PREOMICS

Double the insight: Unified tissue homogenization for quantitative metabolomics and in-depth proteome analysis

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INTRODUCTION

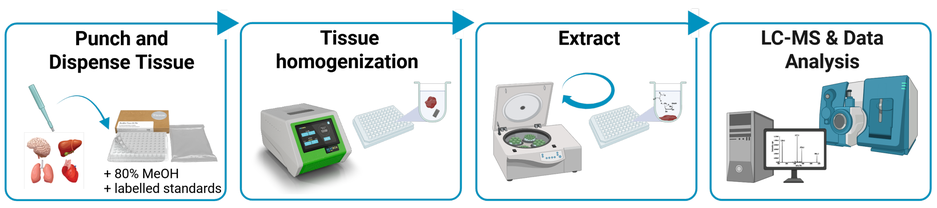
The BeatBox® tissue homogenizer and cell lyser, originally optimized for proteomics applications, has since evolved into a robust tool for high-throughput multi-omics applications, enabling efficient extraction of biomolecules from scarce, challenging samples. It provides rapid, homogeneous lysis of 1–96 samples in just 10 minutes, delivering 2.5× higher reproducibility compared to traditional methods. BeatBox seamlessly pairs with PreOmics® iST kits for automated, streamlined proteomic sample prep, offering a fast and reliable solution for large-scale analyses.

Supported "omics" applications:

- **Cells & Tissues:** Flexible, reproducible across diverse sample types.
- **FFPE Proteomics:** Avoids toxic deparaffinization, boosts protein IDs by 14–43%, and delivers clean peptides from 96 samples in a couple of hours.
- **Metabolomics & Lipidomics:** Enables efficient extraction of metabolites and lipids from even limited samples.

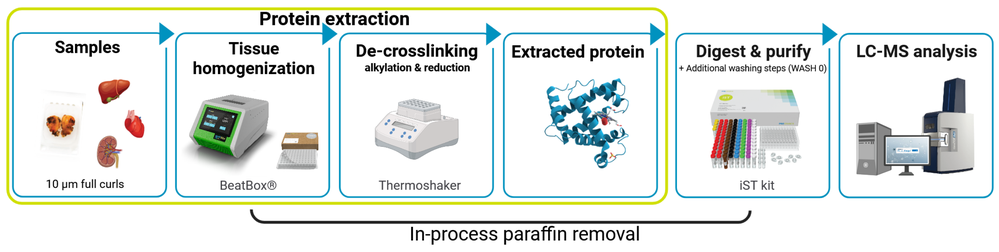
WORKFLOWS AND KEY RESULTS

High-throughput quantitative metabolomics



Metabolomics workflow: 5 mg mouse tissue punches were homogenized in 80% cold methanol with BeatBox. After centrifugation, the extracted analytes in the supernatants were analyzed using a Vanquish™ Duo HPLC coupled with a SCIEX Triple Quad 7500 System and processed in Skyline/MetaboAnalyst.

Proteomics insights from various tissues

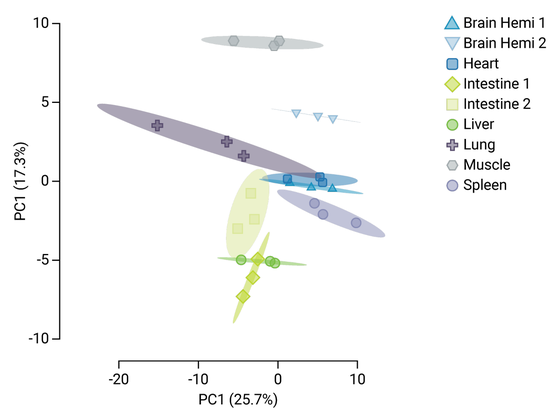


Proteomics workflow: FFPE tissues were homogenized with BeatBox, boiled, and further processed with the iST workflow. Fresh-frozen mouse tissues were prepared similarly, without boiling. Peptides were analyzed on an EASY-nLC™ 1200–timsTOF HT in diaPASEF® mode and processed in Bruker ProteoScape™.

PCA of polar analytes extracted from various tissues

To determine the robustness of metabolite extraction from samples with low input, a pool (12 polar metabolites, 21 non-polar lipids) of different stable isotope-labeled standards (IS) was spiked to the samples before homogenization. Overall, the extraction efficiency resulted in a CV of the extracted metabolites below 20%, indicating a robust and reproducible workflow.

