

## Highly efficient and reproducible sample homogenization for proteomic analysis of various organs up to 50 mg

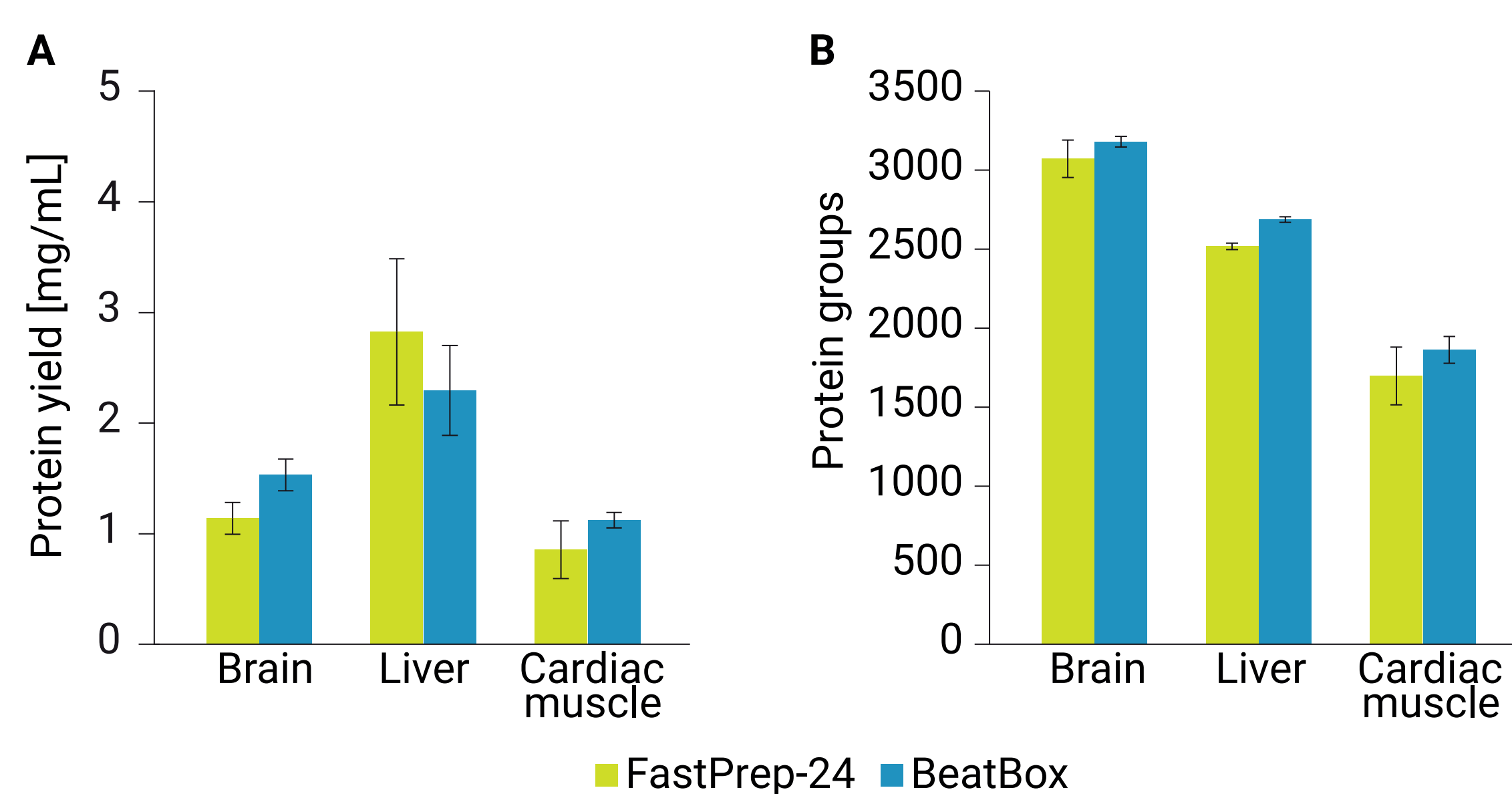
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### Spotlight

- Up to 24 samples homogenized in 10 minutes
- For tissues and cell derived samples
- Quiet homogenization with little to no temperature increase
- Can be combined with PreOmics' iST kit for bottom-up protein analysis

