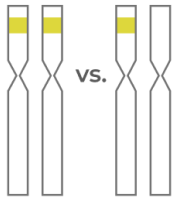
mission bio

ASK THE QUESTIONS
YOU COULD NEVER ASK BEFORE

Tapestri Single-cell Genome Editing Solution

Streamlined analysis for gene editing – no bioinformatics needed

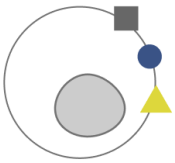
Genome engineering strategies, like CRISPR, result in heterogeneous outcomes including off-target edits, co-occurring multiplex edits, and variations in zygosity. These outcomes cannot be easily measured using traditional sequencing without lengthy clonal outgrowth steps and hours of computational work. With the Tapestri single-cell platform you can rapidly capture genome editing outcomes and confidently validate your engineered cell therapy or CRISPR-based disease model.



Zygosity

Co-Occurrence of Intended Targets

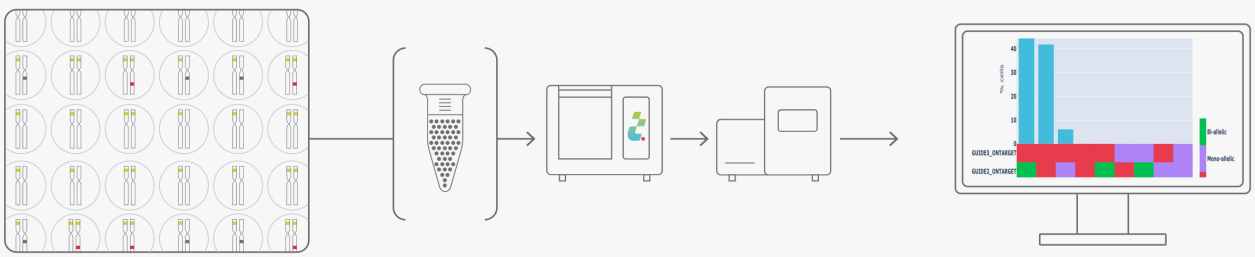
Co-Occurrence of On/Off Targets



Immunophenotype

The Tapestri Genome Editing Solution measures these attributes at single-cell resolution.

THE TAPESTRI GENOME EDITING SOLUTION WORKFLOW



Heterogeneous Edits

Cell Prep

Tapestri Encapsulation + Barcoding

Library Prep + NGS

Software and Automated Reporting

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Streamlined analysis for gene editing – no bioinformatics needed (cont.)

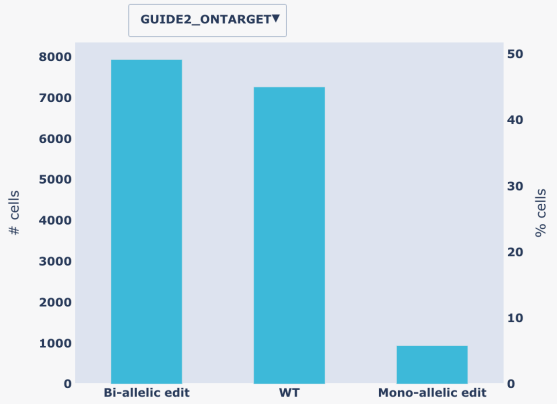
The end-to-end Tapestri workflow for single-cell genome editing analysis. A sample of gene-edited cells are processed on the Tapestri Platform, sequenced using NGS, and analyzed using Tapestri Genome Editing software. The assessment at single-cell resolution of on-targets, predicted off-targets, zygosity of edits, co-occurring (multiplex) edits, predicted translocations and cell-surface proteins is possible. The Solution can be used to analyze gene knockouts (via non-homologous end joining) and base edits.

Step 1 - Design Panel & Run Edited Samples on Tapestri®
Step 2 - Sequence Libraries on NGS
Step 3 - Software Runs Automated Analysis and Generates Intuitive Data Report

GENOME EDITING REPORT SAMPLE DATA

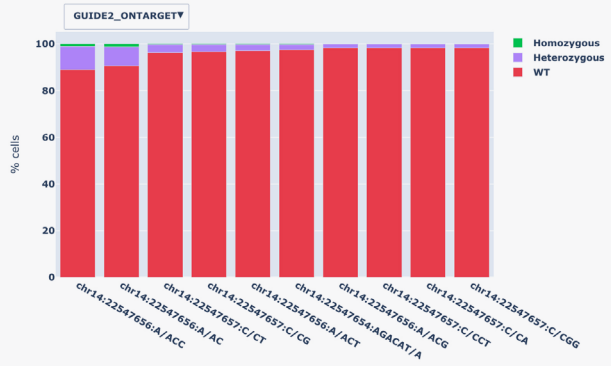
Simplify analysis of your editing outcomes with easy-to-interpret reports. The Genome Editing Solution requires no bioinformatics support, saving you hours of computational time.

