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(54) Benævnelse: **FREMGANGSMÅDER TIL DETEKTERING AF CANCER**

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WO-A1-2009/096903
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Fortsættes ...

DESCRIPTION

BACKGROUND

[0001] Cancer is a major cause of death and suffering and is a major cost to medical systems in the U.S. and across the world. Various studies have been carried out in an attempt to increase understanding in this area. Dessi et al (Oncology, S. Karger, Basel, CH, Vol. 49, No. 6, 1 January 1992, pages 436-441) refers to studies showing an altered pattern of lipid metabolism in patients with lung cancer. Shah et al (Integrative Cancer Therapies, Vol. 7, No. 1, March 2008, pages 33-41) relates to alterations in plasma lipid profiles in breast cancer. Srivastava et al (NMR in Biomedicine, 1 January 2009, pages 113-122) relates to in vitro, high resolution 1H and 31P NMR based analysis of the lipid components in the tissue, serum and cerebrospinal fluid of patients with primary brain tumours. Qadir et al (European Journal of Gynaecological Oncology, Vol. 29, No. 2, 2008, pages 158-161) relates to plasma lipid profile in gynaelogical cancers. Halton et al (1998 American Cancer Society, Vol. 83, No. 2, 15 July 1998, pages 379-384) relates to blood lipid profiles in children with acute lymphoblastic leukemia. WO2009/096903 relates to a method of generating a classification model capable of distinguishing between two biological states; such as a normal and a cancerous or tumour state. Early detection of cancer is associated with better treatment options and improved outcome. Therefore, early detection of cancer can help minimize both the suffering and the cost, while typically increasing the chance of survival. Thus, some embodiments of the invention are methods to determine the presence of cancers in animals.

SUMMARY

[0002] According to a first aspect, the invention relates to a method for determining the presence or absence of at least one cancer type in an animal comprising

- determining lipids amounts of lipids in a lipid set in a sample from the animal, and
- determining the presence or absence of at least one cancer type in the animal with a predictive model;
  wherein
  - the lipid amounts of lipids in the lipid set comprise an input of the predictive model,
  - the sample comprises a bodily fluid or treatment thereof;
  - the at least one cancer type is selected from the group consisting of carcinomas, sarcomas, hematologic cancers, neurological malignancies, thyroid cancer, neuroblastoma, melanoma, renal cell carcinoma, hepatocellular carcinoma, breast cancer, colon cancer, lung cancer, pancreatic cancer, brain cancer, prostate cancer, chronic lymphocytic leukemia, acute lymphoblastic leukemia, rhabdomyosarcoma, Glioblastoma multiforme, meningioma, bladder cancer, gastric cancer, Glioma, oral cancer, nasopharyngeal carcinoma, kidney cancer, rectal cancer, lymph node cancer, bone marrow cancer, stomach cancer, uterine cancer, leukemia, basal cell carcinoma, cancers related to epithelial cells, cancers that can alter the regulation or activity of Pyruvate Carboxylase, and tumors associated with any of the aforementioned cancer types;
  - the lipid set comprises a lipid from the class of BMP, preferably BMP (30:1), BMP (32:1), BMP (34:1), BMP (35:4), BMP (36:3), BMP (37:1), BMP (37:7), BMP (38:1), BMP (38:2), BMP (38:4), BMP (39:1), BMP (39:4), BMP (40:1), BMP (40:2), BMP (40:3), BMP (40:4), BMP (40:7), BMP (42:10), BMP (42:2), BMP (42:5), or BMP (44:8), and
  - the predictive model comprises one or more of dimension reduction method, clustering method, machine learning method, principle component analysis, soft independent modeling of class analogy, partial least squares regression, orthogonal least squares regression, partial least squares discriminant analysis, orthogonal partial least squares discriminant analysis, mean centering, median centering, Pareto scaling, unit variance scaling, orthogonal signal correction, integration, differentiation, cross validation, or receiver operating characteristic curves.

[0003] Preferably, the bodily fluid is selected from the group consisting of plasma vomit, cerumen, gastric juice, breast milk, mucus, saliva, sebum, semen, sweat, tears, vaginal secretion, blood serum, aqueous humor, vitreous humor, endolymph, perilymph, peritoneal fluid, pleural fluid, cerebrospinal fluid, blood, plasma, nipple aspirate fluid, urine, stool, and bronchioalveolar lavage fluid.

[0004] Preferably, the sample comprises a lipid microvesicle fraction.

[0005] Preferably, the lipid set comprises at least 10, at least 50, at least 100, at least 200 or no more than 100,000 lipids.

[0006] Preferably, the lipid set further comprises one or more lipids selected from the one or more classes of lipids selected from the group consisting of CE, Cer, DAG, DH-LTB4, FA, GA2, GM3, HexCer, HexDHCer, LacCer, LysoPA, LysoPC, LysoPC-pmg, LysoPE, LysoPE-pmg, LysoPS, MAG, PC, PC-pmg, PE, PE-pmg, PGA1, PGB1, SM, Sphingosine, TAG, and TH-12-keto-LTB4.

[0007] Preferably, the lipid set further comprises one or more lipids selected from the one or more classes of lipids selected from the group consisting of FA, MAG, DAG, TAG, PI, PE, PS, PI, PG, PA, LysoPC, LysoPE, LysoPS, LysoPI, LysoPG, LysoPA, LysoPC, LysoPE, SM, Cer, Cer-P, HexCer, GA1, GA2, GD1, GD2, GM1, GM2, GM3, GT1, and CE.

[0008] Preferably, one or more lipids in the lipid set are further selected from the group consisting of CE (16:2), CE (18:2), CE (18:3), CE

(18:4), CE (20:2), CE (20:4), CE (20:5), Cer (32:1), Cer (34:1), Cer (36:1), Cer (38:1), Cer (38:4), Cer (40:2), Cer (40:4), DAG (28:0), DAG (32:0), DAG (32:2), DAG (34:0), DAG (34:3), DAG (34:5), DAG (36:0), DAG (36:1), DAG (36:2), DAG (36:3), DAG (36:8), DAG (38:1), DAG (38:10), DAG (38:2), DAG (38:3), DAG (38:5), DAG (40:1), DAG (40:2), DAG (40:5), DH-LTB4 (20:3), FA (16:3), FA (19:1), GA2 (30:0), GA2 (33:2), GA2 (35:2), GA2 (37:2), GM3 (41:1), HexCer (32:1), HexDHCer (34:0), LacCer (30:0), LacCer (30:1), LacCer (32:2), LysoPA (16:2), LysoPA (16:3), LysoPA (18:1), LysoPA (22:0), LysoPA (22:1), LysoPC (16:0), LysoPC (18:0), LysoPC (18:1), LysoPC (18:4), LysoPC (20:4), LysoPC (20:5), LysoPC (26:6), LysoPC-pmg (12:0), LysoPC-pmg (18:3), LysoPC-pmg (24:4), LysoPC-pmg (26:0), LysoPE (10:1), LysoPE (16:2), LysoPE (18:2), LysoPE-pmg (18:4), LysoPS (24:1), MAG (18:0), MAG (20:3), MAG (24:2), PC (32:0), PC (32:1), PC (34:1), PC (34:1), PC (34:2), PC (34:3), PC (34:4), PC (34:6), PC (36:1), PC (36:2), PC (36:3), PC (36:4), PC (36:5), PC (36:6), PC (36:9), PC (38:2), PC (38:3), PC (38:4), PC (38:5), PC (38:6), PC (38:7), PC (38:8), PC (38:9), PC (40:5), PC (40:6), PC (40:7), PC (40:8), PC (40:9), PC (44:12), PC-pmg (30:1), PC-pmg (36:4), PC-pmg (38:5), PC-pmg (38:7), PC-pmg (40:11), PC-pmg (42:1), PE (34:7), PE (36:5), PE (36:7), PE (38:2), PE (38:3), PE (38:4), PE (38:5), PE (38:7), PE (40:4), PE (40:9), PE (42:12), PE (44:11), PE-pmg (28:2), PE-pmg (30:3), PE-pmg (34:6), PE-pmg (34:8), PE-pmg (36:5), PE-pmg (36:6), PE-pmg (40:7), PE-pmg (40:8), PE-pmg (42:10), PE-pmg (42:12), PE-pmg (42:4), PE-pmg (42:7), PE-pmg (42:8), PE-pmg (42:9), PE-pmg (44:10), PE-pmg (44:11), PE-pmg (44:12), PE-pmg (44:7), PE-pmg (44:8), PE-pmg (44:9), PGA1 (20:1), PGB1 (20:1), SM (34:1), SM (34:2), SM (36:1), SM (38:1), SM (40:1), SM (40:2), SM (42:1), SM (42:2), SM (42:3), Sphingosine (18:0), TAG (44:1), TAG (44:3), TAG (46:0), TAG (46:1), TAG (46:2), TAG (46:3), TAG (46:4), TAG (48:0), TAG (48:1), TAG (48:2), TAG (48:3), TAG (48:4), TAG (48:5), TAG (49:1), TAG (49:2), TAG (49:3), TAG (50:0), TAG (50:1), TAG (50:2), TAG (50:3), TAG (50:4), TAG (50:5), TAG (50:6), TAG (51:2), TAG (51:4), TAG (52:2), TAG (52:3), TAG (52:4), TAG (52:5), TAG (52:6), TAG (52:7), TAG (53:4), TAG (54:2), TAG (54:3), TAG (54:4), TAG (54:5), TAG (54:6), TAG (54:7), TAG (54:8), TAG (55:5), TAG (55:6), TAG (55:7), TAG (56:4), TAG (56:5), TAG (56:6), TAG (56:7), TAG (56:8), TAG (56:9), TAG (58:10), TAG (58:6), TAG (58:8), TAG (58:9), TAG (60:12), and TH-12-keto-LTB4(20:2).

[0009] Preferably, the at least one cancer type comprises lung cancer and one or more lipids in the lipid set are further selected from the group consisting of LysoPA (22:0), PE-pmg (42:9), FA (16:3), FA (19:1), CE (18:2), Cer (36:1), Cer (38:4), PC (38:5), Cer (38:1), and TAG (44:3).

[0010] Preferably, the at least one cancer type comprises lung cancer and one or more lipids in the lipid set are further selected from the group consisting of TAG (44:3), PC (36:5), PC (38:5), Cer (38:4), PE-pmg (42:9), PC (38:7), LysoPA (22:0), Cer (38:1), Cer (34:1), Cer (36:1), PC (40:7), TAG (54:5), TAG (54:6), CE (18:2), PC (36:4), FA (16:3), PE-pmg (44:11), TAG (52:5), Cer (40:4), CE (20:5), PC (38:6), TAG (50:2), MAG (18:0), FA (19:1), TAG (52:2), LysoPA (22:1), MAG (24:2), TAG (54:7), TAG (50:3), TAG (50:1), DAG (36:3), PC (34:1), TAG (52:6), PE-pmg (44:12), CE (20:4), PE (44:11), PC (40:8), TAG (56:9), PE-pmg (34:6), PE (36:7), PE (36:5), TAG (56:7), TAG (56:8), DAG (34:3), TAG (56:6), TAG (52:3), TAG (54:3), TAG (56:5), TAG (54:8), PC (34:6), PC (40:6), DAG (36:0), LysoPE (10:1), DAG (40:5), Cer (32:1), TAG (50:5), TAG (50:4), PE-pmg (36:6), TAG (46:3), and PE (38:5).

[0011] Preferably, the at least one cancer type comprises lung cancer and one or more lipids in the lipid set are further selected from the group consisting of TAG (44:3), PC (36:5), PC (38:5), Cer (38:4), PE-pmg (42:9), PC (38:7), LysoPA (22:0), Cer (38:1), Cer (34:1), and Cer (36:1).

[0012] Preferably, the at least one cancer type comprises breast cancer and one or more lipids in the lipid set are further selected from the group consisting of LysoPA (22:1), PE-pmg (42:9), CE (20:5), TAG (52:3), LysoPA (22:0), PC (36:3), PC (36:4), PC (36:2), PC (34:2), and PC (34:1).

[0013] Preferably, the at least one cancer type comprises breast cancer and one or more lipids in the lipid set are further selected from the group consisting of PC (34:2), PC (34:1), PC (36:2), PC (36:4), PC (36:3), PC (38:4), LysoPA (22:1), PE-pmg (42:9), LysoPA (22:0), CE (20:5), Cer (36:1), CE (18:2), DAG (34:0), SM (34:1), DAG (32:0), PE-pmg (40:8), PC (38:3), DAG (36:0), PC (36:1), TAG (54:5), TAG (54:6), PE-pmg (44:11), PE-pmg (42:8), TAG (52:2), SM (42:2), PC (38:6), TAG (54:7), PC (40:6), PC (40:7), LysoPC (16:0), FA (16:3), TAG (52:5), TAG (44:3), SM (40:1), PE-pmg (42:10), PE-pmg (40:7), SM (36:1), PE (38:2), PC (34:3), PC (36:5), PC (32:0), PC (32:1), PC (36:9), SM (42:3), PC-pmg (36:4), PC-pmg (38:5), PC (40:9), TAG (54:3), PE-pmg (44:12), FA (19:1), TAG (50:3), PC (34:6), GA2 (35:2), TAG (58:9), PE-pmg (42:7), and LysoPC (18:0).

[0014] Preferably, the at least one cancer type comprises breast cancer and one or more lipids in the lipid set are further selected from the group consisting of PC (34:2), PC (34:1), PC (36:2), PC (36:4), PC (36:3), PC (38:4), LysoPA (22:1), PE-pmg (42:9), LysoPA (22:0), and CE (20:5).

[0015] Preferably, the at least one cancer type comprises lung cancer and breast cancer, and one or more lipids in the lipid set are further selected from the group consisting of LysoPA (22:1), PC (36:5), TAG (52:3), PC (38:5), CE (20:5), TAG (50:2), PC (34:2), CE (18:2), and PC (34:1).

[0016] Preferably, the at least one cancer type comprises lung cancer and breast cancer, and one or more lipids in the lipid set are further selected from the group consisting of PC (34:2), PC (36:2), TAG (44:3), CE (18:2), PC (34:1), LysoPA (22:1), PC (36:5), Cer (36:1), CE (20:5), PC (36:3), PC (38:4), PC (36:4), Cer (38:4), PC (38:5), PC (38:7), Cer (38:1), TAG (50:2), Cer (34:1), SM (34:1), Cer (40:4), MAG (18:0), MAG (24:2), PC (38:3), PE-pmg (40:8), PE-pmg (42:8), TAG (50:1), DAG (32:0), PC (36:1), DAG (34:0), LysoPC (16:0), PE-pmg (34:6), DAG (36:3), PC (36:9), PE (36:5), TAG (52:6), FA (19:1), PE-pmg (44:11), PE (44:11), TAG (48:2), SM (42:2), PE-pmg (42:10), PE (36:7), PE-pmg (40:7), PE-pmg (36:6), PE (38:5), PC (32:0), PE (38:2), GA2 (35:2), DAG (34:3), PE-pmg (44:12), MAG (16:0), PC (32:1), LysoPE (10:1), SM (36:1), TAG (56:7), and PE-pmg (42:9).

[0017] Preferably, the at least one cancer type comprises lung cancer and breast cancer, and one or more lipids in the lipid set are further selected from the group consisting of PC (34:2), PC (36:2), TAG (44:3), CE (18:2), PC (34:1), LysoPA (22:1), PC (36:5), Cer (36:1), CE (20:5), and PC (36:3).

[0018] Preferably, the lipid amounts are determined using mass spectrometry, such as a Fourier transform ion cyclotron resonance mass analyzer.

[0019] Preferably, the sample is a treatment of a bodily fluid and the treatment comprises one or more extractions using one or more solutions comprising acetonitrile, water, chloroform, methanol, butylated hydroxytoluene, trichloroacetic acid, or combinations thereof.

[0020] Preferably, the predictive model comprises one or more dimension reduction methods.

[0021] Preferably, the predictive model comprises one or more methods selected from the group consisting of principal component analysis (PCA), soft independent modeling of class analogy (SIMCA), partial least squares discriminant analysis (PLS-DA), and orthogonal partial least squares discriminant analysis (OPLS-DA).

[0022] Preferably, the animal is selected from the group consisting of human, dog, cat, horse, cow, pig, sheep, chicken, turkey, mouse, and rat.

[0023] Preferably, the at least one cancer type is lung or breast cancer.

BRIEF DESCRIPTION OF THE DRAWINGS

[0024] The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the description of specific embodiments presented herein.

Figure 1. Diacylglycerols in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 2. Phosphatidylcholines in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 3. Phosphatidylcholines in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 4. Phosphatidylcholines in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 5. Phosphatidylcholines in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 6. Phosphatidylethanolamines in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 7. Phosphatidylethanolamines in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 8. Phosphatidylethanolamines in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 9. Phosphatidylethanolamines-pmg in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 10. Phosphatidylethanolamines-pmg in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 11. Triacylglycerols in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 12. Monoacylglycerols in samples from humans with lung cancer, breast cancer, and no cancer (control).

Figure 13. Lipid classes in samples from humans comparing cancer type.

Figure 14. PC1-PC3 PCA scores plot for breast cancer, control, and lung cancer samples - 4 components, $R^2X = 0.475$, $Q^2 = 0.296$.

Figure 15. PC1-PC3 PCA loadings plot for breast cancer, control, and lung cancer samples - 4 components, $R^2X = 0.475$, $Q^2 = 0.296$.

Figure 16. OPLS-DA scores plot separating lung cancer and control samples - 1+1 orthogonal components, $R^2X = 0.253$, $R^2Y = 0.619$, $Q^2 = 0.345$.

Figure 17. OPLS-DA coefficients plot separating lung cancer and control samples - 1+1 orthogonal components, $R^2X = 0.253$, $R^2Y = 0.619$, $Q^2 = 0.345$. The coefficients plot indicates lipids elevated in control samples.

Figure 18. OPLS-DA coefficients plot separating lung cancer and control samples - 1+1 orthogonal components, $R^2X = 0.253$, $R^2Y = 0.619$, $Q^2 = 0.345$. The coefficients plot indicates lipids elevated in lung cancer samples.

Figure 19. OPLS-DA scores plot separating breast cancer and control samples - 1+1 orthogonal components, $R^2X = 0.281$, $R^2Y = 0.762$,

Q^2 = 0.625.

Figure 20. OPLS-DA coefficients plot separating breast cancer and control samples - 1+1 orthogonal components, R^2X = 0.281, R^2Y = 0.762, Q^2 = 0.625. The coefficients plot indicates lipids elevated in control samples.

Figure 21. OPLS-DA coefficients plot separating breast cancer and control samples - 1+1 orthogonal components, R^2X = 0.281, R^2Y = 0.762, Q^2 = 0.625. The coefficients plot indicates lipids elevated in breast cancer samples.

Figure 22. OPLS-DA scores plot separating lung cancer and breast cancer samples - 1+1 orthogonal components, R^2X = 0.309, R^2Y = 0.816, Q^2 = 0.725.

Figure 23. OPLS-DA coefficients plot separating lung cancer and breast cancer samples - 1+1 orthogonal components, R^2X = 0.309, R^2Y = 0.816, Q^2 = 0.725. The coefficients plot indicates lipids elevated in lung cancer samples.

Figure 24. OPLS-DA coefficients plot separating lung cancer and breast cancer samples - 1+1 orthogonal components, R^2X = 0.309, R^2Y = 0.816, Q^2 = 0.725. The coefficients plot indicates lipids elevated in breast cancer samples.

Figure 25. A flow chart representing an embodiment of one of the methods disclosed herein. Cancer status can include the presence or absence of one or more cancer types.

DETAILED DESCRIPTION

[0025] Some embodiments of the invention include methods for detecting the presence or absence of one or more cancer types by determining the amount of lipids in as lipid set in a sample. The sample can be a bodily fluid (or treatment thereof) from an animal. In some instances, the sample (e.g., a bodily fluid extract) comprises a concentration of lipid microvesicles that is higher than normally found in a bodily fluid. The lipid amounts in the lipid set are analyzed using a predictive model to determine the presence or absence of one or more cancer types.

[0026] Lipids are designated according to the following notation XXX (YY:ZZ). XXX is the abbreviation for the lipid group (in many instances indicating the lipid headgroup) as provided, for example in Table 1. YY is the number of carbons in the acyl chain. ZZ is the number of double bonds in the acyl chains.

[0027] The term lipid, as used herein, is defined as a collection of one or more isomers. For example, PC (36:1) is a lipid and is the collection of one or more of the phosphatidylcholine isomers that have 36 carbons in the acyl chain and one double bond in either of the two acyl chains; these isomers have identical molecular weights. Although the term lipid can encompass the entire collection of isomers, the sample may, in fact, have only one isomer, several isomers, or any number of isomers less than the total number of all possible isomers in a collection. Accordingly, lipid can refer to one or more of the isomers that make up the entire collection of possible isomers.

[0028] The term lipid set is defined to include one or more lipids.

[0029] The term lipid amount (and similar phrases such as, amounts of lipids or amount of a lipid) is defined to encompass an absolute amount of a lipid (e.g., in mmoles) or a relative amount of a lipid (e.g., in % relative intensity).

[0030] Table 1 provides lipid name abbreviations used in the data; other abbreviations are provided in the text as needed.

