# ResolveOME™

BioSkryb GENOMICS

# Decipher Mechanisms of Gene Expression Changes with Single-Cell Multiomics

## ResolveOME Whole Genome and Transcriptome Amplification System

### Whole genome or exome and transcriptome sequencing from a single cell

Uses a single cell for the construction of a whole-genome and full-length mRNA transcriptome library. Workflow available for hybrid capture compatibility.

### Provides 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%.[1,2]

### Superior transcriptome capture and coverage

Increases gene body coverage, representation across transcript sizes, and variant calling versus droplet-based RNA sequencing methods.[3,4]

### Fits into established laboratory protocols

Compatible with various methods of single-cell singulation, sequencing platforms, and downstream applications, including whole exome and panel-based sequencing.[4]

### Scales to experiment size

Low-cost, automation-compatible, scalable approach with up to 384 reactions.

### Bioinformatics analysis available with BaseJumper®

Bioinformatics analysis and data visualization through BaseJumper bioinformatics platform and computational biology custom services.


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

| ResolveOME WGS DNA Performance | |
|---|---|
| Accuracy | 99.99% |
| Sensitivity | 96.65% |
| Specificity | 99.99% |
| Allelic Balance | 91.20% |
| Genomic Coverage | 97.59% |
| **ResolveOME WTS RNA Performance** | |
| Protein Coding Genes | 3451 ± 732 |
| Concordance | 0.97 |
| Variance (CV) | 32.9% |

**Figure 1: Assay Performance Characteristics.** Analysis of NA12878 single cells prepared with ResolveOME Whole Genome Single-Cell Core Kit versus gold standard reference. WGS: whole genome sequencing, WTS: whole transcriptome sequencing.

## A Revolution in Resolution From Each Cell

### DNA

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

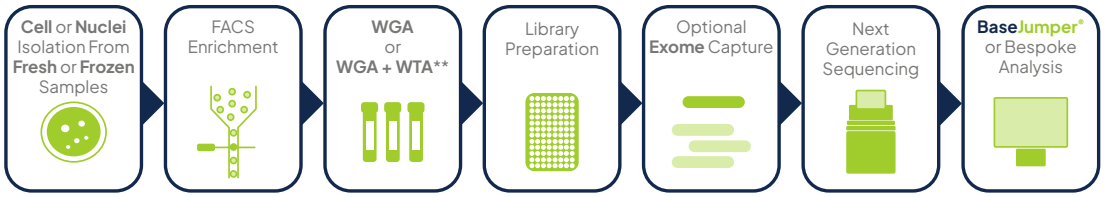
### DNA + RNA

- Resolve Transcriptomes
- Resolve Isoforms
- Resolve Cell ID
- Resolve Fusions

**Resolve More.**

## 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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