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RNA-seq (Eukaryotic Poly-A | With Reference Genome) BT-EPAM-MDL

Applications

Method utilizes directional RNA libraries to process poly(A)+-enriched RNA into NGS libraries. Suitable for profiling changes in gene expression for biological discovery. The project can involve understanding differences between control vs treatment, or profiling changes across time-course or developmental series. Projects often use multiple biological replicates, analyzed to provide precision in inference of gene expression changes.

Pros

- High sensitivity for mRNA
- Accurate quantification of >98% of mRNA
- Cost-effective
- Ideal for differential expression studies of mRNA to infer gene regulation

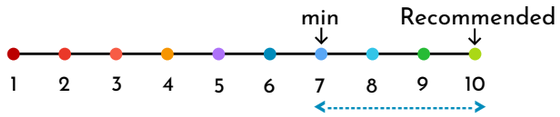
Notes

- Misses a small fraction of lncRNA, histone RNA, and non-polyadenylated RNAs
- Not suitable for degraded RNA due to 3' bias
- Reference genome/transcriptome required for read mapping

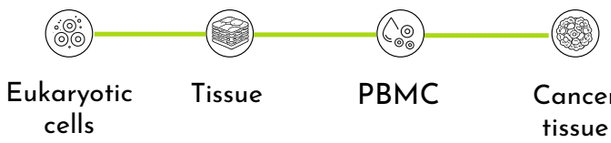
Input

Total-RNA Conc: 100ng - 500ng

RNA Integrity (RIN)



Sample Types



Platform Illumina platforms | 150 x 2

Process Map

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Mapped data(.BAM) files sample and related QC reports
- Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts
- Sample clustering reports
- Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTOME pathways)
- Supporting visualization each step (PCA/UMAP plots, Heatmaps, Volcano plots, Functional enrichment gradient plots, KEGG pathview maps*)
- *KEGG Pathview maps for pathways selected according to the interest of the study

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.

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RNA-seq (Eukaryotic Poly-A | Non-Model Organism - De Novo) BT-EPAN-NMD

Applications

Strain variations or lack of an available nearest reference require creation of a de novo transcriptome assembly. De novo transcriptome assembly improves read mapping and annotation, especially for plant and fungal samples where reference variation limits suitability. Suitable for projects where an isolate is characterized for changes across treatments or developmental stages.

Pros

- Suitable for samples requiring reference genome creation
- High sensitivity for polyadenylated RNA
- Accurate expression quantification after assembly
- Suitable for evolutionary and ecological studies

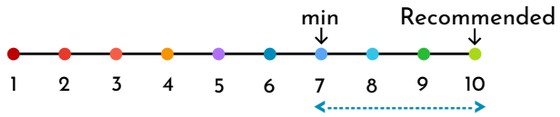
Notes

- Higher computational complexity than reference-based RNA-seq
- Not suitable for highly degraded RNA

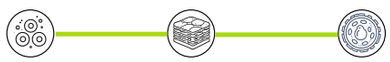
Input

Total-RNA Conc: 100ng - 500ng

RNA Integrity (RIN)



Sample Types



Eukaryotic cells | Plant Tissue | Fungal Cells

Platform

Illumina platforms | 150 x 2

Process Map

Sample Extraction > Sample QC > Library Prep/QC > NGS Data Acquisition > Primary Data QC > De novo Assembly > Annotation > Reference Mapping > DEG

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Mapped data(.BAM) files sample and related QC reports
- Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts
- Sample clustering reports
- Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTOME pathways)
- Supporting visualization each step (PCA/UMAP plots, Heatmaps, Volcano plots, Functional enrichment gradient plots, KEGG pathview maps*)
- *KEGG Pathview maps for pathways selected according to the interest of the study

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.

RNA-seq (Total RNA | Human / Mouse /Rat) BT-TRNA-HMR

Applications

Suitable for comprehensive profiling of total RNA when requirements span non-polyadenylated RNAs such as histone RNA, tRNA, and other RNA species. The method uses rRNA depletion, followed by generation of directional RNA libraries for NGS profiling. Total RNA profiling is suitable for partially degraded RNA where RIN values do not meet criteria for poly(A)-based RNA profiling.

