

Rapid Metabolomics in Blood

Microsamples: Optimization and Biomarker Discovery Feasibility

Marlene N. Thaitumu

Doctoral candidate,

Department of Medicine, School of Health Sciences,

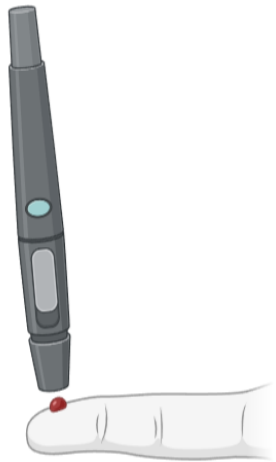
Aristotle University of Thessaloniki, Greece.

Outline

- ✓ Background and significance:
 - ✓ Rapid microbore metabolic profiling (RAMMP).
 - ✓ Blood microsampling/microsamples (B μ S).
- ✓ Optimization and evaluation of a RAMMP assay.
- ✓ Feasibility of RAMMP to identify biomarkers discriminating B μ S and traditional blood matrices (liquid venous blood and plasma).
- ✓ Summary and conclusions.

Background and significance

- ✓ **Microbore** (≤ 1 mm column internal diameter) analysis is a high throughput LC-MS technique.
 - ✓ A common **Microbore** application is rapid microbore metabolic profiling (**RAMMP**):
 - Reduced solvent and sample consumption.
 - Fast chromatography (**RAMMP** 1.5 min – 3.8 min vs **conventional LC-MS** 7.5 min – 30 min).
- ✓ Blood microsampling (B μ S):



Collection of < 100 μ l of capillary blood.

Background and significance

RAMMP

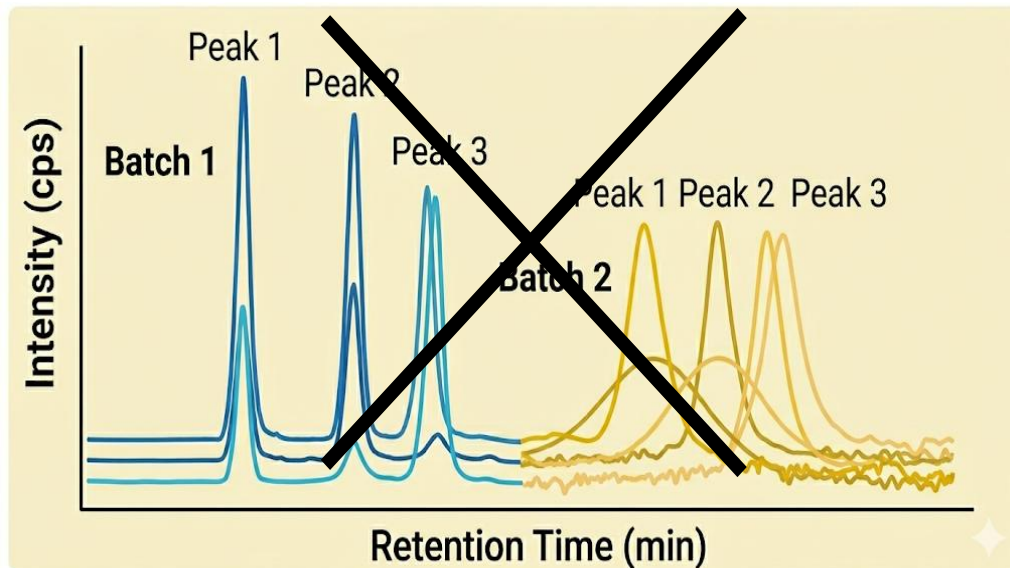
Low reagent and sample consumption



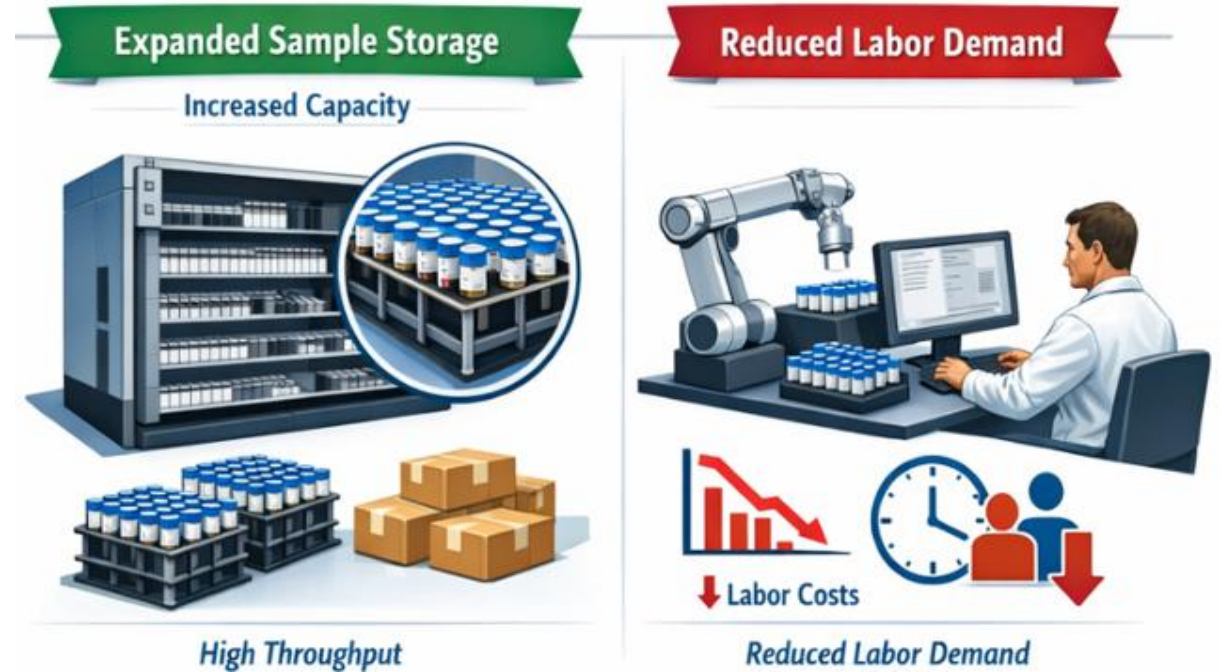
\$\$



Mitigation of batch effects

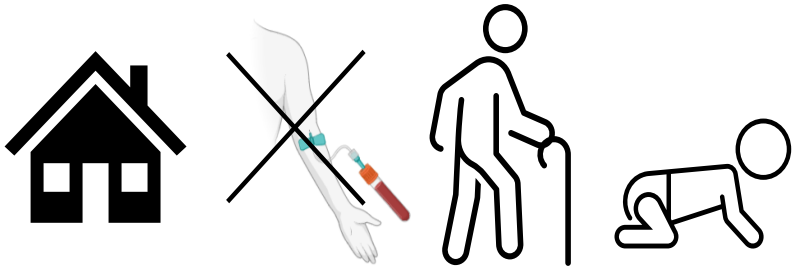


Improved laboratory logistics.



Background and significance

B μ S

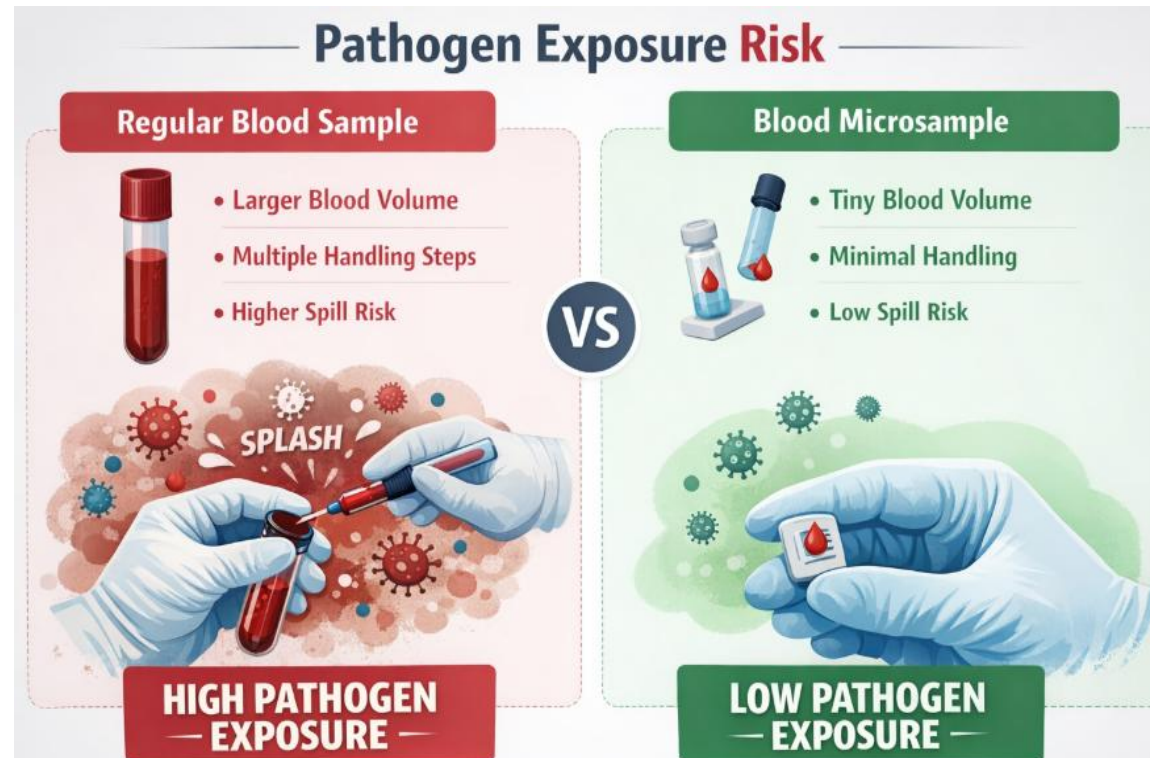


“Patient centric” (ease and convenience).
Feasibility for longitudinal research.

Enhanced stability for certain metabolites
e.g., up to 10 years.



✓ Improved transportation logistics



Low risk of
pathogen
exposure.

Background and significance

RAMMP + B μ S

Can provide a paradigm shift in the analysis of
LARGE PHENOTYPIC STUDIES.

Optimization and evaluation of a RAMMP assay



Conventional LC-QTOF

Waters Acquity UPLC-Synapt G2S QTOF

Department of Metabolism, Digestion, and Reproduction
Imperial College London.

