Supporting Figure 1: Density of technical replicate differences among the triplicate replicates of each of the TOCPA PRM analyses of the ten biomarker proteins in sera from six ovarian cancer (red) and seven control patients (black).
Supporting Figure 2: Log₂-transformed, normalized cancer/control peptide ratios as determined by DIA of sera from six ovarian cancer and seven control (healthy) individuals. (A) DIA technical replicate #1, (B) DIA technical replicate #2, and (C) DIA technical replicate #3.
Supporting Figure 3: Boxplots depicting the relative abundance of 11 ApoA-IV peptides quantified by DIA mass spectrometry analysis of sera from six ovarian cancer and seven control (healthy) patients.
Supporting Figure 4: Retention Times for ApoA-IV tryptic peptides quantified in three technical replicates by DIA mass spectrometry of sera from six ovarian cancer and seven control (healthy) patients.
Supporting Figure 5: Plots depicting the Log2 cancer/control fold-change for targeted peptides from three technical replicate PRM analyses of three (AFM, ApoA-I, and ApoA-IV) of the ten biomarkers in the TOPCA assay. The error bars indicate 95% confidence intervals that were determined by Skyline for the triplicate PRM analyses of each peptide.
Supporting Figure 6: Plots depicting the Log₂ cancer/control fold-change for targeted peptides from three technical replicate PRM analyses of five (ApoC-III, CRP, HP, IGF-II, and SAA) of the ten biomarkers in the TOPCA assay. The error bars indicate 95% confidence intervals that were determined by Skyline for the triplicate PRM analyses of each peptide.
Supporting Figure 7: Plots depicting the Log₂ cancer/control fold-change for targeted peptides from three technical replicate PRM analyses of two (TF and TTR) of the ten biomarkers and of the five PRTC internal standard peptides in the TOPCA assay. The error bars indicate 95% confidence intervals that were determined by Skyline for the triplicate PRM analyses of each peptide.
Supporting Figure 8: Bar graph of the rank-ordered protein Mean Decrease in GINI index from RF analyses of TOPCA proteins. The arrows indicate two apparent break points in the decreasing MDG indexes while the red line indicates the monotonic decrease in MDG indexes from ApoA-I to ApoC-III.
Supporting Figure 9: Relative significance of peptides in Random Forest analyses of PRM data for 10 ovarian cancer biomarkers in sera ranked by MDG index.
Supporting Figure 10: Protein MDG Index as a function of Fold-Change p-value.
Supporting Figure 1: Scatter plots depicting the mean total transition peak areas (Supporting Table 14) from three technical replicate PRM analyses of the ten biomarkers in the TOPCA assay. As indicated by the red arrowhead line in the Apolipoprotein A-IV plot, a breakpoint of 5.95E+07 provides perfect classification of sera from ovarian cancer versus control patients.
Supporting Figure 12: Three dimensional plot depicting the accuracy of Random Forest (RF) classification of sera from seven control and six ovarian cancer patients based on triplicate TOCPA analyses of ten biomarker proteins. The RF analyses were carried out with either 500 (blue) or 10,000 trees (red).
Supporting Figure 13: Box plot of mean transition peak areas for TOCPA proteins. The pink (cancer) and green (control) boxes depict the first and third quartiles for each of the indicated proteins while the lines indicate the range or inner fence (when there are outliers). The inner fence is equal to 1.5x range of first and third quartiles. The pink and green dots indicate outliers while the black dot indicates the values for ovarian cancer sample R827.
Supporting Figure 14: Trajectory of mean ApoA-IV transition peak area in technical replicates of sera from six patients with ovarian cancer as a function of disease stage. On the above graph 1 = stage IC, 2 = stage IIC, 3 = stage IIIC, 4 = stage IVC, and 5 = stage “X” which is advanced disease with disseminated carcinomatosis throughout the peritoneal cavity that cannot be removed by surgery.