### Results & Discussion

#### Increased protein extraction efficiency for specific tissue types and increased number of proteins identified compared to a bead beating workflow

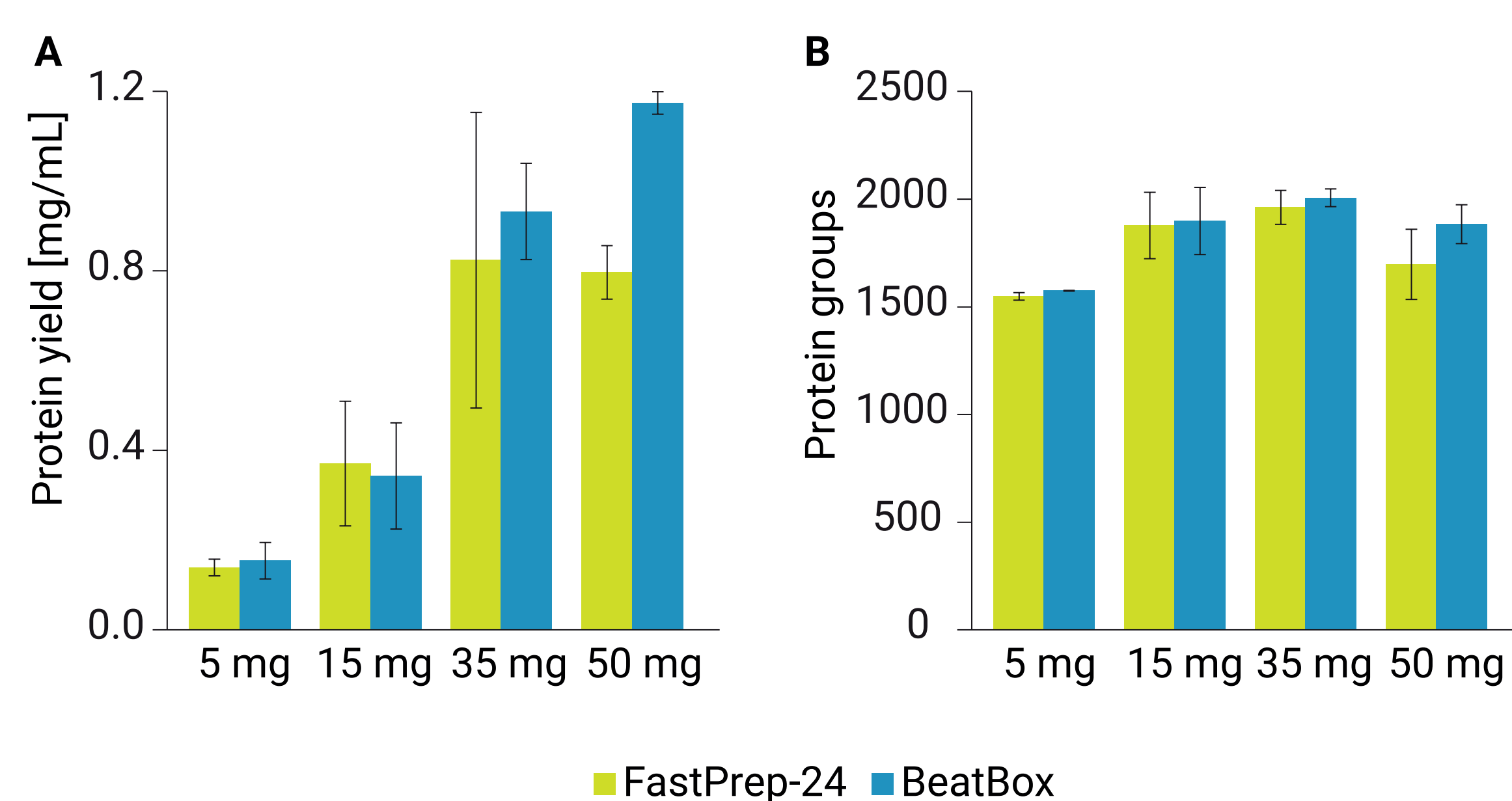


Comparing BeatBox and bead beating homogenization techniques using three mouse tissue types.

Mouse brain, liver and cardiac muscle of 50 mg of wet weight were processed in quadruplicate. Shown are A) protein extraction yields and B) protein groups identified per tissue type.

