

Cost efficient, fully automated high throughput sample preparation with Evokits and Evosep Lupo for large scale discovery proteomics

Salla Keskitalo, Iulia Macavei, Magnus Huusfeldt, Stine R. Friberg, Maurine Fucito, Stoyan Stoychev, Nicolai Bache, Dorte Bekker-Jensen

Evosep Biosystems, Denmark

Highlights

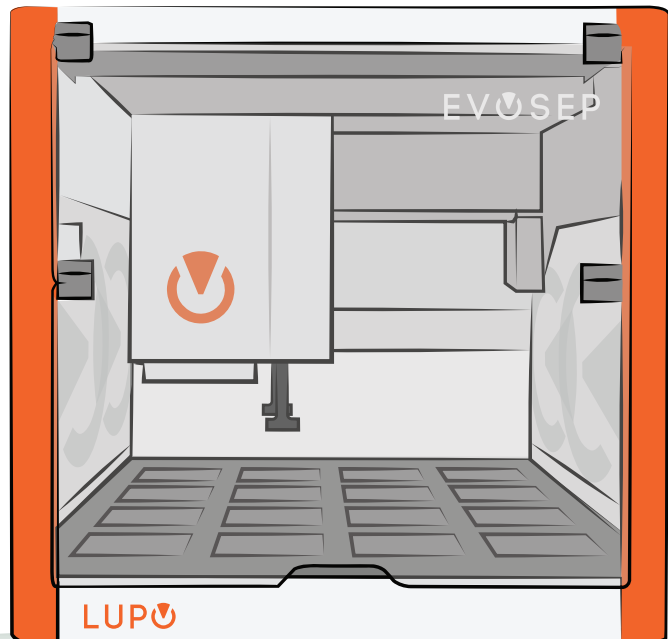
- Evosep Proteomics enables a high-performance Sample to Separation solution for standardized and scalable mass spectrometry.
- Evokits with built-in quality control samples run on Evosep Lupo, with automated setup and consumable checks for seamless sample preparation.
- Robust protein quantification in the Evosep ecosystem with <13% protein CVs across ten sample matrices using the Evosep Eno 500 SPD method.

Robust sample preparation is key to scalable proteomics

Built-in controls and walk-away automation for robust results

For proteomics to operate reliably in large-scale and regulated environments, reproducibility must be continuously verified – not assumed. This requires integrated quality control, full traceability, and automation that reduces risk at every step. Evosep Proteomics embeds these capabilities directly into the workflow.

Automation through the Evosep Lupo platform reduces variability and operational risk through intelligent checks for consumables, plate positioning, and workflow execution, minimizing human error. Combined with a simplified interface and predefined workflows, it enables true walk-away operation and reproducible, high-quality data generation without specialized expertise.



Starting point
Protein lysate, reduced and alkylated
≤ 1 µg protein lysate
≤ 0.5% SDS final conc.
≤ 5 µl sample volume

Standardized kits
No preparation needed. Consumables stored under required conditions.

Error-free setup
Built-in verification of correct position, orientation and expiry.

Built-in QC
Automated monitoring kit and LC-MS performance. Supports additional study QCs.

