

Age-related neurodegenerative disease associated pathways identified in retinal and vitreous proteome from human glaucoma eyes

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Supplementary information

Supplementary dataset 1- The list of proteins identified in the retina samples, pairwise comparison test of glaucoma vs. control

The combined set of proteins identified from two separate TMT experiments performed on retinal samples in glaucoma and control conditions, as well as the list of differentially expressed proteins obtained from a t-test comparison test between glaucoma and control.

Supplementary dataset 2- The list of proteins identified in the vitreous samples- pairwise comparison test of glaucoma vs. control

The combined set of proteins identified from two separate TMT experiments performed on vitreous samples in glaucoma and control conditions as well as the list of differentially expressed proteins obtained from a t-test comparison test between glaucoma and control.

Supplementary Figure S1- Sample densities and box plots of TMT experiments

A series of descriptive statistical analyses were performed to confirm the reproducibility of the data. The overall distribution of median-normalized and log-transformed protein abundances were visualised in density (A) and box plots (B). Within each tissue (retina and vitreous), the boxplots showed similar median and 95% confidence intervals. Moreover, comparison of density plots for each individual biological sample showed similar and highly overlapping patterns, with no major asymmetric bias, satisfying the normality assumption for further analysis. Overall, these statistical metrics confirm the similarity in overall protein abundance distributions of individual biological replicates, and demonstrate the reproducibility of measurements within sample groups.

Supplementary Figure S2-Vitreous functional protein network clustered by Reactome

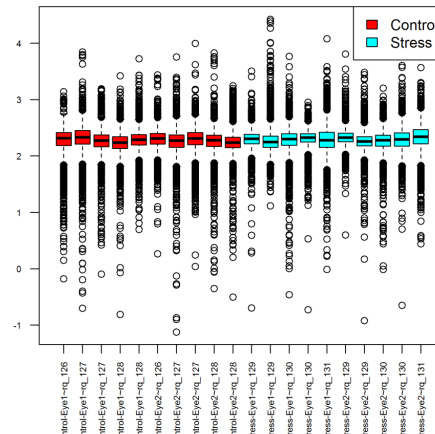
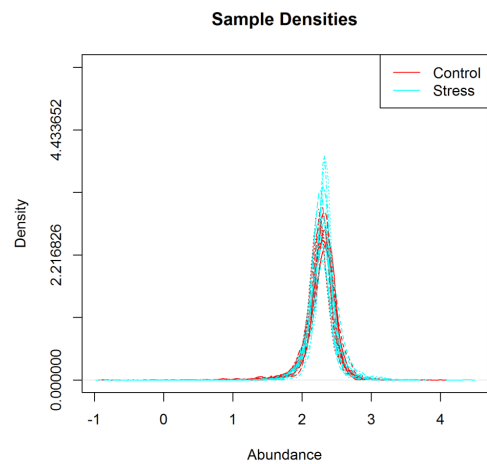
Vitreous Reactome functional interaction networks analyzed by the Reactome FI Cytoscape plugin. Of 1153 vitreous differentially expressed proteins, 568 proteins were had at least one other known functional connection. Network nodes are labeled with gene symbols. The Reactome plugin was used to assign functional clusters, which were color-coded and labeled with representative broad functions. Large number of network clusters was identified representing wide array of cellular pathways in the vitreous.

Supplementary Figure S3-Abundance-coded vitreous reactome functional network

The Reactome plugin was used to assign functional clusters and color-coded (based on their abundance) and labeled with representative broad functions. Yellow represent up-regulation and blue denote upregulation.

Figure S1

Retina



Vitreous

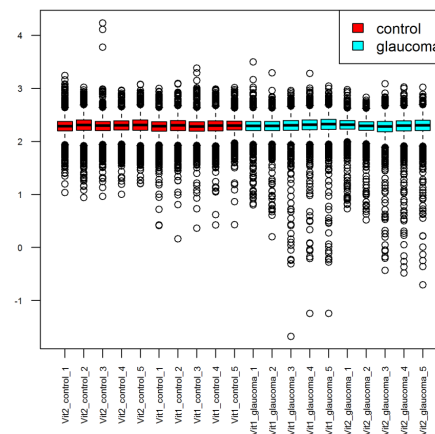
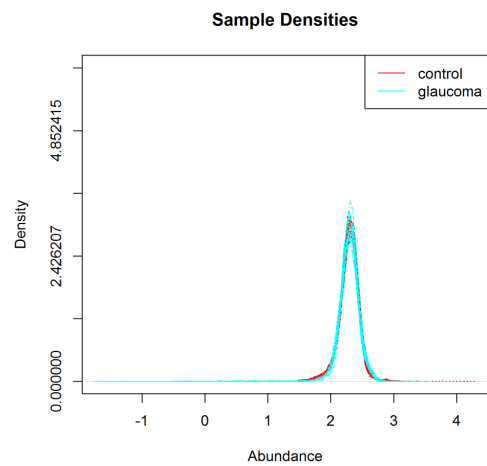


