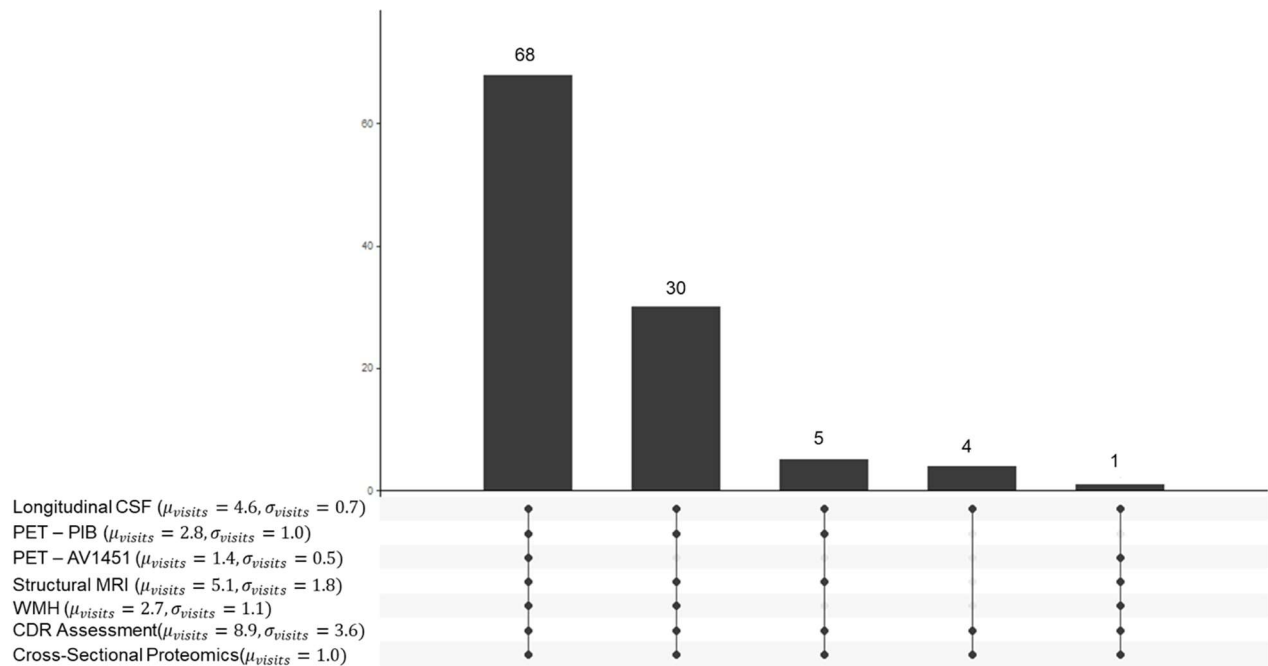
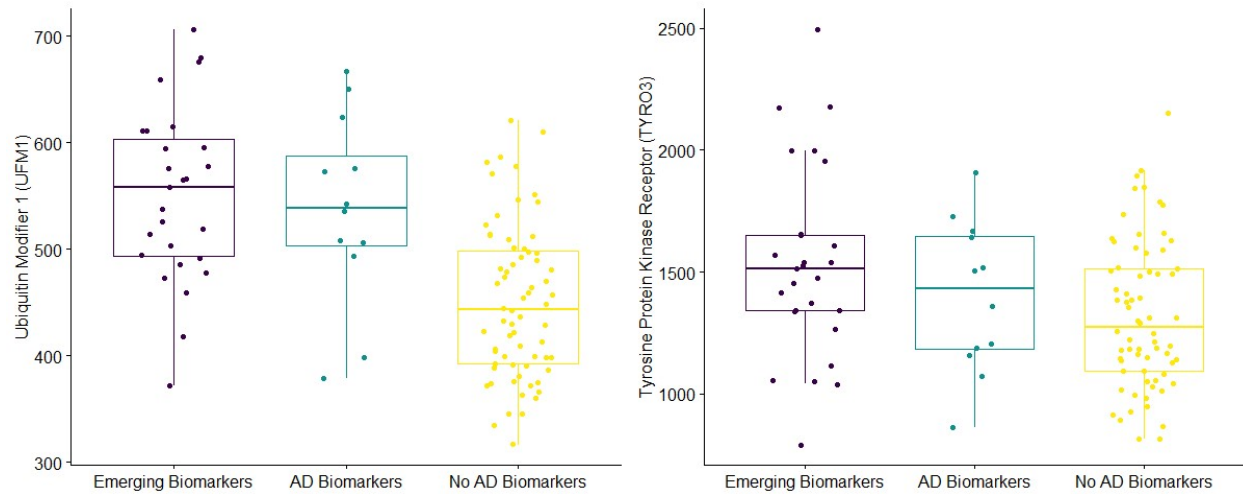


