mirxes | genomics

Actionable. Accessible. Affordable.

Whole Genome Sequencing

Reduce the Cost of Sequencing To Maximise your Research Output

Human whole genome sequencing (hWGS) offers the ability to interrogate the entire genomic DNA sequences, providing the most comprehensive characterization of the human genome.

Mirxes utilizes unique DNA nanoball sequencing technology coupled with PCR-free library preparation to deliver results with high accuracy and low sequencing artefacts. Variant calling based on best practices is provided complementary with every hWGS service.

> **"I am impressed with the quality of data, level of service and cost effectiveness provided by the Mirxes team. Their customer centric approach makes the entire experience very smooth and pleasant."**

Professor Liu Jianjun

Deputy Executive Director
Genome Institute of Singapore, A*STAR

High Quality Data

Q30 score of >80% for PE150 and >85% for PE100

Highly Scalable Sequencing Capacity

Up to 640 genomes in one run with PCR-free library

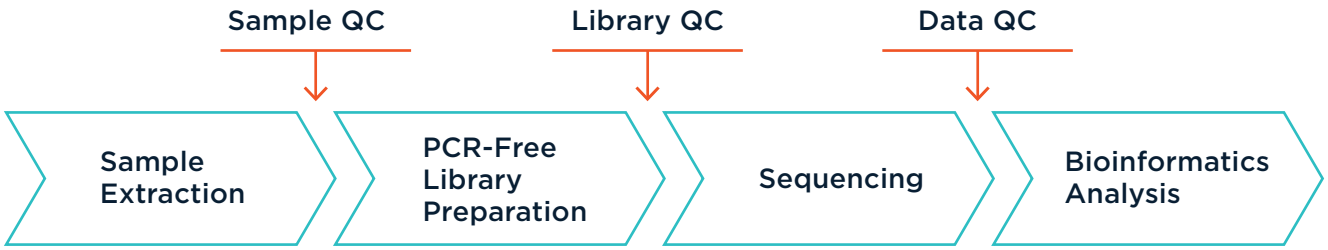
Strong Bioinformatics Support

Experienced experimental planning and customized analysis

Reliable Service and Turnaround Time

All operations based in Singapore, using certified manufacturers' workflows

hWGS Service Workflow



Suggested Sequencing Depths	Sequencing Platforms	Turnaround Time
Rare diseases 30x (90Gb)	DNBSEQ-T7 or DNBSEQ-T10	2-4 weeks for T7 3-6 weeks for T10 from successful sample QC to data delivery
Oncology Tumour: ≥50x (≥150Gb) Adjacent or blood normal: 30x (90Gb)		

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concen-tration	Purity and Quality
hWGS (PCR-free)	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 1.5 µg	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7
hWGS (PCR-based)	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 500 ng	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7
	gDNA	FFPE	≥ 800 ng	≥ 20 µl	≥ 20 ng/µl	Main band of > 1,500 bp (Q Score > 0.5 DIN ≥ 4)

Please note that these requirements serve only as a guide. Please contact us for further assessment if your samples do not meet the requested amounts.

Bioinformatics Analysis and Support

Secondary Analysis Package

- Data Quality Control: Filtering reads with adapter or low-quality sequence data
- Alignment to reference genome using BWA
- Summary statistics of sequencing depth and coverage
- Germline variant calling based on best practices
- Somatic variant calling for tumour alone and/or tumour-normal paired based on best practices

Additional Tertiary Analysis

- Full annotation services
- Joint calling for SNPs and InDels
- Tumour Purity
- Tumour Mutation Burden
- Microsatellite Instability
- **Many other options!**

Contact Us

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