



(51) International Patent Classification:

G01N 33/53 (2006.01) G01N 33/574 (2006.01)
G01N 33/68 (2006.01) G01N 33/532 (2006.01)

(21) International Application Number:

PCT/US2012/024997

(22) International Filing Date:

14 February 2012 (14.02.2012)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

61/463,870 24 February 2011 (24.02.2011) US

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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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(54) Title: BIOMARKER PANELS, DIAGNOSTIC METHODS AND TEST KITS FOR OVARIAN CANCER

FIG. 6A

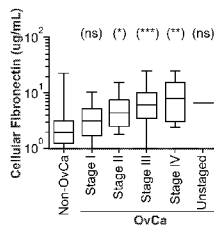
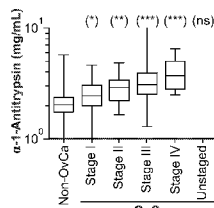
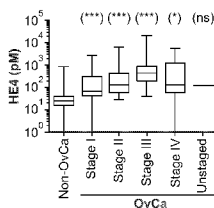
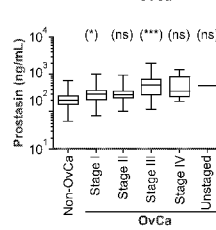
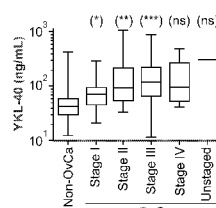
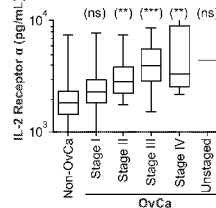
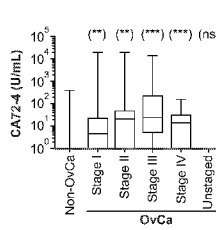
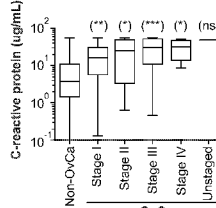
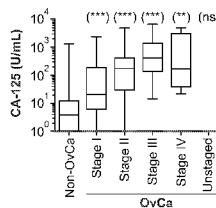


FIG. 6B



(57) Abstract: Methods are provided for predicting the presence, subtype and stage of ovarian cancer, as well as for assessing the therapeutic efficacy of a cancer treatment and determining whether a subject potentially is developing cancer. Associated test kits, computer and analytical systems as well as software and diagnostic models are also provided.



Published:

- *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

BIOMARKER PANELS, DIAGNOSTIC METHODS AND TEST KITS FOR OVARIAN CANCER

Related Applications

5 This application claims the benefit of U.S. Provisional Application Ser. No. 61/463,870, filed February 24, 2011 the entire contents of which are hereby incorporated herein by reference.

Statement of Government Support:

10 The subject matter of the present application includes work supported by SBIR Award No. HHSN261200800045C entitled "Improvement of a Promising MAP for Ovarian Cancer" from the National Cancer Institute.

Field of the Invention:

15 This invention provides methods for predicting and diagnosing ovarian cancer, particularly epithelial ovarian cancer, and it further provides associated analytical reagents, diagnostic models, test kits and clinical reports.

Background:

20 The American Cancer Society estimates that ovarian cancer will strike 22,430 women and take the lives of 15,280 women in 2007 in the United States. Ovarian cancer is not a single disease, however, and there are actually more than 30 types and subtypes of ovarian malignancies, each with its own pathology and clinical behavior. Most experts therefore group ovarian cancers within three major categories, according to the kind of cells from which they were formed: epithelial tumors arise from cells that line or cover the ovaries; germ cell tumors originate from cells that are destined
25 to form eggs within the ovaries; and sex cord-stromal cell tumors begin in the connective cells that hold the ovaries together and produce female hormones.

 Common epithelial tumors begin in the surface epithelium of the ovaries and account for about 90 percent of all ovarian cancers in the U.S. (and the following percentages reflect U.S. prevalence of these cancers). They are further divided into a

number of subtypes -- including serous, endometrioid, mucinous, and clear cell tumors -- that can be further subclassified as benign or malignant tumors. Serous tumors are the most widespread forms of ovarian cancer. They account for 40 percent of common epithelial tumors. About 50 percent of these serous tumors are malignant, 5 33 percent are benign, and 17 percent are of borderline malignancy. Serous tumors occur most often in women who are between 40 and 60 years of age.

Endometrioid tumors represent approximately 20 percent of common epithelial tumors. In about 20 percent of individuals, these cancers are associated with endometrial carcinoma (cancer of the womb lining). In 5 percent of cases, they 10 also are linked with endometriosis, an abnormal occurrence of endometrium (womb lining tissue) within the pelvic cavity. The majority (about 80 percent) of these tumors are malignant, and the remainder (roughly 20 percent) usually is borderline malignancies. Endometrioid tumors occur primarily in women who are between 50 and 70 years of age.

15 Clear cell tumors account for about 6 percent of common epithelial tumors. Nearly all of these tumors are malignant. Approximately one-half of all clear cell tumors are associated with endometriosis. Most patients with clear cell tumors are between 40 and 80 years of age.

Mucinous tumors make up about 1 percent of all common epithelial tumors. 20 Most (approximately 80 percent) of these tumors are benign, 15 percent are of borderline malignancy, and only 5 percent are malignant. Mucinous tumors appear most often in women between 30 to 50 years of age.

Ovarian cancer is by far the most deadly of gynecologic cancers, accounting for more than 55 percent of all gynecologic cancer deaths. But ovarian cancer is also 25 among the most treatable -- if it is caught early. When ovarian cancer is caught early and appropriately treated, the 5-year survival rate is 93 percent. See, for example, Luce et al, "Early Diagnosis Key to Epithelial Ovarian Cancer Detection," *The Nurse Practitioner*, Dec 2003 at p.41. Extensive background information about ovarian cancer is readily available on the internet, for example, from the "Overview: Ovarian 30 Cancer" of the Cancer Reference Information provided by the American Cancer

Society and the NCCN Clinical Practice Guidelines in Oncology™ Ovarian Cancer V.1.2007.

The current reality for the diagnosis of ovarian cancer is that most cases -- 81 percent of all cases of ovarian cancer -- are not caught in earliest stage. This is because early stage ovarian cancer is very difficult to diagnose. Its symptoms may not appear or be noticed at this point. Or, symptoms -- such as bloating, indigestion, diarrhea, constipation and others -- may be vague and associated with many common and less serious conditions. Most importantly, there has been no effective test for early detection. An effective tool for early and accurate detection of ovarian cancer is a critical unmet medical need.

What has been urgently needed in the field of gynecologic oncology is a minimally invasive (preferably serum-based) clinical test for assessing and predicting the presence of ovarian cancer that is based on a robust set of biomarkers and sample features identified from a large and diverse set of samples, together with methods and associated computer systems and software tools to predict, diagnose and monitor ovarian cancer with high accuracy at its various stages.

Summary of the Invention:

The present invention generally relates to cancer biomarkers and particularly to biomarkers associated with ovarian cancer. It provides methods to predict, evaluate, diagnose, and monitor cancer, particularly ovarian cancer, by measuring certain biomarkers, and further provides a set or array of reagents to evaluate the expression levels of biomarkers that are associated with ovarian cancer. A preferred set of biomarkers provides a detectable molecular signature of ovarian cancer in a subject. The invention provides a predictive or diagnostic test for ovarian cancer, particularly for epithelial ovarian cancer and more particularly for early-stage ovarian cancer (that is Stage I, Stage II or Stage I and II together).

In one aspect, the present disclosure generally features a method of predicting the ovarian cancer status of a subject, involving the steps of measuring the level of CA-125 and HE4 and measuring the level of one or more biomarkers selected from the group consisting of IL-2 receptor alpha (IL-2R α), Alpha-1-Antitrypsin (AAT), C-

Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), prostaticin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, IL-6, Vascular Endothelial Growth Factor B (VEGF-B), Matrix Metalloproteinase-7 (MMP-7), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1 in a sample of a biological fluid obtained from the subject; and correlating the measurements with ovarian cancer status.

In another aspect, the present disclosure features a kit containing a panel of affinity reagents that each selectively binds to CA-125 and HE4 and one or more biomarkers selected from the group consisting of Interleukin-2 receptor alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostaticin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1; and a panel of containers each comprising CA-125 and HE4 and a one or more biomarkers selected from the group consisting of Interleukin-2 receptor alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostaticin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1.

In a further aspect, the present disclosure features a panel of purified peptides containing CA-125 and HE4 and one or more biomarkers selected from the group consisting of Interleukin-2 receptor alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostaticin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2

(IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1.

In various embodiments of any of the above aspects or any other aspect of the disclosure delineated herein, the methods involve measuring the level of Cancer
5 Antigen 72-4 (CA-72-4). In another embodiment the ovarian cancer status is presence of ovarian cancer. In additional embodiments the ovarian cancer is stage I ovarian cancer. In yet another embodiment the ovarian cancer is stage II ovarian cancer. In other embodiments the ovarian cancer is stage III ovarian cancer. In yet another embodiment the ovarian cancer is stage IV ovarian cancer. In further
10 embodiments the ovarian cancer is stage I, II, III, or IV ovarian cancer. In other embodiments the method further involves managing subject treatment based on the status. In yet another embodiment managing subject treatment is selected from the group consisting of ordering more tests, performing surgery, and taking no further action. In yet another embodiment the method includes measuring the level of CA-
15 125 and HE4 and measuring the level of one or more biomarkers selected from the group consisting of Interleukin-2 receptor alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostasin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial
20 Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1 in a sample of a biological fluid obtained from the subject after subject management; correlating the measurements with ovarian cancer status; and determining if subject management resulted in a change in ovarian cancer status. In
25 other embodiments measuring is selected from detecting the presence or absence of the biomarkers, quantifying the amount of biomarkers, and qualifying the type of biomarker. In certain embodiments the biomarkers are measured by an immunoassay. In further embodiments the correlating is performed by a software classification algorithm. In yet another embodiment the sample is selected from blood, serum, and
30 plasma. In some embodiments the affinity reagent is an antibody. In yet another embodiment the kits further include written instructions for using the affinity reagent to measure the levels of the biomarkers in a sample from a subject. In yet another

embodiment the kits include written instructions for use of the kit for determining a subjects ovarian cancer status. In certain embodiments one or more of the peptides have a detectable label.

In a preferred embodiment of the present invention, a method of predicting the ovarian cancer status of a subject is provided, which comprises the steps of:
5 determining the concentration of CA-125 and HE4 in a sample of a biological fluid from the subject and the age of the subject (collectively, the “biomarkers”); and evaluating the biomarkers, wherein a change in the level or evaluation of the biomarkers, as compared with a control group of patients who do not have ovarian
10 cancer, predicts that the subject has ovarian cancer. In a more preferred embodiment, the foregoing method further comprises the evaluation of a subject’s menopausal status of the subject as being either post-menopausal or not post-menopausal, and the concentrations of CA15-3 and CA72-4 in a sample of a biological fluid from the subject.

15 A variety of additional biomarkers also are evaluated with the foregoing biomarkers in additional embodiments of the present invention. These include: Vascular Endothelial Growth Factor (VEGF), Interleukin-2 receptor alpha (IL-2 receptor alpha), Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Haptoglobin, Ferritin (FRTN), Prostatin, Interleukin-8 (IL- 8), Maspin, Osteopontin,
20 Serum Amyloid P-Component (SAP), Platelet-Derived Growth Factor BB (PDGF-BB) and B cell-activating factor (BAFF). Optionally, certain additional biomarkers are also evaluated: Calprotectin, von Willebrand Factor (vWF), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), Interleukin-6 (IL-6), Leptin, Transthyretin (TTR), Carcinoembryonic Antigen (CEA), Insulin-like Growth Factor-Binding Protein 1
25 (IGFBP-1) and Thyroxine-Binding Globulin (TBG).

In preferred embodiments, the evaluation is made by a method selected from the group consisting of: logistic regression, look-up tables, decision tree, support vector machine, cluster analysis, neighbor analysis, genetic algorithm, Bayesian and non-Bayesian approaches, and the like. Additionally, the sample preferably is
30 selected from the group of fluids and tissues drawn from a patient that include blood, serum, plasma, lymph, cerebrospinal fluid, ascites, urine and tissue biopsy.

In other preferred embodiments, the methods of the present invention also include the step of providing a written or electronic report of the prediction of ovarian cancer and, optionally, the report includes a prediction as to the presence or absence or likelihood of ovarian cancer in the subject or the stratified risk of ovarian cancer for the subject, optionally by stage of cancer.

Other preferred embodiments provide a method in which the a) the sum of sensitivity and specificity for the method is greater than about 150%, when the sensitivity is above about 95%; or b) the sum of sensitivity and specificity for the method is greater than about 170%, when the specificity is above 95%; and c) the foregoing sum of sensitivity and specificity is supported by analysis of a set of samples comprising at least about 50 cancer samples and 150 benign samples.

Sets of reagents, test kits and multianalyte and ELISA panels and kits are provided to accomplish the foregoing methods.

Other biomarkers useful in the methods of the present invention include the following, which may be determined as one or more additional markers in the methods of claims 1 through 4 appended below: Prostatic Acid Phosphatase (PAP), Epidermal Growth Factor Receptor (EGFR), Cathepsin D, YKL-40, Matrix Metalloproteinase-7 (MMP-7), Vascular Endothelial Growth Factor D (VEGF-D), Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), Mesothelin (MSLN), Sortilin, Cellular Fibronectin (cFib), Osteoprotegerin (OPG), EN-RAGE, CD 40 antigen (CD40), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), Neuropilin-1, Fetuin-A, Resistin, Matrix Metalloproteinase-2 (MMP-2), Peroxiredoxin 4 (Prx-IV), Phosphoserine Aminotransferase (PSAT), Alpha-1-Microglobulin (A1Micro), Heparin-Binding EGF-Like Growth Factor (HB-EGF), Hepatocyte Growth Factor (HGF), Trefoil Factor 3 (TFF3), Complement Factor H, Clusterin (CLU), Aldose Reductase, Macrophage Migration Inhibitory Factor (MIF), Amphiregulin (AR), Macrophage Inflammatory Protein-1 alpha (MIP-1 alpha), FASLG Receptor (FAS), Vascular Endothelial Growth Factor Receptor 1 (VEGFR-1), Matrix Metalloproteinase-1 (MMP-1), Monocyte Chemotactic Protein 2 (MCP-2) and Vascular Endothelial Growth Factor B (VEGF-B).

In yet other embodiments of the present invention, any three or more of the following biomarkers are determined and evaluated: HE4, CA-125, IL-2 receptor alpha, AAT, CRP, YKL-40, fibronectin and CA-72-4.

In another embodiment of the invention, the levels of the following
5 biomarkers, optionally including HE4, are determined and evaluated, in some cases with a determination of age: CA-125, CA72-4, VEGF-B, Maspin, VEGF-D and YKL-40; CA-125, CA72-4, VEGF-B, Maspin, VEGF-D, YKL-40, OSP, Age and CRP; CA-125, CA72-4, VEGF-B, Maspin, and OSP; CA-125, CA72-4, VEGF-B, Maspin, YKL-40 and Age; CA-125, Maspin and Age; CA-125, CA72-4, VEGF-B,
10 Maspin, OSP and Age; CA-125, VEGF-B and Age.

In an additional embodiment of the invention, the levels of the following biomarkers, optionally including HE4, are determined and evaluated,,: HE4, Cancer Antigen 125 (CA-125), Cancer Antigen 72-4 (CA-72-4), Cancer Antigen 15-3 (CA-15-3), Age, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Interleukin-2
15 receptor alpha (IL-2 receptor alpha); HE4, Cancer Antigen 125 (CA-125) and YKL-40, optionally also including Age; HE4, Cancer Antigen 72-4(CA-72-4), Cancer Antigen 15-3 (CA-15-3), Age, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), and Interleukin-2 receptor alpha (IL-2 receptor alpha); CA-125, CA-72-4, Prostatin, CA-15-3, Age, IL-2 receptor alpha, IL-8, optionally also including HE4;
20 and CA-125, CA-72-4, Prostatin, CA-15-3, Age, IL-2 receptor alpha, IL-8, FRTN, VEGF, Osteopontin, Maspin, and Haptoglobin, optionally also including Age.

More specifically, predictive tests and associated methods and products also provide useful clinical information regarding the stage of ovarian cancer progression, that is: Stage I, Stage II, Stage III and Stage IV and an advanced stage which reflects
25 relatively advanced tumors that cannot readily be classified as either Stage III or Stage IV. Overall, the invention also relates to newly discovered correlations between the relative levels of expression of certain groups of markers in bodily fluids, preferably blood serum and plasma, and a subject's ovarian cancer status.

In one embodiment, the invention provides a set of reagents to measure the
30 expression levels of a panel or set of biomarkers in a fluid sample drawn from a

patient, such as blood, serum, plasma, lymph, cerebrospinal fluid, ascites or urine. The reagents in a further embodiment are a multianalyte panel assay comprising reagents to evaluate the expression levels of these biomarker panels.

In embodiments of the invention, a subject's sample is prepared from tissue samples such a tissue biopsy or from primary cell cultures or culture fluid. In a further embodiment, the expression of the biomarkers is determined at the polypeptide level. Related embodiments utilize immunoassays, enzyme-linked immunosorbent assays and multiplexed immunoassays for this purpose.

Preferred panels of biomarkers are selected from the group consisting of the following sets of molecules and their measurable fragments: (a) myoglobin, CRP (C reactive protein), FGF basic protein and CA 19-9; (b) Hepatitis C NS4, Ribosomal P Antibody and CRP; (c) CA 19-9, TGF alpha, EN-RAGE, EGF and HSP 90 alpha antibody, (d) EN-RAGE, EGF, CA 125, Fibrinogen, Apolipoprotein CIII, EGF, Cholera Toxin and CA 19-9; (e) Proteinase 3 (cANCA) antibody, Fibrinogen, CA 125, EGF, CD40, TSH, Leptin, CA 19-9 and lymphotactin; (f) CA125, EGFR, CRP, IL-18, Apolipoprotein CIII, Tenascin C and Apolipoprotein A1; (g) CA125, Beta-2 Microglobulin, CRP, Ferritin, TIMP-1, Creatine Kinase-MB and IL-8; (h) CA125, EGFR, IL-10, Haptoglobin, CRP, Insulin, TIMP-1, Ferritin, Alpha-2 Macroglobulin, Leptin, IL-8, CTGF, EN-RAGE, Lymphotactin, TNF-alpha, IGF-1, TNF RII, von Willebrand Factor and MDC; (i) CA-125, CRP, EGF-R, CA-19-9, Apo-AI, Apo-CIII, IL-6, IL-18, MIP-1a, Tenascin C and Myoglobin; (j) CA-125, CRP, EGF-R, CA-19-9, Apo-AI, Apo-CIII, IL-6, MIP-1a, Tenascin C and Myoglobin; and (k) any of the biomarker panels presented in Table II and Table III.

In another embodiment, the reagents that measure such biomarkers may measure other molecular species that are found upstream or downstream in a biochemical pathway or measure fragments of such biomarkers and molecular species. In some instances, the same reagent may accurately measure a biomarker and its fragments.

Another embodiment of the present invention relates to binding molecules (or binding reagents) to measure the biomarkers and related molecules and fragments.

Contemplated binding molecules includes antibodies, both monoclonal and polyclonal, aptamers and the like.

Other embodiments include such binding reagents provided in the form of a test kit, optionally together with written instructions for performing an evaluation of
5 biomarkers to predict the likelihood of ovarian cancer in a subject.

In other of its embodiments, the present invention provides methods of predicting the likelihood of ovarian cancer in a subject based on detecting or measuring the levels in a specimen or biological sample from the subject of the foregoing biomarkers. As described in this specification, a change in the expression
10 levels of these biomarkers, particularly their relative expression levels, as compared with a control group of patients who do not have ovarian cancer, is predictive of ovarian cancer in that subject.

In other of its aspects, the type of ovarian cancer that is predicted is serous, endometrioid, mucinous, and clear cell tumors. And prediction of ovarian cancer
15 includes the prediction of a specific stage of the disease such as Stage I (IA, IB or IC), II, III and IV tumors.

In yet another embodiment, the invention relates to creating a report for a physician of the relative levels of the biomarkers and to transmitting such a report by mail, fax, email or otherwise. In an embodiment, a data stream is transmitted via the
20 internet that contains the reports of the biomarker evaluations. In a further embodiment, the report includes the prediction as to the presence or absence of ovarian cancer in the subject or the stratified risk of ovarian cancer for the subject, optionally by subtype or stage of cancer.

According to another aspect of the invention, the foregoing evaluation of
25 biomarker expression levels is combined for diagnostic purposes with other diagnostic procedures such as gastrointestinal tract evaluation, chest x-ray, HE4 test, CA-125 test, complete blood count, ultrasound or abdominal/pelvic computerized tomography, blood chemistry profile and liver function tests.

Yet other embodiments of the invention relate to the evaluation of samples drawn from a subject who is symptomatic for ovarian cancer or is at high risk for ovarian cancer. Other embodiments relate to subjects who are asymptomatic of ovarian cancer. Symptomatic subjects have one or more of the following: pelvic
5 mass; ascites; abdominal distention; general abdominal discomfort and/or pain (gas, indigestion, pressure, swelling, bloating, cramps); nausea, diarrhea, constipation, or frequent urination; loss of appetite; feeling of fullness even after a light meal; weight gain or loss with no known reason; and abnormal bleeding from the vagina. The levels of biomarkers may be combined with the findings of such symptoms for a
10 diagnosis of ovarian cancer.

Embodiments of the invention are highly accurate for determining the presence of ovarian cancer. By “highly accurate” is meant a sensitivity and a specificity each at least about 85 percent or higher, more preferably at least about 90 percent or 92 percent and most preferably at least about 95 percent or 97 percent
15 accurate. Embodiments of the invention further include methods having a sensitivity of at least about 85 percent, 90 percent or 95 percent and a specificity of at least about 55 percent, 65 percent, 75 percent, 85 percent or 90 percent or higher. Other embodiments include methods having a specificity of at least about 85 percent, 90 percent or 95 percent, and a sensitivity of at least about 55 percent, 65 percent, 75
20 percent, 85 percent or 90 percent or higher.

Embodiments of the invention relating sensitivity and specificity are determined for a population of subjects who are symptomatic for ovarian cancer and have ovarian cancer as compared with a control group of subjects who are symptomatic for ovarian cancer but who do not have ovarian cancer. In another
25 embodiment, sensitivity and specificity are determined for a population of subjects who are at increased risk for ovarian cancer and have ovarian cancer as compared with a control group of subjects who are at increased risk for ovarian cancer but who do not have ovarian cancer. And in another embodiment, sensitivity and specificity are determined for a population of subjects who are symptomatic for ovarian cancer
30 and have ovarian cancer as compared with a control group of subjects who are not symptomatic for ovarian cancer but who do not have ovarian cancer.

In other aspects, the levels of the biomarkers are evaluated by applying a statistical method such as knowledge discovery engine (KDE™), regression analysis, discriminant analysis, classification tree analysis, random forests, ProteomeQuest®, support vector machine, One R, kNN and heuristic naive Bayes analysis, neural nets
5 and variants thereof.

In another embodiment, a predictive or diagnostic model based on the expression levels of the biomarkers is provided. The model may be in the form of software code, computer readable format or in the form of written instructions for evaluating the relative expression of the biomarkers.

10 A patient's physician can utilize a report of the biomarker evaluation, in a broader diagnostic context, in order to develop a relatively more complete assessment of the risk that a given patient has ovarian cancer. In making this assessment, a physician will consider the clinical presentation of a patient, which includes symptoms such as a suspicious pelvic mass and/or ascites, abdominal distention and
15 other symptoms without another obvious source of malignancy. The general lab workup for symptomatic patients currently includes a GI evaluation if clinically indicated, chest x-ray, CA-125 test, CBC, ultrasound or abdominal/pelvic CT if clinically indicated, chemistry profile with LFTs and may include a family history evaluation along with genetic marker tests such as BRCA-1 and BRCA-2. (See,
20 generally, the NCCN Clinical Practice Guidelines in Oncology™ for Ovarian Cancer, V.I.2007.)

The present invention provides a novel and important additional source of information to assist a physician in stratifying a patient's risk of having ovarian cancer and in planning the next diagnostic steps to take. The present invention is also
25 similarly useful in assessing the risk of ovarian cancer in non-symptomatic, high-risk subjects as well as for the general population as a screening tool. It is contemplated that the methods of the present invention may be used by clinicians as part of an overall assessment of other predictive and diagnostic indicators.

The present invention also provides methods to assess the therapeutic efficacy
30 of existing and candidate chemotherapeutic agents and other types of cancer

treatments. As will be appreciated by persons skilled in the art, the relative expression levels of the biomarker panels – or biomarker profiles – are determined as described above, in specimens taken from a subject prior to and again after treatment or, optionally, at progressive stages during treatment. A change in the relative expression of these biomarkers to a non-cancer profile of expression levels (or to a more nearly non-cancer expression profile) or to a stable, non-changing profile of relative biomarker expression levels is interpreted as therapeutic efficacy. Persons skilled in the art will readily understand that a profile of such expressions levels may become diagnostic for cancer or a pre-cancer, pre-malignant condition or simply move toward such a diagnostic profile as the relative ratios of the biomarkers become more like a cancer-related profile than previously.

In another embodiment, the invention provides a method for determining whether a subject potentially is developing cancer. The relative levels of expression of the biomarkers are determined in specimens taken from a subject over time, whereby a change in the biomarker expression profile toward a cancer profile is interpreted as a progression toward developing cancer.

The expression levels of the biomarkers of a specimen may be stored electronically once a subject's analysis is completed and recalled for such comparison purposes at a future time.

The present invention further provides methods, software products, computer systems and networks, and associated instruments that provide a highly accurate test for ovarian cancer.

