US 20100055690A1

(19) **United States**

(12) **Patent Application Publication**

(10) **Pub. No.: US 2010/0055690 A1**

(43) **Pub. Date: Mar. 4, 2010**

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(54) **PROGNOSTIC BIOMARKERS IN PATIENTS WITH OVARIAN CANCER**

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(21) Appl. No.: **12/422,530**

(22) Filed: **Apr. 13, 2009**

Related U.S. Application Data

(63) Continuation of application No. PCT/US2007/021867, filed on Oct. 12, 2007.

(60) Provisional application No. 60/851,520, filed on Oct. 13, 2006.

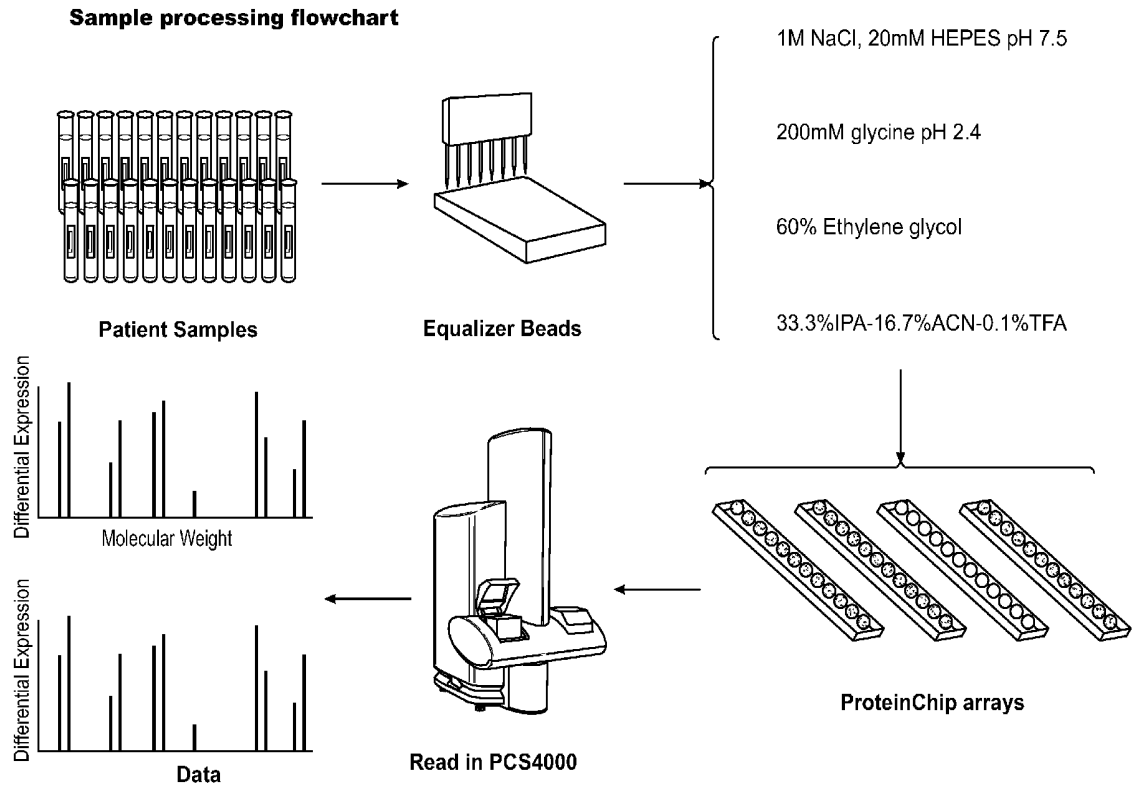
Publication Classification

(51) **Int. Cl.**
C12Q 1/68 (2006.01)
G01N 33/53 (2006.01)

(52) **U.S. Cl.** **435/6**; 435/7.1

(57) **ABSTRACT**

The present invention provides methods for assessing an ovarian cancer patient's survival status. Also, methods for evaluating the ovarian cancer state of a patient are described herein. These methods involve the detection, analysis, and classification of biological patterns in biological samples. The biological patterns are obtained using, for example, mass spectrometry systems and other techniques.



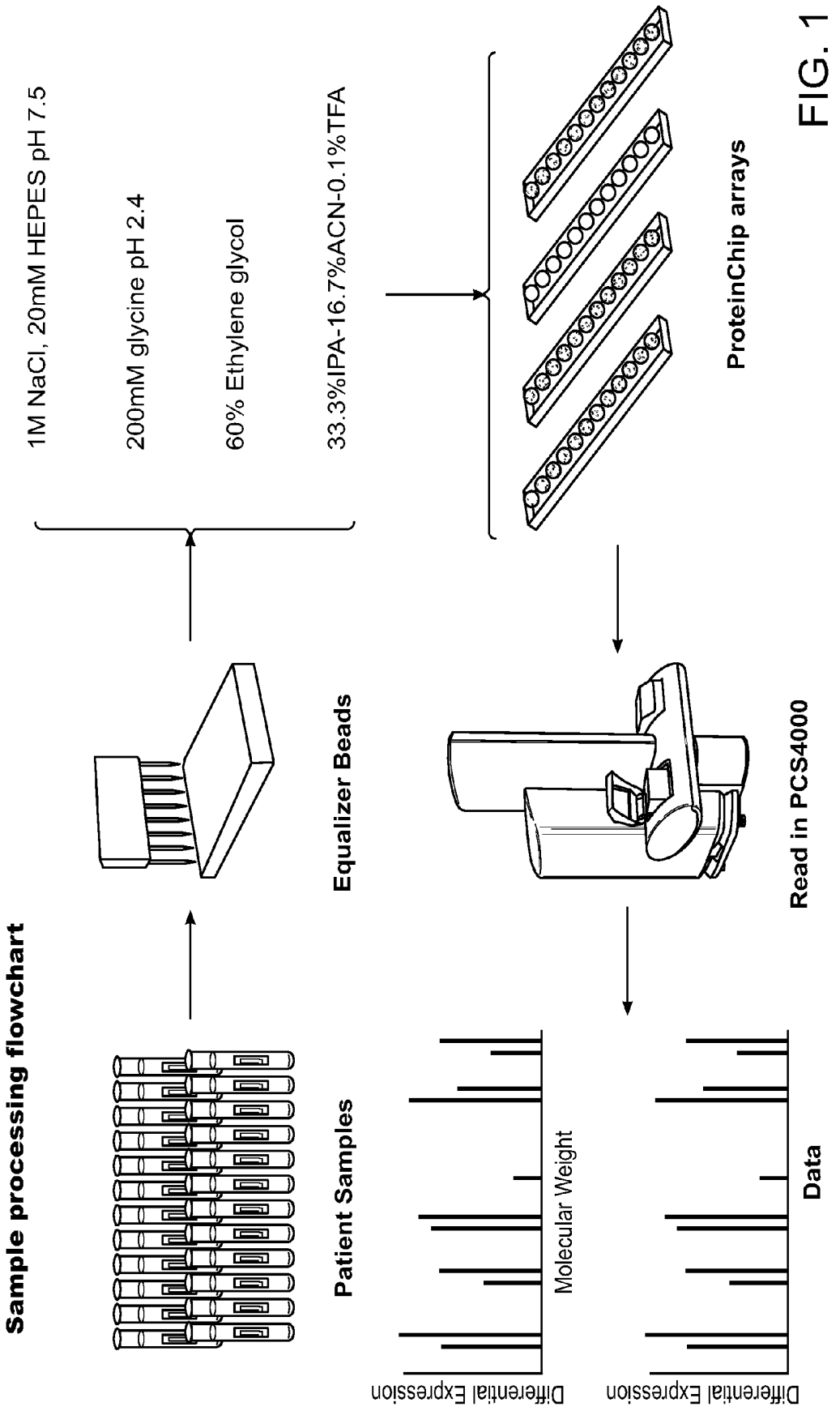

Sample processing flowchart
Patient Samples
Equalizer Beads
1M NaCl, 20mM HEPES pH 7.5
200mM glycine pH 2.4
60% Ethylene glycol
33.3%IPA-16.7%ACN-0.1%TFA
ProteinChip arrays
Read in PCS4000
Data
Molecular Weight
Differential Expression
Differential Expression

FIG. 1

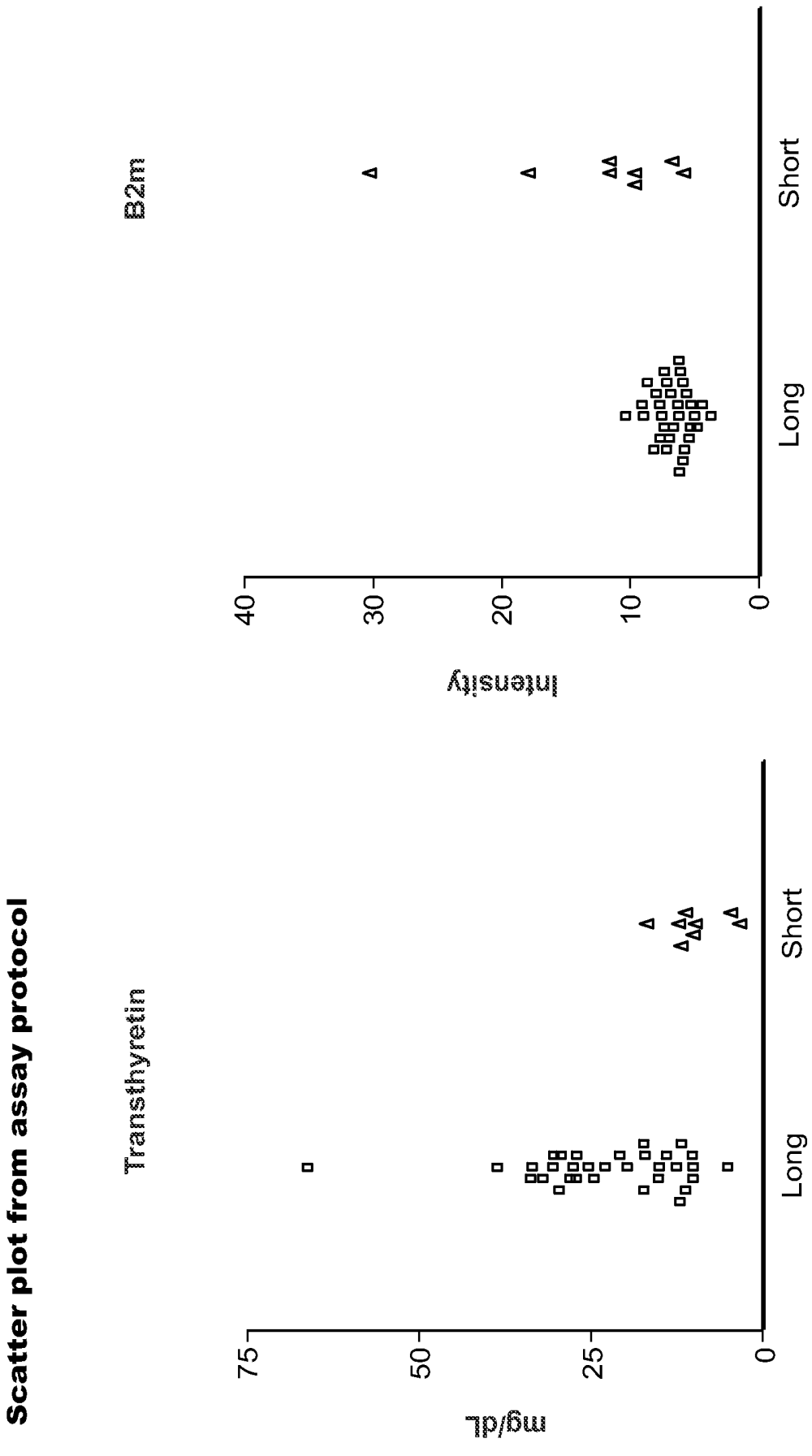

Scatter plot from assay protocol
Transthyretin
mg/dL
75
50
25
0
Long
Short
B2m
Intensity
40
30
20
10
0
Long
Short

FIG. 2

Peak table marker assay

Parameter	p value
Transthyretin	0.0007
B2m	0.0036
Age	0.0084

FIG. 3

Scatter plot of transthyretin

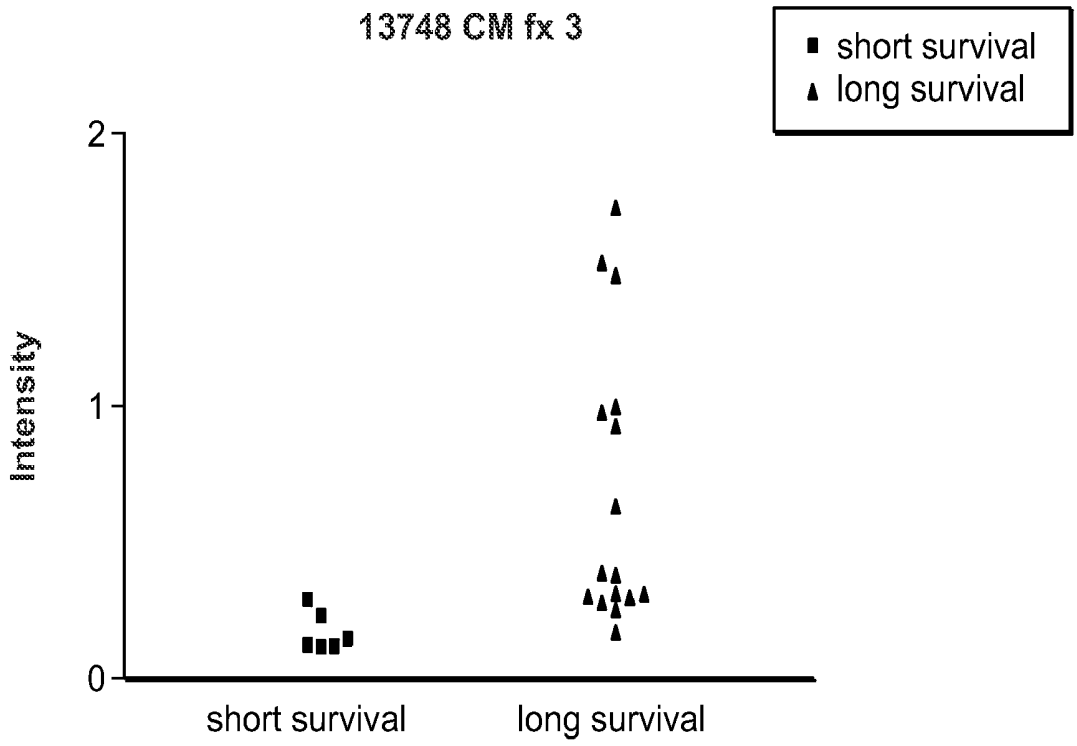


FIG. 4


Scatter plot of SAA
Fx 4 H50 11183
1.50
1.25
1.00
0.75
0.50
0.25
0.00
Short
Long

FIG. 5

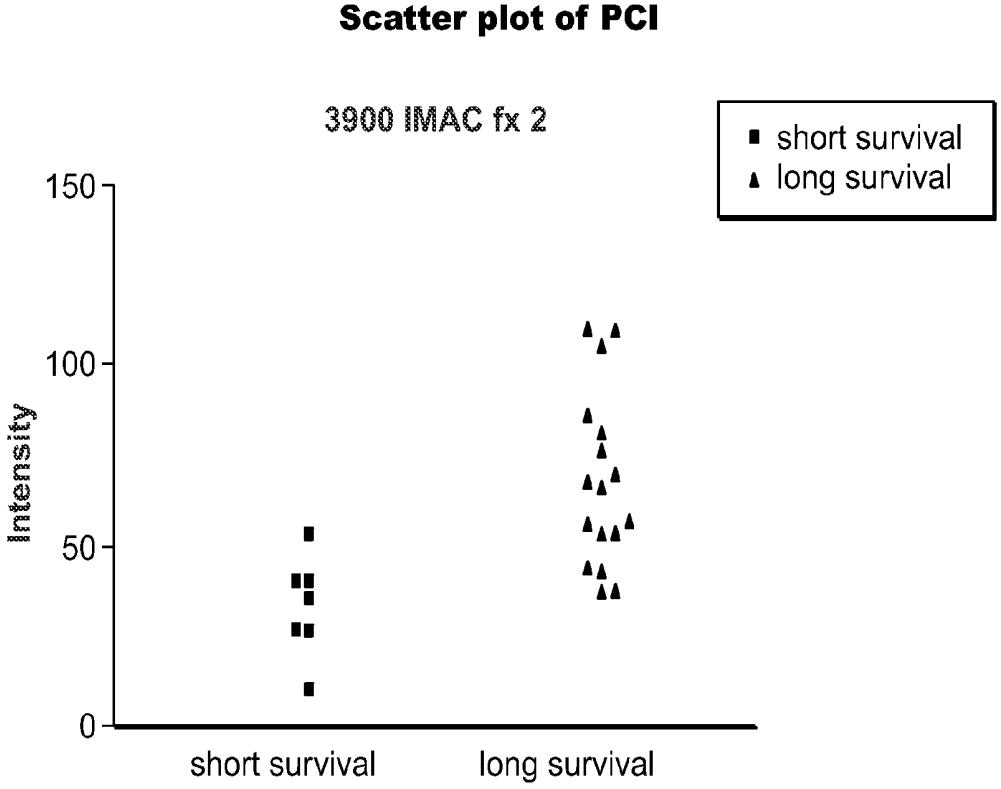

Scatter plot of PCI
3900 IMAC fx 2
short survival
long survival
Intensity
150
100
50
0
short survival
long survival

FIG. 6

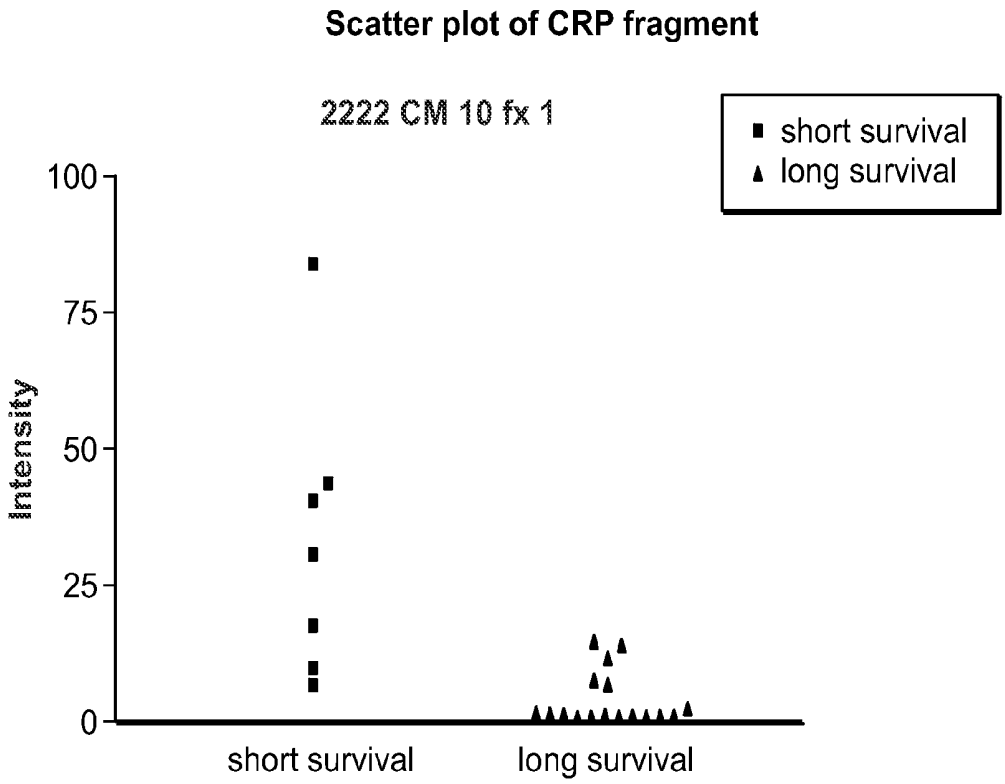

Scatter plot of CRP fragment
2222 CM 10 fx 1
short survival
long survival
100
75
50
25
0
Intensity
short survival
long survival

