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(72) **Inventeurs/Inventors:**
DONOVAN, MICHAEL, US;
KHAN, FAISAL, US;
ALTER, JASON, US;
FERNANDEZ, GERARDO, US;
MESA-TEJADA, RICARDO, US;
POWELL, DOUGLAS A., US;
...

(73) **Propriétaire/Owner:**

(54) **Titre : SYSTEMES ET PROCEDES DE TRAITEMENT, DE DIAGNOSTIC ET DE PREDICTION DE LA SURVENUE D'UN ETAT PATHOLOGIQUE**
(54) **Title: SYSTEMS AND METHODS FOR TREATING, DIAGNOSING AND PREDICTING THE OCCURRENCE OF A MEDICAL CONDITION**

Example 2: Features Selected for Prediction of Favorable
Pathological Stage (Indolent Disease)

Feature	Univariate P Value	Weight in Model
<u>Clinical</u>		
Preoperative PSA	<0.001	-4.232
Biopsy Gleason Score	<0.001	-2.0031
<u>Molecular (Combined)</u>		
Combined AR Dynamic Range at Low bGG, Total Ki67 at High bGG	<0.001	-0.3375
<u>Morphometric</u>		
Area of Epithelial Nuclei Outside Gland Units to Area of Epithelial Nuclei Within Gland Units	<0.001	-6.3303
Area of Epithelial Nuclei Distributed Away From Gland Units	<0.001	-0.8374

(57) **Abrégé/Abstract:**

Clinical information, molecular information and/or computer-generated morphometric information is used in a predictive model for predicting the occurrence of a medical condition. In an embodiment, a model predicts whether a patient is likely to have a favorable pathological stage of prostate cancer, where the model is based on features including one or more (e.g., all) of preoperative PSA, Gleason Score, a measurement of expression of androgen receptor (AR) in epithelial and stromal nuclei and/or a measurement of expression of Ki67-positive epithelial nuclei, a morphometric measurement of a ratio of area of epithelial nuclei outside gland units to area of epithelial nuclei within gland units, and a morphometric measurement of area of epithelial nuclei distributed away from gland units. In some embodiments, quantitative measurements of protein expression in cell lines are utilized to objectively assess assay (e.g., multiplex immunofluorescence (IF)) performance and/or to normalize features for use within a predictive model.

(72) **Inventeurs(suite)/Inventors(continued):** BAYER ZUBEK, VALENTINA, US; HAMANN, STEFAN, US;
CARDON-CARDO, CARLOS, US; COSTA, JOSE, US

(73) **Propriétaires(suite)/Owners(continued):**
FUNDACAO D. ANNA SOMMER CHAMPALIMAUD E DR. CARLOS MONTEZ CHAMPALIMAUD, PT

(74) **Agent:** RIDOUT & MAYBEE LLP

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Filed on 25 July 2008 (25.07.2008)(71) Applicant (for all designated States except US): **AURE-ON LABORATORIES, INC.** [US/US]; 28 Wells Avenue, Yonkers, NY 10701 (US).(72) Inventors; and
(75) Inventors/Applicants (for US only): **DONOVAN, Michael** [US/US]; 10 Museum Way, Cambridge, MA 02110 (US). **KHAN, Faisal** [PK/US]; 931 Huntington Drive, Fishkill, NY 12524 (US). **ALTER, Jason** [US/US]; 17 Cousins Road, Stamford, CT 06903 (US). **FERNANDEZ, Gerardo** [US/US]; 875 Old Granite Springs Rd., Yorktown Heights, NY 10598 (US). **MESA-TEJADA, Ricardo** [US/US]; 7 Greenmeadow Rd., Pleasantville, NY 10570 (US). **POWELL, Douglas, A.** [US/US]; 1078 Midland Avenue, #2, Bronxville, NY 10708 (US). **BAYER ZUBEK, Valentina** [US/US]; 25 Jody Lane, Yonkers, NY 10701 (US). **HAMANN, Stefan** [US/US]; 100 New Roc City Place, New Rochelle, NY 02110 (US). **CORDON-CARDO, Carlos** [US/US]; 860 UN Plaza, Apt. 14F, New York, NY 10017 (US). **COSTA, Jose** [US/US]; 20 Old Quarry Rd., Guilford, CT 06437 (US).

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(54) Title: SYSTEMS AND METHODS FOR TREATING, DIAGNOSING AND PREDICTING THE OCCURRENCE OF A MEDICAL CONDITION

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FIG. 17

(57) Abstract: Clinical information, molecular information and/or computer-generated morphometric information is used in a predictive model for predicting the occurrence of a medical condition. In an embodiment, a model predicts whether a patient is likely to have a favorable pathological stage of prostate cancer, where the model is based on features including one or more (e.g., all) of preoperative PSA, Gleason Score, a measurement of expression of androgen receptor (AR) in epithelial and stromal nuclei and/or a measurement of expression of Ki67-positive epithelial nuclei, a morphometric measurement of a ratio of area of epithelial nuclei outside gland units to area of epithelial nuclei within gland units, and a morphometric measurement of area of epithelial nuclei distributed away from gland units. In some embodiments, quantitative measurements of protein expression in cell lines are utilized to objectively assess assay (e.g., multiplex immunofluorescence (IF)) performance and/or to normalize features for use within a predictive model.



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(74) **Agents:** GERVASE, Richard, G. et al.; Mintz, Levin, Cohn, Ferris, Glovsky & Popeo, P.C., Chrysler Center, 666 Third Avenue, New York, NY 10017 (US).

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SYSTEMS AND METHODS FOR TREATING, DIAGNOSING AND PREDICTING THE OCCURRENCE OF A MEDICAL CONDITION

FIELD OF THE INVENTION

[0002] Embodiments of the present invention relate to methods and systems for predicting the occurrence of a medical condition such as, for example, the presence, indolence, recurrence, or progression of disease (e.g., cancer), responsiveness or unresponsiveness to a treatment for the medical condition, or other outcome with respect to the medical condition. For example, in some embodiments of the present invention, systems and methods are provided that use clinical information, molecular information, and/or computer-generated morphometric information in a predictive model that predicts whether a patient is likely to have a favorable pathological stage (indolent disease) if the patient were to undergo a treatment (e.g., radical prostatectomy) for the disease. In some embodiments, a predictive model is provided that predicts the risk of disease progression in a patient. The morphometric information used in a predictive model according to some embodiments of the present invention may be generated based on image analysis of tissue (e.g., tissue subject to multiplex immunofluorescence (IF)) and may include morphometric information pertaining to a minimum spanning tree (MST) and/or a fractal dimension (FD) observed in the tissue or images of such tissue. In some embodiments, quantitative measurements of protein expression in cell lines are utilized, for example, to objectively assess the performance of an assay (e.g., multiplex IF assay) and/or to normalize measurements derived from the assay prior to inclusion of such features within model development or evaluation of such features with a final predictive model.

BACKGROUND OF THE INVENTION

[0003] Physicians are required to make many medical decisions ranging from, for example, whether and when a patient is likely to experience a medical condition to how a patient should be treated once the patient has been diagnosed with the condition. Determining an appropriate course of treatment for a patient may increase the patient's chances for, for example, survival, recovery, and/or improved quality of life. Predicting the occurrence of an event also allows individuals to plan for the event. For example, predicting whether a patient is likely to experience occurrence (e.g., presence, recurrence, or progression) of a disease may allow a physician to recommend an appropriate course of treatment for that patient.

[0004] When a patient is diagnosed with a medical condition, deciding on the most appropriate therapy is often confusing for the patient and the physician, especially when no single option has been identified as superior for overall survival and quality of life. Traditionally, physicians rely heavily on their expertise and training to treat, diagnose and predict the occurrence of medical conditions. For example, pathologists use the Gleason scoring system to evaluate the level of advancement and aggression of prostate cancer, in which cancer is graded based on the appearance of prostate tissue under a microscope as perceived by a physician. Higher Gleason scores are given to samples of prostate tissue that are more undifferentiated. Although Gleason grading is widely considered by pathologists to be reliable, it is a subjective scoring system. Particularly, different pathologists viewing the same tissue samples may make conflicting interpretations.

[0005] Current preoperative predictive tools have limited utility for the majority of contemporary patients diagnosed with organ-confined and/or intermediate risk disease. For example, prostate cancer remains the most commonly diagnosed non-skin cancer in American men and causes approximately 29,000 deaths each year [1]. Treatment options include radical prostatectomy, radiotherapy, and watchful waiting; there is, however, no consensus on the best therapy for maximizing disease control and survival without over-treating, especially for men with intermediate-risk prostate cancer (prostate-specific antigen 10-20 ng/mL, clinical stage T2b-c, and Gleason score 7). The only completed, randomized clinical study has demonstrated lower rates of overall death in men with T1 or T2 disease treated with radical prostatectomy; however,

the results must be weighed against quality-of-life issues and co-morbidities [2, 3]. It is fairly well accepted that aggressive prostate-specific antigen (PSA) screening efforts have hindered the general utility of more traditional prognostic models due to several factors including an increased (over-diagnosis) of indolent tumors, lead time (clinical presentation), grade inflation and a longer life expectancy [4-7]. As a result, the reported likelihood of dying from prostate cancer 15 years after diagnosis by means of prostate-specific antigen (PSA) screening is lower than the predicted likelihood of dying from a cancer diagnosed clinically a decade or more ago further confounding the treatment decision process [8].

[0006] Several groups have developed methods to predict prostate cancer outcomes based on information accumulated at the time of diagnosis. The recently updated Partin tables [9] predict risk of having a particular pathologic stage (extracapsular extension, seminal vesicle invasion, and lymph node invasion), while the 10-year preoperative nomogram [10] provides a probability of being free of biochemical recurrence within 10 years after radical prostatectomy. These approaches have been challenged due to their lack of diverse biomarkers (other than PSA), and the inability to accurately stratify patients with clinical features of intermediate risk. Since these tools rely on subjective clinical parameters, in particular the Gleason grade which is prone to disagreement and potential error, having more objective measures would be advantageous for treatment planning. Furthermore, biochemical or PSA recurrence alone generally is not a reliable predictor of clinically significant disease [11]. Thus, it is believed by the present inventors that additional variables or endpoints are required for optimal patient counseling.

[0007] Another issue is unnecessary treatment for disease. For example, a man with a truly indolent tumor, typically understood to mean a tumor that is not likely to progress, who is misclassified as having a nonindolent tumor can be subjected to treatments that potentially carry severe side effects. Thus, the need for accurate predictive models for indolent disease status is crucial. Traditionally, research regarding indolent tumors has addressed only standard clinical features. Kattan et al. reported that in a sample of 409 patients, about 20% had indolent cancer [56]. The Kattan predictive nomograms incorporated biopsy Gleason grade, clinical stage and pre-treatment PSA along with the amount of tumor in the biopsy specimen. The reported predictive power of the nomograms ranged from an AUC of 0.64 for the ROC curve to an AUC

of 0.79. Gibod et al., while identifying 29% of patients as having “insignificant cancer,” reported that no specific feature in their study could identify the indolent patients prior to surgery [57]. Gofrit et al. studied cases of “Gleason score upgrades,” where the patient has a biopsy Gleason score of 6 but is actually harboring a more aggressive tumor. It was suggested that both preoperation PSA levels and the greatest percent cancer in a core (GPC) can predict the phenomenon of Gleason score upgrade by employing decision tree methodology [58]. The reported overall accuracy was about 62%.

[0008] Ochiai et al. also purported to predict so-called “insignificant cancer” by using the number of positive biopsy cores, tumor length in a core, Gleason score and prostate volume in a multiple logistic regression model. The reported sensitivity and specificity was about 84% and 62%, respectively [59]. Similar results were reported in another study by Ochiai and associates [60]. Romelling et al. updated the Kattan nomogram and reported in a study of 432 cancer patients that 27% were classified as having indolent tumors [61]. The percentage of patients reported to have indolent tumors was typically in the 20-30% range in the studies that have been cited. It is believed by the present inventors that a more accurate, stable and comprehensive approach to predicting whether or not a disease (e.g., cancer) is indolent is needed.

[0009] In view of the foregoing, it would be desirable to provide systems and methods for treating, diagnosing and predicting the occurrence of medical conditions, responses, and other medical phenomena with improved predictive power. For example, it would be desirable to provide systems and methods for predicting the likelihood that a disease (e.g., cancer) is indolent and/or a risk of disease progression at, for example, the time of diagnosis prior to treatment for the disease.

SUMMARY OF THE INVENTION

[0010] Embodiments of the present invention provide automated systems and methods for predicting the occurrence of medical conditions. As used herein, predicting an occurrence of a medical condition may include, for example, predicting whether and/or when a patient will experience an occurrence (e.g., presence, recurrence or progression) of disease such as cancer, predicting whether a patient is likely to respond to one or more therapies (e.g., a new pharmaceutical drug), or predicting any other suitable outcome with respect to the medical

condition. Predictions by embodiments of the present invention may be used by physicians or other individuals, for example, to select an appropriate course of treatment for a patient, diagnose a medical condition in the patient, and/or predict the risk of disease progression in the patient.

[0011] In some embodiments of the present invention, systems, apparatuses, methods, and computer readable media are provided that use clinical information, molecular information and/or computer-generated morphometric information in a predictive model for predicting the occurrence of a medical condition. For example, a predictive model according to some embodiments of the present invention may be provided which is based on one or more of the features listed in Tables 1-5 and 9 and Figures 9, 11, and 17 and/or other features.

[0012] For example, in an embodiment, a predictive model is provided that predicts the likelihood of a favorable pathological stage (indolence) of prostate cancer in a patient, where the model is based on one or more (e.g., all) of the features listed in Figure 17 and optionally other features. For example, the predictive model may be based on features including one or more (e.g., all) of preoperative PSA, Gleason Score, at least one of a measurement of expression of androgen receptor (AR) in epithelial nuclei and/or stromal nuclei and a measurement of expression of Ki67-positive epithelial nuclei, a morphometric measurement of a ratio of area of epithelial nuclei outside gland units to area of epithelial nuclei within gland units, and a morphometric measurement of area of epithelial nuclei distributed away from gland units. In some embodiments, the Gleason Score comprises a biopsy Gleason Score.

[0013] In another embodiment, a predictive model is provided predicts a risk of prostate cancer progression in a patient, where the model is based on one or more (e.g., all) of the features listed in Figure 11 and optionally other features. For example, the predictive model may be based on features including one or more (e.g., all) of preoperative PSA, dominant Gleason Grade, Gleason Score, at least one of a measurement of expression of AR in epithelial and/or stromal nuclei (e.g., tumor epithelial and/or stromal nuclei) and a measurement of expression of Ki67-positive epithelial nuclei (e.g., tumor epithelial nuclei), a morphometric measurement of average edge length in the minimum spanning tree (MST) of epithelial nuclei, and a morphometric measurement of area of non-lumen associated epithelial cells relative to total tumor area. In

some embodiments, the dominant Gleason Grade comprises a dominant biopsy Gleason Grade. In some embodiments, the Gleason Score comprises a biopsy Gleason Score.

[0014] In some embodiments of the present invention, two or more features (e.g., clinical, molecular, and/or morphometric features) may be combined in order to construct a combined feature for evaluation within a predictive model. For example, in the embodiments of predictive models predictive of favorable pathological stage (indolent disease) and prostate cancer progression described above, the measurement of the expression of androgen receptor (AR) in nuclei (e.g., epithelial and/or stromal nuclei) may form a combined feature with the measurement of the expression of Ki67-positive epithelial nuclei. When a dominant Gleason Grade for the patient is less than or equal to 3, the predictive model may evaluate for the combined feature the measurement of the expression of androgen receptor (AR) in epithelial and stromal nuclei. Conversely, when the dominant Gleason Grade for the patient is 4 or 5, the predictive model may evaluate for the combined feature the measurement of the expression of Ki67-positive epithelial nuclei.

[0015] Additional examples of combined features according to some embodiments of the present invention are described below in connection with, for example, Figure 9. For example, in the embodiment of a predictive model predictive of prostate cancer progression described above, the morphometric measurement of average edge length in the minimum spanning tree (MST) of epithelial nuclei may form a combined feature with dominant Gleason Grade. When the dominant Gleason Grade for the patient is less than or equal to 3, the predictive model may evaluate for the combined feature the measurement of average edge length in the minimum spanning tree (MST) of epithelial nuclei. Conversely, when the dominant Gleason Grade for the patient is 4 or 5, the predictive model may evaluate the dominant Gleason Grade for the combined feature.

[0016] In some embodiments of the present invention, a model is provided which is predictive of an outcome with respect to a medical condition (e.g., presence, recurrence, or progression of the medical condition), where the model is based on one or more computer-generated morphometric features generated from one or more images of tissue subject to multiplex immunofluorescence (IF). For example, due to highly specific identification of molecular

components and consequent accurate delineation of tissue compartments attendant to multiplex IF (e.g., as compared to the stains used in light microscopy), multiplex IF microscopy may provide the advantage of more reliable and accurate image segmentation. The model may be configured to receive a patient dataset for the patient, and evaluate the patient dataset according to the model to produce a value indicative of the patient's risk of occurrence of the outcome. In some embodiments, the predictive model may also be based on one or more other morphometric features, one or more clinical features, and/or one or more molecular features.

[0017] For example, in some embodiments of the present invention, the predictive model may be based on one or more computer-generated morphometric feature(s) including one or more measurements of the minimum spanning tree (MST) (e.g., the MST of epithelial nuclei) identified in the one or more images of tissue subject to multiplex immunofluorescence (IF). For example, the one or more measurements of the minimum spanning tree (MST) may include the average edge length in the MST of epithelial nuclei. Other measurements of the MST according to some embodiments of the present invention are described below in connection with, for example, Figure 9.

[0018] In some embodiments of the present invention, the predictive model may be based on one or more computer-generated morphometric feature(s) including one or more measurements of the fractal dimension (FD) (e.g., the FD of one or more glands) measured in the one or more images of tissue subject to multiplex immunofluorescence (IF). For example, the one or more measurements of the fractal dimension (FD) may include one or more measurements of the fractal dimension of gland boundaries between glands and stroma. In another example, the one or more measurements of the fractal dimension (FD) may include one or more measurements of the fractal dimension of gland boundaries between glands and stroma and between glands and lumen.

[0019] In an aspect of embodiments of the present invention, systems and methods are provided for segmenting and classifying objects in images of tissue subject to multiplex immunofluorescence (IF). For example, such segmentation and classification may include initial segmentation into primitives, classification of primitives into nuclei, cytoplasm, and background,

and refinement of the classified primitives to obtain the final segmentation, in the manner described below in connection with Figure 6.

[0020] In some embodiments, an apparatus is provided for identifying objects of interest in images of tissue, where the apparatus includes an image analysis tool configured to segment a tissue image into pathological objects comprising glands. Starting with lumens in the tissue image identified as seeds, the image analysis tool is configured to perform controlled region growing on the image including initiating growth around the lumen seeds in the tissue image thus encompassing epithelial cells identified in the image through the growth. The image analysis tool continues growth of each gland around each lumen seed so long as the area of each successive growth ring is larger than the area of the preceding growth ring. The image analysis tool discontinues the growth of the gland when the area of a growth ring is less than the area of the preceding growth ring for the gland. For example, in the embodiment of a model predictive of favorable pathological stage (indolent disease) described above, the measurement of the ratio of the area of epithelial nuclei outside gland units to the area of epithelial nuclei within gland units may be determined, at least in part, based on the identification and segmentation of gland units performed by the image analysis tool.

[0021] In some embodiments, an apparatus is provided for measuring the expression of one or more biomarkers in images of tissue subject to immunofluorescence (IF), where the apparatus includes an image analysis tool configured to measure within an IF image of tissue the intensity of a biomarker (e.g., AR) as expressed within a particular type of pathological object (e.g., epithelial nuclei). Specifically, a plurality of percentiles of the intensity of the biomarker as expressed within the particular type of pathological object are determined. The image analysis tool identifies one of the plurality of percentiles as the percentile corresponding to a positive level of the biomarker in the pathological object. For example, the image analysis tool may identify the percentile corresponding to a positive level of the biomarker based at least in part on an intensity in a percentile of another pathological object (e.g., stroma nuclei). In some embodiments, the image analysis tool is further configured to measure one or more features from the image of tissue, wherein the one or more features includes a difference of intensities of the percentile values (e.g., percentiles 90 and 10 of AR in epithelial nuclei). For example, the

one or more features may include a difference of intensities of the percentile values normalized by an image threshold or another difference in intensities of percentile values (e.g., percentiles 90 and 10 in stroma nuclei).

[0022] In some embodiments, an apparatus is provided for identifying objects of interest in images of tissue, where the apparatus includes an image analysis tool configured to detect the presence of CD34 in an image of tissue subject to immunofluorescence (IF). Based on the detection, the image analysis tool is further configured to detect and segment blood vessels which are in proximity to the CD34.

[0023] In another embodiment of the present invention, a predictive model is provided that predicts a likelihood of responsiveness in a patient to a hormonal therapy for prostate cancer, where the model is based on one or more (e.g., all) of the features listed in Figure 18 and optionally other features. For example, the predictive model may be based on features including one or more (e.g., all) of androgen receptor (AR) area in AMACR-positive tumor epithelial cells, dynamic range of AR intensity in tumor epithelial cells, and median lumen area.

[0024] In yet another embodiment of the present invention, a predictive model is provided that predicts a time to prostate cancer specific mortality (PCSM) for a patient, where the model is based on one or more (e.g., all) of the features listed in Table 14 and/or described in connection with Figure 21 and optionally other features. For example, the predictive model may be based on features including a measurement of a level of nuclear androgen receptor (AR) expression in a prostate cancer tissue specimen obtained from the patient prior to treatment for prostate cancer.

[0025] In another aspect of embodiments of the present invention, apparatuses and methods are provided that utilize quantitative measurements of protein expression in cell lines, for example, to objectively assess the performance of an assay (e.g., multiplex IF assay) and/or to normalize measurements derived from the assay prior to inclusion of such features within model development or evaluation of such features with a final predictive model. For example, in some embodiments, a method for performing a multiplex immunofluorescence assay includes subjecting cell lines known to express high and/or low levels of a protein under consideration to a multiplex immunofluorescence (IF) assay to establish baseline level(s) of such expression of the protein in the cell lines. Subsequently, the cell lines are subject to the same multiplex IF

assay simultaneously with tissue and/or isolated cells for one or more patients under consideration. Then, an image analysis tool is used to measure one or more measurements of the expression of the protein in the cells lines (i.e., the cell lines which were subject to the multiplex IF assay simultaneously with the tissue and/or isolated cells for the patient(s) under consideration). Based on a comparison of the measurement(s) with the baseline expression levels, it is determined whether the multiplex IF assay performed simultaneously on the cell lines and the tissue and/or isolated cells has produced reliable results.

[0026] For example, in some embodiments, results from the multiplex IF assay performed simultaneously on the cell lines and the tissue and/or isolated cells are disregarded when the comparison indicates a difference in (i) the one or more measurements and (ii) the baseline levels of expression of the protein in the cell lines. In some embodiments, the tissue and/or isolated cells for the one or more patients under consideration are re-subjected to the multiplex IF assay when the comparison indicates such a difference.

[0027] In some embodiments, subsequent to the multiplex IF assay, an image analysis tool is used to measure one or more measurements of protein expression from the tissue and/or isolated cells (or one or more images thereof) for the one or more patients under consideration. These measurement(s) are then normalized based on at least one of the baseline levels of expression of the protein in the cell lines, the one or more measurements of the expression of the protein in the cells lines, one or more other measurements relating to the cell lines, or a combination thereof. In some embodiments, the normalized measurement(s) are then used to generate a predictive model and/or to evaluate the corresponding patient's risk with a final predictive model.

[0028] In another aspect of embodiments of the present invention, systems and methods are provided in which data for a patient is measured at each of a plurality of points in time and evaluated by a predictive model of the present invention. A diagnosis or treatment of the patient may be based on a comparison of the results from each evaluation. Such a comparison may be summarized in, for example, a report output by a computer for use by a physician or other individual. For example, systems and methods may be provided for screening for an inhibitor compound of a medical condition. A first dataset for a patient may be evaluated by a predictive model, where the model is based on clinical data, molecular data, and computer-generated

morphometric data. A test compound may be administered to the patient. Following administering of the test compound, a second dataset may be obtained from the patient and evaluated by the predictive model. The results of the evaluation of the first dataset may be compared to the results of the evaluation from the second dataset. A change in the results for the second dataset with respect to the first dataset may indicate that the test compound is an inhibitor compound.

[0029] In still another aspect of embodiments of the present invention, a test kit is provided for treating, diagnosing and/or predicting the occurrence of a medical condition. Such a test kit may be situated in a hospital, other medical facility, or any other suitable location. The test kit may receive data for a patient (e.g., including clinical data, molecular data, and/or computer-generated morphometric data), compare the patient's data to a predictive model (e.g., programmed in memory of the test kit) and output the results of the comparison. In some embodiments, the molecular data and/or the computer-generated morphometric data may be at least partially generated by the test kit. For example, the molecular data may be generated by an analytical approach subsequent to receipt of a tissue sample for a patient. The morphometric data may be generated by segmenting an electronic image of the tissue sample into one or more objects, classifying the one or more objects into one or more object classes (e.g., epithelial nuclei, epithelial cytoplasm, stroma, lumen, red blood cells, etc.), and determining the morphometric data by taking one or more measurements for the one or more object classes. In some embodiments, the test kit may include an input for receiving, for example, updates to the predictive model. In some embodiments, the test kit may include an output for, for example, transmitting data, such as data useful for patient billing and/or tracking of usage, to another device or location.

BRIEF DESCRIPTION OF THE DRAWINGS

[0030] For a better understanding of embodiments of the present invention, reference is made to the following detailed description, taken in conjunction with the accompanying drawings, in which like reference characters refer to like parts throughout, and in which:

[0031] Figures 1A and 1B are block diagrams of systems that use a predictive model to treat, diagnose or predict the occurrence of a medical condition according to some embodiments of the present invention;

[0032] Figure 1C is a block diagram of a system for generating a predictive model according to some embodiments of the present invention;

[0033] Figure 2 is a graph illustrating the probability that a patient will experience an outcome with respect to a medical condition (e.g., disease progression) as indicated by the value or score output by a predictive model according to some embodiments of the present invention;

[0034] Figure 3 is a flowchart of illustrative stages involved in image segmentation and object classification in, for example, digitized images of H&E-stained tissue according to some embodiments of the present invention;

[0035] Figure 4A is an image of prostate tissue obtained via a needle biopsy and subject to staining with hematoxylin and eosin (H&E) according to some embodiments of the present invention;

[0036] Figure 4B is a segmented and classified version of the image in Figure 4A according to some embodiments of the present invention, in which gland unit objects are formed from seed lumen, epithelial nuclei, and epithelial cytoplasm, and in which isolated/non-gland-associated tumor epithelial cells are also identified in the image;

[0037] Figure 5A is an image of tissue subject to multiplex immunofluorescence (IF) in accordance with some embodiments of the present invention;

[0038] Figure 5B shows a segmented and classified version of the image in Figure 4A, in which the objects epithelial nuclei, cytoplasm, and stroma nuclei have been identified according to some embodiments of the present invention;

[0039] Figure 6 is a flowchart of illustrative stages involved in image segmentation and object classification in images of tissue subject to multiplex immunofluorescence (IF) according to some embodiments of the present invention;

[0040] Figure 7 is a flowchart of illustrative stages involved in constructing the minimum spanning tree (MST) of objects within an image of tissue subject to multiplex immunofluorescence (IF) according to some embodiments of the present invention;

[0041] Figure 8A is an image of tissue subject to multiplex immunofluorescence (IF) in which the minimum spanning tree (MST) of epithelial nuclei (EN) is identified in accordance with some embodiments of the present invention;

[0042] Figure 8B is an image of tissue subject to multiplex immunofluorescence (IF) in which the boundaries of glands with stroma and the boundaries of glands with lumen are identified according to some embodiments of the present invention;

[0043] Figure 9 is a listing of minimum spanning tree (MST) features, fractal dimension (FD) features, combined features, and their respective two-sided *p*-values and values of the concordance index, which were identified in images of tissue subject to multiplex immunofluorescence (IF) and which may be used in predictive models according to some embodiments of the present invention;

[0044] Figure 10 is a flowchart of illustrative stages involved in screening for an inhibitor compound in accordance with an embodiment of the present invention;

[0045] Figure 11 is a listing of clinical, molecular, and computer-generated morphometric features used by a model to predict disease progression in a patient according to an embodiment of the present invention;

[0046] Figure 12 are Kaplan-Meier curves illustrating the ability of a feature used in the predictive model of Figure 11 to accurately stratify patients into low and high risk groups, namely the morphometric feature of area of isolated (non-lumen associated) tumor epithelial cells relative to total tumor area;

[0047] Figure 13 is a graph of a Kaplan-Meier curve illustrating the ability of another feature used in the predictive model of Figure 11 to accurately stratify patients into low and high risk groups, namely the morphometric feature of mean edge length in the minimum spanning tree (MST) of all edges connecting epithelial nuclei centroids (for dominant biopsy Gleason grade (bGG) ≤ 3) in combination with the clinical feature of Gleason grade (for bGG = 4 or 5);

[0048] Figure 14 is a graph of a Kaplan-Meier curve illustrating the ability of yet another feature used in the predictive model of Figure 11 to accurately stratify patients into low and high risk groups, namely the molecular feature of AR dynamic range (for bGG ≤ 3) in combination with the molecular feature of total Ki67 (for bGG = 4 or 5);

[0049] Figure 15 is a graph of a Kaplan-Meier curve illustrating the ability of the value or score output by the predictive model of Figure 11 to stratify patients in the training set according to risk;

[0050] Figure 16 is a graph of a Kaplan-Meier curve illustrating the ability of the value or score output by the predictive model of Figure 11 to stratify patients in the validation set according to risk;

[0051] Figure 17 is a listing of clinical, molecular, and computer-generated morphometric features used by a model to predict favorable pathology stage (indolent disease) in a patient according to an embodiment of the present invention;

[0052] Figure 18 is a listing of molecular and computer-generated morphometric features determined to be predictive of responsiveness or unresponsiveness to a therapy and time to clinical progression of a medical condition according to an embodiment of the present invention;

[0053] Figures 19A and 19B are segmented images of cell lines (LNCaP and PC3 cells, respectively) with an applied threshold determining positive and negative nuclear androgen receptor (AR) protein levels according to some embodiments of the present invention;

[0054] Figures 20A and 20B are plots of mean intensity in which the intensity of nuclear androgen receptor (AR; y axis) in cell lines (LNCaP, DU145, and PC3) is plotted against experiment sequence number (x-axis); and

[0055] Figure 21 is a graph of a Kaplan-Meier curve illustrating the ability of a feature representing the expression of nuclear androgen receptor (AR) to stratify patients into low and high risk groups for death-of-disease.

DETAILED DESCRIPTION OF THE INVENTION

[0056] Embodiments of the present invention relate to methods and systems that use computer-generated morphometric information, clinical information, and/or molecular information in a predictive model for predicting the occurrence of a medical condition. For example, in some embodiments of the present invention, clinical, molecular and computer-generated morphometric information are used to predict whether or not and/or the likelihood that a patient would have a favorable pathology (indolent disease) if the patient were to undergo a treatment (e.g., radical prostatectomy) for a disease such as, for example, prostate cancer. In some embodiments, a

predictive model is provided that predicts the likelihood or risk of progression of a disease such as, for example, prostate cancer. In other embodiments, the teachings provided herein are used to predict the occurrence (e.g., presence, recurrence, or progression) of other medical conditions such as, for example, other types of disease (e.g., epithelial and mixed-neoplasms including breast, colon, lung, bladder, liver, pancreas, renal cell, and soft tissue) and the responsiveness or unresponsiveness of a patient to one or more therapies (e.g., pharmaceutical drugs). These predictions may be used by physicians or other individuals, for example, to select an appropriate course of treatment for a patient, diagnose a medical condition in the patient, and/or predict the risk or likelihood of disease progression in the patient.

[0057] In an aspect of the present invention, an analytical tool such as, for example, a module configured to perform support vector regression for censored data (SVRc), a support vector machine (SVM), and/or a neural network may be provided that determines correlations between clinical features, molecular features, computer-generated morphometric features, combinations of such features, and/or other features and a medical condition. The correlated features may form a model that can be used to predict an outcome with respect to the condition (e.g., presence, indolence, recurrence, or progression). For example, an analytical tool may be used to generate a predictive model based on data for a cohort of patients whose outcomes with respect to a medical condition (e.g., time to recurrence or progression of cancer) are at least partially known. The model may then be used to evaluate data for a new patient in order to predict the risk of occurrence of the medical condition in the new patient. In some embodiments, only a subset of clinical, molecular, morphometric, and/or other data (e.g., clinical and morphometric data only) may be used by the analytical tool to generate the predictive model. Illustrative systems and methods for treating, diagnosing, and predicting the occurrence of medical conditions are described in commonly-owned U.S. Patent No. 7,461,048, issued December 2, 2008, U.S. Patent No. 7,467,119, issued December 16, 2008, and PCT Application No. PCT/US2008/004523, filed April 7, 2008.

[0058] The clinical, molecular, and/or morphometric data used by embodiments of the present invention may include any clinical, molecular, and/or morphometric data that is relevant to the diagnosis, treatment and/or prediction of a medical condition. For example, features analyzed

for correlations with favorable pathological stage (indolent disease) in patients who had undergone a radical prostatectomy are described below in connection with Tables 1-4 and 11 and Figure 9. Features analyzed for progression of prostate cancer in order to generate a model predictive of prostate cancer progression are described below in connection with Tables 1-5 and 9 and Figure 9. It will be understood that at least some of these features (e.g., epithelial and mixed-neoplasms) may provide a basis for developing predictive models for other medical conditions (e.g., breast, colon, lung, bladder, liver, pancreas, renal cell, and soft tissue). For example, one or more of the features in Tables 1-5, 9, and 11 and Figure 9 may be assessed for patients having some other medical condition and then input to an analytical tool that determines whether the features correlate with the medical condition. Generally, features that increase the ability of the model to predict the occurrence of the medical condition (e.g., as determined through suitable univariate and/or multivariate analyses) may be included in the final model, whereas features that do not increase (e.g., or decrease) the predictive power of the model may be removed from consideration. By way of example only, illustrative systems and methods for selecting features for use in a predictive model are described below and in commonly-owned U.S. Publication No. 2007/0112716, published May 17, 2007 and entitled "Methods and Systems for Feature Selection in Machine Learning Based on Feature Contribution and Model Fitness,"

[0059] Using the features in Tables 1-5, 9, and 11 and Figure 9 as a basis for developing a predictive model may focus the resources of physicians, other individuals, and/or automated processing equipment (e.g., a tissue image analysis system) on obtaining patient data that is more likely to be correlated with outcome and therefore useful in the final predictive model. Moreover, the features determined to be correlated with favorable pathological stage (indolent disease) are shown in Table 11 and Figure 17. The features determined to be correlated with progression of prostate cancer are shown in Table 9 and Figure 11. It will be understood that these features may be included directly in final models predictive of favorable pathological stage and progression of prostate cancer, respectively, and/or used for developing predictive models for other medical conditions.

[0060] The morphometric data used in predictive models according to some embodiments of the present invention may include computer-generated data indicating various structural, textural, and/or spectral properties of, for example, tissue specimens. For example, the morphometric data may include data for morphometric features of stroma, cytoplasm, epithelial nuclei, stroma nuclei, lumen, red blood cells, tissue artifacts, tissue background, glands, other objects identified in a tissue specimen or a digitized image of such tissue, or a combination thereof.

[0061] In an aspect of the present invention, a tissue image analysis system is provided for measuring morphometric features from tissue specimen(s) (e.g., needle biopsies and/or whole tissue cores) or digitized image(s) thereof. The system may utilize, in part, the commercially-available Definiens Cellenger software. For example, in some embodiments, the image analysis system may receive image(s) of tissue stained with hematoxylin and eosin (H&E) as input, and may output one or more measurements of morphometric features for pathological objects (e.g., epithelial nuclei, cytoplasm, etc.) and/or structural, textural, and/or spectral properties observed in the image(s). For example, such an image analysis system may include a light microscope that captures images of H&E-stained tissue at 20X magnification. Illustrative systems and methods for measuring morphometric features from images of H&E-stained tissue according to some embodiments of the present invention are described below in connection with, for example, Figure 3 and the illustrative studies in which aspects of the present invention were applied to prediction of favorable pathological stage and prostate cancer progression. Computer-generated morphometric features (e.g., morphometric features measurable from digitized images of H&E-stained tissue) which may be used in a predictive model for predicting an outcome with respect to a medical condition according to some embodiments of the present invention are summarized in Table 1.

[0062] In some embodiments of the present invention, the image analysis system may receive image(s) of tissue subject to multiplex immunofluorescence (IF) as input, and may output one or more measurements of morphometric features for pathological objects (e.g., epithelial nuclei, cytoplasm, etc.) and/or structural, textural, and/or spectral properties observed in the image(s). For example, such an image analysis system may include a multispectral camera attached to a microscope that captures images of tissue under an excitation light source. Computer-generated

morphometric features (e.g., morphometric features measurable from digitized images of tissue subject to multiplex IF) which may be used in a predictive model for predicting an outcome with respect to a medical condition according to some embodiments of the present invention are listed in Table 2. Illustrative examples of such morphometric features include characteristics of a minimum spanning tree (MST) (e.g., MST connecting epithelial nuclei) and/or a fractal dimension (FD) (e.g., FD of gland boundaries) measured in images acquired through multiplex IF microscopy. Illustrative systems and methods for measuring morphometric features from images of tissue subject to multiplex IF according to some embodiments of the present invention are described below in connection with, for example, Figures 4B-9 and the illustrative study in which aspects of the present invention were applied to the prediction of prostate cancer progression.

[0063] Clinical features which may be used in predictive models according to some embodiments of the present invention may include or be based on data for one or more patients such as age, race, weight, height, medical history, genotype and disease state, where disease state refers to clinical and pathologic staging characteristics and any other clinical features gathered specifically for the disease process under consideration. Generally, clinical data is gathered by a physician during the course of examining a patient and/or the tissue or cells of the patient. The clinical data may also include clinical data that may be more specific to a particular medical context. For example, in the context of prostate cancer, the clinical data may include data indicating blood concentration of prostate specific antigen (PSA), the result of a digital rectal exam, Gleason score, and/or other clinical data that may be more specific to prostate cancer. Clinical features which may be used in a predictive model for predicting an outcome with respect to a medical condition according to some embodiments of the present invention are listed in Table 3.

[0064] Molecular features which may be used in predictive models according to some embodiments of the present invention may include or be based on data indicating the presence, absence, relative increase or decrease or relative location of biological molecules including nucleic acids, polypeptides, saccharides, steroids and other small molecules or combinations of the above, for example, glycoproteins and protein-RNA complexes. The locations at which these

molecules are measured may include glands, tumors, stroma, and/or other locations, and may depend on the particular medical context. Generally, molecular data is gathered using molecular biological and biochemical techniques including Southern, Western, and Northern blots, polymerase chain reaction (PCR), immunohistochemistry, and/or immunofluorescence (IF) (e.g., multiplex IF). Molecular features which may be used in a predictive model for predicting an outcome with respect to a medical condition according to some embodiments of the present invention are listed in Table 4. Additional details regarding multiplex immunofluorescence according to some embodiments of the present invention are described in commonly-owned U.S. Patent Application Publication No. 2007/0154958, published July 5, 2007 and entitled "Multiplex In Situ Immunohistochemical Analysis".

Further, in situ hybridization may be used to show both the relative abundance and location of molecular biological features. Illustrative methods and systems for in situ hybridization of tissue are described in, for example, commonly-owned U.S. Patent No. 6,995,020, issued February 7, 2006 and entitled "Methods and compositions for the preparation and use of fixed-treated cell-lines and tissue in fluorescence in situ hybridization".

[0065] Generally, when any clinical, molecular, and/or morphometric features from any of Tables 1-5, 9, and 11 and/or Figures 9, 11, and 17 are applied to medical contexts other than the prostate, features from these Tables and/or Figures that are more specific to the prostate may not be considered. Optionally, features more specific to the medical context in question may be substituted for the prostate-specific features. For example, other histologic disease-specific features/manifestations may include regions of necrosis (e.g., ductal carcinoma in situ for the breast), size, shape and regional pattern/distribution of epithelial cells (e.g., breast, lung), degree of differentiation (e.g., squamous differentiation with non-small cell lung cancer (NSCLC, mucin production as seen with various adenocarcinomas seen in both breast and colon)), morphological/microscopic distribution of the cells (e.g., lining ducts in breast cancer, lining bronchioles in NSCLC), and degree and type of inflammation (e.g., having different characteristics for breast and NSCLC in comparison to prostate).

[0066] Figures 1A and 1B show illustrative systems that use a predictive model to predict the occurrence (e.g., presence, indolence, recurrence, or progression) of a medical condition in a patient. The arrangement in Figure 1A may be used when, for example, a medical diagnostics lab provides support for a medical decision to a physician or other individual associated with a remote access device. The arrangement in Figure 1B may be used when, for example, a test kit including the predictive model is provided for use in a facility such as a hospital, other medical facility, or other suitable location.

[0067] Referring to Figure 1A, one or more predictive models 102 are located in diagnostics facility 104. Predictive model (s) 102 may include any suitable hardware, software, or combination thereof for receiving data for a patient, evaluating the data in order to predict the occurrence (e.g., presence, indolence, recurrence, and/or progression) of a medical condition for the patient, and outputting the results of the evaluation. In another embodiment, a model 102 may be used to predict the responsiveness of a patient to particular one or more therapies. Diagnostics facility 104 may receive data for a patient from remote access device 106 via Internet service provider (ISP) 108 and communications networks 110 and 112, and may input the data to predictive model(s) 102 for evaluation. Other arrangements for receiving and evaluating data for a patient from a remote location are of course possible (e.g., via another connection such as a telephone line or through the physical mail). The remotely located physician or individual may acquire the data for the patient in any suitable manner and may use remote access device 106 to transmit the data to diagnostics facility 104. In some embodiments, the data for the patient may be at least partially generated by diagnostics facility 104 or another facility. For example, diagnostics facility 104 may receive a digitized image of H&E-stained tissue from remote access device 106 or other device and may generate morphometric data for the patient based on the image. In another example, actual tissue samples may be received and processed by diagnostics facility 104 in order to generate morphometric data, molecular data, and/or other data. In other examples, a third party may receive a tissue sample or image for a new patient, generate morphometric data, molecular data and/or other data based on the image or tissue, and provide the morphometric data, molecular data and/or other data to diagnostics facility 104. Illustrative embodiments of suitable image processing tools for generating

morphometric data and/or molecular data from tissue images and/or tissue samples according to some embodiments of the present invention are described below in connection with Figures 3-8.

[0068] Diagnostics facility 104 may provide the results of the evaluation to a physician or individual associated with remote access device 106 through, for example, a transmission to remote access device 106 via ISP 108 and communications networks 110 and 112 or in another manner such as the physical mail or a telephone call. The results may include one or more values or “scores” (e.g., an indication of the likelihood that the patient will experience one or more outcomes related to the medical condition such as the presence of the medical condition, favorable or unfavorable pathological stage (indolence or nonindolence of the medical condition) and/or the probability thereof, predicted time to recurrence of the medical condition, or risk or likelihood of progression of the medical condition in the patient), information indicating one or more features analyzed by predictive model(s) 102 as being correlated with the medical condition, image(s) output by the image processing tool, information indicating the sensitivity and/or specificity of the predictive model, explanatory remarks, other suitable information, or a combination thereof. For example, Figure 2 shows at least a portion of a report for a fictional patient that may be output by, or otherwise generated based on the output of, one or more predictive models. As shown, the report may indicate that based on the data for the patient input to a predictive model, the predictive model output a value of 40 corresponding to a 19% probability of disease progression (as indicated by castrate PSA rise, metastasis and/or prostate cancer mortality) within eight years after radical prostatectomy, which may place the patient in a high-risk category. (Conversely, as indicated by the vertical line in the embodiment shown in Figure 2, a values of less than 30.19 output by the predictive model may place the patient in a low-risk category.) Alternatively or additionally, the report may indicate that based on data for the patient input to another predictive model, the predictive model output data indicating that the patient is likely to have “UFP” (unfavorable pathology; or conversely, favorable pathology (“FP”)) and/or the probability that the patient will have UFP or FP (e.g., low probability 32% of FP). Such a report may be used by a physician or other individual, for example, to assist in determining appropriate treatment option(s) for the patient. The report may also be useful in that it may help the physician or individual to explain the patient’s risk to the patient.

[0069] Remote access device 106 may be any remote device capable of transmitting and/or receiving data from diagnostics facility 104 such as, for example, a personal computer, a wireless device such as a laptop computer, a cell phone or a personal digital assistant (PDA), or any other suitable remote access device. Multiple remote access devices 106 may be included in the system of Figure 1A (e.g., to allow a plurality of physicians or other individuals at a corresponding plurality of remote locations to communicate data with diagnostics facility 104), although only one remote access device 106 has been included in Figure 1A to avoid over-complicating the drawing. Diagnostics facility 104 may include a server capable of receiving and processing communications to and/or from remote access device 106. Such a server may include a distinct component of computing hardware and/or storage, but may also be a software application or a combination of hardware and software. The server may be implemented using one or more computers.

[0070] Each of communications links 110 and 112 may be any suitable wired or wireless communications path or combination of paths such as, for example, a local area network, wide area network, telephone network, cable television network, intranet, or Internet. Some suitable wireless communications networks may be a global system for mobile communications (GSM) network, a time-division multiple access (TDMA) network, a code-division multiple access (CDMA) network, a Bluetooth network, or any other suitable wireless network.

[0071] Figure 1B shows a system in which test kit 122 including a predictive model in accordance with an embodiment of the present invention is provided for use in facility 124, which may be a hospital, a physician's office, or other suitable location. Test kit 122 may include any suitable hardware, software, or combination thereof (e.g., a personal computer) that is adapted to receive data for a patient (e.g., at least one of clinical, morphometric and molecular data), evaluate the patient's data with one or more predictive models (e.g., programmed in memory of the test kit), and output the results of the evaluation. For example, test kit 122 may include a computer readable medium encoded with computer executable instructions for performing the functions of the predictive model(s). The predictive model(s) may be predetermined model(s) previously generated (e.g., by another system or application such as the system in Figure 1C). In some embodiments, test kit 122 may optionally include an image

processing tool capable of generating data corresponding to morphometric and/or molecular features from, for example, a tissue sample or image. Illustrative embodiments of suitable image processing tools according to some embodiments of the present invention are described below in connection with Figures 3-8. In other embodiments, test kit 122 may receive pre-packaged data for the morphometric features as input from, for example, an input device (e.g., keyboard) or another device or location. Test kit 122 may optionally include an input for receiving, for example, updates to the predictive model. The test kit may also optionally include an output for transmitting data, such as data useful for patient billing and/or tracking of usage, to a main facility or other suitable device or location. The billing data may include, for example, medical insurance information for a patient evaluated by the test kit (e.g., name, insurance provider, and account number). Such information may be useful when, for example, a provider of the test kit charges for the kit on a per-use basis and/or when the provider needs patients' insurance information to submit claims to insurance providers.

[0072] Figure 1C shows an illustrative system for generating a predictive model. The system includes analytical tool 132 (e.g., including a module configured to perform support vector regression for censored data (SVRc), a support vector machine (SVM), and/or a neural network) and database 134 of patients whose outcomes are at least partially known. Analytical tool 132 may include any suitable hardware, software, or combination thereof for determining correlations between the data from database 134 and a medical condition. The system in Figure 1C may also include image processing tool 136 capable of generating, for example, morphometric data based on H&E-stained tissue or digitized image(s) thereof, morphometric data and/or molecular data based on tissue acquired using multiplex immunofluorescence (IF) microscopy or digitized image(s) of such tissue, or a combination thereof. Tool 136 may generate morphometric data and/or molecular data for, for example, the known patients whose data is included in database 134. Illustrative embodiments of suitable image processing tools according to some embodiments of the present invention are described below in connection with Figures 3-8.

[0073] Database 134 may include any suitable patient data such as data for clinical features, morphometric features, molecular features, or a combination thereof. Database 134 may also

include data indicating the outcomes of patients such as whether and when the patients have experienced a disease or its recurrence or progression. For example, database 134 may include uncensored data for patients (i.e., data for patients whose outcomes are completely known) such as data for patients who have experienced a medical condition (e.g., favorable or unfavorable pathological stage) or its recurrence or progression. Database 134 may alternatively or additionally include censored data for patients (i.e., data for patients whose outcomes are not completely known) such as data for patients who have not shown signs of a disease or its recurrence or progression in one or more follow-up visits to a physician. The use of censored data by analytical tool 132 may increase the amount of data available to generate the predictive model and, therefore, may advantageously improve the reliability and predictive power of the model. Examples of machine learning approaches, namely support vector regression for censored data (SVRc) and a particular implementation of a neural network (NNci) that can make use of both censored and uncensored data are described below.

[0074] In one embodiment, analytical tool 132 may perform support vector regression on censored data (SVRc) in the manner set forth in commonly-owned U.S. Patent No. 7,505,948, issued March 17, 2009 . SVRc

uses a loss/penalty function which is modified relative to support vector machines (SVM) in order to allow for the utilization of censored data. For example, data including clinical, molecular, and/or morphometric features of known patients from database 134 may be input to the SVRc to determine parameters for a predictive model. The parameters may indicate the relative importance of input features, and may be adjusted in order to maximize the ability of the SVRc to predict the outcomes of the known patients.

[0075] The use of SVRc by analytical tool 132 may include obtaining from database 134 multi-dimensional, non-linear vectors of information indicative of status of patients, where at least one of the vectors lacks an indication of a time of occurrence of an event or outcome with respect to a corresponding patient. Analytical tool 132 may then perform regression using the vectors to produce a kernel-based model that provides an output value related to a prediction of time to the event based upon at least some of the information contained in the vectors of information. Analytical tool 132 may use a loss function for each vector containing censored data that is

different from a loss function used by tool 132 for vectors comprising uncensored data. A censored data sample may be handled differently because it may provide only “one-sided information.” For example, in the case of survival time prediction, a censored data sample typically only indicates that the event has not happened within a given time, and there is no indication of when it will happen after the given time, if at all.

[0076] The loss function used by analytical tool 132 for censored data may be as follows:

$$Loss(f(\mathbf{x}), y, s = 1) = \begin{cases} C_s^*(e - \varepsilon_s^*) & e > \varepsilon_s^* \\ 0 & -\varepsilon_s \leq e \leq \varepsilon_s^*, \\ C_s(\varepsilon_s - e) & e < -\varepsilon_s \end{cases}$$

where $e = f(\mathbf{x}) - y$; and

$$f(\mathbf{x}) = \mathbf{W}^T \Phi(\mathbf{x}) + b$$

is a linear regression function on a feature space F . Here, $\mathbf{W}$ is a vector in F , and $\Phi(\mathbf{x})$ maps the input $\mathbf{x}$ to a vector in F .

[0077] In contrast, the loss function used by tool 132 for uncensored data may be:

$$Loss(f(\mathbf{x}), y, s = 0) = \begin{cases} C_n^*(e - \varepsilon_n^*) & e > \varepsilon_n^* \\ 0 & -\varepsilon_n \leq e \leq \varepsilon_n^*, \\ C_n(\varepsilon_n - e) & e < -\varepsilon_n \end{cases}$$

where $e = f(\mathbf{x}) - y$

and $\varepsilon_n^* \leq \varepsilon_n$ and $C_n^* \geq C_n$.

[0078] In the above description, the $\mathbf{W}$ and b are obtained by solving an optimization problem, the general form of which is:

$$\begin{aligned}
& \min_{W, b} \quad \frac{1}{2} \|W^T \phi(x_i) - y_i\|^2 \\
& \text{s.t.} \quad y_i - (W^T \phi(x_i) + b) \leq \varepsilon \\
& \quad \quad (W^T \phi(x_i) + b) - y_i \leq \varepsilon
\end{aligned}$$

This equation, however, assumes the convex optimization problem is always feasible, which may not be the case. Furthermore, it is desired to allow for small errors in the regression estimation. It is for these reasons that a loss function is used for SVRc. The loss allows some leeway for the regression estimation. Ideally, the model built will exactly compute all results accurately, which is infeasible. The loss function allows for a range of error from the ideal, with this range being controlled by slack variables ξ and ξ^* , and a penalty C. Errors that deviate from the ideal, but are within the range defined by ξ and ξ^* , are counted, but their contribution is mitigated by C. The more erroneous the instance, the greater the penalty. The less erroneous (closer to the ideal) the instance is, the less the penalty. This concept of increasing penalty with error results in a slope, and C controls this slope. While various loss functions may be used, for an epsilon-insensitive loss function, the general equation transforms into:

$$\begin{aligned}
& \min_{W, b} \quad P = \frac{1}{2} W^T W + C \sum_{i=1}^l (\xi_i + \xi_i^*) \\
& \text{s.t.} \quad y_i - (W^T \Phi(x_i) + b) \leq \varepsilon + \xi_i \\
& \quad \quad (W^T \Phi(x_i) + b) - y_i \leq \varepsilon + \xi_i^* \\
& \quad \quad \xi_i, \xi_i^* \geq 0, \quad i = 1 \dots l
\end{aligned}$$

For an epsilon-insensitive loss function in accordance with the invention (with different loss functions applied to censored and uncensored data), this equation becomes:

$$\begin{aligned}
& \min_{W, b} \quad P_c = \frac{1}{2} W^T W + \sum_{i=1}^l (C_i \xi_i + C_i^* \xi_i^*) \\
& \text{s.t.} \quad y_i - (W^T \Phi(x_i) + b) \leq \varepsilon_i + \xi_i \\
& \quad \quad (W^T \Phi(x_i) + b) - y_i \leq \varepsilon_i^* + \xi_i^* \\
& \quad \quad \xi_i^{(*)} \geq 0, \quad i = 1 \dots l \\
& \text{where} \quad C_i^{(*)} = s_i C_s^{(*)} + (1 - s_i) C_n^{(*)} \\
& \quad \quad \varepsilon_i^{(*)} = s_i \varepsilon_s^{(*)} + (1 - s_i) \varepsilon_n^{(*)}
\end{aligned}$$

[0079] The optimization criterion penalizes data points whose y -values differ from $f(x)$ by more than ε . The slack variables, ξ and ξ^* , correspond to the size of this excess deviation for positive and negative deviations respectively. This penalty mechanism has two components, one for uncensored data (i.e., not right-censored) and one for censored data. Here, both components are represented in the form of loss functions that are referred to as ε -insensitive loss functions.

[0080] In another embodiment, analytical tool 132 may include a module configured to perform binary logistic regression utilizing, at least in part, a commercially-available SAS computer package configured for regression analyses.

[0081] In yet another embodiment, analytical tool 132 may include a neural network. In such an embodiment, tool 132 preferably includes a neural network that is capable of utilizing censored data. Additionally, the neural network preferably uses an objective function substantially in accordance with an approximation (e.g., derivative) of the concordance index (CI) to train an associated model (NNci). Though the CI has long been used as a performance indicator for survival analysis [12], the use of the CI to train a neural network was proposed in commonly-owned U.S. Patent No. 7,321,881, issued January 22, 2008.

The difficulty of using the CI as a training

objective function in the past is that the CI is non-differentiable and cannot be optimized by gradient-based methods. As described in U.S. Patent No. 7,321,881, this obstacle may be overcome by using an approximation of the CI as the objective function.

[0082] For example, when analytical tool 132 includes a neural network that is used to predict prostate cancer progression, the neural network may process input data for a cohort of patients whose outcomes with respect to prostate cancer progression are at least partially known in order to produce an output. The particular features selected for input to the neural network may be selected through the use of the above-described SVRc (e.g., implemented with analytical tool 132) or any other suitable feature selection process. An error module of tool 132 may determine an error between the output and a desired output corresponding to the input data (e.g., the difference between a predicted outcome and the known outcome for a patient). Analytical tool 132 may then use an objective function substantially in accordance with an approximation of the CI to rate the performance of the neural network. Analytical tool 132 may adapt the

weighted connections (e.g., relative importance of features) of the neural network based upon the results of the objective function.

[0083] The concordance index may be expressed in the form:

$$CI = \frac{\sum_{(i,j) \in \Omega} I(\hat{t}_i, \hat{t}_j)}{|\Omega|}$$

where

$$I(\hat{t}_i, \hat{t}_j) = \begin{cases} 1: \hat{t}_i > \hat{t}_j \\ 0: otherwise \end{cases},$$

and may be based on pair-wise comparisons between the prognostic estimates $\hat{t}_i$ and $\hat{t}_j$ for patients i and j , respectively. In this example, Ω consists of all the pairs of patients $\{i,j\}$ who meet the following conditions:

- both patients i and j experienced recurrence, and the recurrence time t_i of patient i is shorter than patient j 's recurrence time t_j ; or
- only patient i experienced recurrence and t_i is shorter than patient j 's follow-up visit time t_j .

The numerator of the CI represents the number of times that the patient predicted to recur earlier by the neural network actually does recur earlier. The denominator is the total number of pairs of patients who meet the predetermined conditions.

[0084] Generally, when the CI is increased, preferably maximized, the model is more accurate. Thus, by preferably substantially maximizing the CI, or an approximation of the CI, the performance of a model is improved. In accordance with some embodiments of the present invention, an approximation of the CI is provided as follows:

$$C = \frac{\sum_{(i,j) \in \Omega} R(\hat{t}_i, \hat{t}_j)}{|\Omega|}$$

where

$$R(\hat{t}_i, \hat{t}_j) = \begin{cases} (-(\hat{t}_i - \hat{t}_j - \gamma))^n : \hat{t}_i - \hat{t}_j < \gamma \\ 0 : otherwise \end{cases},$$

and where $0 < \gamma \leq 1$ and $n > 1$. $R(\hat{t}_i, \hat{t}_j)$ can be regarded as an approximation to $I(-\hat{t}_i, -\hat{t}_j)$.

[0085] Another approximation of the CI provided in accordance with some embodiments of the present invention which has been shown empirically to achieve improved results is the following:

$$C_\omega = \frac{\sum_{(i,j) \in \Omega} -(\hat{t}_i - \hat{t}_j) \bullet R(\hat{t}_i, \hat{t}_j)}{D},$$

where

$$D = \sum_{(i,j) \in \Omega} -(\hat{t}_i - \hat{t}_j)$$

is a normalization factor. Here each $R(\hat{t}_i, \hat{t}_j)$ is weighted by the difference between $\hat{t}_i$ and $\hat{t}_j$.

The process of minimizing the C_ω (or C) seeks to move each pair of samples in Ω to satisfy $\hat{t}_i - \hat{t}_j > \gamma$ and thus to make $I(\hat{t}_i, \hat{t}_j) = 1$.

[0086] When the difference between the outputs of a pair in Ω is larger than the margin γ , this pair of samples will stop contributing to the objective function. This mechanism effectively overcomes over-fitting of the data during training of the model and makes the optimization preferably focus on only moving more pairs of samples in Ω to satisfy $\hat{t}_i - \hat{t}_j > \gamma$. The influence of the training samples is adaptively adjusted according to the pair-wise comparisons during training. Note that the positive margin γ in R is preferable for improved generalization performance. In other words, the parameters of the neural network are adjusted during training by calculating the CI after all the patient data has been entered. The neural network then adjusts the parameters with the goal of minimizing the objective function and thus maximizing the CI. As used above, over-fitting generally refers to the complexity of the neural network.

Specifically, if the network is too complex, the network will react to “noisy” data. Overfitting is risky in that it can easily lead to predictions that are far beyond the range of the training data.

[0087] Morphometric Data Obtained from H&E-Stained Tissue

[0088] As described above, an image processing tool (e.g., image processing tool 136) in accordance with some embodiments of the present invention may be provided that generates digitized images of tissue specimens (e.g., H&E-stained tissue specimens) and/or measures morphometric features from the tissue images or specimens. For example, in some embodiments, the image processing tool may include a light microscope that captures tissue images at 20X magnification using a SPOT Insight QE Color Digital Camera (KAI2000) and produces images with 1600 x 1200 pixels. The images may be stored as images with 24 bits per pixel in Tiff format. Such equipment is only illustrative and any other suitable image capturing equipment may be used without departing from the scope of the present invention.

[0089] In some embodiments, the image processing tool may include any suitable hardware, software, or combination thereof for segmenting and classifying objects in the captured images, and then measuring morphometric features of the objects. For example, such segmentation of tissue images may be utilized in order to classify pathological objects in the images (e.g., classifying objects as cytoplasm, lumen, nuclei, epithelial nuclei, stroma, background, artifacts, red blood cells, glands, other object(s) or any combination thereof). In one embodiment, the image processing tool may include the commercially-available Definiens Cellenger Developer Studio (e.g., v. 4.0) adapted to perform the segmenting and classifying of, for example, some or all of the various pathological objects described above and to measure various morphometric features of these objects. Additional details regarding the Definiens Cellenger product are described in [13].

[0090] For example, in some embodiments of the present invention, the image processing tool may classify objects as background if the objects correspond to portions of the digital image that are not occupied by tissue. Objects classified as cytoplasm may be the cytoplasm of a cell, which may be an amorphous area (e.g., pink area that surrounds an epithelial nucleus in an image of, for example, H&E stained tissue). Objects classified as epithelial nuclei may be the nuclei present within epithelial cells/luminal and basal cells of the glandular unit, which may appear as

round objects surrounded by cytoplasm. Objects classified as lumen may be the central glandular space where secretions are deposited by epithelial cells, which may appear as enclosed white areas surrounded by epithelial cells. Occasionally, the lumen can be filled by prostatic fluid (which typically appears pink in H&E stained tissue) or other “debris” (e.g., macrophages, dead cells, etc.). Together the lumen and the epithelial cytoplasm and nuclei may be classified as a gland unit. Objects classified as stroma may be the connective tissue with different densities that maintains the architecture of the prostatic tissue. Such stroma tissue may be present between the gland units, and may appear as red to pink in H&E stained tissue. Objects classified as stroma nuclei may be elongated cells with no or minimal amounts of cytoplasm (fibroblasts). This category may also include endothelial cells and inflammatory cells, and epithelial nuclei may also be found scattered within the stroma if cancer is present. Objects classified as red blood cells may be small red round objects usually located within the vessels (arteries or veins), but can also be found dispersed throughout tissue.

[0091] In some embodiments, the image processing tool may measure various morphometric features of from basic relevant objects such as epithelial nuclei, epithelial cytoplasm, stroma, and lumen (including mathematical descriptors such as standard deviations, medians, and means of objects), spectral-based characteristics (e.g., red, green, blue (RGB) channel characteristics such as mean values, standard deviations, etc.), texture, wavelet transform, fractal code and/or dimension features, other features representative of structure, position, size, perimeter, shape (e.g., asymmetry, compactness, elliptic fit, etc.), spatial and intensity relationships to neighboring objects (e.g., contrast), and/or data extracted from one or more complex objects generated using said basic relevant objects as building blocks with rules defining acceptable neighbor relations (e.g., ‘gland unit’ features). In some embodiments, the image processing tool may measure these features for every instance of every identified pathological object in the image, or a subset of such instances. The image processing tool may output these features for, for example, evaluation by predictive model 102 (Figure 1A), test kit 122 (Figure 1B), or analytical tool 132 (Figure 1C). Optionally, the image processing tool may also output an overall statistical summary for the image summarizing each of the measured features.

