

USE OF MARKERS IN THE DIAGNOSIS AND TREATMENT OF
PROSTATE CANCER

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority to US Provisional Application Serial No. 61/665201, filed June 27, 2012; US Provisional Application Serial No. 61/672090, filed July 16, 2012; US Provisional Application Serial No. 61/673094, filed July 18, 2012; US Provisional Application Serial No. 61/702523, filed September 18, 2012, and US Provisional Application Serial Nos. 61/718064, 61/718080, and 61/718081 all filed on October 24, 2012. Each of the applications is incorporated herein by reference in its entirety.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on June 25, 2013, is named 119992-06620_SL.txt and is 461,537 bytes in size.

FIELD OF THE INVENTION

The invention relates to treatment, prevention, reduction, diagnosis, monitoring, and prognosis of abnormal prostate states, including benign prostate hyperplasia and oncological disorders, especially prostate cancer, in humans using filamin B, lymphocyte antigen 9 (LY9), keratins and tubulin, specifically using keratins 4, 7, 8, 15, 18, and 19, and tubulin-beta 3, particularly keratins 7, 15, or 19. The filamin B, lymphocyte antigen 9 (LY9), keratins and tubulin can further be used in conjunction with prostate specific antigen (PSA) for the treatment, prevention, reduction, diagnosis, monitoring, and prognosis of abnormal prostate states, including benign prostate hyperplasia and oncological disorders, especially prostate cancer. The invention also relates to panels and kits for use in practicing the methods of the invention.

BACKGROUND OF THE INVENTION

Oncological disorders, such as cancer, are presently one of the leading causes of death in developed nations and is a serious threat to modern society. Cancer can develop in any tissue of any organ at any age. Worldwide, more than 10 million people are diagnosed with cancer every year and it is estimated that this number will grow to 15 million new cases every year by 2020. It is believed that cancer causes six million deaths every year or 12% of the deaths worldwide.

Prostate cancer is a form of cancer that develops in the prostate, a gland in the male reproductive system. Most prostate cancers are slow growing. However, there are cases of aggressive prostate cancers. The cancer cells may metastasize from the prostate to other parts of the body, particularly to the bones and lymph nodes. Prostate cancer may cause pain, difficulty in urinating, problems during sexual intercourse, or erectile dysfunction. Other symptoms can potentially develop during later stages of the disease.

Rates of detection of prostate cancers vary widely across the world, with detection rates in south and east Asia being lower than those in Europe, and especially in the United States. Prostate cancer tends to develop in men over the age of fifty and, although it is one of the most prevalent types of cancer in men, many never have symptoms or undergo therapy for prostate cancer, and eventually die of other causes. Further, treatment of prostate cancer may do more harm to the subject than the prostate cancer itself. Prostate specific antigen (PSA) screening has lead to a significant rise in the number of men diagnosed with prostate cancer with an associated increase in potentially unnecessary biopsies preformed. Despite its limitations, including a positive predictive value of only 25-40%, PSA remains the only generally accepted biomarker for prostate cancer.

Prostate cancer is, in most cases, slow-growing and symptom-free. Moreover, since men with the condition are typically older, they often die of causes unrelated to the prostate cancer, such as heart/circulatory disease, pneumonia, other unrelated cancers, or old age. On the other hand, the more aggressive prostate cancers account for more cancer-related deaths among men in the United States than any other cancer except lung cancer.

About two-thirds of prostate cancer cases are slow growing, whereas the other third are more aggressive and fast developing. It is important to be able to distinguish between aggressive and non-aggressive forms of the disease, and further, to distinguish prostate cancer

from benign prostate hyperplasia (BPH). Commonly used screening tests, e.g., for prostate specific antigen (PSA) cannot distinguish between prostate cancer and BPH.

SUMMARY OF THE INVENTION

The present invention is based, at least in part, on Applicants' discovery that keratins 4, 7, 8, 15, 18, and 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) are differentially regulated in prostate cancer cells.

Accordingly, the invention provides methods for diagnosing, monitoring (*e.g.*, of disease progression or treatment), prognosing, treating, alleviating symptoms of, inhibiting progression of, or preventing, an oncological disease state, *e.g.*, prostate cancer, in a mammal. The invention further provides panels and kits for practicing the methods of the invention.

In one aspect, the invention provides methods for diagnosing an abnormal prostate state in a subject comprising:

(1) determining a level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in a biological sample from the subject; and

(2) comparing the level of the one or more prostate cancer related markers in the biological sample with the level of the one or more prostate cancer related markers in a normal control sample, wherein an altered level of the one or more prostate cancer related markers in the biological sample relative to the normal control sample is indicative of an abnormal prostate state in the subject.

In certain embodiments, the one or more prostate cancer related markers is selected from the group consisting of filamin B, LY9, and keratin 19. In certain embodiments, an increased level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to a normal control sample is indicative of an abnormal prostate state in the subject.

In certain embodiments, no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to a normal control sample is indicative of a normal prostate state in the subject. In such embodiments, levels of one, two, or all three of filamin B, LY9, and keratin 19 can be detected. For the marker levels detected, none of the markers have increased levels.

In certain embodiments, the method further comprises detecting the level of prostate specific antigen (PSA) in the biological sample and preferably further comprising comparing the level of PSA in the biological sample to the level of PSA in a normal control sample. In certain embodiments, an increase in the level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to the normal control sample, in combination with an increase in the level of PSA in the biological sample as compared to the level of PSA in the normal control sample has greater predictive value of the subject having an abnormal prostate state than the predictive value of a single marker alone. In certain embodiments, no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to the normal control sample, in combination with a decreased or normal level of PSA in the biological sample as compared to the level of PSA in the normal control sample has a greater predictive value of the subject having a normal prostate state than any single marker alone.

Throughout the methods, kits, and panels of the invention, one or more of filamin B, LY9 and keratin 19 is understood as any of filamin B; LY9; keratin 19; filamin B and LY9; filamin B and keratin 19; LY9 and keratin 19; or filamin B, LY9, and keratin 19.

In certain embodiments of the invention, the abnormal prostate state is prostate cancer.

In certain embodiments of the invention, the prostate cancer is androgen-dependent prostate cancer. In certain embodiments of the invention, the prostate cancer is androgen-independent prostate cancer. In certain embodiments of the invention, the prostate cancer is aggressive prostate cancer. In certain embodiments of the invention, the prostate cancer is non-aggressive prostate cancer.

In certain embodiments of the invention, the abnormal prostate state is benign prostate hyperplasia.

In another aspect, the invention provides a method for identifying a subject as being at increased risk for developing prostate cancer, the method comprising:

(1) determining a level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in a biological sample from the subject; and

(2) comparing the level of the one or more prostate cancer related markers in the biological sample with the level of the one or more prostate cancer related markers in a normal control sample, wherein an altered level of the one or more prostate cancer related markers in the biological sample relative to the control sample is indicative of an increased risk for developing prostate cancer in the subject.

In certain embodiments, the one or more prostate cancer related markers is selected from the group consisting of filamin B, LY9, and keratin 19. In certain embodiments, an increased level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to the normal control sample is indicative of an increased risk for developing prostate cancer in the subject. In certain embodiments, no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to the normal control sample is indicative of no increased risk for developing prostate cancer in the subject.

In certain embodiments, the method further comprises detecting the level of prostate specific antigen (PSA) in the biological sample and preferably further comprises comparing the level of PSA in the biological sample to the level of PSA in a normal control sample. In certain embodiments, an increase in the level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to the normal control sample, in combination with an increase in the level of PSA in the biological sample as compared to the level of PSA in the normal control sample has greater predictive value of an increased risk for developing prostate cancer in the subject than an increase in any of the individual markers alone. In certain embodiments, no increase in the detected level of expression of each of the one or more prostate-cancer related markers

selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample relative to the normal control sample, in combination with a decreased or normal level of PSA in the biological sample as compared to the level of PSA in the normal control sample, has greater predictive value of no increased risk for developing prostate cancer in the subject than any single marker alone.

In the embodiments of the invention, one or more prostate cancer markers selected from the group consisting of filamin B, LY9 and keratin 19 is: filamin B; LY9; keratin 19; filamin B and LY9; filamin B and keratin 19; LY9 and keratin 19; or filamin B, LY9, and keratin 19.

In certain embodiments of the diagnostic or prognostic methods of the invention, one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3. In certain embodiments, one or more prostate cancer related markers is selected from the group consisting of keratin 7, keratin 8, and keratin 15. In certain embodiments, one or more prostate cancer related markers is selected from the group consisting of keratin 7 and keratin 15. In certain embodiments, one or more prostate cancer markers is selected from the group consisting of keratin 7, 15, and 19. In certain embodiments, the diagnostic and prognostic methods of the invention further comprise detecting the level of prostate specific antigen (PSA) in the biological sample, and preferably further comprise comparing the level of PSA in the biological sample to a level of PSA in a control sample.

In certain embodiments, the control sample for PSA is the same control sample as for the other prostate cancer related markers of the invention. In certain embodiments, the control sample for PSA is different from the control sample for the other prostate cancer related markers of the invention.

In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of an abnormal prostate state in the subject. In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin

15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of an abnormal prostate state in the subject. In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of a normal prostate state in the subject. In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of a normal prostate state in the subject.

In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of an increased risk of developing prostate cancer in the subject. In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of an increased risk of developing prostate cancer in the subject. In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of no increased risk of developing prostate cancer in the subject. In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the biological sample relative to a normal control sample is indicative of no increased risk of developing prostate cancer in the subject.

In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, the method further comprises detecting the level of prostate specific antigen (PSA) in the biological sample, and preferably further comprises comparing the level of PSA in the biological sample to the level of PSA in a normal control sample. In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increase in the level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with an increase in the level of PSA in the biological sample as compared to the level of PSA in the normal control sample is indicative of an abnormal prostate state in the subject wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone. In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an decrease in the level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with an increase in the level of PSA in the biological sample as compared to the level of PSA in the normal control sample is indicative of an abnormal prostate state in the subject wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone. In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with a decreased or normal level of PSA in the biological sample as compared to the level of PSA in the normal control sample, is indicative of a normal prostate state in the subject. In certain embodiments of the diagnostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased or normal level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with a decreased or normal level of PSA in the biological sample as compared to the level of PSA in the normal control sample, is indicative of a normal prostate state in the subject.

In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, the method further comprises detecting the level of prostate specific antigen (PSA) in the biological sample, and preferably further comprises comparing the level of PSA in the biological sample to the level of PSA in a normal control sample. In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increase in the level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with an increase in the level of PSA in the biological sample as compared to the level of PSA in the normal control sample is indicative of an increased risk for the subject of developing prostate cancer wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone. In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an decrease in the level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with an increase in the level of PSA in the biological sample as compared to the level of PSA in the normal control sample is indicative of an increased risk for the subject of developing prostate cancer wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone. In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with a decreased or normal level of PSA in the biological sample as compared to the level of PSA in the normal control sample, is indicative of an decreased risk or normal risk of developing prostate cancer in the subject wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone.. In certain embodiments of the prognostic methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased or normal level of one or more of the prostate cancer related markers in the biological sample relative to the normal control sample, in combination with a decreased or normal level of PSA in the biological sample as compared

to the level of PSA in the normal control sample, is indicative of a decreased risk or normal risk of developing prostate cancer in the subject wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone..

In various embodiments of any of the diagnostic or prognostic methods of the invention, the method may further comprise comparing the level of the one or more prostate cancer related markers in the biological sample with the level of the one or more prostate cancer related markers in a control sample selected from the group consisting of: a sample obtained from the same subject at an earlier time point than the biological sample, a sample from a subject with benign prostatic hyperplasia (BPH), a sample from a subject with non-metastatic prostate cancer, a sample from a subject with metastatic prostate cancer, a sample from a subject with androgen sensitive prostate cancer, a sample from a subject with androgen insensitive prostate cancer, a sample from a subject with aggressive prostate cancer, and a sample from a subject with non-aggressive prostate cancer. In such embodiments, comparison with one or more additional control sample can facilitate differentiating between two prostate cancer states selected from the group consisting of: normal prostate and prostate cancer, benign prostate hyperplasia and prostate cancer, benign prostate hyperplasia and normal prostate, androgen dependent and androgen independent prostate cancer, aggressive prostate cancer and non-aggressive prostate cancer, and metastatic prostate cancer and non-metastatic prostate cancer; or differentiating between any two or more of normal prostate, prostate cancer, benign prostate hyperplasia, androgen dependent prostate cancer, androgen independent prostate cancer, aggressive prostate cancer, non-aggressive prostate cancer, metastatic prostate cancer, and non-metastatic prostate cancer.

In certain embodiments of the invention, when a tumor is present, the method further comprises detecting the size of the prostate tumor in the subject.

In certain embodiments of the diagnostic and prognostic methods the invention, the method further comprises obtaining a sample from a subject.

In certain embodiments of the diagnostic and prognostic methods the invention, the method further comprises selecting a subject who has or is suspected of having prostate cancer.

In certain embodiments of the invention, the method further comprises selecting a treatment regimen for the subject based on the level of the one or more prostate cancer

markers. In certain embodiments of the invention, the method further comprises treating the subject with a treatment regimen based on the level of the one or more prostate cancer markers. In certain embodiments, a treatment regimen comprises one or more treatments selected from the group consisting of surgery, radiation, hormone therapy, antibody therapy, growth factor therapy, cytokine therapy, and chemotherapy.

In yet another aspect, the invention provides methods for monitoring prostate cancer in a subject, the method comprising

(1) determining a level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in a first biological sample obtained at a first time from a subject having prostate cancer;

(2) determining a level of expression of the one or more prostate cancer related markers in a second biological sample obtained from the subject at a second time, wherein the second time is after or later than, the first time; and

(3) comparing the level of the one or more prostate cancer related markers in the second sample with the level of the one or more prostate cancer related markers in the first sample, wherein a change in the level of the one or more prostate cancer related markers in the second sample as compared to the first sample is indicative of a change in prostate cancer status in the subject.

In certain embodiments, the subject is actively treated for prostate cancer prior to obtaining the second sample. That is, the subject is undergoing active treatment for prostate cancer.

In certain embodiments, the subject is not actively treated for prostate cancer prior to obtaining the second sample. That is, the subject is being monitored using watchful waiting.

In certain embodiments, one or more prostate cancer related markers is selected from the group consisting of filamin B, LY9, and keratin 19. In certain embodiments, an increased level of one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second biological sample as compared to the first biological sample is indicative of progression of the prostate cancer in the subject. In

certain embodiments, no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second biological sample as compared to the first biological sample is indicative of non-progression of the prostate cancer in the subject.

In certain embodiments, the methods further comprise determining the level of prostate specific antigen (PSA) in the first biological sample and the second biological sample and preferably, further comprising comparing the level of PSA in the second biological sample to the level of PSA in the first biological sample. In certain embodiments, an increased level of the one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second biological sample relative to the level of the one or more prostate cancer related markers in the first biological sample, in combination with an increase in the level of PSA in the second biological sample relative to the level of PSA in the first biological sample has greater predictive value of progression of the prostate cancer in the subject than any single marker alone. In certain embodiments, no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second biological sample relative to the level of the one or more prostate cancer related markers in the first biological sample, in combination with a decreased or same level of PSA in the second biological sample relative to the level of PSA in the first biological sample has greater predictive value of non-progression of the prostate cancer in the subject than any single marker alone.

In embodiments of the invention, the one or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 is: filamin B; LY9; keratin 19; filamin B and LY9; filamin B and keratin 19; LY9 and keratin 19; or filamin B, LY9, and keratin 19.

In certain embodiments of the monitoring methods of the invention, the one or more prostate cancer markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3. In certain embodiments of the monitoring methods of the invention, the one or more prostate cancer related markers is selected from the group consisting of keratin 7, keratin 8, and keratin 15. In certain embodiments of the monitoring methods of the invention, the one or more prostate cancer related markers is selected from the group consisting of keratin 7, keratin 15, and keratin 19. In certain embodiments of the

monitoring methods of the invention, the one or more prostate cancer related markers is selected from the group consisting of keratin 7 and keratin 15.

In certain embodiments of the monitoring methods of the invention, wherein the one or more prostate cancer markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, the methods further comprise determining the level of prostate specific antigen (PSA) in the first biological sample and the second biological sample, and preferably further comprise comparing the level of PSA in the second biological sample to the level of PSA in the first biological sample.

In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased level of one or more of the prostate cancer related markers in the second sample relative to a first sample is indicative of prostate tumor progression in the subject. In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the second sample relative to a first sample is indicative of prostate tumor progression in the subject. In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased level of one or more of the prostate cancer related markers in the second sample relative to a first sample is indicative of no prostate tumor progression in the subject. In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the second sample relative to a first sample is indicative of no prostate tumor progression in the subject.

In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, the method further comprises detecting the level of prostate specific antigen (PSA) in the second sample, and preferably further comprises comparing the level of PSA in the second sample to the level of PSA in a

first sample. In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increase in the level of one or more of the prostate cancer related markers in the second sample relative to the first sample, in combination with an increase in the level of PSA in the second sample as compared to the level of PSA in the first sample is indicative of prostate tumor progression in the subject wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone. In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an decrease in the level of one or more of the prostate cancer related markers in the second sample relative to the first sample, in combination with an increase in the level of PSA in the second sample as compared to the level of PSA in the first sample is indicative of prostate tumor progression in the subject wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone. . In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, a decreased or normal level of one or more of the prostate cancer related markers in the second sample relative to the first sample, in combination with a decreased or normal level of PSA in the second sample as compared to the level of PSA in the first sample, is indicative of no prostate tumor progression in the subject. In certain embodiments of the monitoring methods of the invention, wherein one or more prostate cancer related markers is selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3, an increased or normal level of one or more of the prostate cancer related markers in the second sample relative to the first sample, in combination with a decreased or normal level of PSA in the second sample as compared to the level of PSA in the first sample, is indicative of no prostate tumor progression in the subject wherein the method has greater diagnostic or predictive value than the value of any of the individual markers alone. .

In certain embodiments of the monitoring methods of the invention, the methods further comprise comparing the level of the one or more prostate cancer related markers in the first biological sample or the second biological sample with the level of the one or more

prostate cancer related markers in a control sample selected from the group consisting of: a normal control sample, a sample from a subject with benign prostatic hyperplasia (BPH), a sample from a subject with non-metastatic prostate cancer, a sample from a subject with metastatic prostate cancer, a sample from a subject with androgen sensitive prostate cancer, a sample from a subject with androgen insensitive prostate cancer, a sample from a subject with aggressive prostate cancer, and a sample from a subject with non-aggressive prostate cancer.

In certain embodiments of the monitoring methods of the invention, the methods further comprise detecting the size of the prostate tumor in the subject.

In certain embodiments of the monitoring methods of the invention, the methods further comprise obtaining a first sample and a second sample from the subject.

In certain embodiments of the monitoring methods of the invention, the methods further comprise selecting and/or administering a different treatment regimen for the subject based on progression of the prostate cancer in the subject.

In certain embodiments of the monitoring methods of the invention, the methods further comprise maintaining a treatment regimen for the subject based on non-progression of the prostate cancer in the subject.

In certain embodiments, the treatment regimens comprise one or more treatments selected from the group consisting of: surgery, radiation, hormone therapy, antibody therapy, growth factor therapy, cytokine therapy, and chemotherapy.

In certain embodiments of the monitoring methods of the invention, the methods further comprise withholding an active treatment of the prostate cancer in the subject based on non-progression of the prostate cancer in the subject. In certain embodiments, the active treatment is one or more treatments selected from the group consisting of: surgery, radiation, hormone therapy, antibody therapy, growth factor therapy, cytokine therapy, and chemotherapy.

In still another aspect, the invention provides methods for detecting a set of prostate cancer related markers, the method comprising:

(1) analyzing a biological sample from a subject for a level of two or more prostate cancer related markers of a set of prostate cancer related markers, wherein the set of prostate cancer related markers comprises filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3;

(2) detecting each of the two or more prostate specific makers in the biological sample, thereby detecting the set of prostate cancer related biomarkers.

In certain embodiments, the set of prostate cancer related markers comprises filamin B, LY9, and keratin 19. In certain embodiments, the two or more prostate cancer related markers are: filamin B and LY9; filamin B and keratin 19; LY9 and keratin 19; or filamin B, LY9, and keratin 19. In certain embodiments, the set of prostate cancer related markers comprises keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3. In certain embodiments, the set of prostate cancer related markers comprises keratin 7, keratin 8, and keratin 15. In certain embodiments, the set of prostate cancer related markers comprises keratin 7, keratin 15, and keratin 19. In certain embodiments, the set of prostate cancer related markers comprises keratin 7 and keratin 15.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises isolating a component of the biological sample.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises labeling a component of the biological sample.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises processing the biological sample.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises contacting a prostate cancer related marker to be detected with a prostate cancer related marker binding agent.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises forming a complex between a prostate cancer related marker to be detected and a prostate cancer related marker binding agent.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises contacting each of the one or more prostate cancer related markers with a prostate cancer related marker binding agent.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises forming a complex between each of the one or more prostate cancer related markers and a prostate cancer related marker binding agent.

In various embodiments of any of the methods of the invention, the step of detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises attaching a prostate cancer related marker to be detected to a solid surface.

In yet another aspect, the invention provides a panel of reagents for use in a detection method, the panel comprising at least two detection reagents, wherein each detection reagent is specific for the detection of at least one prostate cancer related marker of a set of prostate cancer related markers, wherein the set of prostate cancer specific markers comprises two or more prostate cancer related markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3 and PSA.

In certain embodiments, the set of prostate cancer specific markers comprises two or more prostate cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19. In certain embodiments, the two or more prostate cancer related markers is: filamin B and LY9; filamin B and keratin 19; LY9 and keratin 19; or filamin B, LY9, and keratin 19.

In certain embodiments, the set of prostate cancer specific markers comprises two or more prostate cancer related markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3. In certain embodiments, the set of prostate cancer specific markers comprises two or more prostate cancer related markers

selected from the group consisting of keratin 7, keratin 8, and keratin 15. In certain embodiments, the set of prostate cancer specific markers comprises keratin 7 and keratin 15.

In certain embodiments, the set of prostate cancer specific markers further comprises PSA. In certain embodiments, the panel of reagents comprises a detection reagent specific for the detection of PSA.

In yet another aspect, the invention provides for the use of any of the foregoing panels of the invention in any of the methods provided by the invention.

In still another aspect, the invention provides a kit for the diagnosis, monitoring, or characterization of an abnormal prostate state, comprising: at least one reagent specific for the detection of a level of at least one prostate cancer related marker selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, filamin B, and LY9.

In certain embodiments, the kit further comprises instructions for the diagnosis, monitoring, or characterization of an abnormal prostate state based on the level of the at least one prostate cancer related marker selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, filamin B, and LY9 detected.

