTG CTGATTCCACTCAACGG
ABCC4	NM_005845	21	AGCGCCTGGAATC TACAACT	22	AGAGCCCCTGGAGAG AAGAT	23	CGGAGTCCAGTGTTTTCCCA CTTA	24	AGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTC CCACTTATCATCTTCTCTCCAGGGGCTCT
ABCC8	NM_000352	25	CGTCTGTCACTGT GGAGTGG	26	TGATCCGGTTTAGCA GGC	27	AGTCTCTTGGCCACCTTCAG CCCT	28	CGTCTGTCACTGTGGAGTGGACAGGGCTGAAGGTGG CCAAGAGACTGCACCGCAGCCTGCTAAACCGGATCA
ABCG2	NM_004827	29	GGTCTCAACGCCA TCCTG	30	CTTGGATCTTTCCTTG CAGC	31	ACGAAGATTTGCCTCCACCT GTGG	32	GGTCTCAACGCCATCCTGGGACCCAGGTGGAGGC AAATCTTCGTTATTAGATGTCTTAGCTGCAAGGAAAG
ABHD2	NM_007011	33	GTAGTGGGTCTGC ATGGAATGT	34	TGAGGGTTGGCACTC AGG	35	CAGGTGGCTCCTTTGATCCC TGA	36	GTAGTGGGTCTGCATGGATGTTTCAGGGATCAAAGG AGCCACCTGGGCGCCTGAGTGCCAACCCTCA
ACE	NM_000789	37	CCGCTGTACGAGG ATTTCA	38	CCGTGTCTGTGAAGC CGT	39	TGCCCTCAGCAATGAAGCCT ACAA	40	CCGCTGTACGAGGATTTCACTGCCCTCAGCAATGAA GCCTACAAGCAGGACGGCTTCACAGACACGG
ACOX2	NM_003500	41	ATGGAGGTGCCCA GAACAC	42	ACTCCGGGTAACTGT GGATG	43	TGCTCTCAACTTTCCTGCGG AGTG	44	ATGGAGGTGCCCAGAACACTGCACTCCGCAGGAAAG TTGAGAGCATCATCCACAGTTACCCGGAGT
ACTR2	NM_005722	45	ATCCGCATTGAAG ACCAC	46	ATCCGCTAGAACTGC ACCAC	47	CCCGCAGAAAGCACATGGTA TTCC	48	ATCCGCATTGAAGACCCACCCCGCAGAAAGCACATG GTATTCCTGGGTGGTGCAGTTCTAGCGGAT
ADAM15	NM_003815	49	GGCGGGATGTGGT	50	ATTTCTGGGCCTCCG	51	TCAGCCACAATCACCAACTC	52	GGCGGGATGTGGTAACAGAGACCAAGACTGTGGAGT
ADAMTS1	NM_006988	53	GGACAGGTGCAAG CTCATCTG	54	ATCTACAACCTTGGG CTGCAA	55	CAAGCCAAAGGCATTGGCTA CTTCTTCG	56	GGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCAT TGGCTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGAT
ADH5	NM_000671	57	ATGCTGTCATCATT	58	CTGCTTCCTTTCCCTT	59	TGTCTGCCCATTATCTTCAT	60	ATGCTGTCATCATTGTCACGGTTTGTCTGCCCATTAT
AFAP1	NM_198595	61	GATGTCCATCCTT	62	CAACCCTGATGCCTG	63	CCTCCAGTGCTGTGTTCCCA	64	GATGTCCATCCTTGAAACAGCCTCTTCTGGGAACACA
AGTR1	NM_000685	65	AGCATTGATCGAT	66	CTACAAGCATTGTGC	67	ATTGTTCACCCAATGAAGTC	68	AGCATTGATCGATACCTGGCTATTGTTCACCCAATGA
AGTR2	NM_000686	69	ACTGGCATAGGAA	70	ATTGACTGGGTCTCTT	71	CCACCCAGACCCCATGTAGC	72	ACTGGCATAGGAAATGGTATCCAGAATGGAATTTTG
AIG1	NM_016108	73	CGACGGTTCTGCC	74	TGCTCCTGCTGGGAT	75	AATCGAGATGAGGACATCGC	76	CGACGGTTCTGCCCTTTATATTAATCGAGATGAGGAC
AKAP1	NM_003488	77	TGTGGTTGGAGAT	78	GTCTACCCACTGGGC	79	CTCCACCAGGGACCGGTTTA	80	TGTGGTTGGAGATGAAGTGGTGTTGATAAACCGGTC
AKR1C1	BC040210	81	GTGTGTGAAGCTG	82	CTCTGCAGGCGCATA	83	CCAAATCCCAGGACAGGCAT	84	GTGTGTGAAGCTGAATGATGGTCACTTCATGCCTGTC
AKR1C3	NM_003739	85	GCTTTGCCTGATG TCTACCAGAA	86	GTCCAGTCACCGGCA TAGAGA	87	TGCGTCACCATCCACACACA GGG	88	GCTTTGCCTGATGTCTACCAGAAGCCCTGTGTGTGGA TGGTGACGCAGAGGACGTCTCTATGCCGGTGACTGG
AKT1	NM_005163	89	CGCTTCTATGGCG	90	TCCCGGTACACCACG	91	CAGCCCTGGACTACCTGCAC	92	CGCTTCTATGGCGCTGAGATTGTGTCAGCCCTGGACT
AKT2	NM_001626	93	TCCTGCCACCCTTC	94	GGCGGTAAATTCATC	95	CAGGTCACGTCCGAGGTCGA	96	TCCTGCCACCCTTCAAACCTCAGGTCACGTCCGAGGT
AKT3	NM_005465	97	TTGTCTCTGCCTTG CAACTATC	98	CCAGCATTAGATTCTC	99	TCACGGTACACAATCTTTCC GGA	100	TTGTCTCTGCCTTGGACTATCTACATTCCGGAAAGAT TGTGTACCGTGATCTAAGTTGGAGAATCTAATGCTG
ALCAM	NM_001627	101	GAGGAATATGGAA	102	GTGGCGGAGATCAAG	103	CCAGTTCCTGCCGTCTGCTC	104	GAGGAATATGGAATCCAAGGGGGCCAGTTCCTGCCG
ALDH18A1	NM_002860	105	GATGCAGCTGGAA CCCAA	106	CTCCAGCTCAGTGGG GAA	107	CCTGAAACTTGCATCTCCTG CTGC	108	GATGCAGCTGGAACCCAAGCTGCAGCAGGAGATGCA AGTTTCAGGATGTTCCCCACTGAGCTGGAG
ALDH1A	NM_170696	109	CACGTCTGTCCCT	110	GACCGTGGCTCAACT	111	TCTCTGTAGGGCCCAGCTCT	112	CACGTCTGTCCCTCTCTCTGCTTTCTCTGTAGGGCCCAG
ALKBH3	NM_139178	113	TCGCTTAGTCTGC	114	TCTGAGCCCCAGTTTT	115	TAAACAGGGCAGTCACTTTC	116	TCGCTTAGTCTGCACCTCAACCGTGCGGAAAGTGACT
ALOX12	NM_000697	117	AGTTCCTCAATGG	118	AGCACTAGCCTGGAG	119	CATGCTGTTGAGACGCTCGA	120	AGTTCCTCAATGGTGCCAACCCCATGCTGTTGAGACG
ALOX5	NM_000698	121	GAAGCCTGAGGACTT	122	GAAGCCTGAGGACTTCGTAGA	123	CCGCATGCCGTACACGTAGA	124	GAAGCCTGAGGACTTCGTGAACGAGTGTCTACGTGTAC
AMACR	NM_203382	125	GTCTCTGGGCTGT CAGCTTT	126	TGGGTATAAGATCCA GAACTTGC	127	TCCATGTGTTTGATTTCTCCT CAGGC	128	GTCTCTGGGCTGTCAGCTTTCCTTTCTCCATGTGTTT GATTTCTCCTCAGGCTGGTAGCAAGTTCTGGATCTTA

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
AMPD3	NM_000480	129	TGGTTCATCCAGC ACAAGG	130	CATAAATCCGGGGCA CCT	131	TACTCTCCCAACATGCGCTG GATC	132	TGGTTCATCCAGCACAAGGTCTACTCTCCCAACATGC GCTGGATCATCCAGGTGCCCCGGATTTATG
ANGPT2	NM_001147	133	CCGTGAAAGCTGC	134	TTTGCAGTGGGAAGAA	135	AAGCTGACACAGCCCTCCCA	136	CCGTGAAAGCTGCTCTGTAAAAGCTGACACAGCCCT
ANLN	NM_018685	137	TGAAAGTCCAAAA	138	CAGAACCAAGGCTAT	139	CCAAAGAACTCGTGTCCCTC	140	TGAAAGTCCAAAACCAGGAAAATTCCAAAGAACTCG
ANPEP	NM_001150	141	CCACCTTGGACCA AAGTAAAGC	142	TCTCAGCGTCACCTG GTAGGA	143	CTCCCCAACACGCTGAAACC CG	144	CCACCTTGGACCAAAGTAAAGCGTGAATCGTTACC GCCTCCCCAACACGCTGAAACCCGATTCCTACCGGG
ANXA2	NM_004039	145	CAAGACACTAAGG GCGACTACCA	146	CGTGTCGGGCTTCAG TCAT	147	CCACCACACAGGTACACAGCAG CGCT	148	CAAGACACTAAGGGCGACTACCAGAAAGCGCTGCTG TACCTGTGTGGTGGAGATGACTGAAGCCCGACACG
APC	NM_000038	149	GGACAGCAGGAAT	150	ACCCACTCGATTTGTT	151	CATTGGCTCCCCGTGACCTG	152	GGACAGCAGGAATGTGTTTCTCCATACAGGTCACGG
APEX1	NM_001641	153	GATGAAGCCTTTC	154	AGGTCTCCACACAGC	155	CTTTCGGGAAGCCAGGCCCT	156	GATGAAGCCTTTCGCAAGTTCCTGAAGGGCCTGGCTT
APOC1	NM_001645	157	CCAGCCTGATAAA	158	CACTCTGAATCCTTGC	159	AGGACAGGACCTCCCAACCA	160	CCAGCCTGATAAAGGTCCTGCGGGCAGGACAGGACC
APOE	NM_000041	161	GCCTCAAGAGCTG GTTCG	162	CCTGCACCTTCTCCAC CA	163	ACTGGCGCTGCATGTCTTCC AC	164	GCCTCAAGAGCTGCATGTCTTCCTGCAGCCCAGTGGCCGGGCTGGTGGAGAAGGTGC TGCAGCGCCAGTGGGCCGGGCTGGTGGAGAAGGTGC
APRT	NM_000485	165	GAGGTCCTGGAGT	166	AGGTGCCAGCTTCTC	167	CCTTAAGCGAGGTCAGCTCC	168	GAGGTCCTGGAGTGCGTGAGCCTGGTGGAGCTGACC
AQP2	NM_000486	169	GTGTGGGTGCCAG	170	CCCTTCAGCCCTCTCA	171	CTCCTTCCCTTCCCCTTCTCC	172	GTGTGGGTGCCAGTCCTCCTCAGGAGAAGGGGAAGG
AR	NM_000044	173	CGACTTCACCGCA	174	TGACACAAGTGGGAC	175	ACCATGCCGCCAGGGTACCA	176	CGACTTCACCGCACCTGATGTGTGGTACCCTGGCGG
ARF1	NM_001658	177	CAGTAGAGATCCC	178	ACAAGCACATGGCTA	179	CTTGTCCTTGGGTCACCCTG	180	CAGTAGAGATCCCCGCAACTCGCTTGTCCTTGGGTCA
ARHGAP29	NM_004815	181	CACGGTCTCGTGG TGAAGT	182	CAGTTGCTTGCCCAG GAC	183	ATGCCAGACCCAGACAAAG CATCA	184	CACGGTCTCGTGGTGAAGTCAATGCCAGACCCAGAC AAAGCATCAGCTTGTCCTGGGCAAGCAACTG
ARHGDI	NM_001175	185	TGGTCCCTAGAAC	186	TGATGGAGGATCAGA	187	TAAAACCGGGCTTTCACCCA	188	TGGTCCCTAGAACAAGAGGCTTAAAACCGGGCTTTC
ASAP2	NM_003887	189	CGGCCCATCAGCT	190	CTCTGGCCAAAGATA	191	CTGGGCTCCAACCAGCTTCA	192	CGGCCCATCAGCTTCTACCAGCTGGGCTCCAACCAG
ASPN	NM_017680	193	TGGACTAATCTGT	194	AAACACCCTTCAACA	195	AGTATCACCCAGGGTGCAGC	196	TGGACTAATCTGTGGGAGCAGTTTAATTCCAGTATCAC
ATM	NM_000051	197	TGCTTTCTACACAT	198	GTTGTGGATCGGCTC	199	CCAGCTGTCTTCGACACTTC	200	TGCTTTCTACACATGTTCAGGGATTTTTCACCAGCTG
ATP5E	NM_006886	201	CCGCTTTCGCTAC	202	TGGGAGTATCGGATG	203	TCCAGCCTGTCTCCAGTAGG	204	CCGCTTTCGCTACAGCATGGTGGCCTACTGGAGACA
ATP5J	NM_0010037 03	205	GTCGACCGACTGA AACGG	206	CTCTACTTCCGGCCCT GG	207	CTACCCGCCATCGCAATGCA TTAT	208	GTCGACCGACTGAAACGGCGGCCCATAATGCATTGC GATGGCGGGTAGGCGTGTGGGGGCGGAGCCAGGGCC
ATXN1	NM_000332	209	GATCGACTCCAGC	210	GAACTGTATCACGGC	211	CGGGCTATGGCTGTCTTCAA	212	GATCGACTCCAGCACCGTAGAGAGGATTGAAGACAG
AURKA	NM_003600	213	CATCTTCCAGGAG	214	TCCGACCTTCAATCAT	215	CTCTGTGGCACCCTGGACTA	216	CATCTTCCAGGAGGACCACTCTCTGTGGCACCCTGGA
AURKB	NM_004217	217	AGCTGCAGAAGAG	218	GCATCTGCCAACTCC	219	TGACGAGCAGCGAACAGCC	220	AGCTGCAGAAGAGCTGCACATTTGACGAGCAGCGAA
AXIN2	NM_004655	221	GGCTATGTCTTTG	222	ATCCGTCAGCGCATC	223	ACCAGCGCCAACGACAGTG	224	GGCTATGTCTTTGCACCAGCGCCAACGAC
AZGP1	NM_001185	225	GAGGCCAGCTAGG	226	CAGGAAGGGCAGCTA	227	TCTGAGATCCCACATTGCCT	228	GAGGCCAGCTAGGAAGCAAGGGTTGGAGGCAATGTG
BAD	NM_032989	229	GGGTCAGGGGCCT	230	CTGCTCACTCGGCTC	231	TGGGCCCAGAGCATGTTCCA	232	GGGTCAGGGGCCTCGAGATCGGGCTTGGGCCCAGAG
BAG5	NM_0010150 49	233	ACTCCTGCAATGA ACCCTGT	234	ACAAACAGCTCCCCA CGA	235	ACACCGGATTTAGCTCTTGT CGGC	236	ACTCCTGCAATGAACCCGGATTTAGCT CTTGTCGGCCTTCGTGGGGAGCTGTTTGT
BAK1	NM_001188	237	CCATTCCCACCATT	238	GGGAACATAGACCCA	239	ACACCCCAGACGTCCTGGCC	240	CCATTCCCACCATTCTACCTGAGGCCAGGACGTCTGG
BAX	NM_004324	241	CCGCCGTGGACAC	242	TTGCCGTCAGAAAAC	243	TGCCACTCGGAAAAAGACCT	244	CCGCCGTGGACACAGACTCCCCCCGAGAGGTCTTTTT
BBC3	NM_014417	245	CCTGGAGGGTCCT GTACAAT	246	CTAATTGGGCTCCAT CTCG	247	CATCATGGGACTCCTGCCCT TACC	248	CCTGGAGGGTCCTGTACAATCTCATCATGGGACTCCT GCCCTTACCCAGGGGCCACAGAGCCCCCGAGATGGA
BCL2	NM_000633	249	CAGATGGACCTAG TACCCACTGAGA	250	CCTATGATTTAAGGG CATTTTTCC	251	TTCCACGCCGAAGGACAGCG AT	252	CAGATGGACCTAGTACCCACTGAGATTTCCACGCCG AAGGACAGCGATGGGAAAAATGCCCTTAAATCATAG
BDKRB1	NM_000710	253	GTGGCAGAAATCT	254	GAAGGGCAAGCCCAA	255	ACCTGGCAGCCTCTGATCTG	256	GTGGCAGAAATCTACCTGGCCAACCTGGCAGCCTCT
BGN	NM_001711	257	GAGCTCCGCAAGG	258	CTTGTTGTTCACCAGG	259	CAAGGGTCTCCAGCACCTCT	260	GAGCTCCGCAAGGATGACTTCAAGGGTCTCCAGCAC
BIK	NM_001197	261	ATTCCTATGGCTCT GCAATTGTC	262	GGCAGGAGTGAATGG CTCTTC	263	CCGGTTAACTGTGGCCTGTG CCC	264	ATTCCTATGGCTCTGCAATTGTCACCGGTTAACTGTG GCCTGTGCCCAGGAAGAGCCATTCACTCCTGCC
BIN1	NM_004305	265	CCTGCAAAAGGGA ACAAGAG	266	CGTGGTTGACTCTGA TCTCG	267	CTTCGCCTCCAGATGGCTCC C	268	CCTGCAAAAGGGAACAAGAGCCCTTCGCCTCCAGATT GGCTCCCCTGCCGCCACCCCCGAGATCAGAGTCAAC
BIRC5	NM_0010122 71	269	TTCAGGTGGATGA GGAGACA	270	CACACAGCAGTGGCA AAAG	271	TCTGCCAGACGCTTCCTATC ACTCTATTC	272	TTCAGGTGGATGAGGAGACAGAATAGAGTGATAGGA AGCGTCTGGCAGATACTCCTTTGCCACTGCTGTGTG
BMP6	NM_001718	273	GTGCAGACCTTGG	274	CTTAGTTGGCGCACA	275	TGAACCCCGAGTATGTCCCC	276	GTGCAGACCTTGGCCATCCCTTGCATTTGGGGCCGCTATG
BMPR1B	NM_001203	277	ACCACTTTGGCCA	278	GCGGTGTTTGTACCC	279	ATTCACATTACCATAGCGGC	280	ACCACTTTGGCCATCCCTTGCATTTGGGGCCGCTATGG

TABLE A

Official Symbol:	Accession Number:	SEQ ID NO	Forward Primer Sequence:	SEQ ID NO	Reverse Primer Sequence:	SEQ ID NO	Probe Sequence:	SEQ ID NO	Amplicon Sequence:
BRCA1	NM_007294	281	TCAGGGGGCTAGA	282	CCATTCCAGTTGATCT	283	CTATGGGCCCTTCACCAACA	284	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAC
BRCA2	NM_000059	285	AGTTCGTGCTTTG	286	AAGGTAAGCTGGGTC	287	CATTCTTCACTGCTTCATAA	288	AGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAA
BTG1	NM_001731	289	GAGGTCCGAGCGA	290	AGTTATTTTCGAGAC	291	CGCTCGTCTCTTCCTCTCTC	292	GAGGTCCGAGCGATGTGACCAGGCCGCCATCGCTCG
BTG3	NM_006806	293	CCATATCGCCCAA	294	CCAGTGATTCCGGTC	295	CATGGGTACCTCCTCCTGGA	296	CCATATCGCCCAATTCCAGTGACATGGGTACCTCCTC
BTRC	NM_033637	297	GTTGGGACACAGT	298	TGAAGCAGTCAGTTG	299	CAGTCGGCCCAGGACGGTCT	300	GTTGGGACACAGTTGGTCTGCAGTCGGCCCAGGACG
BUB1	NM_004336	301	CCGAGGTTAATCC	302	AAGACATGGCGCTCT	303	TGCTGGGAGCCTACACTTGG	304	CCGAGGTTAATCCAGCACGTATGGGGCCAAGTGTAG
C7	NM_000587	305	ATGTCTGAGTGTG	306	AGGCCTTATGCTGGT	307	ATGCTCTGCCCTCTGCATCT	308	ATGTCTGAGTGTGAGGCGGGCGCTCTGAGATGCAGA
CACNA1D	NM_000720	309	AGGACCCAGCTCCATGTG	310	CCTACATTCCGTGCCATTG	311	CAGTACACTGGCGTCCATTCCCTG	312	AGGACCCAGCTCCATGTGCGTTCTCAGGGAATGGACGCCAGTGTACTGCCAATGGCACGGAATGTAGG
CADM1	NM_014333	313	CCACCACCATCCT	314	GATCCACTGCCCTGA	315	TCTTCACCTGCTCGGGAATC	316	CCACCACCATCCTTACCATCATCACAGATTCCCGAGC
CADPS	NM_003716	317	CAGCAAGGAGACT	318	GGTCCTCTTCTCCACG	319	CTCCTGGATGGCCAAATTTG	320	CAGCAAGGAGACTGTGCTGAGCTCCTGGATGGCCAA
CASP1	NM_001223	321	AACTGGAGCTGAG	322	CATCTACGCTGTACC	323	TCACAGGCATGACAATGCTG	324	AACTGGAGCTGAGGTTGACATCACAGGCATGACAAT
CASP3	NM_032991	325	TGAGCCTGAGCAG	326	CCTTCCTGCGTGGTCC	327	TCAGCCTGTTCCATGAAGGC	328	TGAGCCTGAGCAGAGACATGACTCAGCCTGTTCCAT
CASP7	NM_033338	329	GCAGCGCCGAGAC	330	AGTCTCTCTCCGTCGC	331	CTTTCGCTAAAGGGGCCCCA	332	GCAGCGCCGAGACTTTTAGTTTCGCTTTCGCTAAAGG
CAV1	NM_001753	333	GTGGCTCAACATT	334	CAATGGCCTCCATTTT	335	ATTTCAGCTGATCAGTGGGC	336	GTGGCTCAACATTGTGTTCCCATTTCAGCTGATCAGT
CAV2	NM_198212	337	CTTCCCTGGGACG	338	CTCCTGGTCACCCTTC	339	CCCGTACTGTCATGCCTCAG	340	CTTCCCTGGGACGACTTGCCAGCTCTGAGGCATGAC
CCL2	NM_002982	341	CGCTCAGCCAGATGCAATC	342	GCACTGAGATCTTCCTATTGGTGAA	343	TGCCCCAGTCACCTGCTGTTA	344	CGCTCAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATCTCAGTGC
CCL5	NM_002985	345	AGGTTCTGAGCTC	346	ATGCTGACTTCCTTCC	347	ACAGAGCCCTGGCAAAGCC	348	AGGTTCTGAGCTCTGGCTTTGCCTTGGCTTTGCCAGG
CCNB1	NM_031966	349	TTCAGGTTGTTGCAGGAGAC	350	CATCTTCTTGGGCACACAAT	351	TGTCTCCATTATTGATCGGTTCATGCA	352	TTCAGGTTGTTGCAGGAGACCATGTACATGACTGTCTCCATTATTGATCGGTTCATGCAGAATAATTGTGTGCC
CCND1	NM_001758	353	GCATGTTCGTGGC	354	CGGTGTAGATGCACA	355	AAGGAGACCATCCCCCTGAC	356	GCATGTTCGTGGCCTCTAAGATGAAGGAGACCATCC
CCNE2	NM_057749	357	ATGCTGTGGCTCCTTCCTAACT	358	ACCCAAATTGTGATATACAAAAAGGTT	359	TACCAAGCAACCTACATGTCAAGAAAGCCC	360	ATGCTGTGGCTCCTTCCTAACTGGGGCTTTCTTGACATGTAGGTTGCTTGGTAATAACCTTTTTGTATATCACA
CCNH	NM_001239	361	GAGATCTTCGGTG	362	CTGCAGACGAGAACC	363	CATCAGCGTCCTGGCGTAAA	364	GAGATCTTCGGTGGGGGTACGGGTGTTTTACGCCAG
CCR1	NM_001295	365	TCCAAGACCCAAT	366	TCGTAGGCTTTCGTG	367	ACTCACCACACCTGCAGCCT	368	TCCAAGACCCAATGGGAATTCACTCACCACACCTGC
CD164	NM_006016	369	CAACCTGTGCGAA	370	ACACCCAAGACCAGG	371	CCTCCAATGAAACTGGCTGC	372	CAACCTGTGCGAAAGTCTACCTTTGATGCAGCCAGTT
CD1A	NM_001763	373	GGAGTGGAAGGAACTGGAAA	374	TCATGGGCGTATCTACGAAT	375	CGCACCATTCGGTCATTTGAGG	376	GGAGTGGAAGGAACTGGAAACATTATTCCGTATACGCACCATTCGGTCATTTGAGGGAATTCGTAGATACGCC
CD276	NM_001024736	377	CCAAAGGATGCGATACACAG	378	GGATGACTTGGGAATCATGTC	379	CCACTGTGCAGCCTTATTTCTCCAATG	380	CCAAAGGATGCGATACACAGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCC
CD44	NM_000610	381	GGCACCACTGCTT	382	GATGCTCATGGTGAA	383	ACTGGAACCCAGAAGCACA	384	GGCACCACTGCTTATGAAGGAAACTGGAACCCAGAA
CD68	NM_001251	385	TGGTTCCCAGCCC	386	CTCCTCCACCCTGGGT	387	CTCCAAGCCCAGATTCAGAT	388	TGGTTCCCAGCCCTGTGTCCACCTCCAAGCCCAGATT
CD82	NM_002231	389	GTGCAGGCTCAGGTGAAGTG	390	GACCTCAGGGCGATTCATGA	391	TCAGCTTCTACAACTGGACAGACAACGCTG	392	GTGCAGGCTCAGGTGAAGTGCTGCGGCTGGGTCAGCTTCTACAACTGGACAGACAACGCTGAGCTCATGAAT
CDC20	NM_001255	393	TGGATTGGAGTTC	394	GCTTGCACTCCACAG	395	ACTGGCCGTGGCACTGGACA	396	TGGATTGGAGTTCTGGGAATGTACTGGCCGTGGCAC
CDC25B	NM_021873	397	GCTGCAGGACCAG	398	TAGGGCAGCTGGCTT	399	CTGCTACCTCCCTTGCCTTT	400	GCTGCAGGACCAGTGAGGGGCCTGCGCCAGTCCTGC
CDC6	NM_001254	401	GCAACACTCCCCA	402	TGAGGGGGACCATTC	403	TTGTTCTCCACCAAAGCAAG	404	GCAACACTCCCCATTTACCTCCTTGTTCTCCACCAAA
CDH1	NM_004360	405	TGAGTGTCCCCCGGTATCTTC	406	CAGCCGCTTTCAGATTTTCAT	407	TGCCAATCCCGATGAAATTGGAAATTT	408	TGAGTGTCCCCCGGTATCTTCCCCGCCCTGCCAATCCCGATGAAATTGGAAATTTTATTGATGAAAATCTGAAA
CDH10	NM_006727	409	TGTGGTGCAAGTC	410	TGTAAATGACTCTGG	411	ATGCCGATGACCCTTCATAT	412	TGTGGTGCAAGTCACAGCTACAGATGCCGATGACCC
CDH11	NM_001797	413	GTCGGCAGAAGCA	414	CTACTCATGGGCGGG	415	CCTTCTGCCCATAGTGATCA	416	GTCGGCAGAAGCAGGACTTGTACCTTCTGCCCATAG
CDH19	NM_021153	417	AGTACCATAATGC	418	AGACTGCCTGTATAG	419	ACTCGGAAAACCACAAGCG	420	AGTACCATAATGCGGGAACGCAAGACTCGGAAAACC
CDH5	NM_001795	421	ACAGGAGACGTGT	422	CAGCAGTGAGGTGGT	423	TATTCTCCCGGTCCAGCCTC	424	ACAGGAGACGTGTTCGCCATTGAGAGGCTGGACCGG
CDH7	NM_033646	425	GTTTGACATGGCT	426	AGTCACATCCCTCCG	427	ACCTCAACGTCATCCGAGAC	428	GTTTGACATGGCTGCACTGAGAAACCTCAACGTCATC
CDK14	NM_012395	429	GCAAGGTAAATGG	430	GATAGCTGTGAAAGG	431	CTTCCTGCAGCCTGATCACC	432	GCAAGGTAAATGGGAAGTTGGTAGCTCTGAAGGTGA
CDK2	NM_001798	433	AATGCTGCACTACGACCCTA	434	TTGGTCACATCCTGGAAGAA	435	CCTTGGCCGAAATCCGCTTGT	436	AATGCTGCACTACGACCCTAACAAGCGGATTTCGGCCAAGGCAGCCCTGGCTCACCCTTTCTTCCAGGATGTG
CDK3	NM_001258	437	CCAGGAAGGGACT	438	GTTGCATGAGCAGGT	439	CTCTGGCTCCAGATTGGGCA	440	CCAGGAAGGGACTGGAAGAGATTGTGCCCAATCTGG
CDK7	NM_001799	441	GTCTCGGGCAAAG	442	CTCTGGCCTTGTAAA	443	CCTCCCCAAGGAAGTCCAGC	444	GTCTCGGGCAAAGCGTTATGAGAAGCTGGACTTCCT

