

Advancing DNA methylation to single cell resolution

Scale Bio's Single Cell Methylation Kit revolutionizes epigenetics research as the first commercial solution for detecting single cell DNA methylation states. This groundbreaking technology provides unprecedented insight into epigenetic heterogeneity using massively parallelized barcoding to examine methylation across thousands of cells simultaneously. Ideal for oncology, neuroscience, and aging studies, the kit offers a deeper understanding of cellular diversity in complex tissues.

The workflow begins with sample fixation to preserve the epigenetic state and simplify downstream processing. Built-in multiplexing allows for simultaneous processing of multiple samples, streamlining laboratory time. Thoughtfully designed consumables reduce pipetting steps and hands-on time, with no specialized equipment required. This accessible and efficient technology opens new avenues for researchers to explore epigenetic complexity at the cellular level.

Highlights

High-resolution epigenetic profiling: Illuminate cell type-specific methylation signatures.

Powerful chemistry: Interrogate hundreds of thousands of CpG and CH sites per cell.

Scalable insights: Capture thousands of cells per run with seamless sample multiplexing.

Target enrichment compatibility: Maximize your sequencing budget by focusing on specific regions of interest.

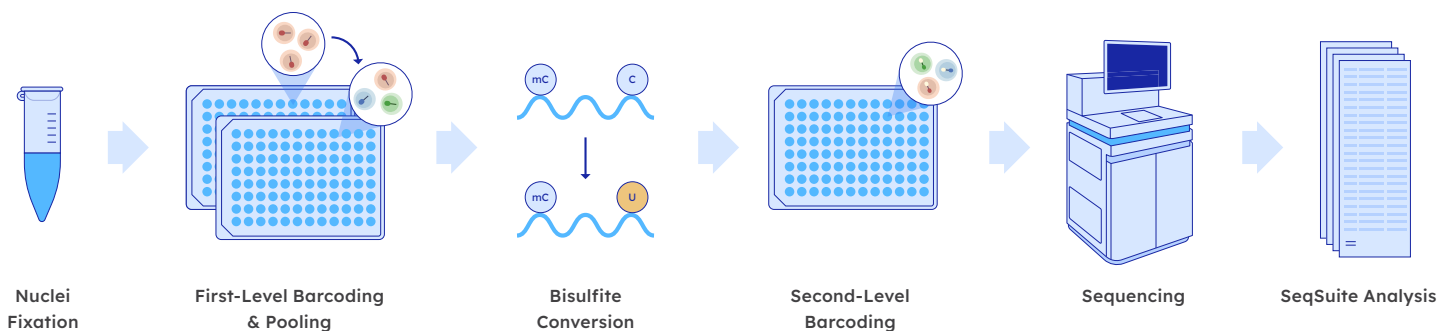


Figure 1. Scalable and efficient workflow for single cell methylation analysis. Start by fixing nuclei to preserve biology and enable processing flexibility. Library construction utilizes massively parallelized single cell barcoding, which leverages the cell as the reaction compartment, to uniquely label DNA fragments in sequential barcoding steps. The first barcoding step occurs via in situ tagmentation after nucleosome depletion, in 96-well plates. Wells are then pooled and redistributed for bisulfite conversion and a second barcoding step. The unique combination of the first and second barcoding steps enables detection of single cells. After sequencing, process data with SeqSuite, our integrated analysis pipeline, to generate a single cell methylation matrix.