The combinations of markers described in this specification provide sensitive, specific and accurate methods for predicting the presence of or detecting ovarian cancer at various stages of its progression. The evaluation of samples as described may also correlate with the presence of a pre-malignant or a pre-clinical condition in a patient. Thus, it is contemplated that the disclosed methods are useful for predicting or detecting the presence of ovarian cancer in a sample, the absence of ovarian cancer in a sample drawn from a subject, the stage of an ovarian cancer, the grade of an ovarian cancer, the benign or malignant nature of an ovarian cancer, the metastatic

potential of an ovarian cancer, the histological type of neoplasm associated with the ovarian cancer, the indolence or aggressiveness of the cancer, and other characteristics of ovarian cancer that are relevant to prevention, diagnosis, characterization, and therapy of ovarian cancer in a patient.

- 5 It is further contemplated that the methods disclosed are also useful for assessing the efficacy of one or more test agents for inhibiting ovarian cancer, assessing the efficacy of a therapy for ovarian cancer, monitoring the progression of ovarian cancer, selecting an agent or therapy for inhibiting ovarian cancer, monitoring the treatment of a patient afflicted with ovarian cancer, monitoring the inhibition of
10 ovarian cancer in a patient, and assessing the carcinogenic potential of a test compound by evaluating biomarkers of test animals following exposure.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a table showing the demographics of the study subjects.

Figure 2 is a table showing the biomarkers assayed in the study.

- 15 Figure 3 is a table showing the Area Underneath the Curve (AUC) values from Receiver Operating Characteristic (ROC) curve analysis of the top 20 markers.

Figure 4 is a table listing the informative biomarkers identified with Area Underneath the Curve (AUC) values statistically greater than 0.5.

- 20 Figure 5 is a set of graphs showing the Receiver Operating Characteristic curves for the nine most informative biomarkers with area under the curve values greater than 0.800.

- 25 Figure 6 is a set of graphs showing the serum level distributions broken out by International Federation of Gynecology and Obstetrics (FIGO) ovarian cancer stage for the nine most informative biomarkers with area underneath the curve values greater than 0.800.

Figure 7 is a set of graphs showing the serum level distributions broken out by subtype of ovarian cancer stage for the nine most informative biomarkers with area underneath the curve values greater than 0.800.

5 Figure 8 is a correlation matrix for biomarkers with area underneath the curve values greater than 0.600.

Figure 9 is a table listing the identities of markers in clusters A through D.

Figure 10 is a table showing the correlation data of the markers in cluster A.

Figure 11 is a table showing the correlation data of the markers in cluster B.

Figure 12 is a table showing the correlation data of the markers in cluster C.

10 Figure 13 is a table showing the correlation data of the markers in cluster D.

Figure 14 is a table showing the sensitivity at landmark threshold specificity values of logistic regression models using the nine most informative markers and the OVA1 biomarkers.

15 Figure 15 is a table showing the specificity at landmark threshold sensitivity values of logistic regression models using the nine most informative markers and the OVA1 biomarkers.

Figure 16 is a table showing the Area Underneath the Curve (AUC) values from Receiver Operating Characteristic (ROC) curve analysis of the top 20 markers broken out by menopausal status.

20 **DEFINITIONS**

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*
25 *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.

“Biomarker panel” refers to one of the biomarker panels set forth herein. A preferred biomarker panel comprises CA-125 and HE4 and one or more biomarkers
5 selected from the group consisting of Interleukin-2 receptor alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostaticin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth
10 Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1.

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

“Analyte” refers to any component of a sample that is desired to be detected. The term can refer to a single component or a plurality of components in the sample.

“Molecular binding partners” and “specific binding partners” refer to pairs of
20 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.

“Monitoring” refers to recording changes in a continuously varying parameter.

“Marker” in the context of the present invention refers to a polypeptide (of a
25 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.”

30 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.

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. 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.

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.

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.

“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.

5 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.*, $\mu\text{g/ml}$) or a relative amount (*e.g.*, relative intensity of signals).

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
10 amount can be either in absolute amount (*e.g.*, $\mu\text{g/ml}$) or a relative amount (*e.g.*, relative intensity of signals).

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.
15 A control amount can be either in absolute amount (*e.g.*, $\mu\text{g/ml}$) or a relative amount (*e.g.*, relative intensity of signals).

“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
20 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.
25 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
30 that comprises one or more heavy chain constant region domains, CH₁, CH₂ and CH₃, but does not include the heavy chain variable region.

As used herein by the term a "sample" is meant material which can be specifically related to a patient and from which specific information about the patient can be determined, calculated or inferred. A sample can be composed in whole or in part of biological material from of the patient. A sample can also be material that has
5 contacted the patient in a way that allows tests to be conducted on the sample which provides information about the patient. A sample may also be material that has contacted other material that is not of the patient but allows the first material to then be tested to determine information about the patient. A sample can contact sources of biologic material other than the patient provided that one skilled in the art can
10 nevertheless determine information about the patient from the sample. It is also understood that extraneous material or information that is not the sample could be utilized to conclusively link the patient to the sample. For a non-limiting example, a double blind test requires a chart or database to match a sample with a patient.

As used herein the term "body fluid" it is meant a material obtained from a
15 patient that is substantially fluid in consistency, but may have solid or particulate matter associated with it. A body fluid can also contain material and portions that are not from the patient. For instance a body fluid can be diluted with water, or can contain preservative, such as EDTA. Non-limiting examples of body fluids blood, serum, serosal fluids, plasma, lymph, urine, cerebrospinal fluid, saliva, mucosal
20 secretions of the secretory tissues and organs, vaginal secretions, breast milk, tears, and ascites fluids such as those associated with non-solid tumors. Additional examples include fluids of the pleural, pericardial, peritoneal, abdominal and other body cavities, and the like. Biological fluids may further include liquid solutions contacted with a subject or biological source, for example, cell and organ culture
25 medium including cell or organ conditioned medium, lavage fluids and the like.

"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.
30 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.

The term “stage” or “cancer stage” is intended to mean a classification of ovarian cancer that is based on the size, invasiveness, progression, migration, etc. of cancer in a subject. The stages of ovarian cancer are well defined. Stage I refers to ovarian cancer wherein the cancer is still contained within the ovary (or ovaries). Specifically, stage IA cancer has developed in one ovary, and the tumor is confined to the inside of the ovary. There is no cancer on the outer surface of the ovary.

Laboratory examination of washings from the abdomen and pelvis did not find any cancer cells. Stage IB cancer has developed within both ovaries without any tumor on their outer surfaces. Laboratory examination of washings from the abdomen and pelvis did not find any cancer cells. Stage IC cancer is present in one or both ovaries and 1 or more of the following are present: cancer on the outer surface of at least one of the ovaries; in the case of cystic tumors (fluid-filled tumors), the capsule (outer wall of the tumor) has ruptured (burst); or laboratory examination found cancer cells in fluid or washings from the abdomen.

Stage II cancer is in one or both ovaries and has involved other organs (such as the uterus, fallopian tubes, bladder, the sigmoid colon, or the rectum) within the pelvis. Specifically, stage IIA cancer has spread to or has actually invaded the uterus or the fallopian tubes, or both. Laboratory examination of washings from the abdomen did not find any cancer cells. Stage IIB cancer has spread to other nearby pelvic organs such as the bladder, the sigmoid colon, or the rectum. Laboratory examination of fluid from the abdomen did not find any cancer cells. Stage IIC cancer has spread to pelvic organs as in stages IIA or IIB and laboratory examination of the washings from the abdomen found evidence of cancer cells.

Stage III cancer involves 1 or both ovaries, and 1 or both of the following are present: (1) cancer has spread beyond the pelvis to the lining of the abdomen; (2) cancer has spread to lymph nodes. The cancer is Stage IIIA if, during the staging operation, the surgeon can see cancer involving the ovary or ovaries, but no cancer is grossly visible (can be seen without using a microscope) in the abdomen and the cancer has not spread to lymph nodes. However, when biopsies are checked under a microscope, tiny deposits of cancer are found in the lining of the upper abdomen. Stage IIIB cancer is in one or both ovaries, and deposits of cancer large enough for

the surgeon to see, but smaller than 2 cm (about 3/4 inch) across, are present in the abdomen. Cancer has not spread to the lymph nodes. For a cancer to be stage IIIC the cancer is in one or both ovaries, and one or both of the following are present: cancer has spread to lymph nodes and/or deposits of cancer larger than 2 cm (about 3/4 inch) across are seen in the abdomen.

Stage IV cancer is the most advanced stage of ovarian cancer. The cancer is in one or both ovaries. Distant metastasis (spread of the cancer to the inside of the liver, the lungs, or other organs located outside of the peritoneal cavity) has occurred. Finding ovarian cancer cells in pleural fluid (from the cavity that surrounds the lungs) is also evidence of stage IV disease.

As used herein, the term “recurrent ovarian cancer” is intended to mean that the disease has come back (recurred) after completion of treatment.

Biomarkers

15

By “CA-125” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers NP_078966.2 or AAL65133 or a fragment thereof. An exemplary sequence of CA-125 is:

1 mlkpsglpgs ssptrrslmtg srstkatpem dsdltgatls pktstgaivv
 20 tehtlpftsp
 61 dktlasptss vvgrrttqslg vmssalpest srgmthseqr tpslspqvn
 gtpsrnypat
 121 smvsglsspr trtsstegnf tkeastytlv vettsgpvte kyvptetst
 tegdstetpw
 25 181 dtryipvkit spmktfadst askenapvsm tpaettvtds htpgrtnpsf
 gtlyssfldl
 241 spkgtpnsrg etslelilst tgyfsspep gsaghsrist saplsssasv
 ldnkisetsi
 301 fsgqsltspl spgvpearas tmpnsaipfs mtlснаetsa ervrstissl
 30 gtpsisstkqt
 361 aetiltfhaf aetmdipsth iaktlasewl gspgtlggts tsalsttsp
 ttlvseent
 421 hhstsgkete gtlntsmtp l etsapgeese mtatlvptlg fttldskirs
 psqvssshpt
 35 481 relrttgsts grqssstaah gssdilratt sstskasswt sestaqqfse
 pqhtqvwets

541 psmkterppa stsvaapitt svpsvvsqft tlktsstkgi wleetsadtl
 igestagptt
 601 hqfavptgis mtggsstrgs qgtthlltra tassetsadl tlatngvpvs
 vspavsktaa
 5 661 gssppggtkp sytmvssvip etsslqssaf regtsgltp lntrhpfssp
 epdsaghtki
 721 stsipllssa svledkvsat stfshhkats sittgtpeis tktkpssavl
 ssmtlsnaat
 781 spervrnats plthpspsge etagsvltls tsaettdspn ihptgtltse
 10 ssespstlsl
 841 psvsgvkttf ssstpsthlf tsgeeteets npsvsqpets vsrvrtllas
 tsvptpvfpt
 901 mdtwptrsaq fssshlvsel ratsstsvtn stgsalpkis hltgtatmsq
 tnrdtfnasa
 15 961 apqsttwpet sprfktglps atttvstsat slsatvmvsk ftspatssme
 atsirepstt
 1021 ilttettnqp gsmavastni pigkgyiteg rldtshlpig ttassetsmd
 ftmakesvsm
 1081 svspsqmda agsstpgrts qfvdtfsddv yhltsreiti prdgtssalt
 20 pqmtathpps
 1141 pdpgsarstw lgilssspss ptpkvmsst fstqrvttsm imdtvetsrw
 nmpnlpstts
 1201 ltpsniptsg aigkstlvpl dtspatsle aseggptls typestntps
 ihlgahasse
 25 1261 spstikltma svvkpgsytp ltfpsiethi hvstarmays sgsspemtap
 getntgstwd
 1321 pttiyitttdp kdtssaqvst phsvrtlrtt enhpktesat paaysgspki
 ssspnltspa
 1381 tkawtitdtt ehstqlhytk laekssgfet qsapgpvsv iptspitgss
 30 tleltsdvpq
 1441 eplvlapseq ttitlpmatw lstslteema stdldissps spmstfaifp
 pmstpsshels
 1501 kseadtsair ntdsttldqh lgirslgrtg dlttvpitpl tttwtsviah
 stqaqdtlsa
 35 1561 tmspthvtqs lkdqtsipas aspshltevy pelgtqgrss seattfwkps
 tdtlsreiet
 1621 gpntniqstpp mdntttgsss sgvtlgiahl pigtsspaet stnmalerrs
 statvsmagt
 1681 mgllvtsapg rsisqslgrv ssvlseste gvtddsskgss prlntqgnta
 40 lssslepsy

1741 egsqmstsis ltsspttpdv efiggstfwt kevttvmtsd iskssartes
 ssatlmstal

1801 gstentgkek lrtasmdlps ptpsmevtpw isltlsnapn ttdslldlshg
 vhtssagtla

5 1861 tdrslntgvt rasrlengsd tsskslsmgn sthtsmtyte ksevsssihp
 rpetsapgae

1921 tltstpgnr aisltlpfss ipveevistg itsgpdinsa pmthspitpp
 tivwtstgti

1981 eqstqplhav ssekvsvtqg stpyvnsvav saspthensv ssgsstsspy
 10 ssasleslds

2041 tisrrnaitis wlwdltslp tttwpstsls ealssghsgv snpssttief
 plfsaastsa

2101 akqrnppet hgpqntaast lntdassvtg lsetpvgasi ssevplpmi
 tsrsdvsglt

15 2161 sestansplg tassagtklt rtislptses lvsfrmknkp wtvsiplgsh
 pttntetsip

2221 vnsagppgls tvasdvidtp sdgaesiptv sfspdpdev ttishfpekt
 thsfrtissl

2281 theltsrvtp ipgdwmssam stkptgasps itlgeretit saapttspiv
 20 ltasftetst

2341 vsldnettvk tsdildarkt nelpsdssss sdlintsias stmdvktas
 isptsisgmt

2401 asspslffs drpqvptstt etntatpsv ssntysldgg snvggtpstl
 ppftithpve

25 2461 tssallawsr pvrtfstmvs tdtasgenpt ssnsvvtsvp apgtwtsvgs
 ttdlpamgfl

2521 ktspageahs llastiepat aftphlsaav vtgssatsea slttteska
 ihsspqtptt

2581 ptsganwets atpesllvvt etsdttltsk ilvtdtilfs tvstppskfp
 30 stgtlsgasf

2641 ptllpdtpai pltateptss latsfdstpl vtiasdslgt vpettlmse
 tsngdalvlk

2701 tvsnpdrsip gitiqgvtes plhpsstspv kivaprntty egsitvalst
 lpagttgslv

35 2761 fsqssenset talvdssagl erasvmltt gsqgmassgg irsgsthstg
 tktfsslplt

2821 mnpgevtams eittnrlltat qstapkgipv kptsaesgll tpsasssps
 kafaslttap

2881 ptwgipqstl tfefsevpsl dtksaslptp gqslntipds dastasssls
 40 kspeknprar

2941 mmtstkaisa ssfqstgfte tpegsaspsm agheprvpts gtgdpryase
smsypdpska

3001 ssamtstsla sklttlftstg qaarsgssss pislsteket sflsptasts
rktslflgps

5 3061 marqpnilvh lqtsaltlsp tstlnmsqee ppeltssqti aeeegttaet
qtlftftpset

3121 ptsllpvssp teptarrkss petwassiv paktslvett dgltvttikm
ssqaaqgnst

10 3181 wpapaeetgs spagtspgsp emsttlkims skepsispei rstvrnspwk
tpettvpmet

3241 tvepvtlqst algsgstsis hlptgttspt ksptenmlat ervslspssp
eawtnlysgt

3301 pggtrqslat mssvslespt arsitgtgqq sspelvsktt gmefsmwhgs
tggttgdhv

15 3361 slstssnile dpvtspnsvs sltdkshkht etwvsttaip stvlmnkima
aeqtsrsvd

3421 eaysstssws dqtsgsditl gaspdvntnl yitstaqtts lvslpsgdqg
itsltnpsgg

20 3481 ktssassvts psigletlra nvsavksdia ptaghlsqts spaevsildv
ttaptpgist

3541 tittmgtnsi stttnpevg mstmdstpat errttstehp stwsstaasd
swtvtdmtsn

3601 lkvarspgti stmhttsfla ssteldsmst phgritvigt slvtpssdas
avktetstse

25 3661 rtlspsdtta stpistfsrv qrmsisvpdi lstswtpsst eaedvpvsmv
stdhastktd

3721 pntplstflf dslstldwdt grslssatat tsapqgattp qeltletmis
patsqlpfsi

30 3781 ghitsavtpa amarssgvtf srpdptsikka eqtstqlptt tsahpgqvpr
saattldvip

3841 htaktpdatf qrqqqtaltt earatsdsw n ekekstpsap witemmnsvs
edtikevtss

3901 ssvlrtlntl dinlesgtts spswksspye riapsettd keaihpstnt
vettgwtss

35 3961 ehashstipa hsassklts vvtststreqa ivsmsttwp estrartepn
sfltielrdv

4021 spymdtsstt qtsiisspgs taitkgprte itsskriss flagsmrssd
spseaitrls

40 4081 nfpamtesgg milamqtspp gatslsaptl dtsataswtg tplattqrft
ysekttlfsk

4141 gpedtsqpsp psveetssss slvpiahatts psnilltsqg hpsstppvt
 svflsetsgl
 4201 gktttdmsris lepgtstlppn lsstageals tyeasrdtka ihhsadtavt
 nmeatsseys
 5 4261 pipghatkpsk atsplvtshi mgditsstsv fgsetteie tvssvnqglq
 erstsqvass
 4321 atatstwith vssgdatthv tktqatfssg tsissphqfi tstntftdvs
 tnpstslimt
 4381 essgvttittq tgptgaatqg pylltdstmp yltetplavt pdfmqsekt
 10 liskgpkdvs
 4441 wtspssvaet syssstltpfl vttippatst lggqhtsspv satsvltsgl
 vkttddlnts
 4501 mepvtnsqpn lnnpsneila tlaattdiet ihpsinkavt nmgtassahv
 lhstlpvsse
 15 4561 pstatspmvp assmgdaldas isipgsettd iegeptssl agrkenstlq
 emnsttesni
 4621 ilsnvsvgai teatkmevps fdatfiptpa qstkfpdifs vassrlsnp
 pmtisthmtt
 4681 tqtgssgats kiplaldtst letsagtpsv vtegfahski ttamnndvkd
 20 vsqtnppfqd
 4741 easspssqap vlvttlpssv aftpqwhsts spvsmssvlt sslvktagkv
 dtsletvtss
 4801 pqmsntltd isvtsaattd ietthpsint vvtnvgttgs afeshstvsa
 ypepskvtsp
 25 4861 nvttstmedt tisrsipkss kttrtetett ssltpklret sisqeitsst
 etstvpysel
 4921 tgattevsrt dvtsssstf pgpdqstvsl distetnrl stspimtesa
 eitittqtgp
 4981 hgatsqdtft mdpsnttpqa gihsamthgf sqldvttlms ripqdvswts
 30 ppsvdktspp
 5041 ssflsspamt tpslisstlp edklsspmts lltsglvkit dilrtrlep
 tsslpnfsst
 5101 sdkilatskd skdtkeifps inteetnvka nnsgheshsp aladsetpka
 ttqmvittv
 35 5161 gdpapstsmv vhgsettni kreptyfltp rlrretstsqe ssfptdtsfl
 lskvptgtit
 5221 evsstgvnss skistpdhdk stvppdtftg eiprvftssi ktksaemt
 tqasppesas
 5281 hstlpldtst tllsqgthst vtqgfpvsev tllmgmgpgn vswmtppe
 40 etssvsslms