The error bars represent the standard deviation (SD).

#### Reliable processing of different tissue input amounts from 5 to 50 mg with comparable results to bead beating



Efficiency of homogenization from different starting amounts of cardiac muscle tissue using BeatBox and bead beating technique.

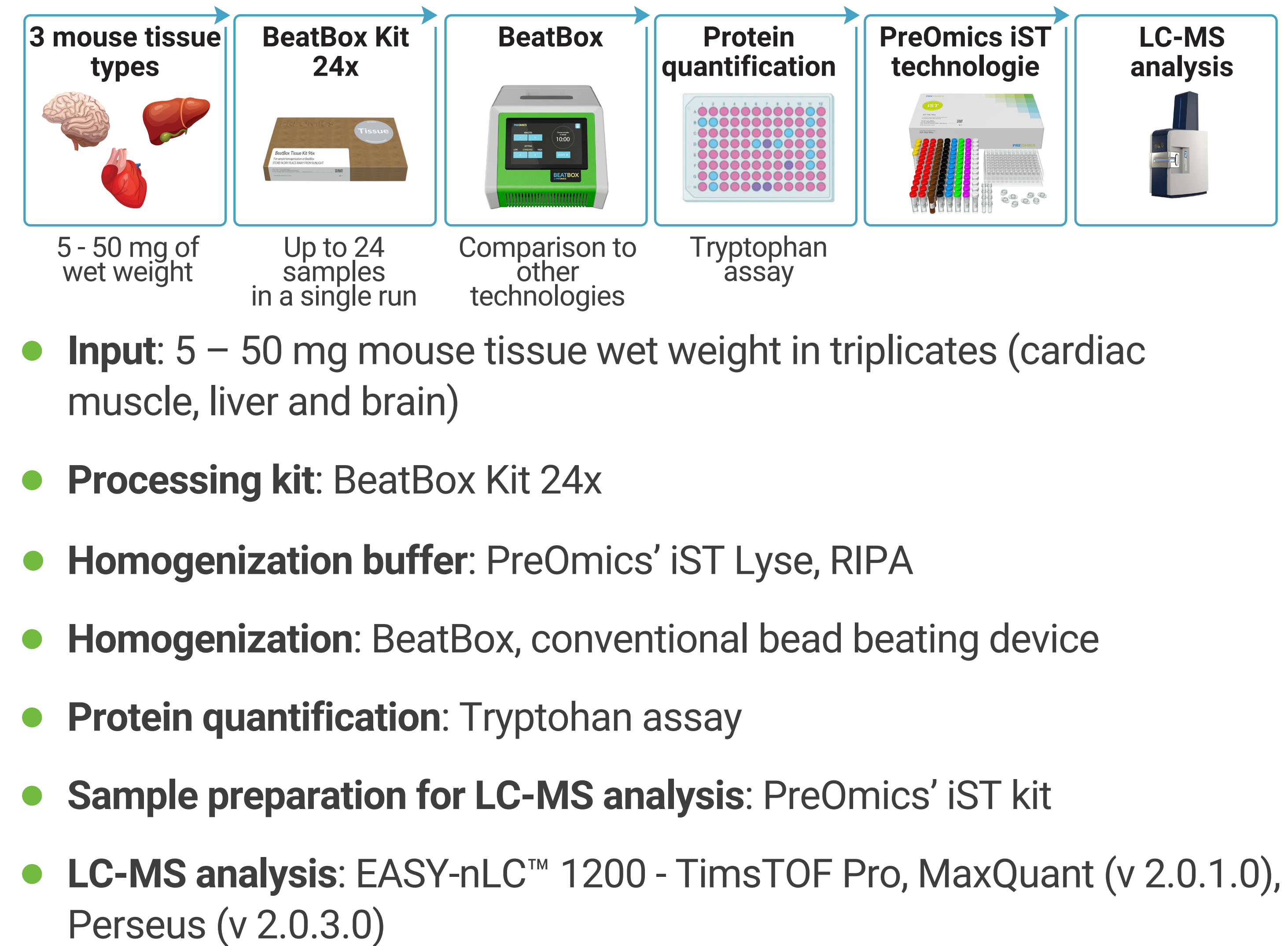
Tissue samples from 5 to 50 mg were processed in triplicate.

