

Supplementary figure legends

Supplementary figure 1:

For the analysis of data distribution, the SQ-SRM based protein ratios (x-axis) were plotted within a 0.5 window against the number of animals displaying the respective ratios (y-axis). Student's T-test, Wilcoxon rank sum test, and the Kolmogorov-Smirnov test were performed to calculate the significance of differences between the groups. Apoe, Mbl2, and Psp exhibited the highest significance in group differences among the set of 13 candidates tested.

Supplementary figure 2:

The Scaffold software (version 3_00_03, Proteome Software Inc.) was used to generate spectra from QTrap4000 MS/MS validation of the 6 heavy peptides used for the absolute quantification of Apoe, Mbl2, and Psp.

Supplementary figure 3:

A response curve for each of the six heavy peptides was generated in depleted and digested NZO plasma. Three technical repetitions were performed at nine concentration points, complemented by blanks and double blank runs. Peak area values were averaged across transitions and replicates. First order polynomial regression was used to fit the serial dilution data points for each curve, using a 1/y weighting on all points having a correlation coefficient of > 0.99 (Prism software, version 5, GraphPad). All curves are plotted on a logarithmic scale. The curves demonstrate a linear range of the assays of up to 3 - 4 orders of magnitude. The limits of detection (LOD) and limits of quantification (LOQ) were calculated according to Whiteaker et al. (4) as averaged background signals from the blank runs plus three times the standard deviation (LOD, indicated as green dot) or ten times the standard deviation (LOQ, indicated as red dot).