WHAT IS CLAIMED IS:

1. A method for diagnosing a patient's pancreatic cancer health state, or change in pancreatic cancer health state, or for diagnosing risk of developing pancreatic cancer or the presence of pancreatic cancer in a patient, comprising the steps of:

a) analyzing a sample from said patient by high resolution mass spectrometry to obtain accurate mass intensity data;

b) comparing the accurate mass intensity data to corresponding data obtained from one or more than one reference sample to identify an increase or decrease in accurate mass intensity; and

c) using said increase or decrease in accurate mass intensity for diagnosing said patient's pancreatic cancer health state, or change in pancreatic cancer health state, or for diagnosing risk of developing pancreatic cancer or the presence of pancreatic cancer in said patient,

wherein the accurate mass intensity is measured, in Daltons, at or substantially equivalent to a hydrogen and electron adjusted accurate mass, or neutral accurate mass, selected from the group consisting of: 78.0516; 84.0575; 112.0974; 116.5696; 191.5055; 197.0896; 200.1389; 202.045; 203.1155; 214.1204; 214.1205; 232.1309; 233.1345; 240.0997; 243.0714; 244.0554; 254.1127; 255.1161; 256.2403; 260.0033; 262.0814; 268.1284; 270.0323; 270.0867; 276.0948; 280.2403; 280.2404; 281.2432; 281.2435; 282.2558; 282.2559; 283.2591; 283.2595; 284.9259; 300.1186; 300.2067; 302.0945; 302.222; 302.2457; 304.2375; 304.2407; 317.9613; 318.0931; 326.2048; 326.2458; 327.9902; 328.2403; 328.2408; 328.2627; 329.2439; 329.2658; 330.2559; 332.1473; 338.0189; 348.1191; 350.2222; 360.1782; 360.1792; 361.1828; 366.3593; 368.1057; 382.1083; 382.1601; 418.2204; 428.2404; 428.3647; 446.2526; 446.3395; 468.2336; 468.3581; 468.3807; 469.237; 469.3616; 481.315; 484.3527; 485.904; 494.4321; 495.3325; 496.3373; 505.3146; 508.2256; 517.3141; 518.321; 519.3295; 520.448; 522.4638; 522.4639; 523.3661; 523.4675; 538.4237; 540.4381; 541.3134; 541.3361; 542.3394; 545.3454; 562.4962; 564.5121; 565.3373; 566.3403; 569.3682; 570.372; 572.4798; 573.4833; 574.4952; 575.4985; 576.4751; 576.5113; 577.5149; 578.5169; 578.5284; 579.5313; 587.3214; 588.3269; 589.3368; 590.3408; 592.4709; 594.4852; 594.4863; 595.4892; 595.4897; 596.5017; 596.5027; 597.5066; 598.4955; 599.4993; 600.5117; 601.5151; 602.5269; 603.5297; 606.5591; 609.3259; 613.3379; 615.3535; 627.5656; 628.5438; 630.799; 631.798; 633.3245; 635.7525; 636.7532; 645.7958; 657.7337; 658.7372; 670.5696; 671.5731; 681.5858; 702.5709; 715.6959; 719.6256; 720.6272; 721.5035; 723.5203; 723.521; 724.5252; 724.5477; 725.7228; 733.5054; 735.6582; 743.5396; 744.5425; 745.5631; 746.5128; 746.5705; 748.527; 749.5374; 749.5388; 750.5425; 751.5511; 751.5539; 752.5574;

755.5497; 757.556; 757.5587; 758.562; 758.5626; 759.5383; 759.5733; 760.5792; 763.5578; 765.5678; 766.4792; 771.5699; 773.5276; 774.5419; 775.5522; 775.5532; 775.5532; 777.0402; 777.5709; 779.5405; 779.5416; 780.5452; 780.5454; 781.5029; 781.5566; 782.5612; 783.569; 783.5755; 784.5742; 784.5806; 785.5913; 785.5929; 785.5931; 786.593; 786.5972; 787.5989; 791.5841; 793.7091; 795.5181; 796.5212; 801.5147; 801.5262; 801.5523; 802.5291; 803.5373; 803.5414; 803.5677; 804.5422; 804.5456; 804.5714; 804.7208; 805.5549; 806.5632; 807.5734; 807.5739; 807.5764; 808.5783; 808.5791; 809.5796; 810.5867; 811.5729; 811.608; 812.6774; 813.5888; 819.5177; 823.5411; 824.69; 825.5522; 826.5561; 826.7047; 827.5401; 827.5678; 827.7082; 828.5397; 828.5721; 829.5516; 829.5532; 829.5843; 830.5591; 830.5879; 831.5652; 831.572; 831.5997; 832.6031; 833.5864; 834.5868; 835.598; 837.7209; 838.7284; 838.7435; 839.7464; 847.531; 850.7061; 850.7326; 851.6694; 851.7107; 851.7337; 852.7368; 853.573; 854.7358; 854.7397; 855.5721; 855.7392; 855.7436; 856.7505; 856.754; 857.6923; 857.7543; 857.7574; 858.7644; 861.749; 865.752; 866.7585; 867.7649; 868.7704; 871.5547; 873.7819; 874.7066; 874.787; 875.7108; 879.7629; 889.7537; 889.8147; 894.7911; 898.7043; 898.7325; 902.7629; 903.7636; 907.7847; 908.7907; 909.7882; 910.7272; 916.7735; 919.6496; 921.813; 922.7081; 922.7285; 922.8222; 923.7295; 924.7233; 925.727; 933.8137; 937.7542; 946.8194; 947.8263; 948.836; 950.7364; 960.7432; 970.733; 972.7481; 973.7482; 984.7406; 986.7568; 996.7518; 997.7397; 998.7566; 999.7632; 1010.765; 1011.669; 1011.77; 1012.781; 1016.931; 1017.935; 1018.944; 1019.951; 1020.957; 1038.915; 1039.705; 1039.921; 1040.933; 1041.935; 1199.084; 1200.088; 1201.09; 1202.098; 1223.09; 1224.096; 1225.096; 1226.599; 1227.112; 1228.117; 1229.12; 1230.125; 1247.084; 1249.105; 1250.108; 1251.119; 1252.12; 1253.123; 1253.134; 1254.137; 1255.153 and combinations thereof.

2. The method of claim 1, wherein the quantifying data is obtained using a Fourier transform ion cyclotron resonance, time of flight, magnetic sector, quadrupole or triple quadrupole mass spectrometer.

