

Computational Multiplexed Transcriptomic Analysis: Modes of Action In the Fungal Plant Pathogen Botrytis Cinerea

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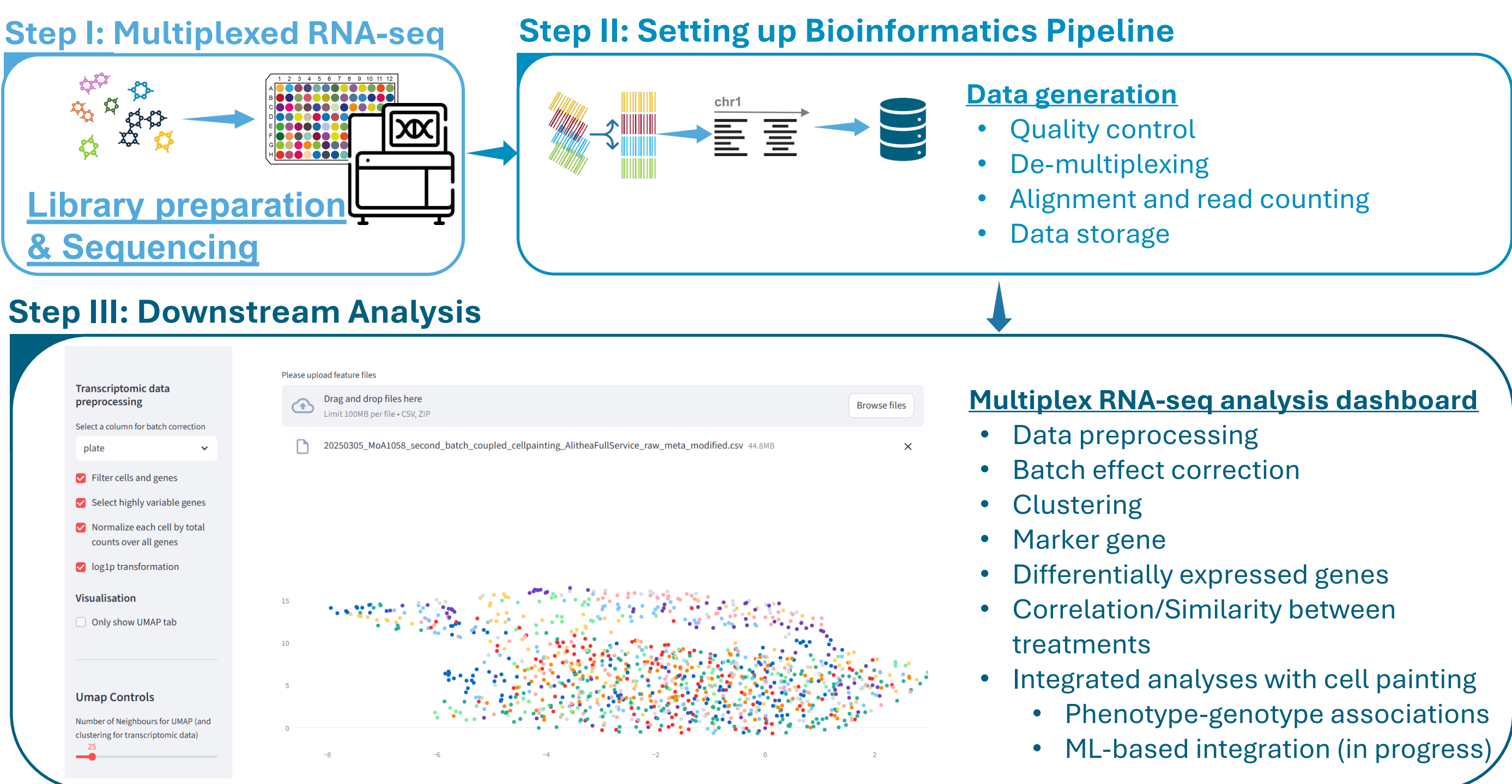
1 Abstract

Crop protection options are increasingly limited by resistance development and stricter safety requirements, driving the need for novel and sustainable modes of action (MoA).

Here, we present an approach that combines transcriptomics and artificial intelligence to rapidly identify the MoAs of bioactive molecules in non-model organisms using Alithea's proprietary sequencing technology. Using plant pathogens as a case study, multidimensional transcriptomic readouts from cell-based screens enabled unbiased profiling, classification of known MoAs, and identification of novel starting points for discovery.

This strategy provides deeper mechanistic insight early in development and supports the discovery of safe, resistance-breaking crop protection solutions.

