



What if your cell or gene therapy characterization could be more conclusive?

Characterize your cell and gene therapies better.

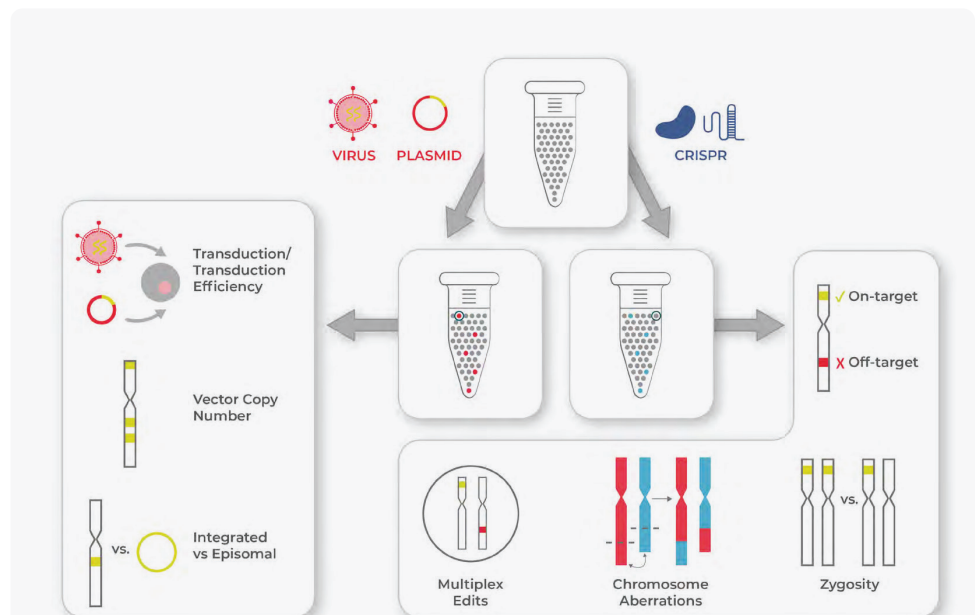
Cell and gene therapies are notoriously difficult to characterize. Yet, early and thorough characterization is key to advancing therapeutic programs quickly with minimal risk of safety issues or clinical holds.

Whether a therapy utilizes gene transfer technologies or gene editing tools, both approaches result in heterogeneity. Some cells have the desired changes while others do not, and some may even have alterations that pose a safety risk.

Measure multiple genetic attributes in a single assay.

A deeper understanding of cell and gene therapeutic agents requires a high-resolution approach.

With this data, you can optimize protocols, identify critical quality attributes, and accelerate your progress to commercialization.



MEASURING GENE TRANSFER

For therapies that involve gene transfer, Tapestri co-measures the transduction/transfection efficiency, vector copy number (VCN), and integrated vs. episomal transgenes at single-cell resolution.

Unlike bulk PCR approaches that report population averages, you will gain visibility into rare events in individual cells.

MEASURING GENE EDITING

For therapies modified by CRISPR or other gene-editing tools, Tapestri co-measures on- and off-target editing in each cell. Additionally, the co-occurrence of multiple edits, zygosity, and chromosomal aberrations can be assessed.

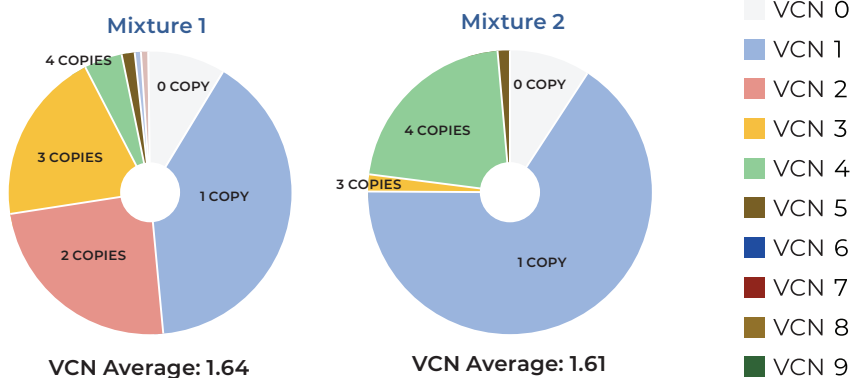
In contrast to traditional bulk NGS, qPCR, or ddPCR analysis, Tapestri delivers data from individual cells so you can understand cell-to-cell variability in your product.

Single-cell multi-omics for simultaneous DNA and protein.

The Tapestri Platform is the world's first and only single-cell solution that provides both genotype and phenotype data from individual cells. Measure genetic alterations along with targeted proteins in a single assay to achieve an even deeper understanding of your therapeutic. You can ensure your genetic changes have not altered the cell type or state (immunophenotype), or you can co-measure the transduction of a transgene and its associated protein expression.

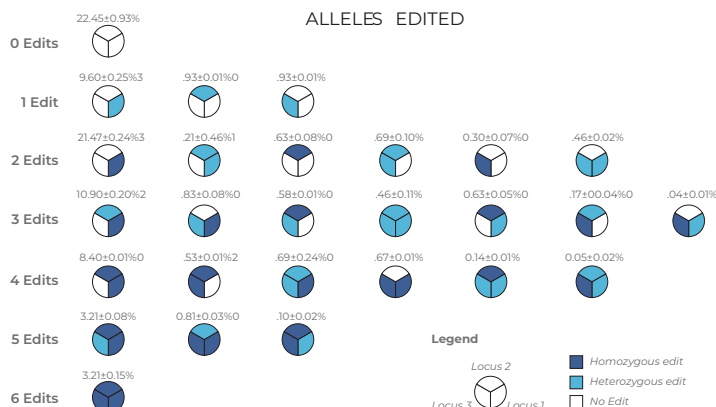
VECTOR COPY NUMBER

Tapestri measured average VCN, consistent with ddPCR (data not shown). However, single-cell Tapestri analysis demonstrated that VCN distributions per mixture varied dramatically, despite similar average populational VCN values.



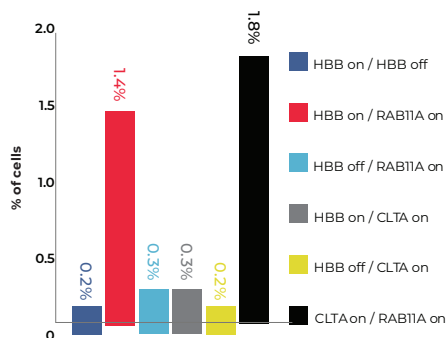
MULTIPLEXED EDITS & ZYGOSITY

Tapestri was used to analyze a CRISPR multiplex editing experiment (3 targets) in PBMCs, where it resolved the percentage of alleles edited, zygosity, and mutation co-occurrence in all 27 possible combinations.



CHROMOSOME ABERRATIONS

Tapestri analysis detected translocation events with high sensitivity (0.2-1.8% of cells) for three genes (HBB, CLTA, & RAB11A) that were co-edited using CRISPR/Cas9 in a cancer cell line.



ON/OFF-TARGET EDITING

Tapestri analysis detected on-target and predicted off-target editing (as % indels) for three genes (HBB, CLTA, & RAB11A) that were co-edited using CRISPR/Cas9 in a cancer cell line.

