Transcriptomic Analysis Tool: Revealing Gene Regulation Dynamics
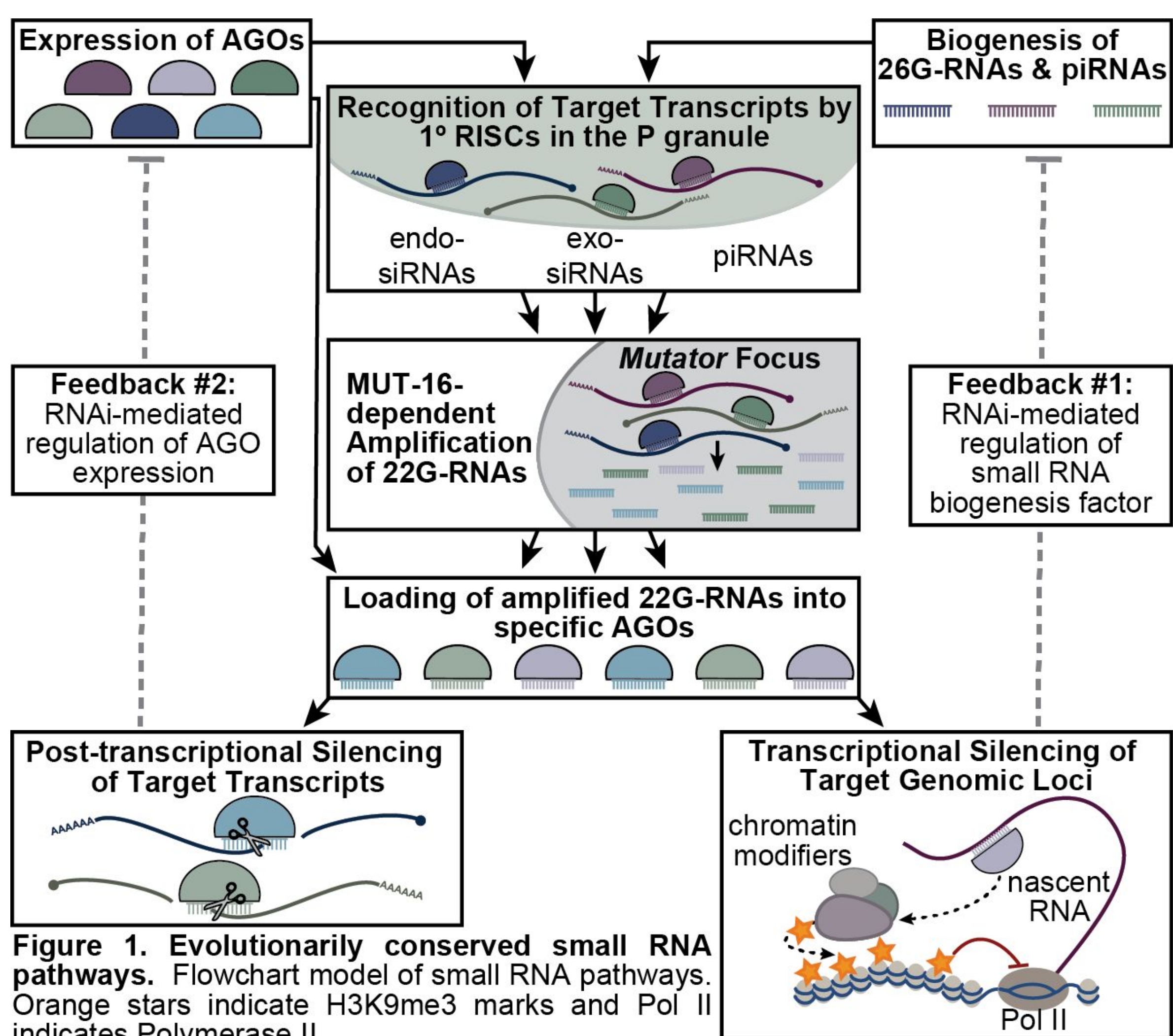