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
CDKN1A	NM_000389	445	TGGAGACTCTCAG	446	GGCGTTTGGAGTGGT	447	CGGCGGCAGACCAGCATGA	448	TGGAGACTCTCAGGGTCGAAAACGGCGGCAGACCAG
CDKN1C	NM_000076	449	CGGCGATCAAGAA	450	CAGGCGCTGATCTCT	451	CGGGCCTCTGATCTCCGATT	452	CGGCGATCAAGAAGCTGTCCGGGCCTCTGATCTCCG
CDKN2B	NM_004936	453	GACGCTGCAGAGC	454	GCGGGAATCTCTCCT	455	CACAGGATGCTGGCCTTTGC	456	GACGCTGCAGAGCACCTTTGCACAGGATGCTGGCCT
CDKN2C	NM_001262	457	GAGCACTGGGCAA	458	CAAAGGCGAACGGGA	459	CCTGTAACTTGAGGCAATCGTTACGACCTGTAACTTGAGG
CDKN3	NM_005192	461	TGGATCTCTACCA	462	ATGTCAGGAGTCCCT	463	ATCACCCATCATCATCCAAT	464	TGGATCTCTACCAGCAATGTGGAATTATCACCCATCA
CDS2	NM_003818	465	GGGCTTCTTTGCT	466	ACAGGGCAGACAAAG	467	CCCGGACATCACATAGGACA	468	GGGCTTCTTTGCTACTGTGGTGTTTGGCCTTCTGCTG
CENPF	NM_016343	469	CTCCCGTCAACAG	470	GGGTGAGTCTGGCCT	471	ACACTGGACCAGGAGTGCAT	472	CTCCCGTCAACAGCGTTCTTTCCAAACACTGGACCAG
CHAF1A	NM_005483	473	GAACTCAGTGTAT	474	GCTCTGTAGCACCTG	475	TGCACGTACCAGCACATCCT	476	GAACTCAGTGTATGAGAAGCGGCCTGACTTCAGGAT
CHN1	NM_001822	477	TTACGACGCTCGT	478	TCTCCCTGATGCACAT	479	CCACCATTGGCCGCTTAGTG	480	TTACGACGCTCGTGAAAGCACATACCACTAAGCGGC
CHRAC1	NM_017444	481	TCTCGCTGCCTCTA	482	CCTGGTTGATGCTGG	483	ATCCGGGTCATCATGAAGAG	484	TCTCGCTGCCTCTATCCCGCATCCGGGTCATCATGAA
CKS2	NM_001827	485	GTGTTGAGCGTGGT	486	CGCTGCAGAAAATGA	487	CTGTGACGTGGTTTTGTCTGCGCCGCTCTTCG	488	GGCTGACGTCCCGCTCTTCG
CLDN3	NM_001306	489	ACCAACTGCGTGC	490	GGCGAGAAGGAACAG	491	CAAGGCCAAGATCACCATCG	492	ACCAACTGCGTGCAGGACGACACGGCCAAGGCCAAG
CLTC	NM_004859	493	ACCGTATGGACAG	494	TGACTACAGGATCAG	495	TCTCACATGCTGTACCCAAA	496	ACCGTATGGACAGCCACAGCCTGGCTTTGGTACAG
COL11A	NM_001854	497	GCCCAAGAGGGTA	498	GGACCTGGGTCTCCA	499	CTGCTCGACCTTTGGGTCCT	500	GCCCAAGAGGGGAAGATGGCCCTGAAGGACCCAAAG
COL1A1	NM_000088	501	GTGGCCATCCAGC	502	CAGTGGTAGGTGATG	503	TCCTGCGCCTGATGTCCAC	504	GTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCA
COL1A2	NM_000089	505	CAGCCAAGAACTG GTATAGGAGCT	506	AAACTGGCTGCCAGC ATTG	507	TCTCCTAGCCAGACGTGTTT CTTGTCCTTG	508	CAGCCAAGAACTGGTATAGGAGCTCCAAGGACAAGA AACACGTCTGGCTAGGAGAAACTATCAATGCTGGCA
COL3A1	NM_000090	509	GGAGGTTCTGGAC	510	ACCAGGACTGCCACG	511	CTCCTGGTCCCCAAGGTGTC	512	GGAGGTTCTGGACCTGCTGGTCCTCTGGTCCCCAAG
COL4A1	NM_001845	513	ACAAAGGCCTCCC	514	GAGTCCCAGGAAGAC	515	CTCCTTTGACACCAGGGATG	516	ACAAAGGCCTCCCAGGATGGCATCCCTGGTG
COL5A1	NM_000093	517	CTCCCTGGGAAAG	518	CTGGACCAGGAAGCC	519	CCAGGGAAACCACGTAATCC	520	CTCCCTGGGAAAGATGGCCCTCCAGGATTACGTGGT
COL5A2	NM_000393	521	GGTCGAGGAACCC	522	GCCTGGAAGGTCCAAC	523	CCAGGAAATCCTGTAGCACC	524	GGTCGAGGAACCCAAGGTCCGCCTGGTGCTACAGGA
COL6A1	NM_001848	525	GGAGACCCTGGTG	526	TCTCCAGGGACACCA	527	CTTCTCTTCCCTGATCACCC	528	GGAGACCCTGGTGAAGCTGGCCCGCAGGGTGATCAG
COL6A3	NM_004369	529	GAGAGCAAGCGAG	530	AACAGGGAACTGGCC	531	CCTCTTTGACGGCTCAGCCA	532	GAGAGCAAGCGAGACATTCTGTTCCTCTTTGACGGCT
COL8A1	NM_001850	533	TGGTGTTCCAGGG	534	CCCTGTAAACCCTGA	535	CCTAAGGGAGAGCCAGGAA	536	TGGTGTTCCAGGGCTTCTCGGACCTAAGGGAGAGCC
COL9A2	NM_001852	537	GGGAACCATCCAG	538	ATTCCGGGTGGACAG	539	ACACAGGAAATCCGCACTGC	540	GGGAACCATCCAGGGTCTGGAAGGCAGTGCGGATTT
CRISP3	NM_006061	541	TCCCTTATGGAACA	542	AACCATTGGTGCATA	543	TGCCAGTTGCCCAGATAACT	544	TCCCTTATGGAACAAGGAGCACCTTGTGCCAGTTGCCC
CSF1	NM_000757	545	TGCAGCGGCTGAT TGACA	546	CAACTGTTCCTGGTCT ACAAACTCA	547	TCAGATGGAGACCTCGTGCC AAATTACA	548	TGCAGCGGCTGATTGACAGTCAGATGGAGACCTCGT GCCAAATTACATTTGAGTTTGTAGACCAGGAACAGTT
CSK	NM_004383	549	CCTGAACATGAAG	550	CATCACGTCTCCGAA	551	TCCCGATGGTCTGCAGCAGC	552	CCTGAACATGAAGGAGCTGCTGCAGACCAT
CSRP1	NM_004078	553	ACCCAAGACCCTG	554	GCAGGGGTGGAGTGA	555	CCACCCTTCTCCAGGGACCC	556	ACCCAAGACCCTGCCCTCTTCCACTCCACCCTTCTCCA
CTGF	NM_001901	557	GAGTTCAAGTGCC CTGACG	558	AGTTGTAATGGCAGG CACAG	559	AACATCATGTTCTTCTTCAT GACCTCGC	560	GAGTTCAAGTGCCCTGACGGCGAGGTCATGAAGAAG AACATGATGTTCATCAAGACCTGTGCCTGCCATTACA
CTHRC1	NM_138455	561	TGGCTCACTTCGG	562	TCAGCTCCATTGAAT	563	CAACGCTGACAGCATGCATT	564	TGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGT
CTNNA1	NM_001903	565	CGTTCCGATCCTCT ATACTGCAT	566	AGGTCCCTGTTGGCC TTATAGG	567	ATGCCTACAGCACCCTGATG TCGCA	568	CGTTCCGATCCTCTATACTGCATCCCAGGCATGCCTA CAGCACCCTGATGTCGCAGCCTATAAGGCCAACAGG
CTNNB1	NM_001904	569	GGCTCTTGTGCGT ACTGTCCTT	570	TCAGATGACGAAGAG CACAGATG	571	AGGCTCAGTGATGTCTTCCC TGTCACCAG	572	GGCTCTTGTGCGTACTGTCCTTCGGGCTGGTGACAGG GAAGACATCACTGAGCCTGCCATCTGTGCTCTTCGTC
CTNND1	NM_001331	573	CGGAAACTTCGGG	574	CTGAATCCTTCTGCCC	575	TTGATGCCCTCATTTTCATT	576	CGGAAACTTCGGGAATGTGATGGTTTAGTTGATGCC
CTNND2	NM_001332	577	GCCCGTCCCTACA	578	CTCACACCCAGGAGT	579	CTATGAAACGAGCCACTACC	580	GCCCGTCCCTACAGTGAACTATGAAACGAGC
CTSB	NM_001908	581	GGCCGAGATCTAC	582	GCAGGAAGTCCGAAT	583	CCCCGTGGAGGGAGCTTTCT	584	GGCCGAGATCTACAAAAACGGCCCCGTGGAGGGAGC
CTSD	NM_001909	585	GTACATGATCCCC TGTGAGAAGGT	586	GGGACAGCTTGTAGC CTTTGC	587	ACCCTGCCCGCGATCACACT GA	588	GTACATGATCCCCTGTGAGAAGGTGTCCACACCCTGCCC GCGATCACACTGAAGCTGGGAGGCAAAGGCTACAAG
CTSK	NM_000396	589	AGGCTTCTCTTGG	590	CCACCTCTTCACTGGT	591	CCCCAGGTGGTTCATAGCCA	592	AGGCTTCTCTTGGTGTTCCATACATATGAACTGGCTAT
CTSL2	NM_001333	593	TGTCTCACTGAGC	594	ACCATTGCAGCCCTG	595	CTTGAGGACGCGAACAGTCC	596	TGTCTCACTGAGCGAGCAGAATCTGGTGGACTGTTC
CTSS	NM_004079	597	TGACAACGGCTTT	598	TCCATGGCTTTGTAG	599	TGATAACAAGGGCATCGACT	600	TGACAACGGCTTTCCAGTACATCATTGATAACAAGG
CUL1	NM_003592	601	ATGCCCTGGTAAT	602	GCGACCACAAAGCCTT	603	CAGCCACAAAGCCAGCGTCA	604	ATGCCCTGGTAATGTCTGCATTCAACAATGACGCTGG
CXCL12	NM_000609	605	GAGCTACAGATGC	606	TTTGAGATGCTTGAC	607	TTCTTCGAAAGCCATGTTGC	608	GAGCTACAGATGCCCATGTTCTTCGAAAGCCA
CXCR4	NM_003467	609	TGACCGCTTCTTC TAC	610	AGGATAAGGCCAACC	611	CTGAAACTGGAACACAACCA	612	TGACCGCTTCTTCTACCCCAATGACTTGTGGGTGGTTGTG
CXCR7	NM_020311	613	CGCCTCAGAACGA TGGAT	614	GTTGCATGGCCAGCT GAT	615	CTCAGAGCCAGGGAACTTCT CGGA	616	CGCCTCAGAACGATGGATCTGCATCTCTTCGACTACT CAGAGCCAGGGAACTTCTCGGACATCAGCTGGCCAT

TABLE A

Official Symbol:	Accession Number:	SEQ ID NO	Forward Primer Sequence:	SEQ ID NO	Reverse Primer Sequence:	SEQ ID NO	Probe Sequence:	SEQ ID NO	Amplicon Sequence:
CYP3A5	NM_000777	617	TCATTGCCCAGTA	618	GACAGGCTTGCCTTT	619	TCCCGCCTCAAGTTTCTCAC	620	TCATTGCCCAGTATGGAGATGTATTGGTGAGAAACTT
CYR61	NM_001554	621	TGCTCATTCTTGAG	622	GTGGCTGCATTAGTG	623	CAGCACCCTTGGCAGTTTCG	624	TGCTCATTCTTGAGGAGCATTAAGGTATTTCGAAACT
DAG1	NM_004393	625	GTGACTGGGCTCA	626	ATCCCACTTGTGCTCC	627	CAAGTCAGAGTTTCCCTGGT	628	GTGACTGGGCTCATGCCTCCAAGTCAGAGTTTCCCTG
DAP	NM_004394	629	CCAGCCTTTCTGG	630	GACCAGGTCTGCCTC	631	CTCACCAGCTGGCAGACGTG	632	CCAGCCTTTCTGGTGCTGTTCTCCAGTTCACGTCTGC
DAPK1	NM_004938	633	CGCTGACATCATG	634	TCTCTTTCAGCAACGA	635	TCATATCCAAACTCGCCTCC	636	CGCTGACATCATGAATGTTCCTCGACCGGCTGGAGG
DARC	NM_002036	637	GCCCTCATTAGTC	638	CAGACAGAAGGGCTG	639	TCAGCGCCTGTGCTTCCAAG	640	GCCCTCATTAGTCCTTGGCTCTTATCTTGGAAGCACA
DDIT4	NM_019058	641	CCTGGCGTCTGTC	642	CGAAGAGGAGGTGGA	643	CTAGCCTTTGGGACCGCTTC	644	CCTGGCGTCTGTCCTCACCATGCCTAGCCTTTGGGAC
DDR2	NM_001014796	645	CTATTACCGGATCCAGGGC	646	CCCAGCAAGATACTCTCCCA	647	AGTGCTCCCTATCCGCTGGATGTC	648	CTATTACCGGATCCAGGGCCGGGCAGTGCTCCCTATCCGCTGGATGTCTTGGGAGAGTATCTTGCTGGG
DES	NM_001927	649	ACTTCTCACTGGC	650	GCTCCACCTTCTCGTT	651	TGAACCAGGAGTTTCTGACC	652	ACTTCTCACTGGCCGACGCGGTGAACCAGGAGTTTCT
DHRS9	NM_005771	653	GGAGAAAGGTCTC	654	CAGTCAGTGGGAGCC	655	ATCAATAATGCTGGTGTTCC	656	GGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGG
DHX9	NM_001357	657	GTTCGAACCATCT	658	TCCAGTTGGATTGTG	659	CCAAGGAACCACACCCACTT	660	GTTCGAACCATCTCAGCGACAAAACCAAGTGGGTGT
DIAPH1	NM_005219	661	CAAGCAGTCAAGG	662	AGTTTTGCTCGCCTCA	663	TTCTTCTGTCTCCCGCCGCT	664	CAAGCAGTCAAGGAGAACCAGAAGCGGCGGGAGAC
DICER1	NM_177438	665	TCCAATTCCAGCA	666	GGCAGTGAAGGCGAT	667	AGAAAAGCTGTTTGTCTCCC	668	TCCAATTCCAGCATCACTGTGGAGAAAAGCTGTTTGT
DIO2	NM_013989	669	CTCCTTTCACGAG	670	AGGAAGTCAGCCACT	671	ACTCTTCCACCAGTTTGCGG	672	CTCCTTTCACGAGCCAGCTGCCAGCCTTCCGCAAACT
DLC1	NM_006094	673	GATTCAGACGAGG	674	CACCTCTTGCTGTCCC	675	AAAGTCCATTTGCCACTGAT	676	GATTCAGACGAGGATGAGCCTTGTGCCATCAGTGGC
DLGAP1	NM_004746	677	CTGCTGAGCCCAG	678	AGCCTGGAAGGAGTT	679	CGCAGACCACCCATACTACA	680	CTGCTGAGCCCAGTGGAGCACCACCCCGCAGACCAC
DLL4	NM_019074	681	CACGGAGGTATAA	682	AGAAGGAAGGTCCAG	683	CTACCTGGACATCCCTGCTC	684	CACGGAGGTATAAGGCAGGAGCCTACCTGGACATCC
DNM3	NM_015569	685	CTTTCCCACCCGG	686	AAGGACCTTCTGCAG	687	CATATCGCTGACCGAATGGG	688	CTTTCCCACCCGGCTTACAGACATATCGCTGACCGAA
DPP4	NM_001935	689	GTCCTGGGATCGG	690	GTACTCCCACCGGGA	691	CGGCTATTCCACACTTGAAC	692	GTCCTGGGATCGGGAAGTGGCGTGTTCAAGTGTGGA
DPT	NM_001937	693	CACCTAGAAGCCT	694	CAGTAGCTCCCCAGG	695	TTCCTAGGAAGGCTGGCAGA	696	CACCTAGAAGCCTGCCCACGATTCCTAGGAAGGCTG
DUSP1	NM_004417	697	AGACATCAGCTCC	698	GACAAACACCCTTCC	699	CGAGGCCATTGACTTCATAG	700	AGACATCAGCTCCTGGTTCAACGAGGCCATTGACTTC
DUSP6	NM_001946	701	CATGCAGGGACTG	702	TGCTCCTACCCTATCA	703	TCTACCCTATGCGCCTGGAA	704	CATGCAGGGACTGGGATTCGAGGACTTCCAGGCGCA
DVL1	NM_004421	705	TCTGTCCCACCTG	706	TCAGACTGTTGCCGG	707	CTTGGAGCAGCCTGCACCTT	708	TCTGTCCCACCTGCTGCTGCCCCTTGGAGCAGCCTGC
DYNLL1	NM_001037494	709	GCCGCCTACCTCACAGAC	710	GCCTGACTCCAGCTCTCCT	711	ACCCACGTCAGTGAGTGCTCACAA	712	GCCGCCTACCTCACAGACTTGTGAGCACTCACTGACGTGGGTAGCGCCCAGGGCCTGCGGGGCGCAGGAGAG
EBNA1BP2	NM_006824	713	TGCGGCGAGATGGACACT	714	GTGACAAGGGATTCATCGGATT	715	CCCGCTCTCGGATTCGGAGTCG	716	TGCGGCGAGATGGACACTCCCCCGCTCTCGGATTCGGAGTCGGAATCCGATGAATCCCTTGTCAC
ECE1	NM_001397	717	ACCTTGGGATCTG	718	GGACCAGGACCTCCA	719	TCCACTCTCGATACCCTGCA	720	ACCTTGGGATCTGCCTCCAAGCTGGTGCAGGGTATC
EDN1	NM_001955	721	TGCCACCTGGACA	722	TGGACCTAGGGCTTC	723	CACTCCCGAGCACGTTGTTC	724	TGCCACCTGGACATCATTTGGGTCAACACTCCCGAGC
EDNRA	NM_001957	725	TTTCCTCAAATTTG	726	TTACACATCCAACCA	727	CCTTTGCCTCAGGGCATCCT	728	TTTCCTCAAATTTGCCTCAAGATGGAAACCCTTTGCC
EFNB2	NM_004093	729	TGACATTATCATCCCGCTAAGGA	730	GTAGTCCCCGCTGACCTTCTC	731	CGGACAGCGTCTTCTGCCCTCACT	732	TGACATTATCATCCCGCTAAGGACTGCGGACAGCGTCTTCTGCCCTCACTACGAGAAGGTCAGCGGGGACTA
EGF	NM_001963	733	CTTTGCCTTGCTCTGTCACAGT	734	AAATACCTGACACCCTTATGACAAATT	735	AGAGTTTAACAGCCCTGCTCTGGCTGACTT	736	CTTTGCCTTGCTCTGTCACAGTGAAGTCAGCCAGAGCAGGGCTGTTAAACTCTGTGAAATTTGTCATAAGGGTG
EGR1	NM_001964	737	GTCCCCGCTGCAGATCTCT	738	CTCCAGCTTAGGGTAGTTGTCCAT	739	CGGATCCTTTCCTCACTCGCCCA	740	GTCCCCGCTGCAGATCTCTGACCCGTTCGGATCCTTTCCTCACTCGCCCACCATGGACAACTACCCTAAGCTGG
EGR3	NM_004430	741	CCATGTGGATGAATGAGGTG	742	TGCCTGAGAAGAGGTGAGGT	743	ACCCAGTCTCACCTTCTCCCCACC	744	CCATGTGGATGAATGAGGTGTCTCCTTTCCATACCCAGTCTCACCTTCTCCCCACCCTACCTCACCTCTTCTCA
EIF2C2	NM_012154	745	GCACTGTGGGCAG	746	ATGTTTGGTGACTGG	747	CGGGTCACATTGCAGACACG	748	GCACTGTGGGCAGATGAAGAGGAAGTACCGCGTCTG
EIF2S3	NM_001415	749	CTGCCTCCCTGATT	750	GGTGGCAAGTGCCTG	751	TCTCGTGCTTCAGCCTCCCA	752	CTGCCTCCCTGATTCAAGTGATTCTCGTGCTTCAGCC
EIF3H	NM_003756	753	CTCATTGCAGGCCAGATAAA	754	GCCATGAAGAGCTTGCCTA	755	CAGAACATCAAGGAGTTCACTGCCCA	756	CTCATTGCAGGCCAGATAAACACTTACTGCCAGAACATCAAGGAGTTCACTGCCCAAAACTTAGGCAAGCTC
EIF4E	NM_001968	757	GATCTAAGATGGCGACTGTCGAA	758	TTAGATTCCGTTTTCTCCTCTTCTG	759	ACCACCCCTACTCCTAATCCCCCGACT	760	GATCTAAGATGGCGACTGTCGAACCGGAAACCACCCCTACTCCTAATCCCCCGACTACAGAAGAGGAGAAAA
EIF5	NM_001969	761	GAATTGGTCTCCA	762	TCCAGGTATATGGCT	763	CCACTTGCACCCGAATCTTG	764	GAATTGGTCTCCAGCTGCCTTTGATCAAGATTCGGGT
ELK4	NM_001973	765	GATGTGGAGAATG	766	AGTCATTGCGGCTAG	767	ATAAACCACCTCAGCCTGGT	768	GATGTGGAGAATGGAGGGAAAGATAAACCACCTCAG
ENPP2	NM_006209	769	CTCCTGCGCACTA	770	TCCCTGGATAATTGG	771	TAACTTCCTCTGGCATGGTT	772	CTCCTGCGCACTAATACCTTCAGGCCAACCATGCCAG
ENY2	NM_020189	773	CCTCAAAGAGTTG	774	CCTCTTTACAGTGTGC	775	CTGATCCTTCCAGCCACATT	776	CCTCAAAGAGTTGCTGAGAGCTAAATTAATTGAATGT
EPHA2	NM_004431	777	CGCCTGTTCACCA	778	GTGGCGTGCCTCGAA	779	TGCGCCCGATGAGATCACCG	780	CGCCTGTTCACCAAGATTGACACCATTGCGCCCGATG