RAMMP

HSS T3 C18 column
1.8 μm , 1 mm X 50 mm

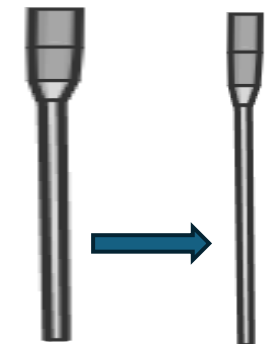
Conventional

HSS T3 C18 column
1.8 μm , 2.1 mm X 150 mm

For RAMMP
Shorter
Narrower peek tubing
Narrower MS probe

0.004 inches

0.0025 inches



125 μm to 50 μm

7

RAMMP SETUP



Optimization and evaluation of a RAMMP assay

Geometrically scaled down conventional LC method (by Gray et al. 2015).

$$\text{RAMMP flowrate} = \text{Conventional flowrate} \times \frac{\text{RAMMP ID}^2}{\text{Conventional ID}^2}$$

$$\text{RAMMP Inj Vol} = \text{Conventional flowrate} \times \frac{(\text{RAMMP ID}^2 \times \text{RAMMP Column Length})}{(\text{Conventional ID}^2 \times \text{Conventional Column length})}$$

$$\text{Difference in RAMMP gradient timepoints} = \text{Difference in conventional gradient timepoints} \times \frac{(\text{RAMMP Column vol})}{(\text{Conventional Column vol})} \times \frac{\text{Conventional flowrate}}{\text{RAMMP flowrate}}$$

$$\text{RAMMP gradient timepoints} = \text{Previous timepoint} + \text{Difference in RAMMP gradient timepoints}$$

Conventional

Flow rate 0.35 mL/min

Injection vol 10 µL

Gradient 17 min

Scaled RAMMP

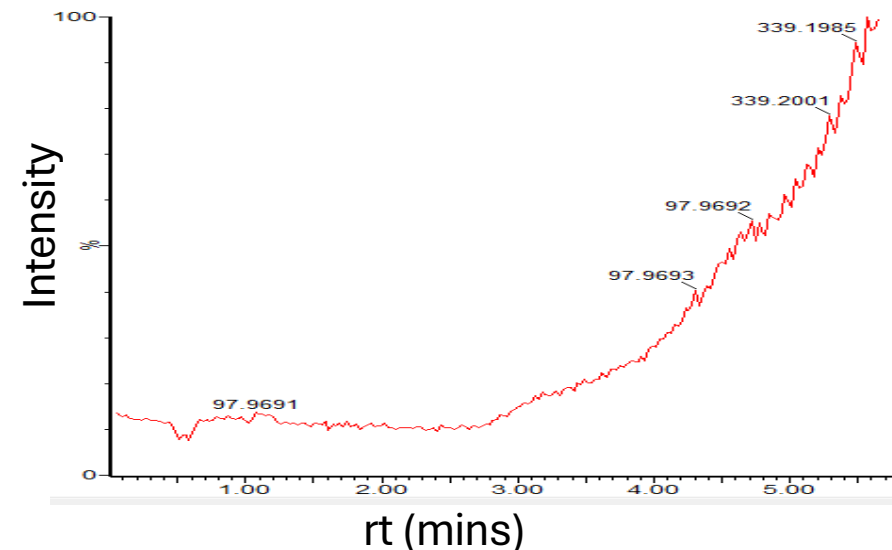
Flowrate 0.1 mL/min

Injection vol 0.8 µL

Gradient 5.7 min

Same **MS parameters** used for both assays.

No **signal** observed using the scaled **RAMMP** assay



Optimization and evaluation of a RAMMP assay

Scaled RAMMP

Flowrate 0.1 mL/min

Injection vol 0.76 μ L

Gradient 5.7 min

Optimized RAMMP

Flowrate 0.2 mL/min

Injection vol 5 μ L

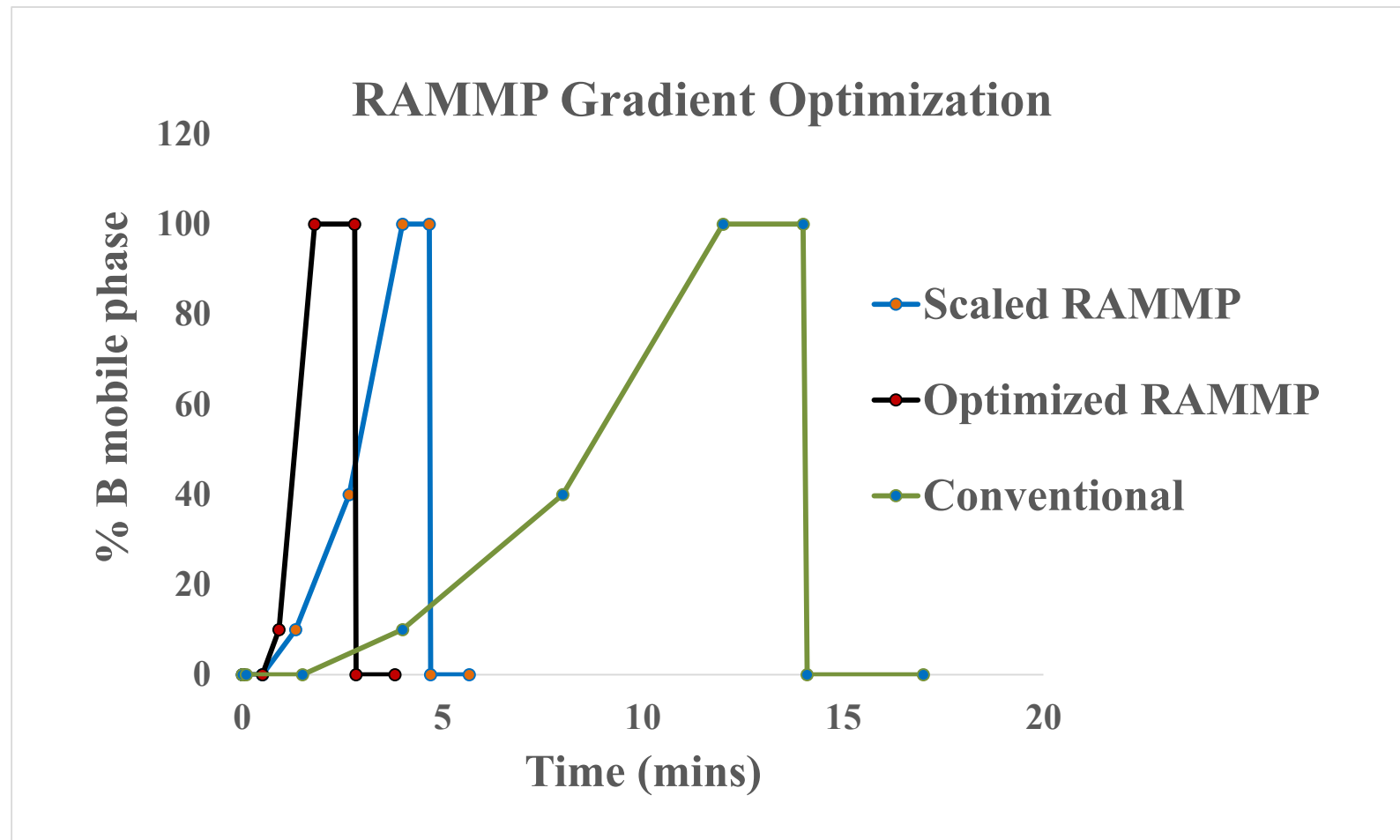
Gradient 3.8min

Conventional

Flow rate 0.35 mL/min

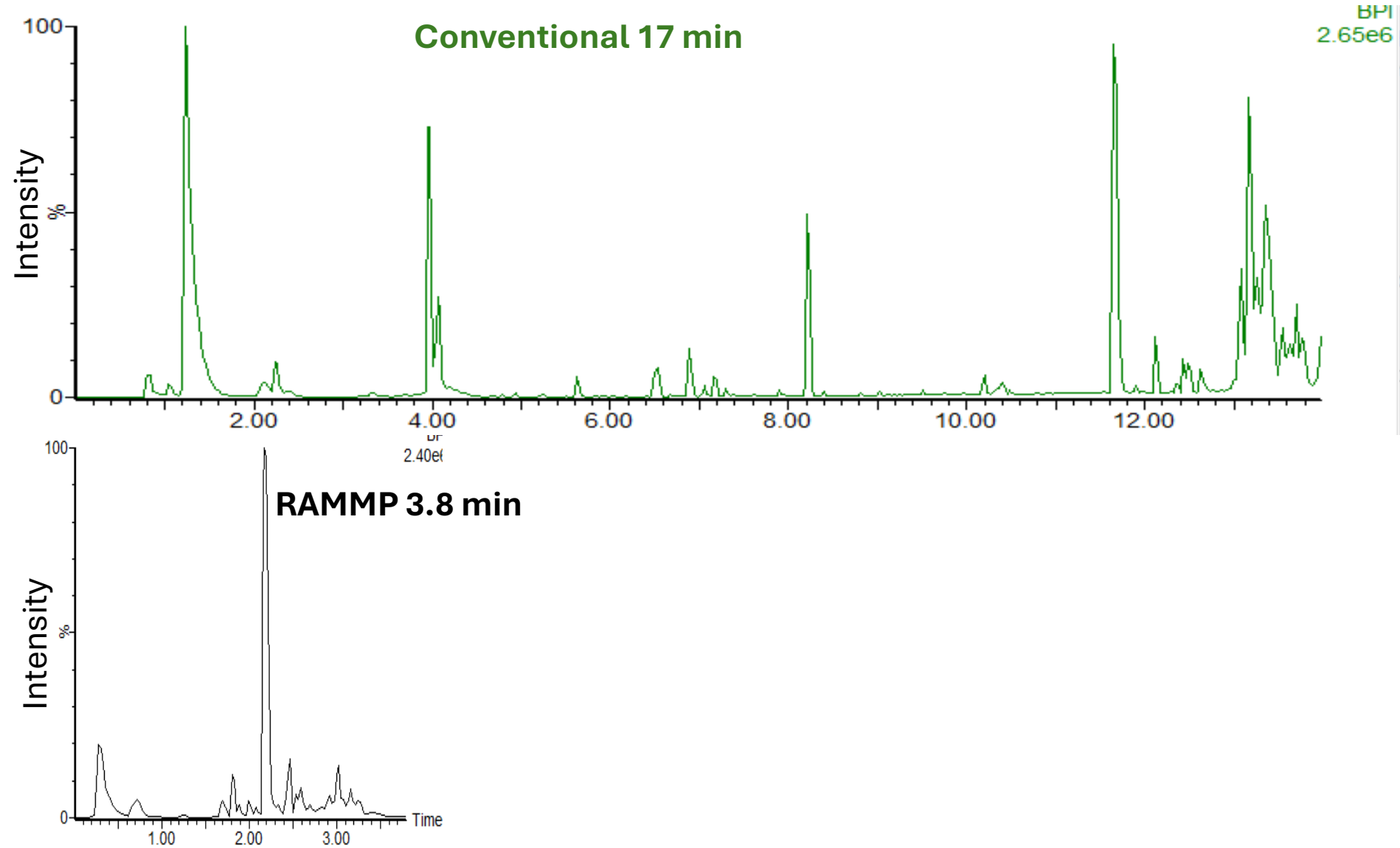
Injection vol 10 μ L

Gradient 17 min



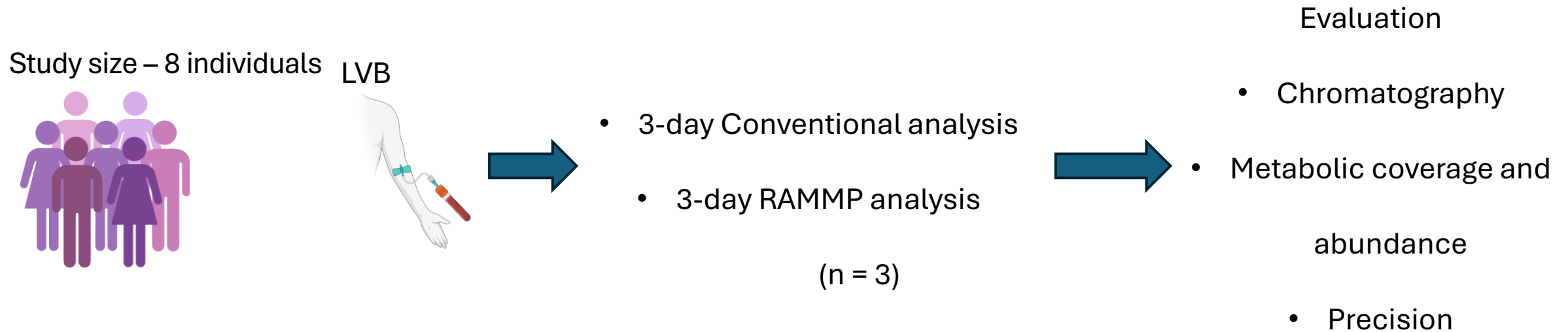
Optimization and evaluation of a RAMMP assay

Comparison of a base peak chromatogram (BPC)



Optimization and evaluation of a RAMMP assay

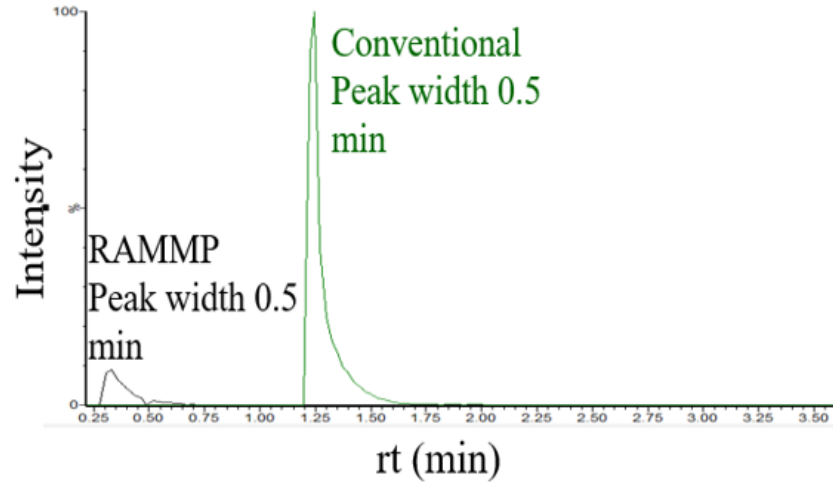
Evaluate **RAMMP's performance** against a **conventional** assay.



