#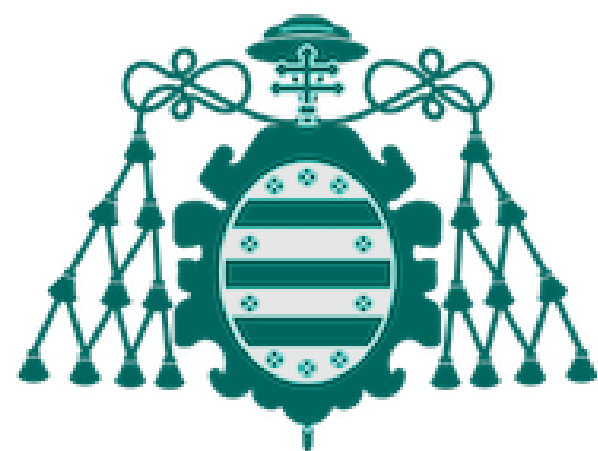 Fostering Proteomics for Histone Code Analysis: A Step Toward Universal Application for Any Species with Reference Genomes and Histone Annotations

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INTRODUCTION

The histone code refers to the array of over 200 post-translational modifications (PTMs) on histone proteins that regulate DNA packaging and gene expression.
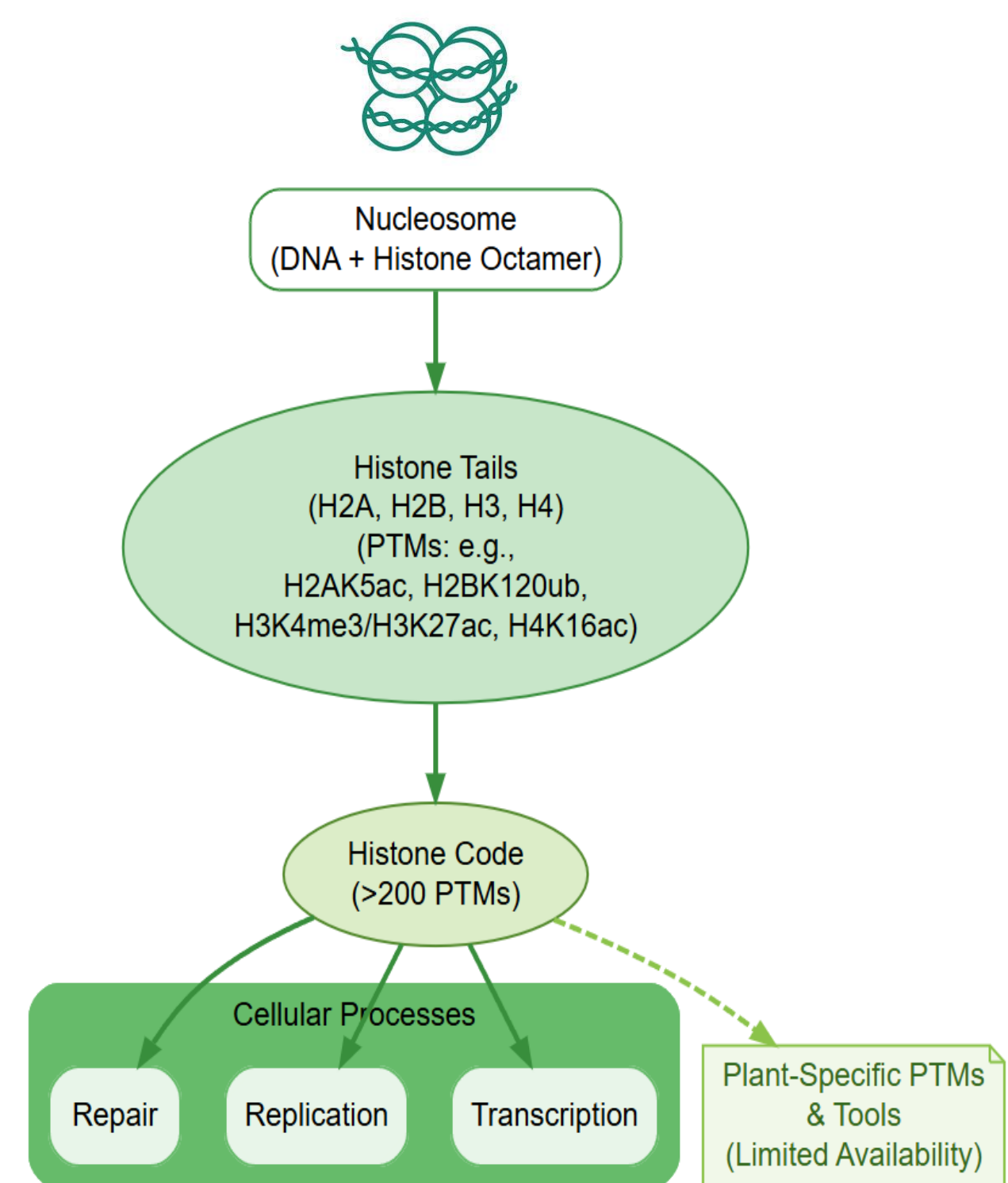
ABSTRACT