FIG. 7

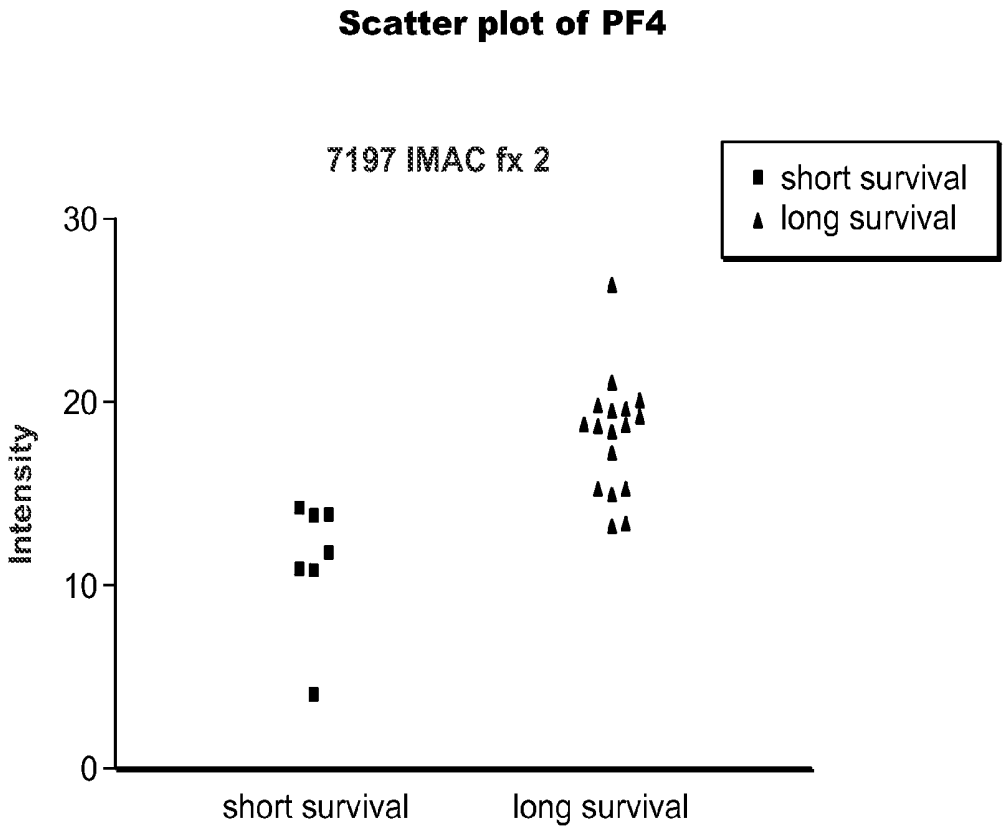

Scatter plot of PF4
7197 IMAC fx 2
short survival
long survival
30
20
10
0
Intensity
short survival
long survival

FIG. 8

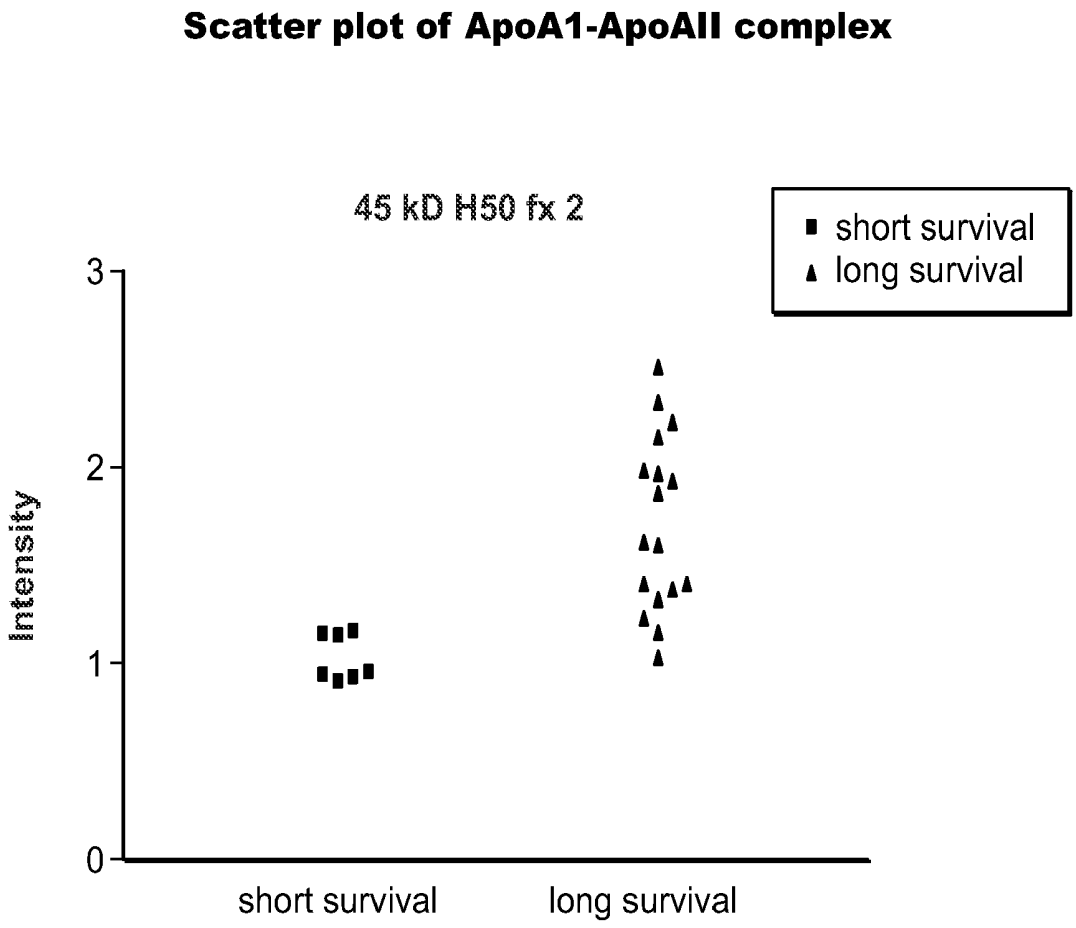

Scatter plot of ApoA1-ApoAII complex
45 kD H50 fx 2
short survival
long survival
Intensity
3
2
1
0
short survival
long survival

FIG. 9

Peak table — equalizer bead results

p value	AUC	m/z	Array	Fraction	ID
0.000538	0.05	45635.89	H50	2	ApoAI-ApoAII dimer
0.000679	0.05	7197.615	IMAC30	2	PF4, N-term. truncation
0.000855	0.08	6889.985	CM10	1	Transthyretin 2+
0.001072	0.92	2222.962	CM10	1	CRP N-terminal fragment
0.001072	0.05	3897.378	IMAC30	2	Protein C inhibitor fragment
0.001100	0.07	11183.28	H50	4	truncated SAA
0.001180	0.06	13748.71	CM10	3	Transthyretin
0.002555	0.08	7900.679	IMAC30	1	PF4, sodium adduct
0.003400	0.16	23068.54	IMAC30	2	Apo-A-I, C-term. degradation

P value calculated using Mann-Whitney test comparing long survivors (defined as surviving > 1 year) versus short survivors (defined as surviving < 1 year).
AUC <.5 indicates protein is lower in short survival group. AUC >.5 indicates protein is higher in short survival group.

FIG. 10

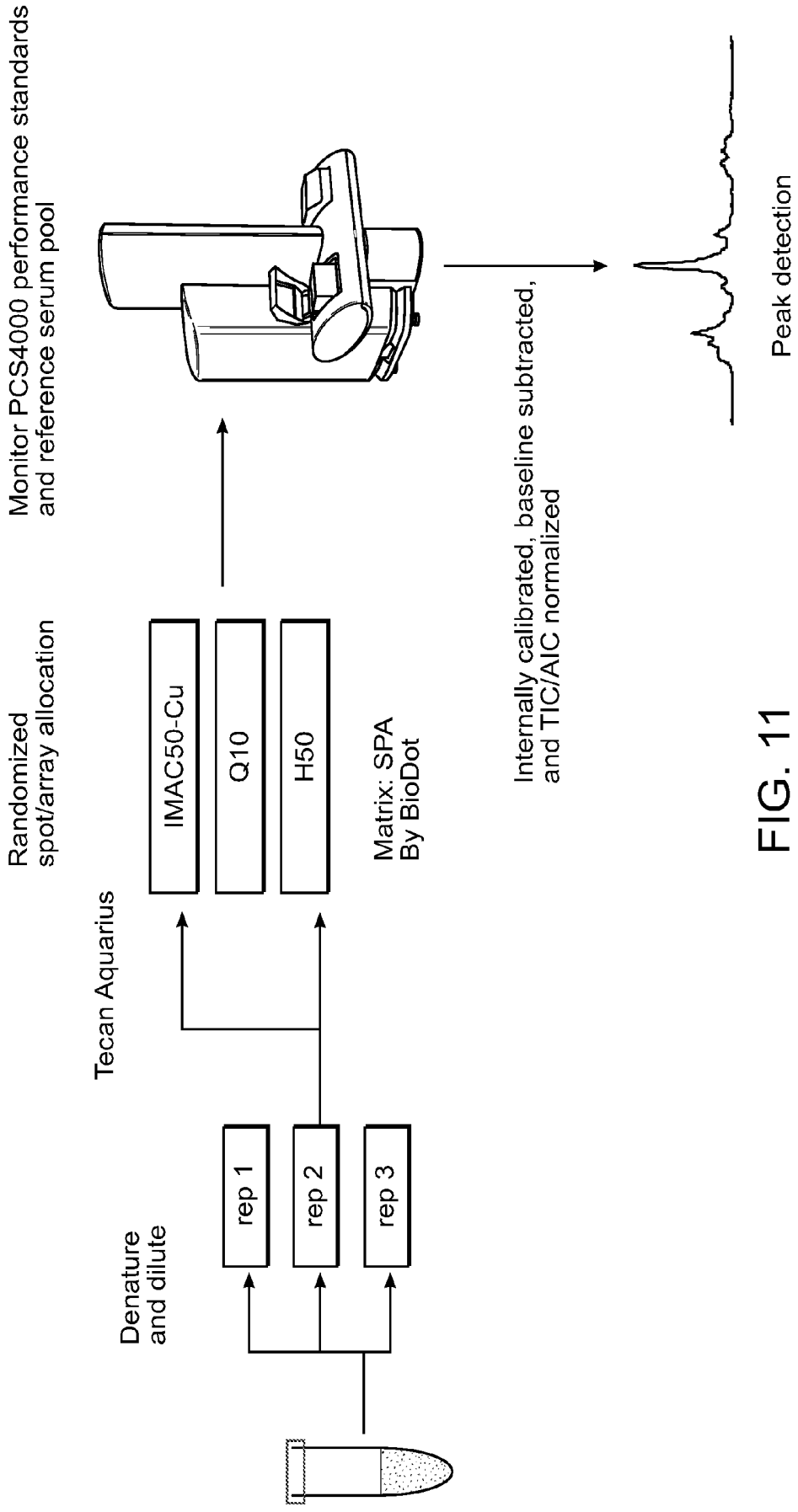

Denature and dilute
rep 1
rep 2
rep 3
Tecan Aquarius
Randomized spot/array allocation
IMAC50-Cu
Q10
H50
Matrix: SPA By BioDot
Monitor PCS4000 performance standards and reference serum pool
Internally calibrated, baseline subtracted, and TIC/AIC normalized
Peak detection

FIG. 11

	Long Survivors	Short survivors
N	68	25
Survival time (months) Median (IQ range)	21.3 (17.6-27.9)	3.7 (1.6-10.0)
Age Median (IQ range)	62.8 (55.4-71.5)	73.6 (65.1-81.7)
CA125 Median (IQ range)	496 (136-1694)	825 (415-1857)
Stage		
1	13	1
2	16	4
3	28	11
4	11	9

FIG. 12

Parameter	p value
B2m	<.0001
Age	0.0007
Transthyretin	0.0015
Hepcidin	0.0463
Transferrin	0.0430
Stage	0.0539
Apo A1	0.0708
CA125	0.0894
CTAP3	0.7191

FIG. 13

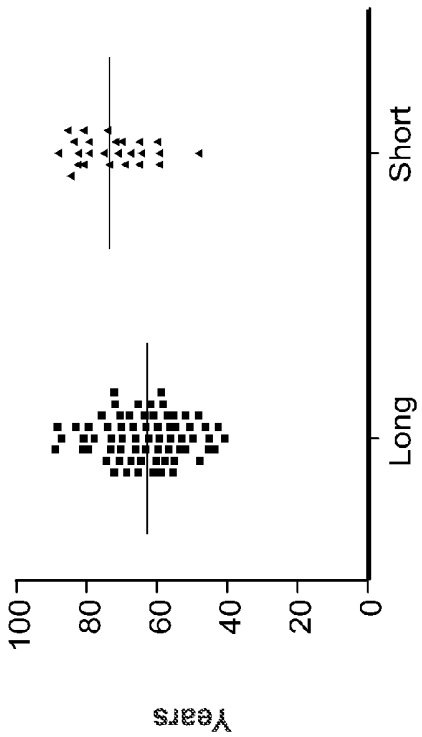


FIG. 14B

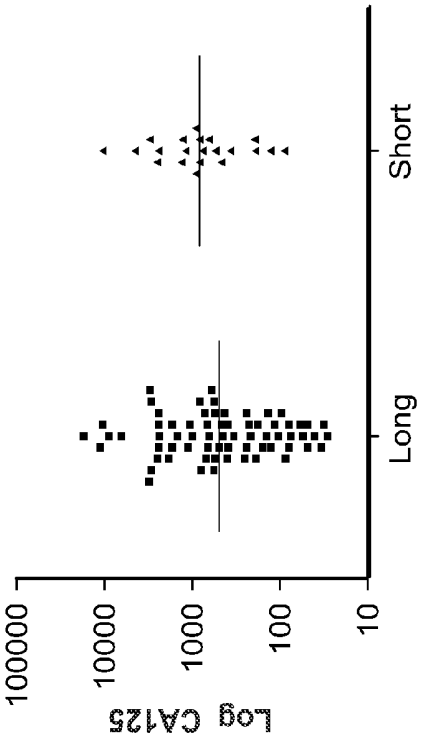


FIG. 14A

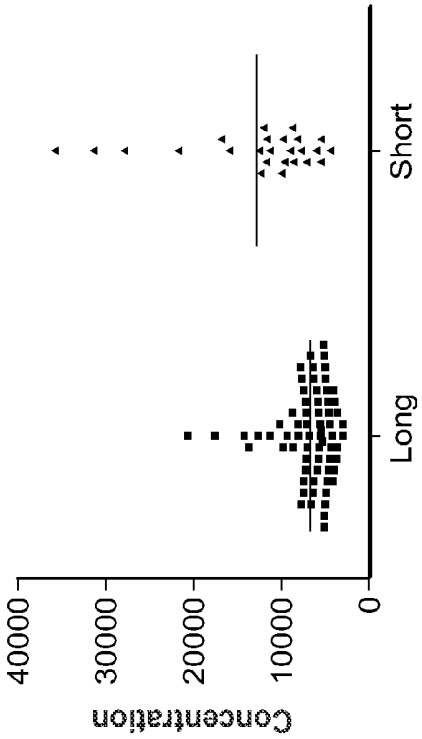


FIG. 14D

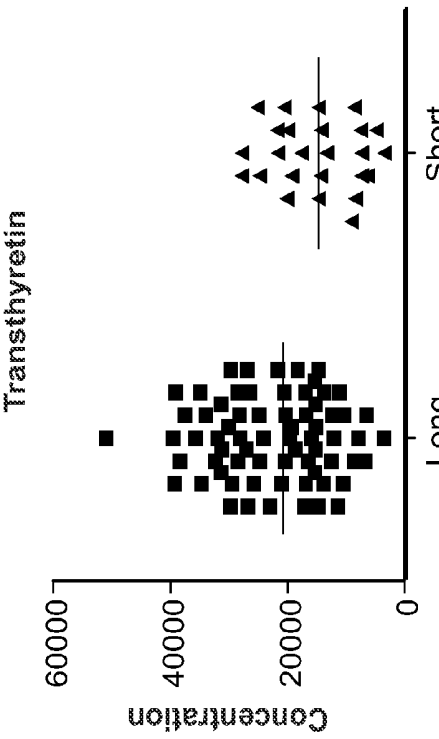


FIG. 14C

FIG. 15A

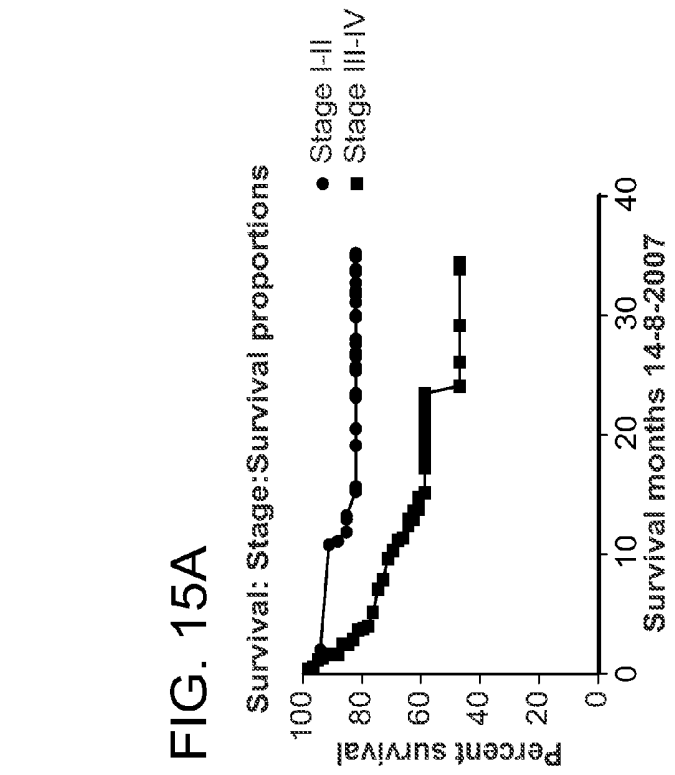


FIG. 15B

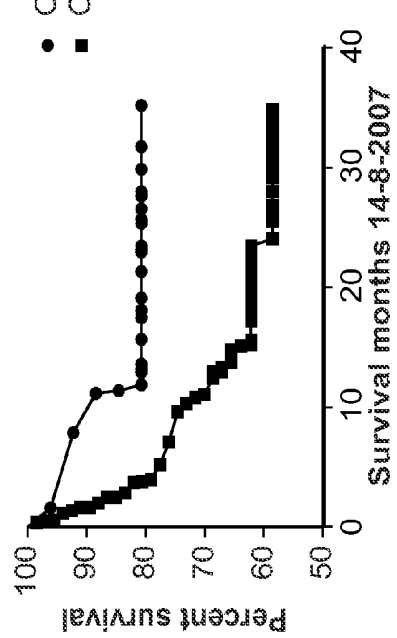


FIG. 15C

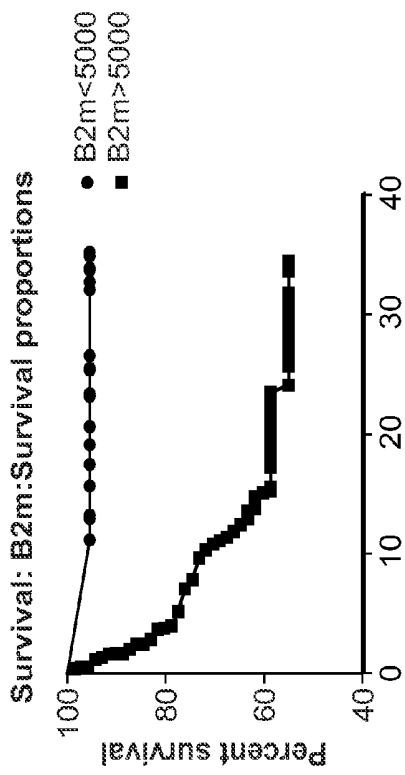
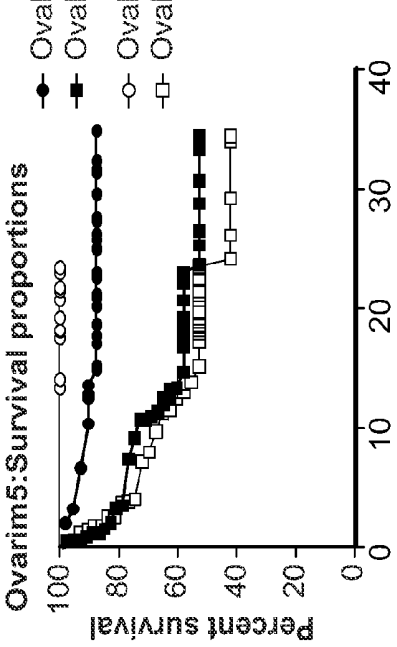


FIG. 15D



PROGNOSTIC BIOMARKERS IN PATIENTS WITH OVARIAN CANCER

RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 60/851,520, filed Oct. 13, 2007. The entire contents of the aforementioned application are hereby incorporated herein by reference.

