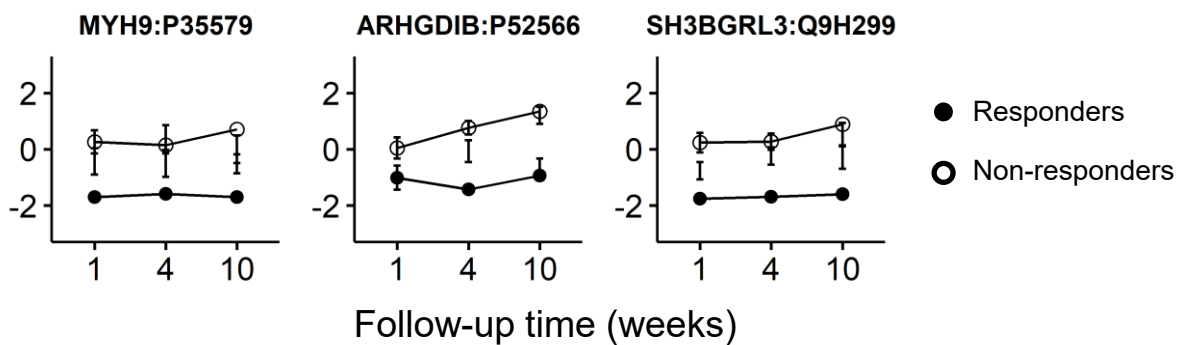


Figure S1: Box plots for protein abundances in each LC-MS/MS run. Protein abundances (a) before and (b) after endogenous protein-based normalization. (c) Two-dimensional global t-SNE map comparing the responders (blue) and non-responders (red) at each sampling time (1, 4, and 10 weeks) and 3 t-SNE parameters of perplexity. (d) Plasma protein log₂ abundances (ng/mL) in the Plasma Proteome Database (bottom) and normalized protein abundance (right).

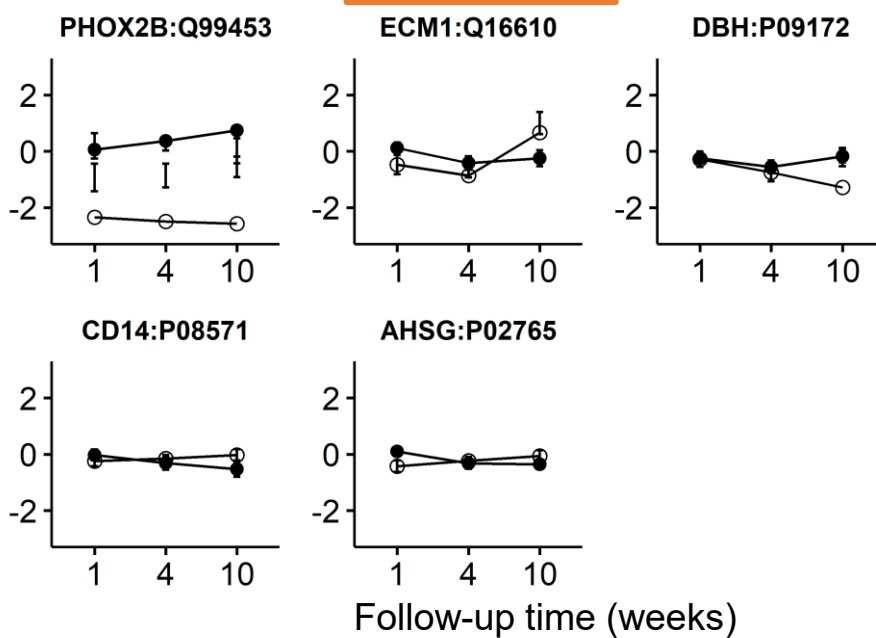
Log_2 (fold difference vs. T_0)