3. The method of claim 1, wherein the sample is a blood sample.

4. The method of claim 1, wherein the sample is a blood serum sample.

5. The method of claim 1, wherein the sample is a cerebral spinal fluid sample.

6. The method of claim 1, wherein the accurate mass intensities represent ionized metabolites.

7. The method of claim 1, wherein a liquid/liquid extraction is performed on the sample whereby non-polar metabolites are dissolved in an organic solvent and polar metabolites are dissolved in an aqueous solvent.

8. The method of claim 7, wherein the accurate mass intensities are obtained from the ionization of the extracted samples using an ionization method selected from the group consisting of: positive electrospray ionization, negative electrospray ionization, positive atmospheric pressure chemical ionization, negative atmospheric pressure chemical ionization, and combinations thereof.

9. The method of claim 1, wherein the quantifying data is obtained using a Fourier transform ion cyclotron resonance mass spectrometer.

10. The method of claim 1, wherein said one or more than one reference sample is from one or more pancreatic cancer-negative humans.

11. The method of claim 1, further comprising:

analyzing a sample from said patient by mass spectrometry to obtain accurate mass intensity data for one or more than one internal standard molecule; and

calculating a ratio for each of the accurate mass intensities obtained in step (a) to the accurate mass intensities obtained for the one or more than one internal standard molecule;

wherein the comparing step (b) comprises comparing each ratio to one or more corresponding ratios obtained for one or more than one reference sample.

12. The method of claim 1, wherein the hydrogen and electron adjusted accurate mass, or neutral accurate mass, is selected from the group consisting of: 519.3295; 523.3661; 541.3134; 702.5709; 724.5477; 757.556; 779.5405; 783.569; 785.5913; 803.5373; 805.5549; 807.5734; 809.5796; 812.6774; 829.5516; 833.5864; 576.4751; 594.4863; 596.5017; and combinations thereof.

13. The method of claim 12, wherein a decrease in accurate mass intensity is identified in the comparing step (b).

14. The method of claim 1, wherein the hydrogen and electron adjusted accurate mass, or neutral accurate mass, is 600.5117.

15. The method of claim 14, wherein an increase in accurate mass intensity is identified in the comparing step (b).

16. The method of any one of claims 1 to 15, wherein substantially equivalent refers to ± 5 ppm of the hydrogen and electron adjusted accurate mass, or neutral accurate mass.

17. The method of any one of claims 1 to 15, wherein substantially equivalent refers to ± 1 ppm of the hydrogen and electron adjusted accurate mass, or neutral accurate mass.

18. A method for diagnosing a patient's pancreatic cancer health state, or change in pancreatic cancer health state, or for diagnosing risk of developing pancreatic cancer or the presence of pancreatic cancer in a patient, comprising the steps of:

a) analyzing a sample from said patient to obtain quantifying data for one or more than one metabolite marker;

b) comparing the quantifying data for said one or more than one metabolite marker to corresponding data obtained for one or more than one reference sample to identify an increase or decrease in the level of said one or more than one metabolite marker in said sample; and

c) using said increase or decrease in the level of said one or more than one metabolite marker in said sample for diagnosing said patient's pancreatic cancer health state, or change in pancreatic cancer health state, or for diagnosing risk of developing pancreatic cancer or the presence of pancreatic cancer in said patient,

wherein the one or more metabolite marker comprises one or more molecule selected from the molecular formulae consisting of: $C_{36}H_{62}O_4$, $C_{36}H_{62}O_5$, $C_{36}H_{64}O_5$, $C_{36}H_{66}O_5$, $C_{36}H_{64}O_6$, $C_{36}H_{66}O_6$, $C_{36}H_{68}O_6$, $C_{22}H_{46}NO_7P$, $C_{22}H_{48}NO_7P$, $C_{24}H_{50}NO_7P$, $C_{24}H_{48}NO_7P$, $C_{24}H_{46}NO_7P$, $C_{26}H_{54}NO_7P$, $C_{26}H_{52}NO_7P$, $C_{26}H_{50}NO_7P$, $C_{26}H_{48}NO_7P$, $C_{28}H_{56}NO_7P$, $C_{28}H_{54}NO_7P$, $C_{28}H_{52}NO_7P$, $C_{28}H_{50}NO_7P$, $C_{28}H_{48}NO_7P$, $C_{28}H_{46}NO_7P$, $C_{30}H_{56}NO_7P$, $C_{30}H_{54}NO_7P$, $C_{30}H_{52}NO_7P$, $C_{30}H_{50}NO_7P$, $C_{32}H_{58}NO_7P$, $C_{32}H_{54}NO_7P$, $C_{38}H_{76}NO_7P$, $C_{40}H_{82}NO_7P$, $C_{40}H_{80}NO_7P$, $C_{40}H_{78}NO_7P$, $C_{40}H_{70}NO_7P$, $C_{42}H_{78}NO_8P$, $C_{42}H_{80}NO_8P$, $C_{42}H_{82}NO_8P$, $C_{42}H_{84}NO_8P$, $C_{44}H_{78}NO_8P$, $C_{44}H_{80}NO_8P$, $C_{44}H_{82}NO_8P$, $C_{44}H_{84}NO_8P$, $C_{44}H_{86}NO_8P$, $C_{44}H_{88}NO_8P$, $C_{46}H_{78}NO_8P$, $C_{46}H_{80}NO_8P$, $C_{46}H_{82}NO_8P$, $C_{46}H_{84}NO_8P$, $C_{48}H_{80}NO_8P$, $C_{48}H_{82}NO_8P$, $C_{48}H_{84}NO_8P$, $C_{48}H_{86}NO_8P$, $C_{42}H_{80}NO_7P$, $C_{42}H_{82}NO_7P$, $C_{42}H_{84}NO_7P$, $C_{44}H_{82}NO_7P$, $C_{44}H_{84}NO_7P$, $C_{44}H_{86}NO_7P$, $C_{44}H_{88}NO_7P$, $C_{46}H_{82}NO_7P$, $C_{46}H_{84}NO_7P$, $C_{46}H_{86}NO_7P$, $C_{48}H_{84}NO_7P$, $C_{48}H_{86}NO_7P$, $C_{39}H_{79}N_2O_6P$, $C_{39}H_{80}N_2O_6P^+$, $C_{41}H_{81}N_2O_6P$, $C_{41}H_{82}N_2O_6P^+$, $C_{41}H_{83}N_2O_6P$, $C_{41}H_{84}N_2O_6P^+$, $C_{47}H_{93}N_2O_6P$, $C_{47}H_{94}N_2O_6P^+$, $C_{47}H_{95}N_2O_6P$, $C_{47}H_{96}N_2O_6P^+$, and combinations thereof.