5341 spamtspspv sstspqsips splpvta1pt svlvtttdvl gttspevts
sppnlssith

5401 erpatykda hteaamhhst ntavtnvgts gsgghksqssv ladsetskat
plmsttstlg

5 5461 dtsvststpn isqtnqiqte ptaslprlr esstsektss ttetntafsy
vptgaitqas

5521 rteissrsts isdldrptia pdistgmitr lftspimtk s aemtvttqtt
tpgatsqgil

5581 pwdtsttlfq ggthstvsqg fphseittlr srtpgdvswm ttpvveetss
10 gfsmlpsmt

5641 spspvsstsp esipssplpv talltsvlvt ttnvlgttsp eptvssppnl
ssptqerl1t

5701 ykdahteam hasmhtntav anvgtsisgh esqssvpads htskatspmg
itfamgdtsv

15 5761 ststpaffet riqtestssl ipglrdtrts eeintvtets tvlsevpttt
ttevsrtevi

5821 tssrttisgp dhskmspyis tetitrlstf pfvtgstema itnqtgpigt
isqatl1ldt

5881 sstaswegth spvtqrfphs eett1tmsrst kgvswqspps veetsspspp
20 vplpaitshs

5941 slysavsgss ptsalpvtsl ltsgrrrktid mldthselvt sslpsassfs
geiltseast

6001 ntetihfsen taetnmgttn smhklhssvs ihsqpsg1tp pkvtgsmmed
aivststpgs

25 6061 petknvdrds tspltpelke dstalvmnst tesntvfssv sldaatevsr
aevtyy1ptf

6121 mpasaqstks pdispeasss hsnsp1tis thktiatqtg psgvtslgql
tldtstiats

6181 agtpsartqd fvdsettsvm nnd1ndv1kt spfsaeeans lssqapllvt
30 tpspvtstl

6241 qehstsslvs vtsvptptla kitdmdtnle pvtrspqnlr ntlatseatt
dthtmhpsin

6301 tavanvg1ts spnefyftvs pdsdpykats avvitstsgd sivstsmprs
samkkieset

35 6361 tfs1lifr1re tstsqkigss sdtstvfdka ftaattevsr teltssrsts
iqgtektms

6421 pdtstrsvtm lstfag1tks eertiatqtg phratsqgtl twdtsittsq
agthsamthg

6481 fsqld1st1t srvpeyisgt sppsvektss sss1lslpai tpspvp1t1l
40 pesrpsspvh

6541 ltslptsglv kttmdlasva slppnlgsts hkipttsedi kdtekmypst
niavtnvgtt

6601 tsekesyssv payseppkvt spmvtsfnir dtivstsmg sseitrieme
stfslahglk

5 6661 gtstsqdpiv steksavlhk lttgatetsr tevassrrts ipgpdhstes
pdistevips

6721 lpislgites snmtiitrtg pplgstsqgt ftldtpttss ragthsmatq
efphsemttv

10 6781 mnkdpeilsw tippsiekts fssslmpspa mtsppvsstl pktihttpsp
mtslltpslv

6841 mtttdtlgtsp epttssppnl sstsheilitt dedttaieam hpststaant
vettssghgs

6901 qssvladsek tkatapmddt stmghttvtst smsvssettk ikrestyslt
pglretsisq

15 6961 nasfsttdtsi vlsevptggt aevsrtevtst sgrtsipggs qstvlpeist
rtmtrlfasp

7021 tmtesaemti ptqtgpgsgt sqdtltdts ttksqakths tltqrfphse
mttlmsrgpg

20 7081 dmswqsspsl enpsslpall slpattsppt isstlpvtis ssplpvtall
tsspvttttdm

7141 lhtspelvtst sppklshtsd erlittgkddt nteavhpstn taasnveips
sghespsal

7201 adsetskats pmfitstqed ttvaistphf letsriqkes isslspklre
tgssvetssa

25 7261 ietsavlsev sigatteisr tevtsssrts isgsaestml peisttrkii
kfptspilae

7321 ssemiktqt sppgstsest ftldtsttps lvithstmtq rlpheittl
vsrgagdvpr

30 7381 psslpveets ppssqlslsa mispspvsst lpashhssa svtslltpgq
vkttevlidas

7441 aepetsspps lsstsveila tsevttdtek ihpfsntavt kvgtsssghe
spssvlpdse

7501 ttkatsamgt isimgdtsvs tltpalsntr kiqsepassl ttrlretstst
eetslatean

35 7561 tvlskvstga ttevsrteai sfsrtsmgsp eqstmsqdis igtiprisas
svltesakmt

7621 ittqtgppses tlestlnlnt attpswveth siviqqfphp emttsmgrgp
ggvswpsppf

40 7681 vketsppssp lslpavtsph pvsttflahi ppslpvtst ltsgpatttd
ilgtstepgt

7741 ssssslstts herlttykdt ahteavhpst ntggtnvatt ssgyksqssv
ladsspmctt

7801 stmgdtsvlt stpafletrr iqtelasslt pglressgse gtssgtkmst
vlsvkvtgat

5 7861 teiskedvts ipgpaqstis pdistrtvsw fstspvmtes aaitmthts
plgattqgts

7921 tldtssttsl tmthstisqg fshsqmstlm rrgpedvswm sppllektrp
sfslmsspat

10 7981 tpspvsstl pesisssplp vtslltsgla kttmhlkss epvtnspanl
sstsvailat

8041 sevttdekt hpssnrtvtd vgtsssghes tsfvladsgt skvtspmvit
stmedtsvst

8101 stpgffetsr iqteptsslt lglrktssse gtlatemst vlsgvptgat
aevsrtevts

15 8161 ssrtsisgfa qltvspetst etitrlptss imtesaemmi ktqtdppgst
pesthtvdis

8221 ttpnwveths tvtqrfishse mttlvsrspg dmlwpsqssv eetssassll
slpattspsp

20 8281 vsstlvedfp saslpvtsll npglvittdr mgisrepqts stsnlsstsh
erlittledtv

8341 dtedmqpsth tavtnvrtsi sghesqssvl sdsetpkats pmgttytmg
tsvsistsdf

8401 fetsriqiep tssltsglre tssserissa tegstvlsev psgattevsr
tevissrgts

25 8461 msgpdqftis pdisteaitr lstspimtes aesaitietg spgatsegtl
tldtstttfw

8521 sgthstaspg fshsemttlm srtpgdvpwp slpsveeass vssslsspan
tstsfstlp

30 8581 esisssphpv talltlgpvk ttdmlrtsse petssppnls stsaailats
evtkdrekih

8641 pssntpvvvn gtviykhls pssvladlvtt kptspmatss tlgntsvsts
tpafpetmmt

8701 qptssltsgl reistsqets satersasls gmptgattkv srtealslgr
tstpgpaqst

35 8761 ispeistetl tristplttt gsaemtltk tghsgassqg tftldtssra
swpgthsaat

8821 hrsphsgmtt pmsrgpedvs wpsrpsvekt sppsslvsls avtspsply
tpsesshssp

40 8881 lrvtslftpv mmkttmldt slepvttsp smnitsdesl atskatmete
aiqlsentav

8941 tqmgtisarq efyssyppglp epskvtspvv tsstikdivs ttipasseit
riemeststl

9001 tptpretsts qeihsatkps tpykaltsa tiedsmtqvm sssrgpspdq
stmsqdiste

5 9061 vitrlstspi ktestemtit tqtgspgats rgtltldtst tfmsgthsta
sqqfshsqmt

9121 almsrtpgdv pwlshpsvee assasfslss pvmtssspvs stlpdsihss
slpvtslits

9181 glvkttellg tssepetssp pnlsstsaai laitevttdt eklemtnvvt
10 sgythespss

9241 vladsvttkka tssmgitypt gdtvnltstp afsdtsriqt ksklsltpgl
metsiseets

9301 satekstvls svptgattev srteaissr tsipgpaqt mssdtsmeti
tristpltrk

15 9361 estdmaitpk tgpsgatsqg tftldsssta swpgthsatt qrfpqsvvtt
pmsrgpedvs

9421 wpsplsvekn sppsslvsss svtspsplys tpsgsshssp vpvtslftsi
mmkatdmla

9481 slepettsap nmnitsdesl aaskattete aihvfentaa shvettsate
20 elysssppgfs

9541 eptkvispvv tsssirdnmv sttmpgssgi trieiesmss ltpglretrt
sqditsstet

9601 stvlykmpsg atpevsrtev mpssrtsipg paqstmsldi sdevvtrlst
spimtesaei

25 9661 tittqtgysl atsqvtlplg tsmtflsgth stmsqglshs emtnlmsrgp
eslswtsprf

9721 vettrssssl tslplttsls pvsstlldss pssplpvtsl ilpglvkte
vldtssepkt

9781 ssspnlssts veipatseim tdtekihps ntaavakvrts ssvheshssv
30 ladsettiti

9841 psmgitsavd dttvftsnpa fsetrripte ptfsltpgfr etstseetts
itetsavlyg

9901 vptsattevs mteimssnri hipdsdqstm spdiitevit rlssssmmse
stqmtittqk

35 9961 sspgataqst ltlatttapl arthstvppr flhsemttlm srspenpswk
sslfvektss

10021 sssllslpvt tpsvsstlp qsipsssfsv tslltpgmvk ttdtstepgt
slspnlsqts

10081 veilaasevt tdtekihps smavtnvgtt ssghelyssv sihsepskat
40 ypvgtppssma

10141 etsistsmpa nfettgfeae pfshltsgfr ktnmsldtss vtptntpssp
gsthllqssk

10201 tdftssakts spdwpasqy teipvdiitp fnaspsites tgitsfpesr
ftmsvtesth

5 10261 hlstdllpsa etistgtvmp slseamtsfa ttgvpraisg sgspfsrtes
gpgdatlsti

10321 aeslpsstpv pfssstfttt dsstipalhe itsssatpyr vdtslgtess
ttegrlvmvs

10381 tldtssqpggr tssspildtr mtesvelgtv tsayqvpsls trlrtdgim
10 ehitkipnea

10441 ahrgtirpvk gpqtstspas pkglhtggtk rmettttalk ttttalktts
ratlittsvyt

10501 ptlgtltpln asmqmastip temmittpyv fpdvpettss latslgaets
talprttpsv

15 10561 fnresettas lvrsrgaers pviqtdvss sepdttaswv ihpaetiptv
skttpnffhs

10621 eldtvsstat shgadvssai ptnispseld altplvtisg tdtsttfptl
tksphetetr

10681 ttwlthpaet sstiprtipn fshhesdatp siatspgaet ssaipimtv
20 pgaedlvtsq

10741 vtssgtdrnm tiptltlspg epktiaslvt hpeaqtssai ptstispavs
rlvtsmvtsl

10801 aaktsttnra ltinspgepat tvslvthpaq tsptvpwts iffhsksdt
psmttshgae

25 10861 sssavptptv stevpgvvtv lvtssravis ttipiltlsp gepettpsma
tshgeeassa

10921 iptptvspgv pgvvtslvts sravtsttip iltfslgepe ttpsmatshg
teagsavptv

10981 lpevpqmvts lvassravts ttlptltlsp gepettpsma tshgaeas
30 vptvspevpg

11041 vvtslvtsss gvnstsiptl ilspgelett psmatshgae assavptptv
spgvsgvvtv

11101 lvtssravts ttipiltlss sepettpsma tshgveassa vltvspevpg
mvtslvtssr

35 11161 avtsttiptl tissdepett tslvthseak misaiptlav sptvqglvts
lvtssgsets

11221 afsnltvass qpetidswva hpgteassvv ptltvstgep ftnislvt
aessstlprt

11281 tsrfshseld tmpstvtspe aesssaistt ispgipgvt slvtssgrdi
40 satfptvpes

11341 pheseatasw vthpavtstt vprttpnys h sepdttpsia tspgaeatsd
 fptitvspdv

11401 pdmvtsgvts sgt dtsitip tltlssgepe tttsfityse thtssaip t l
 pvspgaskml

5 11461 tslvissgtd stttfptlte tpyepettai qlihpaetnt mvprttpkfs
 hsksdttlpv

11521 aitspgpeas savstttisp dmsdlvtslv pssgtdtstt fptlsetpye
 pettatwlth

11581 paetsttvsg tipnfshrgs dtapsmvtsp gvdrtrsgvpt ttippsipgv
 10 vtsqvtssat

11641 dtstaip tlt pspgepetta ssathpgtqt gftvpirtvp ssepdtmasw
 vthppqtstp

11701 vsrttssfish sspdatpvma tsprteassa vlttispgap emvtsqitss
 gaatsttvpt

15 11761 lthspgmpet tallsthprt etsktfpast vfpqvsetta sltirpgaet
 stalptqtts

11821 slftllvtgt srvdlsptas pgvsaktapl sthpgtetst miptstlslg
 llettgllat

11881 sssaetstst ltlvtspavs glssasitt d kpqvtswnt etspsvtsvg
 20 ppefsrtvtg

11941 ttmtlipsem ptppktshge gvspttilrt tmveatnlat tgssptvakt
 tttfntlags

12001 lftplttpgm stlasesvts rtsynhrswi sttssynrry wtpatstpvt
 stfsgists

25 12061 sipsstaatv pfmvpftlnf titnlqyeed mrhpgsrkfn aterelqgll
 kplfrnssle

12121 ylysgcrlas lrpek dssat avdaicthrp dpedlgldre rlywelsnlt
 ngiqelgpyt

12181 ldrnslyvng fthrssmptt stpgtstvdv gtsgtpsssp spttagpllm
 30 pftlnftitn

12241 lqyeedmr rt gsrk fntmes vlqgllkplf kntsvgp lys gcr ltlrpe
 kdgaatgvda

12301 icthrl dpks pgl nreqlyw elsklndie elgpytldr n slyvngfthq
 ssvsttstpg

35 12361 tstvd lrtsg tpsslsspti maagpllvpf tlnftitnlq ygedmghpgs
 rkfnttervl

12421 qgllgpifkn tsvgp lysgc rltslrsek d gaatgvdaic ihhldpkspg
 lnrerlywel

12481 sqltngikel gpytldr nsl yvngfthrts vptsstpgts tvdlgtsgtp
 40 fslpspatag

12541 pllvlftlnf titnlkyeed mhrpgsrkfn ttervlqtll gpmfkntsvg
 llysgcrltl
 12601 lrsekdgat gvdaicthrl dpkspgvdre qlywelsqlt ngikelgpyt
 ldrnslyvng
 5 12661 fthwipvpts stpgtstvd l gsgtpsslps pttagpllvp ftlnftitnl
 kyeedmhcpq
 12721 srkfnntterv lqsllygpmfk ntsvgplysg crltllrsek dgaatgv dai
 cthrl dpksp
 12781 gvdreqlywe lsqlyngike lgyptldrns lyvngfthqt sapntstpgt
 10 stvdlgtsgt
 12841 psslpsptsa gppllvpftln ftitnlqyee dmhhpgsrkf nttervlqgl
 lgpmfkntsv
 12901 gllysgcrlt llrpekngaa tgmdaicshr ldpkspglr eglywelsql
 thgikelgpy
 15 12961 tldrnslyvn gfthrssvap tstpgtstvd lgtsgtpssl pspttavpll
 vpftlnftit
 13021 nlqygedmrh pgsrkfntte rvlqglgpl fknssvgply sgcrllslrs
 ekdgaatgv
 13081 aicthhlnpq spgldreqly wqlsqmtngi kelgpytldr nslyvngfth
 20 rsglittstp
 13141 wtstvdlgts gtpspvpspt ttgpllvpft lnftitnlqy eenmghpgsr
 kfnitesvlq
 13201 gllkplfkst svgplysgcr ltllrpekdg vatrvaict hrpdkipgl
 drqqlywels
 25 13261 qlthsitelg pytldrdsly vngftqrssv pttstpgtft vqpetsetps
 slpgptatgp
 13321 vllpftlnft itnlqyeedm rrpgrskfnt tervlqglm plfkntsvss
 lysgcrltll
 13381 rpekdgatr vdavcthrpd pkspglrdr lywklsqlyth gitelgpytl
 30 drhslyvngf
 13441 thqssmttr tpdstmhla tsrtpaslsg pmtaspllv ftinftitnl
 ryeenmhpg
 13501 srkfnntterv lqglrpvfk ntsvgplysg crltllrpkk dgaatkvdai
 ctyrpdpksp
 35 13561 gldreqlywe lsqlythsite lgyptldrds lyvngftqrs svpttsipgt
 ptvdlgtsgt
 13621 pvskpgpsaa splllvftln ftitnlryee nmqhpgsrkf nttervlqgl
 lrslfkstsv
 13681 gplysgcrlt llrpekdgta tgvdacihh pdpkspldr eglywelsql
 40 thnitelgpy

13741 aldndslfvn gfthrsvst tstpgtptvy lgasktpasi fgpsaashll
ilftlnftit

13801 nlryeenmwp gsrkfnntter vlqgllrplf kntsvgplys gcrlltllrpe
kdgeatgvda

5 13861 icthrpdpdg pglrdreqlyl elsqlyhsit elgpytldrd slyvngfthr
ssvpttstgv

13921 vseepftlnf tinnlrymad mgqpgslkfn itdnvmqhl1 splfqrsslg
arytgcrvia

10 13981 lrsvkngaet rvdllctylq plsgpglpik qvfhelsqqt hgitrlgpys
ldkdslylng

14041 ynepgpdepp ttpkpattfl pplseattam gyhlktltln ftisnlqysp
dmgkgsatfn

14101 stegvlqhl1 rplfqkssmg pfylgcqlis lrpekdgat gvdttctyhp
dpvgpgldiq

15 14161 qlywelsqlt hgvtqlgyfv ldrdslfing yapqnlsirg eyqinfhivn
wnlsnbdpts

14221 seyitllrldi qdkvttlykg sqlhdtfrfc lvtnltdsv lvtvkalfss
nldpslveqv

20 14281 fldktnasf hwlgstyqlv dihvtemess vyqptssst qhfylnftit
nlpysqdkaq

14341 pgttnyqrnk rniedalnql frnssiksyf sdcqvstfrs vprnhhtgvd
slcnfsplar

14401 rvdrvaiyee flrmtrngtq lqnftldrss vlvdygspnr nepltgnsdl
pfwaviligl

25 14461 agllgvitcl icgvlvttrr rkkegeynvq qqcpgyyqsh ldledlq

By “HE4” is meant a polypeptide biomarker having at least 85% sequence
identity to NCBI accession numbers AA052683 or CAA44869 or a fragment thereof.

An exemplary sequence of HE4 is:

30 1 mpacrlgpla aalllslllf gftlvsgtga ektgvcpelq adqnetqecv
sdsecadnlk

61 ccsagcatfc slpndkegsc pqvninfpql glcrdqcvd sqcpqmkcc
rngcgkvscv

121 tpnf

35

By “IL-2 receptor alpha (IL-2R α)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers CAK26553 or NP_000408 or a fragment thereof. An exemplary sequence of IL-2R α is:

```

1 mdsyllmwgl ltfimvpgcq aelcdddpe iphatfkama ykegtmlnce
5 ckrqfrriks
61 gslymlctgn sshsswdnqc qctssatrnt tkqvtpqpee qkerkttemq
spmqpvdqas
121 lpghcreppp weneateriy hfvvgqmvyq qcvqgyralh rgpaesvckm
thgktrwtqp
10 181 qlictgemet sqfpgeekpq aspegrpese tsclvttttdf qiqtemaatm
etsiftteyq
241 vavagcvfll isvlllsglt wqrrqrksrr ti

```

By “Alpha-1-Antitrypsin (AAT)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers AAB59495 or CAJ15161 or a fragment thereof. An exemplary sequence of AAT is:

```

1 mpssvswgil llaglcclvp vslaedpqqd aaqktdtshh dqdhptfnki
tpnlaefafs
61 lyrqlahqsn stniffspvs iatafamsl gkadhthdei leglnfnlte
20 ipeaqihegf
121 qellrtlnqp dsqqlttgn glflsegkl vdkfledvkk lyhseaftvn
fgdteeakkq
181 indyvekgtq gkivdlvkel drdtvfalvn yiffkgkwer pfevkdtee
dfhvdqvttv
25 241 kvpmmkrlgm fniqhckkls swvllmkylg nataifflpd egklqhlvne
lthdiitkfl
301 enedrrsas1 hlpklsitgt ydlksvlgql gitkvfsnga dlsgvteeap
lklskavhka
361 vltidekgte aagamfleai pmsippevkf nkpfvflmie qntksplfmg
30 kvvnptqk

```

By “C-Reactive Protein (CRP)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers CAA39671 or P02741 or a fragment thereof. An exemplary sequence of CRP is:

```

35 1 mekllocflvl tslshafgqt dmsrkafvfp kesdtsyvsl kapltkplka
ftvclhfyte

```

61 lsstrgvtvfs rmprrdktmr ffifwskdig ysftvvggsei lfevpevtva
 pvhictswes
 121 asgivefwvd gkprvrkslk kgytvgaeas iilgqeqsdf ggnfegsqs
 vgdignvnmw
 5 181 dfvlspdein tiylggpfsp nvlnwralky evqgevftkp qlwp

By “YKL-40” also know as “chitinase-3-like protein” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P36222 or NP_001267 or a fragment thereof. An exemplary sequence of YKL-40 is:

10 1 mgvkasqtgf vvlvllqccs ayklvcyyts wsqyregdgs cfpdaldrfl
 cthiiysfan
 61 isndhidtwe wndvtlygml ntlknrnpnl ktllsvggwn fgsqrfskia
 sntqsrrtffi
 121 ksvppflrth gfdgldlawl ypgrrdkqhf ttlikemkae fikeaqpqgk
 15 qlllsaalsa
 181 gkvtidssyd iakisqhldf isimtydfhg awrgttghhs plfrgqedas
 pdrfsntdya
 241 vgymlrlgap asklvmgipt fgrsftlass etgvgapisg pgipgrftke
 agtlayyeic
 20 301 dflrgatvhr ilgqqvpyat kgnqvwgydd qesvkskvqy lkdrqlagam
 vwaldddfq
 361 gsfcgqdlrf pltnaikdal aat

By “Cellular Fibronectin (cFib)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P02751 or a fragment thereof. An exemplary sequence of cFib is:

1 mlrgpqpql1 llavqclgta vpstgasksk rqaqqmvqpq spvavsqskp
 gcydngkhyq
 61 inqqwertyl gnalvctcyg gsergfncesk peaeetcfdk ytgntyrvgd
 30 tyerpkdsmi
 121 wdctcigagr grisctianr cheggqsyki gdtwrrphet ggymlecvcl
 gngkgewtck
 181 piaekcftha agtsyvvget wekpyqgwm vdctclgegs gritctsrnr
 cndqdtrtsy
 35 241 rigdtwskkd nrgnllqcic tgnrgewkc erhtsvqtts sgsgpftdvr
 aavyqpqphp

301 qpppyghcvt dsgevvyvsgm qwlktqgnkq mlctclngv scqetavtqt
 yggnsngepc
 361 vlpftyngrt fyscttegrq dghlwcstts nyeqdqkysf ctdhtvltvt
 rggnsngalc
 5 421 hfpflynnhn ytdctsegrr dnmkwcggttq nydadqkfgf cpmaaheeic
 ttnegvmyri
 481 gdqwdkqhdm ghmmrctcvg nrggewtcia ysqlrdqciv dditynvndt
 fhkrheeghm
 541 lnctcfggqr grwkcdpvdq cqdssetgtfy qigdswekyv hgvryqcycy
 10 grgigewhcq
 601 plqtypsssg pvevfitetp sqpnshpiqw napqpshisk yilrwrpkns
 vgrwkeatip
 661 ghlnsytikg lkpgvvyegq lisiqqyghq evtrfdfttt ststpvtstnt
 vtgettpfsp
 15 721 lvatsesvte itassfvvsw vsasdtvsgf rveyelseeg depqyldlps
 tatsvnipl
 781 lpgrkyivnv yqisedgeqs lilstsqtta pdappdttd qvddtsivvr
 wsrpqapitg
 841 yrivyspsve gsstelnlpe tansvtlsdl qpgvqyniti yaveenqest
 20 pvviqgettq
 901 tprsdvpsp rdlqfvevtd vkvtimwtp esavtgyrvd vipvnlpgeh
 gqrlpisrnt
 961 faevtqlspg vtyyfkvfav shgreskplt aqqttkldap tnlqfvnetd
 stvlvrwtp
 25 1021 raqitgyrlt vgltrrgqpr qynvgpsvsk yplrnlqpas eytvslvaik
 gnqespkatg
 1081 vfttlqpgss ippyntevte ttivitwtpa prigfklgvr psqggeapre
 vtsdsgsivv
 1141 sgltpgvveyv ytiqvlrdgq erdapivnkvtplspptnl hleanpdtgv
 30 ltvswerstt
 1201 pditgyritt tptngqqgns leevvhadqs sctfdnlspg leynsvyvtv
 kddkesvpis
 1261 dtiipavppp tdlrftnigp dtmrvtwapp psidltflv ryspvkneed
 vaelsispsd
 35 1321 navvltnllp gteyvsvsvs vyeqhestpl rgrqktglds ptgidfsdit
 ansftvhwia
 1381 pratitgyri rhhpehfsgr predrvphsr nsitltnltp gteyvsvsiva
 lngreespll
 1441 igqqstvsdv prdlevvaat ptslliswda pavtvryyri tygetggnsp
 40 vqeftvpgsk

1501 statisglkp gvdytitvya vtgrgdspas skpisinyrt eidkpsqmqv
 tdvqdnsisv
 1561 kwlpssspvt gyrvtttpkn gpgptkktka gpdqtemtie glqptveyvv
 svyaqnpdge
 5 1621 sqplvqtavt nidrpkglaf tdvdvdsiki awespqqqvs ryrvtyspe
 dgihelfpap
 1681 dgeedtaelq glrpgseytv svvalhddme sqpligtqst aipaptdlkf
 tqvtptslsa
 1741 qwtppnvqlt gyrvrvtpke ktgpmkeinl apdsssvvvs glmvatkyev
 10 svyalkdtlt
 1801 srpaqgvvtt lenvsprra rvtdatetti tiswrktet itgfqvдав
 angqtpiqrt
 1861 ikpdvrsyti tglqpgtdyk iylytlndna rsspvidas taidapsnlr
 flattpnsll
 15 1921 vswqpprari tgyiikyekp gspprevvpr prpgvteati tglepgteyt
 iyvialknnq
 1981 ksepligrkk tdelpqlvtl phpnlhgpei ldvpstvqkt pfvthpgydt
 gngiqlpqts
 2041 gqqpsvgqqm ifeehgfrt tppttatpir hrprpyppnv geeiqighip
 20 redvdyhlyp
 2101 hpgplnplas tgqealsqtt iswapfqdts eyiischpvg tdeepqfrv
 pgtstsatlt
 2161 gltrgatynv ivealkdqqr hkvreevvtv gnsvneglnq ptddscfdpy
 tvshyavgde
 25 2221 wermsesgfk llcqcclgfgs ghfrcdssrw chdngvnyki gekwdrqgen
 gqmmsetclg
 2281 ngkgefkdcp heatcyddgk tyhvgeqwqk eylgaicsct cfggqrgwrc
 dncrrpgep
 2341 spegttgqsy nqysqryhqr tntnvnpcie cfmpldvqad redsre
 30

By “Cancer Antigen 72-4 (CA-72-4)” also referred to as “TAG-72” is meant a glycoprotein biomarker which is recognized by monoclonal antibody B72.3.

By “prostasin” is meant a polypeptide biomarker having at least 85% sequence
 35 identity to NCBI accession numbers AAB19071 or AAC41759 or a fragment thereof.
 An exemplary sequence of prostasin is:

1 maqkgvlgpg qlgavailly lgllrsgtga egaeapcgva pparitggss
avagqwpwqv

61 sityegvhvc ggslvseqwv lsaahcfpse hhkeayevkl gahqldsyste
dakvstlkdi

5 121 iphpsylqeg sqgdiallql srpitfsryi rpiclpaana sfpnglhctv
tgwghvapsv

181 slltpkplqq levplisret cnclynidak peephfvqed mvcagyvegg
kdacqgdsgg

10 241 plscpveglw yltgivswgd acgarnrpgv ytlassyasw iqskvtelqp
rvvpqtqesq

301 pdsnlcgshl afssapaqgl lrpilflplg lalgllspwl seh

By “Tissue Inhibitor of Metalloproteinases 1 (TIMP-1)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers NP_003245 or P01033 or a fragment thereof. An exemplary sequence of TIMP-1 is:

1 mapfeplasg illllwliap sractcvpph pqtafcnsdl virakfvgtg
evnqttlyqr

20 61 yeikmtkmyk gfqalgdaad irfvytpame svcgyfhrsh nrseefliag
klqdgllhit

121 tcsfvapwns lslaqrngft ktytvgeec tvfpclsipc klqsgthclw
tdqllqgsek

181 gfgsrhlacl prepqlctwq slrsqia

25 By “Interleukin 8 (IL-8)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P10145 or AAH13615 or a fragment thereof. An exemplary sequence of IL-8 is:

1 mtsklavall aafllisaalc egavlprsak elrcqckty skpfhpkfik
elrviesgph

30 61 canteiivkl sdgrelcldp kenwvqrve kflkraens

By “Matrix Metalloproteinase-7 (MMP-7)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P09237 or NP_002414 or a fragment thereof. An exemplary sequence of MMP-7 is:

1 mrltvlcavc llpgslalpl pqaaggmsel qweqaqdyk rfylydsetk
nansleaklk

61 emqkffglpi tgmlnsrvie imqkprcgvp dvaeyslfpn spkwtskvvt
yrivsytrdl

5 121 phitvdrllvs kalnmwgkei plhfrkvvvg tadimigfar gahgdsypfd
gpgntlahaf

181 apgtgllgda hfdederwtd gsslginfly aathelghsl gmghssdpna
vmyptygngd

241 pqnfklsqdd ikgiqklygk rsnsrkk

10

By “Interleukin 6 (IL-6)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P05231, NP_000591, or AAH15511 or a fragment thereof. An exemplary sequence of IL-6 is:

1 mnsfstsafg pvafslglll vlpaafpapv ppgedskdva aphrqpltss
15 eridkqiryi

61 ldgisalrke tcnksnmces skealaennl nlpkmaekdg cfqsgfneet
clvkiitgll

121 efevyleylq nrfesseeqa ravqmstkv1 iqflqkkakn ldaittpdpt
tnaslltklq

20 181 aqnqwlqdm t hlilrsfke flqsslralr qm

By “Vascular Endothelial Growth Factor B (VEGF-B)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P49765, AAC50721, or AAB06274 or a fragment thereof. An exemplary sequence of VEGF-

25 B is:

1 msp11rrlll aallqlapaq apvsqpdapg hqrkvsvwid vytratcqpr
evvvpltvel

61 mgtvakqlvp scvtvqrcgg ccpddglecv ptgqhqvrmq ilmirypssq
lgemsleehs

30 121 qcecrpkkkd savkpdraat phhrpqprsv pgwdsapgap spadithptp
apgpsahaap

181 sttsaltpgp aaaaadaaas svakgga

By “calprotectin” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers AAB33355, AAB25118, or P06702 or a fragment thereof. An exemplary sequence of calprotectin is:

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1 mtckmsqler nietiintfh qysvklghpd tlnqgefkel vrkdlnflk
5 kenknekie
61 himedldtna dkqlsfeefi mmarltwas hekmhegdeg pghhkpplg egtp

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By “Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers AAA03246 or AAA36048 or a fragment thereof. An exemplary sequence of IGFBP-2 is:

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1 mlprvgcpal plppplllpl lpllllllga sgggggarae vlfrcppctp
erlaacgppp
15 61 vappaavaav aggarmcae lvrepgcgcc svcarlegea cgvytprcgq
glrcyphpgs
121 elplqalvmg egtcekrda eygaspeqva dngddhsegg lvenhvdstm
nmlggggsag
181 rkplksgmke lavfrekvt e qhrqmkggk hhlgleepkk lrpppartpc
20 qqeldqvler
241 istmrlpder gplehlyslh ipncdkhgly nlkqckmsln gqrgecwcvn
pntgkcliqga
301 ptirgdpech lfyneqqear gvhtqrmq

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By “Lectin-Like Oxidized LDL Receptor 1 (LOX-1)” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P78380 or NP_002534 or a fragment thereof. An exemplary sequence of LOX-1 is:

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1 mtfddlkiqt vkdqpdeksn gkkakglqfl yspwwclaaa tlglvclglv
vtimvlgmql
30 61 sqvsdlltqe qanlthqkkk legqisarq aeeasqesen elkemietla
rklnekskeq
121 melhhqnl nl qetlkrvanc sapcpqdwiw hgencylfss gsfnweksqe
kclsl dakll
181 kinstadldf iqqaisysf pfwmglsrrn psypwlwedg splmphi frv
35 rgavsqtyps

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241 gtcayiqrga vyaencilaa fsicqkkanl raq

By “neuropilin-1” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers AAP80144, AAP78927, AAG41895, or ABY87548 or a fragment thereof. An exemplary sequence of neuropilin-1 is:

1 mergplllca vlalvlapag afrndkcgdt ikiespgytl spgyphsyhp
 sekcewliqa
 61 pdpyqrimin fnphfdledr dckydyvevf dgenenghfr gkfcgkiapp
 pvvssgpflf
 10 121 ikfvdsyeth gagfsiryei fkrqpecsqn yttpsgviks pgfpekypns
 lectyivfap
 181 kmseiilefe sfdlepdsnp pggmfcrydr leiwdgfpdv gphigrycgg
 ktpgrirsss
 241 gilsmvfytd saiakegfsa nysvlqssvs edfkmealg mesgeihsdq
 15 itassqystn
 301 wsaersrlny pengwtpged syrewiqvdl gllrfvtavg tggaisketk
 kkyvkytyki
 361 dvssngedwi tikegnkpvf fqqntnptdv vvavfpkpli trfvrikpat
 wetgismrfe
 20 421 vvgckitdyp csgmlgmvsq lisdqitss nqgdrnwmpc nirlvtstrsq
 walppaphsy
 481 inewlqidlg eekivrgiii qggkhrenkv fmrkfkigys nngsdwkmim
 ddskrkaksf
 541 egnnnydtpe lrtfpalstr firiyperat hgglgirmel lgceveapta
 25 gpttpngnlv
 601 decdddqanc hsgtgddfql tggttvlate kptvidstiq sefptygfn
 efgwgshktf
 661 chwehdnhvq lkswvltskt gpiqdhtgdg nfiysqaden qkgkvarlvs
 pvvysqnsah
 30 721 cmtfwyhmsg shvgtlrvkl ryqkpeeydq lvwmaighqg dhwkegrvll
 hkslklyqvi
 781 fegeigkgnl ggiavddisi nnhisqedca kpadldkkn
 eikidetgst
 pgyegeged
 841 knisrkpgnv lktldpilit iiamsalgv
 lgavcgvvly cacwhngmse
 35 rnlsalenyn
 901 felvdgvklk kdklntqsty sea

By “TNFR2” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers P20333 or NP_001057 or a fragment thereof. An exemplary sequence of TNFR2 is:

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1 mapvavwaal avglelwaaa halpaqvaft pyapepgstc rlreyydqta
5 qmccskcspg
  61 qhakvfctkt sdtvcdsced stytqlwnwv peclscgsrc ssdqvetqac
  treqnrietc
  121 rpgwycalsk qegcrlcapl rkcrpgfgva rpgtetsdvv ckpcapgtfs
  nttssstdicr
10  181 phqicnvvai pgnasmdavc tstsptrsma pgavhlpqpv strsqhtqpt
  pepstapsts
  241 fllpmgppspp aegstgdfal pvglivgvta lglliigvvn cvimtvkvvk
  plclqreakv
  301 phlpadkarg tqgpeqhll itapssssss lessasaldr raptrnqpqa
15  pgveasgag
  361 arastgssds spgghgtqvn vtcivnvcss dhssqcassq asstmgtdds
  spsespkdeq
  421 vpfskeecaf rsqletpetl lgsteekplp lgvpdagmkp s

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20 By “MPIF-1” is meant a polypeptide biomarker having at least 85% sequence identity to NCBI accession numbers AAB51134 or P55773 or a fragment thereof. An exemplary sequence of MPIF-1 is:

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1 mkvsvaalsc lmlvtalgsq arvtdaete fmmsklplen pvlldrfhat
  sadccisytp
25  61 rsipcslles yfetnsecsk pgvifltkkg rrfcanpsdk qvqvcmrmlk
  ldtriktrkn

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DETAILED DESCRIPTION:

The biomarker panels and associated methods and products were
30 identified through the analysis of analyte levels of various molecular species in human blood serum drawn from subjects having ovarian cancer of various stages and subtypes, subjects having non-cancer gynecological disorders and normal subjects. The immunoassays described below were courteously performed by our colleagues at Rules-Based Medicine of Austin, TX using their Multi-Analyte Profile (MAP)
35 Luminex® platform.