[0092] Figure 3 is a flowchart of illustrative stages involved in image segmentation and object classification (e.g., in digitized images of H&E-stained tissue) according to some embodiments of the present invention.

[0093] *Initial Segmentation.* In a first stage, the image processing tool may segment an image (e.g., an H&E-stained needle biopsy tissue specimen, an H&E stained tissue microarray (TMA) image or an H&E of a whole tissue section) into small groups of contiguous pixels known as objects. These objects may be obtained by a region-growing method which finds contiguous regions based on color similarity and shape regularity. The size of the objects can be varied by adjusting a few parameters [14]. In this system, an object rather than a pixel is typically the smallest unit of processing. Thus, some or all of the morphometric feature calculations and operations may be performed with respect to objects. For example, when a threshold is applied to the image, the feature values of the object are subject to the threshold. As a result, all the pixels within an object are assigned to the same class. In one embodiment, the size of objects may be controlled to be 10-20 pixels at the finest level. Based on this level, subsequent higher and coarser levels are built by forming larger objects from the smaller ones in the lower level.

[0094] *Background Extraction.* Subsequent to initial segmentation, the image processing tool may segment the image tissue core from the background (transparent region of the slide) using intensity threshold and convex hull. The intensity threshold is an intensity value that separates image pixels in two classes: "tissue core" and "background." Any pixel with an intensity value greater than or equal the threshold is classified as a "tissue core" pixel, otherwise the pixel is classified as a "background" pixel. The convex hull of a geometric object is the smallest convex set (polygon) containing that object. A set S is convex if, whenever two points P and Q are inside S , then the whole line segment PQ is also in S .

[0095] *Coarse Segmentation.* In a next stage, the image processing tool may re-segment the foreground (e.g., TMA core) into rough regions corresponding to nuclei and white spaces. For example, the main characterizing feature of nuclei in H&E stained images is that they are stained blue compared to the rest of the pathological objects. Therefore, the difference in the red and blue channels ($R-B$) intensity values may be used as a distinguishing feature. Particularly, for every image object obtained in the initial segmentation step, the difference between average red

and blue pixel intensity values may be determined. The length/width ratio may also be used to determine whether an object should be classified as nuclei area. For example, objects which fall below a $(R-B)$ feature threshold and below a length/width threshold may be classified as nuclei area. Similarly, a green channel threshold can be used to classify objects in the tissue core as white spaces. Tissue stroma is dominated by the color red. The intensity difference d , “red ratio” $r = R/(R + G + B)$ and the red channel standard deviation σ_R of image objects may be used to classify stroma objects.

[0096] *White Space Classification.* In the stage of coarse segmentation, the white space regions may correspond to both lumen (pathological object) and artifacts (broken tissue areas) in the image. The smaller white space objects (area less than 100 pixels) are usually artifacts. Thus, the image processing tool may apply an area filter to classify them as artifacts.

[0097] *Nuclei De-fusion and Classification.* In the stage of coarse segmentation, the nuclei area is often obtained as contiguous fused regions that encompass several real nuclei. Moreover, the nuclei region might also include surrounding misclassified cytoplasm. Thus, these fused nuclei areas may need to be de-fused in order to obtain individual nuclei.

[0098] The image processing tool may use two different approaches to de-fuse the nuclei. The first approach may be based on a region growing method that fuses the image objects constituting nuclei area under shape constraints (roundness). This approach has been determined to work well when the fusion is not severe.

[0099] In the case of severe fusion, the image processing tool may use a different approach based on supervised learning. This approach involves manual labeling of the nuclei areas by an expert (pathologist). The features of image objects belonging to the labeled nuclei may be used to design statistical classifiers.

[0100] In some embodiments, the input image may include different kinds of nuclei: epithelial nuclei, fibroblasts, basal nuclei, endothelial nuclei, apoptotic nuclei and red blood cells. Since the number of epithelial nuclei is typically regarded as an important feature in grading the extent of the tumor, it may be important to distinguish the epithelial nuclei from the others. The image processing tool may accomplish this by classifying the detected nuclei into two classes: epithelial nuclei and “the rest” based on shape (eccentricity) and size (area) features.

[0101] In one embodiment, in order to reduce the number of feature space dimensions, feature selection may be performed on the training set using two different classifiers: the Bayesian classifier and the k nearest neighbor classifier [12]. The leave-one-out method [13] may be used for cross-validation, and the sequential forward search method may be used to choose the best features. Finally, two Bayesian classifiers may be designed with number of features equal to 1 and 5, respectively. The class-conditional distributions may be assumed to be Gaussian with diagonal covariance matrices.

[0102] The image segmentation and object classification procedure described above in connection with Figure 3 is only illustrative and any other suitable method or approach may be used to measure morphometric features of interest in tissue specimens or images in accordance with the present invention. For example, in some embodiments, a digital masking tool (e.g., Adobe Photoshop 7.0) may be used to mask portion(s) of the tissue image such that only infiltrating tumor is included in the segmentation, classification, and/or subsequent morphometric analysis. Alternatively or additionally, in some embodiments, lumens in the tissue images are manually identified and digitally masked (outlined) by a pathologist in an effort to minimize the effect of luminal content (e.g., crystals, mucin, and secretory concretions) on lumen object segmentation. Additionally, these outlined lumens can serve as an anchor for automated segmentation of other cellular and tissue components, for example, in the manner described below.

[0103] In some embodiments of the present invention, the segmentation and classification procedure identifies gland unit objects in a tissue image, where each gland unit object includes lumen, epithelial nuclei, and epithelial cytoplasm. The gland unit objects are identified by uniform and symmetric growth around lumens as seeds. Growth proceeds around these objects through spectrally uniform segmented epithelial cells until stroma cells, retraction artifacts, tissue boundaries, or other gland unit objects are encountered. These define the borders of the glands, where the accuracy of the border is determined by the accuracy of differentiating the cytoplasm from the remaining tissue. In this example, without addition of stop conditions, uncontrolled growth of connected glands may occur. Thus, in some embodiments, firstly the small lumens (e.g., very much smaller than the area of an average nucleus) are ignored as gland

seeds. Secondly, the controlled region-growing method continues as long as the area of each successive growth ring is larger than the preceding ring. Segments of non-epithelial tissue are excluded from these ring area measurements and therefore effectively dampen and halt growth of asymmetric glands. The epithelial cells (including epithelial nuclei plus cytoplasm) thus not captured by the gland are classified as outside of, or poorly associated with, the gland unit. In this manner, epithelial cells (including epithelial nuclei plus cytoplasm) outside of the gland units are also identified.

[0104] In some embodiments, an image processing tool may be provided that classifies and clusters objects in tissue, which utilizes biologically defined constraints and high certainty seeds for object classification. In some embodiments, such a tool may rely less on color-based features than prior classification approaches. For example, a more structured approach starts with high certainty lumen seeds (e.g., based on expert outlined lumens) and using them as anchors, and distinctly colored object segmented objects. The distinction of lumens from other transparent objects, such as tissue tears, retraction artifacts, blood vessels and staining defects, provides solid anchors and object neighbor information to the color-based classification seeds. The probability distributions of the new seed object features, along with nearest neighbor and other clustering techniques, are used to further classify the remaining objects. Biological information regarding of the cell organelles (e.g., their dimensions, shape and location with respect to other organelles) constrains the growth of the classified objects. Due to tissue-to-tissue irregularities and feature outliers, multiple passes of the above approach may be used to label all the segments. The results are fed back to the process as new seeds, and the process is iteratively repeated until all objects are classified. In some embodiments, since at 20x magnification the nuclei and sub-nuclei objects may be too coarsely resolved to accurately measure morphologic features, measurements of nuclei shape, size and nuclei sub-structures (chromatin texture, and nucleoli) may be measured at 40x magnification (see e.g., Table 1). To reduce the effect of segmentation errors, the 40x measurements may differentiate the feature properties of well defined nuclei (based on strongly defined boundaries of elliptic and circular shape) from other poorly differentiated nuclei.

[0105] Figure 4A is an image of typical H&E-stained prostate tissue obtained via a needle biopsy. Figure 4B is a segmented and classified version of the image in Figure 4A according to some embodiments of the present invention, showing gland units 402 formed from seed lumen 404, epithelial nuclei 406, and epithelial cytoplasm 408. Also segmented and classified in the processed image are isolated/non-gland-associated tumor epithelial cells 410, which include epithelial nuclei and epithelial cytoplasm. Although in the original image the seed lumen 404, epithelial nuclei 406, and epithelial cytoplasm 408 of the gland units are red, dark blue, and light blue, respectively, and the epithelial nuclei and epithelial cytoplasm of the isolated/non-gland-associated tumor epithelial cells are green and clear, respectively, the image is provided in gray-scale in FIG. 4B for ease of reproducibility. Black/gray areas represent benign elements and tissue artifacts which have been digitally removed by the pathologist reviewing the case.

[0106] Illustrative computer-generated morphometric features measurable from, for example, digitized images of H&E-stained tissue, are listed in Table 5. As described in greater detail below, all of the features listed in Table 5 were found to be correlated with prostate cancer progression in univariate analysis. Each feature denoted “IF/H&E” is a combined feature formed by mathematically combining one or more features measured from image(s) of H&E-stained tissue with one or more features measured from image(s) of tissue subject to multiplex immunofluorescence (IF).

Table 5. H&E Morphometric Features

Feature Name	Feature Domain	Description
HE02_Lum_Are_Median	H&E	Median area of lumens
orig_approximation_4	H&E	Variance of pixel values in the approximation sub-band after applying 4 stages of undecimated wavelet transform to a mask of glands
orig_diag_detail_6	H&E	Variance of pixel values in the diagonal detail sub-band after applying 6 stages of undecimated wavelet transform

		to a mask of glands
HEx2_nta_Lum_Are_Tot	H&E	Relative area of lumens to total tumor area outlined or otherwise identified
HEx2_EpiNucAre2LumMeanAre	H&E	Ratio of the total epithelial nuclear area to the average size of lumens
HEx2_nrm_ENWinGU_Are_Tot	H&E	Relative area of epithelial nuclei that are inside (within) gland units
HEx2_nrm_ENOutGU_Are_Tot	H&E	Relative area of epithelial nuclei that are outside of gland units
HEx2_nrm_CytWinGU_Are_Tot	H&E	Relative area of epithelial cytoplasm inside (within) gland units
HEx2_nrm_CytOutGU_Are_Tot	H&E	Relative area of epithelial cytoplasm outside of gland units
HEx2_RelArea_EpiNuc_Out2WinGU	H&E	Ratio of the area of epithelial nuclei outside of gland units to the area of epithelial nuclei inside gland units
HEx2_RelArea_Cyt_Out2WinGU	H&E	Ratio of the area of epithelial cytoplasm outside of gland units to the area of epithelial cytoplasm within (inside) gland units
HEx2_RelArea_ENCyt_Out2WinGU	H&E	Ratio of the area of epithelial cells (nuclei + cytoplasm) outside of gland units to the area of epithelial cells (nuclei + cytoplasm) inside of gland units
HEx2_ntaENCYtOutGU2Tumor	H&E	Area of epithelial cells (nuclei plus cytoplasm) not associated with lumens normalized to the total tumor area
HEx2_nrmLUM_ENOutGU_Are_Tot	H&E	Relative area of epithelial nuclei outside of gland units to the total area of lumens
HEx2_nrmLUM_CytWinGU_Are_Tot	H&E	Relative area of epithelial

		cytoplasm within gland units to the total lumen area
HEx2_nrmLUM_CytOutGU_Are_Tot	H&E	Relative area of epithelial cytoplasm outside of gland units to the total lumen area
HEx2_nrmLUM_EpiNucCytOutGU	H&E	Relative area of epithelial cells (nuclei + cytoplasm) to the total area of lumens
HEx2_nrm_ENCytWinGULum_Are_Tot	H&E	Ratio of the area of epithelial cells (nuclei + cytoplasm) within gland units and the total area of lumens to the tumor area
HEx2_RelArea_ENCytLum_Out2WinGU	H&E	Relative area of epithelial cells (nuclei + cytoplasm) outside of gland units to the glandular area, calculated as the sum of epithelial cell (nuclei + cytoplasm) area within gland units and the total area of lumens
HEx2_RelArea_EpiNucCyt_Lum	H&E	Ratio of the area of epithelial cells (nuclei + cytoplasm) to the area of lumens
HEx2_ntaLumContentArea	H&E	Relative area of luminal content, i.e., non-whitespace constrained within the luminal mask
HEx2_nrmEpiNucBand5minus3	H&E	Measures the areas of epithelial nuclei distributed away from gland units. Calculated by measuring the areas of epithelial nuclei with centers that are in a band a certain distance away from lumen borders. The band includes all epithelial nuclei that are at least three units away from the lumen border but within 5 units of the lumen border; a unit is a fixed number set to be approximately the diameter of

min_orig_L_detail5	H&E	one epithelial nucleus. Minimum of the variances of pixel values in the horizontal and vertical detail sub-bands after applying 5 stages of undecimated wavelet transform to a mask of lumens
RelAreaKi67post_2Lumen	IF/ H&E	Ratio of the relative area of Ki67 positive epithelial nuclei in IF images to the relative area of lumens in H&E images
RelAreapAKTpos_2Lumen	IF/ H&E	Ratio of the relative area of pAKT positive epithelial nuclei in IF images to the relative area of lumens in H&E images
RelAreaIFM2EpiNuc_2Lumen	IF/ H&E	Ratio of the relative area of epithelial nuclei in IF images to the relative area of lumens in H&E images
RelAreARpAMACRp2Lumen	IF/ H&E	Ratio of the relative area of AR positive and AMACR positive epithelial nuclei in IF images to the relative area of lumens in H&E images

[0107] It will be understood that the computer-generated morphometric features listed in Table 5 are only illustrative and that any suitable computer-generated morphometric features may be utilized without departing from the scope of the present invention. For example, additional computer-generated morphometric features (e.g., morphometric features measurable from digitized images of H&E-stained tissue) which may be used in a predictive model for predicting an outcome with respect to a medical condition are listed in Tables 1 and 11. It is believed that additional experimentation in the field of prostate cancer, its indolence, recurrence, progression, or other outcome with respect to prostate cancer, may provide additional insight regarding the types of features which may be more likely to correlate with outcome. The inventors expect that continued experimentation and/or the use of other suitable hardware, software, or combination thereof will yield various other sets of computer-generated features (e.g., a subset of the features in Tables 1, 5, and 11) that may correlate with these and other medical conditions.

[0108] Additional details regarding image segmentation and measuring morphometric features of the classified pathological objects according to some embodiments of the present invention are described in U.S. Patent No. 7,461,048, issued December 2, 2008, U.S. Patent No. 7,467,119, issued December 16, 2008, and PCT Application No. PCT/US2008/004523, filed April 7, 2008, as well as commonly-owned U.S. Publication No. 2006/0064248, published March 23, 2006 and entitled "Systems and Methods for Automated Grading and Diagnosis of Tissue Images," and U.S. Patent No. 7,483,554, issued January 27, 2009 and entitled "Pathological Tissue Mapping".

[0109] Morphometric Data And/or Molecular Data Obtained from Multiplex IF

[0110] In some embodiments of the present invention, an image processing tool (e.g., image processing tool 136) is provided that generates digitized images of tissue specimens subject to immunofluorescence (IF) (e.g., multiplex IF) and/or measures morphometric and/or molecular features from the tissue images or specimens. In multiplex IF microscopy [15], multiple proteins in a tissue specimen are simultaneously labeled with different fluorescent dyes conjugated to antibodies specific for each particular protein. Each dye has a distinct emission spectrum and binds to its target protein within a tissue compartment such as nuclei or cytoplasm. Thus, the labeled tissue is imaged under an excitation light source using a multispectral camera attached to a microscope. The resulting multispectral image is then subjected to spectral unmixing to separate the overlapping spectra of the fluorescent labels. The unmixed multiplex IF images have multiple components, where each component represents the expression level of a protein in the tissue.

[0111] In some embodiments of the present invention, images of tissue subject to multiplex IF are acquired with a CRI Nuance spectral imaging system (CRI, Inc., 420-720 nm model) mounted on a Nikon 90i microscope equipped with a mercury light source (Nikon) and an Opti Quip 1600 LTS system. In some embodiments, DAPI nuclear counterstain is recorded at 480 nm wavelength using a bandpass DAPI filter (Chroma). Alexa 488 may be captured between 520 and 560 nm in 10 nm intervals using an FITC filter (Chroma). Alexa 555, 568 and 594 may be recorded between 570 and 670 nm in 10 nm intervals using a custom-made longpass filter

(Chroma), while Alexa 647 may be recorded between 640 and 720 nm in 10 nm intervals using a second custom-made longpass filter (Chroma). Spectra of the pure dyes were recorded prior to the experiment by diluting each Alexa dye separately in SlowFade Antifade (Molecular Probes). In some embodiments, images are unmixed using the Nuance software Version 1.4.2, where the resulting images are saved as quantitative grayscale tiff images and submitted for analysis.

[0112] For example, Figure 5A shows a multiplex IF image of a tissue specimen labeled with the counterstain 4'-6-diamidino-2-phenylindole (DAPI) and the biomarker cytokeratin 18 (CK18), which bind to target proteins in nuclei and cytoplasm, respectively. Although the original image was a pseudo-color image generally exhibiting blue and green corresponding to DAPI and CK18, respectively, the image is provided in gray-scale in FIG. 5A for ease of reproducibility.

[0113] In some embodiments of the present invention, as an alternative to or in addition to the molecular features which are measured in digitized images of tissue subject to multiplex IF, one or more morphometric features may be measured in the IF images. IF morphometric features represent data extracted from basic relevant histologic objects and/or from graphical representations of binary images generated from, for example, a specific segmented view of an object class (e.g., a segmented epithelial nuclei view may be used to generate minimum spanning tree (MST) features as described below). Because of its highly specific identification of molecular components and consequent accurate delineation of tissue compartments—as compared to the stains used in light microscopy—multiplex IF microscopy offers the advantage of more reliable and accurate image segmentation. In some embodiments of the present invention, multiplex IF microscopy may replace light microscopy altogether. In other words, in some embodiments (e.g., depending on the medical condition under consideration), all morphometric and molecular features may be measured through IF image analysis thus eliminating the need for, for example, H&E staining (e.g., some or all of the features listed in tables 1 and 2 could be measured through IF image analysis).

[0114] In an immunofluorescence (IF) image, objects are defined by identifying an area of fluorescent staining above a threshold and then, where appropriate, applying shape parameters and neighborhood restrictions to refine specific object classes. In some embodiments, the

relevant morphometric IF object classes include epithelial objects (objects positive for cytokeratin 18 (CK18)) and complementary epithelial nuclei (DAPI objects in spatial association with CK18). Specifically, for IF images, the process of deconstructing the image into its component parts is the result of expert thresholding (namely, assignment of the 'positive' signal vs. background) coupled with an iterative process employing machine learning techniques. The ratio of biomarker signal to background noise is determined through a process of intensity thresholding. For the purposes of accurate biomarker assignment and subsequent feature generation, supervised learning is used to model the intensity threshold for signal discrimination as a function of image background statistics. This process is utilized for the initial determination of accurate DAPI identification of nuclei and then subsequent accurate segmentation and classification of DAPI objects as discrete nuclei. A similar process is applied to capture and identify a maximal number of CK18+ epithelial cells, which is critical for associating and defining a marker with a specific cellular compartment. These approaches are then applied to the specific markers of interest, resulting in feature generation which reflects both intensity-based and area-based attributes of the relevant protein under study. Additional details regarding this approach, including sub-cellular compartment co-localization strategies, are described in

PCT Application No. PCT/US2008/004523, filed April 7, 2008.

[0115] Multiplex IF Image Segmentation. In some embodiments of the present invention, the image processing tool performs multiplex IF image segmentation as follows. To enable feature extraction, epithelial nuclei (EN) and cytoplasm are segmented from IF images using the Definiens image analysis platform [16, 17]. Figure 6 is a flowchart 600 of illustrative stages involved in segmenting and classifying multiplex IF images according to some embodiments of the present invention. The segmentation method performed by the image processing tool may consist of three stages of initial segmentation into primitives 602; classification of primitives into nuclei, cytoplasm, and background 604; and refinement of classified primitives to obtain the final segmentation 606. In some embodiments, the segmentation and feature extraction operations may be applied to regions of interest (ROI's) in the image. In some embodiments, these ROI's may be identified by a pathologist and may be free of non-tumor tissue and artifacts. In other embodiments, these regions may be identified automatically. Figure 5B shows the

image in Figure 5A segmented into epithelial nuclei (EN) 502, cytoplasm 504, and stroma nuclei 506. Although in the original, segmented and classified image the segmented EN 502 are shown in blue, the segmented cytoplasm 504 are shown in green, and the segmented stroma nuclei 506 are shown in purple, the image is provided in gray-scale in Figure 5B for ease of reproducibility.

[0116] Referring to FIG. 6, in a first stage of segmentation 602 image pixels are grouped into small primitive objects. This grouping is based on the similarity of intensity values and shape characteristics of the resulting objects. To obtain the initial primitives, the quad-tree procedure is first applied to the image. The resulting primitives are then grouped further using a multiresolution segmentation procedure [16]. The quad-tree procedure uses color similarity to group pixels, and the multiresolution method uses color similarity and shape regularity to form primitives. A scale parameter controls the average size of the primitives in both methods.

[0117] At stage 604, the primitives in the CK18 image are classified into cytoplasm and background prototype objects, where background consists of autofluorescence and non-specific binding of the fluorescent dye to the tissue. This is accomplished via intensity thresholding, wherein the average intensities of primitives are compared to thresholds computed from the intensity statistics of all primitives in the CK18 image. If the average intensity of a primitive is below a threshold T_{low} , it is classified as a background prototype object. If the average intensity of the primitive is above a threshold T_{high} , it is classified as a cytoplasm prototype object.

Thresholds T_{low} and T_{high} are derived from a threshold T as $T_{\text{low}} = \alpha_{\text{low}}T$ and $T_{\text{high}} = \alpha_{\text{high}}T$. Threshold T is modeled as a linear function $T = \mathbf{A}^T \mathbf{X} + b$, where $\mathbf{A} = [a_1, \dots, a_n]^T$ and $\mathbf{X} = [x_1, \dots, x_n]^T$ are model parameters and intensity statistics of all image primitives, respectively, and b is a constant. Parameters $\{\mathbf{A}, b\}$ are obtained by fitting the model to a set of reference thresholds selected by two pathologists on a training image set. To avoid model over-fitting, feature selection is performed on $\mathbf{X}$ and thus very few elements of $\mathbf{A}^T$ are non-zero. Parameters α_{low} and α_{high} control the classification accuracy for the resulting class prototypes. In an illustrative example, conservative values $\alpha_{\text{low}} = 0.33$ and $\alpha_{\text{high}} = 1.5$ were used to obtain reliable class prototypes.

[0118] The class prototypes obtained using thresholding drive the classification of the rest of the primitives using the nearest neighbor (NN) classification rule. The NN rule classifies each

primitive as being a cytoplasm or background object if the closest prototype object to it is a cytoplasm or background object, respectively. The metric for the NN rule is the Euclidean distance and objects are represented using the vector $[m \ s]^T$, where m and s denote the average and standard deviation of the intensity of the object.

[0119] At stage 606, the class labels of the cytoplasm and background objects are further refined using neighborhood analysis. Background objects smaller than, for example, 12 pixels in area whose border length with cytoplasm relative to their total border length is 0.6 or more are reclassified as cytoplasm.

[0120] Referring back to stage 604, in the first stage of EN segmentation nuclei prototype objects are identified via intensity thresholding. The intensity threshold model is constructed using a similar procedure to that described for classifying cytoplasm prototype objects. Next, background objects whose relative border length to nuclei is 0.66 or more are reclassified as nuclei prototype objects. Moreover, isolated background objects smaller than, for example, 50 pixels in area are reassigned as nuclei prototype objects.

[0121] To build individual nuclei, nuclei prototype objects are subjected to two stages of region growing, a multiresolution segmentation stage, and a final cleanup stage. Generally, region growing consists of using brighter prototype objects as seeds and merging the darker neighboring objects with the seeds to form individual nuclei. In the following example, the super-object for a given object is obtained by merging the object with all of its connected neighbors. In the first stage of region growing, prototype objects whose average brightness relative to the brightness of their super-object is 0.66 or more are identified as seeds. These objects are classified as nuclei if they meet certain shape criteria (e.g., width and length ≤ 25 pixels, elliptic fit ≥ 0.6 , $35 \text{ pixels} < \text{area} \leq 350 \text{ pixels}$), where elliptic fit [16] measures the similarity of the object to a perfect ellipse. Each identified nucleus is then grown by merging the darker neighboring objects with it. The above process is repeated on the remaining prototype objects using objects with a relative brightness of 0.9 or more as seeds. Following the above region growing stages, multi-resolution segmentation is applied to the remaining prototype objects to build more nuclei. In the cleanup stage, the remaining prototype objects are merged with the individual nuclei identified in previous stages if possible, or otherwise classified as

background. Finally, nuclei whose area has an overlap of, for example, 50% or more with cytoplasm are classified as EN. Otherwise, they are classified as stroma nuclei.

[0122] In some embodiments of the present invention, morphometric features for evaluation or use within a predictive model are provided which are derived from (i) the minimum spanning tree (MST) connecting the epithelial nuclei (EN) in multiplex IF image(s) and/or (ii) the fractal dimension (FD) of gland boundaries in multiplex IF image(s). Such features have been determined by the present inventors to be effective for the quantification of tissue architecture and morphology. Fluorescent labels utilized in multiplex IF microscopy enable more reliable and accurate segmentation of tissue compartments over conventional stains used in light microscopy, thus allowing for more robust feature extraction. By way of example only, using univariate analysis and multivariate modeling, the efficacy and robustness of the MST and FD features were demonstrated in the large-scale, multi-institution study described below.

[0123] In some embodiments, two or more features (e.g., clinical, molecular, and/or morphometric features) may be combined in order to construct a combined feature for evaluation within a predictive model. For example, a morphometric feature such as, for example, a minimum spanning tree (MST) feature and/or a fractal dimension (FD) feature, may be combined with a clinical feature to form a combined feature. In one embodiment, a combined feature constructed using the mean edge length of the MST (a morphometric feature) and the patient's Gleason grade (a clinical feature) was selected in a multivariate model for the prediction of disease progression. Other suitable combinations of features are of course possible and are fully contemplated as being within the scope of embodiments of the present invention. Additional examples of combined features are described below in connection with, for example, Figure 9.

[0124] Minimum Spanning Tree (MST) Features. In some embodiments of the present invention, one or more morphometric features used in a predictive model may include or be based on characteristic(s) of a minimum spanning tree (MST) observed in digitized image(s) of tissue subject to multiplex immunofluorescence (IF). As described above, generally IF microscopy offers the advantage of more reliable and accurate image segmentation when compared to traditional light microscopy. For example, features characterizing tissue

architecture may be extracted from the MST connecting the centroids of all epithelial nuclei (EN) in a tissue specimen. In some embodiments, after segmentation of an IF image into CK18-positive DAPI objects, this segmented image may be used to create a graph for the derivation of all MST features. The MST of a graph is defined as the tree connecting all vertices (here, EN centroids) such that the sum of the lengths of the lines (edges) connecting the vertices is minimized. Several methods exist for constructing the MST of a graph. In some embodiments of the present invention, Prim's method may be used [35]. In other embodiments of the present invention, other methods of constructing the MST may be utilized.

[0125] Figure 7 is a flowchart 700 of illustrative stages involved in constructing a minimum spanning tree (MST) of objects within a digitized image of tissue subject to multiplex immunofluorescence (IF) in accordance with some embodiments of the present invention. Let $G = \{V, E\}$ denote a graph with vertices V and edges E , and let $G_{\text{MST}} = \{V_{\text{MST}}, E_{\text{MST}}\}$ denote the MST of G . Such a procedure may be performed by an image processing tool (e.g., image processing tool 136) or any other suitable hardware, software, or combination thereof. The method starts at stage 702 by adding an arbitrary vertex v in V to V_{MST} , that is, $V_{\text{MST}} = \{v\}$. Then, at stage 704, the method determines the nearest vertex in the rest of the graph to the current G_{MST} . That is, the shortest edge e connecting the vertices u and v is found such that $u \in V_{\text{MST}}$ and $v \notin V_{\text{MST}}$. In some embodiments, the length of each edge is the Euclidean distance between the pair of vertices (e.g., EN centroids) that it connects. Then, at stage 706, G_{MST} is updated by adding v to V_{MST} and adding e to E_{MST} . The process of adding vertices is continued at stage 608 until all of them are included in V_{MST} . As indicated at stage 710, the MST is complete once all of the vertices in the graph have been included.

[0126] Figure 8A shows an instance of the MST of epithelial nuclei (EN) identified in an image of tissue subject to multiplex immunofluorescence (IF) according to some embodiments of the present invention. As shown, the MST includes vertices (here, EN centroids) 802. The MST also includes intra-gland MST edges 804 and inter-gland edges 806. Although in the original, segmented and classified image the EN centroids 802 and intra-gland MST edges 804 are marked in yellow, the inter-gland edges 806 are marked in red, and the segmented EN and

cytoplasm are marked in dark and light gray, respectively (with degree 1 and 3 EN outlined in green and red, respectively, as described below), the image is provided in gray-scale in Figure 8A for ease of reproducibility. Other compartments in the image are masked out for clarity.

[0127] A number of characteristics of the MST of EN have been considered in the literature for cancer diagnosis and prognosis [19-23]; however, a fundamental limitation of the studies was that image analysis was performed on light microscopy images of tissue specimens stained using conventional stains such as hematoxylin and eosin (H&E). In an illustrative example according to some embodiments of the present invention, five MST characteristics from images of tissue subject to multiplex immunofluorescence (IF) were selected for potential use as features within a predictive model. Alternatively or additionally, in other embodiments of the present invention, other MST characteristics can be selected for evaluation or use within a model predictive of a medical condition. The five MST features selected were the mean and standard deviation of edge lengths, and the degree distribution for vertices with degrees 1, 2 and 3 (see Figure 9). The degree of a vertex refers to the number of edges incident on the vertex. For example, the degree of vertex (EN centroid) 802 in Figure 8A is 3. Vertex 808 in Figure 8A has a degree of 1. Here, the degree distribution of an MST, d_i , is defined as $d_i = n_i / n$, where n_i denotes the number of vertices with degree i , and n is the total number of vertices. In this example, the degree distribution up to degree 3 was considered as vertices with higher degrees were rare and thus estimates of their proportions were unreliable. In other embodiments of the present invention, degrees of 4 and higher can be selected as features for evaluation or use within a predictive model.

[0128] In the illustrative embodiment shown in Figure 8A, the MST edges connect epithelial nuclei (EN) within glands (e.g., edge 704) as well as across glands (e.g., edge 706). The present inventors have determined that these intra- and inter-gland edges quantify different tissue characteristics. While the lengths of the intra-gland edges characterize the degree to which the EN are invading the stroma surrounding the gland, inter-gland edges measure the separation between glands, which, for a given Gleason grade, is in part due to the biochemical response of the stroma to cancer resulting in the formation of scar tissue. To decouple these two characteristics, the edges of the MST were classified as being intra- or inter-glandular, and the

mean and standard deviation of the edge lengths were separately obtained for each of the two classes of edges. In this illustrative study, the degree distribution for vertices connecting inter-gland edges was uninformative and thus was not considered, although it could be considered in other embodiments. To classify MST edges, connected component analysis was performed on gland regions, where gland regions consisted of the union of EN and cytoplasm regions. Edges connecting EN belonging to the same connected component were classified as intra-glandular. The remaining edges were classified as being inter-glandular. The inter-glandular mean edge length was able to distinguish good and poor outcome patients. In addition, it was correlated with the outcome in the same direction as the MST mean edge length obtained from all EN.

[0129] In some embodiments, the MST approach as described above is a graph-based method that operates on a binary mask. For example, such an approach can be applied to binary masks from lumens identified (e.g., in H&E-stained images) or DAPI/CK18 objects in tissue images subject to immunofluorescence (IF). In other embodiments of the present invention, any other suitable graph-based approach(es) and/or mask(s) could be used in connection with measuring features of interest in tissue or image(s) thereof.

[0130] **Fractal Dimension of Gland Boundaries.** The present inventors have determined that the fractal dimension (FD) of the boundaries between the glands and the surrounding stroma provides a quantitative measure of the irregularity of the shape of the boundary. In general, the FD is a measure of the space-filling capacity of an object. The FD of a straight line is one, whereas the FD of a more irregular planar curve is between 1 and 2. Gland boundaries with lumen and stroma are defined as pixels that have at least one non-gland and one gland pixel among their 4-connected neighbors (Figure 8B). As lumens and stroma can appear similar in multiplex IF images, morphological operations were used to distinguish them. Lumens were defined as pixels belonging to holes in the gland regions, namely, pixels that cannot be reached by flood-filling the non-gland region starting from pixels on the edge of the image. Two FD features were considered in an illustrative study: the FD of gland-stroma boundaries, and the FD of gland boundaries with both stroma and lumens (see Figure 9). Figure 8B shows boundaries of the glands with stroma 810 and boundaries of the glands with lumen 812 as identified in an image of tissue subject to multiplex immunofluorescence (IF) according to some embodiments of

the present invention. Although in the image processed by the image processing tool the boundaries of the glands with stroma 810 and the boundaries of the glands with lumen 812 were shown in yellow and red, respectively, the image is provided in gray-scale in Figure 8B for ease of reproducibility. The FD was estimated using the box-counting algorithm described below.

[0131] In box counting, grids of varying size are placed on the curve of interest and for each grid the grid cells occupied by the curve are counted. For each grid size, the grid is shifted to find the covering of the curve with the smallest number of occupied cells. Let the pair (s_i, N_i) , $i = 1, \dots, p$, denote the grid size and the corresponding cell count, respectively, where p is the number of pairs. The relationship between $\log(N)$ and $\log(s)$ is modeled as a linear function $\log(N) = a \log(s) + b$ via least squares, where a and b denote the slope and intercept of the line. The FD f is then obtained as $f = -a$.

[0132] A practical consideration in the estimation of FD is the choice of the range of s . In the present study, due to the finite resolution of digital images, a small s tends to underestimate the FD. On the other hand, because of the finite extent of images, large s values result in few occupied grid cells, causing the FD estimate to have a large variance. Determination of the optimal s is also confounded by the fact that in some instances tumor boundaries may not exhibit fractal behavior at all or do so over a finite range of scales.

[0133] The range of s was selected based on the constraints imposed by the finite resolution and size of the images, as well as the predictive power of the resulting feature. Initially, the minimum and maximum box size was set to 2 and 64, respectively, where the choice of maximum size was made empirically to ensure that N was at least 50 for most images. Next, the box sizes were set to $s \in \{2, 3, 4, 6, 8, 12, 16, 24, 32, 48, 64\}$, roughly following a power law. Then, for each pair of consecutive box sizes (i.e., $(2, 3)$, $(3, 4)$, $\dots$, $(48, 64)$), the FD was estimated. The predictive power of the FD estimates was then assessed via univariate analysis as described below. The optimal range of s was selected as the range over which the predictive power of the FD remained statistically significant. The final FD feature was obtained based on this range of s .

[0134] **Analysis of MST and FD Features in IF Images.** Biopsy specimens of tissue were

labeled with the DAPI counterstain and multiple biomarkers, including the CK18 biomarker, and were imaged using a CRI Nuance multispectral imaging system yielding 12-bit 1280×1024-pixel images. Multiple (typically three) regions of interest (ROI's) were imaged for each patient. Biomarker images obtained from spectral unmixing were segmented and the MST and FD features were extracted from the segmented images. Finally, feature values extracted from the patient's multiple ROI's were aggregated into a single value per feature by taking their median.

[0135] The predictive value of the proposed MST and FD features was first established via univariate analysis. This was accomplished by training a univariate Cox proportional hazards model [24] on each feature and testing the significance of the coefficient of the trained model using the Wald χ^2 test. Figure 8 shows the two-sided p -values and CI's of the minimum spanning tree (MST) and fractal dimension (FD) features on the training set, where the concordance index (CI) values range from 0 to 1. A CI of 0.5 indicates no relationship between the feature and outcome, whereas CI values below and above 0.5 correspond to negative and positive relationships with outcome, respectively. As the table indicates, except for d_2 , a larger feature value corresponds to a shorter time to clinical failure (CF). Moreover, the present inventors have determined that both FD features and the MST degree distribution for degree 3 (d_3) were highly effective for predicting CF in terms of both χ^2 test p -value and CI. It is noted that the two FD features had similar performance. It is believed that the same carcinogenesis process underlying the uninhibited proliferation of epithelial cells drives the irregularity of gland boundaries with both stroma and lumen, resulting in similar feature performance.

[0136] The intra-gland and overall mean edge length of the MST also had comparable predictive power. This is believed to be because both features are dominated by intra-gland edges whose number is far larger than that of inter-gland edges. On the other hand, the correlation between the inter-gland mean edge length and CF was not significant in this example. To evaluate whether the inter-gland feature would be useful when considered within a group of patients with similar Gleason grades, particularly Grade 3, the correlation within the grade 3 patient group was evaluated. This correlation was insignificant as well in this example. It is suspected that the relatively small number of inter-gland distances that drive the feature is insufficient for obtaining a stable feature. Thus, larger ROI's or a larger number of ROI's may be

needed.

[0137] The present inventors have determined that MST degree distribution has an intuitive interpretation in terms of tumor architecture. As shown in Figure 8A, degree 1 vertices typically occur when an epithelial nuclei (EN) is fairly isolated from other EN. This usually is the case for EN invading the surrounding stroma. Degree 2 vertices, on the other hand, typically correspond to EN regularly arranged within the gland. Finally, degree 3 (and higher degree) vertices usually belong to clusters of EN resulting from uninhibited proliferation. Thus, d_1 and d_3 are both expected to be negatively correlated with the time to clinical failure (CF), whereas the opposite is expected of d_2 .

[0138] **Combined Features.** The present inventors noted that the fractal dimension (FD) features were the most effective for patients with Gleason grades 3 and lower (CI = 0.395). This was the motivation for creating a combined feature. For Gleason grades 4 or higher, the combined feature was set to the Gleason grade. Otherwise, it was set to the FD feature linearly scaled to the range 0 to 3. The mean edge length of the MST and the degree distribution for degree 3 were also most effective for Gleason grades 3 and lower (CI = 0.415 and 0.434, respectively). Thus, a combined feature was constructed for each of these two features by setting the combined feature to the Gleason grade for grades 4 and higher, and setting it to the MST feature scaled linearly to the range 0 to 3 for grades 3 and lower. The univariate CI's for these combined features are also shown in Figure 9. In other embodiments in accordance with the present invention, any other suitable combined features may be utilized such as, for example, any combination of features listed in Tables 1-5, 9, and 11 and Figure 9 which is correlated with an outcome of interest (e.g., correlated with the outcome in univariate analysis).

[0139] In an aspect of the present invention, systems and methods are provided for screening for an inhibitor compound of a medical condition (e.g., disease). Figure 10 is a flowchart of illustrative stages involved in screening for an inhibitor compound in accordance with an embodiment of the present invention. At stage 1002, a first dataset for a patient may be obtained that includes one or more of clinical data, morphometric data and molecular data (e.g., morphometric data and/or clinical data corresponding to one or more of the features listed in Figure 9). A test compound may be administered to the patient at stage 1004. Following stage

1004, a second dataset may be obtained from the patient at stage 1006. The second dataset may or may not include the same data types (i.e., features) included in the first dataset. At stage 1008, the second dataset may be compared to the first dataset, where a change in the second dataset following administration of the test compound indicates that the test compound is an inhibitor compound. Stage 1008 of comparing the datasets may include, for example, comparing an output generated by a predictive model according to an embodiment of the present invention responsive to an input of the first dataset with an output generated by the predictive model responsive to an input of the second dataset, where the predictive model is predictive of the medical condition under consideration. For example, the inhibitor compound may be a given drug and the present invention may determine whether the drug is effective as a medical treatment for the medical condition.

[0140] EXAMPLE 1: Prediction of Prostate Cancer Progression

[0141] In accordance with an illustrative embodiment of the present invention, a predictive model was developed for use on diagnostic biopsy cores of prostate tissue, where the model predicts the likelihood of advanced prostate cancer progression even after a curative-intent radical prostatectomy. This predictive model was developed from data on a multi-institutional patient cohort followed for a median of 8 years. Features evaluated in connection with generating the model included morphometric features extracted from the diagnostic prostate needle biopsy, molecular features corresponding to an expanded in-situ biomarker profile, and several clinical features. The predictive model may be utilized, for example, at the time of diagnosis of prostate cancer and before treatment, to provide an objective assessment of the patient's risk of prostate cancer progression. It is believed that the model resulting from this study, which accurately predicts outcome, will assist in identifying patients who, for example, may benefit from risk-adjusted therapies.

[0142] A prospectively designed method was applied retrospectively to a cohort of patients with clinically localized or locally advanced prostate cancer. The study subjects consisted of 1027 men treated with radical prostatectomy between 1989 and 2003 at 5 university hospitals. The model predictive of clinical progression (distant metastasis, androgen-independent recurrence, and/or prostate cancer mortality) was derived from features selected through

supervised multivariate learning. Performance of the predictive model was measured by the concordance index.

[0143] A risk stratification model was developed using a training set of 686 patients with 87 clinical failure events. Generally, the predictive model includes androgen receptor and Ki67 levels, preoperative PSA, biopsy Gleason score, predominant Gleason grade, and 2 quantitative histomorphometric characteristics of the prostate tissue specimen. The model had a concordance index of 0.74, sensitivity of 78%, specificity of 69%, and hazard ratio 5.12 for predicting clinical progression within 8 years after prostatectomy. Validation on an independent cohort of 341 patients with 44 clinical failure events yielded a concordance index of 0.73, sensitivity 76%, specificity 64%, and hazard ratio 3.47. This was significantly higher than the accuracy (concordance index of 0.69) of the commonly used pre-operative nomogram.

[0144] As demonstrated by the present study, the incorporation of morphometry and space-related biomarker data is superior to clinical variables alone (including clinical stage, biopsy Gleason score and PSA) for, for example, predicting disease progression within 8 years after prostatectomy. Biopsy assessment of androgen receptor signaling and proliferative activity is important for accurate patient stratification. Significantly, this study also demonstrated the predictive power of a characteristic of the minimum spanning tree (MST) as obtained from digitized images of tissue subject to multiplex immunofluorescence (IF).

[0145] Patients and Samples. Information was compiled on 1487 patients treated with radical prostatectomy between 1989 and 2003 for localized or locally advanced prostate cancer for whom tissue samples were available. Patients were excluded who were treated for prostate cancer before prostatectomy. The cohort (67%-33%) was randomized and split between training and validation sets with similar proportions of clinical failure events and balanced demographically.

[0146] Clinical failure (CF) was pre-specified as any of three events: 1) unequivocal radiographic or pathologic evidence of metastasis, castrate or non-castrate (including skeletal disease or soft tissue disease in lymph nodes or solid organs); 2) rising PSA in a castrate state; or 3) death attributed to prostate cancer. The time to clinical failure was defined as the time from radical prostatectomy to the first of these events. If a patient did not experience clinical failure

as of his last visit, or his outcome at the time of his most recent visit was unknown, then the patient's outcome was considered censored.

[0147] Dominant biopsy Gleason grade (bGG) and Gleason score were obtained from re-evaluation of the primary diagnostic biopsy sections obtained from paraffin block(s) selected by the pathologist. Clinical stage was assessed by retrospective review of clinical records.

[0148] Only patients with complete clinicopathologic, morphometric, and molecular data, as well as non-missing outcome information, were further studied; evaluable patients totaled 686 in the training set and 341 in the validation set (See Table 6 below). The characteristics of these 1027 patients were similar to those of the 1487 in the original cohort. 340 (33%) of 1027 patients had PSA recurrence and 338 (33%) had received secondary therapy. 12 of 1027 (1%) died of disease and 157 (15%) died of other causes. Patients were excluded due to poor quality of the biopsy specimen and/or incomplete clinical data. Table 7 below provides a complete review of patient accounting.

Table 6. Characteristics of patients in the training and validation cohorts.

Characteristic	Training n=686	Validation n=341
Mean age, years	63.6	64
Pre-operative PSA		
≤10 ng/ml	460 (67.1%)	231 (67.7%)
>10 ng/ml	226 (32.9%)	110 (32.3%)
Dominant Gleason grade		
2	25 (3.6%)	8 (2.3%)
3	524 (76.4%)	246 (72.1%)
4	130 (19.0%)	85 (24.9%)
5	7 (1.0%)	2 (0.6%)
Gleason Score		
4	5 (0.7%)	4 (1.2%)
5	31 (4.5%)	7 (2.1%)
6	294 (42.9%)	159 (46.6%)
7	287 (41.8%)	137 (40.2%)
8	46 (6.7%)	25 (7.3%)
9	17 (2.5%)	8 (2.3%)
10	6 (0.9%)	1 (0.3%)
Clinical Stage		
T1a	6 (0.9%)	3 (0.9%)
T1c	263 (38.3%)	116 (34.0%)
T2	374 (54.5%)	198 (58.1%)

T3	27 (3.9%)	15 (4.4%)
Missing	16 (2.3%)	9 (2.6%)
Clinical failure events	87 (12.7%)	44 (12.9%)
Castrate rise in PSA	77 (11.2%)	40 (11.7%)
Bone scan positive	9 (1.3%)	4 (1.2%)
Death of prostate cancer	1 (0.1%)	0

Table 7. Patients in full and final cohorts, and clinical failure events in the final cohort.

Patients	Institution					Total
	1	2	3	4	5	
Full Cohort	74	501	600	233	79	1487
Final Cohort	50	267	565	131	14	1027
% Included	67.6	53.3	94.2	56.2	17.7	69.1
Training Set						
Number of Patients	50	182	359	87	8	686
Number of CF Events	9	26	41	11	0	87
% Events	18.0	14.3	11.4	12.6	0	12.7
Validation Set						
Number of Patients	0	85	206	44	6	341
Number of CF Events	0	10	27	6	1	44
% CF Events	0	11.8	13.1	13.6	16.7	12.9

[0149] Up to 7 unstained slides and/or paraffin blocks were obtained for each patient. Slides and sections obtained from blocks were stained with hematoxylin and eosin (H&E). Sections with maximum tumor content and representative of the patient's Gleason score, including areas of the patient's highest Gleason grade, were selected for further analysis.

[0150] **Image Analysis of H&E-Stained Tissue.** Up to three digitized H&E images were acquired from whole-section biopsy specimens and independently assessed for overall tumor content, Gleason grade, and quality (staining properties, morphological detail, and artifacts) by three pathologists. Using a digital masking tool (here, Adobe Photoshop 7.0), only infiltrating tumor was included for morphometric analysis. The outline of the lumen of individual tumor-glands was used to accurately reflect overall gland architecture. An image analysis tool was used to generate morphometric features, specifically including quantitative histologic features based

on cellular properties of the prostate cancer (e.g., relationship of epithelial nuclear area to gland lumen area.) For a given patient, the final value for each morphometric feature was the median value across a patient's entire tumor available for study.

[0151] In the morphometric analysis of H&E-stained tissue, although the "gland unit" object approximates a true gland unit, it is perhaps a misnomer. The intended relationship captured in this object is that between lumens and closely associated epithelial nuclei. Defining such object and therefore a nuclear subclass (here, those closely associated with lumens) allows one, by subtraction, to study nuclei not closely associated with or distant from lumens. It is the variety of possible relationships between the described objects, nuclear subclasses (by extension epithelial cytoplasm subclasses), and total tumor area that comprise features associated (directly or indirectly) with the gland unit. Gland unit objects according to some embodiments of the present invention are created by uniform and symmetric growth around lumens as seeds in the manner described above, which identifies not only gland units but also epithelial cells not captured by the gland, namely, epithelial cells outside of or poorly associated with the gland unit.

[0152] The specific H&E feature selected in the multivariate model described in this example (Figure 11) represents the relative area of the epithelial cells which are poorly associated with the gland units. Specifically, this feature is defined as the area of epithelial cells (nuclei plus cytoplasm) not associated with lumens normalized to the total tumor area. Pathophysiologically this feature as well as most of its variants capture a progression in prostate tumor grade. Most intuitive is the simple progression from a low-grade Gleason pattern 3, in which the majority of epithelial nuclei are closely associated with lumens, to a high-grade Gleason pattern 5, in which most epithelial nuclei are not associated with lumens. Slightly more subtle is the progression of a simple Gleason pattern 3 to a pattern 4. In pattern 4, increased numbers of glands will have very small or no lumens, with epithelial cancer cells either as 'lumen-less' nests or asymmetrically surrounding small lumens, both leading to an increased feature value.

[0153] A distinct feature targeting similar tumor characteristics as the gland unit features is the 'epithelial nuclear band 5 minus 3' feature. This feature measures epithelial nuclear area within static concentric rings (bands) around lumens. Subtracting the content of the innermost rings from the outermost rings gives area of nuclei distant from lumens. As expected, the direction of

univariate correlation changes for epithelial nuclear area closely associated with lumens (band 1) vs. area more distant from lumens (band 5 minus 3). What differentiates 'band 5 minus 3' from the 'gland unit' feature previously described is that 'band 5 minus 3' includes only epithelial nuclear area associated with a lumen whereas the gland unit includes nuclear area quite distant from or completely unassociated with lumens. These two features therefore overlap, particularly in Gleason pattern 4.

[0154] Quantitative Multiplex Immunofluorescence. Multiple antigens were quantified in single tissue sections by immunofluorescence. Two multiplex assays were performed on prostate needle biopsies with Alexa-fluorochrome-labeled antibodies for the following antigens: a) Multiplex 1: androgen receptor (AR), racemase (AMACR), cytokeratin 18 (CK18), TP73L (p63), and high molecular weight keratin; b) Multiplex 2: Ki67, phosphorylated AKT, CD34, CK18 and AMACR (Table 8). Both multiplexes contained 4'-6-diamidino-2-phenylindole (DAPI) to stain nuclei. Based on the distinctive spectral profiles of the fluorochromes, antigen-specific gray-scale images were acquired. An image analysis tool was used to localize the individual antigens. Utilizing antigen distribution and pixel-based intensity maps, the image analysis tool identified cell types and cellular compartments (e.g. luminal epithelial cells, epithelial/stromal nuclei) and quantified AR, Ki67, phosphorylated AKT, CD34, and AMACR in prostate tumor, benign glands, and stroma. Machine learning statistical modeling was employed to determine optimal thresholds for fluorescence intensity and assign classification schemes for positive and negative profiles. For a given patient, the final value for each immunofluorescence feature was the median value across a patient's entire tumor available for study.

[0155] Prior to incorporation into immunofluorescent multiplexes, all antibodies were titrated using both immunohistochemical and immunofluorescent standard operating procedures.

[0156] De-paraffinization and re-hydration of tissue samples were performed per standard operating procedures. Antigen retrieval was performed by boiling the slides in a microwave oven for 7.5 minutes in 1X Reveal Solution (BioCare Medical). The slides were allowed to cool for 20 minutes at room temperature and then were rinsed under running dH₂O. All subsequent steps were performed on a Nemesis 7200 Automated Slide Stainer (BioCare Medical).

[0157] The tissue samples underwent the following pre-hybridization treatment steps. To help permeate the cellular structures of the tissue, the samples were incubated in PBT (PBS + 0.2% Triton-X 100) at room temperature for thirty minutes, followed by a three minute rinse in TBS. To help reduce tissue auto-fluorescence, the samples were incubated in acid alcohol (1% HCl in 70% ethanol) at room temperature for twenty minutes, followed by a three minute rinse in TBS. Blocking of non-specific binding sites was performed by incubating the slides in IF Blocking Reagent (0.5mg/ml BSA in PBS) at room temperature for twenty minutes. No washes were performed between the blocking step and the subsequent hybridization step.

[0158] Two sets of 5 antibodies each (Table 8) were combined with DAPI into multiplex 'quintplex' assays. The "Multiplex-1" analysis includes a cocktail of anti-racemase (AMACR; clone 13H4, Zeta Corporation) at a 1:50 dilution with high molecular weight cytokeratin (HMW CK; clone 34 β E12, Dako) at a 1:50 dilution and p63 (clone BC4A4, BioCare Medical) at a 1:10 dilution made in 1% Blocking Reagent. 400 μ l of this antibody mixture was applied to the tissue sample, and the antibodies were allowed to bind at room temperature for one hour. Incubation was followed by one rinse of three minutes in TBS.

[0159] For the labeling step, a cocktail of Zenon Alexa Fluor 488 anti-Rabbit IgG Fab fragment, Zenon Alexa Fluor 555 anti-mouse IgG1 Fab fragment, and Zenon Alexa Fluor 594 anti-mouse IgG2a Fab fragment was made in 1% Blocking Reagent at twice the concentrations recommended by the manufacturer (1:50 dilution for each Fab fragment). Approximately 400 μ l of this labeling cocktail was applied to the tissue samples, and the tissue samples were incubated at room temperature for 30 minutes. The labeling reaction was followed by one rinse of three minutes in TBS.

[0160] The tissue samples were then treated to a second round of antibody binding and labeling. A cocktail of anti-CK-18 (synthetic peptide, CalBiochem) at a 1:1250 dilution and anti-Androgen Receptor (AR, clone AR441, Fisher (LabVision)) at a 1:10 dilution was made in 1% Blocking Reagent. Approximately 400 μ l of this antibody cocktail was applied to the tissue sample, and the antibodies were allowed to bind at room temperature for one hour. Hybridization was followed by one rinse of three minutes in TBS.

[0161] For the second labeling step, a cocktail of Zenon Alexa Fluor 647 anti-Rabbit IgG Fab fragment and Zenon Alexa Fluor 568 anti-mouse IgG1 Fab fragment was made in 1% Blocking Reagent at twice the concentrations recommended by the manufacturer (1:50 dilution for each Fab fragment). Approximately 400 µl of this labeling cocktail was applied to the tissue samples, and the tissue samples were incubated and rinsed as described for the first labeling step.

[0162] The “Multiplex-2” analysis includes a cocktail of anti-racemase (AMACR; clone 13H4, Zeta Corporation) at a 1:50 dilution and Ki67 (clone K2, Ventana) at a 1:2 dilution made in 1% Blocking Reagent. 400 µl of this antibody mixture was applied to the tissue sample, and the antibodies were allowed to bind at room temperature for one hour. Incubation was followed by one rinse of three minutes in TBS.

[0163] For the labeling step, a cocktail of Zenon Alexa Fluor 488 anti-Rabbit IgG Fab fragment and Zenon Alexa Fluor 555 anti-mouse IgG1 Fab fragment was made in 1% Blocking Reagent at twice the concentrations recommended by the manufacturer (1:50 dilution for each Fab fragment). Approximately 400 µl of this labeling cocktail was applied to the tissue samples, and the tissue samples were incubated at room temperature for 30 minutes. The labeling reaction was followed by one rinse of three minutes in TBS.

[0164] The tissue samples were then treated to a second round of antibody binding and labeling. A cocktail of anti-CK-18 (synthetic peptide, CalBiochem) at a 1:1250 dilution and anti-CD34 (clone QBEnd-10, Dako) at a 1:100 dilution was made in 1% Blocking Reagent. Approximately 400 µl of this antibody cocktail was applied to the tissue sample, and the antibodies were allowed to bind at room temperature for one hour. Hybridization was followed by one rinse of three minutes in TBS.

[0165] For the second labeling step, a cocktail of Zenon Alexa Fluor 647 anti-Rabbit IgG Fab fragment and Zenon Alexa Fluor 568 anti-mouse IgG1 Fab fragment was made in 1% Blocking Reagent at twice the concentration recommended by the manufacturer (1:50 dilution for the anti-Rabbit IgG Fab fragment) or at the manufacturer’s recommended concentration (1:100 dilution for the anti-Mouse IgG1 fragment). Approximately 400 µl of this labeling cocktail was applied to the tissue samples, and the tissue samples were incubated and rinsed as described for the first labeling step.

[0166] The tissue samples were then treated to a third round of antibody binding and labeling. Phospho-AKT (clone 736E11, Cell Signaling) was diluted at 1:100 in 1% Blocking Reagent. Approximately 400 µl of this antibody dilution was applied to the tissue sample, and the antibody was allowed to bind at room temperature for one hour. Hybridization was followed by one rinse of three minutes in TBS.

[0167] For the third labeling step, Zenon Alexa Fluor 594 anti-Rabbit IgG Fab fragment was made in 1% Blocking Reagent at the manufacturer's recommended concentration (1:100 dilution for the anti-Rabbit IgG fragment). Approximately 400 µl of this labeling cocktail was applied to the tissue samples, and the tissue samples were incubated and rinsed as described for the first labeling step.

[0168] A fixation step was performed on all tissue samples by incubating the samples in 10% formalin at room temperature for 10 minutes, followed by one rinse of three minutes in TBS. Samples were then incubated in 0.15 µg/ml DAPI dilactate (Invitrogen) at room temperature for 10 minutes, followed by one rinse of three minutes in TBS.

[0169] Approximately 30.0µl of *SlowFade* Gold antifade reagent mounting solution (Invitrogen) was applied to the samples, which were then cover slipped. Samples were stored at -20°C until analysis could be performed.

[0170] Images were acquired with the CRI Nuance spectral imaging system (CRI, Inc., 420-720 nm model) described above. Spectra of the pure dyes were recorded prior to the experiment by diluting each Alexa dye separately in *SlowFade* Antifade (Molecular Probes). The diluted dye was then spread out on a glass slide, covered with a coverslip and scanned with the same range and interval as the respective dye in the tissue experiment. Representative regions of background fluorescence were allocated in order to complete the spectral libraries for the spectral unmixing process.

Table 8. Antibodies used for quintplex-immunofluorescent multiplexes.

Multiplex	Antibody	Vendor	Catalog #	Clone	Isotype	Dilution
				Synthetic		
Multiplex-1	CK-18	CalBiochem	AP1021	peptide	RIgG	1:1250
	AMACR	Zeta Corp.	Z2001	13H4	RIgG	1:50

	HMW CK	Dako	M0630	34 β E12	MIgG1	1:50
		Biocare				
	p63	Medical	CM163	BC4A4	MIgG2a	1:10
	AR	Fisher (LV)	MS-443-P	AR441	MIgG1	1:10
				Synthetic		
Multiplex-2	CK-18	CalBiochem	AP1021	peptide	RIgG	1:1250
	AMACR	Zeta Corp.	Z2001	13H4	RIgG	1:50
	Ki67	Ventana	790-2910	K2	MIgG1	1:2
	CD34	Dako	M7165	QBEnd-10	MIgG1	1:100
	Phospho-AKT	Cell Signaling	3787	736E11	RIgG	1:100

[0171] From the IF images, the concentration and distribution of biomarkers in tissue can be evaluated by measuring brightness of the elements of the images. Evaluation of IF images allows for objective, automatic evaluation of biomarkers for, for example, prognosis and diagnostics purposes. One of the challenges encountered with IF images is that measured intensity can be associated not only with the particular biomarker for which the antibody is intended, but with nonspecific binding, which often can be stronger than specific binding. For example, nuclei biomarkers are located in epithelial nuclei. In this example, binding of antibody of the nuclear biomarker in stroma would be nonspecific binding. Nonspecific binding of nuclear biomarker can be observed not only outside, but inside nuclei as well, which can cause the measured intensity of biomarker within nuclei to be contaminated by noise.

[0172] The measurement of the biomarker within, for example, epithelial nuclei can be presented as sum of two components: noise and signal. “Noise” is the part of the measured intensity attributable to nonspecific binding. “Signal” is the part of intensity in, for example, epithelial nuclei attributable to specific binding and related with the medical condition under consideration. All intensity observed outside of, for example, the epithelial nuclei can be considered “noise” as well. For example, based on observations regarding the AR biomarker,

the following hypotheses are made: 1. the noise in the epithelial nuclei is proportional to the noise outside of epithelial nuclei; 2. the same factors affect nonspecific binding in epithelial and stroma nuclei; 3. it is assumed that, for each image, there is a threshold value of intensity of biomarker in the epithelial nuclei such that most of epithelial nuclei with intensity above the threshold contain some excess of the biomarker (even though, nuclei with measured intensity may have some biomarker as well, its level is hard to evaluate, because the measurement is affected by random noise); 4. the excess of the biomarker in epithelial nuclei is related with the progression of the disease, while the noise is not. These hypotheses were supported by analyses on data.

[0173] Two types of thresholds were considered: 1. low threshold: nuclei with intensity above this threshold have various levels of concentration of biomarker. To evaluate abundance of biomarker with the low threshold, it is better to use features which take into account variability of the intensity across nuclei. For example, average intensity may be used for this purpose; and 2. high threshold: nuclei with the intensity above this threshold have similar intensity, close to the highest observed. Proportion of nuclei with intensity above the high threshold may be used for estimate abundance of AR in epithelial nuclei. Based hypothesis 2 above, it is proposed to find these thresholds using the values of noise in stroma nuclei.

[0174] On each image, a series of percentiles of intensity of biomarker in stroma nuclei were calculated. Usually, the second percentile, all percentiles from fifth to ninety fifth are calculated with the step 5 and the 99th percentile. The goal is to select the same stroma nuclei percentile on all images, as a low threshold (high threshold) for separation of epithelial nuclei with excess of biomarker. To achieve this goal, for each percentile of the intensity in stroma nuclei, all epithelial nuclei are determined having the intensity above the threshold. For these nuclei, their average intensity and relative area are evaluated. Correlation of these characteristics with, for example, the disease progression on our training data is also evaluated. The percentile of stroma nuclei which produce the most strongly correlated average intensity is selected as low threshold, the percentile which produces the most strongly correlated relative area feature is selected as high threshold.

[0175] In various embodiments of the present invention, different approaches may be used to measure features of interest from the IF images and/or to prepare the images for such measurements. For example, in some embodiments, artifacts in tissue images may be outlined by a pathologist or automatically to exclude them from segmentation (e.g., for Mplex-1 described above). In some embodiments, tumor area to segment may be outlined by a pathologist or automatically (e.g., for Mplex-2 described above). In some embodiments, no artifacts or tumor mask may be used (e.g., segmentation may be performed on the entire image). In some embodiments, initial segmentation may be done with a quad-tree approach (e.g., for Mplex-1 and/or Mplex-2 described above) which may result in faster initial segmentation. In other embodiments, a multi-resolution approach to initial segmentation may be used.

[0176] In some embodiments, an image-derived CK-18 threshold may be used to classify cytoplasm (e.g., Mplex-1). In other embodiments, an image-derived CK-18 threshold may be used to seed nearest neighbor classification (e.g., Mplex-2), which may make cytoplasm detection more robust across a variety of images.

