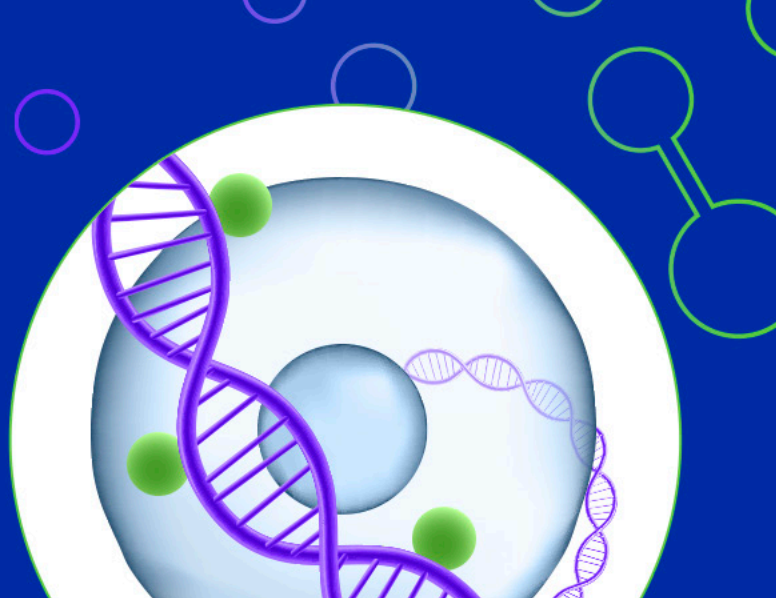


## Single Cell Methylation Kit

# Single cell methylation at scale. Finally.



Our Single Cell Methylation Kit is empowering researchers with the unprecedented ability to capture crucial insights with high-quality data. As the first ever commercial solution for single-cell resolution into methylation states, you'll get a revolutionary view into cellular heterogeneity.

## Why Single Cell Methylation?

Single Cell Methylation is the largest, fastest-growing application in epigenetics research, however current profiling methods only provide a limited picture—with bulk profiling averaging methylation states and masks rare or undiscovered cell type and state specific signatures.

## Redefining single cell research

Our Kit changes the way you look at single cells—revealing a comprehensive view of different cell type methylation states with sample heterogeneity through a high-throughput readout.

Paired with our easy-to-use data analysis pipeline, you can achieve results quickly and efficiently.

## Highlights

### Maximum Scalability

Profile single-cell methylation states across tens of thousands of cells

### Utmost Flexibility

Adapt sample collection, storage, and transport to process samples on your own time

### Powerful Chemistry

Detection of hundreds of thousands of CpG sites per cell in a single run

### Streamlined workflow

Complete the workflow without the need for new instrument using equipment already in your lab or institution.

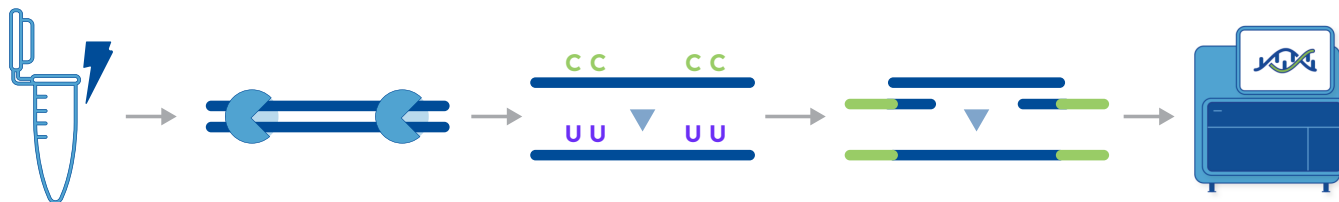
Fix Sample &  
Nucleosome Depletion

In situ  
Tagmentation

Bisulfite  
Conversion

Library  
Generation

Sequencing  
& Analysis



## Forge new pathways

Our single-cell methylation workflow begins with fixed nuclei. Nuclei samples are barcoded upfront in tagmentation, enabling sample multiplexing. 24 nuclei are deposited per well, and then distributed across a 96-well plates to profile >18,000 single cell methylomes in a single run. Bisulfite conversion is then performed, followed by cleanup and the addition of adaptors. Finally, a second barcode is added across plates to complete library construction.

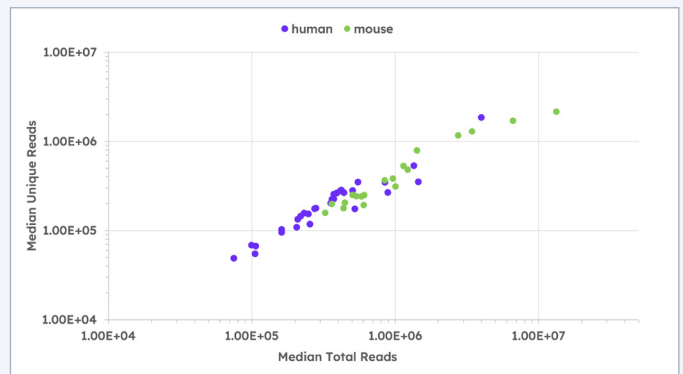
Using the ScaleBio™ Seq Suite, libraries are then sequenced and data is processed to produce a single-cell methylation matrix. The workflow provides many convenient stopping points and can be performed without any additional instrumentation using common lab equipment.