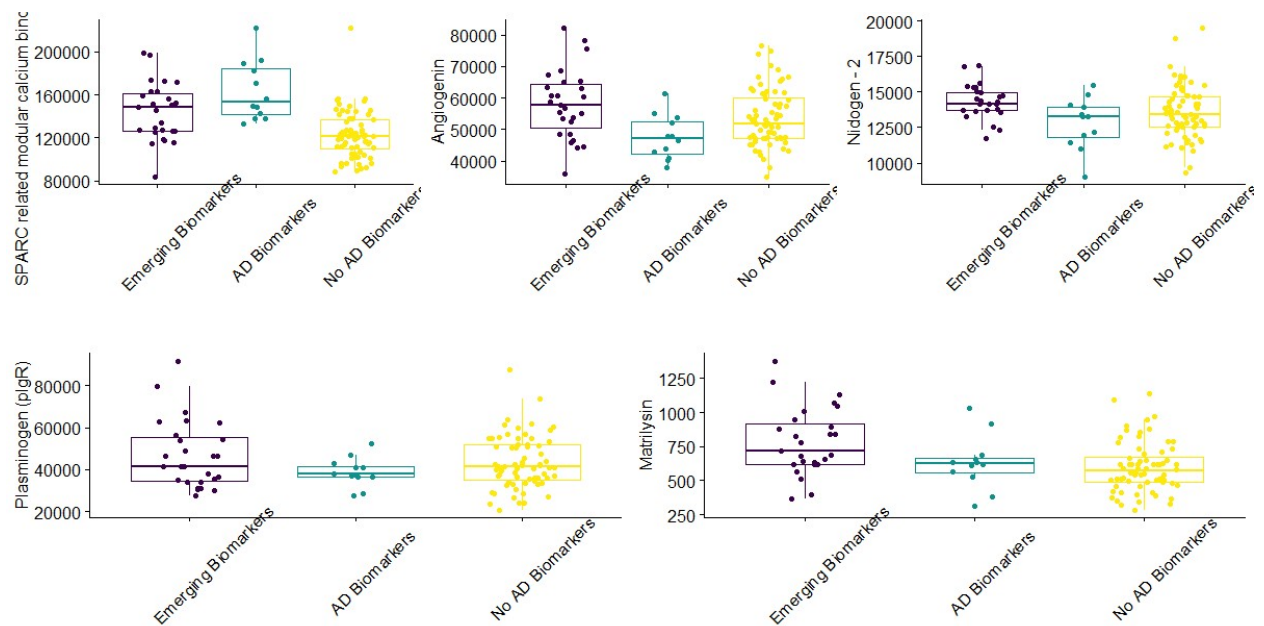
SUPPLEMENTAL MATERIALS



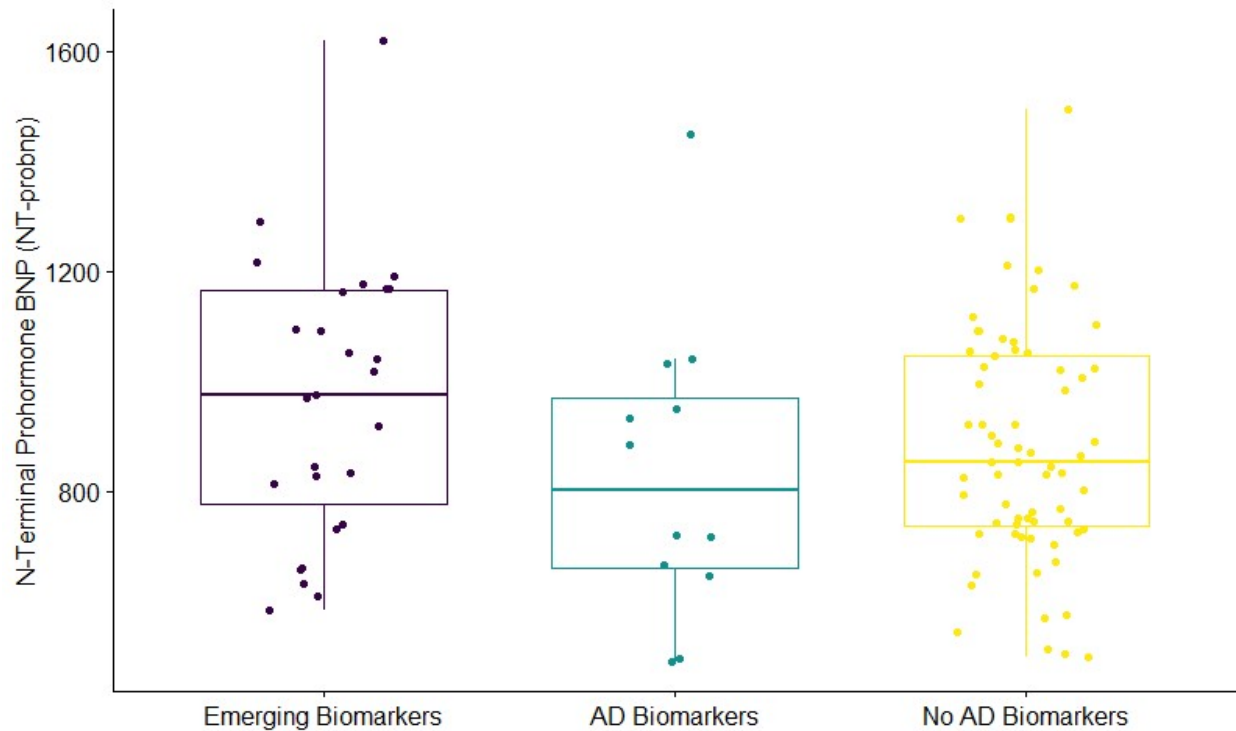
Supplemental Figure 1. Most (N = 68) participants provided all biomarkers and cognitive measures considered in this manuscript. The most frequent missing biomarker was PET – Tau (N = 39). For all measures considered except proteomics, longitudinal data was included where available. The mean number of visits is included in the image.