[0177] In some embodiments, an image-derived DAPI threshold, ratio of DAPI signal to super-object, multiple passes of multi-resolution segmentation and growing of nuclei may be used to segment nuclei (e.g., Mplex-1 and/or Mplex-2), which may result in, for example, improved nuclei segmentation. In other embodiments, only an image-derived DAPI threshold and multiple passes of multi-resolution segmentation may be used to segment nuclei.

[0178] In some embodiments, HMWCK and P63 may be used to find basal cells and exclude them measuring AR in epithelial measurements, which may improve measurement accuracy. In some embodiments, gland units and non-gland units associated epithelial nuclei may be detected (e.g., Mplex-1 and/or Mplex-2). In some embodiments, AMACR association may be evaluated on gland units (e.g., Mplex-1 and/or Mplex-2) or small CK-18 objects.

[0179] In some embodiments, epithelial nuclei AR positive classification may be based on a stromal nuclei AR percentiles derived AR threshold (e.g., Mplex-1). In other embodiments, epithelial nuclei AR positive classification may be based on presence of small and bright AR positive sub-objects found using an image-derived threshold. In some embodiments, epithelial

nuclei Ki67 positive classification may be performed based on an image Ki67 percentiles derived threshold.

[0180] In some embodiments, multiple percentiles of AR signal in epithelial and stromal nuclei are determined for analysis (e.g., Mplex-1 and Mplex-2). In some embodiments, individual nuclei measurements may include area, position and AR mean of each nuclei (e.g., Mplex-1). In some embodiments, individual nuclei measurements may include area, position and Ki67 mean of each nuclei (e.g., Mplex-2) for use in, for example, determining the MST in the image(s).

[0181] In some embodiments, epithelial nuclei are binned by AR intensity and nuclei density (e.g., Mplex-1). In some embodiments, blood vessels are detected using CD34 (e.g., Mplex-2). In some embodiments, multiple biomarkers per nuclei may be detected, for example, nuclei expressing Ki67 and pAKT simultaneously (e.g., Mplex-2).

[0182] Statistical Analysis. In this example, the predictive model was constructed using support vector regression for censored data (SVRc), which is an approach that takes advantage of the ability of support vector regression to handle high dimensional data but is adapted for use with censored data. This approach can increase a model's predictive accuracy over that of the Cox model.

[0183] In conjunction with SVRc, a Bootstrap Feature Selection was employed which was developed specifically for SVRc. In the SVRc with Bootstrap Feature Selection method, an initial filtering step removes features which do not univariately correlate with the outcome of interest. Next, N different splits are made of the training data; in each split approximately two-thirds of the total training instances are randomly assigned to a training subset and approximately one-third of the total training instances are randomly assigned to a testing subset. In this study, N=25 splits were generated.

[0184] The method begins with a "greedy-forward" feature selection process starting with all the features which passed the initial filter. Models are built by increasing the number of features, such that the first model is built on a single feature. For each feature, N models are built using this feature on the training subsets across all the splits, then tested on the N respective testing subsets. The overall performance for each feature is averaged across the N runs. The feature with the best overall performance is selected. In the next step, each feature is added to the

selected feature and again N models are built and tested across the splits. The feature whose addition resulted in the best overall performance is selected. The method continues in this fashion until there are no more features which will improve the performance.

[0185] Subsequently, a “greedy-backward” feature selection approach is employed. Each feature is removed, and N models without that feature across the splits are built and tested. The feature whose removal results in the best overall performance is removed, and the procedure is repeated until the model’s performance ceases to improve due to the removal of features. This step simplifies model complexity and removes features which may have initially been significant, but their information contribution is encapsulated within a feature added subsequently.

[0186] Finally, the complete SVRc model is trained using all the selected features on the complete training cohort. The weight of each feature within the final model is a measure of the relative contribution of that feature’s information in predicting a patient’s outcome. A positive weight implies a positive correlation with outcome (increasing values of the feature are associated with longer survival time) whereas a negative weight implies a negative correlation with outcome (increasing values of the feature are associated with shortened time to event).

[0187] Four metrics were employed to assess a model’s performance: the concordance index (c-index), sensitivity, and specificity, and hazard ratio. The c-index estimates the probability that, of a pair of randomly chosen comparable patients, the patient with the higher predicted time to clinical failure (CF) from the model will experience CF within a shorter time than the other patient. The concordance index is based on pairwise comparisons between two randomly selected patients who meet either of the following criteria: 1) both patients experienced the event and the event time of one patient is shorter than that of the other patient, or 2) only one patient experienced the event and his event time is shorter than the other patient’s follow-up time. The concordance index for a multivariable model ranges from 0.5 (model performs the same as a coin toss) to 1.0 (model has perfect ability to discriminate).

[0188] In order to estimate sensitivity and specificity, typically evaluated for binary output, a clinically meaningful timeframe (CF within 8 years) was selected to separate early from late events. Patients whose outcome was censored before 8 years were excluded from this

estimation. The model's output was inversely scaled to a score between 0 and 100 (longer CF-free times having a lower score and shorter survival times having a higher score). Thereafter every value of the model's score was taken one after another as a potential cut point of the prediction. For each of these potential cut points, the sensitivity and specificity of the classification were evaluated. Sensitivity was defined as the percentage of patients who experienced CF within 8 years that were correctly predicted; specificity was defined as the percentage of patients who did not experience CF within 8 years that were correctly predicted. Every cut point was evaluated by the product of its sensitivity and specificity. The cut point with the highest value of the product was selected as the predictive cut point, and its sensitivity and specificity were considered to be the sensitivity and specificity of the model. In this model, a cut-point of 30.195 was selected, indicating that, if patients with a scaled score above 30.195 are considered as experiencing CF within 8 years post radical-prostatectomy, and patients with a scaled score below 30.195 are considered as being CF-free for 8 years, the model will have a sensitivity and specificity of 78% and 69% in training and 76% and 64% in validation.

[0189] The hazard ratio was also calculated to compare stratification for patients at low risk/high risk for CF within 8 years using the same cut-point employed for sensitivity/specificity. The hazard ratio in training was 5.12 and in validation was 3.47.

[0190] The c-index was also used to measure univariate correlation with CF for each predictive feature. The interpretation of the c-index for univariate correlation is similar to that for the aforementioned model c-indexes. For univariate correlation, a c-index of 0.5 indicates random correlation. Values between 0.5 and 0 indicate negative correlation with outcome; the closer to 0 the better the predictive power. Values between 0.5 and 1 indicate positive correlation with outcome; the closer to 1 the better the predictive power. A heuristic rule used was that features with a concordance index above 0.6 (for positively correlating features) or below 0.4 (for negatively correlating features) are significant. Values of 0.4 and 0.6 approximate a p-value of 0.05.

[0191] A probability for each SVRc model score was generated by analyzing the probability of CF within 8 years in each percentile of the SVRc model scores in the training data. A

probability function was then computed to generate a probability of CF within 8 years for each model score.

[0192] RESULTS

[0193] Patient characteristics in the training set. In the training set of 686 patients, 87 (12.7%) had clinical failure after prostatectomy: 9 with a positive bone scan, 77 with a castrate rise in PSA, and 1 with death from prostate cancer. These 686 patients were followed for a median of 96 months after prostatectomy. Patient characteristics are detailed in Table 6 above. In univariate analyses, preoperative PSA, biopsy Gleason score, and dominant biopsy Gleason grade (bGG) were the only clinical variables associated with clinical failure (concordance index ≤ 0.4 or ≥ 0.6 ; Table 9). In Table 9, the features listed in bold were ultimately selected in the final predictive model. The H&E and IF/H&E features are described above in connection with Table 5. The MST/IF features are described above in connection with Figure 9. In addition, feature “CombIFEpiNucMeanEdgeLengthInter” is a combined feature representing the mean edge length of epithelial nuclei for inter-gland edges for Gleason grades 3 and lower, and the Gleason grade itself for Gleason grades 4 and 5. The MST/IF feature “CombIFEpiNucMeanEdgeLengthIntra” is a combined feature representing the mean edge length of epithelial nuclei for intra-gland edges for Gleason grades 3 and lower, and the Gleason grade itself for Gleason grades 4 and 5. The IF feature “IFx1_RelAreEpi_ARpAMACRp2EN” is a normalized area and intensity feature representing proportion of epithelial nuclei that express positive levels of both AR and AMACR. The feature “CombinedIF_ARepinucnormint” is a combined feature representing the normalized level of AR intensity in epithelial nuclei for Gleason grades 3 and lower, and the Gleason grade itself for Gleason grades 4 and 5. The feature “CombinedIFx1_RelAreNGA2Cyt_4lowGl” is a combined feature representing the relative area of non-gland associated content to cytoplasm for Gleason grades 3 and lower, and the Gleason grade itself for grades 4 and 5. The feature “CombLowGleARpAMACRplum_HighGLKi67” is a combined feature which is different depending on the relative area of lumens in a patient’s tissue or image thereof (e.g., image of H&E-stained tissue). An optimal cutpoint is derived for the relative area of lumens. For patients with a value less than or equal to the cutpoint, the IF feature representing the relative area of AR

positive and AMACR positive epithelial nuclei is used. For patients with a value greater than the cutpoint, the IF feature representing the proportion of Ki67 positive epithelial nuclei is used.

Table 9. Features used as input for model development. Inclusion was based on concordance index for predicting clinical failure in the training cohort in univariate analysis.

Feature	Feature Domain	Concordance Index
Preoperative PSA	clinical	0.373
Dominant biopsy Gleason grade	clinical	0.371
Biopsy Gleason score	clinical	0.336
IFx1_RelAreEpi_ARpAMACRp2EN	IF	0.375
proportion_edge_2_epinuc	MST/IF	0.606
proportion_edge_3_epinuc	MST/IF	0.364
HE02_Lum_Are_Median	H&E	0.654
orig_approximation_4	H&E	0.637
orig_diag_detail_6	H&E	0.654
HEx2_nta_Lum_Are_Tot	H&E	0.635
HEx2_EpiNucAre2LumMeanAre	H&E	0.388
HEx2_nrm_ENWinGU_Are_Tot	H&E	0.645
HEx2_nrm_ENOutGU_Are_Tot	H&E	0.355
HEx2_nrm_CytWinGU_Are_Tot	H&E	0.638
HEx2_nrm_CytOutGU_Are_Tot	H&E	0.362
HEx2_RelArea_EpiNuc_Out2WinGU	H&E	0.353
HEx2_RelArea_Cyt_Out2WinGU	H&E	0.360
HEx2_RelArea_ENCyt_Out2WinGU	H&E	0.348
HEx2_ntaENCYtOutGU2Tumor	H&E	0.347
HEx2_nrmLUM_ENOutGU_Are_Tot	H&E	0.353
HEx2_nrmLUM_CytWinGU_Are_Tot	H&E	0.341
HEx2_nrmLUM_CytOutGU_Are_Tot	H&E	0.340
HEx2_nrmLUM_EpiNucCytOutGU	H&E	0.343
HEx2_nrm_ENCytWinGULum_Are_Tot	H&E	0.610
HEx2_RelArea_ENCytLum_Out2WinGU	H&E	0.345
HEx2_RelArea_EpiNucCyt_Lum	H&E	0.341
HEx2_ntaLumContentArea	H&E	0.643
HEx2_nrmEpiNucBand5minus3	H&E	0.378

min_orig_L_detail5	H&E	0.646
CombinedIFEpiNucMeanEdgeLength	MST/IF	0.330
CombinedIF_ARepinucnormint	IF	0.324
CombLowGleAR_HighGLKi67	IF	0.306
CombinedIFx1_RelAreNGA2Cyt_4lowGl	IF	0.331
RelAreaKi67post_2Lumen	IF/ H&E	0.315
RelAreapAKTpos_2Lumen	IF/ H&E	0.344
RelAreaIFM2EpiNuc_2Lumen	IF/ H&E	0.383
RelAreARpAMACRp2Lumen	IF/ H&E	0.342
CombLowGleARpAMACRp2Lumen_HighGLKi67	IF	0.313
CombIFEpiNucMeanEdgeLengthInter	MST/IF	0.349
CombIFEpiNucMeanEdgeLengthIntra	MST/IF	0.328

[0194] Histologic image analysis. From areas of tumor in digitized images of each patient's H&E-stained biopsy cores, a series of morphometric features were generated, reflecting overall tissue architecture, including distribution of tumor cells and their relationship to glandular structures. Twenty-seven histologic features displayed significant association with clinical failure in univariate analyses (concordance index ≤ 0.4 or ≥ 0.6 ; see Table 9).

[0195] Quantitative immunofluorescence. AMACR as a marker can be used to identify and characterize individual tumor cells [25]. In the current study, AR, Ki67, and phosphorylated AKT were quantified in AMACR-positive and AMACR-negative epithelial tumor cells, and then multiple features related to levels of AR, Ki67, phosphorylated AKT, and AMACR were generated. An endothelial marker, CD34, was also used to assess overall vascularity within the prostate cancer stroma and constructed features of total vessel area and features that related vessel distribution to glandular and epithelial objects. Finally, DAPI and CK18 immunofluorescence were used to quantify tumor morphometry by minimum spanning tree (MST) functions. Generally, the MST characteristics represent proximity between tumor cells and their distribution with respect to glands and each other. For MST characteristics, AR, and Ki67, a series of compound features were constructed that incorporate a clinical trigger, dominant bGG, for determination of marker assessment (e.g. if $bGG \leq 3$ use AR feature; $bGG > 3$ use Ki67 feature). One goal was to identify subtle changes in the morphology and biology

between dominant bGG 3 and 4 tumors that may affect outcome.

[0196] In training, 10% of non-censored patients (36 of 303) with a bGG ≤ 3 had clinical progression within 8 years of prostatectomy. Of this group, 19 of 36 cases (52%) had high levels of AR suggesting that AR expression importantly discriminates significant from indolent disease, especially in low-grade cancers. By comparison, 31 out of 55 non-censored patients (36%) with bGG > 3 had clinical progression within 8 years of prostatectomy. In this group, increasing levels of Ki67 were determined to be additive with bGG regarding shortened time to clinical progression.

[0197] **Model Development.** A SVRc model to predict clinical failure was developed from the data on the 686 training-set patients. The modeling began with the 40 variables that displayed association with clinical failure in univariate analyses (Table 9). Supervised multivariate learning resulted in an optimized model containing 6 features (shown in bold in Table 9), which are listed in Figure 11 in the order of their importance in the final predictive model.

[0198] The clinical features selected by the model were preoperative PSA, biopsy Gleason score, and dominant bGG. Generally, the two imaging features, single infiltrating cells and cellular topology, reflect cellular and tissue architecture at the transition between a dominant Gleason pattern 3 and 4. The first, based on H&E in this example, quantifies the proportion of tumor epithelial cells that are not directly associated with an intact gland structure. The second is an MST combined feature, which relies on the dominant bGG as a trigger (≤ 3 use MST function; > 3 use actual Gleason grade (dominant bGG)) and quantifies proximity between tumor cells as affected by degree of differentiation and stromal content. When bGG is evaluated the combined feature it has a negative weight, whereas the standalone bGG feature evaluated in the model has a positive weight.

[0199] Figures 12 and 13 are Kaplan-Meier curves for the two imaging features which illustrate their ability to accurately stratify patients. Figure 12 shows the Kaplan-Meier curves for the morphometric feature of area of isolated (non-lumen associated) tumor epithelial cells relative to total tumor area (cut-point 0.31, $p < 0.00001$), as measured in an images of needle biopsy tissue specimens after H&E staining. Figure 13 shows the Kaplan-Meier curves for the

morphometric feature of mean edge length in the minimum spanning tree (MST) of all edges connecting epithelial nuclei centroids, in combination with the clinical feature of Gleason grade (cut-point 3.93, $p < 0.00001$), as measured in an images of needle biopsy tissue specimens subject to multiplex immunofluorescence (IF). In both instances, the optimal cut-point values were calculated using the log rank test.

[0200] From the biomarker-based features, the SVRc bootstrap method selected only the combined immunofluorescence (IF) feature of dynamic range of AR and total Ki67 content. Shorter time to clinical failure was predicted by increasing proportion of tumor cells with high AR expression in specimens with clinical bGG ≤ 3 , and high Ki67 levels in specimens with bGG 4-5. For AR, the feature calculates the ratio between the 90th and 10th intensity percentiles of AR in epithelial and stromal nuclei, respectively. It was demonstrated that intensity values of stromal nuclei within the entire tumor compartment were not associated with outcome and represent a good measure of background, namely non-specific fluorescence in the images. This allows for the identification of a true positive signal as well as the distribution of that signal in the epithelial compartment. The AR value is scaled between 0 and 3. Greater values were associated with a shorter time to progression in patients with dominant biopsy Gleason grade of ≤ 3 . For Ki67, the relative area of epithelial nuclei was measured that contains a positive Ki67 signal relative to the total number of epithelial nuclei in the tumor-only area of the needle biopsy. The Ki67 'positive' assignment was based on machine learning models which incorporate mean intensity values for Ki67 in epithelial nuclei followed by thresholding using the stromal nuclei as a baseline for the background fluorescent signal. This Ki67 feature is scaled between 3 and 5. Increasing values in patients with dominant biopsy Gleason grade 4 and 5 were associated with a shortened time to disease progression. In this embodiment, the infiltrative tumor area as denoted for both AR and Ki67 was previously identified and outlined by the pathologist during initial image processing. In other embodiments, such tumor area may be identified automatically.

[0201] Figure 14 shows the Kaplan-Meier curves for patients stratified according to this combined AR-Ki67 molecular feature, where the combined feature cut-point was 0.943 calculated using the log rank test ($p < 0.00001$). Typical immunofluorescence results (e.g., viewed at magnification X200) for AR show AR in epithelial nuclei with increasing intensity

from blue (least), red (moderate) to yellow (high), gold corresponding to AMACR+, green corresponding to AMACR-, and purple corresponding to stromal nuclei. Typical immunofluorescence results (e.g., viewed at magnification X200) for Ki67 show Ki67 (yellow) in tumor epithelial nuclei (blue) and purple corresponding to stromal nuclei.

[0202] The training model had a concordance index of 0.74. When patients were stratified by model score below vs. above 30.19 (corresponding to a 13.82% model-predicted probability of clinical failure), the hazard ratio was 5.12, sensitivity 78%, and specificity 69% for correctly predicting clinical failure within 8 years. Figure 15 shows the Kaplan-Meier curves for patients in the training set stratified by the value or score output by the predictive model, which illustrates the ability of the model to separate patients from the training set according to risk (hazard ratio 5.12). Low risk was predicted for model scores ≤ 30.19 , whereas high risk was predicted for model scores > 30.19 . The probability of remaining free of clinical progression is provided by the y-axis and follow-up time (in months) is given by the x-axis. The p-value (<0.0001) was estimated using the log-rank test.

[0203] Validation. The model was validated using data from 341 patients with a median follow-up of 72 months. Forty-four patients (12.9%) had clinical failure, 4 with a positive bone scan, and 40 with a castrate rise in PSA. The model's performance resulted in a concordance index of 0.73, hazard ratio 3.47, sensitivity 76%, and specificity 64% for predicting clinical failure. Separate Kaplan-Meier curves were generated for patients whose model scores were above or below 30.19 (Figure 16; hazard ratio 3.47). These two patient groups differed significantly in time to clinical failure (log-rank test $P<0.0001$).

[0204] DISCUSSION

[0205] One of the major challenges in the management of patients diagnosed with localized prostate cancer is determining whether a given patient is at high risk for dying of his disease. To address this issue, a predictive tool according to some embodiments of the present invention is provided that can be used at the time of diagnosis: a pre-treatment model using clinical variables and features of prostate needle biopsy specimens to predict the objective end-point of clinical failure after prostatectomy. The model performed in validation with a concordance index of 0.73, hazard ratio 3.47 ($p<0.0001$), sensitivity 76%, and specificity 64%. By comparison, the

10-year biochemical preoperative recurrence nomogram [9] when applied to the same cohort yielded a concordance index of 0.69, and hazard ratio of 2.34 ($p=0.01$), demonstrating the improved accuracy with a more clinically relevant end-point, obtained with the systems approach. Furthermore, the model, as compared with the 10-year postoperative PSA recurrence nomogram [26], was able to identify twice the number of high-risk patients classified by traditional clinical criteria as intermediate risk group. It is believed that a systems pathology model employing multiple robust tumor characteristics will yield a more objective risk assessment of contemporary patients, particularly in a community practice, where selected pathologic variables are prone to subjectivity.

[0206] A strength of the approach was the use of a large cohort from 5 centers in the United States and Europe, which should confer broad applicability. In addition, the features selected in the final model performed uniformly across all cohorts, thus constituting a robust patient profile that should be useful for assessing probable disease course at a time crucial for treatment decisions.

[0207] The clinical variables selected in the model were pretreatment PSA, biopsy Gleason score, and dominant bGG. Both PSA and biopsy Gleason score were found to be important predictors for overall survival in an untreated, conservatively managed population-based cohort from the U.K.[27, 28]. In that study, clinical stage also predicted survival, albeit more weakly. In the example presented above, clinical stage was not found to be a significant parameter in univariate analysis, and therefore it was not included in the multivariate model.

[0208] Higher bGG was associated with worse outcome in univariate analysis; however, it was associated with better outcome in the multivariate model. This phenomenon illustrates the “reversal paradox” known in statistics; the variable is acting as a control for other factors during modeling [29-32]. It is believed that the reversal in the disease progression model described herein resulted primarily from the impact of the two combined features, which contain the dominant bGG as a trigger (i.e., if $bGG \leq 3$ use MST or AR values). Interestingly, several studies have questioned the utility of dominant bGG, especially for 3+4 and 4+3 patterns, given that the associated probabilities of biochemical recurrence overlap substantially, and that bGG is often down-graded upon analysis of the radical prostatectomy specimen [33-35].

[0209] A key component for the current study described above is the morphometric and image analysis strategies to assess tissue architecture and cellular distribution. The MST feature in the model (Figure 11) reflects the spatial distribution of tumor epithelial nuclei in a stromal matrix. It was optimized for bGG ≤ 3 patterns to identify subtle morphologic changes that may relate to properties of de-differentiation. The H&E feature evaluates tumor organization where intact gland structures and cell-to-cell boundaries begin to deteriorate, as identified in progression of Gleason grade 3 to 4 tumors. In the final model, increasing levels for both features were associated with a shortened time to clinical progression, suggesting a more aggressive phenotype capable of invasion within the prostate. By comparison, in this example, morphometric features that were significant in a previous, post-prostatectomy model for clinical failure (e.g., lumen size, tumor cell composition) [36] were not selected by the biopsy model.

[0210] A central role has been demonstrated for both AR and Ki67 in prostate cancer growth and progression [25, 36, 37-42]. The current model reveals the importance of AR and Ki67 specifically in specimens of low and high Gleason grade, respectively. It is believed that this differential assessment of AR and Ki67 constitutes a biologic tumor grade that is important for understanding behavior, and that utilizing the dominant bGG as a classifier for feature annotation allows for discrimination of disease progression risk among intermediate-grade cancers. It is further believed that the aberrant activation of AR, possibly combined with an early chromosomal translocation (e.g., TMPRSS2:ERG) may affect downstream signaling pathways, thereby contributing to the evolution of castrate metastatic disease [43].

[0211] Prior evidence in both biopsy and prostatectomy specimens has linked Ki67 labeling index with bGG and outcome. However, as with AR, clinical adoption has been challenged due primarily to lack of reproducibility, lack of standardized laboratory practices, and the need for determination of an accurate and generalizable cut-point. The approach of incorporating quantitative immunofluorescence standards and machine learning to normalization and choice of threshold(s) may well have circumvented these limitations.

[0212] Finally, although associated with outcome, phosphorylated AKT was not selected in the multivariate model. In addition, the features derived from the CD34 vessel content did not reach univariate statistical significance, although trends were noted. Several studies have

demonstrated involvement of phosphorylated AKT in proliferation and survival pathways in prostate cancer, and have linked increased phosphorylated AKT with Ki-67, activated AR, and a hormone-refractory phenotype [44-47]. The role of CD34 is more controversial, primarily due to differing methods for identifying and counting vessels in various sample types [48-50]. In other embodiments, phosphorylated AKT and CD34 could be included as having prognostic and predictive significance in prostate cancer progression and/or with respect to other medical conditions.

[0213] To address the robustness of our current model results, the model (generated based on SVRc and systems integration of clinicopathologic data with quantitative H&E image and immunofluorescence analyses) was compared with the traditional clinicopathologic factors, independently and in the Kattan nomograms. There are no available tools for predicting clinical disease progression at the time of diagnosis, thus for comparison the Kattan pre-operative nomograms were used, which predict PSA recurrence at 5- and 10-year intervals. Table 10 illustrates the performance of each method for predicting CF in the validation cohort. Hazard ratios were calculated by identifying the optimal cut-point in the training set and applying it to the validation set, as described above. Additionally, a sensitivity and specificity analysis of the nomograms versus the systems method according to an embodiment of the present invention in low- and intermediate-risk groups (as defined by AUA criteria) indicates that the systems method is twice as effective at identifying patients who are at high risk for CF within 8 years but appear to be low to intermediate risk based on clinical profiles.

Table 10. Univariate and Multivariate Results for Predicting CF within 8 years in the validation cohort.

Predictor	C-Index	Hazard Ratio	Hazard Ratio p-value
Age at biopsy	0.47	0.81	0.521
Pre-Operative PSA	0.67	1.93	0.030
Clinical Stage	0.53	1.19	0.769
Dominant Gleason Grade	0.60	2.29	0.007
Gleason Score	0.68	2.92	0.002
Kattan 5-year PSA	0.69	2.34	0.0053

Recurrence Nomogram			
Kattan 10-year PSA	0.69	2.62	0.0098
Recurrence Nomogram			
SVRc-based Systems	0.73	3.47	<0.0001
Pathology Model			

[0214] In conclusion, a highly accurate, robust tool for predicting disease progression at the time of initial diagnosis was provided as a result of this study. It is believed that the biologic and morphologic attributes within the model represent a phenotype that will supplement current practice in determining appropriate treatment options and patient follow-up.

[0215] **EXAMPLE 2: Prediction of Favorable Pathology (Indolent Disease)**

[0216] In accordance with another illustrative embodiment of the present invention, a predictive model was developed for use on diagnostic biopsy cores of prostate tissue, where the model predicts the likelihood that a patient's disease is indolent, namely the likelihood that a patient would have a favorable pathology (indolent disease) if the patient were to undergo a radical prostatectomy to treat prostate cancer in the patient. Generally, predictions by the model may assist patients and/or their physicians with determining whether to undergo a radical prostatectomy or other course of treatment. For example, a prediction indicative of an indolent disease (favorable pathology) may weigh in favor of watchful waiting or other, comparatively less aggressive course of treatment. Conversely, a model prediction indicative of a nonindolent disease (unfavorable pathology) may weigh in favor of a radical prostatectomy or other, comparatively more aggressive treatment. As another example, an assessment of favorable pathology may lead a physician and patient to seek dual treatments, such as hormonal therapy in conjunction with a radical prostatectomy. In this study, only features obtained from data available at the time of biopsy were employed as predictor variables.

[0217] **Patients and Samples**. Information was collected on a total of 1487 patients who were treated by radical prostatectomy between 1989 and 2003 (i.e., the same patients described above in connection with Example 1). Patients who were treated for prostate cancer prior to prostatectomy were not included. Only patients with complete data for all relevant features (see

Independent Variables, below) and only those with non-missing data for indolent disease as assessed by favorable pathology (see Definition of Endpoint, below) were eligible for the study. They were randomly divided between training and validation sets with demographic balance maintained. Researchers otherwise not involved in any aspect of the study conducted this split. The final number in the training set totaled 628 and the final size of the validation set was 280.

[0218] Definition of Endpoint. A patient was defined as having indolent disease if and only if he: (a) had a pathological stage as assessed by prostatectomy data as T2 or less, (b) had a total Gleason score as assessed at prostatectomy of six (6) or less with each component of the Gleason score (dominant and secondary) being three (3) or less and (c) if his PSA “nadired” after surgery, meaning that the first PSA reading was zero post-surgery. Patients who met this definition were coded as a ‘1’ for indolent disease and those who did not were coded as a ‘0’. This binary variable was the sole dependent measure of the study.

[0219] Independent Variables. Clinical features, morphometric features (based on H&E and immunofluorescence (IF)), and molecular features (based on IF) were screened for possible inclusion in the set of features to be subjected to feature selection for the final model. All of the features listed in Tables 1-4 provided (i.e., the features which were used as the starting point for the Disease Progression model) were tested for univariate associations with favorable pathological stage (FPS). For example, “IF01” and “IF02” features were analyzed that were measured through the use of MPLEX 1 and MPLEX 2 described above. Based on expert input, various features were also removed from consideration. A set of twenty-six (26) features, which are listed and described in Table 11, was chosen based on their univariate associations with the dependent variable, i.e., favorable pathological stage in this example. Features were processed so that the range for all features was -1 to 1. All of the Wald-Chi Squared values provided in Table 11 had a p value of less than 0.00000001 and one degree of freedom.

Table 11: Input Feature Set for Favorable Pathological Stage (FPS) Model Development

Feature Name	Type/ Domain	Univari- ate Signifi- cance to FPS (Wald- Chi- Square Value)	Feature Description
preop_psa	Clinical	38.176	Pre-operative PSA measurement (ng/ml)
bxgg1	Clinical	29.730	Dominant Biopsy Gleason Grade
bxgscore	Clinical	62.075	Dominant Biopsy Gleason Score
fd_3_8	Morph./ IF	22.270	Fractal dimension of gland boundaries assessed by a box size range of 3 to 8 pixels
proportion_edge_2_epinuc	Morph./ IF/MST	30.294	Proportion of epithelial nuclei with an edge count of 2 in a minimum spanning tree (MST) of all epithelial nuclei
proportion_edge_3_epinuc	Morph./ IF/MST	40.731	Proportion of epithelial nuclei with an edge count of 3 in a minimum spanning tree (MST) of all epithelial nuclei
IFx2_RelAreEN_Ki67p_Area2EN	Molec./ IF	20.834	Relative area of epithelial nuclei that are Ki67 positive
HE02_Lum_Are_Median	Morph./ H&E	21.490	Median area of lumens
orig_approximation_1	Morph/ IF	34.849	Variance of pixel values in the approximation sub-band after applying 1 stage of undecimated wavelet transform to a mask of glands
orig_diag_detail_5	Morph./ IF	38.624	Variance of pixel values in the diagonal detail sub-band after applying 5 stages of undecimated wavelet transform to a mask of glands
HEx2_nta_Lum_Are_Tot	Morph./ H&E	31.855	Relative area of lumens
HEx2_EpiNucAre2LumMeanAre	Morph./ H&E	29.422	Ratio of the total epithelial nuclear area to the average size of lumens

Feature Name	Type/ Domain	Univariate Significance to FPS (Wald- Chi- Square Value)	Feature Description
HEx2_nrm_ENWinGU_Are_Tot	Morph./ H&E	49.146	Relative area of epithelial nuclei that are inside (within) gland units
HEx2_nrm_ENOutGU_Are_Tot	Morph./ H&E	49.146	Relative area of epithelial nuclei that are outside of gland units
HEx2_RelArea_EpiNuc_Out2WinGU	Morph./ H&E	32.205	Ratio of the area of epithelial nuclei outside of a gland unit to the area of epithelial nuclei inside a gland unit
HEx2_RelArea_ENCyt_Out2WinGU	Morph./ H&E	27.800	Ratio of the area of epithelial cells (nuclei + cytoplasm) outside of a gland unit to the area of epithelial cells (nuclei + cytoplasm) inside of a gland unit
HEx2_ntaENCytWinGU2Tumor	Morph./ H&E	18.289	Ratio of the area of epithelial cells (nuclei + cytoplasm) within a gland unit to the tumor area
HEx2_nrm_ENCytWinGU_Lum_Are_Tot	Morph./ H&E	27.967	Ratio of the area of epithelial cells (nuclei + cytoplasm) within a gland unit and the total area of lumens to the tumor area
HEx2_RelArea_EpiNucCyt_Lum	Morph./ H&E	28.797	Ratio of the area of epithelial cells (nuclei + cytoplasm) to the area of lumens
HEx2_sub_EpiNucDen1_3_Lum	Morph./ H&E	24.816	Measures the area of low density epithelial nuclei relative to lumens by evaluating each epithelial nuclei neighborhood, and calculating the percentage area that is epithelial nuclei. These areas are binned into deciles of 10%, and each decile is divided by the total area of epithelial nuclei and further divided by the total lumen area. This feature is sum of deciles 1 to 3.

Feature Name	Type/ Domain	Univari- -ate Signifi- cance to FPS (Wald- Chi- Square Value)	Feature Description
HEX2_nrmEpiNucBand5mi nus3	Morph./ H&E	47.970	Measures the areas of epithelial nuclei distributed away from gland units. Calculated by measuring the areas of epithelial nuclei with centers that are in a band a certain distance away from lumen borders. The band includes all epithelial nuclei that are at least three units away from the lumen border but within 5 units of the lumen border; a unit is a fixed number set to be approximately the diameter of one epithelial nucleus.
min_orig_L_detail4	Morph./ H&E	32.124	Minimum of the variances of pixel values in the horizontal and vertical detail sub-bands after applying 4 stages of undecimated wavelet transform to a mask of lumens
CombinedIFEpiNucMeanE dgeLength	Morph. (Combined)/ IF/MST	44.196	Combined feature. If the dominant biopsy Gleason Grade is ≤ 3 , is the average edge length between epithelial nuclei in a minimum spanning tree (MST) of all epithelial nuclei scaled between 0 and 3, if the Gleason Grade is ≥ 4 , is the Gleason Grade instead.

Feature Name	Type/ Domain	Univariate Significance to FPS (Wald- Chi- Square Value)	Feature Description
CombLowGleAR_HighGL Ki67	Molecular (Combined)/ IF	39.608	Combined feature. If the dominant biopsy Gleason Grade is ≤ 3 , is the dynamic range of AR scaled between 0 and 3. If the Grade is ≥ 4 , is the relative area of epithelial nuclei that are Ki67 positive (scaled between 3 and 5). The dynamic AR range is determined by calculating the area percentiles of AR intensity in epithelial and stroma nuclei. The difference between the 90 th and 10 th percentiles of epithelial nuclei is normalized by the difference between the 90 th and 10 th percentiles of stroma nuclei.
CombLowGleARpAMACRplum _HighGLKi67	Molecular (Combined)/ IF	37.011	Combined feature. If the dominant biopsy Gleason Grade is ≤ 3 , is the ratio of the area of AR positive and AMACR positive epithelial nuclei to lumen area (scaled between 0 and 3). If the Grade is ≥ 4 , is the relative area of epithelial nuclei that are Ki67 positive (scaled between 4 and 5).
CombIFEpiNucMeanEdgeL engthInter	Morph. (Combined)/ MST/IF	34.348	Combined feature, if the dominant biopsy Gleason Grade is ≤ 3 , after computing an MST of all epithelial nuclei, is the average edge length between epithelial nuclei of different glands scaled between 0 and 3, if the Gleason Grade is ≥ 4 , is the Gleason Grade instead.

[0220] **Summary of Modeling and Analysis.** Logistic regression analysis was employed to establish a model for indolent disease with the set of twenty-six (26) features listed in Table 11

as possible predictors. Binary logistic regression is described generally in [62]. The logistic procedure (PROC LOGISTIC) with the stepwise feature selection method from a commercially-available SAS statistical analysis package was used to model. According to the stepwise method, a series of models was fit until the best fitting model was determined. Predictors were added one at a time if they met the criterion of statistical significance (e.g., 0.05 for the model in this example) in order of the smallness of their p-values, given all other predictors in the model. If at any stage a predictor failed to be significant at the 0.05 level given other predictors now in the model, it was removed from consideration. Convergence occurred when no predictors could either be added or removed. In other words, convergence took place when all predictors in the model were significant and no other potential predictors would be significant if added to the model.

[0221] The final model consisted of five features as predictors of favorable pathological stage (FPS), sometimes called indolent disease. Together these features formed a model that was clearly significant by the likelihood ratio chi-square test ($\chi^2 = 161.34$ with five degrees of freedom, $p < 0.0001$). The features and their respective parameter estimates that formed the best fitting model based on training data are listed in Figure 17. The model was fit using only the training set ($n = 628$). Of these 628 patients, 238 (37.90%) had prostatectomy results indicating the condition of Favorable Pathological Stage. The remaining 390 patient (62.1%) did not have this condition, and thus were characterized as having Unfavorable Pathological Stage. During generation of the model, the intercept parameter in SAS was given a weight of -10.5317.

[0222] Results. The model was validated on a validation set ($N = 280$). Of the 280 patients, 102 (36.43%) had the condition of favorable pathological stage.

[0223] Epidemiological indices as shown in Table 12 were computed for the model based on the training and validation data. The evaluative statistics computed were: sensitivity, specificity and AUC (area under receiver operator characteristic curve). Based on the training data, the AUC was 0.78 and the sensitivity and specificity were 0.75 and 0.69, respectively. The epidemiological indices on validation were: AUC = 0.74, sensitivity = 0.74 and specificity = 0.65. These results confirmed the predictive power of the FPS model.

Table 12: Favorable Pathological Stage (Indolent Disease) Model Performance

Model Characteristic	Training (n = 628)	Validation (n = 280)
Sensitivity	0.75	0.74
Specificity	0.69	0.65
AUC	0.78	0.74

[0224] With reference to Figure 17, the five features in the model capture all three systems pathology domains (clinical, morphometric (H&E in this example), and molecular (IF MPLEX in this example)). The two clinical features selected for inclusion in the model were pre-operative PSA (estimate of regression weight = -4.232) and biopsy Gleason Score (estimate of regression weight = -2.0031).

[0225] Two H&E morphometric features were also selected for inclusion in the model. The first is the ratio of the area of epithelial nuclei that are outside of gland units to the area of epithelial nuclei that are inside (within) gland units (estimate of regression weight = -6.3303). The second H&E feature represents the areas of epithelial nuclei with centers that are in a band a certain distance away from lumen borders (estimate of regression weight = -0.8374). The band includes all epithelial nuclei that are at least three units away from the lumen border but within five units of the lumen border, where a unit is a fixed number set to be approximately the diameter of one epithelial nucleus.

[0226] The IF MPLEX molecular feature selected for inclusion in the model is a combined feature that involves AR and Ki67 measurements (estimate of regression weight = -0.3375). Depending on the patient's dominant biopsy Gleason grade, one or the other is used. If the Gleason Grade is ≤ 3 , the dynamic range of AR is measured (and scaled between 0 and 3). If the Gleason Grade is ≥ 4 , then the relative area of epithelial nuclei that are Ki67 positive is used (and scaled between 3 and 5).

[0227] **Statistical Methodology.** Binary logistic regression of the type used to generate the Favorable Pathological Stage (Indolent Disease) model is a member of the class of Generalized Linear Models (GLIMs) that permit a wide range of dependent variable types to be modeled via a linear composite of independent variables that has been subjected to a linking transformation.

[0228] Generally, in binary logistic regression the dependent variable is a dichotomous categorical variable and is typically coded as either '0' or '1'. A coding of '1' implies an event

has occurred or an experimental unit is in a particular state or condition. A coding of '0' on the other hand implies an event has not occurred or that an experimental unit is not in the particular state or condition. For example, individuals might be classified as a '1' if he/she has suffered a heart attack before his/her fifty-fifth birthday and as a '0' if he/she has not suffered a heart attack prior to his/her fifty-fifth birthday.

[0229] The independent variables in binary logistic regression can be either categorical or continuous. They are used to build a linear combination that is useful in predicting the probability of the dependent variable being equal to one. For example, if the dependent variable was whether an individual had suffered a heart attack before age 55, a likely good predictor would be the categorical independent variable of smoking status (i.e., '1' if the person is a smoker and '0' if The person is not a smoker). Another predictor, of the continuous variety, that would probably be useful in prediction, is the individual's blood cholesterol level. Other predictors might include the categorical predictor of family history ('1' if a family history of heart disease and '0' if not) and the continuous predictor of percent body fat.

[0230] In a binary logistic regression model, the dependent variable is denoted as Y and the predictors (independent variables) are denoted by X's (typically X_1 , X_2 , etc. for multiple predictors). As previously stated, the logistic regression model endeavors to predict the probability that the dependent variable is equal to one. In doing so, it employs the following equation for any given experimental unit:

$$\Pr(Y = 1) = 1/[1 + \exp(-b_0 - \sum_{i=1}^p b_i X_i)] \quad (1)$$

where: $\Pr(Y = 1)$ is the probability that Y is equal to one for any individual, $\exp(u)$ is the exponential function ($\exp(u) = e^u$), X_i is the value of the i th predictor, p is the total number of predictors in the model (the summation is from 1 to p), b_0 is the model intercept, and b_i is the slope coefficient for the i th predictor. The intercept term is a centering term for the model and the value of $1/[1 + \exp(-b_0)]$ gives in essence a baseline probability that Y is equal to one when all the predictors have a simultaneous value of zero. The slope coefficients indicate the weighted impact of each predictor in the model. Together the intercept and slope terms can be referred to as the model's parameters.

[0231] The negation of the exponentiated term is called the logit term and is sometimes designated as L . The logit has a special interpretation and also aids in the interpretation of the parameters of the model. The ratio of the probability of an event to one minus the probability of that event is called the odds of the event. The natural logarithm of the odds of an event is called the log odds of an event. There is a one-to-one correspondence between probability, odds and log odds. In other words, if any one of these three terms is known (probability, odds or log odds), the other two will be uniquely determined. For example if the probability of an event is 0.50 then the odds of the event would be $0.5/(1-0.5) = 1.0$ and the log odds would be $\log(1.0) = 0$. In explicit terms:

$$\text{If Log Odds} = R, \text{ Odds} = e^R \text{ and Probability} = 1/(1 + e^{-R}) \quad (2)$$

[0232] The logit term for an individual gives the log odds that Y equals one for that individual. The intercept thus gives the predicted log odds that Y equals one when all predictors are equal to zero. The slope coefficients give the change in predicted log odds that Y is equal to one as their respective predictors increase by one unit. Thus, although the logistic regression model is a nonlinear model for the prediction of probability, through transformations this model can be linked back to a linear model for the prediction of a quantity that is readily convertible to probability, to wit, log odds.

[0233] In order for the model to be of use in prediction, the proper values of the model's parameters must be determined. In the training stage of the model, data is provided that contains values for the dependent variable (Y) and for various features that can be employed as potential predictors (X 's) for modeling purposes. Once a set of features have been selected, the optimum values for the parameters can be determined by a method known as Maximum Likelihood Estimation, which is described generally in [63]. In this method, a likelihood function for the data is constructed as a function of the model parameters. Using either analytic or iterative techniques of optimization, numeric estimates are obtained for model parameters that maximize the likelihood function. The likelihood function itself is, in the case of logistic regression, equivalent to the joint probability that all cases in the dataset have their observed values on Y given their values on X . Assuming a dataset with n cases of which n_1 have a value of '1' on Y

and n_2 have a value of '0' on Y, then the likelihood function for the data is:

$$L(B) = \prod_{j=1}^n \Pr(Y = Y_j | X_{j1}, \dots, X_{jp}) \quad (3)$$

$$L(B) = \left\{ \prod_{j=1}^{n_1} \frac{1}{1 + \exp(-b_0 - \sum_{i=1}^p b_i X_{ij})} \right\} *$$

$$\left\{ \prod_{j=1}^{n_2} \frac{\exp(-b_0 - \sum_{i=1}^p b_i X_{ij})}{1 + \exp(-b_0 - \sum_{i=1}^p b_i X_{ij})} \right\} \quad (4)$$

where B is the vector of model parameters = $[b_0 \ b_1 \ \dots \ b_p]$, and X_{ij} is the value of the i th predictor for the j th observation in the dataset. The maximization of the likelihood function is rarely so simple a task that the solution is analytic. As a simplification, the natural logarithm of the likelihood function is maximized as opposed to the likelihood function itself. This step is justified by the monotonicity of the logarithm function. Iterative techniques are required, where typical choices involve the Newton-Raphson Method and Weighted Least Squares Methods [63].

[0234] These methods yield estimates not only for the parameters but also for their standard errors. As a result and assuming reasonably large sample sizes, two classes of statistical tests are available for model testing purposes. An omnibus test of model fit is the likelihood ratio test. In this test the final log-likelihood for a model is subtracted from the log-likelihood of a null model that involves only the intercept term and no predictors. If this difference is multiplied by negative two the likelihood ratio test statistic is obtained. This statistic will have an asymptotic chi-square distribution with degrees of freedom equal to the number of predictors in the model. If this value is statistically significant at a preset alpha level (e.g., 0.05), the null hypothesis that none of the variables in the model have predictive power is rejected and the researcher can conclude at least one of the model's independent variables is a useful predictor of the probability that the dependent variable equals one. Additionally, the ratio of each predictor's slope estimate to its respective standard error will follow an asymptotic standard normal distribution, under the null hypothesis that the predictor's slope coefficient has a true value of zero. This is called the Wald test and is employed to test the significance of individual predictors.

[0235] Once a model is established, a set of evaluative indices can be computed to give a more precise view of the model's predictive accuracy. The model yields a probability that each

individual has a value of one on Y. It would seem natural to classify each individual as a '1' if his probability exceeded 0.50 and as a '0' if his probability was less than or equal to 0.50. However, while 0.50 seems intuitively correct, it is not necessarily the best criterion for classifying cases. Rather, the point that is used as a "cutpoint" for classification is the probability value that maximizes the product of the model's sensitivity and specificity. The sensitivity of a classifier is equal to the proportion of actual cases of the condition in question that are correctly classified. Similarly, the specificity of a classifier is the proportion of cases that do not have the condition that are correctly classified. Different cutpoints are applied to the training data until the value that yields the highest product of these two proportions is obtained, subject to the constraint that the difference does not exceed 0.15.

[0236] In the case of the logistic model, sensitivity amounts to the proportion of individuals with a value of one on Y that are classified as having a value of one on Y. In this context, specificity means the proportion of individuals that have a zero on Y that are classified as having a zero on Y. Related indices are the PPV (Positive Predictive Value), or the proportion of individuals that are classified as a '1' that are actually a '1' and the NPV (Negative Predictive Value), or the proportion of individuals that are classified as a '0' that are actually a '0'.

[0237] All of the aforementioned indices depend on the establishment of a cutpoint as a basis for classifying cases. The AUC (Area Under the Curve) is an index that does not depend on the choice of a cutpoint. The term is named for the area under the Receiver's Operating Characteristic (ROC) curve. This curve is a graph, computed across all possible cutpoints, of all coordinates where the abscissa is equal to one minus the classifier's specificity and the ordinate is equal to the classifier's sensitivity. By Theorem it is always equal to the ratio of concordant pair counts to the product of positive counts times negative counts. A concordant pair of observations is a pair where one member of the pair has a Y value of one and the other has a Y value of zero and also where the model probabilities are concordant (i.e., the probability that the pair member that is truly one is greater than the probability of the pair member that is truly zero). If the probabilities are equal in such a case, 0.5 is added to the count of concordant pairs. The count of concordant pairs is then divided by the product of positive and negative counts to yield the AUC. For example, suppose the dataset contained fifty observations with thirty instances of

Y equal to one and twenty instances of Y equal to zero. The product of positive and negative counts would thus be: $20 \times 30 = 600$. Suppose the count of concordant pairs is equal to 360. The AUC would then be equal to $360/600 = 0.60$. An AUC of 0.50 would arise by pure chance agreement and is thus a benchmark for a useless classifier, while a value of 1.0 indicates that the model probability is always in agreement with the actual value of the dependent variable. The closer the AUC is to one, the greater the predictive power of the logistic regression model.

[0238] In summary, the favorable pathological stage (indolent disease) model generated according to this example was generated based on binary logistic regression. In this example, binary logistic regression was used to predict the probability that a dichotomous dependent variable (favorable pathological stage) will assume a value of one. This was accomplished by conceiving of the log odds of an event occurring being predictable from a linear composite of independent variables (features). This linear composite predicted a probability by means of a transformation that yields the logistic model equation (see equation 3, above). Model parameters were estimated by maximum likelihood. Overall model adequacy was assessed by the likelihood ratio chi-square test and each predictor's adequacy was assessed by the Wald test. The model's power to predict was confirmed by computing the sensitivity, specificity, PPV, NPV and AUC of the model.

[0239] **EXAMPLE 3: Androgen Receptor (AR) Studies And Cell Line Control**

[0240] In accordance with additional illustrative embodiments of the present invention, two studies were performed demonstrating the association of androgen receptor (AR) with responsiveness or unresponsiveness to hormonal therapy for prostate cancer (Study 1) and prostate cancer specific mortality (PCSM) (Study 2), also referred to as death from prostate cancer. In connection with Study 2, three prostate cancer cell lines known to express high (LNCaP) and low to absent (DU145 and PC3) AR protein were incorporated into the immunofluorescence (IF) analyses in order to provide a measure of reproducibility for the multiplex IF assay. Although Study 2 relating to PCSM provides an illustrative example of the use of cell line controls, it will be understood that cell line controls can be applied in other embodiments of the present invention relating to, for example, other cell lines (e.g., cell lines other than LNCaP, DU145, and PC3) and/or other outcomes under consideration (e.g., outcomes

other than PCSM).

[0241] Generally, the use of cell line controls involves establishing baseline or expected intensities of protein expression (i.e., nuclear AR expression, in the example of Study 2) in the cell lines by subjecting the cell lines to a multiplex IF assay (e.g., subjecting the cell lines to the assay in multiple experiments to establish mean intensities for the cell lines). The same cell lines are then subject to the same multiplex IF assay simultaneously with tissue (and/or isolated cells) for one or more patients under consideration. Based on qualitative and/or quantitative analysis of the cell lines subject to the multiplex IF assay, it can be determined whether the multiplex IF assay performed on the cell lines (and simultaneously performed on the tissue and/or isolated cells for patient(s) under consideration) has produced reliable results.

[0242] In some embodiments of the present invention, if an irregularity is detected in the multiplex IF assay results based on, for example, qualitative and/or quantitative comparison of the baseline or expected intensities in the cells lines versus the actual intensities measured in the cell lines from the assay run simultaneously with tissue and/or isolated cells for the patient(s) under consideration, the results from the assay involving the patient tissue and/or isolated cells may be disregarded (e.g., not considered during model generation and/or in evaluating a risk of a medical condition in the patient with a final predictive model). Alternatively or additionally, in some embodiments, the tissue and/or isolated cells for the patient(s) under consideration (e.g., and the cell lines) may be re-subjected to the multiplex IF assay one or more times until reliable results are achieved. An irregularity may result from and may identify the need to correct, for example, defective or out-of-specification reagents and/or other factor(s) affecting assay performance.

[0243] In some embodiments of the present invention, one or more features measured from the tissue and/or isolated cells for the patient(s) under consideration (e.g., features to be used in model generation and/or in evaluation of risk by a final predictive model) may be normalized by a measurement of the intensit(ies) or other measurement relating to one or more of the cell lines including, for example, the intensit(ies) of the cell line(s) measured in the assay performed simultaneously with the tissue and/or isolated cells for the patient(s), the baseline or expected intensit(ies), one or more other measurements relating to the cell lines, or a combination thereof.

For example, in some embodiments, as a result of the normalization, measurements from the tissue and/or isolated cells for the patient(s) may be useable in subsequent analysis (e.g., as features for use in model generation and/or evaluation with a final predictive model) without having to re-subject the tissue and/or isolated cells to the multiplex IF assay. The features derived from the AR negative cell population have also been used in the construction of the positive AR threshold and such values can also be applied when assessing the level / degree of background fluorescence signal which will impact both cultured cells and tissues during any given assay.

[0244] In another aspect of embodiments of the present invention, cultured cells (e.g., castrate resistant cells) with known biochemical and physiologic profiles can be used to identify a phenotype of disease. Such a phenotype may be characterized, for example, by the presence or absence of certain values for one or more immunofluorescent (IF) features measurable from IF images, or other features. Thus, by subjecting tissue or cells for such patient(s) to the same IF analyses, such features can be identified as being present or absent within the tissue or cells for the patient(s) (e.g., thus, determining a patient's disease state, risk of experiencing an outcome with respect to the disease, or likely responsiveness or unresponsiveness to a therapy for the disease). For example, a multiplex IF assay can be performed on the tissue or cells for the patient(s) (e.g., simultaneously with the cultured cells as a control), and an image analysis tool can be used to measure one or more IF features within IF images resulting from such analysis. An illustrative application of this approach is to evaluate AR levels in androgen independent cell lines (known to drive cell proliferation and growth) and to compare / contrast with AR in cell populations within tissue specimens and extrapolate to a more aggressive phenotype. Other pharmacodynamic studies, for example, on isolated tumor cell populations (i.e., circulating tumor cells) are of course possible, where overall protein levels can be assessed and dynamic range of protein content (e.g., AR protein content) within patient materials can be compared to the known protein content within cultured cells. In addition, the ability to accurately measure protein content within cultured and isolated cell populations allows for the direct extrapolation and comparison with intensity values in cell populations within tissue samples. Thus, such analyses can be used to generate dynamic biomarker profiles from discrete in situ tissue cell

populations and to drive disease specific phenotyping.

[0245] Study 1: AR Predicts Response to Hormonal Therapy. In this study, elevated androgen receptor levels in tumor cells within a biopsy were determined to be highly significant ($p < 0.0001$) for predicting resistance to a therapy (in this example, androgen ablation with or without salvage radiotherapy). Previously, it was demonstrated that AR levels in prostatectomy samples were predictive of response to therapy post-recurrence [25]. In this study, biopsy specimens from 219 patients (training cohort) who had received hormonal therapy (+/- salvage radiotherapy) were analyzed, of which 77 (35%) progressed with castrate PSA rise. In this analysis, the features listed in Figure 18 were determined in univariate analyses to be predictive of responsiveness or unresponsiveness to hormonal therapy post-recurrence of prostate cancer. Generally, features indicative of increasing levels of AR were significantly associated with a reduced time to failure ($p < 0.0001$ log-rank test). One such feature was the immunofluorescence (IF) feature of the area of AR in AMACR(+) tumor epithelial cells (Table 3, "IFx1_RelAreEpi_ARpAMACRp2EN"; p value < 0.0001). Another such feature was the IF feature of the dynamic range of AR intensity in tumor epithelial cells (Table 3, "IFx1_RelRise_EpiNuc_AR_StrNuc"; p value < 0.0001). In addition, the morphometric feature of median lumen area as measured in an image of H&E-stained tissue (Table 1, "HE02_Lum_Are_Median") was associated with outcome ($p < 0.01$ log-rank test) which supports a further role for morphometry as a surrogate for Gleason grading. In this example, clinical variables including preoperative PSA, biopsy Gleason grade and score were not significant.

[0246] In some embodiments of the present invention, a model (e.g., multivariate model) predictive of responsiveness or unresponsiveness to a therapy (e.g., androgen ablation) for a medical condition (e.g., prostate cancer) is provided, which includes one or more (e.g., all) of the features listed in Figure 18 and/or other features (e.g., one or more features listed in Tables 1-4). For example, based on features derived from or otherwise available at the time of a tissue biopsy for a patient, the model may output a value or score indicative of whether the patient's disease will be responsive or unresponsive to the therapy and/or a time to progression of the disease after the therapy is administered to the patient.

[0247] Study 2: AR Predicts Time to Prostate Cancer Specific Mortality (PCSM).

Androgen Receptor (AR) levels in prostate cancer have been associated with disease progression including PSA recurrence and systemic metastasis. This study investigated whether baseline pre-treatment clinical variables and tumor specimen characteristics (including AR) from a castrate resistant metastatic disease cohort are predictive of time to prostate cancer specific mortality and overall survival.

[0248] Hematoxylin and Eosin (H&E) slides / blocks and outcome data from a castrate metastatic disease cohort of 106 patients (35 prostatectomy and 71 prostate needle biopsy samples) were independently reviewed. H&E morphometry and quantitative immunofluorescence were performed. Sections were analyzed with a multiplex quantitative (IF) assay for CK18 (epithelial cells), DAPI (nuclei), p63/HMWK (basal cells), AR and alpha-methyl CoA – racemase (AMACR). Images acquired with spectral imaging software and processed for quantitation of IF features.

[0249] The advanced disease cohort had a median follow-up of 12 years from diagnosis, 49 men (47%) had baseline PSA levels ≥ 20 ng/ml, 55 men (53%) had Gleason sum 8, 63 men (60%) were dead from disease and 40% were alive (censored). 66 patients had evaluable immunofluorescent features, and association with outcome was performed by univariate Cox modeling and support vector regression (SVRc). PSA was the only clinical variable associated with outcome (CI 0.41; $p < 0.05$ log-rank test). The amount of AR present within tumor nuclei (regardless of tissue provenance and primary treatment) significantly correlated with a greater risk for shortened time to prostate cancer specific mortality (CI 0.36; $p < 0.05$ log-rank test). There were no H&E features that correlated.

[0250] All of the features listed in Tables 1-4 were tested for univariate correlation with the PCSM endpoint in this study. By such univariate analysis, increased nuclear AR expression in either the diagnostic biopsy and/or radical prostatectomy specimen, from an advanced disease cohort, was associated with a reduced time to prostate cancer specific mortality (PCSM). A list of the correlated features is provided in Table 14 below.

[0251] Introduction. The growth of prostate cancer is the result of androgen signaling through the androgen receptor (AR) with primary treatment for recurrence including LHRH

agonists, ligand blockade, inhibition of receptor activation and orchiectomy [65, 66]. The response however is quite variable, and dependent on stage, prior therapy and individual tumor characteristics. Although initially successful, the cancer eventually progresses to an androgen resistant state which heralds the development of a malignant phenotype. In addition to castrate PSA secretion, a number of studies have documented molecular events, including mutations and amplification of the AR gene and hyper-activation of AR signaling [66].

[0252] Recent evidence has shown that AR RNA and protein in the primary prostatectomy sample was associated with disease progression [67, 68, 36, 37]. Furthermore, it was previously demonstrated that high nuclear AR (nAR) in prostatectomy specimens was predictive of systemic disease and that increased levels were associated with a reduced durable response to hormonal therapy and a shortened time to disease relapse [25]. Together these observations support the hypothesis for AR deregulation in the primary sample, possibly restricted to stem cells and/or clonal populations, which promotes tumor growth and metastasis [69].

[0253] The investigation of AR in diagnostic prostate tissue both as an indicator for innate tumor aggressiveness and association with response to hormonal therapy has been studied for over 25 years. The initial strategies incorporated biochemical assays to isolate nuclear AR protein from diagnostic biopsy tissues [70]. This was quickly followed by more standard immunohistochemical (IHC) methods which included the assessment of AR in both prostatectomy (n=640) and metastatic samples [71, 72]. Collectively, these efforts illustrate the importance of understanding AR levels in prostate tissue prior to treatment, with some obvious similarities to the estrogen receptor in breast cancer, but also highlight the importance of having an assay which is both reproducible, and quantitative.

[0254] The present inventors believe to be the first to have associated levels of nAR protein in an untreated prostate cancer specimen with prostate cancer specific survival. Initial studies [25] emphasized a composite end-point of disease progression in a local to locally advanced prostatectomy-only cohort, with an emphasis on a castrate-resistant state potentially relevant for clinical intervention. To further characterize the significance of nAR levels in the manifestation of disease progression from adjuvant hormone response to death, the present inventors sought a more advanced disease cohort with extensive follow-up to determine whether nAR protein levels

were associated with either prostate cancer specific mortality (PCSM) and/or overall survival (OS).

[0255] Patients and Methods. Formalin-fixed, paraffin-embedded (FFPE) tissue sections representing either the diagnostic prostate needle biopsy (n=71) or radical prostatectomy specimen (n=35) were obtained from a castrate metastatic disease cohort. Gleason scores were represented as three categories (i.e. $\leq$, $=$ and >7) and obtained after a re-evaluation of the primary diagnostic biopsy and or prostatectomy specimen. The patients had been followed for a median of 12 years. Prostate cancer specific mortality (PCSM) and overall survival (OS) were calculated in months from diagnosis and death certificates were reviewed to verify cause of death. All patients still alive at last follow-up were censored at that date. Disease progression was defined as clinical, histologic or radiographic evidence of metastatic disease (lymph node, bone, or soft tissue); or initiation of hormone therapy (at physician discretion), radiation, surgery, chemotherapy, or death certified to be from prostate cancer. Patients who had received neoadjuvant therapy were excluded from the analysis.

[0256] Patients with complete clinical, pathologic and biometric (morphometry and immunofluorescent) as well as outcome data (i.e., PCSM/OS) were further studied. As a result of applied quality control metrics outlined below, the total number of patients within each group (i.e., morphometry and immunofluorescence) varied. Demographics of the entire cohort are shown in Table 13.

[0257] Hematoxylin and Eosin Morphometry. Individual sections were stained with Hematoxylin and Eosin (H&E). Triplicate images were acquired with an Olympus bright-field microscope at $\times 20$ magnification using a SPOT Insight QE Color Digital Camera (KAI2000; Diagnostic Instruments Inc.) and reviewed by two pathologists (blinded to outcome) for image quality, and tumor content prior to image analysis. All images were digitally masked using Adobe Photoshop 7.0 to isolate infiltrative tumor from high-grade intraepithelial neoplasia (HGPIN) and normal tissue elements. H&E image processing and feature extraction are described above in connection with Figures 3-8. A minimum of 20% tumor content within two 20X microscopic fields per prostate cancer specimen was required for inclusion. 61 of the 104 patients (59%; 21 radical prostatectomy and 40 biopsy specimens) had sufficient tumor quality

and invasive component (minimum 20%) for H&E feature extraction with the image analysis tool.

[0258] Spectral Multiplex Immunofluorescence. The MPLEX-1 assay described above was used for evaluation of multiple antigens in a single section. Briefly, Alexa fluorochrome-labeled antibodies for the androgen receptor (AR), racemase (AMACR), cytokeratin 18 (CK18), TP73L (p63), and high molecular weight keratin (HMWK) were used, along with 4'-6-diamidino-2-phenylindole (DAPI) as nuclear stain, in a 'quint-plex' assay. Triplicate images were acquired from representative areas which included both infiltrating tumor and HGPIN, un-mixed using spectral imaging software (CRI, Woburn, MA) and digitally masked with Adobe Photoshop 7.0 to remove artifacts including all benign (AMACR negative), non tumor tissue elements. All images were then processed with the fluorescent image analysis tool to derive quantitative features from cellular compartments (e.g. epithelial nuclei, cytoplasm, and stromal nuclei). The IF features include measurements of the mean, medium, maximum, and standard deviation of AR protein intensity and distribution in epithelial and stromal nuclei. AR intensity represents the concentration of the antigen and is developed using a continuous pixel scale allowing for an expanded dynamic range to be constructed [25, 36]. In brief, supervised learning was used to discriminate signal intensity from background. Using object-oriented image analysis, expert thresholds for individual markers were established by a pathologist and linear regression models constructed with feature output to guide accuracy. Once complete, the method for the threshold design was applied to the entire cohort image set and evaluated for qualitative segmentation performance prior to data extraction.