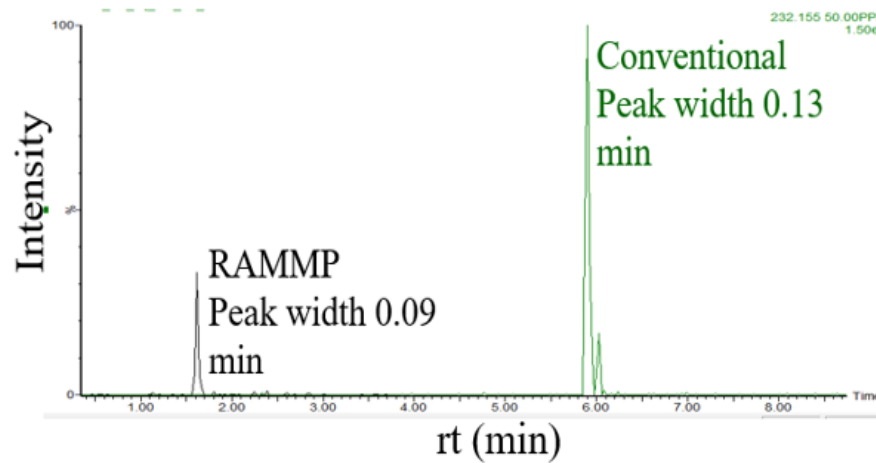
Optimization and evaluation of a RAMMP assay

Chromatography comparison: Four metabolites representing different classes and spanning the gradient compared.

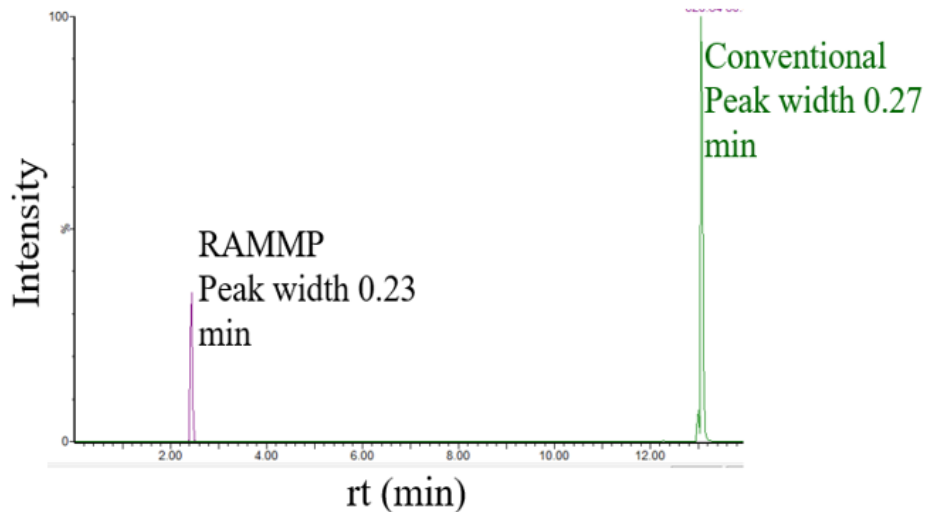
4-Hydroxyproline



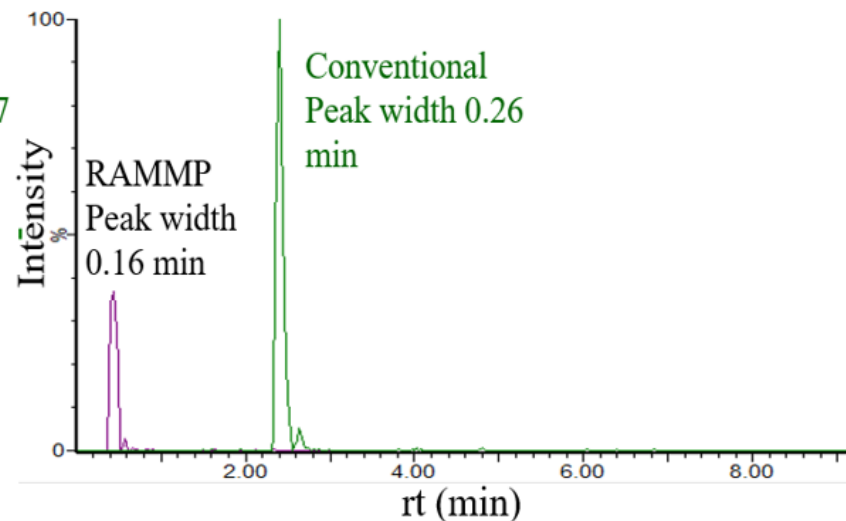
Butyrylcarnitine



Lysophosphatidylcholine 18:2



Hypoxanthine

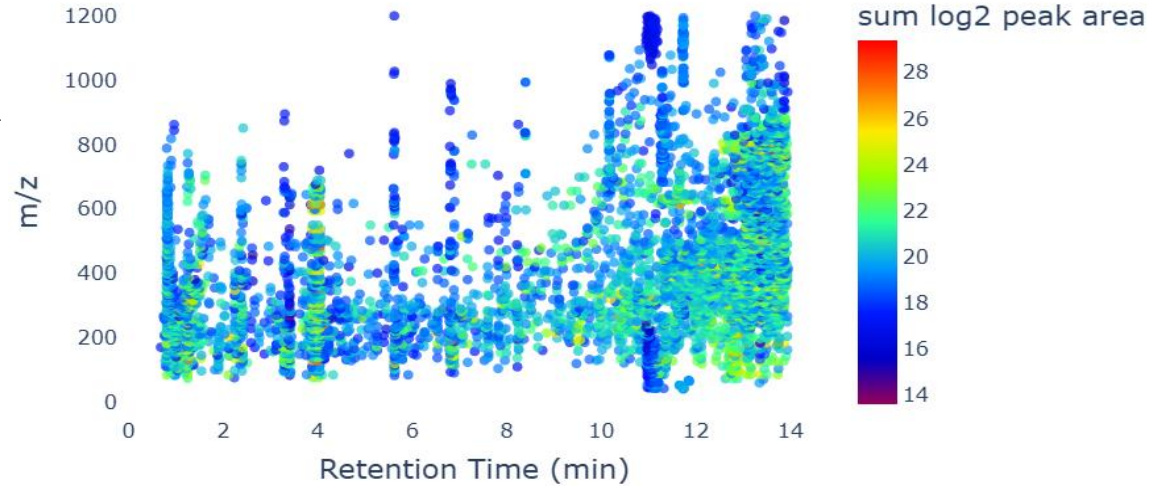


- ✓ Slightly narrower peaks in **RAMMP**; no isomeric resolution.
- ✓ Shorter gradient and column = lower peak capacity and loss of isomeric resolution.

Optimization and evaluation of a RAMMP assay

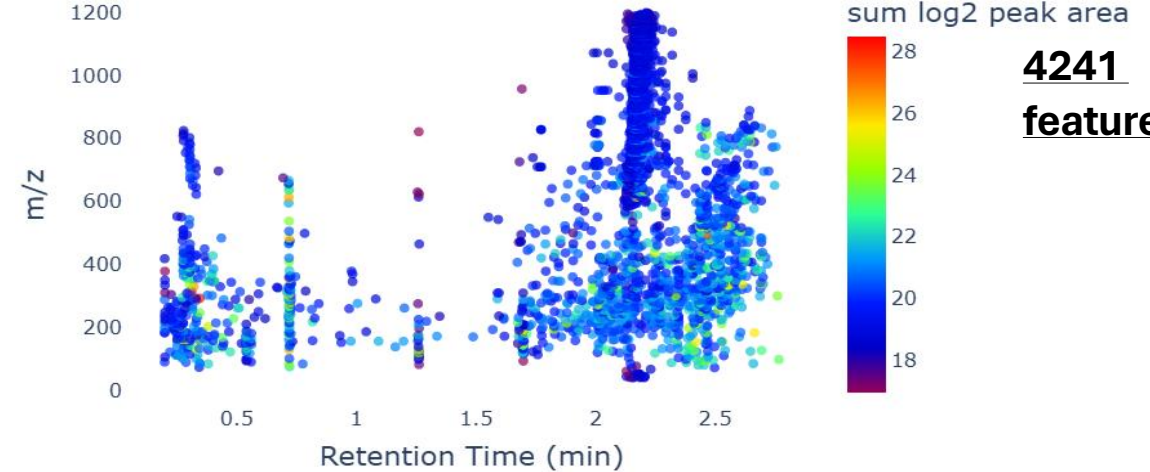
Metabolic coverage comparison

Conventional metabolic profile



6001
features

RAMMP metabolic profile



4241
features

✓ Significant loss (30%) of metabolic coverage using **RAMMP**:

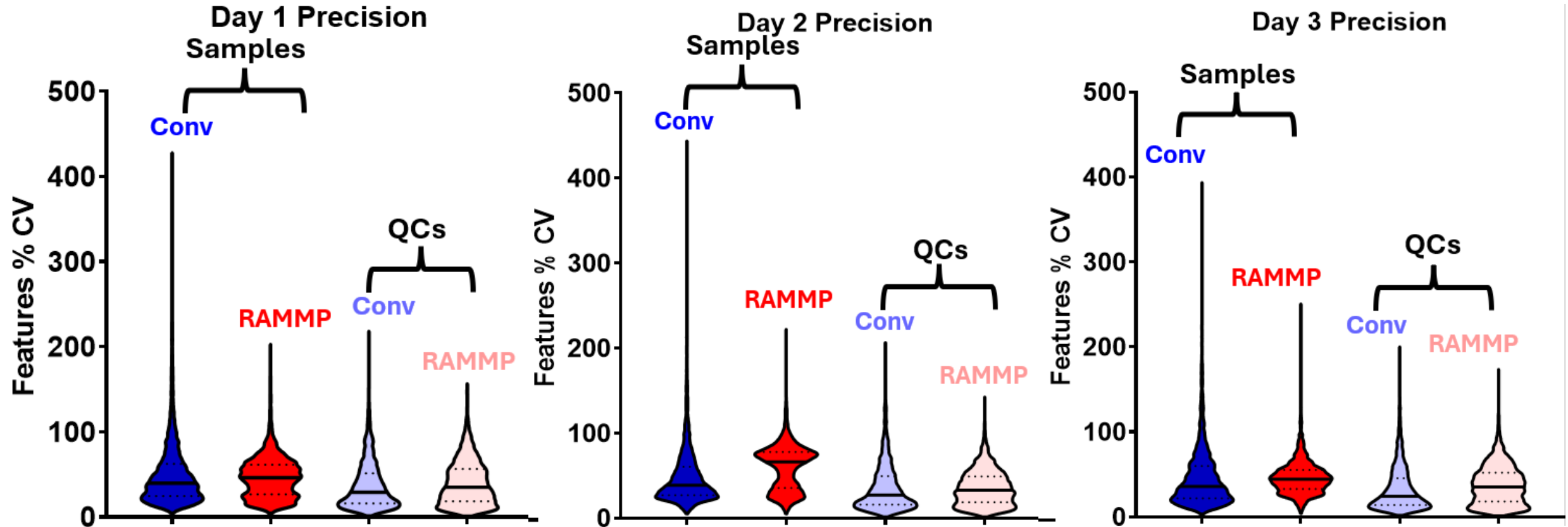
- Low abundant features in the **conventional** assay are undetected in **RAMMP**.
- Loss of metabolic coverage and abundance are attributed to the scaling down of the chromatography.

