



**Figure S2.**

A) Heatmap showing significance of associations for all 1297 protein changes with clinical variable changes using only the surgery group. Clustering of values results in 6 major clusters for proteins and 9 major clusters for clinical variables.

B) Heatmap showing proteins from A) with the most significant associations with a clinical variable and their functional annotation. Significance level is Bonferroni-corrected p-value ( $p \leq 0.05/1297/20 = 1.9 \times 10^{-6}$ ) for 1297 proteins and 20 clinical variables. DMINC is not shown as it only has one protein (RBM39) significantly associated with it.

Values in the first column represent  $(\text{sign}(\beta) \cdot (-1) \log_{10}(\text{p-value}))$  from a regression model. Red indicates high significance of the association of a 12-year increase in protein with weight loss or with a decrease in the clinical variable (negative beta coefficient). Blue indicates high significance of the association of a 12-year decrease in protein with weight loss or with a decrease in the clinical variable (positive beta coefficient). Green indicates the functional annotation for the protein.

FM: fat mass; FFM: fat free mass; FRS: REE: resting energy expenditure; TG: triglycerides; SBP and DBP: systolic and diastolic blood pressure; Framingham risk score for 10-year CAD risk; DMINC and DMREM: diabetes incidence and remission at 12 years.