Table 1

Abbreviation	Name
BMP	Bis(monoacylglycero)phosphates
CE	Cholesterol Esters
Cer	Ceramides
DAG	Diacylglycerols
DH-LTB4	Dihydroleukotriene b4
FA	Fatty Acids
GA2	Gangliosides A2
GM3	Gangliosides M3
HexCer	Hexose Ceramides
HexDHCer	Hexosyl dihydroceramide
LacCer	Lactosylceramide

Abbreviation	Name
LysoPA	Lysophosphatidic acid
LysoPC	Lysophosphatidylcholines
LysoPC-pmg	Lysophosphatidylcholines-plasmalogens
LysoPE	Lysophosphatidylethanolamines
LysoPE-pmg	Lysophosphatidylethanolamines-plasmalogens
LysoPS	Lysophosphatidylserines
MAG	Monoacylglycerols
PC	Phospahtidylcholines
PC-pmg	Phosphatidylcholines-plasmalogens
PE	Phosphatidylethanolamines
PE-pmg	Phosphatidylethanolamines-plasmalogens
PGA1	Prostaglandin A1
PGB1	Prostaglandin B1
SM	Sphingomyelins
Sphingosine	Sphingosine
TAG	Triacylglycerols
TH-12-keto-LTB4	Tetrahydro-12-keto-leukotriene b4

[0031] Bodily fluids can be any suitable bodily fluid for the determination of cancer and include but are not limited to vomit, cerumen (earwax), gastric juice, breast milk, mucus (e.g., nasal drainage and phlegm), saliva, sebum (skin oil), semen (including prostatic fluid), sweat, tears, vaginal secretion, blood serum, aqueous humor, vitreous humor, endolymph, perilymph, peritoneal fluid, pleural fluid, cerebrospinal fluid, blood, plasma, nipple aspirate fluid, urine, stool, bronchioalveolar lavage fluid, peripheral blood, sera, plasma, ascites, cerebrospinal fluid (CSF), sputum, bone marrow, synovial fluid, aqueous humor, amniotic fluid, Cowper's fluid or pre-ejaculatory fluid, female ejaculate, fecal matter, hair, cyst fluid, pleural and peritoneal fluid, pericardial fluid, lymph, chyme, chyle, bile, interstitial fluid, menses, pus, vaginal secretions, mucosal secretion, stool water, pancreatic juice, lavage fluids from sinus cavities, bronchopulmonary aspirates, or other lavage fluids.

[0032] The bodily fluid can originate from any animal tissue (e.g., mammalian tissues) including, but not limited to connective tissue, muscle tissue, nervous tissue, adipose tissue, endothelial tissue, or epithelial tissue. The tissue can be at least part of an organ or part of an organ system. Organs can include, but are not limited to heart, blood, blood vessels, salivary glands, esophagus, stomach, liver, gallbladder, pancreas, large intestines, small intestines, rectum, anus, colon, endocrine glands (e.g., hypothalamus, pituitary, pineal body, thyroid, parathyroids and adrenals), kidneys, ureters, bladder, urethraskin, hair, nails, lymph, lymph nodes, lymph vessels, leukocytes, tonsils, adenoids, thymus, spleen, muscles, brain, spinal cord, peripheral nerves, nerves, sex organs (e.g., ovaries, fallopian tubes, uterus, vagina, mammary glands (e.g., breasts), testes, vas deferens, seminal vesicles, prostate and penis), pharynx, larynx, trachea, bronchi, lungs, diaphragm, bones, cartilage, ligaments, or tendons. Organ systems can include, but are not limited to circulatory system, digestive system, endocrine system, excretory system, integumentary system, lymphatic system, muscular system, nervous system, reproductive system, respiratory system, or skeletal system.

[0033] Bodily fluids can be frozen in liquid nitrogen. Preparation of the removed bodily fluids can be performed in any suitable manner.

[0034] In some embodiments, the bodily fluid is the sample. In other embodiments, the bodily fluid is treated to provide the sample. Treatment can include any suitable method, including but not limited to extraction, centrifugation (e.g., ultracentrifugation), lyophilization, fractionation, separation (e.g., using column or gel chromatography), or evaporation. In some instances, this treatment can include one or more extractions with solutions comprising any suitable solvent or combinations of solvents, such as, but not limited to acetonitrile, water, chloroform, methanol, butylated hydroxytoluene, trichloroacetic acid, toluene, hexane, benzene, or combinations thereof. For instance, in some embodiments, fractions from blood are extracted with a mixture comprising methanol and butylated hydroxytoluene. In some instances, the sample (e.g., a bodily fluid extract or a lipid microvesicle fraction of blood plasma) comprises a concentration of lipid microvesicles that is higher than normally found in a bodily fluid.

[0035] The volume of the sample (e.g., the bodily fluid or treatment thereof) used for analyzing can be in the range of about 0.1 mL to about 20 mL, such as no more than about 20, about 15, about 10, about 9, about 8, about 7, about 6, about 5, about 4, about 3, about 2, about 1, or about 0.1 mL.

[0036] Broad classes of lipids that can be part of a lipid set include, but are not limited to, fatty acids (characterized by a carboxyl group and an acyl chain), Glycerolipids (characterized by the presence of a glycerol backbone with one - monoacylglycerols (MAG), two - diacylglycerols (DAG) or three - triacylglycerols (TAG) ester linked fatty acyl chains), glycerophospholipids (GPL) (characterized by a glyceryl backbone with two ester-linked acyl chains and a phosphate-linked polar headgroup - GPLs include phosphatidylcholines (PC), phosphatidylethanolamines (PE), phosphatidylserines (PS), phosphatidylglycerols (PG), phosphatidylinositols (PI), inositol, and

phosphatidic acids), Lysoglycerophospholipids (LGPL) (LGPLs are missing one of the acyl chains at the glycerol backbone, e.g., at the C2 position - LGPLs include include lysophospahtidylcholines (LysoPC), lysophosphatidylethanolamines (LysoPE), lysophosphatidylserines (LysoPS), lysophosphatidylglycerols (LysoPG), lysophosphatidylinositols (LysoPI), lysoinositol, and lysophosphatidic acids), sphingolipids (SPL) (characterized by a sphingosine base backbone with a trans double bond between C4 and C5 of an acyl chain linked to the amino group via an amide linkage), Bis(monoacylglycero)phosphate (BMP), Ceramides, Gangliosides, Sterols, Prenols, Saccharolipids, and Polyketides. In some instances, the lipid group is based on the acyl chain composition which can vary in any number of ways including the number of carbons in the acyl chain and the number of double bonds in the acyl chain.

[0037] In other embodiments, lipids in the lipid set can come from one or more classes of lipids, such as, BMP, CE, Cer, DAG, DH-LTB4, FA, GA2, GM3, HexCer, HexDHCer, LacCer, LysoPA, LysoPC, LysoPC-pmg, LysoPE, LysoPE-pmg, LysoPS, MAG, PC, PC-pmg, PE, PE-pmg, PGA1, PGB1, SM, Sphingosine, TAG, or TH-12-keto-LTB4. In still other embodiments, lipids in the lipid set can come from one or more classes of lipids, such as, FA, MAG, DAG, TAG, PC, PE, PS, PI, PG, PA, LysoPC, LysoPE, LysoPS, LysoPI, LysoPG, LysoPA, LysoPC, LysoPE, BMP, SM, Cer, Cer-P, HexCer, GA1, GA2, GD1, GD2, GM1, GM2, GM3, GT1, or CE.

[0038] In some embodiments, the lipid set used in the predictive model is limited to those that have a higher probability to be found in human lipid pools. In other embodiments, the lipid set excludes very short and very long acyl chains (e.g., less that 10 carbons and more than 26 carbons within a chain). In still other embodiments, the lipid set lipids (e.g., GPLs or LGPL) are limited to those containing an even number of carbons in the acyl chain. In other embodiments, the lipid set included one or more lipids listed in Table 2.

Table 2

Lipid Class	Lipid Group	Abbrev	Acyl Chain Range	Unsaturated sites (# double bonds)	Additional features or comments	Total # of structures considered
Fatty Acids	Fatty Acids	FA	10-26	0-6		79
Glycerolipids	Monoacylglycerols	MAG	10-26	0-6	Even # of carbons only	43
Glycerolipids	Diacylglycerols	DAG	22-46	0-12	Even # of carbons only	120
Glycerolipids	Triacylglycerols	TAG	44-66	0-18		316
Glycerophospholipids	Phosphatidylcholines	PC	28-44	0-12	Even # of carbons only	77
Glycerophospholipids	Phosphatidylethanolamines	PE	28-44	0-12	Even # of carbons only	77
Glycerophospholipids	Phosphatidylserines	PS	28-44	0-12	Even # of carbons only	77
Glycerophospholipids	Phosphatidylinositols	PI	28-44	0-12	Even # of carbons only	77
Glycerophospholipids	Phosphatidylglycerols	PG	28-44	0-12	Even # of carbons only	77
Glycerop hospholipids	Phosphatidic acid	PA	28-44	0-12	Even # of carbons only	77
Lysoglycerophospholipids	Lysophosphatidylcholines	LysoPC	10-26	0-6	Even # of carbons only	43
Lysoglycerophospholipids	Lysophosphatidylethanolamines	LysoPE	10-26	0-6	Even # of carbons only	43
Lysoglycerophospholipids	Lysophosphatidylserines	LysoPS	10-26	0-6	Even # of carbons only	43
Lysoglycerophospholipids	Lysophosphatidylinositols	LysoPI	10-26	0-6	Even # of carbons only	43
Lysoglycerophospholipids	Lysophosphatidylglycerols	LysoPG	10-26	0-6	Even # of carbons only	43

Lipid Class	Lipid Group	Abbrev	Acyl Chain Range	Unsaturated sites (# double bonds)	Additional features or comments	Total # of structures considered
Lysoglycerophospholipids	Lysophosphatidic acid	LysoPA	10-26	0-6	Even # of carbons only	43
Lysoglycerophospholipids	Lysophosphatidylcholines-pmg	LysoPC	10-26	0-6	Even # of carbons only	43
Lysoglycerophospholipids	Lysophosphatidylethanolamines-pmg	LysoPE	10-26	0-6	Even # of carbons only	43
Bis(monoacylglycero)phosphates		BMP	28-48	0-12		211
Sphingolipids	Sphingomyelins	SM	30-42	0-3		25
Sphingolipids	Ceramides	Cer	30-44	0-3		33
Sphingolipids	Ceramide phosphates	Cer-P	30-44	0-3		33
Sphingolipids	Hexose Ceramides	HexCer	30-44	0-3		33
Sphingolipids	Gangliosides A1	GA1	28-46	0-2		57
Sphingolipids	Gangliosides A2	GA2	28-46	0-2		57
Sphingolipids	Gangliosides D1	GD1	28-46	0-2		57
Sphingolipids	Gangliosides D2	GD2	28-46	0-2		57
Sphingolipids	Gangliosides M1	GM1	28-46	0-2		57
Sphingolipids	Gangliosides M2	GM2	28-46	0-2		57
Sphingolipids	Gangliosides M3	GM3	28-46	0-2		57
Sphingolipids	Gangliosides A1	GT1	28-46	0-2		57
Cholesterol Esters	Cholesterol Esters	CE	10-26	0-6		79

[0039] In some embodiments, the lipids in the lipid set can include one or more of BMP (30:1), BMP (32:1), BMP (34:1), BMP (35:4), BMP (36:3), BMP (37:1), BMP (37:7), BMP (38:1), BMP (38:2), BMP (38:4), BMP (39:1), BMP (39:4), BMP (40:1), BMP (40:2), BMP (40:3), BMP (40:4), BMP (40:7), BMP (42:10), BMP (42:2), BMP (42:5), BMP (44:8), CE (16:2), CE (18:2), CE (18:3), CE (18:4), CE (20:2), CE (20:4), CE (20:5), Cer (32:1), Cer (34:1), Cer (36:1), Cer (38:1), Cer (38:4), Cer (40:2), Cer (40:4), DAG (28:0), DAG (32:0), DAG (32:2), DAG (34:0), DAG (34:3), DAG (34:5), DAG (36:0), DAG (36:1), DAG (36:2), DAG (36:3), DAG (36:8), DAG (38:1), DAG (38:10), DAG (38:2), DAG (38:3), DAG (38:5), DAG (40:1), DAG (40:2), DAG (40:5), DH-LTB4 (20:3), FA (16:3), FA (19:1), GA2 (30:0), GA2 (33:2), GA2 (35:2), GA2 (37:2), GM3 (41:1), HexCer (32:1), HexDHCer (34:0), LacCer (30:0), LacCer (30:1), LacCer (32:2), LysoPA (16:2), LysoPA (16:3), LysoPA (18:1), LysoPA (22:0), LysoPA (22:1), LysoPC (16:0), LysoPC (18:0), LysoPC (18:1), LysoPC (18:4), LysoPC (20:4), LysoPC (20:5), LysoPC (26:6), LysoPC-pmg (12:0), LysoPC-pmg (18:3), LysoPC-pmg (24:4), LysoPC-pmg (26:0), LysoPE (10:1), LysoPE (16:2), LysoPE (18:2), LysoPE-pmg (18:4), LysoPS (24:1), MAG (18:0), MAG (20:3), MAG (24:2), PC (32:0), PC (32:1), PC (34:1), PC (34:1), PC (34:2), PC (34:3), PC (34:4), PC (34:6), PC (36:1), PC (36:2), PC (36:3), PC (36:4), PC (36:5), PC (36:6), PC (36:9), PC (38:2), PC (38:3), PC (38:4), PC (38:5), PC (38:6), PC (38:7), PC (38:8), PC (38:9), PC (40:5), PC (40:6), PC (40:7), PC (40:8), PC (40:9), PC (44:12), PC-pmg (30:1), PC-pmg (36:4), PC-pmg (38:5), PC-pmg (38:7), PC-pmg (40:11), PC-pmg (42:1), PE (34:7), PE (36:5), PE (36:7), PE (38:2), PE (38:3), PE (38:4), PE (38:5), PE (38:7), PE (40:4), PE (40:9), PE (42:12), PE (44:11), PE-pmg (28:2), PE-pmg (30:3), PE-pmg (34:6), PE-pmg (34:8), PE-pmg (36:5), PE-pmg (36:6), PE-pmg (40:7), PE-pmg (40:8), PE-pmg (42:10), PE-pmg (42:12), PE-pmg (42:4), PE-pmg (42:7), PE-pmg (42:8), PE-pmg (42:9), PE-pmg (44:10), PE-pmg (44:11), PE-pmg (44:12), PE-pmg (44:7), PE-pmg (44:8), PE-pmg (44:9), PGA1 (20:1), PGB1 (20:1), SM (34:1), SM (34:2), SM (36:1), SM (38:1), SM (40:1), SM (40:2), SM (42:1), SM (42:2), SM (42:3), Sphingosine (18:0), TAG (44:1), TAG (44:3), TAG (46:0), TAG (46:1), TAG (46:2), TAG (46:3), TAG (46:4), TAG (48:0), TAG (48:1), TAG (48:2), TAG (48:3), TAG (48:4), TAG (48:5), TAG (49:1), TAG (49:2), TAG (49:3), TAG (50:0), TAG (50:1), TAG (50:2), TAG (50:3), TAG (50:4), TAG (50:5), TAG (50:6), TAG (51:2), TAG (51:4), TAG (52:2), TAG (52:3), TAG (52:4), TAG (52:5), TAG (52:6), TAG (52:7), TAG (53:4), TAG (54:2), TAG (54:3), TAG (54:4), TAG (54:5), TAG (54:6), TAG (54:7), TAG (54:8), TAG (55:5), TAG (55:6), TAG (55:7), TAG (56:4), TAG (56:5), TAG (56:6), TAG (56:7), TAG (56:8), TAG (56:9), TAG (58:10), TAG (58:6), TAG (58:8), TAG (58:9), TAG (60:12), or TH-12-keto-LTB4(20:2).

[0040] In some embodiments (e.g., to determine lung cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:0), PE-pmg (42:9), FA (16:3), FA (19:1), CE (18:2), PE-pmg (44:11), BMP (30:1), PE-pmg (44:12), BMP (42:10), BMP (36:3), PC (34:6), BMP (40:3), TAG (50:2), BMP (39:1), DAG (38:3), BMP (37:1), PC-pmg (40:11), DAG (40:5), DAG (32:2), TAG (46:2), BMP (42:5), PE-pmg (42:8), PC (44:12), GA2 (35:2), TAG (50:1), CE (20:5), DAG (40:2), TAG (49:2), LysoPE (18:2), BMP (40:7), DAG (36:8), LysoPC (18:1), PE-pmg (36:5), PE-pmg (42:7), DH-LTB4 (20:3), PGA1 (20:1), PGB1 (20:1), BMP (38:4), BMP (35:4), BMP (44:8), TAG (46:1), TAG (44:1), LysoPC (18:4), DAG (36:0), DAG (38:2), LysoPC (20:4), DAG (38:1), LysoPC (26:6), DAG (36:2), DAG (34:5), TAG (49:1), TAG (56:7), DAG (38:5), Cer (40:2), BMP (40:4), GA2 (30:0), LysoPC-pmg (12:0), LysoPC-pmg (26:0), PC-pmg (30:1), LysoPC (20:5), PE-pmg (44:10), PE-pmg (34:8), PE-pmg (44:7), GM3 (41:1), BMP (37:7), PC (38:9), CE (20:4), SM (36:1), LysoPC-pmg (18:3), TAG (54:2), PE

(38:5), PC (34:4), PC (34:3), TAG (48:0), TAG (50:5), DAG (32:0), PC (36:3), LysoPA (18:1), TAG (48:3), TAG (50:4), TAG (54:3), LysoPA (16:3), PC (36:1), TAG (58:9), PE-pmg (36:6), TAG (54:7), TAG (56:5), SM (42:1), LysoPA (16:2), DAG (28:0), TAG (46:3), TAG (54:8), SM (42:2), PC (40:8), LysoPE (10:1), PE (44:11), TAG (56:9), PC (40:6), SM (40:1), PE (36:5), Cer (32:1), BMP (39:4), PE-pmg (34:6), DAG (34:3), TAG (54:4), TAG (54:6), TAG (52:6), PE (36:7), PC (38:4), DAG (36:3), PC (36:2), PC (38:6), Cer (40:4), TAG (52:4), MAG (24:2), TAG (54:5), PC (36:5), TAG (50:3), TAG (52:5), MAG (18:0), LysoPA (22:1), TAG (52:3), PC (36:4), PC (40:7), PC (34:2), PC (34:1), Cer (34:1), PC (38:7), Cer (36:1), Cer (38:4), PC (38:5), Cer (38:1), or TAG (44:3).

[0041] In some embodiments (e.g., to determine lung cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:0), PE-pmg (42:9), FA (16:3), FA (19:1), CE (18:2), Cer (36:1), Cer (38:4), PC (38:5), Cer (38:1), or TAG (44:3).

[0042] In some embodiments (e.g., to determine lung cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:0), PE-pmg (42:9), FA (16:3), FA (19:1), CE (18:2), PE-pmg (44:11), BMP (30:1), PE-pmg (44:12), BMP (42:10), BMP (36:3), PC (34:6), BMP (40:3), TAG (50:2), BMP (39:1), DAG (38:3), BMP (37:1), PC-pmg (40:11), DAG (40:5), DAG (32:2), TAG (46:2), BMP (42:5), PE-pmg (42:8), PC (44:12), GA2 (35:2), TAG (50:1), PE (36:7), PC (38:4), DAG (36:3), PC (36:2), PC (38:6), Cer (40:4), TAG (52:4), MAG (24:2), TAG (54:5), PC (36:5), TAG (50:3), TAG (52:5), MAG (18:0), LysoPA (22:1), TAG (52:3), PC (36:4), PC (40:7), PC (34:2), PC (34:1), Cer (34:1), PC (38:7), Cer (36:1), Cer (38:4), PC (38:5), Cer (38:1), or TAG (44:3).

[0043] In some embodiments (e.g., to determine lung cancer), the lipids in the lipid set include, but are not limited to TAG (44:3), PC (36:5), PC (38:5), Cer (38:4), PE-pmg (42:9), PC (38:7), LysoPA (22:0), Cer (38:1), Cer (34:1), Cer (36:1), PC (40:7), TAG (54:5), TAG (54:6), CE (18:2), PC (36:4), FA (16:3), PE-pmg (44:11), TAG (52:5), Cer (40:4), CE (20:5), PC (38:6), TAG (50:2), MAG (18:0), FA (19:1), TAG (52:2), LysoPA (22:1), MAG (24:2), TAG (54:7), TAG (50:3), TAG (50:1), DAG (36:3), PC (34:1), TAG (52:6), BMP (30:1), PE-pmg (44:12), CE (20:4), BMP (40:3), PE (44:11), PC (40:8), TAG (56:9), PE-pmg (34:6), PE (36:7), PE (36:5), TAG (56:7), TAG (56:8), DAG (34:3), TAG (56:6), BMP (42:10), TAG (52:3), BMP (39:4), BMP (36:3), TAG (54:3), TAG (56:5), TAG (54:8), PC (34:6), PC (40:6), DAG (36:0), LysoPE (10:1), DAG (40:5), Cer (32:1), TAG (50:5), TAG (50:4), PE-pmg (36:6), BMP (42:5), TAG (46:3), or PE (38:5).

[0044] In some embodiments (e.g., to determine lung cancer), the lipids in the lipid set include, but are not limited to TAG (44:3), PC (36:5), PC (38:5), Cer (38:4), PE-pmg (42:9), PC (38:7), LysoPA (22:0), Cer (38:1), Cer (34:1), or Cer (36:1).