✓ However, **RAMMP** had similar level of annotation:

- **Conventional = 51** and **RAMMP = 49** (**butyrylcarnitine isomer** and **3-methylxanthine** were undetected).

Optimization and evaluation of a RAMMP assay

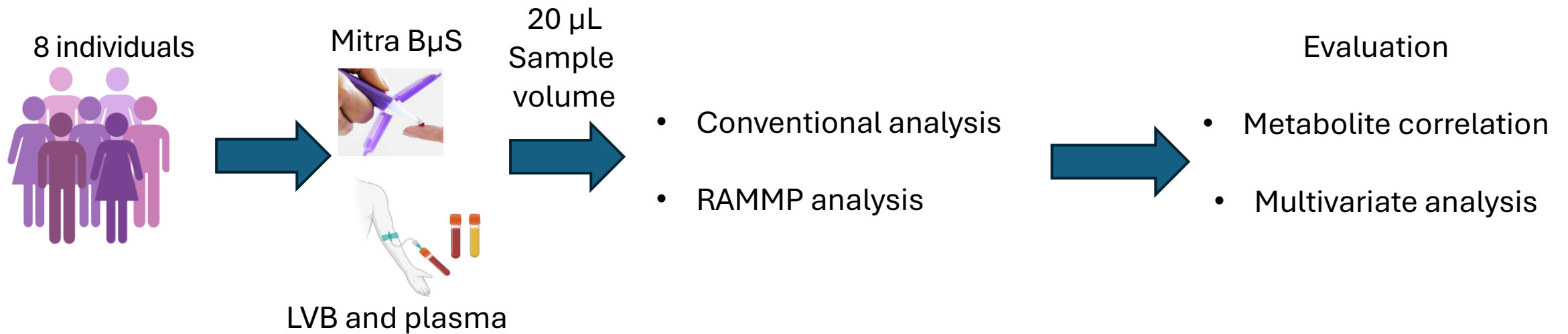
Precision comparison: Intra (within-day) and inter day (day-to-day) comparison.



✓ **RAMMP** demonstrated similar precision relative to the **conventional** assay.

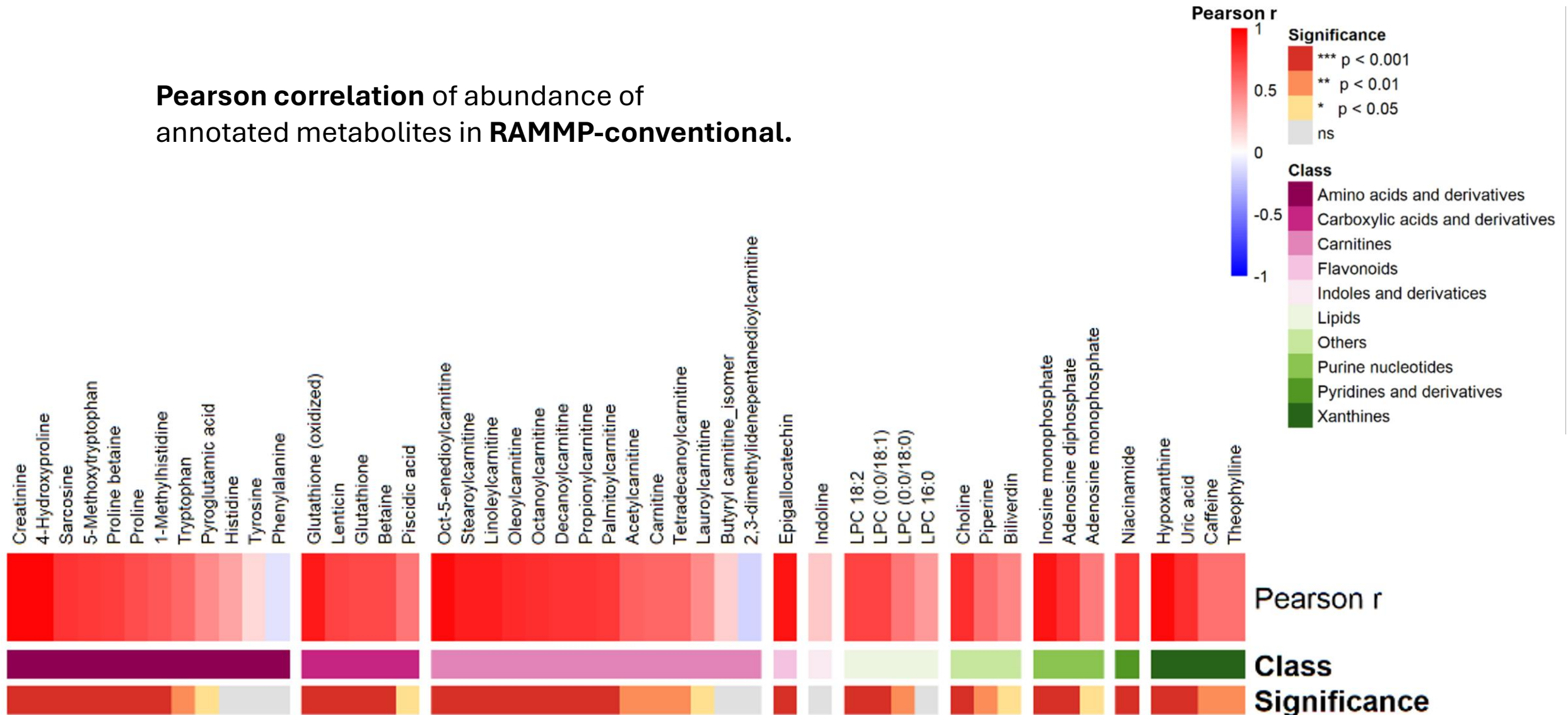
RAMMP's Biomarker Discovery Feasibility

- ✓ **RAMMP** performed similar relative to the conventional assay except for loss of metabolic coverage.
- ✓ Biomarker feasibility study:
 - can **RAMMP** capture discriminating features between **Mitra B μ S** and **traditional blood matrices** despite the loss of metabolic coverage?



RAMMP's Biomarker Discovery Feasibility

Pearson correlation of abundance of annotated metabolites in **RAMMP-conventional**.

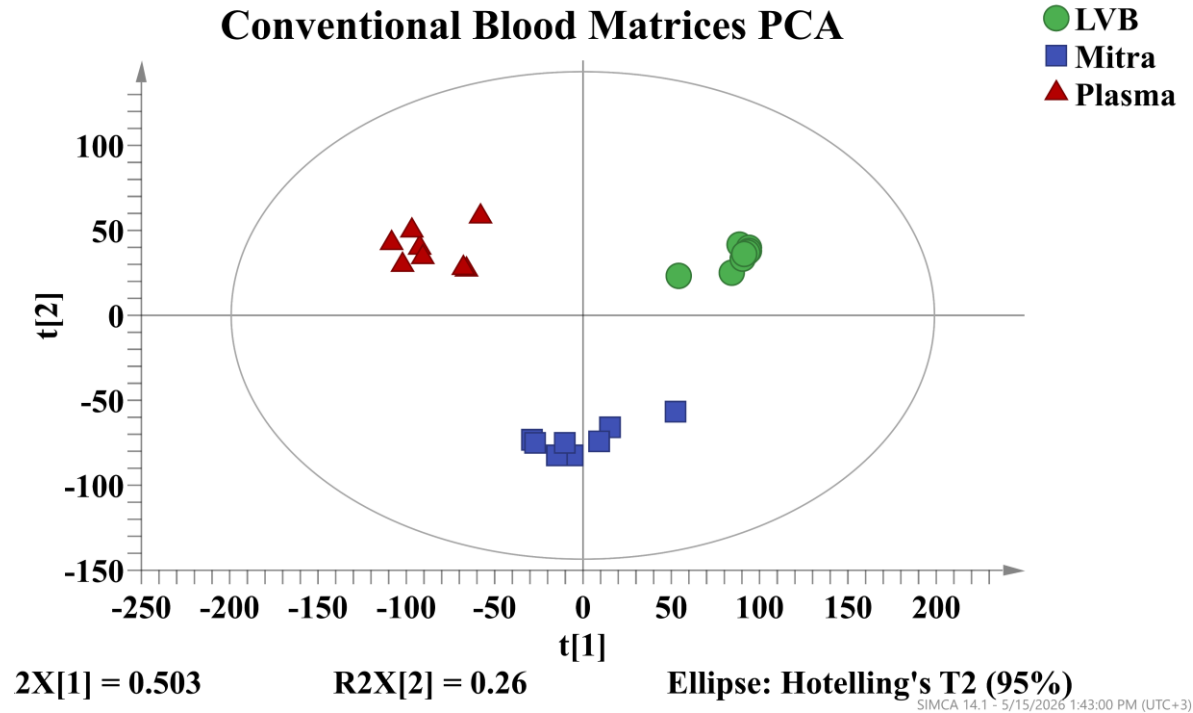


✓ **RAMMP** assay can qualitatively capture similar information.

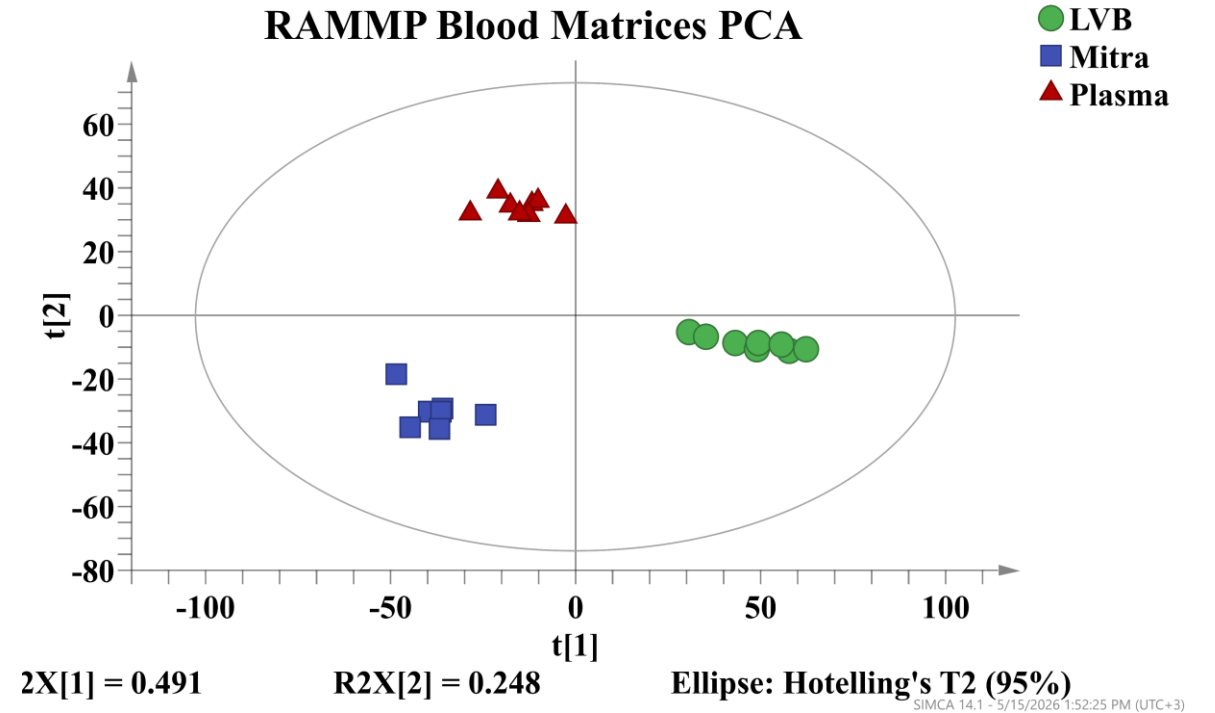
RAMMP's Biomarker Discovery Feasibility

Variance in the metabolic profiles.

