

## Single-cell Clarity

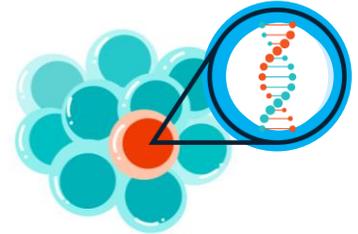
# Single-cell Whole Genome Sequencing

## Capture somatic mosaicism and unravel cell lineage

Single-cell Whole Genome Sequencing (scWGS) empowers the **identification of somatic mutations present at remarkably low mosaicism levels**, which is challenging for bulk sequencing. With its ability to capture the cellular heterogeneity within tissues, scWGS stands at the forefront of genomic research. From uncovering developmental pathways to elucidating cancer progression, scWGS offers invaluable insights into the intricacies of biology and disease.

Mirxes offers the groundbreaking scWGS service utilising Primary Template-directed Amplification (PTA), which addresses key challenges associated with whole genome amplification (WGA) and demonstrates reduced error propagation.

With expert experimental and bioinformatics support from Mirxes, researchers can readily harness scWGS to achieve extraordinary single-cell clarity.



**Exceptional WGA Performance**

PTA achieves excellent coverage, high uniformity and low error



**Sequencing Advantage**

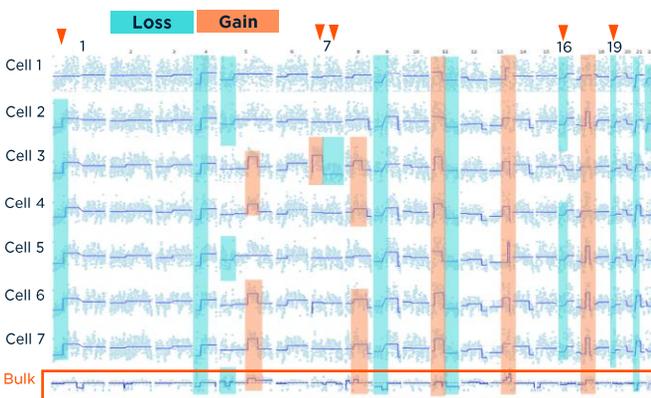
High sequencing throughput and low optical duplication rate



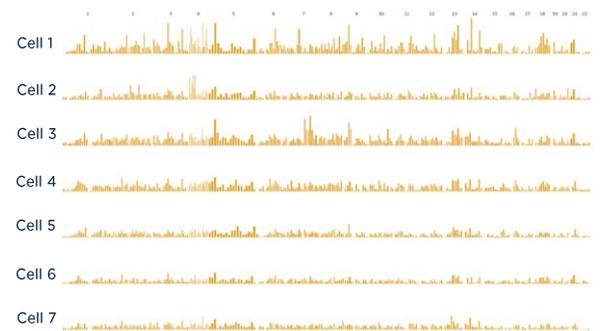
**Expert Bioinformatics Service**

Experienced team providing customised single-cell analysis

### Discovery of somatic mutations



Genomic region



Horizontal axis - 10mb bins sorted by chromosome number and position  
Vertical axis - variant count

#### Heatmap of CNV analysis (500kb bin size):

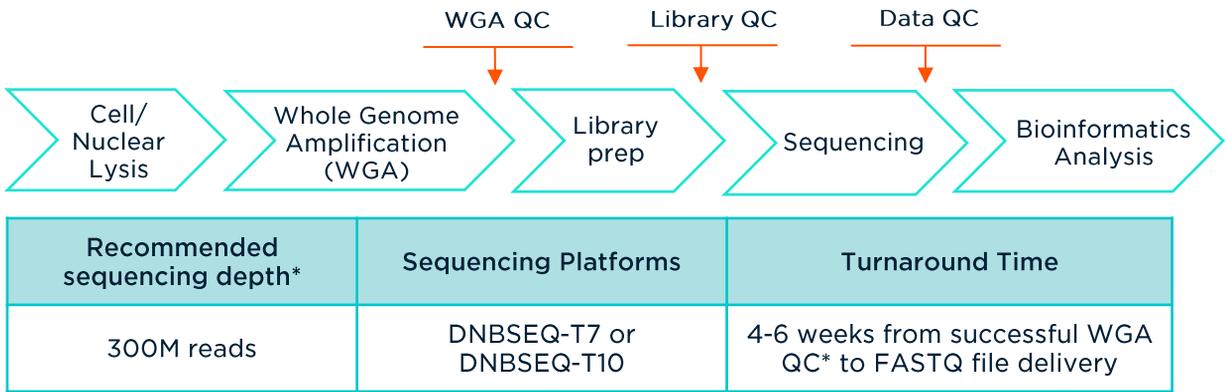
Identify somatic CNVs in single cells undetected in the bulk sample (denoted by ▼)

Detect heterogeneity between single cells

#### Somatic variant analysis (10mb bin size):

Distribution of variants (SNV and indels) across chromosomal bins

## scWGS Service Workflow



\*This serves only as a guide. Please contact us for further discussion.

## Sample Submission Guidelines

Sample Type	Sample Source	Brief Sample Preparation Guideline*
Single intact cells	Fresh tissue, Fresh frozen tissue, Cell line	<ul style="list-style-type: none"> <li>- Single cells/nuclei should be dispensed into Lobind 384-well plate</li> <li>- After cell dispensing, the plate should be spun down and stored at -80°C until use</li> <li>- Note: DAPI staining is not compatible with this assay</li> </ul>
Single nuclei		

Kindly note that this serves as a brief reference only.

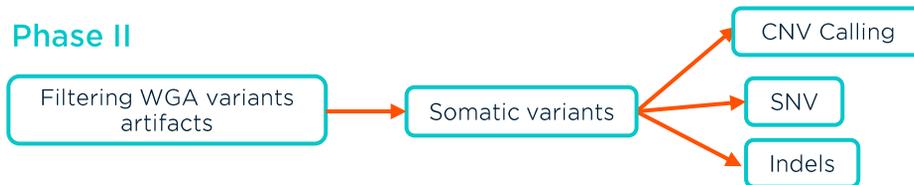
\* Please contact us for the complete sample preparation and submission instructions.

## Bioinformatics Analysis and Support

### Phase I



### Phase II



### Secondary Analysis Package

- Data Quality Control: Filtering reads with adapter or low-quality sequence data
- Alignment to reference genome using BWA
- Summary statistics

### Additional Tertiary Analysis

- Joint calling (Bulk and Single cells)
- Hard filtering of variant calls and removal of germline variants using paired normal bulk WGS data
- Filtering whole genome amplified variant artifacts
- Final variants: SNV, Indels and CNV
- Annotations and mutational signatures

## Contact Us

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