

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%.^{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}



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

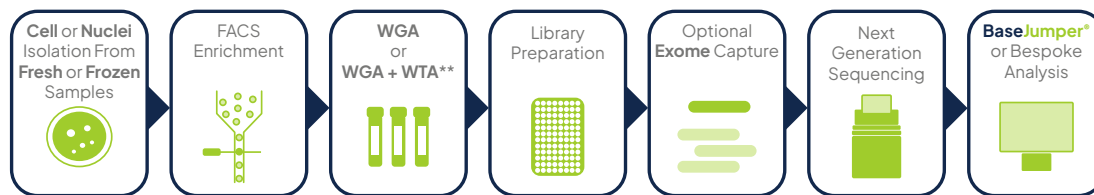
| Characteristic | Observed Values |
|------------------|-----------------|
| Accuracy | 99.99% |
| Sensitivity | 96.65% |
| Specificity | 99.99% |
| Allelic Balance | 91.20% |
| Genomic Coverage | 97.59% |

| 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.

ResolveServicesSM

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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