otherwise be diagnosed with ovarian cancer are not and thereby fail to receive proper follow-up medical attention.

[005] As an alternative, mass spectroscopy (MS) offers sensitive and precise measurement of cancer-specific biomarkers including glycopeptides. *See*, for example, Ruhaak, L.R., *et al.*, Protein-Specific Differential Glycosylation of Immunoglobulins in Serum of Ovarian Cancer Patients DOI: 10.1021/acs.jproteome.5b01071; *J. Proteome Res.*, 2016, 15, 1002−1010 (2016); also Miyamoto, S., *et al.*, Multiple Reaction Monitoring for the Quantitation of Serum Protein Glycosylation Profiles: Application to Ovarian Cancer, DOI: 10.1021/acs.jproteome.7b00541, J. Proteome Res. 2018, 17, 222−233 (2017), the entire contents of which are herein incorporated by reference in its entirety for all purposes. However, using MS to diagnose cancer, generally, or ovarian cancer specifically, has not been demonstrated to date in a clinically relevant manner.

[006] What is needed are new biomarkers and new methods of using MS to diagnose disease states such as cancer using these biomarkers. Set forth herein in the disclosure below are such biomarkers comprising glycans, peptides, and glycopeptides, as well as fragments thereof, and methods of using the biomarkers with MS to diagnose ovarian cancer.

SUMMARY

[006a] In one aspect, provided herein is 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.

[006b] In another aspect, provided herein is 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 as described herein.

[006c] In another aspect, provided herein is 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.

[006d] In another aspect, provided herein is 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.

[006e] In another aspect, provided herein is a glycopeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76, and combinations thereof.

[006f] In another aspect, provided herein is a glycopeptide consisting essentially an amino acid sequence selected from the group consisting essentially of SEQ ID NOs: 1 - 76, and combinations thereof.

[006g] In another aspect, provided herein is 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.

[006h] In another aspect, provided herein is 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.

[006i] In another aspect, provided herein is 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.

[007] In another embodiment, set forth herein is a glycopeptide or peptide consisting of, or consisting essentially of, an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 76.

[008] In another embodiment, set forth herein is a method for detecting one or more MRM transitions, comprising: obtaining a biological sample from a patient; digesting and/or fragmenting a glycopeptide in the sample; and detecting a multiple-reaction-monitoring (MRM) transition selected from the group consisting of transitions 1 - 76, as described herein.

[009] In another embodiment, set forth herein 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 an output probability; determining if the output probability is above or below a threshold for a classification; and identifying a