Cluster 1



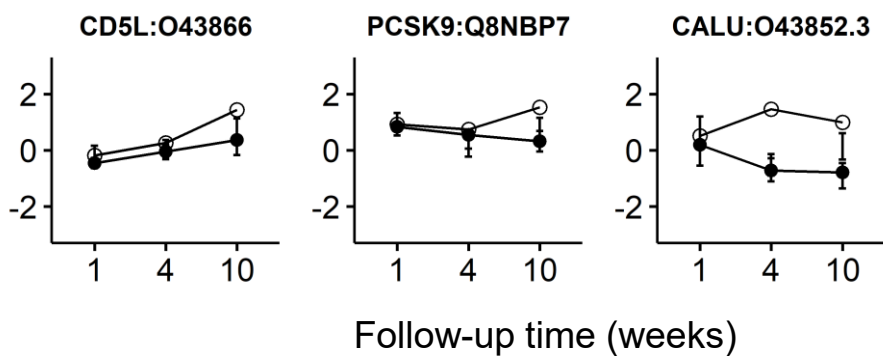
Log_2 (fold difference vs. T_0)

Cluster 2

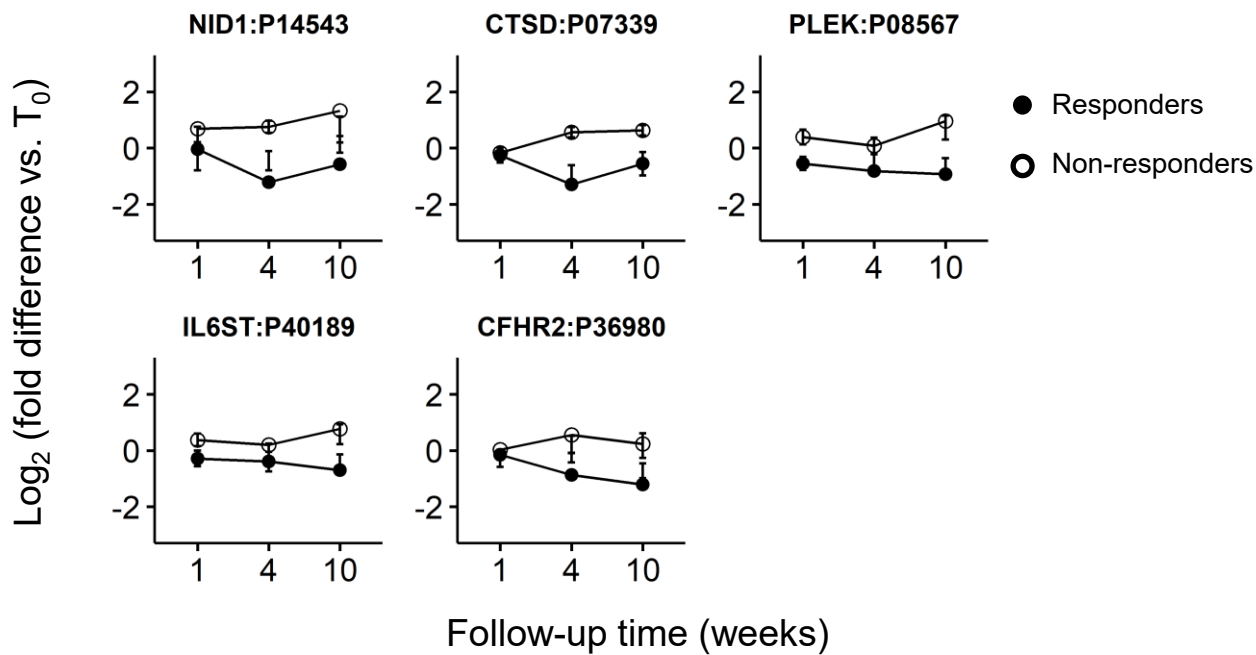


Log_2 (fold difference vs. T_0)