Conventional Blood Matrices PCA



RAMMP Blood Matrices PCA



✓ Similar clustering captured using RAMMP.

RAMMP's Biomarker Discovery Feasibility



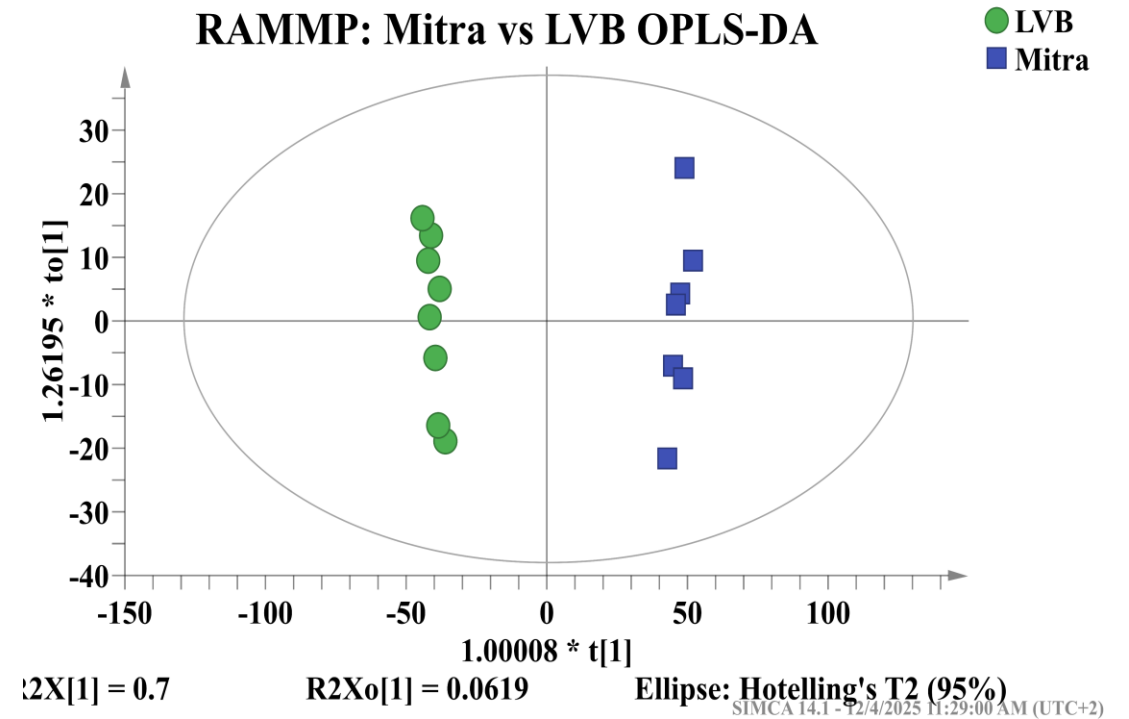
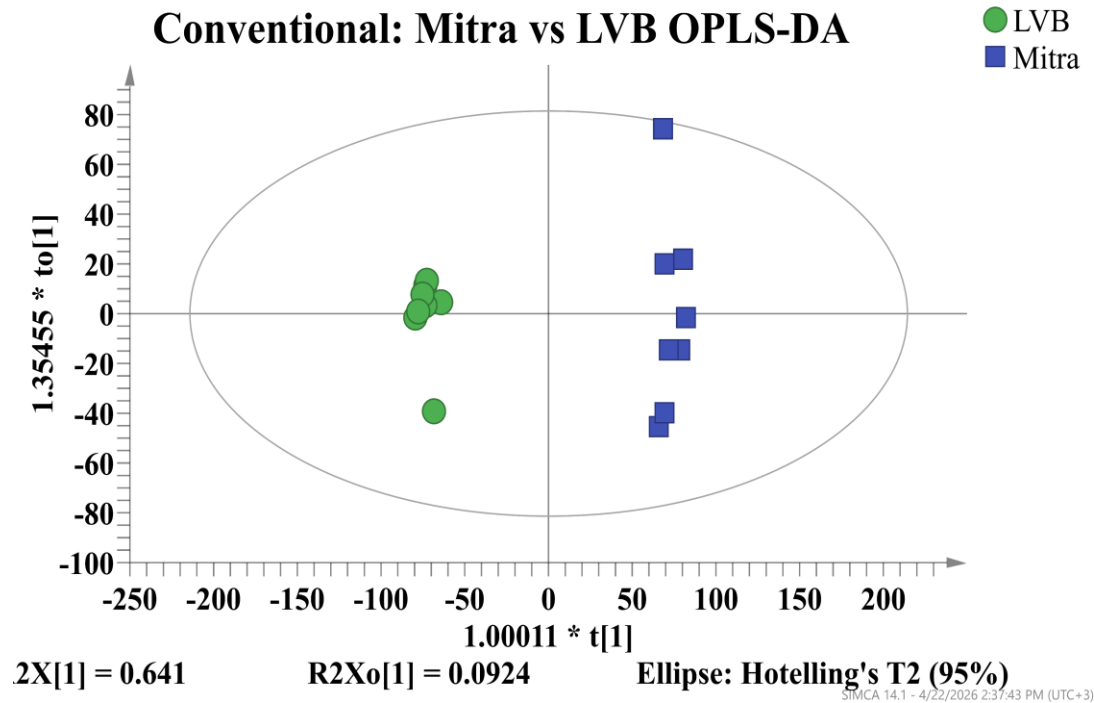
Mitra BpS

VS



LVB

Significance of discrimination analysis using OPLS-DA.



✓ Reliable models: CV ANOVA $p < 0.05$.

✓ Valid and predictive: Permutations R^2 and $Q^2 < \text{original models } R^2 \text{ and } Q^2$.

RAMMP's Biomarker Discovery Feasibility



vs

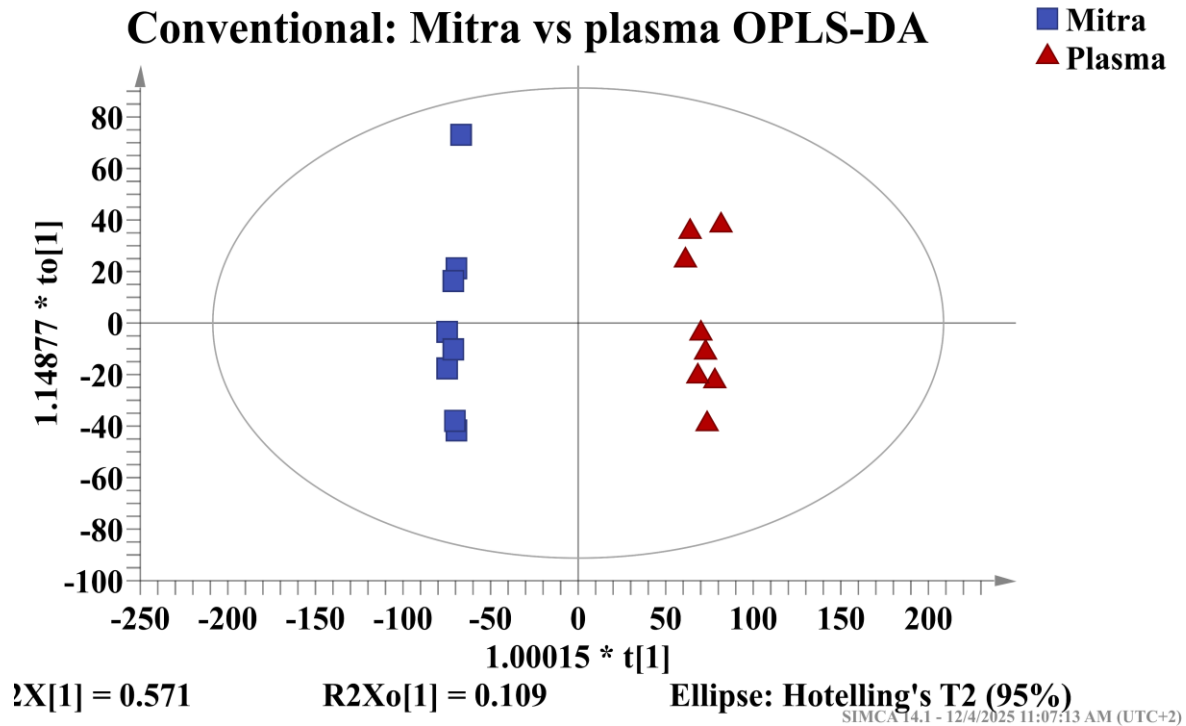


Plasma

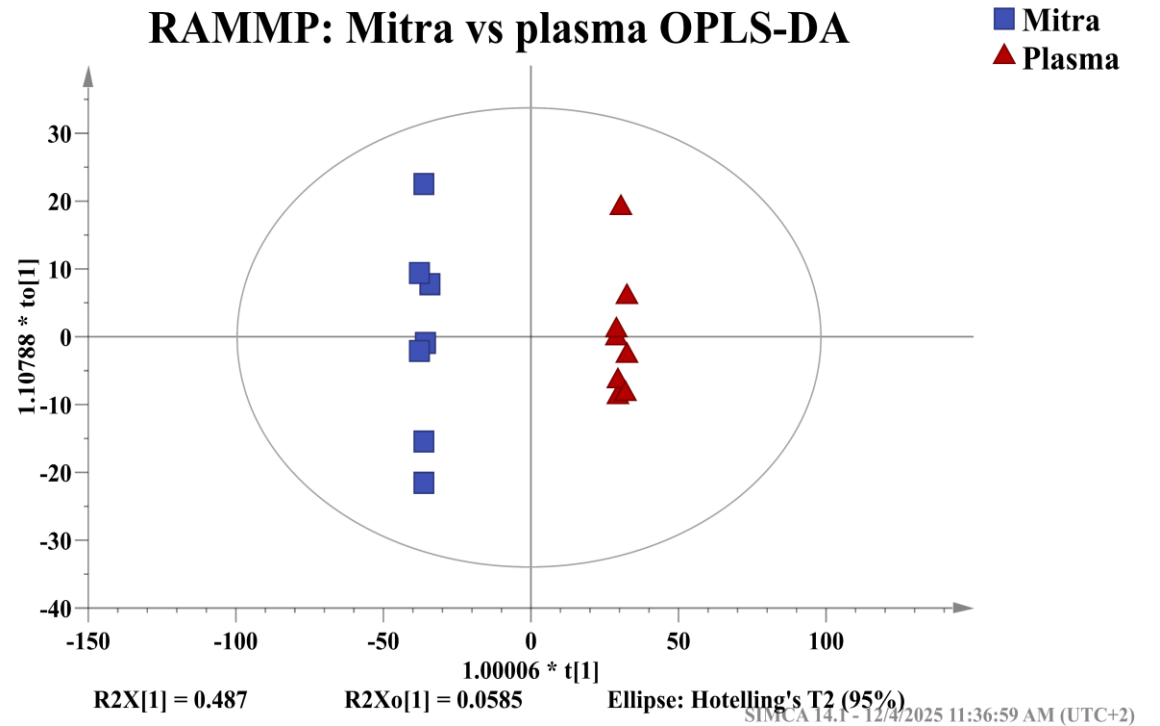
Significance of discrimination analysis using OPLS-DA.

Mitra B μ S

Conventional: Mitra vs plasma OPLS-DA



RAMMP: Mitra vs plasma OPLS-DA



✓ Reliable models: CV ANOVA $p < 0.05$.

