

# The Next Generation Single-Cell Technology



## Whole genome and transcriptome sequencing from a single cell

Uses a single cell for the construction of a whole-genome and full-length mRNA transcriptome library.



## Industry-leading genomic coverage and resolution

Leverages a novel patented technology, primary template-directed amplification (PTA), to dramatically increase genomic capture and coverage to 97%.<sup>1,2</sup>



## Superior transcriptome capture and coverage

Increases gene body coverage, representation across transcript sizes, and variant calling versus droplet-based RNA sequencing methods.<sup>3,4</sup>



## DNA, RNA, and targeted protein analysis from individual cells

Provides integrated DNA-informed multiomic data on a single cell level.

### A Revolution in Resolution From Each Cell

#### DNA

Resolve SNV	Resolve Panels
Resolve SV	Resolve Exomes
Resolve CNV	Resolve Genomes
Resolve Ploidy	Resolve Edits

#### DNA + RNA

Resolve Transcriptomes	Resolve Fusions
Resolve Isoforms	Resolve Cell ID

#### DNA + RNA + Targeted Proteins

Resolve Multiomes

### Research Areas Include:

- Oncology
- Cell and Gene Therapy
- Neurology
- Reproductive Health
- Foundational Research

**Resolve More.**

#### References:

1. Gonzalez-Pena V, et al. Proc. Natl. Acad. Sci. U.S.A. 2021; 118 (24): e2024176118; doi: 10.1073/pnas.2024176118
2. Luquette L, et al. Nat Gen. 2022; 54: 1564-1571. doi: 10.1038/s41588-022-01180-2
3. Marks JR, et al. bioRxiv. 2023; doi: <https://doi.org/10.1101/2022.04.29.489440>
4. Data on file

## Assay Performance

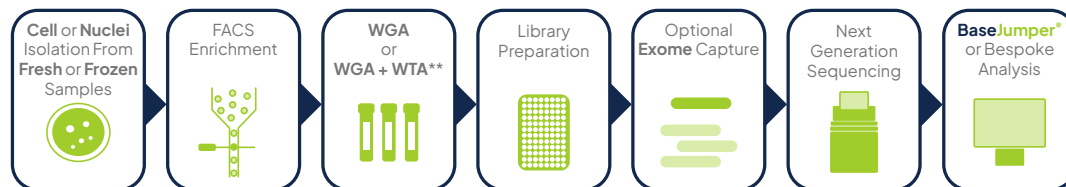
Table 1: ResolveOME WGS DNA Performance	
Characteristic	Observed Values
Accuracy	99.99%
Sensitivity	96.65%
Specificity	99.99%
Allelic Balance	91.20%
Genomic Coverage	97.59%

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<sup>SM</sup>

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
<b>ResolveOMETM</b> 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
<b>ResolveDNA®</b> Whole Genome Single-Cell Core Kit	PTA-based kit for whole genome amplification plus NGS library preparation from single cells.	100954	96
		100955	384
<b>ResolveDNA®</b> Whole Genome Amplification Kit	PTA-based kit for whole genome amplification from as little as 4 pg input DNA.	100545	Up to 384*
<b>BaseJumper®</b> Bioinformatics Platform	A platform for multiomic data analysis.	100605	-
<b>ResolveXOMETM</b> 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](mailto:info@bioskryb.com)

## BioSkryb GENOMICS

All data on file.

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