mirxes | genomics

Actionable. Accessible. Affordable.

Whole Genome Sequencing

Reduce the Cost of Sequencing To Maximize 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 artifacts. 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

Guaranteed 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 preperations

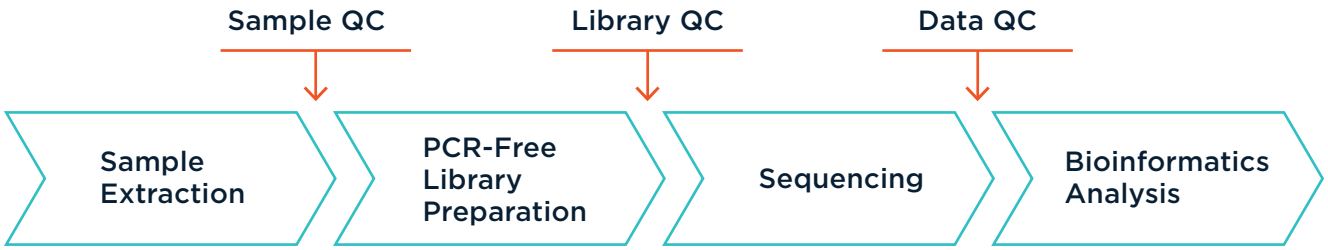
Strong Bioinformatics Support

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 Tumor: ≥50x (≥150Gb) Adjacent or blood normal: 30x (90Gb)		

Sample Type	Amount; Concentration	Minimum Volume	Purity and Quality
Genomic DNA (PCR-free)	≥ 1.5 µg; ≥ 20ng/µl	20 µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7
Genomic DNA (PCR-based)	≥ 250 ng; ≥ 20ng/µl	20 µl	
FFPE DNA	≥ 700 ng; ≥ 20ng/µl	20 µl	Main band of > 1500bp (Q > 0.5) DIN ≥ 4

Bioinformatics Analysis and Support

Standard 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 tumor alone and/or tumor-normal paired based on best practices

Additional Tertiary Analysis

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

Contact Us

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