What is claimed is:

1. A method of detecting one or more multiple-reaction-monitoring (MRM) transitions in a biological sample obtained from a patient, wherein said sample comprises one or more glycans or glycopeptides, comprising:

digesting and/or fragmenting a glycopeptide in the sample; and

detecting a MRM transition selected from the group consisting of transitions 1 - 76.

2. The method of claim 1, wherein the fragmenting a glycopeptide in the sample occurs after introducing the sample, or a portion thereof, into the mass spectrometer.

3. The method of any one of claims 1 or 2, wherein the fragmenting a glycopeptide in the sample produces a glycopeptide ion, a peptide ion, a glycan ion, a glycan adduct ion, or a glycan fragment ion.

4. The method of any one of claims 1-3, wherein the digesting and/or fragmenting a glycopeptide in the sample produces a peptide or glycopeptide:

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76, and combinations thereof;

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 6, 7, 8, 10, 15, 21, 22, 23, 42, 47, 48, 51, 56, 57, 58, 62, 74, and 76, and combinations thereof;

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, 4, 5, 8, 11, 12, 13, 14, 16, 17, 18, 19, 20, 22, 23, 24, 25, 27, 30, 32, 34, 43, 45, 51, 54, 55, 65, 68, 71, 73, 74, 75, and combinations thereof; or

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 36, 56, 62, 66, 73, and 74, and combinations thereof.

5. The method of any one of claims 1-4, wherein the digesting a glycopeptide in the sample produces a peptide or glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76, and combinations thereof.

6. The method of any one of claims 1-4, wherein the fragmenting a glycopeptide in the sample produces a peptide or glycopeptide:

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76, and combinations thereof;

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 6, 7, 8, 10, 15, 21, 22, 23, 42, 47, 48, 51, 56, 57, 58, 62, 74, and 76, and combinations thereof;

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, 4, 5, 8, 11, 12, 13, 14, 16, 17, 18, 19, 20, 22, 23, 24, 25, 27, 30, 32, 34, 43, 45, 51, 54, 55, 65, 68, 71, 73, 74, 75, and combinations thereof; or

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 36, 56, 62, 66, 73, and 74, and combinations thereof.

7. The method of any one of claims 1-6, wherein the MRM transition is selected from the transitions, or any combinations thereof, in any one of Tables 1-5.

8. The method of any one of claims 1-7, further comprising conducting tandem liquid chromatography-mass spectroscopy on the biological sample.

9. The method of any one of claims 1-8, wherein detecting a MRM transition selected from the group consisting of transitions 1 - 76 comprises conducting multiple-reaction-monitoring mass spectroscopy (MRM-MS) mass spectroscopy on the biological sample.

10. The method of any one of claims 1-3 and 7-9, wherein the one or more glycopeptides comprises a peptide or glycopeptide:

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76, and combinations thereof;

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 6, 7, 8, 10, 15, 21, 22, 23, 42, 47, 48, 51, 56, 57, 58, 62, 74, and 76, and combinations thereof;

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, 4, 5, 8, 11, 12, 13, 14, 16, 17, 18, 19, 20, 22, 23, 24, 25, 27, 30, 32, 34, 43, 45, 51, 54, 55, 65, 68, 71, 73, 74, 75, and combinations thereof; or

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 36, 56, 62, 66, 73, and 74, and combinations thereof.