[0045] In some embodiments (e.g., to determine breast cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:1), PE-pmg (42:9), CE (20:5), TAG (52:3), LysoPA (22:0), TAG (52:2), DAG (32:0), TAG (54:4), DAG (34:0), DAG (36:0), TAG (54:3), PE-pmg (44:11), TAG (44:3), BMP (30:1), TAG (52:4), BMP (40:3), PC (36:5), PC (36:9), PC (34:6), PE-pmg (44:12), BMP (42:10), BMP (36:3), PC-pmg (40:11), FA (16:3), DAG (38:3), TAG (54:2), BMP (42:5), HexDHCer (34:0), DAG (40:5), Cer (40:4), PC-pmg (30:1), PC (44:12), PE (38:5), PE (42:12), TAG (48:0), PE (36:5), PE-pmg (34:6), MAG (24:2), PE-pmg (36:6), TAG (56:4), TAG (49:3), CE (18:3), FA (19:1), DAG (38:5), TAG (50:0), BMP (38:4), TAG (46:3), TAG (51:4), BMP (35:4), PE-pmg (36:5), PE (44:11), DAG (38:2), TAG (48:3), CE (20:4), CE (18:4), LysoPC-pmg (18:3), BMP (44:8), LysoPC (20:4), TAG (60:12), LysoPC (18:4), PE-pmg (28:2), PE (40:4), PC-pmg (42:1), Sphingosine (18:0), LacCer (32:2), LysoPC (18:0), PE (38:3), MAG (20:3), SM (34:2), PC (40:5), SM (42:1), PE (38:7), LacCer (30:1), TAG (44:1), TAG (58:8), PC (40:9), CE (16:2), TAG (58:10), PE-pmg (44:10), SM (40:2), TAG (50:4), LysoPE-pmg (18:4), GA2 (37:2), PC-pmg (38:5), PC-pmg (36:4), PC (38:2), LacCer (30:0), GA2 (33:2), SM (42:3), PE (38:4), TAG (46:1), PC (32:1), BMP (42:2), LysoPC (16:0), SM (38:1), PE (38:2), TAG (50:3), TAG (58:9), PC (40:6), TAG (48:1), TAG (50:2), BMP (38:2), PE-pmg (40:7), PE-pmg (42:10), LysoPC-pmg (24:4), PC (34:3), PE-pmg (44:9), SM (36:1), PE-pmg (42:12), TAG (48:2), BMP (40:1), PE-pmg (44:8), DAG (36:1), TAG (56:7), LysoPC (26:6), PE-pmg (40:8), CE (18:2), PC (32:0), TAG (54:8), Cer (36:1), GA2 (35:2), TAG (56:6), TAG (56:9), DAG (36:8), PE-pmg (42:7), BMP (40:2), PC (38:3), PC (40:7), DAG (32:2), SM (42:2), SM (40:1), MAG (18:0), TAG (56:8), PE-pmg (42:8), TAG (52:5), DAG (40:1), PC (36:1), SM (34:1), DAG (38:1), TAG (54:7), Cer (38:1), BMP (39:1), BMP (37:1), Cer (34:1), TAG (54:6), PC (38:4), TAG (54:5), PC (36:3), PC (36:4), PC (36:2), PC (34:2), or PC (34:1).

[0046] In some embodiments (e.g., to determine breast cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:1), PE-pmg (42:9), CE (20:5), TAG (52:3), LysoPA (22:0), PC (36:3), PC (36:4), PC (36:2), PC (34:2), or PC (34:1).

[0047] In some embodiments (e.g., to determine breast cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:1), PE-pmg (42:9), CE (20:5), TAG (52:3), LysoPA (22:0), TAG (52:2), DAG (32:0), TAG (54:4), DAG (34:0), DAG (36:0), TAG (54:3), PE-pmg (44:11), TAG (44:3), BMP (30:1), TAG (52:4), BMP (40:3), PC (36:5), PC (36:9), PC (34:6), PE-pmg (44:12), BMP (42:10), BMP (36:3), PC-pmg (40:11), FA (16:3), DAG (38:3), PC (40:7), DAG (32:2), SM (42:2), SM (40:1), MAG (18:0), TAG (56:8), PE-pmg (42:8), TAG (52:5), DAG (40:1), PC (36:1), SM (34:1), DAG (38:1), TAG (54:7), Cer (38:1), BMP (39:1), BMP (37:1), Cer (34:1), TAG (54:6), PC (38:4), TAG (54:5), PC (36:3), PC (36:4), PC (36:2), PC (34:2), or PC (34:1).

[0048] In some embodiments (e.g., to determine breast cancer), the lipids in the lipid set include, but are not limited to PC (34:2), PC (34:1), PC (36:2), PC (36:4), PC (36:3), PC (38:4), LysoPA (22:1), PE-pmg (42:9), LysoPA (22:0), CE (20:5), Cer (36:1), CE (18:2), DAG (34:0), SM (34:1), DAG (32:0), PE-pmg (40:8), PC (38:3), DAG (36:0), PC (36:1), TAG (54:5), TAG (54:6), PE-pmg (44:11), PE-pmg (42:8), TAG (52:2), SM (42:2), PC (38:6), TAG (54:7), PC (40:6), PC (40:7), LysoPC (16:0), FA (16:3), TAG (52:5), TAG (44:3), BMP (38:2), BMP (30:1), SM (40:1), PE-pmg (42:10), BMP (40:2), PE-pmg (40:7), SM (36:1), PE (38:2), PC (34:3), PC (36:5), PC (32:0), PC (32:1), BMP (37:1), BMP (40:3), PC (36:9), SM (42:3), PC-pmg (36:4), PC-pmg (38:5), PC (40:9), TAG (54:3), PE-pmg (44:12), BMP (36:3), FA (19:1), BMP (39:1), TAG (50:3), BMP (42:10), PC (34:6), GA2 (35:2), TAG (58:9), PE-pmg (42:7), or LysoPC (18:0).

[0049] In some embodiments (e.g., to determine breast cancer), the lipids in the lipid set include, but are not limited to PC (34:2), PC

(34:1), PC (36:2), PC (36:4), PC (36:3), PC (38:4), LysoPA (22:1), PE-pmg (42:9), LysoPA (22:0), or CE (20:5).

[0050] In some embodiments (e.g., to determine breast cancer and lung cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:1), PC (36:5), TAG (52:3), PC (38:5), CE (20:5), TAG (44:3), PC (38:7), TAG (52:2), TAG (54:4), TAG (52:4), Cer (38:4), DAG (32:0), MAG (24:2), DAG (34:0), TAG (54:3), PC (38:6), Cer (40:4), TAG (52:6), PE-pmg (34:6), PE (36:5), DAG (36:0), Cer (36:1), CE (20:4), PC (36:9), PE-pmg (36:6), PE (38:5), PE (36:7), TAG (50:5), TAG (46:3), TAG (48:3), DAG (36:3), TAG (48:0), PC (40:7), CE (18:3), LysoPE (10:1), TAG (56:5), TAG (52:7), PE (44:11), Cer (38:1), TAG (54:2), LysoPA (16:2), TAG (52:5), TAG (48:4), LysoPA (16:3), DAG (28:0), LysoPC-pmg (18:3), HexDHCer (34:0), Cer (32:1), DAG (34:3), TAG (50:3), BMP (39:4), LysoPA (18:1), TAG (49:3), DAG (38:3), MAG (18:0), TAG (56:4), PC (40:8), PE-pmg (42:4), TAG (50:0), TAG (48:5), TAG (50:6), DAG (38:10), BMP (34:1), PC (36:6), BMP (37:7), TAG (55:6), PC (34:4), BMP (32:1), PC (38:8), PC-pmg (38:7), TAG (46:0), TAG (46:4), PC (38:9), TAG (53:4), TAG (55:5), TAG (55:7), TAG (58:6), TAG (58:9), BMP (38:1), TH-12-keto-LTB4(20:2), PC (34:6), HexCer (32:1), LysoPE (16:2), PE (34:7), LysoPS (24:1), PC (40:5), LysoPC (18:0), TAG (51:2), PE (38:3), Sphingosine (18:0), PC-pmg (38:5), PC-pmg (36:4), BMP (40:4), LacCer (30:1), SM (40:2), BMP (30:1), PC-pmg (42:1), PE-pmg (28:2), PE-pmg (30:3), PE (38:2), CE (20:2), DAG (34:5), BMP (42:2), Cer (34:1), PC (32:1), PE-pmg (44:12), GA2 (37:2), GA2 (33:2), LysoPA (22:0), DAG (40:2), TAG (56:7), TAG (54:5), LysoPE (18:2), LysoPE-pmg (18:4), CE (16:2), TAG (56:6), BMP (40:7), PE-pmg (40:7), BMP (38:2), MAG (20:3), TAG (49:2), PE (38:4), TAG (49:1), PE-pmg (42:10), DAG (36:2), BMP (42:10), TAG (44:1), LysoPC (16:0), PC (38:2), SM (42:2), PE-pmg (44:9), BMP (40:1), PE-pmg (44:8), PE-pmg (44:11), TAG (46:2), LysoPC-pmg (24:4), SM (40:1), PE-pmg (42:9), DAG (40:5), PE (40:9), PE-pmg (40:8), PE-pmg (42:12), PC (38:3), TAG (46:1), BMP (40:2), PC (32:0), TAG (56:8), PE-pmg (42:7), DAG (36:1), GA2 (35:2), LysoPC (26:6), TAG (54:6), TAG (48:1), TAG (54:7), PE-pmg (42:8), DAG (36:8), PC (36:1), SM (34:1), TAG (48:2), DAG (40:1), DAG (32:2), TAG (50:1), FA (16:3), PC (36:4), DAG (38:1), PC (38:4), FA (19:1), PC (36:3), PC (36:2), BMP (37:1), TAG (50:2), BMP (39:1), PC (34:2), CE (18:2), or PC (34:1).

[0051] In some embodiments (e.g., to determine breast cancer and lung cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:1), PC (36:5), TAG (52:3), PC (38:5), CE (20:5), TAG (50:2), BMP (39:1), PC (34:2), CE (18:2), or PC (34:1).

[0052] In some embodiments (e.g., to determine breast cancer and lung cancer), the lipids in the lipid set include, but are not limited to LysoPA (22:1), PC (36:5), TAG (52:3), PC (38:5), CE (20:5), TAG (44:3), PC (38:7), TAG (52:2), TAG (54:4), TAG (52:4), Cer (38:4), DAG (32:0), MAG (24:2), DAG (34:0), TAG (54:3), PC (38:6), Cer (40:4), TAG (52:6), PE-pmg (34:6), PE (36:5), DAG (36:0), Cer (36:1), CE (20:4), PC (36:9), PE-pmg (36:6), LysoPC (26:6), TAG (54:6), TAG (48:1), TAG (54:7), PE-pmg (42:8), DAG (36:8), PC (36:1), SM (34:1), TAG (48:2), DAG (40:1), DAG (32:2), TAG (50:1), FA (16:3), PC (36:4), DAG (38:1), PC (38:4), FA (19:1), PC (36:3), PC (36:2), BMP (37:1), TAG (50:2), BMP (39:1), PC (34:2), CE (18:2), or PC (34:1).

[0053] In some embodiments (e.g., to determine breast cancer and lung cancer), the lipids in the lipid set include, but are not limited to PC (34:2), PC (36:2), TAG (44:3), CE (18:2), PC (34:1), LysoPA (22:1), PC (36:5), Cer (36:1), CE (20:5), PC (36:3), PC (38:4), PC (36:4), Cer (38:4), PC (38:5), PC (38:7), Cer (38:1), TAG (50:2), Cer (34:1), SM (34:1), Cer (40:4), MAG (18:0), MAG (24:2), PC (38:3), PE-pmg (40:8), PE-pmg (42:8), TAG (50:1), DAG (32:0), PC (36:1), DAG (34:0), LysoPC (16:0), PE-pmg (34:6), DAG (36:3), PC (36:9), PE (36:5), TAG (52:6), FA (19:1), PE-pmg (44:11), BMP (38:2), PE (44:11), TAG (48:2), SM (42:2), BMP (40:2), PE-pmg (42:10), PE (36:7), PE-pmg (40:7), BMP (39:1), BMP (37:1), PE-pmg (36:6), PE (38:5), PC (32:0), PE (38:2), GA2 (35:2), DAG (34:3), PE-pmg (44:12), MAG (16:0), PC (32:1), LysoPE (10:1), SM (36:1), BMP (39:4), TAG (56:7), or PE-pmg (42:9).

[0054] In some embodiments (e.g., to determine breast cancer and lung cancer), the lipids in the lipid set include, but are not limited to PC (34:2), PC (36:2), TAG (44:3), CE (18:2), PC (34:1), LysoPA (22:1), PC (36:5), Cer (36:1), CE (20:5), or PC (36:3).

[0055] In some embodiments, the number of lipids in the lipid set can include at least 10, at least 50, at least 100, at least 150, at least 200, at least 500, or at least 1000 lipids. In some embodiments, the number of lipids in the lipid set can include no more than 200, no more than 500, no more than 1,000, no more than 5,000, no more than 10,000, or no more than 100,000 lipids.

[0056] Animals include but are not limited to primates (e.g., humans), canine, equine, bovine, porcine, ovine, avian, or mammalian. Animals include those as pets or in zoos and include domesticated swine and horses (including race horses). In addition, any animal connected to commercial activities are also included such as those animals connected to agriculture and aquaculture and other activities in which disease monitoring, diagnosis, and therapy selection are routine practice in husbandry for economic productivity and/or safety of the food chain. In some embodiments, the animal is a human, dog, cat, horse, cow, pig, sheep, chicken, turkey, mouse, or rat.

[0057] The cancer types (including cancerous tumors) can include but are not limited to carcinomas, sarcomas, hematologic cancers, neurological malignancies, thyroid cancer, neuroblastoma, melanoma, renal cell carcinoma, hepatocellular carcinoma, breast cancer, colon cancer, lung cancer, pancreatic cancer, brain cancer, prostate cancer, chronic lymphocytic leukemia, acute lymphoblastic leukemia, rhabdomyosarcoma, Glioblastoma multiforme, meningioma, bladder cancer, gastric cancer, Glioma, oral cancer, nasopharyngeal carcinoma, kidney cancer, rectal cancer, lymph node cancer, bone marrow cancer, stomach cancer, uterine cancer, leukemia, basal cell carcinoma, cancers related to epithelial cells, or cancers that can alter the regulation or activity of Pyruvate Carboxylase. Cancerous tumors include, for example, tumors associated with any of the above mentioned cancers.

[0058] In some embodiments, determining the presence or absence of one or more cancer types includes determining the presence or absence of each cancer type.

[0059] The amount of a lipid can be determined using any suitable technique, including, for example, any of the mass spectrometry

methods described herein.

[0060] Using a mass spectrometry system, the mass spectrometry spectrum of the sample is obtained. The mass spectrometry system can comprise the usual components of a mass spectrometer (e.g., ionization source, ion detector, mass analyzer, vacuum chamber, and pumping system) and other components, including but not limited to separation systems, such as interfaced chromatography systems. The mass spectrometer can be any suitable mass spectrometer for determining a lipid amount. The mass analyzer system can include any suitable system including but not limited to, time of flight analyzer, quadrupole analyzer, magnetic sector, Orbitrap, linear ion trap, or fourier transform ion cyclotron resonance (FTICR). In some instances, the mass analyzer system (e.g., FTICR) has sufficient resolution to determine lipid identity without further experimental means. The ion source can include, but is not limited to electron impact ionization, electrospray, chemical ionization, photoionization, atmospheric pressure chemical ionization, collisional ionization, natural ionization, thermal ionization, fast atom bombardment ionization, particle-beam ionization, or matrix-assisted laser desorption ionization (MALDI). In some instances, electrospray can be a non-ionizing ion source. Interfaced chromatography systems can include any suitable chromatography system, including but not limited to gas chromatography (GC), liquid chromatography (LC), or ion mobility (which can be combined with LC or GC methods). In some instances, direct infusion can be used. In some instances the mass spectrometry system is GC/MS or LC/MS.

[0061] In some instances, once the MS spectra are obtained, the spectra can be analyzed to determine the identity and amount (e.g., the presence) of lipids in the sample.

[0062] For MS spectra, analysis can include any suitable analysis to determine the identity and/or amount of a lipid including analysis of one or more characteristics, which include but are not limited to comparison of masses to known masses, chromatographic retention times (e.g., for GC/MS or LC/MS), and mass fragmentation patterns. In some instances, the analysis can include a comparison of characteristics with that of a database (e.g., a database of standards). In some instances, PREMISE (Lane, A.N., T.W.-M. Fan, X. Xie, H.N. Moseley, and R.M. Higashi, Stable isotope analysis of lipid biosynthesis by high resolution mass spectrometry and NMR Anal. Chim. Acta, 2009. 651: p. 201-208.) can be used to identify lipids. The lipid amount (e.g., the relative amount) can be determined by any suitable method, including but not limited to the response function of the ion detector, by reference to spiked standards, or by isotope dilution.

[0063] In some embodiments, before the data are input into the predictive model, the data can be pre-processed. Pre-processing methods can include one or more of any suitable method such as normalization methods or scaling methods. In some embodiments, scaling methods can include but are not limited to centering, unit variance, unit variance without centering, Pareto, and Pareto without centering.

[0064] A predictive model can comprise any suitable model for determining the presence or absence of one or more cancer types. For example, the predictive model can comprise one or more dimension-reduction methods. In some embodiments, the predictive model comprises one or more of clustering methods (e.g, K-means clustering and K-nearest neighbor clustering), machine learning methods (e.g., artificial neural networks (ANN) and support vector machines (SVM)), principal component analysis (PCA), soft independent modeling of class analogy (SIMCA), partial least squares (PLS) regression, orthogonal least squares (OPLS) regression, partial least squares discriminant analysis (PLS-DA), or orthogonal partial least squares discriminant analysis (OPLS-DA). These techniques may, if desired, include or be supplemented with one or more suitable methods including mean centering, median centering, Pareto scaling, unit variance scaling, orthogonal signal correction, integration, differentiation, cross validation, and receiver operating characteristic (ROC) curves. In some embodiments, the predictive model can be developed using a set of training data, where the training data is designed to produce a set of applicable parameters and coefficients. In some embodiments, the set of parameters and coefficients can be used to determine if an animal has cancer and in some instances the type of cancer. The training data can include negative control data (e.g., when no cancer is present in the animal) and positive control data (where one or more cancer types are present in the animal). The training data set can be used to establish a predictive model that can determine two or more cancer types.

[0065] Figure 25 shows some embodiments of the method. It illustrates that, in some instances, once a predictive model has been established using a training data set, determination of the presence of one or more cancer types can be made from the predictive model without any additional training.

[0066] The methods of the present invention can further comprise the determination of the protein expression, gene expression, or both of proteins or their genes. Any suitable protein (or its gene) expression can be determined, including but not limited to pyruvate carboxylase, succinyl CoA synthetase, phosphoenolpyruvate carboxykinase, transketolase, transaldolase, pyruvate dehydrogenase, a dehydrogenase, glutaminase, isocitrate dehydrogenase, α-ketoglutarate dehydrogenase, mitochondrial malate dehydrogenase, succinate dehydrogenase, fumarate hydratase, hexokinase II, glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate kinase 1, lactate dehydrogenase 5, phosphofructokinase 1 and 2, glutathione peroxidase, or glutathione-S-transferase, or proteins associated with metabolic pathways such as, but are not limited to Krebs cycle (also known as the citric acid cycle), glycolysis, pentose phosphate pathway (oxidative and non-oxidative), gluconeogenesis, lipid biosynthesis, amino acid syntheses (e.g., synthesis of non-essential amino acids), catabolic pathways, urea cycle, Cori cycle or glutamate/glutamine cycle. Protein expression can be determined by any suitable technique including, but not limited to techniques comprising gel electrophoresis techniques (e.g., Western blotting), chromatographic techniques, antibody-based techniques, centrifugation techniques, or combinations thereof. Gene expression can be determined by any suitable technique including, but not limited to techniques comprising PCR based techniques (e.g., real-time PCR), gel electrophoresis techniques, chromatographic techniques, antibody-based techniques, centrifugation techniques, or combinations thereof. Methods for measuring gene expression can comprise measuring amounts of cDNA made from tissue-isolated RNA.

EXAMPLES

[0067] Plasma preparation: Blood from humans diagnosed with breast cancer, diagnosed with the lung cancer non-small-cell lung carcinoma (NSCLC), and healthy (cancer-free) humans (also referred to as control or normal) was collected into K-EDTA containing vacutainer tubes (purple top) for anti-coagulation and immediately placed on ice and centrifuged at 3500xg for 15 min at 4°C. The supernatant (plasma) was aliquoted before flash freezing in liquid N_2 and kept at -80°C until fraction preparation.

[0068] Fraction preparation: Plasma was thawed and 0.8 ml transferred to a 1 ml polyallomer ultracentrifuge tubes using cold PBS to adjust for exact volume (entire volume of ultracentrifuge tubes must be filled to within 5 mm of the top to avoid collapse upon centrifugation). The rotor SWTi55 with buckets was precooled to 4°C. Ultracentrifuge tubes plus cap in bucket was weighed for adjusting all sample masses to within 10 mg of variation using PBS. Samples were then centrifuged in SWTi55 rotor at 70,000xg (27,172 rpm) for 1 h at 4°C. The supernatant was centrifuged again in SWTi55 at 100,000xg (32,477 rpm) for 1 h at 4°C to pellet the lipid microvesicle fraction. The pellet from the first centrifugation (microvesicle fraction) and the lipid microvesicle fraction pellet were washed in cold PBS by resuspension and centrifuged in SWTi55 at 100,000xg (32,477 rpm) for 1 h at 4°C. The supernatant was removed and both tubes were inverted on paper towel to drain excess PBS. The pellets were resuspended in 2x100 µl 18 MOhm water for transfer to 2 ml microfuge tubes and lyophilized overnight. The lyophilized pellets were kept at -80°C until lipid extraction.

[0069] Lipid Extraction: The lipid microvesicle fraction pellet was extracted in 0.5 ml methanol (mass spectrometry-grade)+1mM butylated hydroxytoluene by homogenization with 3x3 mm glass beads in a mixer mill (e.g. MM200, Retsch) for 1 minute at 30 Hz. The homogenate was then shaken in a rocker for 30 min before centrifugation at 14,000 rpm for 30 min at 4°C in a microcentrifuge. The supernatant was transferred into a 1.5 ml screw-cap glass vial with Teflon-faced silicone septum and the extract weight is recorded. The lipid extract was stored at -80°C until FT-ICR-MS analysis.