While a preferred sample is blood serum, it is contemplated that an appropriate sample can be derived from any biological source or sample, such as tissues, extracts, cell cultures, including cells (for example, tumor cells), cell lysates, and physiological fluids, such as, for example, whole blood, plasma, serum, saliva, ductal lavage, ocular lens fluid, cerebral spinal fluid, sweat, urine, milk, ascites fluid, synovial fluid, peritoneal fluid and the like. The sample can be obtained from animals, preferably mammals, more preferably primates, and most preferably humans using species specific binding agents that are equivalent to those discussed below in the context of human sample analysis. It is further contemplated that these techniques and marker panels may be used to evaluate drug therapy in rodents and other animals, including transgenic animals, relevant to the development of human and veterinary therapeutics.

The sample can be treated prior to use by conventional techniques, such as preparing plasma from blood, diluting viscous fluids, and the like. Methods of sample treatment can involve filtration, distillation, extraction, concentration, inactivation of interfering components, addition of chaotropes, the addition of reagents, and the like. Nucleic acids (including silencer, regulatory and interfering RNA) may be isolated and their levels of expression for the analytes described below also used in the methods of the invention.

20 **Samples and Analytical Platform.**

The set of blood serum samples that was analyzed to generate most of the data discussed below contained 150 ovarian cancer samples and 150 non-ovarian cancer samples. The ovarian cancer sample samples further comprised the following epithelial ovarian cancer subtypes: serous (64), clear cell (22), endometrioid (35), mucinous (15), mixed, that is, consisting of more than one subtype (14). The stage distribution of the ovarian cancer samples was: Stage I (41), Stage II (23), Stage III (68), Stage IV (12) and unknown stage (6).

The non-ovarian cancer sample set includes the following ovarian conditions: benign (104), normal ovary (29) and "low malignant potential/borderline (3). The sample set also includes serum from patients with other cancers: cervical cancer (7), endometrial cancer (6) and uterine cancer (1).

Antibodies that are specific for a biomarker antigen polypeptide of the invention are readily generated as monoclonal antibodies or as polyclonal antisera, or may be produced as genetically engineered immunoglobulins (Ig) that are designed to have desirable properties using methods well known in the art. For example, by way of illustration and not limitation, antibodies may include recombinant IgGs, chimeric fusion proteins having immunoglobulin derived sequences or "humanized" antibodies (see, e.g., U.S. Pat. Nos. 5,693,762; 5,585,089; 4,816,567; 5,225,539; 5,530,101; and references cited therein) that may all be used for detection of a human biomarker polypeptide according to the methods described herein. Such antibodies may be prepared as provided herein, including by immunization with biomarker polypeptides as described below. For example, as provided herein, nucleic acid sequences encoding biomarker polypeptides are disclosed, such that those skilled in the art may routinely prepare these polypeptides for use as immunogens.

The term "antibodies" includes polyclonal antibodies, monoclonal antibodies, fragments thereof such as F(ab').sub.2, and Fab fragments, as well as any naturally occurring or recombinantly produced binding partners, which are molecules that specifically bind a biomarker polypeptide. Antibodies are defined to be "immunospecific" or specifically binding if they bind HE4a polypeptide with a K.sub.a of greater than or equal to about 10^{-4} M, preferably of greater than or equal to about 10^{-5} M, more preferably of greater than or equal to about 10^{-6} M, and still more preferably of greater than or equal to about 10^{-7} M. Affinities of binding partners and antibodies can be readily determined using conventional techniques, for example those described by Scatchard et al., Ann. N.Y. Acad. Sci. 51:660 (1949). Determination of other proteins as binding partners of a biomarker polypeptide can be performed using any of a number of known methods for identifying and obtaining proteins that specifically interact with other proteins or polypeptides, for example, a yeast two-hybrid screening system such as that described in U.S. Pat. No. 5,283,173 and U.S. Pat. No. 5,468,614, or the equivalent. The methods described herein also includes the use of a biomarker polypeptide, and peptides based on the amino acid sequence of a biomarker polypeptide, to prepare binding partners and antibodies that specifically bind to a biomarker polypeptide.

Antibodies may generally be prepared by any of a variety of techniques known to those of ordinary skill in the art (see, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988). In one such technique, an immunogen comprising a biomarker polypeptide, for example a cell having a biomarker polypeptide on its surface or an isolated biomarker polypeptide is initially injected into a suitable animal (e.g., mice, rats, rabbits, sheep and goats), preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the biomarker polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for biomarker polypeptides or variants thereof may be prepared, for example, using the technique of Kohler and Milstein (1976 *Eur. J. Immunol.* 6:511-519), and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the mesothelin polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. For example, the spleen cells and myeloma cells may be combined with a membrane fusion promoting agent such as polyethylene glycol or a nonionic detergent for a few minutes, and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred. Hybridomas that generate monoclonal antibodies that specifically bind to biomarker polypeptides are contemplated by the methods described herein.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to

enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse or other suitable host.

Monoclonal antibodies may then be harvested from the ascites fluid or the blood.

Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. For example,
5 antibodies may be purified by chromatography on immobilized Protein G or Protein A using standard techniques.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be
10 prepared using standard techniques (e.g., by digestion with papain to yield Fab and Fc fragments). The Fab and Fc fragments may be separated by affinity chromatography (e.g., on immobilized protein A columns), using standard techniques. Such techniques are well known in the art, see, e.g., Weir, D. M., Handbook of Experimental Immunology, 1986, Blackwell Scientific, Boston.

15 Multifunctional fusion proteins having specific binding affinities for pre-selected antigens by virtue of immunoglobulin V-region domains encoded by DNA sequences linked in-frame to sequences encoding various effector proteins are known in the art, for example, as disclosed in EP-B1-0318554, U.S. Pat. No. 5,132,405, U.S. Pat. No. 5,091,513 and U.S. Pat. No. 5,476,786. Such effector
20 proteins include polypeptide domains that may be used to detect binding of the fusion protein by any of a variety of techniques with which those skilled in the art will be familiar, including but not limited to a biotin mimetic sequence (see, e.g., Luo et al., 1998 J. Biotechnol. 65:225 and references cited therein), direct covalent modification with a detectable labeling moiety, non-covalent binding to a specific labeled reporter
25 molecule, enzymatic modification of a detectable substrate or immobilization (covalent or non-covalent) on a solid-phase support.

Single chain antibodies for use in the methods described herein may also be generated and selected by a method such as phage display (see, e.g., U.S. Pat. No. 5,223,409; Schlebusch et al., 1997 Hybridoma 16:47; and references cited
30 therein). Briefly, in this method, DNA sequences are inserted into the gene III or gene VIII gene of a filamentous phage, such as M13. Several vectors with multicloning

sites have been developed for insertion (McLafferty et al., *Gene* 128:29-36, 1993; Scott and Smith, *Science* 249:386-390, 1990; Smith and Scott, *Methods Enzymol.* 217:228-257, 1993). The inserted DNA sequences may be randomly generated or may be variants of a known binding domain for binding to a biomarker polypeptide. Single chain antibodies may readily be generated using this method. Generally, the inserts
5 encode from 6 to 20 amino acids. The peptide encoded by the inserted sequence is displayed on the surface of the bacteriophage. Bacteriophage expressing a binding domain for a biomarker polypeptide are selected by binding to an immobilized biomarker polypeptide, for example a recombinant polypeptide prepared using
10 methods well known in the art and nucleic acid coding sequences as disclosed herein. Unbound phage are removed by a wash, typically containing 10 mM Tris, 1 mM EDTA, and without salt or with a low salt concentration. Bound phage are eluted with a salt containing buffer, for example. The NaCl concentration is increased in a step-wise fashion until all the phage are eluted. Typically, phage binding with higher
15 affinity will be released by higher salt concentrations. Eluted phage are propagated in the bacteria host. Further rounds of selection may be performed to select for a few phage binding with high affinity. The DNA sequence of the insert in the binding phage is then determined. Once the predicted amino acid sequence of the binding peptide is known, sufficient peptide for use herein as an antibody specific for a
20 biomarker polypeptide may be made either by recombinant means or synthetically. Recombinant means are used when the antibody is produced as a fusion protein. The peptide may also be generated as a tandem array of two or more similar or dissimilar peptides, in order to maximize affinity or binding.

To detect an antigenic determinant reactive with an antibody specific
25 for a biomarker polypeptide, the detection reagent is typically an antibody, which may be prepared as described herein. There are a variety of assay formats known to those of ordinary skill in the art for using an antibody to detect a polypeptide in a sample, including but not limited to enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA), immunofluorimetry, immunoprecipitation, equilibrium
30 dialysis, immunodiffusion and other techniques. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988; Weir, D. M., *Handbook of Experimental Immunology*, 1986, Blackwell Scientific, Boston. For

example, the assay may be performed in a Western blot format, wherein a protein preparation from the biological sample is submitted to gel electrophoresis, transferred to a suitable membrane and allowed to react with the antibody. The presence of the antibody on the membrane may then be detected using a suitable detection reagent, as
5 is well known in the art and described below.

In another embodiment, the assay involves the use of an antibody immobilized on a solid support to bind to the target biomarker polypeptide and remove it from the remainder of the sample. The bound biomarker polypeptide may then be detected using a second antibody reactive with a distinct biomarker
10 polypeptide antigenic determinant, for example, a reagent that contains a detectable reporter moiety. Alternatively, a competitive assay may be utilized, in which a biomarker polypeptide is labeled with a detectable reporter moiety and allowed to bind to the immobilized biomarker polypeptide specific antibody after incubation of the immobilized antibody with the sample. The extent to which components of the
15 sample inhibit the binding of the labeled polypeptide to the antibody is indicative of the reactivity of the sample with the immobilized antibody, and as a result, indicative of the level of biomarker polypeptides in the sample.

The solid support may be any material known to those of ordinary skill in the art to which the antibody may be attached, such as a test well in a microtiter
20 plate, a nitrocellulose filter or another suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic such as polystyrene or polyvinylchloride. The antibody may be immobilized on the solid support using a variety of techniques known to those in the art, which are amply described in the patent and scientific literature.

In certain preferred embodiments, the assay for detection of biomarker antigen polypeptide in a sample is a two-antibody sandwich assay. This assay may be performed by first contacting a biomarker polypeptide-specific antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the biological sample, such that a soluble molecule naturally occurring in the sample and
30 having an antigenic determinant that is reactive with the antibody is allowed to bind to the immobilized antibody (e.g., a 30 minute incubation time at room temperature is

generally sufficient) to form an antigen-antibody complex or an immune complex. Unbound constituents of the sample are then removed from the immobilized immune complexes. Next, a second antibody specific for a biomarker antigen polypeptide is added, wherein the antigen combining site of the second antibody does not

5 competitively inhibit binding of the antigen combining site of the immobilized first antibody to a biomarker polypeptide. The second antibody may be detectably labeled as provided herein, such that it may be directly detected. Alternatively, the second antibody may be indirectly detected through the use of a detectably labeled secondary (or "second stage") anti-antibody, or by using a specific detection reagent as provided

10 herein. The methods described herein are not limited to any particular detection procedure, as those having familiarity with immunoassays will appreciate that there are numerous reagents and configurations for immunologically detecting a particular antigen (e.g., a mesothelin polypeptide) in a two-antibody sandwich immunoassay.

In certain preferred embodiments of the methods described herein

15 using the two-antibody sandwich assay described above, the first, immobilized antibody specific for a biomarker antigen polypeptide is a polyclonal antibody and the second antibody specific for a biomarker antigen polypeptide is a polyclonal antibody. Any combination of non-competitive biomarker antibodies could be used with the methods described herein. Including monoclonal antibodies, polyclonal antibodies

20 and combinations thereof. In certain other embodiments of the methods described herein the first, immobilized antibody specific for a biomarker antigen polypeptide is a monoclonal antibody and the second antibody specific for a biomarker antigen polypeptide is a polyclonal antibody. In certain other embodiments of the methods described herein the first, immobilized antibody specific for a biomarker antigen

25 polypeptide is a polyclonal antibody and the second antibody specific for a biomarker antigen polypeptide is a monoclonal antibody. In certain other highly preferred embodiments of the methods described herein the first, immobilized antibody specific for a biomarker antigen polypeptide is a monoclonal antibody and the second antibody specific for a biomarker antigen polypeptide is a monoclonal antibody. In

30 other preferred embodiments of the methods described herein the first, immobilized antibody specific for a biomarker antigen polypeptide and/or the second antibody specific for a biomarker antigen polypeptide may be any of the kinds of antibodies

known in the art and referred to herein, for example by way of illustration and not limitation, Fab fragments, F(ab').sub.2 fragments, immunoglobulin V-region fusion proteins or single chain antibodies. Those familiar with the art will appreciate that the methods described herein encompass the use of other antibody forms, fragments, derivatives and the like in the methods disclosed and claimed herein.

In certain particularly preferred embodiments, the second antibody may contain a detectable reporter moiety or label such as an enzyme, dye, radionuclide, luminescent group, fluorescent group or biotin, or the like. Any reporter moiety or label could be used with the methods described herein, so long as the signal of such is directly related or proportional to the quantity of antibody remaining on the support after wash. The amount of the second antibody that remains bound to the solid support is then determined using a method appropriate for the specific detectable reporter moiety or label. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Antibody-enzyme conjugates may be prepared using a variety of coupling techniques (for review see, e.g., Scouten, W. H., Methods in Enzymology 135:30-65, 1987). Spectroscopic methods may be used to detect dyes (including, for example, colorimetric products of enzyme reactions), luminescent groups and fluorescent groups. Biotin may be detected using avidin or streptavidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic, spectrophotometric or other analysis of the reaction products. Standards and standard additions may be used to determine the level of antigen in a sample, using well known techniques.

In another embodiment, the methods described herein involve use of a biomarker antigen polypeptide as provided herein to screen for the presence of a malignant condition by detection of immunospecifically reactive antibodies in a biological sample from a biological source or subject. According to this embodiment, a biomarker antigen polypeptide (or a fragment or variant thereof including a truncated biomarker antigen polypeptide as provided herein) is detectably labeled and contacted with a biological sample to detect binding to the biomarker antigen

polypeptide of an antibody naturally occurring in soluble form in the sample. For example, the biomarker antigen polypeptide may be labeled biosynthetically by using the sequences disclosed herein in concert with well known methods such as incorporation during in vitro translation of a readily detectable (e.g. radioactively
5 labeled) amino acid, or by using other detectable reporter moieties such as those described above. Without wishing to be bound by theory, this embodiment of the methods described herein contemplates that certain biomarker polypeptides such as the biomarker fusion polypeptides disclosed herein, may provide peptides that are particularly immunogenic and so give rise to specific and detectable antibodies. For
10 example, according to this theory certain biomarker fusion polypeptides may represent "non-self" antigens that provoke an avid immune response, while biomarker polypeptides that lack fusion domains may be viewed by the immune system as more resembling "self" antigens that do not readily elicit humoral or cell-mediated immunity.

15 Analyte levels in the samples discussed in this specification were measured using a high-throughput, multi-analyte immunoassay platform. A preferred platform is the Luminex® MAP system as developed by Rules-Based Medicine, Inc. in Austin, TX. It is described on the company's website and also, for example, in publications such as Chandler et al., "Methods and kits for the diagnosis of acute
20 coronary syndrome, U.S. Patent Application 2007/0003981, published January 4, 2007, and a related application of Spain et al., "Universal Shotgun Assay," U.S. Patent Application 2005/0221363, published Oct. 6, 2005. This platform has previously been described in Lokshin (2007) and generated data used in other analyses of ovarian cancer biomarkers. However, any immunoassay platform or
25 system may be used.

In brief, to describe a preferred analyte measurement system, the MAP platform incorporates polystyrene microspheres that are dyed internally with two spectrally distinct fluorochromes. By using accurate ratios of the fluorochromes, an array is created consisting of 100 different microsphere sets with specific spectral
30 addresses. Each microsphere set can display a different surface reactant. Because microsphere sets can be distinguished by their spectral addresses, they can be

combined, allowing up to 100 different analytes to be measured simultaneously in a single reaction vessel. A third fluorochrome coupled to a reporter molecule quantifies the biomolecular interaction that has occurred at the microsphere surface.

5 Microspheres are interrogated individually in a rapidly flowing fluid stream as they pass by two separate lasers in the Luminex® analyzer. High-speed digital signal processing classifies the microsphere based on its spectral address and quantifies the reaction on the surface in a few seconds per sample.

In another embodiment, an immunoassay can be used to detect and analyze markers in a sample. This method comprises: (a) providing an antibody that
10 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.

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
15 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
20 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
25 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.

30 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
5 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.

10 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.

15 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
20 sample to the antibody.

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
25 detectable labels include magnetic beads (*e.g.,* DYNABEADS[™]), fluorescent dyes, radiolabels, enzymes (*e.g.,* horse radish peroxidase, 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
30 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.

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*.

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.

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.

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.

5

Another method of measuring the biomarkers includes the use of a combinatorial ligand library synthesized on beads as described in USSN: 11/495,842, filed July 28, 2006 and entitled "Methods for Reducing the range in Concentrations of Analyte Species in a Sample"; hereby incorporated by reference in its

10

Skilled artisans will recognize that a wide variety of analytical techniques may be used to determine the levels of biomarkers in a sample as is described and claimed in this specification. Other types of binding reagents available to persons skilled in the art may be utilized to measure the levels of the indicated analytes in a sample. For example, a variety of binding agents or binding reagents appropriate to evaluate the levels of a given analyte may readily be identified in the scientific literature. Generally, an appropriate binding agent will bind specifically to an analyte, in other words, it reacts at a detectable level with the analyte but does not react detectably (or reacts with limited cross-reactivity) with other or unrelated analytes. It is contemplated that appropriate binding agents include polyclonal and monoclonal antibodies, aptamers, RNA molecules and the like. Spectrometric methods also may be used to measure the levels of analytes, including immunofluorescence, mass spectrometry, nuclear magnetic resonance and optical spectrometric methods. Depending on the binding agent to be utilized, the samples may be processed, for example, by dilution, purification, denaturation, digestion, fragmentation and the like before analysis as would be known to persons skilled in the art. Also, gene expression, for example, in a tumor cell or lymphocyte also may be determined.

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It is also contemplated that the identified biomarkers may have multiple epitopes for immunassays and/or binding sites for other types of binding agents. Thus, it is contemplated that peptide fragments or other epitopes of the identified biomarkers, isoforms of specific proteins and even compounds upstream or

downstream in a biological pathway or that have been post-translationally modified may be substituted for the identified analytes or biomarkers so long as the relevant and relative stoichiometries are taken into account appropriately. Skilled artisans will recognize that alternative antibodies and binding agents can be used to determine the
5 levels of any particular analyte, so long as their various specificities and binding affinities are factored into the analysis.

A variety of algorithms may be used to measure or determine the levels of expression of the analytes or biomarkers used in the methods and test kits of the present invention. It is generally contemplated that such algorithms will be capable of
10 measuring analyte levels beyond the measurement of simple cut-off values. Thus, it is contemplated that the results of such algorithms will generically be classified as multivariate index analyses by the U.S. Food and Drug Administration. Specific types of algorithms include: knowledge discovery engine (KDE™), regression analysis, discriminant analysis, classification tree analysis, random forests,
15 ProteomeQuest®, support vector machine, One R, kNN and heuristic naive Bayes analysis, neural nets and variants thereof.

While there are many very sophisticated algorithms that calculate the probability of an unknown sample being a cancer, a simple logistic regression model typically works quite well for building a diagnostic model based on the measurement
20 of a few markers (preferably less than about five). The theory behind that is well known to persons skilled in the art. There are also many options regarding which software can be use --- both commercial and free (and open source) packages.

The training of a logistic model consists of separating the samples into cases and controls and then use the software chosen to optimize the regression
25 coefficients, one for each marker, plus one bias parameter, so as to maximize the likelihood of the logistic model applied to the training data.

Once trained, the set of regression coefficients defines the logistic model. A person skilled in the art can easily use this type of diagnostic model to predict the probability of any new samples being identified as a case or control, by
30 plugging the levels of the biomarkers into the logistic equation. Furthermore, an ROC

can also be constructed by computing the sensitivities and specificities as the cutoff value of the computed probability varies from 0 to 1. The use of Logistic Regression to calculate a probability comprises the following steps: 1) Measure the levels of the biomarkers:

- 5 For each biomarker, its level is measured and recorded. As guidance to practitioners, the following discussion assumes the use of N biomarkers, and their designated measured levels are x_1, x_2, \dots, x_n –

2) Compute the ‘z’ value:

10 A central quantity to compute in a logistic regression model is the ‘z’ parameter. It is defined as follows,

$$z = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_n x_n . \quad \text{eq(1)}$$

15 The parameter β_0 is called the bias or intercept, while $\beta_1, \beta_2, \dots, \beta_n$ are called weights. Specifying the β s would define a logistic regression model. Typically, a training process determines the β s where samples with a known state of either “disease” or “benign” are used to optimize a likelihood function by varying the β s. Once the training process is completed, the values of the β s will be chosen to yield the optimal likelihood of a correct determination.

20 For an unknown sample with measured biomarker levels: x_1, x_2, \dots, x_n and a predetermined set of β s, a person skilled in the art can compute the value of z according eq(1).

3) Compute the value of the Logistic Function:

The Logistic Function, $f(z)$, is defined as

$$f(z) = e^z / (e^z + 1) \quad \text{eq(2)}$$

25 Given the value of z computed in 2), one can evaluate $f(z)$ according to eq(2). In some applications, the natural logarithm of z is used instead of just z in eq(2).

4) Make A Diagnostic Call:

The Logistic Function yields a value between (0.0 and 1.0), for any value of z . In a typical application, a cutoff of 0.5 is used to differentiate between the controls and the cases. Thus a sample with a score that is > 0.5 would be called a case, while a sample with a score that is ≤ 0.5 would be called a control. In some applications of the diagnostic process, other cutoff values (for example, 0.65) are used.

EXAMPLES

EXAMPLE 1

The following discussion and examples are provided to describe and illustrate the present invention. As such, they should not be construed to limit the scope of the invention. Those skilled in the art will well appreciate that many other embodiments also fall within the scope of the invention, as it is described in this specification and the claims.