3 Results

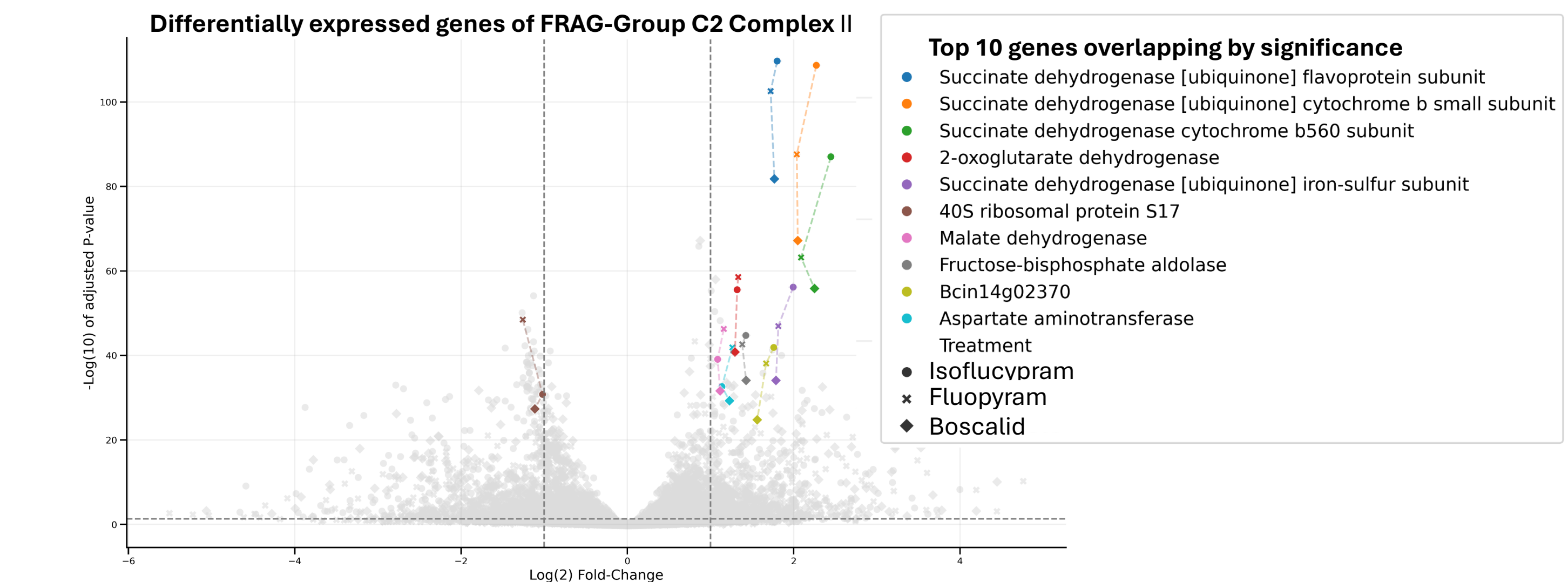
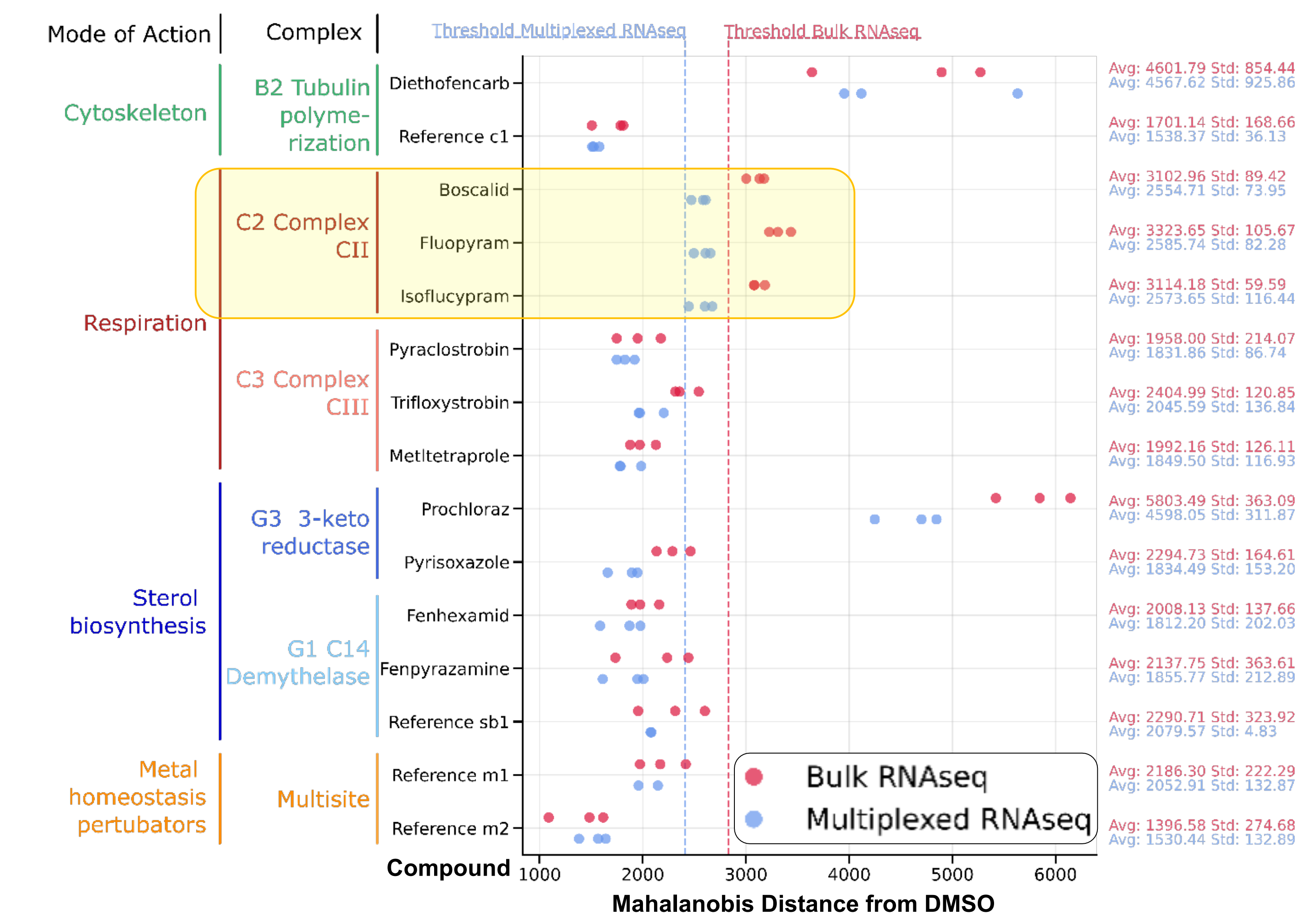
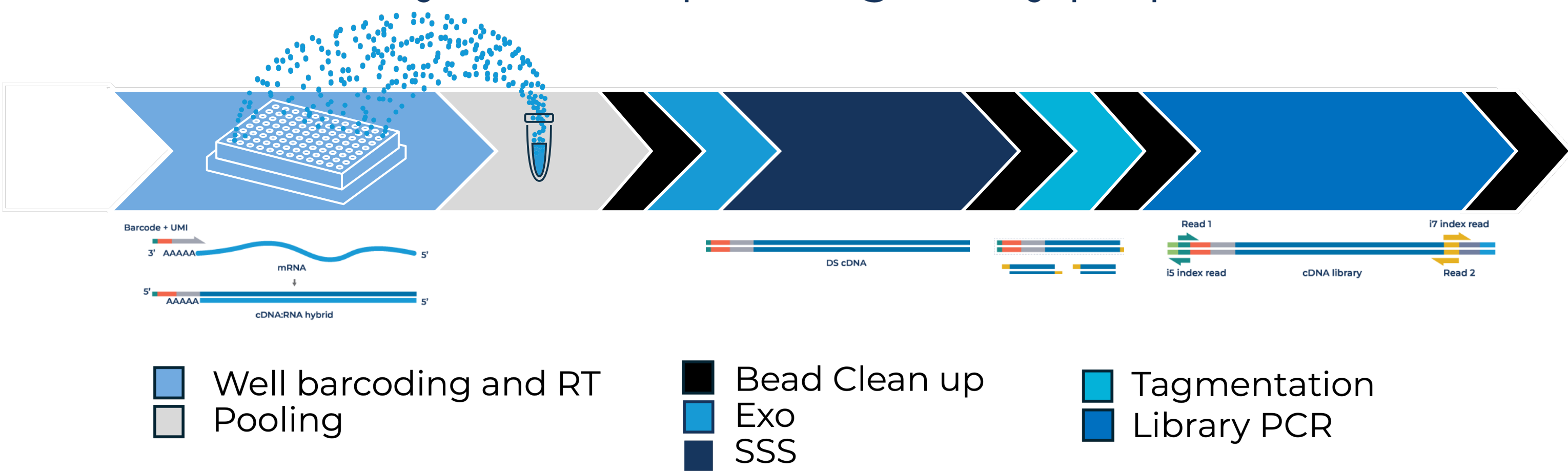