[0259] Prostate Cancer Cell Line Array. In order to provide a measure of reproducibility for the multiplex IF assay, three prostate cancer cell lines known to express high (LNCaP) and low to absent (DU145 and PC3) AR protein were incorporated into this study. In this embodiment, all cells were obtained from the American Tissue Culture Collection (ATCC) and grown to confluency according to provider specifications. Individual cell pellets were resuspended to a desired density in a 1% agar solution (1:1 Invitrogen, Carlsbad, CA), fixed with 10% buffered formalin, and embedded in paraffin molds to create cell suspension arrays which were then sectioned for subsequent IF analysis as described below.

[0260] Statistical Analysis. The primary end point to this study was time to death from prostate cancer (PCSM). Censoring was done only if the patient were alive at last follow-up, regardless of disease progression and patient status was clarified at different follow-up times, i.e., death from prostate cancer and death from other causes. Univariate correlation of individual H&E and IF features with PCSM and OS were assessed according to the Concordance Index (CI) and the log-rank test. Since multiple images were acquired for each patient, an aggregation function (i.e., mean, median, maximum and minimum) was developed to handle respective feature values derived from the individual images. The best aggregating function for a feature was the one in which the CI was farthest from random (0.5). The CI is comparable to the area under the receiver operating characteristic curve, but appropriate for censored data, and estimates the probability that, of a pair of randomly selected comparable patients, the patient with the higher predicted time to PCSM from the model will experience PCSM/OS within a shorter time than the other patient. This function was then applied to all patients. Multivariate models were constructed with support vector regression for censored data (SVRc) which was developed to handle high dimensional data while adapting it for use with censored records. Experience with SVRc has demonstrated that this approach can increase a model's predictive accuracy over that of the Cox model.

[0261] Results. The 104 patients included in the study had local and advanced disease (T1-T4), with 41% (43), 32% (33) and 27% (28) managed with radical prostatectomy, radiation or primary hormonal therapy (within one year of diagnosis), respectively. 47% had PSA levels ≥ 20 ng/ml, and 52% had a Gleason Sum > 7 , at the time of diagnosis. The median follow-up was 12 years. 37.5% of treated patients had developed PSA recurrence and 60.6% had died of their disease with 39.4% censored/alive patients. PCSM and overall survival (OS) were the same for this cohort and therefore only PCSM was evaluated. 85 of 104 patients (82%) had PSA values at the time of diagnosis and by univariate analysis this was the only clinical feature associated with increased risk of a reduced time to PCSM; CI 0.41, (log-rank test $p=0.0004$). In this example, no H&E features were associated with the survival end-point in a univariate analysis.

[0262] Quantitative Immunofluorescence. 66 of 104 patients (63%) had appropriate tumor and staining properties for IF feature extraction. Excluded patient specimens were evenly split

between autofluorescence and poor antigenicity. The 66 IF patients (36 needle biopsy and 30 prostatectomy specimens) were representative by clinical parameters including PSA, GS, treatment and PCSM/OS event status of the entire cohort (see Table 13).

[0263] After image analysis, 10 IF features were generated which represent a variety of tissue and cellular attributes including nuclear AR (nAR) positive and negative intensity and area profiles, AMACR positive and negative tumor and overall tissue architecture including surrogates of tumor volume (e.g., epithelial cytoplasm content). All area features were normalized to the digitally masked tumor area. According to a spectral un-mixing and image analysis process, a composite IF image of infiltrative prostate cancer from a needle biopsy was un-mixed with the CRI software to generate a DAPI-nAR profile, which was then processed with the image analysis tool to segment and classify individual nuclei based on their AR content and association with AMACR expression. In addition to measuring total nAR, three independent IF graded nAR intensity features ranging from low (bin 1-3), medium (bin 4-6) and high (bin 7-10) intensity values were constructed. Selected features were normalized to individual components of the tumor only area.

[0264] Androgen Receptor and Ki-67 in Prostate Cancer Cell Lines. After developing two 5-antigen multiplex (Mutlplex-1 and Multiplex-2, described above) immunofluorescence assays using qualitative tissue controls in formalin-fixed, paraffin-embedded (FFPE) prostate cancer (CaP) tissue sections, control evaluation was performed by quantification of signal-derived features. As is further described below, three CaP cell lines (LNCaP, PC-3, DU-145) were used as substrates for a nuclear antigen in each multiplex [androgen receptor (AR) and Ki-67]. Cells suspended in agar were formalin-fixed, paraffin-embedded (FFPE) as arrays (CSA = cell suspension array) containing all three cell lines. Multiplex results were recorded by a computer-driven microscope system with a Nuance camera (CRI, Woburn MA) and filters to capture serial images 10 nm apart (wave length range: 520 - 720 nm) including emission spectra for all fluors were used. Grey scale images identifying antigen distribution by its spectral profile were created by unmixing fluor signals in each image series. High throughput image analysis scripts were adapted to measure intensity/area features of AR or Ki-67 in CSA nuclei (classified as "DAPI objects"), expressed as (1) mean intensity of all cells, and (2) mean and (3) percentage of

positive cells above a threshold derived from negative control sections. Based on these measurements, results from a test run (e.g., a subsequent test run) were thus validated by control metrics within established antigen/cell line ranges, an objective approach surpassing in accuracy and efficiency subjective visual criteria.

[0265] It was demonstrated that the three prostate cancer cell lines (DU145, PC3, and LNCaP) provide a reliable and unlimited resource of material for detecting and measuring the differential expression of nAR protein in a reproducible and systematic format. To process the immunofluorescence (IF) images derived from the three cell lines and construct threshold parameters for positive and negative AR levels, a cell-specific script was developed which incorporated the mean intensity value of nAR within the nAR negative cell lines (i.e., DU145 and PC3). Figures 19A and 19B illustrate segmented images of LNCaP and PC3 cells, respectively, with the applied threshold determining positive and negative nAR protein levels. The stability of the reagents, assay, script and the incorporation of cells as a routine means of quality control/assay performance was subsequently established. As shown in Figures 20A and 20B, mean intensity plots were also generated where the intensity of nuclear AR (y axis) was plotted against experiment sequence number (x-axis; experiment number recorded as PA1 through PA82). In the plots, intensity of nuclear AR in LNCaP (LN) was shown with green dots, intensity of nuclear AR in DU145 (DU) was shown with red dots, and intensity of nuclear AR in PC3 (PC) was shown with blue dots in immunofluorescence (IF) experiments performed over a 10-week period, although the plots are reproduced in Figures 20A and 20B in black and white for ease of reproducibility. A notable difference was demonstrated between the LNCaP AR positive cell line (green) vs. DU145 (red) and PC3 (blue) and also when compared to the negative control plot (Figure 20B) for all the three cell lines. The mean intensity plots (Figures 20A and 20B) along with the segmented images (Figures 19A and 19B) allow for real-time visual and quantitative quality control assay assessment.

[0266] Cell proliferation marker Ki-67 in prostate cancer cell lines. As Ki-67 is also a nuclear antigen—expressed by all three prostate cancer cell lines (LNCaP, PC-3, DU-145)—the same CSA preparations used for AR control metrics were used in identical manner to obtain Ki-67 control metrics. In these CSA preparations, Ki-67 expression is found to be greater in DU-145

and PC-3 than in LNCaP (DU-145 > PC-3 >> LNCaP). Processing of images, including feature metrics extraction and analysis, was done as described above for AR.

[0267] Generally, cultured cells and tissue sections have been routinely used as controls in IF and other staining techniques (such as Immunohistochemistry) for some time. However, control evaluations are conventionally based on qualitative optical evaluation by the Pathologist or Technician which is subject to a wide margin of error due to observer bias and thus is unsuitable for day-to-day comparison. According to some embodiments of the present invention, a specific set of quantitative signal-derived image features is provided for utilization in combination with a biological substrate (formalin-fixed, paraffin-embedded cell lines initially suspended in soft agar) as an absolute measure for IF consistency. For example, the three cell lines (LNCaP, PC-3 and DU-145) with known status regarding the expression of the biomarkers in question (e.g., the nuclear antigens Androgen Receptor (AR) and Ki-67) are subjected to an IF reaction designed to detect these biomarkers. IF reaction can be done as positive and negative runs, where negative runs lack the primary antibody and thus only report the unspecific binding of the fluorescent dye. Results can be subsequently recorded by a computer-driven spectral microscope system as described above. Grey scale images identifying antigen distribution by its spectral profile can then be created by the process of unmixing fluor signals in each image series. Quantitative features are then computed by establishing a constant threshold that results in 99-100% of nuclei in the negative IF reagent being below that threshold. Nuclei were subsequently segmented (identified) based on their Dapi (4',6-diamidino-2-phenylindole) intensity, resulting in a group of "Dapi objects" in the image. Segmentation/classification of individual nuclei is made possible by adjusting concentration of cells in agar medium to achieve adequate dispersion and separation. In some embodiments, for each positive control image one or more (e.g., all) of the following measurements, or other suitable or similar measurement(s), are collected:

- a. The mean biomarker intensity in total cell nuclei population
- b. The mean biomarker intensity in positive cell nuclei population (nuclei with intensity above corresponding threshold)
- c. Percentage of positive cells nuclei is computed as: $(\text{area of positive cell nuclei} / \text{area of all cell nuclei}) * 100$

[0268] In some embodiments, for each negative control image, the following measurement, or other suitable or similar measurement(s), may be collected:

- a. The mean biomarker intensity in total cell nuclei population

In some embodiments, the various measurements can be plotted for each multiplex run on a continuous graph used to establish acceptable control value ranges (see e.g., Figures 20 and 20B). The limits on these ranges can be used to assess the variability/reproducibility and ultimate validity of the results.

[0269] Univariate Feature Analysis. Given a sample size of 66 patients and a 52% event rate, a statistical power calculation demonstrated that there was sufficient patient number and events (power >0.8 with an $\alpha = 0.05$) to detect moderate to large effect sizes. The correlations observed in this analysis fall within this range. Of the total set of features, 10 out of 22 demonstrated a statistically significant CI 0.37 - 0.69, (log-rank test, $p < 0.05$), as shown in Table 14.

Table 14. Clinical and IF Features Associated With PCSM

Feature	Feature Description	CI	Chi-Square	P-Value
PSA		0.40918	12.4069	0.0004
IFx1_RelAreEpi_ARp2EN	Relative area of AR+ epithelial nuclei	0.36364	4.0963	0.043
The sum of the following features: IFx1_RelAre_EpiNucARp_Density07 IFx1_RelAre_EpiNucARp_Density08 IFx1_RelAre_EpiNucARp_Density09 IFx1_RelAre_EpiNucARp_Density10	Normalized sum AR intensity Bin7-10/total nuclear area. This represents the area of epithelial nuclei with high intensity values.	0.39644	5.8111	0.0159

IFx1_Rati_EpNARpAMACRn2ART	Mean AR intensity in AMACR (-) nuclei	0.40553	4.4371	0.0352
IFx1_Rati_EpNARpAMACRp2ART	Mean AR intensity in AMACR (+) nuclei	0.39684	4.3158	0.0378
IFx1_EN_ARTotInt_Avg	Total AR+ intensity in all Epithelial nuclei	0.3834	6.1746	0.013
IFx1_Sum_BinEN_ARTotInt07_09	Normalized sum of AR intensity in highest bins / total nuclear area	0.38617	4.4839	0.0342
IF01_nExInd_EN_ARp	Normalized AR Intensity in all Epithelial nuclei	0.37154	5.9344	0.0148
IF01_Rati_EN_Flux_ARp2AR	Normalized Average AR intensity/ Total Epithelial Luminance (intensity x brightness)	0.37154	5.6017	0.0179
IFx1_RelAreEpi_ARnAMACRp2EN	Area Epithelial nuclei AR- AMACR+/total epithelial nuclear area	0.6419	6.2762	0.0122
IFx1_EpiNucARn_AreaTotal	Area Epithelial	0.63636	4.0963	0.043

	AR(-) / total nuclear area			
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[0270] The weighted CI is a measure of univariate correlation with overall survival for each predictive feature. An index of 0.5 indicates random correlation, values $<$ or $>$ than 0.5 and 0 indicate a negative and positive correlation with outcome, respectively. This demonstrates that increasing levels of nAR protein, either by area occupied within a DAPI tumor-defined nucleus, or intensity (brightness) are both associated with a greater risk for reduced time to PCSM. These features are irrespective whether the sample was a prostatectomy or needle biopsy specimen and both correlated with outcome.

[0271] Figure 21 is a graph of a Kaplan-Meier curve illustrating the ability of the feature representing the normalized sum of nAR present at the highest levels (i.e., bin 7-10) to stratify patients into low and high risk groups for death-of-disease. 66 patients were stratified by high AR levels (bin 7-10) normalized to the tumor cell nuclear area (cut-point 0.27, $p < 0.0001$). 60 patients were at low risk for death of disease, whereas 6 patients were at high risk for death of disease. The bin level 7-10 represents the maximum nAR intensity measured in tumor cells and exhibited the highest CI value of all bins evaluated for discriminating patients with respect to outcome. By way of comparison, two features which identify the presence of nuclei that do not contain AR protein have a CI > 0.6 , demonstrating that reduced levels of nAR within the tumor is associated with a longer survival time.

[0272] Multivariate models were generated; however, due to the limited number of patients with complete domain features (i.e. Model 1: 66 patients and 10 IF features and Model 2: 56 patients with 10 IF features and 1 (PSA) clinical value), the results although supportive, were inconclusive (Model 1: CI 0.65 and Model 2 CI 0.64, respectively). Of importance, in the combined clinical and IF Model 2, only the relative area of tumor epithelial nuclei which were AR negative and AMACR positive was associated with outcome (greater amount, longer time to PCSM).

[0273] Discussion. The AR signaling axis is one of the most studied pathways in prostate cancer growth, and response to therapy. While androgen withdrawal remains the primary treatment for recurrence, the response is variable and dependent on a number of factors including

stage of the disease, prior treatments and individual tumor characteristics. Unfortunately, many tumors will progress within a 2 year period despite a castrate androgen state, most likely the result of aberrant/reactivation of AR signaling [73, 74]. The morbidity associated with hormonal therapy, and the variable response especially for low and intermediate risk patients, illustrate the necessity for developing a measurable tumor phenotype which would correlate with objective clinical response and survival.

[0274] A cell-specific, object-oriented image analysis approach for identifying and quantifying nAR protein levels in discrete populations of tumor cells in formalin-fixed, paraffin-embedded (FFPE) prostatectomy samples was previously reported [25, 36]. The process automatically corrects for background fluorescence in patient samples while generating unique features which are associated with clinical outcome. In this study, by applying this method to archived diagnostic specimens from patients in a castrate metastatic disease cohort, it was determined that increased nAR in tumor cells was also associated with a greater risk of having a shortened time to death from prostate cancer (PCSM). The only clinical variable which was associated with outcome (univariately) was PSA, regardless of tissue provenance and primary treatment. The lack of an association between the Gleason score and outcome is intriguing; however it is believed that this may reflect both the high frequency of Gleason >7 (i.e. 8-10) in the cohort and the approach used for categorization of the Gleason score in this analysis. A recent study on a population-based, conservatively managed cohort from the United Kingdom also found that PSA was a significant determinant for predicting survival [27]. The known regulation of PSA expression by activity of the AR gene and the utility of PSA in monitoring disease progression, would suggest that these markers are complementary and therefore useful for predicting outcome.

[0275] Prostate cancer is the second most frequently diagnosed cancer in men [1], and although effectively managed with surgery, and/or radiation, up to 70,000 men will experience a PSA-only recurrence requiring some form of therapy including pelvic radiation and/or hormone ablation [75]. The ideal treatment is not clear with current options determined by clinical variables, post-operative nomograms [10, 26] and systems-based pathology algorithms [25, 36]. A recent retrospective analysis on 635 U.S. patients post surgery demonstrated that salvage

radiotherapy given within 2 years of recurrence increased prostate-cancer-specific survival in patients with PSA doubling time of less than 6 months [76]. This observation was independent of other clinical prognostic factors and suggests that residual pelvic disease is more frequent than originally thought and that understanding the biologic factors which drive prostate cancer proliferation and local spread at diagnosis are important for an appropriate treatment plan. The data from this study suggests that even in an advanced disease population, information within the primary tumor is still of prognostic significance and potentially of therapeutic importance. Utilizing image analysis and mathematical modeling, the present inventors have been able to assess tumor heterogeneity in the context of biomarker expression (i.e., AR intensity and area features in this example) and cell phenotype (e.g., AMACR positive and negative tumor cells). It is through these analyses that a number of related features were identified which both directly and inversely correlate with outcome. Of interest, in both preliminary multivariate models an increased number of AMACR positive and nAR negative tumor cells was associated with a longer time to PCSM. This finding agrees with an earlier association of AMACR expression and prostate cancer specific death and further supports a mandate for more comprehensive and thorough tumor characterization, especially at diagnosis [77].

[0276] Traditionally, the biologic mechanisms that link AR in the primary specimen with tumor growth and response to therapy are not entirely understood. The known interaction of AR with several pathways including the PTEN-PI3K-PAKT and the NF-kappaB signaling cascades would support a variety of growth related processes relevant for disease progression [78, 79]. Recent evidence associates nuclear localization of NF-kappaB with lymph node invasion in primary prostate tumors by IHC [80]. The present inventors believe that factors responsible for systemic disease are present within the prostate at diagnosis. Indeed, the observed loss of PTEN and increase in phosphorylated Akt in prostatectomy samples was found to be highly predictive for biochemical recurrence, especially when associated with the prostatectomy Gleason score [81]. A recent report also addresses germline determinants (SNPs) in androgen synthesis pathways and their prognostic significance for hormone therapy response [82]. The present inventors believe that an internal microenvironment is present within the prostate which promotes progression of disease and is predictive of outcome. The present inventors believe that

given the tissue heterogeneity of prostate cancer, analytic approaches which discriminate cell types and assign quantitative values to marker proteins should be more reliable than subjective or derivative based (DNA / RNA) techniques.

[0277] In summary, by establishing a methodology and process for robust protein assessment, including the incorporation of a quantitative biomarker cell line assay, a population of cells has been identified and classified which expresses very high levels of AR and is predictive of a more aggressive phenotype. The present inventors believe that additional study regarding the AR activation axis (e.g., AR phosphorylation, co-factors [47]) will further demonstrate its role as a mechanism for uncontrolled prostate cancer progression.

[0278] Additional Embodiments

[0279] Thus it is seen that methods and systems are provided for treating, diagnosing and predicting the occurrence of a medical condition such as, for example, favorable or unfavorable pathological stage (indolent or nonindolent disease) and/or prostate cancer progression.

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the present inventors that various substitutions, alterations, and modifications may be made without departing from the spirit and scope of the invention as defined by the claims. Other aspects, advantages, and modifications are considered to be within the scope of the following claims. The claims presented are representative of the inventions disclosed herein. Other, unclaimed inventions are also contemplated. The present inventors reserve the right to pursue such inventions in later claims.

[0280] Insofar as embodiments of the invention described above are implementable, at least in part, using a computer system, it will be appreciated that a computer program for implementing at least part of the described methods and/or the described systems is envisaged as an aspect of the present invention. The computer system may be any suitable apparatus, system or device. For example, the computer system may be a programmable data processing apparatus, a general purpose computer, a Digital Signal Processor or a microprocessor. The computer program may

be embodied as source code and undergo compilation for implementation on a computer, or may be embodied as object code, for example.

[0281] It is also conceivable that some or all of the functionality ascribed to the computer program or computer system aforementioned may be implemented in hardware, for example by means of one or more application specific integrated circuits.

[0282] Suitably, the computer program can be stored on a carrier medium in computer usable form, which is also envisaged as an aspect of the present invention. For example, the carrier medium may be solid-state memory, optical or magneto-optical memory such as a readable and/or writable disk for example a compact disk (CD) or a digital versatile disk (DVD), or magnetic memory such as disc or tape, and the computer system can utilize the program to configure it for operation. The computer program may also be supplied from a remote source embodied in a carrier medium such as an electronic signal, including a radio frequency carrier wave or an optical carrier wave.

[0283]

U.S. Application No. 12/462,041, filed on July 27, 2009; PCT Application No. PCT/US09/04364, filed on July 27, 2009; PCT Application No. PCT/US08/004523, filed April 7, 2008, which claims priority from U.S. Provisional Patent Application Nos. 60/922,163, filed April 5, 2007, 60/922,149, filed April 5, 2007, 60/923,447, filed April 13, 2007, and 61/010,598, filed January 9, 2008; U.S. Patent Application No. 11/200,758, filed August 9, 2005; U.S. Patent Application No. 11/581,043, filed October 13, 2006; U.S. Patent Application No. 11/404,272, filed April 14, 2006; U.S. Patent Application No. 11/581,052, filed October 13, 2006, which claims priority from U.S. Provisional Patent Application No. 60/726,809, filed October 13, 2005; and U.S. Patent Application No. 11/080,360, filed March 14, 2005, which is: a continuation-in-part of U.S. Patent Application No. 11/067,066, filed February 25, 2005 (now U.S. Patent No. 7,321,881, issued January 22, 2008), which claims priority from U.S. Provisional Patent Application Nos. 60/548,322, filed February 27, 2004, and 60/577,051, filed June 4, 2004; a continuation-in-part of U.S. Patent Application No. 10/991,897, filed November 17, 2004, which claims priority from U.S. Provisional Patent Application No. 60/520,815, filed November 17, 2003; a continuation-in-part of U.S. Patent Application No. 10/624,233, filed July, 21, 2003

(now U.S. Patent No. 6,995,020, issued February 7, 2006); a continuation-in-part of U.S. Patent Application No. 10/991,240, filed November 17, 2004, which claims priority from U.S. Provisional Patent Application No. 60/520,939 filed November 18, 2003; and claims priority from U.S. Provisional Patent Application Nos. 60/552,497, filed March 12, 2004, 60/577,051, filed June 4, 2004, 60/600,764, filed August 11, 2004, 60/620,514, filed October 20, 2004, 60/645,158, filed January 18, 2005, and 60/651,779, filed February 9, 2005.

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Table 1. Morphometric Features (e.g., measurable in images of H&E-stained tissue)

In some embodiments, features in Table 1 having a prefix of “HE03” or “HEX3” are measured in tissue images at 40x magnification. HE03 features may be measured directly from the images, whereas HEX3 features are derived/calculated from the HE03 features. In some embodiments, features in Table 1 having a prefix of “HE02” or “HEX2” are measured in tissue images at 20x magnification. HE02 features may be measured directly from the images, whereas HEX2 features are derived/calculated from the HE02 features.

Feature	Description
HE02_Art_Are_Mean	Color and morphometric features of identified artifacts
HE02_Art_Are_Std	
HE02_Art_Are_Tot	
HE02_Art_ElpFit_Mean	
HE02_Art_ElpFit_Std	
HE02_Art_LOW_Mean	
HE02_Art_LOW_Std	
HE02_Art_Num	
HE02_Art_OrgBri_Mean	
HE02_Art_OrgBri_Std	
HE02_Art_Ptr_Mean	
HE02_Art_Ptr_Std	
HE02_CluNuc_Are_Mean	Color and morphometric features of clustered nuclei
HE02_CluNuc_Are_Std	

HE02_CluNuc_Are_Tot	
HE02_CluNuc_Num	
HE02_Cra_Are_Mean	Color and morphometric features of luminal content
HE02_Cra_Are_Std	
HE02_Cra_Are_Tot	
HE02_Cra_Num	
HE02_Cra_OrgBlu_MeanMean	
HE02_Cra_OrgBlu_MeanStd	
HE02_Cra_OrgBri_Mean	
HE02_Cra_OrgBri_Std	
HE02_Cra_OrgGre_MeanMean	
HE02_Cra_OrgGre_MeanStd	
HE02_Cra_OrgH_Mean	
HE02_Cra_OrgH_Std	
HE02_Cra_OrgI_Mean	
HE02_Cra_OrgI_Std	
HE02_Cra_OrgQ_Mean	
HE02_Cra_OrgQ_Std	
HE02_Cra_OrgRed_MeanMean	
HE02_Cra_OrgRed_MeanStd	
HE02_Cra_OrgS_Mean	
HE02_Cra_OrgS_Std	
HE02_Cra_OrgV_Mean	
HE02_Cra_OrgV_Std	
HE02_Cra_OrgY_Mean	
HE02_Cra_OrgY_Std	
HE02_CytOGU_Are_Tot	Morphometric and color features of cytoplasm within and outside of gland units.
HE02_CytOutGU_Are_Tot	
HE02_CytOutGU_OrgBlu_MeanMean	
HE02_CytOutGU_OrgBlu_MeanStd	
HE02_CytOutGU_OrgGre_MeanMean	
HE02_CytOutGU_OrgGre_MeanStd	
HE02_CytOutGU_OrgRed_MeanMean	
HE02_CytOutGU_OrgRed_MeanStd	
HE02_CytWIGU_Are_Tot	
HE02_CytWinGU_Are_Tot	
HE02_CytWinGU_OrgBlu_MeanMean	
HE02_CytWinGU_OrgBlu_MeanStd	
HE02_CytWinGU_OrgGre_MeanMean	
HE02_CytWinGU_OrgGre_MeanStd	
HE02_CytWinGU_OrgRed_MeanMean	

HE02_CytWinGU_OrgRed_MeanStd	
HE02_Cyt_Are_Mean	Morphometric and color properties of cytoplasm
HE02_Cyt_Are_Std	
HE02_Cyt_Are_Tot	
HE02_Cyt_Num	
HE02_Cyt_OrgBlu_MeanMean	
HE02_Cyt_OrgBlu_MeanStd	
HE02_Cyt_OrgBri_Mean	
HE02_Cyt_OrgBri_Std	
HE02_Cyt_OrgGre_MeanMean	
HE02_Cyt_OrgGre_MeanStd	
HE02_Cyt_OrgH_Mean	
HE02_Cyt_OrgH_Std	
HE02_Cyt_OrgI_Mean	
HE02_Cyt_OrgI_Std	
HE02_Cyt_OrgQ_Mean	
HE02_Cyt_OrgQ_Std	
HE02_Cyt_OrgRed_MeanMean	
HE02_Cyt_OrgRed_MeanStd	
HE02_Cyt_OrgS_Mean	
HE02_Cyt_OrgS_Std	
HE02_Cyt_OrgV_Mean	
HE02_Cyt_OrgV_Std	
HE02_Cyt_OrgY_Mean	
HE02_Cyt_OrgY_Std	
HE02_DStr_Are_Mean	Morphometric and color properties of dark stroma
HE02_DStr_Are_Std	
HE02_DStr_Are_Tot	
HE02_DStr_Num	
HE02_DStr_OrgBlu_MeanMean	
HE02_DStr_OrgBlu_MeanStd	
HE02_DStr_OrgBri_Mean	
HE02_DStr_OrgBri_Std	
HE02_DStr_OrgGre_MeanMean	
HE02_DStr_OrgGre_MeanStd	
HE02_DStr_OrgH_Mean	
HE02_DStr_OrgH_Std	
HE02_DStr_OrgI_Mean	
HE02_DStr_OrgI_Std	
HE02_DStr_OrgQ_Mean	
HE02_DStr_OrgQ_Std	
HE02_DStr_OrgRed_MeanMean	

HE02_DStr_OrgRed_MeanStd
HE02_DStr_OrgS_Mean
HE02_DStr_OrgS_Std
HE02_DStr_OrgV_Mean
HE02_DStr_OrgV_Std
HE02_DStr_OrgY_Mean
HE02_DStr_OrgY_Std

Morphometric properties of dark nuclei divided into bins, and also of different combinations of those bins.

HE02_DarNucBin0_1_Are_Mean
HE02_DarNucBin0_1_Are_Tot
HE02_DarNucBin0_1_Num
HE02_DarNucBin0_2_Are_Mean
HE02_DarNucBin0_2_Are_Tot
HE02_DarNucBin0_2_Num
HE02_DarNucBin0_3_Are_Mean
HE02_DarNucBin0_3_Are_Tot
HE02_DarNucBin0_3_Num
HE02_DarNucBin0_4_Are_Mean
HE02_DarNucBin0_4_Are_Tot
HE02_DarNucBin0_4_Num
HE02_DarNucBin0_5_Are_Mean
HE02_DarNucBin0_5_Are_Tot
HE02_DarNucBin0_5_Num
HE02_DarNucBin0_6_Are_Mean
HE02_DarNucBin0_6_Are_Tot
HE02_DarNucBin0_6_Num
HE02_DarNucBin0_7_Are_Mean
HE02_DarNucBin0_7_Are_Tot
HE02_DarNucBin0_7_Num
HE02_DarNucBin0_8_Are_Mean
HE02_DarNucBin0_8_Are_Tot
HE02_DarNucBin0_8_Num
HE02_DarNucBin0_Are_Mean
HE02_DarNucBin0_Are_Tot
HE02_DarNucBin0_Num
HE02_DarNucBin1_2_Are_Mean
HE02_DarNucBin1_2_Are_Tot
HE02_DarNucBin1_2_Num
HE02_DarNucBin1_3_Are_Mean
HE02_DarNucBin1_3_Are_Tot
HE02_DarNucBin1_3_Num
HE02_DarNucBin1_4_Are_Mean

HE02_DarNucBin1_4_Are_Tot
HE02_DarNucBin1_4_Num
HE02_DarNucBin1_5_Are_Mean
HE02_DarNucBin1_5_Are_Tot
HE02_DarNucBin1_5_Num
HE02_DarNucBin1_6_Are_Mean
HE02_DarNucBin1_6_Are_Tot
HE02_DarNucBin1_6_Num
HE02_DarNucBin1_7_Are_Mean
HE02_DarNucBin1_7_Are_Tot
HE02_DarNucBin1_7_Num
HE02_DarNucBin1_8_Are_Mean
HE02_DarNucBin1_8_Are_Tot
HE02_DarNucBin1_8_Num
HE02_DarNucBin1_Are_Mean
HE02_DarNucBin1_Are_Tot
HE02_DarNucBin1_Num
HE02_DarNucBin2_3_Are_Mean
HE02_DarNucBin2_3_Are_Tot
HE02_DarNucBin2_3_Num
HE02_DarNucBin2_4_Are_Mean
HE02_DarNucBin2_4_Are_Tot
HE02_DarNucBin2_4_Num
HE02_DarNucBin2_5_Are_Mean
HE02_DarNucBin2_5_Are_Tot
HE02_DarNucBin2_5_Num
HE02_DarNucBin2_6_Are_Mean
HE02_DarNucBin2_6_Are_Tot
HE02_DarNucBin2_6_Num
HE02_DarNucBin2_7_Are_Mean
HE02_DarNucBin2_7_Are_Tot
HE02_DarNucBin2_7_Num
HE02_DarNucBin2_8_Are_Mean
HE02_DarNucBin2_8_Are_Tot
HE02_DarNucBin2_8_Num
HE02_DarNucBin2_Are_Mean
HE02_DarNucBin2_Are_Tot
HE02_DarNucBin2_Num
HE02_DarNucBin3_4_Are_Mean
HE02_DarNucBin3_4_Are_Tot
HE02_DarNucBin3_4_Num
HE02_DarNucBin3_5_Are_Mean

HE02_DarNucBin3_5_Are_Tot
HE02_DarNucBin3_5_Num
HE02_DarNucBin3_6_Are_Mean
HE02_DarNucBin3_6_Are_Tot
HE02_DarNucBin3_6_Num
HE02_DarNucBin3_7_Are_Mean
HE02_DarNucBin3_7_Are_Tot
HE02_DarNucBin3_7_Num
HE02_DarNucBin3_8_Are_Mean
HE02_DarNucBin3_8_Are_Tot
HE02_DarNucBin3_8_Num
HE02_DarNucBin3_Are_Mean
HE02_DarNucBin3_Are_Tot
HE02_DarNucBin3_Num
HE02_DarNucBin4_5_Are_Mean
HE02_DarNucBin4_5_Are_Tot
HE02_DarNucBin4_5_Num
HE02_DarNucBin4_6_Are_Mean
HE02_DarNucBin4_6_Are_Tot
HE02_DarNucBin4_6_Num
HE02_DarNucBin4_7_Are_Mean
HE02_DarNucBin4_7_Are_Tot
HE02_DarNucBin4_7_Num
HE02_DarNucBin4_8_Are_Mean
HE02_DarNucBin4_8_Are_Tot
HE02_DarNucBin4_8_Num
HE02_DarNucBin4_Are_Mean
HE02_DarNucBin4_Are_Tot
HE02_DarNucBin4_Num
HE02_DarNucBin5_6_Are_Mean
HE02_DarNucBin5_6_Are_Tot
HE02_DarNucBin5_6_Num
HE02_DarNucBin5_7_Are_Mean
HE02_DarNucBin5_7_Are_Tot
HE02_DarNucBin5_7_Num
HE02_DarNucBin5_8_Are_Mean
HE02_DarNucBin5_8_Are_Tot
HE02_DarNucBin5_8_Num
HE02_DarNucBin5_Are_Mean
HE02_DarNucBin5_Are_Tot
HE02_DarNucBin5_Num
HE02_DarNucBin6_7_Are_Mean

HE02_DarNucBin6_7_Are_Tot	
HE02_DarNucBin6_7_Num	
HE02_DarNucBin6_8_Are_Mean	
HE02_DarNucBin6_8_Are_Tot	
HE02_DarNucBin6_8_Num	
HE02_DarNucBin6_Are_Mean	
HE02_DarNucBin6_Are_Tot	
HE02_DarNucBin6_Num	
HE02_DarNucBin7_8_Are_Mean	
HE02_DarNucBin7_8_Are_Tot	
HE02_DarNucBin7_8_Num	
HE02_DarNucBin7_Are_Mean	
HE02_DarNucBin7_Are_Tot	
HE02_DarNucBin7_Num	
HE02_DarNucBin8_Are_Mean	
HE02_DarNucBin8_Are_Tot	
HE02_DarNucBin8_Num	
HE02_ENOutGU_Are_Mean	Morphometric and color properties of epithelial nuclei within and outside of gland units.
HE02_ENOutGU_Are_StdMean	
HE02_ENOutGU_Are_Tot	
HE02_ENOutGU_OrgBlu_MeanMean	
HE02_ENOutGU_OrgBlu_MeanStd	
HE02_ENOutGU_OrgGre_MeanMean	
HE02_ENOutGU_OrgGre_MeanStd	
HE02_ENOutGU_OrgRed_MeanMean	
HE02_ENOutGU_OrgRed_MeanStd	
HE02_ENWinGU_Are_Mean	
HE02_ENWinGU_Are_StdMean	
HE02_ENWinGU_Are_Tot	
HE02_ENWinGU_OrgBlu_MeanMean	
HE02_ENWinGU_OrgBlu_MeanStd	
HE02_ENWinGU_OrgGre_MeanMean	
HE02_ENWinGU_OrgGre_MeanStd	
HE02_ENWinGU_OrgRed_MeanMean	
HE02_ENWinGU_OrgRed_MeanStd	
HE02_EpiCluNuc_Are_Mean	Morphometric features of clustered epithelial nuclei
HE02_EpiCluNuc_Are_Std	
HE02_EpiCluNuc_Are_Tot	
HE02_EpiCluNuc_Num	
HE02_EpilsoNuc_Are_Mean	Morphometric features of isolated epithelial nuclei
HE02_EpilsoNuc_Are_Median	

HE02_EpiIsoNuc_Are_Std	
HE02_EpiIsoNuc_Are_Tot	
HE02_EpiIsoNuc_Num	
HE02_EpiNucAt0Dia_Are_Tot	Area of epithelial nuclei certain predefined pixels away from lumens
HE02_EpiNucAt1Dia_Are_Tot	
HE02_EpiNucAt2Dia_Are_Tot	
HE02_EpiNucAt3Dia_Are_Tot	
HE02_EpiNucAt4Dia_Are_Tot	
HE02_EpiNucAt5Dia_Are_Tot	
HE02_EpiNucDen01_Are_Mean	Color and morphometric features of epithelial nuclei divided into bins based on nuclear density/proximity to neighbors.
HE02_EpiNucDen01_Are_Std	
HE02_EpiNucDen01_Are_Tot	
HE02_EpiNucDen01_Num	
HE02_EpiNucDen01_OrgBri_Mean	
HE02_EpiNucDen01_OrgBri_Std	
HE02_EpiNucDen02_Are_Mean	
HE02_EpiNucDen02_Are_Std	
HE02_EpiNucDen02_Are_Tot	
HE02_EpiNucDen02_Num	
HE02_EpiNucDen02_OrgBri_Mean	
HE02_EpiNucDen02_OrgBri_Std	
HE02_EpiNucDen03_Are_Mean	
HE02_EpiNucDen03_Are_Std	
HE02_EpiNucDen03_Are_Tot	
HE02_EpiNucDen03_Num	
HE02_EpiNucDen03_OrgBri_Mean	
HE02_EpiNucDen03_OrgBri_Std	
HE02_EpiNucDen04_Are_Mean	
HE02_EpiNucDen04_Are_Std	
HE02_EpiNucDen04_Are_Tot	
HE02_EpiNucDen04_Num	
HE02_EpiNucDen04_OrgBri_Mean	
HE02_EpiNucDen04_OrgBri_Std	
HE02_EpiNucDen05_Are_Mean	
HE02_EpiNucDen05_Are_Std	
HE02_EpiNucDen05_Are_Tot	
HE02_EpiNucDen05_Num	
HE02_EpiNucDen05_OrgBri_Mean	
HE02_EpiNucDen05_OrgBri_Std	

HE02_EpiNucDen06_Are_Mean
HE02_EpiNucDen06_Are_Std
HE02_EpiNucDen06_Are_Tot
HE02_EpiNucDen06_Num
HE02_EpiNucDen06_OrgBri_Mean
HE02_EpiNucDen06_OrgBri_Std
HE02_EpiNucDen07_Are_Mean
HE02_EpiNucDen07_Are_Std
HE02_EpiNucDen07_Are_Tot
HE02_EpiNucDen07_Num
HE02_EpiNucDen07_OrgBri_Mean
HE02_EpiNucDen07_OrgBri_Std
HE02_EpiNucDen08_Are_Mean
HE02_EpiNucDen08_Are_Std
HE02_EpiNucDen08_Are_Tot
HE02_EpiNucDen08_Num
HE02_EpiNucDen08_OrgBri_Mean
HE02_EpiNucDen08_OrgBri_Std
HE02_EpiNucDen09_Are_Mean
HE02_EpiNucDen09_Are_Std
HE02_EpiNucDen09_Are_Tot
HE02_EpiNucDen09_Num
HE02_EpiNucDen09_OrgBri_Mean
HE02_EpiNucDen09_OrgBri_Std
HE02_EpiNucDen10_Are_Mean
HE02_EpiNucDen10_Are_Std
HE02_EpiNucDen10_Are_Tot
HE02_EpiNucDen10_Num
HE02_EpiNucDen10_OrgBri_Mean
HE02_EpiNucDen10_OrgBri_Std

HE02_EpiNucOGU_Are_Mean	Average area of epithelial nuclei outside of gland units
HE02_EpiNucOGU_Are_Tot	Total area of epithelial nuclei outside of gland units
HE02_EpiNucSizBin0_1_Are_Mean	Morphometric and color features of different combinations of bins where epithelial nuclei have been binned depending on size.
HE02_EpiNucSizBin0_1_Are_Tot	
HE02_EpiNucSizBin0_1_Blu_Mean	
HE02_EpiNucSizBin0_1_Blu_MeanStd	
HE02_EpiNucSizBin0_1_Bri_Mean	
HE02_EpiNucSizBin0_1_Gre_Mean	
HE02_EpiNucSizBin0_1_Gre_MeanStd	

HE02_EpiNucSizBin0_1_Num
HE02_EpiNucSizBin0_1_Red_Mean
HE02_EpiNucSizBin0_1_Red_MeanStd
HE02_EpiNucSizBin0_2_Are_Mean
HE02_EpiNucSizBin0_2_Are_Tot
HE02_EpiNucSizBin0_2_Blu_Mean
HE02_EpiNucSizBin0_2_Blu_MeanStd
HE02_EpiNucSizBin0_2_Bri_Mean
HE02_EpiNucSizBin0_2_Gre_Mean
HE02_EpiNucSizBin0_2_Gre_MeanStd
HE02_EpiNucSizBin0_2_Num
HE02_EpiNucSizBin0_2_Red_Mean
HE02_EpiNucSizBin0_2_Red_MeanStd
HE02_EpiNucSizBin0_3_Are_Mean
HE02_EpiNucSizBin0_3_Are_Tot
HE02_EpiNucSizBin0_3_Blu_Mean
HE02_EpiNucSizBin0_3_Blu_MeanStd
HE02_EpiNucSizBin0_3_Bri_Mean
HE02_EpiNucSizBin0_3_Gre_Mean
HE02_EpiNucSizBin0_3_Gre_MeanStd
HE02_EpiNucSizBin0_3_Num
HE02_EpiNucSizBin0_3_Red_Mean
HE02_EpiNucSizBin0_3_Red_MeanStd
HE02_EpiNucSizBin0_4_Are_Mean
HE02_EpiNucSizBin0_4_Are_Tot
HE02_EpiNucSizBin0_4_Blu_Mean
HE02_EpiNucSizBin0_4_Blu_MeanStd
HE02_EpiNucSizBin0_4_Bri_Mean
HE02_EpiNucSizBin0_4_Gre_Mean
HE02_EpiNucSizBin0_4_Gre_MeanStd
HE02_EpiNucSizBin0_4_Num
HE02_EpiNucSizBin0_4_Red_Mean
HE02_EpiNucSizBin0_4_Red_MeanStd
HE02_EpiNucSizBin0_5_Are_Mean
HE02_EpiNucSizBin0_5_Are_Tot
HE02_EpiNucSizBin0_5_Blu_Mean
HE02_EpiNucSizBin0_5_Blu_MeanStd
HE02_EpiNucSizBin0_5_Bri_Mean
HE02_EpiNucSizBin0_5_Gre_Mean
HE02_EpiNucSizBin0_5_Gre_MeanStd
HE02_EpiNucSizBin0_5_Num
HE02_EpiNucSizBin0_5_Red_Mean

HE02_EpiNucSizBin0_5_Red_MeanStd
HE02_EpiNucSizBin0_6_Are_Mean
HE02_EpiNucSizBin0_6_Are_Tot
HE02_EpiNucSizBin0_6_Blu_Mean
HE02_EpiNucSizBin0_6_Blu_MeanStd
HE02_EpiNucSizBin0_6_Bri_Mean
HE02_EpiNucSizBin0_6_Gre_Mean
HE02_EpiNucSizBin0_6_Gre_MeanStd
HE02_EpiNucSizBin0_6_Num
HE02_EpiNucSizBin0_6_Red_Mean
HE02_EpiNucSizBin0_6_Red_MeanStd
HE02_EpiNucSizBin0_7_Are_Mean
HE02_EpiNucSizBin0_7_Are_Tot
HE02_EpiNucSizBin0_7_Blu_Mean
HE02_EpiNucSizBin0_7_Blu_MeanStd
HE02_EpiNucSizBin0_7_Bri_Mean
HE02_EpiNucSizBin0_7_Gre_Mean
HE02_EpiNucSizBin0_7_Gre_MeanStd
HE02_EpiNucSizBin0_7_Num
HE02_EpiNucSizBin0_7_Red_Mean
HE02_EpiNucSizBin0_7_Red_MeanStd
HE02_EpiNucSizBin0_8_Are_Mean
HE02_EpiNucSizBin0_8_Are_Tot
HE02_EpiNucSizBin0_8_Blu_Mean
HE02_EpiNucSizBin0_8_Blu_MeanStd
HE02_EpiNucSizBin0_8_Bri_Mean
HE02_EpiNucSizBin0_8_Gre_Mean
HE02_EpiNucSizBin0_8_Gre_MeanStd
HE02_EpiNucSizBin0_8_Num
HE02_EpiNucSizBin0_8_Red_Mean
HE02_EpiNucSizBin0_8_Red_MeanStd
HE02_EpiNucSizBin0_Are_Mean
HE02_EpiNucSizBin0_Are_Tot
HE02_EpiNucSizBin0_Blu_Mean
HE02_EpiNucSizBin0_Blu_MeanStd
HE02_EpiNucSizBin0_Bri_Mean
HE02_EpiNucSizBin0_Gre_Mean
HE02_EpiNucSizBin0_Gre_MeanStd
HE02_EpiNucSizBin0_Num
HE02_EpiNucSizBin0_Red_Mean
HE02_EpiNucSizBin0_Red_MeanStd
HE02_EpiNucSizBin1_2_Are_Mean

HE02_EpiNucSizBin1_2_Are_Tot
HE02_EpiNucSizBin1_2_Blu_Mean
HE02_EpiNucSizBin1_2_Blu_MeanStd
HE02_EpiNucSizBin1_2_Bri_Mean
HE02_EpiNucSizBin1_2_Gre_Mean
HE02_EpiNucSizBin1_2_Gre_MeanStd
HE02_EpiNucSizBin1_2_Num
HE02_EpiNucSizBin1_2_Red_Mean
HE02_EpiNucSizBin1_2_Red_MeanStd
HE02_EpiNucSizBin1_3_Are_Mean
HE02_EpiNucSizBin1_3_Are_Tot
HE02_EpiNucSizBin1_3_Blu_Mean
HE02_EpiNucSizBin1_3_Blu_MeanStd
HE02_EpiNucSizBin1_3_Bri_Mean
HE02_EpiNucSizBin1_3_Gre_Mean
HE02_EpiNucSizBin1_3_Gre_MeanStd
HE02_EpiNucSizBin1_3_Num
HE02_EpiNucSizBin1_3_Red_Mean
HE02_EpiNucSizBin1_3_Red_MeanStd
HE02_EpiNucSizBin1_4_Are_Mean
HE02_EpiNucSizBin1_4_Are_Tot
HE02_EpiNucSizBin1_4_Blu_Mean
HE02_EpiNucSizBin1_4_Blu_MeanStd
HE02_EpiNucSizBin1_4_Bri_Mean
HE02_EpiNucSizBin1_4_Gre_Mean
HE02_EpiNucSizBin1_4_Gre_MeanStd
HE02_EpiNucSizBin1_4_Num
HE02_EpiNucSizBin1_4_Red_Mean
HE02_EpiNucSizBin1_4_Red_MeanStd
HE02_EpiNucSizBin1_5_Are_Mean
HE02_EpiNucSizBin1_5_Are_Tot
HE02_EpiNucSizBin1_5_Blu_Mean
HE02_EpiNucSizBin1_5_Blu_MeanStd
HE02_EpiNucSizBin1_5_Bri_Mean
HE02_EpiNucSizBin1_5_Gre_Mean
HE02_EpiNucSizBin1_5_Gre_MeanStd
HE02_EpiNucSizBin1_5_Num
HE02_EpiNucSizBin1_5_Red_Mean
HE02_EpiNucSizBin1_5_Red_MeanStd
HE02_EpiNucSizBin1_6_Are_Mean
HE02_EpiNucSizBin1_6_Are_Tot
HE02_EpiNucSizBin1_6_Blu_Mean

HE02_EpiNucSizBin1_6_Blu_MeanStd
HE02_EpiNucSizBin1_6_Bri_Mean
HE02_EpiNucSizBin1_6_Gre_Mean
HE02_EpiNucSizBin1_6_Gre_MeanStd
HE02_EpiNucSizBin1_6_Num
HE02_EpiNucSizBin1_6_Red_Mean
HE02_EpiNucSizBin1_6_Red_MeanStd
HE02_EpiNucSizBin1_7_Are_Mean
HE02_EpiNucSizBin1_7_Are_Tot
HE02_EpiNucSizBin1_7_Blu_Mean
HE02_EpiNucSizBin1_7_Blu_MeanStd
HE02_EpiNucSizBin1_7_Bri_Mean
HE02_EpiNucSizBin1_7_Gre_Mean
HE02_EpiNucSizBin1_7_Gre_MeanStd
HE02_EpiNucSizBin1_7_Num
HE02_EpiNucSizBin1_7_Red_Mean
HE02_EpiNucSizBin1_7_Red_MeanStd
HE02_EpiNucSizBin1_8_Are_Mean
HE02_EpiNucSizBin1_8_Are_Tot
HE02_EpiNucSizBin1_8_Blu_Mean
HE02_EpiNucSizBin1_8_Blu_MeanStd
HE02_EpiNucSizBin1_8_Bri_Mean
HE02_EpiNucSizBin1_8_Gre_Mean
HE02_EpiNucSizBin1_8_Gre_MeanStd
HE02_EpiNucSizBin1_8_Num
HE02_EpiNucSizBin1_8_Red_Mean
HE02_EpiNucSizBin1_8_Red_MeanStd
HE02_EpiNucSizBin1_Are_Mean
HE02_EpiNucSizBin1_Are_Tot
HE02_EpiNucSizBin1_Blu_Mean
HE02_EpiNucSizBin1_Blu_MeanStd
HE02_EpiNucSizBin1_Bri_Mean
HE02_EpiNucSizBin1_Gre_Mean
HE02_EpiNucSizBin1_Gre_MeanStd
HE02_EpiNucSizBin1_Num
HE02_EpiNucSizBin1_Red_Mean
HE02_EpiNucSizBin1_Red_MeanStd
HE02_EpiNucSizBin2_3_Are_Mean
HE02_EpiNucSizBin2_3_Are_Tot
HE02_EpiNucSizBin2_3_Blu_Mean
HE02_EpiNucSizBin2_3_Blu_MeanStd
HE02_EpiNucSizBin2_3_Bri_Mean

HE02_EpiNucSizBin2_3_Gre_Mean
HE02_EpiNucSizBin2_3_Gre_MeanStd
HE02_EpiNucSizBin2_3_Num
HE02_EpiNucSizBin2_3_Red_Mean
HE02_EpiNucSizBin2_3_Red_MeanStd
HE02_EpiNucSizBin2_4_Are_Mean
HE02_EpiNucSizBin2_4_Are_Tot
HE02_EpiNucSizBin2_4_Blu_Mean
HE02_EpiNucSizBin2_4_Blu_MeanStd
HE02_EpiNucSizBin2_4_Bri_Mean
HE02_EpiNucSizBin2_4_Gre_Mean
HE02_EpiNucSizBin2_4_Gre_MeanStd
HE02_EpiNucSizBin2_4_Num
HE02_EpiNucSizBin2_4_Red_Mean
HE02_EpiNucSizBin2_4_Red_MeanStd
HE02_EpiNucSizBin2_5_Are_Mean
HE02_EpiNucSizBin2_5_Are_Tot
HE02_EpiNucSizBin2_5_Blu_Mean
HE02_EpiNucSizBin2_5_Blu_MeanStd
HE02_EpiNucSizBin2_5_Bri_Mean
HE02_EpiNucSizBin2_5_Gre_Mean
HE02_EpiNucSizBin2_5_Gre_MeanStd
HE02_EpiNucSizBin2_5_Num
HE02_EpiNucSizBin2_5_Red_Mean
HE02_EpiNucSizBin2_5_Red_MeanStd
HE02_EpiNucSizBin2_6_Are_Mean
HE02_EpiNucSizBin2_6_Are_Tot
HE02_EpiNucSizBin2_6_Blu_Mean
HE02_EpiNucSizBin2_6_Blu_MeanStd
HE02_EpiNucSizBin2_6_Bri_Mean
HE02_EpiNucSizBin2_6_Gre_Mean
HE02_EpiNucSizBin2_6_Gre_MeanStd
HE02_EpiNucSizBin2_6_Num
HE02_EpiNucSizBin2_6_Red_Mean
HE02_EpiNucSizBin2_6_Red_MeanStd
HE02_EpiNucSizBin2_7_Are_Mean
HE02_EpiNucSizBin2_7_Are_Tot
HE02_EpiNucSizBin2_7_Blu_Mean
HE02_EpiNucSizBin2_7_Blu_MeanStd
HE02_EpiNucSizBin2_7_Bri_Mean
HE02_EpiNucSizBin2_7_Gre_Mean
HE02_EpiNucSizBin2_7_Gre_MeanStd

HE02_EpiNucSizBin2_7_Num
HE02_EpiNucSizBin2_7_Red_Mean
HE02_EpiNucSizBin2_7_Red_MeanStd
HE02_EpiNucSizBin2_8_Are_Mean
HE02_EpiNucSizBin2_8_Are_Tot
HE02_EpiNucSizBin2_8_Blu_Mean
HE02_EpiNucSizBin2_8_Blu_MeanStd
HE02_EpiNucSizBin2_8_Bri_Mean
HE02_EpiNucSizBin2_8_Gre_Mean
HE02_EpiNucSizBin2_8_Gre_MeanStd
HE02_EpiNucSizBin2_8_Num
HE02_EpiNucSizBin2_8_Red_Mean
HE02_EpiNucSizBin2_8_Red_MeanStd
HE02_EpiNucSizBin2_Are_Mean
HE02_EpiNucSizBin2_Are_Tot
HE02_EpiNucSizBin2_Blu_Mean
HE02_EpiNucSizBin2_Blu_MeanStd
HE02_EpiNucSizBin2_Bri_Mean
HE02_EpiNucSizBin2_Gre_Mean
HE02_EpiNucSizBin2_Gre_MeanStd
HE02_EpiNucSizBin2_Num
HE02_EpiNucSizBin2_Red_Mean
HE02_EpiNucSizBin2_Red_MeanStd
HE02_EpiNucSizBin3_4_Are_Mean
HE02_EpiNucSizBin3_4_Are_Tot
HE02_EpiNucSizBin3_4_Blu_Mean
HE02_EpiNucSizBin3_4_Blu_MeanStd
HE02_EpiNucSizBin3_4_Bri_Mean
HE02_EpiNucSizBin3_4_Gre_Mean
HE02_EpiNucSizBin3_4_Gre_MeanStd
HE02_EpiNucSizBin3_4_Num
HE02_EpiNucSizBin3_4_Red_Mean
HE02_EpiNucSizBin3_4_Red_MeanStd
HE02_EpiNucSizBin3_5_Are_Mean
HE02_EpiNucSizBin3_5_Are_Tot
HE02_EpiNucSizBin3_5_Blu_Mean
HE02_EpiNucSizBin3_5_Blu_MeanStd
HE02_EpiNucSizBin3_5_Bri_Mean
HE02_EpiNucSizBin3_5_Gre_Mean
HE02_EpiNucSizBin3_5_Gre_MeanStd
HE02_EpiNucSizBin3_5_Num
HE02_EpiNucSizBin3_5_Red_Mean

HE02_EpiNucSizBin3_5_Red_MeanStd
HE02_EpiNucSizBin3_6_Are_Mean
HE02_EpiNucSizBin3_6_Are_Tot
HE02_EpiNucSizBin3_6_Blu_Mean
HE02_EpiNucSizBin3_6_Blu_MeanStd
HE02_EpiNucSizBin3_6_Bri_Mean
HE02_EpiNucSizBin3_6_Gre_Mean
HE02_EpiNucSizBin3_6_Gre_MeanStd
HE02_EpiNucSizBin3_6_Num
HE02_EpiNucSizBin3_6_Red_Mean
HE02_EpiNucSizBin3_6_Red_MeanStd
HE02_EpiNucSizBin3_7_Are_Mean
HE02_EpiNucSizBin3_7_Are_Tot
HE02_EpiNucSizBin3_7_Blu_Mean
HE02_EpiNucSizBin3_7_Blu_MeanStd
HE02_EpiNucSizBin3_7_Bri_Mean
HE02_EpiNucSizBin3_7_Gre_Mean
HE02_EpiNucSizBin3_7_Gre_MeanStd
HE02_EpiNucSizBin3_7_Num
HE02_EpiNucSizBin3_7_Red_Mean
HE02_EpiNucSizBin3_7_Red_MeanStd
HE02_EpiNucSizBin3_8_Are_Mean
HE02_EpiNucSizBin3_8_Are_Tot
HE02_EpiNucSizBin3_8_Blu_Mean
HE02_EpiNucSizBin3_8_Blu_MeanStd
HE02_EpiNucSizBin3_8_Bri_Mean
HE02_EpiNucSizBin3_8_Gre_Mean
HE02_EpiNucSizBin3_8_Gre_MeanStd
HE02_EpiNucSizBin3_8_Num
HE02_EpiNucSizBin3_8_Red_Mean
HE02_EpiNucSizBin3_8_Red_MeanStd
HE02_EpiNucSizBin3_Are_Mean
HE02_EpiNucSizBin3_Are_Tot
HE02_EpiNucSizBin3_Blu_Mean
HE02_EpiNucSizBin3_Blu_MeanStd
HE02_EpiNucSizBin3_Bri_Mean
HE02_EpiNucSizBin3_Gre_Mean
HE02_EpiNucSizBin3_Gre_MeanStd
HE02_EpiNucSizBin3_Num
HE02_EpiNucSizBin3_Red_Mean
HE02_EpiNucSizBin3_Red_MeanStd
HE02_EpiNucSizBin4_5_Are_Mean

HE02_EpiNucSizBin4_5_Are_Tot
HE02_EpiNucSizBin4_5_Blu_Mean
HE02_EpiNucSizBin4_5_Blu_MeanStd
HE02_EpiNucSizBin4_5_Bri_Mean
HE02_EpiNucSizBin4_5_Gre_Mean
HE02_EpiNucSizBin4_5_Gre_MeanStd
HE02_EpiNucSizBin4_5_Num
HE02_EpiNucSizBin4_5_Red_Mean
HE02_EpiNucSizBin4_5_Red_MeanStd
HE02_EpiNucSizBin4_6_Are_Mean
HE02_EpiNucSizBin4_6_Are_Tot
HE02_EpiNucSizBin4_6_Blu_Mean
HE02_EpiNucSizBin4_6_Blu_MeanStd
HE02_EpiNucSizBin4_6_Bri_Mean
HE02_EpiNucSizBin4_6_Gre_Mean
HE02_EpiNucSizBin4_6_Gre_MeanStd
HE02_EpiNucSizBin4_6_Num
HE02_EpiNucSizBin4_6_Red_Mean
HE02_EpiNucSizBin4_6_Red_MeanStd
HE02_EpiNucSizBin4_7_Are_Mean
HE02_EpiNucSizBin4_7_Are_Tot
HE02_EpiNucSizBin4_7_Blu_Mean
HE02_EpiNucSizBin4_7_Blu_MeanStd
HE02_EpiNucSizBin4_7_Bri_Mean
HE02_EpiNucSizBin4_7_Gre_Mean
HE02_EpiNucSizBin4_7_Gre_MeanStd
HE02_EpiNucSizBin4_7_Num
HE02_EpiNucSizBin4_7_Red_Mean
HE02_EpiNucSizBin4_7_Red_MeanStd
HE02_EpiNucSizBin4_8_Are_Mean
HE02_EpiNucSizBin4_8_Are_Tot
HE02_EpiNucSizBin4_8_Blu_Mean
HE02_EpiNucSizBin4_8_Blu_MeanStd
HE02_EpiNucSizBin4_8_Bri_Mean
HE02_EpiNucSizBin4_8_Gre_Mean
HE02_EpiNucSizBin4_8_Gre_MeanStd
HE02_EpiNucSizBin4_8_Num
HE02_EpiNucSizBin4_8_Red_Mean
HE02_EpiNucSizBin4_8_Red_MeanStd
HE02_EpiNucSizBin4_Are_Mean
HE02_EpiNucSizBin4_Are_Tot
HE02_EpiNucSizBin4_Blu_Mean

HE02_EpiNucSizBin4_Blu_MeanStd
HE02_EpiNucSizBin4_Bri_Mean
HE02_EpiNucSizBin4_Gre_Mean
HE02_EpiNucSizBin4_Gre_MeanStd
HE02_EpiNucSizBin4_Num
HE02_EpiNucSizBin4_Red_Mean
HE02_EpiNucSizBin4_Red_MeanStd
HE02_EpiNucSizBin5_6_Are_Mean
HE02_EpiNucSizBin5_6_Are_Tot
HE02_EpiNucSizBin5_6_Blu_Mean
HE02_EpiNucSizBin5_6_Blu_MeanStd
HE02_EpiNucSizBin5_6_Bri_Mean
HE02_EpiNucSizBin5_6_Gre_Mean
HE02_EpiNucSizBin5_6_Gre_MeanStd
HE02_EpiNucSizBin5_6_Num
HE02_EpiNucSizBin5_6_Red_Mean
HE02_EpiNucSizBin5_6_Red_MeanStd
HE02_EpiNucSizBin5_7_Are_Mean
HE02_EpiNucSizBin5_7_Are_Tot
HE02_EpiNucSizBin5_7_Blu_Mean
HE02_EpiNucSizBin5_7_Blu_MeanStd
HE02_EpiNucSizBin5_7_Bri_Mean
HE02_EpiNucSizBin5_7_Gre_Mean
HE02_EpiNucSizBin5_7_Gre_MeanStd
HE02_EpiNucSizBin5_7_Num
HE02_EpiNucSizBin5_7_Red_Mean
HE02_EpiNucSizBin5_7_Red_MeanStd
HE02_EpiNucSizBin5_8_Are_Mean
HE02_EpiNucSizBin5_8_Are_Tot
HE02_EpiNucSizBin5_8_Blu_Mean
HE02_EpiNucSizBin5_8_Blu_MeanStd
HE02_EpiNucSizBin5_8_Bri_Mean
HE02_EpiNucSizBin5_8_Gre_Mean
HE02_EpiNucSizBin5_8_Gre_MeanStd
HE02_EpiNucSizBin5_8_Num
HE02_EpiNucSizBin5_8_Red_Mean
HE02_EpiNucSizBin5_8_Red_MeanStd
HE02_EpiNucSizBin5_Are_Mean
HE02_EpiNucSizBin5_Are_Tot
HE02_EpiNucSizBin5_Blu_Mean
HE02_EpiNucSizBin5_Blu_MeanStd
HE02_EpiNucSizBin5_Bri_Mean

HE02_EpiNucSizBin5_Gre_Mean
HE02_EpiNucSizBin5_Gre_MeanStd
HE02_EpiNucSizBin5_Num
HE02_EpiNucSizBin5_Red_Mean
HE02_EpiNucSizBin5_Red_MeanStd
HE02_EpiNucSizBin6_7_Are_Mean
HE02_EpiNucSizBin6_7_Are_Tot
HE02_EpiNucSizBin6_7_Blu_Mean
HE02_EpiNucSizBin6_7_Blu_MeanStd
HE02_EpiNucSizBin6_7_Bri_Mean
HE02_EpiNucSizBin6_7_Gre_Mean
HE02_EpiNucSizBin6_7_Gre_MeanStd
HE02_EpiNucSizBin6_7_Num
HE02_EpiNucSizBin6_7_Red_Mean
HE02_EpiNucSizBin6_7_Red_MeanStd
HE02_EpiNucSizBin6_8_Are_Mean
HE02_EpiNucSizBin6_8_Are_Tot
HE02_EpiNucSizBin6_8_Blu_Mean
HE02_EpiNucSizBin6_8_Blu_MeanStd
HE02_EpiNucSizBin6_8_Bri_Mean
HE02_EpiNucSizBin6_8_Gre_Mean
HE02_EpiNucSizBin6_8_Gre_MeanStd
HE02_EpiNucSizBin6_8_Num
HE02_EpiNucSizBin6_8_Red_Mean
HE02_EpiNucSizBin6_8_Red_MeanStd
HE02_EpiNucSizBin6_Are_Mean
HE02_EpiNucSizBin6_Are_Tot
HE02_EpiNucSizBin6_Blu_Mean
HE02_EpiNucSizBin6_Blu_MeanStd
HE02_EpiNucSizBin6_Bri_Mean
HE02_EpiNucSizBin6_Gre_Mean
HE02_EpiNucSizBin6_Gre_MeanStd
HE02_EpiNucSizBin6_Num
HE02_EpiNucSizBin6_Red_Mean
HE02_EpiNucSizBin6_Red_MeanStd
HE02_EpiNucSizBin7_8_Are_Mean
HE02_EpiNucSizBin7_8_Are_Tot
HE02_EpiNucSizBin7_8_Blu_Mean
HE02_EpiNucSizBin7_8_Blu_MeanStd
HE02_EpiNucSizBin7_8_Bri_Mean
HE02_EpiNucSizBin7_8_Gre_Mean
HE02_EpiNucSizBin7_8_Gre_MeanStd