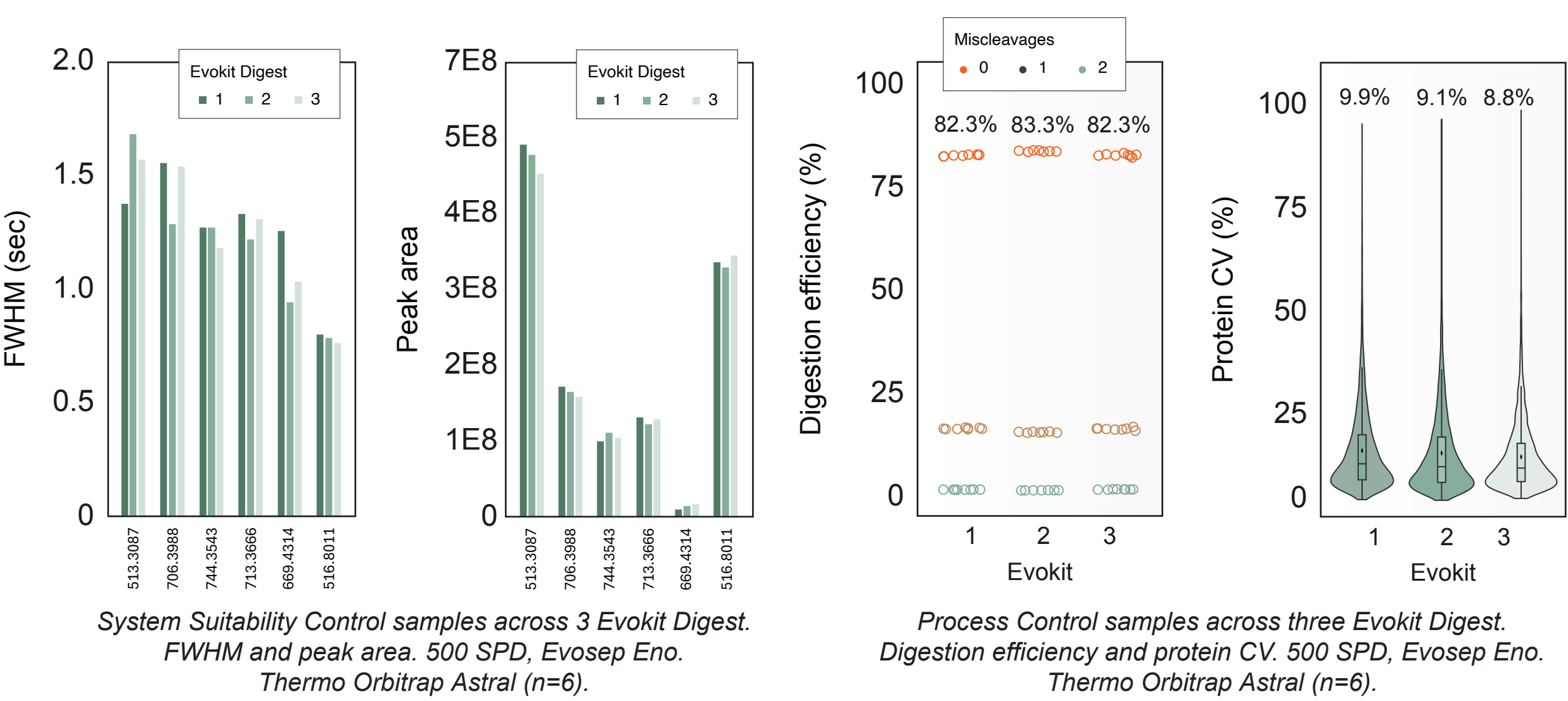
Full traceability
Batch tracking. Easy access to Certificate of Analysis.

MS ready export
Tailored .csv file for your setup. Controlled run order via Evotip positions.

Built-in quality controls incorporated with each Evokit

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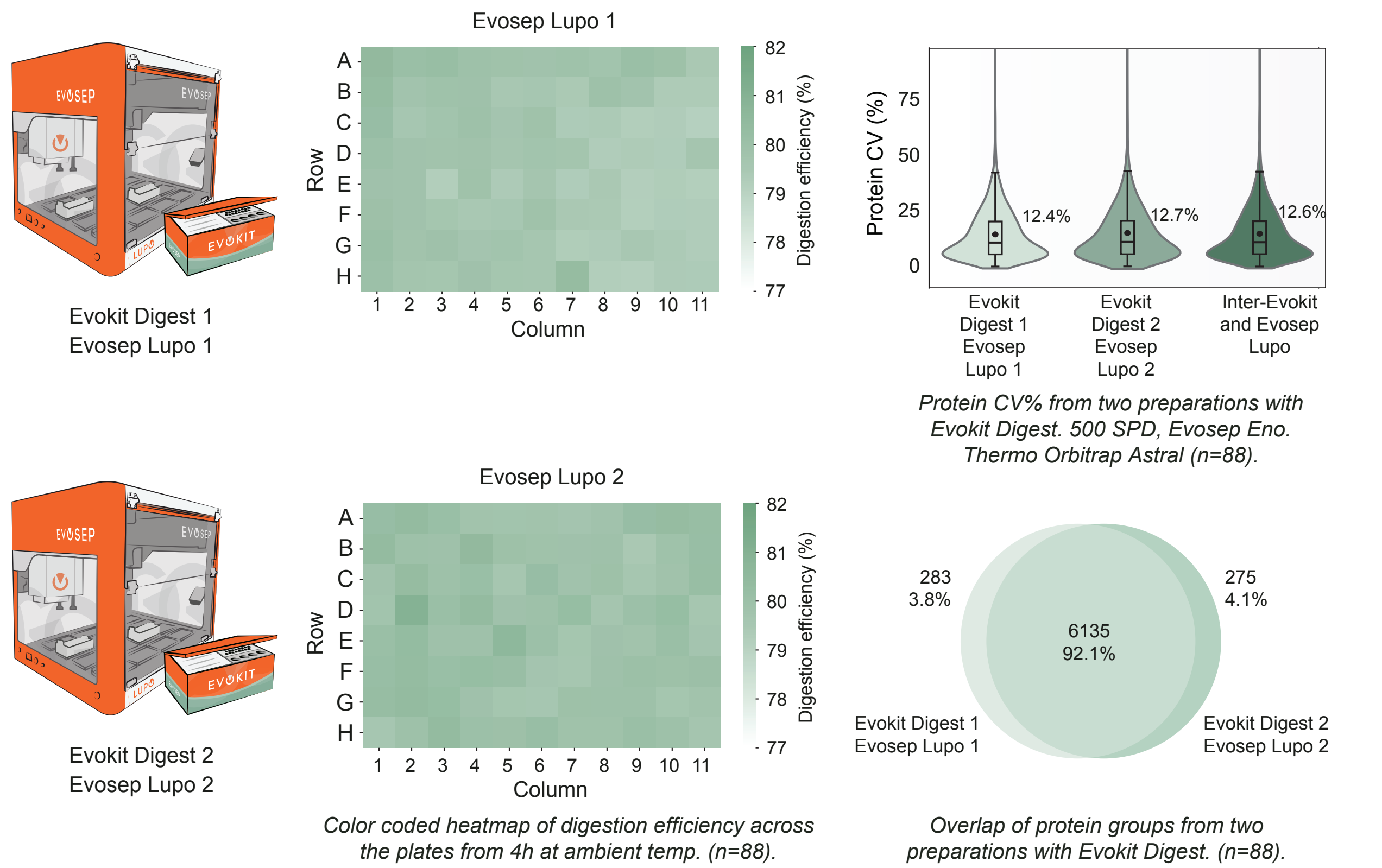
- Each Evokit incorporates built-in quality controls, including:
- Process control samples that monitor the full sample preparation workflow
 - System suitability controls that verify LC–MS performance over time