Pros

- Profiles total RNA, including tRNA, lncRNA, etc.
- Suitable for partially degraded RNA
- Provides broad transcriptome coverage
- Enables isoform-level quantification using a reference genome

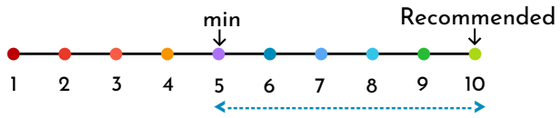
Notes

- Increased data complexity and higher sequencing depth required
- rRNA depletion efficiency impacts data quality

Input

Total-RNA Conc: 100ng - 1 µg

RNA Integrity (RIN)



Sample Types

Tissue PBMC Cancer tissue Serum

Platform Illumina platforms | 150 x 2

Process Map

RNA Extraction → RNA QC → rRNA Depletion → Library WC → Reference alignment → NGS Data Acquisition → Gene, Transcript, lncRNA, Other RNA → DEG → Biological Insights

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Raw Data 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 2000 variant genes, dendrogram and SampleSample correlation plot.
- Differential expression reports for each comparison along with corresponding visualization – Volcano plots.
- Functional overrepresentation (enrichment) analysis per comparison, along with corresponding visualization – Gradient Bar plots for top 20 enriched GO: BP, MF, CC and Reactome Pathways.
- Raw Count and Normalized count of lncRNA for each samples along with Sample Grouping/Clus ering and QC related plots : PCA plot, Heatmap on top 2000 variant genes, dendrogram and SampleSample correlation plot.
- Differential expression reports of known lncRNA for each comparison along with corresponding visualization – Volcano plots..
- Functional over - representation (enrichment) analysis for direct lncRNAs, cis -targets mRNA and mRNA interacting with lncRNA and their supporting plots and tables. 8) Identification of co - expressed mRNA and lncRNA followed by visualization Interaction network for lncRNA and mRNA

- Identification of co - expressed mRNA and lncRNA followed by visualization Interaction network for lncRNA and mRNA.
- Detection of Known and Novel circNAs with the supporting plots
- circRNA expression analysis per comparison. Volcano plot and Heatmap of Significant Circular RNAs
- Summary statistics of Circular RNA and their supporting plots
- Analysis - ASE (Alternative Splicing Event) per and Identification of Novel splice variants
- Overall Volcano plot for Differentially Expressed ASE and Individual Volcano plots for each events
- Scatter plots for showing splicing levels (percent - spliced -in, PSI) between two conditions.
- Unsupervised Heatmap for Top 20 Differentially Expressed ASE
- Gene ontology - Biological process, Molecular Function and Cellular components (overrepresentation analysis using enriched genes of top 10 differential alternative splicing events and their supporting plot.

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.

RNA-seq (bacterial | With Reference Genome) BT-BRNA-REF

Applications

Bacterial RNA-seq is used to profile gene expression changes upon treatment. RNA-seq enables sensitive detection of differential gene expression. Reference-based mapping can be variable and may require de novo assembly to discover transcripts, for example those acquired by horizontal gene transfer or encoded on plasmids/episomes. The process involves microbial rRNA depletion, followed by preparation of directional RNA libraries for NGS.

Pros

- Comprehensive coverage of coding bacterial RNAs
- High-accuracy reference-based alignment
- Suitable for operon- and pathway-level analysis
- Enables condition-specific expression profiling

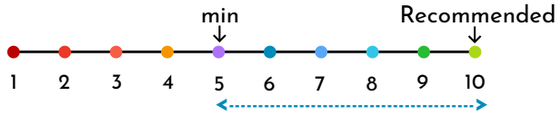
Notes

- Requires high-quality RNA for effective rRNA depletion
- Reference genome quality impacts read mapping
- Not suitable for mixed/highly complex samples

Input

Total-RNA Conc: 100ng - 1µg

RNA Integrity (RIN)



