

## Whole Genome Amplification Kit Covering >95% of the Genome



### Powered by PTA

Leverages a novel patented technology, primary template-directed amplification (PTA)<sup>1</sup>, to dramatically increase genomic coverage to >95%



### Compatible with as little as 4 pg of input DNA

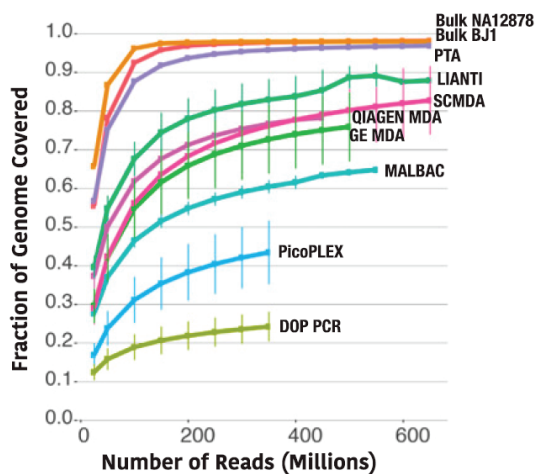
Whole genome amplification from low-input (4 pg to <10 ng) DNA samples



### Uniform and high fidelity genomic coverage

Increases coverage uniformity and reduces experimental artifacts associated with other whole genome amplification methods<sup>1,2</sup>

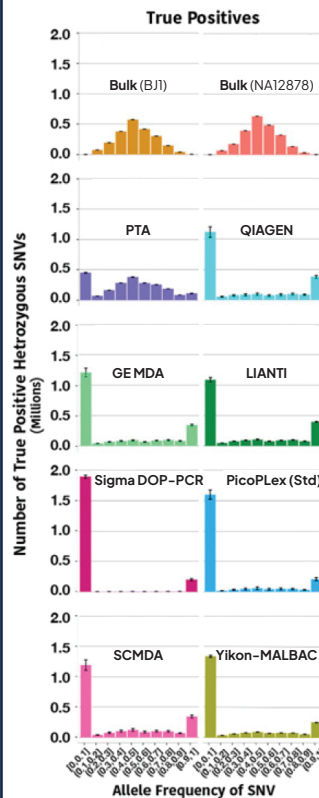
### PTA leads in genomic coverage



**Figure 1. Single-cell genome coverage breadth.**

Genome coverage comparison across different methods at increasing number of single end sequencing reads. PTA approaches the genome coverage obtained in both bulk samples at every sequencing depth. Note that 600 million 150 bp single reads represents about 30x whole genome coverage. Selected panel from Figure 2 of Gonzalez-Pena, et al. PNAS 2021; 118(24): e2024176118.

### PTA provides unparalleled allelic balance



**Figure 2. Improved PTA coverage metrics increase variant detection accuracy.**

Comparison of allele dropout and frequencies of SNVs called heterozygous in the bulk sample. PTA (purple) more evenly amplifies both alleles in the same cell, resulting in significantly diminished allelic dropout and skewing. Selected panel adapted from Figure 2 of Gonzalez-Pena, et al. PNAS 2021; 118(24): e2024176118.



References:

- Gonzalez-Pena V, et al. Proc. Natl. Acad. Sci. U.S.A. 2021; 118 (24): e2024176118; doi: 10.1073/pnas.2024176118
- Luquette L, et al. Nat Gen. 2022; 54: 1564-1571. doi: 10.1038/s41588-022-01180-2

## Workflow Options

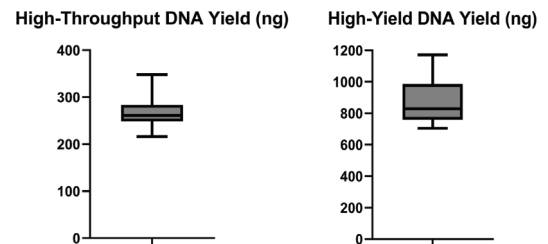
The **ResolveDNA** Whole Genome Amplification Kit is compatible with two workflows:

### High-Throughput Workflow

- Performed in a 384-well plate
- Automation compatible
- Average yield is 260 ng DNA from single human cells

### High-Yield Workflow

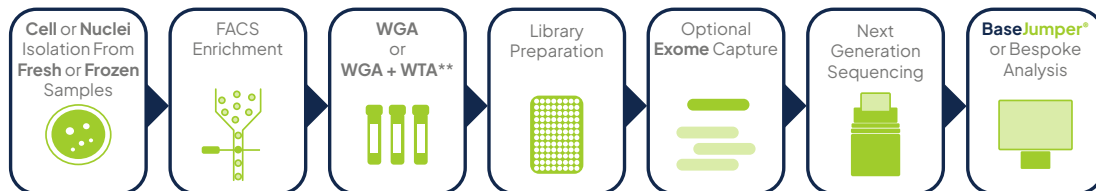
- Performed in a 96-well plate
- Compatible with manual multichannel pipetting
- Average yield is over 800 ng DNA from single human cells



**Figure 3. DNA amplification yield after ResolveDNA WGA.** DNA from single human cells was amplified using either the high-throughput (left) or high-yield (right) workflow. Average yields were 260 ng and >800 ng respectively.

## 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>ResolveOME™</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>ResolveXOME™</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

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