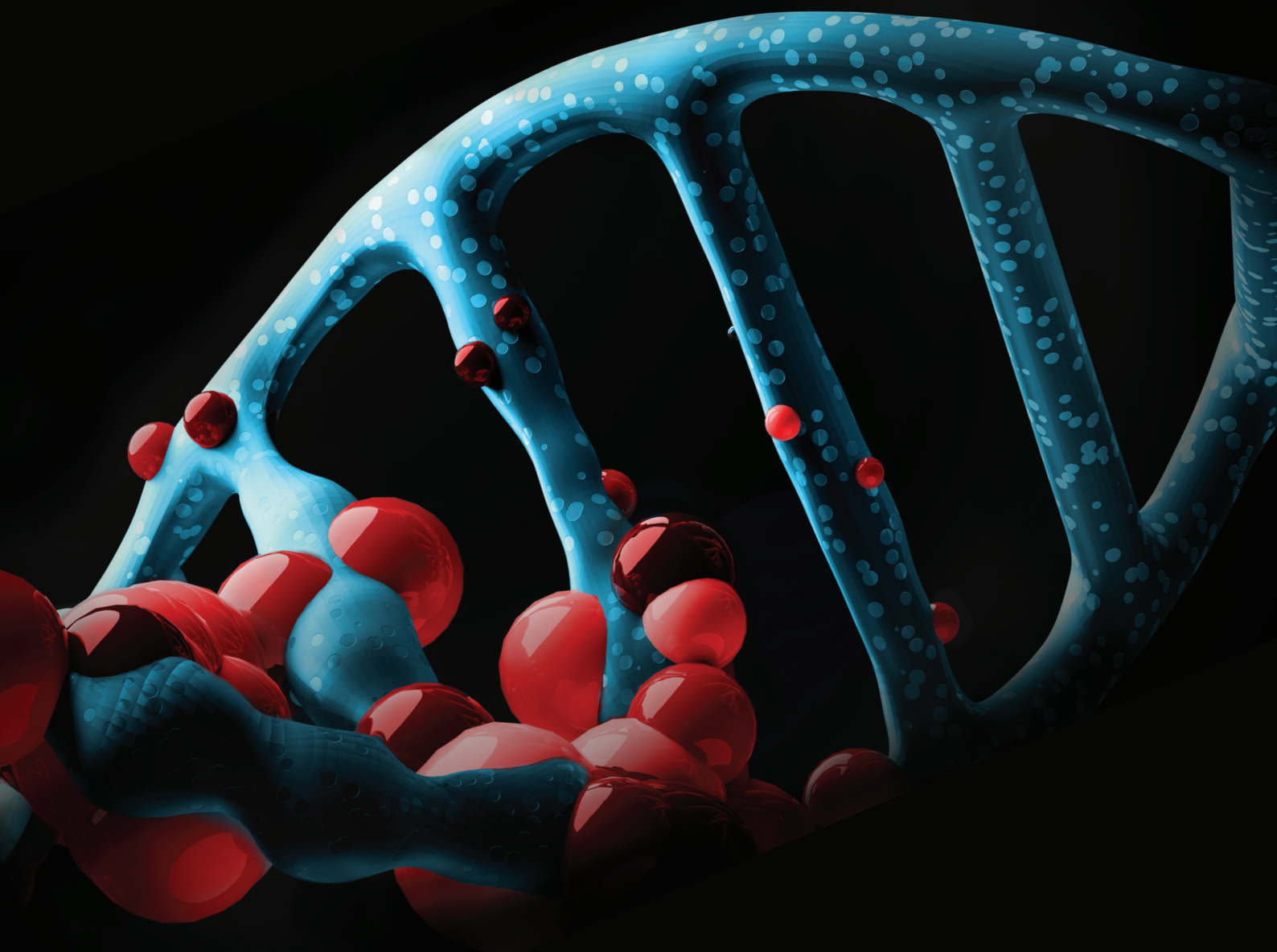


# Simultaneous DNA + Protein + CpG Methylation Analysis on Tapestry®





## Simultaneous DNA + Protein + CpG Methylation Analysis on Tapestri®

A workflow optimized for human samples that reveals clonal architecture, epigenetic states, and differentiation all in the same cells.