In certain embodiments, the kit further comprises instructions to detect the level of PSA in a sample in which the at least one prostate cancer related marker selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, filamin B, and LY9 is detected.

In certain embodiments, the kit further comprises at least one reagent specific for the detection of a level of PSA.

In one embodiment, the invention provides a kit comprising at least one reagent specific for the detection of a level of at least one prostate cancer related marker selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B, and LY9 and at least one reagent specific for the detection of a level of PSA.

Further, the invention provides methods for diagnosing prostate cancer comprising determining a level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers

selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) in a biological sample obtained from a subject; and comparing the level of expression of the one or more markers in the biological sample obtained from the subject with the level of expression of the corresponding one or more markers in a control sample, wherein a modulation in the level of expression of the one or more markers in the biological sample is an indication that the subject is afflicted with prostate cancer. In certain embodiments, an increase in the level of expression of filamin B (FLNB), lymphocyte antigen 9 (LY9), or keratin 19 in the biological sample as compared to a normal control sample is an indication that the subject is afflicted with prostate cancer.

The invention further provides methods prognosing whether a subject is predisposed to developing prostate cancer, the method comprising determining the level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) present in a biological sample obtained from the subject; and comparing the level of expression of the one or more markers present in the biological sample obtained from the subject with the level of expression of the corresponding markers in a control sample, wherein a modulation in the level of expression of the one or more markers in the biological sample obtained from the subject with the level of expression of the corresponding marker in a control sample is an indication that the subject is predisposed to developing prostate cancer. In certain embodiments, an increase in the level of expression of filamin B (FLNB), lymphocyte antigen 9 (LY9), or keratin 19 in the biological sample as compared to a normal control sample is an indication that the subject is predisposed to prostate cancer.

The invention further provides methods for monitoring the treatment of prostate cancer in a subject, the methods comprising determining a level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) present in a first sample obtained from the subject prior to administering at least a portion of a treatment regimen to the subject; determining a level of expression of a corresponding one or more markers in a second sample obtained from the subject following administration of at least a portion of the treatment regimen to the subject;

and comparing the level of expression of the one or more markers in the first sample with the expression level of the corresponding one or more markers in the second sample, wherein a modulation in the level of expression of the one or more in the second sample as compared to the one or more markers in the first sample is an indication of a modulation in prostate cancer status in the subject. In certain embodiments, an decrease in the level of expression of filamin B (FLNB), lymphocyte antigen 9 (LY9), or keratin 19 in the biological sample as compared to the control sample is an indication that the subject is responding to treatment for prostate cancer.

In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) further include detection of prostate specific antigen (PSA) for the diagnosing, prognosing, and monitoring the treatment of prostate cancer.

The invention also provides methods for diagnosing prostate cancer comprising determining a level of expression of keratin 7 or keratin 15 in a biological sample obtained from a subject; and comparing the level of expression of keratin 7 or keratin 15 in the biological sample obtained from the subject with the level of expression of keratin 7 or keratin 15 in a control sample, wherein an modulation in the level of expression of keratin 7 or keratin 15 in the biological sample as compared to the control sample is an indication that the subject is afflicted with prostate cancer.

The invention provides methods of prognosing whether a subject is predisposed to developing prostate cancer, the method comprising determining the level of expression of keratin 7 or keratin 15 present in a biological sample obtained from the subject; and comparing the level of expression of keratin 7 or keratin 15 present in the biological sample obtained from the subject with the level of expression of keratin 7 or keratin 15 in a control sample, wherein a modulation in the level of expression of keratin 7 or keratin 15 in the biological sample obtained from the subject with the level of expression of keratin 7 or keratin 15 in a control sample is an indication that the subject is predisposed to developing prostate cancer.

The invention provides methods for monitoring the treatment of prostate cancer in a subject, the methods comprising determining a level of expression of keratin 7 or keratin 15 present in a first sample obtained from the subject prior to administering at least a portion of a treatment regimen to the subject; determining a level of expression of keratin 7 or keratin 15 in a second sample obtained from the subject following administration of at least a portion of the treatment regimen to the subject; and comparing the level of expression of keratin 7 or keratin 15 in the first sample with the expression level of keratin 7 or keratin 15 in the second sample, wherein a modulation in the level of expression of keratin 7 or keratin 15 in the second sample as compared to keratin 7 or keratin 15 in the first sample is an indication that the therapy is modulating prostate cancer in the subject.

The invention also provides methods for diagnosing prostate cancer comprising determining a level of expression of keratin 19 in a biological sample obtained from a subject; and comparing the level of expression of keratin 19 in the biological sample obtained from the subject with the level of expression of keratin 19 in a control sample, wherein an increase in the level of expression of keratin 19 in the biological sample as compared to a normal control sample is an indication that the subject is afflicted with prostate cancer.

The invention provides methods prognosing whether a subject is predisposed to developing prostate cancer, the method comprising determining the level of expression of keratin 19 present in a biological sample obtained from the subject; and comparing the level of expression of keratin 19 present in the biological sample obtained from the subject with the level of expression of keratin 19 in a control sample, wherein a modulation in the level of expression of keratin 19 in the biological sample obtained from the subject with the level of expression of keratin 19 in a normal control sample is an indication that the subject is predisposed to developing prostate cancer.

The invention provides methods for monitoring the treatment of prostate cancer in a subject, the methods comprising determining a level of expression of keratin 19 present in a first sample obtained from the subject prior to administering at least a portion of a treatment regimen to the subject; determining a level of expression of keratin 19 in a second sample obtained from the subject following administration of at least a portion of the treatment regimen to the subject; and comparing the level of expression of keratin 19 in the first sample with the expression level of keratin 19 in the second sample, wherein a decrease in

the level of expression of keratin 19 in the second sample as compared to keratin 19 in the first sample is an indication that the subject is responding to treatment for prostate cancer.

In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of filamin B for the diagnosing, prognosing, and monitoring the treatment of prostate cancer. In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of LY9 for the diagnosing, prognosing, and monitoring the treatment of prostate cancer. In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of PSA for the diagnosing, prognosing, and monitoring the treatment of prostate cancer. In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of filamin B for the diagnosing, prognosing, and monitoring the treatment of prostate cancer. In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of keratin 4 for the diagnosing, prognosing, and monitoring the treatment of prostate cancer. In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of keratin 8 for the diagnosing, prognosing, and monitoring the treatment of prostate cancer. In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of keratin 18 for the diagnosing, prognosing, and monitoring the treatment of prostate cancer. In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level of keratin 7, 15, or 19 further include detection of tubulin-beta 3 for the diagnosing, prognosing, and monitoring the treatment of prostate cancer.

In certain embodiments, keratin 7, 15, or 19 is keratin 7. In certain embodiments, keratin 7, 15, or 19 is keratin 15. In certain embodiments, keratin 7, 15, or 19 is keratin 19. In certain embodiments, keratin 7, 15, or 19 is keratin 7 and 15. In certain embodiments, keratin 7, 15, or 19 is keratin 7 and 19. In certain embodiments, keratin 7, 15, or 19 is keratin 15 and 19. In certain embodiments, keratin 7, 15, or 19 is keratin 7, 15, and 19.

In certain embodiments, filamin B, LY9, or keratin 19 is filamin B. In certain embodiments, filamin B, LY9, or keratin 19 is LY9. In certain embodiments, filamin B, LY9, or keratin 19 is keratin 19. In certain embodiments, filamin B, LY9, or keratin 19 is filamin B and LY9. In certain embodiments, filamin B, LY9, or keratin 19 is filamin B and keratin 19. In certain embodiments, filamin B, LY9, or keratin 19 is LY9, and keratin 19. In certain embodiments, filamin B, LY9, or keratin 19 is filamin B, LY9, and keratin 19.

In certain embodiments, the control sample is a sample from a normal subject or normal tissue. In certain embodiments, the control sample is a sample from the same subject from an earlier time point than the biological sample. In certain embodiments, the control sample is a sample from a subject with benign prostatic hyperplasia (BPH).

In certain embodiments, diagnosing includes differentiating between normal prostate and prostate cancer. In certain embodiments, diagnosing includes differentiating between benign prostate hyperplasia and prostate cancer.

The invention provides methods of characterizing prostate cancer status in a subject, the method comprising determining the level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) present in a biological sample obtained from the subject; and comparing the level of expression of the one or more markers present in the biological sample obtained from the subject with the level of expression of the one or more markers in a control sample, wherein the level of expression of the one or more markers in the biological sample obtained from the subject compared to the level of expression of the corresponding marker in a control sample is an indication of the prostate cancer status in the subject.

The invention provides methods of characterizing prostate cancer status in a subject, the method comprising determining the level of expression of keratin 7, 15, or 19 present in a biological sample obtained from the subject; and comparing the level of expression of keratin 7, 15, or 19 present in the biological sample obtained from the subject with the level of expression of keratin 7, 15, or 19 in a control sample, wherein the level of expression of keratin 7, 15, or 19 in the biological sample obtained from the subject compared to the level of expression of keratin 7, 15, or 19 in a control sample is an indication of the prostate cancer status in the subject.

In certain embodiments, the methods further comprises detection of the level of expression of prostate specific antigen (PSA) in the biological sample in which the expression level of filamin B or LY9 is detected in the methods of characterization of prostate cancer. In certain embodiments, the method further includes comparing the level of expression of PSA in the biological sample with the level of PSA in a control sample. In certain embodiments, the results from the detection of the expression level of PSA is used in conjunction with the results from detection of the level of one or more (e.g., 1, 2, 3, 4, 5, 6, or 7) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in the methods of characterization of prostate cancer.

In certain embodiments, the control sample is a sample from a normal subject or normal tissue. In certain embodiments, the control sample is a sample from the same subject from an earlier time point than the biological sample. In certain embodiments, the control sample is a sample from a subject with benign prostatic hyperplasia (BPH). In certain embodiments, the control sample is a sample from a subject with androgen dependent prostate cancer. In certain embodiments, the control sample is a sample from a subject with androgen independent prostate cancer. In certain embodiments, the control sample is a sample from a subject with an aggressive prostate cancer. In certain embodiments, the control sample is a sample from a subject with a non-aggressive prostate cancer.

In certain embodiments of the invention, characterizing includes differentiating between normal prostate and prostate cancer. In certain embodiments, characterizing includes differentiating between benign prostate hyperplasia and prostate cancer. In certain embodiments, characterizing includes differentiating between androgen sensitive and androgen insensitive prostate cancer. In certain embodiments, characterizing includes differentiating between aggressive prostate cancer and non-aggressive prostate cancer. In certain embodiments, characterizing includes differentiating between any two or more of normal prostate, prostate cancer, benign prostate hyperplasia, androgen sensitive prostate cancer, androgen insensitive prostate cancer, aggressive prostate cancer, non-aggressive prostate cancer, metastatic prostate cancer and non-metastatic prostate cancer. In certain embodiments, characterizing includes detecting a change in status from androgen independent prostate cancer to androgen dependent prostate cancer. In certain embodiments, characterizing includes detecting a change in status from androgen independent prostate

cancer to androgen dependent prostate cancer in response prior to a change in response to treatment. In certain embodiments, characterizing includes detecting a change in the size or relative aggressiveness of the prostate cancer. In certain embodiments, characterizing includes detecting a change from non-metastatic to metastatic prostate cancer.

In certain embodiments of the invention, an increase in the expression level of keratin 19 is an indication of increased pathology of prostate cancer or increased likelihood of developing prostate cancer. In certain embodiments of the invention, a decrease in the expression level of keratin 19 is an indication of decreased pathology of prostate cancer or decreased likelihood of developing prostate cancer. In certain embodiments of the invention, no significant change in the expression level of keratin 19 is an indication of no significant change in prostate cancer status.

In certain embodiments of the invention, an increase in the expression level of filamin B or LY9 is an indication of increased pathology of prostate cancer or increased likelihood of developing prostate cancer. In certain embodiments of the invention, an decrease in the expression level of filamin B or LY9 is an indication of decreased pathology of prostate cancer or decreased likelihood of developing prostate cancer. In certain embodiments of the invention, no significant change in the expression level of filamin B or LY9 is an indication of no significant change in prostate cancer status.

In certain embodiments, methods of the invention further comprise obtaining a biological sample from a subject.

In certain embodiments, methods of the invention further comprise selecting a subject for having or being suspected of having prostate cancer.

In certain embodiments, methods of the invention further comprise selection of a regimen for treatment of the subject including one or more treatments selected from the group consisting of surgery, radiation, hormone therapy, antibody therapy, therapy with growth factors, cytokines, and chemotherapy.

In certain embodiments, the method further comprises selection of the one ore more specific treatment regimens for the subject based on the results of the methods.

In certain embodiments, the method further comprises changing the treatment regimen of the subject based on the results of the methods.

In certain embodiments, the method further comprises a change in hormone based therapy based on monitoring of the subject based on the results of the methods.

In certain embodiments, the method further comprises not treating the subject with one or more treatments selected from the group consisting of surgery, radiation, hormone therapy, antibody therapy, therapy with growth factors, cytokines, or chemotherapy for an interval prior to performing a subsequent diagnostic, prognostic, or monitoring method provided herein.

The invention provides methods of treating a subject with prostate cancer by determining a level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9), present in a first sample obtained from the subject having prostate cancer; determining a level of expression of the one or more markers in a second sample obtained from the subject after administration of at least a portion of a treatment for prostate cancer; comparing the level of expression of the one or more markers in the first sample with the expression level of the one or more markers in the second sample, wherein a modulated level of expression of the one or more markers in the second sample as compared to the one or more markers in the first sample is an indication that the subject is an indication of modulation of prostate cancer in the subject; and selecting a treatment for the subject based on the expression level of the one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9). For example, a decrease in the level of filamin B, LY9, or keratin 19 is an indication that the subject is responding to treatment. An increase in the level of filamin B, LY9, or keratin 19 is an indication that the subject is not responding to treatment.

As used herein, modulation is understood as a change in an expression level of a marker, particularly a statistically significant change in an expression level of a marker as compared to an appropriate control. The meaning of an increase or a decrease in an expression level of the marker as compared to a control depends, at least, on the specific

identity of the marker and the control used. Such considerations are well understood by those of skill in the art. The meaning of the modulation in the expression level(s) of markers can be determined based on the teachings provided herein.

In certain embodiments, the treatment method further comprises determining a level of expression of PSA in the first sample and determining a level of expression of PSA in the second sample. In certain embodiments, the treatment of the subject is maintained upon detection of a decrease in the expression level of at least one of filamin B, LY9, keratin 19, or PSA in the second sample, indicating that the subject was responsive to the treatment. In certain embodiments, the treatment of the subject is discontinued upon detection of a decrease in the expression level of at least one of filamin B, LY9, keratin 19, or PSA in the second sample, indicating that disease is no longer present or minimized such that treatment is no longer required. In certain embodiments, a new treatment of the subject is initiated upon detection of a decrease in the expression level of at least one of filamin B, LY9, keratin 19, or PSA in the second sample, e.g., resection after shrinkage of the tumor. In certain embodiments, the treatment of the subject is discontinued upon detection of an increase in the expression level of at least one of filamin B, LY9, keratin 19, or PSA in the second sample, indication of a lack of response or discontinuation of response to the treatment. In certain embodiments, a new treatment of the subject is initiated upon detection of an increase in the expression level of at least one of filamin B, LY9, keratin 19, or PSA in the second sample, e.g., due to lack of response or discontinuation of response to treatment. One of skill in the art can select appropriate methods of treatment of a subject based, at least in part, on his response, or non-response, to treatments being used as determined by the expression level of the markers.

The invention provides method of selecting a subject with prostate cancer for administration of active treatment, rather than watchful waiting, by determining a level of expression of filamin B, LY9, or keratin 19, present in a first sample obtained from the subject having prostate cancer wherein the subject has not been actively treated for prostate cancer; determining a level of expression of filamin B, LY9, or keratin 19 in a second sample obtained from the subject; comparing the level of expression of filamin B, LY9, or keratin 19 in the first sample obtained at an earlier time point with the expression level of filamin B, LY9, or keratin 19 in the second sample; wherein a decreased level of expression of filamin B, LY9, or keratin 19 in the second sample as compared to filamin B, LY9, or keratin 19 in

the first sample is an indication that the subject should not be administered active treatment for prostate cancer; and selecting against active treatment of a subject for prostate cancer.

The invention also provides methods of selecting a subject with prostate cancer for administration of active treatment by determining a level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9), present in a first sample obtained from the subject having prostate cancer wherein the subject has not been actively treated for prostate cancer; determining a level of expression of the corresponding one or more markers in a second sample obtained from the subject; comparing the level of expression of the one or more markers in the first sample obtained at an earlier time point with the expression level of the one or more markers in the second sample; wherein an modulated level of expression of the one or more markers in the second sample as compared to the one or more markers in the first sample is considered in determining if a subject should be actively treated for prostate cancer.

In certain embodiments, actively treating the subject for prostate cancer comprises treating the subject with one or more therapies such as hormone therapy, chemotherapy, radiation therapy, and surgery.

In certain embodiments, methods of subject selection further comprise determining a level of expression of PSA in the first sample and determining a level of expression of PSA in the second sample. In certain embodiments, a decreased level of expression of PSA in the second sample as compared to the level of expression of PSA in the first sample is an indication that the subject should not be administered active treatment for prostate cancer. In certain embodiments, an increased level of expression of PSA in the second sample as compared to the level of expression of PSA in the first sample is an indication that the subject should be administered active treatment for prostate cancer.

In certain embodiments of any of the methods provided herein, filamin B or LY9 is understood as filamin B and LY9. In certain embodiments of any of the methods provided herein, filamin B or LY9 is understood as filamin B. In certain embodiments of any of the methods provided herein, filamin B or LY9 is understood as LY9.

In certain embodiments of any of the methods provided herein, keratin 7, 15, or 19 is understood as keratin 7. In certain embodiments of any of the methods provided herein,

keratin 7, 15, or 19 is understood as keratin 15. In certain embodiments of any of the methods provided herein, keratin 7, 15, or 19 is understood as keratin 19. In certain embodiments of any of the methods provided herein, keratin 7, 15, or 19 is understood as keratin 7 and 15. In certain embodiments of any of the methods provided herein, keratin 7, 15, or 19 is understood as keratin 15 and 19. In certain embodiments of any of the methods provided herein, keratin 7, 15, or 19 is understood as keratin 7 and 19. In certain embodiments of any of the methods provided herein, keratin 7, 15, or 19 is understood as keratin 7, 15, and 19.

In certain embodiments, one or more markers selected from any group provided herein does not include keratin 4. In certain embodiments, one or more markers selected from any group provided herein does not include keratin 7. In certain embodiments, one or more markers selected from any group provided herein does not include keratin 8. In certain embodiments, one or more markers selected from any group provided herein does not include keratin 15. In certain embodiments, one or more markers selected from any group provided herein does not include keratin 18. In certain embodiments, one or more markers selected from any group provided herein does not include keratin 19. In certain embodiments, one or more markers selected from any group provided herein does not include tubulin-beta 3. In certain embodiments, one or more markers selected from any group provided herein does not include filamin B. In certain embodiments, one or more markers selected from any group provided herein does not include LY9. In certain embodiments, one or more markers selected from any group provided herein does not include PSA.

In certain embodiments of any of the methods provided herein, the methods further comprising obtaining a biological sample from the subject.

The invention provides methods of identifying a compound for treating prostate cancer comprising obtaining a test cell; contacting the test cell with a test compound; determining the level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) in the test cell; comparing the level of expression of the one or more markers in the test cell with a control cell not contacted by the test compound; and selecting a test compound that modulates the level of expression of the one or more markers in the test cell, thereby identifying a compound for treating a disorder in a subject. In certain embodiments, the methods further include identifying a compound that modulates the level of expression of PSA.

The invention provides methods of identifying a compound for treating prostate cancer comprising obtaining a test cell; contacting the test cell with a test compound; determining the level of expression of keratin 7, 15, or 19 in the test cell; comparing the level of expression of keratin 7, 15, or 19 in the test cell with a control cell not contacted by the test compound; and selecting a test compound that modulates the level of expression of keratin 7, 15, or 19 in the test cell, thereby identifying a compound for treating a disorder in a subject.

The invention provides methods of identifying a compound for treating prostate cancer comprising obtaining a test cell; contacting the test cell with a test compound; determining the level of expression of filamin B or LY9 in the test cell; comparing the level of expression of filamin B or LY9 in the test cell with a control cell not contacted by the test compound; and selecting a test compound that modulates the level of expression of filamin B or LY9 in the test cell, thereby identifying a compound for treating a disorder in a subject.

In certain embodiments, the methods of identifying a compound for treating prostate cancer further include identifying a compound that modulates the level of expression of PSA.

In certain embodiments, the test cell is contacted with the agent in vitro.

In certain embodiments, the test cell is contacted with the agent in vivo. In certain embodiments, the test cell is present in a xenogenic model of cancer. In certain embodiments, the test cell is present in an animal model of prostate cancer. In certain embodiments, the level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) is detected in the test cell by detection of the expression level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) in a biological sample in the organism containing the test cell.

The invention provides kits for the diagnosis, monitoring, or characterization of prostate cancer comprising at least one reagent specific for the detection of the level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) in a sample.

In certain embodiments, the kit further comprises instructions for the diagnosis, monitoring, or characterization of prostate cancer based on the level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9). In certain embodiments, the kit includes instructions to detect the level of expression of PSA in the same sample in which the level of expression of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) is detected. In certain embodiments, the kit includes at least one reagent specific for the detection of the level of expression of PSA. In certain embodiments, the kits include at least one antibody or nucleic acid for binding to f one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) for use in the methods provided herein. In certain embodiments, the kit includes at least one antibody or nucleic acid for binding to keratin 7 and one antibody or nucleic acid for binding to keratin 15. In certain embodiments, the kits further include at least one antibody or nucleic acid for binding to PSA for use in the methods provided herein. The kits may further provide instructions for practicing the methods provided herein.

Where applicable or not specifically disclaimed, any one of the embodiments described herein are contemplated to be able to combine with any other one or more embodiments, even though the embodiments are described under different aspects of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1: Schematic representing the underlying principles of the Interrogative Platform Technology provided in WO2012119129.

Figure 2A-B: Causal associations of Keratins, including KRT8, KRT18 (A) and KRT19 (B) in human prostate cancer cells as inferred by the Interrogative Platform Technology.

Figures 3A-C: Mechanistic insight into regulation of keratins by mitochondrial function inferred by the Interrogative Platform Technology. (A) KRT8-KRT15 association is abolished upon ubidecaronone treatment. Note change of direction of arrow between and positions of KRT7 and KRT15 before treatment (A-1) and after treatment (A-2). (B) Tubulin-beta 3 interacts with a number of proteins. (C) Expression levels of keratin 19 in biological samples from subjects with prostate cancer or control samples.

Figure 4: Inference of filamin B (FLNB) as a hub of activity in prostate cancer and as a biomarker using the Interrogative Platform Technology provided in WO2012119129.

