

Supporting Information

Impact of Preanalytical Factors on Plasma Extracellular Vesicles and Human Plasma Proteome

Patil Shivprasad Suresh,¹ Qibin Zhang^{1,2*}

¹Center for Translational Biomedical Research, University of North Carolina at Greensboro, North Carolina Research Campus, Kannapolis, NC 28081, USA.

²Department of Chemistry & Biochemistry, University of North Carolina at Greensboro, Greensboro, NC 27402, USA.

Corresponding Author

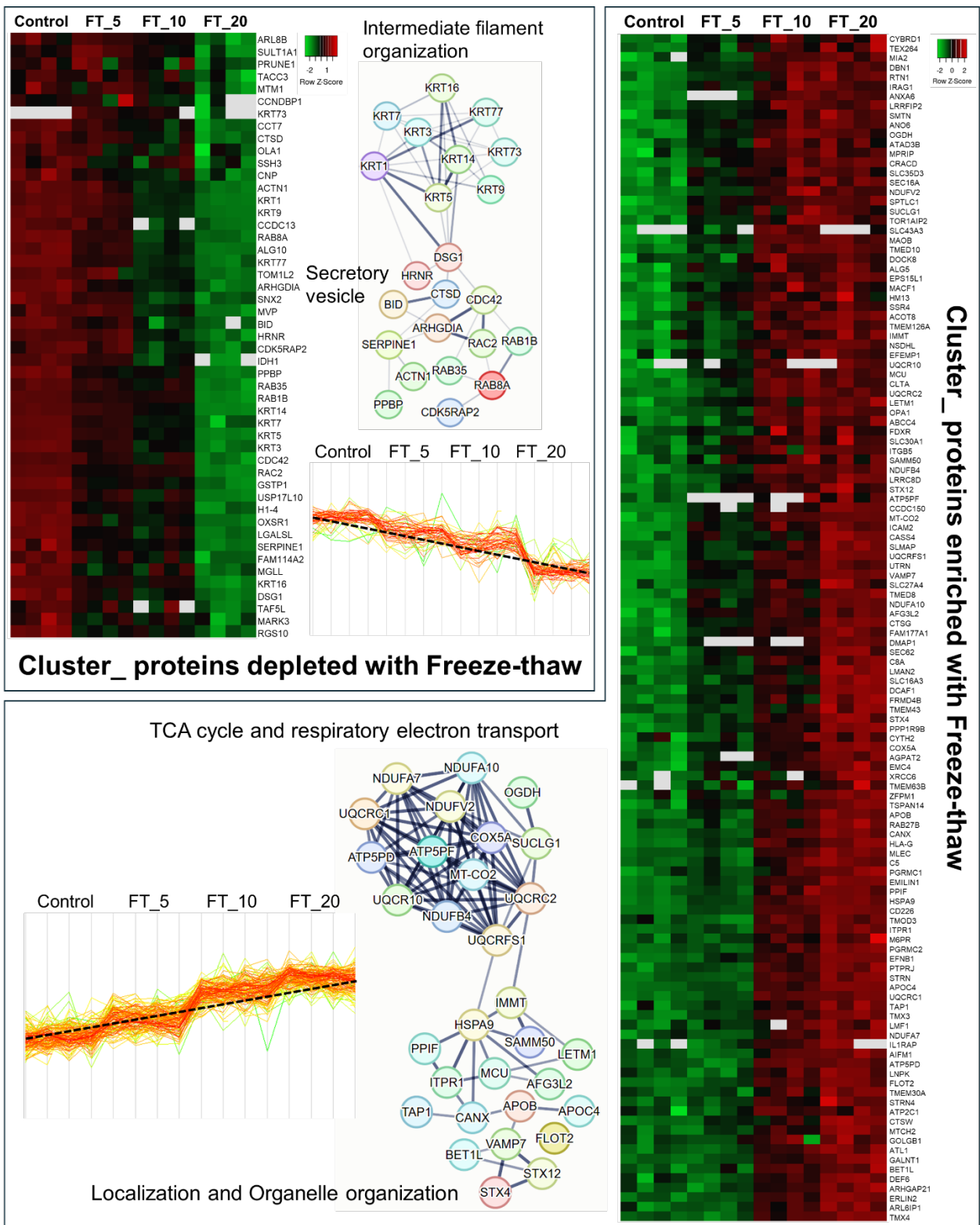
Qibin Zhang – *Center for Translational Biomedical Research, University of North Carolina at Greensboro, Kannapolis, North Carolina 28081, United States; Department of Chemistry & Biochemistry, University of North Carolina at Greensboro, Greensboro, North Carolina 27402, United States.*

orcid.org/0000-0002-6135-8706;