FIELD OF THE INVENTION

[0002] The present invention relates to a method of determining the prognosis of patients with ovarian cancer comprising: (a) measuring biomarkers in a sample from the subject and (b) correlating the measurement with the duration of ovarian cancer survival. The invention further relates to kits for determining prognosis in a subject.

BACKGROUND OF THE INVENTION

[0003] Ovarian cancer is among the most lethal gynecologic malignancies in developed countries. Annually in the United States alone, approximately 23,000 women are diagnosed with the disease and almost 14,000 women die from it. (Jamal, A., et al., CA Cancer J. Clin, 2002; 52:2347). Despite progress in cancer therapy, ovarian cancer mortality has remained virtually unchanged over the past two decades. (Id.) Given the steep survival gradient relative to the stage at which the disease is diagnosed, early detection remains the most important factor in improving long-term survival of ovarian cancer patients.

[0004] The poor prognosis of ovarian cancer diagnosed at late stages, the cost and risk associated with confirmatory diagnostic procedures, and its relatively low prevalence in the general population together pose extremely stringent requirements on the sensitivity and specificity of a test for it to be used for screening for ovarian cancer in the general population.

[0005] The identification of tumor markers suitable for the early detection and diagnosis of cancer holds great promise to improve the clinical outcome of patients. It is especially important for patients presenting with vague or no symptoms or with tumors that are relatively inaccessible to physical examination. Despite considerable effort directed at early detection, no cost effective screening tests have been developed (Paley P J., *Curr Opin Oncol,* 2001; 13(5):399-402) and women generally present with disseminated disease at diagnosis. (Ozols R F, et al., Epithelial ovarian cancer. In: Hoskins W J, Perez C A, Young R C, editors. Principles and Practice of *Gynecologic Oncology.* 3rd ed. Philadelphia: Lippincott, Williams and Wilkins; 2000. p. 981-1057).

[0006] The best-characterized tumor marker, CA125, is negative in approximately 30-40% of stage I ovarian carcinomas and its levels are elevated in a variety of benign diseases. (Meyer T, et al., *Br J Cancer,* 2000; 82(9):1535-8; Buamah P., *J Surg Oncol,* 2000; 75(4):264-5; Tuxen M K, et al., *Cancer Treat Rev,* 1995; 21(3):215-45). Its use as a population-based screening tool for early detection and diagnosis of ovarian cancer is hindered by its low sensitivity and specificity. (MacDonald N D, et al., *Eur J Obstet Gynecol Reprod Biol,* 1999; 82(2):155-7; Jacobs I, et al., *Hum Reprod,* 1989; 4(1):1-12; Shih I-M, et al., Tumor markers in ovarian cancer. In: Diamandis E P, Fritsche, H., Lilja, H., Chan, D. W., and Schwartz, M., editor. Tumor markers physiology, pathobiology, technology and clinical applications. Philadelphia: AACC Press; in press). Although pelvic and more recently vaginal sonography has been used to screen high-risk patients, neither technique has the sufficient sensitivity and specificity to be applied to the general population. (MacDonald N D, et al., supra). Recent efforts in using CA125 in combination with additional tumor markers (Woolas RP XF, et al., *J Natl Cancer Inst,* 1993; 85(21):1748-51; Woolas R P, et al., *Gynecol Oncol,* 1995; 59(1):111-6; Zhang Z, et al., *Gynecol Oncol,* 1999; 73(1):56-61; Zhang Z, et al., Use of Multiple Markers to Detect Stage I Epithelial Ovarian Cancers: Neural Network Analysis Improves Performance. American Society of Clinical Oncology 2001; Annual Meeting, Abstract) in a longitudinal risk of cancer model (Skates S J, et al., *Cancer,* 1995; 76(10 Suppl):2004-10), and in tandem with ultrasound as a second line test (Jacobs I D A, et al., *Br Med J,* 1993; 306(6884):1030-34; Menon U T A, et al., *British Journal of Obstetrics and Gynecology,* 2000; 107(2): 165-69) have shown promising results in improving overall test specificity, which is critical for a disease such as ovarian cancer that has a relatively low prevalence.

[0007] Due to the dismal prognosis of late stage ovarian cancer, it is the general consensus that a physician will accept a test with a minimal positive predictive value of 10%. (Bast, R. C., et al., Cancer Treatment and Research, 2002; 107:61-97). Extending this to the general population, a general screening test would require a sensitivity greater than 70% and a specificity of 99.6%. Currently, none of the existing serologic markers, such as CA 125, CA72-4, or M-CSF, individually delivers such a performance. (Bast, R. C., et al., Int J Biol Markers, 1998; 13:179-87).

[0008] Thus, there is a critical need to identify one or more panels of biomarkers that deliver the required sensitivity and specificity for early detection of ovarian cancer. Without an acceptable screening test, early detection remains the most critical factor in improving long-term survival of patients with ovarian cancer.

[0009] Although the stage of disease is one of the strongest predictors of survival in patients with ovarian cancer, it alone is not adequate to predict survival or outcome in these patients. Better prediction of a patient's prognosis could improve patient management by e.g., identifying patients in whom more aggressive therapy might be warranted.

[0010] Thus, it is desirable to have a reliable and accurate method of determining the ovarian cancer status in patients, the results of which can then be used to manage subject treatment.

SUMMARY

[0011] The present invention provides sensitive and quick methods and kits that are useful for determining the survival status of patients with ovarian cancer by measuring and identifying particular biomarkers. The detection and measurement of these biomarkers in patient samples provides information that diagnosticians can correlate with a survival status of human ovarian cancer patients or a negative diagnosis (e.g., normal or disease-free). The markers are characterized by mass/charge ratio, molecular weight and/or by their known protein identities. The markers can be resolved from other proteins in a sample by using a variety of fractionation techniques, e.g., chromatographic separation coupled with mass spectrometry, protein capture using immobilized antibodies, bead-protein complexes or by traditional immunoassays. In preferred embodiments, the method of resolution involves Surface-Enhanced Laser Desorption/Ionization ("SELDI")

mass spectrometry, in which the surface of the mass spectrometry probe comprises adsorbents that bind the markers.

[0012] More specifically, thirteen (13) biomarkers were discovered and characterized, in accordance with the methods described herein as (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A. In a specific embodiment, a subpanel of seven markers: (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1) is shown to be highly indicative of the prognosis of subjects having ovarian cancer.

[0013] Moreover, the panel of seven biomarkers is predictive of survival independent of the stage of cancer. Additionally, among late stage ovarian cancer patients the panel of seven markers can distinguish between those with longer survival and shorter survival (see Example 2).

[0014] It has also been discovered herein that a single marker beta-2 microglobin (B2M) is predictive of survival in subjects having ovarian cancer.

[0015] The present invention provides a method of assessing an ovarian cancer patient's survival status in a subject comprising (a) measuring the panel of seven biomarkers in a sample from the subject, wherein the biomarkers comprise (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), and (vii) apolipoprotein A1 (ApoA1) (b) and correlating the measurement with ovarian cancer patient survival status. In certain methods, the measuring step comprises detecting the m/z (mass-to-charge ratio) values of markers in the sample.

[0016] In further embodiments, the methods are particularly useful in subjects diagnosed with late stage ovarian cancer wherein most clinical tests can not predict survivability. The instant invention has the surprising ability to predict the length of survival of subjects having late stage ovarian cancer. Specifically, the panel of seven markers is effective for determining this prognosis.

[0017] Preferred methods of the invention also include assessing ovarian cancer patient survival status comprising:

[0018] (a) determining the concentration or expression levels or peak intensity values of a combination of two or more biomarkers in a sample from the subject, wherein the two or more biomarkers are selected from the group consisting of: (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A;

[0019] (b) correlating the corresponding concentration/expression levels/peak intensity values with ovarian cancer patient survival status.

[0020] In such a preferred method, determining may comprise 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or all thirteen of the group of biomarkers.

[0021] In a specific preferred method, the combination is of the following seven biomarkers: (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), and (vii) apolipoprotein A1(ApoA1).

[0022] The invention also relates to methods wherein the measuring step comprises: providing a subject sample of blood or a blood derivative; fractionating proteins in the sample on an anion exchange resin and collecting fractions that contain (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and/or (xiii) truncated serum amyloid A from the fractions on a surface of a substrate comprising capture reagents that bind the protein biomarkers. The blood derivative is, e.g., serum or plasma. In preferred embodiments, the substrate is a SELDI probe comprising an IMAC copper surface and wherein the protein biomarkers are detected by SELDI. In other embodiments, the substrate is a SELDI probe comprising biospecific affinity reagents that bind one or more of the thirteen biomarkers and wherein the protein biomarkers are detected by SELDI. In other embodiments, the substrate is a microtiter plate comprising biospecific affinity reagents that bind (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, (xii) m/z value 7900.679 protein and (xiii) truncated serum amyloid A; and the protein biomarkers are detected by immunoassay. In specific embodiments, the capture reagents specifically bind the following seven biomarkers: (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), and (vii) apolipoprotein A1 (ApoA1).

[0023] In certain embodiments, the methods further comprise managing subject treatment based on the status determined by the method. For example, if the result of the methods of the present invention is inconclusive or there is reason that confirmation of status is necessary, the physician may order more tests. Alternatively, if the status indicates that surgery is appropriate, the physician may schedule the patient for surgery. Furthermore, if the results show that treatment has been successful, no further management may be necessary.

[0024] The invention also provides for such methods where the panel of biomarkers is measured again after subject management. In these instances, the step of managing subject treatment is then repeated and/or altered depending on the result obtained.

[0025] The term "ovarian cancer patient survival status" refers to the status of survival of the patient. Examples of types of ovarian cancer survival statuses include, but are not limited to, disease free or overall survival one year after diagnosis, 2 years after diagnosis, 3 years after diagnosis, 4 years after diagnosis, and 5 or more years after diagnosis. Another type of status is "treatment responsiveness" i.e. whether a patient has a high or low likelihood of responding to a given type of therapy. A third type of status is "remission" i.e. whether a patient is deemed to be free of disease (in remission) or to have cancer after one more therapeutic interventions (in recurrence). Other statuses and degrees of each status are known in the art.

[0026] The biomarkers that are useful in the methods of the present invention are (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4, (xiii) truncated serum amyloid A and/or combinations thereof. The age of the patient is another biomarker of the present invention, wherein the older the patient, the poorer the prognosis for the patient. In certain preferred embodiments, the method further comprises measuring at least one previously known marker (herein referred to as "Marker 14") in a sample from the subject and correlating measurement of the at least one Marker 14 and the measurement of the panel of seven biomarkers cited above with ovarian cancer status.

[0027] In certain embodiments only one Marker 14 is measured, in addition to the markers comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A, while in other embodiments more than one Marker 14 is measured.

[0028] Examples of Marker 14 include known ovarian cancer biomarkers, e.g., but not limited to, CA125, CA125II, CA15-3, CA19-9, CA72-4, CA 195, tumor associated trypsin inhibitor (TATI), CEA, placental alkaline phosphatase (PLAP), Sialyl TN, galactosyltransferase, macrophage colony stimulating factor (M-CSF, CSF-1), lysophosphatidic acid (LPA), 110 kD component of the extracellular domain of the epidermal growth factor receptor (p110EGFR), tissue kallikreins, e.g., kallikrein 6 and kallikrein 10 (NES-1), prostasin, HE4, creatine kinase B (CKB), LASA, HER-2/neu, urinary gonadotropin peptide, Dianon NB 70/K, Tissue peptide antigen (TPA), osteopontin and haptoglobin, and protein variants (e.g., cleavage forms, isoforms) of the markers.

[0029] For the mass values of the markers disclosed herein, the mass accuracy of the spectral instrument is considered to be about within +/−0.15 percent of the disclosed molecular weight value. Additionally, to such recognized accuracy variations of the instrument, the spectral mass determination can vary within resolution limits of from about 400 to 1000 m/dm, where m is mass and dm is the mass spectral peak width at 0.5 peak height. Those mass accuracy and resolution variances associated with the mass spectral instrument and operation thereof are reflected in the use of the term "about" in the disclosure of the mass of each of seven biomarkers. It is also intended that such mass accuracy and resolution variances and thus meaning of the term "about" with respect to the mass of each of the markers disclosed herein is inclusive of variants of the markers as may exist due to sex, genotype and/or ethnicity of the subject and the particular cancer or origin or stage thereof.

[0030] The accuracy of a diagnostic test is characterized by a Receiver Operating Characteristic curve ("ROC curve"). An ROC is a plot of the true positive rate against the false positive rate for the different possible cutpoints of a diagnostic test. An ROC curve shows the relationship between sensitivity and specificity. That is, an increase in sensitivity will be accompanied by a decrease in specificity. The closer the curve follows the left axis and then the top edge of the ROC space, the more accurate the test. Conversely, the closer the curve comes to the 45-degree diagonal of the ROC graph, the less accurate the test. The area under the ROC is a measure of test accuracy. The accuracy of the test depends on how well the test separates the group being tested into those with and without the disease in question. An area under the curve (referred to as "AUC") of 1 represents a perfect test, while an area of 0.5 represents a test of no use. Thus, preferred biomarkers and diagnostic methods of the present invention have an AUC greater than 0.50, more preferred tests have an AUC greater than 0.60, more preferred tests have an AUC greater than 0.70.

[0031] Preferred methods of measuring the biomarkers include use of a biochip array. Biochip arrays useful in the invention include protein and nucleic acid arrays. One or more markers are captured on the biochip array and subjected to laser ionization to detect the molecular weight of the markers. Analysis of the markers is, for example, by molecular weight of the one or more markers against a threshold intensity that is normalized against total ion current. Preferably, logarithmic transformation is used for reducing peak intensity ranges to limit the number of markers detected.

[0032] Another preferred method of measuring the biomarkers includes the use of a combinatorial ligand library synthesized on beads as described in U.S. Ser. No. 11/495,842, filed Jul. 28, 2006 and entitled "Methods for Reducing the range in Concentrations of Analyte Species in a Sample"; hereby incorporated by reference in its entirety.

[0033] In preferred methods of the present invention, the step of correlating the measurement of the biomarkers with ovarian cancer patient survival status is performed by a software classification algorithm. Preferably, data is generated on immobilized subject samples on a biochip array, by subjecting said biochip array to laser ionization and detecting intensity of signal for mass/charge ratio; and, transforming the data into computer readable form; and executing an algorithm that classifies the data according to user input parameters, for

detecting signals that represent markers present in ovarian cancer patients and are lacking in non-cancer subject controls.

[0034] Preferably the biochip surfaces are, for example, ionic, anionic, comprised of immobilized nickel ions, comprised of a mixture of positive and negative ions, comprised of one or more antibodies, single or double stranded nucleic acids, proteins, peptides or fragments thereof, amino acid probes, or phage display libraries.

[0035] In other preferred methods one or more of the markers are measured using laser desorption/ionization mass spectrometry, comprising providing a probe adapted for use with a mass spectrometer comprising an adsorbent attached thereto, and contacting the subject sample with the adsorbent, and; desorbing and ionizing the marker or markers from the probe and detecting the deionized/ionized markers with the mass spectrometer.

[0036] Preferably, the laser desorption/ionization mass spectrometry comprises: providing a substrate comprising an adsorbent attached thereto; contacting the subject sample with the adsorbent; placing the substrate on a probe adapted for use with a mass spectrometer comprising an adsorbent attached thereto; and, desorbing and ionizing the marker or markers from the probe and detecting the desorbed/ionized marker or markers with the mass spectrometer.

[0037] The adsorbent can for example be hydrophobic, hydrophilic, ionic or metal chelate adsorbent, such as, nickel or an antibody, single- or double stranded oligonucleotide, amino acid, protein, peptide or fragments thereof.

[0038] The methods of the present invention can be performed on any type of patient sample that would be amenable to such methods, e.g., blood, serum and plasma.

[0039] The present invention also provides kits comprising (a) capture reagents that bind a biomarkers comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A; and (b) a container comprising the panel of biomarkers. While the capture reagent can be any type of reagent, preferably the reagent is a SELDI probe. The capture reagent may also bind other known biomarkers, e.g., Marker 14.

[0040] The present invention also provides kits comprising (a) capture reagents that bind biomarkers comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), and (vii) apolipoprotein A1 (ApoA1), and (b) a container comprising the panel of biomarkers. While the capture reagent can be any type of reagent, preferably the reagent is a SELDI probe.

[0041] In certain kits of the present invention, the capture reagent comprises an immobilized metal chelate ("IMAC").

[0042] Certain kits of the present invention further comprise a wash solution that selectively allows retention of the bound biomarker to the capture reagent as compared with other biomarkers after washing.

[0043] The invention also provides kits comprising (a) capture reagents that binds at least one biomarkers comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897-378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A; and (b) instructions for using the capture reagent to measure the biomarker. In certain of these kits, the capture reagent comprises an antibody. Furthermore, some kits further comprise an MS probe to which the capture reagent is attached or is attachable. In some kits, the capture reagent comprises an IMAC. The kits may also contain a wash solution that selectively allows retention of the bound biomarker to the capture reagent as compared with other biomarkers after washing. Preferably, the kit comprises written instructions for use of the kit for determining ovarian cancer status and the instructions provide for contacting a test sample with the capture reagents and measuring one or more biomarkers retained by the capture reagents.

[0044] The kit also provides for capture reagents, which are antibodies, single or double stranded oligonucleotide, amino acid, protein, peptide or fragments thereof.

[0045] Measurement of one or more protein biomarkers using the kit, is by mass spectrometry or immunoassays such as an ELISA.

[0046] Purified proteins for detection of ovarian cancer and/or generation of antibodies for further diagnostic assays are also provided for. Purified proteins include purified peptides of biomarkers 1 thru 13. The invention also provides these purified peptides further comprising a detectable label.

[0047] The invention also provides an article manufacture comprising capture reagents bound to the panel of biomarkers. Other embodiments of the article of manufacture of the present invention further comprise a capture reagent that binds other known ovarian cancer markers, i.e., Marker 14, e.g., but not limited to, CA125, CA125 II, CA15-3, CA19-9, CA72-4, CA 195, TATI, CEA, PLAP, Sialyl TN, galactosyltransferase, M-CSF, CSF-1, LPA, p110EGFR, tissue kallikreins, prostasin, HE4, CKB, LASA, HER-2/neu, urinary gonadotropin peptide, Dianon NB 70/K, TPA, osteopontin and haptoglobin, YKL-40, erbB3, M-CAM, mucins (such as MUC16) and protein variants (e.g., cleavage forms, isoforms) of the markers.

[0048] The present invention also provides a system comprising a plurality of capture reagents each of which has bound to it a different biomarker comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A.

[0049] The present invention also provides a system comprising a plurality of capture reagents each of which has bound to it a different biomarker comprising (i) hepcidin, (ii)

inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), and (vii) apolipoprotein A1 (ApoA1).

[0050] Other aspects of the invention are described infra.

BRIEF DESCRIPTION OF THE FIGURES

[0051] FIG. **1** is a schematic illustration of a sample processing flowchart.

[0052] FIG. **2** is a representation of illustrative scatter plots from the assay protocol.

[0053] FIG. **3** is a representation of the results obtained from the peak table marker assay.

[0054] FIG. **4** is a representation of the scatter plot of transthyretin, illustrating the differences in long and short survival.

[0055] FIG. **5** is a representation of the scatter plot of serum amyloid A, illustrating the differences in long and short survival.

[0056] FIG. **6** is a representation of the scatter plot of PCI, illustrating the differences in long and short survival.

[0057] FIG. **7** is a representation of the scatter plot of CRP fragment, illustrating the differences in long and short survival.

[0058] FIG. **8** is a representation of the scatter plot of platelet factor 4, illustrating the differences in long and short survival.

[0059] FIG. **9** is a representation of the scatter plot of Apo A1-ApoAII complex, illustrating the differences in long and short survival.

[0060] FIG. **10** represents a table containing the results obtained using the assays described in Examples 1 and 2 and the equalizer beads.

[0061] FIG. **11** is a schematic representation of the seven biomarker assay system.

[0062] FIG. **12** is a table setting forth the patient distribution of the patients described in Example 2.

[0063] FIG. **13** is a table setting forth the Mann-Whitney p values for markers and clinical parameters (except for stage, which was performed using the Fisher's exact t-test) from Example 2.

[0064] FIG. **14**A-D represents scatter plots of age, CA125, transthyretin, and beta 2 microglobulin levels between long-survival (>1 year) and short survival (<1 year) patients.

