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CELL AND GENE THERAPY

Gene Editing Analysis at Single-cell Resolution

TAPESTRI® SINGLE-CELL MULTI-OMICS PLATFORM

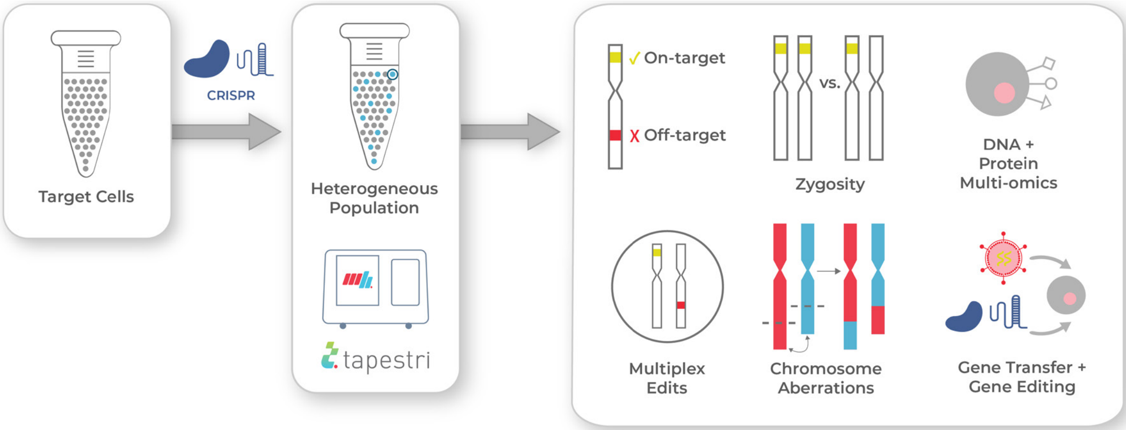
Product Heterogeneity Complicates Characterization

Gene-editing technologies, like CRISPR, are enabling the development of advanced cell and gene therapies. Genome engineering, however, yields heterogeneous cell populations in which cells vary in the edits they contain Moreover, some cells may contain unwanted or even deleterious alterations suchas off-target editing and chromosomal aberrations like translocations.

Tapestri Reveals Gene Edits in 1000s of Single Cells

Single-cell DNA sequencing on the Tapestri Platform provides a high-resolution analysis of gene-edited cells, including on-/off-target editing, multiplex edits, zygosity, and chromosomal aberrations.

For projects that involve gene transfer and gene editing, Tapestri can co-measure these attributes simultaneously in each cell. The platform's powerful multi-omics capability enables the co-analysis of DNA and cell-surface proteins so you can evaluate cell type/ state along with your genomic changes.



Genome engineering yields cell populations with genetic heterogeneity. Single-cell DNA sequencing on Tapestri enables co-measurement of genotypic attributes, including on-/off-target editing, multiplex editing, zygosity, and chromosome aberrations.

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Project Inputs

- Chromosomal coordinates for CRISPR target sites
- Expected Edit(s)
  SNV, short indels,
  long indels, etc.
- Reference genome
- Gene Editing system (e.g., CRISPR)
- Amount of padding sufficient for the analysis
- **Attribute(s) to measure:**
  - On-target site(s)
  - Off-target site(s)
  - Translocations (breakpoint coordinates)
  - Other chromosome aberrations
  - DNA + protein multi-omics
  - Gene transfer*

Project Outputs

- **Raw Data Files**
  - FASTQ files from ILMN
  - h5 files from Tapestri Pipeline
- **Final Project Report**
  - QC analytics: sequencing and amplicon panel performance metrics for experimental and sample QC
  - Project data

*See Gene Transfer flyer for more information

CONTACT US TO LEARN MORE

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Get Higher Resolution Data Than Bulk Sequencing

Unlike bulk technologies that report average editing efficiencies, Tapestri provides information from individual cells — enabling attributes like zygosity and editing co-occurrence to be directly measured in 1000s of individual cells.

	Bulk DNA Sequencing	Tapestri Analysis
Co-occurrence of edits	×	✓
Zygosity of edits	×	✓
Gene editing + gene transfer in individual cells	×	✓
DNA + protein in individual cells	×	✓

Easily Incorporate Single-cell into Your Workflows

Mission Bio offers custom single-cell assay development for gene editing. Our Pharma Assay Development (PAD) team will work closely with you to design an assay that fits your needs. We handle every step of the process — from experimental design to data analysis — and provide a final report upon completion. If desired, we will work with you to transfer the assay to your institution or a qualified CRO/ CDMO. Contact us to learn more about how you can incorporate single-cell analysis of gene editing into your workflow today.

STREAMLINED PAD WORKFLOW