Email: q_zhang2@uncg.edu

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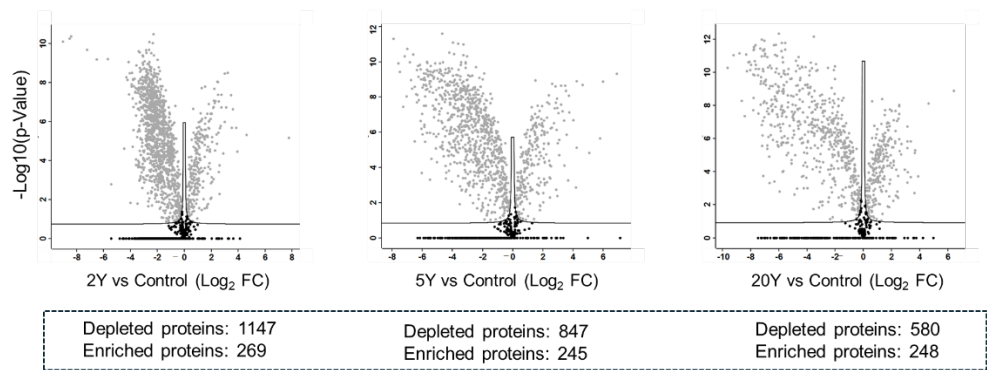
Figure S1: Hierarchical clustering of depleted and enriched proteins over different numbers of freeze-thaw cycles and associated functional enrichment pathways. (FT, freeze-thaw).



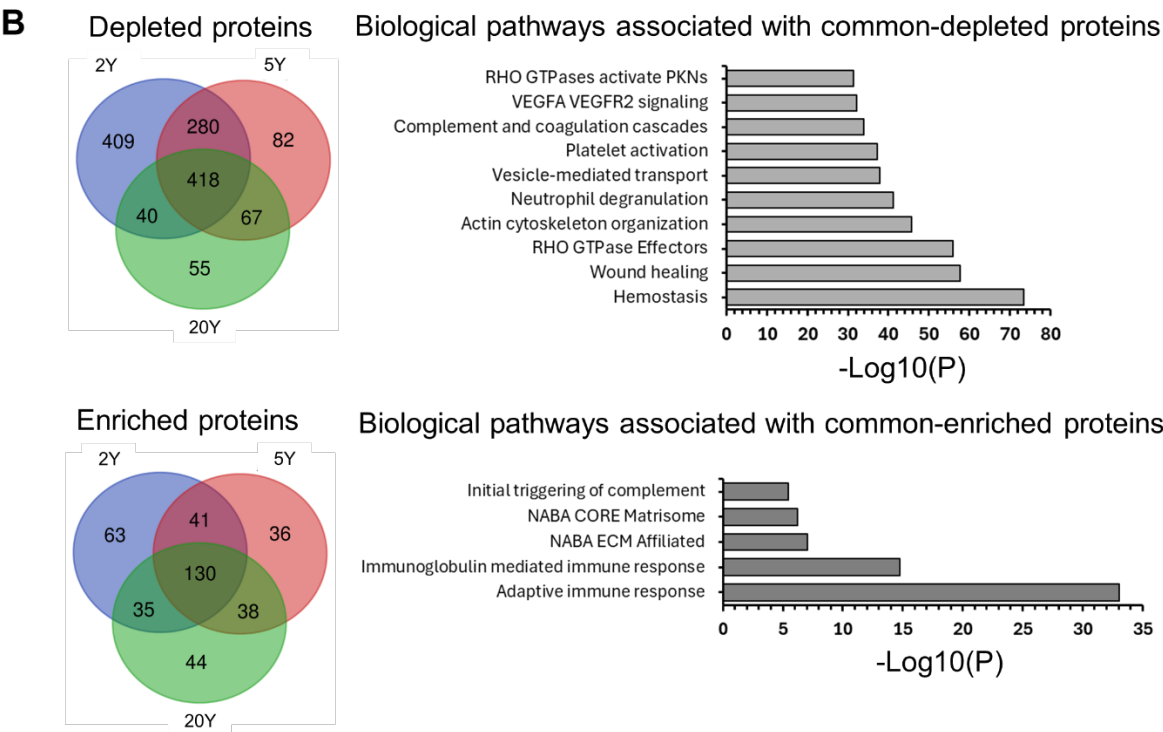
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Figure S2: Enriched and depleted proteins in aged plasma compared to fresh plasma samples and associated biological pathways. **A)** Volcano plot showing significantly enriched and depleted proteins in 2-, 5-, and 20-year storage plasma compared to fresh plasma (control). Student's t-test, with FDR and S0 set at 0.05. The commonly depleted and enriched proteins with fresh plasma are listed for further analysis. **B)** The biological pathways associated with commonly depleted and enriched proteins identified by the volcano plot. (Y, years)

A Volcano Plots of depleted and enriched proteins in different storage time of human plasma compared to fresh human plasma



Among the commonly identified proteins in different storage time plasma, 418 are depleted and 130 are enriched.



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Figure S3: Hierarchical clustering of human plasma with different storage times, fresh plasma (control) and their subcellular localization. (Y, years)

Hierarchical Clustering of Human Plasma with Different Storage Time