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence:	SEQ ID NO	Reverse Primer Sequence:	SEQ ID NO	Probe Sequence:	SEQ ID NO	Amplicon Sequence:
EPHA3	NM_005233	781	CAGTAGCCTCAAG	782	TTCGTCCCATATCCAG	783	TATTCCAAATCCGAGCCCGA	784	CAGTAGCCTCAAGCCTGACACTATATACGTATTCCAA
EPHB2	NM_004442	785	CAACCAGGCAGCT	786	GTAATGCTGTGTCCACG	787	CACCTGATGCATGATGGACA	788	CAACCAGGCAGCTCCATCGGCAGTGTCCATCATGCA
EPHB4	NM_004444	789	TGAACGGGGTATC CTCCTTA	790	AGGTTACCTCTCGGGTC AGTGG	791	CGTCCCAATTTGAGCCTGTCA ATGT	792	TGAACGGGGTATCCTCCTTAGCCACGGGGCCCGTCC CATTTGAGCCTGTCAATGTCACCACTGACCGAGAGGT
ERBB2	NM_004448	793	CGGTGTGAGAAGT	794	CCTCTCGCAAGTGCT	795	CCAGACCATAGCACACTCGG	796	CGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGAGTG
ERBB3	NM_001982	797	CGGTTATGTCATG CCAGATACAC	798	GAACTGAGACCCACT GAAGAAAGG	799	CCTCAAAGGTACTCCCTCCT CCCGG	800	CGGTTATGTCATGCCAGATACACACCTCAAAGGTACT CCCTCCTCCCGGGAAGGCACCCTTTCTTCAGTGGGTC
ERBB4	NM_005235	801	TGGCTCTTAATCA GTTTCGTTACCT	802	CAAGGCATATCGATC CTCATAAAGT	803	TGTCTCTTAATCAGTTTCGTTACCTCTCTGGAGAA AATTCTCCAG	804	TGGCTCTTAATCAGTTTCGTTACCTCTCTGGAGAA TTTACGCATTATTCGTGGGACAAAACTTTATGAGGAT
ERCC1	NM_001983	805	GTCCAGGTGGATG	806	CGGCCAGGATACACA	807	CAGCAGGCCCTCAAGGAGCT	808	GTCCAGGTGGATGTGAAAGATCCCCAGCAGGCCCTC
EREG	NM_001432	809	TGCTAGGTAAACC	810	TGGAGACAAGTCCTG	811	TAAGCCATGGCTGACCTCTG	812	TGCTAGGGTAAACGAAGGCATAATAAGCCATGGCTG
ERG	NM_004449	813	CCAACACTAGGCT	814	CCTCCGCCAGGTCTTT	815	AGCCATATGCCTTCTCATCT	816	CCAACACTAGGCCTTCTCATCTTCCTTCTCA
ESR1	NM_000125	817	CGTGGTGCCCCTC	818	GGCTAGTGGGCGCAT	819	CTGGAGATGCTGGACGCCC	820	CGTGGTGCCCCTCTATGACCTGCTGCTGGAGATGCTG
ESR2	NM_001437	821	TGGTCCATCGCCA GTTATCA	822	TGTTCTAGCGATCTTG CTTCACA	823	ATCTGTATGCGGAACCTCAA AAGAGT	824	TGGTCCATCGCCAGTTATCACATCTGTATGCGGAACC TCAAAAGAGTCCCTGGTGTGAAGCAAGATCGCTAGA
ETV1	NM_004956	825	TCAAACAAGAGCC	826	AACTGCCAGAGCTGA	827	ATCGGGAAGGACCCACATAC	828	TCAAACAAGAGCCAGGAATGTATCGGGAAGGACCCA
ETV4	NM_001986	829	TCCAGTGCCTATG	830	ACTGTCCAAGGGCAC	831	CAGACAAATCGCCATCAAGT	832	TCCAGTGCCTATGACCCCCCCAGACAAATCGCCATCA
EZH2	NM_004456	833	TGGAAACAGCGAA GGATACA	834	CACCGAACACTCCCT AGTCC	835	TCCTGACTTCTGTGAGCTCA TTGCG	836	TGGAAACAGCGAAGGATACAGCCTGTGCACATCCTG ACTTCTGTGAGCTCATTGCGCGGGACTAGGGAGTGTT
F2R	NM_001992	837	AAGGAGCAAACCA	838	GCAGGGTTTCATTGA	839	CCCGGGCTCAACATCACTAC	840	AAGGAGCAAACCATCCAGGTGCCCGGGCTCAACATC
FAAH	NM_001441	841	GACAGCGTAGTGG TGCATGT	842	AGCTGAACATGGACT GTGGA	843	TGCCCTTCGTGCACACCAAT G	844	GACAGCGTAGTGGTGCATGTGCTGAAGCTGCAGGGT GCCGTGCCCTTCGTGCACACCAATGTTCCACAGTCCA
FABP5	NM_001444	845	GCTGATGGCAGAA AAACTCA	846	CTTTCCTTCCCATCCC ACT	847	CCTGATGCTGAACCAATGCA CCAT	848	GCTGATGGCAGAAAAACTCAGACTGTCTGCAACTTT ACAGATGGTGCATTGGTTCAGCATCAGGAGTGGGAT
FADD	NM_003824	849	GTTTTCGCGAGAT	850	CTCCGGTGCCTGATTC	851	AACGCGCTCTTGTCGATTTC	852	GTTTTCGCGAGATAACGGTCGAAAACGCGCTCTTTGTC
FAM107	NM_007177	853	AAGTCAGGGAAAA	854	GCTGGCCCTACAGCT	855	AATTGCCACACTGACCAGCG	856	AAGTCAGGGAAACCTGCGGAGAATTGCCACACTGA
FAM13C	NM_198215	857	ATCTTCAAAGCGG	858	GCTGGATACCACATG	859	TCCTGACTTTCTCCGTGGCT	860	ATCTTCAAAGCGGAGAGCGGGAGGAGCCACGGAGAA
FAM171 B	NM_177454	861	CCAGGAAGGAAAA GCACTGT	862	GTGGTCTGCCCCTTCT TTTA	863	TGAAGATTTTGAAGCTAATA CATCCCCCAC	864	CCAGGAAGGAAAAGCACTGTTGAAGATTTTGAAGCT AATACATCCCCCACTAAAAGAAGGGGCAGACCAC
FAM49B	NM_016623	865	AGATGCAGAAGGC	866	GCTGGATTGCCTCTC	867	TGGCCAGCTCCTCTGTATGA	868	AGATGCAGAAGGCATCTTGGAGGACTTGCAGTCATA
FAM73A	NM_198549	869	TGAGAAGGTGCGC TATTCAA	870	GGCCATTAAAAGCTC AGTGC	871	AAGACCTCATGCAGTTACTCATTCGCCGCACTGAG ATTCGCC	872	TGAGAAGGTGCGCTATTCAAGTACAGAGACTTTAGC TGAAGACCTCATGCAGTTACTCATTCGCCGCACTGAG
FAP	NM_004460	873	GTTGGCTCACGTG	874	GACAGGACCGAAACA	875	AGCCACTGCAAACATACTCG	876	GTTGGCTCACGTGGGTTACTGATGAACGAGTATGTTT
FAS	NM_000043	877	GGATTGCTCAACA ACCATGCT	878	GGCATTAACACTTTTG GACGATAA	879	TCTGGACCCTCCTACCTCTG GTTCTTACGT	880	GGATTGCTCAACAACCATGCTGGGCATCTGGACCCT CCTACCCTCTGGTTCTTACGTCTGTTGCTAGATTATCG
FASLG	NM_000639	881	GCACTTTGGGATT CTTTCCATTAT	882	GCATGTAAGAAGACC CTCACTGAA	883	ACAACATTCTCGGTGCCTGT AACAAAGAA	884	GCACTTTGGGATTCTTTCCATTATGATTCTTTGTTAC AGGCACCGAGAATGTTGTATTCAGTGAGGGTCTTCTT
FASN	NM_004104	885	GCCTCTTCCTGTTC	886	GCTTTGCCGGTAGC	887	TCGCCCACCTACGTACTGGC	888	GCCTCTTCCTGTTCGACGGCTCGCCCACCTACGTACT
FCGR3A	NM_000569	889	GTCTCCAGTGGAA	890	AGGAATGCAGCTACT	891	CCCATGATCTTCAAGCAGGG	892	GTCTCCAGTGGAAGGTGAAAAGCCCATGATCTTCAAG
FGF10	NM_004465	893	TCTTCCGTCCCTGT	894	AGAGTTGGTGGCCTC	895	ACACCATGTCCTGACCAAGG	896	TCTTCCGTCCCTGTCACCTGCCAAGGCCCTTGGTCAGG
FGF17	NM_003867	897	GGTGGCTGTCTCCTC	898	TCTAGCCAGGAGGAG	899	TTCTCGGATCTCCCTCAGTC	900	GGTGGCTGTCTCCTCAAAATCTGCTTCTCGGATCTCCCT
FGF5	NM_004464	901	GCATCGGTTTCCA	902	AACATATTGGCTTCGT	903	CCATTGACTTTGCCATCCGG	904	GCATCGGTTTCCATCTGCAGATCTACCCGGGATGGCAA
FGF6	NM_020996	905	GGGCCATTAATTC TGACCAC	906	CCCGGGACATAGTGA TGAA	907	CATCCACCTTGCCTCTCAGG CAC	908	GGGCCATTAATTCTGACCACGTGCCTGAGAGGCAAG GTGGATGGCCCTGGGACAGAAAACTGTTCATCACTAT
FGF7	NM_002009	909	CCAGAGCAAATGG CTACAAA	910	TCCCCTCCTTCCATGT AATC	911	CAGCCCTGAGCGACACACAA GAAG	912	CCAGAGCAAATGGCTACAAATGTGAACTGTTCCAGC CCTGAGCGACACACAAGAAGTTATGATTACATGGAA
FGFR2	NM_000141	913	GAGGGACTGTTGG CATGCA	914	GAGTGAGAATTCGAT CCAAGTCTTC	915	TCCCAGAGACCAACGTTCAA GCAGTTG	916	GAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACC AACGTTCAAGCAGTTGGATGAAGACTTGGATCGAAT
FGFR4	NM_002011	917	CTGGCTTAAGGAT GGACAGG	918	ACGAGACTCCAGTGC TGATG	919	CCTTTCATGGGGAGAACCGC ATT	920	CTGGCTTAAGGATGGACAGGCCTTTCATGGGGAGAA CCGCATTGGAGGCATTCGGCTGCGCCATCAGCACTG

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
FKBP5	NM_004117	921	CCCACAGTAGAGG	922	GGTTCTGGCTTTCACG	923	TCTCCCCAGTTCCACAGCAG	924	CCCACAGTAGAGGGGTCTCATGTCTCCCCAGTTCCAC
FLNA	NM_001456	925	GAACCTGCGGTGG	926	GAAGACACCCTGGCC	927	TACCAGGCCCATAGCACTGG	928	GAACCTGCGGTGGACACTTCCGGTGTCCAGTGCTAT
HLNC	NM_001458	929	CAGGACAATGGTG	930	TGATGGTGTACCTCGC	931	ATGTGCTGTCAGCTACCTGC	932	CAGGACAATGGTGATGGCTCATGTGCTGTCAGCTAC
FLT1	NM_002019	933	GGCTCCTGAATCT	934	TCCCACAGCAATACT	935	CTACAGCACCAAGAGCGAC	936	GGCTCCTGAATCTATCTTTGACAAAATCTACAGCACC
FLT4	NM_002020	937	ACCAAGAAGCTGA	938	CCTGGAAGCTGTAGC	939	AGCCCGCTGACCATGGAAGA	940	ACCAAGAAGCTGAGGACCTGTGGCTGAGCCCGCTGA
FN1	NM_002026	941	GGAAGTGACAGAC	942	ACACGGTAGCCGGTC	943	ACTCTCAGGCGGTGTCCACA	944	GGAAGTGACAGACGTGAAGGTCACCATCATGTGGAC
FOS	NM_005252	945	CGAGCCCTTTGAT GACTTCCT	946	GGAGCGGGCTGTCTC AGA	947	TCCCAGCATCATCCTGAGCCC	948	CGAGCCCTTTGATGACTTCCTGTTCCCAGCATCATCC AGGCCCAGTGGCTCTGAGACAGCCCGCTCC
FOXO1	NM_002015	949	GTAAGCACCATGC	950	GGGGCAGAGGCACTT	951	TATGAACCGCCTGACCCAAG	952	GTAAGCACCATGCCCCACACCTCGGGTATGAACCGC
FOXP3	NM_014009	953	CTGTTTGCTGTCCG	954	GTGGAGGAACTCTGG	955	TGTTTCCATGGCTACCCCAC	956	CTGTTTGCTGTCCGGAGGCACCTGTGGGGTAGCCAT
FOXQ1	NM_033260	957	TGTTTTTGTCGCAA	958	TGGAAAGGTTCCCTG	959	TGATTTATGTCCCAACTTCCCTC	960	TGTTTTTGTCGCAACTTCCATTGATTTATGTCCCTTCC
FSD1	NM_024333	961	AGGCCTCCTGTCC	962	TGTGTGAACCTGGTC	963	CGCACCCAAACAAGTGCTGCA	964	AGGCCTCCTGTGTCCTTCTACAATGCCCGCACCAAACAA
FYN	NM_002037	965	GAAGCGCAGATCA	966	CTCCTCAGACACCAC	967	CTGAAGCACGACAAGCTGGT	968	GAAGCGCAGATCATGAAGAAGCTGAAGCACGACAAG
G6PD	NM_000402	969	AATCTGCCTGTGG	970	CGAGATGTTGCTGGT	971	CCAGCCTCAGTGCCACTTGA	972	AATCTGCCTGTGGCCTTGCCCGCCAGCCTCAGTGCCA
GABRG2	NM_198904	973	CCACTGTCCTGAC AATGACC	974	GAGATCCATCGCTGT GACAT	975	CTCAGCACCATTGCCCGGAA AT	976	CCACTGTCCTGACAATGACCACCCTCAGCACCATTGC CCGGAAATCGCTCCCCCAAGGTCTCCTATGTCACAGC
GADD45	NM_001924	977	GTGCTGGTGACGA	978	CCCGGCAAAAACAAA	979	TTCATCTCAATGGAAGAATC	980	GTGCTGGTGACGAATCCACATTCATCTCAATGGAAG
GADD45	NM_015675	981	ACCCTCGACAAGA	982	TGGGAGTTCATGGGT	983	TGGGAGTTCATGGGTACAGA	984	ACCCTCGACAAGACCCACACTTTGGGAGCTTGGGAGCT
GDF15	NM_004864	985	CGCTCCAGACCTA	986	ACAGTGGAAGGACCA	987	TGTTAGCCAAAGACTGCCAC	988	CGCTCCAGACCTATGATGACTTGTTAGCCAAAGACTG
GHR	NM_000163	989	CCACCTCCCACAG	990	GGTGCGTGCCTGTAG	991	CGTGCCTCAGCCTCCTGAGT	992	CCACCTCCCACAGGTTCAGGCGATCCCGTGCCTCAG
GNPTAB	NM_024312	993	GGATTCACATCGC	994	GTTCTTGCATAACAAT	995	CCCTGCTCACATGCCTCACA	996	GGATTCACATCGCGGAAAGTCCCTGCTCACATGCCTC
GNRH1	NM_000825	997	AAGGGCTAAATCC AGGTGTG	998	CTGGATCTCTGTGGCT	999	TCCTGTCCTTCACTGTCCTT GCCA	1000	AAGGGCTAAATCCAGGTGTGACGGTATCTAATGATG TCCTGTCCTTCACTGTCCTTGCCATCACCAGCCACAG
GPM6B	NM_0010019 94	1001	ATGTGCTTGGAGT GGCCT	1002	TGTAGAACATAAACA CGGGCA	1003	CGCTGAGAAACCAAACACAC CCAG	1004	ATGTGCTTGGAGTGGCCTGGCTGGGTGTGTTTGGTTT CTCAGCGGTGCCCGTGTTTATGTTCTACA
GPNMB	NM_0010053 40	1005	CAGCCTCGCCTTT AAGGAT	1006	TGACAAATATGGCCA AGCAG	1007	CAAACAGTGCCCTGATCTCC GTTG	1008	CAGCCTCGCCTTTAAGGATGGCAAACAGTGCCCTGA TCTCCGTTGGCTGCTTGGCCATATTTGTCA
GPR68	NM_003485	1009	CAAGGACCAGATC	1010	GGTAGGGCAGGAAGC	1011	CTCAGCACCGTGGTCATCTT	1012	CAAGGACCAGATCCAGCCGGCTGGGTGCTCAGCACCGT
GPS1	NM_004127	1013	AGTACAAGCAGGC	1014	GCAGCTCAGGGAAGT	1015	CCTCCTGCTGGCTTCCTTTG	1016	AGTACAAGCAGGCTGCCAAGTGCCTCCTGCTGGCTT
GRB7	NM_005310	1017	CCATCTGCATCCA	1018	GGCCACCAGGGTATT	1019	CTCCCCACCCTTGAGAAGTG	1020	CCATCTGCATCCATCTTGTTTGGGCTCCCCACCCTTG
GREM1	NM_013372	1021	GTGTGGGCAAGGA	1022	GACCTGATTTGGCCT	1023	TCCACCCTCCCTTTCTACT	1024	GTGTGGGCAAGGACAAGCAGGATAGTGGAGTGAGAA
GSK3B	NM_002093	1025	GACAAGGACCGGC	1026	TTGTGGCCTGTCTGG	1027	CCAGGAGTTGCCACCACTGT	1028	GACAAGGACCGGCAGCAAGGTGACAACAGTGGTGGCA
GSN	NM_000177	1029	CTTCTGCTAAGCG TTCAC	1030	GGCTCAAAGCCTTGC GTACATCGA	1031	ACCCAGCCAATCGGGATCGG C	1032	CTTCTGCTAAGCGGTACATCGAGACCCAGCCA ATCGGGATCGGCGGACGCCCATCACCGTGGTGAAGC
GSTM1	NM_000561	1033	AAGCTATGAGGAA TTTCA	1034	GGCCCAGCTTGAATT AAGAAGTACACGA	1035	TCAGCCACTGGGCTTCTGTCA TAATCAGGAG	1036	AAGCTATGAGGAAAAGGGGGATTGGAAACCCAGAACCAG TCCTGATTATGACAGAAGCCAGTGGCTGAATGAAAA
GSTM2	NM_000848	1037	CTGCAGGCACTCC	1038	CCAAGAAACCATGGC	1039	CTGAAGCTCTACTCACAGTT	1040	CTGCAGGCACTCCCTGAAATGCTGAAGCTCTACTCAC
HDAC1	NM_004964	1041	CAAGTACCACAGC GATGACTACATTA	1042	GCTTGCTGTTACTCCG ACATGTTT	1043	TTCTTGCGCTCCATCCGTCC AGA	1044	CAAGTACCACAGCGATGACTACATTAAATTCTTGCGC TCCATCCGTCCAGATAACATGTCGGAAGTACAGCAAG
HDAC9	NM_178423	1045	AACCAGGCAGTCA CCTTGAG	1046	CTCTGTCTTCCTGCAT CGC	1047	CCCCCTGAAGCTCTTCCTCT GCTT	1048	AACCAGGCAGTCACCCCTGAAGCTCTTCCTCTGCTT TTCAGGGGGACCAGGCGATGCAGGAAGACAGAG
HGD	NM_000187	1049	CTCAGGTCTGCCC	1050	TTATTGGTGCTCCGTG	1051	CTGAGCAGCTCTCAGGATCG	1052	CTCAGGTCTGCCCCTACAATCTCTATGCTGAGCAGCT
HIP1	NM_005338	1053	CTCAGAGCCCCAC	1054	GGGTTTCCCTGCCAT	1055	CGACTCACTGACCGAGGCCT	1056	CTCAGAGCCCCACCTCACTGACCGACTCACTGACC
HIRIP3	NM_003609	1057	GGATGAGGAAAAG	1058	TCCCTAGCTGACTTTC	1059	CCATTGCTCCTGGTTCTGGG	1060	GGATGAGGAAAAGGGGGGATTGGAAACCCAGAACCAG
HK1	NM_000188	1061	TACGCACAGAGGC	1062	GAGAGAAGTGCTGGA	1063	TAAGAGTCCGGCATCCCCAG	1064	TACGCACAGAGGCAAGCAGCTAAGAGTCCGGCATCC
HLA-G	NM_002127	1065	CCATCCCCATCAT	1066	CCGCAGCTCCAGTGA	1067	CTGCAAGGACAACCAGGCC	1068	CCTGCGCGGCTACTACAACCAGAGCGAGGCCAGTTC
HLF	NM_002126	1069	CACCCTGCAGGTG	1070	GGTACCTAGGAGCAG	1071	TAAGTGATCTGCCCTCCAGG	1072	CACCCTGCAGGTGTCTGAGACTAAGTGATCTGCCCTC
HNF1B	NM_000458	1073	TCCCAGCATCTCA	1074	CGTACCAGGTGTACA	1075	CCCCTATGAAGACCCAGAAG	1076	TCCCAGCATCTCAACAAGGGCACCCCTATGAAGACC
HPS1	NM_000195	1077	GCGGAAGCTGTAT	1078	TTCGGATAAGATGAC	1079	CAGTCACCAGCCCAAAGTGC	1080	GCGGAAGCTGTATGTGCTCAAGTACCTGTTTGAAGT
HRAS	NM_005343	1081	GGACGAATACGAC	1082	GCACGTCTCCCCATC	1083	ACCACCTGCTTCCGGTAGGA	1084	GGACGAATACGACCCCACTATAGAGGATTCCTACCG