19. The method of claim 18, wherein the quantifying data is obtained using a Fourier transform ion cyclotron resonance, time of flight, magnetic sector, quadrupole or triple quadrupole mass spectrometer.

20. The method of claim 18, wherein the quantifying data is obtained using a Fourier transform ion cyclotron resonance mass spectrometer.

21. The method of claim 19, wherein the mass spectrometer is equipped with a chromatographic system.

22. The method of claim 18, wherein the sample is a blood sample.

23. The method of claim 18, wherein the sample is a blood serum sample.

24. The method of claim 18, wherein the sample is a cerebral spinal fluid sample.

25. The method of claim 18, wherein a liquid/liquid extraction is performed on the sample whereby non-polar metabolites are dissolved in an organic solvent and polar metabolites are dissolved in an aqueous solvent.

26. The method of claim 25, wherein the extracted samples are analyzed by positive or negative electrospray ionization, positive or negative atmospheric pressure chemical ionization, or combinations thereof.

27. The method of claim 25, wherein the extracted samples are analyzed by MS/MS transition.

28. The method of claim 25, wherein the extracted samples are analyzed by extracted ion current (EIC) chromatography and MS/MS transition.

29. The method of claim 18, wherein said one or more than one reference sample is from one or more pancreatic cancer-negative humans.

30. The method of claim 18, further comprising:

analyzing a sample from said patient to obtain quantifying data for one or more than one internal standard molecule; and

obtaining a ratio for each of the levels of said one or more than one metabolite marker to the level obtained for the one or more than one internal standard molecule;

wherein the comparing step (b) comprises comparing each ratio to one or more corresponding ratios obtained for the one or more than one reference sample.

31. The method of claim 18, wherein a decrease in the level of said one or more than one metabolite marker in said sample is identified in the comparing step (b).

32. The method of claim 18, wherein the metabolite is a lysophosphatidylcholine (LysoPC) selected from the group consisting of LysoPC 14:0, LysoPC 14:1, LysoPC 16:0, LysoPC 16:1, LysoPC 16:2, LysoPC 18:0, LysoPC 18:1, LysoPC 18:2, LysoPC 18:3, LysoPC 20:1, LysoPC 20:2, LysoPC 20:3, LysoPC 20:4, LysoPC 20:5, LysoPC 20:6, LysoPC 22:3, LysoPC 22:4, LysoPC 22:5, LysoPC 22:6, LysoPC 24:4, LysoPC 24:6, LysoPC 30:1, LysoPC 32:0, LysoPC 32:1, LysoPC 32:2, LysoPC 32:6 and combinations thereof.

33. The method of claim 18, wherein the metabolite is a phosphatidylcholine having a molecular formula selected from the group consisting of $C_{42}H_{78}NO_8P$, $C_{42}H_{80}NO_8P$, $C_{42}H_{82}NO_8P$, $C_{42}H_{84}NO_8P$, $C_{44}H_{78}NO_8P$, $C_{44}H_{80}NO_8P$, $C_{44}H_{82}NO_8P$, $C_{44}H_{84}NO_8P$, $C_{44}H_{86}NO_8P$, $C_{44}H_{88}NO_8P$, $C_{46}H_{78}NO_8P$, $C_{46}H_{80}NO_8P$, $C_{46}H_{82}NO_8P$, $C_{46}H_{84}NO_8P$, $C_{48}H_{80}NO_8P$, $C_{48}H_{82}NO_8P$, $C_{48}H_{84}NO_8P$, $C_{48}H_{86}NO_8P$, and combinations thereof.

34. The method of claim 18, wherein the metabolite is a plasmenylphosphocholine having a molecular formula selected from the group consisting of $C_{42}H_{80}NO_7P$, $C_{42}H_{82}NO_7P$, $C_{42}H_{84}NO_7P$, $C_{44}H_{82}NO_7P$, $C_{44}H_{84}NO_7P$, $C_{44}H_{86}NO_7P$, $C_{44}H_{88}NO_7P$, $C_{46}H_{82}NO_7P$, $C_{46}H_{84}NO_7P$, $C_{46}H_{86}NO_7P$, $C_{48}H_{84}NO_7P$, $C_{48}H_{86}NO_7P$, and combinations thereof.

35. The method of claim 18, wherein the metabolite is a sphingomyelin having a molecular formula selected from the group consisting of $C_{39}H_{79}N_2O_6P$, $C_{39}H_{80}N_2O_6P^+$, $C_{41}H_{81}N_2O_6P$, $C_{41}H_{82}N_2O_6P^+$, $C_{41}H_{83}N_2O_6P$, $C_{41}H_{84}N_2O_6P^+$, $C_{47}H_{93}N_2O_6P$, $C_{47}H_{94}N_2O_6P^+$, $C_{47}H_{95}N_2O_6P$, $C_{47}H_{96}N_2O_6P^+$, and combinations thereof.

36. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{36}H_{62}O_4$, said at least one MS/MS transition in negative ionization mode being selected from the group consisting of 557.4 / 495.4, 557.4 / 539.4, 557.4 / 513.3, 557.4 / 279.2, 557.4 / 277.2, 557.4 / 220.7 and 557.4 / 111.2, and combinations thereof.

37. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{36}H_{62}O_5$, said at least one MS/MS transition in

negative ionization mode being selected from the group consisting of 573.5 / 511.4, 573.5 / 555.3, 573.5 / 537.4, 573.5 / 529.4, 573.5 / 519.4, 573.5 / 493.3, 573.5 / 457.4, 573.5 / 455.3, 573.5 / 443.4, 573.5 / 415.4, 573.5 / 413.3, 573.5 / 411.3, 573.5 / 399.3, 573.5 / 397.3, 573.5 / 389.7, 573.5 / 295.2, 573.5 / 279.2, 573.5 / 277.2, 573.5 / 251.2, 573.5 / 231.1, 573.5 / 223.1, 573.5 / 201.1, 573.5 / 171.1, 573.5 / 169.1, 573.5 / 125.1 and 573.5 / 113.1, and combinations thereof.

38. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{36}H_{64}O_5$, said at least one MS/MS transition in negative ionization mode being selected from the group consisting of 575.5 / 513.5, 575.5 / 557.5, 575.5 / 539.5, 575.5 / 531.5, 575.5 / 499.5, 575.5 / 495.5, 575.5 / 459.4, 575.5 / 417.4, 575.5 / 415.3, 575.5 / 413.3, 575.5 / 403.3, 575.5 / 295.2, 575.5 / 279.2, 575.5 / 260.2, 575.5 / 251.2, 575.5 / 197.9, 575.5 / 119.4, 575.5 / 113.1, and 575.5 / 97.0, and combinations thereof.

39. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{36}H_{66}O_5$, said at least one MS/MS transition in negative ionization mode being selected from the group consisting of 577.5 / 515.4, 577.5 / 559.4, 577.5 / 546.5, 577.5 / 533.5, 577.5 / 497.4, 577.5 / 419.4, 577.5 / 405.5, 577.5 / 297.2 and 577.5 / 281.2, and combinations thereof.

40. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{36}H_{64}O_6$, said at least one MS/MS transition in negative ionization mode being selected from the group consisting of 591.5 / 573.4, 591.5 / 555.4, 591.5 / 528.3, 591.5 / 511.2, 591.5 / 476.1, 591.5 / 419.3, 591.5 / 403.1, 591.5 / 387.3, 591.5 / 297.2, 591.5 / 295.2, 591.5 / 274.0, 591.5 / 255.3, 591.5 / 223.6, 591.5 / 203.5, 591.5 / 201.1, 591.5 / 171.0 and 591.5 / 125.3, and combinations thereof.

41. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{36}H_{66}O_6$, said at least one MS/MS transition in negative ionization mode being selected from the group consisting of 593.5 / 557.5, 593.5 / 575.4, 593.5 / 549.4, 593.5 / 531.5, 593.5 / 513.4, 593.5 / 495.4, 593.5 / 433.3, 593.5 / 421.4, 593.5 / 415.2, 593.5 / 391.4, 593.5 / 371.3, 593.5 / 315.3, 593.5 / 311.1, 593.5 / 297.2, 593.5 / 281.2, 593.5 / 277.2, 593.5 / 251.2, 593.5 / 201.1, 593.5 / 195.3, 593.5 / 171.1, 593.5 / 139.1 and 593.5 / 133.5, and combinations thereof.

42. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{36}H_{68}O_6$, said at least one MS/MS transition in negative ionization mode being selected from the group consisting of 595.5 / 559.5, 595.5 / 577.4, 595.5 / 551.4, 595.5 / 533.4, 595.5 / 515.5, 595.5 / 497.4, 595.5 / 478.4, 595.5 / 433.3, 595.5 / 423.4, 595.5 / 391.3, 595.5 / 372.3, 595.5 / 315.3, 595.5 / 313.2, 595.5 / 298.2, 595.5 / 297.2, 595.5 / 281.2, 595.5 / 279.2, 595.5 / 239.2, 595.5 / 232.9, 595.5 / 171.1, 595.5 / 169.1 and 595.5 / 141.1, and combinations thereof.

43. The method of claim 27, wherein at least one MS/MS transition is identified for the lysophosphatidylcholine metabolite having the molecular formula of $C_{26}H_{50}NO_7P$, said at least one MS/MS transition being selected from the group consisting of 520.3 / 184.2 in positive ionization mode, 564.3 / 504.3 in negative ionization mode, 564.3 / 279.3 in negative ionization mode, and combinations thereof.

44. The method of claim 27, wherein at least one MS/MS transition is identified for the lysophosphatidylcholine metabolite having the molecular formula of $C_{26}H_{54}NO_7P$, said at least one MS/MS transition being selected from the group consisting of 524.3 / 184.2 in positive ionization mode, 568.3 / 508.4 in negative ionization mode, 568.3 / 283.3 in negative ionization mode, and combinations thereof.

45. The method of claim 27, wherein at least one MS/MS transition is identified for the lysophosphatidylcholine metabolite having the molecular formula of $C_{28}H_{48}NO_7P$, said at least one MS/MS transition being selected from the group consisting of 542.3 / 184.2 in positive ionization mode 586.3 / 526.3 in negative ionization mode, 586.3 / 301.2 in negative ionization mode, and combinations thereof.

46. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{42}H_{80}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 758.6 / 184.2 in positive ionization mode 802.6 / 742.6 or 802.6 / 279.2 for PtdCho 16:0/18:2 in negative ionization mode, 802.6 / 742.6 or 802.6 / 255.3 for PtdCho 18:2/16:0 in negative ionization mode, 802.6 / 742.6 or 802.6 / 281.2 for PtdCho 16:1/18:1 in negative ionization mode, 802.6 / 742.6 or 802.6 / 253.2 for PtdCho 18:1/16:1 in negative ionization mode, and combinations thereof.

47. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{44}H_{78}NO_8P$, said at least one MS/MS transition

being selected from the group consisting of 780.6 / 184.2 in positive ionization mode, 824.6 / 764.6 or 824.6 / 279.2 for PtdCho 18:2/18:3 in negative ionization mode, 824.6 / 764.6 or 824.6 / 301.2 for PtdCho 16:0/20:5 in negative ionization mode, 824.6 / 764.6 or 824.6 / 255.2 for PtdCho 20:5/16:0 in negative ionization mode, and combinations thereof.

48. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{44}H_{82}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 784.6 / 184.2 in positive ionization mode, 828.6 / 768.6 or 828.6 / 305.2 for PtdCho 16:0/20:3 in negative ionization mode, 828.6 / 768.6 or 828.6 / 255.2 for PtdCho 20:3/16:0 in negative ionization mode, 828.6 / 768.6 or 828.6 / 279.2 for PtdCho 18:1/18:2 in negative ionization mode, 828.6 / 768.6 or 828.6 / 281.2 for PtdCho 18:2/18:1 in negative ionization mode, and combinations thereof.

49. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{44}H_{84}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 786.6 / 184.2 in positive ionization mode, 830.6 / 770.6 or 830.6 / 279.2 for PtdCho 18:0/18:2 in negative ionization mode, 830.6 / 770.6 or 830.6 / 283.2 for PtdCho 18:2/18:0 in negative ionization mode, 830.6 / 770.6 or 830.6 / 281.2 for PtdCho 18:1/18:1 in negative ionization mode, and combinations thereof.

50. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{46}H_{78}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 804.6 / 184.2 in positive ionization mode, 848.6 / 788.6 or 848.6 / 301.3 for PtdCho 18:2/20:5 in negative ionization mode, 848.6 / 788.6 or 848.6 / 279.2 for PtdCho 20:5/18:2 in negative ionization mode, 848.6 / 788.6 or 848.6 / 327.6 for PtdCho 16:1/22:6 in negative ionization mode, and combinations thereof.

51. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{46}H_{80}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 806.6 / 184.2 in positive ionization mode, 850.6 / 255.2 for PtdCho 22:6/16:0 in negative ionization mode,850.6 / 303.2 for PtdCho 18:2/20:4 in negative ionization mode, and combinations thereof.

52. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{46}H_{82}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 808.6 / 184.2 in positive ionization mode, 852.6 /

792.6 or 852.6 / 301.3 for PtdCho 18:0/20:5 in negative ionization mode, 852.6 / 792.6 or 852.6 / 329.3 for PtdCho 16:0 / 22:5 in negative ionization mode, 852.6 / 792.6 or 852.6 / 303.2 for PtdCho 18:1/20:4 in negative ionization mode, 852.6 / 792.6 or 852.6 / 255.2 for PtdCho 22:5/16:0 in negative ionization mode, and combinations thereof.

53. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{46}H_{84}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 810.6 / 184.2 in positive ionization mode, 854.6 / 794.6 or 854.6 / 303.2 for PtdCho 18:0/20:4 in negative ionization mode, 854.6 / 794.6 or 854.6 / 283.2 for PtdCho 20:4/18:0 in negative ionization mode, 854.6 / 794.6 or 854.6 / 305.3 for PtdCho 18:1/20:3 in negative ionization mode, 854.6 / 794.6 or 854.6 / 307.3 for PtdCho 18:2/20:2 in negative ionization mode, 852.6 / 794.6 or 852.6 / 331.3 for PtdCho 16:0/22:4 in negative ionization mode, and combinations thereof.

54. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{48}H_{80}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 830.6 / 184.2 in positive ionization mode, 874.6 / 814.6 or 874.6 / 327.3 for PtdCho 18:2/22:6 in negative ionization mode, and combinations thereof.

55. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{48}H_{82}NO_8P$, said at least one MS/MS transition being 832.6 / 184.2 in positive ionization mode.

56. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{48}H_{84}NO_8P$, said at least one MS/MS transition being selected from the group consisting of 834.6 / 184.2 in positive ionization mode, 878.6 / 818.6 or 878.6 / 283.2 for PtdCho 22:6/18:0 in negative ionization mode, and combinations thereof.

57. The method of claim 27, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{39}H_{79}N_2O_6P$, said at least one MS/MS transition being selected from the group consisting of 703.6 / 184.2 in positive ionization mode, 747.6 / 687.6 or 747.6 / 168.1 in negative ionization mode, and combinations thereof.

58. The method of claim 25, wherein at least one MS/MS transition is identified for the metabolite having the molecular formula of $C_{47}H_{93}N_2O_6P$, said at least one MS/MS transition

being selected from the group consisting of 813.7 / 184.2 in positive ionization mode, 857.6 / 797.6 or 857.6 / 168.1 in negative ionization mode, and combinations thereof.

59. A method for diagnosing a patient's pancreatic cancer health state, or change in pancreatic cancer health state, or for diagnosing risk of developing pancreatic cancer or the presence of pancreatic cancer in a patient, comprising the steps of:

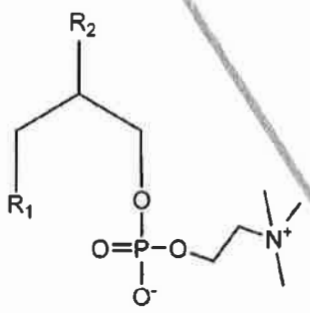
a) analyzing a sample from said patient to obtain quantifying data for one or more than one metabolite marker;

b) comparing the quantifying data for said one or more than one metabolite marker to corresponding data obtained for one or more than one reference sample to identify an increase or decrease in the level of said one or more than one metabolite marker in said sample; and

c) using said increase or decrease in the level of said one or more than one metabolite marker in said sample for diagnosing said patient's pancreatic cancer health state, or change in pancreatic cancer health state, or for diagnosing risk of developing pancreatic cancer or the presence of pancreatic cancer in said patient,

wherein the one or more metabolite marker comprises:

(i) a diacylphosphatidylcholine, plasmanylphosphocholine or plasmenylphosphocholine of Formula (I):



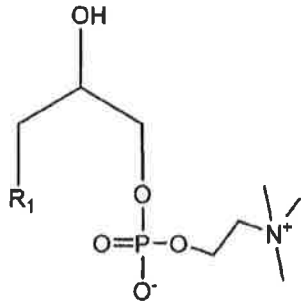
(I)

including adducts or salts thereof, wherein

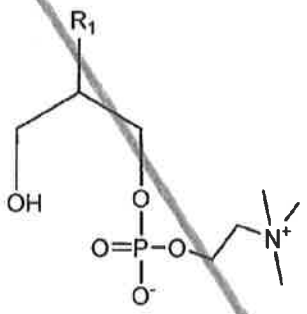
R_1 is a 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:3, 20:4, 20:5, 22:5 or 22:6 fatty acid or alcohol moiety bonded to the glycerol backbone, the bond being an acyl linkage when the metabolite marker comprises a diacylphosphatidylcholine, an ether linkage when the metabolite marker comprises a plasmanylphosphocholine, or a vinyl-ether linkage when the metabolite marker comprises a plasmenylphosphocholine; and

R_2 is a 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:3, 20:4, 20:5, 22:5, or 22:6 fatty acid moiety bonded to the glycerol backbone through an acyl linkage;

(ii) a 2-lysophosphatidylcholine of Formula (II) or 1-lysophosphatidylcholine of Formula (III):



(II)

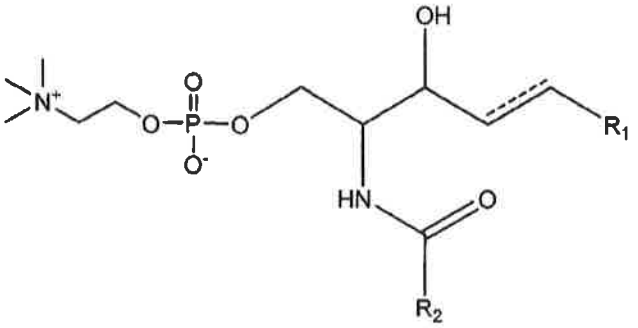


(III)

including adducts or salts thereof, wherein

R_1 is a 14:0, 14:1, 16:0, 16:1, 16:2, 18:0, 18:1, 18:2, 18:3, 20:1, 20:2, 20:3, 20:4, 20:5, 20:6, 22:3, 22:4, 22:5, 22:6, 24:4, 24:6, 30:1, 32:0, 32:1, 32:2 or 32:6 fatty acid moiety bonded to the glycerol backbone through an acyl linkage; or

(iii) a sphingomyelin as defined in Formula (IV):



(IV)

including adducts or salts thereof, wherein the dashed line represents an optional double bond;

R_1 is a C_{13} alkyl group; and

R_2 is a C_{11} to C_{25} alkyl or alkenyl group, said alkenyl group having from 1 to 3 double bonds.