Figure 5: Portion of an inference map showing filamin B is connected directly to LY9, which is, in turn, connected to at least one other marker.

Figure 6: Validation of filamin B levels in human serum samples. Levels of filamin B and PSA were elevated in prostate cancer samples when compared to normal serum. Data represents percent average change, with normal donors set to 100% on a log scale.

Figure 7: Validation of LY9 levels in human serum samples. Levels of LY9 were elevated in prostate cancer samples when compared to normal serum. Data represents percent average change, with normal donors set to 100% on a log scale.

Figure 8: Validation of filamin B, LY9, and PSA levels in human serum samples. Data are shown as ng/ml of the marker in serum.

Figures 9A-B: ROC curve analysis of sensitivity and false positive rate (FPR) of PSA, FLNB and the combination of PSA and FLNB (A) and area under the curve values (AUC) calculated (B) based on the analysis. The combination of PSA and FLNB was more sensitive than either marker alone.

Figures 10A-B: ROC curve analysis of PSA, FLNB, LY9 and combinations of PSA, FLNB, and LY9 using linear (A) and non-linear (B) scoring functions. The combination of PSA, LY9, and FLNB was more sensitive than any marker alone.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

As used herein, each of the following terms has the meaning associated with it in this section.

A “patient” or “subject” to be treated by the method of the invention can mean either a human or non-human animal, preferably a mammal. By “subject” is meant any animal, including horses, dogs, cats, pigs, goats, rabbits, hamsters, monkeys, guinea pigs, rats, mice, lizards, snakes, sheep, cattle, fish, and birds. A human subject may be referred to as a patient. It should be noted that clinical observations described herein were made with human subjects and, in at least some embodiments, the subjects are human.

“Therapeutically effective amount” means the amount of a compound that, when administered to a patient for treating a disease, is sufficient to effect such treatment for the disease, *e.g.*, the amount of such a substance that produces some desired local or systemic effect at a reasonable benefit/risk ratio applicable to any treatment, *e.g.*, is sufficient to ameliorate at least one sign or symptom of the disease, *e.g.*, to prevent progression of the disease or condition, *e.g.*, prevent tumor growth, decrease tumor size, induce tumor cell apoptosis, reduce tumor angiogenesis, prevent metastasis. When administered for preventing a disease, the amount is sufficient to avoid or delay onset of the disease. The “therapeutically effective amount” will vary depending on the compound, its therapeutic index, solubility, the disease and its severity and the age, weight, *etc.*, of the patient to be treated, and the like. For example, certain compounds discovered by the methods of the present invention may be administered in a sufficient amount to produce a reasonable benefit/risk ratio applicable to such treatment. Administration of a therapeutically effective amount of a compound may require the administration of more than one dose of the compound.

“Preventing” or “prevention” refers to a reduction in risk of acquiring a disease or disorder (*i.e.*, causing at least one of the clinical symptoms of the disease not to develop in a patient that may be exposed to or predisposed to the disease but does not yet experience or display symptoms of the disease). Prevention does not require that the disease or condition never occurs in the subject. Prevention includes delaying the onset or severity of the disease or condition.

The term “prophylactic” or “therapeutic” treatment refers to administration to the subject of one or more agents or interventions to provide the desired clinical effect. If it is administered prior to clinical manifestation of the unwanted condition (*e.g.*, disease or other unwanted state of the host animal) then the treatment is prophylactic, *i.e.*, it protects the host against developing at least one sign or symptom of the unwanted condition, whereas if administered after manifestation of the unwanted condition, the treatment is therapeutic (*i.e.*, it is intended to diminish, ameliorate, or maintain at least one sign or symptom of the existing unwanted condition or side effects therefrom).

As used herein, “treatment”, particularly “active treatment” refers to performing an intervention to treat prostate cancer in a subject, *e.g.*, reduce at least one of the growth rate, reduction of tumor burden, reduce or maintain the tumor size, or the malignancy (*e.g.*, likelihood of metastasis) of the tumor; or to increase apoptosis in the tumor by one or more of administration of a therapeutic agent, *e.g.*, chemotherapy or hormone therapy; administration of radiation therapy (*e.g.*, pellet implantation, brachytherapy), or surgical resection of the tumor, or any combination thereof appropriate for treatment of the subject based on grade and stage of the tumor and other routine considerations. Active treatment is distinguished from “watchful waiting” (*i.e.*, not active treatment) in which the subject and tumor are monitored, but no interventions are performed to affect the tumor. Watchful waiting can include administration of agents that alter effects caused by the tumor (*e.g.*, incontinence, erectile dysfunction) that are not administered to alter the growth or pathology of the tumor itself.

The term “therapeutic effect” refers to a local or systemic effect in animals, particularly mammals, and more particularly humans caused by a pharmacologically active substance. The term thus means any substance intended for use in the diagnosis, cure, mitigation, treatment, or prevention of disease, or in the enhancement of desirable physical or mental development and conditions in an animal or human. A therapeutic effect can be understood as a decrease in tumor growth, decrease in tumor growth rate, stabilization or decrease in tumor burden, stabilization or reduction in tumor size, stabilization or decrease in tumor malignancy, increase in tumor apoptosis, and/or a decrease in tumor angiogenesis.

The terms “disorders”, “diseases”, and “abnormal state” are used inclusively and refer to any deviation from the normal structure or function of any part, organ, or system of the body (or any combination thereof). A specific disease is manifested by characteristic symptoms and signs, including biological, chemical, and physical changes, and is often

associated with a variety of other factors including, but not limited to, demographic, environmental, employment, genetic, and medically historical factors. Certain characteristic signs, symptoms, and related factors can be quantitated through a variety of methods to yield important diagnostic information. As used herein the disorder, disease, or abnormal state is an abnormal prostate state, including benign prostate hyperplasia and cancer, particularly prostate cancer. The abnormal prostate state of prostate cancer can be further subdivided into stages and grades of prostate cancer as provided, for example in Prostate. In: Edge SB, Byrd DR, Compton CC, et al., eds.: AJCC Cancer Staging Manual. 7th ed. New York, NY: Springer, 2010, pp 457-68 (incorporated herein by reference). Further, abnormal prostate states can be classified as one or more of benign prostate hyperplasia (BPH), androgen sensitive prostate cancer, androgen insensitive or resistant prostate cancer, aggressive prostate cancer, non-aggressive prostate cancer, metastatic prostate cancer, and non-metastatic prostate cancer.

A subject at “increased risk for developing prostate cancer” may or may not develop prostate cancer. Identification of a subject at increased risk for developing prostate cancer should be monitored for additional signs or symptoms of prostate cancer. The methods provided herein for identifying a subject with increased risk for developing prostate cancer can be used in combination with assessment of other known risk factors or signs of prostate cancer including, but not limited to decreased urinary stream, urgency, hesitancy, nocturia, incomplete bladder emptying, and age.

The term “expression” is used herein to mean the process by which a polypeptide is produced from DNA. The process involves the transcription of the gene into mRNA and the translation of this mRNA into a polypeptide. Depending on the context in which used, “expression” may refer to the production of RNA, or protein, or both.

The terms “level of expression of a gene”, “gene expression level”, “level of a marker”, and the like refer to the level of mRNA, as well as pre-mRNA nascent transcript(s), transcript processing intermediates, mature mRNA(s) and degradation products, or the level of protein, encoded by the gene in the cell.

The term “specific identification” is understood as detection of a marker of interest with sufficiently low background of the assay and cross-reactivity of the reagents used such that the detection method is diagnostically useful. In certain embodiments, reagents for

specific identification of a marker bind to only one isoform of the marker. In certain embodiments, reagents for specific identification of a marker bind to more than one isoform of the marker. In certain embodiments, reagents for specific identification of a marker bind to all known isoforms of the marker.

The term “modulation” refers to upregulation (*i.e.*, activation or stimulation), down-regulation (*i.e.*, inhibition or suppression) of a response, or the two in combination or apart. A “modulator” is a compound or molecule that modulates, and may be, *e.g.*, an agonist, antagonist, activator, stimulator, suppressor, or inhibitor.

The term “control sample,” as used herein, refers to any clinically relevant comparative sample, including, for example, a sample from a healthy subject not afflicted with an oncological disorder, *e.g.*, prostate cancer, or a sample from a subject from an earlier time point, *e.g.*, prior to treatment, an earlier tumor assessment time point, at an earlier stage of treatment. A control sample can be a purified sample, protein, and/or nucleic acid provided with a kit. Such control samples can be diluted, for example, in a dilution series to allow for quantitative measurement of levels of analytes, *e.g.*, markers, in test samples. A control sample may include a sample derived from one or more subjects. A control sample may also be a sample made at an earlier time point from the subject to be assessed. For example, the control sample could be a sample taken from the subject to be assessed before the onset of an oncological disorder, *e.g.*, prostate cancer, at an earlier stage of disease, or before the administration of treatment or of a portion of treatment. The control sample may also be a sample from an animal model, or from a tissue or cell lines derived from the animal model of oncological disorder, *e.g.*, prostate cancer. The level of activity or expression of one or more (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), lymphocyte antigen 9 (LY9), and PSA in a control sample consists of a group of measurements may be determined, *e.g.*, based on any appropriate statistical measure, such as, for example, measures of central tendency including average, median, or modal values. Different from a control is preferably statistically significantly different from a control.

The term “control level” refers to an accepted or pre-determined level of a marker in a subject sample. A control level can be a range of values. Marker levels can be compared to a single control value, to a range of control values, to the upper level of normal, or to the lower level of normal as appropriate for the assay.

In one embodiment, the control is a standardized control, such as, for example, a control which is predetermined using an average of the levels of expression of one or more markers from a population of subjects having no cancer, especially subjects having no prostate cancer. In still other embodiments of the invention, a control level of a marker in a non-cancerous sample(s) derived from the subject having cancer. For example, when a biopsy or other medical procedure reveals the presence of cancer in one portion of the tissue, the control level of a marker may be determined using the non-affected portion of the tissue, and this control level may be compared with the level of the marker in an affected portion of the tissue.

In certain embodiments, the control can be from a subject, or a population of subject, having an abnormal prostate state. For example, the control can be from a subject suffering from benign prostate hyperplasia (BPH), androgen sensitive prostate cancer, androgen insensitive or resistant prostate cancer, aggressive prostate cancer, non-aggressive prostate cancer, metastatic prostate cancer, or non-metastatic prostate cancer. It is understood that not all markers will have different levels for each of the abnormal prostate states listed. It is understood that a combination of marker levels may be most useful to distinguish between abnormal prostate states, possibly in combination with other diagnostic methods. Further, marker levels in biological samples can be compared to more than one control sample (e.g., normal, abnormal, from the same subject, from a population control). Marker levels can be used in combination with other signs or symptoms of an abnormal prostate state to provide a diagnosis for the subject.

A control can also be a sample from a subject at an earlier time point, e.g., a baseline level prior to suspected presence of disease, before the diagnosis of a disease, at an earlier assessment time point during watchful waiting, before the treatment with a specific agent (e.g., chemotherapy, hormone therapy) or intervention (e.g., radiation, surgery). In certain embodiments, a change in the level of the marker in a subject can be more significant than the absolute level of a marker, e.g., as compared to control.

As used herein, a sample obtained at an “earlier time point” is a sample that was obtained at a sufficient time in the past such that clinically relevant information could be obtained in the sample from the earlier time point as compared to the later time point. In certain embodiments, an earlier time point is at least four weeks earlier. In certain embodiments, an earlier time point is at least six weeks earlier. In certain embodiments, an

earlier time point is at least two months earlier. In certain embodiments, an earlier time point is at least three months earlier. In certain embodiments, an earlier time point is at least six months earlier. In certain embodiments, an earlier time point is at least nine months earlier. In certain embodiments, an earlier time point is at least one year earlier. Multiple subject samples (e.g., 3, 4, 5, 6, 7, or more) can be obtained at regular or irregular intervals over time and analyzed for trends in changes in marker levels. Appropriate intervals for testing for a particular subject can be determined by one of skill in the art based on ordinary considerations.

As used herein, “changed as compared to a control” sample or subject is understood as having a level of the analyte or diagnostic or therapeutic indicator (e.g., marker) to be detected at a level that is statistically different than a sample from a normal, untreated, or abnormal state control sample. Changed as compared to control can also include a difference in the rate of change of the level of one or more markers obtained in a series of at least two subject samples obtained over time. Determination of statistical significance is within the ability of those skilled in the art, e.g., the number of standard deviations from the mean that constitute a positive or negative result.

As used herein, the term “obtaining” is understood herein as manufacturing, purchasing, or otherwise coming into possession of.

As used herein, “detecting”, “detection”, “determining”, and the like are understood that an assay performed for identification of a specific marker in a sample, e.g., one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), lymphocyte antigen 9 (LY9), and PSA. The amount of marker expression or activity detected in the sample can be none or below the level of detection of the assay or method.

As used herein, “greater predictive value” is understood as an assay that has significantly greater sensitivity and/or specificity, preferably greater sensitivity and specificity, than the test to which it is compared. The predictive value of a test can be determined using an ROC analysis. In an ROC analysis a test that provides perfect discrimination or accuracy between normal and disease states would have an area under the curve (AUC)=1, whereas a very poor test that provides no better discrimination than random chance would have AUC=0.5. As used herein, a test with a greater predictive value will have

a statistically improved AUC as compared to another assay. The assays are performed in an appropriate subject population.

The articles “a” and “an” are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element.

The term “including” is used herein to mean, and is used interchangeably with, the phrase “including but not limited to.”

The term “or” is used inclusively herein to mean, and is used interchangeably with, the term “and/or,” unless context clearly indicates otherwise. For example, as used herein, filamin B or LY9 is understood to include filamin B alone, LY9 alone, and the combination of filamin B and LY9.

The term “such as” is used herein to mean, and is used interchangeably, with the phrase “such as but not limited to.”

Unless specifically stated or obvious from context, as used herein, the term “about” is understood as within a range of normal tolerance in the art, for example within 2 standard deviations of the mean. About can be understood as within 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1 %, 0.05%, or 0.01% of the stated value. Unless otherwise clear from context, all numerical values provided herein can be modified by the term about.

The recitation of a listing of chemical group(s) in any definition of a variable herein includes definitions of that variable as any single group or combination of listed groups. The recitation of an embodiment for a variable or aspect herein includes that embodiment as any single embodiment or in combination with any other embodiments or portions thereof.

Any compositions or methods provided herein can be combined with one or more of any of the other compositions and methods provided herein.

Ranges provided herein are understood to be shorthand for all of the values within the range. For example, a range of 1 to 50 is understood to include any number, combination of numbers, or sub-range from the group consisting 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50.

As used herein, “one or more” is understood as each value 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, and any value greater than 10.

Reference will now be made in detail to exemplary embodiments of the invention. While the invention will be described in conjunction with the exemplary embodiments, it will be understood that it is not intended to limit the invention to those embodiments. To the contrary, it is intended to cover alternatives, modifications, and equivalents as may be included within the spirit and scope of the invention as defined by the appended claims.

Keratins

Keratin 4

Keratin 4, also known as K4; CK4; CK-4; CYK4, is a member of the keratin gene family. The type II cytokeratins consist of basic or neutral proteins which are arranged in pairs of heterotypic keratin chains coexpressed during differentiation of simple and stratified epithelial tissues. This type II cytokeratin is specifically expressed in differentiated layers of the mucosal and esophageal epithelia with family member KRT13. Mutations in these genes have been associated with White Sponge Nevus, characterized by oral, esophageal, and anal leukoplakia. The type II cytokeratins are clustered in a region of chromosome 12q12-q13.

As used herein, keratin 4 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI Gene ID for human keratin 4 is 3851 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/3851 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority). Homo sapiens keratin 4, GenBank Accession No. NM_002272 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 1 and 2. (The GenBank number is incorporated herein by reference in the version available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of any fragments of keratin 4 sequences as long as the fragment can allow for the specific identification of keratin 4. Moreover, it is understood that there are naturally occurring variants of keratin 4 which may or may not be associated with a specific disease state, the use of which are also included in this application.

Keratin 7

Keratin 7, also known as CK7, K2C7, K7, SCL, CK-7; cytokeratin 7; cytokeratin-7; keratin, 55K type II cytoskeletal; keratin, simple epithelial type I, K7; keratin, type II cytoskeletal 7; keratin-7; sarcolectin; type II mesothelial keratin K7; and type-II keratin Kb7, is a member of the keratin gene family. The type II cytokeratins consist of basic or neutral proteins which are arranged in pairs of heterotypic keratin chains coexpressed during differentiation of simple and stratified epithelial tissues. This type II cytokeratin is specifically expressed in the simple epithelia lining the cavities of the internal organs and in the gland ducts and blood vessels. The genes encoding the type II cytokeratins are clustered in a region of chromosome 12q12-q13. Alternative splicing may result in several transcript variants; however, not all variants have been fully described.

As used herein, keratin 7 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI Gene ID for human keratin 7 is 3855 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/3855 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority). Homo sapiens keratin 7, GenBank Accession No. NM_005556 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 3 and 4. (The GenBank number is incorporated herein by reference in the version available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of any fragments of keratin 7 sequences as long as the fragment can allow for the specific identification of keratin 7. Moreover, it is understood that there are naturally occurring variants of keratin 7 which may or may not be associated with a specific disease state, the use of which are also included in this application.

Keratin 8

Keratin 8, also known as K8; KO; CK8; CK-8; CYK8; K2C8; CARD2 is is a member of the type II keratin family clustered on the long arm of chromosome 12. Type I and type II keratins heteropolymerize to form intermediate-sized filaments in the cytoplasm of epithelial cells. The product of this gene typically dimerizes with keratin 18 to form an intermediate filament in simple single-layered epithelial cells. This protein plays a role in maintaining cellular structural integrity and also functions in signal transduction and cellular

differentiation. Mutations in this gene cause cryptogenic cirrhosis. Alternatively spliced transcript variants have been found for this gene.

As used herein, keratin 8 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI Gene ID for human keratin 8 is 3856 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/3856 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority). Homo sapiens keratin 8, variant 1, GenBank Accession No. NM_001256282 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 5 and 6; and homo sapiens keratin 8, variant 3, GenBank Accession No. NM_001256293 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 7 and 8. (The GenBank numbers are incorporated herein by reference in the version available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of either one or both of the variants of keratin 8 provided in the sequence listing and any fragments of keratin 8 sequences as long as the fragment can allow for the specific identification of keratin 8. Moreover, it is understood that there are naturally occurring variants of keratin 8 which may or may not be associated with a specific disease state, the use of which are also included in this application.

Keratin 15

Keratin 15, also known as K15; CK15; K1CO, is a member of the keratin gene family. The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair keratins. Most of the type I cytokeratins consist of acidic proteins which are arranged in pairs of heterotypic keratin chains and are clustered in a region on chromosome 17q21.2.

As used herein, keratin 15 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI Gene ID for human keratin 15 is 3866 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/3866 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority). Homo sapiens keratin 15, GenBank Accession No. NM_002275 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 9 and 10. (The GenBank number is incorporated herein by reference in the version available on the

filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of any fragments of keratin 15 sequences as long as the fragment can allow for the specific identification of keratin 15. Moreover, it is understood that there are naturally occurring variants of keratin 15 which may or may not be associated with a specific disease state, the use of which are also included in this application.

Keratin 18

Keratin 18, also known as K18; CYK18, encodes the type I intermediate filament chain keratin 18. Keratin 18, together with its filament partner keratin 8, are perhaps the most commonly found members of the intermediate filament gene family. They are expressed in single layer epithelial tissues of the body. Mutations in this gene have been linked to cryptogenic cirrhosis. Two transcript variants encoding the same protein have been found for this gene.

As used herein, keratin 15 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI Gene ID for human keratin 18 is 3875 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/3875 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority). Homo sapiens keratin 18, variant 1, GenBank Accession No. NM_000224 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 11 and 12, and homo sapiens keratin 18, variant 2, GenBank Accession No. 199187 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 13 and 14. (The GenBank numbers are incorporated herein by reference in the version available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of either one or both of the variants of keratin 18 provided in the sequence listing and any fragments of keratin 18 sequences as long as the fragment can allow for the specific identification of keratin 18. Moreover, it is understood that there are naturally occurring variants of keratin 18 which may or may not be associated with a specific disease state, the use of which are also included in this application.

Keratin 19

Keratin 19, also known as K19; CK19; K1CS, is a member of the keratin gene family. The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair keratins. The type I cytokeratins consist of acidic proteins which are arranged in pairs of heterotypic keratin chains. Unlike its related family members, this smallest known acidic cytokeratin is not paired with a basic cytokeratin in epithelial cells. It is specifically expressed in the periderm, the transiently superficial layer that envelopes the developing epidermis. The type I cytokeratins are clustered in a region of chromosome 17q12-q21.

As used herein, keratin 19 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI Gene ID for human keratin 19 is 3880 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/3880 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority). Homo sapiens keratin 19, GenBank Accession No. NM_002276 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 15 and 16. (The GenBank number is incorporated herein by reference in the version available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of any fragments of keratin 19 sequences as long as the fragment can allow for the specific identification of keratin 19. Moreover, it is understood that there are naturally occurring variants of keratin 19 which may or may not be associated with a specific disease state, the use of which are also included in this application.

Tubulin-beta 3

Tubulin-beta 3, also known as CDCBM; TUBB4; beta-4; CFEOM3A, is a class III member of the beta tubulin protein family. Beta tubulins are one of two core protein families (alpha and beta tubulins) that heterodimerize and assemble to form microtubules. This protein is primarily expressed in neurons and may be involved in neurogenesis and axon guidance and maintenance. Mutations in this gene are the cause of congenital fibrosis of the extraocular muscles type 3. Alternate splicing results in multiple transcript variants. A pseudogene of this gene is found on chromosome 6.

As used herein, Tubulin-beta 3 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI Gene ID for human Tubulin-beta 3 is 10381 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/10381 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority). Homo sapiens Tubulin-beta 3, variant 2, GenBank Accession No. NM_001197181 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 17 and 18. Homo sapiens Tubulin-beta 3, variant 1, GenBank Accession No. NM_006086 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 19 and 20. (The GenBank numbers are incorporated herein by reference in the versions available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of any fragments of Tubulin-beta 3 sequences as long as the fragment can allow for the specific identification of Tubulin-beta 3. Moreover, it is understood that there are naturally occurring variants of Tubulin-beta 3 which may or may not be associated with a specific disease state, the use of which are also included in this application.

Filamin B

Filamin B is also known as filamin-3, beta-filamin, ABP-280 homolog, filamin homolog 1, thyroid autoantigen, actin binding protein 278, actin-binding-like protein, Larsen syndrome 1 (autosomal dominant), AOI; FH1; SCT; TAP; LRS1; TABP; FLN-B; FLN1L; ABP-278; and ABP-280. The gene encodes a member of the filamin family. The encoded protein interacts with glycoprotein Ib alpha as part of the process to repair vascular injuries. The platelet glycoprotein Ib complex includes glycoprotein Ib alpha, and it binds the actin cytoskeleton. Mutations in this gene have been found in several conditions: atelosteogenesis type 1 and type 3; boomerang dysplasia; autosomal dominant Larsen syndrome; and spondylocarpotarsal synostosis syndrome. Multiple alternatively spliced transcript variants that encode different protein isoforms have been described for this gene.