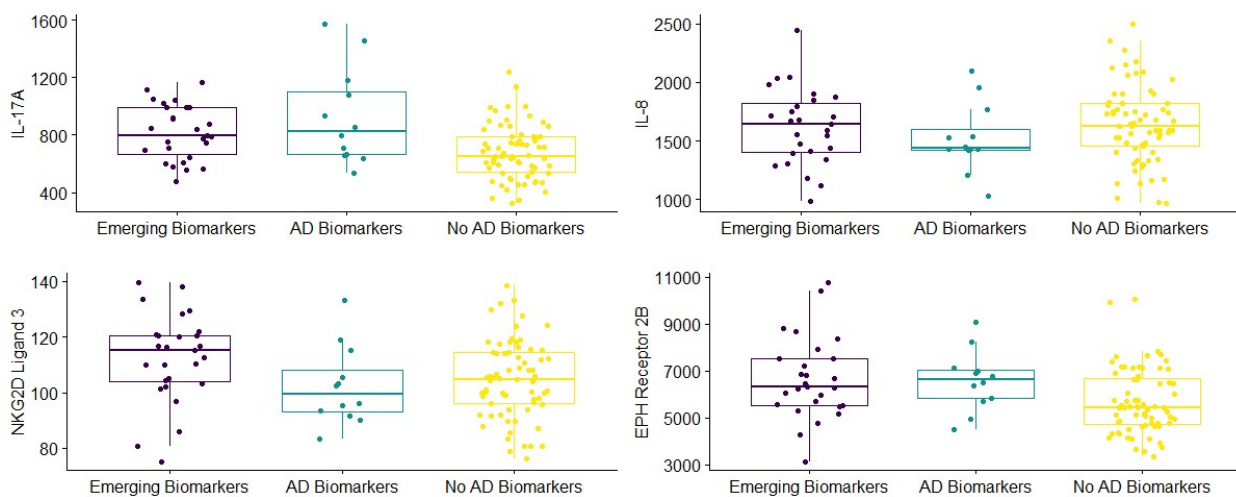
Supplemental Figure 2. Quantification of protein expression for identifying proteins associated with amyloid production and regulation



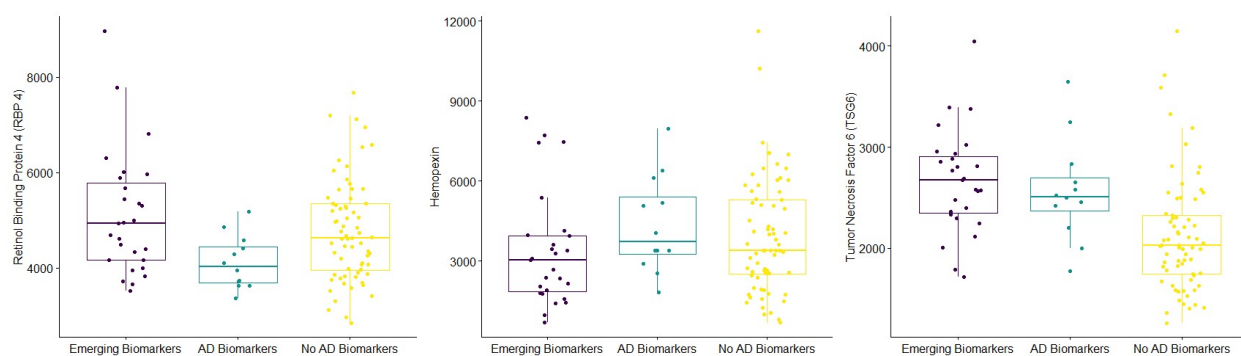
Supplemental Figure 3. Quantification of protein expression for identifying proteins associated with blood brain barrier integrity



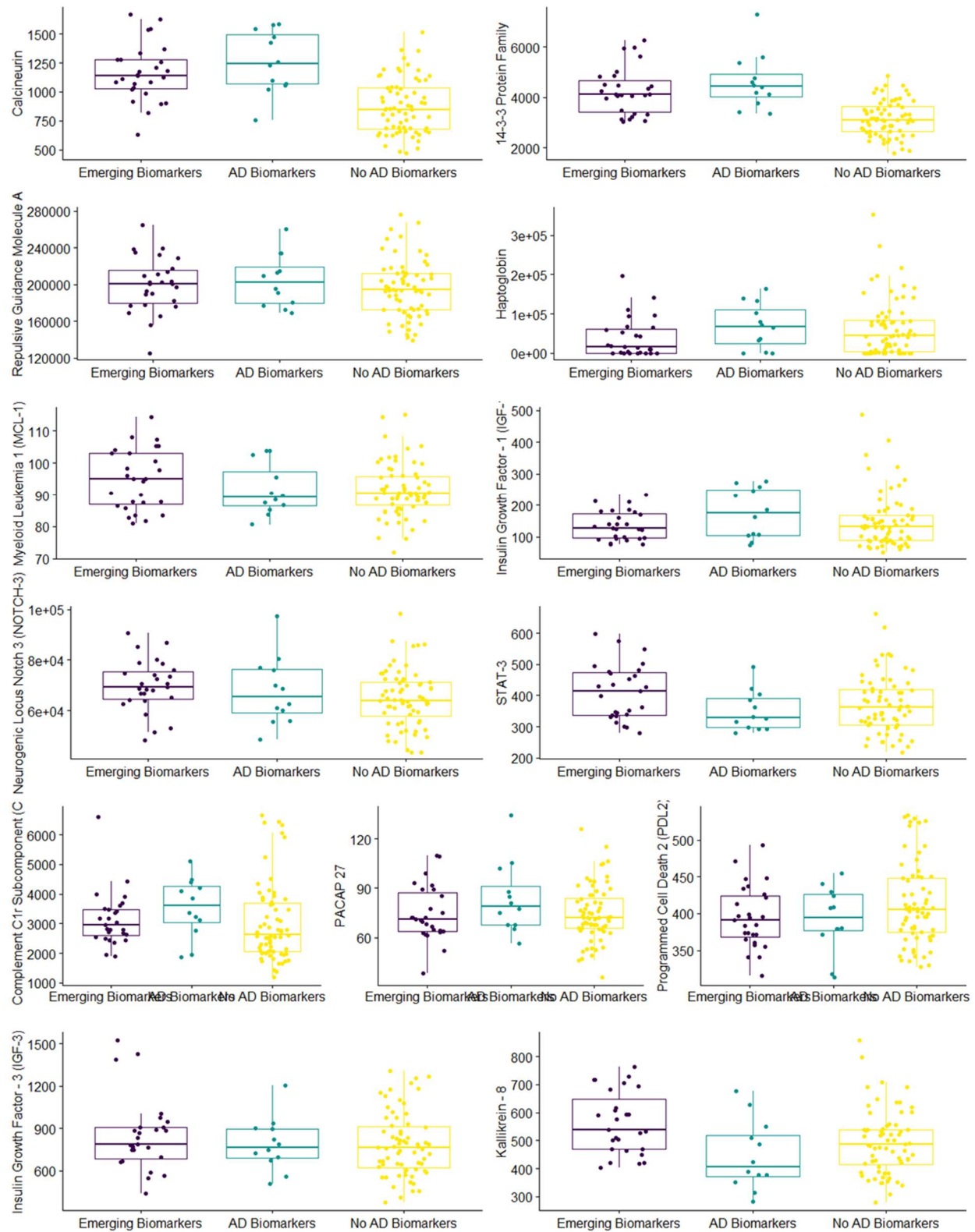
Supplemental Figure 4. Quantification of protein expression for identifying proteins associated with cardiovascular disease.