60. The method of claim 59, wherein the quantifying data is obtained using a Fourier transform ion cyclotron resonance, time of flight, magnetic sector, quadrupole or triple quadrupole mass spectrometer.

61. The method of claim 59, wherein the quantifying data is obtained using a Fourier transform ion cyclotron resonance mass spectrometer.

62. The method of claim 60, wherein the mass spectrometer is equipped with a chromatographic system.

63. The method of claim 59, wherein the sample is a blood sample.

64. The method of claim 59, wherein the sample is a blood serum sample.

65. The method of claim 59, wherein the sample is a cerebral spinal fluid sample.

66. The method of claim 59, wherein a liquid/liquid extraction is performed on the sample whereby non-polar metabolites are dissolved in an organic solvent and polar metabolites are dissolved in an aqueous solvent.

67. The method of claim 66, wherein the extracted samples are analyzed by positive or negative electrospray ionization, positive or negative atmospheric pressure chemical ionization, or combinations thereof.

68. The method of claim 66, wherein the extracted samples are analyzed by MS/MS transition.

69. The method of claim 66, wherein the extracted samples are analyzed by extracted ion current (EIC) chromatography and MS/MS transition.

70. The method of claim 59, wherein said one or more than one reference sample is from one or more pancreatic cancer-negative humans.

71. The method of claim 59, further comprising:

analyzing a sample from said patient to obtain quantifying data for one or more than one internal standard molecule; and

obtaining a ratio for each of the levels of said one or more than one metabolite marker to the level obtained for the one or more than one internal standard molecule;

wherein the comparing step (b) comprises comparing each ratio to one or more corresponding ratios obtained for the one or more than one reference sample.

72. The method of claim 59, wherein a decrease in the level of said one or more than one metabolite marker in said sample is identified in the comparing step (b).

73. The method of claim 59, wherein the metabolite is a lysophosphatidylcholine (LysoPC) selected from the group consisting of LysoPC 14:0, LysoPC 14:1, LysoPC 16:0, LysoPC 16:1, LysoPC 16:2, LysoPC 18:0, LysoPC 18:1, LysoPC 18:2, LysoPC 18:3, LysoPC 20:1, LysoPC 20:2, LysoPC 20:3, LysoPC 20:4, LysoPC 20:5, LysoPC 20:6, LysoPC 22:3, LysoPC 22:4, LysoPC 22:5, LysoPC 22:6, LysoPC 24:4, LysoPC 24:6, LysoPC 30:1, LysoPC 32:0, LysoPC 32:1, LysoPC 32:2, LysoPC 32:6 and combinations thereof.

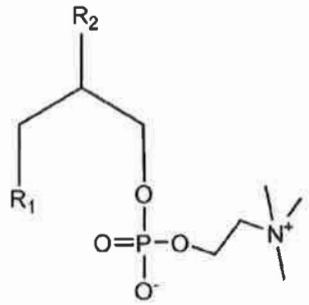
74. The method of claim 59, wherein the metabolite is a phosphatidylcholine having a molecular formula selected from the group consisting of $C_{42}H_{78}NO_8P$, $C_{42}H_{80}NO_8P$, $C_{42}H_{82}NO_8P$, $C_{42}H_{84}NO_8P$, $C_{44}H_{78}NO_8P$, $C_{44}H_{80}NO_8P$, $C_{44}H_{82}NO_8P$, $C_{44}H_{84}NO_8P$, $C_{44}H_{86}NO_8P$, $C_{44}H_{88}NO_8P$, $C_{46}H_{78}NO_8P$, $C_{46}H_{80}NO_8P$, $C_{46}H_{82}NO_8P$, $C_{46}H_{84}NO_8P$, $C_{48}H_{80}NO_8P$, $C_{48}H_{82}NO_8P$, $C_{48}H_{84}NO_8P$, $C_{48}H_{86}NO_8P$ and combinations thereof.

75. The method of claim 59, wherein the metabolite is a plasmenylphosphocholine having a molecular formula selected from the group consisting of $C_{42}H_{80}NO_7P$, $C_{42}H_{82}NO_7P$, $C_{42}H_{84}NO_7P$, $C_{44}H_{82}NO_7P$, $C_{44}H_{84}NO_7P$, $C_{44}H_{86}NO_7P$, $C_{44}H_{88}NO_7P$, $C_{46}H_{82}NO_7P$, $C_{46}H_{84}NO_7P$, $C_{46}H_{86}NO_7P$, $C_{48}H_{84}NO_7P$, $C_{48}H_{86}NO_7P$, and combinations thereof.

76. The method of claim 59, wherein the metabolite is a sphingomyelin having a molecular formula selected from the group consisting of $C_{39}H_{79}N_2O_6P$, $C_{39}H_{80}N_2O_6P^+$, $C_{41}H_{81}N_2O_6P$, $C_{41}H_{82}N_2O_6P^+$, $C_{41}H_{83}N_2O_6P$, $C_{41}H_{84}N_2O_6P^+$, $C_{47}H_{93}N_2O_6P$, $C_{47}H_{94}N_2O_6P^+$, $C_{47}H_{95}N_2O_6P$, $C_{47}H_{96}N_2O_6P^+$, and combinations thereof.

77. A standard comprising:

(i) a diacylphosphatidylcholine, plasmanylphosphocholine or plasmenylphosphocholine of Formula (I):



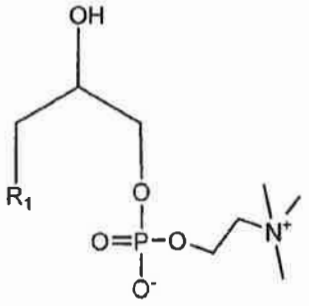
(I)

including adducts or salts thereof, wherein

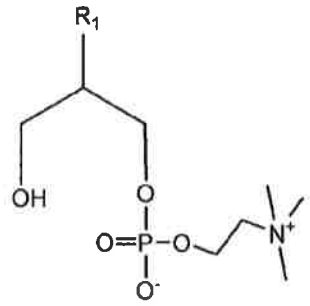
R_1 is a 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:3, 20:4, 20:5 or 22:5 fatty acid or alcohol moiety bonded to the glycerol backbone, the bond being an acyl linkage when the standard comprises a diacylphosphatidylcholine, an ether linkage when the standard comprises a plasmanylphosphocholine, or a vinyl-ether linkage when the standard comprises a plasmenylphosphocholine; and