HE02_EpiNucSizBin7_8_Num	
HE02_EpiNucSizBin7_8_Red_Mean	
HE02_EpiNucSizBin7_8_Red_MeanStd	
HE02_EpiNucSizBin7_Are_Mean	
HE02_EpiNucSizBin7_Are_Tot	
HE02_EpiNucSizBin7_Blu_Mean	
HE02_EpiNucSizBin7_Blu_MeanStd	
HE02_EpiNucSizBin7_Bri_Mean	
HE02_EpiNucSizBin7_Gre_Mean	
HE02_EpiNucSizBin7_Gre_MeanStd	
HE02_EpiNucSizBin7_Num	
HE02_EpiNucSizBin7_Red_Mean	
HE02_EpiNucSizBin7_Red_MeanStd	
HE02_EpiNucSizBin8_Are_Mean	
HE02_EpiNucSizBin8_Are_Tot	
HE02_EpiNucSizBin8_Blu_Mean	
HE02_EpiNucSizBin8_Blu_MeanStd	
HE02_EpiNucSizBin8_Bri_Mean	
HE02_EpiNucSizBin8_Gre_Mean	
HE02_EpiNucSizBin8_Gre_MeanStd	
HE02_EpiNucSizBin8_Num	
HE02_EpiNucSizBin8_Red_Mean	
HE02_EpiNucSizBin8_Red_MeanStd	
HE02_EpiNucWIGU_Are_Mean	Average area of epithelial nuclei within gland units
HE02_EpiNucWIGU_Are_Tot	Total area of epithelial nuclei within gland units
HE02_EpiNuc_Are_Mean	Color and morphometric features of epithelial nuclei
HE02_EpiNuc_Are_Median	
HE02_EpiNuc_Are_Std	
HE02_EpiNuc_Are_Tot	
HE02_EpiNuc_ElpFit_Mean	
HE02_EpiNuc_ElpFit_Median	
HE02_EpiNuc_ElpFit_Std	
HE02_EpiNuc_LOW_Mean	
HE02_EpiNuc_LOW_Median	
HE02_EpiNuc_LOW_Std	
HE02_EpiNuc_Num	
HE02_EpiNuc_OrgBlu_MeanMean	
HE02_EpiNuc_OrgBlu_MeanStd	
HE02_EpiNuc_OrgBri_Mean	
HE02_EpiNuc_OrgBri_Std	
HE02_EpiNuc_OrgGre_MeanMean	
HE02_EpiNuc_OrgGre_MeanStd	

HE02_EpiNuc_OrgH_Mean	
HE02_EpiNuc_OrgH_Std	
HE02_EpiNuc_OrgI_Mean	
HE02_EpiNuc_OrgI_Std	
HE02_EpiNuc_OrgQ_Mean	
HE02_EpiNuc_OrgQ_Std	
HE02_EpiNuc_OrgRed_CF100_MeanStd	
HE02_EpiNuc_OrgRed_CF200_MeanStd	
HE02_EpiNuc_OrgRed_CF300_MeanStd	
HE02_EpiNuc_OrgRed_CF400_MeanStd	
HE02_EpiNuc_OrgRed_CF500_MeanStd	
HE02_EpiNuc_OrgRed_MeanMean	
HE02_EpiNuc_OrgRed_MeanStd	
HE02_EpiNuc_OrgS_Mean	
HE02_EpiNuc_OrgS_Std	
HE02_EpiNuc_OrgV_Mean	
HE02_EpiNuc_OrgV_Std	
HE02_EpiNuc_OrgY_Mean	
HE02_EpiNuc_OrgY_Std	
HE02_IsoEpiNuc_ElpFit_Mean	Color and morphometric features of isolated epithelial nuclei
HE02_IsoEpiNuc_ElpFit_Median	
HE02_IsoEpiNuc_ElpFit_Std	
HE02_IsoEpiNuc_LOW_Mean	
HE02_IsoEpiNuc_LOW_Median	
HE02_IsoEpiNuc_LOW_Std	
HE02_IsoEpiNuc_OrgBlu_MeanMean	
HE02_IsoEpiNuc_OrgBlu_MeanStd	
HE02_IsoEpiNuc_OrgBlu_StdMean	
HE02_IsoEpiNuc_OrgBri_Mean	
HE02_IsoEpiNuc_OrgBri_Std	
HE02_IsoEpiNuc_OrgGre_MeanMean	
HE02_IsoEpiNuc_OrgGre_MeanStd	
HE02_IsoEpiNuc_OrgGre_StdMean	
HE02_IsoEpiNuc_OrgRed_MeanMean	
HE02_IsoEpiNuc_OrgRed_MeanStd	
HE02_IsoEpiNuc_OrgRed_StdMean	
HE02_IsoEpiNuc_ShaInd_Mean	
HE02_IsoEpiNuc_ShaInd_Std	
HE02_IsoNuc_Are_Mean	
HE02_IsoNuc_Are_Std	
HE02_IsoNuc_Are_Tot	

HE02_IsoNuc_Num	
HE02_IsoStrNuc_Are_Mean	
HE02_IsoStrNuc_Are_Std	
HE02_IsoStrNuc_Are_Tot	
HE02_IsoStrNuc_Num	
HE02_LStr_Are_Mean	Color and morphometric features of light stroma
HE02_LStr_Are_Std	
HE02_LStr_Are_Tot	
HE02_LStr_Num	
HE02_LStr_OrgBlu_MeanMean	
HE02_LStr_OrgBlu_MeanStd	
HE02_LStr_OrgBri_Mean	
HE02_LStr_OrgBri_Std	
HE02_LStr_OrgGre_MeanMean	
HE02_LStr_OrgGre_MeanStd	
HE02_LStr_OrgH_Mean	
HE02_LStr_OrgH_Std	
HE02_LStr_OrgI_Mean	
HE02_LStr_OrgI_Std	
HE02_LStr_OrgQ_Mean	
HE02_LStr_OrgQ_Std	
HE02_LStr_OrgRed_MeanMean	
HE02_LStr_OrgRed_MeanStd	
HE02_LStr_OrgS_Mean	
HE02_LStr_OrgS_Std	
HE02_LStr_OrgV_Mean	
HE02_LStr_OrgV_Std	
HE02_LStr_OrgY_Mean	
HE02_LStr_OrgY_Std	
HE02_LigNucBin0_1_Are_Mean	Morphometric features of light nuclei that have been binned
HE02_LigNucBin0_1_Are_Tot	
HE02_LigNucBin0_1_Num	
HE02_LigNucBin0_2_Are_Mean	
HE02_LigNucBin0_2_Are_Tot	
HE02_LigNucBin0_2_Num	
HE02_LigNucBin0_3_Are_Mean	
HE02_LigNucBin0_3_Are_Tot	
HE02_LigNucBin0_3_Num	
HE02_LigNucBin0_4_Are_Mean	
HE02_LigNucBin0_4_Are_Tot	
HE02_LigNucBin0_4_Num	

HE02_LigNucBin0_5_Are_Mean
HE02_LigNucBin0_5_Are_Tot
HE02_LigNucBin0_5_Num
HE02_LigNucBin0_6_Are_Mean
HE02_LigNucBin0_6_Are_Tot
HE02_LigNucBin0_6_Num
HE02_LigNucBin0_7_Are_Mean
HE02_LigNucBin0_7_Are_Tot
HE02_LigNucBin0_7_Num
HE02_LigNucBin0_8_Are_Mean
HE02_LigNucBin0_8_Are_Tot
HE02_LigNucBin0_8_Num
HE02_LigNucBin0_Are_Mean
HE02_LigNucBin0_Are_Tot
HE02_LigNucBin0_Num
HE02_LigNucBin1_2_Are_Mean
HE02_LigNucBin1_2_Are_Tot
HE02_LigNucBin1_2_Num
HE02_LigNucBin1_3_Are_Mean
HE02_LigNucBin1_3_Are_Tot
HE02_LigNucBin1_3_Num
HE02_LigNucBin1_4_Are_Mean
HE02_LigNucBin1_4_Are_Tot
HE02_LigNucBin1_4_Num
HE02_LigNucBin1_5_Are_Mean
HE02_LigNucBin1_5_Are_Tot
HE02_LigNucBin1_5_Num
HE02_LigNucBin1_6_Are_Mean
HE02_LigNucBin1_6_Are_Tot
HE02_LigNucBin1_6_Num
HE02_LigNucBin1_7_Are_Mean
HE02_LigNucBin1_7_Are_Tot
HE02_LigNucBin1_7_Num
HE02_LigNucBin1_8_Are_Mean
HE02_LigNucBin1_8_Are_Tot
HE02_LigNucBin1_8_Num
HE02_LigNucBin1_Are_Mean
HE02_LigNucBin1_Are_Tot
HE02_LigNucBin1_Num
HE02_LigNucBin2_3_Are_Mean
HE02_LigNucBin2_3_Are_Tot
HE02_LigNucBin2_3_Num

HE02_LigNucBin2_4_Are_Mean
HE02_LigNucBin2_4_Are_Tot
HE02_LigNucBin2_4_Num
HE02_LigNucBin2_5_Are_Mean
HE02_LigNucBin2_5_Are_Tot
HE02_LigNucBin2_5_Num
HE02_LigNucBin2_6_Are_Mean
HE02_LigNucBin2_6_Are_Tot
HE02_LigNucBin2_6_Num
HE02_LigNucBin2_7_Are_Mean
HE02_LigNucBin2_7_Are_Tot
HE02_LigNucBin2_7_Num
HE02_LigNucBin2_8_Are_Mean
HE02_LigNucBin2_8_Are_Tot
HE02_LigNucBin2_8_Num
HE02_LigNucBin2_Are_Mean
HE02_LigNucBin2_Are_Tot
HE02_LigNucBin2_Num
HE02_LigNucBin3_4_Are_Mean
HE02_LigNucBin3_4_Are_Tot
HE02_LigNucBin3_4_Num
HE02_LigNucBin3_5_Are_Mean
HE02_LigNucBin3_5_Are_Tot
HE02_LigNucBin3_5_Num
HE02_LigNucBin3_6_Are_Mean
HE02_LigNucBin3_6_Are_Tot
HE02_LigNucBin3_6_Num
HE02_LigNucBin3_7_Are_Mean
HE02_LigNucBin3_7_Are_Tot
HE02_LigNucBin3_7_Num
HE02_LigNucBin3_8_Are_Mean
HE02_LigNucBin3_8_Are_Tot
HE02_LigNucBin3_8_Num
HE02_LigNucBin3_Are_Mean
HE02_LigNucBin3_Are_Tot
HE02_LigNucBin3_Num
HE02_LigNucBin4_5_Are_Mean
HE02_LigNucBin4_5_Are_Tot
HE02_LigNucBin4_5_Num
HE02_LigNucBin4_6_Are_Mean
HE02_LigNucBin4_6_Are_Tot
HE02_LigNucBin4_6_Num

HE02_LigNucBin4_7_Are_Mean	
HE02_LigNucBin4_7_Are_Tot	
HE02_LigNucBin4_7_Num	
HE02_LigNucBin4_8_Are_Mean	
HE02_LigNucBin4_8_Are_Tot	
HE02_LigNucBin4_8_Num	
HE02_LigNucBin4_Are_Mean	
HE02_LigNucBin4_Are_Tot	
HE02_LigNucBin4_Num	
HE02_LigNucBin5_6_Are_Mean	
HE02_LigNucBin5_6_Are_Tot	
HE02_LigNucBin5_6_Num	
HE02_LigNucBin5_7_Are_Mean	
HE02_LigNucBin5_7_Are_Tot	
HE02_LigNucBin5_7_Num	
HE02_LigNucBin5_8_Are_Mean	
HE02_LigNucBin5_8_Are_Tot	
HE02_LigNucBin5_8_Num	
HE02_LigNucBin5_Are_Mean	
HE02_LigNucBin5_Are_Tot	
HE02_LigNucBin5_Num	
HE02_LigNucBin6_7_Are_Mean	
HE02_LigNucBin6_7_Are_Tot	
HE02_LigNucBin6_7_Num	
HE02_LigNucBin6_8_Are_Mean	
HE02_LigNucBin6_8_Are_Tot	
HE02_LigNucBin6_8_Num	
HE02_LigNucBin6_Are_Mean	
HE02_LigNucBin6_Are_Tot	
HE02_LigNucBin6_Num	
HE02_LigNucBin7_8_Are_Mean	
HE02_LigNucBin7_8_Are_Tot	
HE02_LigNucBin7_8_Num	
HE02_LigNucBin7_Are_Mean	
HE02_LigNucBin7_Are_Tot	
HE02_LigNucBin7_Num	
HE02_LigNucBin8_Are_Mean	
HE02_LigNucBin8_Are_Tot	
HE02_LigNucBin8_Num	
HE02_Lum_Are_Mean	Luminal morphometric features
HE02_Lum_Are_Median	
HE02_Lum_Are_Std	

HE02_Lum_Are_Tot	
HE02_Lum_ElpFit_Mean	
HE02_Lum_ElpFit_Std	
HE02_Lum_LOW_Ave	
HE02_Lum_LOW_Mean	
HE02_Lum_LOW_Std	
HE02_Lum_Num	
HE02_Lum_Ptr_Mean	
HE02_Lum_Ptr_Std	
HE02_MDTumor_Are_Tot	Morphometric and color features of the manually defined tumor area.
HE02_MDTumor_Num	
HE02_MDTumor_OrgBlu_MeanMean	
HE02_MDTumor_OrgBlu_MeanStd	
HE02_MDTumor_OrgBri_Mean	
HE02_MDTumor_OrgBri_Std	
HE02_MDTumor_OrgGre_MeanMean	
HE02_MDTumor_OrgGre_MeanStd	
HE02_MDTumor_OrgH_Mean	
HE02_MDTumor_OrgH_Std	
HE02_MDTumor_OrgI_Mean	
HE02_MDTumor_OrgI_Std	
HE02_MDTumor_OrgQ_Mean	
HE02_MDTumor_OrgQ_Std	
HE02_MDTumor_OrgRed_MeanMean	
HE02_MDTumor_OrgRed_MeanStd	
HE02_MDTumor_OrgS_Mean	
HE02_MDTumor_OrgS_Std	
HE02_MDTumor_OrgV_Mean	
HE02_MDTumor_OrgV_Std	
HE02_MDTumor_OrgY_Mean	
HE02_MDTumor_OrgY_Std	
HE02_Nuc_Are_Mean	Nuclear features
HE02_Nuc_Are_Std	
HE02_Nuc_Are_Tot	
HE02_Nuc_Num	
HE02_PDNuc_Are_Mean	Morphometric and color features of poorly defined nuclei
HE02_PDNuc_Are_Std	
HE02_PDNuc_Are_Tot	
HE02_PDNuc_ElpFit_Mean	
HE02_PDNuc_ElpFit_Std	

HE02_PDNuc_LOW_Mean	
HE02_PDNuc_LOW_Std	
HE02_PDNuc_Num	
HE02_PDNuc_OrgBlu_MeanMean	
HE02_PDNuc_OrgBlu_MeanStd	
HE02_PDNuc_OrgBlu_StdMean	
HE02_PDNuc_OrgBri_Mean	
HE02_PDNuc_OrgBri_Std	
HE02_PDNuc_OrgGre_MeanMean	
HE02_PDNuc_OrgGre_MeanStd	
HE02_PDNuc_OrgGre_StdMean	
HE02_PDNuc_OrgRed_MeanMean	
HE02_PDNuc_OrgRed_MeanStd	
HE02_PDNuc_OrgRed_StdMean	
HE02_PDNuc_ShaInd_Mean	
HE02_PDNuc_ShaInd_Std	
HE02_StrNuc_Are_Mean	Morphometric and color features of stroma nuclei
HE02_StrNuc_Are_Median	
HE02_StrNuc_Are_Std	
HE02_StrNuc_Are_Tot	
HE02_StrNuc_ElpFit_Mean	
HE02_StrNuc_ElpFit_Median	
HE02_StrNuc_ElpFit_Std	
HE02_StrNuc_LOW_Mean	
HE02_StrNuc_LOW_Median	
HE02_StrNuc_LOW_Std	
HE02_StrNuc_Num	
HE02_StrNuc_OrgBlu_MeanMean	
HE02_StrNuc_OrgBlu_MeanStd	
HE02_StrNuc_OrgBri_Mean	
HE02_StrNuc_OrgBri_Std	
HE02_StrNuc_OrgGre_MeanMean	
HE02_StrNuc_OrgGre_MeanStd	
HE02_StrNuc_OrgH_Mean	
HE02_StrNuc_OrgH_Std	
HE02_StrNuc_OrgI_Mean	
HE02_StrNuc_OrgI_Std	
HE02_StrNuc_OrgQ_Mean	
HE02_StrNuc_OrgQ_Std	
HE02_StrNuc_OrgRed_MeanMean	
HE02_StrNuc_OrgRed_MeanStd	
HE02_StrNuc_OrgS_Mean	

HE02_StrNuc_OrgS_Std	
HE02_StrNuc_OrgV_Mean	
HE02_StrNuc_OrgV_Std	
HE02_StrNuc_OrgY_Mean	
HE02_StrNuc_OrgY_Std	
HE02_StrPla_Are_Mean	Morphometric features of a combined stroma and cytoplasm object
HE02_StrPla_Are_Tot	
HE02_StrPla_Num	
HE02_StrPla_OrgBlu_MeanMean	
HE02_StrPla_OrgBlu_MeanStd	
HE02_StrPla_OrgBlu_StdMean	
HE02_StrPla_OrgGre_MeanMean	
HE02_StrPla_OrgGre_MeanStd	
HE02_StrPla_OrgGre_StdMean	
HE02_StrPla_OrgH_Mean	
HE02_StrPla_OrgH_Std	
HE02_StrPla_OrgI_Mean	
HE02_StrPla_OrgI_Std	
HE02_StrPla_OrgQ_Mean	
HE02_StrPla_OrgQ_Std	
HE02_StrPla_OrgRed_MeanMean	
HE02_StrPla_OrgRed_MeanStd	
HE02_StrPla_OrgRed_StdMean	
HE02_StrPla_OrgS_Mean	
HE02_StrPla_OrgS_Std	
HE02_StrPla_OrgV_Mean	
HE02_StrPla_OrgV_Std	
HE02_StrPla_OrgY_Mean	
HE02_StrPla_OrgY_Std	
HE02_Str_Are_Mean	Morphometric and color features of stroma
HE02_Str_Are_Std	
HE02_Str_Are_Tot	
HE02_Str_Num	
HE02_Str_OrgBlu_MeanMean	
HE02_Str_OrgBlu_MeanStd	
HE02_Str_OrgBri_Mean	
HE02_Str_OrgBri_Std	
HE02_Str_OrgGre_MeanMean	
HE02_Str_OrgGre_MeanStd	
HE02_Str_OrgH_Mean	
HE02_Str_OrgH_Std	

HE02_Str_OrgI_Mean	
HE02_Str_OrgI_Std	
HE02_Str_OrgQ_Mean	
HE02_Str_OrgQ_Std	
HE02_Str_OrgRed_MeanMean	
HE02_Str_OrgRed_MeanStd	
HE02_Str_OrgS_Mean	
HE02_Str_OrgS_Std	
HE02_Str_OrgV_Mean	
HE02_Str_OrgV_Std	
HE02_Str_OrgY_Mean	
HE02_Str_OrgY_Std	
HE02_TumorWoWS_Are_Tot	Morphometric and color features of the tumor area
HE02_TumorWoWS_Num	without white space
HE02_TumorWoWS_OrgBlu_MeanMean	
HE02_TumorWoWS_OrgBlu_MeanStd	
HE02_TumorWoWS_OrgBri_Mean	
HE02_TumorWoWS_OrgBri_Std	
HE02_TumorWoWS_OrgGre_MeanMean	
HE02_TumorWoWS_OrgGre_MeanStd	
HE02_TumorWoWS_OrgH_Mean	
HE02_TumorWoWS_OrgH_Std	
HE02_TumorWoWS_OrgI_Mean	
HE02_TumorWoWS_OrgI_Std	
HE02_TumorWoWS_OrgQ_Mean	
HE02_TumorWoWS_OrgQ_Std	
HE02_TumorWoWS_OrgRed_MeanMean	
HE02_TumorWoWS_OrgRed_MeanStd	
HE02_TumorWoWS_OrgS_Mean	
HE02_TumorWoWS_OrgS_Std	
HE02_TumorWoWS_OrgV_Mean	
HE02_TumorWoWS_OrgV_Std	
HE02_TumorWoWS_OrgYIQBri_Mean	
HE02_TumorWoWS_OrgYIQBri_Std	
HE02_TumorWoWS_OrgY_Mean	
HE02_TumorWoWS_OrgY_Std	
HE02_WDEpiNuc_Are_Mean	Morphometric and color features of well defined
HE02_WDEpiNuc_Are_Median	epithelial nuclei
HE02_WDEpiNuc_Are_Std	
HE02_WDEpiNuc_Are_Tot	

HE02_WDEpiNuc_ElpFit_Mean	
HE02_WDEpiNuc_ElpFit_Median	
HE02_WDEpiNuc_ElpFit_Std	
HE02_WDEpiNuc_LOW_Mean	
HE02_WDEpiNuc_LOW_Median	
HE02_WDEpiNuc_LOW_Std	
HE02_WDEpiNuc_Num	
HE02_WDEpiNuc_OrgBlu_MeanMean	
HE02_WDEpiNuc_OrgBlu_MeanStd	
HE02_WDEpiNuc_OrgBlu_StdMean	
HE02_WDEpiNuc_OrgBri_Mean	
HE02_WDEpiNuc_OrgBri_Std	
HE02_WDEpiNuc_OrgGre_MeanMean	
HE02_WDEpiNuc_OrgGre_MeanStd	
HE02_WDEpiNuc_OrgGre_StdMean	
HE02_WDEpiNuc_OrgRed_MeanMean	
HE02_WDEpiNuc_OrgRed_MeanStd	
HE02_WDEpiNuc_OrgRed_StdMean	
HE02_WDEpiNuc_ShaInd_Mean	
HE02_WDEpiNuc_ShaInd_Std	
HE02_WSAIgInTumAre_Are_Tot	
'mst_mean_length_lum'	Average MST edge length of lumens
'mst_std_length_lum'	Standard deviation of the MST edge length between lumens
'proportion_edge_1_lum'	Proportion of lumens with one MST connecting edge
'proportion_edge_2_lum'	Proportion of lumens with two MST connecting edges.
'proportion_edge_3_lum'	Proportion of lumens with three MST connecting edges
'proportion_edge_4_lum'	Proportion of lumens with four MST connecting edges
'proportion_edge_5_lum'	Proportion of lumens with five MST connecting edges
'HE02_CytOGU_Are_Tot'	Cytoplasm and epithelial features within and outside fo gland units
'HE02_CytOutGU_Are_Tot'	
'HE02_CytWIGU_Are_Tot'	
'HE02_CytWinGU_Are_Tot'	
'HE02_EpiNucOGU_Are_Mean'	
'HE02_EpiNucOGU_Are_Tot'	
'HE02_EpiNucWIGU_Are_Mean'	
'HE02_EpiNucWIGU_Are_Tot'	

	Normalized morphometric features of various tissue components
'HEX2_RelNumIsoEpiNuc2AreaEpiNuc'	
'HEX2_RelNumIsoEpiNuc2MDTumor'	
'HEX2_RelNumWellDefEpiNuc2MDTumor'	
'HEX2_RelNumIsoEpiNuc2NumEpiNuc'	
'HEX2_RelAre_EpiIsoNuc2EpiNucArea'	
'HEX2RelNum_EpiIsoNuc2EpiNucArea'	
'HEX2_nta_Cyt_Are_Tot'	
'HEX2_nta_EpiNuc_Are_Tot'	
'HEX2_nta_Lum_Are_Tot'	
'HEX2_nta_StrNuc_Are_Tot'	
'HEX2_nta_Str_Are_Tot'	
'HEX2_nta_LStr_Are_Tot'	
'HEX2_nta_DStr_Are_Tot'	
'HEX2_nta_Cra_Are_Tot'	
'HEX2_nta_IsoNuc_Are_Tot'	
'HEX2_nta_Nuc_Are_Tot'	
'HEX2_nta_EpiIsoNuc_Are_Tot'	
'HEX2_nta_IsoStrNuc_Are_Tot'	
'HEX2_nta_WDEpiNuc_Are_Tot'	
'HEX2_RelAre_IsoNuc2EpiNucArea'	
'HEX2RelAre_EpiIsoNuc2EpiNucArea'	
'HEX2_RelAre_WDEpiNuc2EpiNucArea'	
'HEX2_EpiNucAre2LumMeanAre'	
'HEX2_nrm_ENWinGU_Are_Tot'	
'HEX2_nrm_ENOutGU_Are_Tot'	
'HEX2_nrm_CytWinGU_Are_Tot'	
'HEX2_nrm_CytOutGU_Are_Tot'	
'HEX2_RelArea_EpiNuc_Out2WinGU'	
'HEX2_RelArea_Cyt_Out2WinGU'	
'HEX2_RelArea_ENCyt_Out2WinGU'	
'HEX2_ntaENCytWinGU2Tumor'	
'HEX2_ntaENCYtOutGU2Tumor'	
'HEX2_ntaWhiteSpace'	
'HEX2_nrmMDT_ENWinGU_Are_Tot'	Normalized to the tumor area
'HEX2_nrmMDT_ENOutGU_Are_Tot'	
'HEX2_nrmMDT_CytWinGU_Are_Tot'	
'HEX2_nrmMDT_CytOutGU_Are_Tot'	
'HEX2_nrmLUM_ENWinGU_Are_Tot'	Normalized to luminal area
'HEX2_nrmLUM_ENOutGU_Are_Tot'	
'HEX2_nrmLUM_CytWinGU_Are_Tot'	
'HEX2_nrmLUM_CytOutGU_Are_Tot'	

'HEX2_nrmLUM_EpiNucCytWinGU'	
'HEX2_nrmLUM_EpiNucCytOutGU'	
'HEX2_nrm_ENCytWinGULum_Are_Tot'	
'HEX2_RelArea_ENCytLum_Out2WinGU'	
'HEX2_LumenDensity'	
'HEX2_RelArea_EpiNucCyt_Lum'	
'HEX2_RelArea_IsoEpiNuc_Lumen'	
'HEX2_RelArea_Artifact_Lumen'	
'HEX2_RelArea_EpiNuc_Lumen'	
'HEX2_RelArea_Nuc_Lumen'	
'HEX2_RelArea_EpiNuc_Cyt'	
'HEX2_RelArea_LumContent_Lumen'	
'HEX2_ntaLumContentArea'	
'HEX2_nrm_Cyt_OrgRed_MeanStd'	
'HEX2_nrm_Cyt_OrgGre_MeanStd'	
'HEX2_nrm_Cyt_OrgBlu_MeanStd'	
'HEX2_CytOrgSumRGBMeanStd'	
'HEX2_CytNrmSumRGBMeanStd'	
'HEX2_nrm1_CytOutGU_OrgRedMeanStd'	Normalized color features
'HEX2_nrm1_CytOutGU_OrgGreMeanStd'	
'HEX2_nrm1_CytOutGU_OrgBluMeanStd'	
'HEX2_nrm2_CytOutGU_OrgRedMeanStd'	
'HEX2_nrm2_CytOutGU_OrgGreMeanStd'	
'HEX2_nrm2_CytOutGU_OrgBluMeanStd'	
'HEX2_CytOutGUOrgSumRGBMeanStd'	
'HEX2_CytOutGUNrm1SumRGBMeanStd'	
'HEX2_CytOutGUNrm2SumRGBMeanStd'	
'HEX2_nrm1_CytWinGU_OrgRedMeanStd'	
'HEX2_nrm1_CytWinGU_OrgGreMeanStd'	
'HEX2_nrm1_CytWinGU_OrgBluMeanStd'	
'HEX2_nrm2_CytWinGU_OrgRedMeanStd'	
'HEX2_nrm2_CytWinGU_OrgGreMeanStd'	
'HEX2_nrm2_CytWinGU_OrgBluMeanStd'	
'HEX2_CytWinGUOrgSumRGBMeanStd'	
'HEX2_CytWinGUNrm1SumRGBMeanStd'	
'HEX2_CytWinGUNrm2SumRGBMeanStd'	
'HEX2_nrm_EpiNucOrgRed_MeanStd'	
'HEX2_nrm_EpiNucOrgGre_MeanStd'	
'HEX2_nrm_EpiNucOrgBlu_MeanStd'	
'HEX2_nrmSN_EpiNucOrgRed_MeanStd'	
'HEX2_nrmSN_EpiNucOrgGre_MeanStd'	
'HEX2_nrmSN_EpiNucOrgBlu_MeanStd'	

'HEX2_EpiNucOrgSumRGBMeanStd'	
'HEX2_EpiNucNrmSumRGBMeanStd'	
'HEX2_EpiNucNrmSNSumRGBMeanStd'	
'HEX2_nrm1_ENOutGU_OrgRedMeanStd'	
'HEX2_nrm1_ENOutGU_OrgGreMeanStd'	
'HEX2_nrm1_ENOutGU_OrgBluMeanStd'	
'HEX2_nrm2_ENOutGU_OrgRedMeanStd'	
'HEX2_nrm2_ENOutGU_OrgGreMeanStd'	
'HEX2_nrm2_ENOutGU_OrgBluMeanStd'	
'HEX2_ENOutGUOrgSumRGBMeanStd'	
'HEX2_ENOutGUUnrm1SumRGBMeanStd'	
'HEX2_ENOutGUUnrm2SumRGBMeanStd'	
'HEX2_nrm1_ENWinGU_OrgRedMeanStd'	
'HEX2_nrm1_ENWinGU_OrgGreMeanStd'	
'HEX2_nrm1_ENWinGU_OrgBluMeanStd'	
'HEX2_nrm2_ENWinGU_OrgRedMeanStd'	
'HEX2_nrm2_ENWinGU_OrgGreMeanStd'	
'HEX2_nrm2_ENWinGU_OrgBluMeanStd'	
'HEX2_ENWinGUOrgSumRGBMeanStd'	
'HEX2_ENWinGUUnrm1SumRGBMeanStd'	
'HEX2_ENWinGUUnrm2SumRGBMeanStd'	
'HEX2_nrm_EpiNucDen01_Are_Tot'	Density bins normalized by total of all bins
'HEX2_nrm_EpiNucDen02_Are_Tot'	
'HEX2_nrm_EpiNucDen03_Are_Tot'	
'HEX2_nrm_EpiNucDen04_Are_Tot'	
'HEX2_nrm_EpiNucDen05_Are_Tot'	
'HEX2_nrm_EpiNucDen06_Are_Tot'	
'HEX2_nrm_EpiNucDen07_Are_Tot'	
'HEX2_nrm_EpiNucDen08_Are_Tot'	
'HEX2_nrm_EpiNucDen09_Are_Tot'	
'HEX2_nrm_EpiNucDen10_Are_Tot'	
'HEX2_sub_EpiNucDen1_3_Lum'	
'HEX2_RelAreHi2Lo_EpiNucDen_10to2'	
'HEX2_RelAreHi2Lo_EpiNucDen_10to3'	
'HEX2_RelAreHi2Lo_EpiNucDen_10to4'	
'HEX2_RelAreHi2Lo_EpiNucDen_10to5'	
'HEX2_RelAreHi2Lo_EpiNucDen_10to6'	
'HEX2_RelAreHi2Lo_EpiNucDen_10to7'	
'HEX2_RelAreHi2Lo_EpiNucDen_10to8'	
'HEX2_sub_EpiNucDen8_10_Lum'	
'HEX2_nrm_EpiNucAt1Dia_Are_Tot'	
'HEX2_nrm_EpiNucAt2Dia_Are_Tot'	

'HEX2_nrm_EpiNucAt3Dia_Are_Tot'
'HEX2_nrm_EpiNucAt4Dia_Are_Tot'
'HEX2_nrm_EpiNucAt5Dia_Are_Tot'
'HEX2_nrm_EpiNucAt1Dia2MDT'
'HEX2_nrm_EpiNucAt2Dia2MDT'
'HEX2_nrm_EpiNucAt3Dia2MDT'
'HEX2_nrm_EpiNucAt4Dia2MDT'
'HEX2_nrm_EpiNucAt5Dia2MDT'
'HEX2_EpiNucBand5minus4'
'HEX2_EpiNucBand4minus3'
'HEX2_EpiNucBand3minus2'
'HEX2_EpiNucBand2minus1'
'HEX2_nrmEpiNucBand5minus4'
'HEX2_nrmEpiNucBand5minus3'
'HEX2_nrmEpiNucBand5minus2'
'HEX2_nrmEpiNucBand4minus3'
'HEX2_nrmEpiNucBand4minus2'
'HEX2_nrmEpiNucBand3minus2'
'HEX2_nrmEpiNucBand2minus1'
'HEX2_nrmMDT_EpiNucBand5minus4'
'HEX2_nrmMDT_EpiNucBand5minus3'
'HEX2_nrmMDT_EpiNucBand5minus2'
'HEX2_nrmMDT_EpiNucBand4minus3'
'HEX2_nrmMDT_EpiNucBand4minus2'
'HEX2_nrmMDT_EpiNucBand3minus2'
'HEX2_nrmMDT_EpiNucBand2minus1'
'HEX2_EpiNuc_Num1_8'
'HEX2_EpiNuc_Are1_8'
'HEX2_nrmEpiNucSizBin1_Num'
'HEX2_nrmEpiNucSizBin2_Num'
'HEX2_nrmEpiNucSizBin3_Num'
'HEX2_nrmEpiNucSizBin4_Num'
'HEX2_nrmEpiNucSizBin5_Num'
'HEX2_nrmEpiNucSizBin6_Num'
'HEX2_nrmEpiNucSizBin7_Num'
'HEX2_nrmEpiNucSizBin8_Num'
'HEX2_nrmEpiNucSizBin1_Are'
'HEX2_nrmEpiNucSizBin2_Are'
'HEX2_nrmEpiNucSizBin3_Are'
'HEX2_nrmEpiNucSizBin4_Are'
'HEX2_nrmEpiNucSizBin5_Are'
'HEX2_nrmEpiNucSizBin6_Are'

'HEx2_nrmEpiNucSizBin7_Are'	
'HEx2_nrmEpiNucSizBin8_Are'	
'min_orig_L_detail1'	Minimum of the variances in the horizontal and vertical detail sub-bands after applying 1 stage of undecimated wavelet transform to a mask of lumens.
'min_orig_L_detail2'	Minimum of the variances in the horizontal and vertical detail sub-bands after applying 2 stages of undecimated wavelet transform to a mask of lumens.
'min_orig_L_detail3'	Minimum of the variances in the horizontal and vertical detail sub-bands after applying 3 stages of undecimated wavelet transform to a mask of lumens.
'min_orig_L_detail4'	Minimum of the variances in the horizontal and vertical detail sub-bands after applying 4 stages of undecimated wavelet transform to a mask of lumens.
'min_orig_L_detail5'	Minimum of the variances in the horizontal and vertical detail sub-bands after applying 5 stages of undecimated wavelet transform to a mask of lumens.
'min_orig_L_detail6'	Minimum of the variances in the horizontal and vertical detail sub-bands after applying 6 stages of undecimated wavelet transform to a mask of lumens.
'min_orig_L_detail7'	Minimum of the variances in the horizontal and vertical detail sub-bands after applying 7 stages of undecimated wavelet transform to a mask of lumens.
'max_orig_L_detail1'	Maximum of the variances in the horizontal and vertical detail sub-bands after applying 1 stage of undecimated wavelet transform to a mask of lumens.
'max_orig_L_detail2'	Maximum of the variances in the horizontal and vertical detail sub-bands after applying 2 stages of undecimated wavelet transform to a mask of lumens.
'max_orig_L_detail3'	Maximum of the variances in the horizontal and vertical detail sub-bands after applying 3 stages of undecimated wavelet transform to a mask of lumens.
'max_orig_L_detail4'	Maximum of the variances in the horizontal and vertical detail sub-bands after applying 4 stages of undecimated wavelet transform to a mask of lumens.
'max_orig_L_detail5'	Maximum of the variances in the horizontal and vertical detail sub-bands after applying 5 stages of undecimated wavelet transform to a mask of lumens.
'max_orig_L_detail6'	Maximum of the variances in the horizontal and vertical detail sub-bands after applying 6 stages of undecimated wavelet transform to a mask of lumens.

'max_orig_L_detail7'	Maximum of the variances in the horizontal and vertical detail sub-bands after applying 7 stages of undecimated wavelet transform to a mask of lumens.
'sum_orig_L_detail1'	Sum of the variances in the horizontal and vertical detail sub-bands after applying 1 stage of undecimated wavelet transform to a mask of lumens.
'sum_orig_L_detail2'	Sum of the variances in the horizontal and vertical detail sub-bands after applying 2 stages of undecimated wavelet transform to a mask of lumens.
'sum_orig_L_detail3'	Sum of the variances in the horizontal and vertical detail sub-bands after applying 3 stages of undecimated wavelet transform to a mask of lumens.
'sum_orig_L_detail4'	Sum of the variances in the horizontal and vertical detail sub-bands after applying 4 stages of undecimated wavelet transform to a mask of lumens.
'sum_orig_L_detail5'	Sum of the variances in the horizontal and vertical detail sub-bands after applying 5 stages of undecimated wavelet transform to a mask of lumens.
'sum_orig_L_detail6'	Sum of the variances in the horizontal and vertical detail sub-bands after applying 6 stages of undecimated wavelet transform to a mask of lumens.
'sum_orig_L_detail7'	Sum of the variances in the horizontal and vertical detail sub-bands after applying 7 stages of undecimated wavelet transform to a mask of lumens.
'WaveletRatio_Lumendiag_6_5'	Ratio of the variances in the diagonal detail sub-bands after applying 6 and 5 stages of undecimated wavelet transform to a mask of lumens.
HE03_CluNuc_Are_Mean	Measurements on Clustered Nuclei
HE03_CluNuc_Are_Std	
HE03_CluNuc_Are_Tot	
HE03_CluNuc_Num	
HE03_Cyt_Are_Mean	Morphometric and color measurements on cytoplasm
HE03_Cyt_Are_Std	
HE03_Cyt_Are_Tot	
HE03_Cyt_Num	
HE03_Cyt_OrgBlu_MeanMean	
HE03_Cyt_OrgBlu_MeanStd	
HE03_Cyt_OrgBri_Mean	
HE03_Cyt_OrgBri_Std	
HE03_Cyt_OrgGre_MeanMean	
HE03_Cyt_OrgGre_MeanStd	
HE03_Cyt_OrgH_Mean	
HE03_Cyt_OrgH_Std	

HE03_Cyt_OrgI_Mean
HE03_Cyt_OrgI_Std
HE03_Cyt_OrgQ_Mean
HE03_Cyt_OrgQ_Std
HE03_Cyt_OrgRed_MeanMean
HE03_Cyt_OrgRed_MeanStd
HE03_Cyt_OrgS_Mean
HE03_Cyt_OrgS_Std
HE03_Cyt_OrgV_Mean
HE03_Cyt_OrgV_Std
HE03_Cyt_OrgY_Mean
HE03_Cyt_OrgY_Std

Morphometric and color measurements on Dark
Nuclei

HE03_DarNucBin0_3_Are_Mean
HE03_DarNucBin0_3_Are_Tot
HE03_DarNucBin0_3_Num
HE03_DarNucBin0_5_Are_Mean
HE03_DarNucBin0_5_Are_Tot
HE03_DarNucBin0_5_Num
HE03_DarNucBin0_7_Are_Mean
HE03_DarNucBin0_7_Are_Tot
HE03_DarNucBin0_7_Num
HE03_DarNucBin0_Are_Mean
HE03_DarNucBin0_Are_Tot
HE03_DarNucBin0_Num
HE03_DarNucBin1_3_Are_Mean
HE03_DarNucBin1_3_Are_Tot
HE03_DarNucBin1_3_Num
HE03_DarNucBin1_5_Are_Mean
HE03_DarNucBin1_5_Are_Tot
HE03_DarNucBin1_5_Num
HE03_DarNucBin1_7_Are_Mean
HE03_DarNucBin1_7_Are_Tot
HE03_DarNucBin1_7_Num
HE03_DarNucBin1_Are_Mean
HE03_DarNucBin1_Are_Tot
HE03_DarNucBin1_Num
HE03_DarNucBin2_3_Are_Mean
HE03_DarNucBin2_3_Are_Tot
HE03_DarNucBin2_3_Num
HE03_DarNucBin2_5_Are_Mean
HE03_DarNucBin2_5_Are_Tot

HE03_DarNucBin2_5_Num
HE03_DarNucBin2_7_Are_Mean
HE03_DarNucBin2_7_Are_Tot
HE03_DarNucBin2_7_Num
HE03_DarNucBin2_Are_Mean
HE03_DarNucBin2_Are_Tot
HE03_DarNucBin2_Num
HE03_DarNucBin3_5_Are_Mean
HE03_DarNucBin3_5_Are_Tot
HE03_DarNucBin3_5_Num
HE03_DarNucBin3_7_Are_Mean
HE03_DarNucBin3_7_Are_Tot
HE03_DarNucBin3_7_Num
HE03_DarNucBin3_Are_Mean
HE03_DarNucBin3_Are_Tot
HE03_DarNucBin3_Num
HE03_DarNucBin4_5_Are_Mean
HE03_DarNucBin4_5_Are_Tot
HE03_DarNucBin4_5_Num
HE03_DarNucBin4_7_Are_Mean
HE03_DarNucBin4_7_Are_Tot
HE03_DarNucBin4_7_Num
HE03_DarNucBin4_Are_Mean
HE03_DarNucBin4_Are_Tot
HE03_DarNucBin4_Num
HE03_DarNucBin5_7_Are_Mean
HE03_DarNucBin5_7_Are_Tot
HE03_DarNucBin5_7_Num
HE03_DarNucBin5_Are_Mean
HE03_DarNucBin5_Are_Tot
HE03_DarNucBin5_Num
HE03_DarNucBin6_7_Are_Mean
HE03_DarNucBin6_7_Are_Tot
HE03_DarNucBin6_7_Num
HE03_DarNucBin6_Are_Mean
HE03_DarNucBin6_Are_Tot
HE03_DarNucBin6_Num
HE03_DarNucBin7_Are_Mean
HE03_DarNucBin7_Are_Tot
HE03_DarNucBin7_Num
HE03_DarNucBin8_Are_Mean
HE03_DarNucBin8_Are_Tot

HE03_DarNucBin8_Num	
HE03_EpiCluNuc_Are_Mean	Measurements on epithelial clustered nuclei
HE03_EpiCluNuc_Are_Std	
HE03_EpiCluNuc_Are_Tot	
HE03_EpiCluNuc_Num	
HE03_EpiIsoNuc_Are_Mean	Measurements on epithelial isolated nuclei
HE03_EpiIsoNuc_Are_Median	
HE03_EpiIsoNuc_Are_Std	
HE03_EpiIsoNuc_Are_Tot	
HE03_EpiIsoNuc_Num	
HE03_EpiNucEro1_Blu_MeanStd	Color measurements of eroded epithelial nuclei
HE03_EpiNucEro1_Blu_StdMean	
HE03_EpiNucEro1_Bri_MeanStd	
HE03_EpiNucEro1_Bri_StdMean	
HE03_EpiNucEro1_Gre_MeanStd	
HE03_EpiNucEro1_Gre_StdMean	
HE03_EpiNucEro1_Red_MeanStd	
HE03_EpiNucEro1_Red_StdMean	
HE03_EpiNucEro2_Blu_MeanStd	
HE03_EpiNucEro2_Blu_StdMean	
HE03_EpiNucEro2_Bri_MeanStd	
HE03_EpiNucEro2_Bri_StdMean	
HE03_EpiNucEro2_Gre_MeanStd	
HE03_EpiNucEro2_Gre_StdMean	
HE03_EpiNucEro2_Red_MeanStd	
HE03_EpiNucEro2_Red_StdMean	
HE03_EpiNucSizBin0_1_Are_Mean	Color and area measurements of epithelial nuclei divided into different bins based on size.
HE03_EpiNucSizBin0_2_Are_Mean	
HE03_EpiNucSizBin0_3_Are_Mean	
HE03_EpiNucSizBin0_3_Blu_Mean	
HE03_EpiNucSizBin0_3_Blu_MeanStd	
HE03_EpiNucSizBin0_3_Blu_RA	
HE03_EpiNucSizBin0_3_Blu_RASD	
HE03_EpiNucSizBin0_3_Blu_StdMean	
HE03_EpiNucSizBin0_3_Bri_Mean	
HE03_EpiNucSizBin0_3_Bri_MeanStd	
HE03_EpiNucSizBin0_3_Bri_RA	
HE03_EpiNucSizBin0_3_Bri_StdMean	
HE03_EpiNucSizBin0_3_Gre_Mean	
HE03_EpiNucSizBin0_3_Gre_MeanStd	
HE03_EpiNucSizBin0_3_Gre_RA	

HE03_EpiNucSizBin0_3_Gre_RAStd
HE03_EpiNucSizBin0_3_Gre_StdMean
HE03_EpiNucSizBin0_3_Red_Mean
HE03_EpiNucSizBin0_3_Red_MeanStd
HE03_EpiNucSizBin0_3_Red_RA
HE03_EpiNucSizBin0_3_Red_RAStd
HE03_EpiNucSizBin0_3_Red_StdMean
HE03_EpiNucSizBin0_4_Are_Mean
HE03_EpiNucSizBin0_5_Are_Mean
HE03_EpiNucSizBin0_5_Blu_Mean
HE03_EpiNucSizBin0_5_Blu_MeanStd
HE03_EpiNucSizBin0_5_Blu_RA
HE03_EpiNucSizBin0_5_Blu_RAStd
HE03_EpiNucSizBin0_5_Blu_StdMean
HE03_EpiNucSizBin0_5_Bri_Mean
HE03_EpiNucSizBin0_5_Bri_MeanStd
HE03_EpiNucSizBin0_5_Bri_RA
HE03_EpiNucSizBin0_5_Bri_StdMean
HE03_EpiNucSizBin0_5_Gre_Mean
HE03_EpiNucSizBin0_5_Gre_MeanStd
HE03_EpiNucSizBin0_5_Gre_RA
HE03_EpiNucSizBin0_5_Gre_RAStd
HE03_EpiNucSizBin0_5_Gre_StdMean
HE03_EpiNucSizBin0_5_Red_Mean
HE03_EpiNucSizBin0_5_Red_MeanStd
HE03_EpiNucSizBin0_5_Red_RA
HE03_EpiNucSizBin0_5_Red_RAStd
HE03_EpiNucSizBin0_5_Red_StdMean
HE03_EpiNucSizBin0_6_Are_Mean
HE03_EpiNucSizBin0_7_Are_Mean
HE03_EpiNucSizBin0_7_Blu_Mean
HE03_EpiNucSizBin0_7_Blu_MeanStd
HE03_EpiNucSizBin0_7_Blu_RA
HE03_EpiNucSizBin0_7_Blu_RAStd
HE03_EpiNucSizBin0_7_Blu_StdMean
HE03_EpiNucSizBin0_7_Bri_Mean
HE03_EpiNucSizBin0_7_Bri_MeanStd
HE03_EpiNucSizBin0_7_Bri_RA
HE03_EpiNucSizBin0_7_Bri_StdMean
HE03_EpiNucSizBin0_7_Gre_Mean
HE03_EpiNucSizBin0_7_Gre_MeanStd
HE03_EpiNucSizBin0_7_Gre_RA

HE03_EpiNucSizBin0_7_Gre_RAStd
HE03_EpiNucSizBin0_7_Gre_StdMean
HE03_EpiNucSizBin0_7_Red_Mean
HE03_EpiNucSizBin0_7_Red_MeanStd
HE03_EpiNucSizBin0_7_Red_RA
HE03_EpiNucSizBin0_7_Red_RAStd
HE03_EpiNucSizBin0_7_Red_StdMean
HE03_EpiNucSizBin0_8_Are_Mean
HE03_EpiNucSizBin0_Are_Mean
HE03_EpiNucSizBin0_Are_Tot
HE03_EpiNucSizBin0_Blu_Mean
HE03_EpiNucSizBin0_Blu_MeanStd
HE03_EpiNucSizBin0_Bri_Mean
HE03_EpiNucSizBin0_Gre_Mean
HE03_EpiNucSizBin0_Gre_MeanStd
HE03_EpiNucSizBin0_Num
HE03_EpiNucSizBin0_Red_Mean
HE03_EpiNucSizBin0_Red_MeanStd

After dividing epithelial nuclei into different bins based on size, color and area measurements of various combinations of the bins.

HE03_EpiNucSizBin1_2_Are_Mean
HE03_EpiNucSizBin1_3_Are_Mean
HE03_EpiNucSizBin1_3_Blu_Mean
HE03_EpiNucSizBin1_3_Blu_MeanStd
HE03_EpiNucSizBin1_3_Blu_RA
HE03_EpiNucSizBin1_3_Blu_RAStd
HE03_EpiNucSizBin1_3_Blu_StdMean
HE03_EpiNucSizBin1_3_Bri_Mean
HE03_EpiNucSizBin1_3_Bri_MeanStd
HE03_EpiNucSizBin1_3_Bri_RA
HE03_EpiNucSizBin1_3_Bri_StdMean
HE03_EpiNucSizBin1_3_Gre_Mean
HE03_EpiNucSizBin1_3_Gre_MeanStd
HE03_EpiNucSizBin1_3_Gre_RA
HE03_EpiNucSizBin1_3_Gre_RAStd
HE03_EpiNucSizBin1_3_Gre_StdMean
HE03_EpiNucSizBin1_3_Red_Mean
HE03_EpiNucSizBin1_3_Red_MeanStd
HE03_EpiNucSizBin1_3_Red_RA
HE03_EpiNucSizBin1_3_Red_RAStd
HE03_EpiNucSizBin1_3_Red_StdMean
HE03_EpiNucSizBin1_4_Are_Mean

HE03_EpiNucSizBin1_5_Are_Mean
HE03_EpiNucSizBin1_5_Blu_Mean
HE03_EpiNucSizBin1_5_Blu_MeanStd
HE03_EpiNucSizBin1_5_Blu_RA
HE03_EpiNucSizBin1_5_Blu_RAStd
HE03_EpiNucSizBin1_5_Blu_StdMean
HE03_EpiNucSizBin1_5_Bri_Mean
HE03_EpiNucSizBin1_5_Bri_MeanStd
HE03_EpiNucSizBin1_5_Bri_RA
HE03_EpiNucSizBin1_5_Bri_StdMean
HE03_EpiNucSizBin1_5_Gre_Mean
HE03_EpiNucSizBin1_5_Gre_MeanStd
HE03_EpiNucSizBin1_5_Gre_RA
HE03_EpiNucSizBin1_5_Gre_RAStd
HE03_EpiNucSizBin1_5_Gre_StdMean
HE03_EpiNucSizBin1_5_Red_Mean
HE03_EpiNucSizBin1_5_Red_MeanStd
HE03_EpiNucSizBin1_5_Red_RA
HE03_EpiNucSizBin1_5_Red_RAStd
HE03_EpiNucSizBin1_5_Red_StdMean
HE03_EpiNucSizBin1_6_Are_Mean
HE03_EpiNucSizBin1_7_Are_Mean
HE03_EpiNucSizBin1_7_Blu_Mean
HE03_EpiNucSizBin1_7_Blu_MeanStd
HE03_EpiNucSizBin1_7_Blu_RA
HE03_EpiNucSizBin1_7_Blu_RAStd
HE03_EpiNucSizBin1_7_Blu_StdMean
HE03_EpiNucSizBin1_7_Bri_Mean
HE03_EpiNucSizBin1_7_Bri_MeanStd
HE03_EpiNucSizBin1_7_Bri_RA
HE03_EpiNucSizBin1_7_Bri_StdMean
HE03_EpiNucSizBin1_7_Gre_Mean
HE03_EpiNucSizBin1_7_Gre_MeanStd
HE03_EpiNucSizBin1_7_Gre_RA
HE03_EpiNucSizBin1_7_Gre_RAStd
HE03_EpiNucSizBin1_7_Gre_StdMean
HE03_EpiNucSizBin1_7_Red_Mean
HE03_EpiNucSizBin1_7_Red_MeanStd
HE03_EpiNucSizBin1_7_Red_RA
HE03_EpiNucSizBin1_7_Red_RAStd
HE03_EpiNucSizBin1_7_Red_StdMean
HE03_EpiNucSizBin1_8_Are_Mean

HE03_EpiNucSizBin1_Are_Mean
HE03_EpiNucSizBin1_Are_Tot
HE03_EpiNucSizBin1_Blu_Mean
HE03_EpiNucSizBin1_Blu_MeanStd
HE03_EpiNucSizBin1_Bri_Mean
HE03_EpiNucSizBin1_Gre_Mean
HE03_EpiNucSizBin1_Gre_MeanStd
HE03_EpiNucSizBin1_Num
HE03_EpiNucSizBin1_Red_Mean
HE03_EpiNucSizBin1_Red_MeanStd
HE03_EpiNucSizBin2_3_Are_Mean
HE03_EpiNucSizBin2_3_Blu_Mean
HE03_EpiNucSizBin2_3_Blu_MeanStd
HE03_EpiNucSizBin2_3_Blu_RA
HE03_EpiNucSizBin2_3_Blu_RAStd
HE03_EpiNucSizBin2_3_Blu_StdMean
HE03_EpiNucSizBin2_3_Bri_Mean
HE03_EpiNucSizBin2_3_Bri_MeanStd
HE03_EpiNucSizBin2_3_Bri_RA
HE03_EpiNucSizBin2_3_Bri_StdMean
HE03_EpiNucSizBin2_3_Gre_Mean
HE03_EpiNucSizBin2_3_Gre_MeanStd
HE03_EpiNucSizBin2_3_Gre_RA
HE03_EpiNucSizBin2_3_Gre_RAStd
HE03_EpiNucSizBin2_3_Gre_StdMean
HE03_EpiNucSizBin2_3_Red_Mean
HE03_EpiNucSizBin2_3_Red_MeanStd
HE03_EpiNucSizBin2_3_Red_RA
HE03_EpiNucSizBin2_3_Red_RAStd
HE03_EpiNucSizBin2_3_Red_StdMean
HE03_EpiNucSizBin2_4_Are_Mean
HE03_EpiNucSizBin2_5_Are_Mean
HE03_EpiNucSizBin2_5_Blu_Mean
HE03_EpiNucSizBin2_5_Blu_MeanStd
HE03_EpiNucSizBin2_5_Blu_RA
HE03_EpiNucSizBin2_5_Blu_RAStd
HE03_EpiNucSizBin2_5_Blu_StdMean
HE03_EpiNucSizBin2_5_Bri_Mean
HE03_EpiNucSizBin2_5_Bri_MeanStd
HE03_EpiNucSizBin2_5_Bri_RA
HE03_EpiNucSizBin2_5_Bri_StdMean
HE03_EpiNucSizBin2_5_Gre_Mean

HE03_EpiNucSizBin2_5_Gre_MeanStd
HE03_EpiNucSizBin2_5_Gre_RA
HE03_EpiNucSizBin2_5_Gre_RAStd
HE03_EpiNucSizBin2_5_Gre_StdMean
HE03_EpiNucSizBin2_5_Red_Mean
HE03_EpiNucSizBin2_5_Red_MeanStd
HE03_EpiNucSizBin2_5_Red_RA
HE03_EpiNucSizBin2_5_Red_RAStd
HE03_EpiNucSizBin2_5_Red_StdMean
HE03_EpiNucSizBin2_6_Are_Mean
HE03_EpiNucSizBin2_7_Are_Mean
HE03_EpiNucSizBin2_7_Blu_Mean
HE03_EpiNucSizBin2_7_Blu_MeanStd
HE03_EpiNucSizBin2_7_Blu_RA
HE03_EpiNucSizBin2_7_Blu_RAStd
HE03_EpiNucSizBin2_7_Blu_StdMean
HE03_EpiNucSizBin2_7_Bri_Mean
HE03_EpiNucSizBin2_7_Bri_MeanStd
HE03_EpiNucSizBin2_7_Bri_RA
HE03_EpiNucSizBin2_7_Bri_StdMean
HE03_EpiNucSizBin2_7_Gre_Mean
HE03_EpiNucSizBin2_7_Gre_MeanStd
HE03_EpiNucSizBin2_7_Gre_RA
HE03_EpiNucSizBin2_7_Gre_RAStd
HE03_EpiNucSizBin2_7_Gre_StdMean
HE03_EpiNucSizBin2_7_Red_Mean
HE03_EpiNucSizBin2_7_Red_MeanStd
HE03_EpiNucSizBin2_7_Red_RA
HE03_EpiNucSizBin2_7_Red_RAStd
HE03_EpiNucSizBin2_7_Red_StdMean
HE03_EpiNucSizBin2_8_Are_Mean
HE03_EpiNucSizBin2_Are_Mean
HE03_EpiNucSizBin2_Are_Tot
HE03_EpiNucSizBin2_Blu_Mean
HE03_EpiNucSizBin2_Blu_MeanStd
HE03_EpiNucSizBin2_Bri_Mean
HE03_EpiNucSizBin2_Gre_Mean
HE03_EpiNucSizBin2_Gre_MeanStd
HE03_EpiNucSizBin2_Num
HE03_EpiNucSizBin2_Red_Mean
HE03_EpiNucSizBin2_Red_MeanStd
HE03_EpiNucSizBin3_4_Are_Mean

HE03_EpiNucSizBin3_5_Are_Mean
HE03_EpiNucSizBin3_5_Blu_Mean
HE03_EpiNucSizBin3_5_Blu_MeanStd
HE03_EpiNucSizBin3_5_Blu_RA
HE03_EpiNucSizBin3_5_Blu_RAStd
HE03_EpiNucSizBin3_5_Blu_StdMean
HE03_EpiNucSizBin3_5_Bri_Mean
HE03_EpiNucSizBin3_5_Bri_MeanStd
HE03_EpiNucSizBin3_5_Bri_RA
HE03_EpiNucSizBin3_5_Bri_StdMean
HE03_EpiNucSizBin3_5_Gre_Mean
HE03_EpiNucSizBin3_5_Gre_MeanStd
HE03_EpiNucSizBin3_5_Gre_RA
HE03_EpiNucSizBin3_5_Gre_RAStd
HE03_EpiNucSizBin3_5_Gre_StdMean
HE03_EpiNucSizBin3_5_Red_Mean
HE03_EpiNucSizBin3_5_Red_MeanStd
HE03_EpiNucSizBin3_5_Red_RA
HE03_EpiNucSizBin3_5_Red_RAStd
HE03_EpiNucSizBin3_5_Red_StdMean
HE03_EpiNucSizBin3_6_Are_Mean
HE03_EpiNucSizBin3_7_Are_Mean
HE03_EpiNucSizBin3_7_Blu_Mean
HE03_EpiNucSizBin3_7_Blu_MeanStd
HE03_EpiNucSizBin3_7_Blu_RA
HE03_EpiNucSizBin3_7_Blu_RAStd
HE03_EpiNucSizBin3_7_Blu_StdMean
HE03_EpiNucSizBin3_7_Bri_Mean
HE03_EpiNucSizBin3_7_Bri_MeanStd
HE03_EpiNucSizBin3_7_Bri_RA
HE03_EpiNucSizBin3_7_Bri_StdMean
HE03_EpiNucSizBin3_7_Gre_Mean
HE03_EpiNucSizBin3_7_Gre_MeanStd
HE03_EpiNucSizBin3_7_Gre_RA
HE03_EpiNucSizBin3_7_Gre_RAStd
HE03_EpiNucSizBin3_7_Gre_StdMean
HE03_EpiNucSizBin3_7_Red_Mean
HE03_EpiNucSizBin3_7_Red_MeanStd
HE03_EpiNucSizBin3_7_Red_RA
HE03_EpiNucSizBin3_7_Red_RAStd
HE03_EpiNucSizBin3_7_Red_StdMean
HE03_EpiNucSizBin3_8_Are_Mean

HE03_EpiNucSizBin3_Are_Mean
HE03_EpiNucSizBin3_Are_Tot
HE03_EpiNucSizBin3_Blu_Mean
HE03_EpiNucSizBin3_Blu_MeanStd
HE03_EpiNucSizBin3_Bri_Mean
HE03_EpiNucSizBin3_Gre_Mean
HE03_EpiNucSizBin3_Gre_MeanStd
HE03_EpiNucSizBin3_Num
HE03_EpiNucSizBin3_Red_Mean
HE03_EpiNucSizBin3_Red_MeanStd
HE03_EpiNucSizBin4_5_Are_Mean
HE03_EpiNucSizBin4_5_Blu_Mean
HE03_EpiNucSizBin4_5_Blu_MeanStd
HE03_EpiNucSizBin4_5_Blu_RA
HE03_EpiNucSizBin4_5_Blu_RASD
HE03_EpiNucSizBin4_5_Blu_StdMean
HE03_EpiNucSizBin4_5_Bri_Mean
HE03_EpiNucSizBin4_5_Bri_MeanStd
HE03_EpiNucSizBin4_5_Bri_RA
HE03_EpiNucSizBin4_5_Bri_StdMean
HE03_EpiNucSizBin4_5_Gre_Mean
HE03_EpiNucSizBin4_5_Gre_MeanStd
HE03_EpiNucSizBin4_5_Gre_RA
HE03_EpiNucSizBin4_5_Gre_RASD
HE03_EpiNucSizBin4_5_Gre_StdMean
HE03_EpiNucSizBin4_5_Red_Mean
HE03_EpiNucSizBin4_5_Red_MeanStd
HE03_EpiNucSizBin4_5_Red_RA
HE03_EpiNucSizBin4_5_Red_RASD
HE03_EpiNucSizBin4_5_Red_StdMean
HE03_EpiNucSizBin4_6_Are_Mean
HE03_EpiNucSizBin4_7_Are_Mean
HE03_EpiNucSizBin4_7_Blu_Mean
HE03_EpiNucSizBin4_7_Blu_MeanStd
HE03_EpiNucSizBin4_7_Blu_RA
HE03_EpiNucSizBin4_7_Blu_RASD
HE03_EpiNucSizBin4_7_Blu_StdMean
HE03_EpiNucSizBin4_7_Bri_Mean
HE03_EpiNucSizBin4_7_Bri_MeanStd
HE03_EpiNucSizBin4_7_Bri_RA
HE03_EpiNucSizBin4_7_Bri_StdMean
HE03_EpiNucSizBin4_7_Gre_Mean

