ResolveOME™

BioSkryb GENOMICS

Decipher Mechanisms of Gene Expression Changes with Single-Cell Multiomics

ResolveOME Whole Genome and Transcriptome Amplification System

Enables 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

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]

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[3]

Scales to experiment size

Low-cost, scalable approach with up to 96 reactions per kit

Bioinformatics analysis included

Bioinformatics analysis and data visualization through BaseJumper™ bioinformatics platform

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. Data on file

Key Feature: Capture Genomic Alterations and Gene Expression in the Same Cell

ResolveOME | **Droplet DNA-seq** | **Droplet RNA-seq**

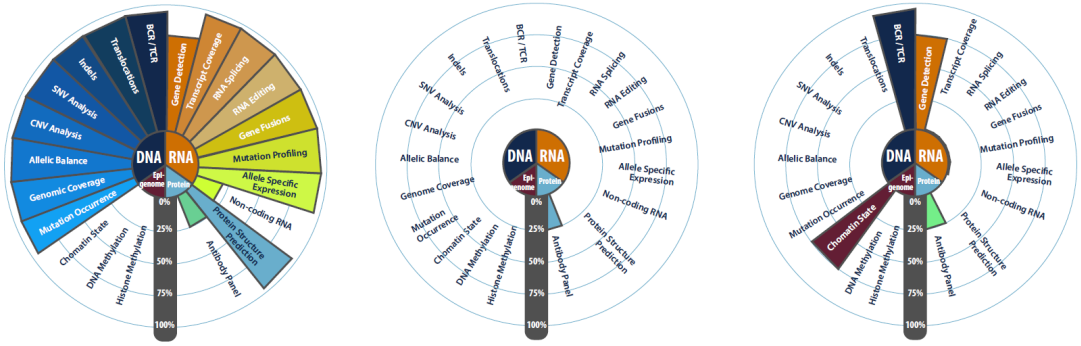

Figure 1: The ResolveOME Whole Genome and Transcriptome Amplification System provides more data from each cell versus other droplet-based approaches. The ResolveOME workflow offers a comprehensive view of the genome, mRNA transcriptome, and inferred impacts of protein sequence alterations. ResolveOME supports more modalities (number of segments), and typically offers more complete coverage within individual modalities (length of segments, normalized to 100%). Although droplet-based methods offer one to two logs higher throughput, the ResolveOME System yields data from a significantly higher proportion (>3-fold) of input cells. Data dials were generated using a combination of quantitative and qualitative internal and published data.

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 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: ResolveOME WTS RNA Performance

Characteristic	Observed Values
Genes Detected	4,546
Reportable Range	6,057
Average Concordance	0.91
Reproducibility (CV)	43.3%

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.

Products

Code	Product	Description
100500	ResolveOME™ Whole Genome and Transcriptome Amplification System	PTA-based kit for accurate and reproducible whole genome and transcriptome amplification.
100605	BaseJumper™ Bioinformatics Platform	A complete bioinformatics solution for multiomic data analysis and visualization. https://www.bioskryb.com/basejumper/

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

BioSkryb GENOMICS

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All data on file.

For Research Use Only. Not for Use in Diagnostic Procedures.