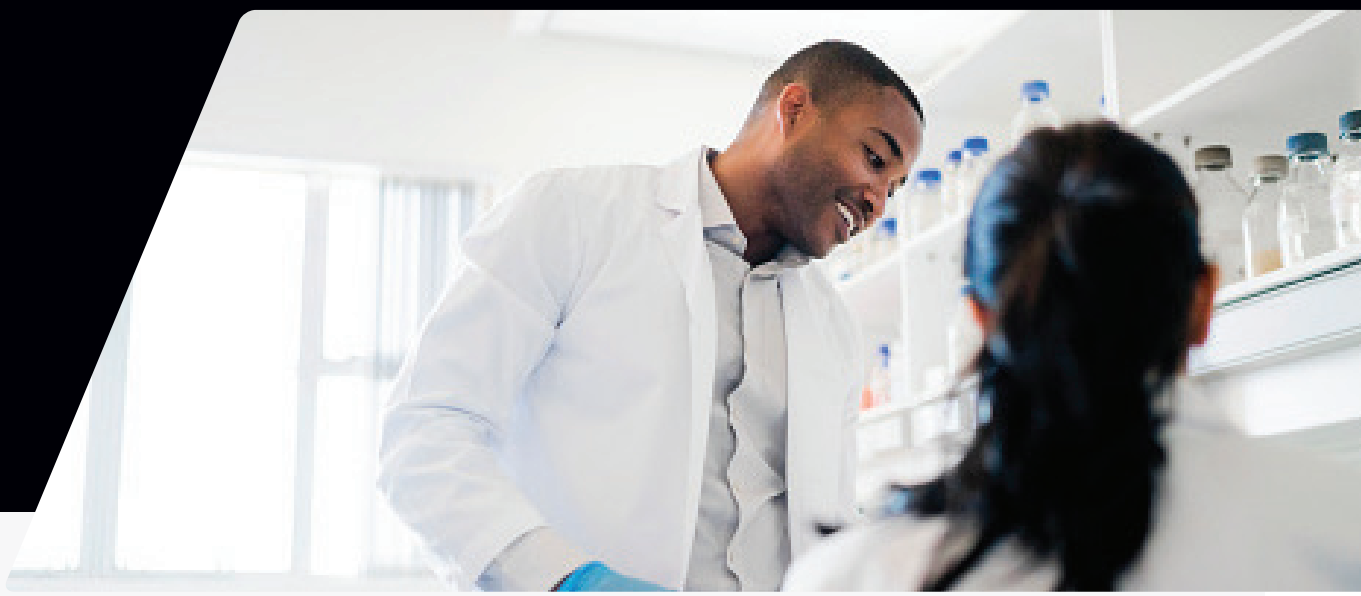
mission bio

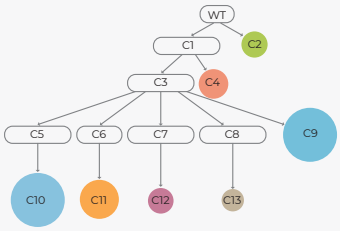
PHARMA ASSAY DEVELOPMENT
BIOMARKER DISCOVERY PILOT PROGRAM:

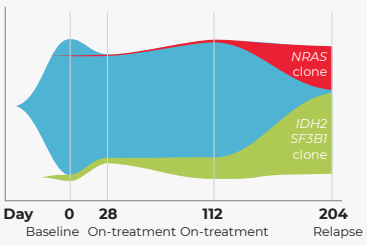
Accelerate your hematologic oncology projects with a dedicated partner across the drug development pipeline.

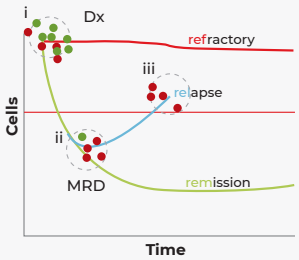


DO BETTER THAN BULK SEQUENCING

The Tapestri® Platform is the only comprehensive, single-cell, multi-omics solution that can untangle therapy resistance mechanisms, help you understand mechanism of actions, better stratify patients, monitor patients while on treatment, and identify better therapies.







