PREOMICS

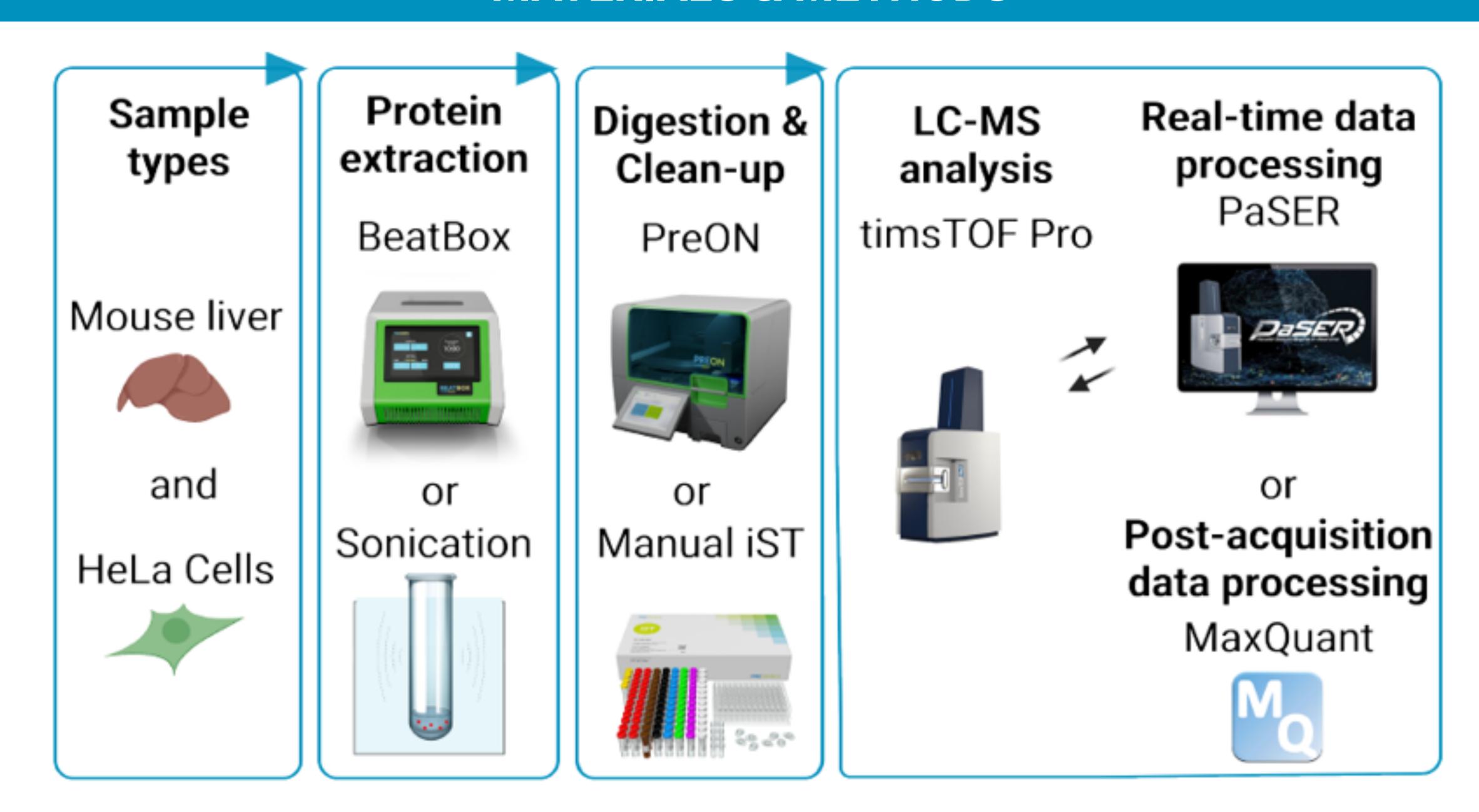
Streamlined and semi-automated proteomics pipeline from protein extraction to data analysis by coupling BeatBox, PreON and PaSER platforms