Histone post-translational modifications (**PTMs**) regulate epigenetic processes, but their study in plants has been limited due to a lack of specialized tools. We adapted open-source software for **Arabidopsis thaliana**, creating plant-specific reference data, including the latest genome and annotated histone sequences. Using in silico digestion, we generated peptide libraries and predicted PTMs, leveraging nucleosome core histone epigenomic marks.
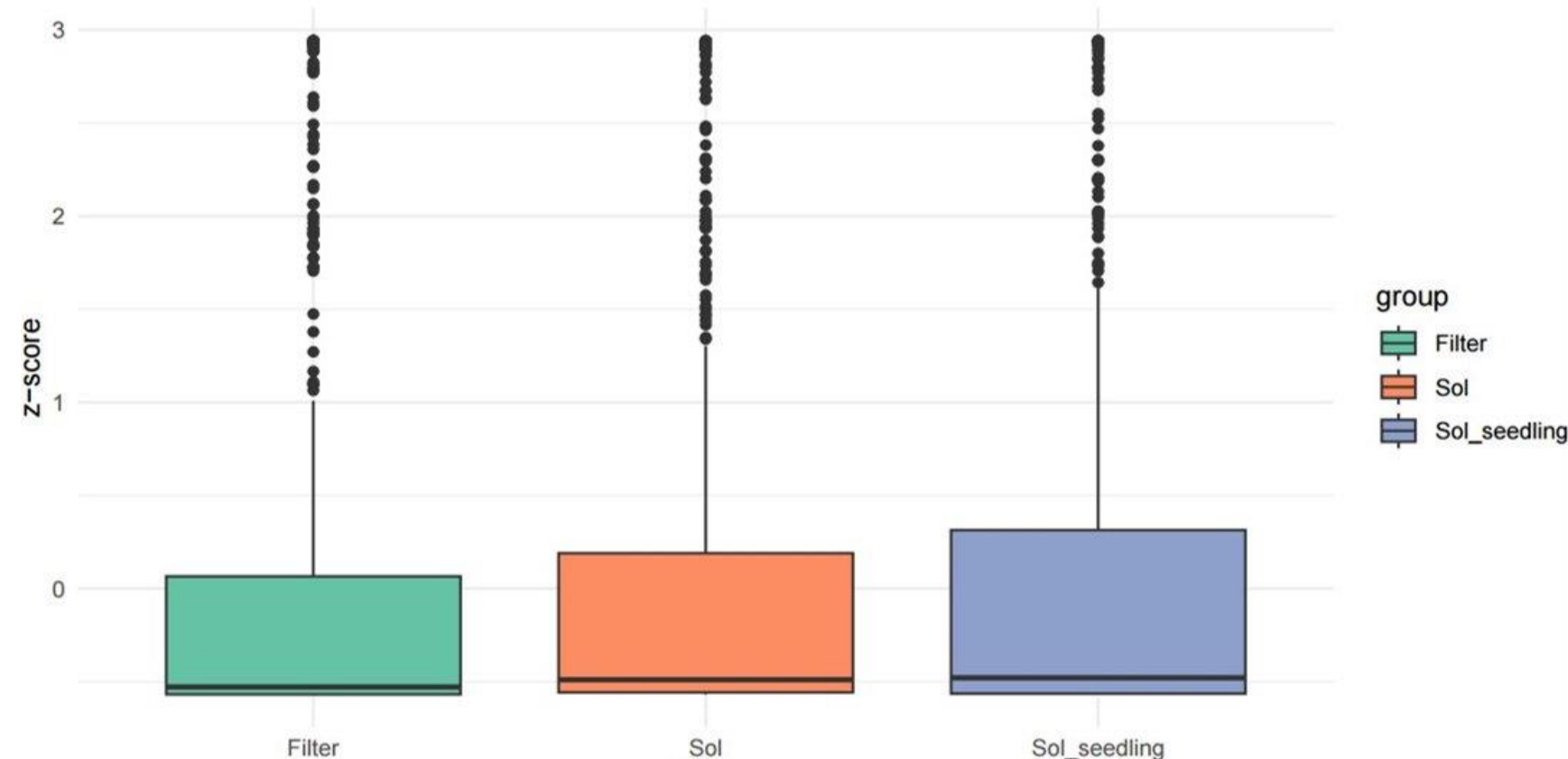
METHODOLOGY
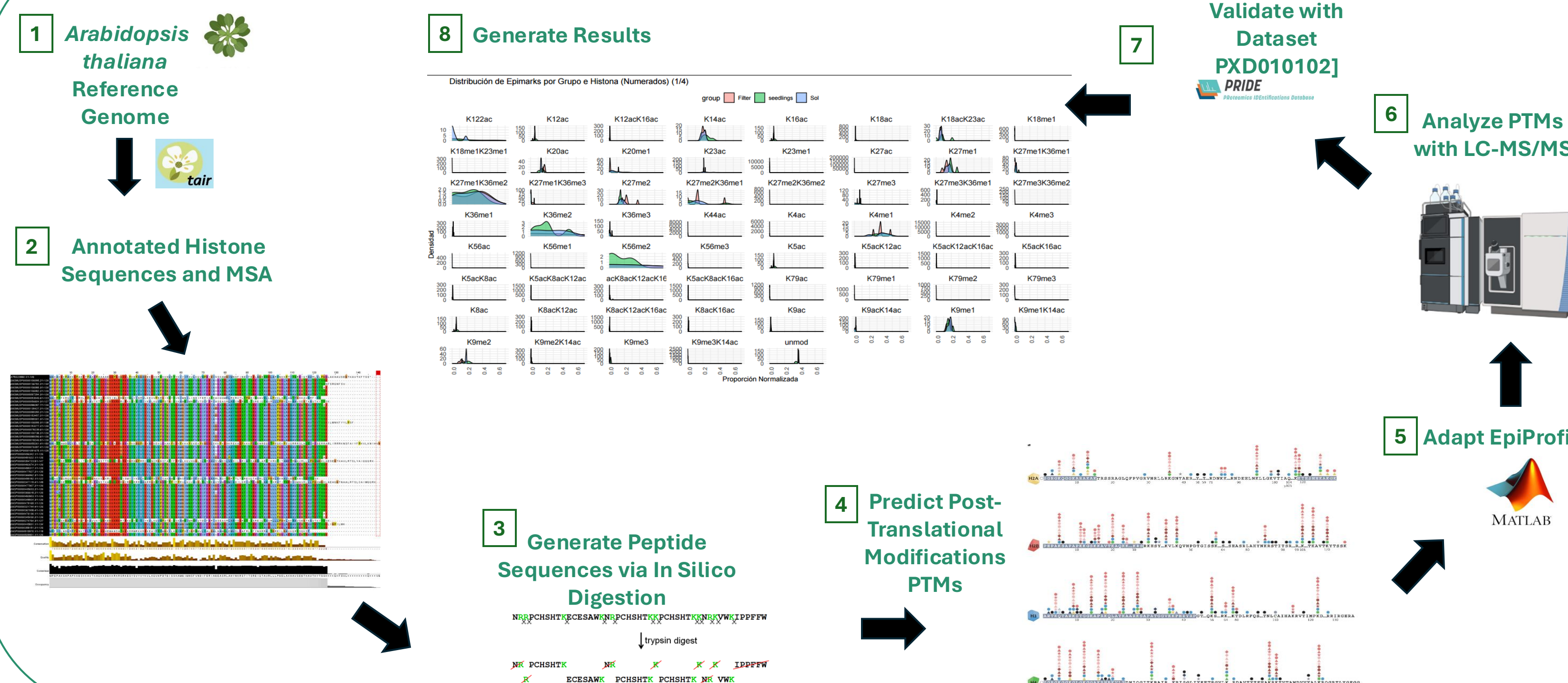
OBJECTIVES

