For SOMAscan, median normalized relative abundances of the 1305 analytes were imported into R (version 3.3.2) using the SomaDataIO package, and were analyzed using empirical Bayesian Analysis (LIMMA, Bioconductor package) that accounted for distribution of global protein expression, outliers, and likely false positives.

Steps for analysis:

1. Log_2 transform the *Somascan* data after adding a pseudo-count of 1. Each column represents a protein and the rows represent the samples for both groups.
2. For each protein, a generalized linear model is fitted to the vector of protein expression values.
3. The protein level model is then linked to a global parameter using empirical Bayes methods. This allows a more robust estimate of the per-protein parameters by sharing the information across the different protein measurements.
4. P-values for the group contrast (adverse vs favorable remodelers) are then extracted from the model fit.
5. A volcano plot of logFC on the x-axis and -log10(P.Value) on the y-axis is then plotted to highlight the proteins differentially expressed between the groups at a significance level of P.Value < 0.05 and a fold change > 1.4