✓ Valid and predictive: Permutations R^2 and $Q^2 < \text{original models}$.

RAMMP's Biomarker Discovery Feasibility



Mitra BμS

vs



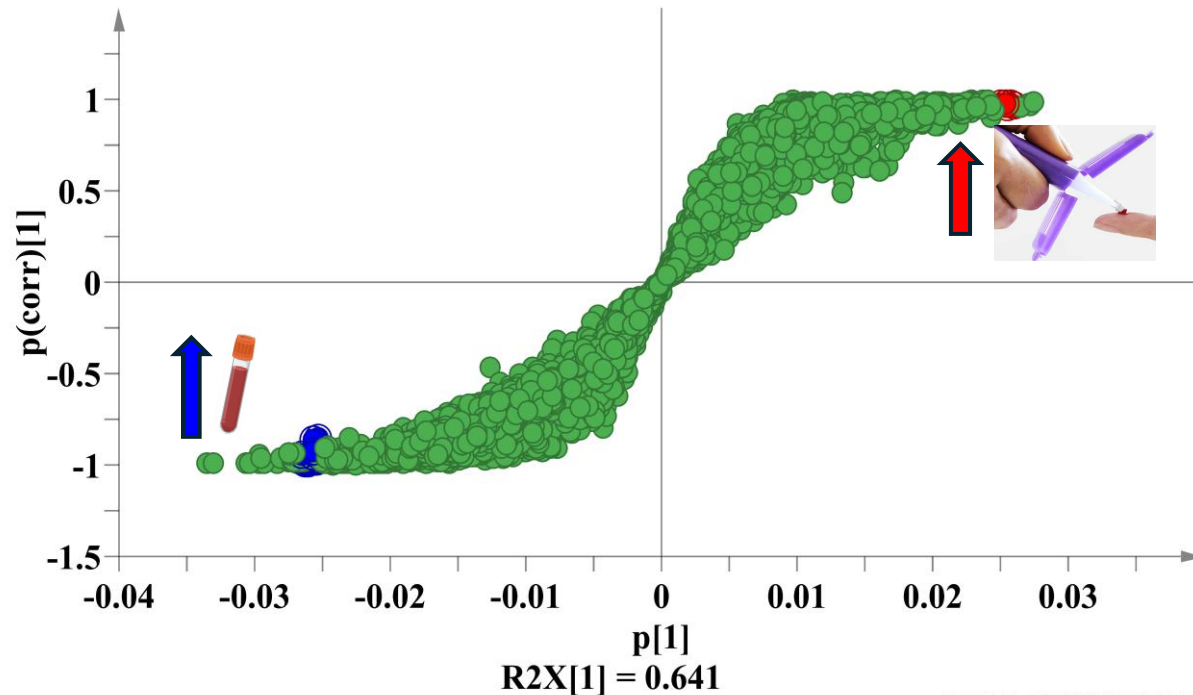
LVB

Statistically significant discriminating features:

- ✓ $VIP > 1.5$, $p(1) > |0.02|$, $p(\text{corr}) > |0.5|$.
- ✓ T-TEST $p < 0.05$; adjusted for false discovery rate (5%) (Benjamini, Krieger, & Yekutieli).

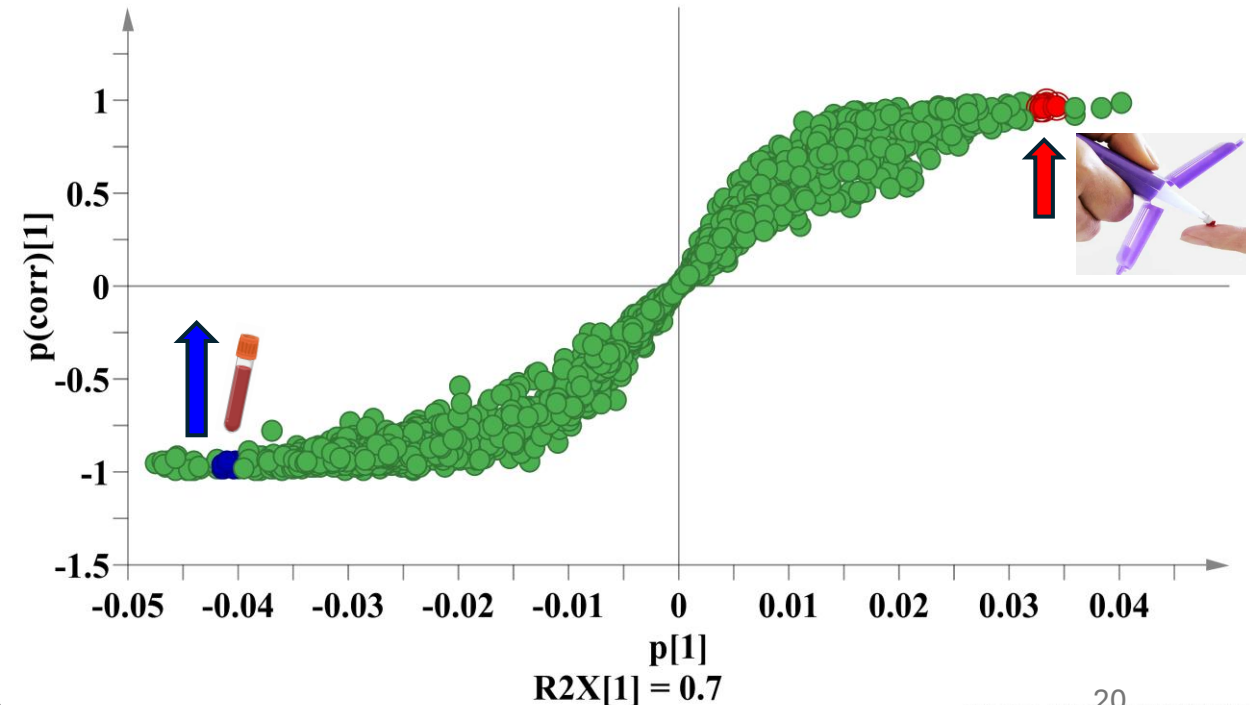
240 (**3.9%**) statistically significant features

S Plot: Conventional Mitra vs LVB



132 (**6.4%**) statistically significant features

S Plot: RAMMP Mitra vs LVB



RAMMP's Biomarker Discovery Feasibility



Mitra BμS

vs



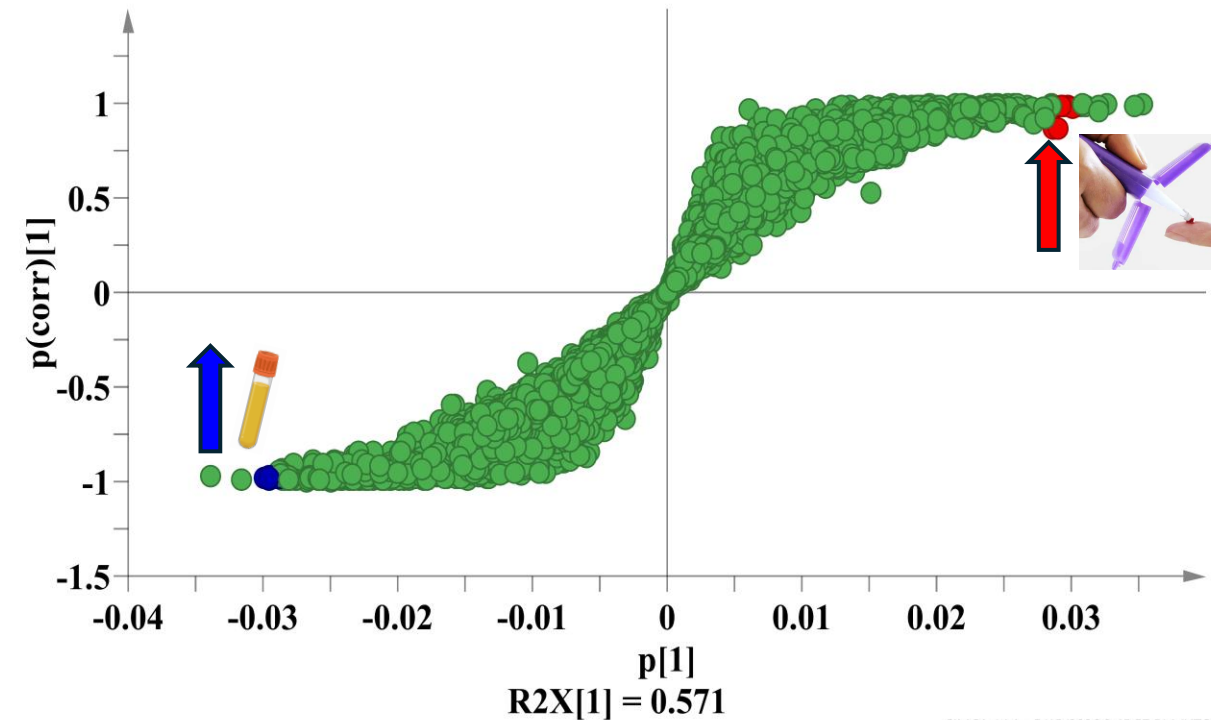
Plasma

Statistically significant discriminating features:

- ✓ $VIP > 1.5$, $p(1) > |0.02|$, $p(\text{corr}) > |0.5|$.
- ✓ T-TEST $p < 0.05$; adjusted for false discovery rate (5%) (Benjamini, Krieger, & Yekutieli).

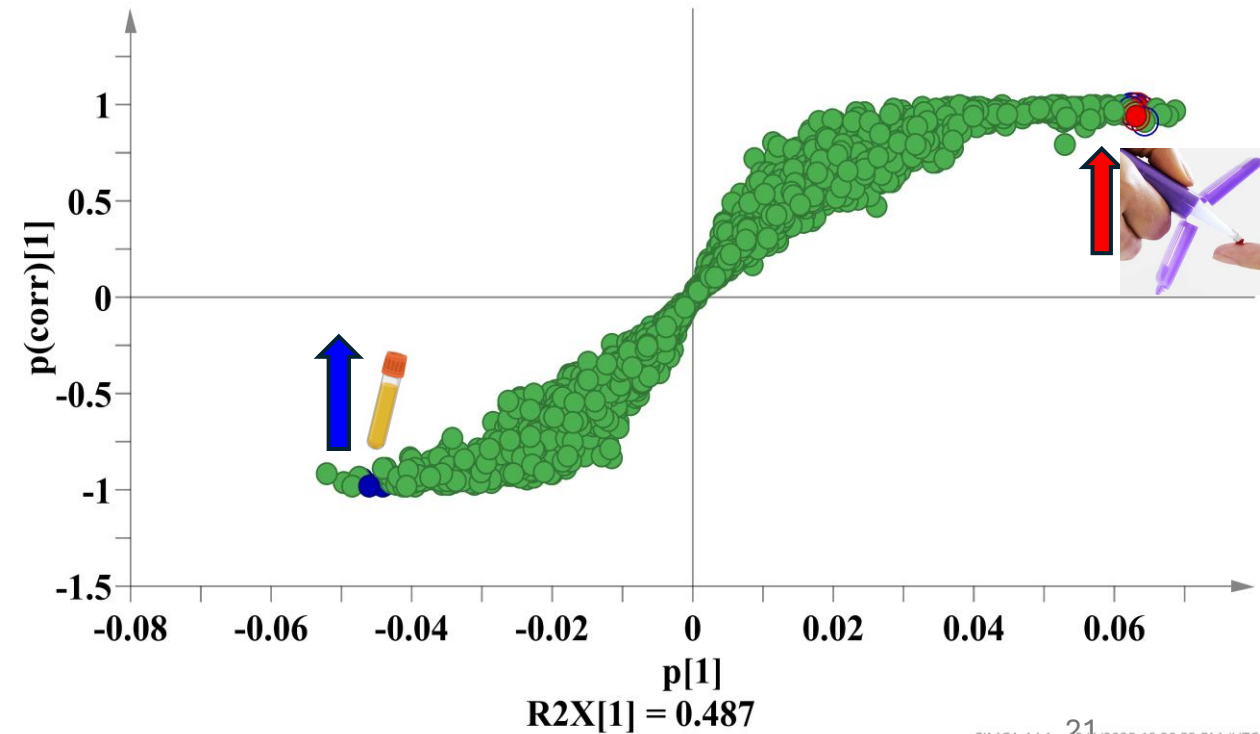
529 (**8.7%**) statistically significant features

S Plot: Conventional Mitra vs Plasma



246 (**12%**) statistically significant features

S Plot: RAMMP Mitra vs Plasma



Summary and conclusions

- ✓ RAMMP and B μ S can provide a paradigm shift in the analysis of large phenotypic studies.
- ✓ RAMMP can capture discriminating features (biomarkers) between B μ S and traditional blood matrices.
- ✓ Although loss of metabolic coverage is expected in RAMMP, results suggest it maybe insignificant.
- ✓ For RAMMP adoption, consider: the goals, budget, target metabolites, lab capacity, and time.