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
HSD17B10	NM_004493	1085	CCAGCGAGTTCTT GATGTGA	1086	ATCTCACCAGCCACC AGG	1087	TCATGGGCACCTTCAATGTG ATCC	1088	CCACCAGACAAGACCGATTCGCTGGCCTCCATTTCTT CAACCCAGTGCCTGTCATGAAACTTGTGG
HSD17B2	NM_002153	1089	GCTTTCCAAGTGG	1090	TGCCTGCGATATTTGT	1091	AGTTGCTTCCAATCCAACCTG	1092	GCTTTCCAAGTGGGGAATTAAAGTTGCTTCCAATCCAA
HSD17B3	NM_000197	1093	GGGACGTCCTGGA ACAGT	1094	TGGAGAATCTCACGC ACTTC	1095	CTTCATCCTCACAGGGCTGC TGGT	1096	GGGACGTCCTGGAACAGTTCTTCATCCTCACAGGGCT GCTGGTGTGCCTGGCCTGCCTGGCGAAGTGCGTGAG
HSD17B4	NM_000414	1097	CGGGAAGCTTCAG	1098	ACCTCAGGCCCAATA	1099	AGGCGGCGTCCTATTTCCTC	1100	CGGGAAGCTTCAGAGTACCTTTGTATTTGAGGAAAT
HSD3B2	NM_000198	1101	GCCTTCCTTTAACC	1102	GGAGTAAATTGGGCT	1103	ACTTCCAGCAGGAAGCCAAT	1104	GCCTTCCTTTAACCCTGATGTACTGGATTGGCTTCCT
HSP90AB1	NM_007355	1105	GCATTGTGACCAG CACCTAC	1106	GAAGTGCCTGGGCTT TCAT	1107	ATCCGCTCCATATTGGCTGT CCAG	1108	GCATTGTGACCAGCACCTACGGCTGGACAGCCAATA TGGAGCGGATCATGAAAGCCCAGGCACTTC
HSPA5	NM_005347	1109	GGCTAGTAGAACT GGATCCCCAACA	1110	GGTCTGCCCAAATGC TTTTC	1111	TAATTAGACCTAGGCCTCAG CTGCACTGCC	1112	GGCTAGTAGAACTGGATCCCCAACACCAAACTCTTAA TTAGACCTAGGCCTCAGCTGCACTGCCCGAAAAGCA
HSPA8	NM_006597	1113	CCTCCCTCTGGTG GTGCTT	1114	GCTACATCTACACTTG GTTGGCTTAA	1115	CTCAGGGCCCACCATTGAAG AGGTTG	1116	CCTCCCTCTGGTGCTTCCTCAGGGCCCACCATTG AAGAGGTTGATTAAGCCAACCAAGTGTAGATGTAGC
HSPB1	NM_001540	1117	CCGACTGGAGGAG CATAAA	1118	ATGCTGGCTGACTCT GCTC	1119	CGCACTTTTCTGAGCAGACG TCCA	1120	CCGACTGGAGGAGCATAAAAGCGCAGCCGAGCCCAG CGCCCCGCACTTTTCTGAGCAGACGTCCAGAGCAGA
HSPB2	NM_001541	1121	CACCACTCCAGAG	1122	TGGGACCAAACCATA	1123	CACCTTTCCCTTCCCCCAAG	1124	CACCACTCCAGAGGTAGCAGCATCCTTGGGGGGAAGG
HSPE1	NM_002157	1125	GCAAGCAACAGTA GTCGCTG	1126	CCAACTTTCAGGCTA ACTGGT	1127	TCTCCACCCTTTCCTTTAGA ACCCG	1128	GCAAGCAACAGTAGTCGCTGTTGGATCGGGTTCTAA AGGAAAGGGGTGGAGAGATTCAACCAGTTAGCGTGAA
HSPG2	NM_005529	1129	GAGTACGTGTGCC	1130	CTCAAATGGTGACCAG	1131	CAGCTCCGTGCCTCTAGAGG	1132	GAGTACGTGTGCCGAGTGTTGGGCAGCTCCGTGCCT
ICAM1	NM_000201	1133	GCAGACAGTGACC ATCTACAGCTT	1134	CTTCTGAGACCTCTG GCTTCGT	1135	CCGGCGCCCAACGTGATTCT	1136	GCAGACAGTGACCATCTACAGCTTTCCGGCGCCCAA CGTGATTCTGACGAAGCCAGAGGTCTCAGAAG
IER3	NM_003897	1137	GTACCTGGTGCGC GAGAG	1138	GCGTCTCCGCTGTAG TGTT	1139	TCAAGTTGCCTCGGAAGTCC CAGT	1140	GTACCTGGTGCGCGAGAGCGTATCCCCAACTGGGAC TTCCGAGGCAACTTGAACTCAGAACACTACAGCGGA
IFI30	NM_006332	1141	ATCCCATGTCTTAGTG	1142	GCACCATTCTTAGTG	1143	AAAATTCCACCCCATGATCA	1144	ATCCCATGAAGCCCAGATACACAAAATTCCACCCCA
IFIT1	NM_001548	1145	TGACAACCAAGCA	1146	CAGTCTGCCCCATGTG	1147	AAGTTGCCCCAGGTCACCAG	1148	TGACAACCAAGCAAATGTGAGGAGTCTGGTGACCTG
IFNG	NM_000619	1149	GCTAAAACAGGGA AGCGAAA	1150	CAACCATTACTGGGA TGCTC	1151	TCGACCTCGAAACAGCATCT GACTCC	1152	GCTAAAACAGGGAAGCGAAAAAGGAGTCAGATGCTG TTTCGAGGTCGAAGAGCATCCCAGTAATGGTTG
IGF1	NM_000618	1153	TCCGGAGCAGAGC	1154	CGGACAGAGGAGAGCT	1155	TGTATTGCGCACCCCTCAAG	1156	TCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATT
IGF1R	NM_000875	1157	GCATGGTAGCCGA GATTTCA	1158	TTTCCGGTAATAGTCT GTCTCATAGATATC	1159	CGCGTCATACCAAAATCTCC GATTTTGA	1160	GCATGGTAGCCGAAGATTTCACAGTCAAAATCGGAG ATTTTGGTATGACGCGAGATATCTATGAGACAGACTA
IGF2	NM_000612	1161	CCGTGCTTCCGGA	1162	TGGACTGCTTCCAGG	1163	TACCCCGTGGGCAAGTTCTT	1164	CCGTGCTTCCGGACAACTTCCCCAGATACCCCGTGGG
IGFBP2	NM_000597	1165	GTGGACAGCACCA	1166	CCTTCATACCCGACTT	1167	CTTCCGGCCAGCACTGCCTC	1168	GTGGACAGCACCATGAACATGTTGGGCGGGGAGGGC
IGFBP3	NM_000598	1169	ACATCCCAACGCA	1170	CCACGCCCTTGTTTCA	1171	ACACCACAGAAGGCTGTGA	1172	ACATCCCAACGCATGCTCCTGAGCTCACAGCCTTCT
IGFBP5	NM_000599	1173	TGGACAAGTACGG	1174	CGAAGGTGTGGCACT	1175	CCCGTCAACGTACTCCATGC	1176	TGGACAAGTACGGGATGAAGCTGCCAGGCATGGAGT
IGFBP6	NM_002178	1177	TGAACCGCAGAGA CCAACAG	1178	GTCTTGGACACCCGC AGAAT	1179	ATCCAGGCACCTCTACCACG CCCTC	1180	TGAACCGCAGAGACCAACAGAGGAATCCAGGCACCT CTACCACGCCCTCCCAGCCCAATTCTGCGGGTGTCCA
IL10	NM_000572	1181	CTGACCACGCTTT	1182	CCAAGCCCAGAGACA	1183	TTGAGCTGTTTTCCCTGACC	1184	CTGACCACGCTTTCTAGCTGTTTGAGCTGTTTTCCCTG
IL11	NM_000641	1185	TGGAAGGTTCCAC	1186	TCTTGACCTTGCAGCT	1187	CCTGTGATCAACAGTACCCG	1188	TGGAAGGTTCCACAAGTCACCCTGTGATCAACAGTA
IL17A	NM_002190	1189	TCAAGCAACACTC	1190	CAGCTCCTTTCTGGGT	1191	TGGCTTCTGTCTGATCAAGG	1192	TCAAGCAACACTCCTAGGGCCTGGCTTCTGTCTGATC
IL1A	NM_000575	1193	GGTCCTTGGTAGA	1194	GGATGGAGCTTCAGG	1195	TCTCCACCCTGGCCCTGTTA	1196	GGTCCTTGGTAGAGGGCTACTTTACTGTAACAGGGC
IL1B	NM_000576	1197	AGCTGAGGAAGAT	1198	GGAAAGAAGGTGCTC	1199	TGCCCACAGACCTTCCAGGA	1200	AGCTGAGGAAGATGCTGGTTCCCTGCCCACAGACCT
IL2	NM_000586	1201	ACCTCAACTCCTG CCACAAT	1202	CACTGTTGTGACAA GTGCAAG	1203	TGCAACTCCTGTCTTGCATT GCAC	1204	ACCTCAACTCCTGCCACAATGTGACAGGATGCAACTCC TGTCTTGCATTGCACTAAGTCTTGCACTTGTCACAAA
IL6	NM_000600	1205	CCTGAACCTTCCA	1206	ACCAGGCAAGTCTCC	1207	CCAGATTGGAAGCATCCATC	1208	CCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATG
IL6R	NM_000565	1209	CCAGCTTATCTCA	1210	CTGGCGTAGAACCTT	1211	CCTTTGGCTTCACGGAAGAG	1212	CCAGCTTATCTCAGGGGTGTGCGGCCTTTGGCTTCAC
IL6ST	NM_002184	1213	GGCCTAATGTTCC	1214	AAAATTGTGCCTTGG	1215	CATATTGCCCAGTGGTCACC	1216	GGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGC
IL8	NM_000584	1217	AAGGAACCATCTC ACTGTGT	1218	ATCAGGAAGGCTGCC AAGAG	1219	TGACTTCCAAGCTGGCCGTG GC	1220	AAGGAACCATCTCACTGTGTGTAAACATGACTTCCAA GCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGAT
ILF3	NM_004516	1221	GACACGCCAAGTG	1222	CTCAAGACCCGGATC	1223	ACACAAGACTTCAGCCCGTT	1224	GACACGCCAAGTGGTTCCAGGCCAGAGCCAACGGGC

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence:	SEQ ID NO	Reverse Primer Sequence:	SEQ ID NO	Probe Sequence:	SEQ ID NO	Amplicon Sequence:
ILK	NM_0010147 94	1225	CTCAGGATTTTCTC GCATCC	1226	AGGAGCAGGTGGAGA CTGG	1227	ATGTGCTCCCAGTGCTAGGT GCCT	1228	CTCAGGATTTTCTCGCATCCAAATGTGCTCCCAGTGC TAGGTGCCTGCCAGTCTCCACCTGCTCCT
IMMT	NM_006839	1229	CTGCCTATGCCAG	1230	GCTTTTCTGGCTTCCT	1231	CAACTGCAIGGCTCTGAACA	1232	CTGCCTAIGCCAGACTCAGAGGAATCGAACAGGCTG
ING5	NM_032329	1233	CCTACAGCAAGTG	1234	CATCTCGTAGGTCTG	1235	CCAGCTGCACTTTGTCGTCA	1236	CCTACAGCAAGTGCAAGGAATACAGTGACGACAAAG
INHBA	NM_002192	1237	GTGCCCGAGCCAT	1238	CGGTAGTGGTTGATG	1239	ACGTCCGGGTCCTCACTGTC	1240	GTGCCCGAGCCATATAGCAGGCACGTCCGGGTCCTC
INSL4	NM_002195	1241	CTGTCATATTGCCC	1242	CAGATTCCAGCAGCC	1243	TGAGAAGACATTCACCACCA	1244	CTGTCATATTGCCCCATGCCTGAGAAGACATTCACCA
ITGA1	NM_181501	1245	GCTTCTTCTGGAG	1246	CCTGTAGATAATGAC	1247	TTGCTGGACAGCCTCGGTAC	1248	GCTTCTTCTGGAGATGTGCTCTATATTGCTGGACAGC
ITGA3	NM_002204	1249	CCATGATCCTCAC	1250	GAAGCTTTGTAGCCG	1251	CACTCCAGACCTCGCTTAGC	1252	CCATGATCCTCACTCTGCTGGTGGACTATACACTCCA
ITGA4	NM_000885	1253	CAACGCTTCAGTG	1254	GTCTGGCCGGGATTC	1255	CGATCCTGCATCTGTAAATC	1256	CAACGCTTCAGTGATCAATCCCGGGCGATTTACAG
ITGA5	NM_002205	1257	AGGCCAGCCCTAC	1258	GTCTTCTCCACAGTCC	1259	TCTGAGCCTTGTCCTCTATC	1260	AGGCCAGCCCTACATTATCAGAGCAAGAGCCGATA
ITGA6	NM_000210	1261	CAGTGACAAACAG	1262	GTTTAGCCTCATGGG	1263	TCGCCATCTTTTGTGGAATT	1264	CAGTGACAAACAGCCCTTCCAACCCAAGGAATCCCA
ITGA7	NM_002206	1265	GATATGATTGGTC ACCAT	1266	AGAACTTCCATTCCCC GCTGCTTTG	1267	CAGCCAGGACCTGGCCATCC G	1268	GATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGACC TGGCCATCCGGGATGAGTTGGATGGTGGGAATGGA
ITGAD	NM_005353	1269	GAGCCTGGTGGAT	1270	ACTGTCAGGATGCCC	1271	CAACTGAAAGGCCTGACGTT	1272	GAGCCTGGTGGATCCCATCGTCCAACTGAAAGGCCT
ITGB3	NM_000212	1273	ACCGGGAGCCCTA CATGAC	1274	CCTTAAGCTCTTTCAC TGACTCAATCT	1275	AAATACCTGCAACCGTTACT GCCGTGAC	1276	ACCGGGAGCCCTACATGACGAAAATACCTGCAACC GTTACTGCCGTGACGAGATTGAGTCAGTGAAAGAGC
ITGB4	NM_000213	1277	CAAGGTGCCCTCA	1278	GCGCACACCTTCATC	1279	CACCAACCTGTACCCGTATT	1280	CAAGGTGCCCTCAGTGGAGCTCACCAACCTGTACCC
ITGB5	NM_002213	1281	TCGTGAAAGATGA	1282	GGTGAACATCATGAC	1283	TGCTATGTTTCTACAAAACC	1284	TCGTGAAAGATGACCAGGAGGCTGTGCTATGTTTCTA
ITPR1	NM_002222	1285	GAGGAGGTGTGGG	1286	GTAATCCCATGTCCG	1287	CCATCCTAACGGAACGAGCT	1288	GAGGAGGTGTGGGTTCCGCTTCCATCCTAACGGGA
ITPR3	NM_002224	1289	TTGCCATCGTGTC	1290	ATGGAGCTGGCGTCA	1291	TCCAGGTCTCGGAATCTCAGA	1292	TTGCCATCGTGTCAGTGCCCGTGTCTGAGAATCCGAGA
ITSN1	NM_003024	1293	TAACTGGGATGCA	1294	CTCTGCCTTAACTGGC	1295	AGCCCTCTCTCACCGTTCCA	1296	TAACTGGGATGCATGGGCAGCCCAGCCCTCTCTCAC
JAG1	NM_000214	1297	TGGCTTACACTGG	1298	GCATAGCTGTGAGAT	1299	ACTCGATTTCCCAGCCAACC	1300	TGGCTTACACTGGCAATGGTAGTTTCTGTGGTTGGCT
JUN	NM_002228	1301	GACTGCAAAGATG GAAACGA	1302	TAGCCATAAGGTCCG CTCTC	1303	CTATGACGATGCCCCTCAACG CCTC	1304	GACTGCAAAGATGGAAACGACCTTCTATGACGATGC CCTCAACGCCTCGTTCCTCCCGTCCGAGAGCGGACCT
JUNB	NM_002229	1305	CTGTCAGCTGCTG	1306	AGGGGGTGTCCGTAA	1307	CAAGGGACACGCCTTCTGAA	1308	CTGTCAGCTGCTGCTTGGGGTCAAGGGACACGCCTT
KCNN2	NM_021614	1309	TGTGCTATTCATCC	1310	GGGCATAGGAGAAGG	1311	TTATACATTCACATGGACGG	1312	TGTGCTATTCATCCCATACCTGGGAATTATACATTCA
KCTD12	NM_138444	1313	AGCAGTTACTGGC	1314	TGGAGACCTGAGCAG	1315	ACTCTTAGGCGGCAGCGTCC	1316	AGCAGTTACTGGCAAGAGGGAGAAAGGACGCTGCCG
KHDRBS	NM_006558	1317	CGGGCAAGAAGAG	1318	CTGTAGAACGCCCTTT	1319	CAAGACACAAGGCACCTTCA	1320	CGGGCAAGAAGAGTGGAACTAACTCAAGACACAAGGC
KIAA019	NM_014846	1321	CAGACACCAGCTC	1322	AACATTGTGAGGCGG	1323	TCCCCAGTGTCCAGGCACAG	1324	CAGACACCAGCTCTGAGGCCAGTTAATCATCCCCCAG
KIAA024	NM_014734	1325	CCGTGGGACATGG	1326	GAAGCAAGTCCGTCT	1327	TCCGCTAGTGATCCTTTGCA	1328	CCGTGGGACATGGAGTGTTCCTTCCGCTAGTGATCCT
KIF4A	NM_012310	1329	AGAGCTGGTCTCC	1330	GCTGGTCTTGCTCTGT	1331	CAGGTCAGCAAACTTGAAAG	1332	AGAGCTGGTCTCCTCCAAAATACAGGTCAGCAAACT
KIT	NM_000222	1333	GAGGCAACTGCTT ATGGCTTAATTA	1334	GGCACTCGGCTTGAG CAT	1335	TTACAGCGACAGTCATGGCC GCAT	1336	GAGGCAACTGCTTATGGCTTAATTAAGTCAGATGCG GCCATGACTGTCGCTGTAAAGATGCTCAAGCCGAGT
KLC1	NM_182923	1337	AGTGGCTACGGGA	1338	TGAGCCACACAGACTGC	1339	CAACACGCAGCAGAAACTG	1340	AGTGGCTACGGGATGAACTGGCCAACACGCAGCAGA
KLF6	NM_001300	1341	CACGAGACCGGCT	1342	GCTCTAGGCAGGTCT	1343	AGTACTCCTCCAGAGACGGC	1344	CACGAGACCGGCTACTTCTCGGCGCTGCCGTCTCTGG
KLK1	NM_002257	1345	AACACAGCCCAGT TTGTTCA	1346	CCAGGAGGCTCATGT TGAAG	1347	TCAGTGAGAGCTTCCCACAC CCTG	1348	AACACAGCCCAGTTTGTTCATGTCAGTGAGAGCTTCC CACACCCTGGCTTCAACATGAGCCTCCTGG
KLK10	NM_002776	1349	GCCCAGAGGCTCC	1350	CAGAGGTTTGAACAG	1351	CCTCTTCCTCCCCAGTCGGC	1352	GCCCAGAGGCTCCATCGTCCATCCTCTTCCTCCCCAG
KLK11	NM_006853	1353	CACCCCCGGCTTCA	1354	CATCTTCACCAGCAT	1355	CCTCCCCCAACAAAGACCACC	1356	CACCCCGGCTTCAACAACAGCCCTCCCCCAACAAAGAC
KLK14	NM_022046	1357	CCCCTAAAATGTT	1358	CTCATCCTCTTGGCTC	1359	CAGCACTTCAAGTCCTGGCT	1360	CCCCTAAAATGTTCCTCGCTGACAGCACTTCAAGT
KLK2	NM_005551	1361	AGTCTCGGATTGT	1362	TGTACACAGCCACCT	1363	TTGGGAATGCTTCTCACACT	1364	AGTCTCGGATTGTGGGAGGCTGGGAGTGTGAGAAGC
KLK3	NM_001648	1365	CCAAGCTTACCAC	1366	AGGGTGAGGAAGACA	1367	ACCCACATGGTGACACAGCT	1368	CCAAGCTTACCACCTGCACCCGGAGAAGCTGTGTCAC
KLRK1	NM_007360	1369	TGAGAGCCAGGCT	1370	ATCCTGGTCCTCTTTG	1371	TGTCTCAAAATGCCAGCCTT	1372	TGAGAGCCAGGCTTCTTGTATGTCTCAAAATGCCAGC
KPNA2	NM_002266	1373	TGATGGTCCCAAAT	1374	AAGCTTCACAAGTTG	1375	ACTCCTGTTTTCACCACCAT	1376	TGATGGTCCAAATGAACGAATTGGCATGGTGGTGAA
KRT1	NM_006121	1377	TGGACAACAACCG	1378	TATCCTCCGTACTGGG	1379	CCTCAGCAATGATGCTGTCC	1380	TGGACAACAACCGCAGTCTCGACCTGGACAGCATCA
KRT15	NM_002275	1381	GCCTGGTTCTTCA	1382	CTTGCTGGTCTGGATC	1383	TGAACAAAGAGGTGGCCTCC	1384	GCCTGGTTCTTCAGCAAGACTGAGGAGCTGAACAAA
KRT18	NM_000224	1385	AGAGATCGAGGCT	1386	GGCCTTTTACTTCCTC	1387	TGGTTCTTCTTCATGAAGAG	1388	AGAGATCGAGGCTCTTCTTGAGGAGGAGCTGCTTCAT
KRT2	NM_000423	1389	CCAGTGACGCCTC	1390	GGGCATGGCTAGAAG	1391	ACCTAGACAGCACAGATTCC	1392	CCAGTGACGCCTCTGTGTTCTGGGGCGGAATCTGTGC
KRT5	NM_000424	1393	TCAGTGGAGATCCAGAGG	1394	TGCCATATCCAGAGG	1395	CCAGTCAACATCTCTGTTGT	1396	TCAGTGGAGAAGGAGTTGGACCAGTCAACATCTCTG

