miRNAseq NGS - Differential profiling

TC-S-BT-MIR-DIFF

Applications

Method utilizes small RNA–enriched, strand-specific library preparation to selectively capture microRNAs (miRNAs) and other small regulatory RNAs for next-generation sequencing. This workflow is optimized for comparative miRNA expression analysis across defined biological conditions. Multiple biological replicates are recommended to ensure accurate statistical inference of miRNA-level expression changes.
miRNA profiling is a method of choice to analyze total miRNA expression for discovery or validation. miRNA profiling enables identification of differentially modulated miRNAs across treatments, during development or disease progression, and in case–control cohorts. The method can be applied to infer functional modulation through target RNA analysis, and is ideally used paired with mRNA or total RNA sequencing.

Pros

- Highly sensitive detection of miRNA expression changes on disease/treatments
- Accurate quantification of known miRNAs
- Ideal for biomarker discovery and validation studies

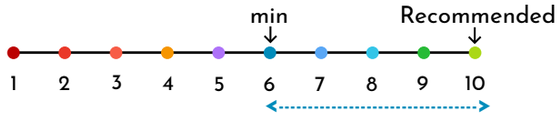
Notes

- miRNA profiling on treatment or disease
- Annotation on reference miRNA databases
- Functional insights are inferred via target prediction, ideal with oaired mRNA/total RNA-seq

Input

Total RNA / Small RNA–enriched RNA
Conc: 50 ng – 500 ng

RNA Integrity (RIN)



Sample Types

*RNA for small RNA, should not be prepared with total isolation-TROZOl/Mirvana

Platform

Illumina platforms | 50 PE/50 SE/75 SE/150 PE

Process Map

Standard Deliverables

Download Sample Report

- Raw Data QC and Raw Data counts across all samples.
- Normalized read count for each samples along with Sample Grouping/Clus ering and QC related plots : PCA plot, Heatmap based on top 500 variant miRNAs. dendrogram and Sample - Sample correlation
- Known and Novel miRNAs identified by miRDeep2
- Differential expression reports for each comparison along with corresponding visualization – Volcano plots.
- Validated targets of Known miRNA identified by miRTarbase
- Functional over - representation (enrichment) analysis per comparison, along with corresponding visualization – Dot plots for top 20 enriched GO: BP, MF, CC and Reactome Pathways.
- Network for miRNA and mRNA (Validated targets)

References

- Sharma E et al. Front Mol Neurosci. 2025; PMID:40636521.
- Nilawar S, Chatterjee K. Biomacromolecules. 2022; doi:10.1021/acs.biomac.1c01235.
- Lalitha AV et al. Indian J Crit Care Med. 2024; PMID:39360202.