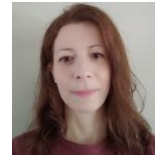
Acknowledgements



Ass Prof. Elizabeth Want



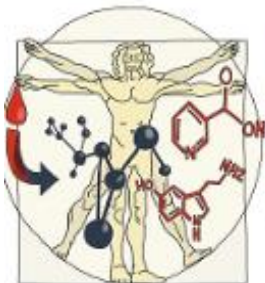
Anna Sanchez Lorenzo



Ass Prof. Helen Gika



Prof. Georgios Theodoridis



HUMAN Harmonising and Unifying Blood
Metabolomic Analysis Networks

Marie Skłodowska-Curie Actions Doctoral Networks 2021



European
Commission

Horizon 2020
European Union funding
for Research & Innovation

Questions?

Let Connect



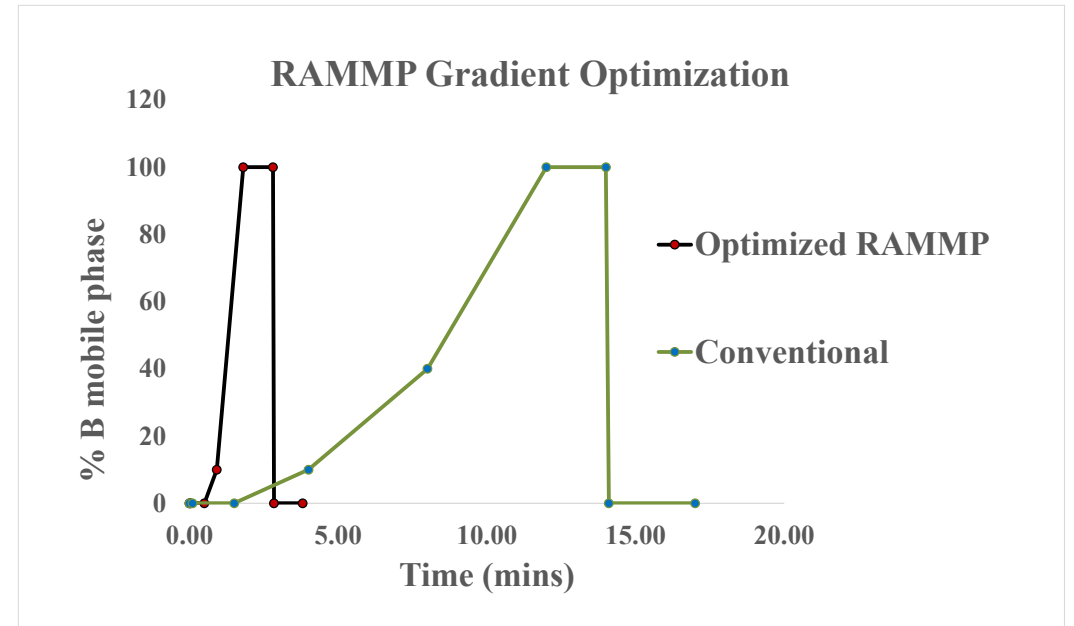
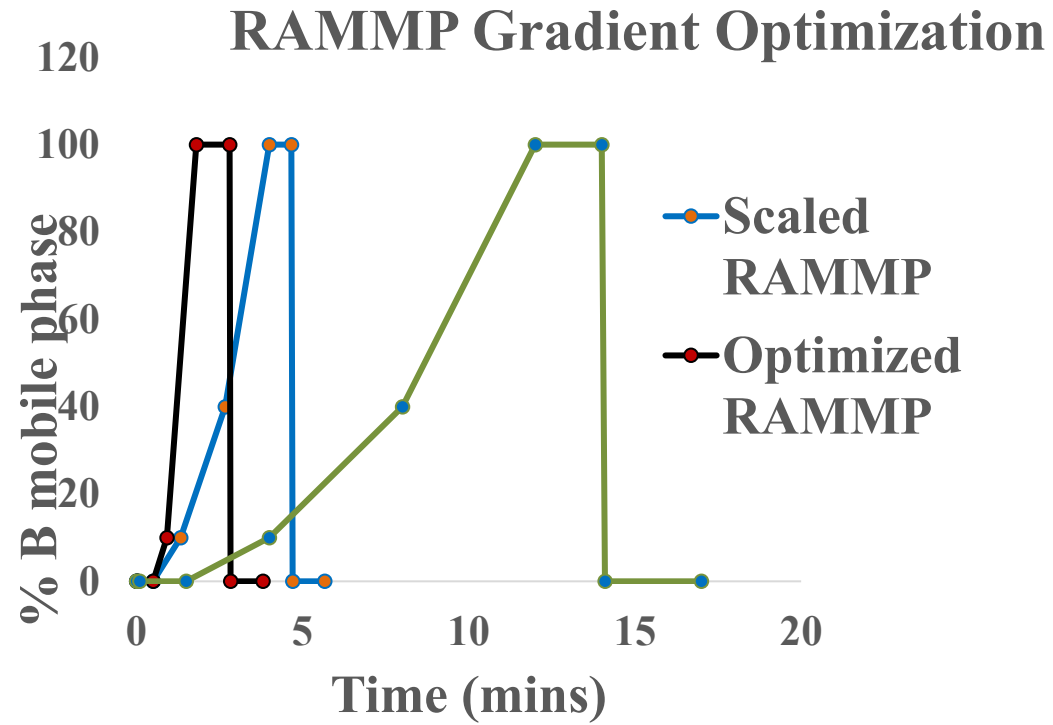
Marlene Thaitumu

Doctoral Researcher

HUMAN Doctoral Network: Marie Skłodowska Curie



Extra slides



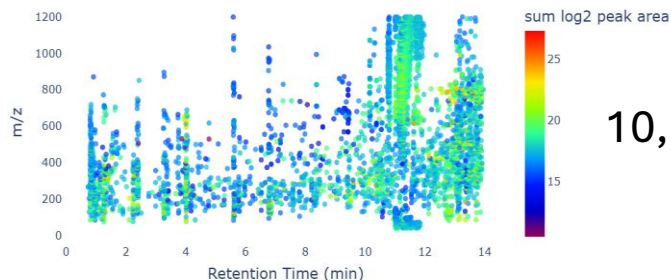
Biomarker discovery feasibility of RAMMP: Mitra B μ S compared to LVB and plasma

Conventional metabolic profiles

LVB-conventional metabolic profile



LVB

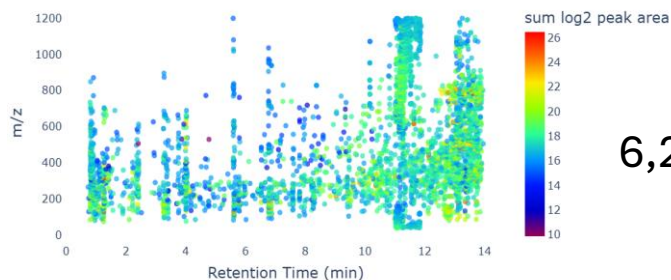


10,618 features

Plasma-conventional metabolic profile



Plasma

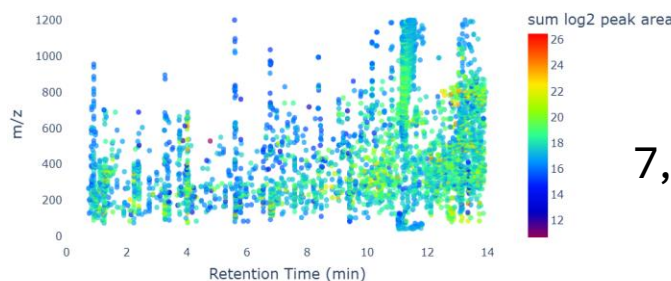


6,228 features

Mitra-conventional metabolic profile



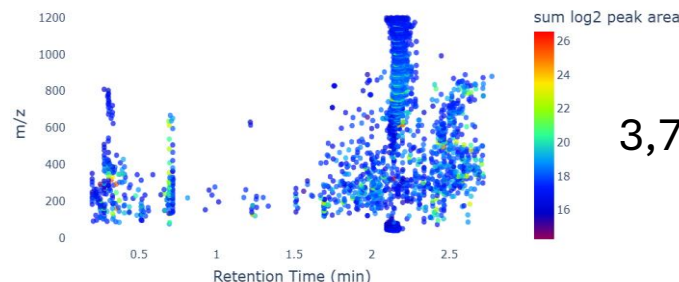
Mitra



7,040 features

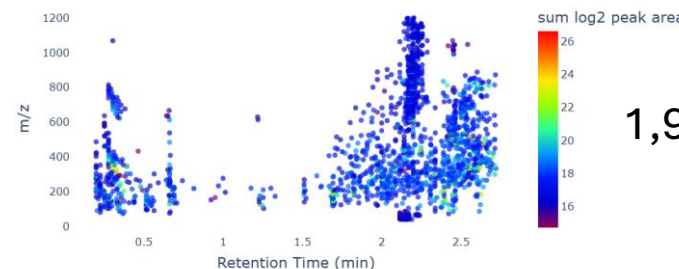
RAMMP metabolic profiles

LVB-RAMMP metabolic profile



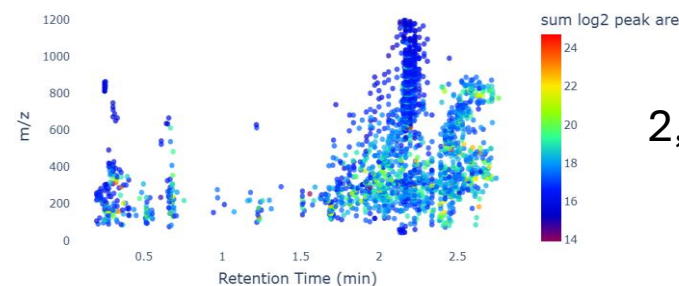
3,798 features

Plasma-RAMMP metabolic profile



1,906 features

Mitra-RAMMP metabolic profile



2,342 features

✓ **RAMMP** showed loss in metabolic coverage as previously discussed.

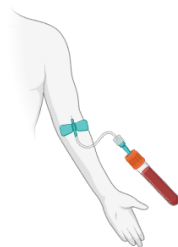
✓ Despite loss in metabolic coverage, **RAMMP** can capture important information compared to the conventional.

RAMMP vs conventional assay in LVB metabolic profiling

Validate **RAMMP's** performance against a **conventional** assay.