[0070] FT-ICR-MS analysis: Samples were diluted 1:5 in methanol+1 mM BHT+ 1ng/nl reserpine before analysis on a hybrid linear ion trap-FT-ICR mass spectrometer (ThermoFisher LTQ FT, Thermo Electron, Bremen, Germany), as described previously (Lane, A.N., T.W.-M. Fan, X. Xie, H.N. Moseley, and R.M. Higashi, Stable isotope analysis of lipid biosynthesis by high resolution mass spectrometry and NMR Anal. Chim. Acta, 2009. 651: p. 201-208). The FT-ICR-MS was equipped with a TriVersa NanoMate ion source (Advion BioSciences, Ithaca, NY) with an "A" electrospray chip (nozzle inner diameter 5.5µm). The TriVersa NanoMate was operated by applying 2.0 kV with 0.1 psi head pressure in positive ion mode and 1.5 kV and 0.5 psi in the negative mode. MS runs were recorded over a mass range from 150 to 1600 Da. Initially, low resolution MS scans were acquired for 1 min to ensure the stability of ionization, after which high mass accuracy data were collected using the FT-ICR analyzer where MS scans were acquired for 8.5 min and at the target mass resolution of 200,000 at 400 m/z. The AGC (automatic gain control) maximum ion time was set to 500ms (but typically utilized <10 ms) and five "µscans" were acquired for each saved spectrum; thus the cycle time for each transformed and saved spectrum was about 10 s. The LTQ-FT was tuned and calibrated according to the manufacturer's default standard recommendations, which achieved better than 1ppm mass accuracy. FT-ICR mass spectra were exported as exact mass lists into a spreadsheet file using QualBrowser 2.0 (Thermo Electron), typically exporting all of the observed peaks. Lipid species were assigned based on their accurate mass, by first applying a small (typically <0.0005) linear correction based on the observed mass of the internal standard (reserpine), then using an in-house software tool PREMISE (PRecaculated Exact Mass Isotopologue Search Engine) (Lane, A.N., T.W.-M. Fan, X. Xie, H.N. Moseley, and R.M. Higashi, Stable isotope analysis of lipid biosynthesis by high resolution mass spectrometry and NMR Anal. Chim. Acta, 2009. 651: p. 201-208) which was manually validated. PREMISE is a routine that matches observed with theoretical m/z values, subject to a selectable window that was 0.0014 Da or smaller. For lipids, the exact masses of a large number (>3500) of possible GPLs and their ion forms (principally H+ and Na+ - positive mode and -H+ - negative mode) were pre-calculated into a spreadsheet lookup table. The overall method was sufficient to assign a GPL to a particular total acyl chain length, degree of saturation, and headgroup identity.

[0071] Chemometrics Analysis: The normalized FT-ICR-MS data were imported into SimcaP (version 11.5, Umetrics, Umeå, Sweden). The data were mean centered and scaled to Pareto variance ($1/\sqrt{sd}$). Principal component analysis (PCA) was then performed on the resulting data. This was done to find outlier samples or variables. No samples were determined to be outliers and one variable was. The variable Sphingosine (18:1) was excluded from further analysis. The PCA scores and loadings plots are shown in Figures 14 and 15.

[0072] Orthogonal partial least squares discriminant analysis (OPLS-DA) models were created from three subsets of data: normal (i.e., cancer-free) and lung cancer, normal (i.e., cancer-free) and breast cancer, and lung cancer and breast cancer. This analysis determined a dimension in multivariate space which maximizes group separation (for example, the control group and the lung cancer group) while removing one dimension orthogonal to the mentioned dimension which has maximum sample variance unrelated to class separation. This analysis determined which of the many variables are most different between the classes of data.

[0073] OPLS-DA showed good separation of the total lipid profiles from the three classes of plasma. Some of the lipids were essentially the same in each source of lipid microvesicle fraction (the common components). The major classes that gave rise to the discrimination were obtained from the loading and coefficient plots, which are visualized in the 3D plots shown in Figures 1-13. The OPLS-DA scores and coefficients plots are provided in Figures 16-24.

[0074] The intensities of the lipids species were normalized to the total lipid response to generate "mol fractions." Different lipid classes varied in their abundances, and within a class some acyl chain length and number of double bonds also vary substantially, which was part

of the classification. Most of the variance arose from intersubject variability rather than analytical variance. The difference in abundance between classes for discrimination was >4 fold with a coefficient of variation within a class of up to 50%. For example, the PC (36:3) showed mean and sd of 1.38±0.34 (BrCA) versus 0.23±0.1 (healthy) versus 0.19±0.28 (NSCLC). This single instance provided statistical separation with p values of <0.0001 (BrCA versus healthy), <0.0001 (BrCa versus NSCLC). NSCLC versus healthy did not reach statistical significance. However, other lipids gave high statistical separation between NSCLC and healthy. Therefore, several classes together were used to discriminate among healthy individuals and those with cancer. Optimal segregation was achieved using sets of lipids where at least two of the subject classes differed with p values better than 0.01, and a minimum of ten such lipid classes were used for reliable discrimination

REFERENCES CITED IN THE DESCRIPTION

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Patentkrav

1. Fremgangsmåde til at bestemme tilstedeværelse eller fravær af mindst en cancertype i et dyr, hvilken fremgangsmåde omfatter:

- at bestemme lipidmængder af lipider i et sæt af lipider i en prøve fra dyret, og
- at bestemme tilstedeværelse eller fravær af mindst en cancertype i dyret med en prædiktiv model;

hvor

- lipidmængderne af lipider i lipidsættet omfatter et input af den prædiktive model,
- prøven omfatter en kropsvæske eller behandling deraf,
- den mindst ene cancertype er valgt fra gruppen, der består af carcinomer, sarcomer, hæmatologiske cancerformer, neurologiske maligniteter, skjoldbruskcancer, neuroblastom, melanom, nyrecellecarcinom, hepatocellulært carcinom, brystcancer, tyktarmscancer, lungecancer, cancer i bugspytkirtlen, hjernecancer, prostatacancer, kronisk lymfocytisk leukæmi, akut lymfoblastisk leukæmi, rhabdomyosarcoma, glioblastom multiforme, meningiom, blærecancer, gastrisk cancer, gliom, oral cancer, nasopharyngeal carcinoma, nyrecancer, rektal cancer, lymfeknudecancer, knoglemarvscancer, mavecancer, livmodercancer, leukæmi, basalcellecarcinom, cancer relateret til epithelceller, cancer, som kan ændre reguleringen eller aktiviteten af pyruvatcarboxylase og tumorer associeret med en hvilken som helst af de førnævnte cancertyper;
- lipidsættet omfatter et lipid fra klassen BMP, fortrinsvis BMP (30: 1), BMP (32: 1), BMP (34: 1), BMP (35: 4), BMP (36: 3), BMP (37: 1), BMP (37: 7), BMP (38: 1), BMP (38: 2), BMP (38: 4), BMP (39: 1), BMP (39: 4), BMP 40: 1), BMP (40: 2), BMP (40: 3), BMP (40: 4), BMP (40: 7), BMP (42:10), BMP (42: 2), BMP: 5) eller BMP (44: 8) og
- den prædiktive model omfatter en eller flere af følgende: dimensionsreducerende fremgangsmåder, klyngefremgangsmåder, maskinindlæringsfremgangsmåder, principalkomponentanalyse, blød uafhængig modellering af klasseanalogi, partielle mindste kvadraters regression, ortogonale mindste kvadraters regression, partielle mindste kvadraters diskriminantanalyse, ortogonale partielle mindste kvadraters

diskriminantanalyse, gennemsnitlig centrering, mediancentrering, Pareto-skalering, enhedsvarianskalering, ortogonal signalkorrektion, integration, differentiering, krydsvalidering eller modtageroperationskarakteristiske kurver.

2. Fremgangsmåden ifølge krav 1, hvor kropsvæsken er valgt fra gruppen, der består plasmaopkastning, cerumen, mavesaft, modermælk, slim, spyt, talg, sæd, sved, tårer, vaginal sekretion, blodserum, vandig legemsvæske, glaslegemevæske, endolymfe, perilymfe, peritonealvæske, lungehindevæske, cerebrospinalvæske, blod, plasma, brystvorte-aspiratvæske, urin, afføring og bronchoalveolær skyllevæske.

3. Fremgangsmåde ifølge krav 1 eller 2, hvor prøven omfatter en lipidmikrovesikelfraktion.

4. Fremgangsmåde ifølge krav 1, 2 eller 3, hvor lipidsættet omfatter mindst 10, mindst 50, mindst 100, mindst 200 eller ikke mere end 100.000 lipider.

5. Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor lipidsættet yderligere omfatter et eller flere lipider, der er udvalgt fra den ene eller de nævnte flere klasser af lipider, som er valgt fra gruppen, der består af CE, Cer, DAG, DH-LTB4, FA, GA2, GM3, HexCer, HexDHCer, LacCer, LysoPA, LysoPC, LysoPC-pmg, LysoPE, LysoPE-pmg, LysoPS, MAG, PC, PC-pmg, PE, PE-pmg, PGA1, PGB1, SM, Sphingosin, TAG og TH-12-keto -LTB4.

6. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor lipidsættet yderligere omfatter et eller flere lipider, der er udvalgt fra den ene eller de nævnte flere klasser af lipider, som er valgt fra gruppen, der består af FA, MAG, DAG, TAG, PI, PE, PS, PI LysoPC, LysoPI, LysoPD, LysoPi, LysoPP, LysoPa, LysoPC, LysoPE, SM, Cer, Cer-P, HexCer, GA1, GA2, GD1, GD2, GM1, GM2, GM3, GT1 og CE.

7. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor et eller flere lipider i lipidsættet er yderligere valgt fra gruppen bestående af CE (16: 2),

CE (18: 2), CE (18: 3), CE 18: 4), CE (20: 2), CE (20: 4), CE (20: 5), Cer (32: 1), Cer (34: 1), Cer (36: 1), Cer (38: 1), Cer (38: 4), Cer (40; 2), Cer (40: 4), DAG (28: 0), DAG (32: 0), DAG (32: 2), DAG (34: 0), DAG (34: 3), DAG (34: 5), DAG (36: 0), DAG (36: 1), DAG (36: 2), DAG (36: 3), DAG (36: 8), DAG (38: 1), DAG (38: 10), DAG (38: 2), DAG (38: 3), DAG (38: 5), DAG (40: 1), DAG (40: 2) , DAG (40: 5), DH-LTB4 (20: 3), FA (16: 3), FA (19: 1), GA2 (30: 0), GA2 (33: 2), GA2 (35: 2), GA2 (37: 2), GM3 (41: 1), HexCer (32: 1), HexDHCer (34: 0), LacCer (30: 0), LacCer (30: 1), LacCer (32: 2) LysoPA (16: 2), LysoPA (16: 3), LysoPA (18: 1), LysoPA (22: 0), LysoPA (22: 1), LysoPC (16: 0), LysoPC (18: 0) LysoPC (18: 1), LysoPC (18: 4), LysoPC (20: 4), LysoPC (20: 5), LysoPC (26: 6), LysoPC-pmg (12: 0), LysoPC-pmg (18:3), LysoPC-pmg (24: 4), LysoPC-pmg (26: 0), LysoPE (10: 1), LysoPE (16: 2), LysoPE (18: 2), Lyso PE-pmg (18: 4), LysoPS (24: 1), MAG (18: 0), MAG (20: 3), MAG (24: 2), PC (32: 0), PC (32: 1) , PC (34: 1), PC (34: 2), PC (34: 3), PC (34: 4), PC (34: 6), PC (36: 1), PC (36: 2) PC (36: 3), PC (36: 4), PC (36: 5), PC (36: 6), PC (36: 9), PC(38:2), PC (38:3), PC (38: 4), PC (38: 5), PC (38: 6), PC (38: 7), PC (38: 8), PC (38: 9), PC (40: 5), PC (40: 6), PC (40;7), PC 40: 8), PC (40: 9), PC (44:12), PC-pmg (30: 1), PC-pmg (36: 4) , PC-pmg (38: 5), PC-pmg (38: 7), PC-pmg (40:11), PC-pmg (42: 1), PE (34: 7), PE (36: 5), PE (36: 7), PE (38: 2), PE (38: 3), PE (38: 4), PE (38: 5), PE (38: 7), PE (40: 4), PE (40: 9), PE (42:12), PE (44:11), PE-pmg (28: 2), PE-pmg (30: 3), PE-pmg (34: 6), PE- pmg (34: 8), PE-pmg (36: 5), PE-pmg (36: 6), PE-pmg (40: 7), PE-pmg (40: 8), PE-pmg (42: 10), PE-pmg (42:12), PE-pmg (42: 4), PE-pmg (42: 7), PE-pmg (42: 8), PE-pmg (42: 9), PE-pmg (44:10), PE-pmg (44:11), PE-pmg (44:12), PE-pmg (44: 7), PE-pmg (44: 8), PE-pmg (44: 9) , PGA1 (20: 1), PGB1 (20: 1), SM (34: 1), SM (34: 2), SM (36: 1), SM (38: 1), SM (40: 1) SM (40: 2), SM (42: 1), SM (42: 2), SM (42: 3), sfingosin (18: 0), TAG (44: 1), TAG (44: 3), TAG (46: 0), TAG (46: 1), TAG (46: 2), TAG (46: 3), TAG (46: 4), TAG (48: 0), TAG (48: 1), TAG (48: 2), TAG (48: 3), TAG (48: 4), TAG (48: 5), TAG (49: 1), TAG (49: 2), TAG (49: 3), TAG (50: 0), TAG (50: 1), TAG (50: 2), TAG (50: 3), TAG (50: 4), TAG (50: 5), TAG (50: 6), TAG (51: 2), TAG (51: 4), TAG (52: 2), TAG (52: 3), TAG (52: 4), TAG (52: 5), TAG (52: 6), TAG (52: 7), TAG (53: 4) TAG (54: 2), TAG (54: 3), TAG (54: 4), TAG (54: 5), TAG (54: 6), TAG (54: 7), TAG (54: 8) TAG (55: 5), TAG (55: 6), TAG (55:

7), TAG (56: 4), TAG (56: 5), TAG (56: 6), TAG (56: 7), TAG (56: 8), TAG (56: 9), TAG (58:10), TAG (58: 6), TAG (58: 8), TAG (58: 9), TAG (60:12) og TH -12-keto-LTB4 (20: 2).

8. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter lungecancer, og en eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af LysoPA (22: 0), PE-pmg (42: 9), FA (16: 3), FA (19: 1), CE (18: 2), Cer (36: 1), Cer (38: 4), PC (38: 5), Cer (38: 1), og TAG (44: 3).

9. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter lungecancer, og et eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af TAG (44: 3), PC (36: 5), PC (38: 5), Cer (38: 4), PE-pmg (42: 9), PC (38: 7), LysoPA (22: 0), Cer (38: 1), Cer (34: 1), Cer (36: 1), PC (40: 7), TAG (54: 5), TAG (54: 6), CE (18: 2), PC (36: 4), FA (16: 3), PE-pmg (44:11), TAG (52: 5), Cer (40: 4), CE (20: 5), PC (38: 6), TAG (50: 2), MAG (18: 0), FA (19: 1), TAG (52: 2), LysoPA (22: 1), MAG (24: 2), TAG (54: 7), TAG (50: 3), TAG (50: 1), DAG (36: 3), PC (34: 1), TAG (52: 6), PE-pmg (44:12), CE (20: 4), PE (44:11), PC (40: 8), TAG (56: 9), PE-pmg (34: 6), PE (36: 7), PE (36: 5), TAG (56: 7), TAG (56: 8), DAG (34: 3), TAG (56: 6), TAG (52: 3), TAG (54: 3), TAG (56: 5), TAG (54: 8), PC (34: 6), PC (40: 6), DAG (36: 0), LysoPE (10: 1), DAG (40: 5), Cer (32: 1), TAG (50: 5), TAG (50: 4), PE-pmg (36: 6), TAG (46: 3) og PE (38: 5).

10. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter lungecancer og et eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af TAG (44: 3), PC (36: 5), PC (38: 5), Cer (38: 4), PE-pmg (42: 9), PC (38: 7), LysoPA (22: 0), Cer (38: 1), Cer (34: 1) og Cer (36: 1).

11. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancer type omfatter brystcancer, og en eller flere lipider i lipidsættet er yderligere valgt fra gruppen, der består af LysoPA (22: 1), PE-pmg

(42: 9), CE (20: 5), TAG (52: 3), LysoPA (22: 0), PC (36: 3), PC (36: 4), PC (36: 2) PC (34: 2) og PC (34: 1).

12. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter brystcancer, og en eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af PC (34: 2), PC (34: 1), PC (36: 2), PC (36: 4), PC (36: 3), PC (38: 4), LysoPA (22: 1), PE-pmg (42: 9), LysoPA (22: 0), CE (20: 5), Cer (36: 1), CE (18: 2), DAG (34: 0), SM (34: 1), DAG (32: 0), PE-pmg (40: 8), PC (38: 3), DAG (36: 0), PC (36: 1), TAG (54: 5), TAG (54: 6), PE-pmg (44:11), PMG (42: 8), TAG (52: 2), SM (42: 2), PC (38: 6), TAG (54: 7), PC (40: 6), PC (40: 7), LysoPC (16: 0), FA (16: 3), TAG (52: 5), TAG (44: 3), SM (40: 1), PE-pmg (42:10), PE-pmg (40: 7), SM (36: 1), PE (38: 2), PC (34: 3), PC (36: 5), PC (32: 0), PC (32: 1) , PC (36: 9), SM (42: 3), PC-pmg (36: 4), PC-pmg (38: 5), PC (40: 9), TAG (54: 3), PE-pmg (44:12), FA (19: 1), TAG (50: 3), PC (34: 6), GA2 (35: 2), TAG (58: 9), PE-pmg (42: 7) og LysoPC (18: 0) .

13. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter brystcancer, og en eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af PC (34: 2), PC (34: 1), PC (36: 2), PC (36: 4), PC (36: 3), PC (38: 4), LysoPA (22: 1), PE-pmg (42: 9), LysoPA 0) og CE (20: 5).

14. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter lungecancer og brystcancer, og en eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af LysoPA (22: 1), PC (36: 5), TAG (52: 3), PC (38: 5), CE (20: 5), TAG (50: 2), PC (34: 2), CE (18: 2) og PC (34: 1).

15. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter lungecancer og brystcancer, og en eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af PC (34: 2), PC (36: 2), TAG (44: 3), CE (18: 2), PC (34: 1), LysoPA (22: 1), PC (36: 5), Cer (36: 1), CE 20: 5), PC (36: 3), PC (38: 4), PC (36: 4), Cer (38: 4), PC (38: 5), PC

(38: 7), Cer (38: 1), TAG (50: 2), Cer (34: 1), SM (34: 1), Cer (40: 4), MAG (18: 0), MAG (24: 2) PC (38: 3), PE-pmg (40: 8), PE-pmg (42: 8), TAG (50: 1), DAG (32: 0), PC (36: 1), DAG (34: 0), LysoPC (16: 0), PE-pmg (34: 6), DAG (36: 3), PC (36: 9), PE (36: 5), TAG (52: 6), FA (19: 1), PE-pmg (44:11), PE (44:11), TAG (48: 2), SM (42: 2), PE-pmg (42:10), PE (36: 7), PE-pmg (40: 7), PE-pmg (36: 6), PE (38: 5), PC (32: 0), PE (38: 2), GA2 (35: 2), DAG (34: 3), PE-pmg (44:12), MAG (16: 0), PC (32: 1), LysoPE (10: 1), SM (36: 1), TAG (56: 7) og PE-pmg (42: 9).

16. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor den mindst ene cancertype omfatter lungecancer og brystcancer, og en eller flere lipider i lipidsættet er yderligere udvalgt fra gruppen, der består af PC (34: 2), PC (36: 2), TAG (44: 3), CE (18: 2), PC (34: 1), LysoPA (22: 1), PC (36: 5), Cer (36: 1), CE (20: 5) og PC (36: 3).

17. Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor lipidmængderne bestemmes under anvendelse af massespektrometri, såsom en Fourier-transform-ion-cyklotron-resonansmasseanalysator.

18. Fremgangsmåden ifølge et hvilket som helst af de foregående krav, hvor prøven er en behandling af en kropsvæske, og behandlingen omfatter en eller flere ekstraktioner under anvendelse af en eller flere opløsninger, der omfatter acetonitril, vand, chloroform, methanol, butyleret hydroxytoluen, trichloreddikesyre eller kombinationer deraf.

19. Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor den prædiktive model omfatter en eller flere dimensionsreduktionsfremgangsmåder.

20. Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor den prædiktive model omfatter en eller flere fremgangsmåder, der er valgt fra gruppen, som består af principal komponentanalyse (PCA), blød uafhængig modellering af klasseanalogi (SIMCA), partielle mindste kvadraters diskriminantanalyse (PLS-DA), og ortogonale partielle mindste kvadrater

diskriminantanalyse (OPLS-DA).

21. Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor dyret er valgt fra gruppen bestående af human, hund, kat, hest, ko, gris, får, kylling, kalkun, mus og rotte.

22. Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor den mindst ene cancertype er lunge- eller brystcancer.