## Your Benefits

Bulk assays and plate-based methods miss rare clones and can't connect **genotype ↔ epigenetic state ↔ lineage** in the same cells.

Aging and disease reshape hematopoiesis through subtle clonal dynamics that require high cell throughput and multi-omic context to see.

### With CpG Methylation Profiling on Tapestri, you can:

- **Reveal clonal hematopoiesis earlier** by pairing **single-cell DNA variants/CNVs** with **CpG methylation** enabling the ability to detect early heme malignancies.
- **Track lineage trajectories retrospectively** in human samples with **no transgenics** required.
- **Confidently identify and prioritize new therapeutic or monitoring targets** with single-cell multi-omic insights.

# Applications & Clinical Implications for Single-Cell Multi-Omics Methylation Analysis

## ONCOLOGY APPLICATIONS

### Tumor Classification & Clonal Subtyping

- Methylation defined subtypes and associations with BRAF mutation status in colorectal cancers

### Prognostic Biomarker Development

- CpG methylation profiling in GBM as a predictive therapy related biomarker

### Predicting Therapy Response

- Profiling of methylation state of therapeutic targets (hypomethylating agents) along with co-occurring genetic lesions that might modulate response

## NON-ONCOLOGY APPLICATIONS

### Aging & Longevity Biomarker Research

- Tracking CHIP via combined genotyping (“DTA”) and epigenetic drift profiling via CpG signatures

### Cell and Gene Therapy

- Ensure engineered cell lines don’t retain aberrant methylation patterns linked to malfunction

### Immunology & Autoimmune Disorders

- Linking specific CpG patterns to immune activation states and mutational subgroups in a lineage-specific manner

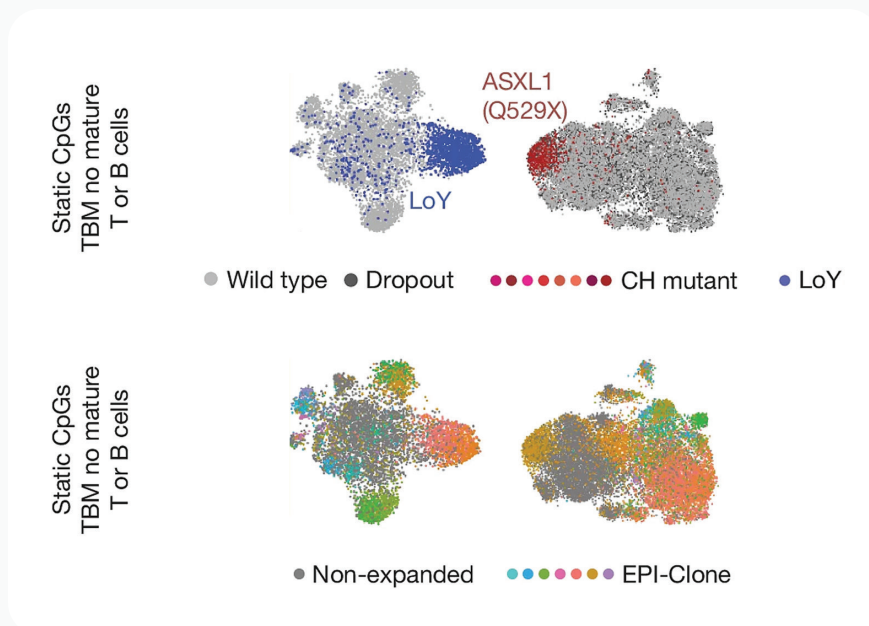


Figure 1: Single-cell DNA and CpG methylation maps showing clonal architecture and lineage composition.

(Top) UMAPs computed per donor on a consensus set of static CpGs, highlighting distinct cell populations containing the specified CH mutations: Loss of Y chromosome (LoY) (A.6, blue) and ASXL1 Q529X mutation (A.7, red).

(Bottom) UMAPs as above, highlighting clonal populations identified using EPI-Clone.

Figure 1 adapted from Scherer M., Singh, I., Braun, M.M et al. Clonal tracing with somatic epimutations reveals dynamics of blood ageing. Nature 643, 478 (2025).