15 Analysis of Data Using the Knowledge Discovery Engine.

Correlogic has described the use of evolutionary and pattern recognition algorithms in evaluating complex data sets, including the Knowledge Discovery Engine (KDE™) and ProteomeQuest®. See, for example, Hitt et al., U.S. Patent No. 6,925,389, "Process for Discriminating Between Biological States Based on Hidden Patterns From Biological Data" (issued August 2, 2005); Hitt, U.S. Patent No. 7,096,206, "Heuristic Method of Classification," (issued August 22, 2006) and Hitt, U.S. Patent No. 7,240,038, "Heuristic Method of Classification," (to be issued July 3, 2007). The use of this technology to evaluate mass spectral data derived from ovarian cancer samples is further elucidated in Hitt et al., "Multiple high-resolution serum proteomic features for ovarian cancer detection," U.S. Published Patent Application 2006/0064253, published March 23, 2006.

When analyzing the data set by Correlogic's Knowledge Discovery Engine, the following five-biomarker panels were found to provide sensitivities and specificities for various stages of ovarian cancer as set forth in Table I. Specifically,

KDE Model 1 [2_0008_20] returned a relatively high accuracy for Stage I ovarian cancer and included these markers: Cancer Antigen 19-9 (CA19-9, Swiss-Prot Accession Number: Q9BXJ9), C Reactive Protein (CRP, Swiss-Prot Accession Number: P02741), Fibroblast Growth Factor-basic Protein (FGF-basic, Swiss-Prot Accession Number: P09038) and Myoglobin (Swiss-Prot Accession Number: P02144). KDE Model 2 [4_0002-10] returned a relatively high accuracy for Stage III, IV and “advanced” ovarian cancer and included these markers: Hepatitis C NS4 Antibody (Hep C NS4 Ab), Ribosomal P Antibody and CRP. KDE Model 3 [4_0009_140] returned a relatively high accuracy for Stage I and included these markers: CA 19-9, TGF alpha, EN-RAGE (Swiss-Prot Accession Number: P80511), Epidermal Growth Factor (EGF, Swiss-Prot Accession Number: P01133) and HSP 90 alpha antibody. KDE Model 4 [4_0026_100] returned a relatively high accuracy for Stage II and Stages III, IV and “advanced” ovarian cancers and included these markers: EN-RAGE, EGF, Cancer Antigen 125 (CA125, Swiss-Prot Accession Number: Q14596), Fibrinogen (Swiss-Prot Accession Number: Alpha chain P02671; Beta chain P02675; Gamma chain P02679), Apolipoprotein CIII (ApoCIII, Swiss-Prot Accession Number: P02656), Cholera Toxin and CA 19-9. KDE Model 5 [4_0027_20] also returned a relatively high accuracy for Stage II and Stages III, IV and “advanced” ovarian cancers and included these markers: Proteinase 3 (cANCA) antibody, Fibrinogen, CA 125, EGF, CD40 (Swiss-Prot Accession Number: Q6P2H9), Thyroid Stimulating Hormone (TSH, Swiss-Prot Accession Number: Alpha P01215; Beta P01222 P02679, Leptin (Swiss-Prot Accession Number: P41159), CA 19-9 and Lymphotoxin (Swiss-Prot Accession Number: P47992). It is contemplated that skilled artisans could use the KDE analytical tools to identify other, potentially useful sets of biomarkers for predictive or diagnostic value based on the levels of selected analytes. Note that the KDE algorithm may select and utilize various markers based on their relative abundances; and that a given marker, for example the level of cholera toxin in Model IV may be zero but is relevant in combination with the other markers selected in a particular grouping.

Skilled artisans will recognize that a limited size data set as was used in this specification may lead to different results, for example, different panels of markers and varying accuracies when comparing the relative performance of KDE

with other analytical techniques. These particular KDE models were built on a relatively small data set using 40 stage I ovarian cancers and 40 normal/benigns and were tested blindly on the balance of the stage II, III/IV described above. Thus, the specificity of the stage I samples reflects sample set size and potential overfitting.

5 The drop in specificity for the balance of the non-ovarian cancer samples also is expected given the relatively larger size of the testing set relative to the training set. Overall, the biomarker panel developed for the stage I samples also provides potentially useful predictive and diagnostic assays for later stages of ovarian cancer given the high sensitivity values.

10 However, these examples of biomarker panels illustrate that there are a number of parameters that can be adjusted to impact model performance. For instance in these cases a variety of different numbers of features are combined together, a variety of match values are used, a variety of different lengths of evolution of the genetic algorithm are used and models differing in the number of nodes are
 15 generated. By routine experimentation apparent to one skilled in the art, combinations of these parameters can be used to generate other models of clinically relevant performance.

Table I. Results of Analysis Using Knowledge Discovery Engine to develop a stage I specific classification model.

Model Name	Feature	Match	Generation	Node	Sensitivity Stage I	Specificity Stage I	Accuracy Stage I	Sensitivity Stage II	Sensitivity Stage III-IV	Specificity
2_0008_20	4	0.9	20	12	75	100	87.5	60.9	46.5	82.6
4_0002_10	3	0.7	10	4	75	100	87.5	69.6	82.6	56
4_0009_140	5	0.6	140	5	75	100	87.5	43.5	39.5	71.6
4_0026_100	9	0.7	100	5	87.5	100	93.8	78.3	84.9	67
4_0027_20	9	0.8	20	5	87.5	100	93.8	78.3	84.9	60.6

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Methods and Analysis Using Random Forests.

A preferred analytical technique, known to skilled artisans, is that of Breiman, Random Forests. Machine Learning, 2001. 45:5-32; as further described by
 25 Segel, Machine Learning Benchmarks and Random Forest Regression, 2004; and Robnik-Sikonja, Improving Random Forests, in Machine Learning, ECML, 2004 Proceedings, J.F.B.e. al., Editor, 2004, Springer: Berlin. Other variants of Random

Forests are also useful and contemplated for the methods of the present invention, for example, Regression Forests, Survival Forests, and weighted population Random Forests.

5 Since each of the analyte assays is an independent measurement of a variable, under some circumstances, known to those skilled in the art, it is appropriate to scale the data to adjust for the differing variances of each assay. In such cases, biweight, MAD or equivalent scaling would be appropriate, although in some cases, scaling would not be expected to have a significant impact. A bootstrap layer on top of the Random Forests was used in obtaining the results discussed below.

10 In preferred embodiments of the present invention, contemplated panels of biomarkers are:

- a. Cancer Antigen 125 (CA125, Swiss-Prot Accession Number: Q14596) and Epidermal Growth Factor Receptor (EGF-R, Swiss-Prot Accession Number: P00533).
- 15 b. CA125 and C Reactive Protein (CRP, Swiss-Prot Accession Number: P02741).
- c. CA125, CRP and EGF-R.
- d. Any one or more of CA125, CRP and EGF-R, plus any one or more of Ferritin (Swiss-Prot Accession Number: Heavy chain P02794; Light chain
20 P02792), Interleukin-8 (IL-8, Swiss-Prot Accession Number: P10145), and Tissue Inhibitor of Metalloproteinases 1 (TIMP-1, Swiss-Prot Accession Number: P01033),
- e. Any one of the biomarker panels presented in Table II and Table III.
- f. Any of the foregoing panels of biomarkers (a – e) plus any one
25 or more of the other biomarkers in the following list if not previously included in the foregoing panels (a - e): Alpha-2 Macroglobulin (A2M, Swiss-Prot Accession Number: P01023), Apolipoprotein A1-1 (ApoA1, Swiss-Prot Accession Number: P02647), Apolipoprotein C-III (ApoCIII, Swiss-Prot Accession Number: P02656),

Apolipoprotein H (ApoH, Swiss-Prot Accession Number: P02749), Beta-2
Microglobulin (B2M, Swiss-Prot Accession Number: P23560), Betacellulin (Swiss-
Prot Accession Number: P35070), C Reactive Protein (CRP, Swiss-Prot Accession
Number: P02741). Cancer Antigen 19-9 (CA19-9, Swiss-Prot Accession Number:
5 Q9BXJ9), Cancer Antigen 125 (CA125, Swiss-Prot Accession Number: Q14596),
Collagen Type 2 Antibody, Creatine Kinase-MB (CK-MB, Swiss-Prot Accession
Number: Brain P12277; Muscle P06732), C Reactive Protein (CRP, Swiss-Prot
Accession Number: P02741), Connective Tissue Growth Factor (CTGF, Swiss-Prot
Accession Number: P29279), Double Stranded DNA Antibody (dsDNA Ab), EN-
10 RAGE (Swiss-Prot Accession Number: P80511), Eotaxin (C-C motif chemokine 11,
small-inducible cytokine A11 and Eosinophil chemotactic protein, Swiss-Prot
Accession Number: P51671), Epidermal Growth Factor Receptor (EGF-R, Swiss-
Prot Accession Number: P00533), Ferritin (Swiss-Prot Accession Number: Heavy
chain P02794; Light chain P02792), Follicle-stimulating hormone (FSH, Follicle-
15 stimulating hormone beta subunit, FSH-beta, FSH-B, Follitropin beta chain,
Follitropin subunit beta, Swiss-Prot Accession Number: P01225), Haptoglobin
(Swiss-Prot Accession Number: P00738), HE4 (Major epididymis-specific protein
E4, Epididymal secretory protein E4, Putative protease inhibitor WAP5 and WAP
four-disulfide core domain protein 2, Swiss-Prot Accession Number: Q14508),
20 Insulin (Swiss-Prot Accession Number: P01308), Insulin-like Growth Factor 1 (IGF-
1, Swiss-Prot Accession Number: P01343), Insulin like growth factor II (IGF-II,
Somatomedin-A, Swiss-Prot Accession Number: P01344), Insulin Factor VII (Swiss-
Prot Accession Number: P08709), Interleukin-6 (IL-6, Swiss-Prot Accession
Number: P05231), Interleukin-8 (IL-8, Swiss-Prot Accession Number: P10145),
25 Interleukin-10 (IL-10, Swiss-Prot Accession Number: P22301), Interleukin-18 (IL-
18, Swiss-Prot Accession Number: Q14116), Leptin (Swiss-Prot Accession Number:
P41159), Lymphotoxin (Swiss-Prot Accession Number: P47992), Macrophage-
derived Chemokine (MDC, Swiss-Prot Accession Number: O00626), Macrophage
Inhibitory Factor (SWISS PROT), Macrophage Inflammatory Protein 1 alpha (MIP-
30 1alpha, Swiss-Prot Accession Number: P10147), Macrophage migration inhibitory
factor (MIF, Phenylpyruvate tautomerase, Glycosylation-inhibiting factor, GIF,
Swiss-Prot Accession Number: P14174), Myoglobin (Swiss-Prot Accession Number:
P02144), Ostopontin (Bone sialoprotein 1, Secreted phosphoprotein 1, SPP-1, Urinary

stone protein, Nephropontin, Uropontin, Swiss-Prot Accession Number: P10451), Pancreatic Islet Cells (GAD) Antibody, Prolactin (Swiss-Prot Accession Number: P01236), Stem Cell Factor (SCF, Swiss-Prot Accession Number: P21583), Tenascin C (Swiss-Prot Accession Number: P24821), Tissue Inhibitor of Metalloproteinases 1
5 (TIMP-1, Swiss-Prot Accession Number: P01033), Tumor Necrosis Factor-alpha (TNF-alpha, Swiss-Prot Accession Number: P01375), Tumor Necrosis Factor RII (TNF-RII, Swiss-Prot Accession Number: Q92956), von Willebrand Factor (vWF, Swiss-Prot Accession Number: P04275) and the other biomarkers identified as being informative for cancer in the references cited in this specification.

10 Using the Random Forests analytical approach, a preferred seven biomarker panel was identified that has a high predictive value for Stage I ovarian cancer. It includes: ApoA1, ApoCIII, CA125, CRP, EGF-R, IL-18 and Tenascin. In the course of building and selecting the relatively more accurate models for Stage I
15 I ovarian cancers generated by Random Forests using these biomarkers, the sensitivity for Stage I ovarian cancers ranged from about 80 % to about 85%. Sensitivity was also about 95 for Stage II and about 94 % sensitive for Stage III/IV. The overall specificity was about 70 %.

 Similarly, a preferred seven biomarker panel was identified that has a high predictive value for Stage II. It includes: B2M, CA125, CK-MB, CRP, Ferritin,
20 IL-8 and TIMP1. A preferred model for Stage II had a sensitivity of about 82 % and a specificity of about 88 %.

 For Stage III, Stage IV and Advanced ovarian cancer, the following 19 biomarker panel was identified: A2M, CA125, CRP, CTGF, EGF-R, EN-RAGE, Ferritin, Haptoglobin, IGF-1, IL-8, IL-10, Insulin, Leptin, Lymphotactin, MDC,
25 TIMP-1, TNF-alpha, TNF-RII, vWF. A preferred model for Stage III/IV had a sensitivity of about 86 % and a specificity of about 89%.

 Other preferred biomarker or analyte panels for detecting, diagnosing and monitoring ovarian cancer are shown in Table II and in Table III. These panels include CA-125, CRP and EGF-R and, in most cases, CA19-9. In Table II, 20 such
30 panels of seven analytes each selected from 20 preferred analytes are displayed in

columns numbered 1 through 20. In Table III, another 20 such panels of seven analytes each selected from 23 preferred analytes are displayed in columns numbered 1 through 20.

	Table II. Additional Biomarker Panels																				
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
CA125	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
CRP	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
EGF-R	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
CA19-9	x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	
Haptoglobin																					
Serum Amyloid P			x			x			x												
Apo A1							x		x												
IL-6			x	x				x		x									x	x	
Myoglobin					x					x	x	x		x	x	x	x	x	x	x	
MIP-1a	x	x	x	x			x	x	x	x	x	x	x			x					
EN-RAGE																					
CK-MB																					
vWF		x		x			x														
Leptin																x	x				
Apo CIII					x	x														x	
Growth Hormone											x		x	x	x		x	x			
IL-10																					
IL-18	x				x	x		x				x		x						x	x
Myeloperoxidase											x			x							
VCAM-1	x	x														x					

	Table III. Additional Biomarker Panels																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
CA125	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
CRP	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
EGF-R	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
CA19-9	x	x	x	x	x	x	x	x	x	x			x	x	x	x	x	x	x	x
Haptoglobin																				
Serum Amyloid P							x					x					x			
Apo A1			x							x										
IL-6											x	x		x	x			x	x	
Myoglobin	x	x	x	x	x	x	x	x	x	x										
MIP-1a	x		x	x	x	x	x	x	x			x		x	x	x		x		x
EN-RAGE																				
CK-MB																				x
vWF											x		x			x				x
Leptin	x	x								x										
Apo CIII								x			x		x			x	x	x		
Growth Hormone																				
IL-10															x					x
IL-18																				
Myeloperoxidase		x				x						x								
VCAM-1																				
Insulin				x																
Ferritin					x								x	x			x			x
Haptoglobin									x											

Other preferred biomarker panels (or models) for all stages of ovarian cancer include: (a) CA-125, CRP, EGF-R, CA-19-9, Apo-AI, Apo-CIII, IL-6, IL-18, MIP-1a, Tenascin C and Myoglobin; (b) CA125, CRP, CA19-9, EGF-R, Myoglobin, IL-18, Apo CIII; and (c) CA125, CRP, EGF-R, CA19-9, Apo CIII, MIP-1a, Myoglobin, IL-18, IL-6, Apo AI, Tenascin C, vWF, Haptoglobin, IL-10. Optionally, any one or more of the following biomarkers may be added to these or to any of the other biomarker panels disclosed above in text or tables (to the extent that any such panels are not already specifically identified therein): vWF, Haptoglobin, IL-10, IGF-I, IGF-II, Prolactin, HE4, ACE, ASP and Resistin.

It is contemplated by the present inventors that additional, informative sets of analytes (or biomarkers) include any one or more, two or more, three or more and for or more of the analytes presented below in Table IV, as well as any of the biomarker sets in Tables I, II or III combined with any one or more of the analytes in Table IV, and any one or more of the markers in Table IV combined with any of the other biomarker sets discussed in Paragraphs 70 – 75, above, or identified elsewhere in this specification. Additional set of informative analytes for use in the test kits and methods of the present invention include any one or more of CA-125, CRP, ECG-R and HE-4 together with any one or more of the biomarkers in Table IV.

Thus, contemplated sets of biomarkers include combinations such as: CA-125, CRP and one or more (or two or more) of the biomarkers in Table IV; CA-125, EGF-R and any one or more (or two or more) of the biomarkers in Table IV; CA-125, HE-4 and any one or more (or two or more) of the biomarkers in Table IV; CRP, EGF-R and any one or more (or two or more) of the biomarkers in Table IV; CRP, HE-4 and any one or more (or two or more) of the biomarkers in Table IV; and EGF-R, HE-4 and any one or more (or two or more) of the biomarkers in Table IV. It is contemplated that markers of informative value in the foregoing biomarker sets according to the present invention include VCAM-1, IL-6R, IL-18R and sortillin.

Additionally, biomarker panels comprising any one or more (or two or more) of the biomarkers in Table IV together with any two or more, three or more and four or more of these three sets of biomarkers: (a) CA125, Transthyretin, ApoA-I, B2-microglobulin and Transferrin; (b) CA125 and leptin, prolactin, osteopontin, and

insulin-like growth factor-II; and (c) OvaPlex: CA125, C-reactive protein, serum amyloid A, IL-6 and IL-8.

In general, soluble forms of these analytes are contemplated, including protein and peptide fragments and domains that are shed into the circulating blood and lymph streams. These analytes may be detected and analyzed in blood, lymph, serum, urine and other bodily fluids. Also contemplated in the compositions and methods of the present invention are autoantibodies against any of the disclosed biomarkers, as well as nucleotides that encode these biomarkers, and that may be detected and quantified as another indirect way to assess the levels of these markers. Aptamers and other compounds useful for the detection of such molecular species are well known to persons skilled in the art.

Table IV.

Analyte #	Informative Analytes
1	CA 15-3 (MUC-1)
2	Her2/Neu (erbB-2)
3	Kallikrein-5
4	Macrophage Inhibitory Factor (MIF)
5	Osteopontin
6	TAG-72
7	Total IGF-II
8	HE4
9	IL6-R
10	IL6-R shedded form of full-length IL6-R
11	IL18-R
12	IL-18BP
13	VCAM-1
14	IP-10 (interferon-gamma inducible 10kD protein)
15	SMRP
16	TgII (tissue transglutaminase)
17	Exotaxin-1
18	Cyfra 21-1(cytokeratin 19 fragment)
19	IGF2BP3
20	TIMP-1
21	Alpha-1 Antitrypsin
22	MMP7
23	TAG-72

Analyte #	Informative Analytes
24	IL-8
25	IL-6
26	Sortillin
27	CD40
28	CA 15-3
29	Alpha 1-Antichymotrypsin
30	VEGF
21	TTR (pre-albumin)
22	Haptoglobin

Any two or more of the preferred biomarkers described above will have predictive value, however, adding one or more of the other preferred markers to any of the analytical panels described herein may increase the panel's predictive value for clinical purposes. For example, adding one or more of the different biomarkers listed above or otherwise identified in the references cited in this specification may also increase the biomarker panel's predictive value and are therefore expressly contemplated. Skilled artisans can readily assess the utility of such additional biomarkers. It is contemplated that additional biomarker appropriate for addition to the sets (or panels) of biomarkers disclosed or claimed in this specification will not result in a decrease in either sensitivity or specificity without a corresponding increase in either sensitivity or specificity or without a corresponding increase in robustness of the biomarker panel overall. A sensitivity and/or specificity of at least about 80 % or higher are preferred, more preferably at least about 85 % or higher, and most preferably at least about 90 % or 95 % or higher.

The results of the disclosed diagnostic may be output for the benefit of the user or diagnostician, or may otherwise be displayed on a medium such as, but not limited to, a computer screen, a computer readable medium, a piece of paper, or any other visible medium.

The foregoing embodiments and advantages of this invention are set forth, in part, in the preceding description and examples and, in part, will be apparent to persons skilled in the art from this description and examples and may be further realized from practicing the invention as disclosed herein. For example, the

techniques of the present invention are readily applicable to monitoring the progression of ovarian cancer in an individual, by evaluating a specimen or biological sample as described above and then repeating the evaluation at one or more later points in time, such that a difference in the expression or dysregulation of the relevant biomarkers over time is indicative of the progression of the ovarian cancer in that individual or the responsiveness to therapy. All references, patents, journal articles, web pages and other documents identified in this patent application are hereby incorporated by reference in their entireties.

10 **EXAMPLE 2**

Sera were from a prospective collection undertaken specifically to develop and validate the performance of an ovarian cancer test. All samples were collected under a uniform protocol from 11 different sites, which were monitored for adherence. The Western Institutional Review Board (Olympia, WA) and the IRBs of the individual sites approved the studies under FDA Investigational Device Exemption (IDE) number G050132. The collection sites (and IRBs) were: Cedars-Sinai Medical Center, Los Angeles, CA (Cedars-Sinai Institutional Review Board); Florida Gynecologic Oncology, Fort Meyers, FL (Lee Memorial Health System Institutional Review Committee); Florida Hospital Cancer Institute, Orlando, FL (Florida Hospital Institutional Review Board); The Harry and Jeanette Weinberg Cancer Institute at Franklin Square Hospital, Baltimore, MD (MedStar Research Institute Georgetown Oncology Institutional Review Board); Holy Cross Hospital, Silver Spring, MD (Holy Cross Institutional Review Board); North Shore – Long Island Jewish Health System, Manhasset, NY (Institutional Review Board North Shore-Long Island Jewish Health System); SUNY at Stony Brook, NY, Stony Brook, NY (Committee on Research Involving Human Subjects SUNY Stony Brook); University of Alabama at Birmingham, Birmingham, AL (The University of Alabama at Birmingham Institutional Review Board for Human Use); University of Southern California, Norris Cancer Center, Los Angeles, CA and Women's and Children's Hospital, Los

Angeles, CA (University of Southern California Health Sciences Campus Institutional Review Board); Wake Forest University Health Sciences, Winston-Salem, NC (Institutional Review Board Wake Forest University School of Medicine); and Women and Infants Hospital of Rhode Island, Providence, RI (Institutional Review Board Women and Infants' Hospital of Rhode Island). The study inclusion criteria were women, at least 18 years of age, symptomatic of ovarian cancer according to the National Comprehensive Cancer Network (NCCN) Ovarian Cancer Treatment Guidelines for Patients, which includes women with or without a pelvic mass. Participants had to be scheduled for gynecologic surgery based on concern they had ovarian cancer, and post-surgical pathological evaluation of the ovaries and excised tissues was required to establish clinical truth of disease status. Exclusion criteria were women who did not meet the inclusion criteria, could not provide informed consent, were pregnant, or previously treated for ovarian cancer. Written informed consent was obtained for each participant in the study. All data were de-identified and no results were returned to the physicians or patients.

149 samples were used from the patients with pathology-confirmed ovarian cancer and 350 samples from the patients with pathology-confirmed benign conditions (Figure 1). The ovarian cancer samples included all stages and common subtypes of the disease. The benign samples included the common types of benign conditions seen in the entire study population. Complete clinicopathology reports, obtained following surgery, along with the patient age, race, staging, subtype and coded collection site accompanied each sample.

Prior to any intervention, blood samples (10 ml) were collected into red top glass Vacutainer tubes. The blood was clotted for at least 30 minutes at room temperature, centrifuged at 3,500 g for 10 minutes, and the resulting serum removed into pre-labeled cryotubes, and stored promptly at -80°C . Processing from blood draw to freezing was completed within 2 hours. All samples were shipped on dry ice to a single designated site for storage. To aliquot, all samples were thawed in a water and ice slurry then transferred into sample tubes labeled with coded identifiers that blinded all subsequent experimenters to the sample disease status.

Multiplex Immunoassays

Two hundred and fifty nine serum biomarkers were measured using a set of proprietary multiplexed immunoassays (Human DiscoveryMAP® v1.0 and Human OncologyMAP® v1.0; (Figure 2). Each assay was calibrated using an 8-point standard curve, performed in duplicate. Median Fluorescence Intensity (MFI) measurements were interpolated into final protein concentrations using curve-fitting software. Assay performance was verified using quality control (QC) samples at low, medium and high levels for each analyte in duplicate. All standard and QC samples were in a complex serum-based matrix to match the sample background matrix. Since sera were analyzed at a previously optimized dilution, any reading above the maximum concentration of the calibration curve was assigned the concentration of the highest standard, whereas any below the minimum concentration was assigned the value 0. For analysis, the sample run order was randomized to avoid any sequential bias due to presence or absence of disease, subtype or stage of disease, patient age, or age of serum sample.

Data Analysis

Descriptive statistics, Receiver Operating Characteristic (ROC) curves and graphical displays (dot plots) for serum analyte concentrations were performed using commercially available software packages. Statistical differences were determined using the nonparametric Kruskal-Wallis test (ANOVA) followed by Dunn's multiple comparison post-test. For all statistical comparisons a P-value <0.05 was interpreted as statistically significant. A Pearson correlation matrix was created using a multi-spectral analysis application.

Using multiplexed immunoassays, the levels of 259 molecules were simultaneously measured in sera from 149 patients with pathology-confirmed epithelial ovarian cancer and 350 individuals with benign ovarian conditions (Figure 1). To facilitate the determination of the ability of biomarkers to differentiate between symptomatically similar cancer and benign gynecological conditions, all

samples were obtained from the same clinical population – women presenting for surgery primarily based on the presence of an adnexal mass. All samples were collected before any intervention and before the disease status was known. Disease status was subsequently identified by pathology exams of the excised tissue. Sera were collected using a single sample collection protocol that was monitored for compliance. The study was conducted prospectively at 11 sites that were also monitored for protocol adherence. This assured sample quality and removed the possibility of any collection, processing or biological biases in the sample set, a concern for many other studies. No normal healthy samples were used in this study, as they are typically easier to classify than benign conditions and introduce confounding factors such as lower stress levels compared to patients facing surgery. As expected, the median patient age was higher in individuals with ovarian cancer (61 years) than those with benign conditions (51 years) and increased with the stage of disease present (Figure 1). The distribution of the ovarian cancer subtypes was similar to the distribution seen for all ovarian cancer cases in the US population as a whole, with a larger proportion of serous carcinoma (55%) than other subtypes (Figure 1). The benign controls in the study were representative of common benign ovarian conditions including cystadenoma, cystadenofibroma and fibroma.