R_2 is a 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:3, 20:4, 20:5, 22:5, or 22:6 fatty acid moiety bonded to the glycerol backbone through an acyl linkage;

(ii) a 2-lysophosphatidylcholine of Formula (II) or a 1-lysophosphatidylcholine of Formula (III):



(II)

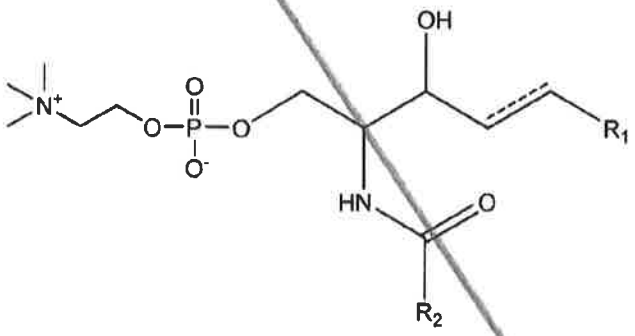


(III)

including adducts or salts thereof, wherein

R_1 is a 14:0, 14:1, 16:0, 16:1, 16:2, 18:0, 18:1, 18:2, 18:3, 20:1, 20:2, 20:3, 20:4, 20:5, 20:6, 22:3, 22:4, 22:5, 22:6, 24:4, 24:6, 30:1, 32:0, 32:1, 32:2 or 32:6 fatty acid moiety bonded to the glycerol backbone through an acyl linkage; or

(iii) a sphingomyelin as defined in Formula (IV):



(IV)

including adducts or salts thereof, wherein the dashed line represents an optional double bond;

R_1 is a C_{13} alkyl group; and

R_2 is a C_{11} to C_{25} alkyl or alkenyl group, said alkenyl group having from 1 to 3 double bonds,

wherein the diacylphosphatidylcholine, plasmanylphosphocholine, plasmenylphosphocholine, lysophosphatidylcholine or sphingomyelin is labeled with a detectable marker.

78. The standard of claim 77, wherein R_2 of the sphingomyelin is a C_{11} alkyl group, a C_{13} alkyl group, a C_{15} alkyl group, a C_{17} alkyl group, a C_{17} alkenyl group with 3 double bonds, a C_{19} alkyl group, a C_{21} alkyl group, a C_{23} alkenyl group with 1 double bond, a C_{23} alkyl group, a C_{24} alkyl group, a C_{25} alkenyl group with 1 double bond, or a C_{25} alkyl group.

79. The standard of claim 77, wherein the lysophosphatidylcholine is selected from the group consisting of LysoPC 14:0, LysoPC 14:1, LysoPC 16:0, LysoPC 16:1, LysoPC 16:2, LysoPC 18:0, LysoPC 18:1, LysoPC 18:2, LysoPC 18:3, LysoPC 20:1, LysoPC 20:2, LysoPC 20:3, LysoPC 20:4, LysoPC 20:5, LysoPC 20:6, LysoPC 22:3, LysoPC 22:4, LysoPC 22:5, LysoPC 22:6, LysoPC 24:4, LysoPC 24:6, LysoPC 30:1, LysoPC 32:0, LysoPC 32:1, LysoPC 32:2, and LysoPC 32:6.

80. The standard of claim 77, wherein the diacylphosphatidylcholine has a molecular formula selected from the group consisting of $C_{42}H_{78}NO_8P$, $C_{42}H_{80}NO_8P$, $C_{42}H_{82}NO_8P$, $C_{42}H_{84}NO_8P$, $C_{44}H_{78}NO_8P$, $C_{44}H_{80}NO_8P$, $C_{44}H_{82}NO_8P$, $C_{44}H_{84}NO_8P$, $C_{44}H_{86}NO_8P$, $C_{44}H_{86}NO_8P$, $C_{46}H_{78}NO_8P$, $C_{46}H_{80}NO_8P$, $C_{46}H_{82}NO_8P$, $C_{46}H_{84}NO_8P$, $C_{48}H_{80}NO_8P$, $C_{48}H_{82}NO_8P$, $C_{48}H_{84}NO_8P$ and $C_{48}H_{86}NO_8P$.

81. The standard of claim 77, wherein the plasmenylphosphocholine has a molecular formula selected from the group consisting of $C_{42}H_{80}NO_7P$, $C_{42}H_{82}NO_7P$, $C_{42}H_{84}NO_7P$, $C_{44}H_{82}NO_7P$, $C_{44}H_{84}NO_7P$, $C_{44}H_{86}NO_7P$, $C_{44}H_{88}NO_7P$, $C_{46}H_{82}NO_7P$, $C_{46}H_{84}NO_7P$, $C_{46}H_{86}NO_7P$, $C_{48}H_{84}NO_7P$, and $C_{48}H_{86}NO_7P$.

82. The standard of claim 77, wherein the sphingomyelin has a molecular formula selected from the group consisting of $C_{39}H_{79}N_2O_6P$, $C_{39}H_{80}N_2O_6P^+$, $C_{41}H_{81}N_2O_6P$, $C_{41}H_{82}N_2O_6P^+$, $C_{41}H_{83}N_2O_6P$, $C_{41}H_{84}N_2O_6P^+$, $C_{47}H_{93}N_2O_6P$, $C_{47}H_{94}N_2O_6P^+$, $C_{47}H_{95}N_2O_6P$, and $C_{47}H_{96}N_2O_6P^+$.

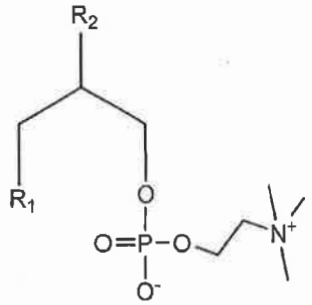
83. The standard of claim 77, wherein the detectable marker is a stable isotope, an enzyme or a protein that enables detection *in vitro*.

84. A kit comprising a standard according to claim 77 and instructions for quantitating an analyte or performing a diagnostic test.