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SPOTLIGHT

- Streamlined LC-MS-based proteomics workflow rom sample homogenization to data analysis
- Efficient protein extraction on the BeatBox platform combined with robust iST sample preparation automated on the PreON platform (PreOmics)
- Real-time results with the PaSER technology (Bruker) for improved and accelerated data processing

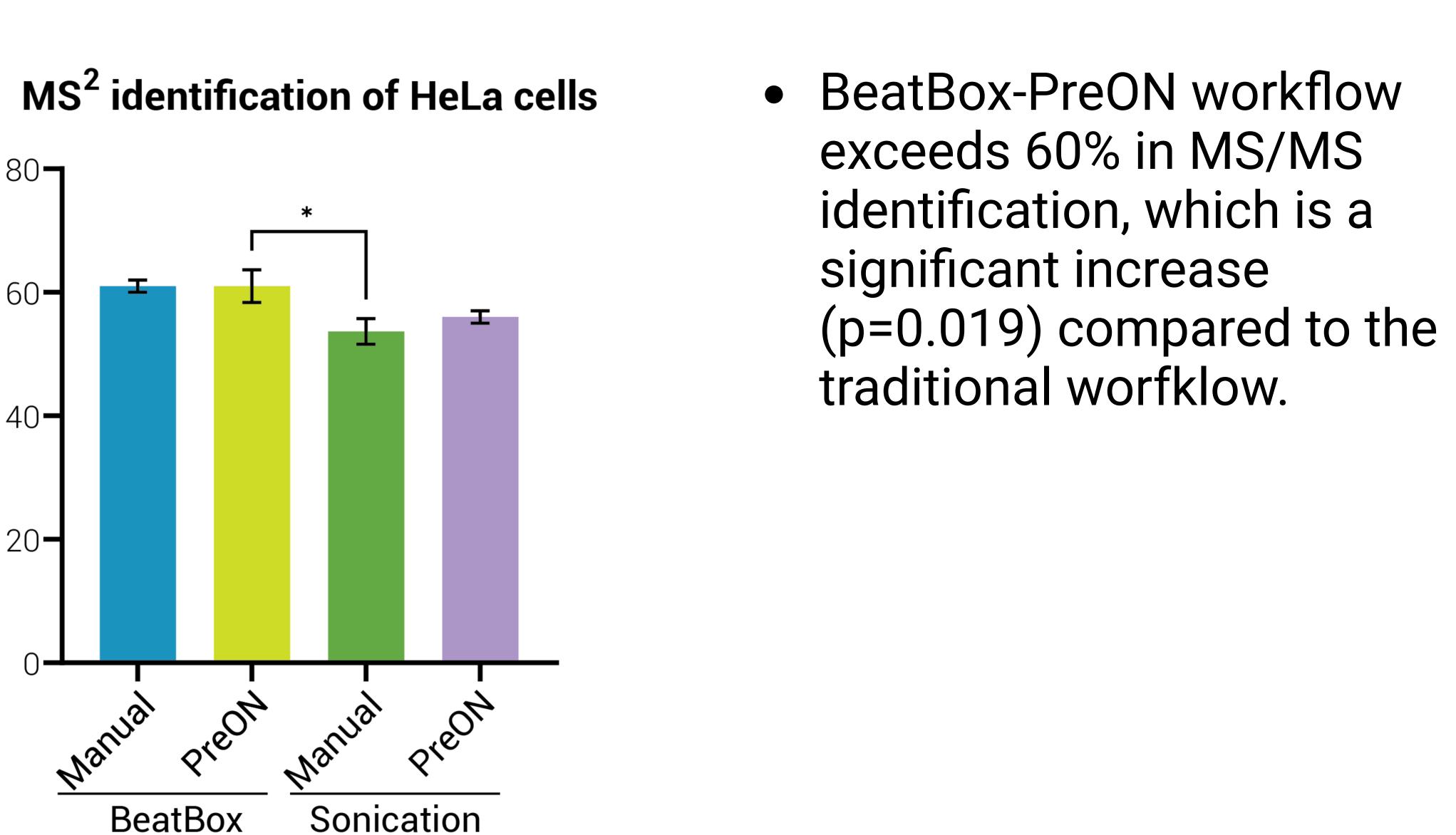
MATERIALS & METHODS

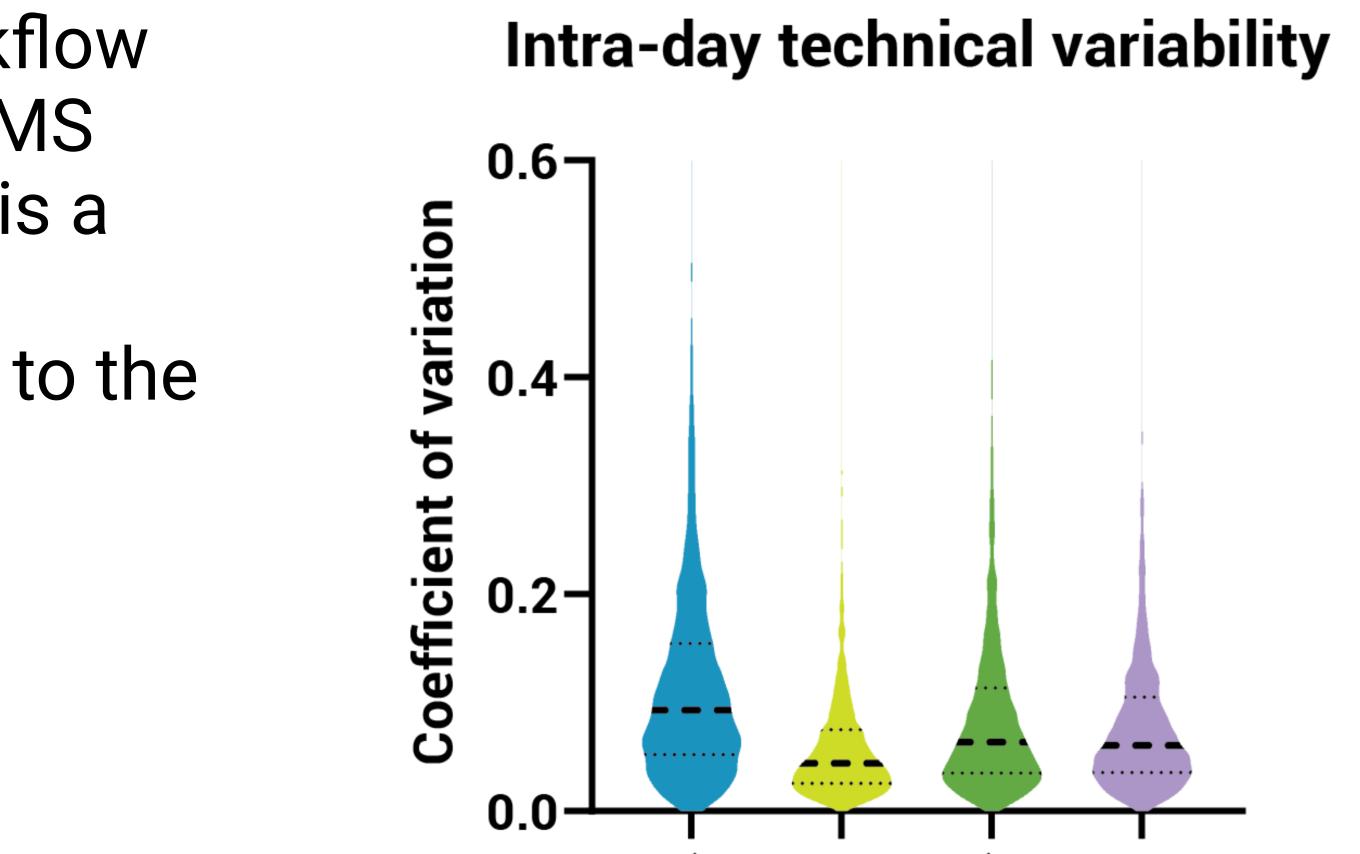


- Input: Mouse liver tissue (5 mg for sonication; 50 mg for BeatBox) and HeLa cells (1.6E6 cells)
- Homogenization: BeatBox (10 min, standard power settings) with BeatBox Tissue 24x kit or boiling (10 min, 95 °C) plus sonication (10 cycles; 30 sec on / off)
- Protein assay: Micro BCA™ Protein Assay (Thermo)