Sample Types

Frozen RNA later Inactivated

Platform Illumina platforms | 150 x 2

Process Map

Sample Extraction > Sample QC > Ribodepletion > Library prep > NGS Data Acquisition > Primary Data QC > Reference mapping and annotation > DEG > Biological insights

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Raw & QC Trimmed data (.fastq files) and QC reports per sample Mapped data (.BAM) files sample and related QC reports
- Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts Sample clustering reports Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTO ME pathways)
- Supporting visualization each step (PCA/UMAP/tS NE plots, Heatmaps, Volcano plots, Functional enrichment gradient plots, KEGG pathview map

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.

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RNA-seq (Blood | 3' End Tagging) BT-BACT-BLD

Applications

Cost-effective, high-throughput RNA sequencing for gene expression profiling from blood samples using 3′ end-tag RNA-seq, optimized for large-scale studies requiring robust expression quantification from whole blood. The method involves globin mRNA removal, followed by directional RNA library preparation. Blood RNA sequencing is suitable for whole-blood transcriptome profiling, particularly in biomarker discovery studies, where globin removal improves gene profiling and enhances coverage of low-abundance blood transcripts.

Pros

- Cost-effective for high sample numbers
- Optimized sequencing requirements to focus on genes of interest
- Robust gene-level quantification
- High reproducibility across samples

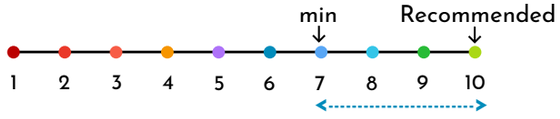
Notes

- Limited information on splice variants and isoforms
- Reference genome–dependent

Input

Total-RNA/Blood-derived RNA
Conc: 10ng - 100ng

RNA Integrity (RIN)



Sample Types

Whole Blood

Stabalized Blood
PAXgene/Tempus

Platform Illumina platforms | 150 x 2

Process Map

Whole Blood RNA Extraction | RNA QC | Globin Depletion | Library QC | NGS Data Acquisition | Primary Data QC | Reference mapping | DEG | Biological insights

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Raw & QC Trimmed data (.fastq files) and QC reports per sample
- Mapped data(.BAM) files sample and related QC reports
- Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts
- Sample clustering reports
- Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTOME pathways)
- Supporting visualization each step (PCA/UMAP plots, Heatmaps, Volcano plots, Functional enrichment gradient plots, KEGG pathview maps*)
- *KEGG Pathview maps for pathways selected according to the interest of the study

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.

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RNA-seq (FFPE | Human | With Reference Genome) BT-FFPE-HUM

Applications

Optimized RNA sequencing for formalin-fixed, paraffin-embedded (FFPE) human samples, enabling reliable gene expression profiling from degraded RNA. Designed for translational, clinical, and retrospective studies using well-annotated human reference genomes.

Pros

- Compatible with degraded and fragmented RNA
- Enables analysis of valuable archived samples
- Robust gene-level expression quantification
- Reference-based alignment ensures accuracy
- Ideal for clinical and translational research

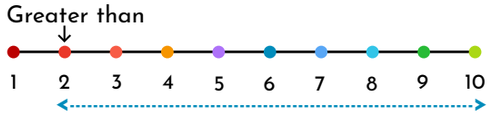
Notes

- Limited isoform and splice-variant detection
- Lower complexity compared to fresh-frozen
- Quality dependent on fixation and storage conditions
- Reference-genome dependent

Input

FFPE derived Total-RNA: %DV 200

RNA Integrity (RIN)



Sample Types

FFPE Tissue sections | Archived tumor samples | Clinical biopsy samples

Platform

Illumina platforms | 150 x 2

Process Map

FFPE Curls → RNA Extraction → RNA QC → Ribodepletion + Directional NGS → NGS Data Acquisition → Data QC → Reference alignment → DEG → Biological Insights

