

GAGE-seq: Integrated Profiling of 3D Genome Organization and Gene Expression in Single Cells

GAGE-seq is a single-cell technology that simultaneously measures 3D genome structure and gene expression, providing comprehensive insights into cellular functions and identity.

What is the Problem?

The mammalian genome is highly organized, characterized by genomic architecture such as topologically associating domains and chromatin loops. Understanding the complex relationship between genome organization and gene expression at the single-cell level is crucial for advancing our knowledge of cellular functions, development, and disease progression. Traditional methods often analyze these aspects separately, missing the intricate interplay between 3D genome architecture and transcriptional activities. This gap limits our ability to fully comprehend how genomic structures influence gene regulation and cellular behavior.

What is the Solution?

GAGE-seq (Genome Architecture and Gene Expression by Sequencing) addresses this challenge by concurrently profiling 3D genome organization and gene expression within the same single cell. This innovative co-assay integrates single-cell Hi-C (a method to study 3D genome structure) and single-cell RNA sequencing (scRNA-seq) to provide a holistic view of cellular functions. By applying GAGE-seq to various cell types, such as mouse brain cortex and human bone marrow CD34+ cells, researchers can uncover the relationships between genome architecture and gene expression, enhancing our understanding of cell-type-specific gene regulation and identity.

What is the Competitive Advantage?

Comprehensive Analysis: GAGE-seq offers simultaneous measurement of 3D genome structure and gene expression, providing a more complete picture of cellular functions compared to methods that analyze these aspects separately.

Single-Cell Resolution: The technology captures data at the single-cell level, revealing cellular heterogeneity and uncovering variations that bulk analyses might miss.

Scalability and Robustness: GAGE-seq is designed to be scalable and robust, making it suitable for diverse biological contexts and large-scale studies.

Technology ID

BDP 8852

Category

Research Tools

Selection of Available

Technologies

Authors

Zhijun Duan

[Learn more](#)



Integration with Other Data: The ability to integrate GAGE-seq data with spatial transcriptomics and other single-cell datasets enhances the depth and breadth of biological insights.

References

1. Zhou, T., Zhang, R., Jia, D., Doty, R. T., Munday, A. D., Gao, D., Xin, L., Abkowitz, J. L., Duan, Z., Ma, J.(2024) , <https://pmc.ncbi.nlm.nih.gov/articles/PMC11323187/>, <https://www.nature.com/ng/>, 56, 1701-1711