DRAWINGS

Figure 1

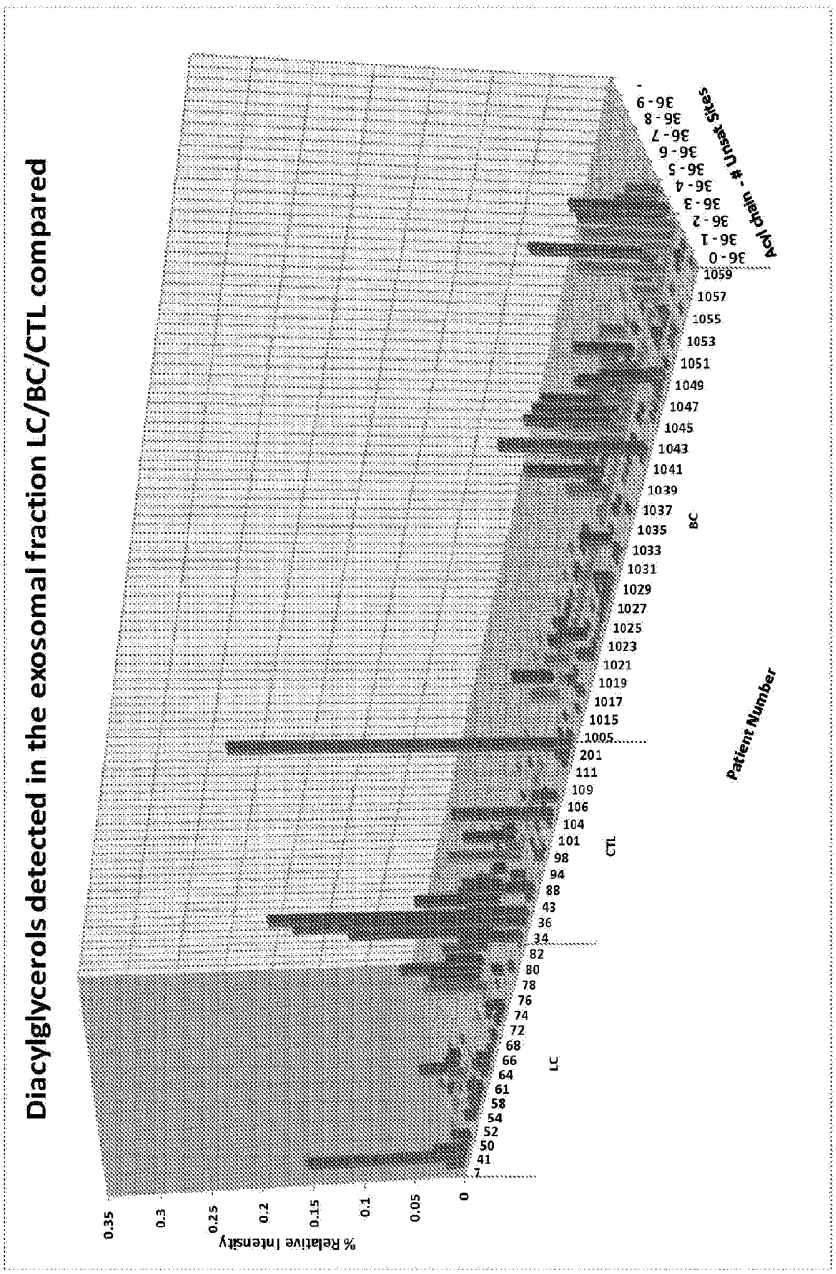


Figure 2

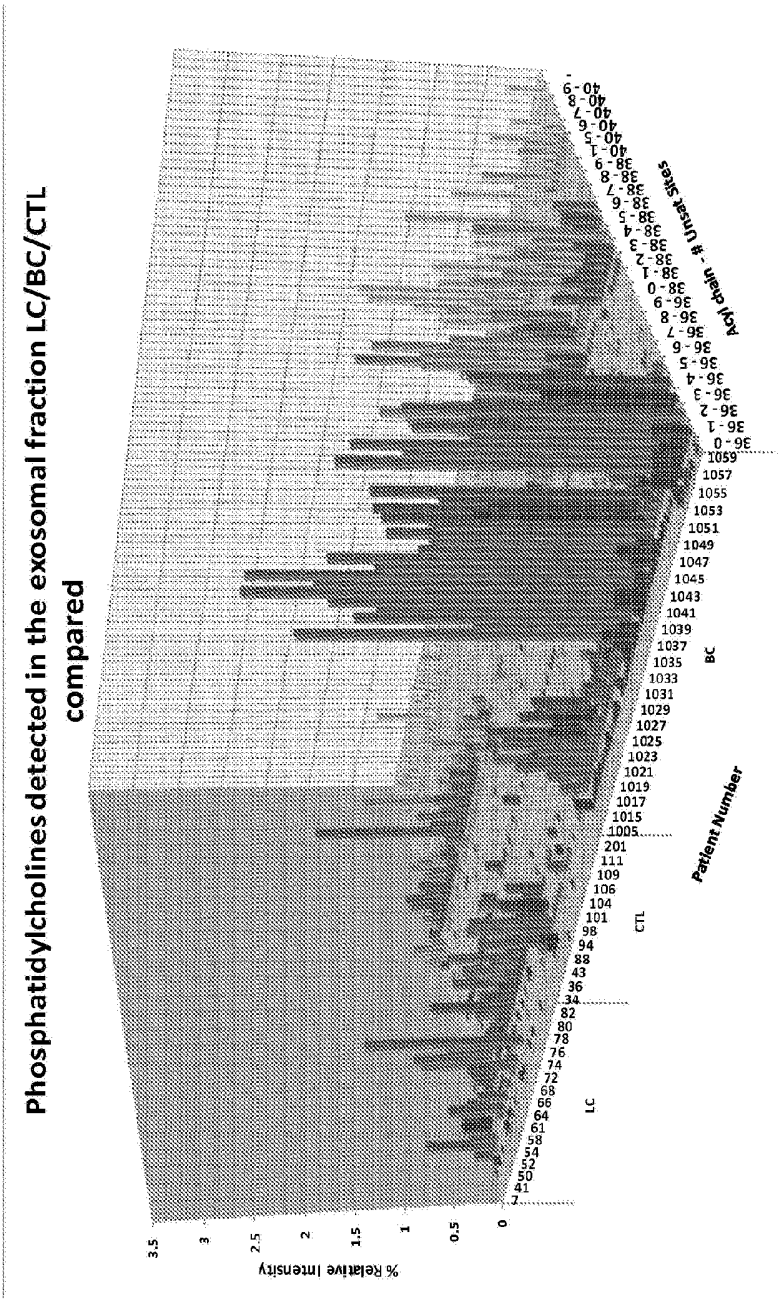

Phosphatidylcholines detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
3.5
3
2.5
2
1.5
1
0.5
0
LC
CTL
BC
Patient Number
Acyl chain - # Unsat Sites

Figure 3

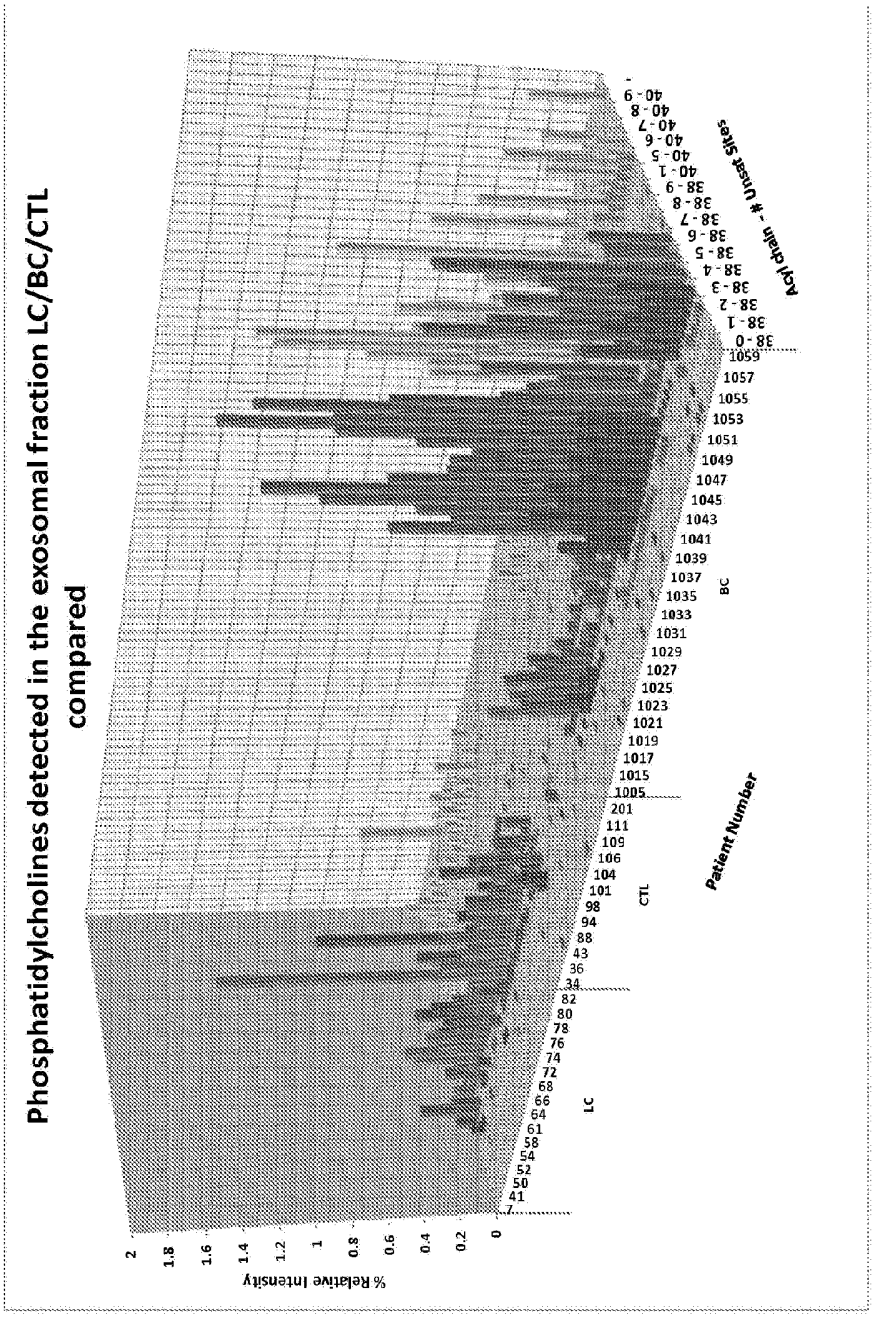

Phosphatidylcholines detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
LC
7
41
50
52
54
58
61
64
66
68
72
74
76
78
80
82
34
36
43
88
94
98
101
104
106
109
111
201
CTL
1005
1015
1017
1019
1021
1023
1025
1027
1029
1031
1033
1035
1037
1039
1041
1043
1045
1047
1049
1051
1053
1055
1057
1059
BC
Patient Number
38-0
38-1
38-2
38-3
38-4
38-5
38-6
38-7
38-8
38-9
40-1
40-5
40-6
40-7
40-8
40-9
Acl chain - # unsat Sites

Figure 4

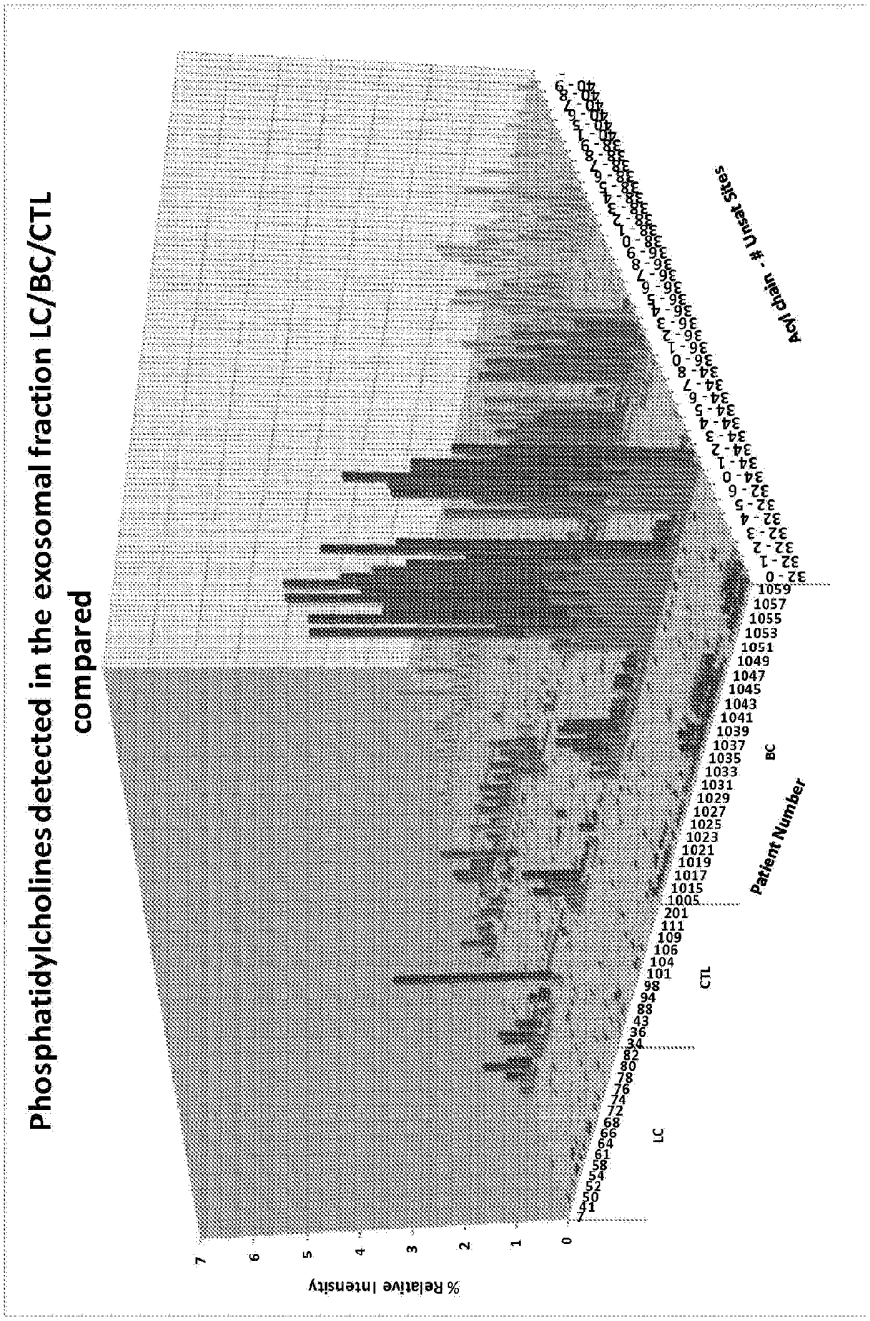

Phosphatidylcholines detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
Patient Number
LC
BC
CTL
Acyl chain - # Unsat Sites

Figure 5

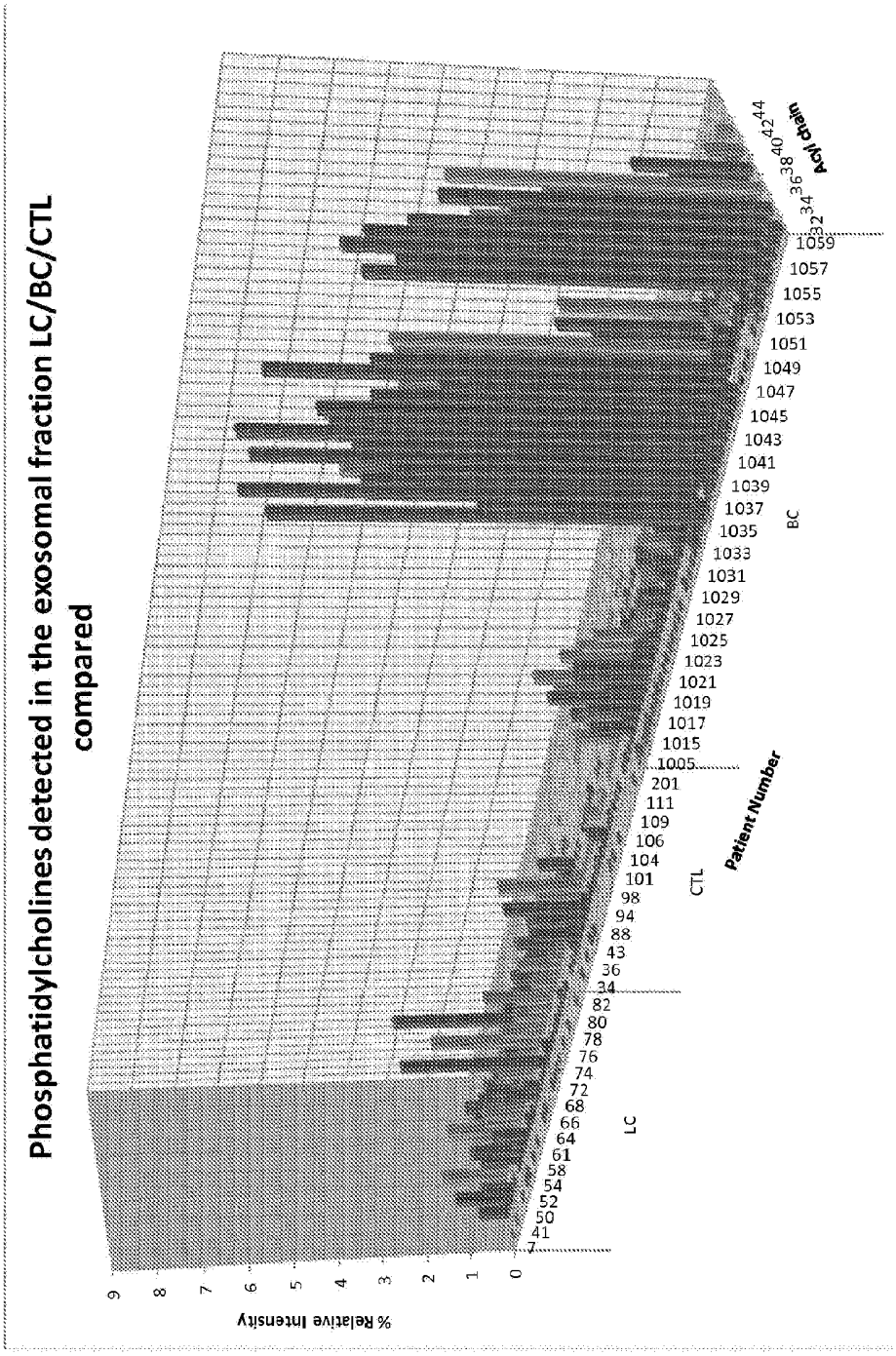

Phosphatidylcholines detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
0
1
2
3
4
5
6
7
8
9
Acyl chain
32
34
36
38
40
42
44
BC
1059
1057
1055
1053
1051
1049
1047
1045
1043
1041
1039
1037
1035
1033
1031
1029
1027
1025
1023
1021
1019
1017
1015
1005
CTL
201
111
109
106
104
101
98
94
88
43
36
34
LC
82
80
78
76
74
72
68
66
64
61
58
54
52
50
41
Patient Number

Figure 6

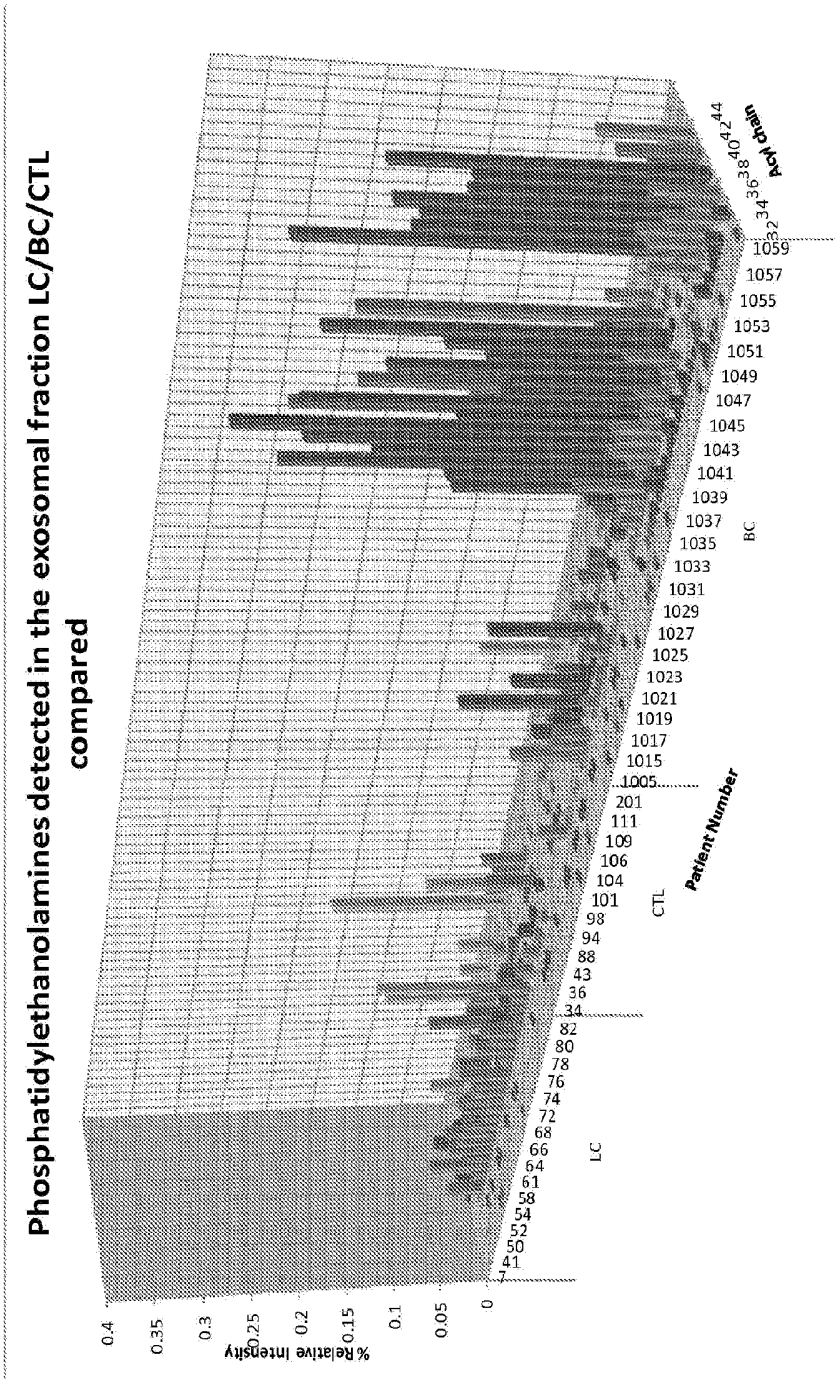

Phosphatidylethanolamines detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Acyl Chain
32 34 36 38 40 42 44
LC
41 50 52 54 58 61 64 66 68 72 74 76 78 80 82
CTL
34 36 43 88 94 98 101 104 106 109 111 201 1005
BC
1015 1017 1019 1021 1023 1025 1027 1029 1031 1033 1035 1037 1039 1041 1043 1045 1047 1049 1051 1053 1055 1057 1059
Patient Number