[0065] FIGS. **15**A-D set forth Kaplan-Meier curve analysis of stage, CA125, beta-2 microglobulin, and the OvaRI for the seven marker panel. For the OvaRI score, patients were analyzed in total and also for the late stage patients alone (in red). Mantel-Cox P value for these comparisons are stage, 0.0095; CA125, 0.075; beta 2 microglobulin, 0.002; OvaRI index (all patients), 0.0018; OvaRI index (late stage) 0.0093.

DEFINITIONS

[0066] Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton et al. *Dictionary of Microbiology and Molecular Biology* (2nd ed. 1994); *The Cambridge Dictionary of Science and Technology* (Walker ed., 1988); *The Glossary of Genetics,* 5th Ed., R. Rieger et al. (eds.), Springer Verlag (1991); and Hale & Marham, *The Harper Collins Dictionary of Biology* (1991). As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

[0067] "Gas phase ion spectrometer" refers to an apparatus that detects gas phase ions. Gas phase ion spectrometers include an ion source that supplies gas phase ions. Gas phase ion spectrometers include, for example, mass spectrometers, ion mobility spectrometers, and total ion current measuring devices. "Gas phase ion spectrometry" refers to the use of a gas phase ion spectrometer to detect gas phase ions.

[0068] "Mass spectrometer" refers to a gas phase ion spectrometer that measures a parameter that can be translated into mass-to-charge ratios of gas phase ions. Mass spectrometers generally include an ion source and a mass analyzer. Examples of mass spectrometers are time-of-flight, magnetic sector, quadrupole filter, ion trap, ion cyclotron resonance, electrostatic sector analyzer and hybrids of these. "Mass spectrometry" refers to the use of a mass spectrometer to detect gas phase ions.

[0069] "Laser desorption mass spectrometer" refers to a mass spectrometer that uses laser energy as a means to desorb, volatilize, and ionize an analyte.

[0070] "Tandem mass spectrometer" refers to any mass spectrometer that is capable of performing two successive stages of m/z-based discrimination or measurement of ions, including ions in an ion mixture. The phrase includes mass spectrometers having two mass analyzers that are capable of performing two successive stages of m/z-based discrimination or measurement of ions tandem-in-space. The phrase further includes mass spectrometers having a single mass analyzer that is capable of performing two successive stages of m/z-based discrimination or measurement of ions tandem-in-time. The phrase thus explicitly includes Qq-TOF mass spectrometers, ion trap mass spectrometers, ion trap-TOF mass spectrometers, TOF-TOF mass spectrometers, Fourier transform ion cyclotron resonance mass spectrometers, electrostatic sector—magnetic sector mass spectrometers, and combinations thereof.

[0071] "Mass analyzer" refers to a sub-assembly of a mass spectrometer that comprises means for measuring a parameter that can be translated into mass-to-charge ratios of gas phase ions. In a time-of-flight mass spectrometer the mass analyzer comprises an ion optic assembly, a flight tube and an ion detector.

[0072] "Ion source" refers to a sub-assembly of a gas phase ion spectrometer that provides gas phase ions. In one embodiment, the ion source provides ions through a desorption/ionization process. Such embodiments generally comprise a probe interface that positionally engages a probe in an interrogatable relationship to a source of ionizing energy (e.g., a laser desorption/ionization source) and in concurrent communication at atmospheric or subatmospheric pressure with a detector of a gas phase ion spectrometer.

[0073] Forms of ionizing energy for desorbing/ionizing an analyte from a solid phase include, for example: (1) laser energy; (2) fast atoms (used in fast atom bombardment); (3) high energy particles generated via beta decay of radionucleides (used in plasma desorption); and (4) primary ions generating secondary ions (used in secondary ion mass spectrometry). The preferred form of ionizing energy for solid phase analytes is a laser (used in laser desorption/ionization), in particular, nitrogen lasers, Nd-Yag lasers and other pulsed laser sources. "Fluence" refers to the energy delivered per unit area of interrogated image. A high fluence source, such as

a laser, will deliver about 1 mJ/mm2 to 50 mJ/mm2. Typically, a sample is placed on the surface of a probe, the probe is engaged with the probe interface and the probe surface is struck with the ionizing energy. The energy desorbs analyte molecules from the surface into the gas phase and ionizes them.

[0074] Other forms of ionizing energy for analytes include, for example: (1) electrons that ionize gas phase neutrals; (2) strong electric field to induce ionization from gas phase, solid phase, or liquid phase neutrals; and (3) a source that applies a combination of ionization particles or electric fields with neutral chemicals to induce chemical ionization of solid phase, gas phase, and liquid phase neutrals.

[0075] "Solid support" refers to a solid material which can be derivatized with, or otherwise attached to, a capture reagent. Exemplary solid supports include probes, microtiter plates and chromatographic resins.

[0076] "Probe" in the context of this invention refers to a device adapted to engage a probe interface of a gas phase ion spectrometer (e.g., a mass spectrometer) and to present an analyte to ionizing energy for ionization and introduction into a gas phase ion spectrometer, such as a mass spectrometer. A "probe" will generally comprise a solid substrate (either flexible or rigid) comprising a sample presenting surface on which an analyte is presented to the source of ionizing energy.

[0077] "Seven biomarker panel" refers to a subset of the 13 biomarkers identified herein. Specifically, the seven biomarkers are (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating pep tide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1).

[0078] "Surface-enhanced laser desorption/ionization" or "SELDI" refers to a method of desorption/ionization gas phase ion spectrometry (e.g., mass spectrometry) in which the analyte is captured on the surface of a SELDI probe that engages the probe interface of the gas phase ion spectrometer. In "SELDI MS," the gas phase ion spectrometer is a mass spectrometer. SELDI technology is described in, e.g., U.S. Pat. No. 5,719,060 (Hutchens and Yip) and U.S. Pat. No. 6,225,047 (Hutchens and Yip).

[0079] "Surface-Enhanced Affinity Capture" or "SEAC" is a version of SELDI that involves the use of probes comprising an absorbent surface (a "SEAC probe").

[0080] "Adsorbent surface" refers to a surface to which is bound an adsorbent (also called a "capture reagent" or an "affinity reagent"). An adsorbent is any material capable of binding an analyte (e.g., a target polypeptide or nucleic acid). "Chromatographic adsorbent" refers to a material typically used in chromatography. Chromatographic adsorbents include, for example, ion exchange materials, metal chelators (e.g., nitriloacetic acid or iminodiacetic acid), immobilized metal chelates, hydrophobic interaction adsorbents, hydrophilic interaction adsorbents, dyes, simple biomolecules (e.g., nucleotides, amino acids, simple sugars and fatty acids) and mixed mode adsorbents (e.g., hydrophobic attraction/electrostatic repulsion adsorbents). "Biospecific adsorbent" refers an adsorbent comprising a biomolecule, e.g., a nucleic acid molecule (e.g., an aptamer), a polypeptide, a polysaccharide, a lipid, a steroid or a conjugate of these (e.g., a glycoprotein, a lipoprotein, a glycolipid, a nucleic acid (e.g., DNA)-protein conjugate). In certain instances the biospecific adsorbent can be a macromolecular structure such as a multiprotein complex, a biological membrane or a virus. Examples of biospecific adsorbents are antibodies, receptor proteins and nucleic acids. Biospecific adsorbents typically have higher specificity for a target analyte than chromatographic adsorbents. Further examples of adsorbents for use in SELDI can be found in U.S. Pat. No. 6,225,047 (Hutchens and Yip, "Use of retentate chromatography to generate difference maps," May 1, 2001).

[0081] In some embodiments, a SEAC probe is provided as a pre-activated surface which can be modified to provide an adsorbent of choice. For example, certain probes are provided with a reactive moiety that is capable of binding a biological molecule through a covalent bond. Epoxide and carbodiimidizole are useful reactive moieties to covalently bind biospecific adsorbents such as antibodies or cellular receptors.

[0082] "Adsorption" refers to detectable non-covalent binding of an analyte to an adsorbent or capture reagent.

[0083] "Surface-Enhanced Neat Desorption" or "SEND" is a version of SELDI that involves the use of probes comprising energy absorbing molecules chemically bound to the probe surface. ("SEND probe.") "Energy absorbing molecules" ("EAM") refer to molecules that are capable of absorbing energy from a laser desorption/ionization source and thereafter contributing to desorption and ionization of analyte molecules in contact therewith. The phrase includes molecules used in MALDI, frequently referred to as "matrix", and explicitly includes cinnamic acid derivatives, sinapinic acid ("SPA"), cyano-hydroxy-cinnamic acid ("CHCA") and dihydroxybenzoic acid, ferulic acid, hydroxyacetophenone derivatives, as well as others. It also includes EAMs used in SELDI. SEND is further described in U.S. Pat. No. 5,719,060 and U.S. patent application 60/408,255, filed Sep. 4, 2002 (Kitagawa, "Monomers And Polymers Having Energy Absorbing Moieties Of Use In Desorption/Ionization Of Analytes").

[0084] "Surface-Enhanced Photolabile Attachment and Release" or "SEPAR" is a version of SELDI that involves the use of probes having moieties attached to the surface that can covalently bind an analyte, and then release the analyte through breaking a photolabile bond in the moiety after exposure to light, e.g., laser light. SEPAR is further described in U.S. Pat. No. 5,719,060.

[0085] "Eluant" or "wash solution" refers to an agent, typically a solution, which is used to affect or modify adsorption of an analyte to an adsorbent surface and/or remove unbound materials from the surface. The elution characteristics of an eluant can depend, for example, on pH, ionic strength, hydrophobicity, degree of chaotropism, detergent strength and temperature.

[0086] "Analyte" refers to any component of a sample that is desired to be detected.

[0087] The term can refer to a single component or a plurality of components in the sample.

[0088] The "complexity" of a sample adsorbed to an adsorption surface of an affinity capture probe means the number of different protein species that are adsorbed.

[0089] "Molecular binding partners" and "specific binding partners" refer to pairs of molecules, typically pairs of biomolecules that exhibit specific binding. Molecular binding partners include, without limitation, receptor and ligand, antibody and antigen, biotin and avidin, and biotin and streptavidin.

[0090] "Monitoring" refers to recording changes in a continuously varying parameter.

[0091] "Biochip" refers to a solid substrate having a generally planar surface to which an adsorbent is attached. Frequently, the surface of the biochip comprises a plurality of addressable locations, each of which location has the adsorbent bound there. Biochips can be adapted to engage a probe interface and, therefore, function as probes.

[0092] "Protein biochip" refers to a biochip adapted for the capture of polypeptides. Many protein biochips are described in the art. These include, for example, protein biochips produced by Ciphergen Biosystems (Fremont, Calif.), Packard BioScience Company (Meriden Conn.), Zyomyx (Hayward, Calif.) and Phylos (Lexington, Mass.). Examples of such protein biochips are described in the following patents or patent applications: U.S. Pat. No. 6,225,047 (Hutchens and Yip, "Use of retentate chromatography to generate difference maps," May 1, 2001); International publication WO 99/51773 (Kuimelis and Wagner, "Addressable protein arrays," Oct. 14, 1999); U.S. Pat. No. 6,329,209 (Wagner et al., "Arrays of protein-capture agents and methods of use thereof," Dec. 11, 2001) and International publication WO 00/56934 (Englert et al., "Continuous porous matrix arrays," Sep. 28, 2000).

[0093] Protein biochips produced by Ciphergen Biosystems comprise surfaces having chromatographic or biospecific adsorbents attached thereto at addressable locations. Ciphergen ProteinChip® arrays include NP20, H4, H50, SAX-2, WCX-2, CM-10, IMAC-3, IMAC-30, LSAX-30, LWCX-30, IMAC40, PS-10, PS-20 and PG-20. These protein biochips comprise an aluminum substrate in the form of a strip. The surface of the strip is coated with silicon dioxide.

[0094] In the case of the NP-20 biochip, silicon oxide functions as a hydrophilic adsorbent to capture hydrophilic proteins.

[0095] H4, H50, SAX-2, WCX-2, CM-10, IMAC-3, IMAC-30, PS-10 and PS-20 biochips further comprise a functionalized, cross-linked polymer in the form of a hydrogel physically attached to the surface of the biochip or covalently attached through a silane to the surface of the biochip. The H4 biochip has isopropyl functionalities for hydrophobic binding. The H50 biochip has nonylphenoxy-poly(ethylene glycol)methacrylate for hydrophobic binding. The SAX-2 biochip has quaternary ammonium functionalities for anion exchange. The WCX-2 and CM-10 biochips have carboxylate functionalities for cation exchange. The IMAC-3 and IMAC-30 biochips have nitriloacetic acid functionalities that adsorb transition metal ions, such as Cu++ and Ni++, by chelation. These immobilized metal ions allow adsorption of peptide and proteins by coordinate bonding. The PS-10 biochip has carboimidizole functional groups that can react with groups on proteins for covalent binding. The PS-20 biochip has epoxide functional groups for covalent binding with proteins. The PS-series biochips are useful for binding biospecific adsorbents, such as antibodies, receptors, lectins, heparin, Protein A, biotin/streptavidin and the like, to chip surfaces where they function to specifically capture analytes from a sample. The PG-20 biochip is a PS-20 chip to which Protein G is attached. The LSAX-30 (anion exchange), LWCX-30 (cation exchange) and IMAC-40 (metal chelate) biochips have functionalized latex beads on their surfaces. Such biochips are further described in: WO 00/66265 (Rich et al., "Probes for a Gas Phase Ion Spectrometer," Nov. 9, 2000); WO 00/67293 (Beecher et al., "Sample Holder with Hydrophobic Coating for Gas Phase Mass Spectrometer," Nov. 9, 2000); U.S. patent application US20030032043A1 (Pohl and Papanu, "Latex Based Adsorbent Chip," Jul. 16, 2002) and U.S. patent application 60/350,110 (Um et al., "Hydrophobic Surface Chip," Nov. 8, 2001).

[0096] Upon capture on a biochip, analytes can be detected by a variety of detection methods selected from, for example, a gas phase ion spectrometry method, an optical method, an electrochemical method, atomic force microscopy and a radio frequency method. Gas phase ion spectrometry methods are described herein. Of particular interest is the use of mass spectrometry and, in particular, SELDI. Optical methods include, for example, detection of fluorescence, luminescence, chemiluminescence, absorbance, reflectance, transmittance, birefringence or refractive index (e.g., surface plasmon resonance, ellipsometry, a resonant mirror method, a grating coupler waveguide method or interferometry). Optical methods include microscopy (both confocal and non-confocal), imaging methods and non-imaging methods. Immunoassays in various formats (e.g., ELISA) are popular methods for detection of analytes captured on a solid phase. Electrochemical methods include voltametry and amperometry methods. Radio frequency methods include multipolar resonance spectroscopy.

[0097] "Marker" in the context of the present invention refers to a polypeptide (of a particular apparent molecular weight), which is differentially present in a sample taken from patients having human cancer as compared to a comparable sample taken from control subjects (e.g., a person with a negative diagnosis or undetectable cancer, normal or healthy subject). The term "biomarker" is used interchangeably with the term "marker."

[0098] The term "measuring" means methods which include detecting the presence or absence of marker(s) in the sample, quantifying the amount of marker(s) in the sample, and/or qualifying the type of biomarker. Measuring can be accomplished by methods known in the art and those further described herein, including but not limited to SELDI and immunoassay. Any suitable methods can be used to detect and measure one or more of the markers described herein. These methods include, without limitation, mass spectrometry (e.g., laser desorption/ionization mass spectrometry), fluorescence (e.g. sandwich immunoassay), surface plasmon resonance, ellipsometry and atomic force microscopy.

[0099] The phrase "differentially present" refers to differences in the quantity and/or the frequency of a marker present in a sample taken from patients having human cancer as compared to a control subject. For example, the IAIH4 fragment is present at an elevated level in samples of ovarian cancer patients compared to samples from control subjects. In contrast, Apo A1 and transthyretin described herein are present at a decreased level in samples of ovarian cancer patients compared to samples from control subjects. Furthermore, a marker can be a polypeptide, which is detected at a higher frequency or at a lower frequency in samples of human cancer patients compared to samples of control subjects. A marker can be differentially present in terms of quantity, frequency or both.

[0100] A polypeptide is differentially present between two samples if the amount of the polypeptide in one sample is statistically significantly different from the amount of the polypeptide in the other sample. For example, a polypeptide is differentially present between the two samples if it is present at least about 120%, at least about 130%, at least about 150%, at least about 180%, at least about 200%, at least about 300%, at least about 500%, at least about 700%, at least

about 900%, or at least about 1000% greater than it is present in the other sample, or if it is detectable in one sample and not detectable in the other.

[0101] Alternatively or additionally, a polypeptide is differentially present between two sets of samples if the frequency of detecting the polypeptide in the ovarian cancer patients' samples is statistically significantly higher or lower than in the control samples. For example, a polypeptide is differentially present between the two sets of samples if it is detected at least about 120%, at least about 130%, at least about 150%, at least about 180%, at least about 200%, at least about 300%, at least about 500%, at least about 700%, at least about 900%, or at least about 1000% more frequently or less frequently observed in one set of samples than the other set of samples.

[0102] "Diagnostic" means identifying the presence or nature of a pathologic condition, i.e., ovarian cancer. Diagnostic methods differ in their sensitivity and specificity. The "sensitivity" of a diagnostic assay is the percentage of diseased individuals who test positive (percent of "true positives"). Diseased individuals not detected by the assay are "false negatives." Subjects who are not diseased and who test negative in the assay, are termed "true negatives." The "specificity" of a diagnostic assay is 1 minus the false positive rate, where the "false positive" rate is defined as the proportion of those without the disease who test positive. While a particular diagnostic method may not provide a definitive diagnosis of a condition, it suffices if the method provides a positive indication that aids in diagnosis.

[0103] A "test amount" of a marker refers to an amount of a marker present in a sample being tested. A test amount can be either in absolute amount (e.g., μg/ml) or a relative amount (e.g., relative intensity of signals).

[0104] A "diagnostic amount" of a marker refers to an amount of a marker in a subject's sample that is consistent with a diagnosis of ovarian cancer. A diagnostic amount can be either in absolute amount (e.g., μg/ml) or a relative amount (e.g., relative intensity of signals).

[0105] A "control amount" of a marker can be any amount or a range of amount, which is to be compared against a test amount of a marker. For example, a control amount of a marker can be the amount of a marker in a person without ovarian cancer.

[0106] A control amount can be either in absolute amount (e.g., μg/ml) or a relative amount (e.g., relative intensity of signals).

[0107] "Antibody" refers to a polypeptide ligand substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof, which specifically binds and recognizes an epitope (e.g., an antigen). The recognized immunoglobulin genes include the kappa and lambda light chain constant region genes, the alpha, gamma, delta, epsilon and mu heavy chain constant region genes, and the myriad immunoglobulin variable region genes. Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. This includes, e.g., Fab' and $F(ab)'_2$ fragments.

[0108] The term "antibody," as used herein, also includes antibody fragments either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA methodologies. It also includes polyclonal antibodies, monoclonal antibodies, chimeric antibodies, humanized antibodies, or single chain antibodies. "Fc" portion of an antibody refers to that portion of an immunoglobulin heavy chain that comprises one or more heavy chain constant region domains, CH_1, CH_2 and CH_3, but does not include the heavy chain variable region.

[0109] "Managing subject treatment" refers to the behavior of the clinician or physician subsequent to the determination of ovarian cancer status. For example, if the result of the methods of the present invention is inconclusive or there is reason that confirmation of status is necessary, the physician may order more tests. Alternatively, if the status indicates that surgery is appropriate, the physician may schedule the patient for surgery. Likewise, if the status is negative, e.g., late stage ovarian cancer or if the status is acute, no further action may be warranted. Furthermore, if the results show that treatment has been successful, no further management may be necessary.

DETAILED DESCRIPTION OF THE INVENTION

[0110] The present invention provides sensitive and quick methods and kits that are useful for determining the survival status of patients with ovarian cancer by measuring and identifying particular biomarkers. The detection and measurement of these biomarkers in patient samples provides information that diagnosticians can correlate with a survival status of human ovarian cancer patients.

[0111] More specifically, thirteen (13) biomarkers were discovered and characterized, in accordance with the methods described herein as (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, (xii) m/z value 7900.679 protein and (xiii) truncated serum amyloid A.

[0112] Some of these biomarkers have been disclosed in PCT/US2005/010783 (WO 2005/098447); US Patent Application Publication 2005/0059013; PCT/US03/00531 (WO03/057014); PCT/US2003/024636 (WO 2004/012588); PCT/US06/08578; and U.S. patent application Ser. No. 11/373,833, all of which documents are incorporated herein by reference in their entirety.

[0113] The m/z values of these thirteen biomarkers measured on mass spectrometer—are centered around (accuracy affected by a mass spectrometer's mass resolving capability).

