

Large-Scale Quantitative Proteomics of Human Retinal Mitochondria-Enriched Fractions Reveals Key Regulators for the Early Pathogenesis of Age-Related Macular Degeneration

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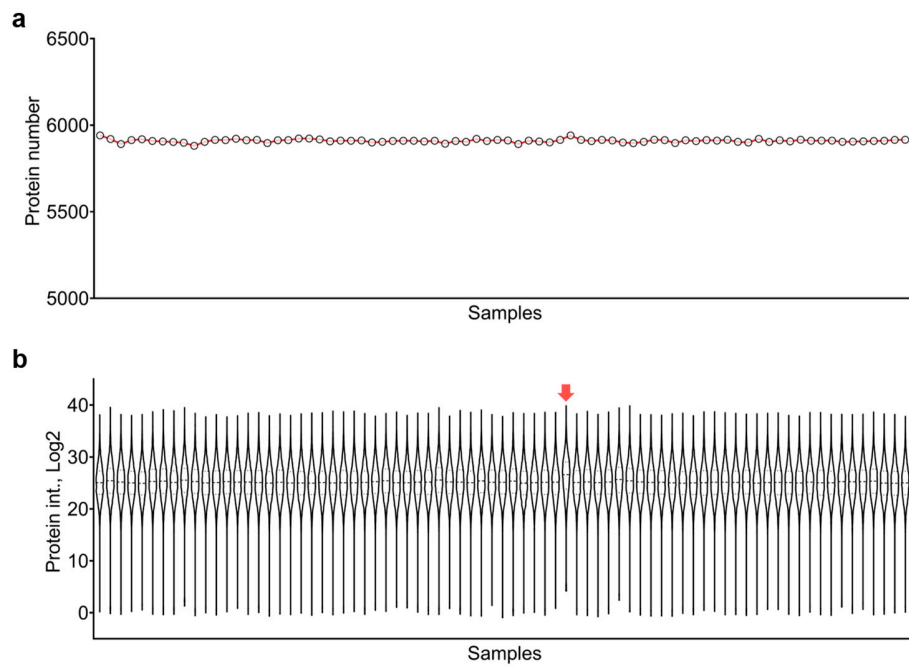
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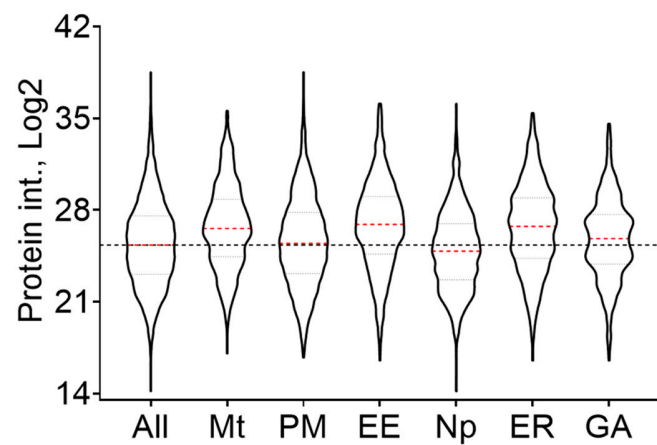
Supplementary Materials

Supplementary Figure S1 – S6

Supplementary Table S1 – S7



Supplementary Figure S1. Proteomic profiles of the 77 retinal pigment epithelium (RPE) mitochondria-enriched fraction samples. (a) Number of proteins quantified in individual samples; (b) Log2 protein mass spectrometry (MS) intensities of individual samples. The red arrow denotes the 1 sample (M2_S2_2) with abnormal MS intensities.

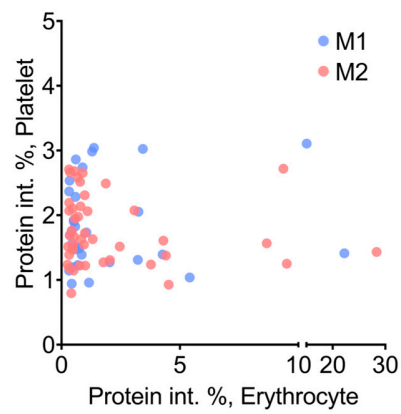


Supplementary Figure S2. MS intensities distribution of proteins enriched in major cellular compartments. All: all proteins; Mt: mitochondrion; PM: plasma membrane; EE: extracellular exosomes; Np: nucleoplasm; ER: endoplasmic reticulum; GA: Golgi apparatus.