Figure 7

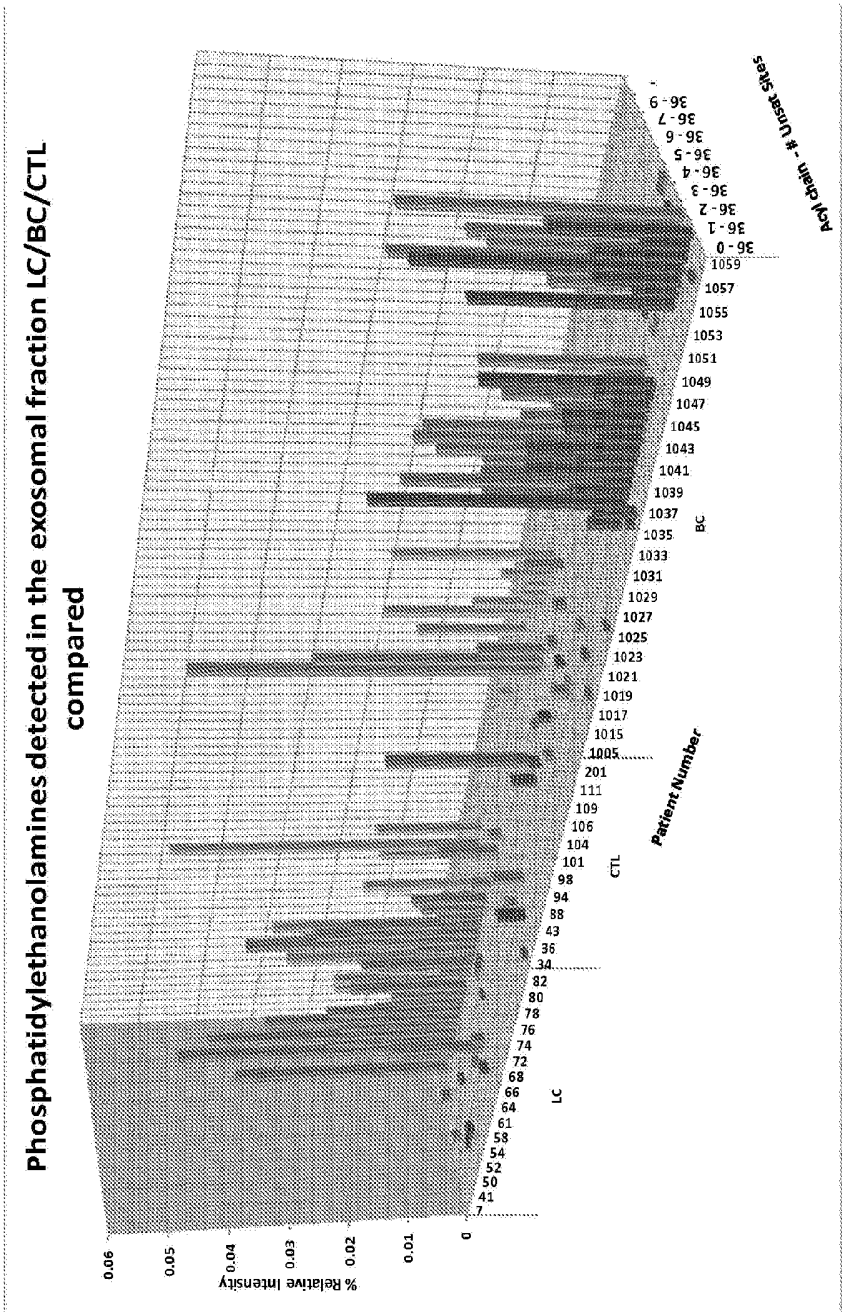

Phosphatidylethanolamines detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
0.06
0.05
0.04
0.03
0.02
0.01
0
Patient Number
LC
CTL
BC
Acyl chain - # Unsat Shes
36-0
36-1
36-2
36-3
36-4
36-5
36-6
36-7
36-9

Figure 8

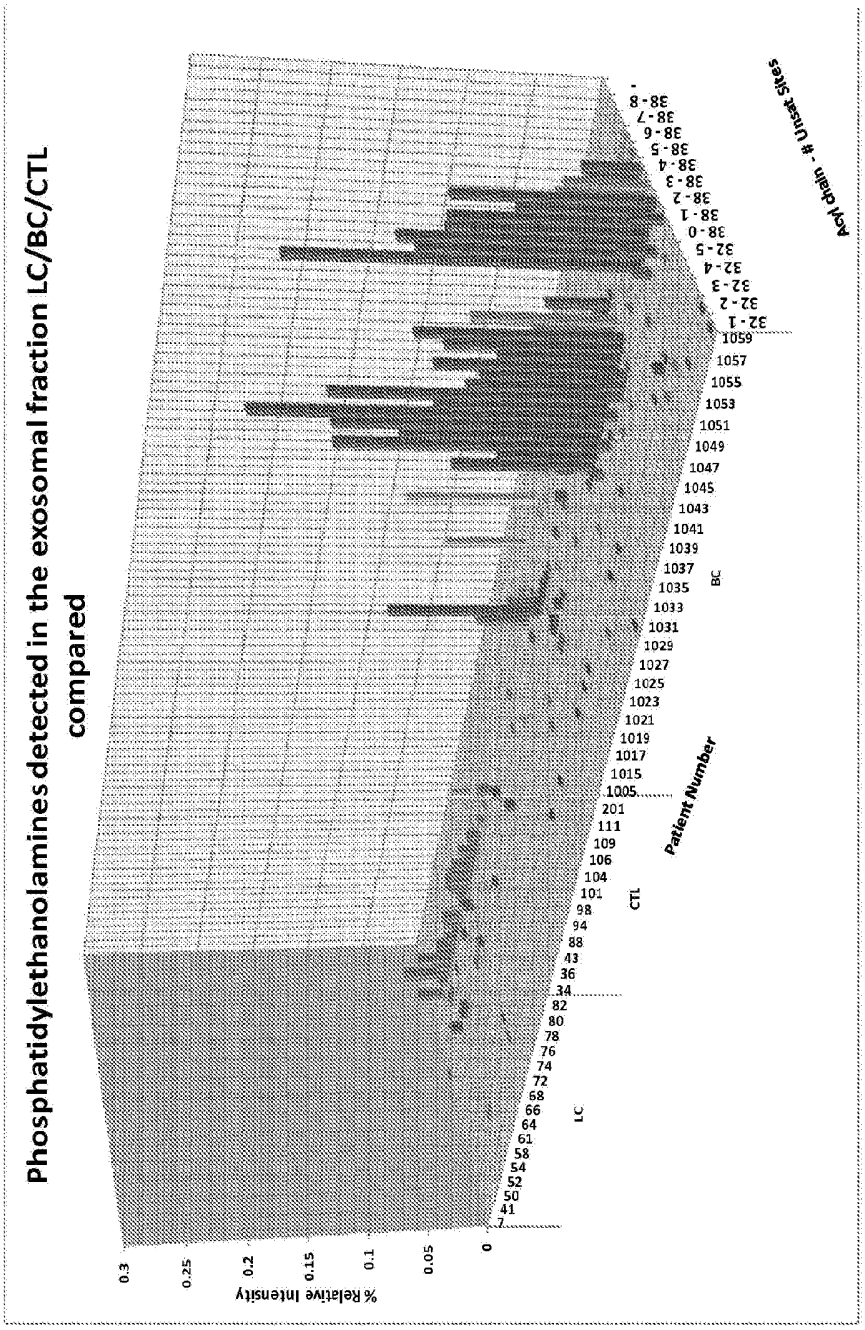

Phosphatidylethanolamines detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
0.3
0.25
0.2
0.15
0.1
0.05
0
LC
CTL
BC
Patient Number
Acyl chain - # unsat sites

Figure 9

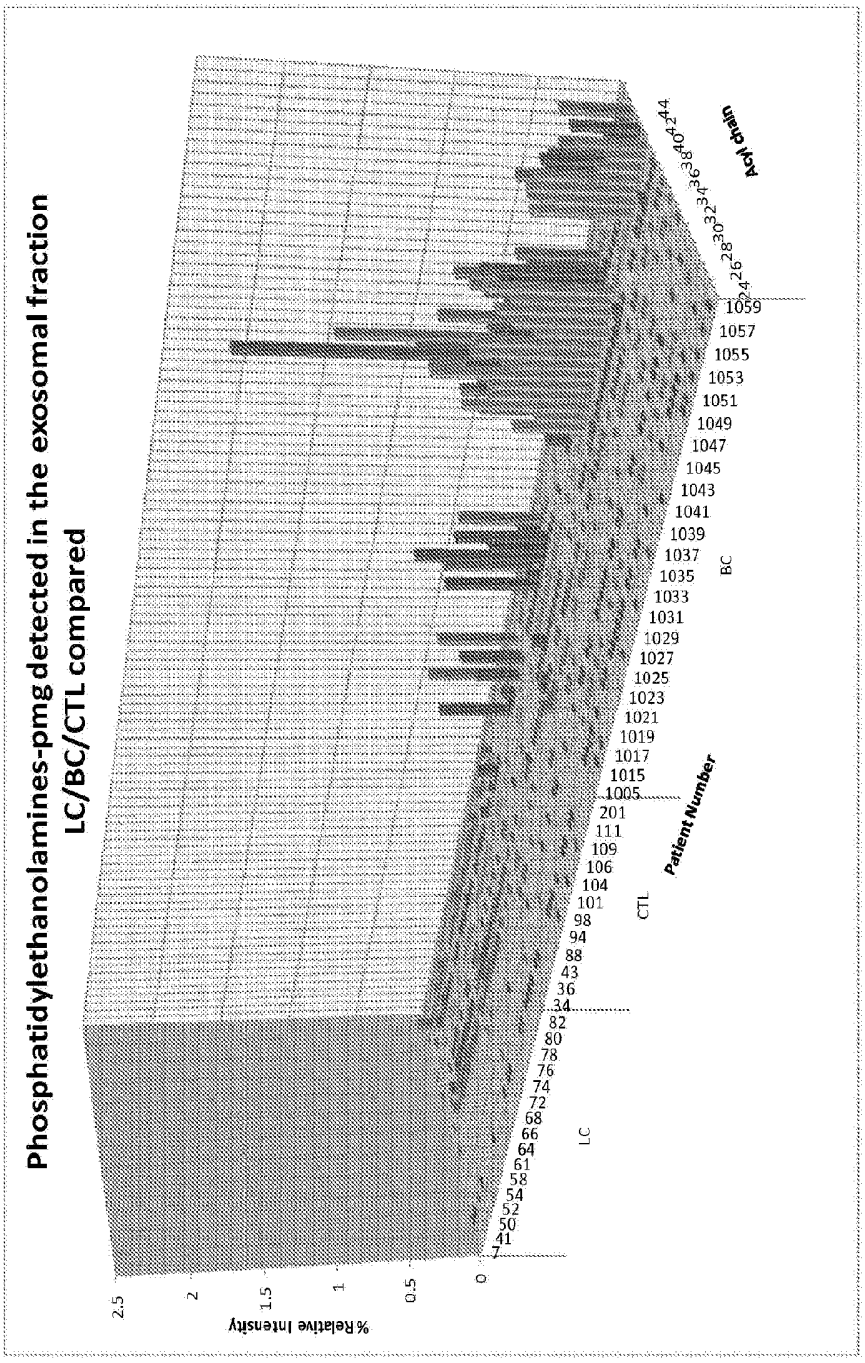

Phosphatidylethanolamines-pmg detected in the exosomal fraction
LC/BC/CTL compared
% Relative Intensity
2.5
2
1.5
1
0.5
0
LC
BC
CTL
Patient Number
Acyl chain
7
41
50
52
54
58
61
64
66
68
72
74
76
78
80
82
34
36
43
88
94
98
101
104
106
109
111
201
1005
1015
1017
1019
1021
1023
1025
1027
1029
1031
1033
1035
1037
1039
1041
1043
1045
1047
1049
1051
1053
1055
1057
1059
24
26
28
30
32
34
36
38
40
44

Figure 10

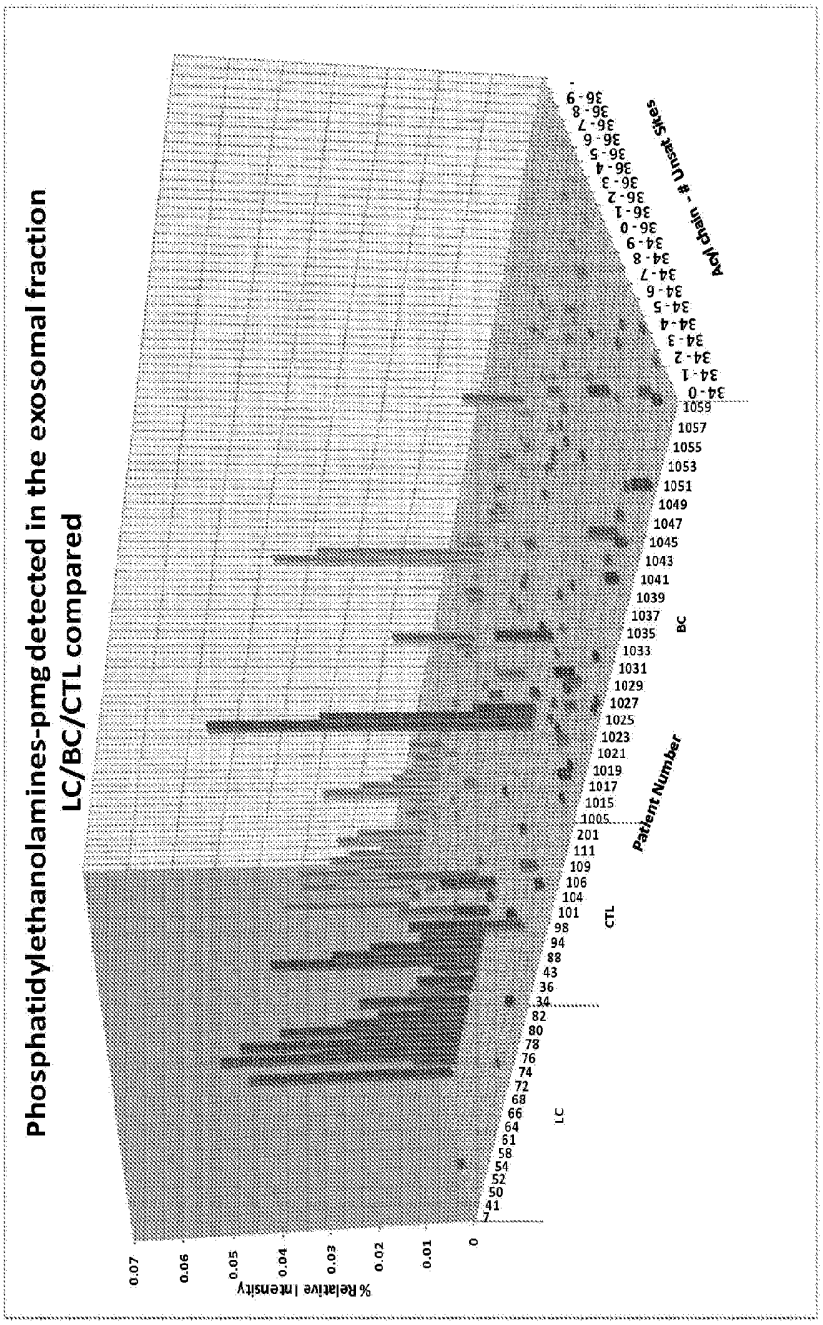

Phosphatidylethanolamines-pmg detected in the exosomal fraction
LC/BC/CTL compared
% Relative Intensity
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
Patient Number
LC
CTL
BC
Acyl chain - # Unsat Sites

Figure 11

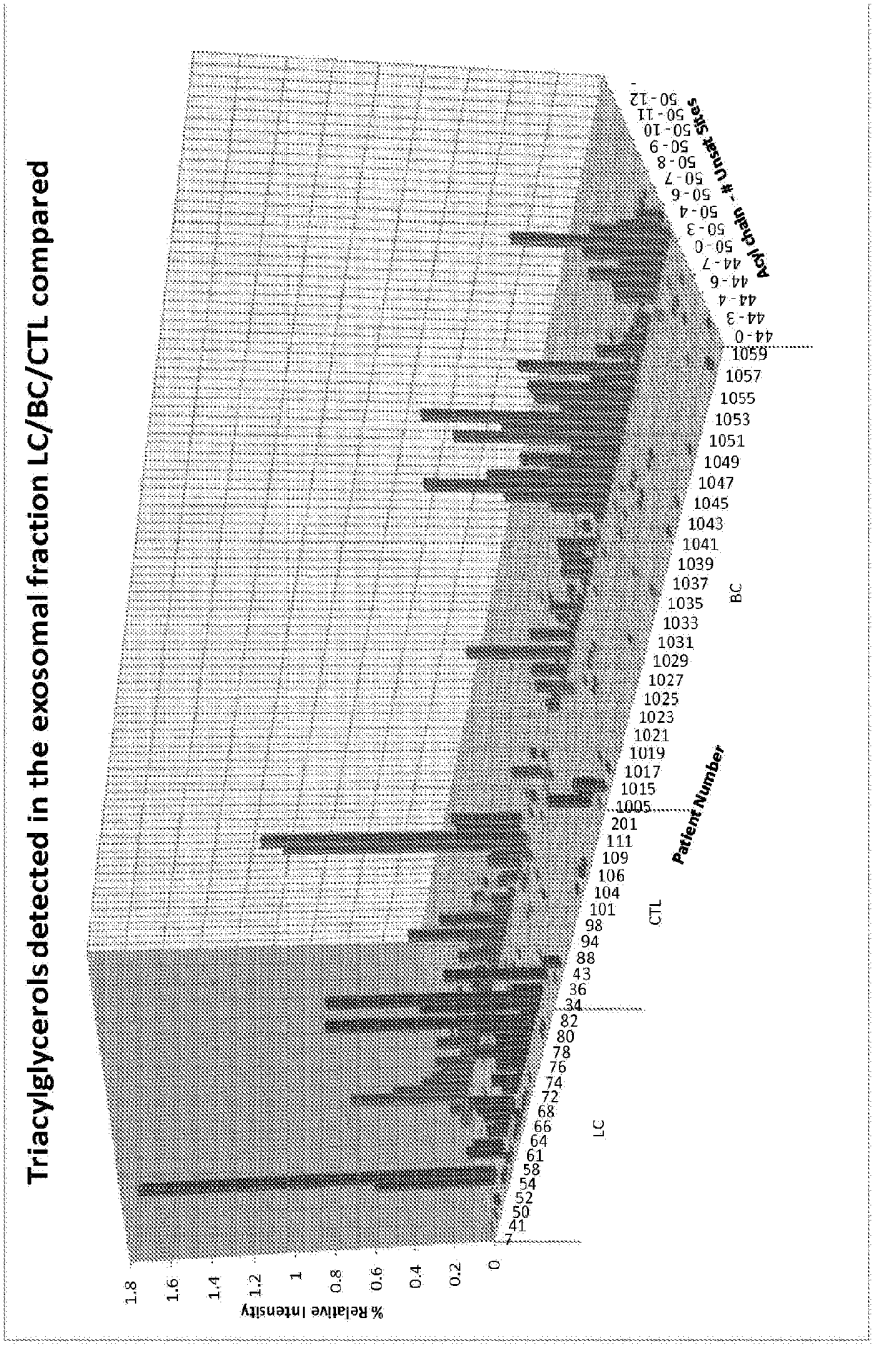

Triacylglycerols detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
LC
CTL
BC
Patient Number
Acyl chain - # Unsat Sites
41
50
52
54
58
61
64
66
68
72
74
76
78
80
82
34
36
43
88
94
98
101
104
106
109
111
201
1005
1015
1017
1019
1021
1023
1025
1027
1029
1031
1033
1035
1037
1039
1041
1043
1045
1047
1049
1051
1053
1055
1057
1059
44-0
44-3
44-4
44-6
44-7
50-0
50-3
50-4
50-6
50-7
50-8
50-9
50-10
50-11
50-12

