PREOMICS

High-performance 96-well tissue homogenization and cell lysis on the BeatBox platform improves protein identification and sample preparation repeatability

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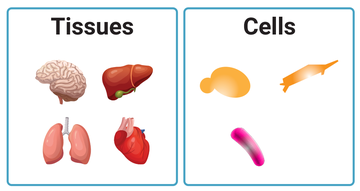
Spotlight

- Up to 96 samples homogenized in 10 minutes
- Quiet homogenization at a steady temperature
- Process a wide variety of tissue types at 1 to 5 mg wet weight
- Supports eukaryotic and prokaryotic cell processing workflows from thousands to ten million cells per well
- Seamlessly coupled with iST technology for global proteomic analysis

Materials & Methods

Sample types



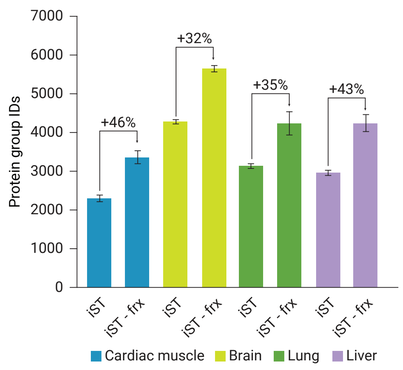
Workflow solution

- **Input**: : Mouse tissue (cardiac muscle, brain, lung and liver) and cell lines (*S.cerevisiae*, *E.coli*, and HEK293)
- **Homogenization**: 10 min using STANDARD mode
- **Sample digestion/peptide clean-up**: iST 96x w/o iST-Fractionation Add-on
- **LC-MS analysis**: EASY-nLC™ 1200 - TimsTOF Pro; ddaPASEF acquisition
- **Data analysis**: MaxQuant (v 2.0.1.0), STRING (v11.5)

Results & Discussion

Tissue homogenization

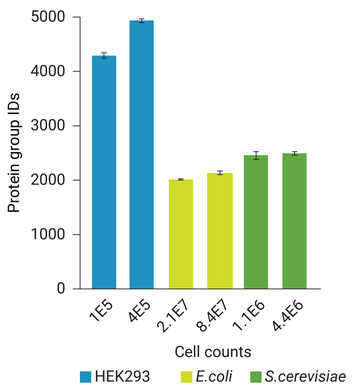
Substantial coverage of various tissue proteomes



BeatBox workflow combined with 3-step peptide fractionation increases proteome depth by ~40% compared to unfractionated samples

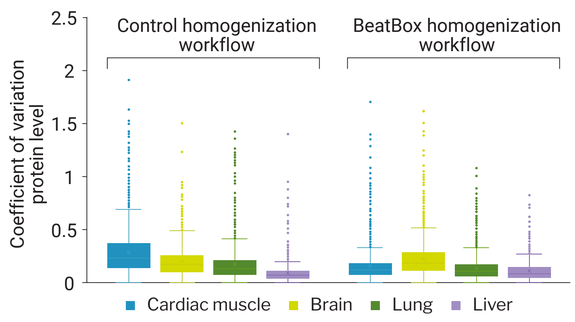
Cell lysis

Highly efficient cell lysis across cell types



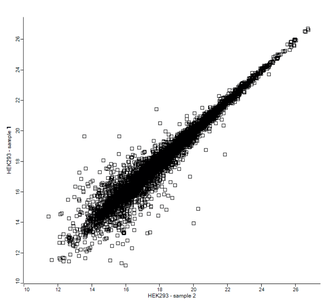
- Effective cell lysis for different cell counts resulted in a similar protein group identification rate
- The same peptide amount (300 ng) was injected from both cell counts

Amended technical variability



Improved repeatability across different tissue types compared to control workflow, CV ~9% on average

Exceptional repeatability of cell lysis



The repeatability of the protein group numbers was less than CV ~3%

Key takeaways

- The BeatBox is a high-throughput and easy-to-use instrument for tissue homogenization and cell lysis
- Efficacious protein extraction and high protein identification rate from various tissue and cell types
- Superb repeatability of the whole tissue and cell sample preparation workflow