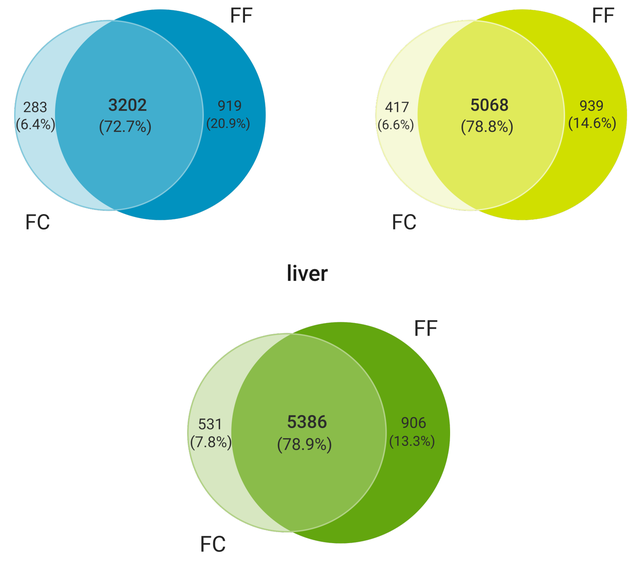
Clustering based on sample origin revealed distinct metabolite and lipid levels across different organs, indicating that information is preserved in this workflow.



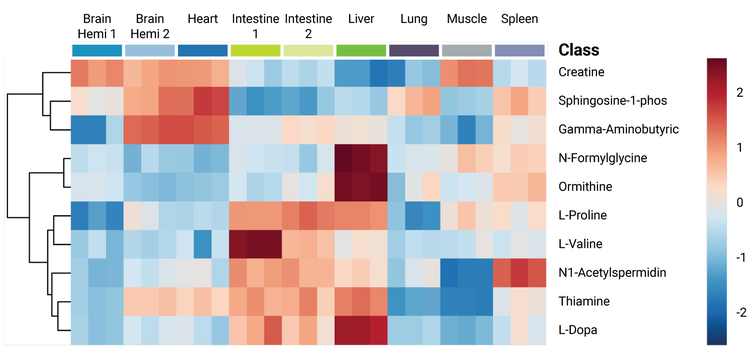
Venn diagrams of identified proteins from FFPE and fresh-frozen tissue

Similar results were obtained when using the BeatBox workflow for FFPE and fresh-frozen tissues. The identified protein for full curls were comparable to those for fresh-frozen tissues.

A high overlap of proteins identified (72–79%) was achieved for full curl FFPE (FC) and fresh-frozen (FF) samples for all three mouse tissue types (three valid values in four replicates).

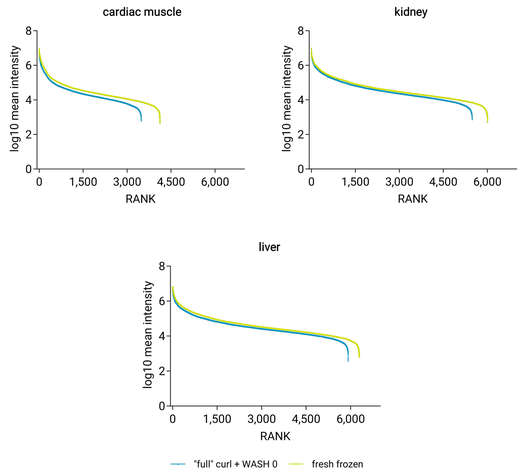


Heatmap of the 10 most abundant polar analytes



The top 10 polar metabolites revealed unique regulation levels throughout various tissues. Creatine is upregulated in the brain, muscle, and cardiac muscle tissues, while ornithine is significantly upregulated in the liver and thiamine upregulated in the intestine, liver, and brain.

Dynamic range of proteins quantified from FFPE and fresh-frozen tissue



Protein quantification in three out of four replicates exhibited similar dynamic ranges, spanning approximately four orders of magnitude. These results confirm the efficiency of protein extraction from FFPE tissue using the BeatBox workflow.

KEY TAKEAWAYS

- **High-throughput & versatile:** Processes 1–96 samples per run from cells, fresh-frozen tissues, and FFPE materials.
- **Comprehensive extraction:** Captures metabolites, lipids, and proteins in a single workflow.
- **Fast & clean prep:** Ready-to-measure metabolites and peptides in a single day; no xylene or separate deparaffinization step required for FFPE processing.
- **Scalable & reproducible:** Standardized procedure with consistent performance across various tissue types, ideal for large clinical cohorts and multi-site studies.

CONTACT & MORE

Metabolomics workflow

FFPE proteomics workflow

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Conflict of Interest Disclosure
ZD, JJ, and SW are employed by PreOmics GmbH, which produces the BeatBox instrument and iST kits used in this work. BN, DI, and JW are employed by Altos Labs. CE is employed by PreOmics Inc.