As used herein, filamin B refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI gene ID for filamin B is 2317 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/2317 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority).

Homo sapiens filamin B, beta (FLNB), RefSeqGene on chromosome 3, locus NG_012801 is shown in SEQ ID NO: 21. Homo sapiens filamin B, beta (FLNB), transcript variant 1, GenBank Accession No. NM_001164317.1 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 22 and 23. Homo sapiens filamin B, beta (FLNB), transcript variant 3, GenBank Accession No. NM_001164318.1 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 24 and 25. Homo sapiens filamin B, beta (FLNB), transcript variant 4, GenBank Accession No. NM_001164319.1 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 26 and 27. Homo sapiens filamin B, beta (FLNB), transcript variant 2, GenBank Accession No. NM_001457.3 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 28 and 29. (Each GenBank number is incorporated herein by reference in the version available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of any combination of one or more of the filamin B sequences provided in the sequence listing or any fragments thereof as long as the fragment can allow for the specific identification of filamin B. Methods of the invention and reagents can be used to detect single isoforms of filamin B, combinations of filamin B isoforms, or all of the filamin B isoforms simultaneously. Unless specified, filamin B can be considered to refer to one or more isoforms of filamin B, including total filamin B. Moreover, it is understood that there are naturally occurring variants of filamin B, which may or may not be associated with a specific disease state, the use of which are also included in the instant application.

Lymphocyte Antigen 9

Lymphocyte antigen 9 (LY9) is also known as RP11-312J18.1, CD229, SLAMF3, hly9, mLY9, T-lymphocyte surface antigen Ly-9; and cell surface molecule Ly-9. LY9 belongs to the SLAM family of immunomodulatory receptors (see SLAMF1; MIM 603492) and interacts with the adaptor molecule SAP (SH2D1A; MIM 300490) (Graham et al., 2006).

As used herein, LY9 refers to both the gene and the protein unless clearly indicated otherwise by context. The NCBI gene ID for LY9 is 4063 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/4063 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority).

Homo sapiens lymphocyte antigen 9 (LY9), transcript variant 2, GenBank Accession

No. NM_001033667 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 30 and 31. Homo sapiens lymphocyte antigen 9 (LY9), transcript variant 3, GenBank Accession No. NM_001261456 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 32 and 33. Homo sapiens lymphocyte antigen 9 (LY9), transcript variant 4, GenBank Accession No. NM_001261457 amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 34 and 35. Homo sapiens lymphocyte antigen 9 (LY9), transcript variant 1, GenBank Accession No. NM_002348 is shown amino acid and nucleotide sequences, respectively, are provided in SEQ ID NOs: 36 and 37. (Each GenBank number is incorporated herein by reference in the version available on the filing date of the application to which this application claims priority.)

It is understood that the invention includes the use of any combination of one or more of the LY9 sequences provided in the sequence listing or any fragments thereof as long as the fragment can allow for the specific identification of LY9. Methods of the invention and reagents can be used to detect single isoforms of LY9, combinations of LY9 isoforms, or all of the LY9 isoforms simultaneously. Unless specified, LY9 can be considered to refer to one or more isoforms of LY9, including total LY9. Moreover, it is understood that there are naturally occurring variants of LY9, which may or may not be associated with a specific disease state, the use of which are also included in the instant application.

Prostate Specific Antigen

Prostate-specific antigen (PSA) is also known as kallikrein-3, seminin, P-30 antigen, semenogelase, gamma-seminoprotein, APS, hK3, and KLK2A1. Kallikreins are a subgroup of serine proteases having diverse physiological functions. Growing evidence suggests that many kallikreins are implicated in carcinogenesis and some have potential as novel cancer and other disease biomarkers. This gene is one of the fifteen kallikrein subfamily members located in a cluster on chromosome 19. Its protein product is a protease present in seminal plasma. It is thought to function normally in the liquefaction of seminal coagulum, presumably by hydrolysis of the high molecular mass seminal vesicle protein. Serum level of this protein, called PSA in the clinical setting, is useful in the diagnosis and monitoring of prostatic carcinoma. Alternate splicing of this gene generates several transcript variants encoding different isoforms.

As used herein, PSA refers to both the gene and the protein, in both processed and unprocessed forms, unless clearly indicated otherwise by context. The NCBI gene ID for PSA is 354 and detailed information can be found at www.ncbi.nlm.nih.gov/gene/354 (incorporated herein by reference in the version available on the filing date of the application to which this application claims priority).

Homo sapiens PSA is located on chromosome 19 at 19q13.41 Sequence : NC_000019.9 (51358171..51364020). Four splice variants of human PSA are known. Prostate-specific antigen isoform 3 preproprotein, NM_001030047.1, is provided in Figure 16. Prostate-specific antigen isoform 4 preproprotein, NM_001030048.1, is provided in Figure 17. Prostate-specific antigen isoform 6 preproprotein, NM_001030050.1, is provided in Figure 18. Prostate-specific antigen isoform 1 preproprotein, NM_001648.2, is provided in Figure 19. (Each GenBank number is incorporated herein by reference in the version available on the filing date of the application to which this application claims priority).

It is understood that the invention includes the use of any combination of one or more of the PSA sequences provided in the sequence listing or any fragments thereof as long as the fragment can allow for the specific identification of PSA. Methods of the invention and reagents can be used to detect single isoforms of PSA, combinations of PSA isoforms, or all of the PSA isoforms simultaneously. Unless specified, PSA can be considered to refer to one or more isoforms of PSA, including total PSA. Moreover, it is understood that there are naturally occurring variants of PSA, which may or may not be associated with a specific disease state, the use of which are also included in the instant application.

Treatment of Disease States

The present invention provides methods for use of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9) to treat disease states in a subject, *e.g.*, a mammal, *e.g.*, a human.

The present invention also provides methods for treatment of a subject with prostate cancer with a therapeutic, *e.g.*, a nucleic acid based therapeutic, that modulates the expression or activity of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9).

The invention also provides methods for selection and/or administration of known treatment agents, especially hormone based therapies vs. non-hormone based therapies, and aggressive or active treatment vs. “watchful waiting”, depending on the detection of a change in the level of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9), as compared to a control. The selection of treatment regimens can further include the detection of PSA to assist in selection of the therapeutic methods. Selection of treatment methods can also include other diagnostic considerations and patient characteristics including results from imaging studies, tumor size or growth rates, risk of poor outcomes, disruption of daily activities, and age.

As used herein, the term “aggressive oncological disorder”, such as aggressive prostate cancer, refers to an oncological disorder involving a fast-growing tumor. An aggressive oncological disorder typically does not respond, responds poorly, or loses response to therapeutic treatment. For example, an prostate cancer may be considered to become an aggressive prostate cancer upon loss of response to hormone therapy, necessitating treatment with chemotherapy, surgery, and/or radiation. As used herein, an aggressive prostate cancer, for example, is one that will likely or has metastasized. As used herein, an aggressive prostate cancer is one that will result in significant changes in quality of life as the tumor grows. Active treatment is therapeutically indicated for an aggressive oncological disorder, e.g., aggressive prostate cancer.

As used herein, the term “non-aggressive oncological disorder” such as a non-aggressive prostate cancer, refers to an oncological disorder involving a slow-growing tumor. A non-aggressive oncological disorder typically responds favorably or moderately to therapeutic treatment or grows so slowly that immediate treatment is not warranted. A non-aggressive prostate tumor is one that a person skilled in the art, e.g., an oncologist, may decide to not actively treat with routine interventions for the treatment of cancer, e.g., chemotherapy, radiation, surgery, as the active treatment may do more harm than the disease, particularly in an older subject. A non-aggressive prostate tumor is one that a person skilled in the art may decide to monitor with “watchful waiting” rather than subjecting the person to any active therapeutic interventions to alter the presence or growth of the tumor (e.g., radiation, surgery, chemotherapy, hormone therapy).

Diagnostic/Prognostic Uses of the Invention

The invention provides methods for diagnosing an abnormal prostate state, e.g., BPH or an oncological disease state, e.g., prostate cancer, in a subject. The invention further provides methods for prognosing or monitoring progression or monitoring response of an abnormal prostate state, e.g., BPH or prostate cancer, to a therapeutic treatment during active treatment or watchful waiting.

The invention provides, in one embodiment, methods for diagnosing an oncological disorder, e.g., prostate cancer. The methods of the present invention can be practiced in conjunction with any other method used by the skilled practitioner to prognose the occurrence or recurrence of an oncologic disorder and/or the survival of a subject being treated for an oncologic disorder. The diagnostic and prognostic methods provided herein can be used to determine if additional and/ or more invasive tests or monitoring should be performed on a subject. It is understood that a disease as complex as an oncological disorder is rarely diagnosed using a single test. Therefore, it is understood that the diagnostic, prognostic, and monitoring methods provided herein are typically used in conjunction with other methods known in the art. For example, the methods of the invention may be performed in conjunction with a morphological or cytological analysis of the sample obtained from the subject, imaging analysis, and/or physical exam. Cytological methods would include immunohistochemical or immunofluorescence detection (and quantitation if appropriate) of any other molecular marker either by itself, in conjunction with other markers. Other methods would include detection of other markers by *in situ* PCR, or by extracting tissue and quantitating other markers by real time PCR. PCR is defined as polymerase chain reaction.

Methods for assessing tumor progression during watchful waiting or the efficacy of a treatment regimen, e.g., chemotherapy, radiation therapy, surgery, hormone therapy, or any other therapeutic approach useful for treating an oncologic disorder in a subject are also provided. In these methods the amount of marker in a pair of samples (a first sample obtained from the subject at an earlier time point or prior to the treatment regimen and a second sample obtained from the subject at a later time point, e.g., at a later time point when the subject has undergone at least a portion of the treatment regimen) is assessed. It is understood that the methods of the invention include obtaining and analyzing more than two samples (e.g., 3, 4, 5, 6, 7, 8, 9, or more samples) at regular or irregular intervals for assessment of marker levels. Pairwise comparisons can be made between consecutive or

non-consecutive subject samples. Trends of marker levels and rates of change of marker levels can be analyzed for any two or more consecutive or non-consecutive subject samples.

The invention also provides a method for determining whether an oncologic disorder, e.g., prostate cancer, is aggressive. The method comprises determining the amount of a marker present in a sample and comparing the amount to a control amount of the marker present in one or more control samples, as defined in Definitions, thereby determining whether an oncologic disorder is aggressive. Marker levels can be compared to marker levels in samples obtained at different times from the same subject or marker levels from normal or abnormal prostate state subjects. A rapid increase in the level of marker may be indicative of a more aggressive cancer than a slow increase or no increase or change in the marker level.

The methods of the invention may also be used to select a compound that is capable of modulating, *i.e.*, decreasing, the aggressiveness of an oncologic disorder, e.g., prostate cancer. In this method, a cancer cell is contacted with a test compound, and the ability of the test compound to modulate the expression and/or activity of a marker in the invention in the cancer cell is determined, thereby selecting a compound that is capable of modulating aggressiveness of an oncologic disorder.

Using the methods described herein, a variety of molecules, may be screened in order to identify molecules which modulate, *e.g.*, increase or decrease the expression and/or activity of a marker of the invention, *i.e.*, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9), optionally in combination with PSA. Compounds so identified can be provided to a subject in order to inhibit the aggressiveness of an oncologic disorder in the subject, to prevent the recurrence of an oncologic disorder in the subject, or to treat an oncologic disorder in the subject.

Markers of the Invention

The invention relates to markers (hereinafter “biomarkers”, “markers” or “markers of the invention”). The preferred markers of the invention are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9). Methods of the invention also include use of the marker PSA in conjunction with one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin

4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9).

The invention provides nucleic acids and proteins (e.g., isolated nucleic acids and isolated proteins or fragments thereof) that are encoded by, or correspond to, the markers (hereinafter “marker nucleic acids” and “marker proteins,” respectively). These markers are particularly useful in screening for the presence of an altered prostate state, e.g., BPH or prostate cancer, in assessing aggressiveness and metastatic potential of an oncologic disorder, assessing the androgen dependent status of an oncological disorder, assessing whether a subject is afflicted with an oncological disorder, identifying a composition for treating an oncological disorder, assessing the efficacy of a compound for treating an oncological disorder, monitoring the progression of an oncological disorder, prognosing the aggressiveness of an oncological disorder, prognosing the survival of a subject with an oncological disorder, prognosing the recurrence of an oncological disorder, and prognosing whether a subject is predisposed to developing an oncological disorder.

In some embodiments of the present invention, other biomarkers can be used in connection with the methods of the present invention. As used herein, the term “one or more biomarkers” is intended to mean that one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B (FLNB), and lymphocyte antigen 9 (LY9), are assayed, optionally in combination with PSA, and, in various embodiments, more than one other biomarker may be assayed, such as two, three, four, five, six, seven, eight, nine, or more biomarkers in the list may be assayed. One or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and keratin 19 can be assayed in combination with one or more of filamin B, LY9, and PSA. Filamin B can be used in conjunction with one or more other biomarkers, e.g., LY9 or PSA, known to be associated with prostate cancer. LY9 can be used in conjunction with one or more other biomarkers, e.g., filamin B or PSA, known to be associated with prostate cancer. That is, any combination of the filamin B and LY9 biomarkers, optionally with PSA can be used, e.g., filamin B; LY9; filamin B and PSA; filamin B and LY9; LY9 and PSA; filamin B, LY9, and PSA; all of which can optionally be combined with other markers, e.g., one or more of keratins 4, 7, 8, 15, 18, 19, or tubulin-beta 3.

Methods, kits, and panels provided herein include any combination of 1, 2, 3, 4, 5, 6, 7, 8, or 9 markers of the set filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3. Such combinations include any of the following marker sets:

Marker sets with one member: filamin B; LY9; keratin 4; keratin 7; keratin 8; keratin 15; keratin 18; keratin 19; and tubulin-beta 3. Any single marker can be used in combination with PSA.

Marker sets with two members: filamin B, LY9; filamin B, keratin 4; filamin B, keratin 7; filamin B, keratin 8; filamin B, keratin 15; filamin B, keratin 18; filamin B, keratin 19; filamin B, tubulin-beta 3; LY9, keratin 4; LY9, keratin 7; LY9, keratin 8; LY9, keratin 15; LY9, keratin 18; LY9, keratin 19; LY9, tubulin-beta 3; keratin 4, keratin 7; keratin 4, keratin 8; keratin 4, keratin 15; keratin 4, keratin 18; keratin 4, keratin 19; keratin 4, tubulin-beta 3; keratin 7, keratin 8; keratin 7, keratin 15; keratin 7, keratin 18; keratin 7, keratin 19; keratin 7, tubulin-beta 3; keratin 8, keratin 15; keratin 8, keratin 18; keratin 8, keratin 19; keratin 8, tubulin-beta 3; keratin 15, keratin 18; keratin 15, keratin 19; keratin 15, tubulin-beta 3; keratin 18, tubulin-beta 3; keratin 18, keratin 19; and keratin 19, tubulin-beta 3. Any marker set can be used in combination with PSA.

Marker sets with three members: filamin B, LY9, keratin 4; filamin B, LY9, keratin 7; filamin B, LY9, keratin 8; filamin B, LY9, keratin 15; filamin B, LY9, keratin 18; filamin B, LY9, keratin 19; filamin B, LY9, tubulin-beta 3; filamin B, keratin 4, keratin 7; filamin B, keratin 4, keratin 8; filamin B, keratin 4, keratin 15; filamin B, keratin 4, keratin 18; filamin B, keratin 4, keratin 19; filamin B, keratin 4, tubulin-beta 3; filamin B, keratin 7, keratin 8; filamin B, keratin 7, keratin 15; filamin B, keratin 7, keratin 18; filamin B, keratin 7, keratin 19; filamin B, keratin 7, tubulin-beta 3; filamin B, keratin 8, keratin 15; filamin B, keratin 8, keratin 18; filamin B, keratin 8, keratin 19; filamin B, keratin 8, tubulin-beta 3; filamin B, keratin 15, keratin 18; filamin B, keratin 15, keratin 19; filamin B, keratin 15, tubulin-beta 3; filamin B, keratin 18, keratin 19; filamin B, keratin 18, tubulin-beta 3; filamin B, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 7; LY9, keratin 4, keratin 8; LY9, keratin 4, keratin 15; LY9, keratin 4, keratin 18; LY9, keratin 4, keratin 19; LY9, keratin 4, tubulin-beta 3; LY9, keratin 7, keratin 8; LY9, keratin 7, keratin 15; LY9, keratin 7, keratin 18; LY9, keratin 7, keratin 19; LY9, keratin 7, tubulin-beta 3; LY9, keratin 8, keratin 15; LY9, keratin 8, keratin 18; LY9, keratin 8, keratin 19; LY9, keratin 8, tubulin-beta 3; LY9, keratin 15, keratin 18;

LY9, keratin 15, keratin 19; LY9, keratin 15, tubulin-beta 3; LY9, keratin 18, keratin 19; LY9, keratin 18, tubulin-beta 3; LY9, keratin 19, tubulin-beta 3; keratin 4, keratin 7, keratin 8; keratin 4, keratin 7, keratin 15; keratin 4, keratin 7, keratin 18; keratin 4, keratin 7, keratin 19; keratin 4, keratin 7, tubulin-beta 3; keratin 4, keratin 8, keratin 15; keratin 4, keratin 8, keratin 18; keratin 4, keratin 8, keratin 19; keratin 4, keratin 8, tubulin-beta 3; keratin 4, keratin 15, keratin 18; keratin 4, keratin 15, keratin 19; keratin 4, keratin 15, tubulin-beta 3; keratin 4, keratin 18, keratin 19; keratin 4, keratin 19, tubulin-beta 3; keratin 7, keratin 8, keratin 15; keratin 7, keratin 8, keratin 18; keratin 7, keratin 8, keratin 19; keratin 7, keratin 8, tubulin-beta 3; keratin 7, keratin 8, tubulin-beta 3; keratin 7, keratin 15, keratin 18; keratin 7, keratin 15, keratin 19; keratin 7, keratin 15, tubulin-beta 3; keratin 7, keratin 18, keratin 19; keratin 7, keratin 18, tubulin-beta 3; keratin 15, keratin 18, keratin 19; keratin 15, keratin 18, tubulin-beta 3; and keratin 18, keratin 19, tubulin-beta 3. Any marker set can be used in combination with PSA.

Marker sets with four members: filamin B, LY9, keratin 4, keratin 7; filamin B, LY9, keratin 4, keratin 8; filamin B, LY9, keratin 4, keratin 15; filamin B, LY9, keratin 4, keratin 18; filamin B, LY9, keratin 4, keratin 19; filamin B, LY9, keratin 4, tubulin-beta 3; filamin B, keratin 4, keratin 7, keratin 8; filamin B, keratin 4, keratin 7, keratin 15; filamin B, keratin 4, keratin 7, keratin 18; filamin B, keratin 4, keratin 7, tubulin-beta 3; filamin B, keratin 4, keratin 7, tubulin-beta 3; filamin B, keratin 7, keratin 8, keratin 15; filamin B, keratin 7, keratin 8, keratin 18; filamin B, keratin 7, keratin 8, keratin 19; filamin B, keratin 7, keratin 8, tubulin-beta 3; filamin B, keratin 8, keratin 15, keratin 18; filamin B, keratin 8, keratin 15, keratin 19; filamin B, keratin 8, keratin 15, tubulin-beta 3; filamin B, keratin 15, keratin 18, keratin 19; filamin B, keratin 15, keratin 18, tubulin-beta 3; filamin B, keratin 18, keratin 19, and tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8; LY9, keratin 4, keratin 7, keratin 15; LY9, keratin 4, keratin 7, keratin 18; LY9, keratin 4, keratin 7, keratin 19; LY9, keratin 4, keratin 7, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 15; LY9, keratin 7, keratin 8, keratin 18; LY9, keratin 7, keratin 8, keratin 19; LY9, keratin 7, keratin 8, tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 18; LY9, keratin 8, keratin 15, keratin 19; LY9, keratin 8, keratin 15, tubulin-beta 3; LY9, keratin 15, keratin 18, keratin 19; LY9, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 18, keratin 19, and tubulin-beta 3; keratin 4, keratin 7, keratin 8, keratin 15; keratin 4, keratin 7, keratin 8, keratin 18; keratin 4, keratin 7, keratin 8, keratin 19; keratin 4, keratin 7, keratin 8, tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 18; keratin 4, keratin 8, keratin 15, keratin 19; keratin 4, keratin 8, keratin 15, tubulin-beta 3; keratin 4, keratin 15, keratin 18, keratin 19; keratin 4, keratin 15, keratin 18, tubulin-beta 3; keratin

4, keratin 18, keratin 19, tubulin-beta 3; keratin 8, keratin 15, keratin 18, keratin 19; keratin 8, keratin 15, keratin 18, tubulin-beta 3; and keratin 15, keratin 18, keratin 19, tubulin-beta 3. Any marker set can be used in combination with PSA.

