

A comprehensive resource on plasma proteome stability under sample handling variations



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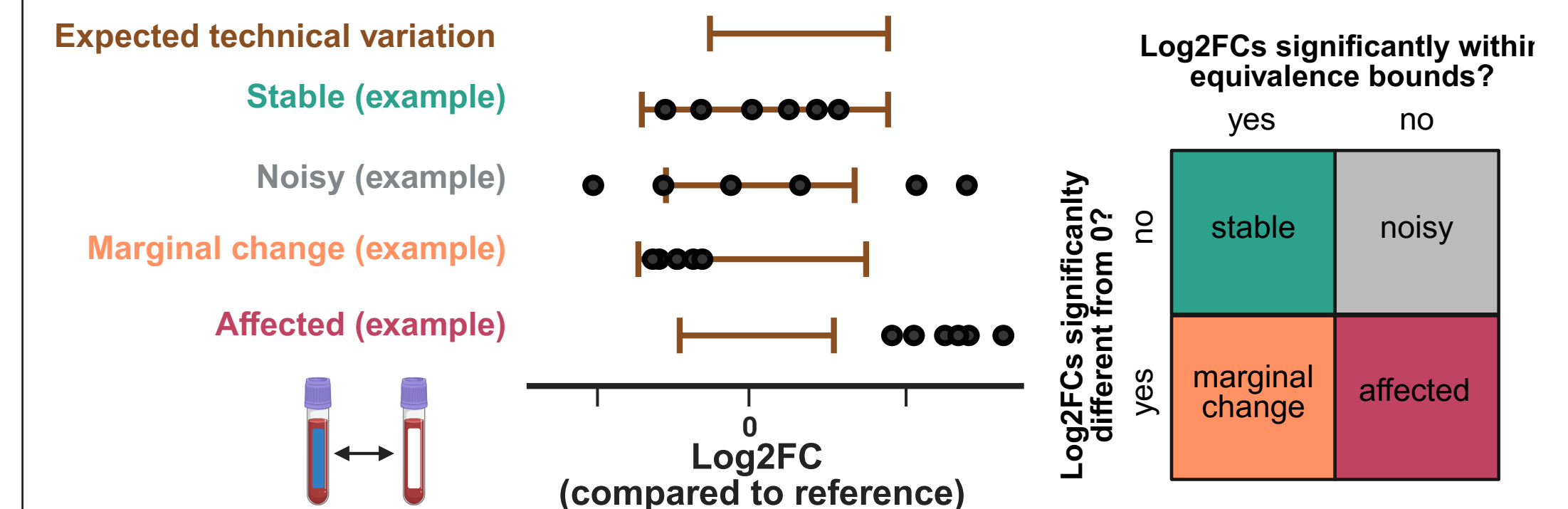
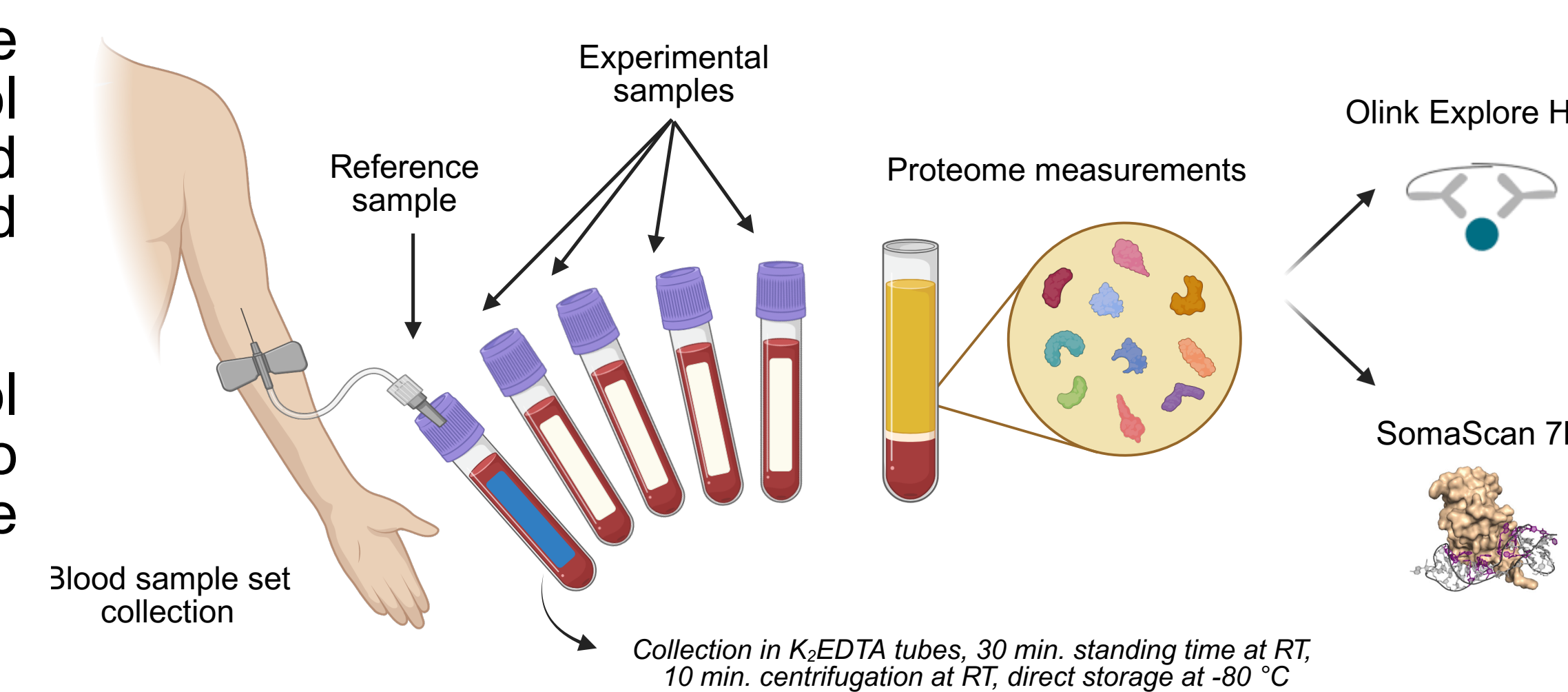
INTRODUCTION