HE03_EpiNucSizBin4_7_Gre_MeanStd
HE03_EpiNucSizBin4_7_Gre_RA
HE03_EpiNucSizBin4_7_Gre_RAStd
HE03_EpiNucSizBin4_7_Gre_StdMean
HE03_EpiNucSizBin4_7_Red_Mean
HE03_EpiNucSizBin4_7_Red_MeanStd
HE03_EpiNucSizBin4_7_Red_RA
HE03_EpiNucSizBin4_7_Red_RAStd
HE03_EpiNucSizBin4_7_Red_StdMean
HE03_EpiNucSizBin4_8_Are_Mean
HE03_EpiNucSizBin4_Are_Mean
HE03_EpiNucSizBin4_Are_Tot
HE03_EpiNucSizBin4_Blu_Mean
HE03_EpiNucSizBin4_Blu_MeanStd
HE03_EpiNucSizBin4_Bri_Mean
HE03_EpiNucSizBin4_Gre_Mean
HE03_EpiNucSizBin4_Gre_MeanStd
HE03_EpiNucSizBin4_Num
HE03_EpiNucSizBin4_Red_Mean
HE03_EpiNucSizBin4_Red_MeanStd
HE03_EpiNucSizBin5_6_Are_Mean
HE03_EpiNucSizBin5_7_Are_Mean
HE03_EpiNucSizBin5_7_Blu_Mean
HE03_EpiNucSizBin5_7_Blu_MeanStd
HE03_EpiNucSizBin5_7_Blu_RA
HE03_EpiNucSizBin5_7_Blu_RAStd
HE03_EpiNucSizBin5_7_Blu_StdMean
HE03_EpiNucSizBin5_7_Bri_Mean
HE03_EpiNucSizBin5_7_Bri_MeanStd
HE03_EpiNucSizBin5_7_Bri_RA
HE03_EpiNucSizBin5_7_Bri_StdMean
HE03_EpiNucSizBin5_7_Gre_Mean
HE03_EpiNucSizBin5_7_Gre_MeanStd
HE03_EpiNucSizBin5_7_Gre_RA
HE03_EpiNucSizBin5_7_Gre_RAStd
HE03_EpiNucSizBin5_7_Gre_StdMean
HE03_EpiNucSizBin5_7_Red_Mean
HE03_EpiNucSizBin5_7_Red_MeanStd
HE03_EpiNucSizBin5_7_Red_RA
HE03_EpiNucSizBin5_7_Red_RAStd
HE03_EpiNucSizBin5_7_Red_StdMean
HE03_EpiNucSizBin5_8_Are_Mean

HE03_EpiNucSizBin5_Are_Mean
HE03_EpiNucSizBin5_Are_Tot
HE03_EpiNucSizBin5_Blu_Mean
HE03_EpiNucSizBin5_Blu_MeanStd
HE03_EpiNucSizBin5_Bri_Mean
HE03_EpiNucSizBin5_Gre_Mean
HE03_EpiNucSizBin5_Gre_MeanStd
HE03_EpiNucSizBin5_Num
HE03_EpiNucSizBin5_Red_Mean
HE03_EpiNucSizBin5_Red_MeanStd
HE03_EpiNucSizBin6_7_Are_Mean
HE03_EpiNucSizBin6_7_Blu_Mean
HE03_EpiNucSizBin6_7_Blu_MeanStd
HE03_EpiNucSizBin6_7_Blu_RA
HE03_EpiNucSizBin6_7_Blu_RASD
HE03_EpiNucSizBin6_7_Blu_StdMean
HE03_EpiNucSizBin6_7_Bri_Mean
HE03_EpiNucSizBin6_7_Bri_MeanStd
HE03_EpiNucSizBin6_7_Bri_RA
HE03_EpiNucSizBin6_7_Bri_StdMean
HE03_EpiNucSizBin6_7_Gre_Mean
HE03_EpiNucSizBin6_7_Gre_MeanStd
HE03_EpiNucSizBin6_7_Gre_RA
HE03_EpiNucSizBin6_7_Gre_RASD
HE03_EpiNucSizBin6_7_Gre_StdMean
HE03_EpiNucSizBin6_7_Red_Mean
HE03_EpiNucSizBin6_7_Red_MeanStd
HE03_EpiNucSizBin6_7_Red_RA
HE03_EpiNucSizBin6_7_Red_RASD
HE03_EpiNucSizBin6_7_Red_StdMean
HE03_EpiNucSizBin6_8_Are_Mean
HE03_EpiNucSizBin6_Are_Mean
HE03_EpiNucSizBin6_Are_Tot
HE03_EpiNucSizBin6_Blu_Mean
HE03_EpiNucSizBin6_Blu_MeanStd
HE03_EpiNucSizBin6_Bri_Mean
HE03_EpiNucSizBin6_Gre_Mean
HE03_EpiNucSizBin6_Gre_MeanStd
HE03_EpiNucSizBin6_Num
HE03_EpiNucSizBin6_Red_Mean
HE03_EpiNucSizBin6_Red_MeanStd
HE03_EpiNucSizBin7_8_Are_Mean

HE03_EpiNucSizBin7_Are_Mean
HE03_EpiNucSizBin7_Are_Tot
HE03_EpiNucSizBin7_Blu_Mean
HE03_EpiNucSizBin7_Blu_MeanStd
HE03_EpiNucSizBin7_Bri_Mean
HE03_EpiNucSizBin7_Gre_Mean
HE03_EpiNucSizBin7_Gre_MeanStd
HE03_EpiNucSizBin7_Num
HE03_EpiNucSizBin7_Red_Mean
HE03_EpiNucSizBin7_Red_MeanStd
HE03_EpiNucSizBin8_Are_Mean
HE03_EpiNucSizBin8_Are_Tot
HE03_EpiNucSizBin8_Blu_Mean
HE03_EpiNucSizBin8_Blu_MeanStd
HE03_EpiNucSizBin8_Bri_Mean
HE03_EpiNucSizBin8_Gre_Mean
HE03_EpiNucSizBin8_Gre_MeanStd
HE03_EpiNucSizBin8_Num
HE03_EpiNucSizBin8_Red_Mean
HE03_EpiNucSizBin8_Red_MeanStd

Morphometric, color and area measurements of
epithelial nuclei

HE03_EpiNuc_Are_Mean
HE03_EpiNuc_Are_Median
HE03_EpiNuc_Are_Std
HE03_EpiNuc_Are_Tot
HE03_EpiNuc_ElpFit_Mean
HE03_EpiNuc_ElpFit_Median
HE03_EpiNuc_ElpFit_Std
HE03_EpiNuc_LOW_Mean
HE03_EpiNuc_LOW_Median
HE03_EpiNuc_LOW_Std
HE03_EpiNuc_Num
HE03_EpiNuc_OrgBlu_MeanMean
HE03_EpiNuc_OrgBlu_MeanStd
HE03_EpiNuc_OrgBri_Mean
HE03_EpiNuc_OrgBri_Std
HE03_EpiNuc_OrgGre_MeanMean
HE03_EpiNuc_OrgGre_MeanStd
HE03_EpiNuc_OrgH_Mean
HE03_EpiNuc_OrgH_Std
HE03_EpiNuc_OrgI_Mean
HE03_EpiNuc_OrgI_Std

HE03_EpiNuc_OrgQ_Mean	
HE03_EpiNuc_OrgQ_Std	
HE03_EpiNuc_OrgRed_MeanMean	
HE03_EpiNuc_OrgRed_MeanStd	
HE03_EpiNuc_OrgS_Mean	
HE03_EpiNuc_OrgS_Std	
HE03_EpiNuc_OrgV_Mean	
HE03_EpiNuc_OrgV_Std	
HE03_EpiNuc_OrgY_Mean	
HE03_EpiNuc_OrgY_Std	
HE03_IsoEpiNuc_ElpFit_Mean	Morphometric, color and area measurements of isolated epithelial and stroma nuclei
HE03_IsoEpiNuc_ElpFit_Median	
HE03_IsoEpiNuc_ElpFit_Std	
HE03_IsoEpiNuc_LOW_Mean	
HE03_IsoEpiNuc_LOW_Median	
HE03_IsoEpiNuc_LOW_Std	
HE03_IsoEpiNuc_OrgBlu_MeanMean	
HE03_IsoEpiNuc_OrgBlu_MeanStd	
HE03_IsoEpiNuc_OrgBlu_StdMean	
HE03_IsoEpiNuc_OrgBri_Mean	
HE03_IsoEpiNuc_OrgBri_Std	
HE03_IsoEpiNuc_OrgGre_MeanMean	
HE03_IsoEpiNuc_OrgGre_MeanStd	
HE03_IsoEpiNuc_OrgGre_StdMean	
HE03_IsoEpiNuc_OrgRed_MeanMean	
HE03_IsoEpiNuc_OrgRed_MeanStd	
HE03_IsoEpiNuc_OrgRed_StdMean	
HE03_IsoEpiNuc_ShaInd_Mean	
HE03_IsoEpiNuc_ShaInd_Std	
HE03_IsoNuc_Are_Mean	
HE03_IsoNuc_Are_Std	
HE03_IsoNuc_Are_Tot	
HE03_IsoNuc_Num	
HE03_IsoStrNuc_Are_Mean	
HE03_IsoStrNuc_Are_Std	
HE03_IsoStrNuc_Are_Tot	
HE03_IsoStrNuc_Num	
HE03_LENSizBin0_Are_Mean	Color and morphometric measurements of likely epithelial nuclei
HE03_LENSizBin0_Are_Tot	
HE03_LENSizBin0_Num	

HE03_LENSizBin1_Are_Mean
HE03_LENSizBin1_Are_Tot
HE03_LENSizBin1_Num
HE03_LENSizBin2_Are_Mean
HE03_LENSizBin2_Are_Tot
HE03_LENSizBin2_Num
HE03_LENSizBin3_Are_Mean
HE03_LENSizBin3_Are_Tot
HE03_LENSizBin3_Num
HE03_LENSizBin4_Are_Mean
HE03_LENSizBin4_Are_Tot
HE03_LENSizBin4_Num
HE03_LENSizBin5_Are_Mean
HE03_LENSizBin5_Are_Tot
HE03_LENSizBin5_Num
HE03_LENSizBin6_Are_Mean
HE03_LENSizBin6_Are_Tot
HE03_LENSizBin6_Num
HE03_LENSizBin7_Are_Mean
HE03_LENSizBin7_Are_Tot
HE03_LENSizBin7_Num
HE03_LENSizBin8_Are_Mean
HE03_LENSizBin8_Are_Tot
HE03_LENSizBin8_Num
HE03_LEN_Are_Mean
HE03_LEN_Are_Q50
HE03_LEN_Are_Q75
HE03_LEN_Are_Q90
HE03_LEN_Are_Q95
HE03_LEN_Are_Tot
HE03_LEN_Com_Mean
HE03_LEN_ElpFit_Mean
HE03_LEN_Num
HE03_LEN_OrgBlu_MeanMean
HE03_LEN_OrgBlu_MeanStd
HE03_LEN_OrgBlu_StdMean
HE03_LEN_OrgBri_MeanMean
HE03_LEN_OrgBri_StdMean
HE03_LEN_OrgGre_MeanMean
HE03_LEN_OrgGre_MeanStd
HE03_LEN_OrgGre_StdMean
HE03_LEN_OrgH_MeanMean

HE03_LEN_OrgH_StdMean
HE03_LEN_OrgI_MeanMean
HE03_LEN_OrgQ_MeanMean
HE03_LEN_OrgRed_MeanMean
HE03_LEN_OrgRed_MeanStd
HE03_LEN_OrgRed_StdMean
HE03_LEN_OrgS_MeanMean
HE03_LEN_OrgS_StdMean
HE03_LEN_OrgV_MeanMean
HE03_LEN_OrgV_StdMean
HE03_LEN_OrgY_MeanMean
HE03_LEN_Rou_Mean
HE03_LEN_ShaInd_Mean
HE03_LENw0N_Are_Mean
HE03_LENw0N_Are_Tot
HE03_LENw0N_Com_Mean
HE03_LENw0N_ElpFit_Mean
HE03_LENw0N_Num
HE03_LENw0N_OrgBlu_MeanMean
HE03_LENw0N_OrgBlu_MeanStd
HE03_LENw0N_OrgBlu_StdMean
HE03_LENw0N_OrgBri_MeanMean
HE03_LENw0N_OrgBri_StdMean
HE03_LENw0N_OrgGre_MeanMean
HE03_LENw0N_OrgGre_MeanStd
HE03_LENw0N_OrgGre_StdMean
HE03_LENw0N_OrgH_MeanMean
HE03_LENw0N_OrgH_StdMean
HE03_LENw0N_OrgI_MeanMean
HE03_LENw0N_OrgQ_MeanMean
HE03_LENw0N_OrgRed_MeanMean
HE03_LENw0N_OrgRed_MeanStd
HE03_LENw0N_OrgRed_StdMean
HE03_LENw0N_OrgS_MeanMean
HE03_LENw0N_OrgS_StdMean
HE03_LENw0N_OrgV_MeanMean
HE03_LENw0N_OrgV_StdMean
HE03_LENw0N_OrgY_MeanMean
HE03_LENw0N_Rou_Mean
HE03_LENw0N_ShaInd_Mean
HE03_LENw1N_Are_Mean
HE03_LENw1N_Are_Tot

HE03_LENw1N_Com_Mean
HE03_LENw1N_ElpFit_Mean
HE03_LENw1N_Num
HE03_LENw1N_OrgBlu_MeanMean
HE03_LENw1N_OrgBlu_MeanStd
HE03_LENw1N_OrgBlu_StdMean
HE03_LENw1N_OrgBri_MeanMean
HE03_LENw1N_OrgBri_StdMean
HE03_LENw1N_OrgGre_MeanMean
HE03_LENw1N_OrgGre_MeanStd
HE03_LENw1N_OrgGre_StdMean
HE03_LENw1N_OrgH_MeanMean
HE03_LENw1N_OrgH_StdMean
HE03_LENw1N_OrgI_MeanMean
HE03_LENw1N_OrgQ_MeanMean
HE03_LENw1N_OrgRed_MeanMean
HE03_LENw1N_OrgRed_MeanStd
HE03_LENw1N_OrgRed_StdMean
HE03_LENw1N_OrgS_MeanMean
HE03_LENw1N_OrgS_StdMean
HE03_LENw1N_OrgV_MeanMean
HE03_LENw1N_OrgV_StdMean
HE03_LENw1N_OrgY_MeanMean
HE03_LENw1N_Rou_Mean
HE03_LENw1N_ShaInd_Mean
HE03_LENw2N_Are_Mean
HE03_LENw2N_Are_Tot
HE03_LENw2N_Com_Mean
HE03_LENw2N_ElpFit_Mean
HE03_LENw2N_Num
HE03_LENw2N_OrgBlu_MeanMean
HE03_LENw2N_OrgBlu_MeanStd
HE03_LENw2N_OrgBlu_StdMean
HE03_LENw2N_OrgBri_MeanMean
HE03_LENw2N_OrgBri_StdMean
HE03_LENw2N_OrgGre_MeanMean
HE03_LENw2N_OrgGre_MeanStd
HE03_LENw2N_OrgGre_StdMean
HE03_LENw2N_OrgH_MeanMean
HE03_LENw2N_OrgH_StdMean
HE03_LENw2N_OrgI_MeanMean
HE03_LENw2N_OrgQ_MeanMean

HE03_LENw2N_OrgRed_MeanMean
HE03_LENw2N_OrgRed_MeanStd
HE03_LENw2N_OrgRed_StdMean
HE03_LENw2N_OrgS_MeanMean
HE03_LENw2N_OrgS_StdMean
HE03_LENw2N_OrgV_MeanMean
HE03_LENw2N_OrgV_StdMean
HE03_LENw2N_OrgY_MeanMean
HE03_LENw2N_Rou_Mean
HE03_LENw2N_ShaInd_Mean

Color and morphometric measurements of light nuclei

HE03_LigNucBin0_3_Are_Mean
HE03_LigNucBin0_3_Are_Tot
HE03_LigNucBin0_3_Num
HE03_LigNucBin0_5_Are_Mean
HE03_LigNucBin0_5_Are_Tot
HE03_LigNucBin0_5_Num
HE03_LigNucBin0_7_Are_Mean
HE03_LigNucBin0_7_Are_Tot
HE03_LigNucBin0_7_Num
HE03_LigNucBin0_Are_Mean
HE03_LigNucBin0_Are_Tot
HE03_LigNucBin0_Num
HE03_LigNucBin1_3_Are_Mean
HE03_LigNucBin1_3_Are_Tot
HE03_LigNucBin1_3_Num
HE03_LigNucBin1_5_Are_Mean
HE03_LigNucBin1_5_Are_Tot
HE03_LigNucBin1_5_Num
HE03_LigNucBin1_7_Are_Mean
HE03_LigNucBin1_7_Are_Tot
HE03_LigNucBin1_7_Num
HE03_LigNucBin1_Are_Mean
HE03_LigNucBin1_Are_Tot
HE03_LigNucBin1_Num
HE03_LigNucBin2_3_Are_Mean
HE03_LigNucBin2_3_Are_Tot
HE03_LigNucBin2_3_Num
HE03_LigNucBin2_5_Are_Mean
HE03_LigNucBin2_5_Are_Tot
HE03_LigNucBin2_5_Num
HE03_LigNucBin2_7_Are_Mean

HE03_LigNucBin2_7_Are_Tot
HE03_LigNucBin2_7_Num
HE03_LigNucBin2_Are_Mean
HE03_LigNucBin2_Are_Tot
HE03_LigNucBin2_Num
HE03_LigNucBin3_5_Are_Mean
HE03_LigNucBin3_5_Are_Tot
HE03_LigNucBin3_5_Num
HE03_LigNucBin3_7_Are_Mean
HE03_LigNucBin3_7_Are_Tot
HE03_LigNucBin3_7_Num
HE03_LigNucBin3_Are_Mean
HE03_LigNucBin3_Are_Tot
HE03_LigNucBin3_Num
HE03_LigNucBin4_5_Are_Mean
HE03_LigNucBin4_5_Are_Tot
HE03_LigNucBin4_5_Num
HE03_LigNucBin4_7_Are_Mean
HE03_LigNucBin4_7_Are_Tot
HE03_LigNucBin4_7_Num
HE03_LigNucBin4_Are_Mean
HE03_LigNucBin4_Are_Tot
HE03_LigNucBin4_Num
HE03_LigNucBin5_7_Are_Mean
HE03_LigNucBin5_7_Are_Tot
HE03_LigNucBin5_7_Num
HE03_LigNucBin5_Are_Mean
HE03_LigNucBin5_Are_Tot
HE03_LigNucBin5_Num
HE03_LigNucBin6_7_Are_Mean
HE03_LigNucBin6_7_Are_Tot
HE03_LigNucBin6_7_Num
HE03_LigNucBin6_Are_Mean
HE03_LigNucBin6_Are_Tot
HE03_LigNucBin6_Num
HE03_LigNucBin7_Are_Mean
HE03_LigNucBin7_Are_Tot
HE03_LigNucBin7_Num
HE03_LigNucBin8_Are_Mean
HE03_LigNucBin8_Are_Tot
HE03_LigNucBin8_Num
HE03_NoWhi_Are_Tot

HE03_NucLikTis_Are_Tot	
HE03_Nuc_Are_Mean	Area features of all nuclei
HE03_Nuc_Are_Std	
HE03_Nuc_Are_Tot	
HE03_Nuc_Num	
HE03_Nuclli_Are_Mean	Area features of nucleoli
HE03_Nuclli_Are_Q50	
HE03_Nuclli_Are_Q75	
HE03_Nuclli_Are_Q90	
HE03_Nuclli_Are_Q95	
HE03_PD Nuc_Are_Mean	Color and morphometric features of poorly defined nuclei
HE03_PD Nuc_Are_Std	
HE03_PD Nuc_Are_Tot	
HE03_PD Nuc_ElpFit_Mean	
HE03_PD Nuc_ElpFit_Std	
HE03_PD Nuc_LOW_Mean	
HE03_PD Nuc_LOW_Std	
HE03_PD Nuc_Num	
HE03_PD Nuc_OrgBlu_MeanMean	
HE03_PD Nuc_OrgBlu_MeanStd	
HE03_PD Nuc_OrgBlu_StdMean	
HE03_PD Nuc_OrgBri_Mean	
HE03_PD Nuc_OrgBri_Std	
HE03_PD Nuc_OrgGre_MeanMean	
HE03_PD Nuc_OrgGre_MeanStd	
HE03_PD Nuc_OrgGre_StdMean	
HE03_PD Nuc_OrgRed_MeanMean	
HE03_PD Nuc_OrgRed_MeanStd	
HE03_PD Nuc_OrgRed_StdMean	
HE03_PD Nuc_ShaInd_Mean	
HE03_PD Nuc_ShaInd_Std	
HE03_StrNuc_Are_Mean	Color and morphometric features of stroma nuclei
HE03_StrNuc_Are_Median	
HE03_StrNuc_Are_Std	
HE03_StrNuc_Are_Tot	
HE03_StrNuc_ElpFit_Mean	
HE03_StrNuc_ElpFit_Median	
HE03_StrNuc_ElpFit_Std	
HE03_StrNuc_LOW_Mean	
HE03_StrNuc_LOW_Median	
HE03_StrNuc_LOW_Std	

HE03_StrNuc_Num	
HE03_StrNuc_OrgBlu_MeanMean	
HE03_StrNuc_OrgBlu_MeanStd	
HE03_StrNuc_OrgBri_Mean	
HE03_StrNuc_OrgBri_Std	
HE03_StrNuc_OrgGre_MeanMean	
HE03_StrNuc_OrgGre_MeanStd	
HE03_StrNuc_OrgH_Mean	
HE03_StrNuc_OrgH_Std	
HE03_StrNuc_OrgI_Mean	
HE03_StrNuc_OrgI_Std	
HE03_StrNuc_OrgQ_Mean	
HE03_StrNuc_OrgQ_Std	
HE03_StrNuc_OrgRed_MeanMean	
HE03_StrNuc_OrgRed_MeanStd	
HE03_StrNuc_OrgS_Mean	
HE03_StrNuc_OrgS_Std	
HE03_StrNuc_OrgV_Mean	
HE03_StrNuc_OrgV_Std	
HE03_StrNuc_OrgY_Mean	
HE03_StrNuc_OrgY_Std	
HE03_Str_Are_Mean	Color and morphometric measurements of stroma
HE03_Str_Are_Std	
HE03_Str_Are_Tot	
HE03_Str_Num	
HE03_Str_OrgBlu_MeanMean	
HE03_Str_OrgBlu_MeanStd	
HE03_Str_OrgBri_Mean	
HE03_Str_OrgBri_Std	
HE03_Str_OrgGre_MeanMean	
HE03_Str_OrgGre_MeanStd	
HE03_Str_OrgH_Mean	
HE03_Str_OrgH_Std	
HE03_Str_OrgI_Mean	
HE03_Str_OrgI_Std	
HE03_Str_OrgQ_Mean	
HE03_Str_OrgQ_Std	
HE03_Str_OrgRed_MeanMean	
HE03_Str_OrgRed_MeanStd	
HE03_Str_OrgS_Mean	
HE03_Str_OrgS_Std	
HE03_Str_OrgV_Mean	

HE03_Str_OrgV_Std	
HE03_Str_OrgY_Mean	
HE03_Str_OrgY_Std	
HE03_WDEpiNuc_Are_Mean	Color and morphometric measurements of well defined epithelial nuclei
HE03_WDEpiNuc_Are_Median	
HE03_WDEpiNuc_Are_Std	
HE03_WDEpiNuc_Are_Tot	
HE03_WDEpiNuc_ElpFit_Mean	
HE03_WDEpiNuc_ElpFit_Median	
HE03_WDEpiNuc_ElpFit_Std	
HE03_WDEpiNuc_LOW_Mean	
HE03_WDEpiNuc_LOW_Median	
HE03_WDEpiNuc_LOW_Std	
HE03_WDEpiNuc_Num	
HE03_WDEpiNuc_OrgBlu_MeanMean	
HE03_WDEpiNuc_OrgBlu_MeanStd	
HE03_WDEpiNuc_OrgBlu_StdMean	
HE03_WDEpiNuc_OrgBri_Mean	
HE03_WDEpiNuc_OrgBri_Std	
HE03_WDEpiNuc_OrgGre_MeanMean	
HE03_WDEpiNuc_OrgGre_MeanStd	
HE03_WDEpiNuc_OrgGre_StdMean	
HE03_WDEpiNuc_OrgRed_MeanMean	
HE03_WDEpiNuc_OrgRed_MeanStd	
HE03_WDEpiNuc_OrgRed_StdMean	
HE03_WDEpiNuc_ShaInd_Mean	
HE03_WDEpiNuc_ShaInd_Std	
HE03_Whi_Are_Tot	
'HEX2_LENwNcli_NumTotal'	Normalized measurements of likely epithelial nuclei
'HEX2_LENwNcli_AreTotal'	
'HEX3_RelNumw0Nucleoli'	Proportions of numbers of nucleoli
'HEX3_RelNumw1Nucleoli'	
'HEX3_RelNumw2Nucleoli'	
'HEX3_RelNumwNucleoli'	
'HEX3_RelAreaw0Nucleoli'	
'HEX3_RelAreaw1Nucleoli'	
'HEX3_RelAreaw2Nucleoli'	
'HEX3_RelAreawNucleoli'	
'HEX3_nrmSN_EpiNuc_OrgRed_MnMn'	Normalized color features of epithelial nuclei. SN indicates normalization by Stroma Nuclei
'HEX3_nrmS_EpiNuc_OrgRed_MnMn'	

'HEX3_nrmSN_EpiNuc_OrgGre_MnMn'
'HEX3_nrmS_EpiNuc_OrgGre_MnMn'
'HEX3_nrmSN_EpiNuc_OrgBlu_MnMn'
'HEX3_nrmS_EpiNuc_OrgBlu_MnMn'
'HEX3_nrmSN_EpiNuc_OrgQ_Mn'
'HEX3_nrmS_EpiNuc_OrgQ_Mn'
'HEX3_nrmSN_EpiNuc_OrgI_Mn'
'HEX3_nrmS_EpiNuc_OrgI_Mn'
'HEX3_nrm_EpiNucOrgRed_MeanStd'
'HEX3_nrm_EpiNucOrgGre_MeanStd'
'HEX3_nrm_EpiNucOrgBlu_MeanStd'
'HEX3_nrmSN_EpiNucOrgRed_MeanStd'
'HEX3_nrmSN_EpiNucOrgGre_MeanStd'
'HEX3_nrmSN_EpiNucOrgBlu_MeanStd'
'HEX3_nrmSN2_EpiNucOrgRed_MeanStd'
'HEX3_nrmSN2_EpiNucOrgGre_MeanStd'
'HEX3_nrmSN2_EpiNucOrgBlu_MeanStd'
'HEX3_nrmS_EpiNucOrgRed_MeanStd'
'HEX3_nrmS_EpiNucOrgGre_MeanStd'
'HEX3_nrmS_EpiNucOrgBlu_MeanStd'
'HEX3_EpiNucOrgSumRGBMeanStd'
'HEX3_EpiNucNrmSumRGBMeanStd'
'HEX3_EpiNucNrmSNSumRGBMeanStd'
'HEX3_nrm_EpNucBin0_7_Red_StdMean'
'HEX3_nrm_EpNucBin0_7_Gre_StdMean'
'HEX3_nrm_EpNucBin0_7_Blu_StdMean'
'HEX3_nrmSN_EpNucBn0_7_RedStdMean'
'HEX3_nrmSN_EpNucBn0_7_GreStdMean'
'HEX3_nrmSN_EpNucBn0_7_BluStdMean'
'HEX3_nrmS_EpNucBn0_7_RedStdMean'
'HEX3_nrmS_EpNucBn0_7_GreStdMean'
'HEX3_nrmS_EpNucBn0_7_BluStdMean'
'HEX3_nrm_EpNucBn4_5_Br_MeanStd'
'HEX3_nrmSN_EpNucB4_5_Br_MeanStd'
'HEX3_nrmSN2_EpNucB4_5_Br_MeanStd'
'HEX3_nrmS_EpNucB4_5_Br_MeanStd'
'HEX3_nrm_EpNucBn4_5_Br_StdMean'
'HEX3_nrmSN_EpNucB4_5_Br_StdMean'
'HEX3_nrmSN2_EpNucB4_5_Br_StdMean'
'HEX3_nrmS_EpNucB4_5_Br_StdMean'
'HEX3_nrm_EpNucBn4_5_Red_StdMean'
'HEX3_nrmSN_EpNucB4_5_Red_StdMean'

'HEX3_nrmS_EpNucB4_5_Red_StdMean'
'HEX3_nrm_EpNucBn4_7_Br_MeanStd'
'HEX3_nrmSN_EpNucB4_7_Br_MeanStd'
'HEX3_nrmSN2_EpNucB4_7_Br_MeanStd'
'HEX3_nrm_EpNucBn3_7_Red_StdMean'
'HEX3_nrmSN_EpNucB3_7_Red_StdMean'
'HEX3_nrmS_EpNucB3_7_Red_StdMean'
'HEX3_nrm_EpiNucEr1_Red_MeanStd'
'HEX3_nrm_EpiNucEr1_Gre_MeanStd'
'HEX3_nrm_EpiNucEr1_Blu_MeanStd'
'HEX3_nrm_EpiNucEr1_Bri_MeanStd'
'HEX3_nrmSN_EpiNucEr1_Red_MeanStd'
'HEX3_nrmSN_EpiNucEr1_Gre_MeanStd'
'HEX3_nrmSN_EpiNucEr1_Blu_MeanStd'
'HEX3_nrmSN_EpiNucEr1_Bri_MeanStd'
'HEX3_nrmSN2_EpNucEr1_Red_MeanStd'
'HEX3_nrmSN2_EpNucEr1_Gre_MeanStd'
'HEX3_nrmSN2_EpNucEr1_Blu_MeanStd'
'HEX3_nrmSN2_EpNucEr1_Bri_MeanStd'
'HEX3_ENEr1orgSumRGBMeanStd'
'HEX3_ENEr1nrmSumRGBMeanStd'
'HEX3_nrm_EpiNucEr2_Red_MeanStd'
'HEX3_nrm_EpiNucEr2_Gre_MeanStd'
'HEX3_nrm_EpiNucEr2_Blu_MeanStd'
'HEX3_ENEr2orgSumRGBMeanStd'
'HEX3_ENEr2nrmSumRGBMeanStd'

Normalized area features of epithelial nuclei in total, clustered, isolated, and likely groups.

'HEX3_nrm_TiEpiNuc_Are_Tot'
'HEX3_nrm_TiEpiCluNuc_Are_Tot'
'HEX3_nrm_TiEpiCluNuc_Num'
'HEX3_nrm_TiEpiIsoNuc_Are_Tot'
'HEX3_nrm_TiEpiIsoNuc_Num'
'HEX3_nrm_TiEpiNuc_Num'
'HEX3_nrm_TiEpiNuc_NucLikTis'
'HEX3_nrm_EpiNuc_Are_Tot2Cyt'
'HEX3_nrm_EpiCluNuc_Are_Tot2Cyt'
'HEX3_nrm_EpiCluNuc_Num2Cyt'
'HEX3_nrm_EpiIsoNuc_Are_Tot2Cyt'
'HEX3_nrm_EpiIsoNuc_Num2Cyt'
'HEX3_nrm_EpiNuc_Num2Cyt'
'HEX3_nrm_NucLikTis2Cyt'
'HEX3_TotArea_EpNucBin'

'HEX3_TotArea_LENucBin'	
'HEX3_nrm_EpiNucSizBin0_Are_Tot'	Normalized bins of epithelial nuclei divided by size
'HEX3_nrm_EpiNucSizBin1_Are_Tot'	
'HEX3_nrm_EpiNucSizBin2_Are_Tot'	
'HEX3_nrm_EpiNucSizBin3_Are_Tot'	
'HEX3_nrm_EpiNucSizBin4_Are_Tot'	
'HEX3_nrm_EpiNucSizBin5_Are_Tot'	
'HEX3_nrm_EpiNucSizBin6_Are_Tot'	
'HEX3_nrm_EpiNucSizBin7_Are_Tot'	
'HEX3_nrm_EpiNucSizBin8_Are_Tot'	
Normalized bins of likely epithelial nuclei divided by size	
'HEX3_nrm_LENSizBin0_Are_Tot'	
'HEX3_nrm_LENSizBin1_Are_Tot'	
'HEX3_nrm_LENSizBin2_Are_Tot'	
'HEX3_nrm_LENSizBin3_Are_Tot'	
'HEX3_nrm_LENSizBin4_Are_Tot'	
'HEX3_nrm_LENSizBin5_Are_Tot'	
'HEX3_nrm_LENSizBin6_Are_Tot'	
'HEX3_nrm_LENSizBin7_Are_Tot'	
'HEX3_nrm_LENSizBin8_Are_Tot'	
'HEX3_A0'	
'HEX3_A1'	
Normalized bins of dark nuclei	
'HEX3_nrm0_DarNucBin0_Are_Tot'	
'HEX3_nrm0_DarNucBin0_3_Are_Tot'	
'HEX3_nrm0_DarNucBin0_5_Are_Tot'	
'HEX3_nrm0_DarNucBin0_7_Are_Tot'	
'HEX3_nrm0_DarNucBin1_Are_Tot'	
'HEX3_nrm0_DarNucBin1_3_Are_Tot'	
'HEX3_nrm0_DarNucBin1_5_Are_Tot'	
'HEX3_nrm0_DarNucBin1_7_Are_Tot'	
'HEX3_nrm0_DarNucBin2_Are_Tot'	
'HEX3_nrm0_DarNucBin2_3_Are_Tot'	
'HEX3_nrm0_DarNucBin2_5_Are_Tot'	
'HEX3_nrm0_DarNucBin2_7_Are_Tot'	
'HEX3_nrm0_DarNucBin3_Are_Tot'	
'HEX3_nrm0_DarNucBin3_5_Are_Tot'	
'HEX3_nrm0_DarNucBin3_7_Are_Tot'	
'HEX3_nrm0_DarNucBin4_Are_Tot'	
'HEX3_nrm0_DarNucBin4_5_Are_Tot'	
'HEX3_nrm0_DarNucBin4_7_Are_Tot'	
'HEX3_nrm0_DarNucBin5_Are_Tot'	
'HEX3_nrm0_DarNucBin5_7_Are_Tot'	

'HEX3_nrm0_DarNucBin6_Are_Tot'
'HEX3_nrm0_DarNucBin6_7_Are_Tot'
'HEX3_nrm0_DarNucBin7_Are_Tot'
'HEX3_nrm0_DarNucBin8_Are_Tot'
'HEX3_nrm1_DarNucBin0_Are_Tot'
'HEX3_nrm1_DarNucBin0_3_Are_Tot'
'HEX3_nrm1_DarNucBin0_5_Are_Tot'
'HEX3_nrm1_DarNucBin0_7_Are_Tot'
'HEX3_nrm1_DarNucBin1_Are_Tot'
'HEX3_nrm1_DarNucBin1_3_Are_Tot'
'HEX3_nrm1_DarNucBin1_5_Are_Tot'
'HEX3_nrm1_DarNucBin1_7_Are_Tot'
'HEX3_nrm1_DarNucBin2_Are_Tot'
'HEX3_nrm1_DarNucBin2_3_Are_Tot'
'HEX3_nrm1_DarNucBin2_5_Are_Tot'
'HEX3_nrm1_DarNucBin2_7_Are_Tot'
'HEX3_nrm1_DarNucBin3_Are_Tot'
'HEX3_nrm1_DarNucBin3_5_Are_Tot'
'HEX3_nrm1_DarNucBin3_7_Are_Tot'
'HEX3_nrm1_DarNucBin4_Are_Tot'
'HEX3_nrm1_DarNucBin4_5_Are_Tot'
'HEX3_nrm1_DarNucBin4_7_Are_Tot'
'HEX3_nrm1_DarNucBin5_Are_Tot'
'HEX3_nrm1_DarNucBin5_7_Are_Tot'
'HEX3_nrm1_DarNucBin6_Are_Tot'
'HEX3_nrm1_DarNucBin6_7_Are_Tot'
'HEX3_nrm1_DarNucBin7_Are_Tot'
'HEX3_nrm1_DarNucBin8_Are_Tot'

Table 2. Morphometric Features (e.g., measurable in images of tissue subject to multiplex immunofluorescence (IF))

Feature	Description
'fd_3_8'	Fractal dimension of gland objects as identified by CK18.
'fd_3_8_fillholes'	Fractal dimension of gland objects as identified by CK18, with luminal holes filled in during pre-processing.
'mst_mean_length_epinuc'	Average MST length between epithelial nuclei
'mst_std_length_epinuc'	Standard Deviation of MST length between epithelial nuclei

'proportion_edge_1_epinuc'	Proportion of epithelial nuclei with one MST connecting edge.
'proportion_edge_2_epinuc'	Proportion of epithelial nuclei with two MST connecting edges.
'proportion_edge_3_epinuc'	Proportion of epithelial nuclei with three MST connecting edges.
'proportion_edge_4_epinuc'	Proportion of epithelial nuclei with four MST connecting edges.
'proportion_edge_5_epinuc'	Proportion of epithelial nuclei with five MST connecting edges.
'mst_mean_length_intra_epinuc'	Average MST length between epithelial nuclei that are restricted to CK18 positive space, i.e. constrained by glands.
'mst_std_length_intra_epinuc'	Standard Deviation of MST length between epithelial nuclei that are restricted to CK18 positive space, i.e. constrained by glands.
'mst_mean_length_strnuc'	Average MST length between stroma nuclei
'mst_std_length_strnuc'	Standard Deviation of MST length between stroma nuclei
'proportion_edge_1_strnuc'	Proportion of stroma nuclei with one MST connecting edge.
'proportion_edge_2_strnuc'	Proportion of stroma nuclei with two MST connecting edges.
'proportion_edge_3_strnuc'	Proportion of stroma nuclei with three MST connecting edges.
'proportion_edge_4_strnuc'	Proportion of stroma nuclei with four MST connecting edges.
'proportion_edge_5_strnuc'	Proportion of stroma nuclei with five MST connecting edges.
'mst_mean_length_endnuc'	Average MST length between endothelial nuclei
'mst_std_length_endnuc'	Standard Deviation of MST length between endothelial nuclei
'proportion_edge_1_endnuc'	Proportion of endothelial nuclei with one MST connecting edge.
'proportion_edge_2_endnuc'	Proportion of endothelial nuclei with two MST connecting edges.
'proportion_edge_3_endnuc'	Proportion of endothelial nuclei with three MST connecting edges.
'proportion_edge_4_endnuc'	Proportion of endothelial nuclei with four MST connecting edges.
'proportion_edge_5_endnuc'	Proportion of endothelial nuclei with five MST connecting edges.

'iforig_approximation_1'	Variance of pixel values in the approximation sub-band after applying 1 stage of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_approximation_2'	Variance of pixel values in the approximation sub-band after applying 2 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_approximation_3'	Variance of pixel values in the approximation sub-band after applying 3 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_approximation_4'	Variance of pixel values in the approximation sub-band after applying 4 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_approximation_5'	Variance of pixel values in the approximation sub-band after applying 5 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_approximation_6'	Variance of pixel values in the approximation sub-band after applying 6 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_approximation_7'	Variance of pixel values in the approximation sub-band after applying 7 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_horiz_detail_1'	Variance of pixel values in the horizontal detail sub-band after applying 1 stage of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_horiz_detail_2'	Variance of pixel values in the horizontal detail sub-band after applying 2 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_horiz_detail_3'	Variance of pixel values in the horizontal detail sub-band after applying 3 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.

'iforig_horiz_detail_4'	Variance of pixel values in the horizontal detail sub-band after applying 4 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_horiz_detail_5'	Variance of pixel values in the horizontal detail sub-band after applying 5 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_horiz_detail_6'	Variance of pixel values in the horizontal detail sub-band after applying 6 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_horiz_detail_7'	Variance of pixel values in the horizontal detail sub-band after applying 7 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_vert_detail_1'	Variance of pixel values in the vertical detail sub-band after applying 1 stage of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_vert_detail_2'	Variance of pixel values in the vertical detail sub-band after applying 2 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_vert_detail_3'	Variance of pixel values in the vertical detail sub-band after applying 3 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_vert_detail_4'	Variance of pixel values in the vertical detail sub-band after applying 4 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_vert_detail_5'	Variance of pixel values in the vertical detail sub-band after applying 5 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_vert_detail_6'	Variance of pixel values in the vertical detail sub-band after applying 6 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.

'iforig_vert_detail_7'	Variance of pixel values in the vertical detail sub-band after applying 7 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_diag_detail_1'	Variance of pixel values in the diagonal detail sub-band after applying 1 stage of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_diag_detail_2'	Variance of pixel values in the diagonal detail sub-band after applying 2 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_diag_detail_3'	Variance of pixel values in the diagonal detail sub-band after applying 3 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_diag_detail_4'	Variance of pixel values in the diagonal detail sub-band after applying 4 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_diag_detail_5'	Variance of pixel values in the diagonal detail sub-band after applying 5 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_diag_detail_6'	Variance of pixel values in the diagonal detail sub-band after applying 6 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'iforig_diag_detail_7'	Variance of pixel values in the diagonal detail sub-band after applying 7 stages of undecimated wavelet transform to a mask of epithelial cytoplasm as identified by CK18.
'min_IForig_detail1'	Minimum of above defined features "iforig_horiz_detail_1" and "iforig_vert_detail_1".
'min_IForig_detail2'	Minimum of above defined features "iforig_horiz_detail_2" and "iforig_vert_detail_2".
'min_IForig_detail3'	Minimum of above defined features "iforig_horiz_detail_3" and "iforig_vert_detail_3".
'min_IForig_detail4'	Minimum of above defined features "iforig_horiz_detail_4" and "iforig_vert_detail_4".
'min_IForig_detail5'	Minimum of above defined features "iforig_horiz_detail_5" and "iforig_vert_detail_5".

'min_IForig_detail6'	Minimum of above defined features "iforig_horiz_detail_6" and "iforig_vert_detail_6".
'min_IForig_detail7'	Minimum of above defined features "iforig_horiz_detail_7" and "iforig_vert_detail_7".
'max_IForig_detail1'	Maximum of above defined features "iforig_horiz_detail_1" and "iforig_vert_detail_1".
'max_IForig_detail2'	Maximum of above defined features "iforig_horiz_detail_2" and "iforig_vert_detail_2".
'max_IForig_detail3'	Maximum of above defined features "iforig_horiz_detail_3" and "iforig_vert_detail_3".
'max_IForig_detail4'	Maximum of above defined features "iforig_horiz_detail_4" and "iforig_vert_detail_4".
'max_IForig_detail5'	Maximum of above defined features "iforig_horiz_detail_5" and "iforig_vert_detail_5".
'max_IForig_detail6'	Maximum of above defined features "iforig_horiz_detail_6" and "iforig_vert_detail_6".
'max_IForig_detail7'	Maximum of above defined features "iforig_horiz_detail_7" and "iforig_vert_detail_7".
'sum_IForig_detail1'	Sum of above defined features "iforig_horiz_detail_1" and "iforig_vert_detail_1".
'sum_IForig_detail2'	Sum of above defined features "iforig_horiz_detail_2" and "iforig_vert_detail_2".
'sum_IForig_detail3'	Sum of above defined features "iforig_horiz_detail_3" and "iforig_vert_detail_3".
'sum_IForig_detail4'	Sum of above defined features "iforig_horiz_detail_4" and "iforig_vert_detail_4".
'sum_IForig_detail5'	Sum of above defined features "iforig_horiz_detail_5" and "iforig_vert_detail_5".
'sum_IForig_detail6'	Sum of above defined features "iforig_horiz_detail_6" and "iforig_vert_detail_6".
'sum_IForig_detail7'	Sum of above defined features "iforig_horiz_detail_7" and "iforig_vert_detail_7".
'IFwaveletratio_diag6_7'	Ratio of the above defined features "iforig_diag_detail_6" and "iforig_diag_detail_7"

Table 3. Molecular Immunofluorescence (IF) Features

In some embodiments, features in Table 3 having the prefix "IF01" are measured through the use of MPLEX 1 as described above, whereas "IFx1" refers to features derived/calculated from the MPLEX 1 features. Similarly, in some embodiments, "IF02" refers to features measured through the use of MPLEX 2 described above, whereas "IFx2" refers to features derived/calculated from the MPLEX 2 features.

Feature	Description
'IF01_AMACR_Threshold'	AMACR Threshold
'IF01_AR_Percentile'	AR specific features
'IF01_AR_Threshold'	
'IF01_AR_Trigger'	
'IF01_BasNuc_Area'	Basil Nuclei features
'IF01_BasNuc_DAPI_Mean'	
'IF01_BasNuc_p63_Mean'	
'IF01_CK18_AMACRpObj_AMACR_Mean'	CK18 alone and with AMACR intensity and morphometric features
'IF01_CK18_AMACRpObj_AreaTotal'	
'IF01_CK18_AreaTotal'	
'IF01_CK18_CK18_Mean'	
'IF01_CK18_Threshold'	
'IF01_CytAMACRn_AMACR_MeanMean'	
'IF01_CytAMACRn_AMACR_StdMean'	
'IF01_CytAMACRn_AMACR_StdStd'	
'IF01_CytAMACRn_AreaTotal'	
'IF01_CytAMACRp_AMACR_MeanMean'	
'IF01_CytAMACRp_AMACR_StdMean'	
'IF01_CytAMACRp_AMACR_StdStd'	
'IF01_CytAMACRp_AreaTotal'	
'IF01_Cyt_AR_Mean'	Intensity features and percentiles of AR in cytoplasm (CK18)
'IF01_Cyt_AR_Perc_02'	
'IF01_Cyt_AR_Perc_05'	
'IF01_Cyt_AR_Perc_10'	
'IF01_Cyt_AR_Perc_15'	
'IF01_Cyt_AR_Perc_20'	
'IF01_Cyt_AR_Perc_25'	
'IF01_Cyt_AR_Perc_30'	
'IF01_Cyt_AR_Perc_35'	
'IF01_Cyt_AR_Perc_40'	
'IF01_Cyt_AR_Perc_45'	
'IF01_Cyt_AR_Perc_50'	
'IF01_Cyt_AR_Perc_55'	
'IF01_Cyt_AR_Perc_60'	
'IF01_Cyt_AR_Perc_65'	
'IF01_Cyt_AR_Perc_70'	
'IF01_Cyt_AR_Perc_75'	
'IF01_Cyt_AR_Perc_80'	

'IF01_Cyt_AR_Perc_85'	
'IF01_Cyt_AR_Perc_90'	
'IF01_Cyt_AR_Perc_95'	
'IF01_Cyt_AR_Perc_99'	
'IF01_CytoAMACRn_AMACR_MeanStd'	
'IF01_CytoAMACRp_AMACR_MeanStd'	
'IF01_DAPI_Threshold'	
'IF01_EpiNucARnAMACRn_AR_Mean2'	Intensity features of AR and AMACR in epithelial nuclei
'IF01_EpiNucARnAMACRn_AR_MeanMean'	
'IF01_EpiNucARnAMACRn_AR_MeanStd'	
'IF01_EpiNucARnAMACRn_AR_StdMean'	
'IF01_EpiNucARnAMACRn_AR_StdStd'	
'IF01_EpiNucARnAMACRn_AreaTotal'	
'IF01_EpiNucARnAMACRp_AR_Mean2'	
'IF01_EpiNucARnAMACRp_AR_MeanMean'	
'IF01_EpiNucARnAMACRp_AR_MeanStd'	
'IF01_EpiNucARnAMACRp_AR_StdMean'	
'IF01_EpiNucARnAMACRp_AR_StdStd'	
'IF01_EpiNucARnAMACRp_AreaTotal'	
'IF01_EpiNucARn_ARFlux_Mean'	
'IF01_EpiNucARn_AR_Mean'	
'IF01_EpiNucARn_Num'	
'IF01_EpiNucARpAMACRn_AR_Mean2'	
'IF01_EpiNucARpAMACRn_AR_MeanMean'	
'IF01_EpiNucARpAMACRn_AR_MeanStd'	
'IF01_EpiNucARpAMACRn_AR_StdMean'	
'IF01_EpiNucARpAMACRn_AR_StdStd'	
'IF01_EpiNucARpAMACRn_AreaTotal'	
'IF01_EpiNucARpAMACRp_AR_Mean2'	
'IF01_EpiNucARpAMACRp_AR_MeanMean'	
'IF01_EpiNucARpAMACRp_AR_MeanStd'	
'IF01_EpiNucARpAMACRp_AR_StdMean'	
'IF01_EpiNucARpAMACRp_AR_StdStd'	
'IF01_EpiNucARpAMACRp_AreaTotal'	
'IF01_EpiNucARp_ARFlux_Mean'	
'IF01_EpiNucARp_AR_Mean'	
'IF01_EpiNucARp_DensityBin01_Area'	
'IF01_EpiNucARp_DensityBin02_Area'	
'IF01_EpiNucARp_DensityBin03_Area'	
'IF01_EpiNucARp_DensityBin04_Area'	
'IF01_EpiNucARp_DensityBin05_Area'	

'IF01_EpiNucARp_DensityBin06_Area'	
'IF01_EpiNucARp_DensityBin07_Area'	
'IF01_EpiNucARp_DensityBin08_Area'	
'IF01_EpiNucARp_DensityBin09_Area'	
'IF01_EpiNucARp_DensityBin10_Area'	
'IF01_EpiNucARp_Num'	Percentiles of AR positive intensity
'IF01_EpiNucARp_Perc_02'	
'IF01_EpiNucARp_Perc_05'	
'IF01_EpiNucARp_Perc_10'	
'IF01_EpiNucARp_Perc_15'	
'IF01_EpiNucARp_Perc_20'	
'IF01_EpiNucARp_Perc_25'	
'IF01_EpiNucARp_Perc_30'	
'IF01_EpiNucARp_Perc_35'	
'IF01_EpiNucARp_Perc_40'	
'IF01_EpiNucARp_Perc_45'	
'IF01_EpiNucARp_Perc_50'	
'IF01_EpiNucARp_Perc_55'	
'IF01_EpiNucARp_Perc_60'	
'IF01_EpiNucARp_Perc_65'	
'IF01_EpiNucARp_Perc_70'	
'IF01_EpiNucARp_Perc_75'	
'IF01_EpiNucARp_Perc_80'	
'IF01_EpiNucARp_Perc_85'	
'IF01_EpiNucARp_Perc_90'	
'IF01_EpiNucARp_Perc_95'	
'IF01_EpiNucARp_Perc_99'	
'IF01_EpiNuc_ARFlux_Mean'	
'IF01_EpiNuc_AR_Mean'	
'IF01_EpiNuc_AR_Perc_02'	
'IF01_EpiNuc_AR_Perc_05'	
'IF01_EpiNuc_AR_Perc_10'	
'IF01_EpiNuc_AR_Perc_15'	
'IF01_EpiNuc_AR_Perc_20'	
'IF01_EpiNuc_AR_Perc_25'	
'IF01_EpiNuc_AR_Perc_30'	
'IF01_EpiNuc_AR_Perc_35'	
'IF01_EpiNuc_AR_Perc_40'	
'IF01_EpiNuc_AR_Perc_45'	
'IF01_EpiNuc_AR_Perc_50'	
'IF01_EpiNuc_AR_Perc_55'	
'IF01_EpiNuc_AR_Perc_60'	

'IF01_EpiNuc_AR_Perc_65'
'IF01_EpiNuc_AR_Perc_70'
'IF01_EpiNuc_AR_Perc_75'
'IF01_EpiNuc_AR_Perc_80'
'IF01_EpiNuc_AR_Perc_85'
'IF01_EpiNuc_AR_Perc_90'
'IF01_EpiNuc_AR_Perc_95'
'IF01_EpiNuc_AR_Perc_99'
'IF01_EpiNuc_AreaTotal'
'IF01_EpiNuc_DAPI_Mean'
'IF01_EpiNuc_DensityBin01_Area'
'IF01_EpiNuc_DensityBin02_Area'
'IF01_EpiNuc_DensityBin03_Area'
'IF01_EpiNuc_DensityBin04_Area'
'IF01_EpiNuc_DensityBin05_Area'
'IF01_EpiNuc_DensityBin06_Area'
'IF01_EpiNuc_DensityBin07_Area'
'IF01_EpiNuc_DensityBin08_Area'
'IF01_EpiNuc_DensityBin09_Area'
'IF01_EpiNuc_DensityBin10_Area'

Features relative to extremely high levels of AR (HOT) that are calculated using the percentiles of AR in epithelial nuclei

'IF01_EpiNuc_Hot2AMACRn_AR_Mean'
'IF01_EpiNuc_Hot2AMACRn_Area'
'IF01_EpiNuc_Hot2AMACRp_AR_Mean'
'IF01_EpiNuc_Hot2AMACRp_Area'
'IF01_EpiNuc_Hot2_AR_Mean'
'IF01_EpiNuc_Hot2_Area'
'IF01_EpiNuc_HotAMACRn_AR_Mean'
'IF01_EpiNuc_HotAMACRn_Area'
'IF01_EpiNuc_HotAMACRp_AR_Mean'
'IF01_EpiNuc_HotAMACRp_Area'
'IF01_EpiNuc_Hot_AR_Mean'
'IF01_EpiNuc_Hot_Area'
'IF01_EpiNuc_NormARIntBin00_Area'
'IF01_EpiNuc_NormARIntBin01_Area'
'IF01_EpiNuc_NormARIntBin02_Area'
'IF01_EpiNuc_NormARIntBin03_Area'
'IF01_EpiNuc_NormARIntBin04_Area'
'IF01_EpiNuc_NormARIntBin05_Area'
'IF01_EpiNuc_NormARIntBin06_Area'
'IF01_EpiNuc_NormARIntBin07_Area'

'IF01_EpiNuc_NormARIntBin08_Area'	
'IF01_EpiNuc_NormARIntBin09_Area'	
'IF01_EpiNuc_NormARIntBin10_Area'	
'IF01_EpiNuc_Num'	
'IF01_GU_Area'	
'IF01_HMWCKSignal_Area'	
'IF01_HMWCKSignal_HMWCK_Mean'	
'IF01_HMWCK_Threshold'	
'IF01_NGA_Area'	Non Gland associated features
'IF01_NGA_Number'	
'IF01_Nuc_DAPI_Mean'	
'IF01_P63_Threshold'	
'IF01_Scene_AMACR_Mean'	
'IF01_Scene_AR_Mean'	
'IF01_Scene_CK18_Mean'	
'IF01_Scene_DAPI_Mean'	
'IF01_Scene_HMWCK_Mean'	
'IF01_Scene_p63_Mean'	
'IF01_StrNuc_AR_Mean'	AR in Stroma Nuclei features
'IF01_StrNuc_AR_Mean2'	
'IF01_StrNuc_AR_Perc_02'	
'IF01_StrNuc_AR_Perc_05'	
'IF01_StrNuc_AR_Perc_10'	
'IF01_StrNuc_AR_Perc_15'	
'IF01_StrNuc_AR_Perc_20'	
'IF01_StrNuc_AR_Perc_25'	
'IF01_StrNuc_AR_Perc_30'	
'IF01_StrNuc_AR_Perc_35'	
'IF01_StrNuc_AR_Perc_40'	
'IF01_StrNuc_AR_Perc_45'	
'IF01_StrNuc_AR_Perc_50'	
'IF01_StrNuc_AR_Perc_55'	
'IF01_StrNuc_AR_Perc_60'	
'IF01_StrNuc_AR_Perc_65'	
'IF01_StrNuc_AR_Perc_70'	
'IF01_StrNuc_AR_Perc_75'	
'IF01_StrNuc_AR_Perc_80'	
'IF01_StrNuc_AR_Perc_85'	
'IF01_StrNuc_AR_Perc_90'	
'IF01_StrNuc_AR_Perc_95'	
'IF01_StrNuc_AR_Perc_99'	
'IF01_StrNuc_AreaTotal'	

'IF01_StrNuc_DAPI_Mean'	
'IF01_StrNuc_Num'	
'IF01_Stroma_AR_Mean'	
'IF01_Stroma_AR_Perc_02'	
'IF01_Stroma_AR_Perc_05'	
'IF01_Stroma_AR_Perc_10'	
'IF01_Stroma_AR_Perc_15'	
'IF01_Stroma_AR_Perc_20'	
'IF01_Stroma_AR_Perc_25'	
'IF01_Stroma_AR_Perc_30'	
'IF01_Stroma_AR_Perc_35'	
'IF01_Stroma_AR_Perc_40'	
'IF01_Stroma_AR_Perc_45'	
'IF01_Stroma_AR_Perc_50'	
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'IF01_Stroma_AR_Perc_60'	
'IF01_Stroma_AR_Perc_65'	
'IF01_Stroma_AR_Perc_70'	
'IF01_Stroma_AR_Perc_75'	
'IF01_Stroma_AR_Perc_80'	
'IF01_Stroma_AR_Perc_85'	
'IF01_Stroma_AR_Perc_90'	
'IF01_Stroma_AR_Perc_95'	
'IF01_Stroma_AR_Perc_99'	
'IFx1_EpiNucARp_AreaTotal'	Normalized Area and intensity features
'IFx1_EpiNucARn_AreaTotal'	
'IFx1_RelAreCyt_AMACRp2Cyt'	
'IFx1_RelAreNGA2Cyt'	
'IFx1_RelAreEpi_ARp2EN'	
'IFx1_RelAreEpi_ARpAMACRp2EN'	
'IFx1_RelAreEpi_ARpAMACRn2EN'	
'IFx1_RelAreEpi_ARnAMACRp2EN'	
'IFx1_RelAreEpi_ARnAMACRn2EN'	
'IFx1_RelAreEpi_Hot22EN'	
'IFx1_RelAreEpi_Hot2EN'	
'IFx1_RelAreEpi_HotAMACRp2EN'	
'IFx1_RelAreEpi_Hot2AMACRp2EN'	
'IFx1_RelAreEpi_HotAMACRn2EN'	
'IFx1_RelAreEpi_Hot2AMACRn2EN'	
'IFx1HotInt_nrmStrNuc85'	
'IFx1_EN_NormARTotIntBin00'	
'IFx1_EN_NormARTotIntBin01'	

'IFx1_EN_NormARTotIntBin02'
'IFx1_EN_NormARTotIntBin03'
'IFx1_EN_NormARTotIntBin04'
'IFx1_EN_NormARTotIntBin05'
'IFx1_EN_NormARTotIntBin06'
'IFx1_EN_NormARTotIntBin07'
'IFx1_EN_NormARTotIntBin08'
'IFx1_EN_NormARTotIntBin09'
'IFx1_EN_NormARTotIntBin10'
'IFx1_Sum_BinEN_ARTotInt01_03'
'IFx1_Sum_BinEN_ARTotInt04_06'
'IFx1_Sum_BinEN_ARTotInt07_09'
'IFx1_EN_ARTotInt_Avg'
'IFx1_RelAre_EpiNucARp_Density01'
'IFx1_RelAre_EpiNucARp_Density02'
'IFx1_RelAre_EpiNucARp_Density03'
'IFx1_RelAre_EpiNucARp_Density04'
'IFx1_RelAre_EpiNucARp_Density05'
'IFx1_RelAre_EpiNucARp_Density06'
'IFx1_RelAre_EpiNucARp_Density07'
'IFx1_RelAre_EpiNucARp_Density08'
'IFx1_RelAre_EpiNucARp_Density09'
'IFx1_RelAre_EpiNucARp_Density10'
'IFx1_Sum_EpiNucARp_Density01_03'
'IFx1_Sum_EpiNucARp_Density04_06'
'IFx1_Sum_EpiNucARp_Density07_09'
'IFx1_RelAre_EpiNuc_Density01'
'IFx1_RelAre_EpiNuc_Density02'
'IFx1_RelAre_EpiNuc_Density03'
'IFx1_RelAre_EpiNuc_Density04'
'IFx1_RelAre_EpiNuc_Density05'
'IFx1_RelAre_EpiNuc_Density06'
'IFx1_RelAre_EpiNuc_Density07'
'IFx1_RelAre_EpiNuc_Density08'
'IFx1_RelAre_EpiNuc_Density09'
'IFx1_RelAre_EpiNuc_Density10'
'IFx1_Sum_EpiNuc_Density01_03'
'IFx1_Sum_EpiNuc_Density04_06'
'IFx1_Sum_EpiNuc_Density07_09'
'IFx1_ExInd_EN_ARp'
'IFx1_RatInt_CytAMACRp2n'
'IFx1_RatInt_AR_EpN2Cyt'

'IFx1_RatiInt_ARp_EpN2Cyt'	
'IFx1_RatiInt_ARp_EpN2CtAMACRp'	
'IFx1_RatiInt_ARp_EpN2CtAMACRn'	
'IFx1_RatInt_ENARpAMACRp2AnAMp'	
'IFx1_RatInt_ENARpAMACRn2AnAMn'	
'IFx1_Rati_EpNARpAMACRp2ART'	
'IFx1_Rati_EpNARpAMACRn2ART'	
'IFx1_Rati_EpNARp2ART'	
'IFx1_Rati_EpNAR2ART'	
'IF01_Rati_EN_Flux_ARp2AR'	
'IF01_Rati_EN_Flux_ARp2ARn'	
'IFx1_ExInd_EN_AMACRp'	
'IFx1_ExInd_EN_AMACRn'	
'IFx1_nExInd_EN_AMACRp'	
'IF01_nExInd_EN_AMACRn'	
'IF01_nExInd_EN_ARp'	
	Dynamic range of AR, difference in epithelial nuclei percentiles relative to stroma nuclei percentiles
'IFx1_RelRise_EpiNuc_AR_StrNuc'	
	Dynamic range of AR, difference in epithelial nuclei percentiles relative to the AR threshold
'IFx1_RelRise_EpiNuc_AR_THR'	
'IF02_AMACR_Threshold'	AMACR Threshold
'IF02_CD34_Area'	
'IF02_CD34ProximalCut05_Area'	Features to detect CD34 proximal to blood vessels
'IF02_CD34Proximal_AMACRn_Area'	
'IF02_CD34Proximal_AMACRp_Area'	
'IF02_CD34Proximal_Area'	
'IF02_CK18_AreaTotal'	
'IF02_CK18_Threshold'	
	Ki67 intensities and percentiles in cytoplasm (CK18)
'IF02_Cyt_Ki67_Mean'	
'IF02_Cyt_Ki67_Perc_02'	
'IF02_Cyt_Ki67_Perc_05'	
'IF02_Cyt_Ki67_Perc_10'	
'IF02_Cyt_Ki67_Perc_15'	
'IF02_Cyt_Ki67_Perc_20'	
'IF02_Cyt_Ki67_Perc_25'	
'IF02_Cyt_Ki67_Perc_30'	