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
KRT75	NM_004693	1397	TCAAAGTCAGGTA CGAAGATGAAATT	1398	ACGTCCTTTTTCAGGG CTACAA	1399	TTCATTCTCAGCAGCTGTGC GCTTGT	1400	TCAAAGTCAGGTACGAAGATGAAATTAACAAGCGCA CAGCTGCTGAGAATGAATTGTAGCCCTGAAAAAGG
KRT76	NM_015848	1401	ATCTCCAGACTGC TGGTTCC	1402	TCAGGGAATTAGGGG ACAGA	1403	TCTGGGCTTCAGATCCTGAC TCCC	1404	ATCTCCAGACTGCTGGTTCCCAGGGAACCCTCCCTAC ATCTGGGCTTCAGATCCTGACTCCCTTCTGTCCCTA
KRT8	NM_002273	1405	GGATGAAGCTTAC ATGAACAAGGTAG	1406	CATATAGCTGCCTGA GGAAGTTGAT	1407	CGTCGGTCAGCCCTTCCAGG C	1408	GGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTC TCGCCTGGAAGGGCTGACCGAGATCAACTTCCT
LJCAM	NM_000425	1409	CTTGCTGGCCAAT	1410	TGATTGTCCGCAGTC	1411	ATCTACGTTGTCCAGCTGCC	1412	CTTGCTGGCCAATGCCTACATCTACGTTGTCCAGCTG
LAG3	NM_002286	1413	GCCTTAGAGCAAG	1414	CGGTTCTTGCTCCAGC	1415	TCTATCTTGCTCTGAGCCTG	1416	GCCTTAGAGCAAGGGATTCACCCTCCGCAGGCTCAG
LAMA3	NM_000227	1417	CCTGTCACTGAAG	1418	TGGGTTACTGGTCAG	1419	ATTCAGACTGACAGGCCCCT	1420	CCTGTCACTGAAGCCTTGGAAGTCCAGGGGCCTGTC
LAMA4	NM_002290	1421	GATGCACTGCGGT	1422	CAGAGGATACGCTCA	1423	CTCTCCATCGAGGAAGGCAA	1424	GATGCACTGCGGTTAGCAGCGCTCTCCATCGAGGAA
LAMA5	NM_005560	1425	CTCCTGGCCAACA	1426	ACACAAGGCCCAGCC	1427	CTGTTCCTGGAGCATGGCCT	1428	CTCCTGGCCAACAGCACTGCACTAGAAGAGGCCATG
LAMB1	NM_002291	1429	CAAGGAGACTGGG	1430	CGGCAGAACTGACAG	1431	CAAGTGCCTGTACCACACGG	1432	CAAGGAGACTGGGAGGTGTCTCAAGTGCCTGTACCA
LAMB3	NM_000228	1433	ACTGACCAAGCCT	1434	GTCACACTTGCAGCA	1435	CCACTCGCCATACTGGGTGC	1436	ACTGACCAAGCCTGAGACCTACTGCACCCAGTATGG
LAMC1	NM_002293	1437	GCCGTGATCTCAG	1438	ACCTGCTTGCCCAAG	1439	CCTCGGTACTTCATTGCTCC	1440	GCCGTGATCTCAGACAGCTACTTTCCTCGGTACTTCA
LAMC2	NM_005562	1441	ACTCAAGCGGAAA TTGAAGCA	1442	ACTCCCTGAAGCCGA GACACT	1443	AGGTCTTATCAGCACAGTCT CCGCCTCC	1444	ACTCAAGCGGAAATTGAAGCAGATAGGTCTTATCAG CACAGTCTCCGCCTCCTCCTGGATTCAGTGTCTCGGCTTC
LAPTM5	NM_006762	1445	TGCTGGACTTCTG	1446	TGAGATAGGTGGGCA	1447	TCCTGACCCTCTGCAGCTCC	1448	TGCTGGACTTCTGCCTGAGCATCCTGACCCTCTGCAG
LGALS3	NM_002306	1449	AGCGGAAAATGGC	1450	CTTGAGGGTTTGGGT	1451	ACCCAGATAACGCATCATGG	1452	AGCGGAAAATGGCAGACAATTTTCGCTCCATGATG
LIG3	NM_002311	1453	GGAGGTGTCATCAGC	1454	ACAGGTGTCATCAGC	1455	CTGGACGCTCAGAGCTCGTC	1456	GGAGGTGGAGAAGGAGCCGGCCAGAGACGAGCTCT
LIMS1	NM_004987	1457	TGAACAGTAATGG	1458	TTCTGGGAACTGCTG	1459	ACTGAGCGCACACGAAACA	1460	TGAACAGTAATGGGGAGCTGTACCATGAGCAGTGTT
LOX	NM_002317	1461	CCAATGGGAGAAC	1462	CGCTGAGGCTGGTAC	1463	CAGGCTCAGCAAGCTGAACA	1464	CCAATGGGAGAACAACGGGCAGGTGTTCAGCTTGCT
LRP1	NM_002332	1465	TTTGGCCCAATGG GCTAAG	1466	GTCTCGATGCGGTCG TAGAAG	1467	TCCCGGCTGGGCGCCTCTAC T	1468	TTTGGCCCAATGGGCTAAGCCTCGGACATCCCGGCTG GGCGCCTCTACTGGGTGGATGCCTTCTCACGACCGCAT
LTBP2	NM_000428	1469	GCACACCCATCCT	1470	GATGGCTGGCCACGT	1471	CTTTGCAGCCCTCAGAACTC	1472	GCACACCCATCCTTGAGTCTCCTTTGCAGCCCTCAGA
LUM	NM_002345	1473	GGCTCTTTTGAAG GATTGGTAA	1474	AAAAGCAGCTGAAAC AGCATC	1475	CCTGACCTTCATCCATCTCC AGCA	1476	GGCTCTTTTGAAGGATTGGTAAACCTGACCTTCATCC ATCTCCAGCACAATCGGCTGAAAGAGGATGCTGTTT
MAGEA4	NM_002362	1477	GCATCTAACAGCC	1478	CAGAGTGAAGAATGG	1479	CAGCTTCCCTTGCCTCGTGT	1480	GCATCTAACAGCCCTGTGCAGCAGCTTCCCTTGCCTC
MANF	NM_006010	1481	CAGATGTGAAGCC	1482	AAGGGAATCCCCTCA	1483	TTCCTGATGATGCTGGCCCT	1484	CAGATGTGAAGCCTGGAGCTTTCCTGATGATGCTGG
MAOA	NM_000240	1485	GTGTCAGCCAAAG	1486	CGACTACGTCGAACA	1487	CCGCGATACTCGCCTTCTCT	1488	GTGTCAGCCAAAGCATGGAGAATCAAGAGAAGGCGA
MAP3K5	NM_005923	1489	AGGACCCAAGAGG	1490	CCTGTGGCCATTTCA	1491	CAGCCCAGAGACCAGATGTC	1492	AGGACCCAAGAGGCTACGGAAAAGCAGCAGACATCTG
MAP3K7	NM_145333	1493	CAGGCAAGAACTA GTTGCAGAA	1494	CCTGTACCAGGCGAG ATGTAT	1495	TGCTGGTCCTTTTCATCCTG GTCC	1496	CAGGCAAGAACTAGTTGCAGAACTGGACCAGGATGA AAAGGACCAGCAAAATACATCTCGCCTGGTACAGG
MAP4K4	NM_004834	1497	TCGCCGAGATTTC	1498	CTGTTGTCTCCGAAG	1499	AACGTTCCTTGTTCTCCTGC	1500	TCGCCGAGATTTCCTGAGACTGCAGCAGGAGAACAA
MAP7	NM_003980	1501	GAGGAACAGAGGT	1502	CTGCCAACTGGCTTTC	1503	CATGTACAACAAACGCTCCG	1504	GAGGAACAGAGGTGTCTGCACTTCCATGTACAACAA
MAPKAPK3	NM_004635	1505	AAGCTGCAGAGAT AATGCGG	1506	GTGGGCAATGTTTATG GCTG	1507	ATTGGCACTGCCATCCAGTT TCTG	1508	AAGCTGCAGAGATAATGCGGGATATTGGCACTGCCA TCCAGTTTCTGCACAGCCATAACATTGCCCAC
MCM2	NM_004526	1509	GACTTTTGCCCGC TACCTTTC	1510	GCCACTAACTGCTTC AGTATGAAGAG	1511	ACAGCTCATTGTTGTCACGC CGGA	1512	GACTTTTGCCCGCTACCTTTCATTCCGGCGTGACAAC AATGAGCTGTTGCTCTTCATACTGAAGCAGTTAGTGG
MCM3	NM_002388	1513	GGAGAAACAATCCC	1514	ATCTCCTGGATGGTG	1515	TGGCCTTTCTGTCTACAAGG	1516	GGAGAACAATCCCCTTGAGACAGAATATGGCCTTTC
MCM6	NM_005915	1517	TGATGGTCCTATG TGTCACATTCA	1518	TGGGACAGGAAACAC ACCAA	1519	CAGGTTTCATACCAACACAG GCTTCAGCAC	1520	TGATGGTCCTATGTGTCACATTCATCACAGGTTTCAT ACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTC
MDK	NM_002391	1521	GGAGCCGACTGCA	1522	GACTTTGGTGCCTGT	1523	ATCACACGCACCCCAGTTCT	1524	GGAGCCGACTGCAAGTTACAAGTTTGAGAACTGGGGT
MDM2	NM_002392	1525	CTACAGGGACGCC	1526	ATCCAACCAATCACC	1527	CTTACACCAGCATCAAGATC	1528	CTACAGGGACGCCATCGAATCCGGATCTTGATGCTG
MELK	NM_014791	1529	AGGATCGCCTGTC	1530	TGCACATAAGCAACA	1531	CCCGGGTTGTCTTCCGTCAG	1532	AGGATCGCCTGTCAGAAGAGGAGACCCGGGTTGTCT
MET	NM_000245	1533	GACATTTCCAGTC CTGCAGTCA	1534	CTCCGATCGCACACA TTTGT	1535	TGCCTCTCTGCCCCACCCTT TGT	1536	GACATTTCCAGTCCTGCAGTCAATGCCTCTCTGCCCC ACCCTTTGTTCAGTGTGGCTGGTGCCACGACAAATGT
MGMT	NM_002412	1537	GTGAAATGAAACG	1538	GACCCTGCTCACAAC	1539	CAGCCCTTTGGGGAAGCTGG	1540	GTGAAATGAAACGCACCACACTGGACAGCCCTTTGG
MGST1	NM_020300	1541	ACGGATCTACCAC ACCATTGC	1542	TCCATATCCAACAAA AAACTCAAAG	1543	TTTGACACCCCTTCCCCAGC CA	1544	ACGGATCTACCACACCATTGCATATTTGACACCCCTT CCCCAGCCAAATAGAGCTTTGAGTTTTTTTGTGGAT
MICA	NM_000247	1545	ATGGTGAATGTCA	1546	AAGCCAGAAGCCCTG	1547	CGAGGCCTCAGAGGGCAAC	1548	ATGGTGAATGTCACCCGCAGCGAGGCCTCAGAGGGC

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
MKI67	NM_002417	1549	GATTGCACCAGGG	1550	TCCAAAGTGCCTCTG	1551	CCACTCTTCCTTGAACACCC	1552	GATTGCACCAGGGCAGAACAGGGGAGGGTGTTCAAG
MLXIP	NM_014938	1553	TGCTTAGCTGGCA	1554	CAGCCTACTCTCCAT	1555	CATGAGATGCCAGGAGACCC	1556	TGCTTAGCTGGCATGTGGCCGCATGAGATGCCAGGA
MMP11	NM_005940	1557	CCTGGAGGCTGCA ACATACC	1558	TACAATGGCTTTGGA GGATAGCA	1559	ATCCTCCTGAAGCCCTTTTC GCAGC	1560	CCTGGAGGCTGCAACAATACCTCAATCCTGTCCCAGG CCGGATCCTCCTGAAGCCCTTTTCGCAGCACTGCTAT
MMP2	NM_004530	1561	CAGCCAGAAGCGG	1562	AGACACCATCACCTG	1563	AAGTCCGAATCTCTGCTCCC	1564	CAGCCAGAAGCGGAAACTTAAAAAGTCCGAATCTCT
MMP7	NM_002423	1565	GGATGGTAGCAGT CTAGGGATTAACT	1566	GGAATGTCCCATACC CAAAGAA	1567	CCTGTATGCTGCAACTCATG AACTTGGC	1568	GGATGGTAGCAGTCTAGGGATTAACTTCCTGTATGCT GCAACTCATGAACTTGGCCATTCTTTGGGTATGGGAC
MMP9	NM_004994	1569	GAGAACCAATCTC	1570	CACCCGAGTGTAACC	1571	ACAGGTATTCCTCTGCCAGC	1572	GAGAACCAATCTCACCCGACAGGCAGCTGGCAGAGTA
MPPED2	NM_001584	1573	CCGACCAACCCTC	1574	AGGGCATTTAGAGCT	1575	ATTTGACCTTCCAAACCCAC	1576	CCGACCAACCCTCCAATTATATTTGACCTTCCAAACC
MRC1	NM_002438	1577	CTTGACCTCAGGA	1578	GGACTGCGGTCACTC	1579	CCAACCGCTGTTGAAGCTCA	1580	CTTGACCTCAGGACTCTGGAATTGGACTTAACAGTCTG
MRPL13	NM_014078	1581	TCCGGTTCCCTTCG	1582	GTGGAAAAACTGCGG	1583	CGGCTGGAAATTATGTCCTC	1584	TCCGGTTCCCTTCGTTTAGGTCGGCTGGAAATTATGT
MSH2	NM_000251	1585	TGATGCAGAATTGA	1586	TCTTGGCAAGTCGGT	1587	CAAGAAGATTTACTTCGTCG	1588	GATGCAGAATTGAGGCAGACTTTACAAGAAGATTTA
MSH3	NM_002439	1589	TGATTACCATCAT GGCTCAGA	1590	CTTGTGAAAATGCCA TCCAC	1591	TCCCAATTGTCGCTTCTTCT GCAG	1592	TGATTACCATCATGGCTCAGATTGGCTCCTATGTTCC TGCAGAAGAAGCGACAATTGGGATTGTGGATGGCAT
MSH6	NM_000179	1593	TCTATTGGGGGAT	1594	CAAATTGCGAGTGGT	1595	CCGTTACCAGCTGGAAATTC	1596	TCTATTGGGGGATTGGTAGGAACCGTTACCAGCTGG
MTA1	NM_004689	1597	CCGCCCTCACCTG AAGAGA	1598	GGAATAAGTTAGCCG CGCTTCT	1599	CCCAGTGTCCGCCAAGGAGC G	1600	CCGCCCTCACCTGCAGAGAAACGCGCTCCTTGGCGG ACACTGGGGAGAGGAAGAAGGCGCGGCTAACTT
MTPN	NM_145808	1601	GGTGGAAGGAAAC	1602	CAGCAGCAGAAATTC	1603	AAGCTGCCCACAATCTGCTG	1604	GGTGGAAGGAAACCTCTTCATTATGCAGCAGATTGT
MTSS1	NM_014751	1605	TTCGGACAAGTCCT	1606	CTTGGAACAATCCGTC	1607	CCAAGAAACAGCGACATCA	1608	TTCGACAAGTCCTCCACCATTCCAAGAAACAGCGAC
MUC1	NM_002456	1609	GGCCAGGATCTGT GGTGGTA	1610	CTCCACGTCGTGGAC ATTGA	1611	CTCTGGCCTTCCGAGAAGGT ACC	1612	GGCCAGGATCTGTGGTGGTACAATTGACTCTGGCCTT CCGAGAAGGTACCATCAATGTCCACGACGTGGAG
MVP	NM_017458	1613	ACGAGAACGAGGG CATCTATGT	1614	GCATGTAGGTGCTTC CAATCAC	1615	CGCACCTTTCCGGTCTTGAC ATCCT	1616	ACGAGAACGAGGGCATCTATGTGCAGGATGTCAAGA CCGGAAAGGTGCGCGCTGTGATTGGAAGCACCTACA
MYBL2	NM_002466	1617	GCCGAGATCGCCA AGATG	1618	CTTTTGATGGTAGAG TTCCAGTGATTC	1619	CAGCATTGTCTGTCCTCCCT GGCA	1620	GCCGAGATCGCCAAGATGTTGCCAGGGAGGACAGAC AATGCTGTGTAAGAAATCACTGGAACTCTACCATCAAA
MYBPC1	NM_002465	1621	CAGCAACCAGGGA	1622	CAGCAGTAAGTGCCT	1623	AAATTCGCAAGCCCCAGCCCC	1624	CAGCAACCAGGGAGTCTGTACCCTGGAAATTCGCAA
MYC	NM_002467	1625	TCCCTCCACTCGG AAGGACTA	1626	CGGTTGTTGCTGATCT GTCTCA	1627	TCTGACACTGTCCAACTTGA CCCTCTT	1628	TCCCTCCACTCGGAAGGACTATCCTGCTGCCAAGAG GGTCAAGTTGGACAGTGTCAGAGTCCTGAGACAGAT
MYLK3	NM_182493	1629	CACCTGACTGAGC TGGATGT	1630	GATGTAGTGCTGGTG CAGGT	1631	CACACCCTCACAGATCTGCC TGGT	1632	CACCTGACTGAGCTGGATGTGGTCCTGTTCACCAGGC AGATCTGTGAGGGTGTGCATTACCTGCACCAGCACT
MYO6	NM_004999	1633	AAGCAGTTCTGGA	1634	GATGAGCTCGGCTTC	1635	CAATCCTCAGGGCCAGCTCC	1636	AAGCAGTTCTGGAGCAGGAGCGCAGGGACCGGGAGC
NCAM1	NM_000615	1637	TAGTTCCCAGCTG	1638	CAGCCTTGTTCTCAGC	1639	CTCAGCCTCGTTCTTTAT	1640	TAGTTCCCAGCTGACCATCAAAAAGGTGGATAAGAA
NCAPD3	NM_015261	1641	TCGTTGCTTAGAC	1642	CTCCAGACAGTGTGC	1643	CTACTGTCCGCAGCAAGGCA	1644	TCGTTGCTTAGACAAGGCGCCTACTGTCCGCAGCAA
NCOR1	NM_006311	1645	AACCGTTACAGCC	1646	TCTGGAGAGACCCTT	1647	CCAGGCTCAGTCTGTCCATC	1648	AACCGTTACAGCCCAGAATCCCAGGCTCAGTCTGTCC
NCOR2	NM_006312	1649	CGTCATCTACGAA	1650	GAGCACTGGGTCACA	1651	CCTCATAGGACAAGACGTGG	1652	CGTCATCTACGAAGGCAAGAAGGGCCACGTCTTGTC
NDRG1	NM_006096	1653	AGGGCAACATTCC	1654	CAGTGCTCCTACTCC	1655	CTGCAAGGACACTCATCACA	1656	AGGGCAACATTCCACAGCTGCCCTGCTGTGATGAG
NDUFS5	NM_004552	1657	AGAAGAGTCAAGG	1658	AGGCCGAACCTTTTC	1659	TGTCCAAGAAAGGCATGGCT	1660	AGAAGAGTCAAGGGCACGAGCATCGGGTAGCCATGC
NEK2	NM_002497	1661	GTGAGGCAGCGCG ACTCT	1662	TGCCAATGGTGTACA ACACTTCA	1663	TGCCTTCCCGGGCTGAGGAC T	1664	GTGAGGCAGCGCGACTCTGGCGACTGGCCCGGCCATG CCTTCCCGGGCTGAGGACTATGAAGTGTTGTACACC
NETO2	NM_018092	1665	CCAGGGCACCATA	1666	AACGGTAAATCAAGG	1667	AGCCAACCCTTTTCTCCCAT	1668	CCAGGGCACCATCAGTCCAGCCAACCCTTTT
NEXN	NM_144573	1669	AGGAGGAGGAAGA	1670	GAGCTCCTGATCTGG	1671	TCATCTTCAGCAGTGGAGCC	1672	AGGAGGAGGAAGAAGGTAGCATCATGAATGGCTCCA
NFAT5	NM_006599	1673	CTGAACCCCTCTC	1674	AGGAAACGATGGCGA	1675	CGAGAATCAGTCCCCGTGGA	1676	CTGAACCCCTCTCCTGGTCACCGAGAATCAGTCCCCG
NFATC2	NM_173091	1677	CAGTCAAGGTCAG	1678	CTTTGGCTCGTGGCAT	1679	CGGGTTCCTACCCCACAGTC	1680	CAGTCAAGGTCAGAGGCTGAGCCCCGGGTTCCTACCC
NFKB1	NM_003998	1681	CAGACCAAGGAGA	1682	AGCTGCCAGTGCTAT	1683	AAGCTGTAAACATGAGCCGC	1684	CAGACCAAGGAGATGGACCTCAGCGTGGTGCGGCTC
NFKBIA	NM_020529	1685	CTACTGGACGACC	1686	CCTTGACCATCTGCTC	1687	CTCGTCTTTCATGGAGTCCA	1688	CTACTGGACGACCGACCACGACAGCGGCCTGGACTCC
NME1	NM_000269	1689	CCAACCCTGCAGA CTCCAA	1690	ATGTATAATGTTCCTG CCAACTTGTATG	1691	CCTGGGACCATCCCGTGGAGA	1692	CCAACCCTGCAGACTCCAAGCCTGGGACCATCCGTG GAGACTTCTGCATACAAGTTGGCAGGAACATTATAC
NNMT	NM_006169	1693	CCTAGGGCAGGGA	1694	CTAGTCCAGCCAAAC	1695	CCCTCTCCTCATGCCCAGAC	1696	CCTAGGGCAGGGATGGAGAGAGAGTCTGGGCATGAG
NOS3	NM_000603	1697	ATCTCCGCCTCGC	1698	TCGGAGCCATACAGG	1699	TTCACTCGCTTCGCCATCAC	1700	ATCTCCGCCTCGCTCATGGGCACGGTGATGGCGAAG

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence:	SEQ ID NO	Reverse Primer Sequence:	SEQ ID NO	Probe Sequence:	SEQ ID NO	Amplicon Sequence:
NOX4	NM_016931	1701	CCTCAACTGCAGC CTTATCC	1702	TGCTTGGAACCTTCTG TGAT	1703	CCGAACACTCTTGGCTTACC TCCG	1704	CCTCAACTGCAGCCTTATCCTTTTACCCATGTGCCGA ACACTCTTGGCTTACCTCCGAGGATCACAGAAGGTTC
NPBWR1	NM_005285	1705	TCACCAACCTGTT	1706	GATGTTGAATGGGCAG	1707	ATCGCCGACGAGCTCTTTCAC	1708	TCACCAACCTGTTCATCCTTCAACCTGGCCATCGCCGA
NPM1	NM_002520	1709	AATGTTGTCCAGG TTCTATTGC	1710	CAAGCAAAGGGTGGA GTTC	1711	AACAGGCATTTTGGACAACA CATTCTTG	1712	AATGTTGTCCAGGTTCTATTGCCAAGAATGTGTTGTC
NRG1	NM_013957	1713	CGAGACTCTCCTC ATAGTGAAAGGTA	1714	CTTGGCGTGTGGAAA TCTACAG	1715	ATGACCACCCCGGCTCGTAT GTCA	1716	CGAGACTCTCCTCATAGTGAAAGGTATGTGTCAGCC ATGACCACCCCGGCTCGTATGTCACCTGTAGATTTCC
NRIP3	NM_020645	1717	CCCACAAGCATGA	1718	TGCTCAATCTGGCCC	1719	AGCTTCTCTACCCCGGCAT	1720	CCCACAAGCATGAAGGAAAAGCTTTCTCTACCCC
NRP1	NM_003873	1721	CAGCTCTCTCCAC GCGATTC	1722	CCCAGCAGCTCCATT CTGA	1723	CAGGATCTACCCCGAGAGAG CCACTCAT	1724	CAGCTCTCTCCACGCGATTCATCAGGATCTACCCCGA GAGAGCCACTCATGGCGGACTGGGGCTCAGAATGGA
NUP62	NM_153719	1725	AGCCTCTTTGCGT CAATAGC	1726	CTGTGGTCACAGGGG TACAG	1727	TCATCTGCCACCACTGGACT CTCC	1728	AGCCTCTTTGCGTCAATAGCAACTGCTCCCAACCTCAT CTGCCACCACTGGACTCTCCCTGTGAC
OAZ1	NM_004152	1729	AGCAAGGACATGGTCGGC	1730	GAAGACATGGTCGGC	1731	CTGCTCCTCAGCGAACTCCA	1732	AGCAAGGACAGCTTTGCAGTTCTCCTGGAGTTCGCTG
OCLN	NM_002538	1733	CCCTCCCATCCGA	1734	GACGCGGGAGTGTAG	1735	CTCCTCCCTCGGTGACCAAT	1736	CCCTCCCATCCGAGTTTCAGGTGAATTGGTCACCGAG
ODC1	NM_002539	1737	AGAGATCACCGGC GTAATCAA	1738	CGGGCTCAGCTATGA TTCTCA	1739	CCAGCGTTGGACAAATACTT TCCGTCA	1740	AGAGATCACCGGCGTAATCAACCCAGCGTTGGACAA ATACTTTCCGTCAGACTCTGGAGTGAGAATCATAGCT
OLFML2	NM_015441	1741	CATGTTGGAAGGA	1742	CACCAGTTTGGTGGT	1743	TGGCCTGGATCTCCTGAAGC	1744	CATGTTGGAAGGAGCGTTCTATGGCCTGGATCTCCTG
OLFML3	NM_020190	1745	TCAGAACTGAGGC	1746	CCAGATAGTCTACCT	1747	CAGACGATCCACTCTCCCGG	1748	TCAGAACTGAGGCCCGACACCATCTCCGGGAGAGTGG
OMD	NM_005014	1749	CGCAAACTCAAGA CTATCCCA	1750	CAGTCACAGCCTCAA TTTCATT	1751	TCCGATGCACATTCAGCAAC TCTACC	1752	CGCAAACTCAAGACTATCCCAAATATTCCGATGCAC ATTCAGCAACTCTACCATCTCCGATGCAC
OR51E1	NM_152430	1753	GCATGCTTTCAGG	1754	AGAAGATGGCCAGCA	1755	TCCTCATCTCCACCTCATCC	1756	GCATGCTTTCAGGCATTGACATCCTCATCTCCACCTC
OR51E2	NM_030774	1757	TATGGTGCCAAAA	1758	GTCCTTGTCACAGCT	1759	ACATAGCCAGCACCCGTGTT	1760	TATGGTGCCAAAACCCAAACAGATCAGAACCACGGGTG
OSM	NM_020530	1761	GTTTCTGAAGGGG	1762	AGGTGTCTGGTTTGG	1763	CTGAGCTGGCCTCCTATGCC	1764	GTTTCTGAAGGGGAGGTCACAGCCTGAGCTGGCCTC
PAGE1	NM_003785	1765	CAACCTGACGAAG TGGAATC	1766	CAGATGCTCCCTCAT CCTCT	1767	CCAACTCAAAGTCAGGATTC TACACCTGC	1768	CAACCTGACGAAGTCAGGATTCTACACCTGCAGTCAG GATTCTACACCTGCTGAAGAGAGAGGATGAGGCA
PAGE4	NM_007003	1769	GAATCTCAGCAAG AGGAACCA	1770	GTTCTTCGATCGGAG GTGTT	1771	CCAACTGACAATCAGGATAT TGAACCTGG	1772	GAATCTCAGCAAGAGGAACCACCAACTGACAATCAG GATATTGAACCTGGACAAGAGAGAGGAAGGAACACCT
PAK6	NM_020168	1773	CCTCCAGGTCACC	1774	GTCCCTTCAGGCCAG	1775	AGTTTCAGGAAGGCTGCCCC	1776	CCTCCAGGTCACCCACAGCCAGTTTCAGGAAGGCTG
PATE1	NM_138294	1777	TGGTAATCCCCTGG	1778	TCCACCTTATGCCTTT	1779	CAGCACAGTTCTTTAGGCAG	1780	TGGTAATCCCTGGTTAACCTTCATGGGCTGCCTAAAG
PCA3	NR_015342	1781	CGTGATTGTCAGG	1782	AGAAAGGGGAGATGC	1783	CTGAGATGCTCCCTGCCTTC	1784	CGTGATTGTCAGGAGCAAGACCTGAGATGCTCCCTG
PCDHGB	NM_018927	1785	CCCAGCGTTGAAG	1786	GAAACGCCAGTCCGT	1787	ATTCTTAAACAGCAAGCCCC	1788	CCCAGCGTTGAAGCAGATAAGAAGATTCTTAAACAG
PCNA	NM_002592	1789	GAAGGTGTTGGAG	1790	GGTTTACACCGCTGG	1791	ATCCCAGCAGGCCTCGTTGA	1792	GAAGGTGTTGGAGGCACTCAAGGACCTCATCAACGA
PDE9A	NM_0010015 70	1793	TTCCACAACTTCC GGCAC	1794	AGACTGCAGAGCCAG ACCA	1795	TACATCATCTGGGCCACGCA GAAG	1796	TTCCACAACTTCCGGCACTGCTTCTGCGTGGCCCAGA TGATGTACAGCATGGTCTGGCTCTGCAGTCT
PDGFRB	NM_002609	1797	CCAGCTCTCCTTC	1798	GGGTGGCTCTCACTT	1799	ATCAATGTCCCTGTCCGAGT	1800	CCAGCTCTCCTTCCAGCTACAGATCAATGTCCCTGTC
PECAM1	NM_000442	1801	TGTATTTCAAGAC CTCTGTGCACTT	1802	TTAGCCTGAGTAATT GCTGTGTT	1803	TTTATGAACCTGCCCCTGCTC CCACA	1804	TGTATTTCAAGACCTCTGTGCACTTATTTATGAACCT GCCCTGCTCCCACAGAACACAGCAATTCCTCAGGCT
PEX10	NM_153818	1805	GGAGAAGTTCCCT CCCCAG	1806	ATCTGTGTCCAGGCC CAC	1807	CTACCTTCGGCACTACCGCT GAGC	1808	GGAGAAGTTCCCTCCCCAGAAGCTCATCTACCTTCGG CACTACCGCTGAGCCGGGTGGGCCTGGAC
PGD	NM_002631	1809	ATTCCCATGCCCT	1810	CTGGCTGGAAGCATC	1811	ACTGCCCTCTCCTTCTATGA	1812	ATTCCCATGCCCTGTTTTACCACTGCCCTCTCCTTCT
PGF	NM_002632	1813	GTGGTTTCCCTCG	1814	AGCAAGGGAACAGCC	1815	ATCTTCTCAGACGTCCCGAG	1816	GTGGTTTCCCTCGGAGCCCCCTGGCTCGGGACGTCT
PGK1	NM_000291	1817	AGAGCCAGTTGCT GTAGAACTCAA	1818	CTGGGCCTACACAGT CCTTCA	1819	TCTCTGCTGGGCAAGGATGT TCTGTTC	1820	AGAGCCAGTTGCTGTGAGAACTCAAATCTCTGCTGGG CAAGGATGTTCTGTTCTTGAAGGACTGTGTAGGCCCA
PGR	NM_000926	1821	GATAAAGGGAGCCG	1822	TCACAAGTCCGGCAC	1823	TAAATTGCCGTCGCAGCCGC	1824	GATAAAGGGAGCCCGCGTGTCACTAAATTGCCGTCGCA
PHTF2	NM_020432	1825	GATATGGCTGATG	1826	GGTTTGGGTGTTCTTG	1827	ACAATCTGGCAATGCCACAGT	1828	GATATGGCTGATGCTGCTCCTGGGAACTGTGCATTGC
PIK3C2A	NM_002645	1829	ATACCAATCACCG CACAAACC	1830	CACACTAGCATTTTCT CCGCATA	1831	TGTGCTGTGTGACTGGACTTAA CAAATAGCCT	1832	ATACCAATCACCGCACACAAACCCAGGCTATTTGTTAAG TCCAGTCACAGCACACAAAGAAACATATGCGGAGAAAA
PIK3CA	NM_006218	1833	GTGATTGAAGAGC	1834	GTCCTGCGTGTGGAAT	1835	TCCTGCTTCTCGGGATACAG	1836	GTGATTGAAGAGCATGCCAATTGGTCTGTATCCCGA
PIK3CG	NM_002649	1837	GGAGAACTCAATG	1838	TGATGCTTAGGCAGG	1839	TTCTGGACAATTACTGCCAC	1840	GGAGAACTCAATGTCCATCTCCATTCTTCTGGACAAT
PIM1	NM_002648	1841	CTGCTCAAGGACA	1842	GGATCCACTCTGGAG	1843	TACACTCGGGTCCCATCGAA	1844	CTGCTCAAGGACACCGTCTACACGGACTTCGATGGG