To ensure consistency and aid in biomarker comparisons, all 259 markers and 499 samples were measured on a single platform at a single site using a panel of rigorously qualified, high-throughput, multiplexed immunoassays. This survey built on our previous profiling of 104 serum biomarkers. The majority of the additional 155 serum biomarkers in the present study were developed as part of two NCI-funded Small Business Innovative Research (SBIR) awards specifically targeted at markers that had reasonable literature support to suggest a significant role in cancer biomarker. The selected biomarkers covered a broad range of biological functions, primarily implicated in cancer including cancer antigens, hormones, clotting factors, tissue modeling factors, lipoprotein constituents, proteases and protease inhibitors, markers of cardiovascular risk, growth factors, cytokine/chemokines, soluble forms of cell-signaling receptors, and inflammatory and acute phase reactants (Figure 2). The

present study is the broadest and most consistent single study of immunoassay profiling of molecules using fully characterized, quality-controlled samples.

For each biomarker, an ROC curve was generated and its area under the curve (AUC) value compared to that of an uninformative marker (AUC = 0.500). A total of 5 175 biomarkers were dysregulated (P-values>0.05) in the ovarian cancer samples relative to the benign gynecological conditions. Of these, 136 biomarkers were up-regulated and 39 down-regulated (Figures 3 and 4). The biomarkers with the greatest AUC values were predominantly up-regulated in ovarian cancer (Figures 3, 4, and 5) with values ranging from 0.599 to 0.933. The most up-regulated markers were HE4 10 and CA-125 with AUC values of 0.933 and 0.907, respectively, followed by interleukin-2 receptor α (IL-2 receptor α), α 1-antitrypsin, C-reactive protein, YKL-40, cellular fibronectin, cancer antigen 72-4 (CA-72-4) and prostaticin, with AUC values between 0.829 and 0.800 (Figure 3). The remaining 127 up-regulated biomarkers had a continuum of AUC values from 0.797 to 0.556 (Figure 4). Thirty-four of the 15 remaining 127 markers had AUC values above 0.700. For down-regulated biomarkers, the AUC values ranged from 0.556 to 0.745 (Figure 4). The two most informative of these stood out as transthyretin (0.745) and apolipoprotein A-IV (0.713), while the remaining biomarkers had AUC values below 0.700.

This is the first time that thirteen of the twenty biomarkers with the highest 20 AUC values, namely HE4, IL-2 receptor α , YKL-40, cellular fibronectin, CA 72-4, prostaticin, MMP-7, VEGF-B, Calprotectin, IGFBP-2, LOX-1, neuropilin-1 and MPIF-1 have been accurately quantified together, on a coherent set of samples, under uniformly controlled analytical conditions, to determine their discriminative power for ovarian cancer. This approach improves biomarker comparisons and should aid in the 25 selection of biomarkers in the development of multi-biomarker panels.

As a comparison between the two most informative biomarkers in this study, the sensitivity for HE4 and CA-125 was determined over a range of specificity values. In addition, the optimal cut-off value, defined as that yielding the greatest sum of specificity and sensitivity was calculated for each biomarker. The sensitivity for HE4

alone decreased from 89.0% to 57.1% as specificity increased from 80% to 99.6%, while for CA-125 alone the sensitivity decreased from 85.2% to 30.2%. The optimal cut-off for HE4 and CA-125 was 54.8 pM and 52.5 U/mL, respectively giving sensitivity values of 86.6% and 74.5%, respectively, and specificity values of 89.4% and 93.7%, respectively. As expected from ROC curves, there are trade-offs when no individual biomarker shows high specificity at a predetermined high sensitivity value. For example, at 100% sensitivity, both HE4 and CA-125 were 0% specific. At 98% sensitivity, HE4 had 30.6% specificity and CA-125 had 35.4% specificity. However, to see relatively good specificity values, the sensitivities had to be lowered to approximately 95%. At 95% sensitivity, HE4 had 50.9% specificity and CA-125 had 45.4% specificity. These values, along with the AUC values, indicated that on this population, HE4 performed slightly better than CA-125. In addition, these results show that none of the biomarkers in this study are sufficiently informative as standalone ovarian cancer biomarkers for broad applications and that biomarker panels are needed to improve performance to clinically acceptable levels.

To determine if some biomarkers might have greater discrimination for different stages of cancer, especially early stage, the nine biomarkers with AUC values above 0.800 on FIGO stage I and II samples were compared where there is the greatest need for marker-based detection (Figure 6). For FIGO stage I samples, both HE4 and CA-125 were highly discriminative (P-values<0.001), followed in descending order by C-reactive protein and CA 72-4 (P-values 0.001–0.01) then α 1-antitrypsin, YKL-40 and prostaticin (P-values 0.01–0.05). For IL2-receptor α and cellular fibronectin, there were no statistical differences between stage I cancer and benign conditions (P-values>0.05). For FIGO stage II samples, both HE4 and CA-125 were again highly discriminative (P-values<0.001), followed by for IL2-receptor α , α 1-antitrypsin, YKL-40 and CA 72-4 (P-values 0.001–0.01) and then C-reactive protein and cellular fibronectin (P-values 0.01–0.05). For prostaticin, there was no statistical difference (P-value>0.05).

The same nine biomarkers were evaluated to determine if there were statistically significant differences between samples from women with benign

conditions and women with each individual subtype of ovarian cancer (Figure 7). For clear cell carcinomas, α 1-antitrypsin and C-reactive protein were highly discriminatory (P-values<0.001), followed in descending order by HE4, CA-125 and IL2-receptor α (P-values 0.01–0.05). For YKL-40, cellular fibronectin, CA 72-4 and prostatic acid phosphatase (PAP) there were no statistical differences (P-value>0.05). For endometrioid carcinomas, there were highly significant differences for HE4 and CA-125 (P-values<0.001) and significant differences for C-reactive protein, cellular fibronectin, CA 72-4 (P-values 0.01–0.05). For α 1-antitrypsin, IL2-receptor α , YKL-40 and PAP there were no statistical differences (P-values>0.05). For mucinous carcinomas, only CA 72-4 had a significant difference (P-value 0.01–0.05). For serous and mixed carcinomas, all nine biomarkers had highly significant differences (P-value<0.001). Therefore, with the exception of mucinous carcinomas, the nine biomarkers are informative for all common ovarian cancer subtypes, however, their different discriminative powers suggests that different combinations of markers may be useful for different subtypes. While it would have been preferential to find more informative biomarkers for the mucinous subtype, it is relatively rare. Indeed, only 6.0% of the cancers in the study were of mucinous subtype (Figure 1).

For simplicity and cost effectiveness, the use of a single biomarker is preferred over multiple biomarkers. However, it is clear that single biomarkers may not be able to capture the inherent diversity of complex diseases such as ovarian cancer. An informative test seeks to combine multiple biomarkers in a way that each marker adds a different type of discrimination either to the entire patient population or the population subdivisions made by the other markers. Simply put, markers with poor correlation with one another have a greater chance of individually contributing to a panel than markers with strong correlation with one another. Therefore, correlation analysis was performed on the strongest ovarian cancer markers - the 124 biomarkers with AUC values greater than 0.600. The co-varying molecules were sorted agglomeratively with hierarchical clustering using Pearson correlation coefficients as the distance measure. The pair-wise results were assembled into a 124×124 matrix (numbered 0–123) and displayed using a heat map where an intense red color

signifies strong positive correlation and blue signifies a negative correlation (Figure 8). There were four major clusters (Clusters A through D; Figures 8-13), each cluster representing markers strongly correlating with each other. Each of these clusters contained markers that are strong ovarian cancer markers. Cluster A (markers 1–10) contained two strong ovarian cancer markers, CA 72-4 and MPIF-1 (Figures 9 and 5 10). TNFR2 was found in Cluster B (markers 58–67; Figures XXX (Tables S3 and S5). Cluster C (markers 79–87) contained the two strongest ovarian cancer markers (HE4, CA-125) as well as prostasin and VEGF-B (Figures 9 and 12). The strongest correlations with CA-125 were mesothelin (Pearson correlation coefficient = 0.600), 10 maspin (0.599), VEGF-D (0.568), prostasin (0.551), kallikrein-7 (0.507) and VEGF-B (0.505). Maspin (0.517) correlated with HE4 the strongest, followed by TIMP-1 (0.470), prostasin (0.463), IL-2 receptor α (0.424), VEGF-B (0.413) and VEGF-D (0.409). Finally, the largest cluster (Cluster D; biomarkers 32–55), was composed of loosely correlated markers that contained several good ovarian cancer markers 15 including calprotectin, LOX-1, IL-6, YKL-40, cellular fibronectin, neuropilin-1, α 1-antitrypsin, TIMP-1, C-reactive protein and IL-2 receptor α (Figures 9 and 13). These correlation data can help drive the development of biomarkers panels and may give insights into pathways that are disrupted in ovarian cancer.

The combined performance of the nine markers with AUC values greater than 20 0.800 were evaluated to determine the predictive value of a simple multi-marker scenario. The nine markers were combined using logistic regression which yielded an AUC of 0.950 (Standard error: 0.01213; 95% CI: 0.926–0.974; P-value: <0.0001). Next this performance was compared against the five markers in the FDA-cleared OVA1 test. The samples in this study were collected by gynecologic oncologists. A 25 similar study population was reported in the OVA1 510(k) summary with 100% sensitivity (invasive ovarian cancer only) and 32.9% specificity. The five markers combined and a logistic regression model was built. Consistent with the OVA1 510(k) summary, with this sample set, at 32.9% specificity, OVA1 biomarkers gave a sensitivity of 98.0%. Interestingly, with these samples, at a specificity of 32.9%, CA- 30 125 alone had a sensitivity of 98.0%. This indicated that the additional OVA1

markers contributed little, if any, to the overall classification. Indeed, the AUC value for the five OVA1 biomarkers was 0.912 (Standard error: 0.0157; 95% CI: 0.881–0.943; P-value: <0.0001), barely higher than CA-125 alone which had an AUC of 0.907 (Standard error: 0.01571; 95% CI: 0.877–0.938; P-value: <0.0001). The two
5 models were further compared by determining the sensitivity of models at fixed specificity values and the specificity of models at fixed sensitivity values (Figures 14 and 15). In general, the logistic regression model built on the top 9 markers outperformed the model built on OVA1 markers at all points of the ROC curve. At fixed specificity values between 80 and 95%, the top 9 model was 8 to 10% more
10 sensitive than the model built on the OVA1 markers. At higher specificity (99%), the top 9 model was approximately 19% more sensitive. At fixed sensitivity between 80 and 99%, the top 9 model was between 8 and 25% more specific than the model built on the OVA1 markers.

As both the top nine and OVA1 panels contained markers that may perform
15 differently for pre- and post-menopausal women, the performance of the two panels were compared by menopausal status. For the top nine panel, the AUC value for pre-menopausal women was lower (0.937) than for post-menopausal women (0.953). This is consistent with the individual marker analysis that demonstrated that the top
20 three individual markers (HE4, CA-125 and IL2-R α) all performed better for the post-menopausal women (0.927, 0.927 and 0.824, respectively; (Figure 16) than for the pre-menopausal women (0.912, 0.907 and 0.812, respectively). For the OVA1 panel, the AUC value for pre-menopausal women was slightly lower (0.920) than for post-menopausal women (0.924). Again, this is consistent with the individual marker
25 analysis that demonstrated that CA-125, the marker that appears to drive the performance of the OVA1 panel, performed worse for the group of pre-menopausal women (0.907) than for post-menopausal women (0.927).

New biomarkers have been identified that are capable of discriminating
between samples drawn from women with benign ovarian conditions and those from
women with ovarian cancer. Preliminary multivariate analysis, using a logistic
30 regression model on the nine most informative biomarkers appeared to have

significantly improved performance over the OVA1 biomarkers. This analysis indicates that our data have the potential to improve on OVA1 and other tests.

Claims:

1. A method of predicting the ovarian cancer status of a subject, comprising the steps of:
measuring the level of CA-125 and HE4 and measuring the level of one or
5 more biomarkers selected from the group consisting of IL-2 receptor alpha (IL-2R α),
Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin
(cFib), prostasin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, IL-6,
Vascular Endothelial Growth Factor B (VEGF-B), Matrix Metalloproteinase-7
(MMP-7), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2),
10 Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1
in a sample of a biological fluid obtained from the subject; and
correlating the measurements with ovarian cancer status.
2. The method of claim 1, further comprising measuring the level of Cancer
15 Antigen 72-4 (CA-72-4).
3. The method of claim 1, wherein the ovarian cancer status is presence of
ovarian cancer.
- 20 4. The method of claim 1 further comprising:
managing subject treatment based on the status.
5. The method of claim 4, wherein managing subject treatment is selected from
the group consisting of ordering more tests, performing surgery, and taking no further
25 action.
6. The method of claim 4 further comprising:
measuring the level of CA-125 and HE4 and measuring the level of
one or more biomarkers selected from the group consisting of Interleukin-2 receptor
30 alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP),
YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostasin,
Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7

(MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1 in a sample of a biological fluid obtained from the subject after subject management;

5 correlating the measurements with ovarian cancer status; and
determining if subject management resulted in a change in ovarian cancer status.

7. The method of claim 1, wherein measuring is selected from detecting the
10 presence or absence of the biomarkers, quantifying the amount of biomarkers, and qualifying the type of biomarker.

8. The method of any of claims 1-7, wherein the biomarkers are measured by an immunoassay.

15

9. The method of any of claims 1-7 wherein the correlating is performed by a software classification algorithm.

10. The method of any one of claims 1-7 wherein the sample is selected from
20 blood, serum, and plasma.

11. A kit comprising:

a) a panel of affinity reagents that each selectively binds to CA-125 and HE4 and one or more biomarkers selected from the group consisting of Interleukin-2 receptor alpha
25 (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostasin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1
30 (LOX-1), neuropilin-1, TNFR2, and MPIF-1; and
b) a panel of containers each comprising CA-125 and HE4 and a one or more biomarkers selected from the group consisting of Interleukin-2 receptor alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40,

Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostasin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1.

12. The kit of claim 11, wherein the affinity reagent is an antibody.

13. The kit of claim 11 further comprising written instructions for using the affinity reagent to measure the levels of the biomarkers in a sample from a subject.

14. The kit of claim 11 further comprising written instructions for use of the kit for determining a subjects ovarian cancer status.

15. A panel of purified peptides comprising CA-125 and HE4 and one or more biomarkers selected from the group consisting of Interleukin-2 receptor alpha (IL-2 receptor alpha), Alpha-1-Antitrypsin (AAT), C-Reactive Protein (CRP), YKL-40, Cellular Fibronectin (cFib), Cancer Antigen 72-4 (CA-72-4), prostasin, Tissue Inhibitor of Metalloproteinases 1 (TIMP-1), IL-8, Matrix Metalloproteinase-7 (MMP-7), IL-6, Vascular Endothelial Growth Factor B (VEGF-B), calprotectin, Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2), Lectin-Like Oxidized LDL Receptor 1 (LOX-1), neuropilin-1, TNFR2, and MPIF-1.

16. The peptides of claim 15, wherein one or more of the peptides comprise a detectable label.

FIG. 1

	Ovarian cancer = FIGO Stage and Subtype					Benign
	I	II	III	IV	X	
Number of Samples (%):						
Ovarian Cancer						
Serous	8	10	60	4	0	82 (55.0) --
Mucinous	7	0	1	1	0	9 (6.0) --
Clear Cell	9	1	3	1	0	14 (9.4) --
Endometrioid	5	4	4	0	0	13 (8.7) --
Brenner	1	0	0	1	0	2 (1.3) --
Poorly/undifferentiated	0	0	2	1	0	3 (2.0) --
Mixed	10	2	13	0	1	26 (17.4) --
Total	40	17	83	8	1	149 --
	(26.8)	(11.4)	(55.7)	(5.4)	(0.7)	(100) --
Benign						
Neoplastic	--	--	--	--	--	105 (30.0)
Non-neoplastic	--	--	--	--	--	155 (44.3)
Mixed	--	--	--	--	--	64 (18.3)
No abnormalities	--	--	--	--	--	26 (7.4)
Total						350 (100)
Population Age						
Median Age (years)	59	61	63	68	76	61 51
Range Age (years)	47-88	33-85	30-84	55-80	76-76	30-88 18-85
Mean Age (years)	61.4	60.5	62.7	67.1	76.0	62.4 52.8
SD	10.5	13.7	11.5	9.6	--	11.4 14.0

FIG. 2A
FIG. 2B
FIG. 2C

FIG. 2

FIG. 2A

6Ckine; Adiponectin; Agouti-Related Protein (AGRP); Aldose Reductase; Alpha-1-Antichymotrypsin (AACT); Alpha-1-Antitrypsin (AAT); Alpha-1-Microglobulin (A1Micro); Alpha-2-Macroglobulin (A2Macro); Alpha-Fetoprotein (AFP); Amphiregulin (AR); Angiogenin; Angiopoietin-2 (ANG-2); Angiotensin-Converting Enzyme (ACE); Annexin A1 (ANXA1); Apolipoprotein A-I (Apo A-I); Apolipoprotein A-II (Apo A-II); Apolipoprotein A-IV (Apo A-IV); Apolipoprotein B (Apo B); Apolipoprotein C-I (Apo C-I); Apolipoprotein C-III (Apo C-III); Apolipoprotein D (Apo D); Apolipoprotein E (Apo E); Apolipoprotein H (Apo H); Apolipoprotein(a) (Lp(a)); AXL Receptor Tyrosine Kinase (AXL); B cell-activating factor (BAFF); B Lymphocyte Chemoattractant (BLC); Bcl-2-like protein 2 (Bcl2-L-2); Beta-2-Microglobulin (B2M); Betacellulin (BTC); Bone Morphogenetic Protein 6 (BMP-6); Brain-Derived Neurotrophic Factor (BDNF); Calbindin; Calcitonin; Calprotectin; Cancer Antigen 125 (CA-125); Cancer Antigen 15-3 (CA-15-3); Cancer Antigen 19-9 (CA-19-9); Cancer Antigen 72-4(CA-72-4); Carcinoembryonic Antigen (CEA); Cathepsin D; CD 40 antigen (CD40); CD40 Ligand (CD40-L); CD5 (CD5L); Cellular Fibronectin (cFib); Chemokine CC-4 (HCC-4); Chromogranin-A (CgA); Ciliary Neurotrophic Factor (CNTF); Clusterin (CLU); Collagen IV; Complement C3 (C3); Complement Factor H; Connective Tissue Growth Factor (CTGF); Cortisol (Cortisol); C-peptide; C-Reactive Protein (CRP); Creatine Kinase-MB (CK-MB); Cystatin-C; Endoglin; Endostatin; Endothelin-1 (ET-1); EN-RAGE; Eotaxin-1; Eotaxin-2; Eotaxin-3; Epidermal Growth Factor (EGF); Epidermal Growth Factor Receptor (EGFR); Epiregulin (EPR); Epithelial cell adhesion molecule (EPCAM); Epithelial-Derived Neurophil-Activating Protein 78 (ENA-78); Erythropoietin (EPO); E-Selectin; Ezrin; Factor VII; Fas Ligand (FasL); FASLG Receptor (FAS); Fatty Acid-Binding Protein, adipocyte (FABP, adipocyte); Fatty Acid-Binding Protein, heart (FABP, heart); Fatty Acid-

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FIG. 2B

Binding Protein, liver (FABP, liver); Ferritin (FRTN); Fetuin-A; Fibrinogen; Fibroblast Growth Factor 4 (FGF-4); Fibroblast Growth Factor basic (FGF-basic); Fibulin-1C (Fib-1C); Folicle-Stimulating Hormone (FSH); Galectin-3; Gelsolin; Glucagon; Glucagon-like Peptide 1, total (GLP-1 total); Glucose-6-phosphate Isomerase (G6PI); Glutamate-Cysteine Ligase Regulatory subunit (GCLR); Glutathione S-Transferase alpha (GST-alpha); Glutathione S-Transferase Mu 1 (GST-M1); Granulocyte Colony-Stimulating Factor (G-CSF); Granulocyte-Macrophage Colony-Stimulating Factor (GM-CSF); Growth Hormone (GH); Growth-Regulated alpha protein (GRO-alpha); Haptoglobin; HE4; Heat Shock Protein 60 (HSP-60); Heparin-Binding EGF-Like Growth Factor (HB-EGF); Hepatocyte Growth Factor (HGF); Hepatocyte Growth Factor receptor (HGF receptor); Hepsin; Human Chorionic Gonadotropin beta (hCG); Human Epidermal Growth Factor Receptor 2 (HER-2); Immunoglobulin A (IgA); Immunoglobulin E (IgE); Immunoglobulin M (IGM); Insulin; Insulin-like Growth Factor Binding Protein 4 (IGFBP4); Insulin-like Growth Factor Binding Protein 5 (IGFBP5); Insulin-like Growth Factor Binding Protein 6 (IGFBP6); Insulin-like Growth Factor I (IGF-I); Insulin-like Growth Factor Binding Protein 1 (IGFBP-1); Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2); Insulin-like Growth Factor-Binding Protein 3 (IGFBP-3); Intercellular Adhesion Molecule 1 (ICAM-1); Interferon gamma (IFN-gamma); Interferon gamma Induced Protein 10 (IP-10); Interferon-inducible T-cell alpha chemoattractant (ITAC); Interleukin-1 alpha (IL-1 alpha); Interleukin-1 beta (IL-1 beta); Interleukin-1 receptor antagonist (IL-1ra); Interleukin-10 (IL-10); Interleukin-12 Subunit p40 (IL-12p40); Interleukin-12 Subunit p70 (IL-12p70); Interleukin-13 (IL-13); Interleukin-15 (IL-15); Interleukin-16 (IL-16); Interleukin-18 (IL-18); Interleukin-2 receptor alpha (IL-2 receptor alpha); Interleukin-25 (IL-25); Interleukin-3 (IL-3); Interleukin-4 (IL-4); Interleukin-5 (IL-5); Interleukin-6 (IL-6); Interleukin-6 receptor (IL-6r); Interleukin-6 receptor subunit beta(IL-6R beta); Interleukin-7 (IL-7); Interleukin-8 (IL-8); Kallikrein 5; Kallikrein-7 (KLLK-7); Kidney Injury Molecule-1 (KIM-1); Lactoylglutathione lyase (LGL); Latency-Associated Peptide of Transforming Growth Factor beta 1 (LAP TGF-b1); Lectin-Like Oxidized LDL Receptor 1 (LOX-1); Leptin; Luteinizing Hormone (LH); Lymphotactin; Macrophage Colony-Stimulating Factor 1 (M-CSF); Macrophage inflammatory protein 3 beta (MIP-3 beta); Macrophage Inflammatory Protein-1 alpha (MIP-1 alpha); Macrophage Inflammatory Protein-1 beta (MIP-1 beta); Macrophage Inflammatory Protein-3 alpha (MIP-3 alpha); Macrophage Migration Inhibitory Factor (MIF); Macrophage-Derived Chemokine (MDC); Macrophage-Stimulating Protein (MSP); Malondialdehyde-Modified Low-Density Lipoprotein (MDA-LDL); Maspin; Matrix Metalloproteinase-1 (MMP-1); Matrix Metalloproteinase-10 (MMP-10); Matrix Metalloproteinase-2 (MMP-2); Matrix Metalloproteinase-3 (MMP-3); Matrix Metalloproteinase-7 (MMP-7); Matrix Metalloproteinase-9 (MMP-9); Matrix Metalloproteinase-9, total (MMP-9, total); Mesothelin (MSLN); MHC class I chain-related protein 1 (MICA); Monocyte Chemotactic Protein 1 (MCP-1); Monocyte Chemotactic Protein 2 (MCP-2); Monocyte

FIG. 2C

Chemotactic Protein 3 (MCP-3); Monocyte Chemotactic Protein 4 (MCP-4); Monokine Induced by Gamma Interferon (MIG); Myeloid Progenitor Inhibitory Factor 1 (MPIF-1); Myeloperoxidase (MPO); Myoglobin; Nerve Growth Factor beta (NGF-beta); Neuron Specific Enolase (NSE); Neuronal Cell Adhesion Molecule (Nr-CAM); Neuropilin-1; Neutrophil Gelatinase-Associated Lipocalin (NGAL); N-terminal prohormone of brain natriuretic peptide (NT proBNP); Nucleoside diphosphate kinase B (NDK B); Osteopontin; Osteoprotegerin (OPG); Pancreatic Polypeptide (PPP); Pepsinogen I (PGI); Peroxiredoxin 4 (Prx-IV); Phosphoserine Aminotransferase (PSAT); Placenta Growth Factor (PLGF); Plasminogen Activator Inhibitor 1 (PAI-1); Platelet-Derived Growth Factor BB (PDGF-BB); Pregnancy-Associated Plasma Protein A (PAPP-A); Progesterone; Proinsulin, Intact; Proinsulin, Total; Prolactin (PRL); Prostatin; Prostate-Specific Antigen, Free (PSA-f); Prostatic Acid Phosphatase (PAP); Protein S100-A4 (S100-A4); Protein S100-A6 (S100-A6); Pulmonary and Activation-Regulated Chemokine (PARC); Receptor for advanced glycosylation end products (RAGE); Receptor tyrosine-protein kinase erbB-3 (ErbB3); Resistin; S100 calcium-binding protein B (S100-B); Serotransferrin (Transferrin); Serum Amyloid P-Component (SAP); Serum Glutamic Oxaloacetic Transaminase (SGOT); Sex Hormone-Binding Globulin (SHBG); Sortilin; Squamous Cell Carcinoma Antigen-1 (SCCA-1); Stem Cell Factor (SCF); Stromal cell-derived factor-1 (SDF-1); Superoxide Dismutase 1, Soluble (SOD-1); T Lymphocyte-Secreted Protein I-309 (I-309); Tamm-Horsfall Urinary Glycoprotein (THP); T-Cell-Specific Protein RANTES (RANTES); Tenascin-C (TN-C); Testosterone, Total; Tetractin; Thrombomodulin (TM); Thrombopoietin; Thrombospondin-1; Thymus-Expressed Chemokine (TECK); Thyroglobulin (TG); Thyroid-Stimulating Hormone (TSH); Thyroxine-Binding Globulin (TBG); Tissue Factor (TF); Tissue Inhibitor of Metalloproteinases 1 (TIMP-1); Tissue type Plasminogen activator (tPA); TNF-Related Apoptosis-Inducing Ligand Receptor 3 (TRAIL-R3); Transforming Growth Factor alpha (TGF-alpha); Transforming Growth Factor beta-3 (TGF-beta-3); Transthyretin (TTR); Trefoil Factor 3 (TFF3); Tumor Necrosis Factor alpha (TNF-alpha); Tumor Necrosis Factor beta (TNF-beta); Tumor Necrosis Factor Receptor 2 (TNFR2); Tumor Necrosis Factor Receptor 1 (TNF RI); Tyrosine kinase with Ig and EGF homology domains 2 (TIE-2); Urokinase-type Plasminogen Activator (uPA); Urokinase-type Plasminogen Activator Receptor (uPAR); Vascular Cell Adhesion Molecule-1 (VCAM-1); Vascular Endothelial Growth Factor (VEGF); Vascular Endothelial Growth Factor B(VEGF-B); Vascular Endothelial Growth Factor C (VEGF-C); Vascular Endothelial Growth Factor D (VEGF-D); Vascular Endothelial Growth Factor Receptor 1 (VEGFR-1); Vascular Endothelial Growth Factor Receptor 2 (VEGFR-2); Vascular Endothelial Growth Factor Receptor 3 (VEGFR-3); Vitamin K-Dependent Protein S (VKDPS); Vitronectin; von Willebrand Factor (vWF); YKL-40.