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Raw & QC Trimmed data (.fastq files) and QC reports per sample
- Mapped data(.BAM) files sample and related QC reports
- Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts
- Sample clustering reports
- Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTOME pathways)
- Supporting visualization each step (PCA/UMAP plots, Heatmaps, Volcano plots, Functional enrichment gradient plots, KEGG pathview maps*)
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- Nilawar S, Chatterjee K. Biomacromolecules. 2022; doi:10.1021/acs.biomac.1c01235.
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FFPE Cancer Transcriptome (Discovery RNA-seq | Human) BT-FFPE-DIS

Applications

Discovery transcriptome is designed to provide multiple layers of information from a tumor sample. The method is optimized to work with fragmented RNA while maintaining broad transcript coverage. The discovery transcriptome is generated by multiplexing multiple libraries to address FFPE-associated biases. The computational methods enable detection of gene fusions, alternative splice forms, estimation of tumor signatures, tumor immune cell composition, and neoantigens.

Pros

- Discovery research from archived FFPE samples
- Broad transcriptome coverage
- Optimized for fragmented RNA
- Reference-based analysis for high confident results
- Ideal for in detail tumor profiling

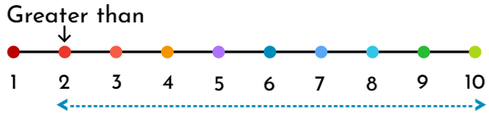
Notes

- RNA fragmentation may impact low-abundance transcripts
- FFPE sample quality leads to variations in discovery
- Reference-genome dependent

Input

FFPE derived Total-RNA: %DV 200

RNA Integrity (RIN)

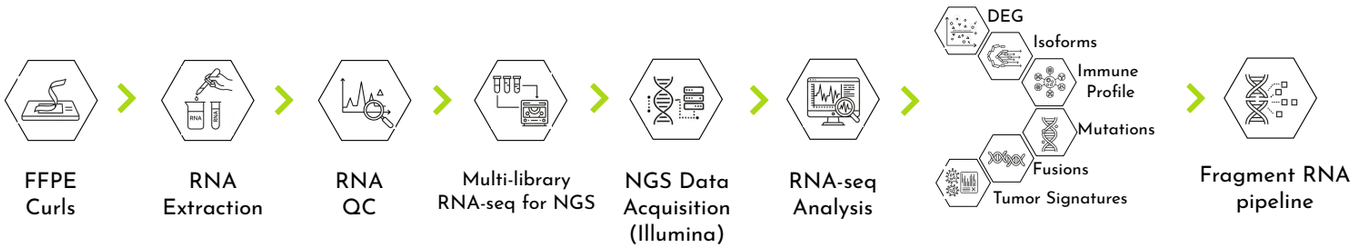


Sample Types

FFPE Tissue sections | Archived tumor samples | Clinical biopsy samples

Platform Illumina platforms | 150 x 2

Process Map



Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Raw & QC Trimmed data (.fastq files) and QC reports per sample
- Mapped data(.BAM) files sample and related QC reports
- Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts
- Sample clustering reports
- Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTOME pathways)
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- Nilawar S, Chatterjee K. Biomacromolecules. 2022; doi:10.1021/acs.biomac.1c01235.
- Lalitha AV et al. Indian J Crit Care Med. 2024; PMID:39360202.

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RNA-seq (Plant / Microbial | Host-pathogen Co-expression) BT-HPCE-PLT

Applications

The method utilizes multistage profiling of RNA, in eukaryotes with plant-fungal interaction to analyze the directional poly A enriched library for host and pathogen gene expression alteration, upon infection/treatment as single or muti-time point studies. When the pathogen is bacterial Total RNA seq with dual ribosomal RNA depletion is applied, prior to directional library preparation..