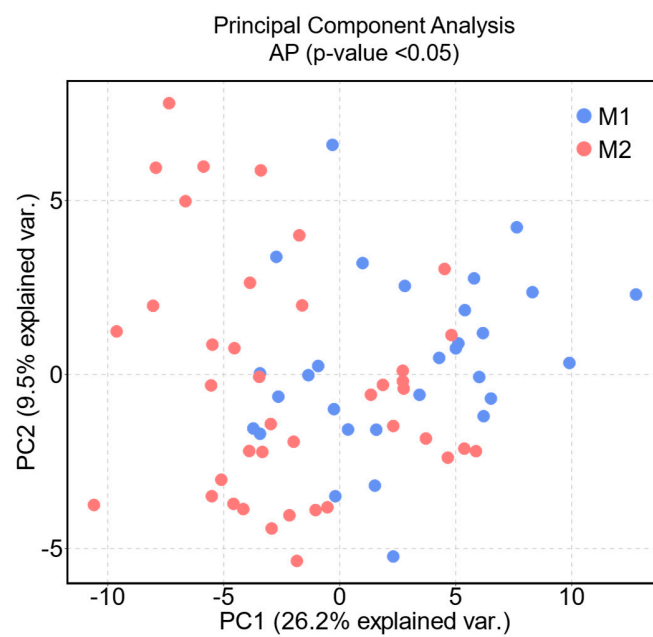


- Benchmark samples (Human cancer cell line digest) for system performance evaluation
- Quality control (QC) samples (pooled aliquots of randomly selected samples) for LC-MS stability monitoring
- Analytical samples, analyzed in a random order

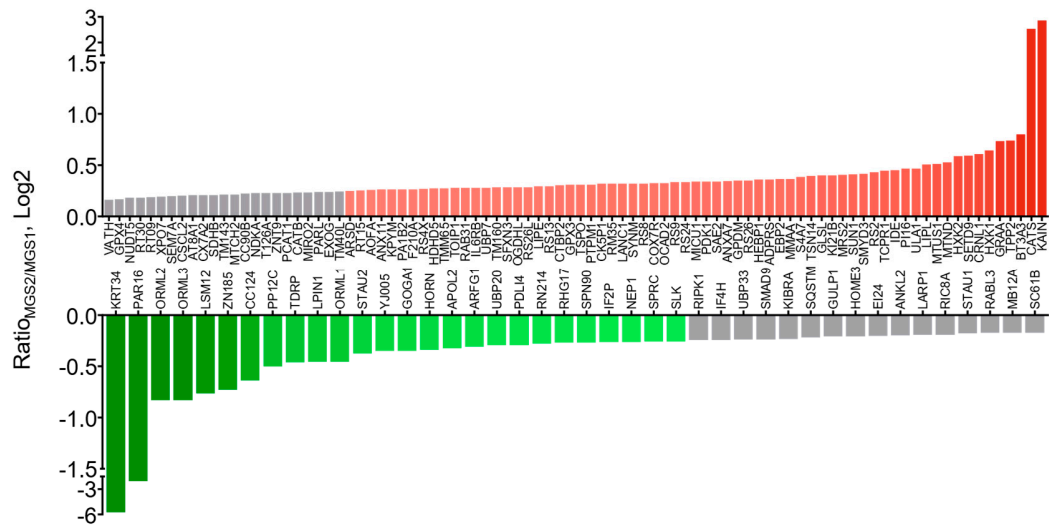
Supplementary Figure S3. A standardized LC-MS scheme allowing monitoring and evaluation of reproducibility during the analysis queue.



Supplementary Figure S4. Correlation plot between the percentage of erythrocyte- and platelet-specific proteins in all samples.



Supplementary Figure S5. Principal Component Analysis (PCA) of M1 and M2 samples using the 132 altered proteins (APs).



Supplementary Table S1. Demographic profiles of donors involved in the current study.

Supplementary Table S2. Quantification results of 5,941 proteins in 77 RPE mitochondria-enriched fractions from human donors w/ and w/o AMD.

Supplementary Table S3. Proteomic quantification results of the 5 QC sample runs.

Supplementary Table S4. Percentage of MS intensities of the 16 quality markers within each sample. Samples removed are highlighted in red.

Supplementary Table S5. Quantification results of 5,941 proteins after removing 7 outlier samples with high blood protein percentages and abnormal MS intensities.

Supplementary Table S6. A total of 132 altered proteins (APs) determined by Welch's t-test.

****All Supplementary Tables are provided as separate Excel files.**