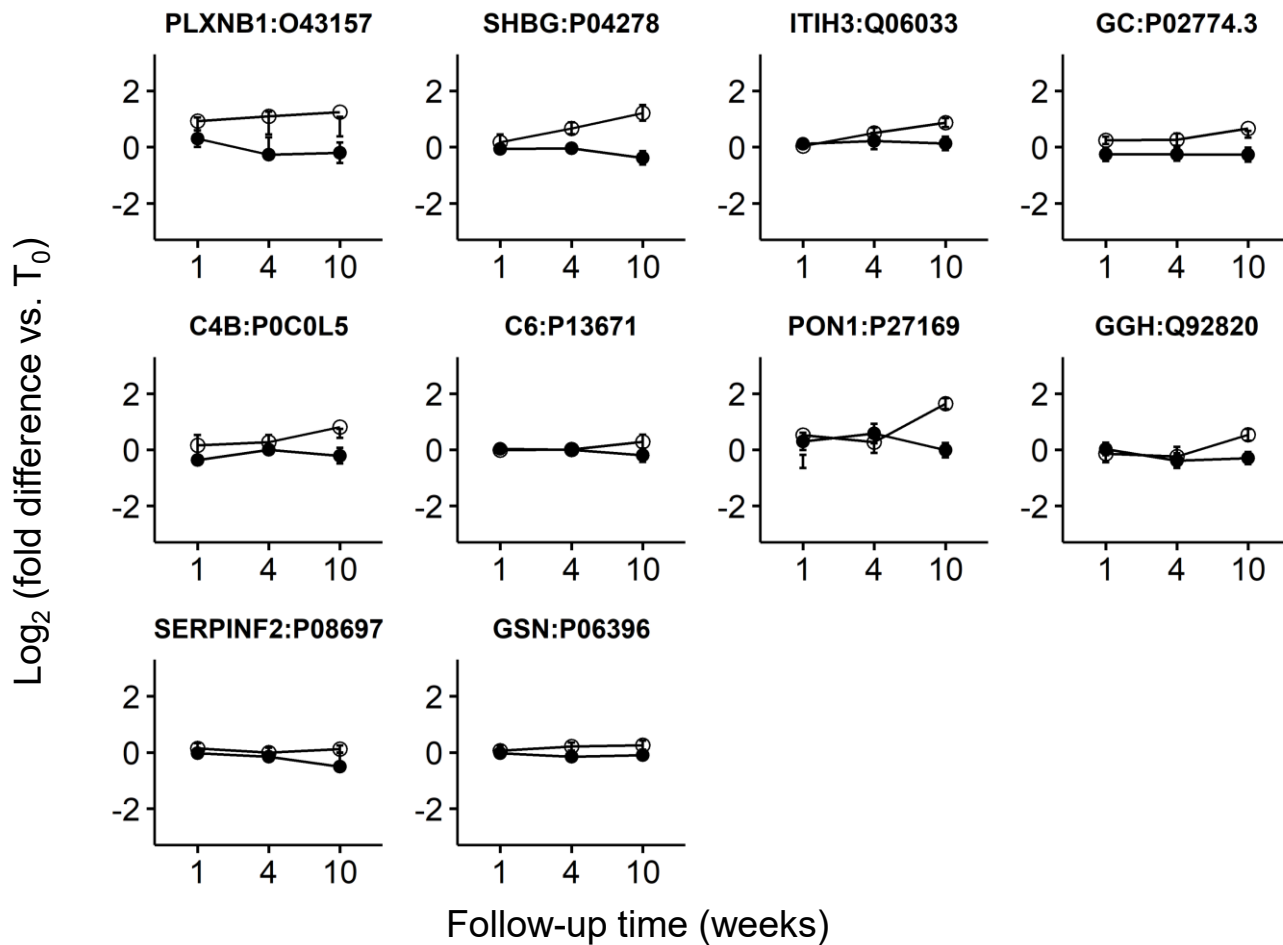
Cluster 3



Cluster 4



Cluster 5



Cluster 6

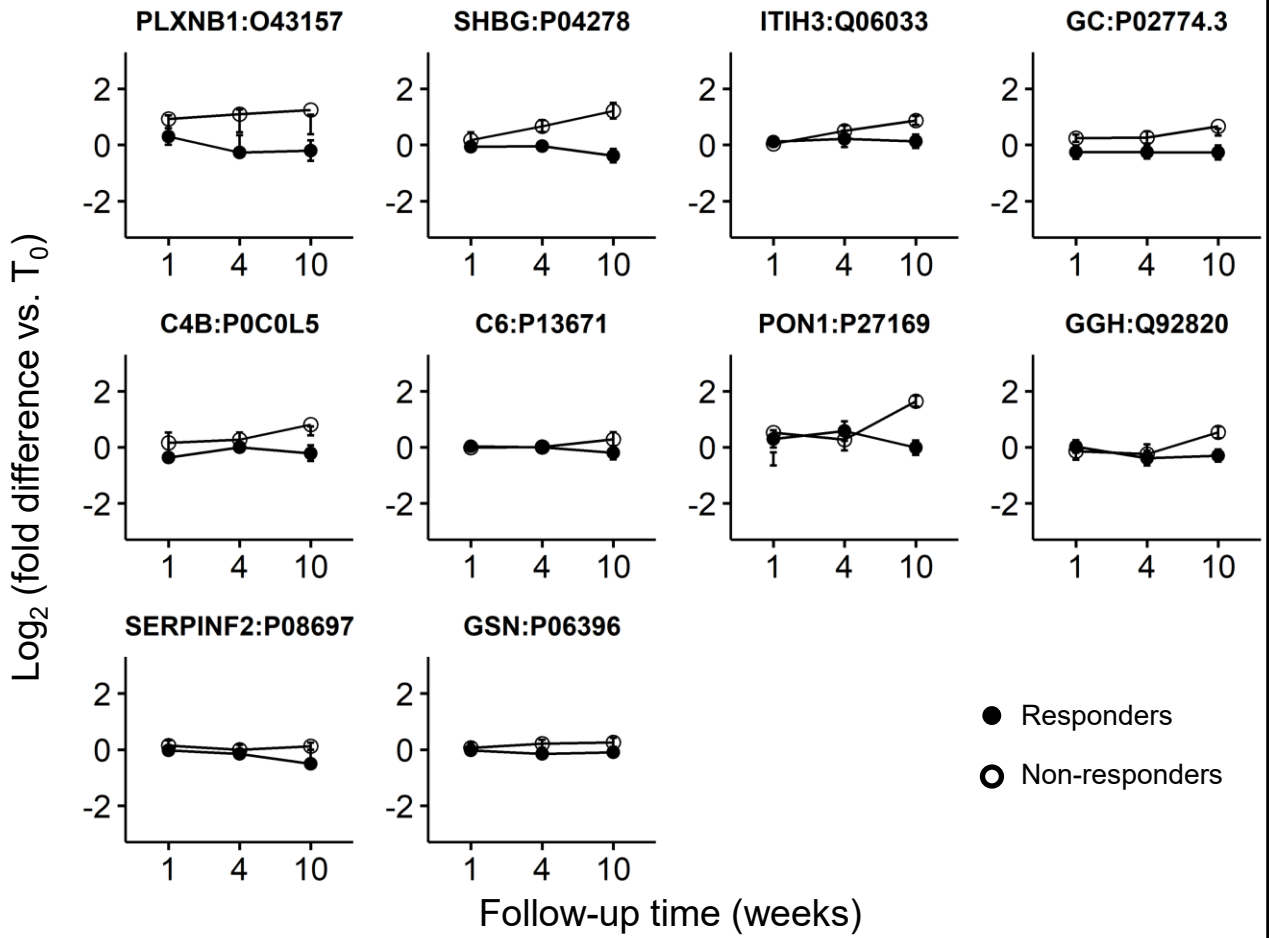


Figure S2: Changes in responders over time to the amounts of 37 significant proteins belonging to six clusters, as determined by response/time interaction. Clusters 1 through 6 included 3, 5, 3, 5, 10 and 11 proteins, respectively.