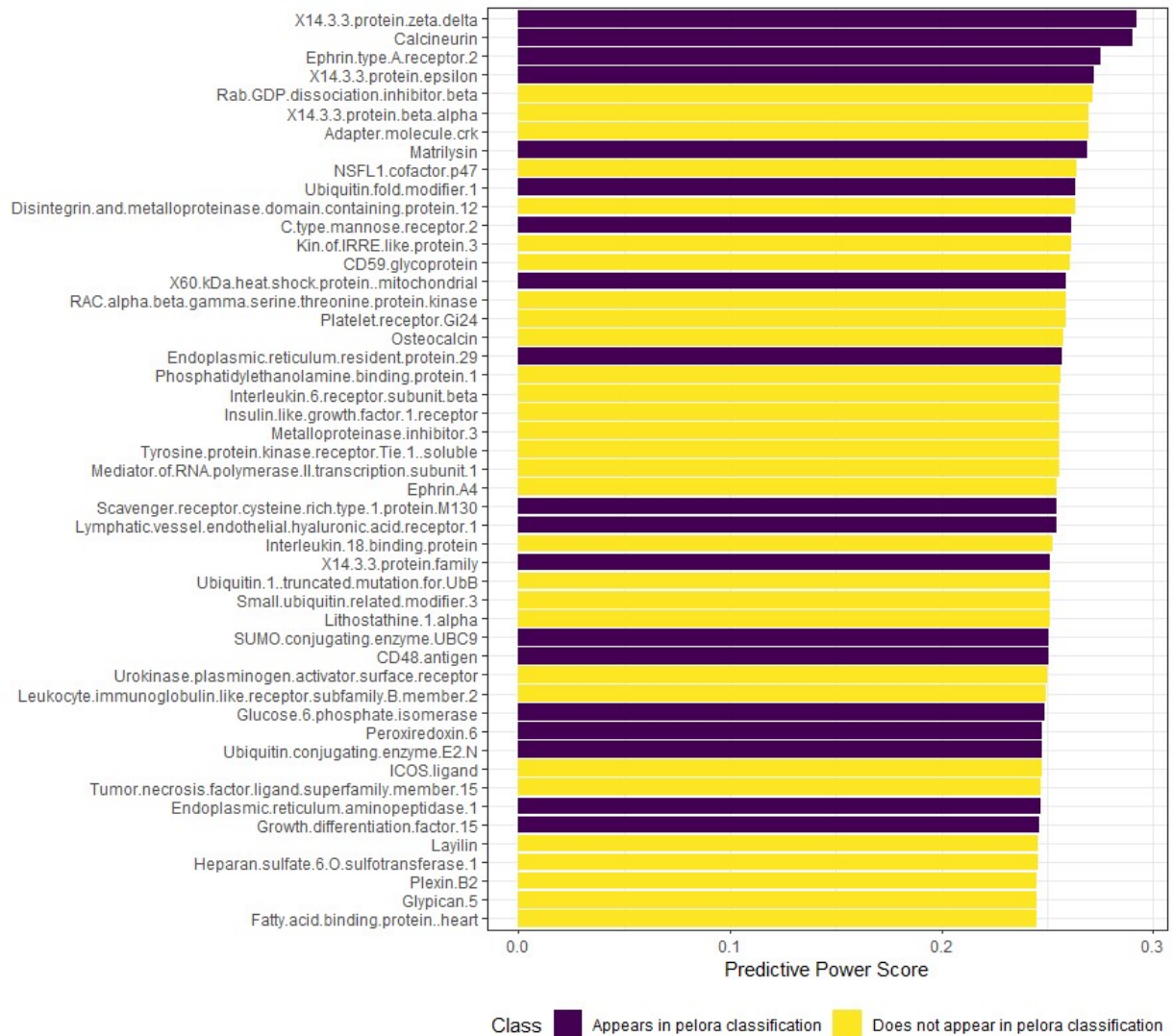
Supplemental Figure 5. Quantification of protein expression for identifying proteins associated with inflammation.