Pros

- Simultaneous host-pathogen transcript profiling
- Dynamic interaction and response signatures
- Cross species regulatory pathway discovery
- Efficient sample and sequencing utilization
- Ideal for discovery and hypothesis-driven studies

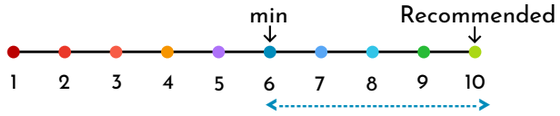
Notes

- Requires careful library design and sequencing depth
- Host RNA often dominates total reads
- Requires accurate reference genomes
- Complex data analysis and interpretation

Input

Total-RNA Conc: 200ng - 1µg

RNA Integrity (RIN)



Sample Types

Infected Plant tissues (leaf, root, stem) | Plant-bacteria interaction samples | Plant-fungal interaction samples | Mixed host-pathogen RNA preparations

Platform Illumina platforms | 150 x 2

Process Map (Fungal-Host)

Total RNA Extraction → RNA QC → Poly A Enrichment → Library Prep & QC → NGS Data Acquisition → Primary Data QC → Host Reference + Pathogen Reference → De Novo Annotation → Refmapping → DEG → Biological Insights

Process Map (Bacterial-Host)

Total RNA Extraction → RNA QC → Ribodepletion → Library Prep & QC → NGS Data Acquisition → Reference Alignment → De Novo Annotation → DEG → Biological Insights

Standard Deliverables

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Sequencing (Reference based*) – only protein coding genes - Raw & QC Trimmed data (.fastq files) and QC reports per sample
- Extraction of data for host and pathogen Mapped data (.BAM) files sample and related QC reports, host and pathogen
- Analysis performed separately for Host and pathogen : Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts Sample clustering reports
- Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTO ME pathways) Interaction between the pathogen and host transcriptome using WGCNA networks Protein - interaction network analysis
- Supporting visualization each step (PCA/UMAP plots, Heatmaps, Volcano plots, Functional enrichment gradient plots, KEGG pathview maps* and many more..!)
- *KEGG Pathview maps for pathways selected according to the interest of the study *Reference genome/transc riptome must be known for the organism,

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.

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RNA-seq (Plant / Microbial | De Novo Transcriptome) BT-DNVO-PLT

Applications

Plant and fungal isolates show significant variation across ecotypes and strains. To address this, we provide an option to generate a de novo transcriptome assembly, which is annotated and used for differential gene expression analysis. The process uses poly(A)+ RNA or total RNA, prepared as directional RNA libraries, to generate a de novo assembly. This approach supports both transcript discovery and gene expression profiling.

Pros

- No reference genome required
- Enables discovery of novel genes and transcripts
- Broad transcriptome coverage
- Suitable for emerging and understudied species
- Flexible for diverse plant and microbial systems

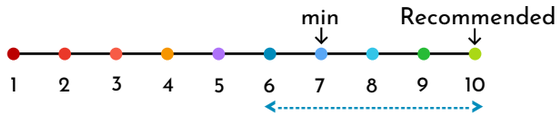
Notes

- Assembly quality depends on RNA quality and sequencing depth
- Higher computational complexity than reference-based RNA-seq
- Isoform resolution may vary across organisms

Input

Total-RNA Conc: 200ng - 1µg

RNA Integrity (RIN)



Sample Types

Plant tissues (leaf, root, stem) | Fungal Samples | Bacterial Cultures | Algal Samples

Platform Illumina platforms | 150 x 2

Process Map (Fungal-Host)

RNA Extraction → RNA QC → Library Prep & QC → NGS Data Acquisition → Primary Data QC → De Novo Assembly & Annotation → DEG → Biological Insights

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Sequencing (Reference based*) – only protein coding genes - Raw & QC Trimmed data (.fastq files) and QC reports per sample
- Extraction of data for host and pathogen Mapped data (.BAM) files sample and related QC reports, host and pathogen
- Analysis performed separately for Host and pathogen : Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts Sample clustering reports
- Differential gene expression report
- Functional enrichment reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTO ME pathways) Interaction between the pathogen and host transcriptome using WGCNA networks Protein - interaction network analysis
- Supporting visualization each step (PCA/UMAP plots, Heatmaps, Volcano plots, Functional enrichment gradient plots, KEGG pathview maps* and many more..!)
- *KEGG Pathview maps for pathways selected according to the interest of the study *Reference genome/transc riptome must be known for the organism,

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.

