

Single-cell Clarity, Multi-omic Insights

scWGS+scRNAseq

Single-cell Whole Genome Sequencing and Single-cell RNA Sequencing (same cell)



Integrated Genomic and Transcriptomic Insights from the Same Cell

Experience the power of single-cell multi-omics, by performing Single-cell Whole Genome Sequencing (scWGS) and Single-cell RNA sequencing (scRNA-seq) on the same cell.

With Primary Template-directed Amplification (PTA) as the whole genome amplification (WGA) method, scWGS can be performed with reduced amplification artifacts, high genomic uniformity and low error propagation.

Mirxes offers **scWGS+scRNAseq** as an **end-to-end** service, supporting seamless integration of genomic variation data with transcriptional information to generate unparalleled insights into the drivers and consequences of cell heterogeneity.



Single-cell Multi-omics

Whole Genome and mRNA Transcriptome information obtained from single-cell input



Exceptional WGA Performance

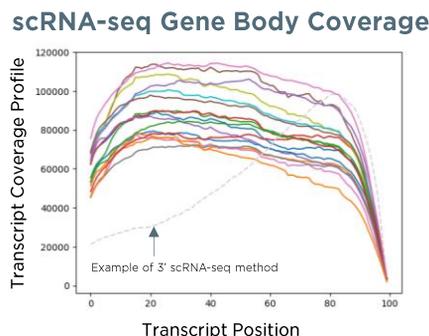
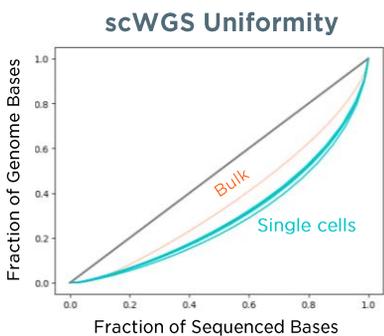
PTA achieves excellent coverage, high uniformity and low error



Expert Bioinformatics Service

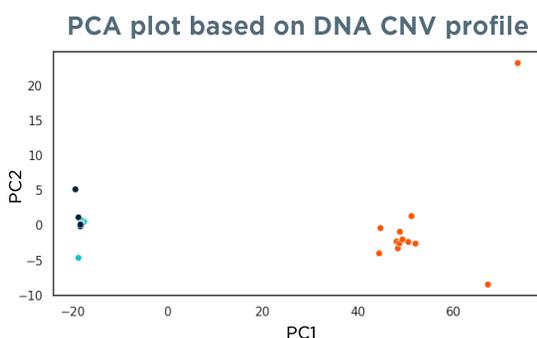
Experienced team providing customised single-cell multi-omic analysis

QC Performance of scWGS+scRNAseq



- scWGS shows remarkable **genome coverage uniformity**
- scRNA-seq shows **full gene body coverage** compared to 3' scRNA-seq methods (example labelled as -----)

Concordance between Genotype and mRNA levels in the Same Cell

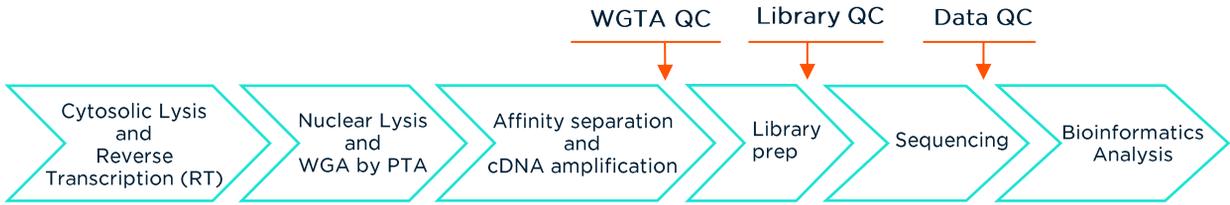


Legend:

- Cell type-I
- Cell type-II
- Cell type-III (based on gene expression)

Clear concordance is observed between the clustering of cells based on **DNA CNV profile** and the cell types identified by **gene expression**.

scWGS+scRNAseq Service Workflow



*WGTA: Whole Genome and Transcriptome Analysis

Recommended Sequencing Depth*	Sequencing Platforms	Turnaround Time
300M reads for DNA; 1M reads for RNA	DNBSEQ-T7 or DNBSEQ-T10	4-6 weeks from successful WGTA 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 (viable) cells	Fresh tissue, Cell line	<ul style="list-style-type: none"> - Single cells should be dispensed into Lobind 96-well or 384-well plate - 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

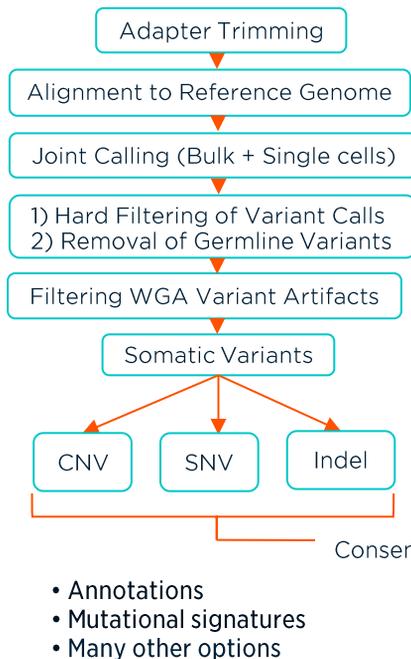
Kindly note that this serves as a brief reference only.

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

Bioinformatics Analysis and Support



scWGS Analysis



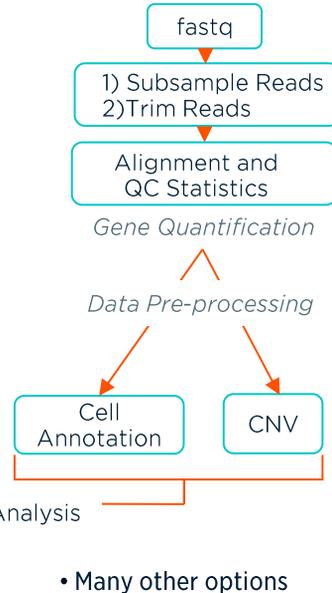
Secondary Analysis Deliverables

- QC statistics
- BAM

Additional Tertiary Analysis



scRNA-seq Analysis



Secondary Analysis Deliverables

- QC statistics
- BAM + Gene Count

Additional Tertiary Analysis

Contact Us

Email: genomics@mirxes.com

Phone: +65 6950 5864

Website: mirxes.com