[0114] 1. hepcidin: 2791D,

[0115] 2. ITIH4: 3272D,

[0116] 3. CTAPIII: 9293D,

[0117] 4. TTR: 13.8 KD,

[0118] 5. TFR: 79.9 KD,

[0119] 6. B2M: 11.7 KD, and

[0120] 7. ApoA1: 28K.

[0121] 8. CRP N-terminal fragment: 2222.962

[0122] 9. ApoAI-ApoAII dimer: 45635.89

[0123] 10. Platelet Factor 4, N-terminal truncation: 7197.615

[0124] 11. Protein: 3897.378

[0125] 12. Protein: 7900.679

[0126] 13. Truncated Serum Amyloid A: 11183.28

[0127] These biomarkers assess a patient's survival status after having developed ovarian cancer and could potentially provide additional information to physicians for clinical decision-making. This is supported by Receiver-Operating Characteristic (ROC) curve analysis in an independent validation.

For example, several large-scale studies have suggested that ovarian cancer patients with surgical procedures operated by gynecological oncologists tend to have a better long-term survival. However, other studies concluded that currently only about one third of ovarian cancer patients undergoing surgical procedures in the US are treated by gynecological oncologists. With the current total number of gynecological oncologists available, it is still not practical to have all patients undergoing surgery for suspected ovarian cancer be operated by gynecologic oncologists. The biomarkers have the potential to be used to identify patients with the lower probability of surviving ovarian cancer and recommend them for treatment by gynecologic oncologists.

[0128] High-throughput protein profiling combined with effective use of bioinformatics tools provides a useful approach to screening for cancer markers. Briefly, the system used in the present invention utilizes chromatographic ProteinChip® Arrays to assay samples using SELDI (Surface Enhanced Laser Desorption/Ionization). Proteins bound to the arrays are read in a ProteinChip® Reader, a time-of-flight mass spectrometer.

[0129] The present invention is based upon the discovery of protein markers that are differentially present in samples of ovarian cancer patients and control subjects, and the application of this discovery in methods and kits for determining ovarian cancer status. These protein markers are found in samples from ovarian cancer patients at levels that are different than the levels in samples from women in whom human cancer is undetectable. Accordingly, the amount of one or more markers found in a test sample compared to a control, or the presence or absence of one or more markers in the test sample provides useful information regarding the ovarian cancer status of the patient.

I. DESCRIPTION OF THE BIOMARKERS

1. Hepcidin

[0130] Hepcidin was originally identified as a 25 amino acid peptide (hepcidin-25) in human plasma and urine, exhibiting antimicrobial activity. The full-length hepcidin precursor is an 84 amino acid protein (SwissProt Accession No. P81172) comprising a signal sequence and a pro-region (see Kulaksiz, H. et al. (2004) Gut 53:735-743). The hepcidin biomarkers of the present invention are derived from the C-terminus of the full-length hepcidin protein. Hepcidin is recognized by antibodies available from, e.g., U.S. Biological (catalog H2008-51) (www.usbio.net, Swampscott, Mass.). Four different variants of hepcidin useful as biomarkers of this invention are characterized by calculated mass-to-charge ratios of 2789, 2673, 2436, and 2191.

[0131] Hepcidin was discovered to be a biomarker for ovarian and endometrial cancer using SELDI technology employing ProteinChip arrays from Ciphergen Biosystems, Inc. (Fremont, Calif.) ("Ciphergen"). More specifically, hepcidin levels can distinguish ovarian cancer from each of non-cancer, cervical cancer and benign ovarian disease. It also can distinguish between endometrial cancer and non-cancer. Urine and serum samples were collected from subjects diagnosed with ovarian cancer, endometrial cancer, cervical cancer and subjects diagnosed as normal or as having benign disease. The samples were applied to SELDI biochips, with or without co-immunoprecipitation with the ITIH4 3272 m/z fragment (see International Publication Number WO 2004/099432), using an antibody raised against ITIH4 fragment 1 (discussed in more detail below), and spectra of polypeptides in the samples were generated by time-of-flight mass spectrometry on a Ciphergen PBSIIc or PCS4000 mass spectrometer. The spectra thus obtained were analyzed by Ciphergen Express™ Data Manager Software with Biomarker Wizard and Biomarker Pattern Software from Ciphergen Biosystems, Inc. The mass spectra for each group were subjected to scatter plot analysis. A Mann-Whitney test analysis was employed to compare ovarian cancer and control groups for each protein cluster in the scatter plot, and proteins were selected that differed significantly ($p<0.01$) between the two groups.

[0132] The amino acid sequences of hepcidin-25, -24, -22 and -20 are:

```
Hepcidin-25
(SEQ ID NO: 1):    DTHFPICIFCCGCCHRSKCGMCCKT

Hepcidin-24
(SEQ ID NO: 2):     THFPIGTFCCGCCHRSKCGMCCKT

Hepcidin-22
(SEQ ID NO: 3):       FPICIFCCGCCHRSKCGMCCKT

Hepcidin-20
(SEQ ID NO: 4):         ICIFCCGCCHRSKCGMCCKT
```

[0133] The biomarkers of this invention are further characterized by their binding properties on chromatographic surfaces. Hepcidin binds to cation exchange adsorbents (e.g., the Ciphergen® CM10 ProteinChip® array) after washing with 100 mM sodium acetate at pH 4. Hepcidin also binds to metal chelate adsorbents (e.g., the Ciphergen® IMAC-Cu^{++} ProteinChip® array) after washing with 100 mM sodium phosphate, 0.5 M NaCl, pH 7 or organic buffer. Hepcidin may be visualized in the same assay as used to visualize ITIH4, as described below.

[0134] The preferred biological sources for detection of hepcidin is urine or serum. Hepcidin may also be detected in ascites fluid and cyst fluid, tissues and organs such as liver, and in specific cells, such as macrophages.

2. IAIH4 Fragments

[0135] Other biomarkers that are useful in the methods of the present invention one or more of a closely related set of cleavage fragments of inter-α-trypsin inhibitor heavy chain H4 precursor, also referred to alternatively herein as "ITIH4 fragments." ITIH4 fragments are described as biomarkers for ovarian cancer in US patent publication 2005-0059013 A1, International Patent Publication WO 2005/098447 and Fung et al., Int. J. Cancer 115:783-789 (2005). ITIH4 fragments can be selected from the group consisting of ITIH4 fragment no. 1, ITIH4 fragment no. 2, and ITIH4 fragment no. 3.

[0136] The amino acid sequences of the ITIH4 fragments were determined to be: ITIH4 fragment 1 (SEQ ID NO: 5): MNFRPGVLSSRQLGLPGPPDVPDHAAYHPF ITIH4 fragment 2 (SEQ ID NO: 6): PGVLSSRQLGLPGPPDVPDHAAYHPF ITIH4 fragment 3 (SEQ ID NO: 7): GVLSSRQLGLPGPPDVPDHAAYHPF. The present invention also includes all other known fragments of ITIHA4.

[0137] ITIH4 precursor is a 930 amino acid protein (SwissProt Q14624). ITIH4 fragment 1 spans amino acids 658-687 of human ITIH4 precursor. ITIH4 fragment 2 spans amino acids 662-687 of ITIH4 precursor. ITIH4 fragment 3 spans amino acids 663-687 of ITIH4 precursor.

[0138] Additionally, preferred methods of the present invention include the use of modified forms of ITIH4 fragment. Modification of ITIH4 fragment may include the post-translational addition of various chemical groups, for example, glycosylation, lipidation, cysteinylation, and glutathionylation.

3. CTAPIII

[0139] Another biomarker that is useful in the methods of the present invention is CTAP-III (connective tissue activating peptide III), derived from platelet basic protein. CTAP-III is described as a biomarker for ovarian cancer in U.S. provisional patent application 60/693,324, filed Jun. 22, 2005 (Zhang et al.). CTAP-III is an 85 amino acid protein (SwissProt P02775) (SEQ ID NO: 8). CTAP-III is recognized by antibodies available from, e.g., Chemicon International (catalog 1484P) (www.chemicon.com, Temecula, Calif.) CTAP-III is a fragment of platelet basic protein and includes amino acids 44-128 of platelet basic protein.

3. Transthyretin

[0140] Transthyretin, also called "pre-albumin" is another biomarker that is useful in the methods of the present invention. Transthyretin and variants thereof are described as biomarkers for ovarian cancer in US patent publication 2005-0059013 A1 and International Patent Publication WO 2005/098447. Unmodified transthyretin is a 127 amino acid protein deriving from a 147 amino acid precursor (SwissProt Accession No. P02766) (SEQ ID NO: 9). The transthyretin biomarkers of the present invention include any or all of unmodified transthyretin and various modified forms. Transthyretin is recognized by antibodies available from, e.g., Dako (catalog A0002) (www.dako.com, Glostrup, Denmark).

[0141] In mass spectra of serum, transthyretin appears as a cluster of peaks around 13.9K Daltons. This cluster includes several forms of transthyretin including unmodified transthyretin, S-sulfonated thransthyretin, S-cysteinylated transthyretin, S-Gly-Cys transthyretin and S-glutathionylated transthryetin. Any and/or all of these is useful as a biomarker for ovarian cancer. However, the S-cysteinylated version represents the dominant form in the spectrum and is a preferred biomarker when using mass spectrometry. Another variant of transthyretin useful as a biomarker is transthyretin ΔN10.

5. Transferrin

[0142] Another biomarker that is useful in the methods of the present invention is transferrin. Transferrin is described as a biomarker for ovarian cancer in US patent publication 2005-0214760 A1. Transferrin is a 679 amino acid protein derived from a 698 amino acid precursor (GenBank Accession No. NP_001054 GI:4557871; SwissProt Accession No. P02787) (SEQ ID NO: 10). Transferrin is recognized by antibodies available from, e.g., Dako (catalog A006) (www.dako.com, Glostrup, Denmark). Transferrin is glycosylated. Therefore, the measured molecular weight is higher than the theoretical weight, which does not take glycosylation into account.

6. Beta-2 Microglobin

[0143] Another biomarker that is useful in the methods of the present invention is β2-microglobulin. β2-microglobulin is described as a biomarker for ovarian cancer in U.S. provisional patent publication 60/693,679, filed Jun. 24, 2005 (Fung et al.). β2-microglobulin is a 99 amino acid protein derived from an 119 amino acid precursor (GI: 179318; SwissProt Accession No. P61769) (SEQ ID NO: 11). β2-microglobulin is recognized by antibodies available from, e.g., Abcam (catalog AB759) (www.abcam.com, Cambridge, Mass.).

7. Apolipoprotein A1

[0144] Another biomarker that is useful in the methods of the present invention is apolipoprotein A1, also referred to as Apo A1. Apo A1 is described as a biomarker for ovarian cancer in US patent publication 2005-0059013 A1 and International Patent Publication WO 2005/098447. Apo A1 is a 243 amino acid protein derived from a 267 amino acid precursor (SwissProt Accession No. P02647) SEQ ID NO: 12). Apo A1 is recognized by antibodies available from, e.g., EMD Biosciences, Inc. (catalog 178474) (www.emdbiosciences.com/home.asp, San Diego, Calif.). ApoA1 can be visualized on H50 arrays or IMAC30 or IMAC50 arrays, but is preferentially visualized on H50 arrays.

[0145] Preferred methods of the present invention include the use of modified forms of Apo A1, such as C-terminal truncation of Apo A1 (amino acids-1 thru 190-200). Modification of Apo A1 may include the post-translational addition of various chemical groups, for example, glycosylation and lipidation.

8. CRP N-Terminal Fragment

[0146] C-reactive protein (CRP) and fragments thereof, is a well-known acute phase protein. C-reactive protein (CRP) is a plasma protein, an acute phase protein produced by the liver. It is a member of the pentraxin family of proteins. It should not be confused with C-peptide or Protein C. The Genebank accession number is CAA39671 and SwissProt No. P02741 (fragment bolded). Amino acid sequence:

mekllcflvl tslshafgqt **dmsrkafvfp kesdtsy**vsl

kapltkplka ftvclhfyte lsstrgtvfs rmpprdktmr

ffifwskdig ysftvggsei lfevpevtva pvhictswes

asgivefwvd gkprvrkslk kgytvgaeas iilgqeqdsf

ggnfegsqsl vgdignvnmw dfvlspdein tiylggpfsp

nvlnwralky evqgevftkp qlwp.

9. APOA1-APOAII Dimer

[0147] Apolipoproteins are well known to form dimers. The Genebank accession number for Apo AII CAA26665. The amino acid sequence is:

mkllaatvll lticslegal vrrqakepcv eslvsqyfqt

vtdygkdlme kvkspelqae aksyfekske qltplikkag

telvnflsyf velgtqpatq.

10. Platelet Factor 4

[0148] Platelet factor 4 (PF4), a 30,000 dalton high-affinity heparin-binding protein, is produced in megakaryocytes and stored in platelet alpha granules.[1] It is secreted by stimulated platelets and its plasma biological half-life is <5 minutes. It

constitutes 5% of the protein found in circulating platelets. It is a member of the chemokine family of proteins. Platelet factor 4 is released from activated platelets and in vivo, it is stored both in the endothelium and on hepatocyte surfaces. The primary function of platelet factor 4 is to neutralize the anticoagulant effect of heparin. Heparin neutralization occurs by the binding of platelet factor 4 to heparin at sites that are different from heparin's antithrombin binding site. Heparin therapy induces the release of platelet factor 4 from endothelial cells, and levels are markedly increased during the initiation of therapy but diminish with time as stores are exhausted. In vivo release of PF4 occurs with platelet hyperactivity and this may result from platelet interaction with subendothelial structures, artificial surfaces, atherosclerotic plaques, and thrombin. Increased levels of platelet factor 4 are observed in a variety of clinical states that are associated with activation of platelets. The Genebank accession number is AAK29643. The amino acid sequence is:

```
mssaagfcas rpgllflgll Ilplvvafas aeaeedgdlq

clcvkttsqv rprhitslev ikagphcpta qliatlkngr

kicldlqapl ykkiikklle s.
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11. PCI

[0149] Protein C inhibitor (PCI) and fragments thereof, a plasma serine protease inhibitor (Genebank accession No. AAB30461), inhibits several proteases including the anticoagulant enzyme, activated protein C (APC), and the coagulation enzymes, thrombin and factor Xa and occurs at high concentration in seminal plasma. Amino acid sequence:

```
mqlflllclv llspqgaslh rhhpremkkr vedlhvgatv

apssrrdftf dlyralasaa psqniffspv sismslamls

lgagsstkmq ileglglnlq kssekelhrg fqqllqelnq

prdgfqlslg nalftdlvvd lqdtfvsamk tlyladtfpt

nfrdsagamk qindyvakqt kgkivdllkn ldsnavvimv

nyiffkakwe tsfnhkgtqe qdfyvtsetv vrvpmmsred

qyhylldrnl scrvvgvpyq gnatalfilp segkmqqven

glsektlrkw lkmfkkrqle lylpkfsieg syqlekvlps

lgisnvftsh adlsgisnhs niqvsemvhk avvevdesg

raaaatgtif tfrsarlnsq rlvfnrpflm fivdnnilfl

gkvnrp.
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12. Protein M/Z 7900.679: Platelet Factor IV sodium Adduct

[0150] Sodium adducts are mass spectrometry-induced byproducts often seen in IMAC array profiling since the binding buffer contains 0.5 M NaCl. These adducts are detectable even with tandem MS instruments.

