mirxes | genomics

Actionable. Accessible. Affordable.

RNA Sequencing

Reduce the Cost of Sequencing To Maximize your Research Output

RNA sequencing (RNASeq) is an indispensable tool for transcriptome-wide analysis of differential gene expression and structural analysis of RNAs.
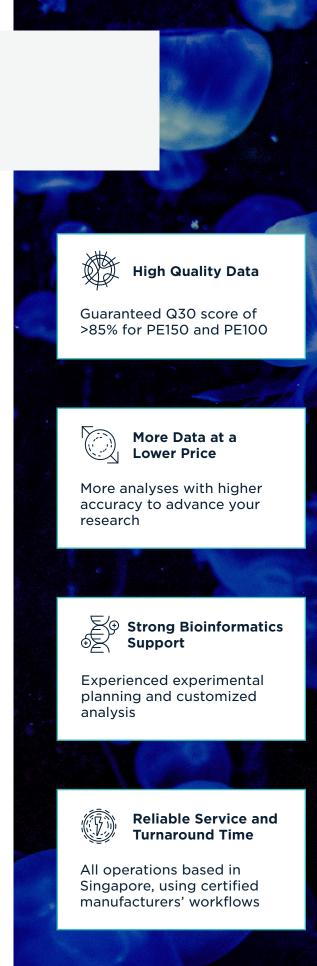
MiRXES Genomics offers an efficient package for rRNA depletion with synthesis of cDNA libraries from a wide input range of total RNA. These libraries are then sequenced using DNA nanoball sequencing technology, generating high quality data for comprehensive analysis of gene expression analysis and discovery of alternative splicing events, gene fusions and other transcriptomic aberrations.
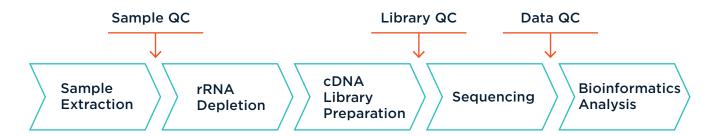
" "I am impressed with the quality of data, level of service and cost effectiveness provided by the MiRXES team. Their customer centric approach makes the entire experience very smooth and pleasant."

Professor Liu Jianjun

Deputy Executive Director
Genome Institute of Singapore
A*STAR

High Quality Data

Guaranteed 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

RNASeq Service Workflow

Sample QC → Sample Extraction → rRNA Depletion → cDNA Library Preparation ← Library QC | Sequencing ← Data QC | Bioinformatics Analysis

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)		

Sample Type	Amount; Concentration	Minimum Volume	Purity and Quality
Total RNA	≥ 200 ng; ≥ 20ng/μl	20 μl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 2.0 RIN ≥ 6
Total RNA (Directional)	≥ 400 ng; ≥ 20ng/μl	20 μl	
FFPE RNA	≥ 400 ng; ≥ 20ng/μl	20 μl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 2.0 RIN ≥ 2 , DV200 > 50%

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
- Gene counting matrix

Additional Tertiary Analysis

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

Contact Us

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