mirxes | genomics

Actionable. Accessible. Affordable.

Whole Exome Sequencing

Reduce the Cost of Sequencing To Maximise your Research Output

Human whole exome sequencing (hWES) is a widely used genomic technique targeting protein-coding regions of the human genome, presenting as a cost-efficient approach for increased coverage of regions of interest.

Customise your panels for comprehensive capture of coding sequences and 100% of the mitochondrial genome for discovery, or focus on coding sequences with guaranteed >99% coverage. Complementary variant calling based on best practices is provided with every hWES 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 >85% for PE150 and PE100

Flexible Choice of Exomes

From large discovery panels to focused exome covering >99% protein coding genes

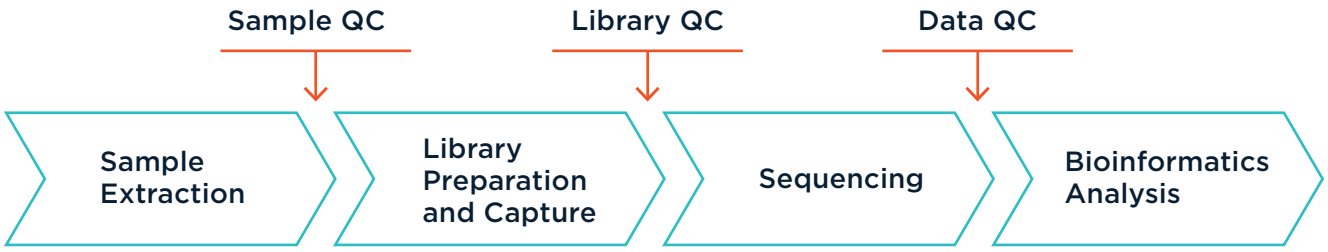
Strong Bioinformatics Support

Experienced experimental planning and customized analysis

Reliable Service and Turnaround Time

All operations based in Singapore, using certified manufacturers' workflows

hWES Service Workflow



Suggested Sequencing Depths	Sequencing Platforms	Turnaround Time
Rare diseases 100x	DNBSEQ-T7	2-4 weeks from successful sample QC to data delivery
Oncology Tumour: ≥300x		

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concen-tration	Purity and Quality
hWES	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 500 ng	≥ 20 µl	≥ 10 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7
	gDNA	FFPE	≥ 500 ng	≥ 20 µl	≥ 10 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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