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
PLA2G7	NM_005084	1845	CCTGGCTGTGGTT	1846	TGACCCATGCTGATG	1847	TGGCAATACATAAATCCTGT	1848	CCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATA
PLAU	NM_002658	1849	GTGGATGTGCCCT	1850	CTGCGGATCCAGGGT	1851	AAGCCAGGCGTCTACACGAG	1852	GTGGATGTGCCCTGAAGGACAAGCCAGGCGTCTACA
PLALR	NM_002659	1853	CCCATGGATGCTC	1854	CCGGTGGCTACCAGA	1855	CATTGACTGCCGAGGCCCCA	1856	CCCATGGATGCTCCTCTGAAGAGACTTCCTCATTGA
PLG	NM_000301	1857	GGCAAAATTTCCA	1858	ATGTATCCATGAGCG	1859	TGCCAGGCCTGGGACTCTCA	1860	GGCAAAATTTCCAAGACCATGTCTGGACTGGAATGC
PLK1	NM_005030	1861	AATGAATACAGTA TTCCCAAGCACAT	1862	TGTCTGAAGCATCTTC TGGATGA	1863	AACCCCGTGGCCGCCTCC	1864	AATGAATACAGTATTCCCAAGCACATCAACCCCGTG GCCGCCTCCCTCATCCAGAAGATGCTTCAGACA
PLOD2	NM_000935	1865	CAGGGAGGTGGTT GCAAAT	1866	TCTCCCAGGATGCAT GAAG	1867	TCCAGCCTTTTCGTGGTGAC TCAA	1868	CAGGGAGGTGGTTGCAAATTTCTAAGGTACAATTGC TCTATTGAGTCACCACGAAAAGCTTGGAGCTTCATG
PLP2	NM_002668	1869	CCTGATCTGCTTCA	1870	GCAGCAAGGATCATC	1871	ACACCAGGCTACTCCTCCCT	1872	CCTGATCTGCTTCAGTGCCTCCACACCAGGCTACTCC
PNLIPRP	NM_005396	1873	TGGAGAAGGTGAA	1874	CACGGCTTGGGTGTA	1875	ACCCGTGCCTCCAGTCCACA	1876	TGGAGAAGGTGAACTGCATCTGTGTGGACTGGAGGC
POSTN	NM_006475	1877	GTGGCCCAATTAG	1878	TCACAGGTGCCAGCA	1879	TTCTCCATCTGGCCTCAGAG	1880	GTGGCCCAATTAGGCTTGGCATCTGCTCTGAGGCCA
PPAP2B	NM_003713	1881	ACAAGCACCATCC	1882	ACCAGGGCTCCTTGAGCAAA	1883	ACCAGGGCTCCTTGAGCAAATGTTCTGGCAGGATTTGC
PPFIA3	NM_003660	1885	CCTGGAGCTCCGT	1886	AGCCACATAGGGATC	1887	CACCCACTTTACCTTCTGGT	1888	CCTGGAGCTCCGTTACTCTCAGGCACCCACTTTACCT
PPP1R12A	NM_002480	1889	CGGCAAGGGGTTG ATATAGA	1890	TGCCTGGCATCTCTA AGCA	1891	CCGTTCTTCTTCCTTTCGAG CTGC	1892	CGGCAAGGGGTTGATATAGAAGCAGCTCGAAAGGAA GAAGAACGGATCATGCTTAGAGATGCCAGGCA
PPP3CA	NM_000944	1893	ATACTCCGAGTCC	1894	GGAAGCCTGTTGTTT	1895	TACATGCGGTACCCTGCATC	1896	ATACTCCGAGCCCACGAAGCCCAAGATGCAGGGTAC
PRIM1	NM_178013	1897	ATCCTCTTCCCTGA	1898	CCCAGCTGAGAGGGA	1899	TGACGCATCCAGGGCTCTAG	1900	ATCCTCTTCCCTGAGCCGCTGACGCATCCAGGGCTCT
PRKAR1	NM_002735	1901	ACAAAACCCATGAC	1902	TGTCATCCAGGTGAG	1903	AAGGCCATCTCCAAGAACGT	1904	ACAAAACCCATGACTGCGCTGGCCAAGGCCATCTCCA
PRKAR2B	NM_002736	1905	TGATAATCGTGGG AGTTTCG	1906	GCACCAGGAGAGGTA GCAGT	1907	CGAACTGGCCTTAATGTACA ATACACCCA	1908	TGATAATCGTGGCGAGTTTCGGCGAACTGGCCTTAAT GTACAATACACCCAGAGCAGCTACAATCACTGCTAC
PRKCA	NM_002737	1909	CAAGCAATGCGTC	1910	GTAAATCCGCCCCCT	1911	CAGCCTCTGCGGAATGGATC	1912	CAAGCAATGCGTCATCAATGTCCCCAGCCTCTGCGG
PRKCB	NM_002738	1913	GACCCAGCTCCAC	1914	CCCATTCACGTACTCC	1915	CCAGACCATGGACCGCCTGT	1916	GACCCAGCTCCACTCCTGCTTCCAGACCATGGACCGC
PROM1	NM_006017	1917	CTATGACAGGCAT	1918	CTCCAACCATGAGGA	1919	ACCCGAGGCTGTGTCTCCAA	1920	CTATGACAGGCATGCCACCCCGACCACCCGAGGCTG
PROS1	NM_000313	1921	GCAGCACAGGAAT	1922	CCCACCTATCCAACCT	1923	CTCATCCTGACAGACTGCAG	1924	GCAGCACAGGAATCTTCTTCTTGGCAGCTGCAGTCTG
PSCA	NM_005672	1925	ACCGTCATCAGCA AAGGCT	1926	CGTGATGTTCTTCTTG CCC	1927	CCTGTGAGTCATCCACCGCAG TTCA	1928	ACCGTCATCAGCAAAGGCTGCAGCTTGAACTGCGTG GATGACTCACAGGACTACTACGTGGGCAAGAAGAAC
PSMD13	NM_002817	1929	GGAGGAGCTCTAC ACGAAGAAG	1930	CGGATCCTGCACAAA ATCA	1931	CCTGAAGTGTCAGCTGATGC CACA	1932	GGAGGAGCTCTACACGAAGAAGTTGTGGCATCAGCT GACACTTCAGGTGCTTGATTTTGTGCAGGATCCG
PTCH1	NM_000264	1933	CCACGACAAAGCC	1934	TACTCGATGGGCTCT	1935	CCTGAAACAAGCCGACTACATGCCTGAAACAAGCT	1936	CCACGACAAAGCCGACTACATGCCTGAAACAAGCT
PTEN	NM_000314	1937	TGGCTAAGTGAAG ATGACAATCATG	1938	TGCACATATCATTAC ACCAGTTCGT	1939	CCTTTCCAGCTTTACAGTGA ATTGCTGCA	1940	TGGCTAAGTGAAGATGACAATCATGTTGCAGCAATT CACTGTAAAGCTGGAAAGGGACGAACTGGTGTGTAATG
PTGER3	NM_000957	1941	TAACTGGGGCAAC	1942	TTGCAGGAAAAAGGTG	1943	CCTTTGCCTTCCTGGGGCTC	1944	TAACTGGGGCAACCTTTTCTTCGCCTCTGCCTTTGCC
PTGS2	NM_000963	1945	GAATCATTCACCA GGCAAAATTG	1946	CTGTACTGCGGGTGG AACAT	1947	CCTACCACCAGGCAAACCCTGC CA	1948	GAATCATTCACCAGGCAAATTGCTGGCAGGGTTGCT GGTGGTAGGAAATGTTCCACCCGCAGTACAG
PTHIR	NM_000316	1949	CGAGGTACAAGCT GAGATCCAAGAA	1950	GCGTGCCTTTCGCTTG AA	1951	CCAGTGCCAGTGTCCAGCGG CT	1952	CGAGGTACAAGCTGAGATCAAGAAATCTTGGAGCCG CTGGACACTGGCACTGGACTTCAAGCGAAAGGCACG
PTHLH	NM_002820	1953	AGTGACTGGGAGT GGGCTAGAA	1954	AAGCCTGTTACCGTG AATCGA	1955	TGACACCTCCACACAACGTCGC TGGA	1956	AGTGACTGGGAGTGGGCTAGAAGGGGGACCACCTGTC TGACACCTCCACACAACGTCGCTGGAGCTCGATTCACG
PTK2	NM_005607	1957	GACCGGTCGAATG	1958	CTGGACATCTCGATG	1959	ACCAGGCCCGTCACATTCTC	1960	GACCGGTCGAATGATAAGGTGTACGAGAATGTGACG
PTK2B	NM_004103	1961	CAAGCCCAGCCGA	1962	GAACCTGGAACTGCA	1963	CTCCGCAAACCAACCTCCTG	1964	CAAGCCCAGCCGAACCTAAGTACAGACCCCTCCGCA
PTK6	NM_005975	1965	GTGCAGGAAAGGT TCACAAA	1966	GCACACACGATGGAG TAAGG	1967	AGTGTCTGCGTCCAATACAC GCGT	1968	GTGCAGGAAAGGTTCACAAATGTGGAGTGTCTGCGT CCAATACACGCGTGTGCTCCTCTTCCTTACTCCATCGT
PTK7	NM_002821	1969	TCAGAGGACTCAC	1970	CATACACCTCCACGC	1971	CGCAAGGTCCCATTCTTGAA	1972	TCAGAGGACTCACGGTTCGAGGTCTTCAAGAATGGG
PTPN1	NM_002827	1973	AATGAGGAAGTTT	1974	CTTCGATCACAGCCA	1975	CTGATCCAGACAGCCGACCA	1976	AATGAGGAAGTTTCGGATGGGGCTGATCCAGACAGC
PTPRK	NM_002844	1977	TCAAACCCTCCCA	1978	AGCAGCCAGTTCGTC	1979	CCCCATCGTTGTACATTGCA	1980	TCAAACCCTCCCAGTGCTGGCCCCATCGTTGTACATT
PTTG1	NM_004219	1981	GGCTACTCTGATC TATGTTGATAAGG	1982	GCTTCAGCCCATCCTT AGCA	1983	CACACGGGTGCCTGGTTCTC CA	1984	GGCTACTCTGATCTATGTTGATAAGGAAAATGGAGA ACCAGGCACCCGTGTGGTTGCTAAGGATGGCCTGAA
PYCARD	NM_013258	1985	CTTTATAGACCAG	1986	AGCATCCAGCAGCCA	1987	ACGTTTGTGACCCTCGCGAT	1988	CTTTATAGACCAGCACCGGGCTGCGCTTATCGCGAG
RAB27A	NM_004580	1989	TGAGAGATTTAATG	1990	CCGGATGCTTTATTCG	1991	ACAAATTGCTTCTCACCATC	1992	TGAGAGATTAATGGCCATTGTGTACAAATTGCTTCTC
RAB30	NM_014488	1993	TAAAGGCTGAGGC	1994	CTCCCCAGCATCTCAT	1995	CCATCAGGGCCAGTTGCTGAT	1996	TAAAGGCTGAGGCACGGAGAAGAAAAGGAATCAGCA

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
RAB31	NM_006868	1997	CTGAAGGACCCTA	1998	ATGCAAAGCCAGTGT	1999	CTTCTCAAAGTGAGGTGCCA	2000	CTGAAGGACCCTACGCTCGGTGGCCTGGCAACCTCAC
RAD21	NM_006265	2001	TAGGGATGGTATC TGAAACAACA	2002	TCGCGTACACCTCTG CTC	2003	CACTTAAAACGAATCTCAAG AGGGTGACCA	2004	TAGGGATGGTATCTGAAACAACAATGGTCACCCTCTT GAGATTCGTTTTAAGTGTAATTCCATAATGAGCAGAG
RAD51	NM_002875	2005	AGACTACTCGGGT	2006	AGCATCCGCAGAAAC	2007	CTTTGCTGGACGGCCACTTT	2012	AGACTACTCGGGTCGAGGTGAGCTTTCAGCCAGGCA
RAD9A	NM_004584	2009	GCCATCTTCACCA	2010	CGGTGTCTGGAGAGTG	2011	CTTTGCTGGACGGCCACTTT	2012	GCCATCTTCACCATCAAGGACTCTTTGCTGGACGGCC
RAF1	NM_002880	2013	CGTCGTATGCGAG	2014	TGAAGGCGTGAGGTG	2015	TCCAGGATGCCTGTTATAGTTC	2016	CGTCGTATGCGAGAGTCTGTTTCAGGATGCCTGTTA
RAGE	NM_014226	2017	ATTAGGGGACTTT	2018	GGGTGGAGATGTATT	2019	CCGGAGTGTCTATTCCAAGC	2020	ATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCC
RALA	NM_005402	2021	TGGTCCTGAATGT	2022	CCCCATTTCACCTCTT	2023	TTGTGTTTCTTGGGCAGTCT	2024	TGGTCCTGAATGTAGCGTGTAAGCTTGTGTTTCTTGG
RALBP1	NM_006788	2025	GGTGTCAGATATA AATGTGCAAATGC	2026	TTCGATATTGCCAGC AGCTATAAA	2027	TGCTGTCCTGTCGGTCTCAG TACGTTCA	2028	GGTGTCAGATATAAATGTGCAAATGCCTTCTTGCTGT CCTGTCGGTCTCAGTACGTTCACTTTATAGCTGCTGG
RAP1B	NM_0010109 42	2029	TGACAGCGTGAGA GGTACTTAGG	2030	CTGAGCCAAGAACGA CTAGCTT	2031	CACGCATGATGCAAGCTTGT CAAA	2032	TGACAGCGTGAGAGGTACTAGGTTTTGACAAGCTTG CATCATGCGTGAGTATAAGCTAGTCGTTCTTGGCTCA
RARB	NM_000965	2033	ATGAACCCTTGAC CCCAAGT	2034	GAGCTGGGTGAGATG CTAGG	2035	TGTGCTCTGCTGTTCCCA CTTG	2036	ATGAACCCTTGACCCCAAGTTCAAGTGGGAACACAG CAGAGCACAGTCCTAGCATCTCACCCAGCTC
RASSF1	NM_007182	2037	AGGGCACGTGAAG TCATTG	2038	AAAGAGTGCAAACTT GCGG	2039	CACCACCAAGAACTTTCGCA GCAG	2040	AGGGCACGTGAAGTCATTGAGGCCCTGCTGCGAAAG TTCTTGGTGGTGGATGACCCCCGCAAGTTTGCACTCT
RB1	NM_000321	2041	CGAAGCCCTTACA	2042	GGACTCTTCAGGGGT	2043	CCCTTACGGATTCCTGGAGG	2044	CGAAGCCCTTACAAGTTTCTAGTTCACCCTTACGGA
RECK	NM_021111	2045	GTCGCCGAGTGTG	2046	GTGGGATGATGGTT	2047	TCAAGTGTCCTTCGCTCTTG	2048	GTCGCCGAGTGTGCTTCTGTCAAGTGTCCTTCGCTCT
REG4	NM_032044	2049	TGCTAGGTTTCCCCTC ACAGCC	2050	TGCTAACTCCTGCAC TGAA	2051	TCCTCTTCCTTTCTGCTAGCC TGGC	2052	TGCTAACTCCTGCACAGCCCCGTCCTTCTTCTG CTAGCCTGGCTAAATCTGCTCATATTTCAGAGGGGA
RELA	NM_021975	2053	CTGCCGGATGGC	2054	CCAGGTTCTGGAAAC	2055	CTGAGCTCTGCCCGGACCGC	2056	CTGCCGGGATGGCTTCTATGAGGCTGAGCTCTGCCC
RFX1	NM_002918	2057	TCCTCTCCAAGTTC	2058	CAGGCCCTGGTACAG	2059	TCCAATGGACCAAGCACTGT	2060	TCCTCTCCAAGTTCCAGCAGCAGAAGCACAAGCAAA TACCAGAGCTACAGCAGTATGTACCTGCATTAAAGG
RGS10	NM_0010053 39	2061	AGACATCCACGAC AGCGAT	2062	CCATTTGGCTGTGCTC TTG	2063	AGTTCCAGCAGCAGCCACCA GAG	2064	AGACATCCACGACAGCAGATGGCAGTTCCAGCAGCAG CCACCAGAGCCTCAAGAGCACAGCCAAATGG
RGS7	NM_002924	2065	CAGGCTGCAGAGA GCATTT	2066	TTTGCTTGTGCTTTCTG CTTG	2067	TGAAAATGAACTCCCACTTC CGGG	2068	CAGGCTGCAGAGAGCATTTGCCCGGAAGTGGGAGTT CATTTTCATGCAAGCAGAAGCACAAGCAAA
RHOA	NM_001664	2069	TGGCATAGCTCTG	2070	TGCCACAGCTGCATG	2071	AAATGGGCTCAACCAGAAA	2072	TGGCATAGCTCTGGGGGTGGGCAGTTTTTTGAAAATG
RHOB	NM_004040	2073	AAGCATGAACAGG	2074	CCTCCCCAAGTCAGT	2075	CTTTCCAACCCCTGGGGAAG	2076	AAGCATGAACAGGACTTGACCATCTTTCCAACCCCTG
RHOC	NM_175744	2077	CCCGTTCGGTCTG	2078	GAGCACTCAAGGTAG	2079	TCCGGTTCGCCATGTCCCG	2080	CCCGTTCGGTCTGAGGAAGGCCGGGACATGGCGAAC
RLN1	NM_006911	2081	AGCTGAAGGCAGC CCTATC	2082	TTGGAATCCTTTAATG CAGGT	2083	TGAGAGGCAACCATCATTAC CAGAGC	2084	AGCTGAAGGCAGCCCTATCTGAGAGGCAACCATCAT TACCAGAGCTACAGCAGTATGTACCTGCATTAAAGG
RND3	NM_005168	2085	TCGGAATTGGACT	2086	CTGGTTACTCCCCTCC	2087	TTTTAAGCCTGACTCCTCAC	2088	TCGGAATTGGACTTGGGAGGCGCGGTGAGGAGTCAG
RNF114	NM_018683	2089	TGACAGGGAAGT	2090	GGAAGACAGCTTTGG	2091	CCAGGTCAGCCCTTCTCTTC	2092	TGACAGGGAAGTCGGTCCCCAGGTCAGCCCTTCTC
ROBO2	NM_002942	2093	CTACAAGGGCCCAG	2094	CACCAGTGGCTTTTAC	2095	CTGTACCATCCACTGCCAGC	2096	CTACAAGGGCCCAGCCAACCAAACGCTGGCAGTGGAT
RRM1	NM_001033	2097	GGGCTACTGGCAG	2098	CTCTCAGCATCGGTA	2099	CATTGGAATTGCCATTAGTC	2100	GGGCTACTGGCAGCTACATTGCTGGGACTAATGGGCA
RRM2	NM_001034	2101	CAGCGGGATTAAA	2102	ATCTGCCGTTGAAGCA	2103	CCAGCACAGCCAGTTAAAAG	2104	CAGCGGGATTAAACAGTCCTTTAACCAGCACAGCCA
S100P	NM_005980	2105	AGACAAGGATGCC	2106	GAAGTCCACCTGGGC	2107	TTGCTCAAGGACCTGGACGC	2108	AGACAAGGATGCCGTGGATAAATTGCTCAAGGACCT
SAT1	NM_002970	2109	CCTTTTACCACTGC	2110	ACAATGCTGTGTCCTT	2111	TCCAGTGCTCTTTTCGGCACT	2112	CCTTTTACCACTGCCTGGTTGCAGAAGTGGCCGAAAGA
SCUBE2	NM_020974	2113	TGACAATCAGCAC ACCTGCAT	2114	TGTGACTACAGGCCGT GATCCTTA	2115	CAGGCCCTCTTCCGAGCGGT	2116	TGACAATCAGCACACCTGCATTCACCGCTCGGAAGA GGGCCTGAGCTGCATGAATAAGGATCACGGCTGTAG
SDC1	NM_002997	2117	GAAATTGACGAGG	2118	AGGAGCTAACGGAGA	2119	CTCTGAGCGCCTCCATCCAA	2120	GAAATTGACGAGGGGTGTCTTGGGCAGAGCTGGCTC
SDC2	NM_002998	2121	GGATTGAAGTGGC	2122	ACCAGCCACAGTACC	2123	AACTCCATCTCCTTCCCCAG	2124	GGATTGAAGTGGCTGGAAAGAGTGATGCCTGGGGAA
SDHC	NM_003001	2125	CTTCCCTCGGGTCT	2126	TTCCCTCCTGGTAAA	2127	TTACATCCTCCCCTCTCCCCG	2128	CTTCCCTCGGGTCTCAGGCATTTACATCCTCCCCTCTC
SEC14L1	NM_0010395 73	2129	AGGGTTCCCATGT GACCAG	2130	GCAGGCATGCTGTGG AAT	2131	CGGGCTTCTACATCCTGCAG TGG	2132	AGGGTTCCCATGTGACCAGGTGGCCGGGCTTCTACA TCCTGCAGTGGAAATTCCACAGCATGCCTGC
SEC23A	NM_006364	2133	CGTGTGCATTAGA	2134	CCCATTACCATGTATC	2135	TCCTGGAGATGAAATGCTGT	2136	CGTGTGCATTAGATCAGACAGGTCTCCTGGAGATGA
SEMA3A	NM_006080	2137	TTGGAATGCAGTC	2138	CTCTTCATTTCGCCTC	2139	TTGCCAATAGACCAGCGCTC	2140	TTGGAATGCAGTCCGAGATCCAGCTGGTC
SEPT9	NM_006640	2141	CAGTGACCACGAG	2142	CTTCGATGGTACCCC	2143	TTGCCAATAGACCAGCGCTC	2144	CAGTGACCACGAGTACCAGGTCAACGGCAAGAGGAT
SERPINA3	NM_001085	2145	GTGTGGCCCTGTC TGCTTA	2146	CCCTGTGCATGTGAG AGCTAC	2147	AGGGAATCGCTGTCACCTTC CAAG	2148	GTGTGGCCCTGTCTGCTTATCCTTGGAAGGTGACAGC GATTCCCTGTGTAGCTCTCACATGCACAGGG

