

Actionable. Accessible. Affordable.

Whole Genome Methylation Sequencing



High Quality Data

Q30 score of >80% for PE150 and PE100



Highly Scalable Sequencing Capacity

Up to 320 methylated genomes in a single sequencing run



Strong Bioinformatics Support

Experienced experimental planning and customized analysis



Reliable Service and Turnaround Time

All operations based in Singapore, using certified manufacturers' workflows

Reduce the Cost of Sequencing To Maximise your Research Output

Human Whole Genome Methylation Sequencing (hWGMS) is widely used to investigate changes in methylation patterns associated with multiple diseases such as cancer and neurological disorders, at a single base resolution epigenome wide.

With the largest sequencers in the world, Mirxes Genomics provides high-throughput methylation analysis with large data bioinformatics support to lower the cost of sequencing for hWGMS.



“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

hWGMS Service Workflow



Suggested Sequencing Depths	Sequencing Platforms	Turnaround Time
Basic Analysis 30x	DNBSEQ-T7 or DNBSEQ-T10	2-4 weeks for T7 3-6 weeks for T10 From successful sample QC to data delivery
Deep Analysis ≥100x		

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concentration	Purity and Quality
hWGMS	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 1 µg	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7

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
- Methylation extraction report

Additional Tertiary Analysis

- Methylation density
- Distribution analysis
- Clustering analysis
- Differentially methylated regions analysis
- **Many other options!**

Contact Us

Email: genomics@mirxes.com

Phone: +65 6950 5864

Website: mirxes.com