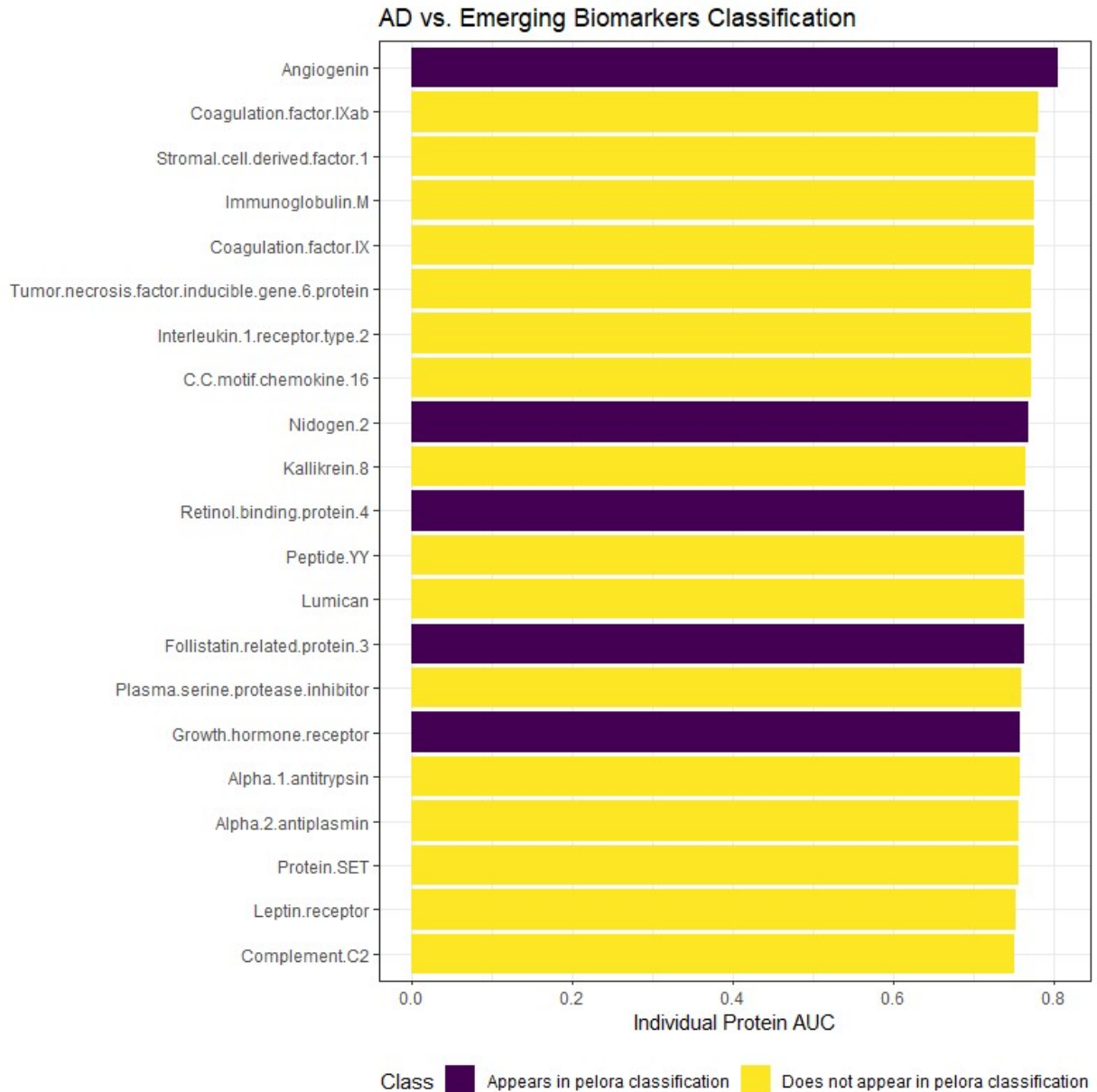
Supplemental Figure 6. Quantification of protein expression for identifying proteins associated with liver function



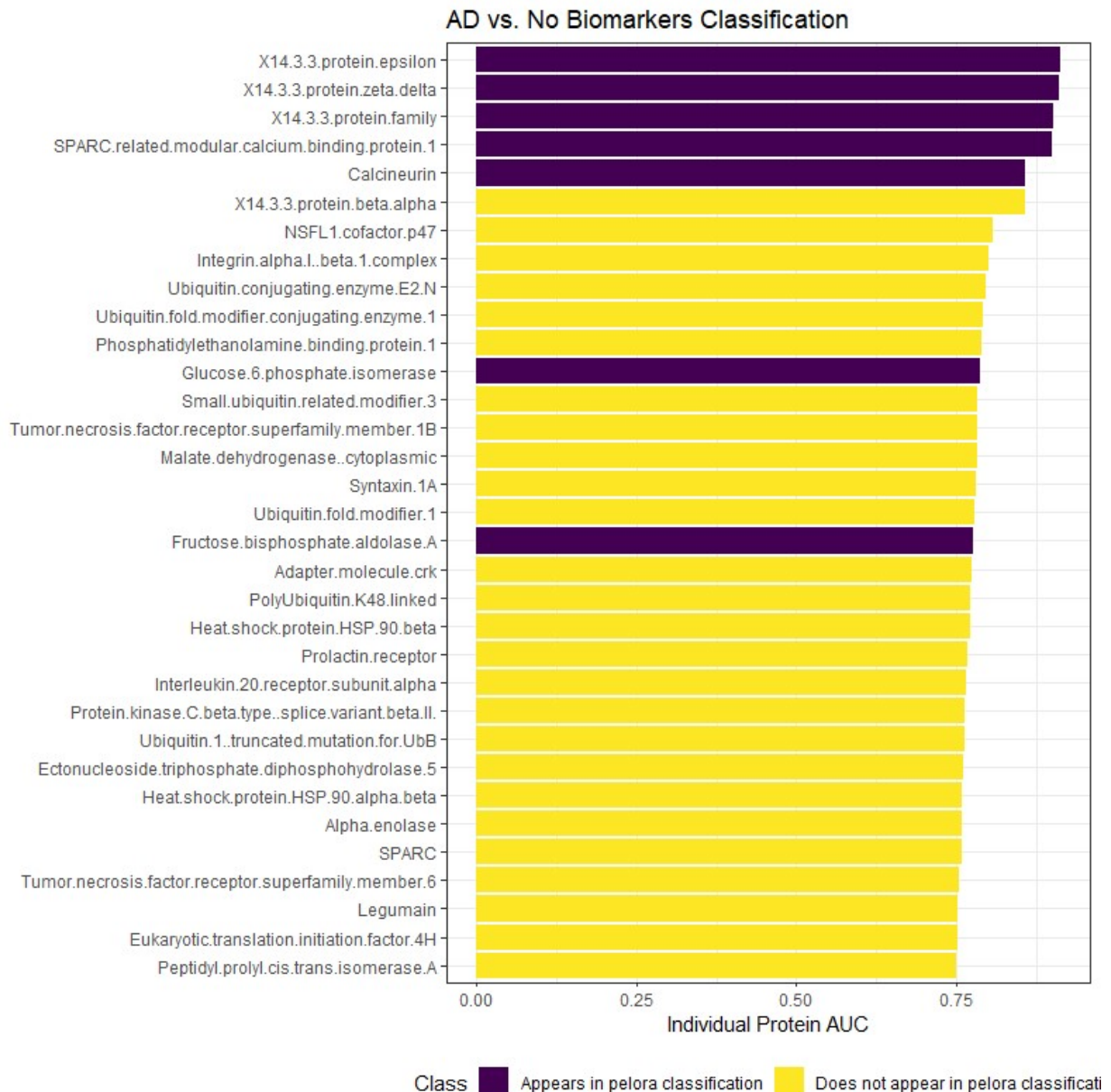
Supplemental Figure 7. Quantification of protein expression for identifying proteins associated with neurodegeneration