Sample preparation at scale with Evokits and Evosep Lupo

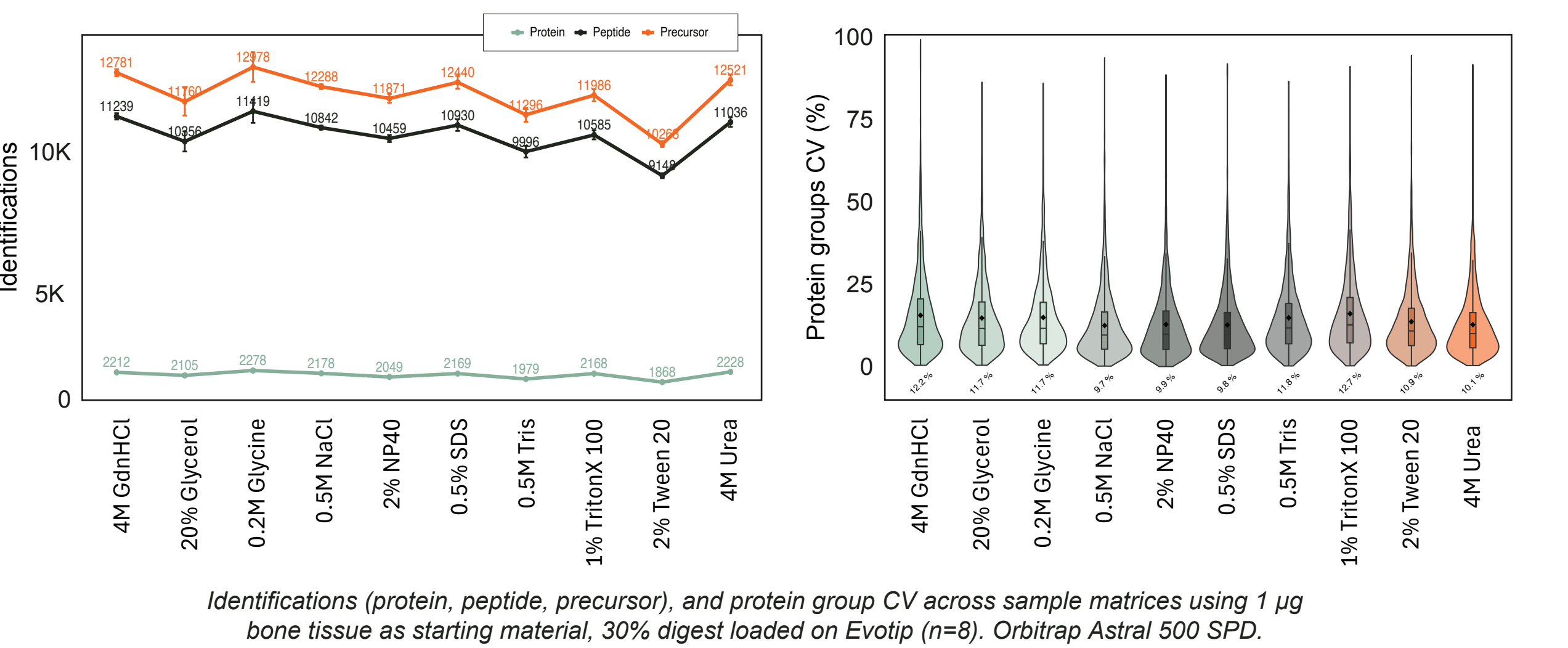
Reproducibility across plates and instruments