Figure S2

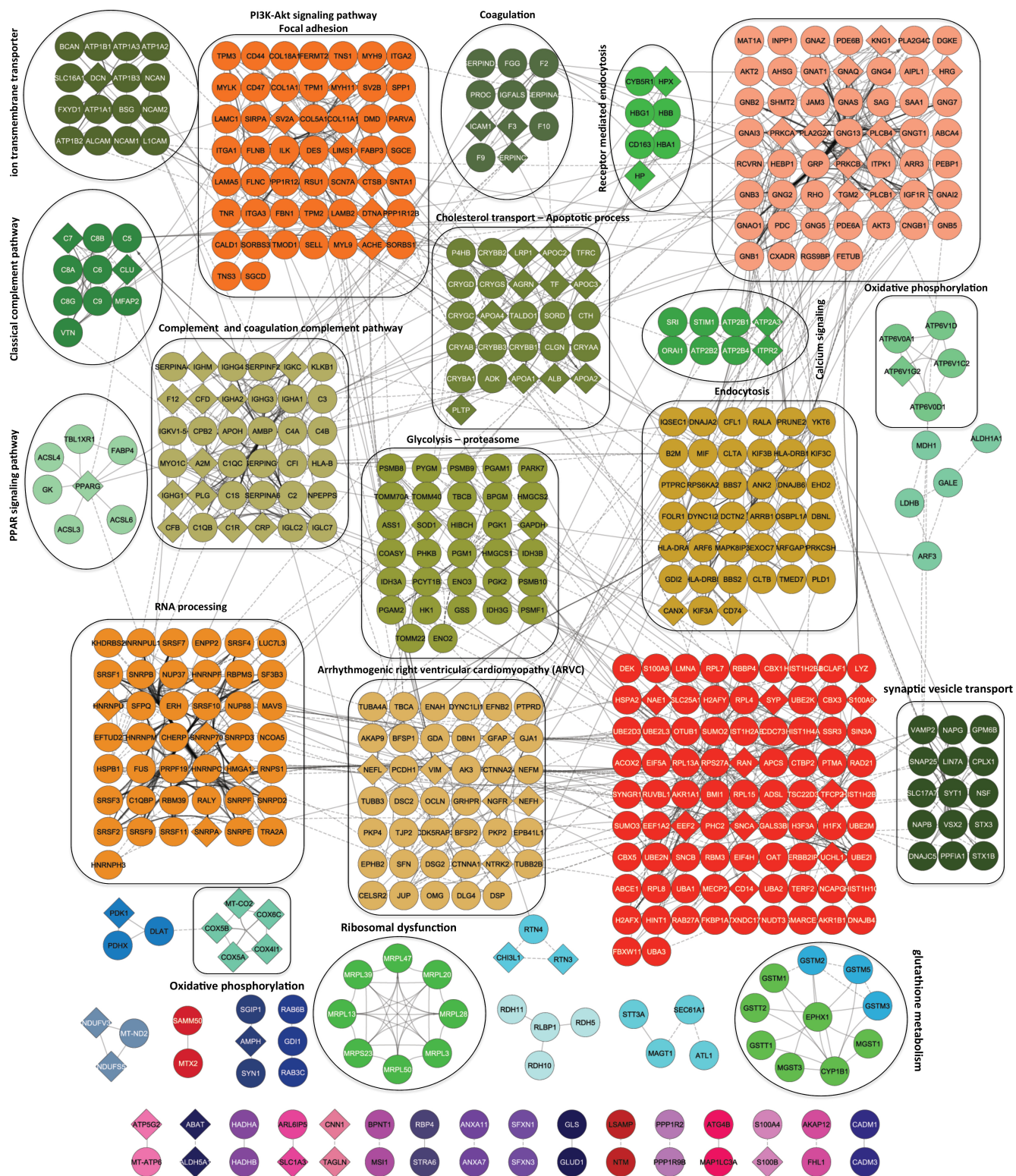


Figure S3