Plasma protein biomarkers are accessible and scalable diagnostic tools, but variations in blood collection and handling can affect the reliability of their measurement. This study systematically examines how such pre-analytical variations impact plasma protein measurements using affinity-based proteomics.

Blood was drawn from 166 individuals. Eleven separate experiments were conducted to assess various pre-analytical factors, each including a control and multiple experimental conditions. Proteomic profiling was performed using antibody-based (Olink Explore HT) as well as aptamer-based (SomaScan 7K) platforms.

Protein stability was evaluated by comparing experimental and control conditions for significant differences, followed by equivalence testing to determine whether observed changes fell within the technical variability of the assays, as estimated from duplicate control measurements.

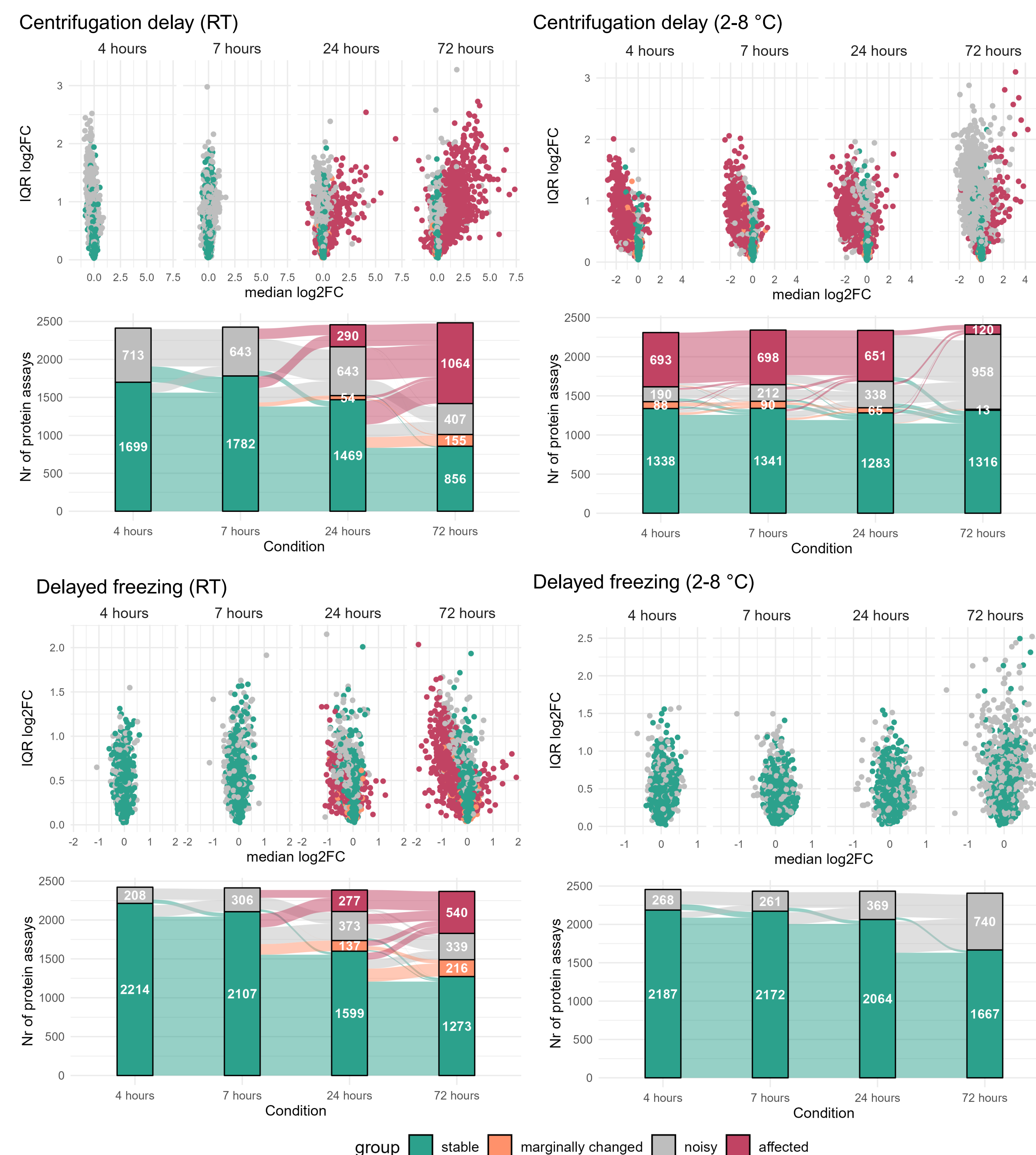