Shown are A) protein extraction yields and B) protein identification from different tissue inputs. The error bars represent the SD.

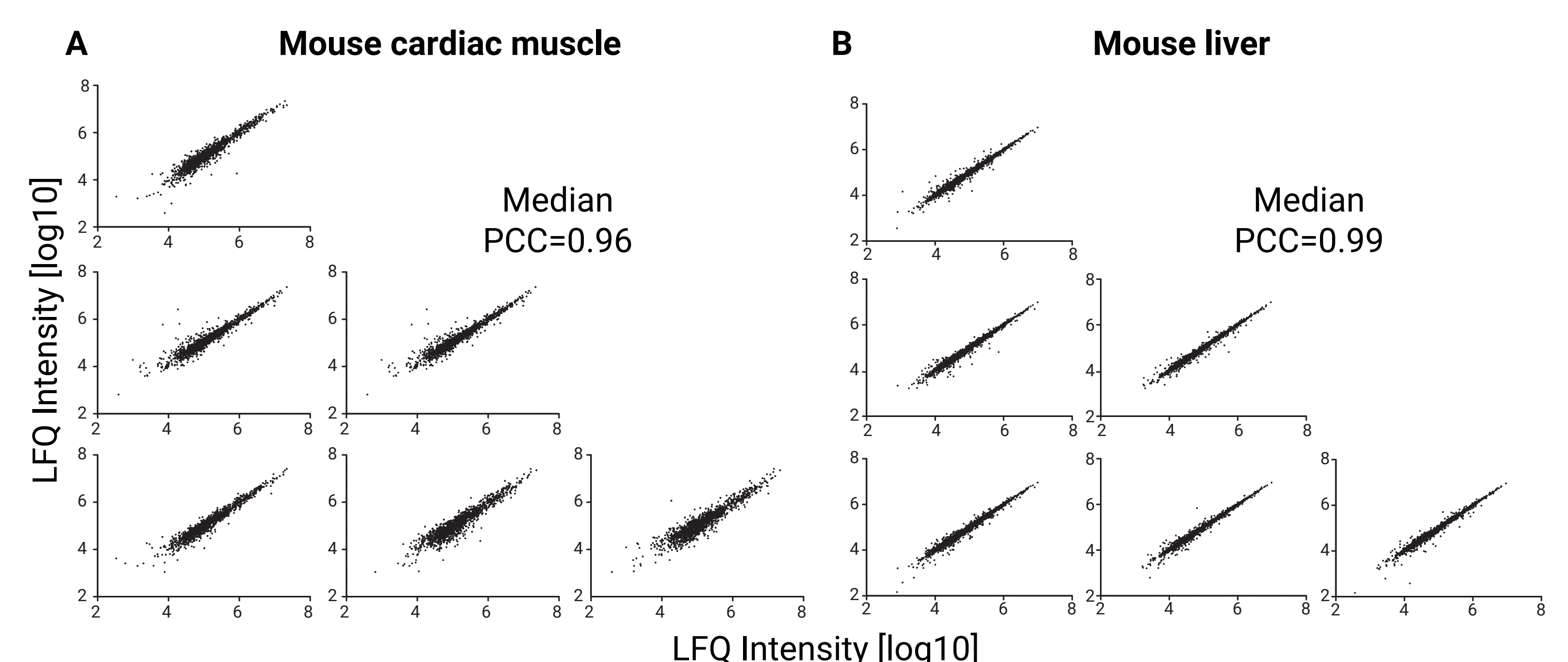
### Conclusions

- BeatBox in combination with the BeatBox Kit 24x provides high-throughput, efficient, and reproducible homogenization results across multiple types of tissue and cell derived samples
- Able to process a variety of tissue types with up to 50 mg of wet weight in PreOmics' iST LYSE or RIPA lysis buffer
- 1 to 24 tissue and cell derived samples can be homogenized in parallel, independently on the position in the tube holder
- BeatBox can be seamlessly combined with the PreOmics' iST kit, providing a complete and reliable proteomic sample preparation workflow from tissue to ready-to-measure peptides in less than 3 hours