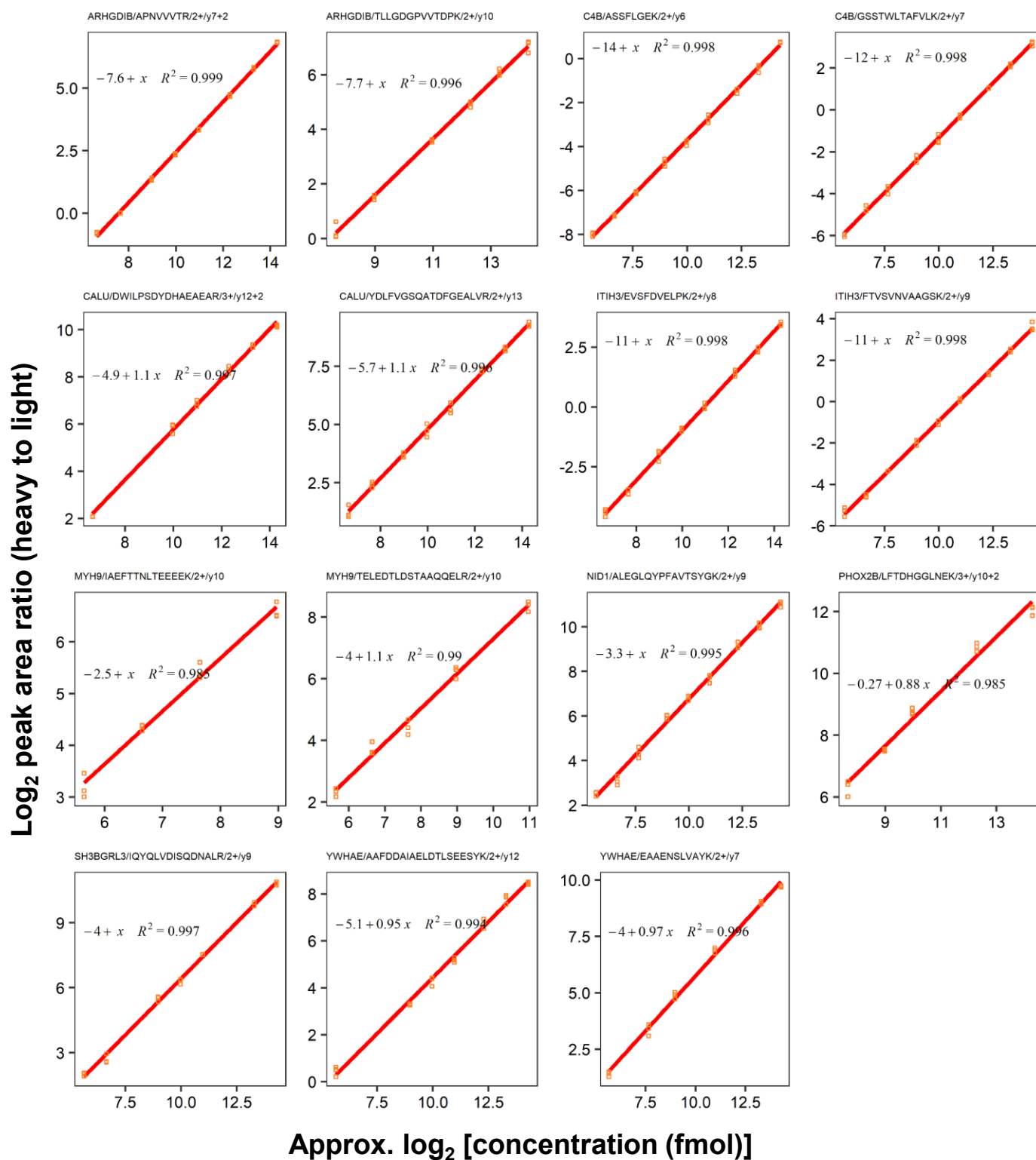


Figure S3: Calibration curves of 15 surrogate peptides relative to nine proteins based on heavy-to-light extracted ion chromatogram ratio.