13. Truncated Serum Amyloid A

[0151] Serum amyloid A (SAA) proteins are a family of apolipoproteins found predominantly associated with high-density lipoprotein (HDL) in plasma, with different isoforms being unequally expressed constitutively and in response to inflammatory stimuli. Although synthesized primarily in the liver, extrahepatic tissue_cellular expression of SAA has been widely documented. SAA has been linked to functions related to inflammation, pathogen defense, HDL metabolism, and cholesterol transport and thereby has been implicated in several pathological conditions including atherosclerosis, rheumatoid arthritis, Alzheimer's disease, and cancer. SAA is known best for its role during the acute phase response to an inflammatory stimulus such as infection, tissue injury, and trauma. During active inflammation the concentration of SAA in plasma can increase up to 1.000-fold within 24 h. It is believed that persistently high levels of SAA during chronic inflammation may contribute to the occasional development of the potentially fatal disease reactive amyloidosis (amyloid A (AA) amyloidosis). The Genebank accession number is P02735. The amino acid sequence is:

```
mklltglvfc slvlgvssrs ffsflgeafd gardmwrays

dmreanyigs dkyfhargny daakrgpggv waaeaisdar

eniqrffghg aedsladqaa newgrsgkdp nhfrpaglpe ky.
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14. Other Biomarkers

[0152] In additional to the above identified biomarkers, other markers such serum tissue factor and p53 are biomarkers of the present invention for ovarian cancer. These markers can be used in conjunction with the biomarkers identified above for determining the prognosis of an ovarian cancer patient.

[0153] Because the biomarker of this invention is characterized by mass-to-charge ratio, binding properties and spectral shape, they can be detected by mass spectrometry without knowing their specific identity. However, if desired, biomarkers whose identity is not determined can be identified by, for example, determining the amino acid sequence of the polypeptides. For example, a biomarker can be peptide-mapped with a number of enzymes, such as trypsin or V8 protease, and the molecular weights of the digestion fragments can be used to search databases for sequences that match the molecular weights of the digestion fragments generated by the various enzymes. Alternatively, protein biomarkers can be sequenced using tandem MS technology. In this method, the protein is isolated by, for example, gel electrophoresis. A band containing the biomarker is cut out and the protein is subject to protease digestion. Individual protein fragments are separated by a first mass spectrometer. The fragment is then subjected to collision-induced cooling, which fragments the peptide and produces a polypeptide ladder. A polypeptide ladder is then analyzed by the second mass spectrometer of the tandem MS. The difference in masses of the members of the polypeptide ladder identifies the amino acids in the sequence. An entire protein can be sequenced this way, or a sequence fragment can be subjected to database mining to find identity candidates.

[0154] U.S. patent application Ser. No. 11/373,833, filed Mar. 10, 2006 is hereby incorporated by reference in its entirety.

[0155] It has been found that proteins frequently exist in a sample in a plurality of different forms characterized by a detectably different mass. These forms can result from either,

or both, of pre- and post-translational modification. Pre-translational modified forms include allelic variants, slice variants and RNA editing forms. Post-translationally modified forms include forms resulting from proteolytic cleavage (e.g., fragments of a parent protein), glycosylation, phosphorylation, lipidation, oxidation, methylation, cystinylation, sulphonation and acetylation. The collection of proteins including a specific protein and all modified forms of it is referred to herein as a "protein cluster." The collection of all modified forms of a specific protein, excluding the specific protein, itself, is referred to herein as a "modified protein cluster." Modified forms of the biomarker of this invention also may be used, themselves, as biomarkers. In certain cases the modified forms may exhibit better discriminatory power in diagnosis than the specific forms set forth herein.

[0156] Modified forms of a biomarker can be initially detected by any methodology that can detect and distinguish the modified from the biomarker. A preferred-method for initial detection involves first capturing the biomarker and modified forms of it, e.g., with biospecific capture reagents, and then detecting the captured proteins by mass spectrometry. More specifically, the proteins arc captured using biospecific capture reagents, such as antibodies, aptarners or Affibodies that recognize the biomarker and modified forms of it. This method also will also result in the capture of protein interactors that are bound to the proteins or that are otherwise recognized by antibodies and that, themselves, can be biomarkers. In certain embodiments, the biospecific capture reagents are bound to a solid phase. Then, the captured proteins can be detected by SELDI mass spectrometry or by eluting the proteins from the capture reagent and detecting the eluted proteins by traditional MALDI or by SELDI. The use of mass spectrometry is especially attractive because it can distinguish and quantify modified forms of a protein based on mass and without the need for labeling.

[0157] Preferably, the biospecific capture reagent is bound to a solid phase, such as a bead, a plate, a membrane or a chip. Methods of coupling biomolecules, such as antibodies, to a solid phase are well known in the art. They can employ, for example, bifunctional linking agents, or the solid phase can be derivatized with a reactive group, such as an epoxide or an imidizole, that will bind the molecule on contact. Biospecific capture reagents against different target proteins can be mixed in the same place, or they can be attached to solid phases in different physical or addressable locations. For example, one can load multiple columns with derivatized beads, each column able to capture a single protein cluster. Alternatively, one can pack a single column with different beads derivatized with capture reagents against a variety of protein clusters, thereby capturing all the analytes in a single place. Accordingly, antibody-derivatized bead-based technologies, such as xMAP technology of Luminex (Austin, Tex.) can be used to detect the protein clusters. However, the biospecific capture reagents must be specifically directed toward the members of a cluster in order to differentiate them.

[0158] In yet another embodiment, the surfaces of biochips can be derivatized with the capture reagents directed against protein clusters either in the same location or in physically different addressable locations. One advantage of capturing different clusters in different addressable locations is that the analysis becomes simpler.

[0159] After identification of modified forms of a protein and correlation with the clinical parameter of interest, the modified form can be used as a biomarker in any of the methods of this invention. At this point, detection of the modified form can be accomplished by any specific detection methodology including affinity capture followed by mass spectrometry, or traditional immunoassay directed specifically the modified form. Immunoassay requires biospecific capture reagents, such as antibodies, to capture the analytes. Furthermore, if the assay must be designed to specifically distinguish protein and modified forms of protein. This can be done, for example, by employing a sandwich assay in which one antibody captures more than one form and second, distinctly labeled antibodies, specifically bind, and provide distinct detection of, the various forms. Antibodies can be produced by immunizing animals with the biomolecules. This invention contemplates traditional immunoassays including, for example, sandwich immunoassays including ELISA or fluorescence-based immunoassays, as well as other enzyme immunoassays.

II. TEST SAMPLES

A) Subject Types

[0160] Samples are collected from subjects, e.g., women, who want to establish ovarian cancer status. The subjects may be women who have been determined to have a high risk of ovarian cancer based on their family history. Other patients include women who have ovarian cancer or women diagnosed with a pelvic mass and the test is being used to determine the effectiveness of therapy or treatment they are receiving. Also, patients could include healthy women who are having a test as part of a routine examination, or to establish baseline levels of the biomarkers. Samples may be collected from women who had been diagnosed with ovarian cancer and received treatment to eliminate the cancer, or perhaps are in remission.

B) Types of Sample and Preparation of the Sample

[0161] The markers can be measured in different types of biological samples. The sample is preferably a biological fluid sample. Examples of a biological fluid sample useful in this invention include blood, blood serum, plasma, vaginal secretions, urine, ovarian cyst fluid, tears, saliva, etc. Because all of the markers are found in blood serum, blood serum is a preferred sample source for embodiments of the invention.

[0162] If desired, the sample can be prepared to enhance detectability of the markers. For example, to increase the detectability of markers, a blood serum sample from the subject can be preferably fractionated by, e.g., Cibacron blue agarose chromatography and single stranded DNA affinity chromatography, anion exchange chromatography, affinity chromatography (e.g., with antibodies) and the like. The method of fractionation depends on the type of detection method used. Any method that enriches for the protein of interest can be used. Sample preparations, such as pre-fractionation protocols, are optional and may not be necessary to enhance detectability of markers depending on the methods of detection used. For example, sample preparation may be unnecessary if antibodies that specifically bind markers are used to detect the presence of markers in a sample.

[0163] Typically, sample preparation involves fractionation of the sample and collection of fractions determined to contain the biomarkers. Methods of pre-fractionation include, for example, size exclusion chromatography, ion exchange chromatography, heparin chromatography, affinity chromatography, sequential extraction, gel electrophoresis

and liquid chromatography. The analytes also may be modified prior to detection. These methods are useful to simplify the sample for further analysis. For example, it can be useful to remove high abundance proteins, such as albumin, from blood before analysis. Examples of methods of fractionation are described in PCT/US03/00531 (incorporated herein in its entirety).

[0164] Preferably, the sample is pre-fractionated by anion exchange chromatography. Anion exchange chromatography allows pre-fractionation of the proteins in a sample roughly according to their charge characteristics. For example, a Q anion-exchange resin can be used (e.g., Q HyperD F, Biosepra), and a sample can be sequentially eluted with eluants having different pH's. Anion exchange chromatography allows separation of biomolecules in a sample that are more negatively charged from other types of biomolecules. Proteins that are eluted with an eluant having a high pH is likely to be weakly negatively charged, and a fraction that is eluted with an eluant having a low pH is likely to be strongly negatively charged. Thus, in addition to reducing complexity of a sample, anion exchange chromatography separates proteins according to their binding characteristics.

[0165] In preferred embodiments, the serum samples are fractionated via anion exchange chromatography. Signal suppression of lower abundance proteins by high abundance proteins presents a significant challenge to SELDI mass spectrometry. Fractionation of a sample reduces the complexity of the constituents of each fraction. This method can also be used to attempt to isolate high abundance proteins into a fraction, and thereby reduce its signal suppression effect on lower abundance proteins. Anion exchange fractionation separates proteins by their isoelectric point (pI). Proteins are comprised of amino acids, which are ambivalent-their charge changes based on the pH of the environment to which they are exposed. A protein's pI is the pH at which the protein has no net charge. A protein assumes a neutral charge when the pH of the environment is equivalent to pI of the protein. When the pH rises above the pI of the protein, the protein assumes a net negative charge. Similarly, when the pH of the environment falls below the pI of the protein, the protein has a net positive charge. The serum samples were fractionated according to the protocol set forth in the Examples below to obtain the markers described herein.

[0166] After capture on anion exchange, proteins were eluted in a series of step washes at pH 9, pH 7, pH 5, pH 4 and pH 3. A panel of three potential biomarkers was discovered by UMSA analysis of profiling data of three fractions (pH 9/flow through, pH 4, and organic solvent). Two of the peaks were from fraction pH 4 at m/z of 12828 and 28043, both down-regulated in the cancer group, and the third was from fraction pH 9/flow through at m/z of 3272, up-regulated in the cancer group. All bound to the immobilized metal affinity chromatography array charged with copper ions (IMAC3-Cu).

[0167] Biomolecules in a sample can also be separated by high-resolution electrophoresis, e.g., one or two-dimensional gel electrophoresis. A fraction containing a marker can be isolated and further analyzed by gas phase ion spectrometry. Preferably, two-dimensional gel electrophoresis is used to generate two-dimensional array of spots of biomolecules, including one or more markers. See, e.g., Jungblut and Thiede, *Mass Spectr. Rev.* 16:145-162 (1997).

[0168] The two-dimensional gel electrophoresis can be performed using methods known in the art. See, e.g., Deutscher ed., *Methods In Enzymology vol.* 182. Typically, biomolecules in a sample are separated by, e.g., isoelectric focusing, during which biomolecules in a sample are separated in a pH gradient until they reach a spot where their net charge is zero (i.e., isoelectric point). This first separation step results in one-dimensional array of biomolecules. The biomolecules in one-dimensional array is further separated using a technique generally distinct from that used in the first separation step. For example, in the second dimension, biomolecules separated by isoelectric focusing are further separated using a polyacrylamide gel, such as polyacrylamide gel electrophoresis in the presence of sodium dodecyl sulfate (SDS-PAGE). SDS-PAGE gel allows further separation based on molecular mass of biomolecules. Typically, two-dimensional gel electrophoresis can separate chemically different biomolecules in the molecular mass range from 1000-200,000 Da within complex mixtures. The pI range of these gels is about 3-10 (wide range gels).

[0169] Biomolecules in the two-dimensional array can be detected using any suitable methods known in the art. For example, biomolecules in a gel can be labeled or stained (e.g., Coomassie Blue or silver staining). If gel electrophoresis generates spots that correspond to the molecular weight of one or more markers of the invention, the spot can be further analyzed by gas phase ion spectrometry. For example, spots can be excised from the gel and analyzed by gas phase ion spectrometry. Alternatively, the gel containing biomolecules can be transferred to an inert membrane by applying an electric field. Then a spot on the membrane that approximately corresponds to the molecular weight of a marker can be analyzed by gas phase ion spectrometry. In gas phase ion spectrometry, the spots can be analyzed using any suitable techniques, such as MALDI or SELDI (e.g., using ProteinChip® array) as described herein.

[0170] Prior to gas phase ion spectrometry analysis, it may be desirable to cleave biomolecules in the spot into smaller fragments using cleaving reagents, such as proteases (e.g., trypsin). The digestion of biomolecules into small fragments provides a mass fingerprint of the biomolecules in the spot, which can be used to determine the identity of markers if desired.

[0171] High performance liquid chromatography (HPLC) can also be used to separate a mixture of biomolecules in a sample based on their different physical properties, such as polarity, charge and size. HPLC instruments typically consist of a reservoir of mobile phase, a pump, an injector, a separation column, and a detector. Biomolecules in a sample are separated by injecting an aliquot of the sample onto the column. Different biomolecules in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase. A fraction that corresponds to the molecular weight and/or physical properties of one or more markers can be collected. The fraction can then be analyzed by gas phase ion spectrometry to detect markers. For example, the spots can be analyzed using either MALDI or SELDI (e.g., using ProteinChip® array) as described herein.

[0172] Optionally, a marker can be modified before analysis to improve its resolution or to determine its identity. For example, the markers may be subject to proteolytic digestion before analysis. Any protease can be used. Proteases, such as trypsin, that are likely to cleave the markers into a discrete number of fragments are particularly useful. The fragments that result from digestion function as a fingerprint for the markers, thereby enabling their detection indirectly. This is

particularly useful where there are markers with similar molecular masses that might be confused for the marker in question. Also, proteolytic fragmentation is useful for high molecular weight markers because smaller markers are more easily resolved by mass spectrometry. In another example, biomolecules can be modified to improve detection resolution. For instance, neuraminidase can be used to remove terminal sialic acid residues from glycoproteins to improve binding to an anionic adsorbent (e.g., cationic exchange ProteinChip® arrays) and to improve detection resolution. In another example, the markers can be modified by the attachment of a tag of particular molecular weight that specifically bind to molecular markers, further distinguishing them. Optionally, after detecting such modified markers, the identity of the markers can be further determined by matching the physical and chemical characteristics of the modified markers in a protein database (e.g., SwissProt).

III. CAPTURE OF MARKERS

[0173] Biomarkers are preferably captured with capture reagents immobilized to a solid support, such as any biochip described herein, a multiwell microtiter plate or a resin. In particular, the biomarkers of this invention are preferably captured on SELDI protein biochips. Capture can be on a chromatographic surface or a biospecific surface. Any of the SELDI protein biochips comprising reactive surfaces can be used to capture and detect the biomarkers of this invention. However, the biomarkers of this invention bind well to immobilized metal chelates. The IMAC-3 and IMAC 30 biochips, which nitriloacetic acid functionalities that adsorb transition metal ions, such as Cu^{++} and Ni^{++} by chelation, are the preferred SELDI biochips for capturing the biomarkers of this invention. Any of the SELDI protein biochips comprising reactive surfaces can be used to capture and detect the biomarkers of this invention. These biochips can be derivatized with the antibodies that specifically capture the biomarkers, or they can be derivatized with capture reagents, such as protein A or protein G that bind immunoglobulins. Then the biomarkers can be captured in solution using specific antibodies and the captured markers isolated on chip through the capture reagent.

[0174] In general, a sample containing the biomarkers, such as serum, is placed on the active surface of a biochip for a sufficient time to allow binding. Then, unbound molecules are washed from the surface using a suitable eluant, such as phosphate buffered saline. In general, the more stringent the eluant, the more tightly the proteins must be bound to be retained after the wash. The retained protein biomarkers now can be detected by appropriate means.

IV. DETECTION AND MEASUREMENT OF MARKERS

[0175] Once captured on a substrate, e.g., biochip or antibody, any suitable method can be used to measure a marker or markers in a sample. For example, markers can be detected and/or measured by a variety of detection methods including for example, gas phase ion spectrometry methods, optical methods, electrochemical methods, atomic force microscopy and radio frequency methods. Using these methods, one or more markers can be detected.

[0176] A) SELDI

[0177] One preferred method of detection and/or measurement of the biomarkers uses mass spectrometry and, in particular, "Surface-enhanced laser desorption/ionization" or "SELDI". SELDI refers to a method of desorption/ionization gas phase ion spectrometry (e.g., mass spectrometry) in which the analyte is captured on the surface of a SELDI probe that engages the probe interface. In "SELDI MS," the gas phase ion spectrometer is a mass spectrometer. SELDI technology is described in more detail above. ApoA1, transthyretin ΔN10 and IAIH4 fragment are detected as peaks at m/z of 28043, m/z of about 12870.9, and m/z of 3272, respectively.

[0178] B) Immunoassay

[0179] In another embodiment, an immunoassay can be used to detect and analyze markers in a sample. This method comprises: (a) providing an antibody that specifically binds to a marker; (b) contacting a sample with the antibody; and (c) detecting the presence of a complex of the antibody bound to the marker in the sample.

[0180] An immunoassay is an assay that uses an antibody to specifically bind an antigen (e.g., a marker). The immunoassay is characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen. The phrase "specifically (or selectively) binds" to an antibody or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies raised to a marker from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with that marker and not with other proteins, except for polymorphic variants and alleles of the marker. This selection may be achieved by subtracting out antibodies that cross-react with the marker molecules from other species.

[0181] Using the purified markers or their nucleic acid sequences, antibodies that specifically bind to a marker can be prepared using any suitable methods known in the art. See, e.g., Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies: A Laboratory Manual* (1988); Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature* 256:495-497 (1975). Such techniques include, but are not limited to, antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (see, e.g., Huse et al., *Science* 246:1275-1281 (1989); Ward et al., *Nature* 341:544-546 (1989)). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

[0182] Generally, a sample obtained from a subject can be contacted with the antibody that specifically binds the marker. Optionally, the antibody can be fixed to a solid support to facilitate washing and subsequent isolation of the complex, prior to contacting the antibody with a sample. Examples of solid supports include glass or plastic in the form of, e.g., a microtiter plate, a stick, a bead, or a microbead. Antibodies can also be attached to a probe substrate or ProteinChip® array described above. The sample is preferably a biological

fluid sample taken from a subject. Examples of biological fluid samples include blood, serum, plasma, nipple aspirate, urine, tears, saliva etc. In a preferred embodiment, the biological fluid comprises blood serum. The sample can be diluted with a suitable eluant before contacting the sample to the antibody.

[0183] After incubating the sample with antibodies, the mixture is washed and the antibody-marker complex formed can be detected. This can be accomplished by incubating the washed mixture with a detection reagent. This detection reagent may be, e.g., a second antibody which is labeled with a detectable label. Exemplary detectable labels include magnetic beads (e.g., DYNABEADS™), fluorescent dyes, radiolabels, enzymes (e.g., horse radish peroxide, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads. Alternatively, the marker in the sample can be detected using an indirect assay, wherein, for example, a second, labeled antibody is used to detect bound marker-specific antibody, and/or in a competition or inhibition assay wherein, for example, a monoclonal antibody which binds to a distinct epitope of the marker is incubated simultaneously with the mixture.

[0184] Methods for measuring the amount of, or presence of, antibody-marker complex include, for example, detection of fluorescence, luminescence, chemiluminescence, absorbance, reflectance, transmittance, birefringence or refractive index (e.g., surface plasmon resonance, ellipsometry, a resonant mirror method, a grating coupler waveguide method or interferometry). Optical methods include microscopy (both confocal and non-confocal), imaging methods and non-imaging methods. Electrochemical methods include voltametry and amperometry methods. Radio frequency methods include multipolar resonance spectroscopy. Methods for performing these assays are readily known in the art. Useful assays include, for example, an enzyme immune assay (EIA) such as enzyme-linked immunosorbent assay (ELISA), a radioimmune assay (RIA), a Western blot assay, or a slot blot assay. These methods are also described in, e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991); and Harlow & Lane, supra.

[0185] Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, preferably from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, marker, volume of solution, concentrations and the like. Usually the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10° C. to 40° C.

[0186] Immunoassays can be used to determine presence or absence of a marker in a sample as well as the quantity of a marker in a sample. The amount of an antibody-marker complex can be determined by comparing to a standard. A standard can be, e.g., a known compound or another protein known to be present in a sample. As noted above, the test amount of marker need not be measured in absolute units, as long as the unit of measurement can be compared to a control.

[0187] The methods for detecting these markers in a sample have many applications. For example, one or more markers can be measured to aid human cancer diagnosis or prognosis. In another example, the methods for detection of the markers can be used to monitor responses in a subject to cancer treatment. In another example, the methods for detecting markers can be used to assay for and to identify compounds that modulate expression of these markers in vivo or in vitro. In a preferred example, the biomarkers are used to differentiate between the different stages of tumor progression, thus aiding in determining appropriate treatment and extent of metastasis of the tumor.

[0188] C) Combinatorial Ligand Library Beads

[0189] Another method of measuring the biomarkers includes the use of a combinatorial ligand library synthesized on beads as described in U.S. Ser. No. 11/495,842, filed Jul. 28, 2006 and entitled "Methods for Reducing the range in Concentrations of Analyte Species in a Sample"; hereby incorporated by reference in its entirety.

V. DATA ANALYSIS

[0190] When the sample is measured and data is generated, e.g., by mass spectrometry, the data is then analyzed by a computer software program. Generally, the software can comprise code that converts signal from the mass spectrometer into computer readable form. The software also can include code that applies an algorithm to the analysis of the signal to determine whether the signal represents a "peak" in the signal corresponding to a marker of this invention, or other useful markers. The software also can include code that executes an algorithm that compares signal from a test sample to a typical signal characteristic of "normal" and human cancer and determines the closeness of fit between the two signals. The software also can include code indicating which the test sample is closest to, thereby providing a probable diagnosis.

[0191] In preferred methods of the present invention, multiple biomarkers are measured. The use of multiple biomarkers increases the predictive value of the test and provides greater utility in diagnosis, toxicology, patient stratification and patient monitoring. The process called "Pattern recognition" detects the patterns formed by multiple biomarkers greatly improves the sensitivity and specificity of clinical proteomics for predictive medicine. Subtle variations in data from clinical samples, e.g., obtained using SELDI, indicate that certain patterns of protein expression can predict phenotypes such as the presence or absence of a certain disease, a particular stage of cancer progression, or a positive or adverse response to drug treatments.

[0192] Data generation in mass spectrometry begins with the detection of ions by an ion detector as described above. Ions that strike the detector generate an electric potential that is digitized by a high speed time-array recording device that digitally captures the analog signal. Ciphergen's ProteinChip® system employs an analog-to-digital converter (ADC) to accomplish this. The ADC integrates detector output at regularly spaced time intervals into time-dependent bins. The time intervals typically are one to four nanoseconds long. Furthermore, the time-of-flight spectrum ultimately analyzed typically does not represent the signal from a single pulse of ionizing energy against a sample, but rather the sum of signals from a number of pulses. This reduces noise and increases dynamic range. This time-of-flight data is then subject to data processing. In Ciphergen's ProteinChip® software, data processing typically includes TOF-to-M/Z transformation, baseline subtraction, high frequency noise filtering.

[0193] TOF-to-M/Z transformation involves the application of an algorithm that transforms times-of-flight into mass-to-charge ratio (M/Z). In this step, the signals are converted

from the time domain to the mass domain. That is, each time-of-flight is converted into mass-to-charge ratio, or M/Z. Calibration can be done internally or externally. In internal calibration, the sample analyzed contains one or more analytes of known M/Z. Signal peaks at times-of-flight representing these massed analytes are assigned the known M/Z. Based on these assigned M/Z ratios, parameters are calculated for a mathematical function that converts times-of-flight to M/Z. In external calibration, a function that converts times-of-flight to M/Z, such as one created by prior internal calibration, is applied to a time-of-flight spectrum without the use of internal calibrants.

[0194] Baseline subtraction improves data quantification by eliminating artificial, reproducible instrument offsets that perturb the spectrum. It involves calculating a spectrum baseline using an algorithm that incorporates parameters such as peak width, and then subtracting the baseline from the mass spectrum.

[0195] High frequency noise signals are eliminated by the application of a smoothing function. A typical smoothing function applies a moving average function to each time-dependent bin. In an improved version, the moving average filter is a variable width digital filter in which the bandwidth of the filter varies as a function of, e.g., peak bandwidth, generally becoming broader with increased time-of-flight. See, e.g., WO 00/70648, Nov. 23, 2000 (Gavin et al., "Variable Width Digital Filter for Time-of-flight Mass Spectrometry").

[0196] Analysis generally involves the identification of peaks in the spectrum that represent signal from an analyte. Peak selection can, of course, be done by eye. However, software is available as part of Ciphergen's ProteinChip® software that can automate the detection of peaks. In general, this software functions by identifying signals having a signal-to-noise ratio above a selected threshold and labeling the mass of the peak at the centroid of the peak signal. In one useful application many spectra are compared to identify identical peaks present in some selected percentage of the mass spectra. One version of this software clusters all peaks appearing in the various spectra within a defined mass range, and assigns a mass (M/Z) to all the peaks that are near the mid-point of the mass (M/Z) cluster.

[0197] Peak data from one or more spectra can be subject to further analysis by, for example, creating a spreadsheet in which each row represents a particular mass spectrum, each column represents a peak in the spectra defined by mass, and each cell includes the intensity of the peak in that particular spectrum. Various statistical or pattern recognition approaches can applied to the data.

[0198] In one example, Ciphergen's Biomarker Patterns® Software is used to detect a pattern in the spectra that are generated. The data is classified using a pattern recognition process that uses a classification model. In general, the spectra will represent samples from at least two different groups for which a classification algorithm is sought. For example, the groups can be pathological v. non-pathological (e.g., cancer v. non-cancer), drug responder v. drug non-responder, toxic response v. non-toxic response, progressor to disease state v. non-progressor to disease state, phenotypic condition present v. phenotypic condition absent.

[0199] The spectra that are generated in embodiments of the invention can be classified using a pattern recognition process that uses a classification model. In some embodiments, data derived from the spectra (e.g., mass spectra or time-of-flight spectra) that are generated using samples such as "known samples" can then be used to "train" a classification model. A "known sample" is a sample that is pre-classified (e.g., cancer or not cancer). Data derived from the spectra (e.g., mass spectra or time-of-flight spectra) that are generated using samples such as "known samples" can then be used to "train" a classification model. A "known sample" is a sample that is pre-classified. The data that are derived from the spectra and are used to form the classification model can be referred to as a "training data set". Once trained, the classification model can recognize patterns in data derived from spectra generated using unknown samples. The classification model can then be used to classify the unknown samples into classes. This can be useful, for example, in predicting whether or not a particular biological sample is associated with a certain biological condition (e.g., diseased vs. non diseased).

[0200] The training data set that is used to form the classification model may comprise raw data or pre-processed data. In some embodiments, raw data can be obtained directly from time-of-flight spectra or mass spectra, and then may be optionally "pre-processed" in any suitable manner. For example, signals above a predetermined signal-to-noise ratio can be selected so that a subset of peaks in a spectrum is selected, rather than selecting all peaks in a spectrum. In another example, a predetermined number of peak "clusters" at a common value (e.g., a particular time-of-flight value or mass-to-charge ratio value) can be used to select peaks. Illustratively, if a peak at a given mass-to-charge ratio is in less than 50% of the mass spectra in a group of mass spectra, then the peak at that mass-to-charge ratio can be omitted from the training data set. Pre-processing steps such as these can be used to reduce the amount of data that is used to train the classification model.

[0201] Classification models can be formed using any suitable statistical classification (or "learning") method that attempts to segregate bodies of data into classes based on objective parameters present in the data. Classification methods may be either supervised or unsupervised. Examples of supervised and unsupervised classification processes are described in Jain, "Statistical Pattern Recognition: A Review", IEEE Transactions on Pattern Analysis and Machine Intelligence, Vol. 22, No. 1, January 2000, which is herein incorporated by reference in its entirety.

[0202] In supervised classification, training data containing examples of known categories are presented to a learning mechanism, which learns one more sets of relationships that define each of the known classes. New data may then be applied to the learning mechanism, which then classifies the new data using the learned relationships. Examples of supervised classification processes include linear regression processes (e.g., multiple linear regression (MLR), partial least squares (PLS) regression and principal components regression (PCR)), binary decision trees (e.g., recursive partitioning processes such as CART-classification and regression trees), artificial neural networks such as backpropagation networks, discriminant analyses (e.g., Bayesian classifier or Fischer analysis), logistic classifiers, and support vector classifiers (support vector machines).

[0203] A preferred supervised classification method is a recursive partitioning process. Recursive partitioning processes use recursive partitioning trees to classify spectra derived from unknown samples. Further details about recur-

sive partitioning processes are provided in U.S. 2002 0138208 A1 (Paulse et al., "Method for analyzing mass spectra," Sep. 26, 2002.

