

Applications

Method utilizes small RNA-enriched library preparation to capture and sequence microRNAs (miRNAs) and other small regulatory RNAs from non-human samples. This discovery-driven approach enables identification, quantification, and comparative profiling of known and novel miRNAs across experimental conditions. miRNA discovery pipelines are applied to identify known and novel miRNAs, often from new isolates, strains, or treatment conditions. The workflow involves mapping to miRBase and computational models to annotate and discover novel small RNAs.

Pros

- Enables discovery of species-specific miRNAs
- High sensitivity for low-abundance small RNAs
- Provides insights into post-transcriptional gene regulation
- Ideal for comparative and evolutionary studies

Notes

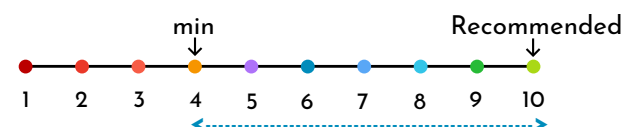
- Requires specialized small RNA library prep, totalRNA does not represent miRNA
- Functional interpretation relies on predicted miRNA targets Validation (qPCR/functional assays) recommended for novel miRNAs

Input



Total RNA / Small RNA-enriched RNA
Conc: 100 ng - 1 µg

RNA Integrity (RIN)



Sample Types



Tissues



Plant tissues



Cell
cultures

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

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

Process Map



Sample
Extraction



Sample
QC



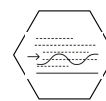
Library
Prep/QC



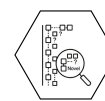
NGS Data
Acquisition



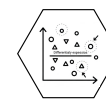
Primary
Data QC



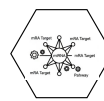
miRNA
Prediction



Known & Novel
miRNA Discovery



DEG



Target Prediction &
Functional Biology
*When Reference is
available

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/Clustering 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.