**Supplementary Figure 1: Replicability of proteome analyses.**

For replicate secretome samples, the label-free quantitative profile of each sample was compared to the other samples from the same group and plotted as log transformed scatterplots. Data from NCM, LR-UM and HR-UM are shown in (A), (B) and (C) respectively.

**Supplementary Figure 2: Correlation heatmap of replicability of proteome analyses.**

For each set of secretome replicates, the Pearson correlation coefficient was high, and this was true also between LR and HR UM subsets. Between sample groups, however, the correlation coefficients were lower.

**Supplementary Figure 3: Subset of proteins differentially expressed in HR-UM only compared with both LR-UM and NCM.**

Box and whisker plots of the 33 proteins up-regulated (**A**) or the 20 proteins that are down-regulated (**B**), between HR-UM and LR-UM/NCMs (see main manuscript for discussion).