11. The method of any one of claims 1-10, comprising detecting one or more MRM transitions indicative of one or more glycans selected from the group consisting of glycan 3200, 3210, 3300, 3310, 3320, 3400, 3410, 3420, 3500, 3510, 3520, 3600, 3610, 3620, 3630, 3700, 3710, 3720, 3730, 3740, 4200, 4210, 4300, 4301, 4310, 4311, 4320, 4400, 4401, 4410, 4411, 4420, 4421, 4430, 4431, 4500, 4501, 4510, 4511, 4520, 4521, 4530, 4531, 4540, 4541, 4600, 4601, 4610, 4611, 4620, 4621, 4630, 4631, 4641, 4650,4700, 4701, 4710, 4711, 4720, 4730, 5200, 5210, 5300, 5301, 5310, 5311, 5320, 5400, 5401, 5402, 5410, 5411, 5412, 5420, 5421, 5430, 5431, 5432, 5500, 5501, 5502, 5510, 5511, 5512, 5520, 5521, 5522, 5530, 5531, 5541, 5600, 5601, 5602, 5610, 5611, 5612, 5620, 5621, 5631, 5650, 5700, 5701, 5702, 5710, 5711, 5712, 5720, 5721, 5730, 5731, 6200, 6210, 6300, 6301, 6310, 6311, 6320, 6400, 6401, 6402, 6410, 6411, 6412, 6420, 6421, 6432, 6500, 6501, 6502, 6503, 6510, 6511, 6512, 6513, 6520, 6521, 6522, 6530, 6531, 6532, 6540, 6541, 6600, 6601, 6602, 6603, 6610, 6611, 6612, 6613, 6620, 6621, 6622, 6623, 6630, 6631, 6632, 6640, 6641, 6642, 6652, 6700, 6701, 6711, 6721, 6703, 6713, 6710, 6711, 6712, 6713, 6720, 6721, 6730, 6731, 6740, 7200, 7210, 7400, 7401, 7410, 7411, 7412, 7420, 7421, 7430, 7431, 7432, 7500, 7501, 7510, 7511, 7512, 7600, 7601, 7602, 7603, 7604, 7610, 7611, 7612, 7613, 7614, 7620, 7621, 7622, 7623, 7632, 7640, 7700, 7701, 7702, 7703, 7710, 7711, 7712, 7713, 7714, 7720, 7721, 7722, 7730, 7731, 7732, 7740, 7741, 7751, 8200, 9200, 9210, 10200, 11200, 12200, and combinations thereof.

12. The method of claim 11, further comprising quantifying a first glycan and quantifying a second glycan; and further comprising comparing the quantification of the first glycan with the quantification of the second glycan.

13. The method of claim 11 or 12, further comprising associating the detected glycan with a peptide residue site, whence the glycan was bonded.

14. The method of claim 13, further comprising quantifying relative abundance of a glycan and/or a peptide.

15. The method of any one of claims 1-14, comprising normalizing the amount of glycopeptide based on the amount of peptide or glycopeptide consisting essentially of an amino acid having a SEQ ID NOs: 1-76.

16. A method for identifying a classification for a sample, the method comprising

quantifying by mass spectroscopy (MS) one or more glycopeptides in a sample wherein the glycopeptides each, individually in each instance, comprises a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76, and combinations thereof; and

inputting the quantification into a trained model to generate a output probability;

determining if the output probability is above or below a threshold for a classification; and

identifying a classification for the sample based on whether the output probability is above or below a threshold for a classification.

17. The method of claim 16, wherein the glycopeptides each, individually in each instance, comprises a glycopeptide:

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 6, 7, 8, 10, 15, 21, 22, 23, 42, 47, 48, 51, 56, 57, 58, 62, 74, and 76, and combinations thereof;

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, 4, 5, 8, 11, 12, 13, 14, 16, 17, 18, 19, 20, 22, 23, 24, 25, 27, 30, 32, 34, 43, 45, 51, 54, 55, 65, 68, 71, 73, 74, 75, and combinations thereof; or

consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 36, 56, 62, 66, 73, and 74, and combinations thereof.

18. The method of claim 16, wherein the sample is a biological sample from a patient or individual having a disease or condition.

19. The method of claim 18, wherein the patient has cancer, an autoimmune disease, or fibrosis.

20. The method of claim 18, wherein the patient has ovarian cancer.

21. The method of claim 18, wherein the individual has an aging condition.

22. The method of claim 18, wherein the disease or condition is ovarian cancer.

23. The method of claim any one of claims 16-22, wherein the trained model was trained used a machine learning algorithm selected from the group consisting of a deep learning algorithm, a neural network algorithm, an artificial neural network algorithm, a supervised machine learning algorithm, a linear discriminant analysis algorithm, a quadratic discriminant analysis algorithm, a support vector machine algorithm, a linear basis function kernel support vector algorithm, a radial basis function kernel support vector algorithm, a random forest algorithm, a genetic algorithm, a nearest neighbor algorithm, k-nearest neighbors, a naive Bayes classifier algorithm, a logistic regression algorithm, or a combination thereof.

24. The method of any one of claims 16-23, wherein the classification is a disease classification or a disease severity classification.

25. The method of claim 24, wherein the classification is identified with greater than 80 % confidence, greater than 85 % confidence, greater than 90 % confidence, greater than 95 % confidence, greater than 99 % confidence, or greater than 99.9999 % confidence.