### Materials & Methods

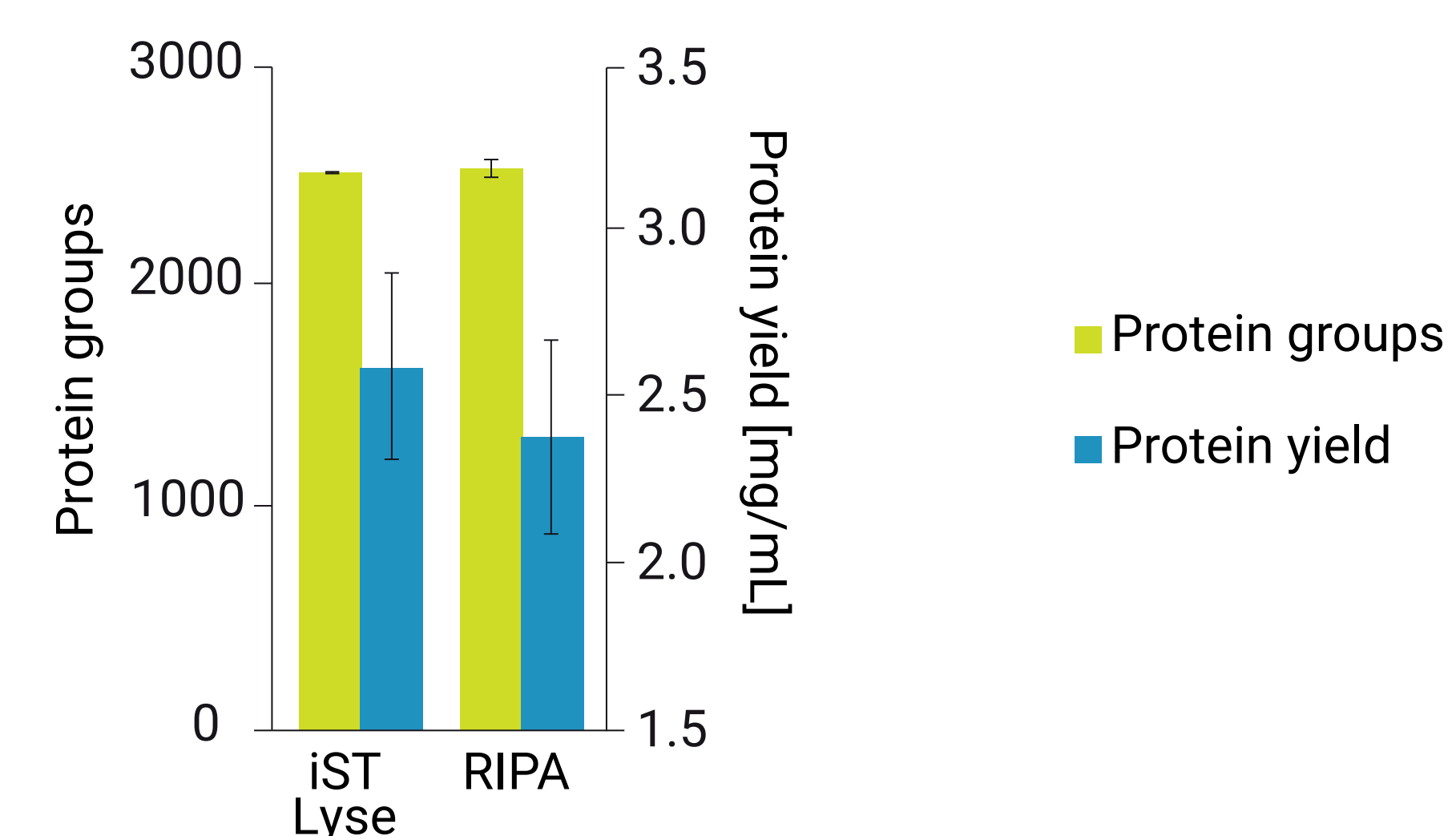


### High reproducibility across different types of tissue



Quantitative reproducibility of A) mouse cardiac muscle and B) liver tissue using the BeatBox Kit 24x. Tissue samples of 50 mg wet weight were processed in quadruplicate.

### Workflow is compatible with RIPA buffer



Comparing PreOmics' iST Lyse and RIPA buffer using mouse liver tissue. Mouse liver tissue samples of 50 mg of wet weight were processed in triplicate. Shown are protein extraction yields and identified protein groups. The error bars represent the SD.