TABLE A

Official Symbol:	Accession Number:	SEQ ID NO	Forward Primer Sequence:	SEQ ID NO	Reverse Primer Sequence:	SEQ ID NO	Probe Sequence:	SEQ ID NO	Amplicon Sequence:
SERPINB 5	NM_002639	2149	CAGATGGCCACTT TGAGAACATT	2150	GGCAGCATTAACCAC AAGGATT	2151	AGCTGACAACAGTGTGAACG ACCAGACC	2152	CAGATGGCCACTTTGAGAACATTTTAGCTGACAACA GTGTGAACGACCAGACCAAAATCCTTGTGGTTAATG
SESN3	NM_144665	2153	GACCCTGGTTTTG	2154	GAGCTCGGAATGTTG	2155	TGCTCTTCTCCTCGTCTGGC	2156	GACCCTGGTTTTGGGTATGAAGACTTTGCCAGACGA
SFRP4	NM_003014	2157	TACAGGATGAGGC	2158	GTTGTTAGGGCAAGG	2159	CCTGGGACAGCCTATGTAAG	2160	TACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTA
SH3RF2	NM_152550	2161	CCATCACAACAGC CTTGAAC	2162	CACTGGGGTGCTGAT CTCTA	2163	AACCGGATGGTCCATTCTCC TTCA	2164	CCATCACAACAGCCTTGAACACTCTCAACCGGATGG TCCATTCTCCTTCAGGGCGCCATATGGTAGAGATCAG
SH3YL1	NM_015677	2165	CCTCCAAAGCCAT	2166	CTTTGAGAGCCAGAG	2167	CACAGCAGTCATCTGCACCA	2168	CCTCCAAAGCCATTGTCAAGACCACAGCAGTCATCT
SHH	NM_000193	2169	GTCCAAGGCACAT	2170	GAAGCAGCCTCCCGA	2171	CACCGAGTTCTCTGCTTTCA	2172	GTCCAAGGCACATATCCACTGCTCGGTGAAAGCAGA
SHMT2	NM_005412	2173	AGCGGGTGCTAGA	2174	ATGGCACTTCGGTCT	2175	CCATCACTGCCAACAAGAAC	2176	AGCGGGTGCTAGAGCTTGTATCCATCACTGCCAACA
SIM2	NM_005069	2177	GATGGTAGGAAGG	2178	CACAAGGAGCTGTGA	2179	CGCCTCTCCACGCACTCAGC	2180	GATGGTAGGAAGGGATGTGCCCGCCTCTCCACGCAC
SIPA1L1	NM_015556	2181	CTAGGACAGCTTG	2182	CATAACCGTAGGGCT	2183	CGCCACAATGCCCTCATAGT	2184	CTAGGACAGCTTGGCTTCCATGTCAACTATGAGGGC
SKIL	NM_005414	2185	AGAGGCTGAATAT	2186	CTATCGGCCTCAGCA	2187	CCAATCTCTGCCTCAGTTCT	2188	AGAGGCTGAATATGCAGGACAGTTGGCAGAACTGAG
SLC22A3	NM_021977	2189	ATCGTCAGCGAGT	2190	CAGGATGGCTTGGGT	2191	CAGCATCCACGCATTGACAC	2192	ATCGTCAGCGAGTTTGACCTTGTCTGTGTCAATGCGT
SLC25A2 1	NM_030631	2193	AAGTGTTTTTCCCC CTTGAGAT	2194	GGCCGATCGATAGTC TCTCTT	2195	TCATGGTGCTGCATAGCAAA TATCCA	2196	AAGTGTTTTTCCCCCTTGAGATAATGGATATTTGCTA TGCAGCACCATGAAGAAGAGAGACTATCGATCGGCC
SLC44A1	NM_080546	2197	AGGACCGTAGCTG	2198	ATCCCATCCCAATGC	2199	TACCATGGCTGCTGCTCTTC	2200	AGGACCGTAGCTGCACAGACATACCATGGCTGCTGC
SMAD4	NM_005359	2201	GGACATTACTGGC	2202	ACCAATACTCAGGAG	2203	TGCATTCCAGCCTCCCATTT	2204	GGACATTACTGGCCTGTTCACAATGAGCTTGCATTCC
SMARCC 2	NM_003075	2205	TACCGACTGAACC CCCAA	2206	GACATCACCCGCTAG GTTTC	2207	TATCTTACCTCTACCGCCTG CCGC	2208	TACCGACTGAACCCCCAAGAGTATCTTACCTCTACCG CCTGCCGCCGAAACCTAGCGGGTGATGTC
SMARC D1	NM_003076	2209	CCGAGTTAGCATA TCCCAGG	2210	CCTTTGTGCCCAGCTG TC	2211	CCCACCCTTGCTGTGTTGAG TCTG	2212	CCGAGTTAGCATATCCCAGGCTCGCAGACTCAACAC AGCAAGGGTGGGAGACAGCTGGGCACAAAGG
SMO	NM_005631	2213	GGCATCCAGTGCC	2214	CGCGATGTAGCTGTG	2215	CTTCACAGAGGCTGAGCACC	2216	GGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCT
SNAI1	NM_005985	2217	CCCAATCGGAAGC	2218	GTAGGGCTGCTGGAA	2219	TCTGGATTAGAGTCCTGCAG	2220	CCCAATCGGAAGCCTAACTACAGCGAGCTGCAGGAC
SNRPB2	NM_003092	2221	CGTTTCCTGCTTTT	2222	AGGTAGAAGGCGCAC	2223	CCCACCTAAGGCCTACGCCG	2224	CGTTTCCTGCTTTTGGTTCTTACAGTAGTCGGCGTAG
SOD1	NM_000454	2225	TGAAGAGAGGCAT	2226	AATAGACACATCGGC	2227	TTTGTCAGCAGTCACATTGC	2228	TGAAGAGAGGCATGTTGGAGACTTGGGCAATGTGAC
SORBS1	NM_015385	2229	GCAGATGAGTGGA	2230	AGCGAGTGAAGAGGG	2231	ATTTCCATTGGCATCAGCAC	2232	GCAGATGAGTGGAGGCTTTCTTCCAGTGCTGATGCC
SOX4	NM_003107	2233	AGATGATCTCGGG	2234	GCGCCCTTCAGTAGG	2235	CGAGTCCAGCATCTCCAACC	2236	AGATGATCTCGGGAGACTGGCTCGAGTCCAGCATCT
SPARC	NM_003118	2237	TCTTCCCTGTACAC TGGCAGTTC	2238	AGCTCGGTGTGGGAG AGGTA	2239	TGGACCAGCACCCCATTGAC GG	2240	TCTTCCCTGTACACTGGCAGTTCGGCCAGCTGGACCA GCACCCCATTGACGGGTACCTCTCCCACACCGAGCT
SPARCL	NM_004684	2241	GGCACAGTGCAAG	2242	GATTGAGCTCTCTCG	2243	ACTTCATCCCAAGCCAGGCC	2244	GGCACAGTGCAAGTGATGACTACTTCATCCCAAGCC
SPDEF	NM_012391	2245	CCATCCGCCAGTA TTACAAG	2246	GGGTGCACGAACTGG TAGA	2247	ATCATCCGGAAGCCAGACAT CTCC	2248	CCATCCGCCAGTATTACAAGAAGGGCATCATCCGGA AGCCAGACATCTCCCAGCGCCTCGTCTACCAGTTCGT
SPINK1	NM_003122	2249	CTGCCATATGACC	2250	GTTGAAAACTGCACC	2251	ACCACGTCTCTTCAGAAGCC	2252	CTGCCATATGACCCTTCCAGTCCCAGGCTTCTGAAGA
SPINT1	NM_003710	2253	ATTCCCAGCACAG	2254	AGATGGCTACCACCA	2255	CTGTCGCAGTGTTCCTGGTC	2256	ATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCA
SPP1	NM_0010400 58	2257	TCACACATGGAAA GCGAGG	2258	GTTCAGGTCCTGGGC AAC	2259	TGAATGGTGCATACAAGGCC ATCC	2260	TCACACATGGAAAGCGAGGAGTTGAATGGTGCATAC AAGGCCATCCCCGTTGCCCAGGACCTGAAC
SQLE	NM_003129	2261	ATTTTCGAGGCCA AAAAATC	2262	CCTGAGCAAGGATAT TCACG	2263	TGGGCAAGAAAAACATCTCA TTCCTTTG	2264	ATTTTCGAGGCCAAAAAATCATTTTACTGGGCAAGA AAAACATCTCATTCCTTTGTCGTGAATATCCTTGCTC
SRC	NM_005417	2265	TGAGGAGTGGTAT TTTGGCAAGA	2266	CTCTCGGGTTCTCTGC ATTGA	2267	AACCGCTCTGACTCCCGTCT GGTG	2268	TGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGA GTCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAG
SRD5A1	NM_001047	2269	GGGCTGGAATCTG	2270	CCATGACTGCACAAT	2271	CCTCTCTCGGAGGCCACAGA	2272	GGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGC
SRD5A2	NM_000348	2273	GTAGGTCTCCTGG CGTTCTG	2274	TCCCTGGAAGGGTAG GAGTAA	2275	AGACACCACTCAGAATCCCC AGGC	2276	GTAGGTCTCCTGGCGTTCTGCCAGCTGGCCTGGGGAT TCTGAGTGGTGTCTGCTTAGAGTTTACTCCTACCCTT
ST5	NM_005418	2277	CCTGTCCTGCCAG	2278	CAGCTGCACAAAACT	2279	AGTCACGAGCACCCAGCGA	2280	CCTGTCCTGCCAGAGCATGGATGAAGTTTCGCTGGGT
STAT1	NM_007315	2281	GGGCTCAGCTTTC AGAAGTG	2282	ACATGTTCAGCTGGT CCACA	2283	TGGCAGTTTTCTTCTGTCAC CAAAA	2284	GGGCTCAGCTTTCAGAAGTGCTGAGTTGGCAGTTTTC TTCTGTCACCAAAAGAGGTCTCAATGTGGACCAGCT
STAT3	NM_003150	2285	TCACATGCCACTTT	2286	CTTGCAGGAAGCGGC	2287	TCCTGGGAGAGATTGACCAG	2288	TCACATGCCACTTTGGTGTTTCATAATCTCCTGGGAG
STAT5A	NM_003152	2289	GAGGCGCTCAACA TGAAATTC	2290	GCCAGGAACACGAGG TTCTC	2291	CGGTTGCTCTGCACTTCGGC CT	2292	GAGGCGCTCAACATGAAATTCAAGGCCGAAGTGCAG AGCAACCGGGGCCTGACCAAGGAGAACCTCGTGTTC
STAT5B	NM_012448	2293	CCAGTGGTGGTGA	2294	GCAAAAGCATTGTCC	2295	CAGCCAGGACAACAATGCG	2296	CCAGTGGTGGTGATCGTTCATGGCAGCCAGGACAAC

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
STMN1	NM_005563	2297	AATACCCAACGCA	2298	GGAGACAATGCAAAC	2299	CACGTTCTCTGCCCCGTTTC	2300	AATACCCAACGCACACAAATGACCGCAACGTTCTCTGCC
STS	NM_000351	2301	GAAGATCCCTTTC CTCCTACTGTTC	2302	GGATGATGTTCGGCC TTTGAT	2303	CTGCGTGGCTCTCGGCTTCC CA	2304	GAAGATCCCTTTCCTCCTACTGTTCTTTCTGTGGGAA GCCGAGAGCCACGCAGCATCAAGGCCGAACATCATC
SULF1	NM_015170	2305	TGCAGTTGTAGGGG AGTCTGG	2306	TCTCAAGAATTGCCG TTGAC	2307	TACCGTGCCAGCAGAAGCCA AAG	2308	TGCAGTTGTAGGGAGTCTGGTTACCGTGCCAGCAGA AGCCAAAGAAAGAGTCAACGGCAATTCTTGAGA
SUMO1	NM_003352	2309	GTGAAGCCACCGT	2310	CCTTCCTTCTTATCCC	2311	CTGACCAGGAGGCAAACCT	2312	GTGAAGCCACCGTCATCATGTCTGACCAGGAGGCAA
SVIL	NM_003174	2313	ACTTGCCCAGCAC	2314	GACACCATCCGTGTC	2315	ACCCCAGGACTGATGTTCAAG	2316	ACTTGCCCAGCACACAAGGAAGACCCCAGGACTGATGT
TAF2	NM_003184	2317	GCGCTCCACTCTC AGTCTTT	2318	CTTGTGCTCATGGTG ATGGT	2319	AGCCTCCAAACACAGTGACC ACCA	2320	GCGCTCCACTCTCAGTCTTTACTAAGGAATCTACAGC CTCCAAACACAGTGACCACCATCACCATCAT
TARP	NM_0010037 99	2321	GAGCAACACGATT CTGGGA	2322	GGCACCGTTAACCAG CTAAAT	2323	TCTTCATGGTGTTCCCCTCC TGG	2324	GAGCAACACGATTCTGGGATCCCAGGAGGGGAACAC CATGAAGACTAACGACACATACATGAAATTTAGCTG
TBP	NM_003194	2325	GCCCGAAACGCCG	2326	CGTGGCTCTCTTATCC	2327	TACCGCAGCAAACCGCTTGG	2328	GCCCGAAACGCCGAATATAATCCCAAGCGGTTTGCT
TFDP1	NM_007111	2329	TGCGAAGTGCTTT TGTTTGT	2330	GCCTTCCAGACAGTC TCCAT	2331	CGCACCCAGCATGGCAATAAG CTTT	2332	TGCGAAGTGCTTTTGTTTGTTTTCGTTTGGTTAA AGCTTATTGCCATGCTGGTGCGGCTATGGAGACTGTC
TFF1	NM_003225	2333	GCCCTCCCAGTGT GCAAAT	2334	CGTCGATGGTATTAG GATAGAAGCA	2335	TGCTGTTTCGACGACACCGT TCG	2336	GCCCTCCCAGTGTGCAAATAAGGGCTGCTGTTTCGAC GACACCGTTCGTGGGGTCCCCTGGTGCTTCTATCCTA
TFF3	NM_003226	2337	AGGCACTGTTCAT CTCAGTTTTTCT	2338	CATCAGGCTCCAGAT ATGAACTTTC	2339	CAGAAGCGCTTGCCGGGAG CAAAGG	2340	AGGCACTGTTCATCTCAGCTTTCTGTCCCTTTGCTC CCGGCAAGCGCTTCTGCTGAAAGTTCATATCTGGAG
TGFA	NM_003236	2341	GGTGTGCCACAGA CCTTCCT	2342	ACGGAGTTCTTGACA GAGTTTTGA	2343	TTGGCCTGTAATCACCTGTG CAGCCTT	2344	GGTGTGCCACAGACCTTCCTACTTGGCCTGTAATCAC CTGTGCAGCCTTTTGTGGGCCTTCAAAACTCTGTCAA
TGFB111	NM_0010424 54	2345	GCTACTTTGAGCG CTTCTCG	2346	GGTCACCATCTTGTGT CGG	2347	CAAGATGTGGCTTCTCGCCAAGATGTGGCTTCTG CAGC	2348	GCTACTTTGAGCGCTTCTCGCCAAGATGTGGCTTCTG CAACCAGCCCATCCGACACAAGATGGTGACC
TGFB2	NM_003238	2349	ACCAGTCCCCCAG	2350	CCTGGTGCTGTTGTA	2351	TCCTGAGCCCGAGGAAGTCC	2352	ACCAGTCCCCCAGAAGACTATCCTGAGCCCGAGGAA
TGFB3	NM_003239	2353	GGATCGAGCTCTT	2354	GCCACCGATATAGCG	2355	CGGCCAGATGAGCACATTGC	2356	GGATCGAGCTCCTTCCAGATCCTTCGGCCAGATGAGC
TGFBR2	NM_003242	2357	AACACCAATGGGT	2358	CCTCTTCATCAGGCC	2359	TTCTGGGCTCCTTGATTGCTC	2360	AACACCAATGGGTTCCATCTTTCTGGGCTCCTCGATTG
THBS2	NM_003247	2361	CAAGACTGGCTAC ATCAGAGTCTTAG	2362	CAGCGTAGGTTTGGT CATAGATAGG	2363	TGAGTCTGCCATGACCTGTT	2364	CAAGACTGGCTACATCAGAGTCTTAGTGCATGAAGG AAAACAGGTCATGGCAGACTCAGGACCTATCTATGA
THY1	NM_006288	2365	GGACAAGACCCTC	2366	TTGGAGGCTGTGGGT	2367	CAAGCTCCCAAGAGCTTCCA	2368	GGACAAGACCCTCTCAGGCTGTTCCCAAGCTCCCAAG
TIAM1	NM_003253	2369	GTCCCTGGCTGAA	2370	GGGCTCCCGAAGTCT	2371	TGGAGCCCTTCTCCCAAGAT	2372	GTCCCTGGCTGAAAATGGCCTGAAGCCCTTCTCCCAA
TIMP2	NM_003255	2373	TCACCCTCTGTGA	2374	TGTGGTTCAGGCTCTT	2375	CCCTGGGACACCCTGAGCAC	2376	TCACCCTCTGTGACTTCATCGTGCCCTGGGACACCCT
TIMP3	NM_000362	2377	CTACCTGCCTTGCT	2378	ACCGAAATTGGAGAG	2379	CCAAGAACGAGTGTCTCTGG	2380	CTACCTGCCTTGCTTTGTGACTTCCAAGAACGAGTGT
TK1	NM_003258	2381	GCCGGGAAGACCG TAATTGT	2382	CAGCGGCACCCAGGTT CAG	2383	CAAATGGCTTCCTCTGGGAAG GTCCCA	2384	GCCGGGAAGACCGTAATTGTGGCTGCACTGGATGGG ACCTTCCAGAGGAAGCCATTTGGGCCATCCTGAAC
TMPRSS	NM_005656	2385	GGACAGTGTGCAC	2386	CTCCCACGAGGAAGG	2387	AAGCACTGTGCATCACCTTG	2388	GGACAGTGTGCACCTCAAAGACTAAGAAAGCACTGT
TMPRSS 2ERGA	DQ204772	2389	GAGGCGGAGGGCG AG	2390	ACTGGTCCTCACTCA CAACT	2391	TAAGGCTTCCTGCCGCGCTC CA	2392	GAGGCGGAGGCGGAGGGCGAGGGCGGGAGCGCC GCCTGGAGCCGCGGCAGGAAGCCTTATCAGTTGTGAG
TMPRSS 2ERGB	DQ204773	2393	GAGGCGGAGGGCG AG	2394	TTCCTCGGGTCTCCAA AGAT	2395	CCTGGAATAACCTGCCGCGC	2396	GAGGCGGAGGCGAGGGGCGGGGAGCGCCGCCTGG AGCGCGCGGCAGGTTATTCCAGGATCTTTGGAGACCCG
TNF	NM_000594	2397	GGAGAAGGGTGAC	2398	TGCCCAGACTCGGCA	2399	CGCTGAGATCAATCGGCCCG	2400	GGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCG
TNFRSF1 0A	NM_003844	2401	TGCACAGAGGGTG AGGGTTAC	2402	TCTTCATCTGATTTAC AAGCTGTACATG	2403	CAATGCTTCCAACAATTTGT TTGCTTGCC	2404	TGCACAGAGGGTGTGGGTTACACCAATGCTTCCAAC AATTTGTTTGCTTGCCTGTGTACAGCTTGTAAAT
TNFRSF1 0B	NM_003842	2405	CTCTGAGACAGTG TTCCTT	2406	CCATGAGGCCCAACT TCCT	2407	CAGACTTGGTGCCCTTTGAC TCC	2408	CTCTGAGACAGTGCTTCGATGACTTTGCAGACTTGGT GCCCTTTGACTCCTGGGAGCCCGCTCATGAGGAAGTT
TNFRSF1 8	NM_148901	2409	CAGAAGCTGCCAG TTCCC	2410	CACCCACAGGTCTCC CAG	2411	CCTTCTCCTCTGCCGATCGC TC	2412	CAGAAGCTGCCAGTCCCCGAGGAAGAGGGGCGGCTGGGAGACCT GCGATCGGCAGAGGAGAAGGGGCGGCTGGGAGACCT
TNFSF10	NM_003810	2413	CTTCACAGTGCTC	2414	CATCTGCTTCAGCTCG	2415	AAGTACACGTAAGTTACAGC	2416	CTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTA
TNFSF11	NM_003701	2417	AACTGCATGTGGG	2418	TGACACCCTCTCCACT	2419	ACATGACCAGGGACCAACCC	2420	AACTGCATGTGGGCTATGGGAGGGGTTGGTCCCTGG
TOP2A	NM_001067	2421	AATCCAAGGGGGA	2422	GTACAGATTTTGCCC	2423	CATATGGACTTTGACTCAGC	2424	AATCCAAGGGGGAGAGTGATGACTTCCATATGGACT
TP53	NM_000546	2425	CTTTGAACCCTTGC	2426	CCCGGGACAAAGCAA	2427	AAGTCCTGGGTGCTTCTGAC	2428	CTTTGAACCCTTGCTTGCAATAGGTGTGCGTCAGAAG
TP63	NM_003722	2429	CCCCCAAGCAGTGC	2430	GAATCGCACAGCATC	2431	CCCGGGTCTCACTGGAGCCC	2432	CCCCCAAGCAGTGCCTCTACAGTCAGTGTGGCTCCA