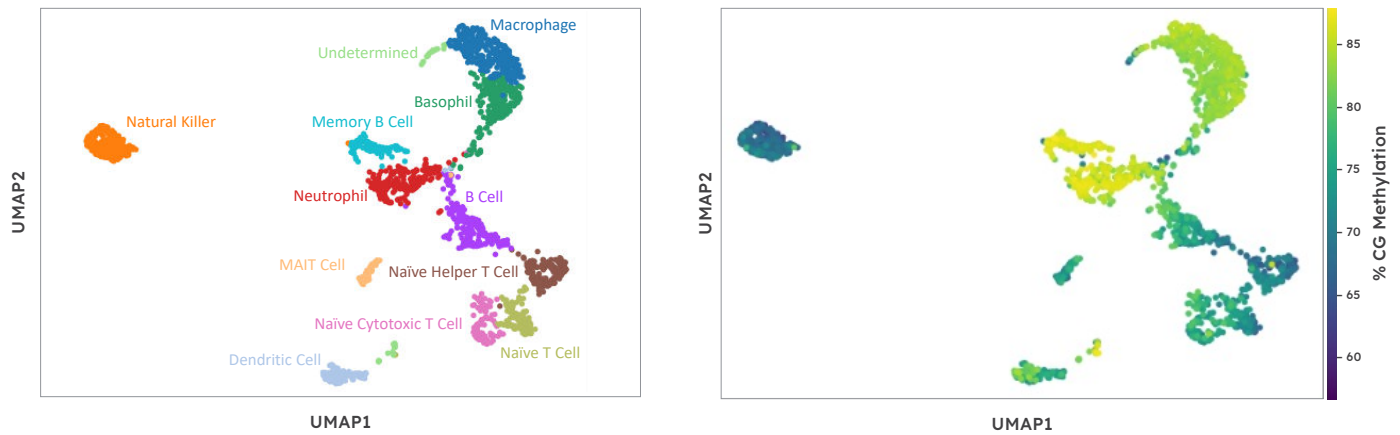


Figure 2. Data generated with Scale Bio’s Single Cell Methylation Kit captures differentially methylated regions to reveal distinct cell populations in PBMCs. Nuclei were processed using the single cell methylation workflow and were analyzed with the SeqSuite methylation pipeline. Methylation status was analyzed in 50 kb bins to generate a methylation status matrix. Differentially methylated regions were used to annotate cell types using cell type-specific methylation markers (left). Also shown is the CG methylation percentage (right).

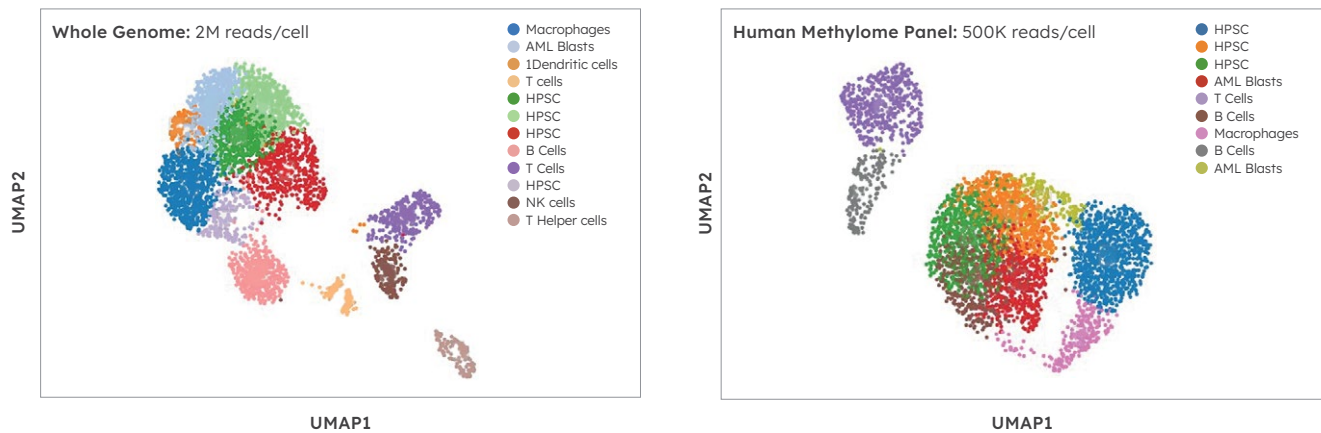


Figure 3. Target enrichment captures similar PBMC cell types. A target-enriched, single cell methylation PBMC library (right) generated using Twist Human Methylome Target Enrichment panel captures similar cell types as whole genome single cell methylation library (left) with 75% fewer sequencing reads.

Product specifications

- Analyze from 4,100 to 16,400 nuclei per run for flexible experimental design
- Interrogate up to hundreds of thousands of CpG and CH sites per cell
- Generate robust data with powerful chemistry and a demonstrated low doublet rate of 8%
- Easily multiplex samples in one run to streamline processing
- Maximize sequencing budget with target enrichment compatibility
- Demonstrated across cell lines, fresh and frozen tissue, and species

Product Code	Product Description
1064637	Scale Bio™ Nuclei Resuspension Kit
1064641	Scale Bio™ Single Cell Methylation Kit v1.1 - Small
1064640	Scale Bio™ Single Cell Methylation Kit v1.1 - Large

To learn more about Scale Bio’s Single Cell Methylation Kit, visit scale.bio/single-cell-methylation-kit.