RECONSTRUCT PHYLOGENIES

Model clonal evolution across multiple analytes with longitudinal samples.

REVEAL RESISTANCE MECHANISMS

Identify resistant clones through the course of therapy.

DETECT MEASURABLE RESIDUAL DISEASE

Detect and characterize measurable residual disease (MRD) that portends relapse.

Resurrect failed clinical trials.

Retrospective analysis of failed clinical trials via Tapestri can elucidate details that more conventional methodologies, like bulk sequencing, may have missed the first time. Resolve clonal heterogeneity, identify co-occurring mutations, measure zygosity, detect rare cell populations, and quantitatively characterize genotype and phenotype at the single cell level.

Make the easy move to single-cell multi-omics.

Implement single-cell multi-omics in your lab with ease through a Pharma Assay Development (PAD) proof of concept study. It is as easy as shipping samples to Mission Bio and getting a fully analyzed report back. As part of the pilot study, you'll have access to Mission Bio's innovative technology, assay development team, R&D organization, and bioinformatics support.

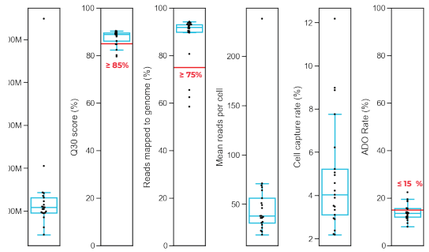
Our oncology experts partner with you to:

- Scope your single cell multi-omics project with the goal of uncovering therapeutic resistance
- Identify high impact longitudinal sample sets that indicate clinical relevance
- Deliver a comprehensive report that highlights therapeutic insights
- Deliver next-generation clinical trial design for better patient stratification

Gain insights with your data.

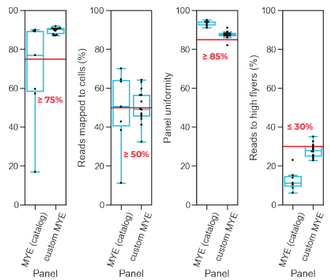
Your raw data will be analyzed by expert bioinformaticians and you'll receive a comprehensive report, summarizing study design and single-cell data interpretation on SNVs, indels, chromosomal rearrangements and CNVs; as well as structural characteristics like zygosity, mutational co-occurrence, and the presence of rare cell populations.

SEQUENCING PERFORMANCE METRICS



Passing criteria indicated in red for critical performance metrics.

PANEL PERFORMANCE METRICS



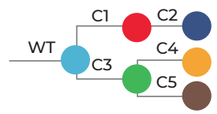
Passing criteria indicated in red for critical performance metrics.

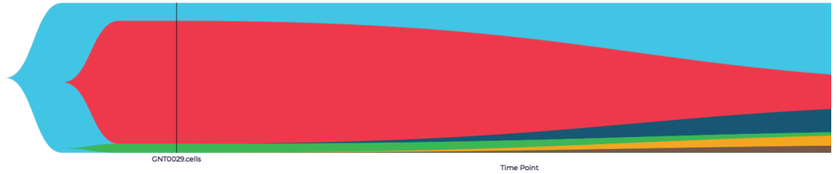
BULK-SEQ COMPARED WITH SINGLE CELL

Sample	Bulk variants in panel	Bulk variants identified by pipeline
x1	2	2
x2	9	7
x3	17	16
x4	9	4
x5	18	17
x6		
x7	13	12
x8		
x9	16	14
x10	10	9
x11		
x12	8	6
x13	16	14
x14		
x15	13	12
Total	**131**	**113 (86.26%)**