Figure 12

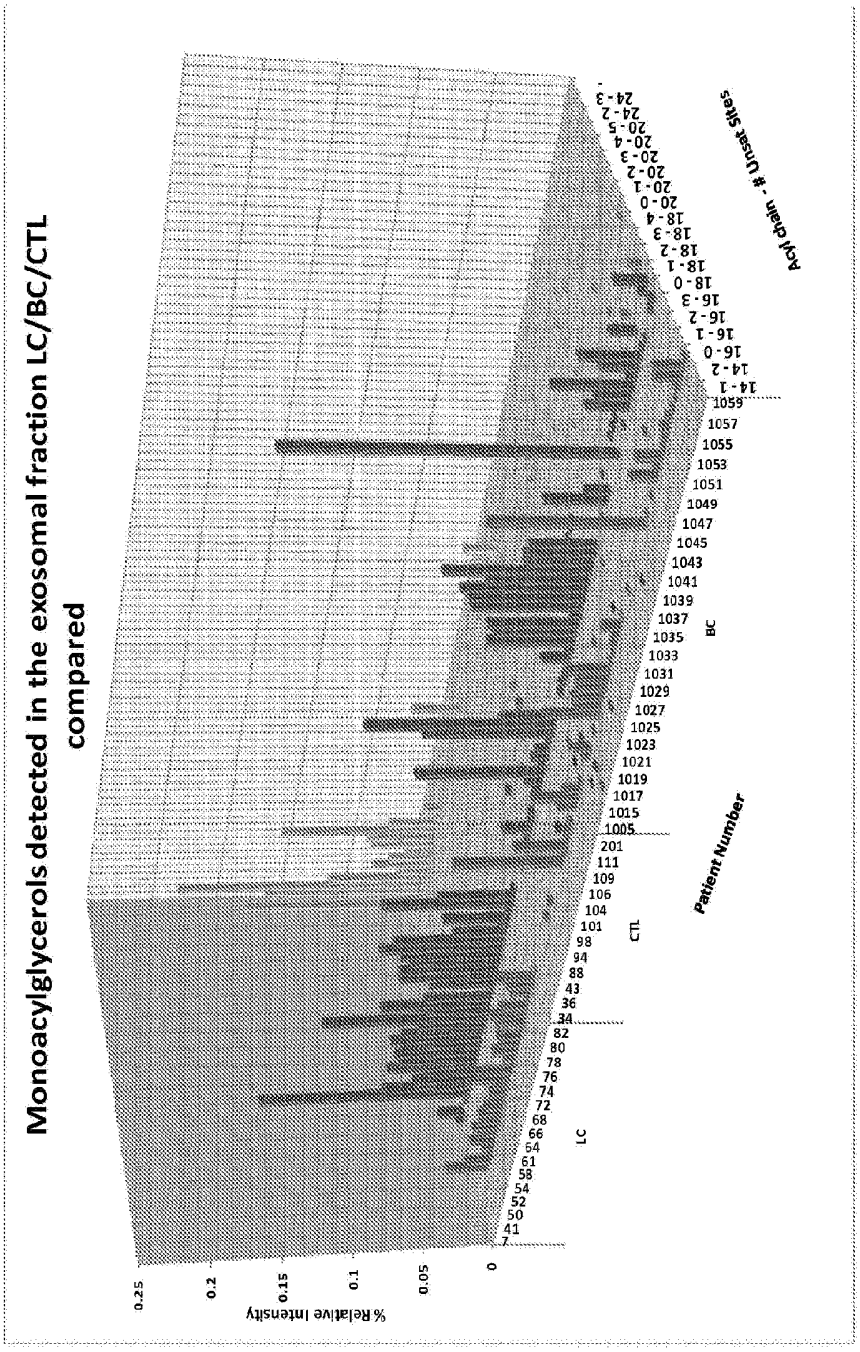

Monoacylglycerols detected in the exosomal fraction LC/BC/CTL compared
% Relative Intensity
0.25
0.2
0.15
0.1
0.05
0
LC
CTL
BC
Patient Number
Acyl chain - # Unsat Sites

Figure 13

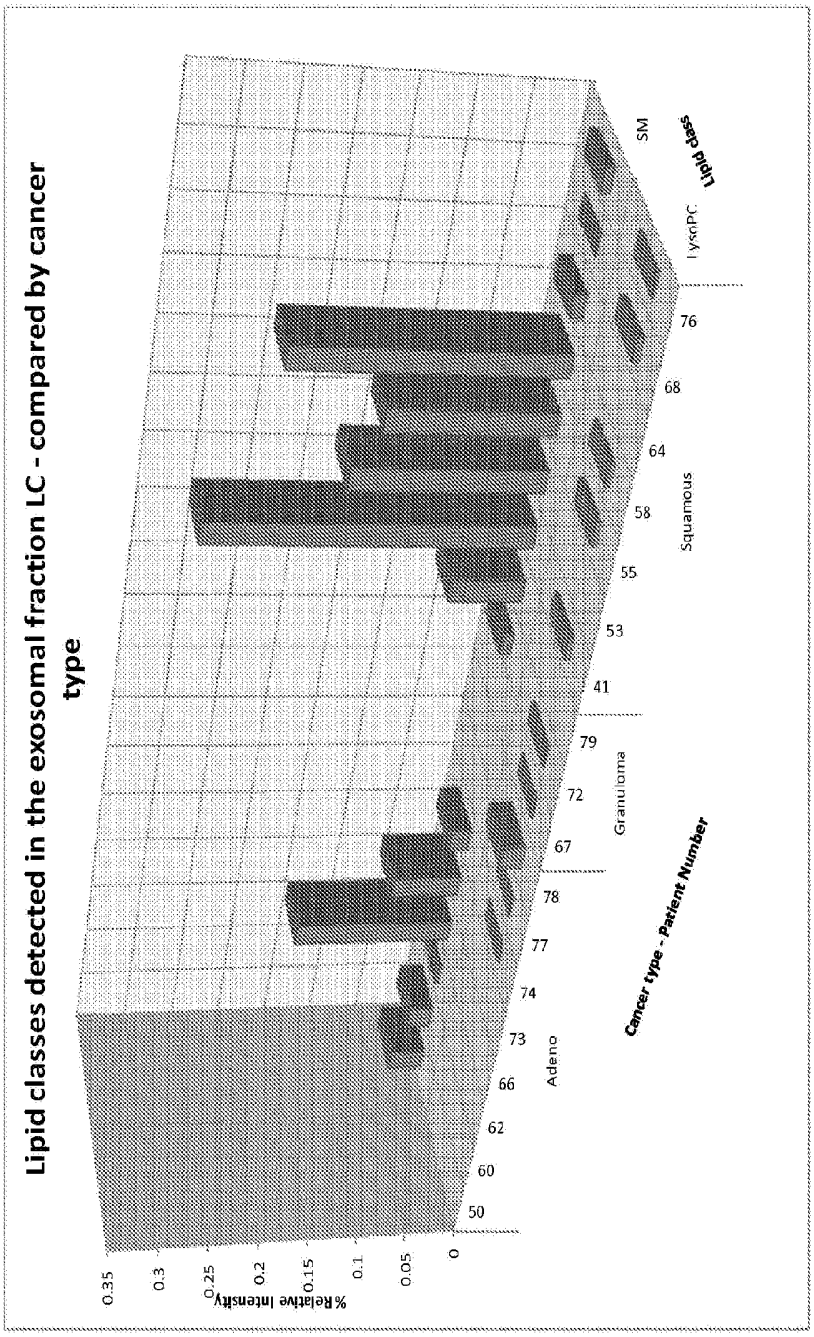

Lipid classes detected in the exosomal fraction LC - compared by cancer type
% Relative Intensity
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Lipid class
SM
LysoPC
Cancer type - Patient Number
Adeno
50
60
62
66
73
74
77
78
67
Granuloma
72
79
41
53
55
Squamous
58
64
68
76

Figure 14

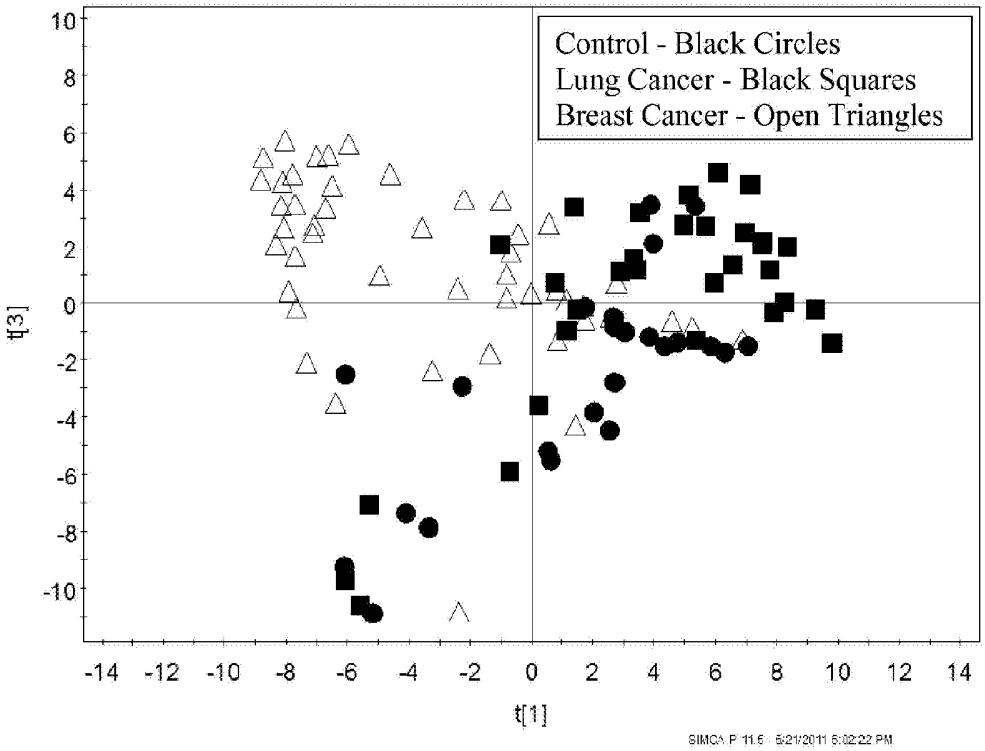

Control - Black Circles
Lung Cancer - Black Squares
Breast Cancer - Open Triangles
t[3]
t[1]
10
8
6
4
2
0
-2
-4
-6
-8
-10
-14
-12
-10
-8
-6
-4
-2
0
2
4
6
8
10
12
14
SIMCA-P 11.5 - 5/21/2011 5:02:22 PM

Figure 15

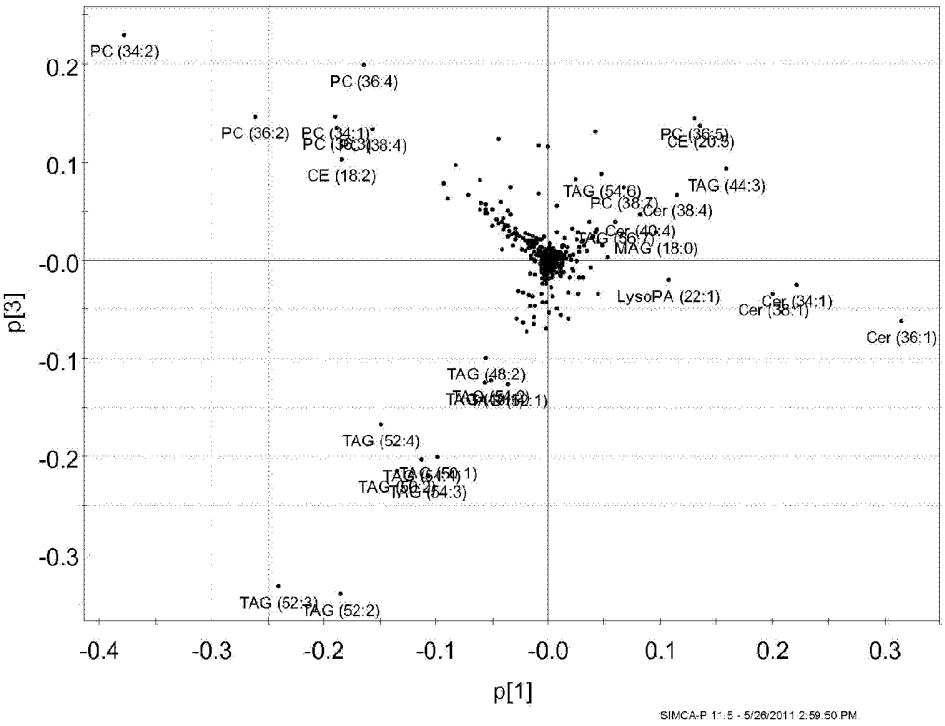

PC (34:2)
PC (36:4)
PC (36:2)
PC (34:1)
PC (38:4)
CE (18:2)
PC (36:5)
CE (20:3)
TAG (54:6)
TAG (44:3)
PC (38:7)
Cer (38:4)
Cer (40:4)
TAG (56:7)
MAG (18:0)
LysoPA (22:1)
Cer (34:1)
Cer (38:1)
Cer (36:1)
TAG (48:2)
TAG (52:4)
TAG (50:1)
TAG (54:3)
TAG (52:3)
TAG (52:2)
0.2
0.1
-0.0
-0.1
-0.2
-0.3
p[3]
-0.4
-0.3
-0.2
-0.1
-0.0
0.1
0.2
0.3
p[1]
SIMCA-P 1

Figure 16

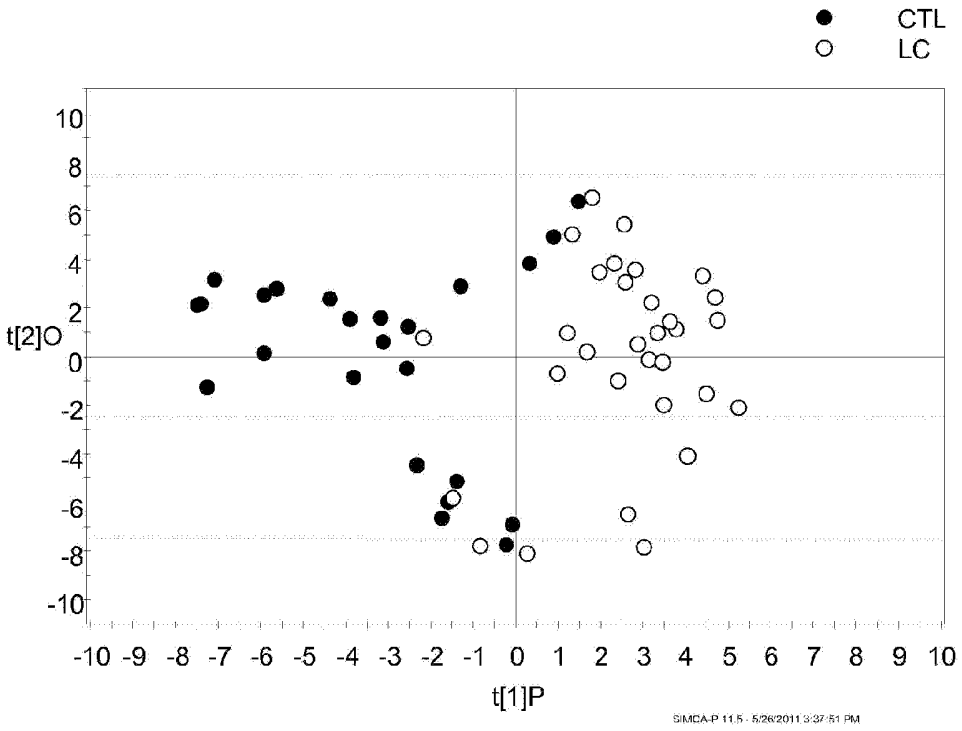

CTL
LC
t[2]O
t[1]P
10
8
6
4
2
0
-2
-4
-6
-8
-10
-10 -9 -8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7 8 9 10
SIMCA-P 11.5 - 5/26/2011 3:37:51 PM

Figure 17

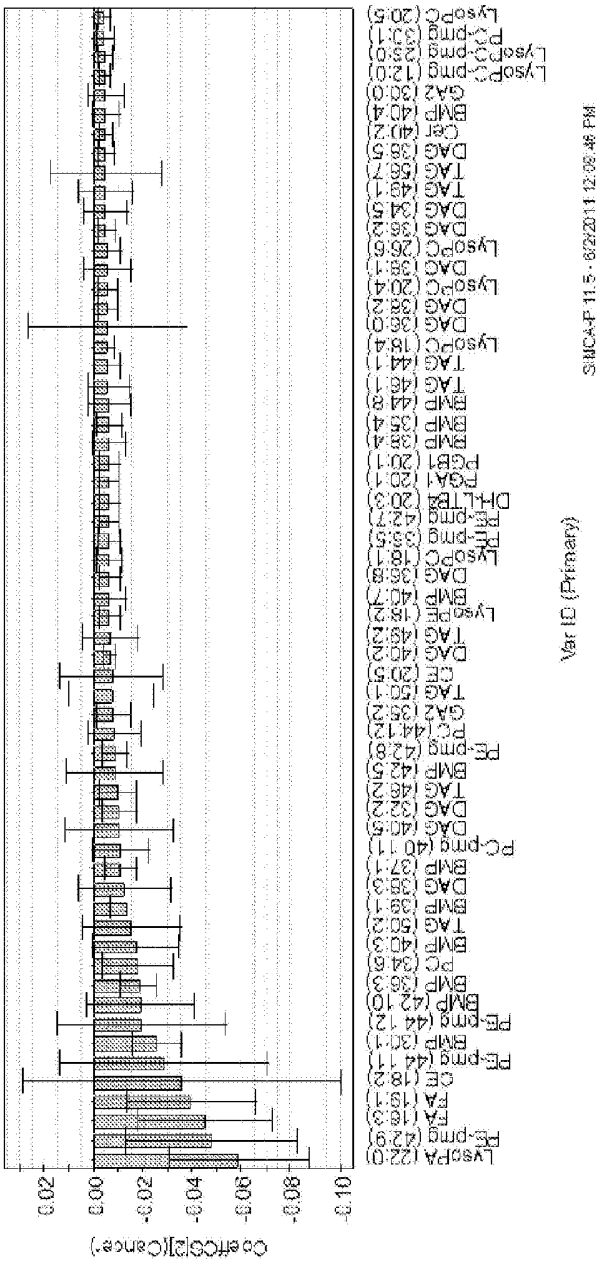

coef(CS[2](Cancer))
0.02
0.00
-0.02
-0.04
-0.06
-0.08
-0.10
LysoPA (22:0)
PE-pmg (42:9)
FA (16:3)
FA (18:1)
CE (18:2)
PE-pmg (44:11)
BMP (20:1)
PE-pmg (44:12)
BMP (42:10)
BMP (36:3)
PC (34:6)
BMP (40:3)
TAG (50:2)
BMP (39:1)
DAG (36:3)
BMP (37:1)
PC-pmg (40:11)
DAG (40:5)
DAG (32:2)
TAG (46:2)
BMP (42:5)
PE-pmg (42:8)
TAG (44:12)
GA2 (36:2)
TAG (50:1)
CE (20:5)
DAG (40:2)
TAG (48:2)
LysoPE (18:2)
BMP (40:7)
DAG (36:6)
LysoPC (18:1)
PE-pmg (36:5)
PE-pmg (42:7)
DHLTB4 (20:3)
PGA1 (20:1)
PGB1 (20:1)
BMP (36:4)
BMP (35:4)
BMP (44:8)
TAG (46:1)
TAG (44:1)
LysoPC (18:4)
DAG (36:0)
DAG (38:2)
LysoPC (20:4)
DAG (38:1)
LysoPC (26:6)
DAG (36:2)
DAG (34:5)
TAG (48:1)
TAG (56:7)
DAG (36:5)
Cer (40:2)
BMP (40:4)
GA2 (36:0)
LysoPC (12:0)
LysoPC (25:0)
PC-pmg (33:1)
LysoPC (20:5)
Var ID (Primary)
SIMCA-P 11.5 - 6/22/2011 12:08:46 PM

Figure 18

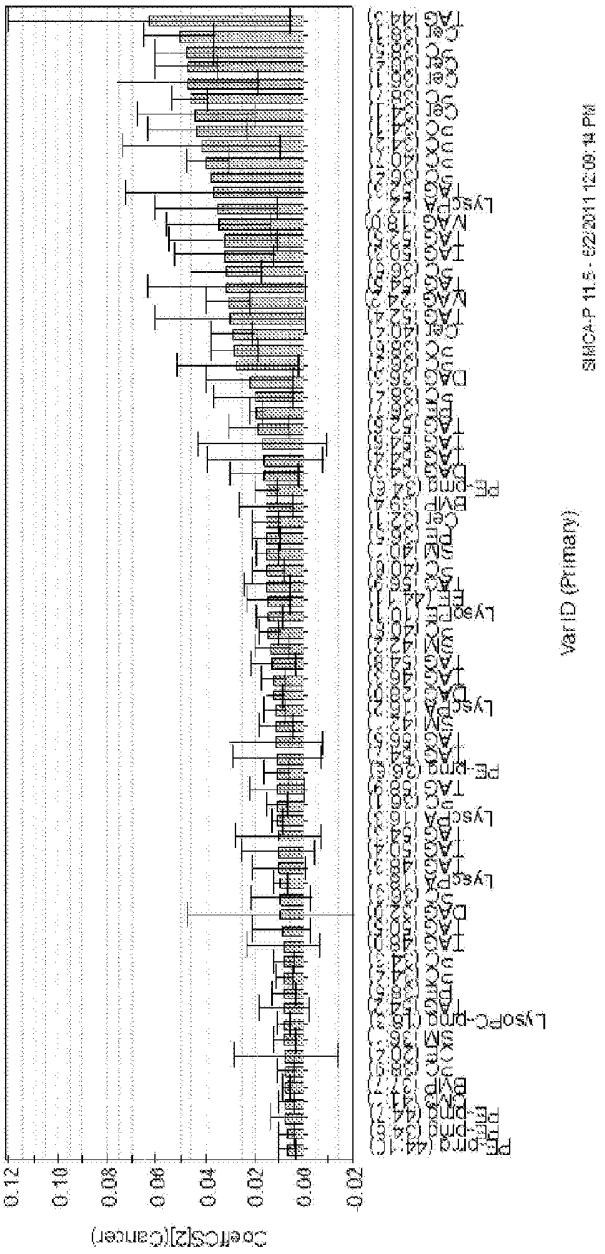

coef[CSIZ](Cancer)
0.12
0.10
0.08
0.06
0.04
0.02
0.00
-0.02
Var ID (Primary)
SIMCA-P 11.5 - 02/2011 12:09:14 PM

