## SUPPLEMENTARY INFORMATION

## Comparative analysis of obesity-related cardiometabolic and renal biomarkers in human plasma and serum

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**Supplementary Figure S1.** Inclusion/exclusion of proteins in the comparative and correlation analyses. Four multiplex panels were selected on the basis of their relevance to obesity-related diseases. Of the 368 proteins analyzed in the four multiplex panels (10 of which were measured in duplicate panels), one protein was excluded due to technical issues, and 9 proteins were excluded because they were undetectable in plasma and serum. For the comparative analysis, 23 additional proteins were excluded because values were missing in >30% of the samples in all of the four groups (lean plasma, lean obese, obese plasma, obese serum). For the correlation analysis, a further 19 proteins were excluded because values were missing in >30% of the samples in any of the four groups. For proteins that passed the cut-off criteria, any missing values were replaced with limit of detection values for that protein.



## **Enrichment Analysis** [25/34, ES=2.2] Neutrophil chemotaxis GO:0030593 Granulocyte chemotaxis, leukocyte Regulation of Ser/Thr kinase activity GO:0071900 [20/27, ES=2.2]chemotaxis, response to IL-1, [17/22, ES=2.3] Cellular calcium ion homeostasis GO:0006874 response to TNF, chemokine Cellular component disassembly GO:0022411 [13/16, ES=2.4] signaling pathway Rheumatoid arthritis hsa05323 [17/24, ES=2.1] [13/17, ES=2.2] Activation of organelle organization GO:0010638 Degradation of the extracellular Regulation of protein complex assembly [10/12 ES=2.4] GO:0043254 matrix, activation of MMPs. Pathways in cancer hsa05200 [19/30, ES=1.9] Wound healing GO:0042060 [26/46, ES=1.7] Regulation of vascular permeability, hsa05219 [8/9, ES = 2.6]Bladder cancer regulation of epithelial cell migration. Regulation of cell division GO:0051302 [9/11, ES=2.4] PID P75 NTR PATHWAY [6/6, ES=2.3] M153 Platelet activation, signaling and Inhibition of endopeptidase activityin apoptosis GO:0043154 [7/8, ES=2.6] aggregation. Phosphatidylinositol-mediated signaling GO:0048015 [12/18, ES=2.0] R-HSA-186797 [6/7, ES=2.5] Signaling by PDGF Regulation of lymphocyte migration GO:2000401 [7/9, ES=2.3] 0 6 2 4 -log10(P)

Supplementary Figure S2. Detectability of proteins in plasma versus serum. Heatmaps showing concentrations of protein biomarkers in plasma versus serum in (a) lean subjects (n = 11) and (b) obese subjects (n = 11). Relative protein concentrations are reported as z-scores. (c) Enrichment analysis of the proteins that exhibited significantly different concentrations in plasma versus serum as shown in Figure 1.



**Supplementary Figure S3.** Obesity-induced increase in PAI-1 concentrations in plasma and serum. PAI-1 concentrations in plasma and serum from lean and obese subjects (n = 11 per group) as detected by (a) the cardiovascular III panel of the proximity extension assay and (b) ELISA. Data are presented as mean ± SEM. In (a), values are reported as normalized protein expression (NPX) values, an arbitrary unit on a log<sub>2</sub> scale. For comparison, ELISA values in (b) are presented on a log<sub>2</sub> scale.



**Supplementary Figure S4.** Inclusion/exclusion of lipids in the comparative and correlation analyses. Of the 76 lipids analyzed, two were excluded from the comparative analysis because values were missing in >30% of the samples in all of the four groups (lean plasma, lean obese, obese plasma, obese serum) and one further lipid was excluded from the correlation analysis because values were missing in >30% of the samples in any of the four groups. For lipids that passed the cut-off criteria, any missing values were replaced with half of the minimum value detected for that lipid.



**Supplementary Figure S5.** Detectability of lipids in plasma versus serum. Heatmaps showing concentrations of lipids in plasma versus serum in (a) lean subjects (n = 11) and (b) obese subjects (n = 11).

**Supplementary Table S1.** The full list and names of the proteins analyzed in the four multiplex panels: inflammation, cardiometabolic, cardiovascular II and cardiovascular III. The number of missing values for respective protein is noted and highlighted if values were missing in >30% of the samples of the groups.

**Supplementary Table S2.** The full list and names of the lipids analyzed. The number of missing values for respective lipid is noted and highlighted if values were missing in >30% of the samples of the groups.

**Supplementary Table S3.** Metascape result from the pathway enrichment analysis of proteins that differed significantly between plasma and serum. The 325 unique proteins that survived the cut-off criteria comprise the background list. A Gene Ontology category was deemed significantly enriched if the p value was lower than 0.01 and displayed a minimum enrichment of 1.5.

**Supplementary Table S4.** Correlations of protein concentrations in plasma versus serum in lean and obese individuals. Proteins that showed significant correlations in Table 3 are shown and are ordered on the basis of difference in correlation between lean and obese (from highest to lowest). p values were adjusted by the Holm-Bonferroni multiple comparison test.

**Supplementary Table S5.** Correlations of lipid concentrations in plasma versus serum in lean and obese individuals. Lipids that showed significant correlations in Table 4 are shown and are ordered on the basis of difference in correlation between lean and obese (from greatest to smallest). p values were adjusted by the Holm-Bonferroni multiple comparison test.