'IF02_Cyt_Ki67_Perc_35'	
'IF02_Cyt_Ki67_Perc_40'	
'IF02_Cyt_Ki67_Perc_45'	
'IF02_Cyt_Ki67_Perc_50'	
'IF02_Cyt_Ki67_Perc_55'	
'IF02_Cyt_Ki67_Perc_60'	
'IF02_Cyt_Ki67_Perc_65'	
'IF02_Cyt_Ki67_Perc_70'	
'IF02_Cyt_Ki67_Perc_75'	
'IF02_Cyt_Ki67_Perc_80'	
'IF02_Cyt_Ki67_Perc_85'	
'IF02_Cyt_Ki67_Perc_90'	
'IF02_Cyt_Ki67_Perc_95'	
'IF02_Cyt_Ki67_Perc_99'	
'IF02_Cyt_pAKT_Mean'	pAKT intensities and percentiles in cytoplasm (CK18)
'IF02_Cyt_pAKT_Perc_02'	
'IF02_Cyt_pAKT_Perc_05'	
'IF02_Cyt_pAKT_Perc_10'	
'IF02_Cyt_pAKT_Perc_15'	
'IF02_Cyt_pAKT_Perc_20'	
'IF02_Cyt_pAKT_Perc_25'	
'IF02_Cyt_pAKT_Perc_30'	
'IF02_Cyt_pAKT_Perc_35'	
'IF02_Cyt_pAKT_Perc_40'	
'IF02_Cyt_pAKT_Perc_45'	
'IF02_Cyt_pAKT_Perc_50'	
'IF02_Cyt_pAKT_Perc_55'	
'IF02_Cyt_pAKT_Perc_60'	
'IF02_Cyt_pAKT_Perc_65'	
'IF02_Cyt_pAKT_Perc_70'	
'IF02_Cyt_pAKT_Perc_75'	
'IF02_Cyt_pAKT_Perc_80'	
'IF02_Cyt_pAKT_Perc_85'	
'IF02_Cyt_pAKT_Perc_90'	
'IF02_Cyt_pAKT_Perc_95'	
'IF02_Cyt_pAKT_Perc_99'	
'IF02_DAPI_Threshold'	
'IF02_EpiNuc_Area'	
'IF02_EpiNuc_Ki67Neg_Area'	Ki67 morphometric and area features in

epithelial nuclei	
'IF02_EpiNuc_Ki67Neg_Ki67_Mean'	
'IF02_EpiNuc_Ki67Neg_Ki67_Std'	
'IF02_EpiNuc_Ki67Pos_Area'	
'IF02_EpiNuc_Ki67Pos_Ki67_Mean'	
'IF02_EpiNuc_Ki67Pos_Ki67_Std'	
'IF02_EpiNuc_Ki67_Mean'	
'IF02_EpiNuc_Ki67_Perc_02'	
'IF02_EpiNuc_Ki67_Perc_05'	
'IF02_EpiNuc_Ki67_Perc_10'	
'IF02_EpiNuc_Ki67_Perc_15'	
'IF02_EpiNuc_Ki67_Perc_20'	
'IF02_EpiNuc_Ki67_Perc_25'	
'IF02_EpiNuc_Ki67_Perc_30'	
'IF02_EpiNuc_Ki67_Perc_35'	
'IF02_EpiNuc_Ki67_Perc_40'	
'IF02_EpiNuc_Ki67_Perc_45'	
'IF02_EpiNuc_Ki67_Perc_50'	
'IF02_EpiNuc_Ki67_Perc_55'	
'IF02_EpiNuc_Ki67_Perc_60'	
'IF02_EpiNuc_Ki67_Perc_65'	
'IF02_EpiNuc_Ki67_Perc_70'	
'IF02_EpiNuc_Ki67_Perc_75'	
'IF02_EpiNuc_Ki67_Perc_80'	
'IF02_EpiNuc_Ki67_Perc_85'	
'IF02_EpiNuc_Ki67_Perc_90'	
'IF02_EpiNuc_Ki67_Perc_95'	
'IF02_EpiNuc_Ki67_Perc_99'	
'IF02_EpiNuc_Ki67_Std'	
'IF02_EpiNuc_Ki67nAMACRn_Area'	Joint Ki67 and AMACR features in epithelial nuclei
'IF02_EpiNuc_Ki67nAMACRn_Ki67_Mn'	
'IF02_EpiNuc_Ki67nAMACRn_Ki67_Std'	
'IF02_EpiNuc_Ki67nAMACRn_Num'	
'IF02_EpiNuc_Ki67nAMACRp_Area'	
'IF02_EpiNuc_Ki67nAMACRp_Ki67_Mn'	
'IF02_EpiNuc_Ki67nAMACRp_Ki67_Std'	
'IF02_EpiNuc_Ki67nAMACRp_Num'	
'IF02_EpiNuc_Ki67nPAKTn_Area'	Joint Ki67 and pAKT features in epithelial nuclei

'IF02_EpiNuc_Ki67nPAKTP_Area'
'IF02_EpiNuc_Ki67pAMACRn_Area'
'IF02_EpiNuc_Ki67pAMACRn_Ki67_Mn'
'IF02_EpiNuc_Ki67pAMACRn_Ki67_Std'
'IF02_EpiNuc_Ki67pAMACRn_Num'
'IF02_EpiNuc_Ki67pAMACRp_Area'
'IF02_EpiNuc_Ki67pAMACRp_Ki67_Mn'
'IF02_EpiNuc_Ki67pAMACRp_Ki67_Std'
'IF02_EpiNuc_Ki67pAMACRp_Num'
'IF02_EpiNuc_Ki67pPAKTn_Area'
'IF02_EpiNuc_Ki67pPAKTP_Area'
'IF02_EpiNuc_Num'

pAKT intensity and morphometric
features

'IF02_EpiNuc_pAKTNeg_pAKT_Mean'
'IF02_EpiNuc_pAKTNeg_pAKT_Std'
'IF02_EpiNuc_pAKTPos_Area'
'IF02_EpiNuc_pAKTPos_pAKT_Mean'
'IF02_EpiNuc_pAKTPos_pAKT_Std'
'IF02_EpiNuc_pAKT_Mean'
'IF02_EpiNuc_pAKT_Perc_02'
'IF02_EpiNuc_pAKT_Perc_05'
'IF02_EpiNuc_pAKT_Perc_10'
'IF02_EpiNuc_pAKT_Perc_15'
'IF02_EpiNuc_pAKT_Perc_20'
'IF02_EpiNuc_pAKT_Perc_25'
'IF02_EpiNuc_pAKT_Perc_30'
'IF02_EpiNuc_pAKT_Perc_35'
'IF02_EpiNuc_pAKT_Perc_40'
'IF02_EpiNuc_pAKT_Perc_45'
'IF02_EpiNuc_pAKT_Perc_50'
'IF02_EpiNuc_pAKT_Perc_55'
'IF02_EpiNuc_pAKT_Perc_60'
'IF02_EpiNuc_pAKT_Perc_65'
'IF02_EpiNuc_pAKT_Perc_70'
'IF02_EpiNuc_pAKT_Perc_75'
'IF02_EpiNuc_pAKT_Perc_80'
'IF02_EpiNuc_pAKT_Perc_85'
'IF02_EpiNuc_pAKT_Perc_90'
'IF02_EpiNuc_pAKT_Perc_95'
'IF02_EpiNuc_pAKT_Perc_99'

'IF02_EpiNuc_pAKT_Std'	
'IF02_EpiNuc_pAKTnAMACRn_Area'	Joint pAKT and AMACR features.
'IF02_EpiNuc_pAKTnAMACRn_Num'	
'IF02_EpiNuc_pAKTnAMACRn_pAKT_Mn'	
'IF02_EpiNuc_pAKTnAMACRn_pAKT_Std'	
'IF02_EpiNuc_pAKTnAMACRp_Area'	
'IF02_EpiNuc_pAKTnAMACRp_Num'	
'IF02_EpiNuc_pAKTnAMACRp_pAKT_Mn'	
'IF02_EpiNuc_pAKTnAMACRp_pAKT_Std'	
'IF02_EpiNuc_pAKTpAMACRn_Area'	
'IF02_EpiNuc_pAKTpAMACRn_Num'	
'IF02_EpiNuc_pAKTpAMACRn_pAKT_Mn'	
'IF02_EpiNuc_pAKTpAMACRn_pAKT_Std'	
'IF02_EpiNuc_pAKTpAMACRp_Area'	
'IF02_EpiNuc_pAKTpAMACRp_Num'	
'IF02_EpiNuc_pAKTpAMACRp_pAKT_Mn'	
'IF02_EpiNuc_pAKTpAMACRp_pAKT_Std'	
'IF02_GU_Area'	
'IF02_Ki67_Percentile'	
'IF02_Ki67_Threshold'	
'IF02_Ki67_Trigger'	
'IF02_NGA_Area'	Non Gland Associated area
'IF02_StrNuc_Area'	
'IF02_StrNuc_Ki67_Mean'	Ki67 features in Stroma Nuclei
'IF02_StrNuc_Ki67_Perc_02'	
'IF02_StrNuc_Ki67_Perc_05'	
'IF02_StrNuc_Ki67_Perc_10'	
'IF02_StrNuc_Ki67_Perc_15'	
'IF02_StrNuc_Ki67_Perc_20'	
'IF02_StrNuc_Ki67_Perc_25'	
'IF02_StrNuc_Ki67_Perc_30'	
'IF02_StrNuc_Ki67_Perc_35'	
'IF02_StrNuc_Ki67_Perc_40'	
'IF02_StrNuc_Ki67_Perc_45'	
'IF02_StrNuc_Ki67_Perc_50'	
'IF02_StrNuc_Ki67_Perc_55'	
'IF02_StrNuc_Ki67_Perc_60'	
'IF02_StrNuc_Ki67_Perc_65'	
'IF02_StrNuc_Ki67_Perc_70'	
'IF02_StrNuc_Ki67_Perc_75'	

'IF02_StrNuc_Ki67_Perc_80'	
'IF02_StrNuc_Ki67_Perc_85'	
'IF02_StrNuc_Ki67_Perc_90'	
'IF02_StrNuc_Ki67_Perc_95'	
'IF02_StrNuc_Ki67_Perc_99'	
'IF02_StrNuc_Num'	
'IF02_StrNuc_pAKT_Mean'	pAKT features in stroma nuclei
'IF02_StrNuc_pAKT_Perc_02'	
'IF02_StrNuc_pAKT_Perc_05'	
'IF02_StrNuc_pAKT_Perc_10'	
'IF02_StrNuc_pAKT_Perc_15'	
'IF02_StrNuc_pAKT_Perc_20'	
'IF02_StrNuc_pAKT_Perc_25'	
'IF02_StrNuc_pAKT_Perc_30'	
'IF02_StrNuc_pAKT_Perc_35'	
'IF02_StrNuc_pAKT_Perc_40'	
'IF02_StrNuc_pAKT_Perc_45'	
'IF02_StrNuc_pAKT_Perc_50'	
'IF02_StrNuc_pAKT_Perc_55'	
'IF02_StrNuc_pAKT_Perc_60'	
'IF02_StrNuc_pAKT_Perc_65'	
'IF02_StrNuc_pAKT_Perc_70'	
'IF02_StrNuc_pAKT_Perc_75'	
'IF02_StrNuc_pAKT_Perc_80'	
'IF02_StrNuc_pAKT_Perc_85'	
'IF02_StrNuc_pAKT_Perc_90'	
'IF02_StrNuc_pAKT_Perc_95'	
'IF02_StrNuc_pAKT_Perc_99'	
'IF02_Stroma_Ki67_Mean'	Ki67 features in Stroma
'IF02_Stroma_Ki67_Perc_02'	
'IF02_Stroma_Ki67_Perc_05'	
'IF02_Stroma_Ki67_Perc_10'	
'IF02_Stroma_Ki67_Perc_15'	
'IF02_Stroma_Ki67_Perc_20'	
'IF02_Stroma_Ki67_Perc_25'	
'IF02_Stroma_Ki67_Perc_30'	
'IF02_Stroma_Ki67_Perc_35'	
'IF02_Stroma_Ki67_Perc_40'	
'IF02_Stroma_Ki67_Perc_45'	
'IF02_Stroma_Ki67_Perc_50'	
'IF02_Stroma_Ki67_Perc_55'	

'IF02_Stroma_Ki67_Perc_60'	
'IF02_Stroma_Ki67_Perc_65'	
'IF02_Stroma_Ki67_Perc_70'	
'IF02_Stroma_Ki67_Perc_75'	
'IF02_Stroma_Ki67_Perc_80'	
'IF02_Stroma_Ki67_Perc_85'	
'IF02_Stroma_Ki67_Perc_90'	
'IF02_Stroma_Ki67_Perc_95'	
'IF02_Stroma_Ki67_Perc_99'	
'IF02_Stroma_pAKT_Mean'	pAKT features in Stroma
'IF02_Stroma_pAKT_Perc_02'	
'IF02_Stroma_pAKT_Perc_05'	
'IF02_Stroma_pAKT_Perc_10'	
'IF02_Stroma_pAKT_Perc_15'	
'IF02_Stroma_pAKT_Perc_20'	
'IF02_Stroma_pAKT_Perc_25'	
'IF02_Stroma_pAKT_Perc_30'	
'IF02_Stroma_pAKT_Perc_35'	
'IF02_Stroma_pAKT_Perc_40'	
'IF02_Stroma_pAKT_Perc_45'	
'IF02_Stroma_pAKT_Perc_50'	
'IF02_Stroma_pAKT_Perc_55'	
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'IF02_Stroma_pAKT_Perc_65'	
'IF02_Stroma_pAKT_Perc_70'	
'IF02_Stroma_pAKT_Perc_75'	
'IF02_Stroma_pAKT_Perc_80'	
'IF02_Stroma_pAKT_Perc_85'	
'IF02_Stroma_pAKT_Perc_90'	
'IF02_Stroma_pAKT_Perc_95'	
'IF02_Stroma_pAKT_Perc_99'	
'IF02_Tumor_Area'	
'IF02_pAKT_Threshold'	
'IFx2_RelAreEN_Ki67p_Area2EN'	Normalized area features
'IFx2_RelAreEN_Ki67p_Area2MDT'	
'IFx2_RelAreEN_Ki67p_Area2GU'	
'IFx2_RelAreEN_Ki67pAMACRp2EN'	
'IFx2_RelAreEN_Ki67pAMACRn2EN'	
'IFx2_RelAreEN_Ki67nAMACRp2EN'	
'IFx2_RelAreEN_Ki67nAMACRn2EN'	
'IFx2_RelAreEN_pAKTp2_Area2EN'	

'IFx2_RelAreEN_pAKTp_Area2MDT'	
'IFx2_RelAreEN_pAKTp_Area2GU'	
'IFx2_RelAreEN_pAKTpAMACRp2EN'	
'IFx2_RelAreEN_pAKTpAMACRn2EN'	
'IFx2_RelAreEN_pAKTnAMACRp2EN'	
'IFx2_RelAreEN_pAKTnAMACRn2EN'	
'IFx2_sumRelAreEN_Ki67_pAKT'	
'IFx2_RelAre_GU2MDT'	
'IFx2_RelAre_CK182MDT'	
'IFx2_RelAre_EN_Ki67nPAKTn2EN'	
'IFx2_RelAre_EN_Ki67nPAKTp2EN'	
'IFx2_RelAre_EN_Ki67pPAKTn2EN'	
'IFx2_RelAre_EN_Ki67pPAKTp2EN'	
'IFx2_RelAre_EN_Ki67nPAKTn2GU'	
'IFx2_RelAre_EN_Ki67nPAKTp2GU'	
'IFx2_RelAre_EN_Ki67pPAKTn2GU'	
'IFx2_RelAre_EN_Ki67pPAKTp2GU'	
'IFx2_RelAre_EN_Ki67nPAKTn2MDT'	
'IFx2_RelAre_EN_Ki67nPAKTp2MDT'	
'IFx2_RelAre_EN_Ki67pPAKTn2MDT'	
'IFx2_RelAre_EN_Ki67pPAKTp2MDT'	
'IFx2_sumRelAreKi67npPAKTpn'	Normalized intensity features
'IFx2_nrmKi67pMean2EpiNucMean'	
'IFx2_nrmKi67pMean2Thrh'	
'IFx2_nrmKi67pMean2StrNucMean'	
'IFx2_nrmKi67pMean2StrNucP50'	
'IFx2_nrmKi67pMean2StrNucP95'	
'IFx2_nrmKi67pAMACRpMean2SNmn'	
'IFx2_nrmKi67pAMACRnMean2SNmn'	
'IFx2_nrmKi67nAMACRpMean2SNmn'	
'IFx2_nrmKi67nAMACRnMean2SNmn'	
'IFx2_nrmKi67pAMACRpMean2Thrh'	
'IFx2_nrmKi67pAMACRnMean2Thrh'	
'IFx2_nrmKi67nAMACRpMean2Thrh'	
'IFx2_nrmKi67nAMACRnMean2Thrh'	
'IFx2_nrmKi67pAMACRpMean2SNp50'	
'IFx2_nrmKi67pAMACRnMean2SNp50'	
'IFx2_nrmKi67nAMACRpMean2SNp50'	
'IFx2_nrmKi67nAMACRnMean2SNp50'	
'IFx2_nrmKi67pAMACRpMean2SNp95'	
'IFx2_nrmKi67pAMACRnMean2SNp95'	
'IFx2_nrmKi67nAMACRpMean2SNp95'	

'IFx2_nrmKi67nAMACRnMean2SNp95'
'IFx2_nrmKi67nMean2Thrh'
'IFx2_nrmKi67EpiNucMean2Thrsh'
'IFx2_nrmEpiNucKi67IntTotal2MDT'
'IFx2_nrmEpiNucKi67pIntTotal2MDT'
'IFx2_nrmEpiNucKi67nIntTotal2MDT'
'IFx2_nrmEpiNucKi67IntTotal2GU'
'IFx2_nrmEpiNucKi67pIntTotal2GU'
'IFx2_nrmEpiNucKi67nIntTotal2GU'
'IFx2_nrmEpiNucKi67IntTotal2EN'
'IFx2_nrmEpiNucKi67pIntTotal2EN'
'IFx2_nrmEpiNucKi67nIntTotal2EN'
'IFx2_RatiEpiNucKi67pInt2MDT'
'IFx2_nrmEpiNuc_Ki67_p02Thrh'
'IFx2_nrmEpiNuc_Ki67_p05Thrh'
'IFx2_nrmEpiNuc_Ki67_p10Thrh'
'IFx2_nrmEpiNuc_Ki67_p15Thrh'
'IFx2_nrmEpiNuc_Ki67_p20Thrh'
'IFx2_nrmEpiNuc_Ki67_p25Thrh'
'IFx2_nrmEpiNuc_Ki67_p30Thrh'
'IFx2_nrmEpiNuc_Ki67_p35Thrh'
'IFx2_nrmEpiNuc_Ki67_p40Thrh'
'IFx2_nrmEpiNuc_Ki67_p45Thrh'
'IFx2_nrmEpiNuc_Ki67_p50Thrh'
'IFx2_nrmEpiNuc_Ki67_p55Thrh'
'IFx2_nrmEpiNuc_Ki67_p60Thrh'
'IFx2_nrmEpiNuc_Ki67_p65Thrh'
'IFx2_nrmEpiNuc_Ki67_p70Thrh'
'IFx2_nrmEpiNuc_Ki67_p75Thrh'
'IFx2_nrmEpiNuc_Ki67_p80Thrh'
'IFx2_nrmEpiNuc_Ki67_p85Thrh'
'IFx2_nrmEpiNuc_Ki67_p90Thrh'
'IFx2_nrmEpiNuc_Ki67_p95Thrh'
'IFx2_nrmEpiNuc_Ki67_p99Thrh'
'IFx2_RelRiseKi67StrNuc'
'IFx2_RelRiseKi67Thrh'
'IFx2_nrmpAKTpMean2EpiNucMean'
'IFx2_nrmpAKTpMean2Thrh'
'IFx2_nrmpAKTpMean2StrNucMean'
'IFx2_nrmpAKTpMean2StrNucP50'
'IFx2_nrmpAKTpMean2StrNucP95'
'IFx2_nrmpAKTpAMACRpMean2SNmn'

'IFx2_nrmpAKTpAMACRpMean2Thrh'	
'IFx2_nrmpAKTpAMACRpMean2SNp50'	
'IFx2_nrmpAKTpAMACRpMean2SNp95'	
'IFx2_nrmpAKTEpiNucMean2Thrsh'	
'IFx2_nrmEpiNucpAKTIntTotal2MDT'	
'IFx2_nrmEpiNucpAKTIntTotal2GU'	
'IFx2_nrmEpiNucpAKTIntTotal2EN'	
'IFx2_nrmEpiNuc_pAKT_p02Thrh'	
'IFx2_nrmEpiNuc_pAKT_p05Thrh'	
'IFx2_nrmEpiNuc_pAKT_p10Thrh'	
'IFx2_nrmEpiNuc_pAKT_p15Thrh'	
'IFx2_nrmEpiNuc_pAKT_p20Thrh'	
'IFx2_nrmEpiNuc_pAKT_p25Thrh'	
'IFx2_nrmEpiNuc_pAKT_p30Thrh'	
'IFx2_nrmEpiNuc_pAKT_p35Thrh'	
'IFx2_nrmEpiNuc_pAKT_p40Thrh'	
'IFx2_nrmEpiNuc_pAKT_p45Thrh'	
'IFx2_nrmEpiNuc_pAKT_p50Thrh'	
'IFx2_nrmEpiNuc_pAKT_p55Thrh'	
'IFx2_nrmEpiNuc_pAKT_p60Thrh'	
'IFx2_nrmEpiNuc_pAKT_p65Thrh'	
'IFx2_nrmEpiNuc_pAKT_p70Thrh'	
'IFx2_nrmEpiNuc_pAKT_p75Thrh'	
'IFx2_nrmEpiNuc_pAKT_p80Thrh'	
'IFx2_nrmEpiNuc_pAKT_p85Thrh'	
'IFx2_nrmEpiNuc_pAKT_p90Thrh'	
'IFx2_nrmEpiNuc_pAKT_p95Thrh'	
'IFx2_nrmEpiNuc_pAKT_p99Thrh'	
'IFx2_RelRisepAKTStrNuc'	
'IFx2_RelRisepAKTThrh'	
'IFx2_RelArea_EpiNuc2Cyt'	
'IFx2_RelAreCD34_ProxArea2EN'	Normalizations of CD34 proximal area to blood vessels
'IFx2_RelAreCD34_ProxAMACRn2EN'	
'IFx2_RelAreCD34_ProxAMACRp2EN'	
'IFx2_RelAreCD34_ProxArea2CK18'	
'IFx2_RelAreCD34_ProxAMACRn2CK18'	
'IFx2_RelAreCD34_ProxAMACRp2CK18'	
'IFx2_RelAre_CD34Prox2CD34'	
'IFx2_RelAre_CD34ProxAMACRn2CD34'	
'IFx2_RelAre_CD34ProxAMACRp2CD34'	

'IFx2_RelAre_Ki67PosArea2CD34'
'IFx2_RelAre_pAKTPosArea2CD34'
'IFx2_RelAr_CD34Proxcut052EN'
'IFx2_RelAr_CD34Proxcut052MDT'
'IFx2_RelAreCD34_ProxArea2EN'
'IFx2_RelAreCD34_ProxAMACRn2EN'
'IFx2_RelAreCD34_ProxAMACRp2EN'
'IFx2_RelAreCD34_ProxArea2CK18'

Table 4. Clinical Features

Feature
Number of total biopsy cores
Percent of positive biopsy cores
Age
Length of tumor in biopsy cores
Percent of tumor in biopsy cores
Clinical Stage
PSA
Dominant Gleason Grade
Secondary Gleason Grade
Gleason Sum

What is claimed is:

1. A system for evaluating a pathological stage of a patient with respect to prostate cancer, the system comprising:

- (1) a fluorescence imaging device configured to record at least one sample image of at least one tissue sample of a patient, the tissue sample treated with a plurality of fluorochrome labeled antibodies, wherein the antibodies are selected to bind with at least androgen receptor and Ki67;
- (2) a database configured to store a dataset containing clinical feature data values for the patient corresponding to at least a value indicative of a biopsy Gleason score (bGS) and a biopsy Gleason grade (bGG) of the patient obtained from a tissue sample of the patient and a value indicative of a blood concentration level of Prostate Specific Antigen (PSA) in the patient;
- (3) a processor configured by code executing therein to implement one or more image analysis applications to evaluate the at least one sample image recorded by the imaging device and generate:
 - (i) molecular feature values indicative of a measurement of expression of androgen receptor (AR) in epithelial nuclei and stromal nuclei (combined androgen receptor dynamic range) where the bGG value is ≤ 3 , and a total Ki67 where the bGG value is ≥ 4 by applying at least a segmentation analysis to the sample image using a quad-tree function to differentiate the sample image into background and non-background objects where the background objects have an average pixel intensity below a predetermined threshold; and
 - (ii) a plurality of morphometric measurements, including: (a) a ratio of area of epithelial nuclei outside gland units to area of epithelial nuclei within gland units, and (b) an area of epithelial nuclei distributed away from gland units;

wherein generation of the plurality of morphometric measurements includes:

- (i) identification within the at least one sample image of a lumen object where the lumen object has an average pixel intensity value above a pre-determined threshold and identification of one or more regions in proximity to the lumen object as a neighboring region where the average pixel intensity of the neighboring region is less than the lumen object;
- (ii) classification of the lumen as a seed object where the relative brightness of the lumen to the neighboring regions is 0.66 or more;
- (iii) combination of the seed object with a neighboring region having an average pixel intensity that is less than the pixel intensity of the seed object to form a merged object,
- (iv) classification of the merged object as a nuclei where the merged object has at least a length < 25 pixels;

the processor further configured to combine the molecular feature values, morphometric measurements and clinical feature data values into a patient dataset and evaluate the patient dataset with a Support Vector Regression for Censored Data (SVRc) analytic tool, where the SVRc analytic tool:

- (a) configures the processor to output a model value corresponding to the probability that a favorable pathological stage will assume a value of 1 according to a support vector regression model generated from a population dataset, where each member of the population has data corresponding to the clinical feature data values, molecular feature values and morphometric measurements of the patient dataset, and where the population includes members where a cancer indolence status is known and members

where a cancer indolence status is unknown, and the model is configured to implement a first loss function on the unknown outcome data such that:

$$\text{Loss}(f(x), y, s=1) = \begin{cases} C_s^* (e - \epsilon_s^*) & e > \epsilon_s^* \\ 0 & -\epsilon_s \leq e \leq \epsilon_s^* \\ C_s (\epsilon_s - e) & e < -\epsilon_s \end{cases}$$

where $e=f(x)-y$; and ϵ and C values differentiate the penalties incurred for $f(x)>0$ versus $f(x)<0$; and a second loss function on the known outcome data such that:

$$\text{Loss}(f(x), y, s=0) = \begin{cases} C_n^* (e - \epsilon_n^*) & e > \epsilon_n^* \\ 0 & -\epsilon_n \leq e \leq \epsilon_n^* \\ C_n (\epsilon_n - e) & e < -\epsilon_n \end{cases}$$

where $e=f(x)-y$ and $\epsilon_n^* \leq \epsilon_n$ and $C_n^* \geq C_n$;

(b) assigns the patient to a high probability of cancer indolence where the output model value is below about 30 and assigns the patient to a low probability of cancer indolence where the model value is above about 30;

(c) generates a report based on the updated patient dataset; and

(d) transmits the report to an output device; and

(4) an output device configured to receive the report from the processor and output the report to a user.

2. The system of claim 1, wherein the morphometric measurement of epithelial nuclei distributed away from gland units comprises a morphometric measurement of the area of

epithelial nuclei with centers in a band located a predetermined distance away from lumen borders.

3. The system of claim 2, wherein the band located a predetermined distance away from the lumen borders comprises the region between three and five units away from a lumen border, wherein a unit is approximately equal to a diameter of one epithelial nucleus.

4. The system of claim 1, wherein the predictive model is generated primarily based on one or more features from each of the molecular feature values, morphometric measurements and clinical feature data values and is further generated based on at least one additional clinical feature, molecular feature, or morphometric measurement.

5. The system of claim 1, wherein the processor is further configured to provide a value indicative of whether the patient is likely to have: (a) a pathological stage as assessed by prostatectomy data of T2 or less, (b) a total Gleason score as assessed at prostatectomy of six or less with each component of the Gleason score being three or less, and (c) a first PSA reading post-prostatectomy of approximately zero.

6. A computer-implemented method for evaluating, with a computing device, a pathological stage of a patient with respect to prostate cancer, the computing device having a processor, a memory, and an occurrence application stored in the memory and executable by the processor, the method comprising the steps of:

- (1) capturing, with a fluorescence imaging device, at least one sample image of a tissue sample treated with a plurality of fluorochrome labeled antibodies, wherein the antibodies are selected to bind with at least androgen receptor and Ki67;
- (2) accessing from a database, using a processor configured by code executing therein, a patient dataset containing clinical feature data values for the patient corresponding to at least a value indicative of a biopsy Gleason score (bGS) and a biopsy Gleason grade (bGG) of the patient obtained from a tissue sample of the patient and a value indicative of a blood concentration_level of Prostate Specific Antigen (PSA) in the patient;

(3) evaluating, using the processor, the at least one sample image recorded by the imaging device and the patient dataset and deriving:

- a. molecular feature values indicative of a measurement of expression of androgen receptor (AR) in epithelial nuclei and stromal nuclei (combined androgen receptor dynamic range) where the bGG value is ≤ 3 , and a total Ki67 where the bGG value is ≥ 4 by applying at least a segmentation analysis to the sample image using a quad-tree function to differentiate the sample image into background and non-background objects where the background objects have an average intensity below a predetermined threshold; and
- b. a plurality of morphometric measurements, including: (a) the ratio of area of epithelial nuclei outside gland units to the area of epithelial nuclei within gland units, and (b) area of epithelial nuclei distributed away from gland units;

wherein deriving the plurality of morphometric measurements includes:

- (i) identifying within the at least one sample image a lumen object where the lumen object has an average pixel intensity value above a pre-determined threshold and identifying one or more regions in proximity to the lumen object as a neighboring region where the average pixel intensity of the neighboring region is less than the lumen object;
- (ii) classifying the lumen as a seed object where the relative brightness of the lumen to the neighboring regions is 0.66 or more;
- (iii) merging the seed object with neighboring region having an average pixel intensity that is less than the pixel intensity of the seed object to form a merged object,

- (iv) classifying the merged object as a nuclei where the merged object has at least a length < 25 pixels;
- (4) updating the patient dataset, using the processor, to include the derived molecular feature values and morphometric measurements;
- (5) evaluating, using the processor, the patient dataset with a Support Vector Regression for Censored Data (SVRc) analytic tool configured as code executing in the processor, where the SVRc analytic tool configures the processor to output a model value corresponding to a risk score for cancer progression according to a support vector regression model generated from a population dataset, where each member of the population has data corresponding to the clinical, molecular and morphometric features of the patient dataset, and where the population includes members where a final health outcome is known (uncensored) and members where the final health outcome is unknown (censored), and the model is configured to evaluate the patient dataset according to the following:

$$\min (W, b) \quad 1/2 \| W \|^2 + \sum_{i=1}^n (C_i \xi_i + C *_{\xi} \xi *_{\xi})$$

given the constraints:

$$y_i - (W * \Phi(x_i) + b) \leq \varepsilon_i + \xi_i$$

$$(W * \Phi(x_i) + b) - y_i \leq \varepsilon *_{\xi} + \xi *_{\xi}$$

$$\xi^{(*)}_i \geq 0, i = 1 \dots n$$

where:

$$s_i = 1 \text{ if censored, } s_i = 0 \text{ if uncensored}$$

$$C^{(*)}_i = s_i C^{(*)}_c + (1-s_i) C^{(*)}_n$$

$$\varepsilon^{(*)}_i = s_i \varepsilon^{(*)}_c + (1-s_i) \varepsilon^{(*)}_n$$

- (6) assigning, using the processor, the patient to a high probability of cancer indolence where the output model value is below about 30 and assigning the patient to a low probability of cancer indolence where the model value is above about 30;
- (7) generating, using the processor, a report based on the updated patient dataset;
- (8) transmitting the report to a remote device over a network; and
- (9) receiving, at the remote device the report from the processor.

7. The method of claim 6, wherein the morphometric measurement of epithelial nuclei distributed away from gland units comprises a morphometric measurement of the area of epithelial nuclei with centers in a band located a predetermined distance away from lumen borders.

8. The method of claim 7, wherein the band located a predetermined distance away from the lumen borders comprises the region between three and five units away from a lumen border, where a unit is approximately equal to a diameter of one epithelial nucleus.

9. The method of claim 6, wherein the model predictive of favorable pathological stage of prostate cancer is predictive of whether the patient is likely to have a pathological stage as assessed by prostatectomy data of T2 or less, a total Gleason score as assessed at prostatectomy of six or less with each component of the Gleason score being three or less, and having a first PSA reading post-prostatectomy of approximately zero.

10. A computer readable medium comprising computer executable instructions recorded thereon for performing the method comprising:

evaluating a dataset for a patient with a model predictive of favorable pathological stage of prostate cancer, wherein the model is based on one or more features selected from the following group of features:

- (1) accessing from a database, using a processor configured by code executing therein, a patient dataset containing clinical feature data values for the patient corresponding to

at least a value indicative of a biopsy Gleason score (bGS) and a biopsy Gleason grade (bGG) of the patient obtained from a tissue sample of the patient and a value indicative of a blood concentration level of Prostate Specific Antigen (PSA) in the patient and at least one sample image of a tissue sample of the patient treated with a plurality of fluorochrome labeled antibodies, wherein the antibodies are selected to bind with at least androgen receptor and Ki67;

(2) evaluating, using the processor, the at least one sample image recorded by the imaging device and the patient dataset and deriving:

- a. one or more molecular feature values indicative of a measurement of expression of androgen receptor (AR) in epithelial nuclei and stromal nuclei (combined androgen receptor dynamic range) where the bGG values is ≤ 3 , and a total Ki67 where the bGG value is ≥ 4 by applying at least a segmentation analysis to the sample image using a quad-tree function to differentiate the sample image into background and non-background objects where the background objects have an average intensity below a predetermined threshold; and
- b. a plurality of morphometric measurements, including: (a) the ratio of area of epithelial nuclei outside gland units to the area of epithelial nuclei within gland units, and (b) area of epithelial nuclei distributed away from gland units;

wherein deriving the plurality of morphometric measurements includes:

- (i) identifying within the at least one sample image a lumen object where the lumen object has an average pixel intensity value above a pre-determined threshold and identifying one or more regions in proximity to the lumen object as a neighboring region where the average pixel intensity of the neighboring region is less than the lumen object;

- (ii) classifying the lumen as a seed object where the relative brightness of the lumen to the neighboring regions is 0.66 or more;
 - (iii) merging the seed object with neighboring region having an average pixel intensity that is less than the pixel intensity of the seed object to form a merged object,
 - (iv) classifying the merged object as a nuclei where the merged object has at least a length < 25 pixels;
- (3) updating the patient dataset, using the processor, to include the derived molecular feature values and morphometric measurements;
- (4) evaluating, using the processor, the patient dataset with a Support Vector Regression for Censored Data (SVRc) analytic tool configured as code executing in the processor, where the SVRc analytic tool configures the processor to output a model value corresponding to a risk score for cancer progression according to a support vector regression model generated from a population dataset, where each member of the population has data corresponding to the clinical, molecular and morphometric features of the patient dataset, and where the population includes members where a final health outcome is known (uncensored) and members where the final health outcome is unknown (censored), and the model is configured to evaluate the patient dataset according to the following:

$$\min (W, b) \quad 1/2 \|W\|^2 + \sum_{i=1}^n (C_i \xi_i + C^*_{*i} \xi^*_{*i})$$

given the constraints:

$$y_i - (W * \Phi(x_i) + b) \leq \varepsilon_i + \xi_i$$

$$(W * \Phi(x_i) + b) - y_i \leq \varepsilon^*_{*i} + \xi^*_{*i}$$

$$\xi^*_{*i} \geq 0, i = 1 \dots n$$

where:

$s_i = 1$ if censored, $s_i = 0$ if uncensored

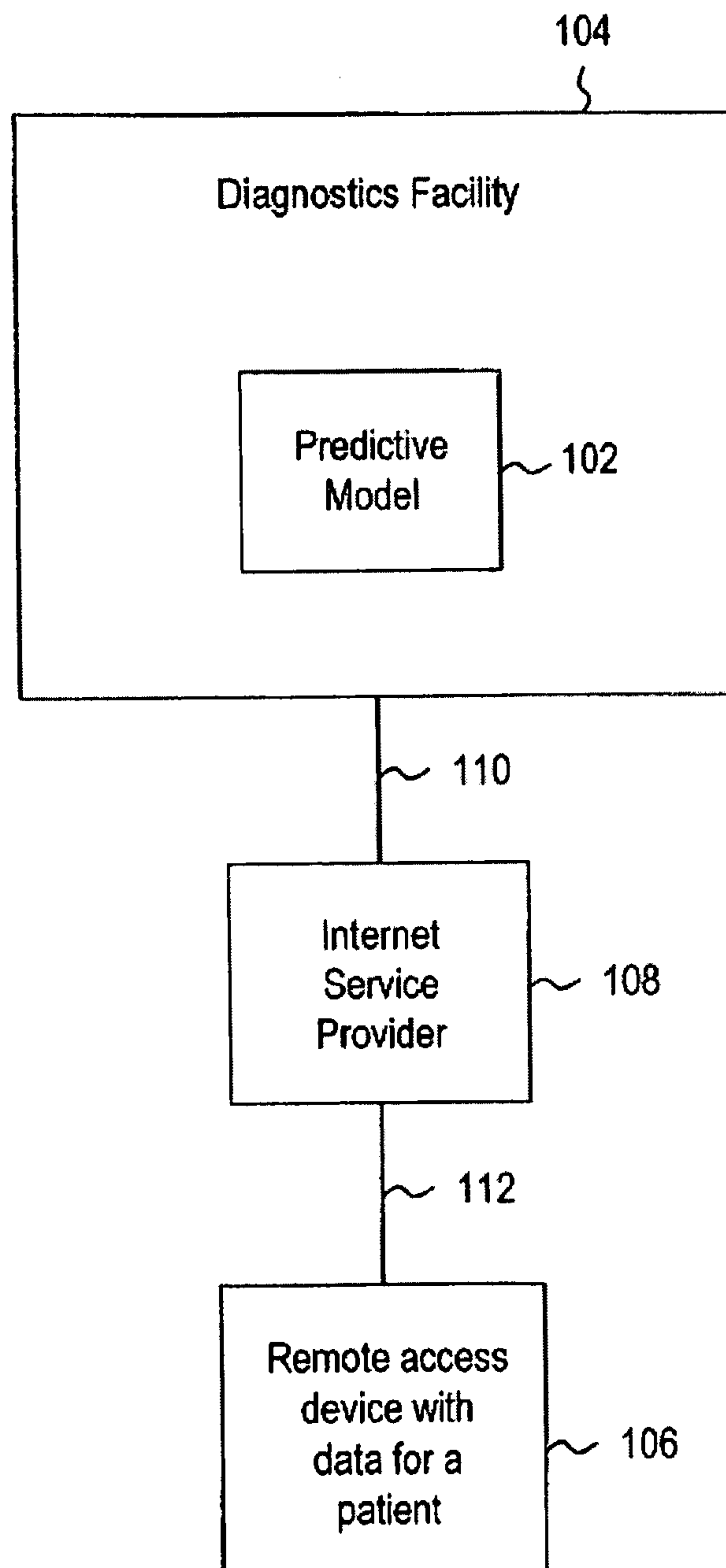
$$C_i^{(*)} = s_i C_c^{(*)} + (1-s_i) C_n^{(*)}$$

$$\varepsilon_i^{(*)} = s_i \varepsilon_c^{(*)} + (1-s_i) \varepsilon_n^{(*)}$$

- (5) assigning, using the processor, the patient to a high probability of cancer indolence where the output model value is below about 30 and assigning the patient to a low probability of cancer indolence where the model value is above about 30;
- (6) generating, using the processor, a report based on the updated patient dataset;
- (7) transmitting the report to a remote device over a network; and
- (8) receiving at the remote device the report from the processor.

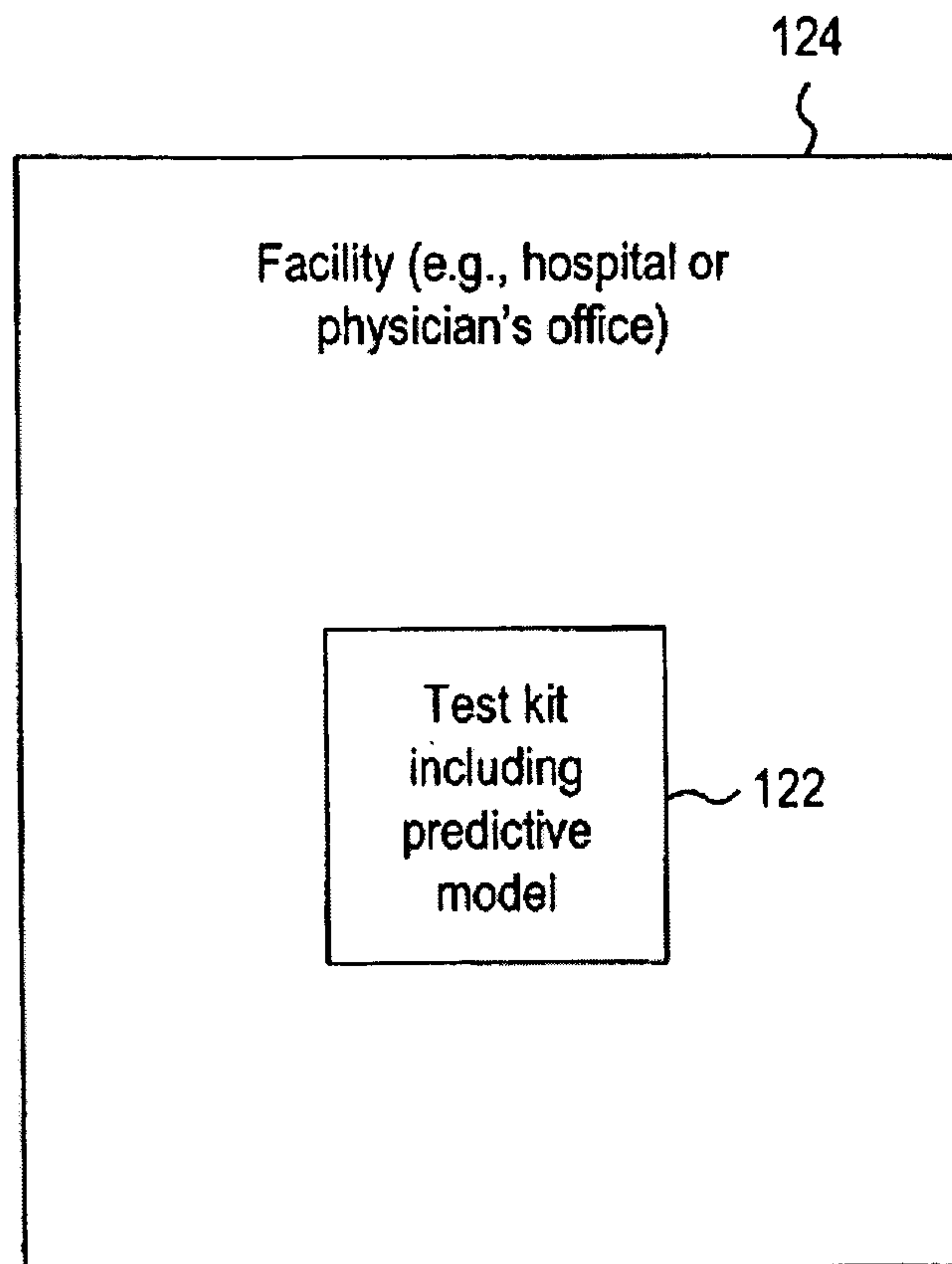
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FIG. 1A



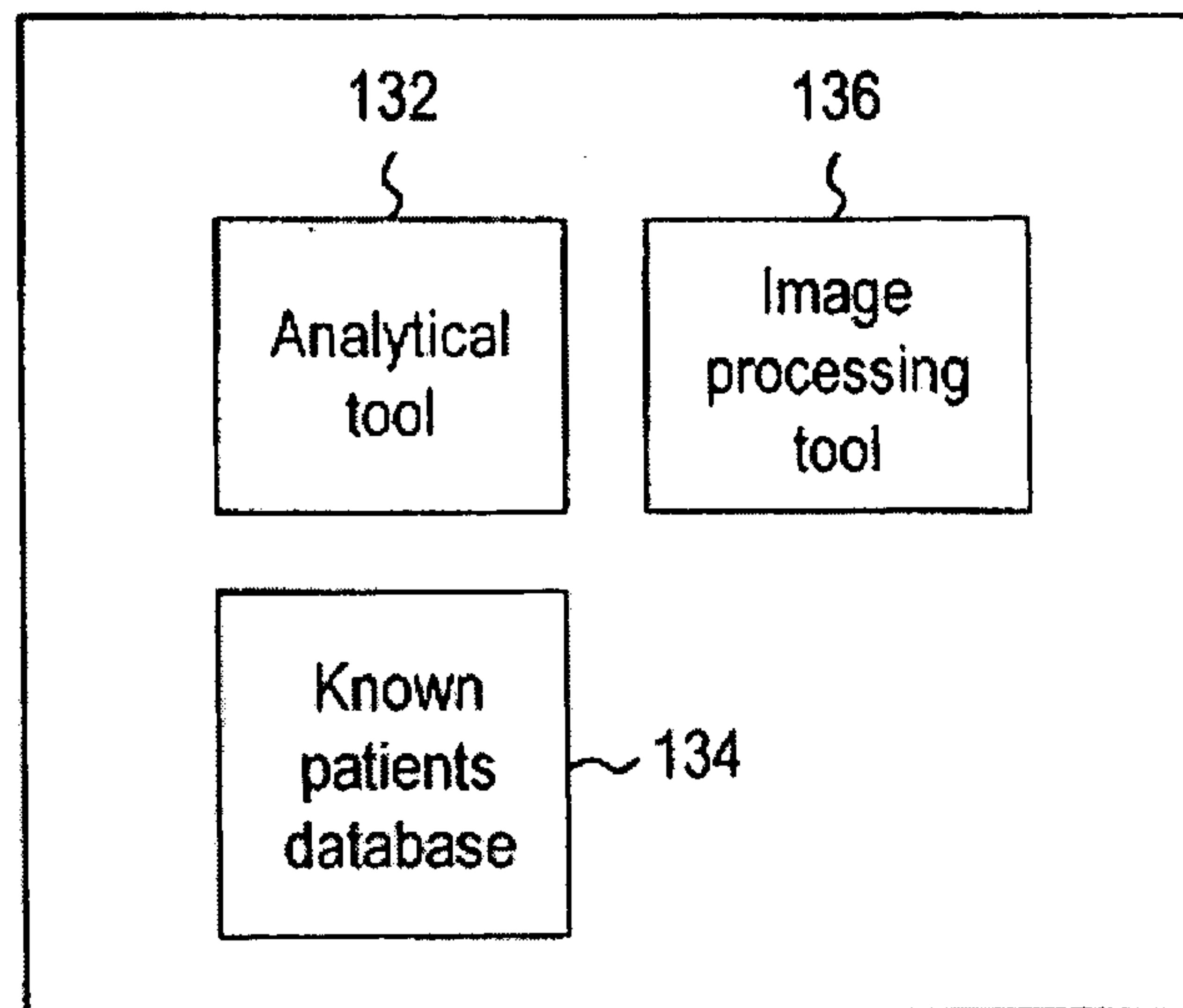
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FIG. 1B



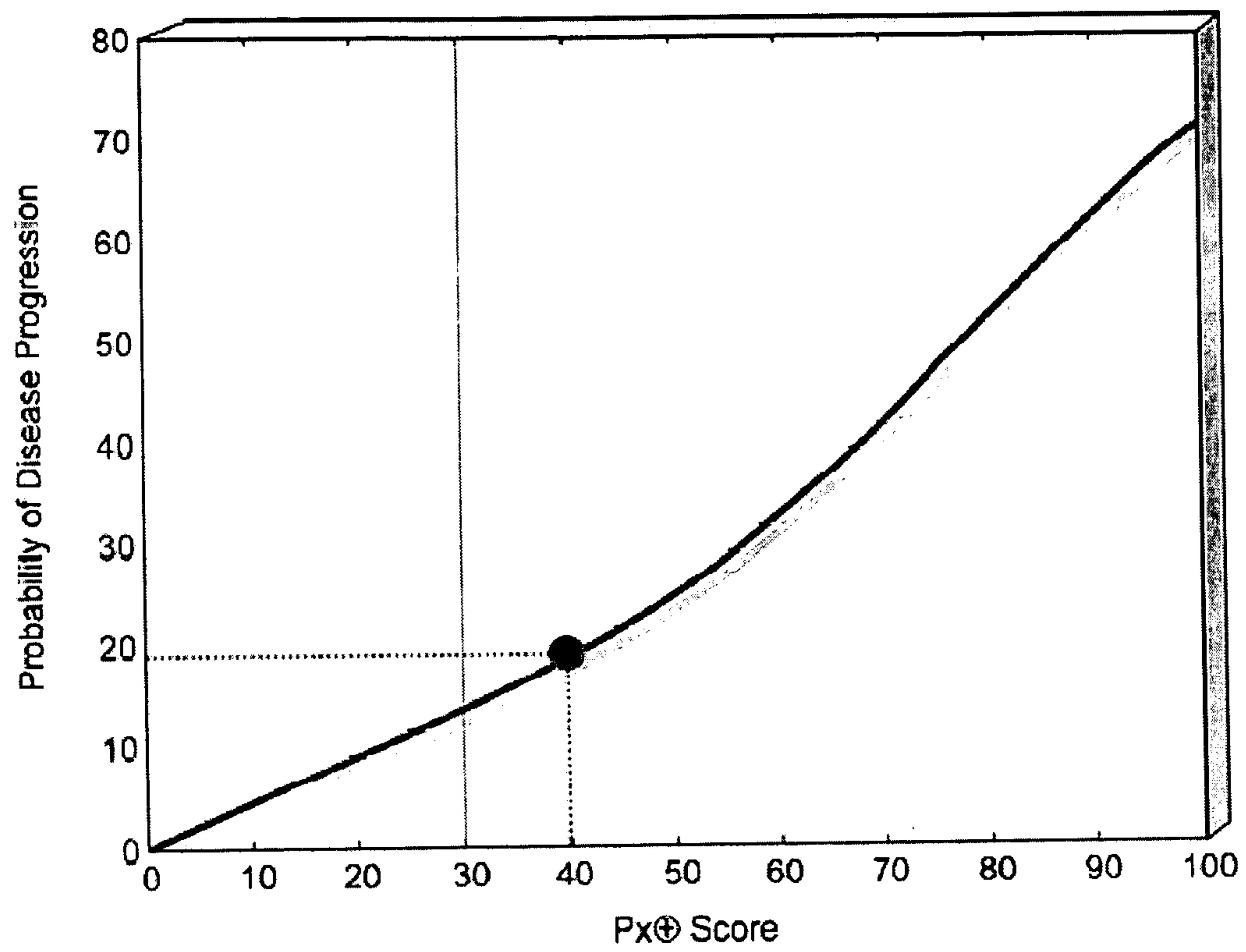
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FIG. 1C



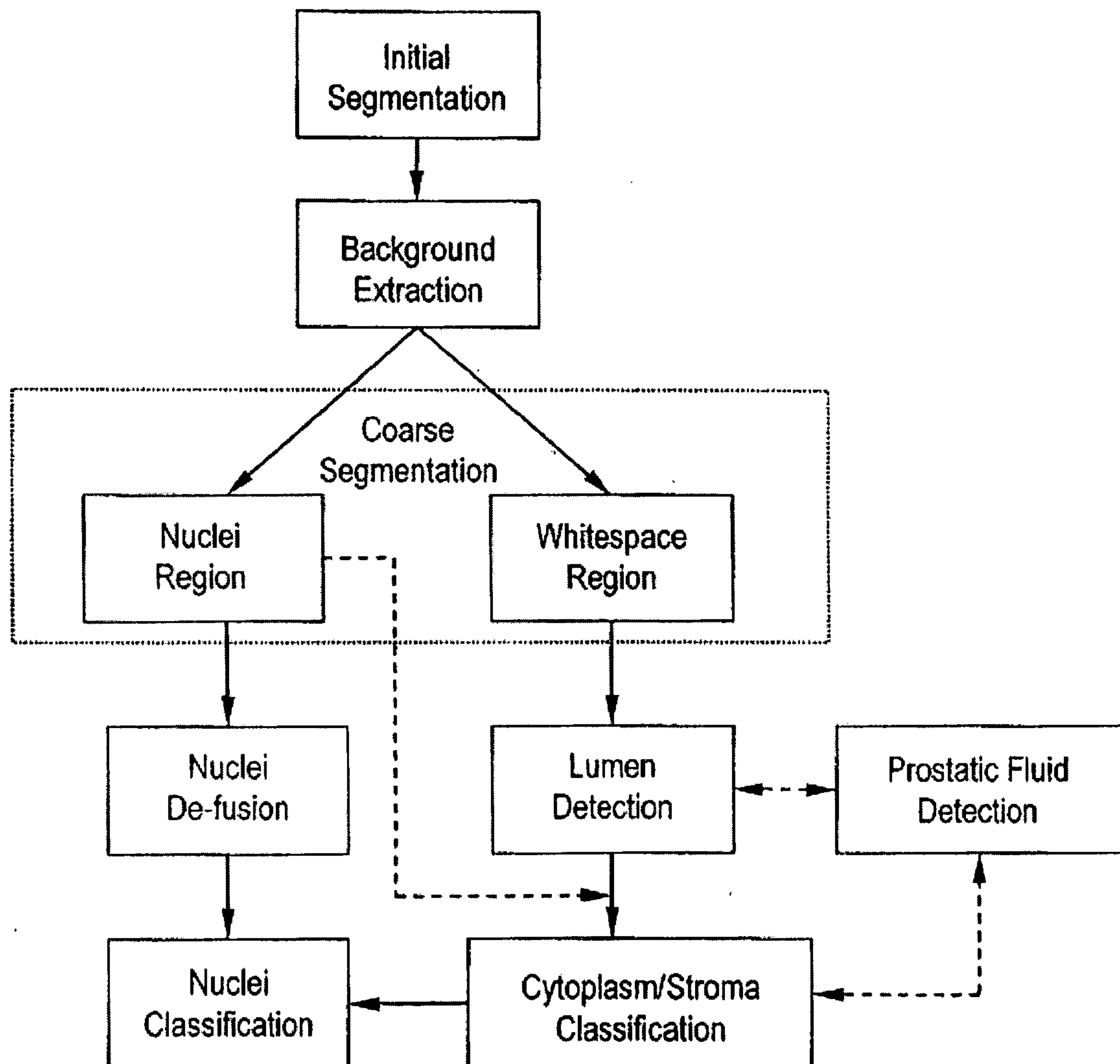
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FIG. 2



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FIG. 3



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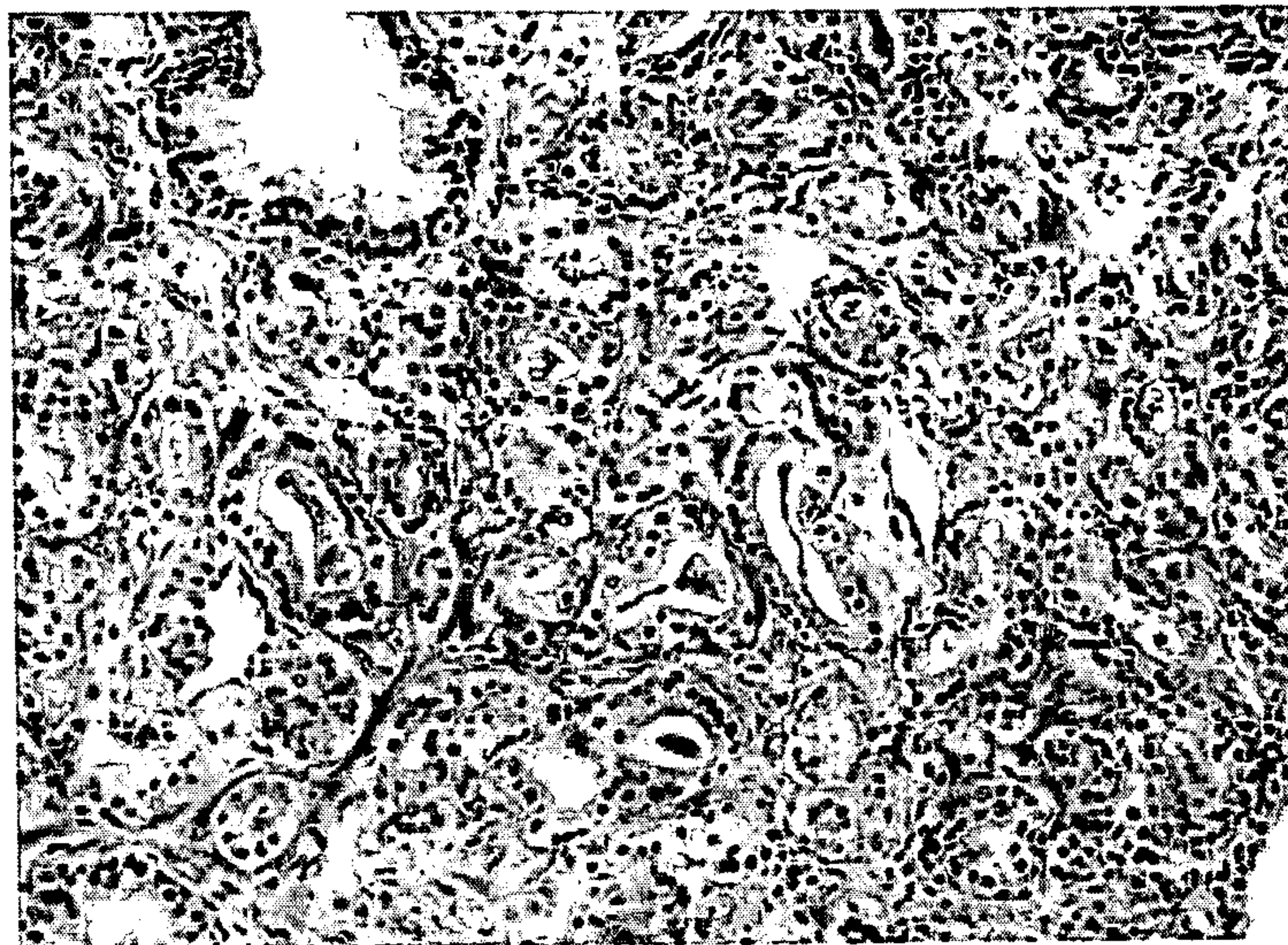


FIG. 4A

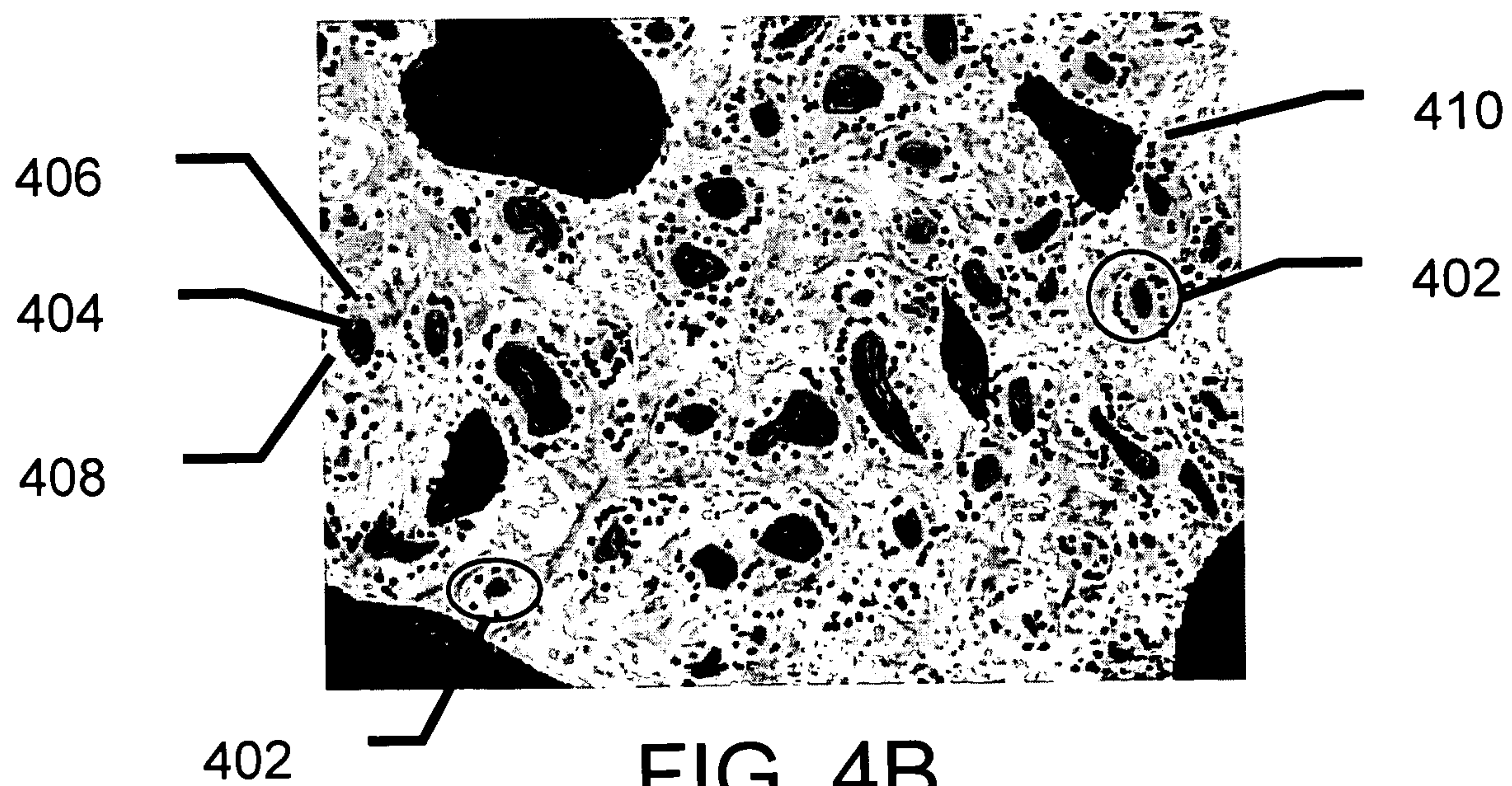


FIG. 4B

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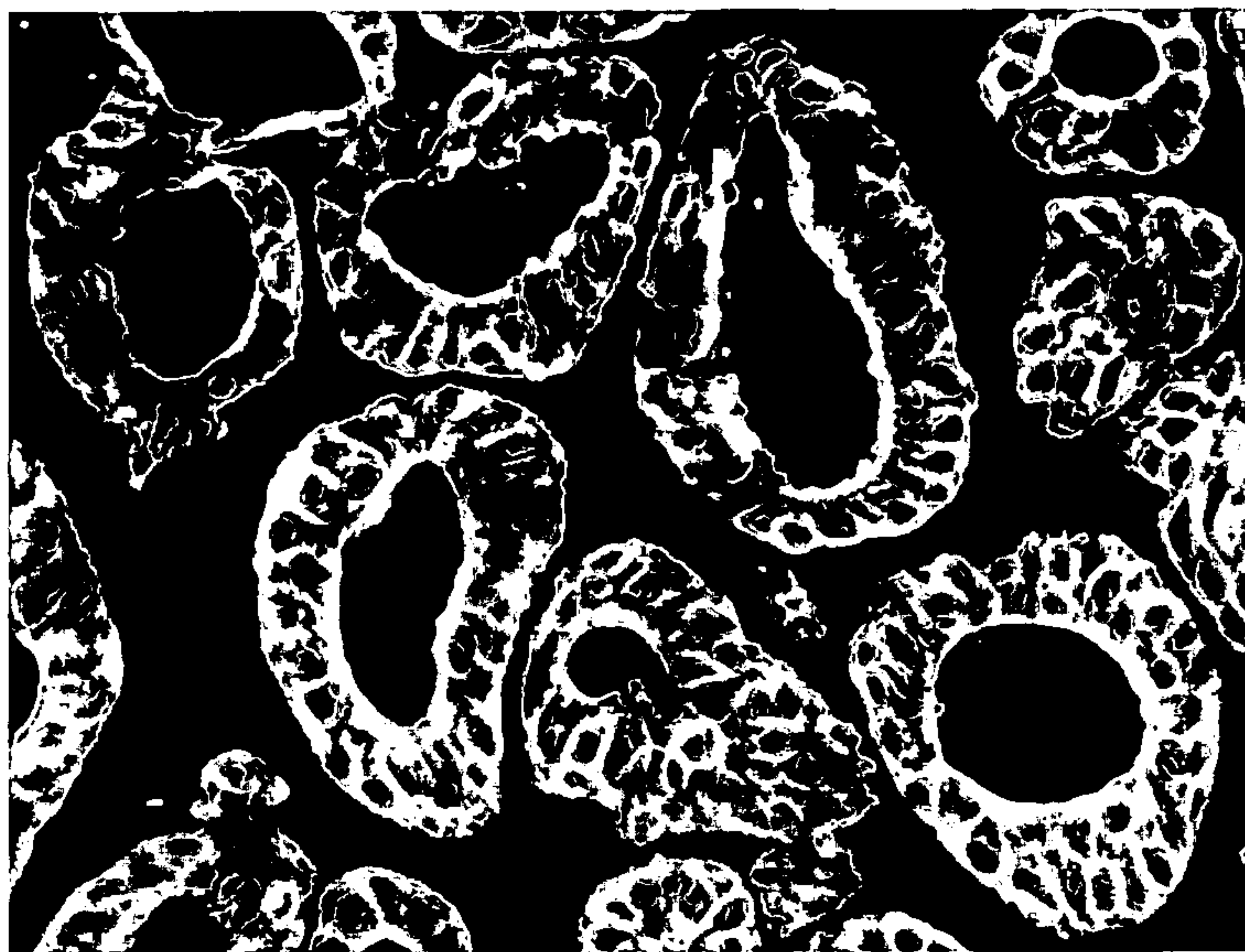