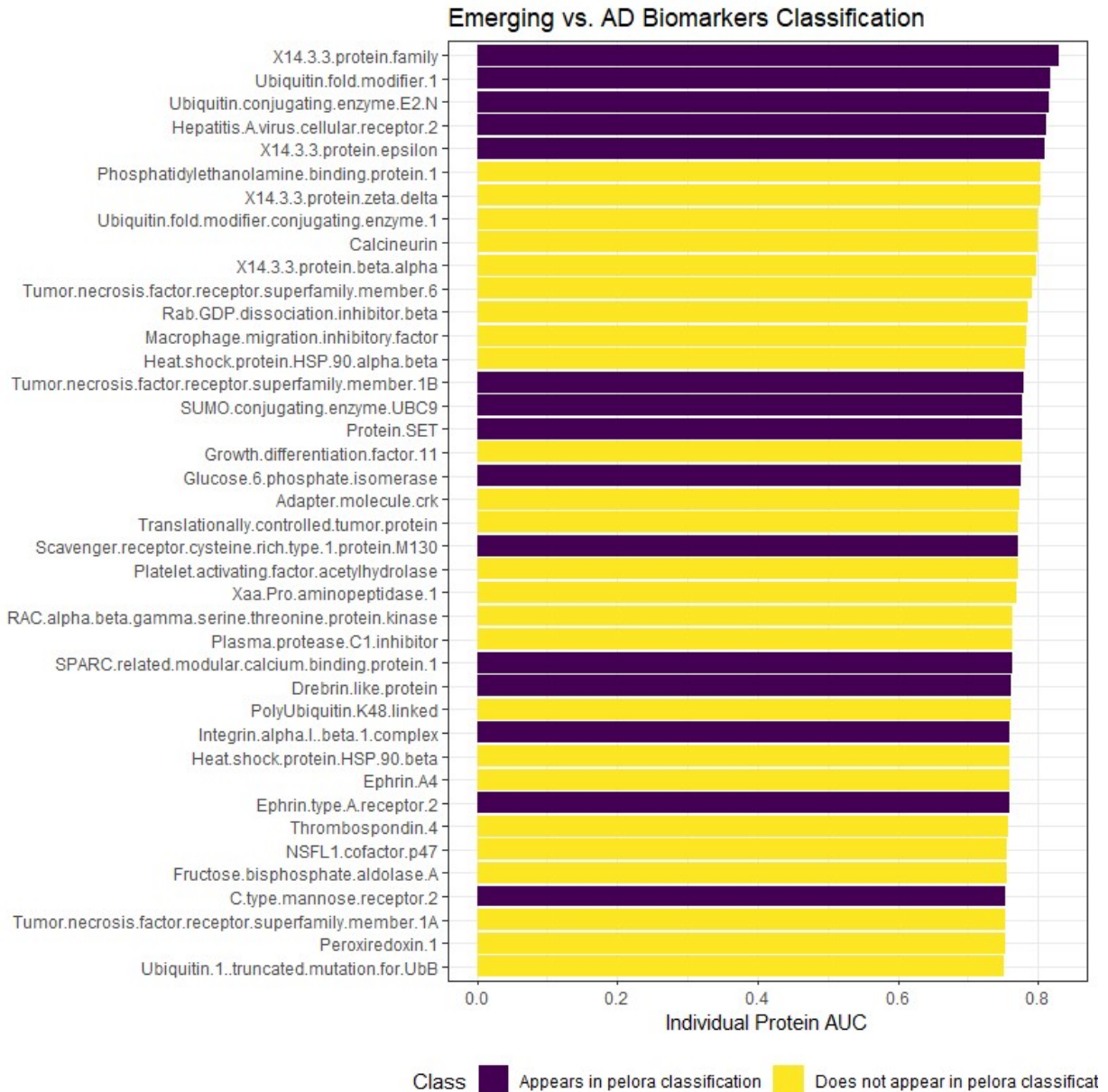
Supplemental Figure 8. The individual predictive power score (PPS) of each protein for classifying individuals for group membership is shown above. PPS is a value that ranges between 0 and 1. The three proteins with the highest individual predictive power (14-3-3 protein zeta-delta, calcineurin and ephrin type A receptor 2) were also identified by the pelora-based classification scheme. This indicates that the individual proteins are strongly tied to group membership, rather than being important by virtue of their interactions with other proteins.