METHODS



RESULTS

Proteome-level insights

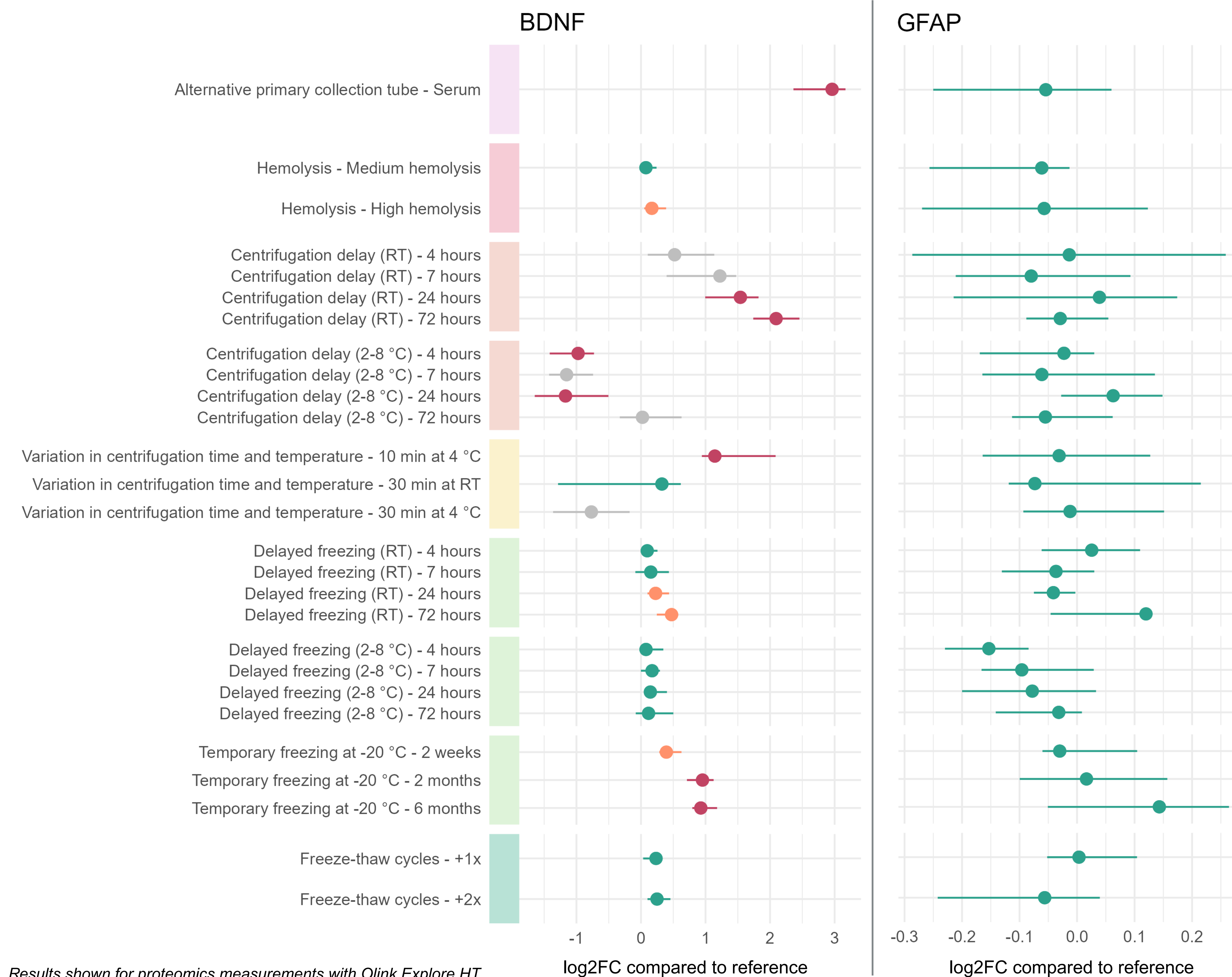
Our resource enables comparisons of the relative impact of different sample-handling variations on overall proteome measurement integrity, thereby supporting protocol development.



Results shown for proteomics measurements with Olink Explore HT

Protein-level insights

Our resource enables comparisons of the pre-analytical stability of protein biomarker candidates, thereby supporting lead selection for biomarker development.



Results shown for proteomics measurements with Olink Explore HT

CONCLUSION

- Variations in pre-analytical sample handling can have a major impact on affinity-based plasma proteome measurements.
- We provide a resource on the pre-analytical stability of thousands of plasma proteins, supporting the selection and development of reliable protein biomarkers for real-world and resource limited settings.