- Explore PTM's within histones in the nucleosome.
- Adapt EpiProfile to specifically study histone modifications in A. thaliana.

KEY MESSAGE

The adapted tool applies to **any species,** as long as there is a **reference genome** and annotated histone sequence.
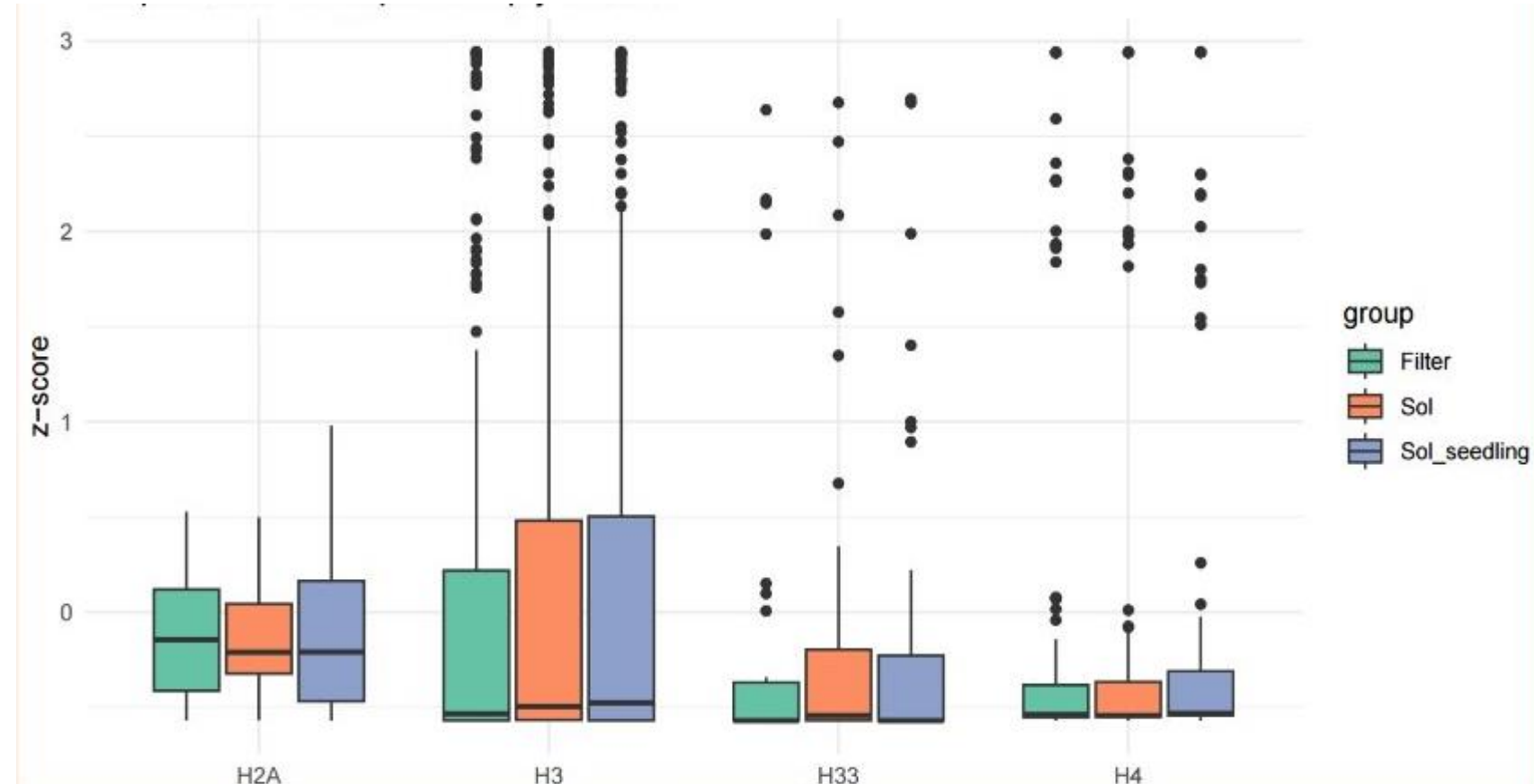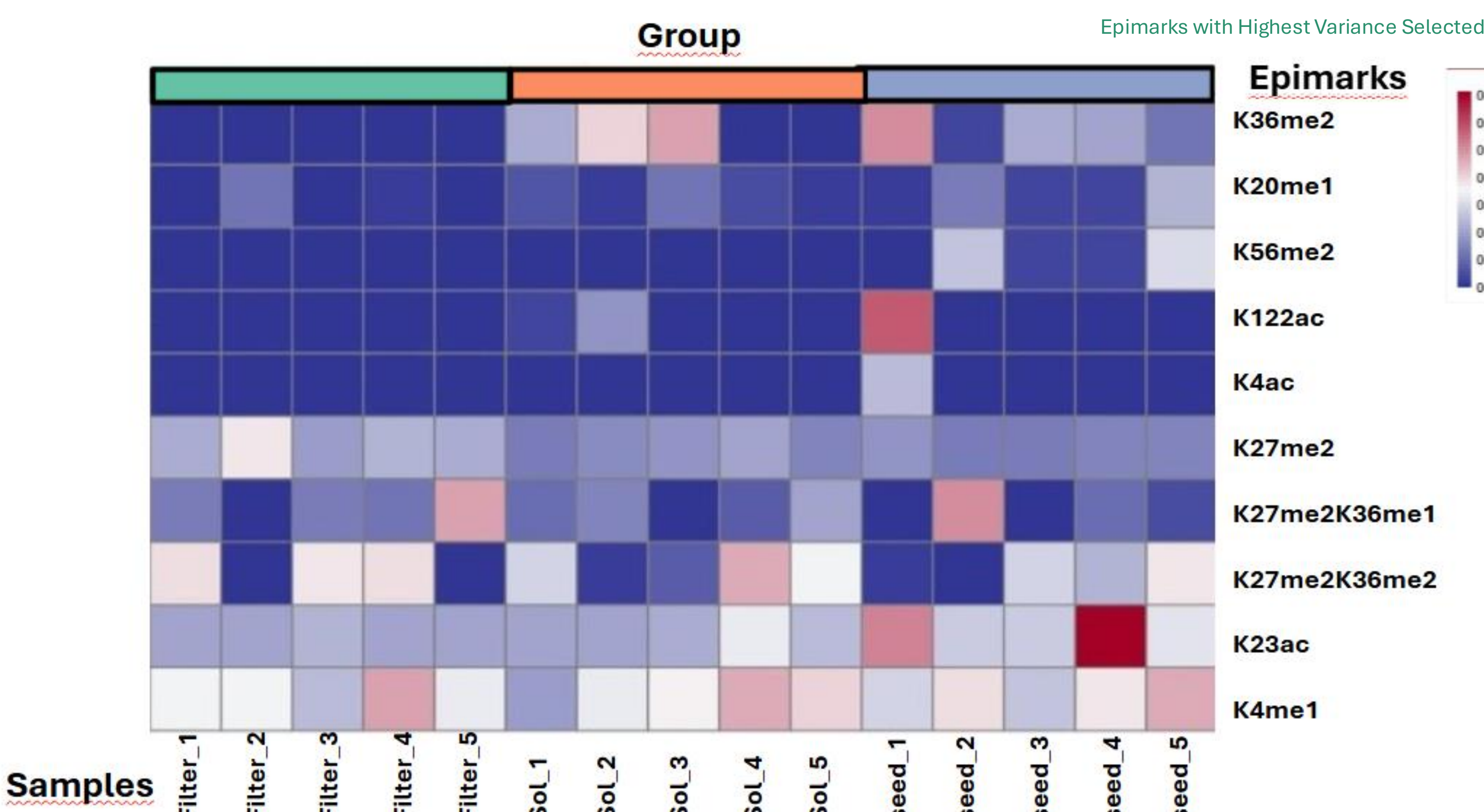
RESULTS

1. Boxplot of z-scores by Group

Z-scores across three experimental groups: Filter, Sol, and seedling

2. Boxplot of z-scores by Group and Histone

Z-scores by both **group** and **histone** type (H2A, H3, H3.3 and H4).

3. Heatmap of Z-scores by High Variance- Epimarks Across Groups

Despite focusing on the most variable epimarks, there is no clear clustering or separation between the groups, indicating no significant differences across conditions. This result supports the hypothesis of no group-based variation previously described for this dataset.
Filter-Aided Sample Preparation Procedure for Mass Spectrometric Analysis of Plant Histones. https://doi.org/10.3389/fpls.2018.01373

CONCLUSIONS

- EpiProfile applied to **Arabidopsis thaliana** provides a powerful tool for studying histone **PTMs**, advancing research in plant epigenetics.
- The method's *applicability across different developmental stages* (seedling and leaf) demonstrates its versatility and potential for broader use in plant biology.

ACKNOWLEDGEMENTS

ON GOING

MSA to create new features: H1

Histone H1 alignment in A. thaliana, M. musculus and H. sapiens