## Specifications

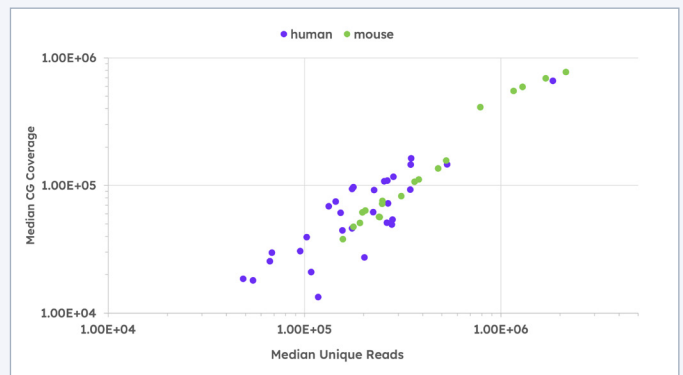
- Demonstrated across diverse sample types, cell lines, fresh and frozen tissue
- Demonstrated across a broad number of tissue types
- Fixation-compatible for sample storage, transport, and batching
- High cell throughput: > 18k nuclei/run
- Low multiplet rate: <4%
- Produces whole genome libraries
- Integrated sample multiplexing: multiplex up to 8 samples in a single run
- Efficient chemistries to maximize quality data from sequencing
- High performance: hundreds of thousands of CpGs detected
- Target enrichment compatible for reduced sequencing costs—maintaining high quality data sample throughput

## Robust performance across different tissue types, sample formats and species

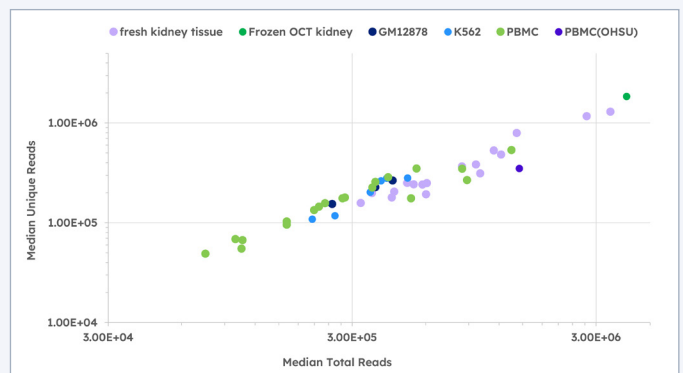
Powerful chemistry generates genome-wide coverage and high quality data for more discovery power



