Research

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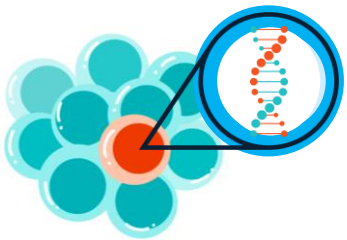
Single-cell Clarity

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

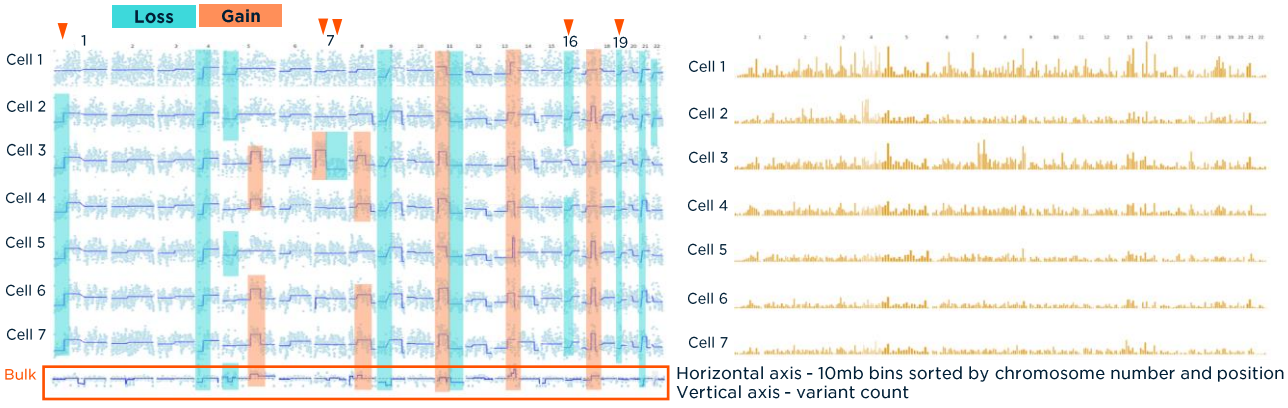
Sequencing Advantage

High sequencing throughput and low optical duplication rate

Expert Bioinformatics Service

Experienced team providing customised single-cell analysis

Discovery of somatic mutations



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

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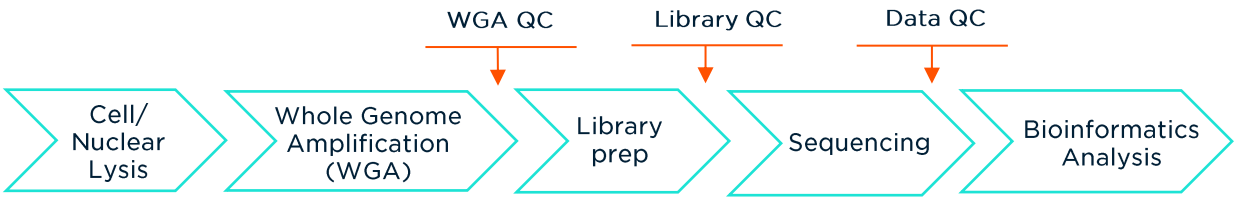
scWGS Service Workflow



Recommended sequencing depth*	Sequencing Platforms	Turnaround Time
300M reads	DNBSEQ-T7 or DNBSEQ-T10	4-6 weeks from successful WGA QC* to FASTQ file delivery

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

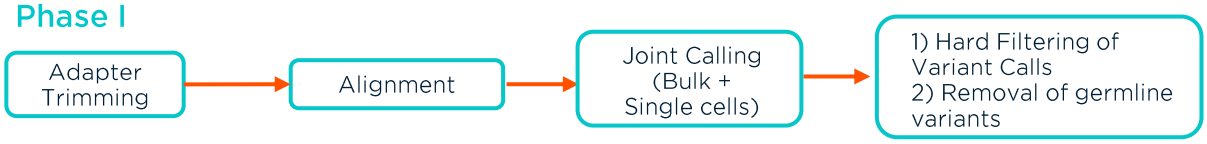
Sample Submission Guidelines

Sample Type	Sample Source	Brief Sample Preparation Guideline*
Single intact cells	Fresh tissue, Fresh frozen tissue, Cell line	- Single cells/nuclei should be dispensed into 384-well plate (Lobind and Optical) - After cell dispensing, the plate should be spun down and stored at -80°C until use - Note: DAPI staining is not compatible with this assay
Single nuclei		

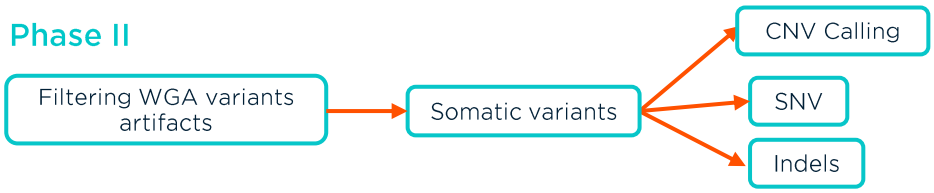
Kindly note that this serves as a brief reference only.
* Please contact us for the complete sample preparation and submission instructions.

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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scWGS Brochure - LB-1327_r01
For Research Use Only.