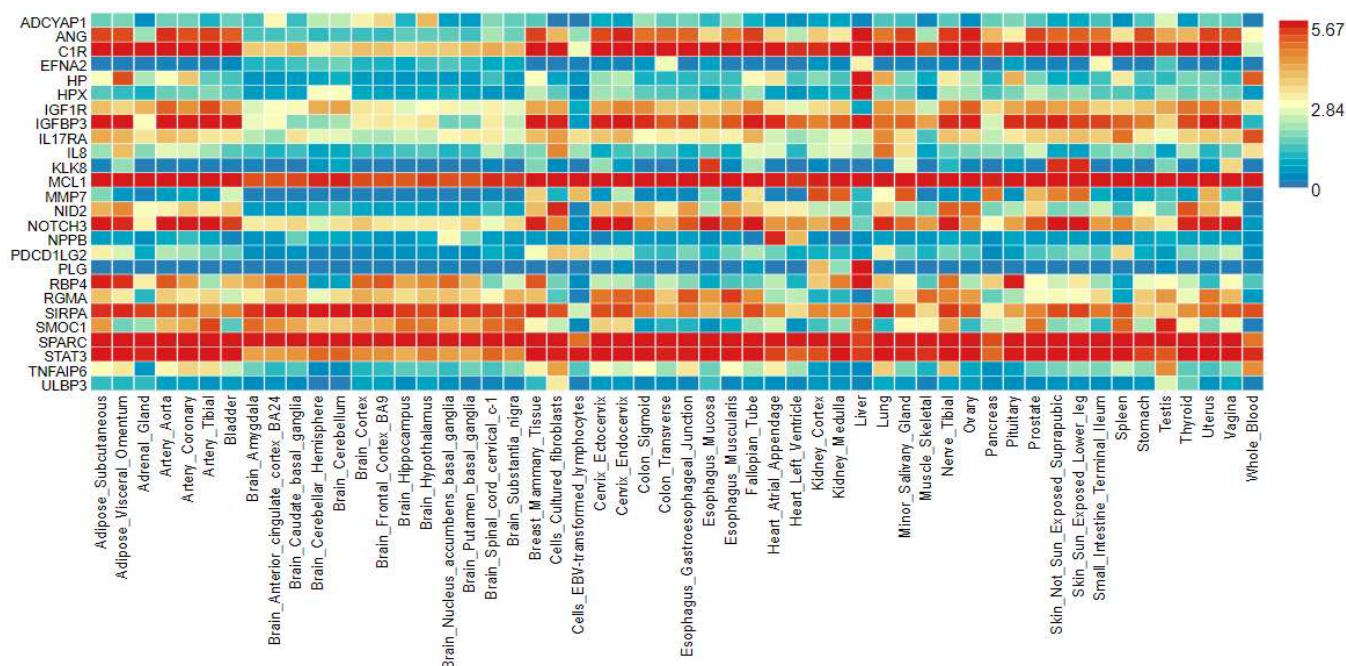
Supplemental Figure 9. All proteins with an individual AUC of greater than 0.75 when classifying individuals as belonging to either the AD Biomarker or Intermediate Biomarker cohort. The protein with the highest individual AUC, angiogenin, is also important for the pelora-based classification algorithm. Recall that the AD Biomarker vs. Intermediate Biomarker classification AUC was 0.75. This means that each of these individual proteins would actually be more useful for classification than the identified groupings of up and down-regulated proteins.



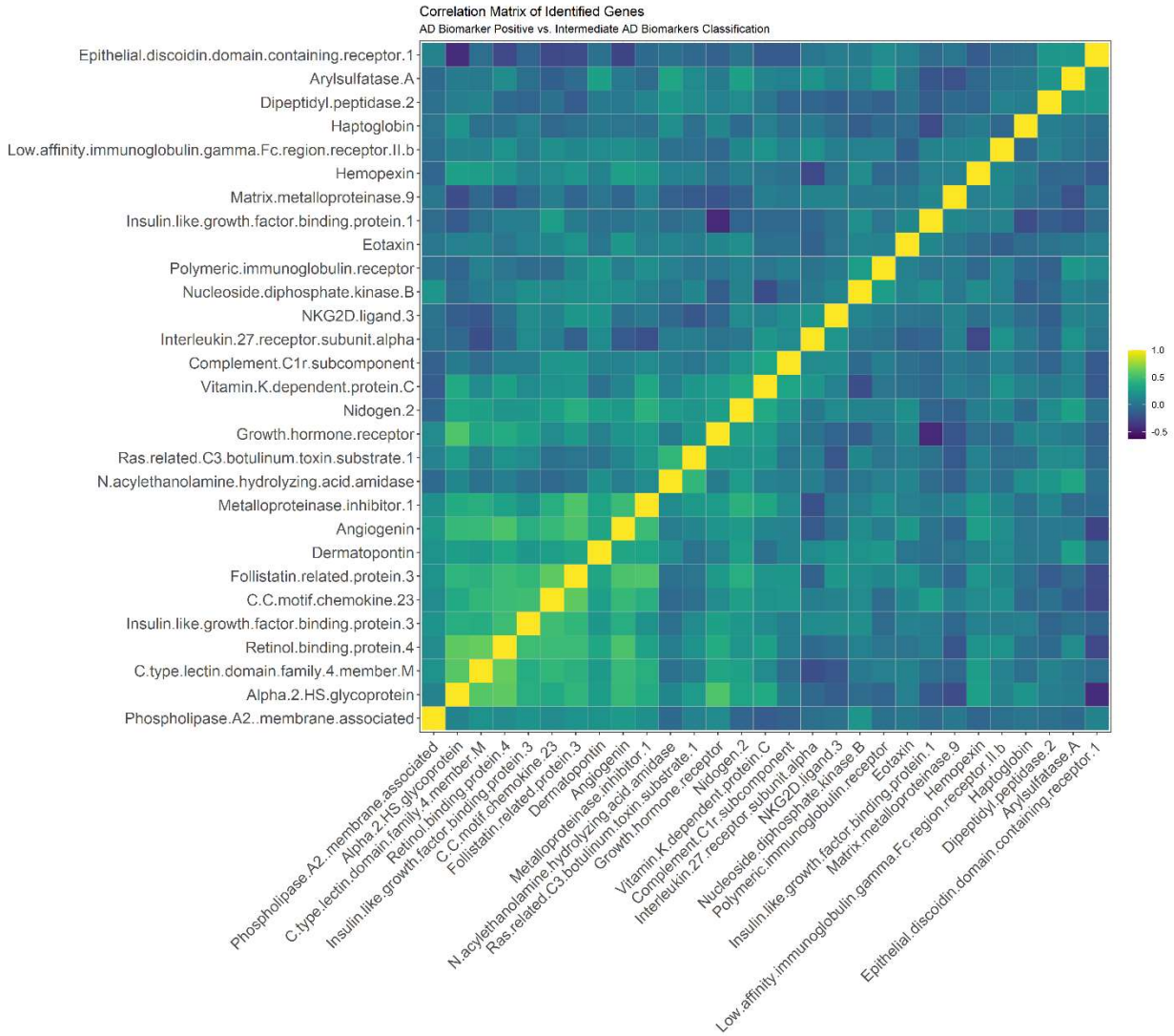
Supplemental Figure 10. All proteins with an individual AUC of greater than 0.75 when classifying individuals as belonging to either the AD Biomarker or AD Biomarker Negative cohort. Recall that the AD Biomarker vs. AD Biomarker Negative classification AUC was 0.98. This means that the combination of proteins identified as useful for classification (including proteins from the 14-3-3 family, SMOC1 and calcineurin) was substantially more powerful than any individual protein for classification.