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
TPD52	NM_005079	2433	GCCTGTGAGATTCC	2434	ATGTGCTTGGACCTC	2435	TCTGCTACCCACTGCCAGAT	2436	GCCTGTGAGATTCCTACCTTTGTTCTGCTACCCACTG
TPM1	NM_0010180 05	2437	TCTCTGAGCTCTG CATTTGTC	2438	GGCTCTAAGGCAGGA TGCTA	2439	TTCTCCAGCTGACCCTGGTT CTCTC	2440	TCTCTGAGCTCTGCATTTGTCTATTCTCCAGCTGACC CTGGTTCTCTCTCTCTTAGCATCCTGCCTTAGAGCC
TPM2	NM_213674	2441	AGGAGATGCAGCT	2442	CCACCTCTTCATATTT	2443	CCAAGCACATCGCTGAGGAT	2444	AGGAGATGCAGCTGAAGGAGGCCAAGCACATCGCTG
TPP2	NM_003291	2445	TAACCGTGGCATC	2446	ATGCCAACGCCATGA	2447	ATCCTGTTCAGGTGGCTGCA	2448	TAACCGTGGCATCTACCTCCGAGATCCTGTTCAGGTG
TPX2	NM_012112	2449	TCAGCTGTGAGCT GCGGATA	2450	ACGGTCCTAGGTTTG AGGTTAAGA	2451	CAGGTCCCATTGCCGGGCG	2452	TCAGCTGTGAGCTGCGGATACCGCCCGGCAATGGGA CCTGCTCTTAACCTCAAACCTAGGACCGT
TRA2A	NM_013293	2453	GCAAATCCAGATC	2454	CTTCACGAAGATCCC	2455	AACTGAGGCCAAACACTTCA	2456	GCAAATCCAGATCCCAACACTTGCCTTGGAGTGTTTG
TRAF3IP	NM_147200	2457	CCTCACAGGAACC	2458	CTGGGGCTGGGAATC	2459	TGGATCTGCCAACCATAGAC	2460	CCTCACAGGAACCGAGCAGGCCTGGATCTGCCAACC
TRAM1	NM_014294	2461	CAAGAAAAGCACC	2462	ATGTCCGCGTGATTCT	2463	AGTGCTGAGCCACGAATTCG	2464	CAAGAAAAGCACCAAGAGCCCCCCAGTGCTGAGCCA
TRAP1	NM_016292	2465	TTACCAGTGGCTTT	2466	CAAGGTACCTTGGCTT	2467	TTCGGCGATTTCAAACACTC	2468	TTACCAGTGGCTTTCAGATGGTTCTGGAGTGTTTGAA
TRIM14	NM_033220	2469	CATTCGCCTTAAG	2470	CAAGGTACCTGGCTT	2471	AACTGCCAGCTCTCAGACC	2472	CATTCGCCTTAAGGAAAGCATAAACTGCCAGCTCTCA
TRO	NM_177556	2473	GCAACTGCCACCC	2474	TGGTGTGGATACTGG	2475	CCACCCAAGGCCAAATTACC	2476	GCAACTGCCACCCATACAGCTACCACACCCAAGGCCAA
TRPC6	NM_004621	2477	CGAGAGCCCAGTAC	2478	TAGCCGTAGCAAGTC AGC	2479	CTTCTCCCAGCTTCCGAGTCC ATG	2480	CGAGAGCCCAGTACTATCTGCTCATGGACTCGGAGCT GGGAGAAGACGGCTGCCCGCAAGCCCCCGCTGCCTTG
TRPV6	NM_018646	2481	CCGTAGTCCCTGC AACCTC	2482	TCCTCACTGTTCACAC AGGC	2483	ACTTTGGGGAGCACCCTTTG TCCT	2484	CCGTAGTCCCTGCAACCTCATCTACTTTGGGGAGCAC CCTTTGTCCTTTGCTGCCTGTGTGAACAGTGAGGA
TSTA3	NM_003313	2485	CAATTTGGACTTCT	2486	CACCTCAAAGGCCGA	2487	AACGTGCACATGAACGACAA	2488	CAATTTGGACTTCTGGAGGAAAAACGTGCACATGAA
TUBB2A	NM_001069	2489	CGAGGACGAGGCT	2490	ACCATGCTTGAGGAC	2491	TCTCAGATCAATCGTGCATC	2492	CGAGGACGAGGCTTAAAAACTTCTCAGATCAATCGT
TYMP	NM_001953	2493	CTATATGCAGCCA GAGAATGTGG	2494	CCACGAGTTTCTTACT CCACGAGTTTCTTACT	2495	ACAGCCTGCCACTCATCACA GCC	2496	CTATATGCAGCCAGAGATGTGACAGCCACCGTGGAC AGCCTGCCACTCATCACAGCCTCCATTCTCAGTAAGA
TYMS	NM_001071	2497	GCCTCGGTGTGCC	2498	CGTGATGTGCGCAAT	2499	CATCGCCAGCTACGCCCTGC	2500	GCCTCGGTGTGCCTTTCAACATCGCCAGCTACGCCCT
UAP1	NM_003115	2501	CTGGAGACGGTCG TAGCTG	2502	GCCAAGCTTTGTAGA AATAGGG	2503	TACCTGTAAACCTTTCTCGG CGCG	2504	CTGGAGACGGTCGTAGCTGCGGTCGCCGAGAAAAG GTTTACAGGTACATACATTACACCCCTATTTCTACAA
UBE2C	NM_007019	2505	TGTCTGGCGATAA	2506	ATGGTCCCTACCCATT	2507	TCTGCCTTCCCTGAATCAGA	2508	TGTCTGGCGATAAAAGGGATTTCTGCCTTCCCTGAATC
UBE2G1	NM_003342	2509	TGACACTGAACGA	2510	AAGCAGAGAGGAATC	2511	TTGTCCCACCAGTGCCTCAT	2512	TGACACTGAACGAGGTGGCTTTGTCCCACCAGTGCC
UBE2T	NM_014176	2513	TGTTCTCAAATTGC	2514	AGAGGTCAACACAGT	2515	AGGTGCTTGGAGACCATCCC	2516	TGTTCTCAAATTGCCACCAAAAGGTGCTTGGAGACC
UGDH	NM_003359	2517	GAAACTCCAGAGG	2518	CTCTGGGAACCCAGT	2519	TATACAGCACACAGGGCCTG	2520	GAAACTCCAGAGGGCCAGAGAGCTGTGCAGGCCCTG
UGT2B1	NM_001076	2521	AAGCCTGAAGTGG	2522	CCTCCATTTAAAACCC	2523	AAAGATGGGACTCCTCCTTT	2524	AAGCCTGAAGTGGAATGACTGAAAGATGGGACTCCT
UGT2B1	NM_001077	2525	TTGAGTTTGTCATG	2526	TCCAGGTGAGGTGT	2527	ACCCGAAGGTGCTTGGCTCC	2528	TTGAGTTTGTCATGCGCCATAAAGGAGCCAAGCACC
UHRF1	NM_013282	2529	CTACAGGGGCAAA	2530	GGTGTCATTCAGGCG	2531	CGGCCATACCCTCTCTCGACT	2532	CTACAGGGGCAAACAGATGGAGGACGGCCATACCCT
UTP23	NM_032334	2533	GATTGCACAAAAA	2534	GGAAAGCAGACATTC	2535	TCGAAATTGTCCTCATTTCA	2536	GATTGCACAAAAATTGCCAAGTTCGAAATTGTCCTCAT
VCAM1	NM_001078	2537	TGGCTTCAGGAGC TGAATACC	2538	TGCTGTCGTGATGAG AAAATAGTG	2539	CAGGCACACAGGTGGGA CACAAAT	2540	TGGCTTCAGGAGCTGAATACCCTCCCAGGCACACAC AGGTGGGACACAAATAAGGGTTTTGGAACCACTATT
VCL	NM_003373	2541	GATACCACAACTC CCATCAAGCT	2542	TCCCTGTTAGGCGCA TCAG	2543	AGTGGCAGCCACGGCGCC	2544	GATACCACAACTCCCATCAAGCTGTTGGCAGTGGCA GCCACGGCGCCTCCTGATGCGCCTAACAGGGA
VCPIP1	NM_025054	2545	TTTCTCCCAGTACC	2546	TGAATAGGGAGCCTT	2547	TGGTCCATCCTCTGCACCTG	2548	TTTCTCCCAGTACCATTCGTGATGGTCCATCCTCTGC
VDR	NM_000376	2549	CCTCTCCTTCCAGC	2550	TCATTGCCAAACACTT	2551	CAGCATGAAGCTAACGCCCC	2552	CCTCTCCTTCCAGCCTGAGTGCAGCATGAAGCTAACG
VEGFA	NM_003376	2553	CTGCTGTCTTGGG	2554	GCAGCCTGGGAACCAC	2555	TTGCCTTGCTGCTCTACCTC	2556	CTGCTGTCTTGGGTGCATTGGAGCCTTGCCTTGCTGC
VEGFB	NM_003377	2557	TGACGATGGCCTG	2558	GGTACCGGATCATGA	2559	CTGGGCAGCACCAAGTCCGG	2560	TGACGATGGCCTGGAGTGTGTCCCACTGGGCAGCA
VEGFC	NM_005429	2561	CCTCAGCAAGACG AACTGATTG	2562	AAGTGTGATTGGCAA TTATTTGAAATT	2563	CCTCTCTCTCAAGGCCCCAA ACCAGT	2564	CCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTC TCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCA
VIM	NM_003380	2565	TGCCCTTAAAGGA	2566	GCTTCAACGGCAAAG	2567	ATTTCACGCATCTGGCGTTC	2568	TGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCA
VTI1B	NM_006370	2569	ACGTTATGCACCC CTGTCTT	2570	CCGATGGAGTTTAGC AAGGT	2571	CTATGAGTGCCACATCCTGA	2572	ACGTTATGCACCCCTGTCTTTCCGAAACCCCATGATG GCTTCG TCTAAGCTTCGAAACTACCGGAAGGACCTTGCTAAA
WDR19	NM_025132	2573	GAGTGGCCCAGAT	2574	GATGCTTGAGGGCTT	2575	CCCCTCGACGTATGTCTCCC	2576	GAGTGGCCCAGATGTCCATAAGAATGGGAGACATAC
WFDC1	NM_021197	2577	ACCCCTGCTCTGT	2578	ATACCTTCGGCCACG	2579	CTATGAGTGCCACATCCTGA	2580	ACCCCTGCTCTGTCCCTCGGGCTATGAGTGCCACATC
WISP1	NM_003882	2581	AGAGGCATCCATG AACTTCACA	2582	CAAACTCCACAGTAC TTGGGTTGA	2583	CGGGCTGCATCAGCACACGC	2584	AGAGGCATCCATGAACTTCACACTTGCGGGCTGCAT CAGCACACGCTCCTATCAACCCAAGTACTGTGGAGTTT

TABLE A

Official Symbol	Accession Number	SEQ ID NO	Forward Primer Sequence	SEQ ID NO	Reverse Primer Sequence	SEQ ID NO	Probe Sequence	SEQ ID NO	Amplicon Sequence
WNT5A	NM_003392	2585	GTATCAGGACCAC ATGCAGTACATC	2586	TGTCGGAATTGATAC TGGCATT	2587	TTGATGCCTGTCTTCGCGCC TTCT	2588	GTATCAGGACCACATGCAGTACATCGGAGAAGGCGC GAAGACAGGCATCAAAGAATGCCAGTATCAATTCCG
WWOX	NM_016373	2589	ATCGCAGCTGGTG	2590	AGCTCCCTGTTGCAT	2591	CTGCTGTTTACCTTGGCGAG	2592	ATCGCAGCTGGTGGGTGTACACACTGCTGTTTACCTT
XIAP	NM_001167	2593	GCAGTTGGAAGAC ACAGGAAAGT	2594	TGCGTGGCACTATTTT CAAGA	2595	TCCCCAAATTGCAGATTTAT CAACGGC	2596	GCAGTTGGAAGACACAGGAAAGTATCCCCAAATTGC AGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCA
XRCC5	NM_021141	2597	AGCCCACTTCAGC	2598	AGCAGGATTCACACT	2599	TCTGGCTGAAGGCAGTGTCA	2600	AGCCCACTTCAGCGTCTCCAGTCTGGCTGAAGGCAG
YY1	NM_003403	2601	ACCCGAGCAACAA	2602	GACCGAGAACTCGCC	2603	TTGATCTGCACCTGCTTCTG	2604	ACCCGAGCAACAAGAAGTGGGAGCAGAAGCAGGTGC
ZFHX3	NM_006885	2605	CTGTGGAGCCTCT	2606	GGAGCAGGGTTGGAT	2607	ACCTGGCCCAACTCTACCAG	2608	CTGTGGAGCCTCTTGCCTGGACCTGGCCCAACTCTA
ZFP36	NM_003407	2609	CATTAACCCACTC	2610	CCCCCACCATCATGA	2611	CAGGTCCCCAAGTGTGCAAG	2612	CATTAACCCACTCCCCTGACCTCACGCTGGGGCAGGT
ZMYND8	NM_183047	2613	GGTCTGGGCCAAA	2614	TGCCCGTCTTTATCCC	2615	CTTTTGCAGGCCAGAATGGA	2616	GGTCTGGGCCAAACTGAAGGGGTTTCCATTCTGGCCT
ZNF3	NM_017715	2617	CGAAGGGACTCTG	2618	GCAGGAGGTCCTCAG	2619	AGGAGGTTCCACACTCGCCA	2620	CGAAGGGACTCTGCTCCAGTGAACTGGCGAGTGTGG
ZNF827	NM_178835	2621	TGCCTGAGGACCC	2622	GAGGTGGCGGAGTGA	2623	CCCGCCTTCAGAGAAGAAC	2624	TGCCTGAGGACCCTCTACCGCCCCGCCTTCAGAGA
ZWINT	NM_007057	2625	TAGAGGCCATCAA	2626	TCCGTTTCCTCTGGGC	2627	ACCAAGGCCCTGACTCAGAT	2628	TAGAGGCCATCAAAATTGGCCTCACCAAGGCCCTGA

TABLE B

microRNA	Sequence	SEQ ID NO
hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	2629
hsa-miR-103	GCAGCAUUGUACAGGGCUAUGA	2630
hsa-miR-106b	UAAAGUGCUGACAGUGCAGAU	2631
hsa-miR-10a	UACCCUGUAGAUCCGAAUUUGUG	2632
hsa-miR-133a	UUUGGUCCCCUUCAACCAGCUG	2633
hsa-miR-141	UAACACUGUCUGGUAAAGAUGG	2634
hsa-miR-145	GUCCAGUUUUCCCAGGAAUCCCU	2635
hsa-miR-146b-5p	UGAGAACUGAAUUCCAUAGGCU	2636
hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	2637
hsa-miR-152	UCAGUGCAUGACAGAACUUGG	2638
hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	2639
hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	2640
hsa-miR-191	CAACGGAAUCCCAAAAGCAGCUG	2641
hsa-miR-19b	UGUAAACAUCCUCGACUGGAAG	2642
hsa-miR-200c	UAAUACUGCCGGGUAAUGAUGGA	2643
hsa-miR-205	UCCUUCAUUCCACCGGAGUCUG	2644
hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	2645
hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	2646
hsa-miR-210	CUGUGCGUGUGACAGCGGCUGA	2647
hsa-miR-22	AAGCUGCCAGUUGAAGAACUGU	2648
hsa-miR-222	AGCUACAUCUGGCUACUGGGU	2649
hsa-miR-26a	UUCAAGUAAUCCAGGAUAGGCU	2650
hsa-miR-27a	UUCACAGUGGCUAAGUUCCGC	2651
hsa-miR-27b	UUCACAGUGGCUAAGUUCUGC	2652
hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	2653
hsa-miR-30a	CUUUCAGUCGGAUGUUUGCAGC	2654
hsa-miR-30e-5p	CUUUCAGUCGGAUGUUUACAGC	2655
hsa-miR-31	AGGCAAGAUGCUGGCAUAGCU	2656
hsa-miR-331	GCCCCUGGGCCUAUCCUAGAA	2657
hsa-miR-425	AAUGACACGAUCACUCCCGUUGA	2658
hsa-miR-449a	UGGCAGUGUAUUGUUAGCUGGU	2659
hsa-miR-486-5p	UCCUGUACUGAGCUGCCCCGAG	2660
hsa-miR-92a	UAUUGCACUUGUCCCGGCCUGU	2661
hsa-miR-93	CAAAGUGCUGUUCGUGCAGGUAG	2662
hsa-miR-99a	AACCCGUAGAUCCGAUCUUGUG	2663

What is claimed is:

1. A method for determining a likelihood of cancer recurrence in a human patient with prostate cancer, comprising:

determining a level of an RNA transcript of Glutathione-S-Transferase Mu 2 (GSTM2) in a fixed, paraffin-embedded biological sample comprising prostate tumor tissue obtained from the patient;

normalizing the level of the RNA transcript of GSTM2 against the level of either all assayed RNA transcripts in the sample or against the level of a reference set of RNA transcripts in the sample to obtain a normalized level of the RNA transcript of GSTM2; and

predicting a likelihood of cancer recurrence for the patient, wherein increases in normalized level of the RNA transcript of GSTM2 are associated with decreases in risk of recurrence.

2. The method of claim 1, wherein the likelihood of cancer recurrence is based on clinical recurrence-free interval (cRFI).

3. The method of claim 1, wherein the likelihood of cancer recurrence is based on biochemical recurrence-free interval (bRFI).

4. A method for determining a likelihood of upgrading or upstaging in a human patient with prostate cancer, comprising:

determining a level of an RNA transcript of Glutathione-S-Transferase Mu 2 (GSTM2) in a fixed, paraffin-embedded biological sample comprising prostate tumor tissue obtained from the patient;

normalizing the level of the RNA transcript of GSTM2 against the level of either all assayed RNA transcripts in the sample or against the level of a reference set of RNA transcripts in the sample to obtain a normalized level of the RNA transcript of GSTM2;

wherein an increased expression level of GSTM2 is negatively associated with an increased risk of upgrading/upstaging.

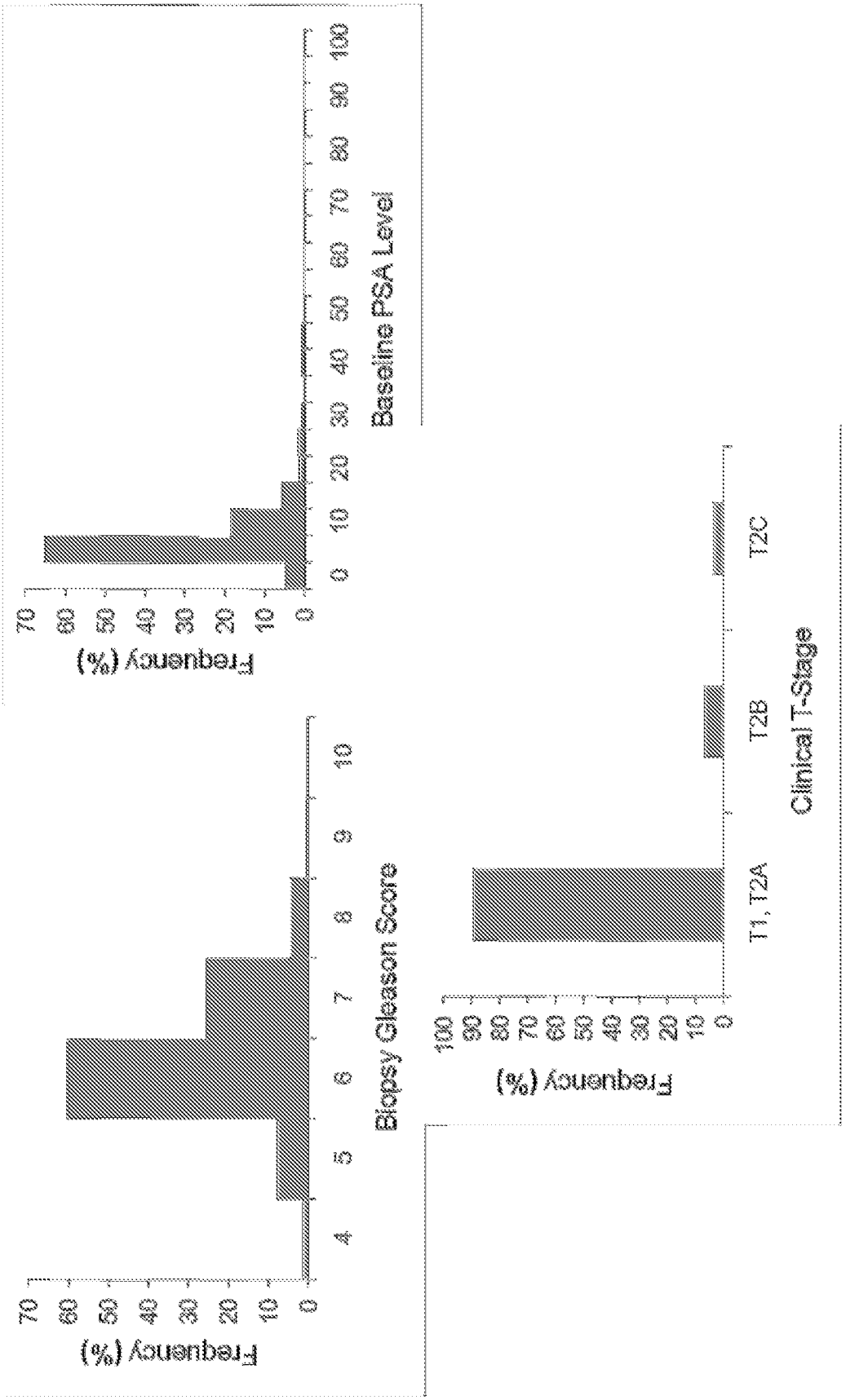
5. The method of any one of claims 1 to 4, wherein the patient has early-stage prostate cancer.

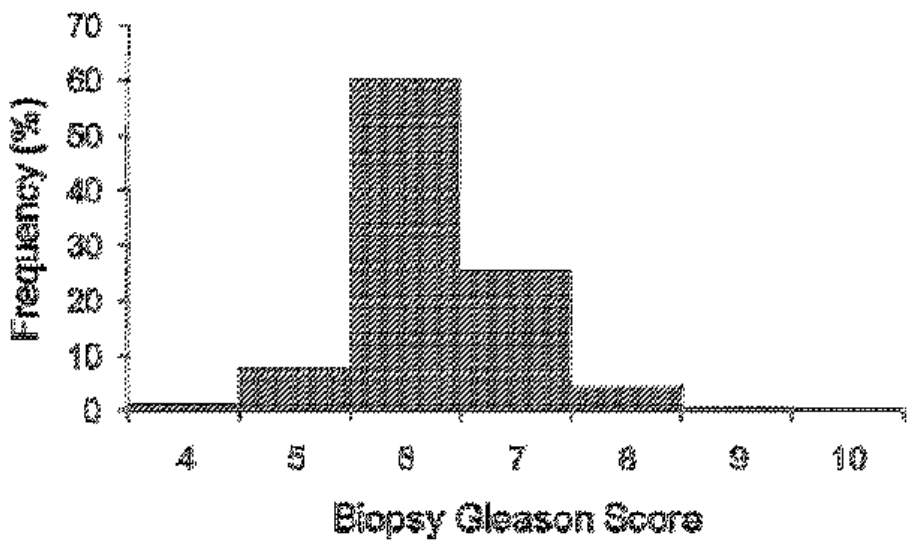
6. The method of any one of claims 1 to 5, wherein the biological sample comprises prostate tumor tissue with the primary Gleason pattern for said prostate tumor.

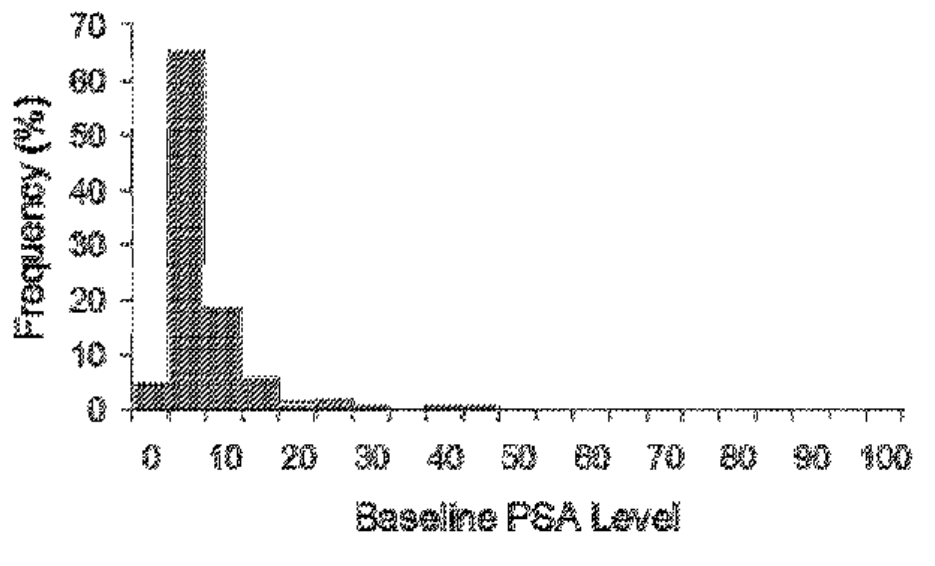
7. The method of any one of claims 1 to 5, wherein the biological sample comprises prostate tumor tissue with the highest Gleason pattern for said prostate tumor.

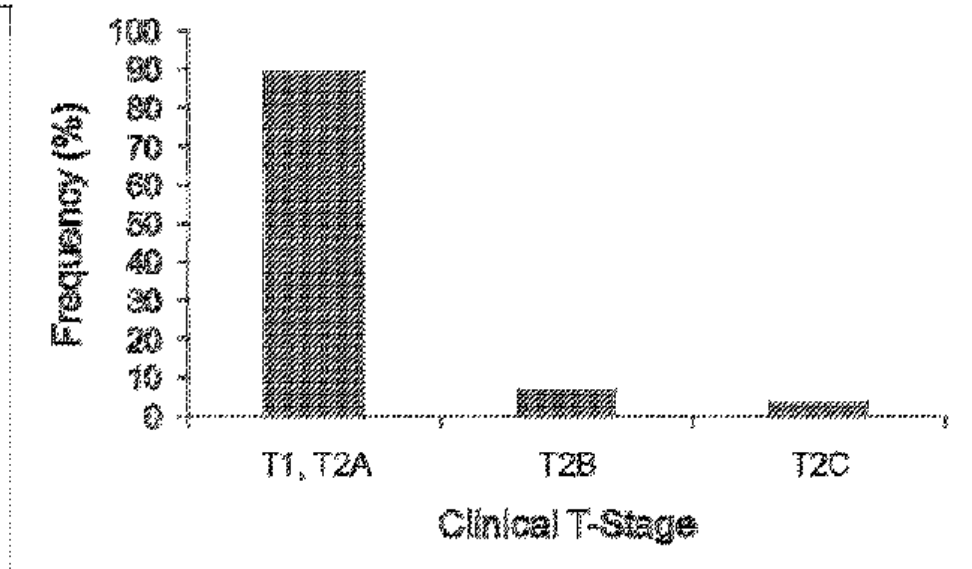
8. The method of any one of claims 1 to 5, wherein the method further comprises measuring an expression level of Inhibin Beta A (INHBA), wherein an increased expression level of INHBA is negatively associated with good prognosis.

FIGURE 1


Frequency (%)
0
10
20
30
40
50
60
70
Baseline PSA Level
0
10
20
30
40
50
60
70
80
90
100
Biopsy Gleason Score
4
5
6
7
8
9
10
Clinical T-Stage
T1, T2A
T2B
T2C


Frequency (%)
70
60
50
40
30
20
10
0
4
5
6
7
8
9
10
Biopsy Gleason Score


Frequency (%)
70
60
50
40
30
20
10
0
0
10
20
30
40
50
60
70
80
90
100
Baseline PSA Level


Frequency (%)
100
90
80
70
60
50
40
30
20
10
0
T1, T2A
T2B
T2C
Clinical T-Stage