Application:

Hematologic Malignancies



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 cooccur 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.

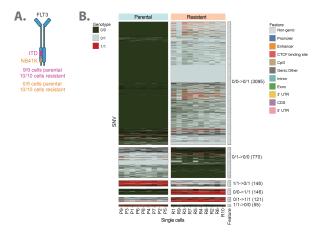


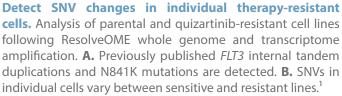
Consequences of SNV, CNV, and SV changes are not always obvious

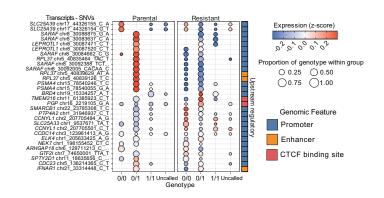
DNA-only approaches can fail to identify the gene expression changes resulting from mutations in both malignant and benign hematologic disorders.

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.







Identify underlying mechanisms of gene expression changes in individual cells. Analysis of parental and drugresistant 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

Reference

1. Marks et al., "Unifying comprehensive genomics and transcriptomics in individual cells to illuminate oncogenic and drug resistance mechanisms". bioRxiv. (2023)

ResolveDNA® and ResolveOME™ Assay Performance

Table 1: ResolveOME WGS DNA Performance*	
Characteristic	Observed Values
Accuracy	99.5%
Sensitivity	97.1%
Specificity	99.2%
Allelic Balance	98.4%
Genomic Coverage	97.1%

Table 2: ResolveOME WTS RNA Performance		
Characteristic	Observed Values	
Genes Detected	4,546	
Reportable Range	6,057	
Average Concordance	0.91	
Reproducibility (CV)	43.3%	

Table 1: Assay performance characteristics of DNA isolated using ResolveOME. Analysis of FACS-sorted NA12878 single cells prepared with ResolveOME versus gold-standard reference. WGS: whole genome sequencing.

Table 2: Assay performance characteristics of RNA isolated using ResolveOME. Analysis of FACS-sorted NA12878 single cells prepared with ResolveOME versus gold-standard reference. WTS: whole transcriptome sequencing.

Custom Services

We offer custom service packages from our end-to-end single-cell multiomic pipeline, from singulating cells to ready-to-publish figures. All services include quality control verification. Services include:

- Cell sorting from fresh or frozen cells and tissues
- Whole genome amplification or whole genome and transcriptome amplification
- · Library preparation for downstream applications, such as whole genome or targeted sequencing
- Sequencing of 550M quality reads capturing >97% of the human genome from each cell
- Analysis using our bioinformatics platform, BaseJumper™

Products

Code	Product	Description
100500	ResolveOME™ Whole Genome and Transcriptome Amplification System	PTA-based kit for accurate and reproducible whole genome and transcriptome amplification from single cells.
100545	ResolveDNA® Whole Genome Amplification Kit	PTA-based kit for accurate and reproducible whole genome amplification from single cells and low-input DNA inputs.
100605	BaseJumper™ Bioinformatics Platform	A complete bioinformatics solution for multiomic data analysis and visualization.

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



All data on file.

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^{*}DNA amplified using ResolveDNA and ResolveOME have comparable DNA performance characteristics. All data on file.