

Actionable. Accessible. Affordable.

Whole Genome Bisulphite Sequencing



High Quality Data

Guaranteed Q30 score of >80% for PE150 and PE100



Highly Scalable Sequencing Capacity

Up to 320 bisulphite 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 Maximize your Research Output

Human whole genome bisulphite sequencing (hWGBS) 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 throughput sequencers in the world, MiRXES Genomics provides unmatched methylation analysis with bioinformatics support to lower sequencing costs for hWGBS

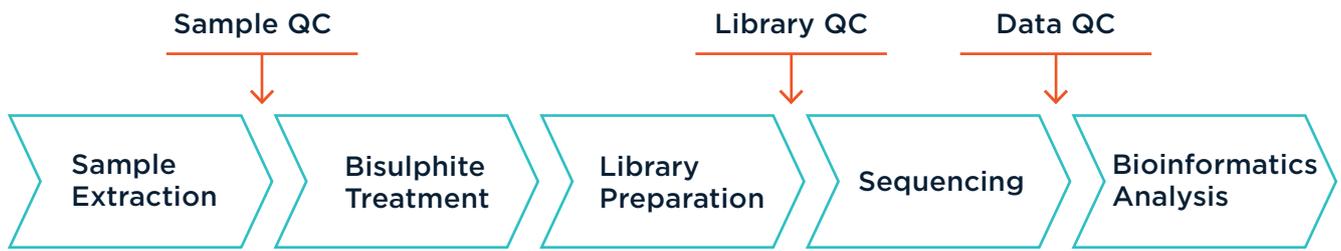


"I am impressed with the quality of data, level of service and cost effectiveness provided by the MiRXES team. Their customer centric approach makes the entire experience very smooth and pleasant."

Professor Liu Jianjun

Deputy Executive Director
Genome Institute of Singapore
A*STAR

hWGBS 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		

Sample Type	Amount; Concentration	Minimum Volume	Purity and Quality
Genomic DNA	≥ 800 ng; ≥ 20ng/μl	20 μl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7

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
- Methylation extraction report
- Methylation tracks generated for visualization in the Integrative Genomics viewer

Additional Tertiary Analysis

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

Contact Us

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