FIG. 5A

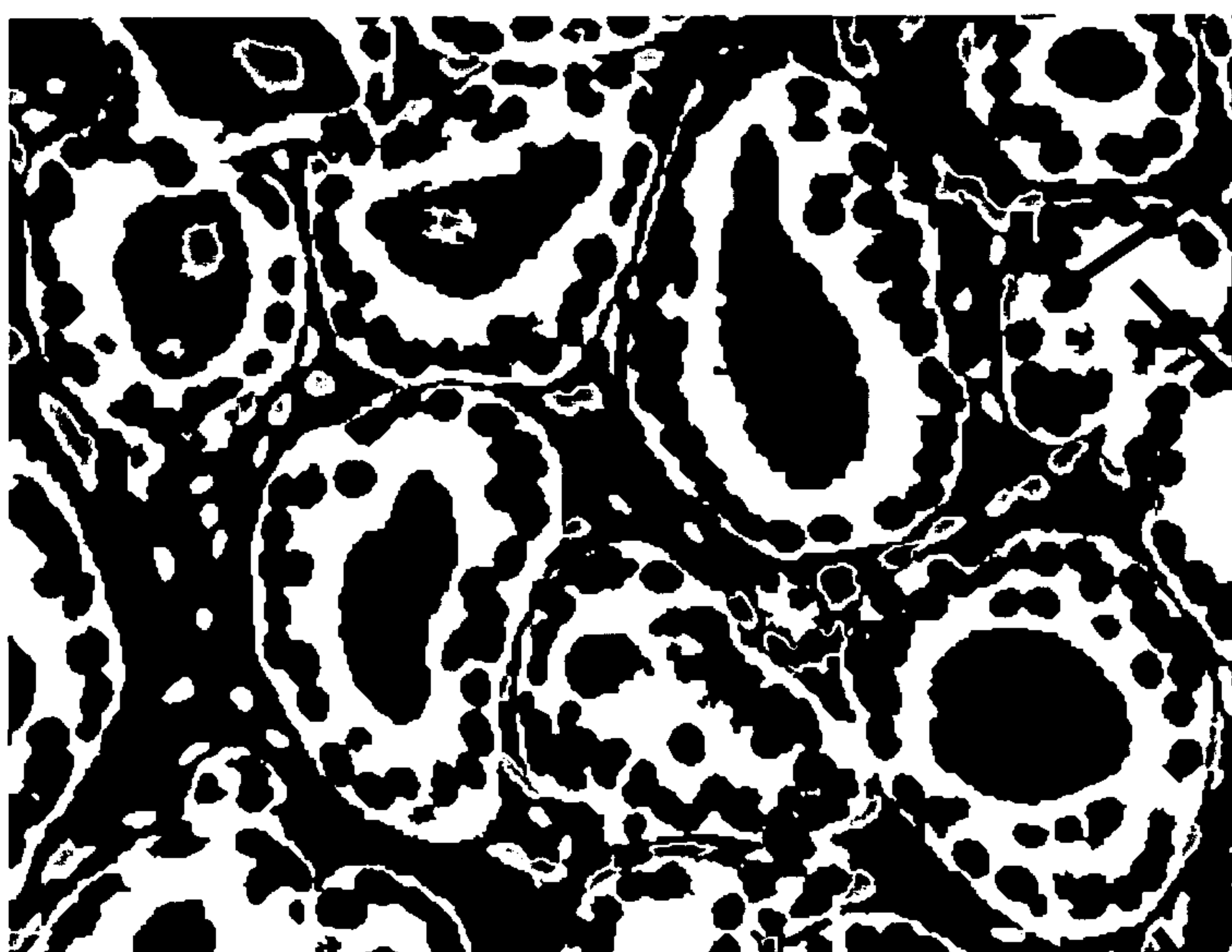


FIG. 5B

502

504

506

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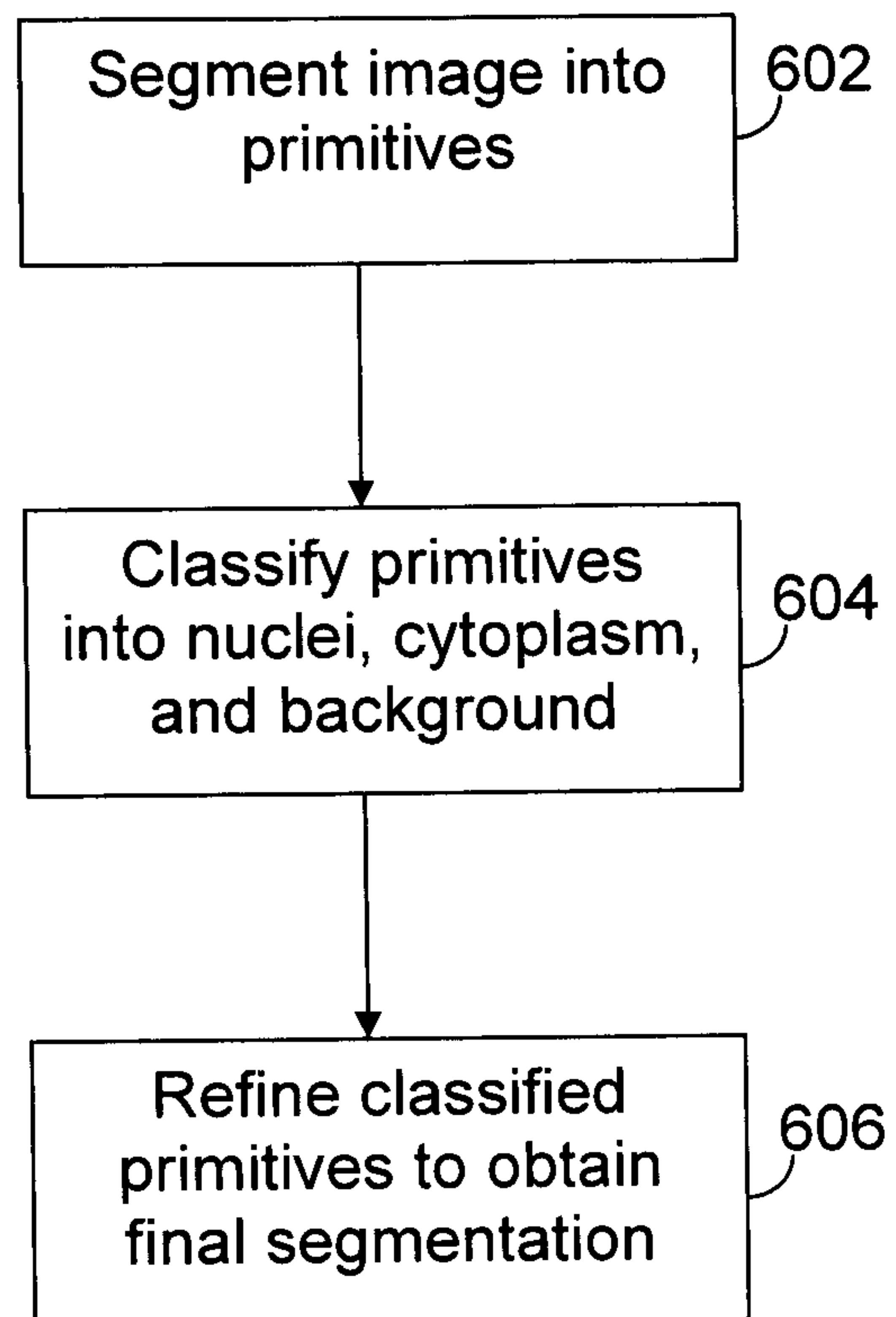
600

FIG. 6

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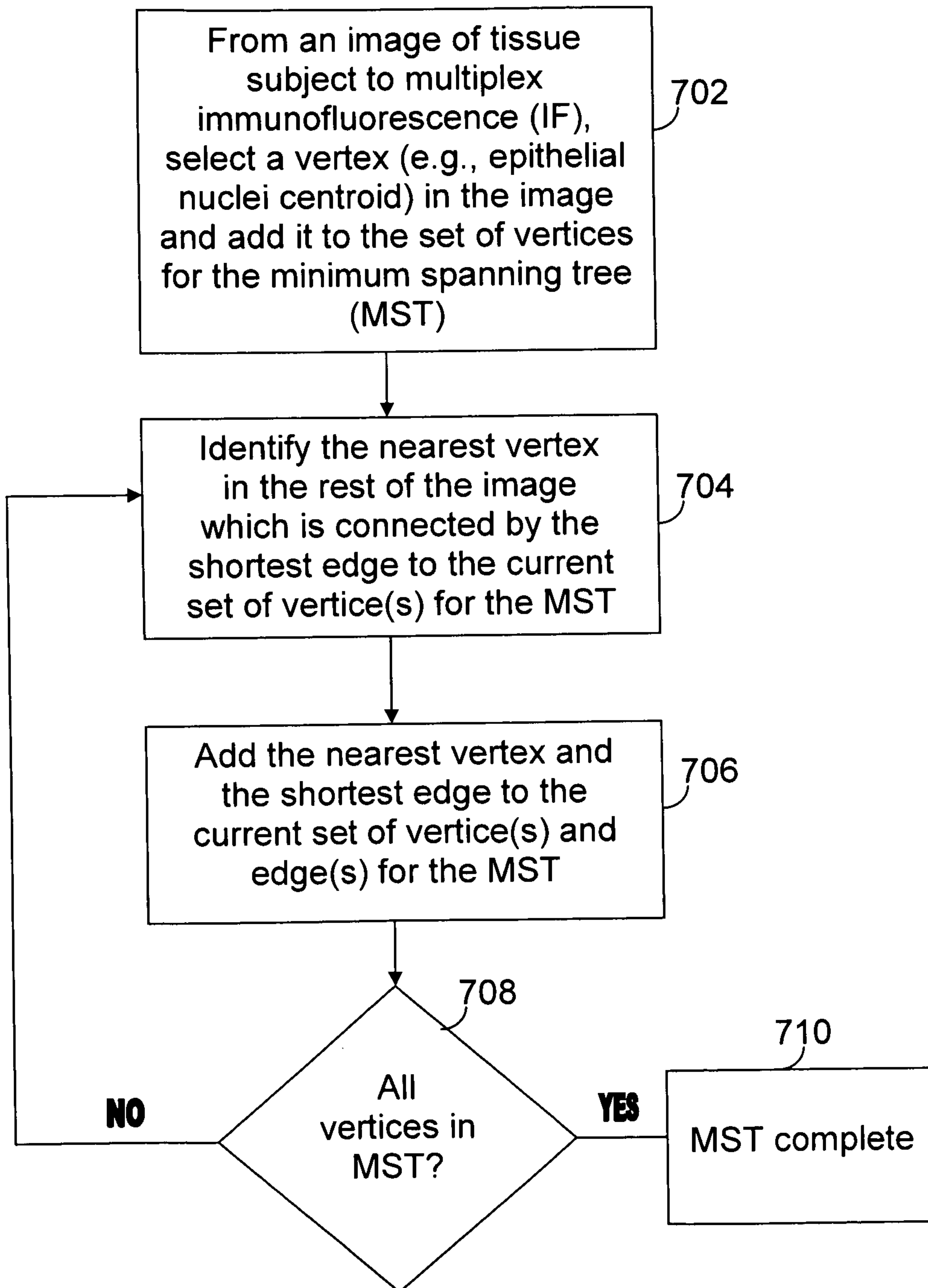
700

FIG. 7

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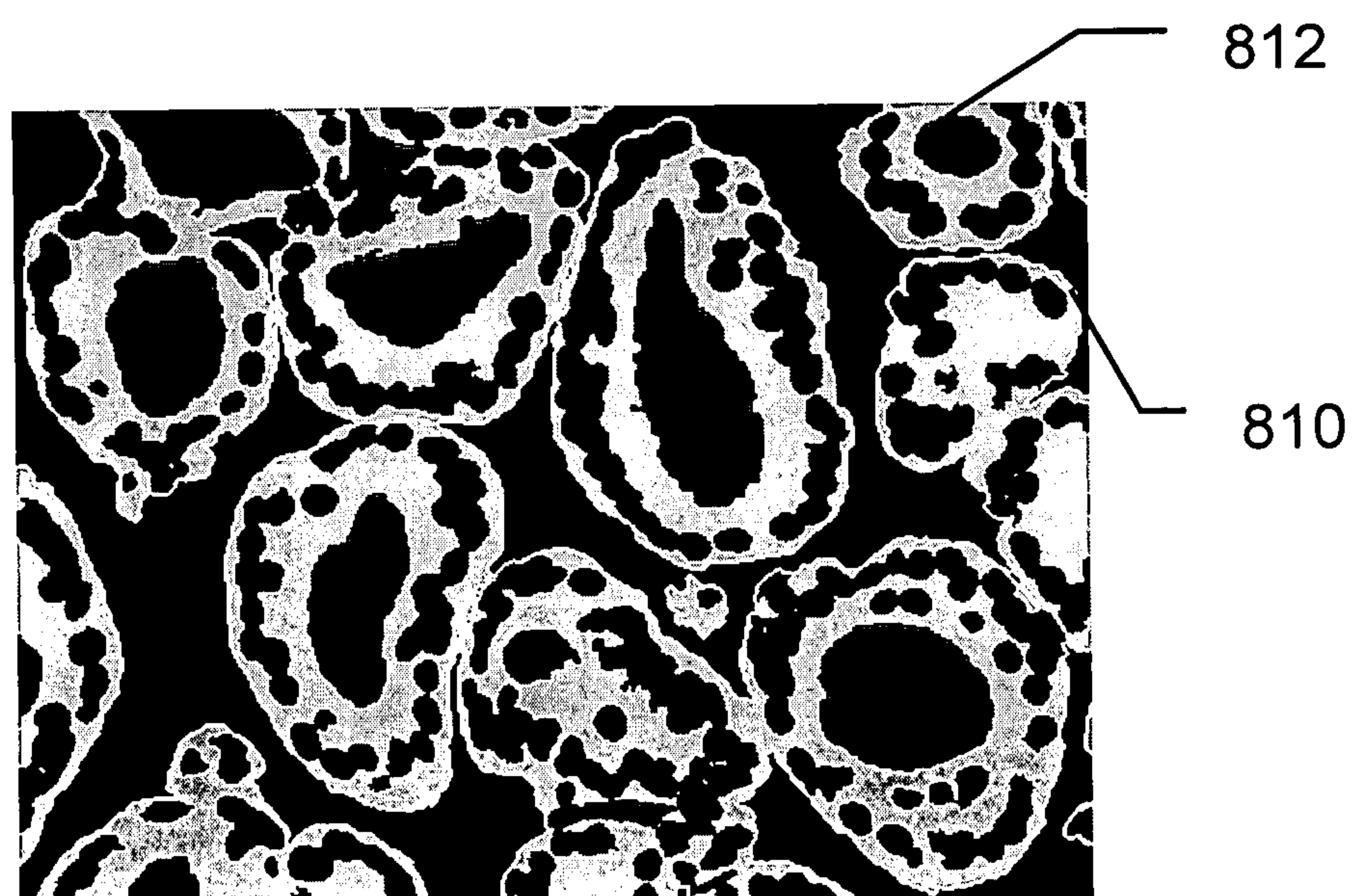
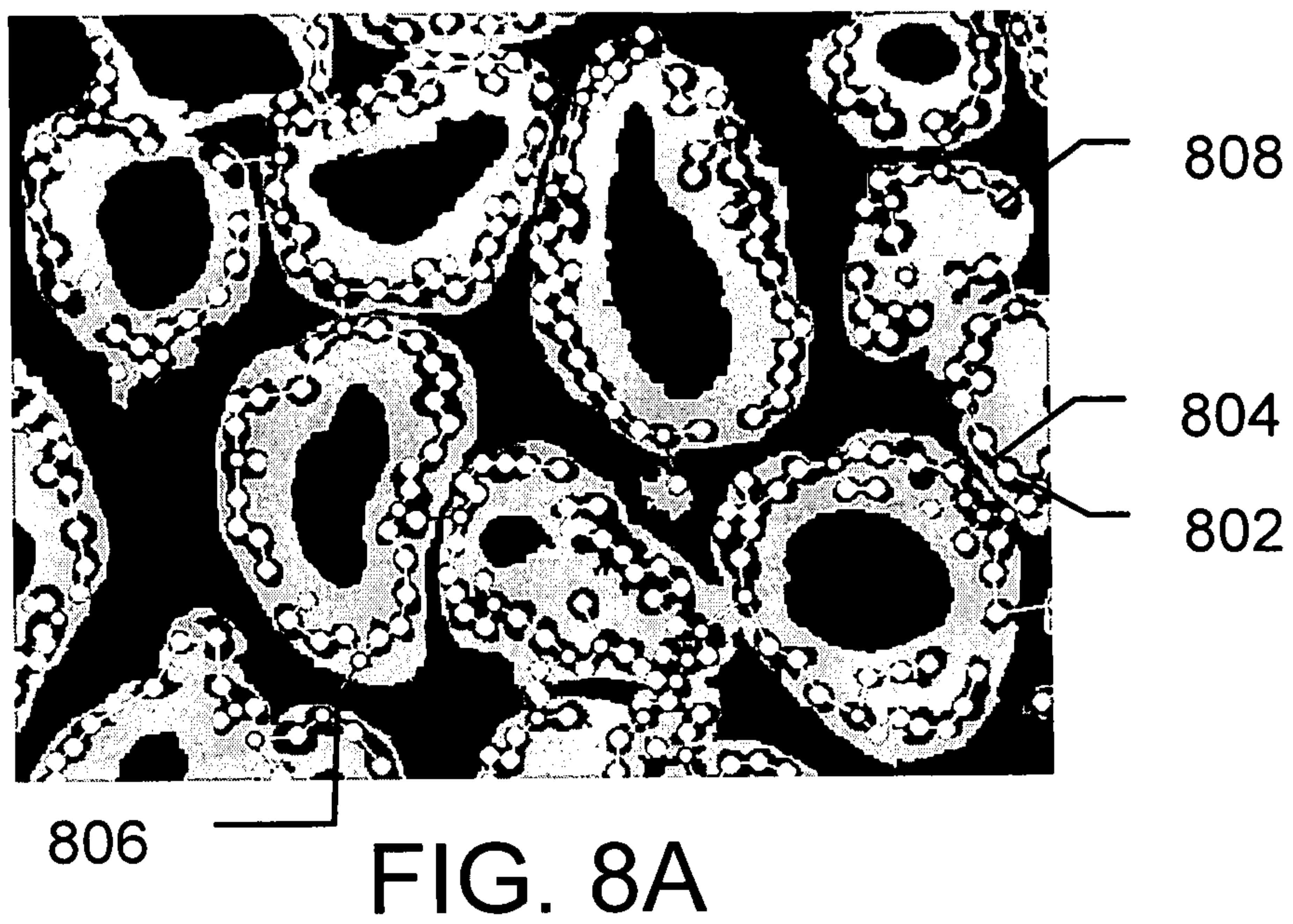


FIG. 8B

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	Feature	χ^2 p-value	CI
FD	Gland Boundaries (w/ Stroma)	< 0.0001	0.348
	Gland Boundaries (All)	< 0.0001	0.343
MST	Mean Edge Length (All)	0.0043	0.416
	Mean Edge Length (Intra-Gland)	0.0044	0.418
	Mean Edge Length (Inter-Gland)	0.3130	0.459
	Std Dev of Edge Lengths (All)	0.1220	0.446
	Std Dev of Edge Lengths (Intra-Gland)	0.0295	0.424
	Std Dev of Edge Lengths (Inter-Gland)	0.2564	0.470
	Degree Distribution for Degree 1 (d_1)	0.0032	0.403
	Degree Distribution for Degree 2 (d_2)	0.0018	0.606
	Degree Distribution for Degree 3 (d_3)	0.0001	0.364
Combined	FD (Gland-Stroma) + Gleason Grade	< 0.0001	0.321
	Mean Edge Length (All) + Gleason Grade	< 0.0001	0.330
	d_3 + Gleason grade	< 0.0001	0.321

FIG. 9

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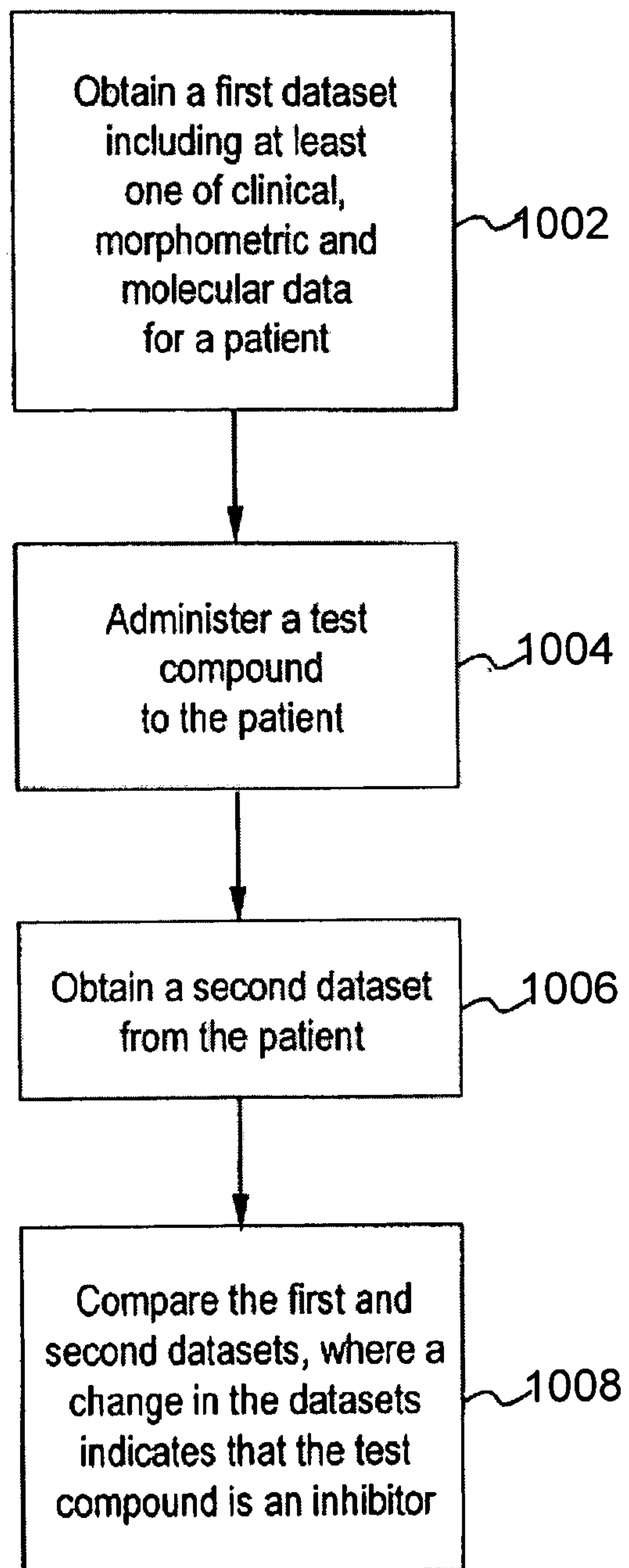
1000

FIG. 10

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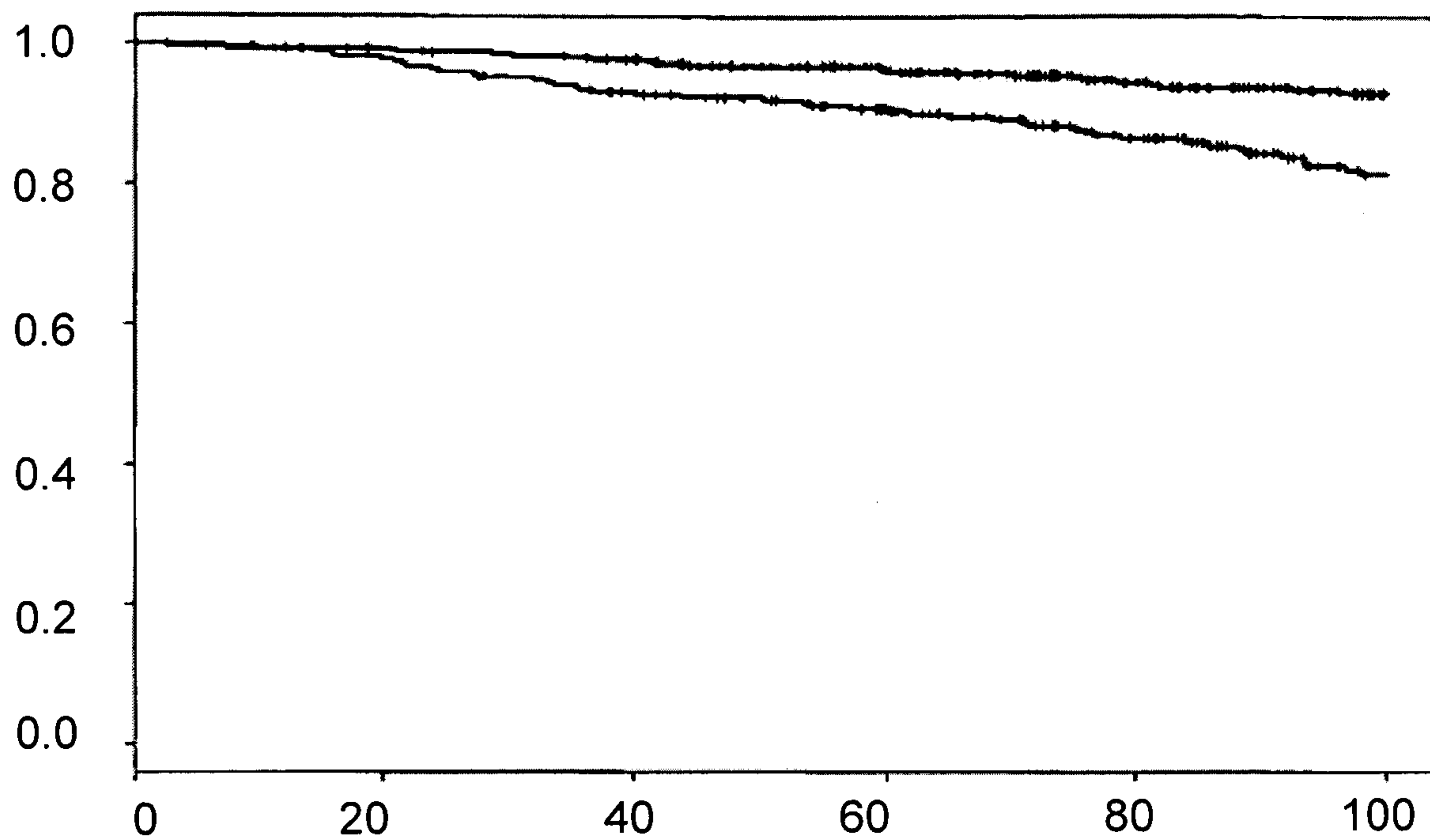
Example 1: Features Selected for Prediction of Disease Progression

Feature	Univariate P Value	Weight in Model
<u>Clinical</u>		
Preoperative PSA	<0.00001	-24.479
Dominant Biopsy Gleason Grade	<0.0001	23.140
Biopsy Gleason Score	<0.00001	-17.512
<u>Molecular (Combined)</u>		
Combined AR Dynamic Range at Low bGG, Total Ki67 at High bGG	<0.00001	-16.005
<u>Morphometric (Combined)</u>		
Combined Mean Distance Between Epithelial Tumor Cells (MST) at Low bGG, Actual Grade at High bGG	<0.00001	-13.521
<u>Morphometric</u>		
Area of Isolated (Non-Lumen Associated) Tumor Epithelial Cells Relative to Total Tumor Area	<0.00001	-6.852

FIG. 11

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Feature: Area of Isolated (Non-Lumen Associated) Tumor Epithelial Cells Relative to Total Tumor Area



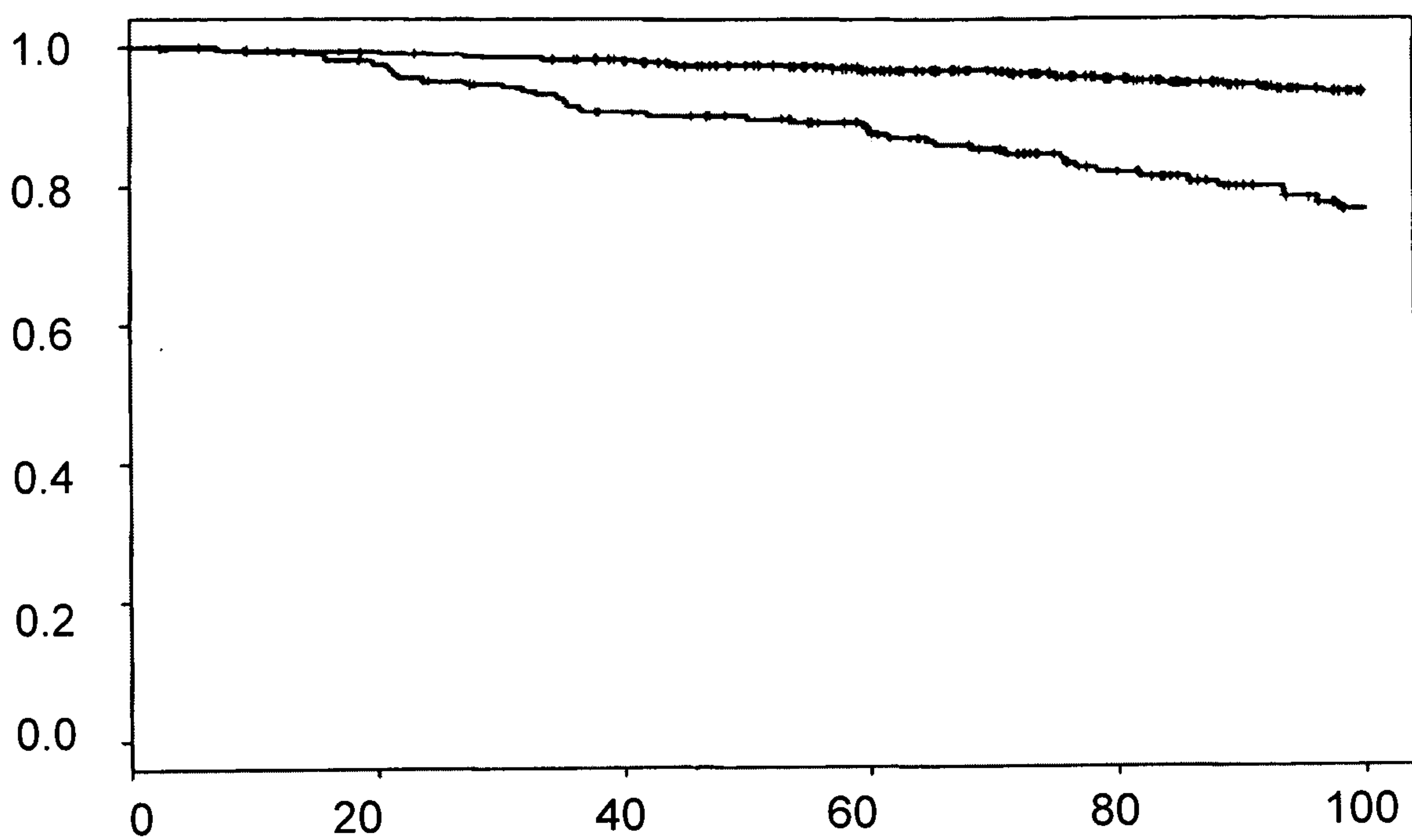
X Axis: Months Post Radical Prostatectomy

Y Axis: Probability of Remaining Disease Progression Free

FIG. 12

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Feature: Combined Mean Distance Between Epithelial Tumor Cells
(MST) at Low bGG, Actual Grade at High bGG



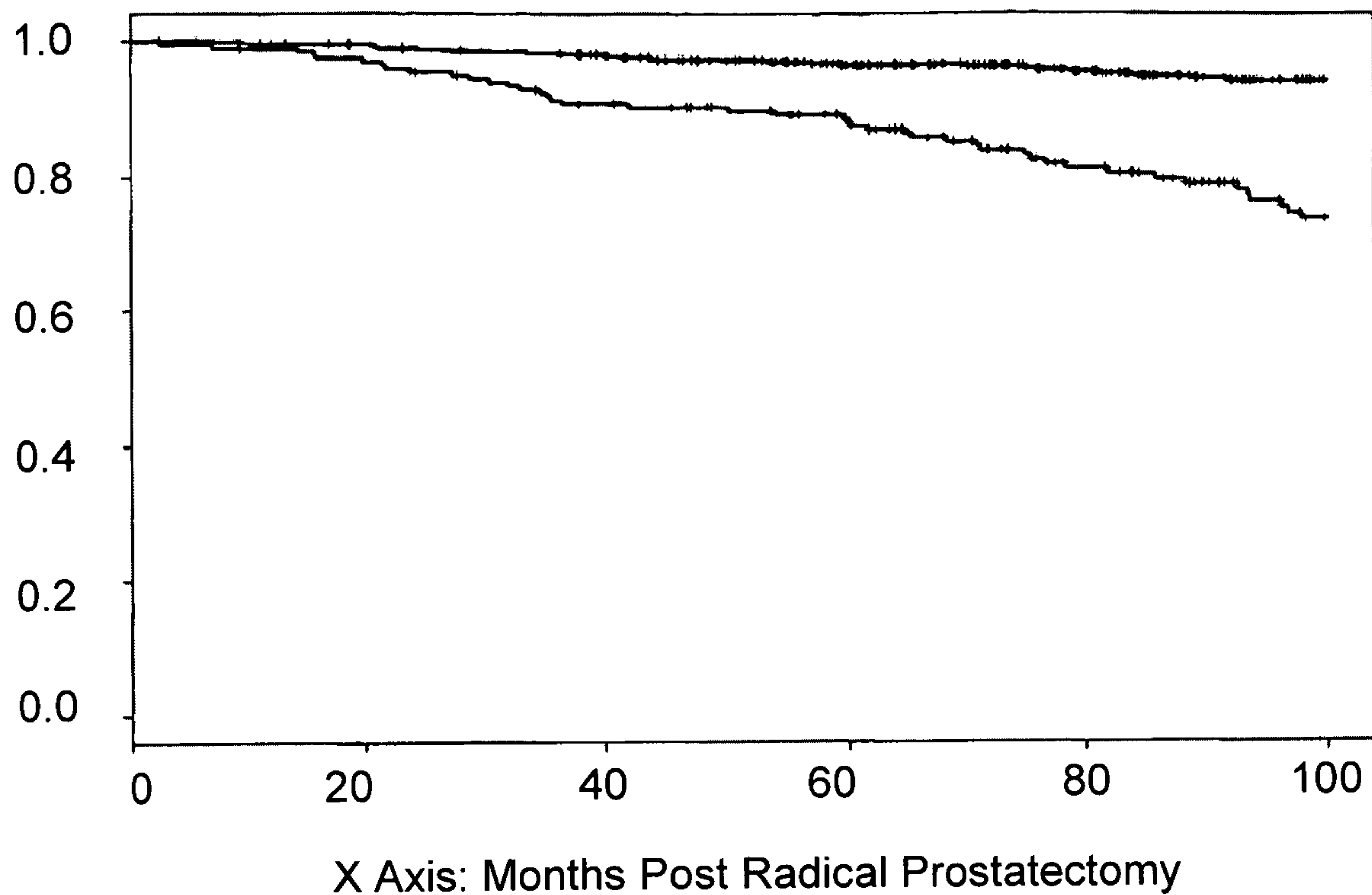
X Axis: Months Post Radical Prostatectomy

Y Axis: Probability of Remaining Disease Progression Free

FIG. 13

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Feature: Combined AR Dynamic Range at Low bGG,
Total Ki67 at High bGG

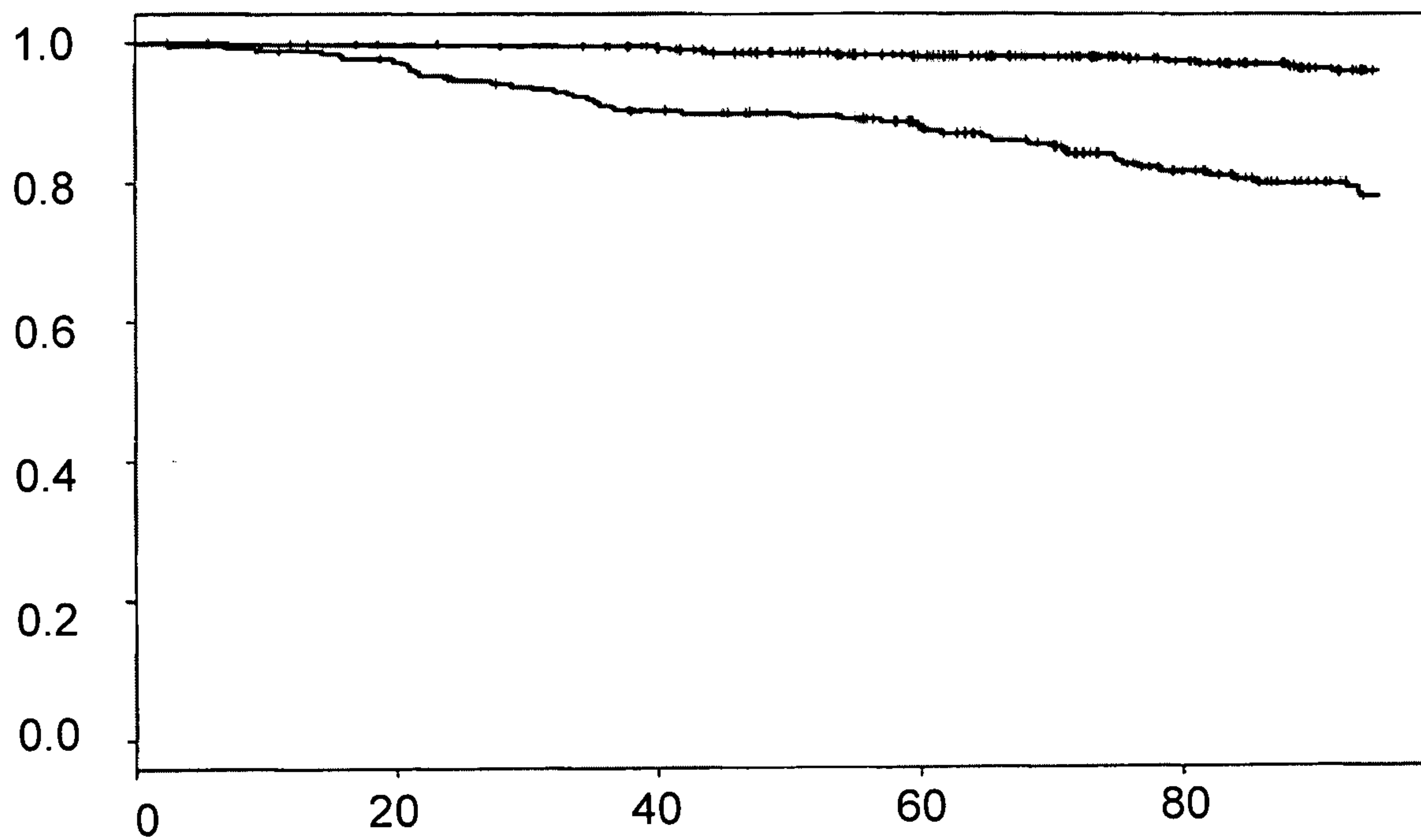


Y Axis: Probability of Remaining Disease Progression Free

FIG. 14

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Output Value of Model Predictive of Disease Progression
Training Set



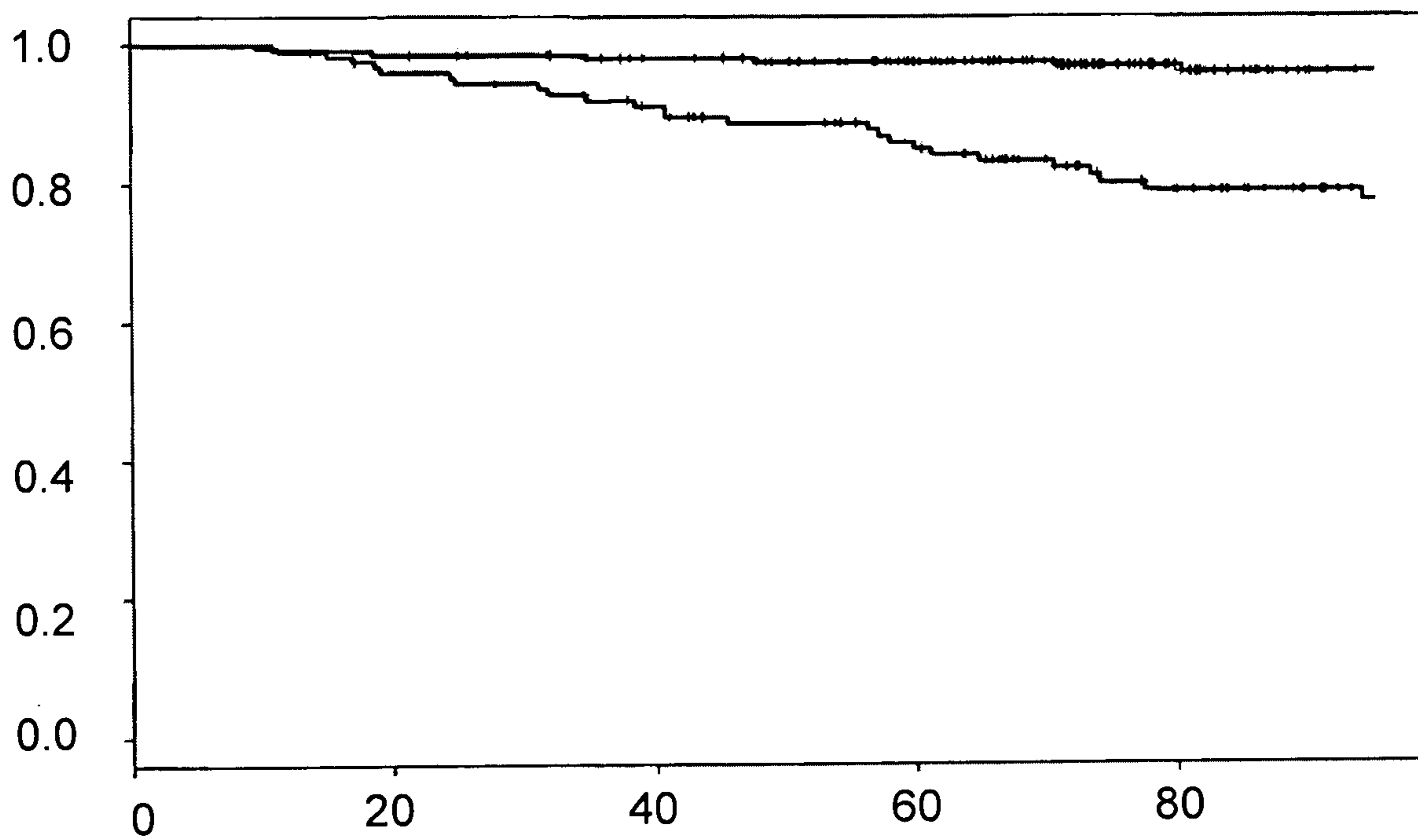
X Axis: Months Post Radical Prostatectomy

Y Axis: Probability of Remaining Disease Progression Free

FIG. 15

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Output Value of Model Predictive of Disease Progression
Validation Set



X Axis: Months Post Radical Prostatectomy

Y Axis: Probability of Remaining Disease Progression Free

FIG. 16

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Example 2: Features Selected for Prediction of Favorable
Pathological Stage (Indolent Disease)

Feature	Univariate P Value	Weight in Model
<u>Clinical</u>		
Preoperative PSA	<0.001	-4.232
Biopsy Gleason Score	<0.001	-2.0031
<u>Molecular (Combined)</u>		
Combined AR Dynamic Range at Low bGG, Total Ki67 at High bGG	<0.001	-0.3375
<u>Morphometric</u>		
Area of Epithelial Nuclei Outside Gland Units to Area of Epithelial Nuclei Within Gland Units	<0.001	-6.3303
Area of Epithelial Nuclei Distributed Away From Gland Units	<0.001	-0.8374

FIG. 17

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Example 3, Study 1: Features Associated With Responsiveness To
Hormonal Therapy And Time To Clinical Progression

Feature	Univariate P Value
<u>Molecular</u>	
AR area in AMACR(+) Tumor Epithelial Cells	<0.0001
Dynamic range of AR intensity in Tumor Epithelial Cells	<0.0001
<u>Morphometric</u>	
Median Lumen Area	<0.01

FIG. 18

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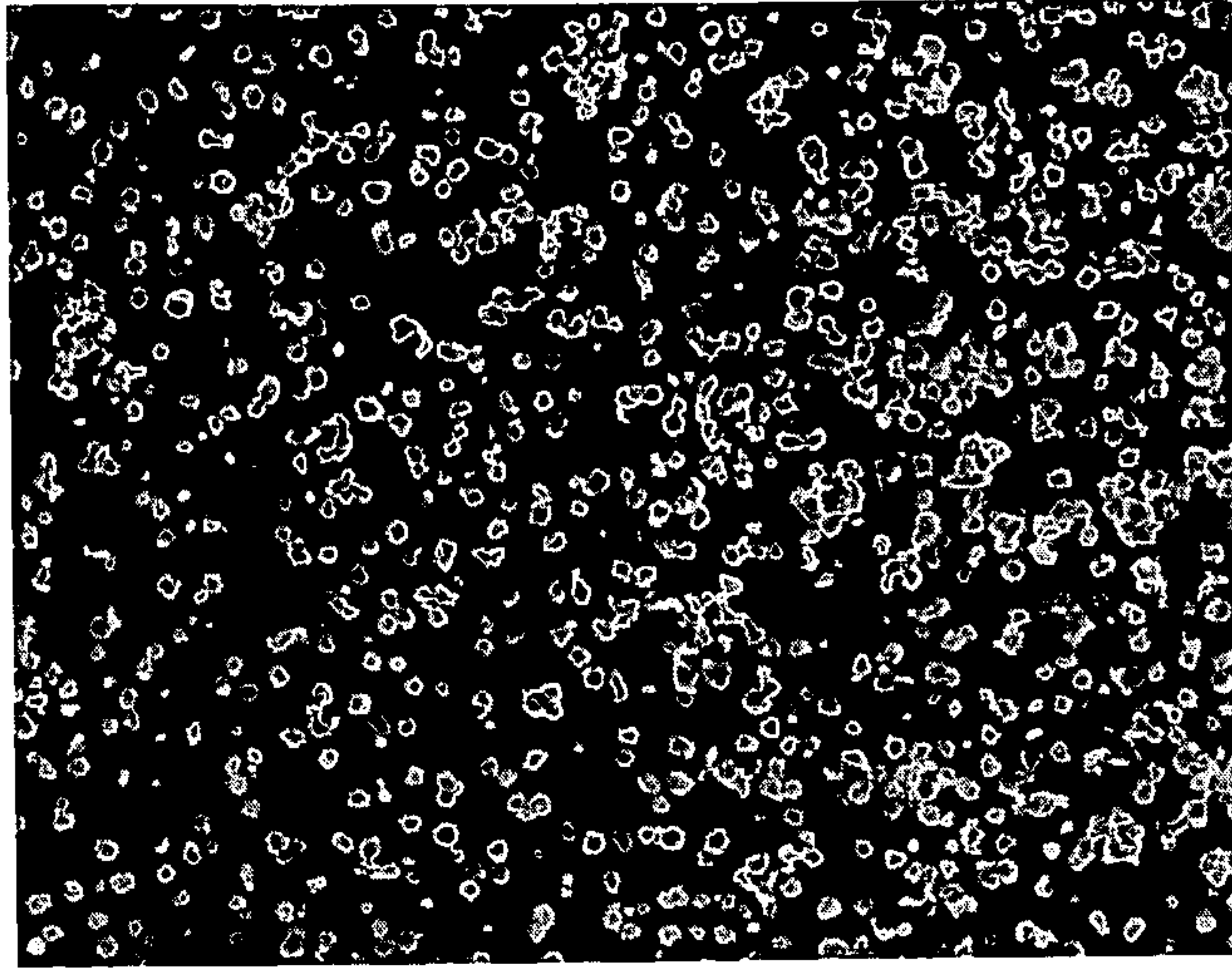


FIG. 19A

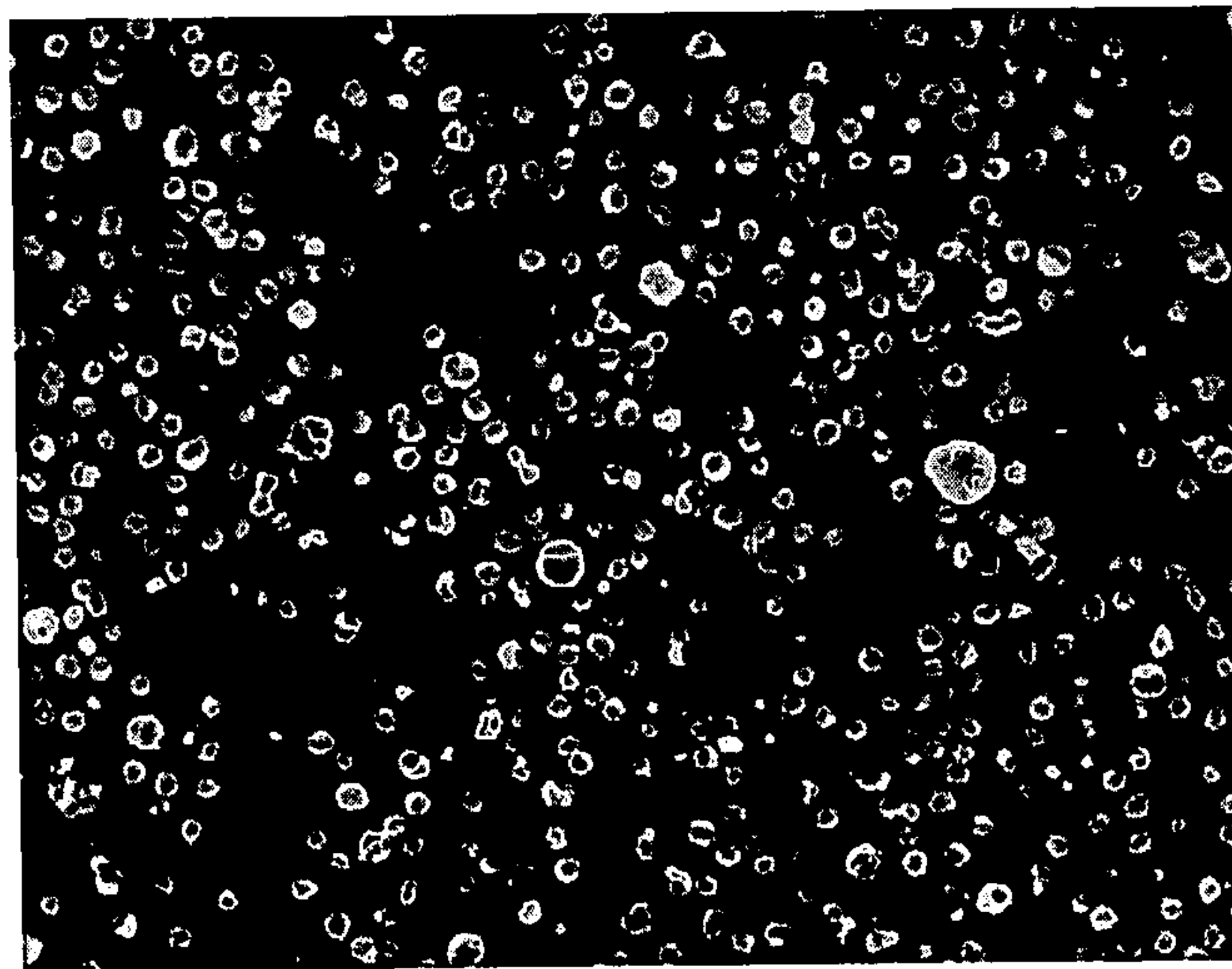


FIG. 19B

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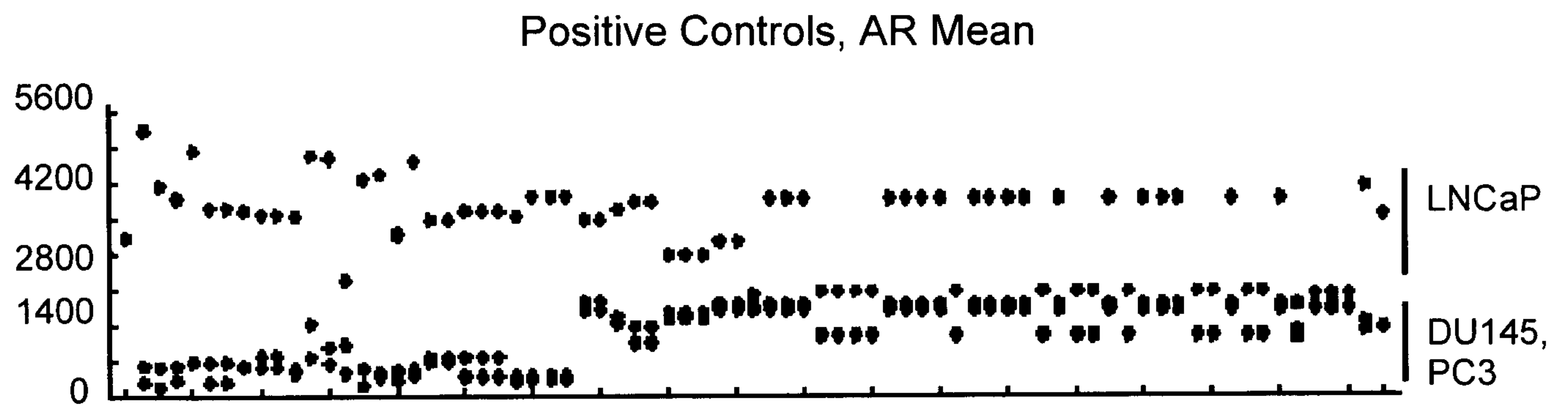


FIG. 20A

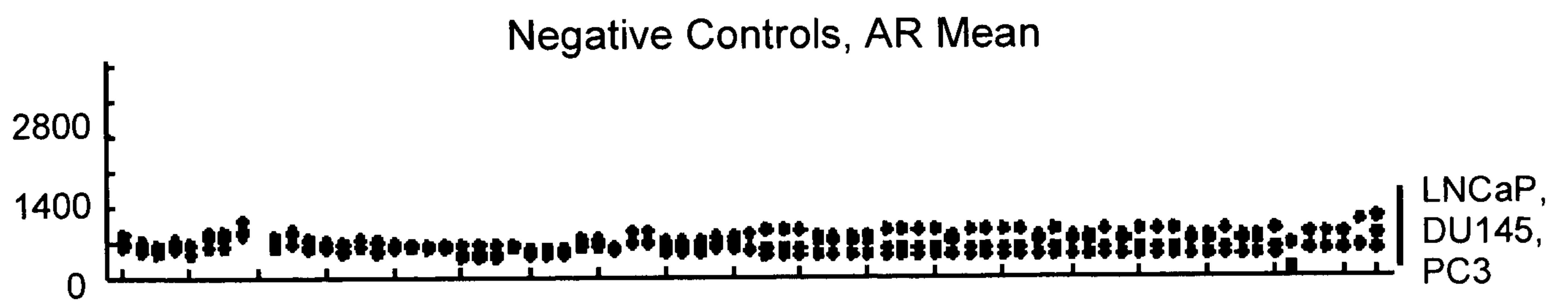
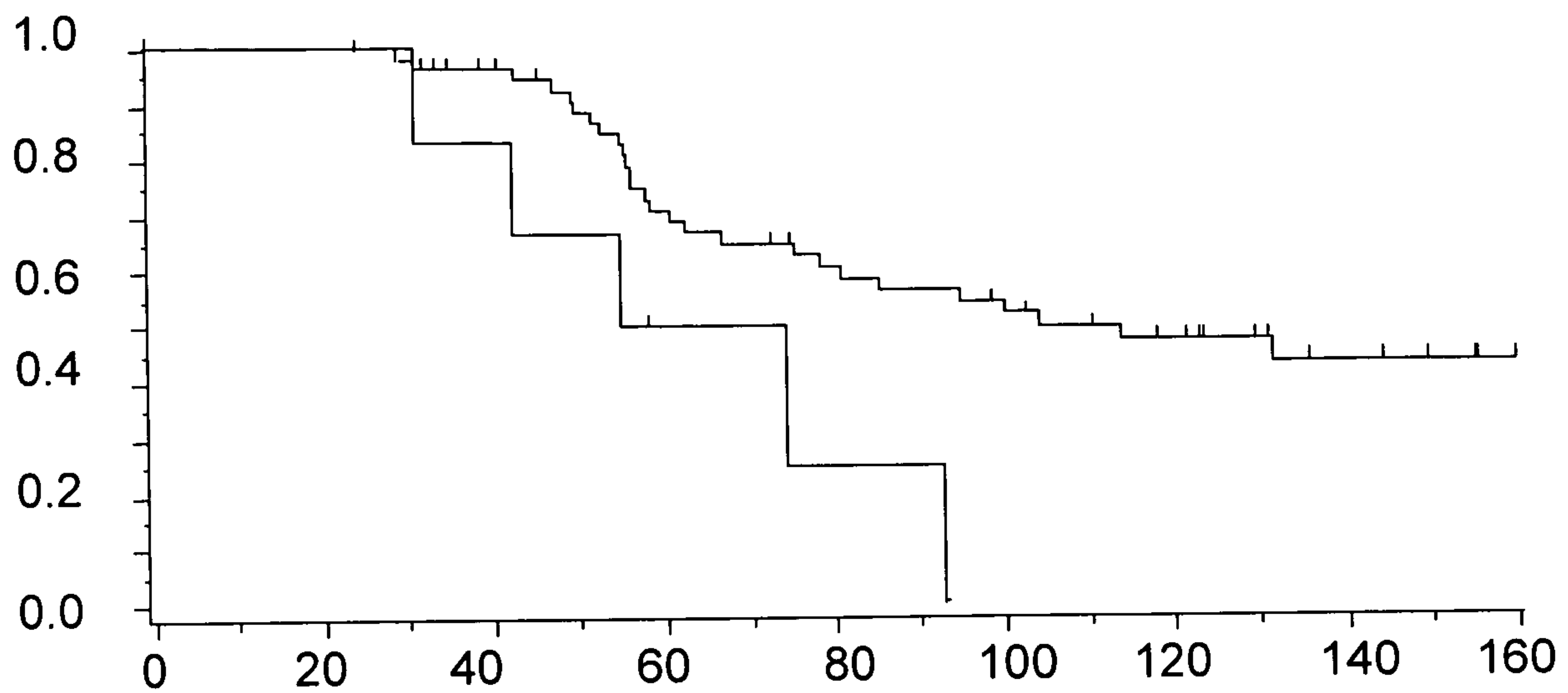


FIG. 20B

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Example 3, Study 2: Stratification of Patients By
Feature Representing Expression of Nuclear AR



X Axis: Actual Time to Death-of-Disease (months)

Y Axis: Probability of Remaining Death-of-Disease Free

FIG. 21

Example 2: Features Selected for Prediction of Favorable Pathological Stage (Indolent Disease)

Feature	Univariate P Value	Weight in Model
<u>Clinical</u>		
Preoperative PSA	<0.001	-4.232
Biopsy Gleason Score	<0.001	-2.0031
<u>Molecular (Combined)</u>		
Combined AR Dynamic Range at Low bGG, Total Ki67 at High bGG	<0.001	-0.3375
<u>Morphometric</u>		
Area of Epithelial Nuclei Outside Gland Units to Area of Epithelial Nuclei Within Gland Units	<0.001	-6.3303
Area of Epithelial Nuclei Distributed Away From Gland Units	<0.001	-0.8374