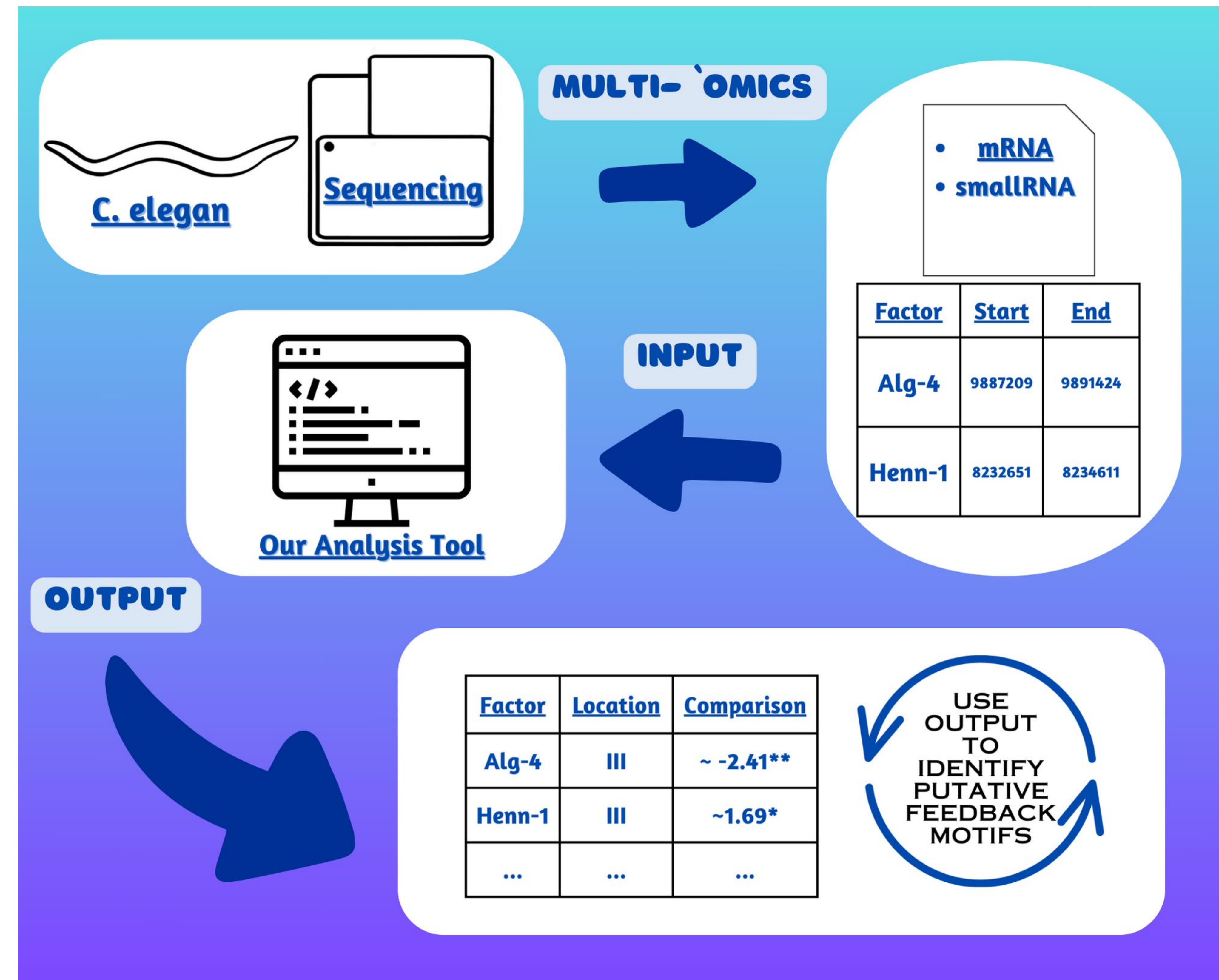
Neeka Mardani-Kamali, Alicia K. Rogers