ZYGOSITY OF ON-TARGET EDITS



The percentage of cells with wild type (WT), monoallelic, or biallelic edits at the on-target site. For multiplex experiments, the target may be selected from the dropdown menu.

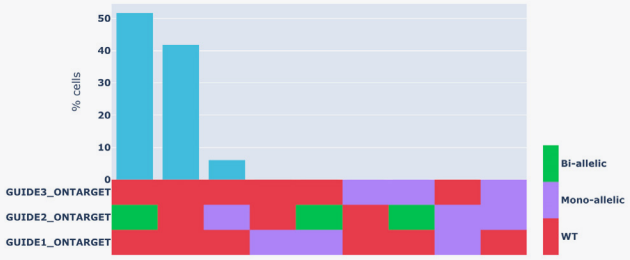
ZYGOSITY OF TOP 10 ON-TARGET VARIANTS



The 10 most frequent variants and the percentage of cells that contain the variant on both alleles (homozygous), one allele (heterozygous), and not at all (wildtype, WT). The variant name (x-axis) is in the format of "chromosome:position:reference bases/alternative bases." If there are multiple on-targets in the same sample, the on-target names may be selected from the drop-down menu.

GENOME EDITING REPORT SAMPLE DATA (CONT.)

CO-OCCURRENCE OF ON-TARGET EDITS



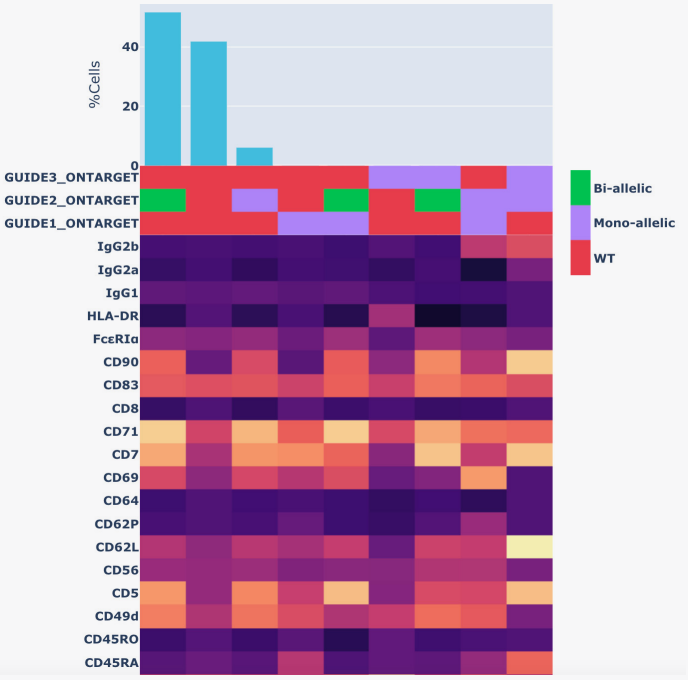
The percentage of cells with the most frequent combinations of multiple on-target edits. The upper portion is a bar plot with each bar representing the percentage of cells with each combination of edits. The lower portion is a heatmap. Each row of the heatmap represents an on-target. Each color square represents zygosity: WT (red), heterozygous edit (purple), homozygous edit (green).

TOP EDIT COMBINATIONS

Group	Edited targets	% cells
GUIDE2	GUIDE2_OFFTARGET4 + GUIDE2_ONTARGET	0.40 %
GUIDE2	GUIDE2_OFFTARGET7 + GUIDE2_ONTARGET	0.30 %
GUIDE2	GUIDE2_ONTARGET + GUIDE2_OFFTARGET12	0.15 %
GUIDE2	GUIDE2_OFFTARGET3 + GUIDE2_ONTARGET	0.13 %
GUIDE2	GUIDE2_OFFTARGET9 + GUIDE2_ONTARGET	0.14 %
GUIDE3	GUIDE3_OFFTARGET1 + GUIDE3_OFFTARGET32	0.01 %
GUIDE3	GUIDE3_OFFTARGET20 + GUIDE3_OFFTARGET9	0.01 %
GUIDE3	GUIDE3_OFFTARGET24 + GUIDE3_OFFTARGET38	0.01 %
GUIDE3	GUIDE3_OFFTARGET25 + GUIDE3_OFFTARGET41	0.01 %

The most frequent combinations of co-occurring on-target(s) and/or off-target(s) within each Group. The percentage values were calculated by: (the number of cells in each combination/ total number of cells with on and above minimum read depth in the on-target(s) and/or off-target(s)) *100. Each bar represents a unique combination of edits. The plot shows a maximum of 5 combinations.

GENOME EDITING + CELL SURFACE PROTEIN



The number of cells with different combinations of edits and cell-surface protein expression. Each column represents cells with the indicated combination of edits and protein expression.

Top: the number of cells with each combination.

Middle: the zygosity of on-target and predicted off-target edits.

Bottom: expression of cell-surface proteins.