Reproducibility was further assessed across two different plates processed on two different Evosep Lupo systems to evaluate transferability and robustness at scale. The comparison showed a high degree of overlap in identified proteins between plates and platforms, as visualized by the Venn diagram, while closely aligned CV distributions confirmed consistent quantitative performance across runs.



Consistent performance with Evokit Digest across diverse sample matrices

The workflow was tested against a number of commonly used sample matrices for preparing samples for proteomics analyses. The performance maintains robustness, precursor identifications and quantitative precision using 1 µg bone tissue lysate as starting amount. 30% of the digest was loaded on Evotips.

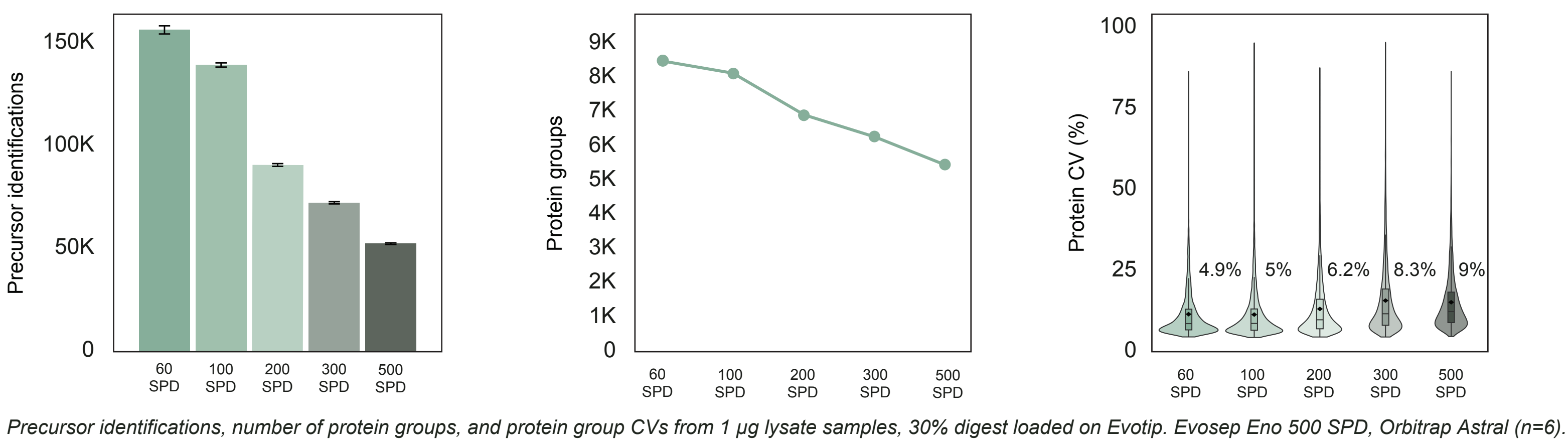


Technical details

All samples analyzed using the 60 and 100 SPD methods were run on an EV1109 column, whereas the 200, 300, and 500 SPD methods were analyzed using an EV1182 column. All columns were maintained at a constant temperature of 40°C in the Evosep Pod and coupled to an EasySpray source on the Orbitrap Astral mass spectrometer. Full MS scans were acquired at a resolution of 240,000 over a precursor mass range of 380–980 m/z. MS2 scans were acquired using 4 m/z isolation window for the 200, 300, and 500 SPD methods, while 2 m/z isolation windows were used for the 60 and 100 SPD methods. An injection time of 3 ms was applied for all methods. Data were processed and searched using DIA-NN version 1.9.2.

Controlled, consistent results across every workflow step

Evokit Digest performance across Evosep Eno standard methods



Read more:



The Evokit Digest performance was assessed using the Evosep Eno standard methods on the Orbitrap Astral MS, providing good proteome coverage and protein CVs. 1 µg K562 lysate was processed, and 30% of the resulting digest was loaded on Evotips.