WHAT IS CLAIMED IS:

1. A standard for use in a method to detect pancreatic cancer, or to quantitate a pancreatic cancer marker, comprising:

(i) a diacylphosphatidylcholine, plasmanylphosphocholine or plasmenylphosphocholine of Formula (I):



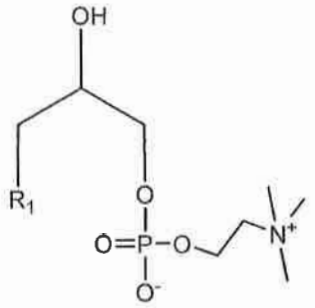
(I)

including adducts or salts thereof, wherein

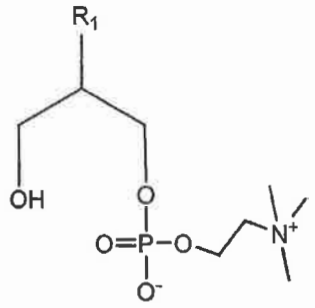
R_1 is a 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:3, 20:4, 20:5 or 22:5 fatty acid or alcohol moiety bonded to the glycerol backbone, the bond being an acyl linkage when the standard comprises a diacylphosphatidylcholine, an ether linkage when the standard comprises a plasmanylphosphocholine, or a vinyl-ether linkage when the standard comprises a plasmenylphosphocholine; and

R_2 is a 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:3, 20:4, 20:5, 22:5, or 22:6 fatty acid moiety bonded to the glycerol backbone through an acyl linkage;

(ii) a 2-lysophosphatidylcholine of Formula (II) or a 1-lysophosphatidylcholine of Formula (III):



(II)

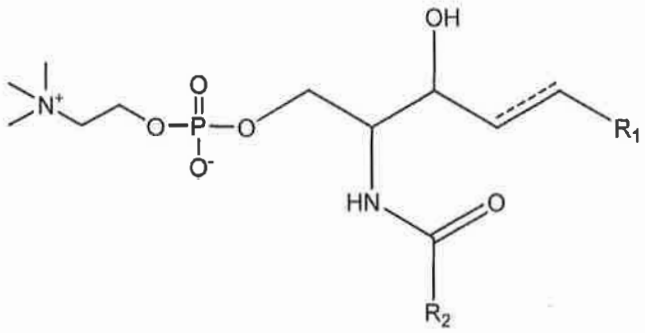


(III)

including adducts or salts thereof, wherein

R_1 is a 14:0, 14:1, 16:0, 16:1, 16:2, 18:0, 18:1, 18:2, 18:3, 20:1, 20:2, 20:3, 20:4, 20:5, 20:6, 22:3, 22:4, 22:5, 22:6, 24:4, 24:6, 30:1, 32:0, 32:1, 32:2 or 32:6 fatty acid moiety bonded to the glycerol backbone through an acyl linkage; or

(iii) a sphingomyelin as defined in Formula (IV):



(IV)

including adducts or salts thereof, wherein the dashed line represents an optional double bond;

R_1 is a C_{13} alkyl group; and

R_2 is a C_{11} to C_{25} alkyl or alkenyl group, said alkenyl group having from 1 to 3 double bonds,

wherein the diacylphosphatidylcholine, plasmanylphosphocholine, plasmenylphosphocholine, lysophosphatidylcholine or sphingomyelin is labeled with a detectable marker.

2. The standard of claim 1, wherein R_2 of the sphingomyelin is a C_{11} alkyl group, a C_{13} alkyl group, a C_{15} alkyl group, a C_{17} alkyl group, a C_{17} alkenyl group with 3 double bonds, a C_{19} alkyl group, a C_{21} alkyl group, a C_{23} alkenyl group with 1 double bond, a C_{23} alkyl group, a C_{24} alkyl group, a C_{25} alkenyl group with 1 double bond, or a C_{25} alkyl group.

3. The standard of claim 1, wherein the lysophosphatidylcholine is selected from the group consisting of LysoPC 14:0, LysoPC 14:1, LysoPC 16:0, LysoPC 16:1, LysoPC 16:2, LysoPC 18:0, LysoPC 18:1, LysoPC 18:2, LysoPC 18:3, LysoPC 20:1, LysoPC 20:2, LysoPC 20:3, LysoPC 20:4, LysoPC 20:5, LysoPC 20:6, LysoPC 22:3, LysoPC 22:4, LysoPC 22:5, LysoPC 22:6, LysoPC 24:4, LysoPC 24:6, LysoPC 30:1, LysoPC 32:0, LysoPC 32:1, LysoPC 32:2, and LysoPC 32:6.

4. The standard of claim 1, wherein the diacylphosphatidylcholine has a molecular formula selected from the group consisting of $C_{42}H_{78}NO_8P$, $C_{42}H_{80}NO_8P$, $C_{42}H_{82}NO_8P$, $C_{42}H_{84}NO_8P$, $C_{44}H_{78}NO_8P$, $C_{44}H_{80}NO_8P$, $C_{44}H_{82}NO_8P$, $C_{44}H_{84}NO_8P$, $C_{44}H_{86}NO_8P$, $C_{44}H_{86}NO_8P$, $C_{46}H_{78}NO_8P$, $C_{46}H_{80}NO_8P$, $C_{46}H_{82}NO_8P$, $C_{46}H_{84}NO_8P$, $C_{48}H_{80}NO_8P$, $C_{48}H_{82}NO_8P$, $C_{48}H_{84}NO_8P$ and $C_{48}H_{86}NO_8P$.

5. The standard of claim 1, wherein the plasmenylphosphocholine has a molecular formula selected from the group consisting of $C_{42}H_{80}NO_7P$, $C_{42}H_{82}NO_7P$, $C_{42}H_{84}NO_7P$, $C_{44}H_{82}NO_7P$, $C_{44}H_{84}NO_7P$, $C_{44}H_{86}NO_7P$, $C_{44}H_{88}NO_7P$, $C_{46}H_{82}NO_7P$, $C_{46}H_{84}NO_7P$, $C_{46}H_{86}NO_7P$, $C_{48}H_{84}NO_7P$, and $C_{48}H_{86}NO_7P$.

6. The standard of claim 1, wherein the sphingomyelin has a molecular formula selected from the group consisting of $C_{39}H_{79}N_2O_6P$, $C_{39}H_{80}N_2O_6P^+$, $C_{41}H_{81}N_2O_6P$, $C_{41}H_{82}N_2O_6P^+$, $C_{41}H_{83}N_2O_6P$, $C_{41}H_{84}N_2O_6P^+$, $C_{47}H_{93}N_2O_6P$, $C_{47}H_{94}N_2O_6P^+$, $C_{47}H_{95}N_2O_6P$, and $C_{47}H_{96}N_2O_6P^+$.

7. The standard of any one of claims 1 to 6, wherein the detectable marker is a stable isotope, an enzyme or a protein that enables detection *in vitro*.

8. A kit for use in a method to detect pancreatic cancer, or to quantitate a pancreatic cancer marker, comprising a standard according to any one of claims 1 to 7, a dilution medium, and instructions for quantitating said marker or performing said detection method.