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Area Underneath the Curve (AUC) values from Receiver Operating Characteristic (ROC) curve analysis of the top 20 markers.

Marker	AUC	Std. Error	95% CI
H64	0.933	0.014	0.905 to 0.961
CA-125	0.907	0.016	0.877 to 0.938
IL-2 receptor alpha	0.829	0.020	0.790 to 0.868
Alpha-1-antitrypsin	0.817	0.023	0.773 to 0.851
C-reactive protein	0.806	0.022	0.763 to 0.850
YKL-40	0.804	0.021	0.763 to 0.845
Cellular Fibronectin	0.803	0.022	0.760 to 0.846
CA-72-4	0.802	0.025	0.753 to 0.850
Prostasin	0.800	0.023	0.755 to 0.845
TIMP-1	0.797	0.024	0.751 to 0.844
IL-8	0.795	0.022	0.752 to 0.837
MMP-7	0.787	0.024	0.741 to 0.834
IL-6	0.786	0.024	0.740 to 0.833
VEGF-B	0.767	0.024	0.720 to 0.815
Calprotectin	0.767	0.024	0.719 to 0.814
IGFBP-2	0.759	0.023	0.714 to 0.805
LOX-1	0.750	0.023	0.704 to 0.796
Neuropilin-1	0.750	0.024	0.702 to 0.798
TNFR2	0.748	0.024	0.700 to 0.796
MPIF-1	0.745	0.025	0.697 to 0.793

FIG. 3

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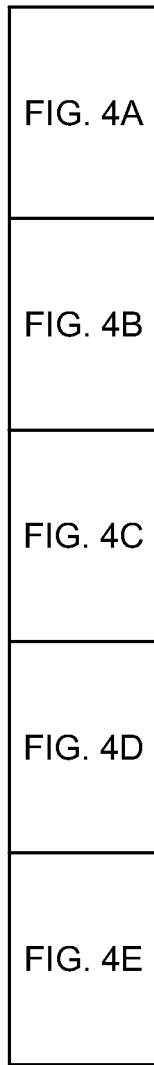


FIG. 4

FIG. 4A

Up-regulated Markers	AUC Value
HE4	0.933
Cancer Antigen 125 (CA-125)	0.907
Interleukin-2 receptor alpha (IL-2 receptor alpha)	0.829
Alpha-1-Antitrypsin (AAT)	0.817
C-Reactive Protein (CRP)	0.806
YKL-40	0.804
Cellular Fibronectin (cFib)	0.803
Cancer Antigen 72-4(CA-72-4)	0.802
Prostasin	0.800
Tissue Inhibitor of Metalloproteinases 1 (TIMP-1)	0.797
Interleukin-8 (IL-8)	0.795
Matrix Metalloproteinase-7 (MMP-7)	0.787

FIG. 4B

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Interleukin-6 (IL-6)	0.786
Vascular Endothelial Growth Factor B (VEGF-B)	0.767
Calprotectin	0.767
Insulin-like Growth Factor-Binding Protein 2 (IGFBP-2)	0.759
Lectin-Like Oxidized LDL Receptor 1 (LOX-1)	0.750
Neuropilin-1	0.750
Tumor Necrosis Factor Receptor 2 (TNFR2)	0.748
Myeloid Progenitor Inhibitory Factor 1 (MPIF-1)	0.745
Maspin	0.744
Cancer Antigen 15-3 (CA-15-3)	0.744
Vascular Endothelial Growth Factor D(VEGF-D)	0.744
EN-RAGE	0.742
B cell-activating factor (BAFF)	0.739
Serum Amyloid P-Component (SAP)	0.733
Endostatin	0.731
CD 40 antigen (CD40)	0.731
Haptoglobin	0.730
Mesothelin (MSLN)	0.728
Osteoprotegerin (OPG)	0.727
Urokinase-type Plasminogen Activator Receptor(uPAR)	0.726
Growth-Regulated alpha protein (GRO-alpha)	0.725
Hepatocyte Growth Factor (HGF)	0.723
Vascular Endothelial Growth Factor (VEGF)	0.720
Macrophage Inflammatory Protein-1 alpha (MIP-1 alpha)	0.720
Ferritin (FRTN)	0.719
von Willebrand Factor (vWF)	0.718
Pulmonary and Activation-Regulated Chemokine (PARC)	0.714
Peroxiredoxin 4 (Prx-IV)	0.706
Tumor Necrosis Factor Receptor I (TNF RI)	0.705
Insulin-like Growth Factor-Binding Protein 1 (IGFBP-1)	0.701
Platelet-Derived Growth Factor BB (PDGF-BB)	0.701
Heparin-Binding EGF-Like Growth Factor (HB-EGF)	0.699
Cathepsin D	0.699
MHC class I chain-related protein 1 (MICA)	0.698
Neutrophil Gelatinase-Associated Lipocalin (NGAL)	0.697
Sortilin	0.697
Beta-2-Microglobulin (B2M)	0.695
Insulin-like Growth Factor Binding Protein 4 (IGFBP4)	0.694
FASLG Receptor (FAS)	0.694
Osteopontin	0.692
Thymus-Expressed Chemokine (TECK)	0.685

FIG. 4C

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Monokine Induced by Gamma Interferon (MIG)	0.683
Neuron Specific Enolase (NSE)	0.683
Plasminogen Activator Inhibitor 1 (PAI-1)	0.683
Human Chorionic Gonadotropin beta (hCG)	0.677
Phosphoserine Aminotransferase (PSAT)	0.677
Interleukin-1 receptor antagonist (IL-1ra)	0.675
Intercellular Adhesion Molecule 1 (ICAM-1)	0.675
Myeloperoxidase (MPO)	0.674
B Lymphocyte Chemoattractant (BLC)	0.674
Tumor Necrosis Factor alpha (TNF-alpha)	0.673
Interferon-inducible T-cell alpha chemoattractant (ITAC)	0.669
Matrix Metalloproteinase-1 (MMP-1)	0.668
Interleukin-10 (IL-10)	0.665
Receptor tyrosine-protein kinase erbB-3 (ErbB3)	0.663
Alpha-1-Antichymotrypsin (AACT)	0.660
Complement C3 (C3)	0.657
Thyroxine-Binding Globulin (TBG)	0.654
Tenascin-C (TN-C)	0.653
Galectin-3	0.652
Trefoil Factor 3 (TFF3)	0.651
Aldose Reductase	0.648
Interferon gamma Induced Protein 10 (IP-10)	0.644
Latency-Associated Peptide of Transforming Growth Factor beta 1 (LAP TGF-b1)	0.640
Monocyte Chemotactic Protein 3 (MCP-3)	0.638
Fibrinogen	0.636
Kallikrein-7 (KLK-7)	0.634
Hepsin	0.632
Matrix Metalloproteinase-2 (MMP-2)	0.629
Vascular Endothelial Growth Factor C (VEGF-C)	0.629
Interleukin-16 (IL-16)	0.629
Tissue type Plasminogen activator (tPA)	0.627
Prostatic Acid Phosphatase (PAP)	0.627
Angiogenin	0.624
Sex Hormone-Binding Globulin (SHBG)	0.623
Epiregulin (EPR)	0.623
Alpha-1-Microglobulin (A1Micro)	0.621
Amphiregulin (AR)	0.620
Collagen IV	0.619
Matrix Metalloproteinase-10 (MMP-10)	0.619
Cystatin-C	0.617
Transforming Growth Factor alpha (TGF-alpha)	0.617

FIG. 4D

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Vitamin K-Dependent Protein S (VKDPS)	0.616
N-terminal prohormone of brain natriuretic peptide (NT proBNP)	0.615
Macrophage inflammatory protein 3 beta (MIP-3 beta)	0.615
Kidney Injury Molecule-1 (KIM-1)	0.613
Fatty Acid-Binding Protein, adipocyte (FABP, adipocyte)	0.613
Angiopoietin-2 (ANG-2)	0.612
Calcitonin	0.611
Complement Factor H	0.611
Human Epidermal Growth Factor Receptor 2 (HER-2)	0.605
Fatty Acid-Binding Protein, heart (FABP, heart)	0.605
Monocyte Chemotactic Protein 1 (MCP-1)	0.605
Apolipoprotein E (Apo E)	0.605
Macrophage Migration Inhibitory Factor (MIF)	0.601
TNF-Related Apoptosis-Inducing Ligand Receptor 3 (TRAIL-R3)	0.601
Placenta Growth Factor (PLGF)	0.600
Luteinizing Hormone (LH)	0.599
Resistin	0.599
Matrix Metalloproteinase-9, total (MMP-9, total)	0.599
Follicle-Stimulating Hormone (FSH)	0.593
Fibroblast Growth Factor basic (FGF-basic)	0.591
CD40 Ligand (CD40-L)	0.591
Macrophage Inflammatory Protein-1 beta (MIP-1 beta)	0.590
Chemokine CC-4 (HCC-4)	0.585
Apolipoprotein(a) (Lp(a))	0.585
Growth Hormone (GH)	0.583
Vascular Endothelial Growth Factor Receptor 3 (VEGFR-3)	0.582
6Ckine	0.582
Carcinoembryonic Antigen (CEA)	0.581
Alpha-Fetoprotein (AFP)	0.580
Erythropoietin (EPO)	0.579
Cortisol (Cortisol)	0.578
Bone Morphogenetic Protein 6 (BMP-6)	0.578
Epidermal Growth Factor (EGF)	0.578
Monocyte Chemotactic Protein 2 (MCP-2)	0.576
Vascular Cell Adhesion Molecule-1 (VCAM-1)	0.576
T-Cell-Specific Protein RANTES (RANTES)	0.575
S100 calcium-binding protein B (S100-B)	0.570
Chromogranin-A (CgA)	0.569
Matrix Metalloproteinase-3 (MMP-3)	0.567
T Lymphocyte-Secreted Protein I-309 (I-309)	0.563
Pancreatic Polypeptide (PPP)	0.560

FIG. 4E

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Pepsinogen I (PGI)	0.559
Down-regulated Biomarkers	AUC Value
Transthyretin (TTR)	0.745
Apolipoprotein A-IV (Apo A-IV)	0.713
Leptin	0.664
Serotransferrin (Transferrin)	0.660
Fetuin-A	0.644
Epidermal Growth Factor Receptor (EGFR)	0.635
Apolipoprotein A-II (Apo A-II)	0.631
Endoglin	0.627
Insulin	0.626
Gelsolin	0.613
Angiotensin-Converting Enzyme (ACE)	0.611
Vascular Endothelial Growth Factor Receptor 2 (VEGFR-2)	0.611
Tetranectin	0.608
Interleukin-13 (IL-13)	0.605
Interleukin-1 alpha (IL-1 alpha)	0.602
Thrombopoietin	0.599
E-Selectin	0.597
Tamm-Horsfall Urinary Glycoprotein (THP)	0.595
Glucagon-like Peptide 1, total (GLP-1 total)	0.591
Alpha-2-Macroglobulin (A2Macro)	0.591
Granulocyte Colony-Stimulating Factor (G-CSF)	0.589
Brain-Derived Neurotrophic Factor (BDNF)	0.586
Interleukin-3 (IL-3)	0.583
Fibulin-1C (Fib-1C)	0.580
Macrophage-Derived Chemokine (MDC)	0.580
Interleukin-2 (IL-2)	0.578
Superoxide Dismutase 1, Soluble (SOD-1)	0.578
Receptor for advanced glycosylation end products (RAGE)	0.575
Interleukin-7 (IL-7)	0.574
Glutathione S-Transferase alpha (GST-alpha)	0.573
Thyroglobulin (TG)	0.573
Interleukin-15 (IL-15)	0.573
Vascular Endothelial Growth Factor Receptor 1 (VEGFR-1)	0.573
Tumor Necrosis Factor beta (TNF-beta)	0.573
Interleukin-5 (IL-5)	0.564
Progesterone	0.563
Monocyte Chemotactic Protein 4 (MCP-4)	0.562
Immunoglobulin E (IgE)	0.558
Insulin-like Growth Factor Binding Protein 6 (IGFBP6)	0.556

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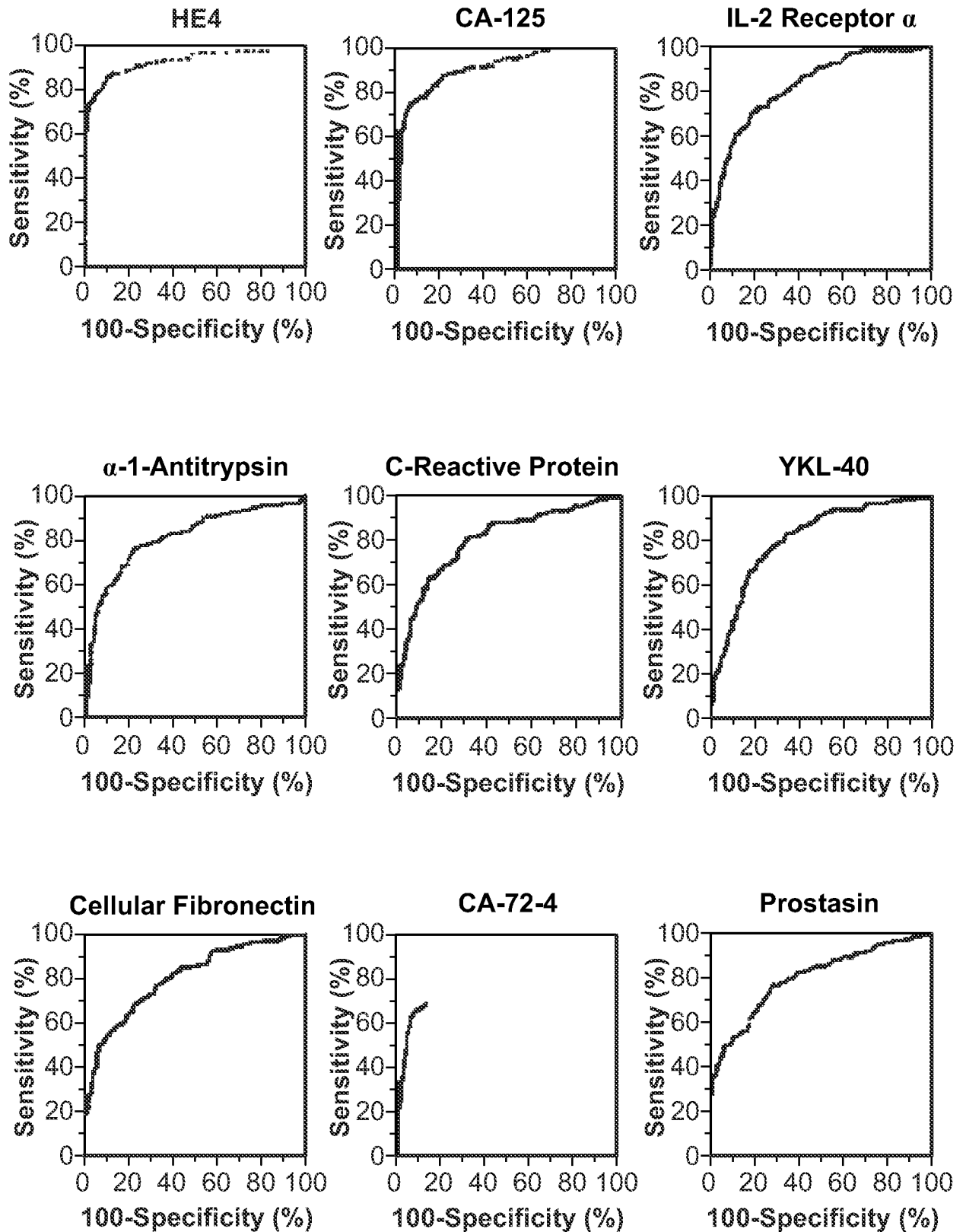


FIG. 5

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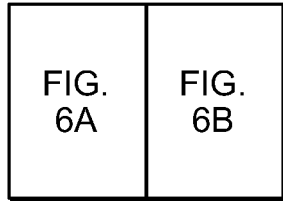


FIG. 6

FIG. 6A

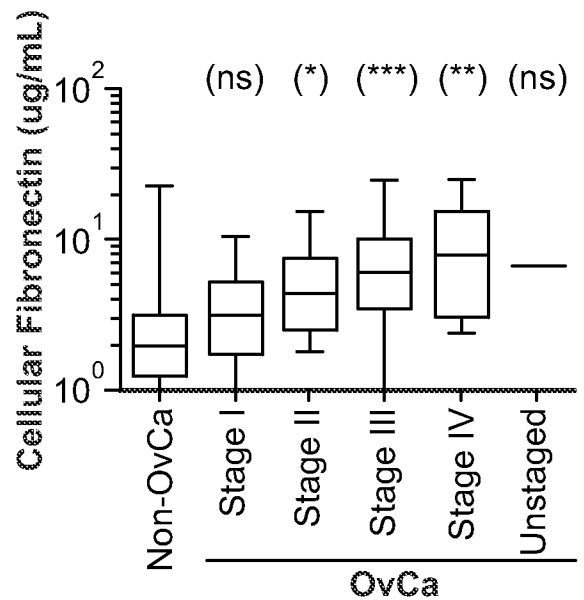
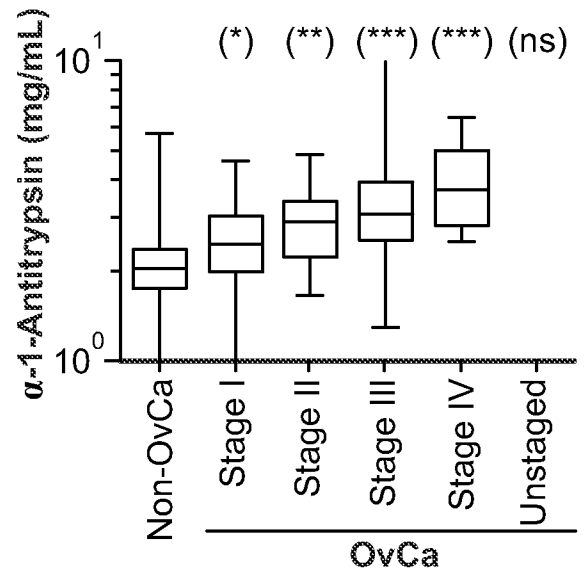
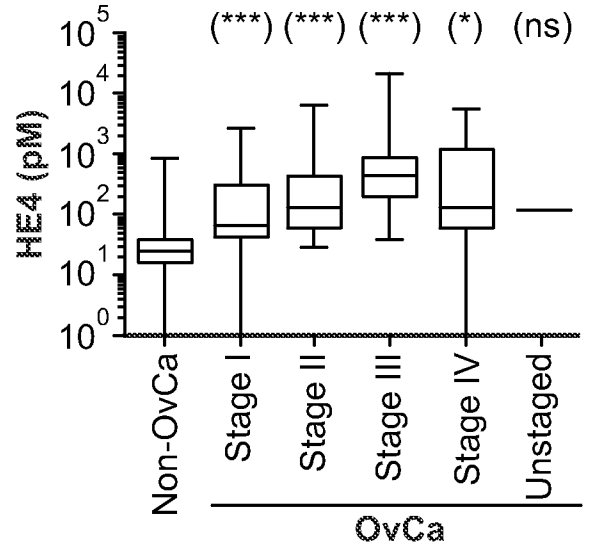
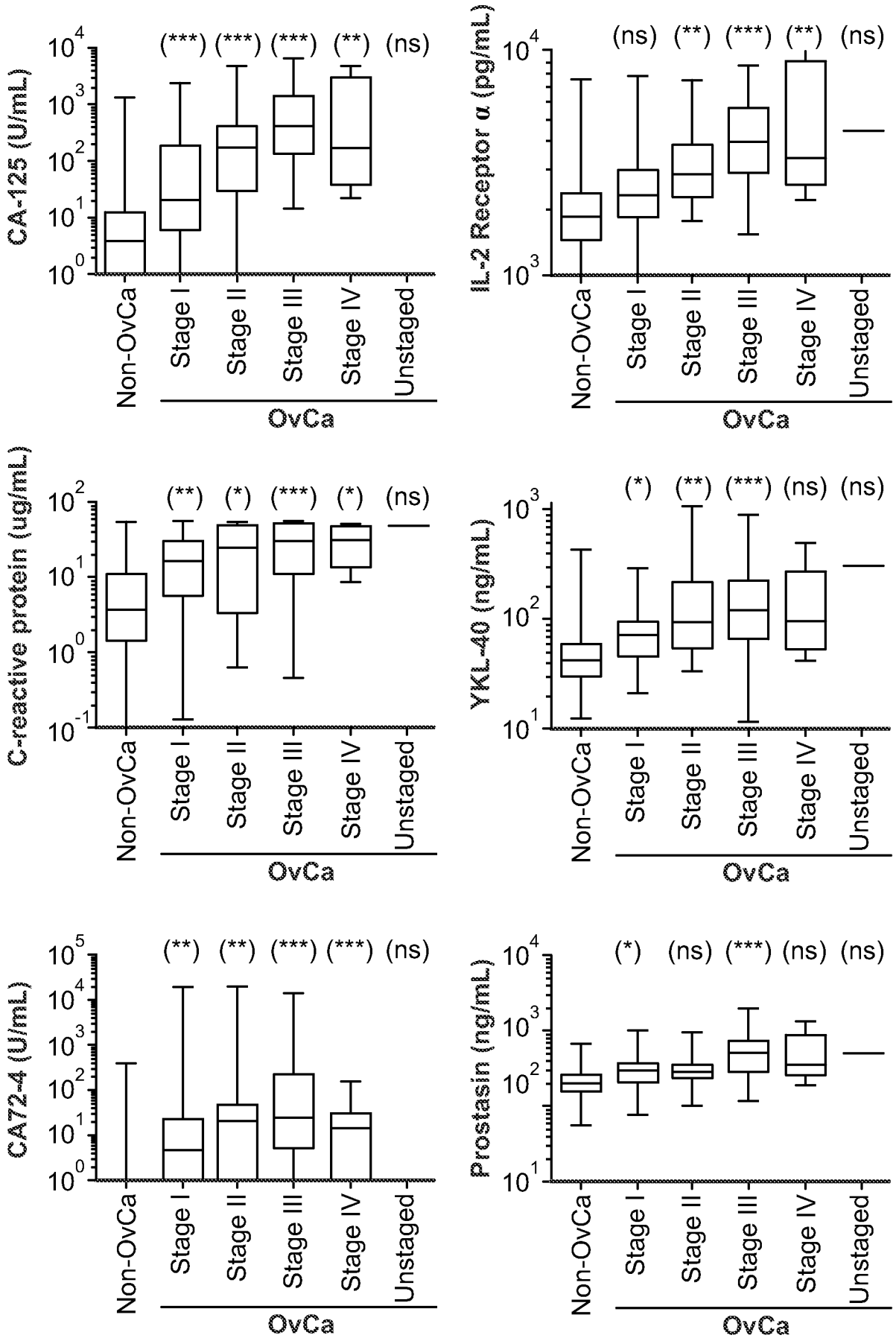


FIG. 6B



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FIG. 7A	FIG. 7B
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FIG. 7