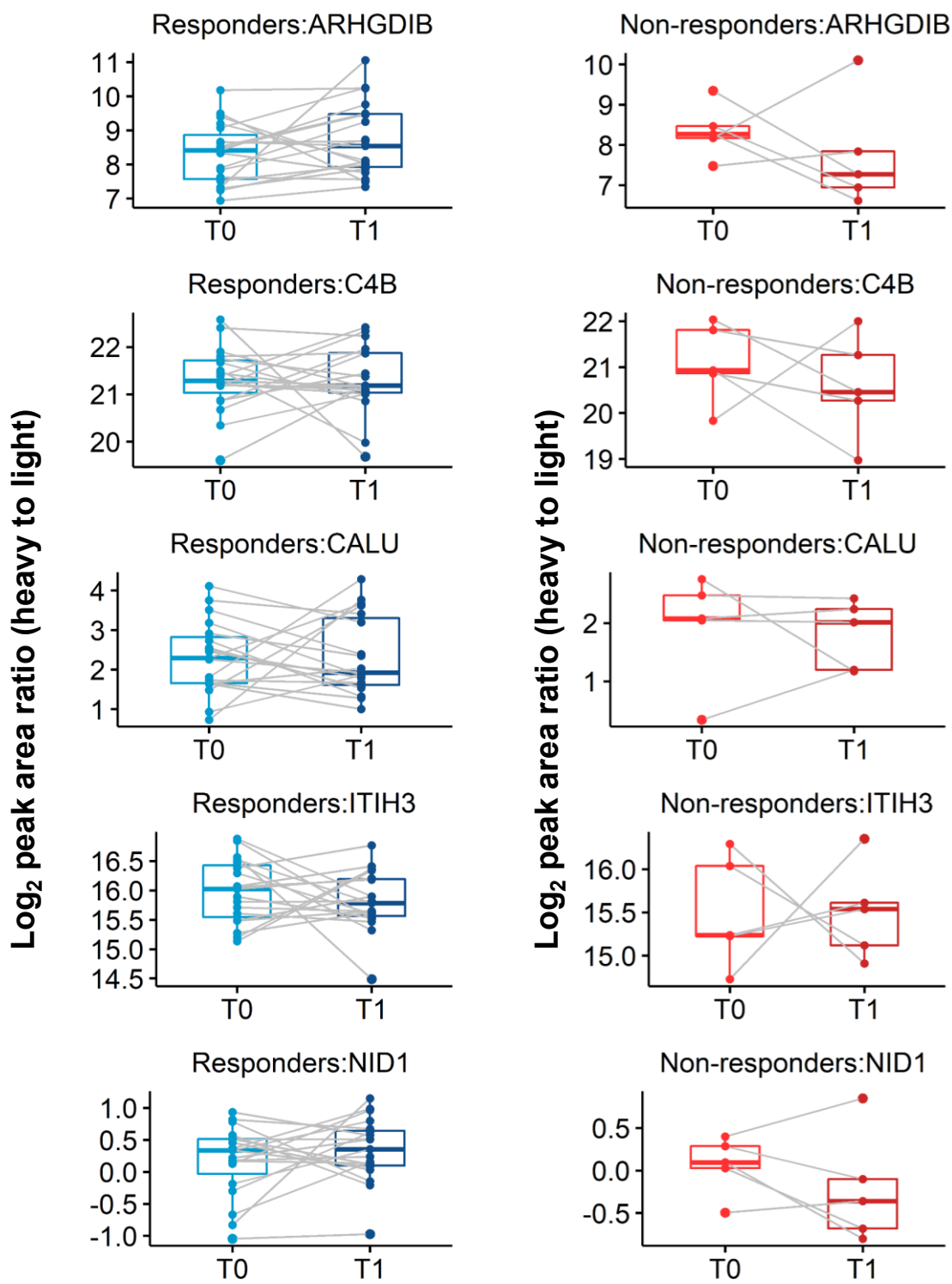


Figure S4: MRM results of five proteins at T₀ vs. T₁. Boxplot of five quantified proteins paired at T₀ and T₁ in responders (blue color) and non-responders (red color).