Study size – 8 individuals

LVB



3-day analysis using:

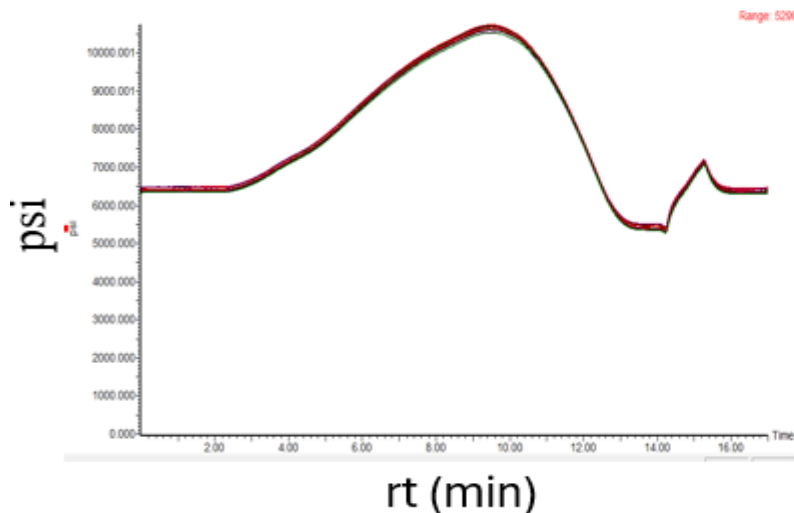
- Conventional
- RAMMP

In triplicate (n = 3)

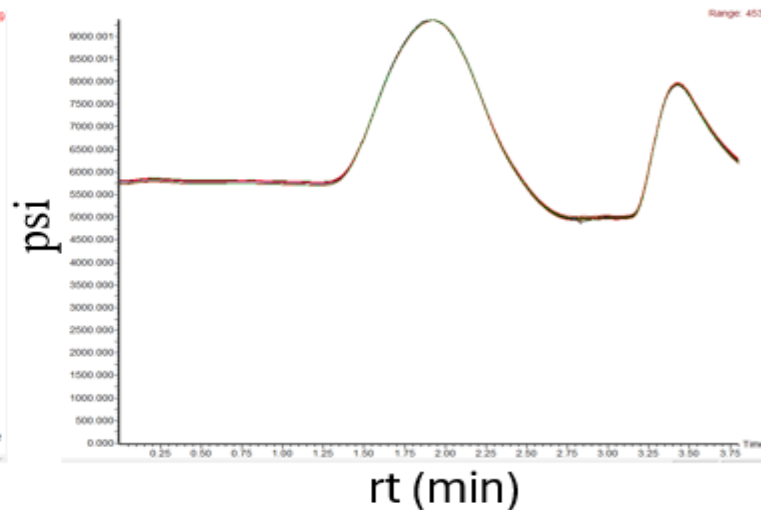
- Robustness
- Chromatography
- Metabolic coverage
- Precision
- Abundance

Robustness

Conventional pressure trace



RAMMP pressure trace



✓ **RAMMP** assay demonstrated comparable robustness despite scale down (1 mm internal diameter).

RAMMP's Biomarker Discovery Feasibility



Mitra BμS

vs



LVB

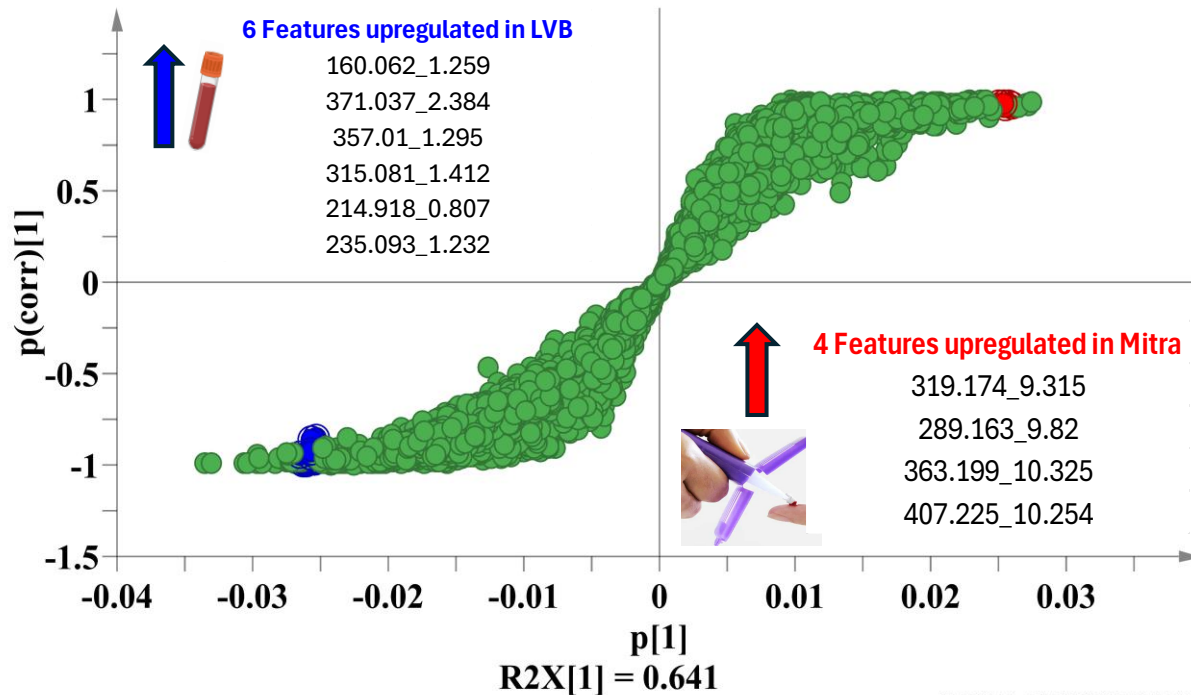
Statistically significant discriminating features in the two assays:

✓ VIP > 1.5, $p(1) > |0.02|$, $p(\text{corr}) > |0.5|$.

✓ T-TEST $p < 0.05$; adjusted for false discovery rate (Benjamini, Krieger, & Yekutieli).

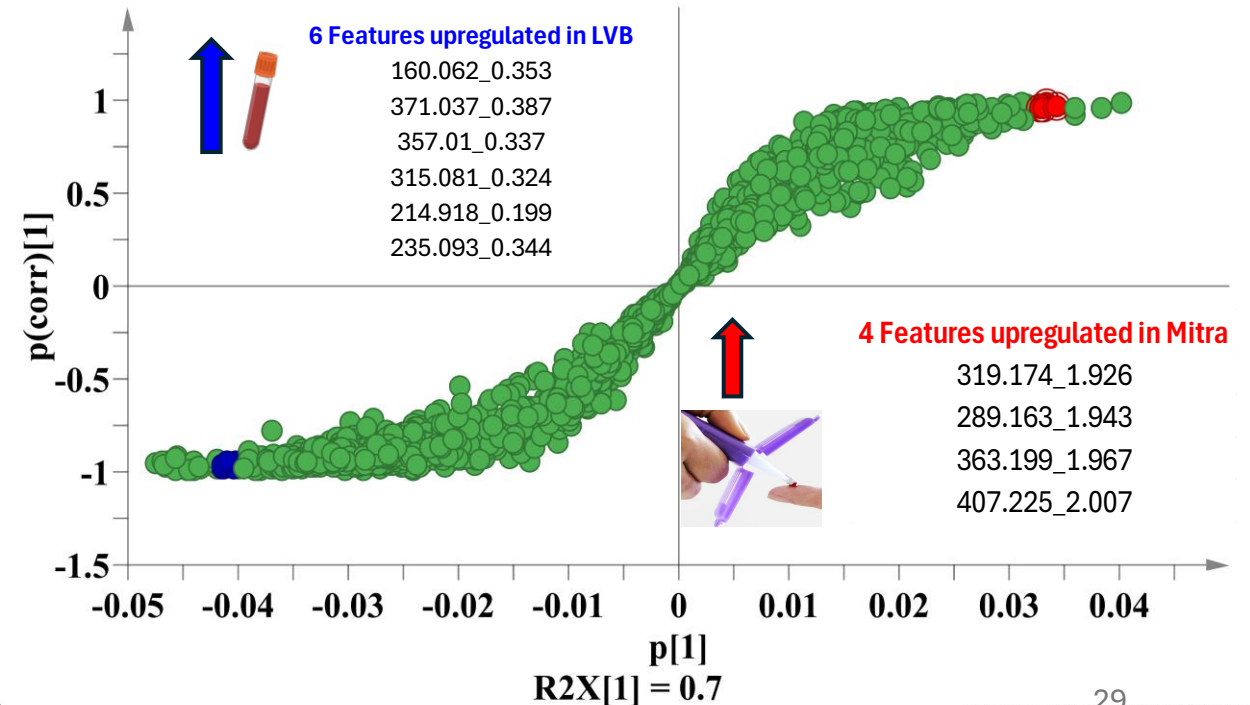
240 (3.9%) statistically significant features

S Plot: Conventional Mitra vs LVB



132 (6.4%) statistically significant features

S Plot: RAMMP Mitra vs LVB



RAMMP's Biomarker Discovery Feasibility



Mitra BμS

VS



Plasma

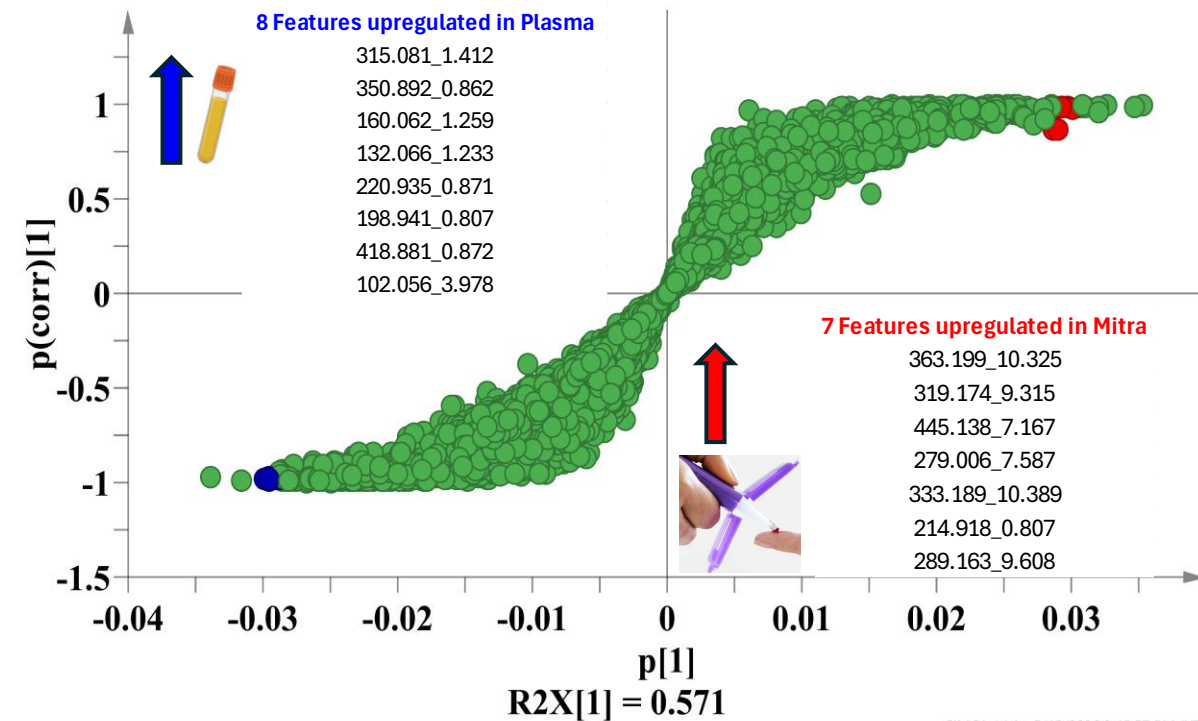
Statistically significant discriminating features in the two assays:

✓ $VIP > 1.5$, $p(1) > |0.02|$, $p(\text{corr}) > |0.5|$.

✓ T-TEST $p < 0.05$; adjusted for false discovery rate (Benjamini, Krieger, & Yekutieli).

529 (8.7%) statistically significant features

S Plot: Conventional Mitra vs Plasma



246 (12%) statistically significant features

S Plot: RAMMP Mitra vs Plasma