Abstract

Understanding gene regulation mechanisms is crucial for unraveling the complexities of biological processes. Our research aims to solve how scientists can effectively analyze gene expression data to comprehend gene regulation in molecular biology. This research addresses these challenges by introducing a program tailored to multi - 'omics sequences of a control and any number of treated species, and using high-throughput methods to compare the gene expression between them at a list of specific locations of the user's choosing. With the log2 fold-change of each comparison presented in a clear format, the users can more easily identify feedback motifs. The program's inherent versatility enables researchers from any background to input their sequencing data and genomic positions, facilitating rapid data analysis for all.
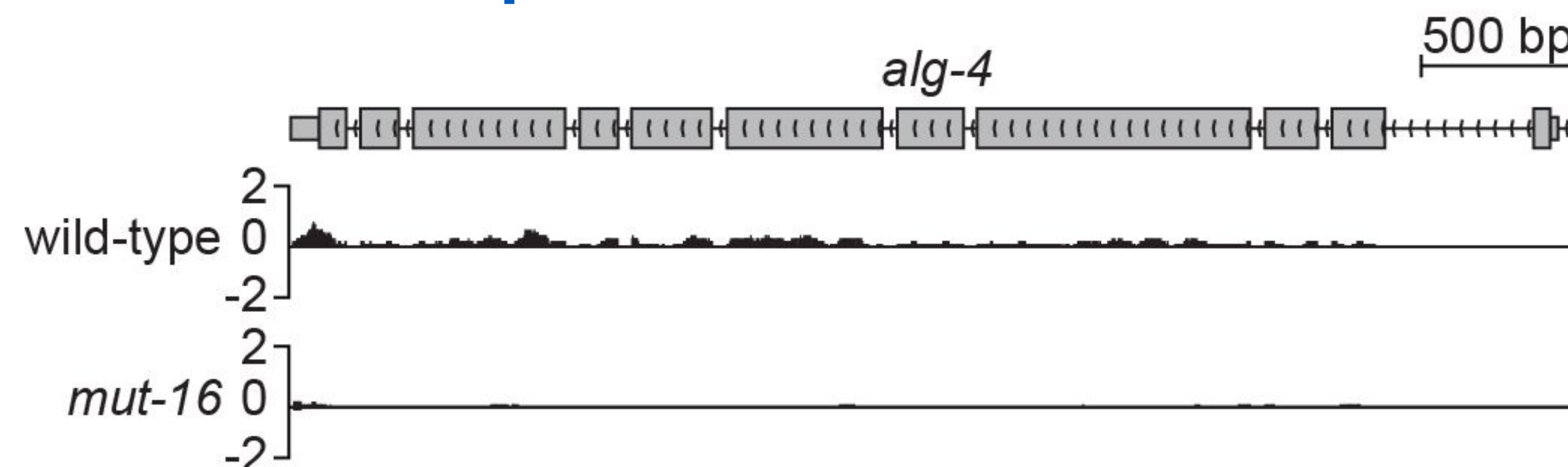
Introduction

Figure 1. Evolutionarily conserved small RNA pathways. Flowchart model of small RNA pathways. Orange stars indicate H3K9me3 marks and Pol II indicates Polymerase II.

Data Analysis and Results

Factor	Start	End
Alg-4	9887209	9891424
Henn-1	8232651	8234611

Factor	Location	Comparison
Alg-4	III	~ -2.41**
Henn-1	III	~1.69*
...	...	...

IGV Visual Representation

Conclusion

- **In summary,** our project developed a user-friendly tool to detect differences between control and treatment species at specific genomic sites.

- **Using transcriptomic data,** our analysis unveiled notable differences in gene expression within C. elegans, particularly in the ALG-4 and HENN-1 factors.

Future Implications

- **Having identified discrepancies in HENN-1 gene expression,** our researchers can delve deeper into this finding.

- **Valuable resource** for other researchers to analyze regulatory mechanisms in their own studies.

References

1. Gazoni, E., & Clark, C. (2024). openpyxl (Version 3.1.2) [Computer Software]. Retrieved from https://pypi.org/project/openpyxl/
2. Maurits, L. (2024). PrettyTable (Version 3.10) [Computer Software]. Available from https://pypi.org/project/PrettyTable/
3. James T. Robinson, Helga Thorvaldsdóttir, Wendy Winckler, Mitchell Guttman, Eric S. Lander, Gad Getz, Jill P. Mesirov. Integrative Genomics Viewer. Nature Biotechnology 29, 24–26 (2011). A public access version is also available: PMC3346182.

Acknowledgements

Contact: Neeka Mardani - Kamali
neeka.mardanikamali@mavs.uta.edu
UTA Department of Biology
https://www.uta.edu/academics/schools-colleges/science/departments/biology

UNIVERSITY OF TEXAS ARLINGTON