Application:
Hematologic Malignancies

BioSkryb GENOMICS

Transform Your Hematology Research with Sensitive and Precise Single-Cell Multiomics

Challenges in Hematologic Oncology Research

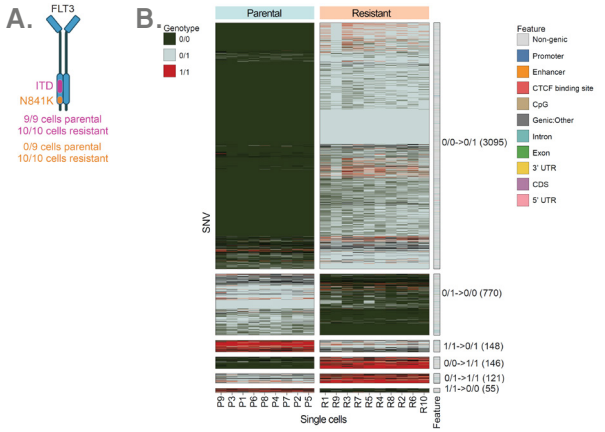
Rare malignant clones and persister cells facilitate resistance and recurrence
Bulk sequencing may miss significant mutations in rare cells and fail to identify which mutations co-occur in the same cell.

Hematologic malignancies are driven by various sizes of genomic alterations
Panel-based DNA approaches struggle to capture single nucleotide variants (SNV), copy number variation (CNV), and structural variants (SV) in one assay.

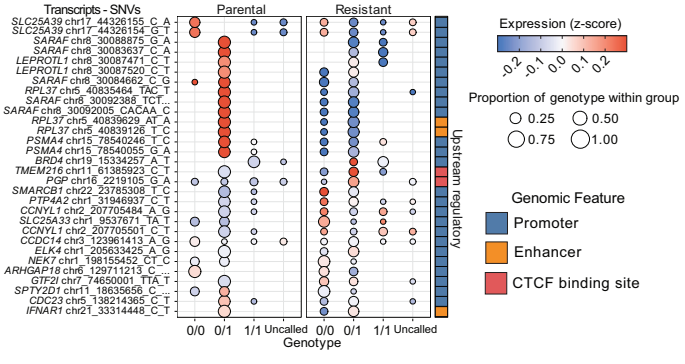
Consequences of SNV, CNV, and SV changes are not always obvious
DNA-only approaches can fail to identify the gene expression changes resulting from mutations in both malignant and benign hematologic disorders.

Solutions from BioSkryb Genomics

ResolveDNA® enables single-cell whole genome sequencing, empowering researchers to sensitively and precisely detect whole genome CNV and SNVs at a single cell resolution. **ResolveOME™** allows investigators to move beyond inference from gene expression and define the genetic mechanisms controlling gene expression at a single-cell level.



Detect SNV changes in individual therapy-resistant cells. Analysis of parental and quizartinib-resistant cell lines following ResolveOME whole genome and transcriptome amplification. **A.** Previously published *FLT3* internal tandem duplications and N841K mutations are detected. **B.** SNVs in individual cells vary between sensitive and resistant lines.[1]



Identify underlying mechanisms of gene expression changes in individual cells. Analysis of parental and drug-resistant cell lines following ResolveOME whole genome and transcriptome amplification reveals SNVs in non-coding upstream regulatory regions that are associated with changes in gene expression.[1]

References:
1. Marks JR, et al. bioRxiv. 2023; doi: https://doi.org/10.1101/2022.04.29.489440

Assay Performance

Table 1: ResolveOME WGS DNA Performance

Characteristic	Observed Values
Accuracy	99.99%
Sensitivity	96.65%
Specificity	99.99%
Allelic Balance	91.20%
Genomic Coverage	97.59%

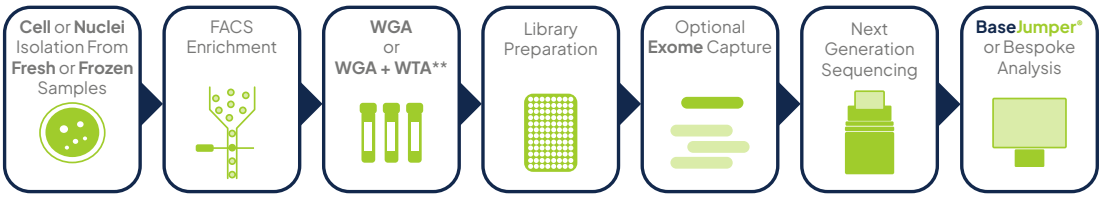
Table 2: ResolveOME WTS RNA Performance

Characteristic	Observed Values
Protein Coding Genes	3451 ± 732
Concordance	0.97
Variance (CV)	32.9%

Assay performance characteristics of DNA (Table 1) and RNA (Table 2) isolated using ResolveOME Whole Genome and Transcriptome Single-Cell Core Kit. Analysis of FACS-sorted NA12878 single cells prepared with ResolveOME versus gold-standard reference. WGS: whole genome sequencing. WTS: whole transcriptome sequencing.

ResolveServices℠

Custom-built service projects, from singulating cells to figures. Services can include:



FACS: Fluorescence-Activated Cell Sorting, WGA: Whole Genome Amplification, WTA: Whole Transcriptome Amplification,
Optional **targeted protein detection available

Products

Product	Description	Codes	Well Format
ResolveOME™ Whole Genome and Transcriptome Single-Cell Core Kit	PTA-based kit for whole genome and transcriptome amplification plus NGS library preparation from single cells.	100956	96
		100957	384
ResolveDNA® Whole Genome Single-Cell Core Kit	PTA-based kit for whole genome amplification plus NGS library preparation from single cells.	100954	96
		100955	384
ResolveDNA® Whole Genome Amplification Kit	PTA-based kit for whole genome amplification from as little as 4 pg input DNA.	100545	Up to 384*
BaseJumper® Bioinformatics Platform	A platform for multiomic data analysis.	100605	-
ResolveXOME™ Exome Capture Module	Exome capture module for use with ResolveDNA or ResolveOME Single-Cell Core Kits.	Early-Access	-

*Dependent on workflow option used

For a complete list of services, products, and pricing, email a member of our team, info@bioskryb.com

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All data on file.

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