FIG. 7A

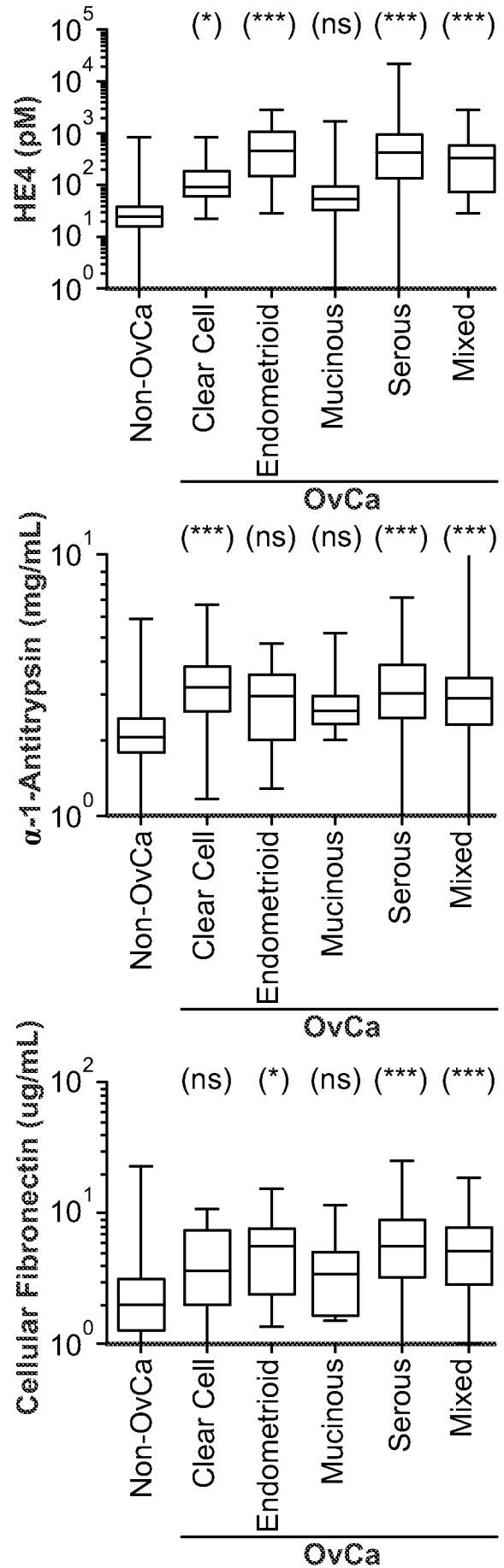
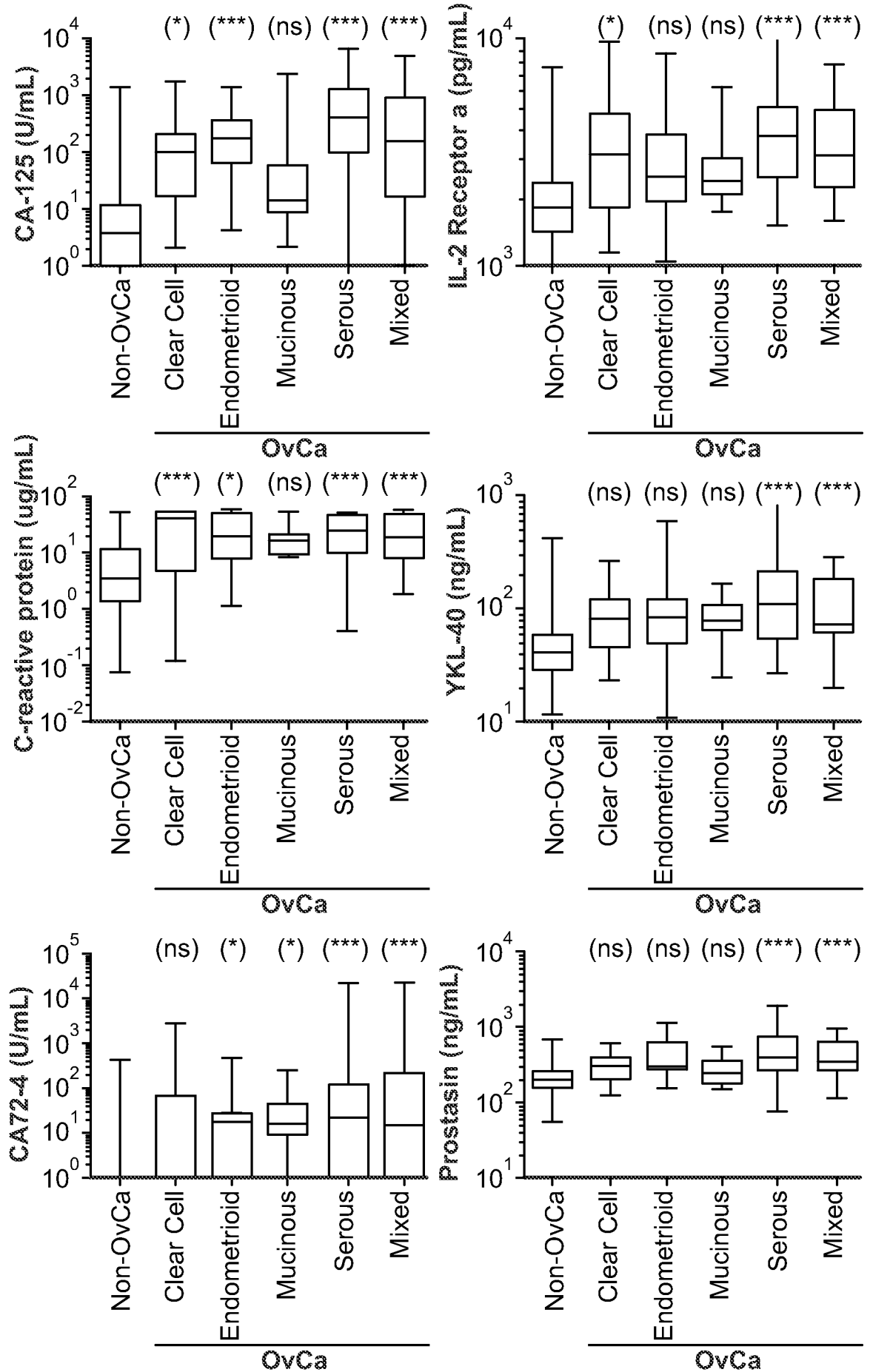


FIG. 7B



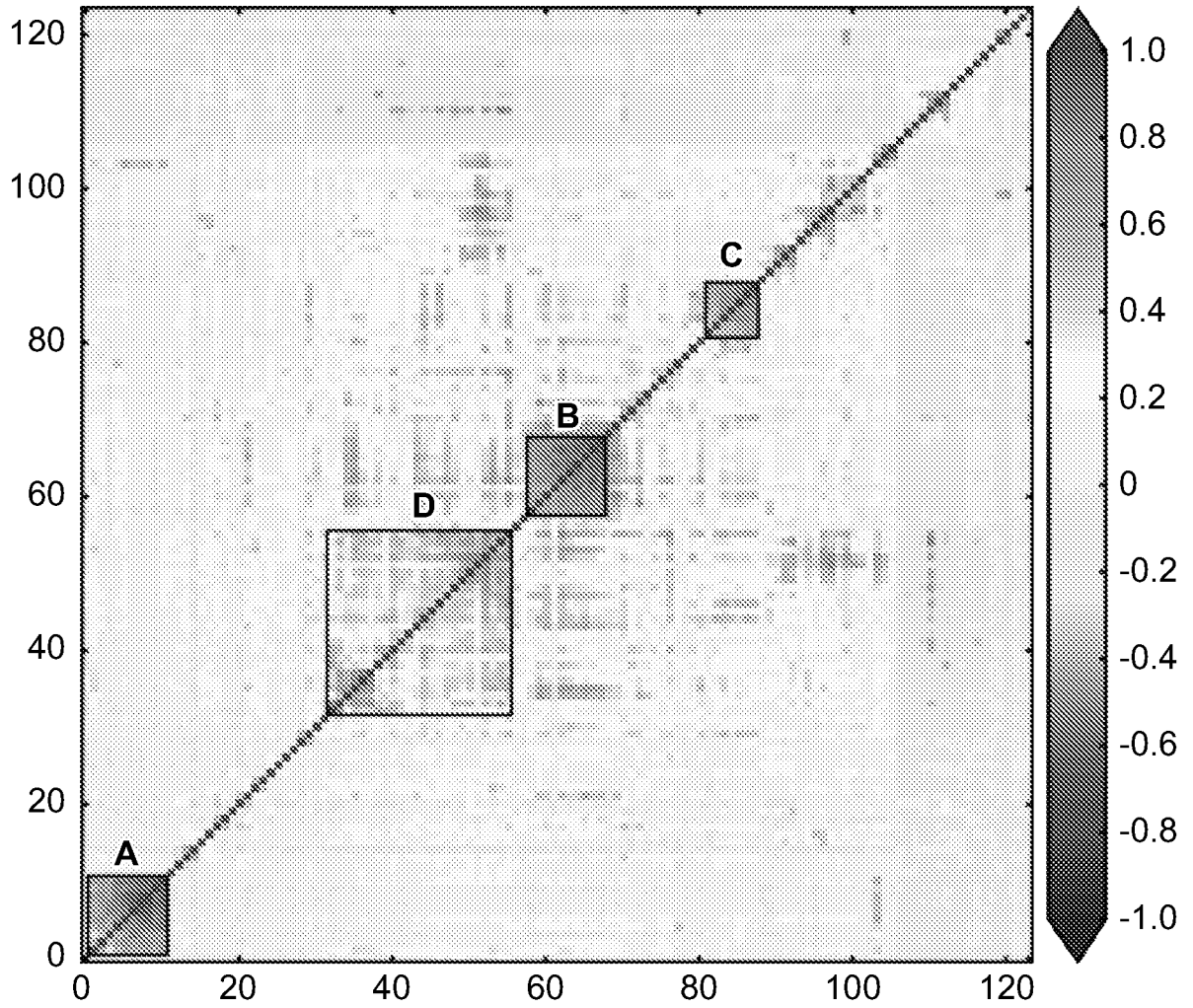


FIG. 8

Cluster	ID	Markers
A	1-10	Matrix metalloproteinase-10, TNF-Related Apoptosis-Inducing Ligand Receptor 3, FASLG Receptor (FAS), CA 72-4, monokine induced by gamma interferon, hepatocyte growth factor, CA 15-3, human epidermal growth factor receptor 2 (HER-2), thymus-expressed chemokine, monocyte chemotactic protein 3, and myeloid progenitor inhibitory factor 1.
B	58-67	Adipocyte fatty acid binding protein (FABP), galectin-3, endostatin, heart FABP, tumor necrosis factor receptor 2 (TNFR2), TNFR1, CD40 antigen, insulin-like growth factor binding protein 4, β 2-Microglobulin and cystatin C.
	68-69	Weak association α -1-Microglobulin and hepsin
C	81-87	Kallikrein 7, CA-125, prostasin, vascular endothelial growth factor-B (VEGF-B), VEGF-D, maspin and mesothelin
	79-80	Weak association HE4 and urokinase-type plasminogen activator receptor
D	32-55	Calprotectin, EN-RAGE, IL-16, neutrophil gelatinase-associated lipocalin, lectin-like oxidized LDL receptor 1, myeloperoxidase, ferritin, IL-1 receptor α , peroxiredoxin 4, IL-6, tenascin C, osteopontin, YKL-40, von Willebrand Factor, cellular fibronectin, pulmonary and activation-regulated chemokine, neuropilin-1, haptoglobin, α 1-antitrypsin, plasminogen activator inhibitor 1, tissue inhibitor of metalloproteinases 1 (TIMP-1), VEGF, C-reactive protein and IL-2 receptor α .

FIG. 9

	MMP-10	TRAILR-3	FAS	CA 72-4	MIG	HGF	CA 15-3	HER-2	TEC	MCP 3	MPIF-1
MMP-10	1.000	0.232	0.179	0.215	0.223	0.269	0.323	0.258	0.251	0.189	0.234
TRAILR-3	0.232	1.000	0.547	0.373	0.528	0.620	0.580	0.575	0.621	0.545	0.651
FAS	0.179	0.547	1.000	0.487	0.600	0.686	0.602	0.662	0.653	0.619	0.654
CA 72-4	0.215	0.373	0.487	1.000	0.533	0.606	0.793	0.701	0.621	0.628	0.616
MIG	0.223	0.528	0.600	0.533	1.000	0.728	0.783	0.799	0.810	0.797	0.830
HGF	0.269	0.620	0.686	0.606	0.728	1.000	0.797	0.843	0.881	0.760	0.829
CA 15-3	0.323	0.580	0.602	0.793	0.783	0.797	1.000	0.921	0.913	0.827	0.851
HER-2	0.258	0.575	0.662	0.701	0.799	0.843	0.921	1.000	0.948	0.873	0.878
TEC	0.251	0.621	0.653	0.621	0.810	0.881	0.913	0.948	1.000	0.853	0.888
MCP 3	0.189	0.545	0.619	0.628	0.797	0.760	0.827	0.873	0.853	1.000	0.914
MPIF-1	0.234	0.651	0.654	0.616	0.830	0.829	0.851	0.878	0.888	0.914	1.000

Abbreviations: MMP-10, Matrix metalloproteinase-10; TRAILR-3, TNF-Related Apoptosis-Inducing Ligand Receptor 3; FAS, FASLG Receptor; MIG, monokine induced by gamma interferon; HGF, hepatocyte growth factor; HER-2, human epidermal growth factor receptor 2; TEC, thymus-expressed chemokine; MCP-3, monocyte chemoattractant protein 3; MPIF-1, myeloid progenitor inhibitory factor.

FIG. 10

	aFABP	Galectin-3	Endostatin	hFABP	TNFR2	TNFR1	CD40a	IGFBP4	β 2M	Cystatin C	α 1M	Hepsin
aFABP	1.000	0.626	0.613	0.619	0.667	0.623	0.668	0.659	0.697	0.533	0.451	1.000
Galectin-3	0.626	1.000	0.655	0.736	0.642	0.680	0.718	0.703	0.706	0.509	0.556	0.626
Endostatin	0.613	0.655	1.000	0.743	0.705	0.729	0.810	0.745	0.773	0.574	0.672	0.613
hFABP	0.572	0.589	0.586	0.733	0.787	0.837	0.755	0.838	0.811	0.482	0.429	0.572
TNFR2	0.619	0.736	0.743	1.000	0.817	0.826	0.821	0.884	0.808	0.591	0.592	0.619
TNFR1	0.667	0.642	0.705	0.817	1.000	0.856	0.835	0.851	0.830	0.535	0.505	0.667
CD40a	0.623	0.680	0.729	0.826	0.856	1.000	0.843	0.887	0.870	0.552	0.539	0.623
IGFBP4	0.668	0.718	0.810	0.821	0.835	0.843	1.000	0.868	0.905	0.624	0.646	0.668
β 2M	0.659	0.703	0.745	0.884	0.851	0.887	0.868	1.000	0.917	0.587	0.555	0.659
Cystatin C	0.697	0.706	0.773	0.808	0.830	0.870	0.905	0.917	1.000	0.617	0.586	0.697
α 1M	0.533	0.509	0.574	0.591	0.535	0.552	0.624	0.587	0.617	1.000	0.634	0.533
Hepsin	0.451	0.556	0.672	0.592	0.505	0.539	0.646	0.555	0.586	0.634	1.000	0.451

Abbreviations: aFABP, Adipocyte fatty acid binding protein; hFABP, Heart FABP; TNFR2, Tumor necrosis factor receptor 2; TNFR1, Tumor necrosis factor receptor 1; CD40a, CD40 antigen; IGFBP4, Insulin-like growth factor binding protein 4; β 2M, β 2Microglobulin; α 1M, α -1-Microglobulin.

FIG. 11

	KLK7	CA-125	Prostasin	VEGF-B	VEBF-D	Maspin	Mesothelin	HE4	uPAR
KLK7	1.000	0.507	0.482	0.539	0.530	0.594	0.590	0.338	0.222
CA-125	0.507	1.000	0.551	0.505	0.568	0.599	0.600	0.280	0.358
Prostasin	0.482	0.551	1.000	0.709	0.757	0.748	0.639	0.463	0.549
VEBF-B	0.539	0.505	0.709	1.000	0.745	0.770	0.718	0.413	0.391
VEBF-D	0.530	0.568	0.757	0.745	1.000	0.821	0.808	0.409	0.453
Maspin	0.594	0.599	0.748	0.770	0.821	1.000	0.878	0.517	0.434
Mesothelin	0.590	0.600	0.639	0.718	0.808	0.878	1.000	0.335	0.377
HE4	0.338	0.280	0.463	0.413	0.409	0.517	0.335	1.000	0.303
uPAR	0.222	0.358	0.549	0.391	0.453	0.434	0.377	0.303	1.000

Abbreviations: KLK7, Kallikrein 7; VEGF-B, vascular endothelial growth factor-B; VEGF-D, vascular endothelial growth factor-D.

FIG. 12

FIG. 13A	FIG. 13B	FIG. 13C	FIG. 13D
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FIG. 13

FIG. 13A

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	Calpro	ENRAGE	IL-16	N-GAL	LOX-1
Calpro	1.000	0.711	0.305	0.472	0.402
ENRAGE	0.711	1.000	0.500	0.622	0.572
IL-16	0.305	0.500	1.000	0.606	0.545
N-GAL	0.472	0.622	0.606	1.000	0.734
LOX-1	0.402	0.572	0.545	0.734	1.000
Myelo	0.406	0.612	0.505	0.621	0.775
Ferritin	0.523	0.449	0.337	0.392	0.344
IL1-R α	0.486	0.368	0.401	0.278	0.332
PER-4	0.494	0.475	0.330	0.364	0.428
IL-6	0.396	0.406	0.195	0.307	0.322
Ten C	0.234	0.292	0.227	0.329	0.302
Osteop	0.153	0.204	0.298	0.291	0.309
YKL-40	0.394	0.390	0.447	0.438	0.424
vWF	0.312	0.322	0.382	0.361	0.328
cFib	0.189	0.317	0.337	0.323	0.315
PARC	0.234	0.310	0.404	0.432	0.406
Neu-1	0.341	0.447	0.309	0.419	0.417
Hapto	0.299	0.422	0.208	0.317	0.381
AAT	0.305	0.454	0.266	0.424	0.439
PAI-1	0.203	0.323	0.178	0.314	0.336
TIMP-1	0.311	0.465	0.356	0.489	0.473
VEGF	0.290	0.363	0.343	0.520	0.431
CRP	0.341	0.501	0.337	0.477	0.486
IL2-R α	0.275	0.365	0.421	0.521	0.490

Abbreviations: Calpro, Calprotectin; N-GAL, Neutrophil gelatinase-associated lipocalin; LOX-1, Lectin-like oxidized LDL receptor 1; Myelo, Myeloperoxidase; IL1-R α , IL-1 receptor α ; PER4, Peroxiredoxin 4; Ten C, Tenascin C; Osteop, Osteoprotegerin; vWF, von Willebrand Factor; cFib, cellular fibronectin; PARC, pulmonary and activation-regulated chemokine; Neu-1, NeHapilin-1, Hapto, Haptoglobin; AAT, α 1-antitrypsin; PAI-1, Plasminogen activator inhibitor 1; TIMP-1, Tissue inhibitor of metalloproteinases 1 (TIMP-1); CRP, C-reactive protein; IL2-R α , IL-2 receptor α .

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Myelo	Ferritin	IL1-R α	PER-4	IL-6	Ten C	Osteop
0.406	0.523	0.486	0.494	0.396	0.234	0.153
0.612	0.449	0.368	0.475	0.406	0.292	0.204
0.505	0.337	0.401	0.330	0.195	0.227	0.298
0.621	0.392	0.278	0.364	0.307	0.329	0.291
0.775	0.344	0.332	0.428	0.322	0.302	0.309
1.000	0.325	0.301	0.353	0.281	0.234	0.223
0.325	1.000	0.392	0.530	0.367	0.242	0.415
0.301	0.392	1.000	0.543	0.241	0.210	0.181
0.353	0.530	0.543	1.000	0.468	0.430	0.416
0.281	0.367	0.241	0.468	1.000	0.402	0.167
0.234	0.242	0.210	0.430	0.402	1.000	0.212
0.223	0.415	0.181	0.416	0.167	0.212	1.000
0.316	0.426	0.491	0.513	0.330	0.351	0.287
0.311	0.334	0.355	0.463	0.309	0.375	0.207
0.221	0.320	0.136	0.370	0.297	0.342	0.269
0.322	0.386	0.203	0.425	0.295	0.324	0.253
0.341	0.373	0.203	0.448	0.375	0.365	0.356
0.360	0.306	0.215	0.423	0.444	0.357	0.128
0.392	0.370	0.188	0.469	0.412	0.423	0.273
0.334	0.283	0.208	0.361	0.294	0.271	0.187
0.425	0.456	0.226	0.525	0.428	0.396	0.334
0.396	0.334	0.167	0.445	0.441	0.402	0.275
0.455	0.452	0.220	0.492	0.500	0.382	0.234
0.359	0.427	0.176	0.454	0.328	0.390	0.471

FIG. 13B

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YKL-40	vWF	cFib	PARC	Neu-1	Hapto	AAT
0.394	0.312	0.189	0.234	0.341	0.299	0.305
0.390	0.322	0.317	0.310	0.447	0.422	0.454
0.447	0.382	0.337	0.404	0.309	0.208	0.266
0.438	0.361	0.323	0.432	0.419	0.317	0.424
0.424	0.328	0.315	0.406	0.417	0.381	0.439
0.316	0.311	0.221	0.322	0.341	0.360	0.392
0.426	0.334	0.320	0.386	0.373	0.306	0.370
0.491	0.355	0.136	0.203	0.203	0.215	0.188
0.513	0.463	0.370	0.425	0.448	0.423	0.469
0.330	0.309	0.297	0.295	0.375	0.444	0.412
0.351	0.375	0.342	0.324	0.365	0.357	0.423
0.287	0.207	0.269	0.253	0.356	0.128	0.273
1.000	0.511	0.412	0.447	0.422	0.466	0.436
0.511	1.000	0.425	0.409	0.451	0.398	0.355
0.412	0.425	1.000	0.409	0.454	0.430	0.449
0.447	0.409	0.409	1.000	0.404	0.429	0.380
0.422	0.451	0.454	0.404	1.000	0.496	0.497
0.466	0.398	0.430	0.429	0.496	1.000	0.606
0.436	0.355	0.449	0.380	0.497	0.606	1.000
0.286	0.230	0.216	0.359	0.378	0.543	0.602
0.526	0.482	0.532	0.540	0.602	0.641	0.708
0.411	0.348	0.375	0.491	0.446	0.456	0.506
0.474	0.454	0.517	0.562	0.494	0.597	0.592
0.529	0.456	0.618	0.552	0.532	0.470	0.563

FIG. 13C

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PAI-1	TIMP-1	VEGF	CRP	IL2-R α
0.203	0.311	0.341	0.275	1.000
0.323	0.465	0.501	0.365	0.711
0.178	0.356	0.337	0.421	0.305
0.314	0.489	0.477	0.521	0.472
0.336	0.473	0.486	0.490	0.402
0.334	0.425	0.455	0.359	0.406
0.283	0.456	0.452	0.427	0.523
0.208	0.226	0.220	0.176	0.486
0.361	0.525	0.492	0.454	0.494
0.294	0.428	0.500	0.328	0.396
0.271	0.396	0.382	0.390	0.234
0.187	0.334	0.234	0.471	0.153
0.286	0.526	0.474	0.529	0.394
0.230	0.482	0.454	0.456	0.312
0.216	0.532	0.517	0.618	0.189
0.359	0.540	0.562	0.552	0.234
0.378	0.602	0.494	0.532	0.341
0.543	0.641	0.597	0.470	0.299
0.602	0.708	0.592	0.563	0.305
1.000	0.761	0.488	0.448	0.203
0.761	1.000	0.662	0.693	0.311
0.506	0.648	0.525	0.609	0.290
0.488	0.662	1.000	0.619	0.341
0.448	0.693	0.619	1.000	0.275

FIG. 13D

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Threshold Specificity (%)	Sensitivity (%)	
	Top 9	OVA1
80	92.6	84.6
90	88.6	79.2
95	83.9	73.2
99	69.1	50.3

Top 9, a logistic regression model was built using the 9 markers which had the highest individual AUC values; OVA1, a logistic regression model was build using the 5 markers in the OVA1 panel.
doi:10.1371/journal.pone.0029533.t003

FIG. 14

Threshold Specificity (%)	Sensitivity (%)	
	Top 9	OVA1
80	96.3	88.3
90	88.9	63.4
95	62.3	52.9
99	20.6	7.1

Top 9, a logistic regression model was built using the 9 markers which had the highest individual AUC values; OVA1, a logistic regression model was build using the 5 markers in the OVA1 panel.
doi:10.1371/journal.pone.0029533.t004

FIG. 15

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Marker	All	95% CI	Pre	95% CI	Post	95% CI
HE4	0.933	0.905-0.961	0.912	0.826-0.997	0.927	0.895-0.959
CA-125	0.907	0.877-0.938	0.907	0.849-0.966	0.927	0.896-0.959
IL-2 receptor alpha	0.829	0.790-0.868	0.812	0.724-0.899	0.824	0.778-0.870
Alpha-1-antitrypsin	0.817	0.773-0.861	0.876	0.806-0.945	0.818	0.768-0.869
C-reactive protein	0.806	0.763-0.850	0.839	0.752-0.926	0.797	0.745-0.849
YKL-40	0.804	0.763-0.845	0.824	0.734-0.913	0.761	0.708-0.814
Cellular Fibronectin	0.803	0.760-0.846	0.835	0.747-0.924	0.776	0.723-0.830
CA-72-4	0.802	0.753-0.850	0.769	0.650-0.888	0.806	0.752-0.861
Prostasin	0.800	0.755-0.845	0.732	0.609-0.855	0.799	0.748-0.850
TIMP-1	0.797	0.751-0.844	0.767	0.664-0.870	0.797	0.744-0.851
IL-8	0.795	0.752-0.837	0.823	0.736-0.910	0.755	0.700-0.810
MMP-7	0.787	0.741-0.834	0.757	0.644-0.870	0.771	0.717-0.826
IL-6	0.786	0.740-0.833	0.791	0.683-0.898	0.778	0.724-0.833
VEGF-B	0.767	0.720-0.815	0.704	0.581-0.826	0.778	0.725-0.832
Calprotectin	0.767	0.719-0.814	0.795	0.698-0.892	0.772	0.718-0.827
IGFBP-2	0.759	0.714-0.805	0.799	0.692-0.906	0.713	0.656-0.769
LOX-1	0.750	0.704-0.796	0.734	0.624-0.844	0.763	0.711-0.816
Neuropilin-1	0.750	0.702-0.798	0.789	0.699-0.879	0.727	0.669-0.784
TNFR2	0.748	0.700-0.796	0.684	0.561-0.806	0.735	0.679-0.791
MPIF-1	0.745	0.697-0.793	0.803	0.709-0.896	0.716	0.658-0.774

Abbreviations: Pre, Pre-menopausal; Post, Post-menopausal; HE4, human epididymis protein-4; CA, cancer antigen; TIMP-1, tissue inhibitor of metalloproteinases 1; IL, interleukin; MMP-7, Matrix Metalloproteinase-7; VEGF-B, vascular endothelial growth factor B; IGFBP-2, insulin-like growth factor-binding protein 2; LOX-1, lectin-like oxidized LDL receptor 1; TNFR2, tumor necrosis factor receptor 2; MPIF-1, myeloid progenitor inhibitory factor 1.

FIG. 16