Marker sets with five members: keratin 8, keratin 15, keratin 18, keratin 19 tubulin-beta 3; keratin 7, keratin 15, keratin 18, keratin 19 tubulin-beta 3; keratin 7, keratin 8, keratin 18, keratin 19 tubulin-beta 3; keratin 7, keratin 8, keratin 15, keratin 19 tubulin-beta 3; keratin 7, keratin 8, keratin 15, keratin 18 tubulin-beta 3; keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; keratin 4, keratin 15, keratin 18, keratin 19 tubulin-beta 3; keratin 4, keratin 8, keratin 18, keratin 19 tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 19 tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 18, keratin 19; LY9, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 8, keratin 18, keratin 19 tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 19 tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 18, and tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 18, keratin 19; filamin B, keratin 15, keratin 18, keratin 19 tubulin-beta 3; filamin B, keratin 8, keratin 18, keratin 19 tubulin-beta 3; filamin B, keratin 8, keratin 15, keratin 19 tubulin-beta 3; filamin B, keratin 8, keratin 15, keratin 18, and tubulin-beta 3; filamin B, keratin 8, keratin 15, keratin 18, keratin 19; filamen B, LY9, keratin 18, keratin 19 tubulin-beta 3; filamen B, LY9, keratin 15, keratin 19 tubulin-beta 3; filamen B, LY9, keratin 15, keratin 18, tubulin-beta 3; filamen B, LY9, keratin 15, keratin 18, keratin 19; filamen B, keratin 4, keratin 18, keratin 19 tubulin-beta 3; filamen B, keratin 4, keratin 15, keratin 19 tubulin-beta 3; filamen B, keratin 4, keratin 15, keratin 18, tubulin-beta 3; filamen B, keratin 4, keratin 15, keratin 18, keratin 19; filamen B keratin 7, keratin 18, keratin 19 tubulin-beta 3; filamen B keratin 7, keratin 15, keratin 19, tubulin-beta 3; filamen B keratin 7, keratin 15, keratin 18, tubulin-beta 3; filamen B keratin 7, keratin 15, keratin 18, keratin 19; filamen B, keratin 8, keratin 18, keratin 19 tubulin-beta 3; filamen B, keratin 8, keratin 15, keratin 19 tubulin-beta 3; filamen B, keratin 8, keratin 15, keratin 18 tubulin-beta 3; filamen B, keratin 8, keratin 15, keratin 18, keratin 19; LY9, keratin 4, keratin 18, keratin 19 and tubulin-beta 3; LY9, keratin 4, keratin 15, keratin 19 tubulin-beta 3; LY9, keratin 4, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 15, keratin 18, keratin 19; LY9, keratin 7, keratin 18, keratin 19 tubulin-beta 3; LY9, keratin 7, keratin 15, keratin 19 tubulin-beta 3; LY9, keratin 7, keratin 15, keratin 18, and tubulin-beta 3; LY9, keratin 7, keratin 15, keratin 18, keratin 19; LY9, keratin 8, keratin 18, keratin 19 tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 19 tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 18, and tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 18, keratin 19; keratin 4, keratin 7, keratin 18, keratin 19 tubulin-beta 3;

keratin 4, keratin 7, keratin 15, keratin 19 tubulin-beta 3; keratin 4, keratin 7, keratin 15, keratin 18, and tubulin-beta 3; keratin 4, keratin 7, keratin 15, keratin 18, keratin 19; keratin 4, keratin 8, keratin 18, keratin 19 tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 19 tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 18, and tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 18, keratin 19; keratin 7, keratin 8, keratin 18, keratin 19 tubulin-beta 3; keratin 7, keratin 8, keratin 15, keratin 19 tubulin-beta 3; keratin 7, keratin 8, keratin 15, keratin 18, and tubulin-beta 3; keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; filamen B, LY9, keratin 4, keratin 19, tubulin-beta 3; filamen B, LY9, keratin 4, keratin 18, tubulin-beta 3; filamen B, LY9, keratin 4, keratin 18, keratin 19; filamen B, LY9, keratin 7, keratin 19, tubulin-beta 3; filamen B, LY9, keratin 7, keratin 18, tubulin-beta 3; filamen B, LY9, keratin 7, keratin 18, keratin 19; filamen B, LY9, keratin 8, keratin 19, tubulin-beta 3; filamen B, LY9, keratin 8, keratin 18, tubulin-beta 3; filamen B, LY9, keratin 8, keratin 18, keratin 19; filamen B, LY9, keratin 15, keratin 19, tubulin-beta 3; filamen B, LY9, keratin 15, keratin 18, tubulin-beta 3; filamen B, LY9, keratin 15, keratin 18, keratin 19; filamen B, keratin 4, keratin 7, keratin 19, tubulin-beta 3; filamen B, keratin 4, keratin 7, keratin 18, tubulin-beta 3; filamen B, keratin 4, keratin 7, keratin 18, keratin 19; filamen B, keratin 4, keratin 8, keratin 19, tubulin-beta 3; filamen B, keratin 4, keratin 8, keratin 18, tubulin-beta 3; filamen B, keratin 4, keratin 8, keratin 18, keratin 19; filamen B, keratin 4, keratin 15, keratin 19, tubulin-beta 3; filamen B, keratin 4, keratin 15, keratin 18, keratin 19; filamen B, keratin 7, keratin 8, keratin 19, tubulin-beta 3; filamen B, keratin 7, keratin 8, keratin 18, tubulin-beta 3; filamen B, keratin 7, keratin 8, keratin 18, keratin 19; filamen B, keratin 8, keratin 15, keratin 19, tubulin-beta 3; filamen B, keratin 8, keratin 15, keratin 18, tubulin-beta 3; filamen B, keratin 8, keratin 15, keratin 18, keratin 19; LY9, keratin 4, keratin 7, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 18, keratin 19; LY9, keratin 4, keratin 8, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 8, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 8, keratin 18, keratin 19; LY9, keratin 4, keratin 15, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 15, keratin 18, keratin 19; LY9, keratin 7, keratin 8, keratin 19, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 18, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 18, keratin 19; LY9, keratin 7, keratin 15, keratin 19, tubulin-beta 3; LY9, keratin 7, keratin 15, keratin 18, keratin 19; LY9, keratin 8, keratin 15, keratin 19, tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 8, keratin 15, keratin 18, keratin 19; keratin 4, keratin 7, keratin 8, keratin 19, tubulin-beta 3; keratin 4, keratin 7, keratin 8, keratin 18, tubulin-beta 3;

keratin 4, keratin 7, keratin 8, keratin 18, keratin 19; keratin 4, keratin 7, keratin 15, keratin 19, tubulin-beta 3; keratin 4, keratin 7, keratin 15, keratin 18, tubulin-beta 3; keratin 4, keratin 7, keratin 15, keratin 18, keratin 19; keratin 4, keratin 8, keratin 15, keratin 19, tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 18, tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 18, keratin 19; keratin 7, keratin 8, keratin 15, keratin 19, tubulin-beta 3; keratin 7, keratin 8, keratin 15, keratin 18, tubulin-beta 3; and keratin 7, keratin 8, keratin 15, keratin 18, keratin 19. Any marker set can be used in combination with PSA.

Marker sets with six members: keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3; keratin 4, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3; keratin 4, keratin 7, keratin 15, keratin 18, keratin 19, tubulin-beta 3; keratin 4, keratin 7, keratin 8, keratin 18, keratin 19, tubulin-beta 3; keratin 4, keratin 7, keratin 8, keratin 15, keratin 19, tubulin-beta 3; keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, tubulin-beta 3; keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; LY9, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 7, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 15, keratin 19, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; LY9, keratin 4, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 8, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 8, keratin 15, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 8, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19; LY9, keratin 4, keratin 7, keratin 18, keratin 19, and tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 15, keratin 19, and tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 15, keratin 18, keratin 19; LY9, keratin 4, keratin 7, keratin 8, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 18, keratin 19; LY9, keratin 4, keratin 7, keratin 8, keratin 15, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 19; and LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18. Any marker set can be used in combination with PSA.

Marker sets with seven members: keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 15, keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 15, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; and LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3.

keratin 18, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 19, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, tubulin-beta 3; LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; filamin B, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, keratin 4, keratin 7, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, keratin 4, keratin 7, keratin 8, keratin 18, keratin 19, tubulin-beta 3; filamin B, keratin 4, keratin 7, keratin 8, keratin 15, keratin 19, tubulin-beta 3; filamin B, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, tubulin-beta 3; filamin B, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; filamin B, LY9, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 7, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 7, keratin 8, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 7, keratin 8, keratin 15, keratin 18, tubulin-beta 3; filamin B, LY9, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19; filamin B, LY9, keratin 4, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19; filamin B, LY9, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19; filamin B, LY9, keratin 4, keratin 7, keratin 15, keratin 18, keratin 19, and tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 15, keratin 19, and tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 15, keratin 18, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 15, keratin 18, keratin 19; filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 18, keratin 19; filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 19; and filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18. Any marker set can be used in combination with PSA.

Marker sets with eight members: LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 15, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 18, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 19, tubulin-beta 3; filamin B, LY9, keratin 4, keratin 7,

keratin 8, keratin 15, keratin 18, tubulin-beta 3; and filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19. Any marker set can be used in combination with PSA.

Marker sets with nine members: filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3.

Any marker set can be used in combination with PSA.

The invention provides for the use of various combinations and sub-combinations of markers. It is understood that any single marker or combination of the markers provided herein can be used in the invention unless clearly indicated otherwise. Further, any single marker or combination of the markers of the invention can be used in conjunction with PSA.

Throughout the application, one or more of filamin B, LY9 and keratin 19 is understood as any of: filamin B; LY9; keratin 19; filamin B and LY9; filamin B and keratin 19; LY9 and keratin 19; or filamin B, LY9, and keratin 19. Further, any single marker or combination of the markers of the invention can be used in conjunction with PSA.

Throughout the application, combination of the filamin B and LY9 with PSA is understood as any of filamin B; LY9; filamin B and PSA; filamin B and LY9; LY9 and PSA; filamin B, LY9, and PSA.

Throughout the application, one or more prostate cancer markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 is understood as any of keratin 4; keratin 7; keratin 8; keratin 15; keratin 18; tubulin beta-3; keratin 4 and keratin 7; keratin 4 and keratin 8; keratin 4 and keratin 15; keratin 4 and keratin 18; keratin 4 and tubulin beta-3; keratin 7 and keratin 8; keratin 7 and keratin 15; keratin 7 and keratin 18; keratin and tubulin beta-3; keratin 8 and keratin 15; keratin 8 and keratin 18; keratin 8 and tubulin beta-3; keratin 15 and keratin 18; keratin 15 and tubulin beta-3; keratin 18 and tubulin beta-3; keratin 4, keratin 7 and keratin 8; keratin 4, keratin 7 and keratin 15; keratin 4, keratin 7 and keratin 18; keratin 4, keratin 7 and tubulin beta-3; keratin 4, keratin 8 and keratin 15; keratin 4, keratin 8 and keratin 18; keratin 4, keratin 8 and tubulin beta-e; keratin 4, keratin 15 and keratin 18; keratin 4, keratin 15 and tubulin beta-e; keratin 4, keratin 18 and tubulin beta-3; kertain 4, keratin 7, keratin 8 and keratin 15; keratin 4, keratin 7, keratin 8 and keratin 18; keratin 4, keratin 7, keratin 8 and tubulin beta-3; keratin 4, keratin 8, keratin 15 and keratin 18; keratin 4, keratin 8, keratin 15 and tubulin beta-3; keratin 4, keratin 15,

keratin 18 and tubulin beta-3; keratin 4, keratin 7, keratin 8, keratin 15 and keratin 18; keratin 4, keratin 7, keratin 8, keratin 15, and tubulin beta-3; keratin 4, keratin 7, keratin 8, keratin 18, and tubulin beta-3; keratin 4, keratin 7, keratin 15, keratin 18, and tubulin beta-3; keratin 4, keratin 8, keratin 15, keratin 18, and tubulin beta-3; or keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3. Further, any single marker or combination of the markers of the invention can be used in conjunction with PSA.

Throughout the application, one or more prostate cancer markers selected from the group consisting of keratin 7, 15, and 19 is understood as any of keratin 7; keratin 15; keratin 19; keratin 7 and 15; keratin 7 and 19; keratin 15 and 19; and keratin 7, 15, and 19. Further, any single marker or combination of the markers of the invention can be used in conjunction with PSA.

Throughout the application, one or more prostate cancer markers selected from the group consisting of keratin 7, 8, and 15 is understood as any of keratin 7; keratin 8; keratin 15; keratin 7 and 8; keratin 7 and 15; keratin 8 and 15; and keratin 7, 8, and 15. Further, any single marker or combination of the markers of the invention can be used in conjunction with PSA.

Throughout the application, one or more prostate cancer markers selected from the group consisting of keratin 7 and 15 is understood as any of keratin 7; keratin 15; or keratin 7 and 15. Further, any single marker or combination of the markers of the invention can be used in conjunction with PSA.

Throughout the application, one or more prostate cancer markers selected from the group consisting filamin B, LY9, or keratin 19 is understood as any of filamin B; LY9; keratin 19; filamin B and LY9; filamin B and keratin 19; LY9, and keratin 19; and filamin B, LY9, and keratin 19. Further, any single marker or combination of the markers of the invention can be used in conjunction with PSA.

In certain embodiments, methods of diagnosing, prognosing, and monitoring the treatment of prostate cancer by detecting the level sets of markers including of keratin 7, 15, or 19 and filamin B; keratin 7, 15, 19 or LY9; keratin 7, 15, 19, or PSA; keratin 4, 7, 15, or 19; keratin 7, 8, 15, or 19; keratin 7, 15, 18, or 19; and keratin 7, 15, 19, or tubulin-beta 3.

A "marker" is a gene whose altered level of expression in a tissue or cell from its expression level in normal or healthy tissue or cell is associated with a disease state, such as an abnormal prostate state. In a preferred embodiment, the marker is detected in a blood sample, e.g., serum or plasma. In one embodiment, the marker is detected in serum. In one embodiment, the marker is detected in plasma. In certain embodiments, the serum or plasma can be further processed to remove abundant blood proteins (e.g., albumin) or proteins that are not marker proteins prior to analysis. A "marker nucleic acid" is a nucleic acid (e.g., mRNA, cDNA) encoded by or corresponding to a marker of the invention. Such marker nucleic acids include DNA (e.g., cDNA) comprising the entire or a partial sequence of any of the nucleic acid sequences provided herein or the complement of such a sequence. The marker nucleic acids also include RNA comprising the entire or a partial sequence of any of the nucleic acid sequences provided herein or the complement of such a sequence, wherein all thymidine residues are replaced with uridine residues. A "marker protein" is a protein encoded by or corresponding to a marker of the invention. A marker protein comprises the entire or a partial sequence of any of the amino acid sequences provided herein. The terms "protein" and "polypeptide" are used interchangeably.

A "biological sample" or a "subject sample" is a body fluid or tissue in which a prostate cancer related marker may be present. In certain embodiments the sample is blood or a blood product (e.g., serum or plasma). In certain embodiments, the sample is a tissue sample, e.g., a tissue sample from at or near the site of the prostate hyperplasia or tumor, or the suspected prostate hyperplasia or tumor. A tissue sample can be obtained, for example, during biopsy or surgical resection of the prostate. A tissue sample can include one or more of normal tissue, hyperplasia, and cancerous tissue. Methods of distinguishing between such tissue types are known, e.g., histological analysis, immunohistochemical analysis. In certain embodiments, the control sample can be a normal portion of sample tissue removed from a subject.

An "oncological disorder-associated" body fluid is a fluid which, when in the body of a subject, contacts, or passes through oncological cells or into which cells or proteins shed from oncological cells are capable of passing. Exemplary oncological disorder-associated body fluids include blood fluids (e.g. whole blood, blood serum, blood having platelets removed therefrom), and are described in more detail below. Many oncological disorder-associated body fluids can have oncological cells therein, particularly when the cells are

metastasizing. Cell-containing fluids which can contain oncological cells include, but are not limited to, whole blood, blood having platelets removed therefrom, lymph, prostatic fluid, urine, and semen.

The "normal" level of expression of a marker is the level of expression of the marker in cells of a human subject or patient or a population of subjects not afflicted with an oncological disorder or an abnormal prostate state, e.g., BPH or prostate cancer.

An "over-expression", "higher level of expression", "higher level", and the like of a marker refers to an expression level in a test sample that is greater than the standard error of the assay employed to assess expression, and is preferably at least 25% more, at least 50% more, at least 75% more, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten times the expression level of the marker in a control sample (*e.g.*, sample from a healthy subject not having the marker associated disease, *i.e.*, an abnormal prostate state) and preferably, the average expression level of the marker or markers in several control samples.

A "lower level of expression" or "lower level" of a marker refers to an expression level in a test sample that is less than 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, or 10% of the expression level of the marker in a control sample (*e.g.*, sample from a healthy subjects not having the marker associated disease, *i.e.*, an abnormal prostate state) and preferably, the average expression level of the marker in several control samples.

A "transcribed polynucleotide" or "nucleotide transcript" is a polynucleotide (*e.g.* an mRNA, hnRNA, a cDNA, or an analog of such RNA or cDNA) which is complementary to or having a high percentage of identity (*e.g.*, at least 80% identity) with all or a portion of a mature mRNA made by transcription of a marker of the invention and normal post-transcriptional processing (*e.g.* splicing), if any, of the RNA transcript, and reverse transcription of the RNA transcript.

"Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a

cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Identical" or "identity" as used herein, refers to nucleotide sequence similarity between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are identical at that position. A first region is identical to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Identity between two regions is expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% identity. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

"Proteins of the invention" encompass marker proteins and their fragments; variant marker proteins and their fragments; peptides and polypeptides comprising an at least a 15 amino acid segment of a marker or variant marker protein; and fusion proteins comprising a marker or variant marker protein, or an at least a 15 amino acid segment of a marker or variant marker protein. In certain embodiments, a protein of the invention is a peptide sequence or epitope large enough to permit the specific binding of an antibody to the marker.

The invention further provides antibodies, antibody derivatives and antibody fragments which specifically bind with the marker proteins and fragments of the marker proteins of the present invention. Unless otherwise specified herewithin, the terms "antibody" and "antibodies" broadly encompass naturally-occurring forms of antibodies (*e.g.*, IgG, IgA, IgM, IgE) and recombinant antibodies such as single-chain antibodies, chimeric and humanized antibodies and multi-specific antibodies, as well as fragments and derivatives of all of the foregoing, which fragments and derivatives have at least an antigenic binding site. Antibody derivatives may comprise a protein or chemical moiety conjugated to an antibody.

In certain embodiments, the positive or negative fold change refers to that of any gene described herein.

As used herein, "positive fold change" refers to "up-regulation" or "increase (of expression)" of a gene that is listed herein.

As used herein, "negative fold change" refers to "down-regulation" or "decrease (of expression)" of a gene that is listed herein.

Various aspects of the invention are described in further detail in the following subsections.

Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules, including nucleic acids which encode a marker protein or a portion thereof. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify marker nucleic acid molecules, and fragments of marker nucleic acid molecules, *e.g.*, those suitable for use as PCR primers for the amplification of a specific product or mutation of marker nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. In one

embodiment, an "isolated" nucleic acid molecule (preferably a protein-encoding sequences) is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. In another embodiment, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. A nucleic acid molecule that is substantially free of cellular material includes preparations having less than about 30%, 20%, 10%, or 5% of heterologous nucleic acid (also referred to herein as a "contaminating nucleic acid").

A nucleic acid molecule of the present invention can be isolated using standard molecular biology techniques and the sequence information in the database records described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, ed., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, nucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which has a nucleotide sequence complementary to the nucleotide sequence of a marker nucleic acid or to the nucleotide sequence of a nucleic acid encoding a marker protein. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker nucleic acid or which encodes a marker protein. Such nucleic acids can be used, for example, as a probe or primer. The probe/primer typically is used as one or more substantially purified oligonucleotides. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 15, more preferably at least about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. In certain embodiments, the probes hybridize to nucleic acid sequences that traverse splice junctions. The probe comprises a label group attached thereto, *e.g.*, a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit or panel for identifying cells or tissues which express or mis-express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, *e.g.*, detecting mRNA levels or determining whether a gene encoding the protein or its translational control sequences have been mutated or deleted.

The invention further encompasses nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a marker protein (*e.g.*, protein having the sequence provided in the sequence listing), and thus encode the same protein.

It will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation and changes known to occur in cancer. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist that may affect the overall expression level of that gene (*e.g.*, by affecting regulation or degradation).

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a polypeptide corresponding to a marker of the invention. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent conditions to a marker nucleic acid or to a nucleic acid encoding a marker protein. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% (65%, 70%, preferably 75%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

Nucleic Acid Therapeutics

Nucleic acid therapeutics are well known in the art. Nucleic acid therapeutics include both single stranded and double stranded (i.e., nucleic acid therapeutics having a complementary region of at least 15 nucleotides in length that may be one or two nucleic acid strands) nucleic acids that are complementary to a target sequence in a cell. Nucleic acid therapeutics can be delivered to a cell in culture, e.g., by adding the nucleic acid to culture media either alone or with an agent to promote uptake of the nucleic acid into the cell.

Nucleic acid therapeutics can be delivered to a cell in a subject, i.e., in vivo, by any route of administration. The specific formulation will depend on the route of administration.

As used herein, and unless otherwise indicated, the term “complementary,” when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Such conditions can, for example, be stringent conditions, where stringent conditions may include: 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50°C or 70°C for 12-16 hours followed by washing. Other conditions, such as physiologically relevant conditions as may be encountered inside an organism, can apply. The skilled person will be able to determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

Sequences can be “fully complementary” with respect to each when there is base-pairing of the nucleotides of the first nucleotide sequence with the nucleotides of the second nucleotide sequence over the entire length of the first and second nucleotide sequences. However, where a first sequence is referred to as “substantially complementary” with respect to a second sequence herein, the two sequences can be fully complementary, or they may form one or more, but generally not more than 4, 3 or 2 mismatched base pairs upon hybridization, while retaining the ability to hybridize under the conditions most relevant to their ultimate application. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs as is common in double stranded nucleic acid therapeutics, such overhangs shall not be regarded as mismatches with regard to the determination of complementarity. For example, a dsRNA comprising one oligonucleotide 21 nucleotides in length and another oligonucleotide 23 nucleotides in length, wherein the longer oligonucleotide comprises a sequence of 21 nucleotides that is fully complementary to the shorter oligonucleotide, may yet be referred to as “fully complementary” for the purposes described herein.

“Complementary” sequences, as used herein, may also include, or be formed entirely from, non-Watson-Crick base pairs and/or base pairs formed from non-natural and modified nucleotides, in as far as the above requirements with respect to their ability to hybridize are

fulfilled. Such non-Watson-Crick base pairs includes, but not limited to, G:U Wobble or Hoogsteen base pairing.

The terms “complementary,” “fully complementary,” and “substantially complementary” herein may be used with respect to the base matching between the sense strand and the antisense strand of a dsRNA, or between an antisense nucleic acid or the antisense strand of dsRNA and a target sequence, as will be understood from the context of their use.

As used herein, a polynucleotide that is “substantially complementary to at least part of” a messenger RNA (mRNA) refers to a polynucleotide that is substantially complementary to a contiguous portion of the mRNA of interest (*e.g.*, an mRNA encoding filamin B, LY9, a keratin, tubulin-beta 3, or PSA) including a 5' UTR, an open reading frame (ORF), or a 3' UTR. For example, a polynucleotide is complementary to at least a part of filamin B, LY9, a keratin, tubulin-beta 3, or PSA mRNA if the sequence is substantially complementary to a non-interrupted portion of an mRNA encoding filamin B, LY9, a keratin, tubulin-beta 3, or PSA.

Nucleic acid therapeutics typically include chemical modifications to improve their stability and to modulate their pharmacokinetic and pharmacodynamic properties. For example, the modifications on the nucleotides can include, but are not limited to, LNA, HNA, CeNA, 2'-methoxyethyl, 2'-O-alkyl, 2'-O-allyl, 2'-C-allyl, 2'-fluoro, 2'-deoxy, 2'-hydroxyl, and combinations thereof.