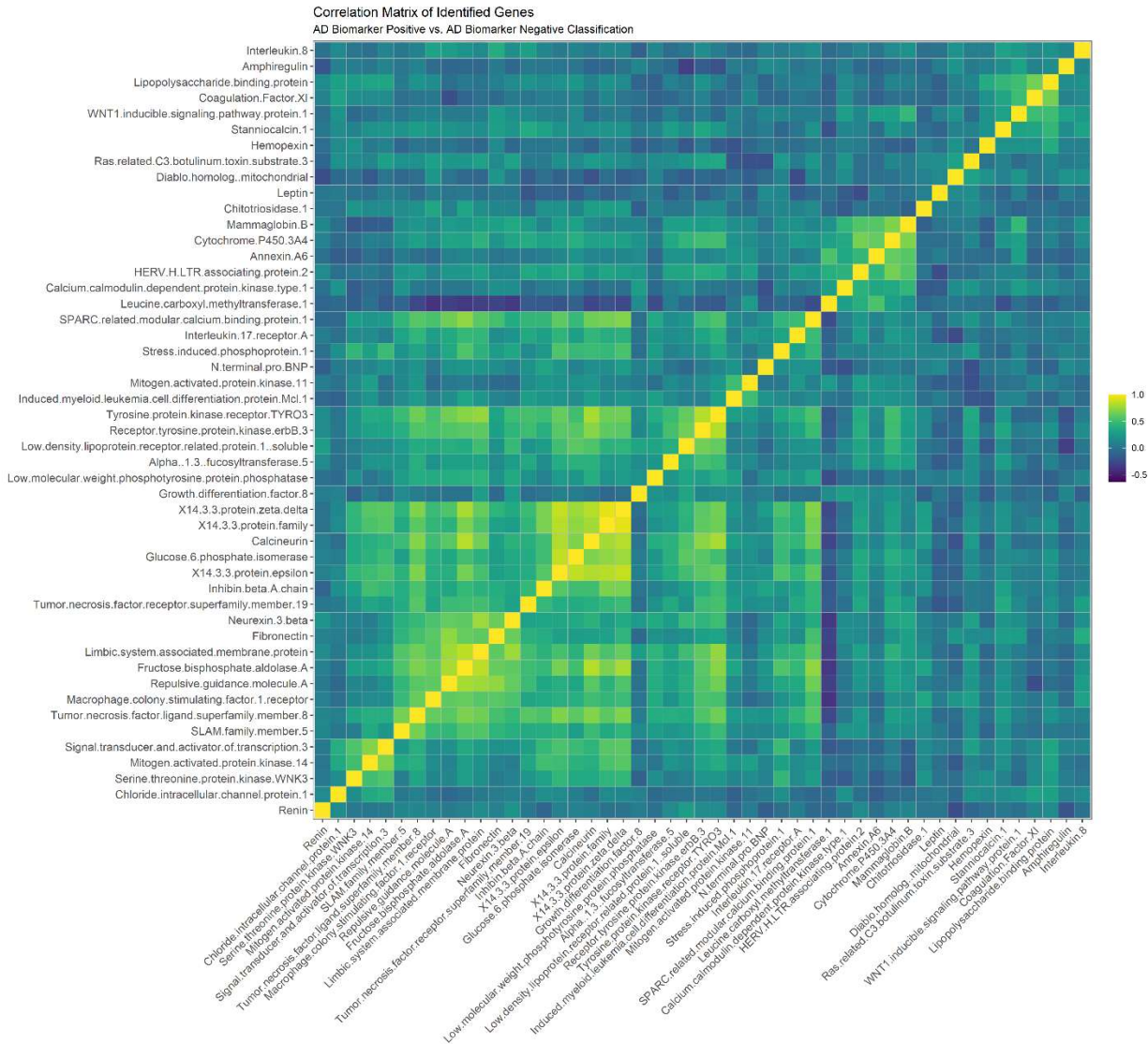
Supplemental Figure 11. All proteins with an individual AUC of greater than 0.75 when classifying individuals as belonging to either the Intermediate Biomarker or AD Biomarker Negative cohort. Recall that the Intermediate Biomarker vs. AD Biomarker Negative classification AUC was 0.68. This means that each of these individual proteins would actually be more useful for classification than the identified groupings of up and down-regulated proteins.



Supplemental Figure 12. Heatmap showing the average expression per protein (log2 transformed). This is the product of the pathway analysis conducted on the proteins identified as important for classification via pelora.



Supplemental Figure 13. Correlations between all proteins identified by Pelora as important for the AD Biomarker Positive – Intermediate AD Biomarker classification.



Supplemental Figure 14. Correlations between all proteins identified by Pelora as important for the AD Biomarker Positive – AD Biomarker Negative classification.