26. The method of any one of claims 13-25, further comprising:
quantifying by MS a first glycopeptide in a sample at a first time point;
quantifying by MS a second glycopeptide in a sample at a second time point; and
comparing the quantification at the first time point with the quantification at the second time point.

27. The method of claim 26, further comprising:
quantifying by MS a third glycopeptide in a sample at a third time point;
quantifying by MS a fourth glycopeptide in a sample at a fourth time point; and
comparing the quantification at the fourth time point with the quantification at the third time point.

28. The method of any one of claims 16-27, further comprising monitoring the health status of a patient.

29. The method of any one of claims 16-28, further comprising quantifying by MS a glycopeptide from whence the amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76 was fragmented.

30. The method of any one of claims 16-29, further comprising diagnosing a patient with a disease or condition based on the classification.

31. The method of claim 30, further comprising diagnosing the patient as having ovarian cancer based on the classification.

32. Use of a therapeutic agent selected from the group consisting of a chemotherapeutic, an immunotherapy, a hormone therapy, a targeted therapy, and combinations thereof in the manufacture of a medicament for the treatment of a patient diagnosed as having ovarian cancer according to the method of any one of claims 16-31.

33. Use of a therapeutic agent in the manufacture of a medicament for treating a patient having ovarian cancer, wherein the patient is classified based on an output probability comprising the steps of:

digesting and/or fragmenting one or more glycopeptides in a sample obtained from the patient;

detecting and quantifying one or more multiple-reaction-monitoring (MRM) transitions selected from the group consisting of transitions 1 - 76;

inputting the quantification into a trained model to generate the output probability;

determining if the output probability is above or below a threshold for a classification; and

classifying the patient based on whether the output probability is above or below a threshold for a classification, wherein the classification is selected from the group consisting of:

(A) a patient in need of a chemotherapeutic agent;

(B) a patient in need of a immunotherapeutic agent;

(C) a patient in need of hormone therapy;

(D) a patient in need of a targeted therapeutic agent;

(E) a patient in need of surgery;

(F) a patient in need of neoadjuvant therapy;

(G) a patient in need of chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, before surgery;

(H) a patient in need of chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, after surgery;

(I) or a combination thereof; and

wherein the therapeutic agent is selected from chemotherapy if classification A or I is determined; or

wherein the therapeutic agent is selected from immunotherapy if classification B or I is determined; or

wherein the therapeutic agent is selected from hormone therapy if classification C or I is determined; or

wherein the therapeutic agent is selected from targeted therapy if classification D or I is determined; or

wherein the therapeutic agent is selected from neoadjuvant therapy if classification F or I is determined; or

wherein the therapeutic agent is selected from chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof if classification G or I is determined; or

wherein the therapeutic agent is selected from chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof if classification H or I is determined.

34. A method for diagnosing a patient having ovarian cancer; the method comprising:

performing mass spectroscopy of a biological sample obtained from a patient using MRM-MS with a QQQ and/or qTOF spectrometer to detect and quantify one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-76; or to detect one or more MRM transitions selected from transitions 1-76;

inputting the quantification of the detected glycopeptides or the MRM transitions into a trained model to generate an output probability,

determining if the output probability is above or below a threshold for a classification; and

identifying a diagnostic classification for the patient based on whether the output probability is above or below a threshold for a classification; and

diagnosing the patient as having ovarian cancer based on the diagnostic classification.

35. A glycopeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76, and combinations thereof.

36. A glycopeptide consisting essentially an amino acid sequence selected from the group consisting essentially of SEQ ID NOs: 1 - 76, and combinations thereof.

37. A glycopeptide consisting essentially an amino acid sequence selected from the group consisting essentially of SEQ ID NOs: 1, 6, 7, 8, 10, 15, 21, 22, 23, 42, 47, 48, 51, 56, 57, 58, 62, 74, and 76, and combinations thereof.

38. A glycopeptide consisting essentially an amino acid sequence selected from the group consisting essentially of SEQ ID NOs: 1, 3, 4, 5, 8, 11, 12, 13, 14, 16, 17, 18, 19, 20, 22, 23, 24, 25, 27, 30, 32, 34, 43, 45, 51, 54, 55, 65, 68, 71, 73, 74, 75, and combinations thereof.

39. A glycopeptide consisting essentially an amino acid sequence selected from the group consisting essentially of SEQ ID NOs: 9, 36, 56, 62, 66, 73, and 74, and combinations thereof.