To deliver comprehensive BRB-seq data analysis, we built a standardized and reproducible workflow. Our online dashboard enables fast, flexible data analysis without requiring computational skills. Moreover, we are developing a machine-learning cell painting and transcriptomic data integration algorithm, enabling deeper insights into mechanisms via phenotype-genotype relationships.

Our benchmarking study demonstrates the robustness of BRB-seq in comparison with bulk RNA-seq, using 120 RNA samples from a plant pathogen species, botrytis cinerea (*B. cinerea*) treated with 19 different compounds. We found large overlap in differentially expressed gene analyses for compounds within the same MoA, particularly for the succinate dehydronase inhibitors (SDHIs) Fluopyram, Boscalid, and Isoflucypram. Notably, we provide the first direct transcriptomic evidence for the effect of Isoflucypram on SDH in its target organism, *B. cinerea*.

2 Method - Transcriptomics

MERCURIUS™ Bulk RNA Barcoding and Sequencing (BRB-seq) is an ultra-high-throughput bulk 3' mRNA-seq technology that uses early-stage sample barcoding and unique molecular identifiers (UMIs) to allow the pooling of up to 384 samples in one tube early in the sequencing library preparation workflow.



4 Conclusions

BRB-seq enables a parallelized and cost-efficient gene regulations profiling under chemical perturbations. It facilitates mechanistic studies and target identification across diverse compounds, transforming plant pathogen transcriptomic research for crop protection.

Presentation Details

Date and Time: Monday, January 12, 2026: 4:00 PM - 6:10 PM

Room: Pacific C

Booth #527

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