Nucleic acid therapeutics may further comprise at least one phosphorothioate or methylphosphonate internucleotide linkage. The phosphorothioate or methylphosphonate internucleotide linkage modification may occur on any nucleotide of the sense strand or antisense strand or both (in nucleic acid therapeutics including a sense strand) in any position of the strand. For instance, the internucleotide linkage modification may occur on every nucleotide on the sense strand or antisense strand; each internucleotide linkage modification may occur in an alternating pattern on the sense strand or antisense strand; or the sense strand or antisense strand may contain both internucleotide linkage modifications in an alternating pattern. The alternating pattern of the internucleotide linkage modification on the sense strand may be the same or different from the antisense strand, and the alternating pattern of

the internucleotide linkage modification on the sense strand may have a shift relative to the alternating pattern of the internucleotide linkage modification on the antisense strand.

Single Stranded Nucleic Acid Therapeutics

Antisense nucleic acid therapeutic agent single stranded nucleic acid therapeutics, typically about 16 to 30 nucleotides in length and are complementary to a target nucleic acid sequence in the target cell, either in culture or in an organism.

Patents directed to antisense nucleic acids, chemical modifications, and therapeutic uses are provided, for example, in U.S. Patent No. 5,898,031 related to chemically modified RNA-containing therapeutic compounds, and U.S. Patent No. 6,107,094 related methods of using these compounds as therapeutic agent. U.S. Patent No. 7,432,250 related to methods of treating patients by administering single-stranded chemically modified RNA-like compounds; and U.S. Patent No. 7,432,249 related to pharmaceutical compositions containing single-stranded chemically modified RNA-like compounds. U.S. Patent No. 7,629,321 is related to methods of cleaving target mRNA using a single-stranded oligonucleotide having a plurality RNA nucleosides and at least one chemical modification. Each of the patents listed in the paragraph are incorporated herein by reference.

Double Stranded Nucleic Acid Therapeutics

In many embodiments, the duplex region is 15-30 nucleotide pairs in length. In some embodiments, the duplex region is 17-23 nucleotide pairs in length, 17-25 nucleotide pairs in length, 23-27 nucleotide pairs in length, 19-21 nucleotide pairs in length, or 21-23 nucleotide pairs in length.

In certain embodiments, each strand has 15-30 nucleotides.

The RNAi agents that are used in the methods of the invention include agents with chemical modifications as disclosed, for example, in Publications WO 2009/073809 and WO/2012/037254, the entire contents of each of which are incorporated herein by reference.

An “RNAi agent,” “double stranded RNAi agent,” double-stranded RNA (dsRNA) molecule, also referred to as “dsRNA agent,” “dsRNA”, “siRNA”, “iRNA agent,” as used interchangeably herein, refers to a complex of ribonucleic acid molecules, having a duplex structure comprising two anti-parallel and substantially complementary, as defined below,

nucleic acid strands. As used herein, an RNAi agent can also include dsRNA (see, e.g., US Patent publication 20070104688, incorporated herein by reference). In general, the majority of nucleotides of each strand are ribonucleotides, but as described herein, each or both strands can also include one or more non-ribonucleotides, *e.g.*, a deoxyribonucleotide and/or a modified nucleotide. In addition, as used in this specification, an “RNAi agent” may include ribonucleotides with chemical modifications; an RNAi agent may include substantial modifications at multiple nucleotides. Such modifications may include all types of modifications disclosed herein or known in the art. Any such modifications, as used in a siRNA type molecule, are encompassed by “RNAi agent” for the purposes of this specification and claims.

The two strands forming the duplex structure may be different portions of one larger RNA molecule, or they may be separate RNA molecules. Where the two strands are part of one larger molecule, and therefore are connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting RNA chain is referred to as a “hairpin loop.” Where the two strands are connected covalently by means other than an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting structure is referred to as a “linker.” The RNA strands may have the same or a different number of nucleotides. The maximum number of base pairs is the number of nucleotides in the shortest strand of the dsRNA minus any overhangs that are present in the duplex. In addition to the duplex structure, an RNAi agent may comprise one or more nucleotide overhangs. The term “siRNA” is also used herein to refer to an RNAi agent as described above.

In another aspect, the agent is a single-stranded antisense RNA molecule. An antisense RNA molecule is complementary to a sequence within the target mRNA. Antisense RNA can inhibit translation in a stoichiometric manner by base pairing to the mRNA and physically obstructing the translation machinery, see Dias, N. *et al.*, (2002) *Mol Cancer Ther* 1:347-355. The antisense RNA molecule may have about 15-30 nucleotides that are complementary to the target mRNA. For example, the antisense RNA molecule may have a sequence of at least 15, 16, 17, 18, 19, 20 or more contiguous nucleotides complementary to the filamin B or LY9 sequences provided herein.

The term “antisense strand” refers to the strand of a double stranded RNAi agent which includes a region that is substantially complementary to a target sequence (*e.g.*, a human TTR mRNA). As used herein, the term “region complementary to part of an mRNA encoding transthyretin” refers to a region on the antisense strand that is substantially complementary to part of a TTR mRNA sequence. Where the region of complementarity is not fully complementary to the target sequence, the mismatches are most tolerated in the terminal regions and, if present, are generally in a terminal region or regions, *e.g.*, within 6, 5, 4, 3, or 2 nucleotides of the 5’ and/or 3’ terminus.

The term “sense strand,” as used herein, refers to the strand of a dsRNA that includes a region that is substantially complementary to a region of the antisense strand.

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A “molecular beacon” nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

Isolated Proteins and Antibodies

One aspect of the invention pertains to isolated marker proteins and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a marker protein or a fragment thereof. In one embodiment, the native marker protein can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, a protein or peptide comprising the whole or a segment of the marker protein is produced by recombinant DNA techniques. Alternative to recombinant expression, such protein or peptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a marker protein include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the marker protein, which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding full-length protein. A biologically active portion of a marker protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the marker protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of the marker protein.

Preferred marker proteins are encoded by nucleotide sequences provided in the sequence listing. Other useful proteins are substantially identical (*e.g.*, at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%) to one of these sequences and retain the functional activity of the corresponding naturally-occurring marker protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. Preferably, the percent identity between the two sequences is calculated using a global alignment. Alternatively, the percent identity between the two sequences is calculated using a local alignment. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions (*e.g.*, overlapping positions) x 100). In one embodiment the two sequences are the same length. In another embodiment, the two sequences are not the same length.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, a newer version of the BLAST algorithm called Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, which is able to perform gapped local alignments for the programs BLASTN, BLASTP and BLASTX. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, BLASTX and BLASTN) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller,

(1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448. When using the FASTA algorithm for comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a k -tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

Another aspect of the invention pertains to antibodies directed against a protein of the invention. In preferred embodiments, the antibodies specifically bind a marker protein or a fragment thereof. The terms "antibody" and "antibodies" as used interchangeably herein refer to immunoglobulin molecules as well as fragments and derivatives thereof that comprise an immunologically active portion of an immunoglobulin molecule, (*i.e.*, such a portion contains an antigen binding site which specifically binds an antigen, such as a marker protein, *e.g.*, an epitope of a marker protein). An antibody which specifically binds to a protein of the invention is an antibody which binds the protein, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the protein. Examples of an immunologically active portion of an immunoglobulin molecule include, but are not limited to, single-chain antibodies (scAb), F(ab) and F(ab')₂ fragments.

An isolated protein of the invention or a fragment thereof can be used as an immunogen to generate antibodies. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of one of the proteins of the invention, and encompasses at least one epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein. Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or

similar analyses can be used to identify hydrophilic regions. In preferred embodiments, an isolated marker protein or fragment thereof is used as an immunogen.

The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope. Preferred polyclonal and monoclonal antibody compositions are ones that have been selected for antibodies directed against a protein of the invention. Particularly preferred polyclonal and monoclonal antibody preparations are ones that contain only antibodies directed against a marker protein or fragment thereof. Methods of making polyclonal, monoclonal, and recombinant antibody and antibody fragments are well known in the art.

Predictive Medicine

The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining the level of expression of one or more marker proteins or nucleic acids, in order to determine whether an individual is at risk of developing a disease or disorder, such as, without limitation, an oncological disorder, e.g., prostate cancer. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the disorder.

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs or other compounds administered either to inhibit an oncological disorder, e.g., prostate cancer, or to treat or prevent any other disorder (*i.e.* in order to understand any carcinogenic effects that such treatment may have)) on the expression or activity of a marker of the invention in clinical trials. These and other agents are described in further detail in the following sections.

A. Diagnostic Assays

An exemplary method for detecting the presence or absence or change of expression level of a marker protein or nucleic acid in a biological sample involves obtaining a

biological sample (e.g. an oncological disorder-associated body fluid) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (e.g., mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample in vitro as well as in vivo.

Methods provided herein for detecting the presence, absence, change of expression level of a marker protein or nucleic acid in a biological sample include obtaining a biological sample from a subject that may or may not contain the marker protein or nucleic acid to be detected, contacting the sample with a marker-specific binding agent (i.e., one or more marker-specific binding agents) that is capable of forming a complex with the marker protein or nucleic acid to be detected, and contacting the sample with a detection reagent for detection of the marker—marker-specific binding agent complex, if formed. It is understood that the methods provided herein for detecting an expression level of a marker in a biological sample includes the steps to perform the assay. In certain embodiments of the detection methods, the level of the marker protein or nucleic acid in the sample is none or below the threshold for detection.

The methods include formation of either a transient or stable complex between the marker and the marker-specific binding agent. The methods require that the complex, if formed, be formed for sufficient time to allow a detection reagent to bind the complex and produce a detectable signal (e.g., fluorescent signal, a signal from a product of an enzymatic reaction, e.g., a peroxidase reaction, a phosphatase reaction, a beta-galactosidase reaction, or a polymerase reaction).

In certain embodiments, all markers are detected using the same method. In certain embodiments, all markers are detected using the same biological sample (e.g., same body fluid or tissue). In certain embodiments, different markers are detected using various methods. In certain embodiments, markers are detected in different biological samples.

1. Protein detection

In certain embodiments of the invention, the marker to be detected is a protein. Proteins are detected using a number of assays in which a complex between the marker protein to be detected and the marker specific binding agent would not occur naturally, for example, because one of the components is not a naturally occurring compound or the marker

for detection and the marker specific binding agent are not from the same organism (e.g., human marker proteins detected using marker-specific binding antibodies from mouse, rat, or goat). In a preferred embodiment of the invention, the marker protein for detection is a human marker protein. In certain detection assays, the human markers for detection are bound by marker-specific, non-human antibodies, thus, the complex would not be formed in nature. The complex of the marker protein can be detected directly, e.g., by use of a labeled marker-specific antibody that binds directly to the marker, or by binding a further component to the marker--marker-specific antibody complex. In certain embodiments, the further component is a second marker-specific antibody capable of binding the marker at the same time as the first marker-specific antibody. In certain embodiments, the further component is a secondary antibody that binds to a marker-specific antibody, wherein the secondary antibody preferably linked to a detectable label (e.g., fluorescent label, enzymatic label, biotin). When the secondary antibody is linked to an enzymatic detectable label (e.g., a peroxidase, a phosphatase, a beta-galactosidase), the secondary antibody is detected by contacting the enzymatic detectable label with an appropriate substrate to produce a colorimetric, fluorescent, or other detectable, preferably quantitatively detectable, product. Antibodies for use in the methods of the invention can be polyclonal, however, in a preferred embodiment monoclonal antibodies are used. An intact antibody, or a fragment or derivative thereof (e.g., Fab or F(ab')₂) can be used in the methods of the invention. Such strategies of marker protein detection are used, for example, in ELISA, RIA, western blot, and immunofluorescence assay methods.

In certain detection assays, the marker present in the biological sample for detection is an enzyme and the detection reagent is an enzyme substrate. For example, the enzyme can be a protease and the substrate can be any protein that includes an appropriate protease cleavage site. Alternatively, the enzyme can be a kinase and the substrate can be any substrate for the kinase. In preferred embodiments, the substrate which forms a complex with the marker enzyme to be detected is not the substrate for the enzyme in a human subject.

In certain embodiments, the marker--marker-specific binding agent complex is attached to a solid support for detection of the marker. The complex can be formed on the substrate or formed prior to capture on the substrate. For example, in an ELISA, RIA, immunoprecipitation assay, western blot, immunofluorescence assay, in gel enzymatic assay the marker for detection is attached to a solid support, either directly or indirectly. In an

ELISA, RIA, or immunofluorescence assay, the marker is typically attached indirectly to a solid support through an antibody or binding protein. In a western blot or immunofluorescence assay, the marker is typically attached directly to the solid support. For in-gel enzyme assays, the marker is resolved in a gel, typically an acrylamide gel, in which a substrate for the enzyme is integrated.

2. Nucleic acid detection

In certain embodiments of the invention, the marker is a nucleic acid. Nucleic acids are detected using a number of assays in which a complex between the marker nucleic acid to be detected and a marker-specific probe would not occur naturally, for example, because one of the components is not a naturally occurring compound. In certain embodiments, the analyte comprises a nucleic acid and the probe comprises one or more synthetic single stranded nucleic acid molecules, e.g., a DNA molecule, a DNA-RNA hybrid, a PNA, or a modified nucleic acid molecule containing one or more artificial bases, sugars, or backbone moieties. In certain embodiments, the synthetic nucleic acid is a single stranded is a DNA molecule that includes a fluorescent label. In certain embodiments, the synthetic nucleic acid is a single stranded oligonucleotide molecule of about 12 to about 50 nucleotides in length. In certain embodiments, the nucleic acid to be detected is an mRNA and the complex formed is an mRNA hybridized to a single stranded DNA molecule that is complementary to the mRNA. In certain embodiments, an RNA is detected by generation of a DNA molecule (i.e., a cDNA molecule) first from the RNA template using the single stranded DNA that hybridizes to the RNA as a primer, e.g., a general poly-T primer to transcribe poly-A RNA. The cDNA can then be used as a template for an amplification reaction, e.g., PCR, primer extension assay, using a marker-specific probe. In certain embodiments, a labeled single stranded DNA can be hybridized to the RNA present in the sample for detection of the RNA by fluorescence in situ hybridization (FISH) or for detection of the RNA by northern blot.

For example, in vitro techniques for detection of mRNA include northern hybridizations, in situ hybridizations, and rtPCR. In vitro techniques for detection of genomic DNA include Southern hybridizations. Techniques for detection of mRNA include PCR, northern hybridizations and in situ hybridizations. Methods include both qualitative and quantitative methods.

A general principle of such diagnostic, prognostic, and monitoring assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways known in the art, e.g., ELISA assay, PCR, FISH.

3. Detection of expression levels

Marker levels can be detected based on the absolute expression level or a normalized or relative expression level. Detection of absolute marker levels may be preferable when monitoring the treatment of a subject or in determining if there is a change in the prostate cancer status of a subject. For example, the expression level of one or more markers can be monitored in a subject undergoing treatment for prostate cancer, e.g., at regular intervals, such as monthly intervals. A modulation in the level of one or more markers can be monitored over time to observe trends in changes in marker levels. Expression levels of one or more of filamin B, LY9, or keratin 19 in the subject may be higher than the expression level of those markers in a normal sample, but may be lower than the prior expression level, thus indicating a benefit of the treatment regimen for the subject. Similarly, rates of change of marker levels can be important in a subject who is not subject to active treatment for prostate cancer (e.g., watchful waiting). Changes, or not, in marker levels may be more relevant to treatment decisions for the subject than marker levels present in the population. Rapid changes in marker levels in a subject who otherwise appears to have a normal prostate may be indicative of an abnormal prostate state, even if the markers are within normal ranges for the population.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a gene that is not a marker, e.g., a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level in one sample, e.g., a patient sample, to another sample, e.g., a non-cancer sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative expression level as compared to an appropriate control, e.g., population control, adjacent normal tissue control, earlier time point control, etc.. Preferably, the samples used in the baseline determination will be from non-cancer cells. The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether the marker assayed is cancer specific (versus normal cells). In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from cancer cells provides a means for grading the severity of the cancer state.

Diagnostic, Prognostic, and Treatment Methods

The invention provides methods for detecting an abnormal prostate state in a subject by

(1) contacting a biological sample from a subject with a panel of one or more detection reagents wherein each detection reagent is specific for one prostate-cancer related protein; wherein the prostate-cancer related proteins are selected from the prostate-cancer related protein set as follows: filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3;

(2) measuring the amount of each prostate-cancer related marker detected in the biological sample by each detection reagent; and

(3) comparing the level of expression of the one or more prostate-cancer related protein in the biological sample obtained from the subject with a level of expression of the one or more prostate-cancer related protein in a normal control sample, thereby detecting an abnormal prostate state.

In certain embodiments, detecting an abnormal prostate state comprises diagnosing prostate cancer status in a subject. In certain embodiments, an abnormal prostate state comprises identifying a predisposed to developing prostate cancer.

The invention provides methods for monitoring the treatment of prostate cancer in a subject by

(1) contacting a first biological sample obtained from the subject prior to administering at least a portion of a treatment regimen to the subject with a panel of one or more detection reagents wherein each detection reagent is specific for one prostate-cancer related protein; wherein the prostate-cancer related proteins are selected from the prostate protein set as follows: filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3;

(2) contacting a second biological sample obtained from the subject after administering at least a portion of a treatment regimen to the subject with a panel of one or more detection reagents wherein each detection reagent is specific for one prostate-cancer related protein; wherein the prostate-cancer related proteins are selected from the prostate protein set as follows: filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3;

(3) measuring the amount of prostate-cancer related marker detected in each the first biological sample and the second biological sample by each detection reagent; and

(4) comparing the level of expression of the one or more prostate-cancer related markers in the first sample with the expression level of the one or more prostate-cancer related markers in the second sample, thereby monitoring the treatment of prostate cancer in the subject.

The invention provides method of selecting for administration of active treatment or against administration of active treatment of prostate cancer in a subject by

(1) contacting a first biological sample obtained from the subject prior to administering a treatment regimen to the subject with a panel of one or more detection reagents wherein each detection reagent is specific for one prostate-cancer related protein; wherein the prostate-cancer related proteins are selected from the prostate protein set as follows: filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3;

(2) contacting a second biological sample obtained from the subject prior to administering a treatment regimen to the subject with a panel of one or more detection reagents wherein each detection reagent is specific for one prostate-cancer related protein; wherein the prostate-cancer related proteins are selected from the prostate protein set as

follows: filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3;

(3) measuring the amount of prostate-cancer related marker detected in each the first biological sample and the second biological sample by each detection reagent; and

(4) comparing the level of expression of the one or more prostate-cancer related markers in the first sample with the expression level of the one or more prostate-cancer related markers in the second sample, wherein selecting for administration of active treatment or against administration of active treatment of prostate cancer is based on the presence or absence of changes in the level of expression of one or more markers between the first sample and the second sample.

In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is two or more markers. In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is three or more markers. In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is four or more markers. In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is five or more markers. In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is six or more markers. In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is seven or more markers. In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is eight or more markers. In certain embodiments of the diagnostic and monitoring methods provided herein, one or more prostate-cancer related markers is nine or more markers.

In certain embodiments of the diagnostic methods provided herein, an increase in the level of expression of one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample as compared to the level of expression of the one or more prostate-cancer related markers in a normal control sample is an indication that the subject is afflicted with prostate cancer. In certain embodiments of the diagnostic methods provided herein, no increase in the detected expression level of one or more of filamin B, LY9, and keratin 19 in the biological sample as compared to the

expression level in a normal control sample is an indication that the subject is not afflicted with prostate cancer or not predisposed to developing prostate cancer.

In certain embodiments of the diagnostic methods provided herein, an increase in the level of expression of one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the biological sample as compared to the level of expression of the one or more prostate-cancer related markers in a normal control sample is an indication that the subject is predisposed to developing prostate cancer.

In certain embodiments of the monitoring methods provided herein, no increase in the detected level of expression of any of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second sample as compared to the level of expression of the one or more prostate-cancer related markers in the first sample is an indication that the therapy is efficacious for treating prostate cancer in the subject. In certain embodiments the monitoring methods provided herein, further comprise comparing the level of expression of one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the first sample or the level of expression of one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second sample with the expression of the one or more prostate-cancer related markers in a control sample.

In certain embodiments of the monitoring methods provided herein, an increase in the level of expression of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second sample as compared to the level of expression of the one or more prostate-cancer related markers in the first sample is an indication for selection of active treatment of prostate cancer in the subject. In certain embodiments of the monitoring methods provided herein, no increase in the detected level of expression of any of the one or more prostate-cancer related markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second sample as compared to the level of expression of the one or more prostate-cancer related markers in the first sample is an indication against selection of active treatment of prostate cancer in the subject. In certain embodiments of the monitoring methods provided herein, wherein an increased expression level of one or more of filamin B, LY9, and keratin 19 in the second sample as compared to the expression level in the first sample is an indication that the therapy is not efficacious in the treatment of prostate cancer.

In certain embodiments of the diagnostic and monitoring methods provided herein, the one or more prostate-cancer related markers is selected from the group of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3. In certain embodiments of the diagnostic and monitoring methods provided herein, the one or more prostate-cancer related markers is selected from the group of keratin 7, keratin 8, and keratin 15. In certain embodiments of the diagnostic and monitoring methods provided herein, the one or more prostate-cancer related markers is selected from the group of keratin 7, keratin 15, and keratin 19. In certain embodiments of the diagnostic and monitoring methods provided herein, the one or more prostate-cancer related markers is keratin 7 or keratin 15. In certain embodiments of the diagnostic and monitoring methods provided herein, the one or more prostate-cancer related markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the biological sample is compared to the level of the one or more prostate-cancer related markers in a normal control sample is indicative of a modulation in prostate cancer status.

In certain embodiments of the monitoring methods provided herein, modulation of the level of expression of the one or more prostate-cancer related markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the second sample as compared to the level of expression of the one or more prostate-cancer related markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the first sample is indicative of a change in prostate cancer status in response to treatment of the prostate cancer in the subject. In certain embodiments of the monitoring methods provided herein, the methods further comprise comparing the level of expression of one or more prostate-cancer related markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the first sample; or the level of expression of one or more prostate-cancer related markers selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the second sample to the level of expression of one or more prostate-cancer related markers in a normal control sample.

In certain embodiments the diagnostic methods provided herein further comprise detecting the level of expression of prostate specific antigen (PSA) in the biological sample and preferably further comprise comparing the level of expression of PSA in the biological sample to a PSA expression level in a normal control sample. In certain embodiments, the

combination of PSA level with one or more of the prostate-cancer marker levels increases the predictive value of the method.

In certain embodiments the monitoring methods provided herein further comprise detecting the level of expression of prostate specific antigen (PSA) in the first sample and the second sample, and preferably further comprising comparing the level of expression of PSA in the first sample with the level of expression of PSA in the second sample. In certain monitoring methods, the change in PSA level in combination with the change in prostate-cancer marker level increases the predictive value of the method.

