

Actionable. Accessible. Affordable.

RNA Sequencing

Reduce the Cost of Sequencing To Maximise your Research Output

RNA sequencing (RNA-Seq) is an indispensable tool for transcriptome-wide analysis of differential gene expression and structural analysis of RNAs.

Mirxes Genomics offers an efficient package for rRNA depletion with synthesis of cDNA libraries from a wide input range of total RNA. These libraries are then sequenced using DNA nanoball sequencing technology, generating high quality data for comprehensive analysis of gene expression analysis and discovery of alternative splicing events, gene fusions and other transcriptomic aberrations.



“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



More Data at a Lower Price

More analyses with higher
accuracy to advance your
research



Strong Bioinformatics Support

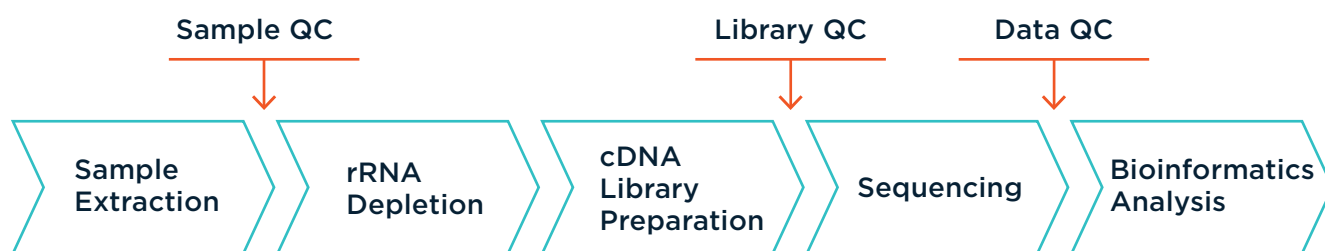
Experienced experimental
planning and customized
analysis



Reliable Service and Turnaround Time

All operations based in
Singapore, using certified
manufacturers' workflows

RNA-Seq Service Workflow



Suggested Sequencing Depths	Sequencing Platforms	Turnaround Time
Deep gene expression analysis ≥40M reads (≥12Gb)	DNBSEQ-T7	2-4 weeks from successful sample QC to data delivery
Novel transcripts, alternative splicing analysis ≥100M (≥30Gb)		

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concentration	Purity and Quality
RNA-Seq	Total RNA	Fresh frozen tissue, cell line, saliva, blood	≥ 500 ng	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 2.0 RIN ≥ 6
	Total RNA	FFPE	≥ 500 ng	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 2.0 DV200 > 50% RIN ≥ 2
RNA-Seq (Directional)	Total RNA	Fresh frozen tissue, cell line, saliva, blood	≥ 1 ug	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 2.0 RIN ≥ 6
	Total RNA	FFPE	≥ 1 ug	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 2.0 DV200 > 50% RIN ≥ 2

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

Standard Analysis Package

- Data Quality Control: Filtering reads with adapter or low-quality sequence data
- Alignment to reference genome
- Summary statistics
- Gene count matrix
- Differential gene expression analysis (DEGs)
- GO enrichment analysis of DEGs
- KEGG enrichment analysis of DEGs

Secondary Analysis Package

- Data Quality Control: Filtering reads with adapter or low-quality sequence data
- Alignment to reference genome
- Summary statistics
- Gene count matrix

Additional Tertiary Analysis

- Gene ontology enrichment
- Biomarker prediction
- Full annotations
- Pathway analysis
- **Many other options!**

Contact Us

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