[0204] In other embodiments, the classification models that are created can be formed using unsupervised learning methods. Unsupervised classification attempts to learn classifications based on similarities in the training data set, without pre classifying the spectra from which the training data set was derived. Unsupervised learning methods include cluster analyses. A cluster analysis attempts to divide the data into "clusters" or groups that ideally should have members that are very similar to each other, and very dissimilar to members of other clusters. Similarity is then measured using some distance metric, which measures the distance between data items, and clusters together data items that are closer to each other. Clustering techniques include the MacQueen's K-means algorithm and the Kohonen's Self-Organizing Map algorithm.

[0205] Learning algorithms asserted for use in classifying biological information are described in, for example, WO 01/31580 (Barnhill et al., "Methods and devices for identifying patterns in biological systems and methods of use thereof," May 3, 2001); U.S. 2002/0193950 A1 (Gavin et al., "Method or analyzing mass spectra," Dec. 19, 2002); U.S. 2003/0004402 A1 (Hitt et al., "Process for discriminating between biological states based on hidden patterns from biological data," Jan. 2, 2003); and U.S. Pat. No. 7,113,896 A1 (Zhang and Zhang, "Systems and methods for processing biological expression data" Mar. 20, 2003). More specifically, to obtain the biomarkers, the peak intensity data of samples from cancer patients and healthy controls were used as a "discovery set." This data were combined and randomly divided into a training set and a test set to construct and test multivariate predictive models.

[0206] Generally, the data generated from Section IV above is inputted into a diagnostic algorithm (i.e., classification algorithm as described above). The classification algorithm is then generated based on the learning algorithm. The process involves developing an algorithm that can generate the classification algorithm. The methods of the present invention generate a more accurate classification algorithm by accessing a number of ovarian cancer and normal samples of a sufficient number based on statistical sample calculations. The samples are used as a training set of data on learning algorithm.

[0207] The generation of the classification, i.e., diagnostic, algorithm is dependent upon the assay protocol used to analyze samples and generate the data obtained in Section IV above. It is imperative that the protocol for the detection and/or measurement of the markers (e.g., in step IV) must be the same as that used to obtain the data used for developing the classification algorithm. The assay conditions, which must be maintained throughout the training and classification systems include chip type and mass spectrometer parameters, as well as general protocols for sample preparation and testing. If the protocol for the detection and/or measurement of the markers (step IV) is changed, the learning algorithm and classification algorithm must also change. Similarly, if the learning algorithm and classification algorithm change, then the protocol for the detection and/or measurement of markers (step IV) must also change to be consistent with that used to generate classification algorithm. Development of a new classification model would require accessing a sufficient number of ovarian cancer and normal samples, developing a new training set of data based on a new detection protocol, generating a new classification algorithm using the data and finally, verifying the classification algorithm with a multi-site study.

[0208] The classification models can be formed on and used on any suitable digital computer. Suitable digital computers include micro, mini, or large computers using any standard or specialized operating system such as a Unix, Windows™ or Linux™ based operating system. The digital computer that is used may be physically separate from the mass spectrometer that is used to create the spectra of interest, or it may be coupled to the mass spectrometer. If it is separate from the mass spectrometer, the data must be inputted into the computer by some other means, whether manually or automated.

[0209] The training data set and the classification models according to embodiments of the invention can be embodied by computer code that is executed or used by a digital computer. The computer code can be stored on any suitable computer readable media including optical or magnetic disks, sticks, tapes, etc., and can be written in any suitable computer programming language including C, C++, visual basic, etc.

VI. EXAMPLES OF PREFERRED EMBODIMENTS

[0210] In a preferred embodiment, a serum sample is collected from a patient and then fractionated using an anion exchange resin as described above. The biomarkers in the sample are captured using an IMAC copper ProteinChip array. The markers are then detected using SELDI. In such a test one can detect (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A, and/or respective fragment thereof. The results are then entered into a computer system, which contains an algorithm that is designed using the same parameters that were used in the learning algorithm and classification algorithm to originally determine the biomarkers. The algorithm produces a diagnosis based upon the data received relating to each biomarker.

[0211] The diagnosis is determined by examining the data produced from the SELDI tests with the classification algorithm that is developed using the biomarkers. The classification algorithm depends on the particulars of the test protocol used to detect the biomarkers. These particulars include, for example, sample preparation, chip type and mass spectrometer parameters. If the test parameters change, the algorithm must change. Similarly, if the algorithm changes, the test protocol must change.

[0212] In another embodiment, the sample is collected from the patient. The biomarkers are captured using an antibody ProteinChip array as described above. The markers are detected using a biospecific SELDI test system. In such a test one can detect (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TrR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-ter-

minal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A, and/or respective fragment thereof. The results are then entered into a computer system, which contains an algorithm that is designed using the same parameters that were used in the learning algorithm and classification algorithm to originally determine the biomarkers. The algorithm produces a diagnosis based upon the data received relating to each biomarker.

[0213] In yet other preferred embodiments, the markers are captured and tested using non-SELDI formats. In one example, the sample is collected from the patient. The biomarkers are captured on a substrate using other known means, e.g., antibodies to the markers. The markers are detected using methods known in the art, e.g., optical methods and refractive index. Examples of optical methods include detection of fluorescence, e.g., ELISA. Examples of refractive index include surface plasmon resonance. The results for the markers are then subjected to an algorithm, which may or may not require artificial intelligence. The algorithm produces a diagnosis based upon the data received relating to each biomarker.

[0214] In any of the above methods, the data from the sample may be fed directly from the detection means into a computer containing the diagnostic algorithm. Alternatively, the data obtained can be fed manually, or via an automated means, into a separate computer that contains the diagnostic algorithm.

VII. DIAGNOSIS OF SUBJECT AND DETERMINATION OF OVARIAN CANCER SURVIVAL STATUS

[0215] This panel of biomarkers comparing (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A, and/or respective fragment thereof, is useful in aiding in the determination of ovarian cancer status. First, the selected biomarkers are measured in a subject sample using the methods described herein, e.g., capture on a SELDI biochip followed by detection by mass spectrometry. Then, the measurements is compared with a diagnostic amount or control that distinguishes an ovarian cancer status from a non-cancer status. The diagnostic amounts will reflect the information herein that the particular biomarkers are up-regulated or down-regulated in a cancer status compared with a non-cancer status. As is well understood in the art, the particular diagnostic amounts used can be adjusted to increase sensitivity or specificity of the diagnostic assay depending on the preference of the diagnostician. The test amounts as compared with the diagnostic amount thus indicates ovarian cancer status.

[0216] While individual biomarkers are useful diagnostic markers, it has been found that a combination of biomarkers provides greater predictive value than single markers alone. Specifically, the detection of a plurality of markers in a sample increases the percentage of true positive and true negative diagnoses and would decrease the percentage of false positive or false negative diagnoses. Thus, methods of the present invention comprise the measurement of more than one biomarker. For example, the methods of the present invention have an AUC from ROC analysis greater than 0.50, more preferred methods have an AUC greater than 0.60, more preferred methods have an AUC greater than 0.70. Especially preferred methods have an AUC greater than 0.70 and most preferred methods have an AUC greater than 0.80.

[0217] In some embodiments, the mere presence or absence of a marker detected with a detection cutoff, without quantifying the amount of marker, is useful and can be correlated with a probable diagnosis of ovarian cancer. For example, ITIH4 fragment can be more frequently detected in human ovarian cancer patients than in normal subjects. Equally, for example, biomarkers Apo A1 and transthyretin, can be less frequently detected in human ovarian cancer patients than in normal subjects. Thus, a detected presence or absence, respectively, of these markers in a subject being tested indicates that the subject has a higher probability of having ovarian cancer.

[0218] In other embodiments, the measurement of markers can involve quantifying the markers to correlate the detection of markers with a probable diagnosis of ovarian cancer. Thus, if the amount of the markers detected in a subject being tested is different compared to a control amount (i.e., higher or lower than the control, depending on the marker), then the subject being tested has a higher probability of having ovarian cancer.

[0219] The correlation may take into account the amount of the marker or markers in the sample compared to a control amount of the marker or markers (up or down regulation of the marker or markers) (e.g., in normal subjects in whom human cancer is undetectable). A control can be, e.g., the average or median amount of marker present in comparable samples of normal subjects in whom human cancer is undetectable. The control amount is measured under the same or substantially similar experimental conditions as in measuring the test amount. The correlation may take into account the presence or absence of the markers in a test sample and the frequency of detection of the same markers in a control. The correlation may take into account both of such factors to facilitate determination of ovarian cancer status.

[0220] In certain embodiments of the methods of qualifying ovarian cancer status, the methods further comprise managing subject treatment based on the status. As aforesaid, such management describes the actions of the physician or clinician subsequent to determining ovarian cancer status. For example, if the result of the methods of the present invention is inconclusive or there is reason that confirmation of status is necessary, the physician may order more tests. Alternatively, if the status indicates that surgery is appropriate, the physician may schedule the patient for surgery. In other instances, the patient may receive chemotherapy or radiation treatments, either in lieu of, or in addition to, surgery. Likewise, if the result is negative, e.g., the status indicates late stage ovarian cancer or if the status is otherwise acute, no further action may be warranted. Furthermore, if the results show that treatment has been successful, no further management may be necessary.

[0221] The invention also provides for such methods where the biomarkers (or specific combination of biomarkers) are measured again after subject management. In these cases, the

methods are used to monitor the status of the cancer, e.g., response to cancer treatment, remission of the disease or progression of the disease. Because of the ease of use of the methods and the lack of invasiveness of the methods, the methods can be repeated after each treatment the patient receives. This allows the physician to follow the effectiveness of the course of treatment. If the results show that the treatment is not effective, the course of treatment can be altered accordingly. This enables the physician to be flexible in the treatment options.

[0222] In another example, the methods for detecting markers can be used to assay for and to identify compounds that modulate expression of these markers in vivo or in vitro.

[0223] The methods of the present invention have other applications as well. For example, the markers can be used to screen for compounds that modulate the expression of the markers in vitro or in vivo, which compounds in turn may be useful in treating or preventing ovarian cancer in patients. In another example, the markers can be used to monitor the response to treatments for ovarian cancer. In yet another example, the markers can be used in heredity studies to determine if the subject is at risk for developing ovarian cancer. For instance, certain markers may be genetically linked. This can be determined by, e.g., analyzing samples from a population of ovarian cancer patients whose families have a history of ovarian cancer. The results can then be compared with data obtained from, e.g., ovarian cancer patients whose families do not have a history of ovarian cancer. The markers that are genetically linked may be used as a tool to determine if a subject whose family has a history of ovarian cancer is predisposed to having ovarian cancer.

VIII. KITS

[0224] In yet another aspect, the present invention provides kits for qualifying ovarian cancer status, wherein the kits can be used to measure the markers of the present invention. For example, the kits can be used to measure any one or more of the markers described herein, which markers are differentially present in samples of ovarian cancer patient and normal subjects. The kits of the invention have many applications. For example, the kits can be used to differentiate if a subject has ovarian cancer or has a negative diagnosis, thus enabling the physician or clinician to diagnose the presence or absence of the cancer. The kits can also be used to monitor the patient's response to a course of treatment, enabling the physician to modify the treatment based upon the results of the test. In another example, the kits can be used to identify compounds that modulate expression of one or more of the markers in in vitro or in vivo animal models for ovarian cancer.

[0225] The present invention therefore provides kits comprising (a) a capture reagent that binds a panel of biomarkers comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A and/or respective fragments thereof; and (b) a container comprising at least one of the biomarkers. The capture reagents may also bind at least one known biomarker, Marker 4, e.g., CA125.

[0226] While the capture reagents can be any type of reagent, preferably the reagent is a SELDI probe. In certain kits of the present invention, the capture reagent comprises an IMAC.

[0227] The invention also provides kits comprising (a) a capture reagents that bind the panel of biomarkers comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A, and/or respective fragments thereof and (b) instructions for using the capture reagent to measure the biomarker. In certain of these kits, the capture reagents comprise antibodies. Furthermore, some of the aforesaid kits further comprise an MS probe to which the capture reagent is attached or is attachable. In some kits, the capture reagent comprises an IMAC. One preferred embodiment of the present invention includes a high-throughput test for early detection of ovarian cancer, which analyzes a patient's sample on the IMAC ProteinChip® array for the seven (7) analytes.

[0228] Certain kits of the present invention further comprise a wash solution, or eluant, that selectively allows retention of the bound biomarkers to the capture reagents as compared with other biomarkers after washing. Alternatively, the kit may contain instructions for making a wash solution, wherein the combination of the adsorbent and the wash solution allows detection of the markers using gas phase ion spectrometry.

[0229] Preferably, the kit comprises written instructions for use of the kit for detection of cancer and the instructions provide for contacting a test sample with the capture reagents and detecting the panel of biomarkers retained by the capture reagents. For example, the kit may have standard instructions informing a consumer how to wash the capture reagents (e.g., probes) after a sample of blood serum contacts the capture reagents. In another example, the kit may have instructions for pre-fractionating a sample to reduce complexity of proteins in the sample. In another example, the kit may have instructions for automating the fractionation or other processes.

[0230] Such kits can be prepared from the materials described above, and the previous discussion of these materials (e.g., probe substrates, capture reagents, adsorbents, washing solutions, etc.) is fully applicable to this section and will not be repeated.

[0231] In another embodiment, a kit comprises (a) antibodies that specifically bind to the panel of biomarkers; and (b) a detection reagent. Such kits can be prepared from the materials described above, and the previous discussion regarding the materials (e.g., antibodies, detection reagents, immobilized supports, etc.) is fully applicable to this section and will not be repeated. Optionally, the kit may further comprise pre-fractionation spin columns. In some embodiments, the kit may further comprise instructions for suitable operation parameters in the form of a label or a separate insert.

[0232] Optionally, the kit may further comprise a standard or control information so that the test sample can be compared with the control information standard to determine if the test

amount of a marker detected in a sample is a diagnostic amount consistent with a diagnosis of ovarian cancer.

[0233] The invention also provides an article manufacture comprising at least one capture reagent bound to at least two biomarkers selected from (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A. Examples of articles of manufacture of the present invention include, but are not limited to, ProteinChip® Arrays, probes, microtitre plates, beads, test tubes, microtubes, and any other solid phase onto which a capture reagent can be incorporated.

[0234] The present invention also provides a system comprising a plurality of capture reagents each of which has bound to it a different biomarker comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, (xii) m/z value 7900.679 protein and (xiii) truncated serum amyloid A, and/or respective fragment thereof. Examples of other systems include those in which the capture reagents are test tubes containing an antibody for each of the biomarkers, either separately, or in groups. One of ordinary skill in the art would readily be able to manufacture other such articles in accordance with the teachings described herein.

[0235] The following examples are offered by way of illustration, not by way of limitation. While specific examples have been provided, the above description is illustrative and not restrictive. Any one or more of the features of the previously described embodiments can be combined in any manner with one or more features of any other embodiments in the present invention. Furthermore, many variations of the invention will become apparent to those skilled in the art upon review of the specification. The scope of the invention should, therefore, be determined not with reference to the above description, but instead should be determined with reference to the appended claims along with their full scope of equivalents.

[0236] All publications and patent documents cited in this application are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent document were so individually denoted. By their citation of various references in this document, Applicants do not admit any particular reference is "prior art" to their invention.

EXAMPLES

Example 1

Equalizer Bead Protocol: Sequential Elution

Swelling of the Beads

[0237] Add 20% methanol to dry beads, allow to swell overnight, gently rocking, at 4° C. Allow to settle by gravity. Remove fines. Add methanol, allow resin to settle, and remove fines. Wash with methanol several times. The beads can be stored swollen at 4° C. or −20° C. in 20% methanol indefinitely.

Preparing E-Bead Filter Plate

[0238] 1. To each well of 96 well filtration plate(s) add 40 μL 50% E beads slurry.

[0239] 2. Apply vacuum for 30 seconds to drain off the organic solvent.

[0240] 3. Add 200 μL of deionized water and incubate with shaking for 5 min.

[0241] 4. Apply vacuum for 30 seconds to drain off the water.

[0242] 5. Add 200 μL of PBS and incubate with shaking for 5 min.

[0243] 6. Apply vacuum to for 30 seconds drain off the PBS.

[0244] 7. Add 200 μL of PBS and apply vacuum to drain off the PBS.

[0245] 8. Repeat the above step a total of 4 times. On the last wash apply the vacuum for 1 minute.

Sample Binding

[0246] 1. Add 200 μL of serum or plasma to a 96 well E-beads filtration plate and incubate for 2 hr at 4° C. with shaking on a Micromix shaker.

Sample Wash

[0247] 1. Place the 96 well collection plate labeled FT underneath filter plate and collect the Flow through.

[0248] 2. Wash the beads with 200 μL of PBS by incubating with shaking for 5 min. Apply vacuum. Repeat once.

[0249] 3. Add 200 μL of PBS and apply vacuum.

[0250] 4. Repeat the above step a total of 4 times.

Collect Fractions (Sequential Elution frome E Beads)

[0251] 1. Add 40 μL of 1 M NaCl, 20 mM HEPES pH 7.5 to each well of the filter plate. Let the sample shake on a Micromix shaker for 15 min.

[0252] 2. Collect the extraction buffer from the filter plate in a collection plate labeled F1 by centrifugation, 2 minutes at 200×g. Repeat steps 1 & 2 and collect all three eluents.

[0253] 3. Add 40 μL of 200 mM glycine pH 2.4 to each well of the filter plate. Let the sample shake on a Micromix shaker for 15 min.

[0254] 4. Collect the extraction buffer from the filter plate in a collection plate labeled F2 by centrifugation, 2 minutes at 200×g. Repeat steps 3 & 4 and collect all three eluents.

[0255] 5. Add 40 μL of 60% ethylene glycol to each well of the filter plate. Let the sample shake on a Micromix shaker for 15 min.

[0256] 6. Collect the extraction buffer from the filter plate in a collection plate labeled F3 by centrifugation, 2 minutes at 200×g. Repeat steps 5 & 6 and collect all three eluents.

[0257] 7. Add 40 μL of 33.3% IPA-16.7% ACN-0.1% TFA to each well of the filter plate. Let the sample shake on a Micromix shaker for 5 min.

[0258] 8. Collect the extraction buffer from the filter plate in a collection plate labeled F4 by centrifugation, 2 minutes at 200×g. Repeat steps 7 & 8 and collect all three eluents.

Profiling

[0259] 5ρL of each fraction can be used for profiling (with 45 μL of binding buffer). Profiling buffers are as shown in the table below.

Array type	Binding buffer
CM10	100 mM Sodium Acetate pH 4.0
IMAC30	100 mM Sodium Phosphate + 0.5M NaCl pH 7.0
H50	10% acetonitrile/0.1% TFA
Q10	50 mM Tris pH 9.0

Example 2

Chip Binding Protocols of E Bead Fractions

Buffer List:

[0260] IMAC3 chip:

[0261] 1. 100 mM Sodium Phosphate+0.5M NaCl pH 7.0 (binding buffer)

[0262] 2. 50 mM $CuSO_4$

CM10 Chip:

[0263] 1. 100 mM Sodium Acetate pH 4.0 (binding buffer)

Q10 chip:

[0264] 1. 50 mM tris, pH8.0 (binding buffer)

H50 Chip:

[0265] 10% acetonitrile 0.1% TFA (binding buffer)

Material List:

Bioprocessors

[0266] IMAC30 chips
CM10 chips
Q10 chips
H50 chips
Place Chips into Bioprocessor
Load IMAC Chips with Copper
Load 50 uL of 100 mM $CuSO_4$ onto each spot of IMAC30 chips

Centrifuge at 800 rpm for 1'

Shake for 5' at Room Temperature (RT)

[0267] Remove $CuSO_4$ after shaking
Add 200 uL water, shake for 1'
Add 50 uL 100 mM sodium acetate pH4 buffer

Shake for 5' at RT

[0268] Remove pH4 buffer
Add 200 uL water, shake for 1'
Chips are ready for buffer equilibration

Pre-Wash H50 Chips

[0269] Add 50 uL of 50% acetonitrile onto each spot on the H50 chips

Centrifuge at 800 rpm for 1'

Shake for 5' at RT

[0270] Remove acetonitrile
Add 200 uL water, shake for 1'
Chips are ready for buffer equilibration

CM10 and Q10 Chips

[0271] No pre-treatment
[0272] Chips are ready for buffer equilibration

Equilibrate Chips

[0273] Add 150 uL of corresponding chip binding buffer (see buffer list above) into each well Centrifuge at 800 rpm for 1'

Shake 5' at Room Temperature (RT)

[0274] Remove buffer
Add 150 uL of corresponding binding buffer into each well

Shake for 5' at Room Temperature (RT)

[0275] Remove buffer

Bind Fractions to Chips

[0276] Add 45 uL of corresponding chip binding buffer into each well
Add 5 uL of E bead fraction
Seal bioprocessor with tape

Shake for 60' at Room Temperature (RT)

[0277] Remove sample samples

Wash Chips

[0278] Add 150 uL of corresponding binding buffer into each well

Shake 5' at Room Temperature (RT)

[0279] Remove buffer
Add 150 uL of corresponding binding buffer into each well

Shake 5' at Room Temperature (RT)

[0280] Remove buffer
Add 200 uL water into each well

Shake 1' at Room Temperature (RT)

[0281] Remove water
Add 200 uL water into each well

Shake 1' at Room Temperature (RT)

[0282] Remove water

Add Matrix

[0283] Remove bioprocessor top and gasket
Flick chip cassette by hand to remove excess water from spots

Allow the chips to dry for 30' at RT

For sinapinic acid matrix

[0284] Add 200 ul of acetonitrile, 200 ul of 1% TFA to 1 tube of sinapinic acid Vortex 5 minutes at RT to dissolve.

[0285] Add 0.75 uL to each spot with Biodot

[0286] Air dry for 10' inside Biodot chamber

[0287] Add 0.75 uL to each spot with Biodot

[0288] Air dry for 30' inside Biodot chamber

Chip Reading

[0289] Read on PCS4000, focus at 7 KDa, mass range 2-200 KDa, collect 10 shots per region, ¼ partition, and a total of 530 shots.

Results

[0290] Using the assays described in Example 1 and 2, biomarkers for ovarian cancer were identified as listed in FIG. **10**.

Example 2

Prognosis of Subjects with Ovarian Cancer using a Panel of Seven Biomarkers

[0291] Ovarian cancer is the most lethal of gynecologic malignancies. The strongest determinant of long-term survival is stage at diagnosis. Patients with early stage disease have five year survival rates approaching 90% whereas patients with late stage disease have five year survival rates of ~30%. Because ovarian cancer is a heterogeneous disease, new prognostic markers that correlate with patient survival may permit better subclassification of patients and therefore more tailored treatment. We have used proteomic profiling in an attempt to identify novel biomarkers that correlate with survival in a prospective cohort of women with newly diagnosed ovarian cancer.

[0292] Materials and Methods:

[0293] Patients: Women for this analysis were part of the Pelvic Mass Study at Rigshospitalet. Informed consent was obtained according to the Helsinki Protocol. Pre-operative serum was obtained, aliquotted, and frozen until the time of analysis.

[0294] Biomarker assays: Semi-quantitative and quantitative assays for seven biomarkers (hepcidin, ITIH4, Apolipoprotein A1, transthyretin, transferrin, CTAP3, and beta-2 microglobulin) were performed using SELDI-TOF-MS. A schematic of the workflow can be found in FIG. **11**.

[0295] Statistical analysis: Survival was assessed at one year post-diagnosis. Deaths were all-cause, although the majority were due to ovarian cancer. The non-parametric Mann-Whitney test was performed to assess statistical significance. Principal component analysis was used to assess the performance of multivariable models.

CONCLUSION

[0296] The panel of seven biomarkers is predictive of survival independent of the stage of the cancer. Moreover, among late stage patients, it can distinguish between those with longer survival and shorter survival.

[0297] The present invention has been described in detail, including the preferred embodiments thereof. However, it will be appreciated that those skilled in the art, upon consideration of the present disclosure, may make modifications and/or improvements of this invention and still be within the scope and spirit of this invention as set forth in the following claims.

[0298] All publications and patent documents cited in this application are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent document were so individually denoted. By their citation of various references in this document, Applicants do not admit any particular reference is "prior art" to their invention.

SEQUENCE LISTING

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Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala Lys Gly
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Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg Cys Met
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Cys Ile Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln Ser Leu
65 70 75 80

Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val Ile Ala
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35 40 45

Ala Val His Val Phe Arg Lys Ala Ala Asp Asp Thr Trp Glu Pro Phe
50 55 60

Ala Ser Gly Lys Thr Ser Glu Ser Gly Glu Leu His Gly Leu Thr Thr
65 70 75 80

Glu Glu Glu Phe Val Glu Gly Ile Tyr Lys Val Glu Ile Asp Thr Lys
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Ser Tyr Trp Lys Ala Leu Gly Ile Ser Pro Phe His Glu His Ala Glu
100 105 110

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His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
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Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
    50                  55                  60

Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
65                  70                  75                  80

Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
                85                  90                  95

Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
            100                 105                 110

Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
        115                 120                 125

Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
    130                 135                 140

Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
145                 150                 155                 160

Pro Arg Lys Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser
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Cys Ala Pro Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu
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Cys Pro Gly Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser
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Gly Ala Phe Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val
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Lys His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp
225                 230                 235                 240

Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu
                245                 250                 255

Tyr Lys Asp Cys His Leu Ala Gln Val Pro Ser His Thr Val Val Ala
            260                 265                 270

Arg Ser Met Gly Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln
        275                 280                 285

Ala Gln Glu His Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe
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Ser Ser Pro His Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly
305                 310                 315                 320

Phe Leu Lys Val Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr
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Ala Pro Thr Asp Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His
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Ile Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn
            420                 425                 430

Lys Ser Asp Asn Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Val
        435                 440                 445

Ala Val Val Lys Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys
    450                 455                 460

Gly Lys Lys Ser Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn
465                 470                 475                 480

Ile Pro Met Gly Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp
                485                 490                 495

Glu Phe Phe Ser Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser
            500                 505                 510

Leu Cys Lys Leu Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn
        515                 520                 525

Asn Lys Glu Gly Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val
    530                 535                 540

Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn
545                 550                 555                 560

Thr Gly Gly Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys
                565                 570                 575

Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu
            580                 585                 590

Tyr Ala Asn Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr
        595                 600                 605

Arg Lys Asp Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln
    610                 615                 620

His Leu Phe Gly Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu
625                 630                 635                 640

Phe Arg Ser Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys
                645                 650                 655

Leu Ala Lys Leu His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu
            660                 665                 670

Glu Tyr Val Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser
        675                 680                 685

Leu Leu Glu Ala Cys Thr Phe Arg Arg Pro
    690                 695


<210> SEQ ID NO 11
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser
1               5                   10                  15

Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg
            20                  25                  30

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser
        35                  40                  45

Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu
    50                  55                  60

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp
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65                  70                  75                  80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp
                85                  90                  95

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile
            100                 105                 110

Val Lys Trp Asp Arg Asp Met
        115
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<210> SEQ ID NO 12
<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

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Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
1               5                   10                  15

Gln Ala Arg His Phe Trp Gln Gln Asp Glu Pro Pro Gln Ser Pro Trp
            20                  25                  30

Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu Lys Asp
        35                  40                  45

Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu Gly Lys
    50                  55                  60

Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr Ser Thr
65                  70                  75                  80

Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu Phe Trp
                85                  90                  95

Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met Ser Lys
            100                 105                 110

Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp Asp Phe
        115                 120                 125

Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys Val Glu
    130                 135                 140

Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu His Glu
145                 150                 155                 160

Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp Arg Ala
                165                 170                 175

Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr Ser Asp
            180                 185                 190

Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys Glu Asn
        195                 200                 205

Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu His Leu
    210                 215                 220

Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu Arg Gln
225                 230                 235                 240

Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu Ser Ala
                245                 250                 255

Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
            260                 265
```