In certain embodiments the diagnostic and monitoring methods provided herein further comprise comparing the detected level of the one or more prostate markers in the biological samples with one or more control samples wherein the control sample is one or more of a sample from the same subject at an earlier time point than the biological sample, a sample from a subject with benign prostatic hyperplasia (BPH), a sample from a subject with non-metastatic prostate cancer, a sample from a subject with metastatic prostate cancer, a sample from a subject with androgen sensitive prostate cancer, a sample from a subject with androgen insensitive prostate cancer, a sample from a subject with aggressive prostate cancer, and sample obtained from a subject with non-aggressive prostate cancer. Comparison of the marker levels in the biological samples with control samples from subjects with various normal and abnormal prostate states facilitates the differentiation between various prostate states including normal prostate and prostate cancer, benign prostate hyperplasia and prostate cancer, benign prostate hyperplasia and normal prostate, androgen dependent and androgen independent prostate cancer, aggressive prostate cancer and non-aggressive prostate cancer, aggressive prostate cancer and non-aggressive prostate cancer, or between any two or more prostate states including normal prostate, prostate cancer, benign prostate hyperplasia, androgen dependent prostate cancer, androgen independent prostate cancer, aggressive prostate cancer, non-aggressive prostate cancer, metastatic prostate cancer, and non-metastatic prostate cancer.

In certain embodiments the diagnostic and monitoring methods provided herein further comprising detecting the size of the prostate tumor in the subject. In certain embodiments the monitoring methods provided herein further comprise detecting a change in the size or relative aggressiveness of the tumor. In certain embodiments, the size of the prostate tumor in the subject is detected prior to administering the at least a portion of a

treatment regimen to the subject. In certain embodiments, the size of the prostate tumor in the subject is detected after administering the at least a portion of a treatment regimen to the subject. Certain monitoring methods, further comprise comparing the size of the prostate tumor in the subject prior to administering the at least a portion of a treatment regimen to the subject to the size of the prostate tumor in the subject after administering the at least a portion of a treatment regimen to the subject.

In certain embodiments the diagnostic and monitoring methods provided herein further comprising obtaining a subject sample.

In certain embodiments the diagnostic and monitoring methods provided herein further comprising selecting a treatment regimen for the subject based on the level expression of one or more of the prostate-cancer related markers provided in claims 1.

In certain embodiments the diagnostic and monitoring methods provided herein further comprising selecting a subject for having or being suspected of having prostate cancer.

In certain embodiments the diagnostic and monitoring methods provided herein further comprising treating the subject with a regimen including one or more treatments selected from the group consisting of surgery, radiation, hormone therapy, antibody therapy, therapy with growth factors, cytokines, and chemotherapy.

In certain embodiments the diagnostic and monitoring methods provided herein further comprising selecting the one or more specific treatment regimens for the subject based on the results of the diagnostic and monitoring methods provided herein. In certain embodiments, the treatment method is maintained based on the results from the diagnostic or prognostic methods. In certain embodiments, the treatment method is changed based on the results from the diagnostic or prognostic methods.

In certain embodiments, a change the treatment regimen comprises changing a hormone based therapy treatment. In certain embodiments, treatments for prostate cancer include one or more of surgery, radiation, hormone therapy, antibody therapy, therapy with growth factors, cytokines, or chemotherapy based on the results of a method of any one of claims 1-64 for an interval prior to performing a subsequent diagnostic, prognostic, or monitoring method provided herein.

In certain embodiments of the diagnostic and monitoring methods provided herein, the method of detecting a level comprises isolating a component of the biological sample.

In certain embodiments of the diagnostic and monitoring methods provided herein, the method of detecting a level comprises labeling a component of the biological sample.

In certain embodiments of the diagnostic and monitoring methods provided herein, the method of detecting a level comprises amplifying a component of a biological sample.

In certain embodiments of the diagnostic and monitoring methods provided herein, the method of detecting a level comprises forming a complex with a probe and a component of a biological sample. In certain embodiments, forming a complex with a probe comprises forming a complex with at least one non-naturally occurring reagent. In certain embodiments of the diagnostic and monitoring methods provided herein, the method of detecting a level comprises processing the biological sample. In certain embodiments of the diagnostic and monitoring methods provided herein, the method of detecting a level of at least two markers comprises a panel of markers. In certain embodiments of the diagnostic and monitoring methods provided herein, the method of detecting a level comprises attaching the marker to be detected to a solid surface.

The invention provides methods of selecting for administration of active treatment or against administration of active treatment of prostate cancer in a subject comprising:

(1) detecting a level of one or more markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta in a first sample obtained from the subject having prostate cancer wherein the subject has not been actively treated for prostate cancer;

(2) detecting a level of one or more markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in a second sample from the subject;

(3) comparing the level of one or more markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in the first sample with the level of one or more markers selected from the group

consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in the second sample;

wherein selecting for administration of active treatment or against administration of active treatment of prostate cancer is based on the presence or absence of changes in the level of expression of one or more markers between the first sample and the second sample.

In certain embodiments, the method further comprising obtaining a third sample obtained from the subject, detecting a level of one or more markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in the third sample, and comparing the level of one or more markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 in the third sample with the level of the one or more markers in the first sample or the one or more markers in the second sample.

In certain embodiments, an increased level of one or more of filamin B, LY9, and keratin 19 in the second sample as compared to the level of one or more of filamin B, LY9, and keratin 19 in the first sample is an indication that the therapy is not efficacious in the treatment of prostate cancer.

In certain embodiments, an increased of one or more of filamin B, LY9, and keratin 19 in the second sample as compared to the level of one or more of filamin B, LY9, and keratin 19 in the first sample is an indication for selecting active treatment for prostate cancer.

In certain embodiments, the method further comprises comparing the level of one or more markers selected from the group consisting of filamin B, LY9, and keratin 19 in the first sample or the level of one or more markers selected from the group consisting of filamin B, LY9, and keratin 19 in the second sample with the level of one or more of filamin B, LY9, and keratin 19 in a control sample. In certain embodiments, the method comprises detecting the level of one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the first sample; detecting the level of one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the second sample; and comparing the level of the one or more of one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the second sample with the one or more of the level of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the first sample. In certain

embodiments, the method comprises detection of a subset of keratins such as keratin 7, keratin 8, and keratin 15; keratin 7, 15, and 19; and keratin 7 or keratin 15. In certain embodiments, the method further comprises comparing the level of one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the first sample; or the level of expression of one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in the second sample to the level of one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, and tubulin beta-3 in a control sample.

In certain embodiments, no change in the level of expression of one or more markers selected from the group consisting of filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3 between the first sample and the second sample is an indication for selecting against active treatment for prostate cancer.

In certain embodiments, the methods further comprise detecting the level of prostate specific antigen (PSA) in the first sample and the second sample, and then preferably further comprising comparing the level of PSA in the first sample with the level of PSA in the second sample.

In certain embodiments, a decrease in the level of one or more of filamin B, LY9, and keratin 19 in the second sample as compared to the level of one or more of filamin B, LY9, and keratin 19 in the first sample in combination with a decrease in the level of PSA in the second sample as compared to the level of PSA in the first sample has greater predictive value that the therapy is efficacious in treating prostate cancer in the subject than analysis of a single marker alone.

In certain embodiments, a decrease in the level of one or more of filamin B, LY9, and keratin 19 in the second sample as compared to the level of one or more of filamin B, LY9, and keratin 19 in the first sample in combination with a decrease in the level of expression of PSA in the second sample as compared to the level of PSA in the first sample has greater predictive value that for selecting against active treatment for prostate cancer than analysis of a single marker alone.

Monitoring Clinical Trials

Monitoring the influence of agents (*e.g.*, drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening or monitoring the

treatment of a single subject, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for an oncological disorder. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one or more selected markers of the invention (*e.g.*, filamin B, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, optionally in combination with PSA) in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased expression of the marker gene(s) during the course of treatment may indicate ineffective dosage and the desirability of increasing the dosage. Conversely, decreased expression of the marker gene(s) may indicate efficacious treatment and no need to change dosage.

Kits

The invention also provides compositions and kits for diagnosing, prognosing, or monitoring a disease or disorder, recurrence of a disorder, or survival of a subject being treated for a disorder (*e.g.*, an abnormal prostate state, BPH, an oncologic disorder, *e.g.*, prostate cancer). These kits include one or more of the following: a detectable antibody that specifically binds to a marker of the invention, a detectable antibody that specifically binds to a marker of the invention, reagents for obtaining and/or preparing subject tissue samples for staining, and instructions for use.

The invention also encompasses kits for detecting the presence of a marker protein or nucleic acid in a biological sample. Such kits can be used to determine if a subject is suffering from or is at increased risk of developing an abnormal prostate state. For example, the kit can comprise a labeled compound or agent capable of detecting a marker protein or nucleic acid in a biological sample and means for determining the amount of the protein or mRNA in the sample (*e.g.*, an antibody which binds the protein or a fragment thereof, or an

oligonucleotide probe which binds to DNA or mRNA encoding the protein). Kits can also include instructions for use of the kit for practicing any of the methods provided herein or interpreting the results obtained using the kit based on the teachings provided herein. The kits can also include reagents for detection of a control protein in the sample not related to the abnormal prostate state, e.g., actin for tissue samples, albumin in blood or blood derived samples for normalization of the amount of the marker present in the sample. The kit can also include the purified marker for detection for use as a control or for quantitation of the assay performed with the kit.

Kits include panel of reagents for use in a method to diagnose prostate cancer in a subject (or to identify a subject predisposed to developing prostate cancer, etc.), the panel comprising at least two detection reagents, wherein each detection reagent is specific for one prostate cancer-specific protein, wherein said prostate cancer-specific proteins are selected from the prostate cancer-specific protein sets provided herein.

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.*, attached to a solid support) which binds to a first marker protein; and, optionally, (2) a second, different antibody which binds to either the first marker protein or the first antibody and is conjugated to a detectable label. In certain embodiments, the kit includes (1) a second antibody (*e.g.*, attached to a solid support) which binds to a second marker protein; and, optionally, (2) a second, different antibody which binds to either the second marker protein or the second antibody and is conjugated to a detectable label. The first and second marker proteins are different. In an embodiment, the first and second markers are markers of the invention, *e.g.*, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B, LY9, and PSA. In certain embodiments, neither the first marker nor the second marker is PSA. In certain embodiments, the kit comprises a third antibody which binds to a third marker protein which is different from the first and second marker proteins, and a second different antibody that binds to either the third marker protein or the antibody that binds the third marker protein wherein the third marker protein is different from the first and second marker proteins.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, *e.g.*, a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a marker protein or (2) a pair of primers useful for amplifying a marker nucleic acid molecule. In certain embodiments, the kit can further include, for example: (1)

an oligonucleotide, *e.g.*, a second detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a second marker protein or (2) a pair of primers useful for amplifying the second marker nucleic acid molecule. The first and second markers are different. In an embodiment, the first and second markers are markers of the invention, *e.g.*, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B, LY9, and PSA. In certain embodiments, neither the first marker nor the second marker is PSA. In certain embodiments, the kit can further include, for example: (1) an oligonucleotide, *e.g.*, a third detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a third marker protein or (2) a pair of primers useful for amplifying the third marker nucleic acid molecule wherein the third marker is different from the first and second markers. In certain embodiments, the kit includes a third primer specific for each nucleic acid marker to allow for detection using quantitative PCR methods.

For chromatography methods, the kit can include markers, including labeled markers, to permit detection and identification of one or more markers of the invention, *e.g.*, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B, LY9, and optionally PSA, by chromatography. In certain embodiments, kits for chromatography methods include compounds for derivatization of one or more markers of the invention. In certain embodiments, kits for chromatography methods include columns for resolving the markers of the method.

Reagents specific for detection of a marker of the invention, *e.g.*, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B, LY9, and PSA, allow for detection and quantitation of the marker in a complex mixture, *e.g.*, serum, tissue sample. In certain embodiments, the reagents are species specific. In certain embodiments, the reagents are not species specific. In certain embodiments, the reagents are isoform specific. In certain embodiments, the reagents are not isoform specific. In certain embodiments, the reagents detect total keratin 8, keratin 18, filamin B, PSA, or LY9.

In certain embodiments, the kits for the diagnosis, monitoring, or characterization of prostate cancer comprise at least one reagent specific for the detection of the level of expression of at least one marker selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, filamin B, and LY9. In certain embodiments, the kits further comprise instructions for the diagnosis, monitoring, or characterization of prostate cancer based on the level of expression of the at least one marker

selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, filamin B, and LY9. In certain embodiments, the kits further comprise instructions to detect the level of PSA in a sample in which the at least one marker selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, filamin B, and LY9 is detected. In certain embodiments, the kits further comprise at least one reagent for the specific detection of PSA.

The invention provides kits comprising at least one reagent specific for the detection of a level of expression of at least one marker selected from the group consisting of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, filamin B, and LY9 and at least one reagent specific for the detection of a level of expression of PSA.

In certain embodiments, the kits can also comprise, *e.g.*, a buffering agents, a preservative, a protein stabilizing agent, reaction buffers. The kit can further comprise components necessary for detecting the detectable label (*e.g.*, an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. The controls can be control serum samples or control samples of purified proteins or nucleic acids, as appropriate, with known levels of target markers. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

The kits of the invention may optionally comprise additional components useful for performing the methods of the invention.

Panels

The invention provides panels of reagents for detection of one or more prostate-related marker in a subject sample and at least one control reagent. In certain embodiments, the control reagent is to detect the marker for detection in the biological sample wherein the panel is provided with a control sample containing the marker for use as a positive control and optionally to quantitate the amount of marker present in the biological sample. In certain embodiments, the panel includes a detection reagent for a marker not related to an abnormal prostate state that is known to be present or absent in the biological sample to provide a positive or negative control, respectively. The panel can be provided with reagents for detection of a control protein in the sample not related to the abnormal prostate state, *e.g.*,

actin for tissue samples, albumin in blood or blood derived samples for normalization of the amount of the marker present in the sample. The panel can be provided with a purified marker for detection for use as a control or for quantitation of the assay performed with the panel.

In a preferred embodiment, the panel includes reagents for detection of two or more markers of the invention (e.g., 2, 3, 4, 5, 6, 7, 8, 9), preferably in conjunction with a control reagent. In the panel, each marker is detected by a reagent specific for that marker. In certain embodiments, the panel further includes a reagent for the detection of PSA. In certain embodiments, the panel includes replicate wells, spots, or portions to allow for analysis of various dilutions (e.g., serial dilutions) of biological samples and control samples. In a preferred embodiment, the panel allows for quantitative detection of one or more markers of the invention.

In certain embodiments, the panel is a protein chip for detection of one or more markers. In certain embodiments, the panel is an ELISA plate for detection of one or more markers. In certain embodiments, the panel is a plate for quantitative PCR for detection of one or more markers.

In certain embodiments, the panel of detection reagents is provided on a single device including a detection reagent for one or more markers of the invention and at least one control sample. In certain embodiments, the panel of detection reagents is provided on a single device including a detection reagent for two or more markers of the invention and at least one control sample. In certain embodiments, multiple panels for the detection of different markers of the invention are provided with at least one uniform control sample to facilitate comparison of results between panels.

Screening Assays

The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, proteins, peptides, peptidomimetics, peptoids, small molecules or other drugs), which modulate the state of the diseased cell by modulating the expression and/or activity of a marker of the invention, *i.e.*, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B, or LY9; optionally in combination with PSA. Such assays typically comprise a reaction between a marker of the invention and one or more assay components. The other

components may be either the test compound itself, or a combination of test compounds and a natural binding partner of a marker of the invention. Compounds identified *via* assays such as those described herein may be useful, for example, for modulating, *e.g.*, inhibiting, ameliorating, treating, or preventing the disease. Compounds identified for modulating the expression level of one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, filamin B, or LY9; optionally in combination with PSA, are preferably further tested for activity useful in the treatment of cancer, preferably prostate cancer, *e.g.*, inhibiting tumor cell growth, inhibiting tumor angiogenesis, inducing tumor cell apoptosis, etc.

The test compounds used in the screening assays of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, *e.g.*, Zuckermann *et al.*, 1994, *J. Med. Chem.* 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992, *Biotechniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor, 1993, *Nature* 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull *et al.*, 1992, *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith, 1990, *Science*

249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla *et al*, 1990, *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici, 1991, *J. Mol. Biol.* 222:301-310; Ladner, *supra.*).

The screening methods of the invention comprise contacting a cell, e.g., a diseased cell, especially a prostate cancer cell, with a test compound and determining the ability of the test compound to modulate the expression and/or activity of filamin B, LY9, or keratin 19, optionally in combination with PSA, in the cell. The expression and/or activity of filamin B, LY9, or keratin 19; optionally in combination with PSA, can be determined using any methods known in the art, such as those described herein.

In another embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a marker of the invention or biologically active portions thereof. In yet another embodiment, the invention provides assays for screening candidate or test compounds which bind to a marker of the invention or biologically active portions thereof. Determining the ability of the test compound to directly bind to a marker can be accomplished, for example, by any method known in the art.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent capable of modulating the expression and/or activity of a marker of the invention identified as described herein can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatment as described above.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references and published patents and patent applications cited throughout the application are hereby incorporated by reference.

Exemplification of the Invention:

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, GenBank Accession and Gene numbers,

and published patents and patent applications cited throughout the application are hereby incorporated by reference.

Example 1 – Identification of Keratins and Tubulin as Prostate Cancer Markers

Extracellular Keratins are known to influence the cell proliferation and metastasis of epithelial derived prostate cancers. Androgen refractory prostate cancers exhibit differential expression keratin 8 (K8) when compared to normal tissue. Modulation and degradation of keratins is in turn mediated by mitochondrial generation of Reactive Oxygen Species (ROS). Despite these advances a systematic approach to understanding of keratins and other EC proteins in prostate cancer metastasis and proliferation is lacking. An interrogative systems biology based discovery platform disclosed in WO2012119129 (incorporated herein by reference), and shown schematically in Figure 1, provides new mechanistic insights into understanding mitochondrial role in behavior of prostate cancer cells. The discovery platform involves discovery across a hierarchy of systems including in vitro human cell based models and human serum samples from prostate cancer patients and downstream data integration and mathematical modeling employing an Artificial Intelligence (AI) based informatic module. For cellular models, androgen sensitive LnCAP cell line and metastatic, androgen refractory PC3 cell line were treated with ubidecarenone (coenzyme Q10) in order to engage the mitochondrial machinery. Proteomic signatures were captured using a 2D LC-MS orbitrap technology. Total protein signatures were input to an AI based informatics module to generate causal protein networks (Figure 2). Wet lab assays that specifically measure mitochondrial ROS, ATP and caspase 3 activation confirmed changes in intracellular levels of these markers. Several novel protein causal interactions that govern induction of mitochondrial machinery by ubidecarenone in PC3 cells were observed. Causal protein maps revealed association of keratins 8 and 15 in PC3 models and not LnCAP. The keratin 8/15 association was lost upon treatment with ubidecarenone, and a direct association of keratins 7 and 15 was established (Figure 3). These results suggest that a change in the interaction among keratins 7, 8, and 15 is particularly useful in demonstrating a response to treatment or a change in prostate cancer status in a subject. Further, keratins 8 and 15 were differentially associated in the androgen refractory, metastatic PC3 cell line and the androgen sensitive LnCAP cell line. This indicates that keratins 8 and 15 could be useful to differentiate

between prostate cancer states, e.g., between androgen sensitive and metastatic, androgen refractory prostate cancer.

An increase in the expression of keratin 19 in relation to prostate cancer was confirmed using a panel of serum samples from subjects suffering from prostate cancer as compared to an appropriate matched control population.

Thus novel mechanistic insight into prostate cancer proliferation and mitochondrial role in modulating metastasis was gained with a novel chemical systems biology approach.

The results provided herein demonstrate that modulation of keratin and potential causal association in androgen refractory prostate cancer was inferred by the Platform technology. This provides a potential mechanisms of keratin regulation in response to modulation of mitochondrial function was deciphered by the Platform technology. Thus, novel drivers of cancer pathophysiology were validated in patient serum samples.

Example 2 – Identification of Filamin B as a Prostate Cancer Marker

An interrogative systems biology based discovery platform was used to obtain mechanistic insights into understanding mitochondrial role in behavior of prostate cancer cells. The Platform technology, which is described in detail in WO2012119129, involves discovery across a hierarchy of systems including in vitro human cell based models and human serum samples from prostate cancer patients and downstream data integration and mathematical modeling employing an Artificial Intelligence (AI) based informatics module.

The results provided herein demonstrate the modulation of filamin B and LY9, and potential causal association in androgen refractory prostate cancer that was inferred using the Platform technology. The application provides potential mechanisms of filamin B and LY9 regulation in response to modulation of mitochondrial function was deciphered by the Platform technology and provides validation of the markers in patient serum samples.

Using the Platform methods, human prostate cancer cells PC3 (androgen insensitive, metastatic) and LnCap (androgen sensitive) were modeled in cancer microenvironments including hypoxia, reduced environments, and hyperglycemia and in presence of coenzyme Q10. Normal cells (human dermal fibroblasts (HDFa) and SV40 transformed human liver cells (THLE2)) were modeled under similar conditions mentioned above. Proteomics of

cellular proteins and proteins secreted in the supernatant were carried out by LCMS. Data were input into the Bayesian Network Inference (BNI) algorithms REFS™.

Causal associations between proteins were derived by the BNI. Differential network analysis was employed to tease out the hubs of activity in prostate cancer when compared to normal cells in normal microenvironments. Filamin B was identified as differential hub of activity in PC3 and not in LnCap and normal cells. That is, Filamin B was found to differ between androgen sensitive LnCAP cell line and metastatic, androgen refractory PC3 cell line. This indicates that Filamin B could be useful to differentiate between prostate cancer states, e.g., between androgen sensitive and metastatic, androgen refractory prostate cancer. The interaction matrix placing filamin B at the center of an interaction hub is shown in Figure 4. The interaction of LY9 with filamin B is shown in Figure 5.

Example 3 – Validation of Filamin B as a Prostate Cancer Marker in Human Samples

Having identified filamin B as a prostate cancer marker using the platform technology, human serum samples from normal subjects and subjects with prostate cancer were used to confirm filamin B as a prostate cancer marker.

Specifically, human serum samples were procured from a commercial vendor that sources human serum. Twenty samples were from normal donors and 20 samples were from patients diagnosed with prostate cancer. Prostate cancer samples were from patients with different prognosis and aggressiveness of cancers reported. Clinical characteristics of the subjects are provided in the table.

	Prostate Cancer	Control Group
Median Age	61 (47-86)	58 (45-72)
Ethnicity		
Caucasian	75%	85%
African American	15%	10%
Hispanic	10%	5%
Tumor Stage		
Stage I	20%	
Stage II	35%	
Stage III	5%	

Stage IV	40%
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Commercially available ELISA tests for filamin B and PSA were procured from commercial source. The assays were performed using the manufactures' instructions. The results from the assay are shown in Figure 6. The results show the differential levels of FlnB and PSA in patients with a diagnosis for prostate cancer as compared to control subjects without prostate cancer.