- Sample digestion/peptide clean-up: iST workflow processed manually or on PreON
- LC-MS analysis: EASY-nLC™ 1200 TimsTOF Pro; ddaPASEF acquisition; 30min gradient
- Data analysis: MaxQuant (v 2.0.1.0) or PaSER (2023)

Protein yields of tissues Protein yields of cells Mouse liver 1.6 E6 HeLa Cells

 BeatBox improves protein extraction efficiency compared to sonicationbased homogenization.



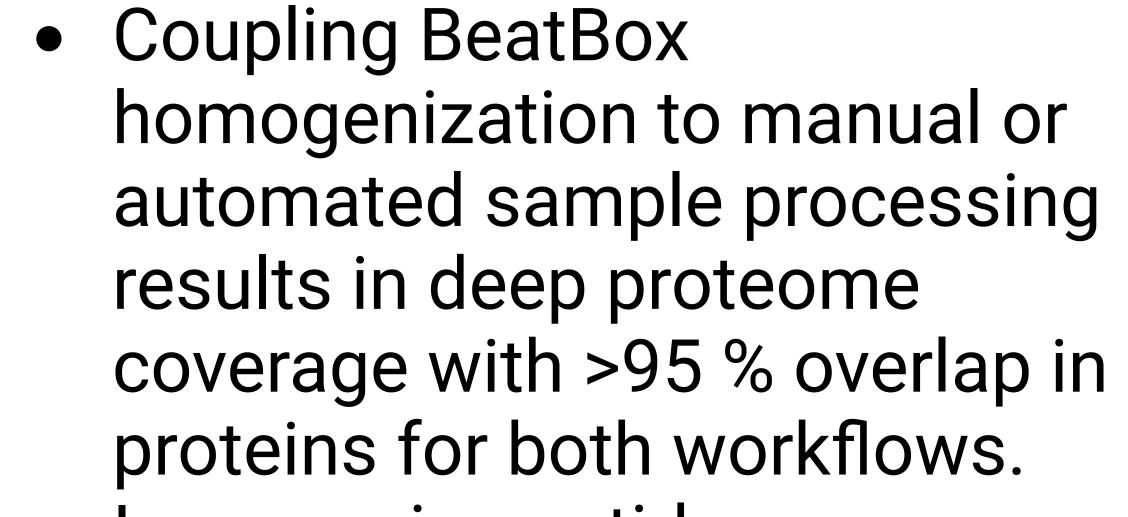


BeatBox-Manual iST BeatBox-PreON Inter-day technical variability

Mouse liver

HeLa cell

Peptide identification



- Increase in peptide identifications applying the optimized PaSER search engine indicating enhanced sequence coverage.
- PreON sample processing starting from pooled BeatBox homogenates provides minimal technical variabilty for both intraday (for mouse liver: CVPreON: CVmanua = 7%:11%) and interday (PreON: CV of <20 % for mouse liver and CV ~10 % for HeLa).

KEY TAKEAWAYS

HeLa cell

RESULTS

Protein groups identification

BeatBox vs. sonication-based homogenization

- BeatBox shortens protein extraction to 10 min with parallel processing of 1 - 96 samples
- BeatBox allows to process large sample quantities
- BeatBox provides excellent protein extraction efficiency

PreON vs. manual iST sample preparation

Mouse liver

- Coupling to BeatBox iST sample preparation provides reliable and improved LC-MS proteome analysis
- PreON improves technical variability
- BeatBox-PreON saves valuable time with less handson steps

PaSER vs. MaxQuant data processing

- PaSER accelerates data processing by making the results available immediatly after the run
- PaSER enhances peptide identifications by an optimized search algorithm