Ratio of CG coverage per Unique reads

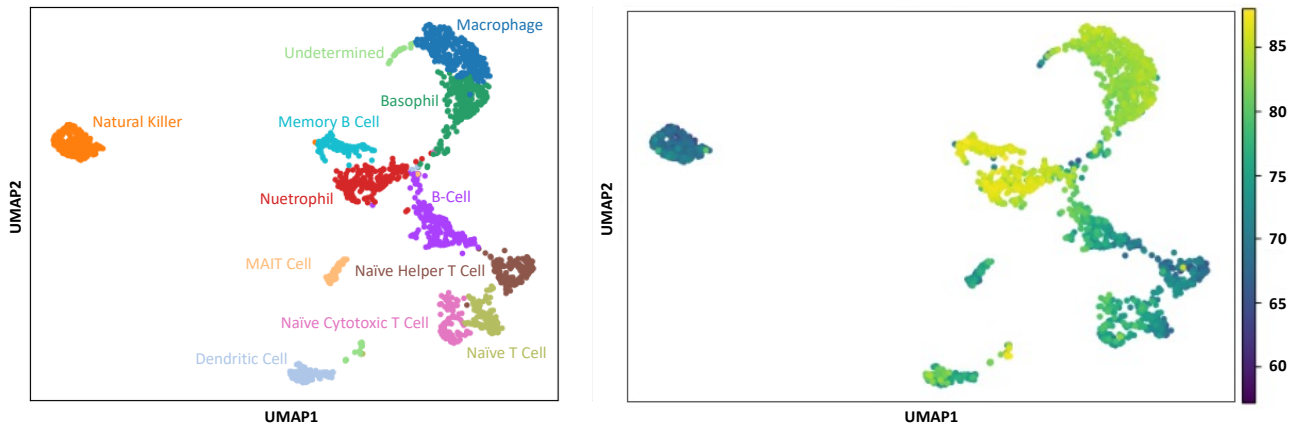


Robust performance demonstrated across diverse sample types

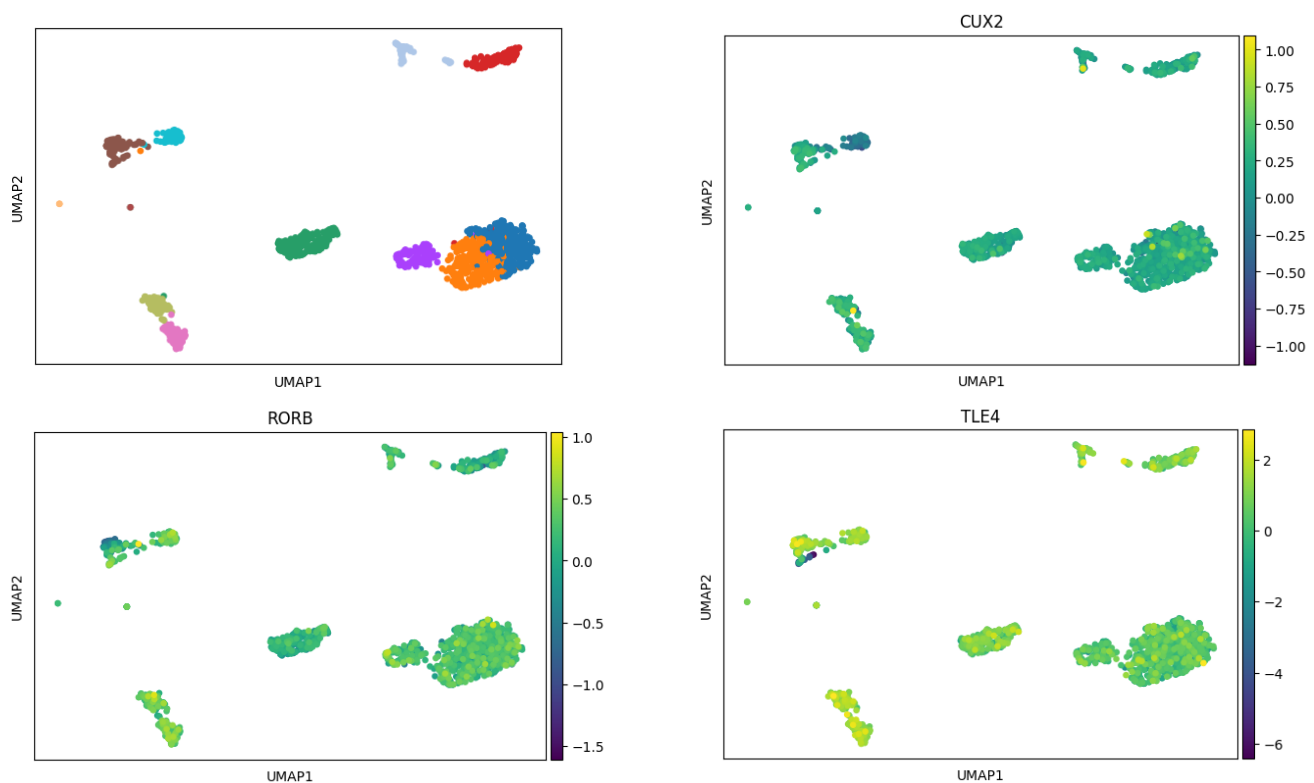


## Single Cell Methylation Data

UMAP clustering of differentially methylated regions reveal heterogeneous PBMC cell types. Nuclei isolated from PBMCs were processed through the Single Cell Methylation workflow and analyzed through the Scale Bio Seq Suite: Methylation Pipeline. Methylation status was analyzed and called across 50kb “bins” to generate a methylation status matrix. Differentially methylated regions were used to annotate cell types using cell-type-specific methylation markers. The righthand figure highlights the differences in CG methylation percentage across various cell type clusters.



Nuclei were isolated from snap-frozen post-mortem human brain tissue and processed through the Single Cell Methylation Kit workflow and analysis pipeline to generate a methylation matrix. UMAP clustering, annotated by methylation state, reveals the diverse cell types present in the population, including oligodendrocytes, cortical layer cells, and inhibitory neuronal cells.





## About Scale Biosciences

Scale Biosciences strives to unlock complex biology by enabling single-cell analysis with our patented combinatorial indexing technology.

We are developing products that enable exploration of novel modalities and unprecedented scale to allow researchers to ask new questions in the biological research.

Our goal is to transform single-cell analysis and to pave the way for new and ground-breaking discoveries in single-cell.

Product Code	Product Description
940554	ScaleBio™ Single Cell Methylation Nuclei Preparation Kit
955251	ScaleBio™ Single Cell Methylation Kit - Small
955253	ScaleBio™ Single Cell Methylation Kit - Large

Learn more about our Single Cell Methylation Kit at:  
[scale.bio/scalebio-single-cell-methylation-kit/](https://scale.bio/scalebio-single-cell-methylation-kit/)