## WHAT YOU CAN UNCOVER

- **Age-linked epigenetic signatures** tied to known and newly detected **clonal hematopoiesis (CH)** mutations.
- **Stable methylation states** that illuminate clonal structure beyond transient differentiation signals.
- **Emergent SNVs with coordinated methylation + lineage shifts** that reveal clone-specific targets to track.

## WHAT THE DATA COULD REVEAL

- CpG profiles capture **age-linked epigenetic signatures**, distinguishing donors by age and aligning with both established and newly discovered CH mutations.
- **Stable methylation states** reveal clonal structure less tied to instantaneous differentiation.
- **Analysis of thousands of cells** exposes emergent SNVs alongside coordinated methylation and lineage shifts, **revealing new targets to track**.

## Tapestri Workflow For CpG Methylation

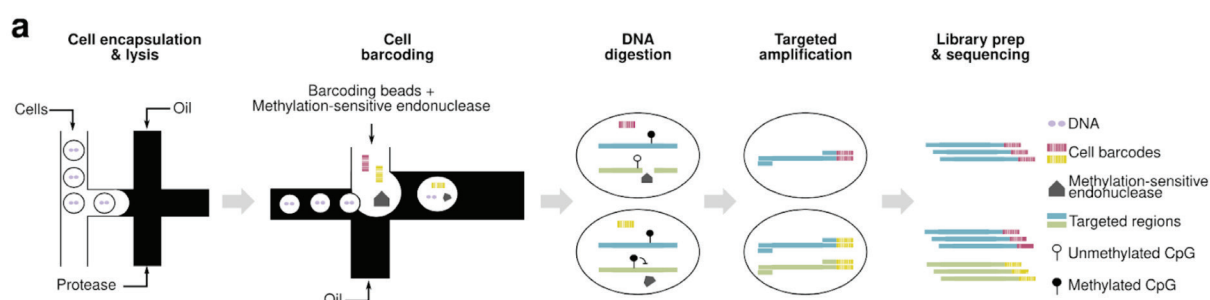


Figure 2: Tapestri CpG methylation workflow overview. Figure 2 adapted from Bianchi, A., Scherer, M., Zaurin, R. et al. scTAM-seq enables targeted high-confidence analysis of DNA methylation in single cells. *Genome Biol* 23, 229 (2022).

1. **Prepare single-cell suspensions** from human bone marrow or blood.
2. **Tapestri DNA (+ Protein optional)** to call **SNVs/CNVs** at single-cell resolution.
3. **Add** methylation-sensitive endonuclease (Single-Cell Targeted Analysis of the Methylome- scTAM-seq) to target informative CpG loci (**bisulfite-free**).
4. **Analyze & visualize** by methylation-specific Tapestri Pipeline and ready-to-use dimension reduction and cluster analysis.

# Made for Teams Like Yours

- **Translational & clinical research teams** monitoring **clonal hematopoiesis (CH) / Acute Myeloid Leukemia (AML) / Multiple Myeloma (MM)** risk, minimal residual disease (MRD), or therapy response.
- **Aging & stem-cell biology** labs mapping differentiation potential across life span.
- **Drug discovery** groups prioritizing clone-specific vulnerabilities.
- **Therapy developers** targeting the epigenome.

## Why Tapestri® for CpG Methylation Profiling



**Targeted sensitivity**  
for variants & CpGs  
that matter.



**Flexible panels** to fit  
your indication and  
study design.



**Scalable workflow**  
with **thousands of**  
**cells** per run.



High-resolution  
**single-cell** analysis.

Ready to see your clones  
and CpGs together?

Visit [support.missionbio.com](https://support.missionbio.com) for additional information.

Contact: [support@missionbio.com](mailto:support@missionbio.com)

## Selected references

- Scherer M. et al., Nature (2025): Clonal tracing with somatic epimutations reveals dynamics of blood ageing.
- Bianchi A. et al., Genome Biology (2022): scTAM-seq enables targeted high-confidence analysis of DNA methylation in single cells.
- Lareau C.A. et al., bioRxiv (2023): Codon affinity in mitochondrial DNA shapes evolutionary and somatic fitness.