Figure 19

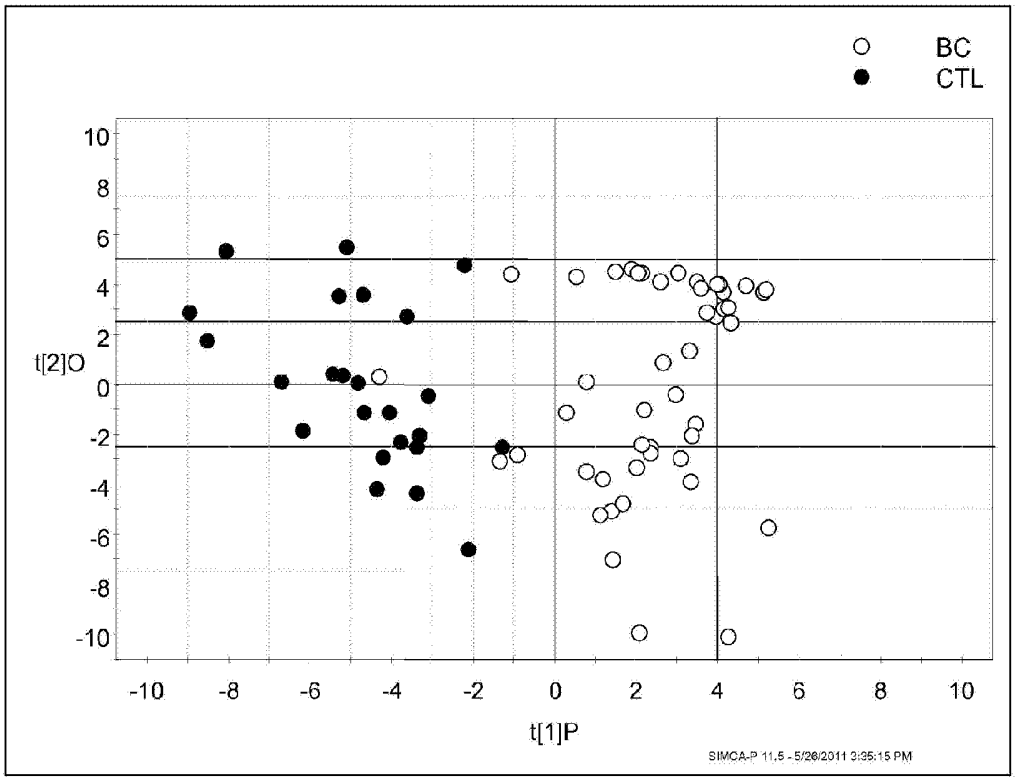

BC
CTL
10
8
6
4
2
0
-2
-4
-6
-8
-10
t[2]O
-10
-8
-6
-4
-2
0
2
4
6
8
10
t[1]P
SIMCA-P 11.5 - 5/26/2011 3:35:15 PM

Figure 20

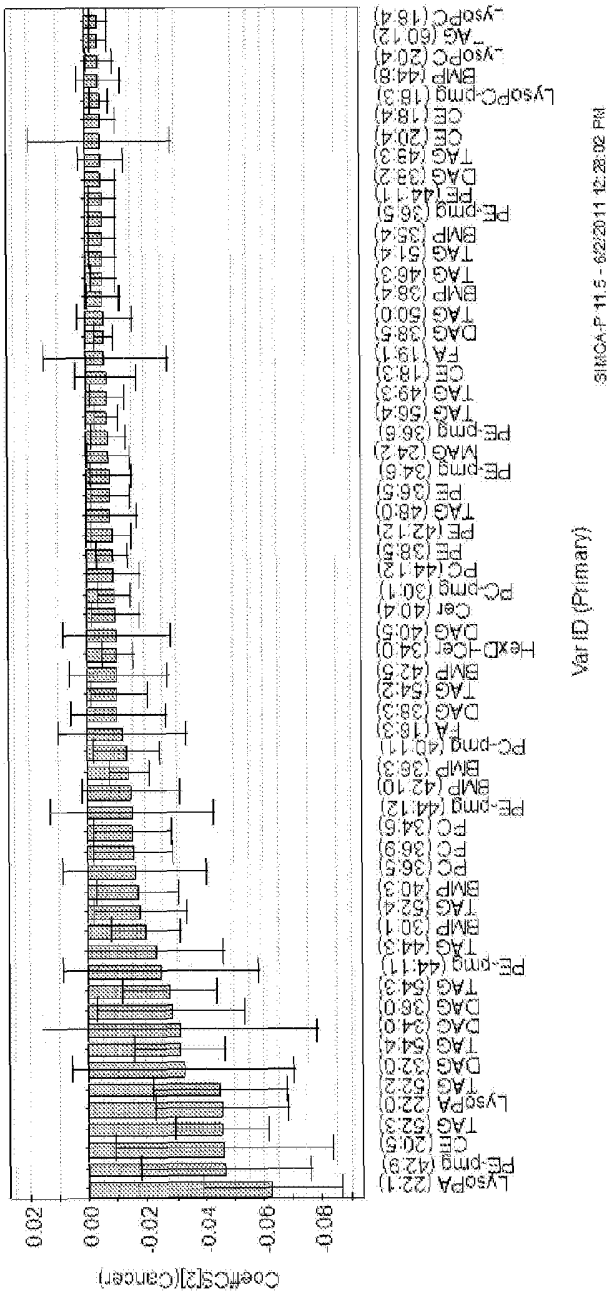

0.02
0.00
-0.02
-0.04
-0.06
-0.08
CoeffCS[2](Cancer)
LysoPA (22:1)
PE-pmg (42:5)
CE (20:5)
TAG (52:2)
LysoPA (22:0)
TAG (52:2)
DAG (54:4)
TAG (54:4)
DAG (36:0)
TAG (54:3)
PE-pmg (44:11)
TAG (44:3)
BMP (30:1)
TAG (52:4)
BMP (40:3)
PC (36:5)
PC (34:5)
PE-pmg (44:12)
BMP (42:10)
BMP (36:3)
PC-pmg (40:11)
PA (18:3)
DAG (38:3)
TAG (54:2)
BMP (42:5)
HexD-Cer (34:0)
DAG (40:5)
Cer (40:4)
PC-pmg (30:1)
PC (44:12)
PE (38:5)
PE (42:12)
TAG (48:0)
PE (36:5)
PE-pmg (34:5)
MAG (24:2)
PE-pmg (36:6)
TAG (56:4)
TAG (49:3)
CE (18:3)
FA (19:1)
DAG (38:5)
TAG (50:0)
BMP (38:4)
TAG (46:3)
TAG (51:4)
BMP (35:4)
PE-pmg (36:5)
PE (44:11)
DAG (38:2)
TAG (49:3)
CE (20:4)
CE (18:4)
LysoPC-pmg (18:3)
BMP (44:8)
LysoPC (20:4)
MAG (60:12)
LysoPC (18:4)
Var ID (Primary)
SIMCA-P 11.5 - 6/2/2011 12:28:02 PM

Figure 21

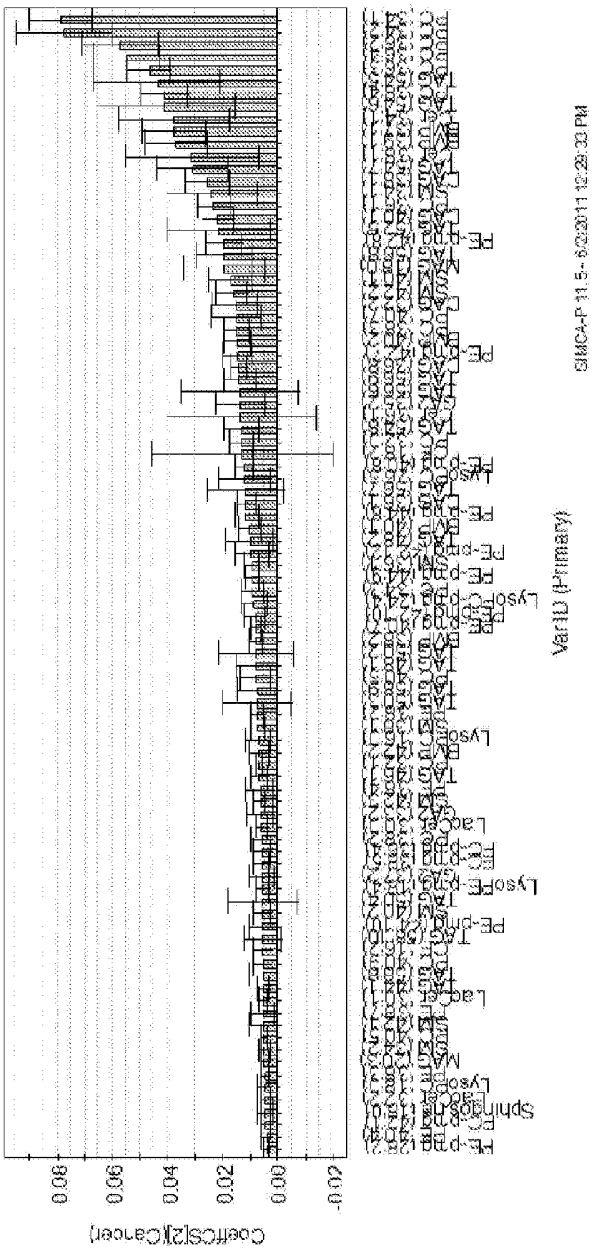

coef(CS[2])(Cancer)
0.08
0.06
0.04
0.02
0.00
-0.02
Var1(U (Primary))
SMC4-P 11.5 - 6/2/2011 12:29:33 PM

Figure 22

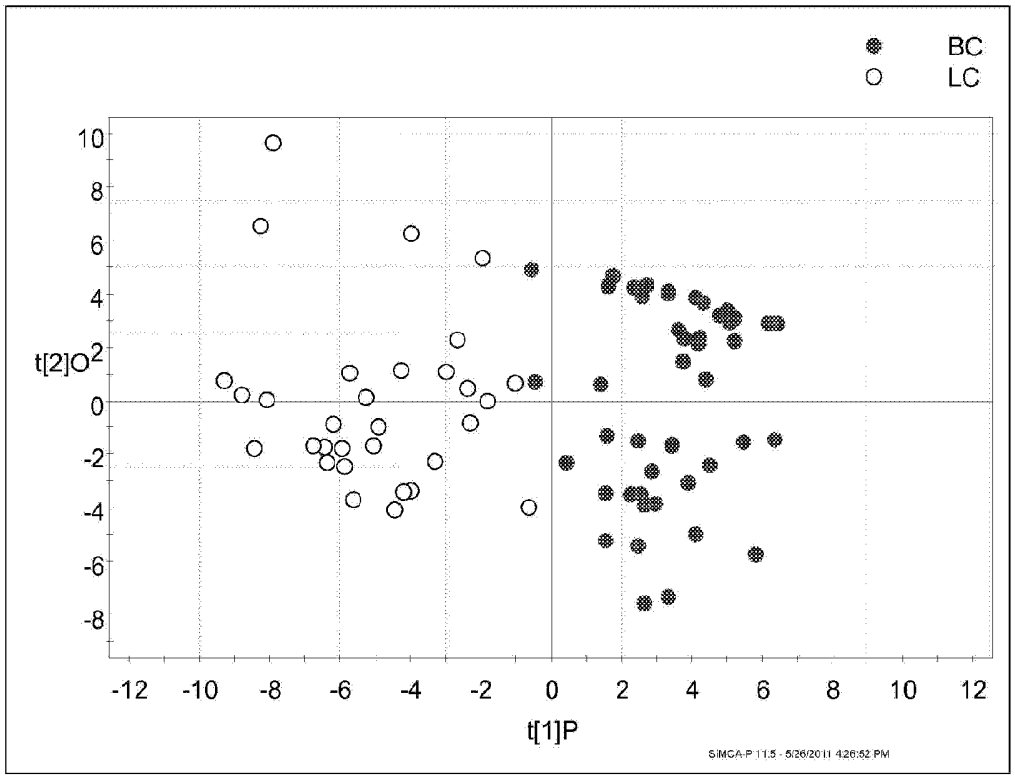

BC
LC
10
8
6
4
t[2]O2
0
-2
-4
-6
-8
-12
-10
-8
-6
-4
-2
0
2
4
6
8
10
12
t[1]P
SIMCA-P 11.5 - 5/26/2011 4:26:52 PM

Figure 23

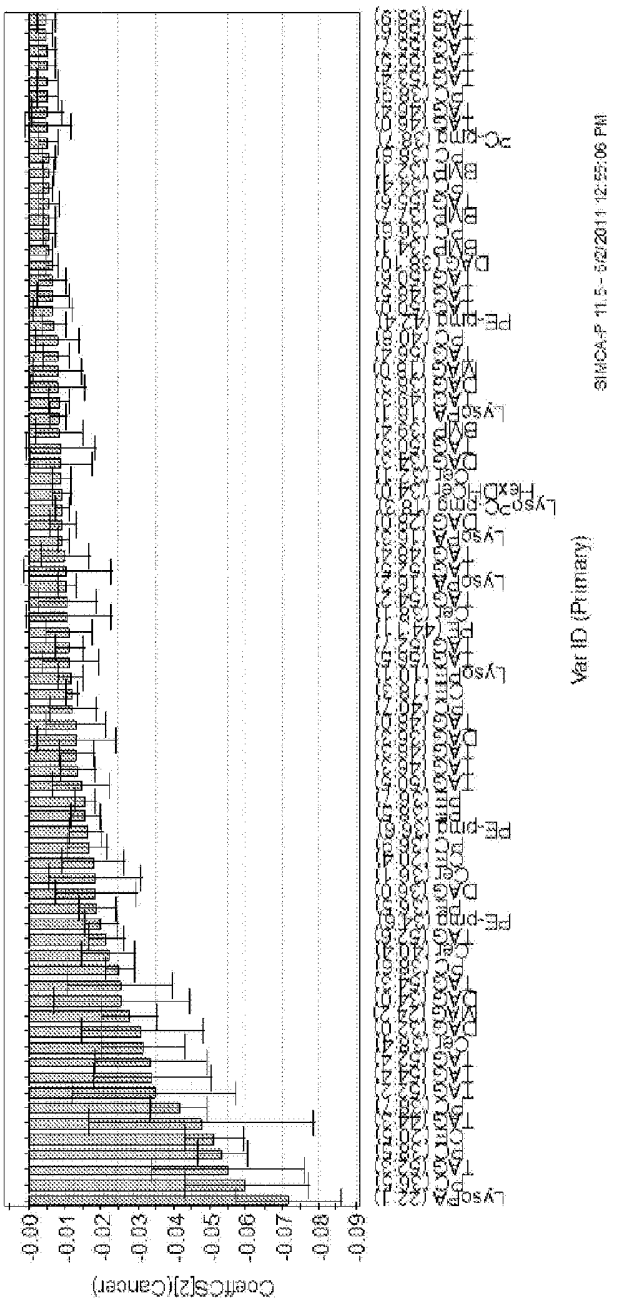

CoefficS[2](Cancer)
-0.00
-0.01
-0.02
-0.03
-0.04
-0.05
-0.06
-0.07
-0.08
-0.09
Var ID (Primary)
SIMCA-P 11.5 - 5/2/2011 12:55:06 PM

Figure 24

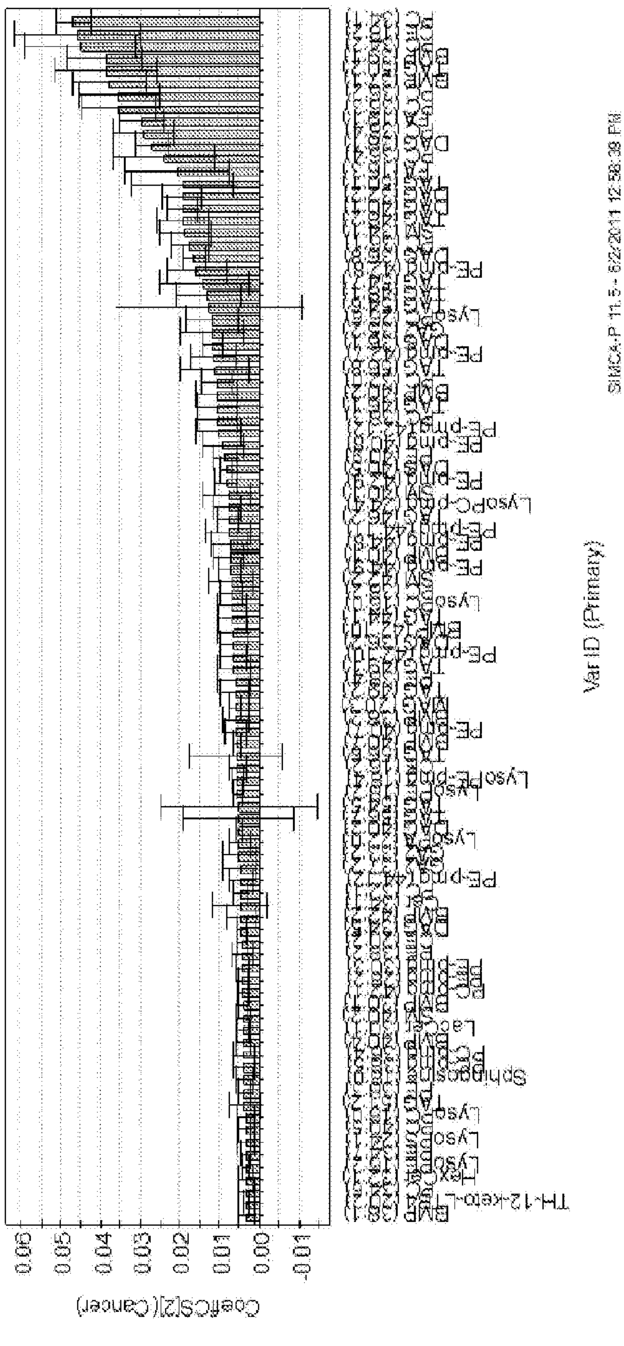
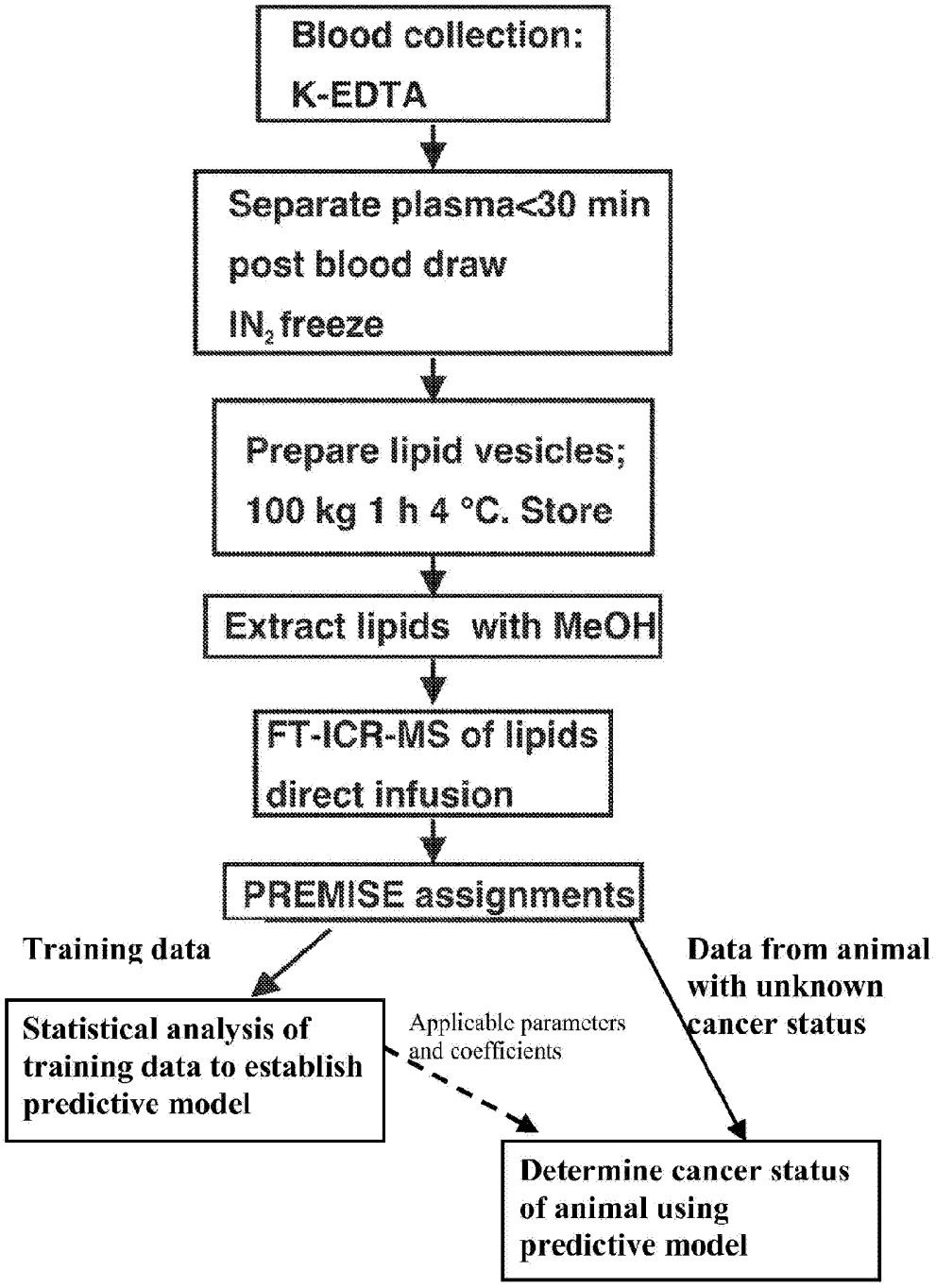

CoeffCS[2](Cancer)
0.06
0.05
0.04
0.03
0.02
0.01
0.00
-0.01
Var ID (Primary)
SIMCA-P 11.5 - 6/2/2011 12:58:38 PM

Figure 25


Blood collection:
K-EDTA
Separate plasma<30 min
post blood draw
IN2 freeze
Prepare lipid vesicles;
100 kg 1 h 4 °C. Store
Extract lipids with MeOH
FT-ICR-MS of lipids
direct infusion
PREMISE assignments
Training data
Data from animal
with unknown
cancer status
Statistical analysis of
training data to establish
predictive model
Applicable parameters
and coefficients
Determine cancer status
of animal using
predictive model