<210> SEQ ID NO 13
<211> LENGTH: 224
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 13

Met Glu Lys Leu Leu Cys Phe Leu Val Leu Thr Ser Leu Ser His Ala
1 5 10 15

Phe Gly Gln Thr Asp Met Ser Arg Lys Ala Phe Val Phe Pro Lys Glu
20 25 30

Ser Asp Thr Ser Tyr Val Ser Leu Lys Ala Pro Leu Thr Lys Pro Leu
35 40 45

Lys Ala Phe Thr Val Cys Leu His Phe Tyr Thr Glu Leu Ser Ser Thr
50 55 60

Arg Gly Thr Val Phe Ser Arg Met Pro Pro Arg Asp Lys Thr Met Arg
65 70 75 80

Phe Phe Ile Phe Trp Ser Lys Asp Ile Gly Tyr Ser Phe Thr Val Gly
85 90 95

Gly Ser Glu Ile Leu Phe Glu Val Pro Glu Val Thr Val Ala Pro Val
100 105 110

His Ile Cys Thr Ser Trp Glu Ser Ala Ser Gly Ile Val Glu Phe Trp
115 120 125

Val Asp Gly Lys Pro Arg Val Arg Lys Ser Leu Lys Lys Gly Tyr Thr
130 135 140

Val Gly Ala Glu Ala Ser Ile Ile Leu Gly Gln Glu Gln Asp Ser Phe
145 150 155 160

Gly Gly Asn Phe Glu Gly Ser Gln Ser Leu Val Gly Asp Ile Gly Asn
165 170 175

Val Asn Met Trp Asp Phe Val Leu Ser Pro Asp Glu Ile Asn Thr Ile
180 185 190

Tyr Leu Gly Gly Pro Phe Ser Pro Asn Val Leu Asn Trp Arg Ala Leu
195 200 205

Lys Tyr Glu Val Gln Gly Glu Val Phe Thr Lys Pro Gln Leu Trp Pro
210 215 220

<210> SEQ ID NO 14
<211> LENGTH: 100
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

Met Lys Leu Leu Ala Ala Thr Val Leu Leu Leu Thr Ile Cys Ser Leu
1 5 10 15

Glu Gly Ala Leu Val Arg Arg Gln Ala Lys Glu Pro Cys Val Glu Ser
20 25 30

Leu Val Ser Gln Tyr Phe Gln Thr Val Thr Asp Tyr Gly Lys Asp Leu
35 40 45

Met Glu Lys Val Lys Ser Pro Glu Leu Gln Ala Glu Ala Lys Ser Tyr
50 55 60

Phe Glu Lys Ser Lys Glu Gln Leu Thr Pro Leu Ile Lys Lys Ala Gly
65 70 75 80

Thr Glu Leu Val Asn Phe Leu Ser Tyr Phe Val Glu Leu Gly Thr Gln
85 90 95

Pro Ala Thr Gln
100

<210> SEQ ID NO 15
<211> LENGTH: 101

-continued

<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
1 5 10 15

Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
20 25 30

Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
35 40 45

Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
50 55 60

Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
65 70 75 80

Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
85 90 95

Lys Leu Leu Glu Ser
100

<210> SEQ ID NO 16
<211> LENGTH: 405
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser Pro Gln Gly
1 5 10 15

Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys Arg Val Glu
20 25 30

Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg Arg Asp Phe
35 40 45

Thr Phe Asp Leu Tyr Arg Ala Leu Ala Ser Ala Ala Pro Ser Gln Asn
50 55 60

Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala Met Leu Ser
65 70 75 80

Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu Gly Leu Gly
85 90 95

Leu Asn Leu Gln Lys Ser Ser Glu Lys Glu Leu His Arg Gly Phe Gln
100 105 110

Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe Gln Leu Ser
115 120 125

Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu Gln Asp Thr
130 135 140

Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr Phe Pro Thr
145 150 155 160

Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn Asp Tyr Val
165 170 175

Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys Asn Leu Asp
180 185 190

Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe Lys Ala Lys
195 200 205

Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln Asp Phe Tyr
210 215 220

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Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser Arg Glu Asp
225                 230                 235                 240

Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg Val Val Gly
                245                 250                 255

Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu Pro Ser Glu
            260                 265                 270

Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys Thr Leu Arg
        275                 280                 285

Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu Tyr Leu Pro
    290                 295                 300

Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val Leu Pro Ser
305                 310                 315                 320

Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu Ser Gly Ile
                325                 330                 335

Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His Lys Ala Val
            340                 345                 350

Val Glu Val Asp Glu Ser Gly Arg Ala Ala Ala Ala Thr Gly Thr Ile
        355                 360                 365

Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg Leu Val Phe Asn
    370                 375                 380

Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile Leu Phe Leu Gly
385                 390                 395                 400

Lys Val Asn Arg Pro
                405


<210> SEQ ID NO 17
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
1               5                   10                  15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
            20                  25                  30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
        35                  40                  45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
    50                  55                  60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
65                  70                  75                  80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
                85                  90                  95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
            100                 105                 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
        115                 120
```

1. A method of determining an ovarian cancer patient's prognosis comprising:

(a) determining the concentration or expression levels or peak intensity values of a combination of two or more biomarkers in a sample from the subject, wherein the one or more biomarkers are selected from the group consisting of: (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900. 679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A; and

(b) correlating the measurements with ovarian cancer patient survival status, wherein the expression or up-regulation of one or more biomarkers represents a lower probability of the patient surviving ovarian cancer.

2. The method of claim **1** comprising determining three or more of the biomarkers.

3. The method of claim **1** comprising determining four or more of the biomarkers.

4.-**16**. (canceled)

17. The method of claim **1** wherein the ovarian cancer patient survival status is selected from the group consisting of one to two years survival post diagnosis; two to five years post diagnosis; and beyond five years post diagnosis.

18. The method of claim **1** further comprising measuring a known biomarker in a sample from the subject and correlating measurement of the known biomarker and the measurements of the panel of biomarkers of claim **1** with ovarian cancer status.

19. A method of qualifying ovarian cancer status in a subject comprising:

(a) providing a subject sample of blood or a blood derivative;

(b) fractionating proteins in the sample on an anion exchange resin and collecting fractions that contain (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900.679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A; and

(c) capturing (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900. 679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A from the fractions on a surface of a substrate comprising capture reagents that bind the protein biomarkers.

20. The method of claim **19** wherein the substrate is a SELDI probe comprising an IMAC copper surface and wherein the protein biomarkers are detected by SELDI.

21.-**27**. (canceled)

28. The method of any one of claims **1** through **13** wherein the panel of protein biomarkers are measured by SELDI.

29. The method of any one of claims **1** through **13** wherein the panel of protein biomarkers are measured by immunoassay.

30. (canceled)

31. The method of claim **1** wherein the sample is selected from blood, serum and plasma.

32.-**33**. (canceled)

34. A kit comprising:

(a) a capture reagent that binds a panel of biomarkers comprising (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900. 679 protein, identified as an sodium adduct of platelet factor 4 and (xiii) truncated serum amyloid A fragments; and

(b) a container comprising at the panel of biomarkers.

35.-**38**. (canceled)

39. The kit of claim **34** further comprising a wash solution that selectively allows retention of the bound biomarker to the capture reagent as compared with other biomarkers after washing.

40.-**41**. (canceled)

42. The kit of claim **34** wherein the capture reagent is an antibody.

43.-**54**. (canceled)

55. A method of determining an ovarian cancer patient's prognosis comprising:

(a) determining the concentration or expression levels or peak intensity values of a combination of two or more biomarkers in a sample from the subject, wherein the one or more biomarkers are selected from the group consisting of: (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1), (viii) CRP N-terminal fragment, (ix) ApoA1-ApoAII dimer, (x) Platelet Factor 4-N-terminal truncation, (xi) m/z value 3897.378 protein, identified as a fragment of protein C inhibitor (xii) m/z value 7900. 679 protein, identified as an sodium adduct of platelet factor 4; (xiii) truncated serum amyloid A and one or more known biomarkers for ovarian cancer; and

(a) correlating the measurements with ovarian cancer patient survival status, wherein the expression or up-regulation of one or more biomarkers represents a lower probability of the patient surviving ovarian cancer.

56. A method of determining an ovarian cancer patient's prognosis comprising:

(a) determining the concentration or expression levels or peak intensity values of a combination of two or more biomarkers in a sample from the subject, wherein the one or more biomarkers are selected from the group consisting of: (i) hepcidin, (ii) inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) (ITIH4), (iii) connective tissue-activating peptide (CTAPIII), (iv) transthyretin (TTR), (v) transferrin (TFR), (vi) beta-2 microglobin (B2M), (vii) apolipoprotein A1 (ApoA1); and

(b) correlating the measurements with ovarian cancer patient survival status, wherein the expression or up-regulation of one or more biomarkers represents a lower probability of the patient surviving ovarian cancer.

57. The method of of claim **56** further comprising determining the age of the patient (b).

58. (canceled)

59. The method of claim **56**, wherein the ovarian cancer is late stage ovarian cancer.

* * * * *

专利名称(译)	卵巢癌患者的预后生物标志物		
公开(公告)号	US20100055690A1	公开(公告)日	2010-03-04
申请号	US12/422530	申请日	2009-04-13
申请(专利权)人(译)	VERMILLION INC.		
当前申请(专利权)人(译)	VERMILLION INC.		
[标]发明人	FUNG ERIC T		
发明人	FUNG, ERIC T.		
IPC分类号	C12Q1/68 G01N33/53		
CPC分类号	G01N33/57449		
优先权	60/851520 2006-10-13 US		
外部链接	Espacenet USPTO		

摘要(译)

本发明提供了评估卵巢癌患者生存状态的方法。此外，本文描述了用于评估患者的卵巢癌状态的方法。这些方法涉及生物样品中生物模式的检测，分析和分类。使用例如质谱系统和其他技术获得生物模式。