As shown, both filamin B and PSA levels were elevated in serum samples from patients diagnosed with prostate cancer. The correlation between PSA and FlnB expression in serum samples is 0.20075, indicating a relatively low correlation between the variables. This demonstrates that filamin B and PSA are useful for the detection of prostate cancer in different subjects. These results demonstrate that filamin B is useful for the diagnosis of prostate cancer, and that filamin B is useful for improving the detection of prostate cancer by PSA. Additional samples can be analyzed to further refine the results.

Example 4 – Stratification of Subjects with Prostate Cancer using LY9

The same human serum samples used in Example 4 were further tested to detect the presence of LY9. A commercially available ELISA test for LY9 was procured from commercial source. The assay was performed using the manufactures' instructions. The results from the assay are shown in Figure 7. The results show the differential levels of LY9 in patients with a diagnosis for prostate cancer as compared to control subjects without prostate cancer. As shown, samples from subjects with prostate cancer were found to have higher levels of LY9 as compared to normal subjects. Results from assays of expression levels of both filamin B and LY9 in human serum with results expressed as ng/ml of protein are shown in Figure 8. Additional samples can be analyzed to further refine the results.

Example 5 – Analysis of Filamin B Levels Improves the Detection of Prostate Cancer as Compared to PSA Alone

Having demonstrated that level of filamin B is increased in the serum of subjects with prostate cancer, the results were analyzed in conjunction with the study of PSA levels in the same samples to determine the predictive value of filamin B and PSA together was better than either of the markers alone. Receiver operating characteristic (ROC) curve analysis of

sensitivity and false positive rate (FPR) of PSA, filamin B, and the combination of PSA and filamin B was generated. The curves and the area under the curve (AUC) values are shown in Figures 9A and B. The goal of this analysis is to gauge the predictive power of the test independent of a specific cut-off. When using an ROC analysis, a test that provides perfect discrimination or accuracy between normal and disease states would have $AUC=1$, whereas a very poor test that provides no better discrimination than random chance would have $AUC=0.5$.

As demonstrated by the analysis, filamin B alone performs very well and most importantly somewhat orthogonal to PSA. PSA is reported to have a very high false positive rate, e.g., about 75% (as reported in, Gilligan, The new data on prostate cancer screening: What should we do now? Cleveland Clin. J. Med. 76: 446-448, 2009, incorporated herein by reference). That is, it has a high sensitivity and low specificity. In the specific study presented, the AUC for FLNB is lower than that for PSA. However, the correlation level of 0.20075 determined in Example 3, indicates a relatively low correlation between the variables. That is, subjects identified as having an elevated filamin B level did not necessarily have a high PSA level, and the reverse was also true, suggesting that the markers in combination can provide a predictive test than either marker alone.

This was confirmed in the ROC analysis. As shown, the combination of PSA and filamin B was found to have a higher AUC indicating better discrimination of the test than PSA alone, and to be more predictive than either of the markers alone. The combination of PSA and filamin B is very good and provides a drastic increase PSA test specificity, which is the main problem with the test.

Example 6 – Analysis of Filamin B, LY9, and PSA Levels Together Improves the Detection of Prostate Cancer as Compared to any Marker Alone

Having demonstrated that each filamin B, LY9, and PSA are all elevated in serum samples from subjects with prostate cancer, the ROC curve analysis was performed comparing each of the three markers individually to the combination of all three markers using a linear scoring function, and comparing the combination of filamin B and LY9, and the combination of filamin B and PSA, against the combination of all three markers using a non-linear scoring function to determine which combinations of the markers were more effective than each single marker for the detection of prostate cancer in a subject. As shown,

the combination of all three markers was more predictive than any of the markers alone (Figure 10A). The combination of filamin B with PSA, either with or without LY9, was more predictive than the combination of filamin B with LY9 (Figure 10B). Additional samples can be analyzed to further refine the results. The AUC results are summarized in the table.

Marker	AUC
LY9	0.85
FLNB	0.78
PSA	0.87
LY9 + FLNB + PSA	0.98

Example 7 – Stratification of Subjects with Prostate Cancer using Keratin 4, Keratin 7, Keratin 8, Keratin 15, Keratin 18, Keratin 19, Tubulin-beta 3

As demonstrated in Examples 3 and 4 respectively, filamin B levels and LY9 levels can be used to distinguish subjects who are or are not suffering from prostate cancer. Further, as demonstrated in Examples 6 and 7, the analysis of both filamin B and PSA, optionally further in combination with LY9, is more sensitive than an analysis based on either marker alone.

A series of subject samples are obtained from an appropriate source, e.g., a commercial source, wherein the samples were obtained from subjects with different stages of prostate cancer, e.g., aggressive prostate cancer, androgen sensitive, androgen insensitive, metastatic; or from subjects not suffering from prostate cancer, e.g., subjects with normal prostate or subjects with BPH. The samples are analyzed for the expression level of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 15, and keratin 19; and optionally further at least one of filamin B, LY9, and PSA. The level of the expression of the makers, alone and in various combinations, correlate with the presence or absence of disease, and with the severity of prostate cancer. For example, an increase in the expression level of one or more of keratin 19, filamin B, LY9, and PSA, as compared to a normal sample from a subject not suffering from prostate cancer, is indicative of prostate cancer in the subject. Expression levels of

keratins 7, 8, and 15 may also be particularly useful in the stratification of subjects with prostate cancer.

Example 8 – Monitoring of Prostate Cancer Treatment using Keratin 4, Keratin 7, Keratin 8, Keratin 15, Keratin 18, Keratin 19, Tubulin-beta 3

At the time of diagnosis with prostate cancer, subjects are invited to participate in a trial. A subject sample, e.g., blood, is obtained. Periodically, throughout the monitoring, watchful waiting, or active treatment of the subject, e.g., chemotherapy, radiation therapy, surgery, hormone therapy, a new subject sample is obtained. At the end of the study, all subject samples are tested for the expression level of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 15, and keratin 19; and optionally further at least one of filamin B, LY9, and PSA. The subject samples are matched to the medical records of the subjects to correlate marker levels with prostate cancer status at the time of diagnosis, rate of progression of disease, response of subjects to one or more interventions, and transitions between androgen dependent and independent status. An increase in the expression level of one or more of keratin 19, filamin B, LY9, and PSA, as compared to a normal sample from a subject not suffering from prostate cancer, is indicative of prostate cancer in the subject. Expression levels of keratins 7, 8, and 15 may also be particularly useful in the diagnosis and monitoring of subjects with prostate cancer.

Example 9 – Detection and Monitoring of Prostate Cancer using keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3

Despite its limitations, including a positive predictive value of only 25-40%, PSA remains the only generally accepted biomarker for prostate cancer. Moreover, as prostate cancer is most commonly a slow growing tumor in men of advanced age, treatment of the cancer may do more harm to the subject than the tumor itself would. Therefore, the tests together for the expression level of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 15, and keratin 19; and optionally further at least one of filamin B, LY9, and PSA are used for the detection and monitoring of prostate cancer. The level of the expression of the markers, alone and in various combinations are used in detection, including in routine, preventative, screening methods in men having an increased risk of prostate cancer (e.g., increased age,

family history, race, etc.) or in monitoring of subjects diagnosed with prostate cancer prior to or during treatment may be useful to better identify subjects in need of further, potentially more invasive, diagnostic tests, e.g., prostate exam or biopsy, digital rectal exam; or more aggressive treatment. Detection of levels of expression of the markers, or various combinations thereof, may also be indicative of a good or poor response to a specific treatment regimen prior to changes in other signs or symptoms, e.g., loss of tumor response to hormone therapy.

In routine screening methods for prostate cancer, a serum sample from a subject is tested for the level of expression of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 15, and keratin 19; and optionally further at least one of filamin B, LY9, and PSA. The levels are compared to one or more appropriate controls, e.g., other normal subjects, subjects with prostate cancer. Detection of an abnormal level of one or more of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 8, keratin 15, and keratin 19; indicates that the subject should be considered for further tests for the presence of prostate cancer. Changes in the level of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 8, keratin 15, and keratin 19, in the subject may be more indicative of a change in prostate cancer status than comparison to a population control.

In determining a therapeutic regimen for a subject with prostate cancer not yet being actively treated for prostate cancer (i.e., watchful waiting) can be tested at regular intervals to determine if there is a change in the level of expression of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 15, and keratin 19; and optionally further at least one of filamin B, LY9, and PSA. An modulation in the level of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 8, keratin 15, and keratin 19; and optionally further at least one of filamin B, LY9, and PSA indicates that the subject should be considered for further tests to monitor the prostate cancer and more active therapeutic interventions should be considered.

In a subject undergoing treatment for prostate cancer (e.g., hormone therapy, chemotherapy, radiation therapy, surgery) is tested prior to the initiation of the treatment and during and/ or after the treatment to determine if the treatment results in a decrease in the

level of expression of at least one of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, tubulin-beta 3, preferably at least one of keratin 7, keratin 15, and keratin 19; and optionally further at least one of filamin B, LY9, and PSA. A decrease in the level of keratin 19, filamin B, LY9, or PSA is indicative of response to treatment. Expression levels of keratins 7, 8, and 15 may also be particularly useful in the diagnosis and monitoring of subjects with prostate cancer.

Example 10 – Stratification of Subjects with Prostate Cancer using Filamin B, PSA, or LY9

As demonstrated in Examples 3 and 4 respectively, filamin B levels and LY9 levels can be used to distinguish subjects who are or are not suffering from prostate cancer. Further, as demonstrated in Examples 6 and 7, the analysis of both filamin B and PSA, optionally further in combination with LY9, is more sensitive than an analysis based on either marker alone.

A series of subject samples are obtained from an appropriate source, e.g., a commercial source, wherein the samples were obtained from subjects with different stages of prostate cancer, e.g., aggressive prostate cancer, androgen sensitive, androgen insensitive, metastatic; or from subjects not suffering from prostate cancer, e.g., subjects with normal prostate or subjects with BPH. The samples are analyzed for the expression level of filamin B and PSA, and optionally the level of LY9, and further with one or more of keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, especially keratin 19. The level of filamin B, LY9, and PSA, alone and in various combinations, optionally with other markers, e.g., keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, especially keratin 19, correlate with the presence or absence of disease, and with the severity of prostate cancer.

Example 11 – Monitoring of Prostate Cancer Treatment using Filamin B, PSA, or LY9

At the time of diagnosis with prostate cancer, subjects are invited to participate in a trial. A subject sample, e.g., blood, is obtained. Periodically, throughout the monitoring, watchful waiting, or active treatment of the subject, e.g., chemotherapy, radiation therapy, surgery, hormone therapy, a new subject sample is obtained. At the end of the study, all subject samples are tested for the level of filamin B, PSA, and optionally in further combination with one or more of LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18,

keratin 19, and tubulin-beta 3. The subject samples are matched to the medical records of the subjects to correlate filamin B, PSA, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, or tubulin-beta 3 levels, as appropriate, with prostate cancer status at the time of diagnosis, rate of progression of disease, response of subjects to one or more interventions, and transitions between androgen dependent and independent status.

Example 12 – Detection and Monitoring of Prostate Cancer using Filamin B, PSA, or LY9

Despite its limitations, including a positive predictive value of only 25-40%, PSA remains the only generally accepted biomarker for prostate cancer. Moreover, as prostate cancer is most commonly a slow growing tumor in men of advanced age, treatment of the cancer may do more harm to the subject than the tumor itself would. As demonstrated herein, there is a low correlation between elevated levels of filamin B and PSA in subjects with prostate cancer. Further, elevated levels of LY9 have been demonstrated to be associated with prostate cancer. Therefore, the tests together, particularly filamin B and PSA, optionally in combination with one or more of LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, especially keratin 19, in detection, including in routine, preventative, screening methods in men having an increased risk of prostate cancer (e.g., increased age, family history, race, etc.) or in monitoring of subjects diagnosed with prostate cancer prior to or during treatment may be useful to better identify subjects in need of further, potentially more invasive, diagnostic tests, e.g., prostate exam or biopsy, digital rectal exam; or more aggressive treatment. Detection of levels of expression of filamin B, PSA, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, especially keratin 19, may also be indicative of a good or poor response to a specific treatment regimen prior to changes in other signs or symptoms, e.g., loss of tumor response to hormone therapy.

In routine screening methods for prostate cancer, a serum sample from a subject is tested for the level of expression of both filamin B and PSA, and optionally one or more of LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, especially keratin 19. The levels are compared to one or more appropriate controls, e.g., other normal subjects, subjects with prostate cancer. Detection of an abnormal level of one or more of filamin B, PSA, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3, especially keratin 19 indicates that the subject should be considered for further tests for the presence of prostate cancer. Changes in the level of filamin B,

optionally in combination with one or more of PSA, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, or tubulin-beta 3, especially keratin 19 with PSA in the subject may be more indicative of a change in prostate cancer status than comparison to a population control.

In determining a therapeutic regimen for a subject with prostate cancer not yet being actively treated for prostate cancer (i.e., watchful waiting) can be tested at regular intervals to determine if there is a change in the level of expression of filamin B, PSA, LY9 keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3. An increase in the level of filamin B, PSA, keratin 19, or LY9 indicates that the subject should be considered for further tests to monitor the prostate cancer and more active therapeutic interventions should be considered.

In a subject undergoing treatment for prostate cancer (e.g., hormone therapy, chemotherapy, radiation therapy, surgery) is tested prior to the initiation of the treatment and during and/ or after the treatment to determine if the treatment results in a change in the level of expression of one or more of filamin B, PSA, LY9, keratin 4, keratin 7, keratin 8, keratin 15, keratin 18, keratin 19, and tubulin-beta 3. A decrease in the level of filamin B, PSA, keratin 19, or LY9 is indicative of response to treatment.

Equivalents:

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

CLAIMS

1. A method for diagnosing prostate cancer in a subject comprising:
 - (1) determining a level of one or more prostate cancer related markers selected from the group consisting of filamin B, and keratin 19 in a biological sample from the subject; and
 - (2) comparing the level of the one or more prostate cancer related markers in the biological sample with the level of the one or more prostate cancer related markers in a non-cancer control sample, wherein an increased level of the one or more prostate cancer related markers in the biological sample relative to the non-cancer control sample is indicative of prostate cancer in the subject.
2. The method of claim 1, wherein no increase in the detected level of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B and keratin 19 in the biological sample relative to the non-cancer control sample is indicative of a normal prostate state in the subject.
3. The method of claim 1 or claim 2, further comprising detecting the level of prostate specific antigen (PSA) in the biological sample.
4. The method of claim 3, further comprising comparing the level of PSA in the biological sample to the level of PSA in a non-cancer control sample.
5. The method of claim 4, wherein an increase in the level of one or more prostate cancer related markers selected from the group consisting of filamin B and keratin 19 in the biological sample relative to the non-cancer control sample, in combination with an increase in the level of PSA in the biological sample relative to the level of PSA in the non-cancer control sample is indicative of prostate cancer in the subject.
6. The method of claim 5, wherein no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B and keratin 19 in the biological sample relative to the non-cancer control sample, in combination with a decreased or normal level of PSA in the biological sample as compared to

the level of PSA in the non-cancer control sample, is indicative of a normal prostate state in the subject.

7. The method of any one of claims 1-6, wherein the one or more prostate cancer markers selected from the group consisting of filamin B and keratin 19 is: filamin B; keratin 19; or filamin B and keratin 19.
8. The method of claim 1, wherein the prostate cancer is androgen-dependent prostate cancer.
9. The method of claim 1, wherein the prostate cancer is androgen-independent prostate cancer.
10. The method of claim 1, wherein the prostate cancer is aggressive prostate cancer.
11. The method of claim 1, wherein the prostate cancer is non-aggressive prostate cancer.
12. A method for identifying a subject as being at increased risk for developing prostate cancer, the method comprising:
 - (1) determining a level of one or more prostate cancer related markers selected from the group consisting of filamin B and keratin 19 in a biological sample from the subject; and
 - (2) comparing the level of the one or more prostate cancer related markers in the biological sample with the level of the one or more prostate cancer related markers in a non-cancer control sample, wherein an increased-level of the one or more prostate cancer related markers in the biological sample relative to the non-cancer control sample is indicative of an increased risk for developing prostate cancer in the subject.
13. The method of claim 12, wherein no increase in the detected level of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B and keratin 19 in the biological sample relative to the non-cancer control sample is indicative of no increased risk for developing prostate cancer in the subject.
14. The method of claim 12 or claim 13, further comprising detecting the level of prostate specific antigen (PSA) in the biological sample.

15. The method of claim 14, further comprising comparing the level of PSA in the biological sample to the level of PSA in a non-cancer control sample.

16. The method of claim 15, wherein an increase in the level of one or more prostate cancer related markers selected from the group consisting of filamin B and keratin 19 in the biological sample relative to the non-cancer control sample, in combination with an increase in the level of PSA in the biological sample as compared to the level of PSA in the non-cancer control sample is indicative of an increased risk for developing prostate cancer in the subject.

17. The method of claim 15, wherein no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B, and keratin 19 in the biological sample relative to the non-cancer control sample, in combination with a decreased or non-cancer level of PSA in the biological sample as compared to the level of PSA in the non-cancer control sample, is indicative of no increased risk for developing prostate cancer in the subject.

18. The method of any one of claims 11-17, wherein the one or more prostate cancer related markers selected from the group consisting of filamin B and keratin 19 is: filamin B; keratin 19; or filamin B and keratin 19.

19. The method of any one of the preceding claims, further comprising comparing the level of the one or more prostate cancer related markers in the biological sample with the level of the one or more prostate cancer related markers in a control sample selected from the group consisting of: a sample obtained from the same subject at an earlier time point than the biological sample, a sample from a subject with benign prostatic hyperplasia (BPH), a sample from a subject with non-metastatic prostate cancer, a sample from a subject with metastatic prostate cancer, a sample from a subject with androgen sensitive prostate cancer, a sample from a subject with androgen insensitive prostate cancer, a sample from a subject with aggressive prostate cancer, and a sample from a subject with non-aggressive prostate cancer.

20. The method of any one of claims 1-11, wherein the method further comprises selecting a subject who has or is suspected of having prostate cancer.

21. The method of any one of claims 1, 3-5, and 7-11, wherein the method further comprises selecting a treatment regimen for the subject based on the level of the one or more prostate cancer markers.

22. The method of any one of claims 1, 3-5, and 7-11, wherein the method further comprises selection of a treatment regimen comprising one or more treatments selected from the group consisting of surgery, radiation, hormone therapy, antibody therapy, growth factor therapy, cytokine therapy, and chemotherapy.

23. A method for monitoring prostate cancer in a subject, the method comprising

(1) determining a level of one or more prostate cancer related markers selected from the group consisting of filamin B and keratin 19 in a first biological sample obtained at a first time from a subject having prostate cancer;

(2) determining a level of expression of the one or more prostate cancer related markers in a second biological sample obtained from the subject at a second time, wherein the second time is later than the first time; and

(3) comparing the level of the one or more prostate cancer related markers in the second sample with the level of the one or more prostate cancer related markers in the first sample, wherein an increase in the level of the one or more prostate cancer related markers in the second sample as compared to the first sample is indicative of progression of the prostate cancer in the subject.

24. The method of claim 23, wherein the subject is actively treated for prostate cancer prior to obtaining the second sample.

25. The method of claim 23, wherein the subject is not actively treated for prostate cancer prior to obtaining the second sample.

26. The method of any of claims 23-25, wherein no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B and keratin 19 in the second biological sample as compared to the first biological sample is indicative of non-progression of the prostate cancer in the subject.

27. The method of any one of claims 23-25, further comprising determining the level of prostate specific antigen (PSA) in the first biological sample and the second biological sample.

28. The method of claim 27, further comprising comparing the level of PSA in the second biological sample to the level of PSA in the first biological sample.

29. The method of claim 28, wherein an increased level of the one or more prostate cancer related markers selected from the group consisting of filamin B, and keratin 19 in the second biological sample relative to the level of the one or more prostate cancer related markers in the first biological sample, in combination with an increase in the level of PSA in the second biological sample relative to the level of PSA in the first biological sample, is indicative of progression of the prostate cancer in the subject.

30. The method of claim 28, wherein no increase in the detected level of expression of each of the one or more prostate-cancer related markers selected from the group consisting of filamin B and keratin 19 in the second biological sample relative to the level of the one or more prostate cancer related markers in the first biological sample, in combination with a decreased or same level of PSA in the second biological sample relative to the level of PSA in the first biological sample, is indicative of non-progression of the prostate cancer in the subject.

31. The method of any one of claims 23-30, further comprising determining the level of prostate specific antigen (PSA) in the first biological sample and the second biological sample.

32. The method of claim 31, further comprising comparing the level of PSA in the second biological sample to the level of PSA in the first biological sample.

33. The method of any one of claims 23-32, further comprising comparing the level of the one or more prostate cancer related markers in the first biological sample or the second biological sample with the level of the one or more prostate cancer related markers in a control sample selected from the group consisting of: a non-cancer control sample, a sample from a subject with benign prostatic hyperplasia (BPH), a sample from a subject with non-metastatic prostate cancer, a sample from a subject with metastatic prostate cancer, a sample from a subject with androgen sensitive prostate cancer, a sample from a subject with androgen insensitive prostate cancer, a sample from a subject with aggressive prostate cancer, and a sample from a subject with non-aggressive prostate cancer.

34. The method of claim 26, wherein the method further comprises withholding an active treatment of the prostate cancer in the subject based on non-progression of the prostate cancer in the subject.

35. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises isolating a component of the biological sample.

36. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises labeling a component of the biological sample.

37. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises processing the biological sample.

38. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises contacting a prostate cancer related marker to be detected with a prostate cancer related marker binding agent.

39. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises forming a complex between a prostate cancer related marker to be detected and a prostate cancer related marker binding agent.

40. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises contacting each of the one or more prostate cancer related markers with a prostate cancer related marker binding agent.

41. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises forming a complex between each of the one or more prostate cancer related markers and a prostate cancer related marker binding agent.

42. The method of any one of the preceding claims, wherein detecting or determining a level of one or more prostate cancer related markers in a biological sample comprises attaching a prostate cancer related marker to be detected to a solid surface.

43. Use of a panel of reagents for the diagnosis of prostate cancer, the panel comprising at least two detection reagents selected from the group consisting of: a detection reagent specific for the detection of filamin B, a detection reagent specific for the detection of LY9, and a detection reagent specific for the detection of keratin 19.

44. The use of claim 43 in the method of anyone of claims 1-42.

45. Use of a kit for the diagnosis of prostate cancer, the kit comprising at least two detection reagents selected from the group consisting of: a detection reagent specific for the detection of filamin B, a detection reagent specific for the detection of LY9, and a detection reagent specific for the detection of keratin 19.

46. The use of claim 45, further comprising at least one detection reagent specific for the detection of PSA.