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10x Genomics Multiome (ATAC + RNA) sequencing for human induced pluripotent stem cells (hiPSCs)

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Fan Li^{1,2}, Dongming Liang^{1,2}, Hao Wu^{1,2}

¹Department of Genetics, Epigenetics Institute, Perelman School of Medicine, University of Pennsylvania, Philadelphia PA 19104, USA;

²The Institute for Regenerative Medicine, Perelman School for Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA

Wu Lab @ UPenn

Tech. support email: haowu2@upenn.edu



Fan Li

University of Pennsylvania

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Protocol status: Working

We use this protocol and it's working

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Keywords: 10x genomics multiome assay, 10x genomics multiome, linking open chromatin region, simultaneous profiling of gene expression, cells with similar transcriptional profile, lineage differentiation from diverse hipsc line, open chromatin region, distinct chromatin landscape, deeper mechanistic insights into dynamic gene, chromatin within the same cell, chromatin, similar transcriptional profile, accessible chromatin, drivers of differential gene expression, directed lineage differentiation, gene expression, differential gene expression, pluripotent stem cell, induced pluripotent stem cell, dynamic gene, integrating rna, gene, rna, comprehensive view of cellular regulation, cellular regulation, sequencing, thousands of cell, diverse hipsc line, same cell

Abstract

The 10x Genomics Multiome assay enables simultaneous profiling of gene expression and open chromatin within the same cell across thousands of cells (ref 1-2), offering a comprehensive view of cellular regulation. By integrating RNA sequencing with assay for transposase-accessible chromatin (ATAC), this multiomic approach enhances the resolution of cell states, identifies drivers of differential gene expression, and reveals cells with similar transcriptional profiles but distinct chromatin landscapes. By linking open chromatin regions to gene expression at single-cell resolution, this technology could provide deeper mechanistic insights into dynamic gene regulatory networks, particularly in the context of directed lineage differentiation from diverse hiPSC lines.



Nuclei isolation

- 1 For 10x multiome sequencing analysis of hiPSCs and their differentiated progenies, we followed the standard protocol of nuclei isolation from 10x Genomics (see below).

1.1  CG000365_DemonstratedProtocol... 744.8KB

Library preparation

- 2 For 10x multiome sequencing analysis of hiPSCs and their differentiated progenies, we followed the standard library preparation protocol from 10x Genomics (see below).

2.1  CG000338_ChromiumNextGEM_M... 4.7MB

Protocol references

1. Nuclei Isolation for Single Cell Multiome ATAC + Gene Expression Sequencing.
<https://www.10xgenomics.com/support/epi-multiome/documentation/steps/sample-prep/nuclei-isolation-for-single-cell-multiome-atac-plus-gene-expression-sequencing>
2. Chromium Next GEM Single Cell Multiome ATAC + Gene Expression Reagent Kits User Guide.
<https://www.10xgenomics.com/support/epi-multiome/documentation/steps/library-prep/chromium-next-gem-single-cell-multiome-atac-plus-gene-expression-reagent-kits-user-guide>