SUBCLONE IDENTIFICATION

Clonal phylogeny





SAMPLE DATA ANNOTATIONS

- All bulk-seq confirmed variants (n=8) detected | 5/8 used for clonal analysis (somatic); 3/8 disregarded (germline character)
- 6 subclones resolved based on 5 somatic variants' co-occurrence pattern and zygosity states
- Rare aaa/bbb double-mut clone (C4, 0.06%) detected at screen, which expands at x time point
- Double mutant aaa/ddd clone (C5, 5.45%) detectable at x time point with ddd zygosity = HOM suggesting either true homozygosity or potential LOH
- Multi-branched clonal evolution pattern with at least two independent trajectories

Pass-filter variants used for downstream analysis

Variant	From bulk	% GT	VAF %	
			Untreated	Treated
aaa	Yes	87%	2.9%	13.5%
bbb	Yes	77%	41.5%	28.1%
ccc	Yes	71%	44.1%	19.5%
ddd	Yes	86%	0.5%	5.5%
eee	Yes	92%	0.0%	13.0%
fff	Yes	76%	49.6%	51.6%
ggg	Yes	90%	52.6%	53.4%
hhh	Yes	64%	51.4%	51.6%

Subclones identified

Variant	C1	WT	C2	C3	C4	C5
aaa	WT	WT	WT	**Het**	**Het**	**Het**
bbb	**Het**	WT	**Het**	WT	Het	WT
ccc	**Het**	WT	**Het**	WT	WT	WT
ddd	WT	WT	WT	WT	WT	**Hom**
eee	WT	WT	**Het**	WT	WT	WT
x	82.12%	11.94%	0.00%	5.87%	**0.06%**	0.00%
a	13.22%	53.75%	18.03%	1.63%	**7.92%**	5.45%

REPORTS INCLUDED

- Sequencing performance metrics
- Target panel performance metrics
- Clonal phylogeny
- SNV analysis
- CNV analysis
- Immunophenotyping & cell lineage
- UMAP clustering & FISH plots

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PARTNERED WITH LEADING PHARMA AND BIOPHARMA COMPANIES

- AbbVie
- Amgen
- Blueprint Medicines
- Bristol Myers Squibb
- Celgene
- Covance
- Genentech
- LabCorp
- Merck
- Servier

CONTACT US TO LEARN MORE

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MISSIONBIO.COM

Pilot Program Catalog Panel: MYE + TotalSeq™-D


16 Samples

8 Patients


2 Timepoints

45-Gene Myeloid Panel

ASXL1	ERG	KDM6A	NRAS	SMC1A
ATM	ETV6	KIT	PHF6	SMC3
BCOR	EZH2	KMT2A	PPM1D	STAG3
BRAF	FLT3	KRAS	PTEN	STAT3
CALR	GATA2	MPL	PTPN11	TET2
CBL	GNAS	MYC	RAD21	TP53
CHEK2	IDH1	MYD88	RUNX1	U2AF1
CSF3R	IDH2	NF1	SET8P1	WT1
DNMT3A	JAK2	NPM1	SF3B1	ZRSR2

Metric	Value
Number of genes	45
Number of targets	1,197
Target type possible	SNVs, Indels, CNVs, LOH
Number of amplicons	312
Coverage	99.0%
Panel size	~65 kb
Amplicon length	125–375 bp
Panel uniformity: % of amplicons >0.2x mean	≥90%
Amplicon completeness: % of amplicons in >80% of cells	≥80%
Verified NGS systems	MiSeq, NextSeq, HiSeq, NovaSeq
Recommended number of reads per sample	~188 M

Heme Oncology Protein Panel

CD1c	CD11c	CD34	CD62P	CD141
CD2	CD14	CD38	CD64	CD163
CD3	CD14	CD44	CD69	CD303
CD4	CD16	CD45	CD71	CD304
CD5	CD19	CD45RA	CD83	FcεRIα
CD7	CD22	CD45RO	CD90	HLA-DR
CD8	CD25	CD49d	cd1171	IgG1 control
CD10	CD30	CD56	CD123	IgG2a control
CD11b	CD33	CD26L	CD138	IgG2b control