LongRNAseq (Discovery) BT-LRNA-DIS

Applications

Long RNA-seq uses cDNA converted from poly(A)-enriched RNA, sequenced using long-read sequencing. The use of long reads improves the ability to resolve structural variants (alternative isoforms, splice variants), long indels, and polyploidy-induced artifacts that are often missed in short-read assemblies. This method can be used to develop reference transcriptomes or for discovery studies.

Pros

- Discovery of splice forms and isoform fusions
- Captures novel transcripts and isoforms beyond annotated genes
- Enables variant discovery and detection of alternative splicing and structure variation
- Suitable for polyploid genomes

Notes

- Reads long cDNA; discovery depends on sequencing depth (million reads)
- Enriched via poly(A) capture
- Suitable for transcript discovery, not ideal for DEG analysis due to limited depth
- Does not detect RNA base modifications

Input

Total-RNA Conc: 200 ng – 1 µg

RNA Integrity (RIN)

Sample Types

Platform ONT cDNA | 0.5 - 3 million+ Reads

Process Map

Standard Deliverables

Download Sample Report

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- Sample QC, Library QC, Method Summary
- Mapped data(.BAM) files sample and related QC reports
- Gene expression matrix (.csv/xlsx format) : Raw counts, Normalized counts
- Sample clustering reports: Transcript clustering, annotation, isoform, SNV/SNP
- Differential gene expression report
- Functional annotation reports (Gene ontology – Biological process, Cellular Component, Molecular Function & KEGG/REACTOME pathways)
- Supporting visualization: functional enrichment gradient plots, KEGG pathview maps*)
- *KEGG Pathview maps for pathways selected according to the interest of the study

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.

miRNAseq NGS – Discovery (Non-Human) BT-MIRD-NHU

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

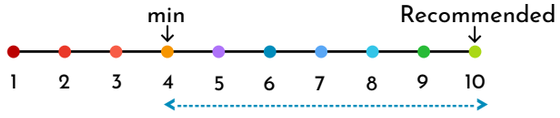
Notes

- Requires specialized small RNA library prep, totalRNA does not represent miRNA
- Functional interpretation relies on predicted miRNA targetsValidation (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 Refernce is available

Standard Deliverables

[Download Sample Report]

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- 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.
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miRNAseq NGS - Differential profiling BT-DIFF-DIR

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

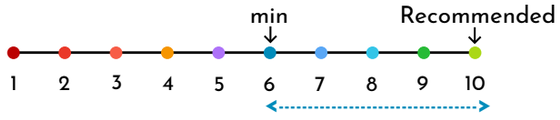
Notes

- 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

- Sample QC, Library QC, Summary of Methods
- Data QC / Sequence Data Pre-processing Summary
- 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
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miRNA–mRNA Integrated Analysis (Human / Mouse) BT-MIRM-INT

Applications

Method integrates small RNA sequencing (miRNA-seq) and whole-transcriptome RNA sequencing (mRNA-seq) to comprehensively investigate post-transcriptional gene regulation. By jointly analyzing miRNA expression and corresponding mRNA targets, this approach enables identification of regulatory miRNA–mRNA interaction networks driving biological phenotypes. Multiple biological replicates are recommended to improve confidence in integrated regulatory inference.

The method uses total RNA extracted with compatible protocols such as TRIzol to generate parallel miRNA/small RNA libraries and total RNA or poly(A) RNA libraries. The co-expression and differential regulation of miRNAs and mRNAs in treated samples or case–control groups are analyzed as a network to unravel underlying biological mechanisms.

Pros

- Enables insight into miRNA gene regulation
- Integrates transcriptional and post-transcriptional layers
- Improves confidence in functional miRNA target identification

Notes

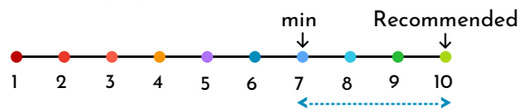
- Requires matched miRNA-seq and mRNA-seq samples
- Integrated analysis based on curated miRNA target databases
- Increased sequencing and analysis depth

Input

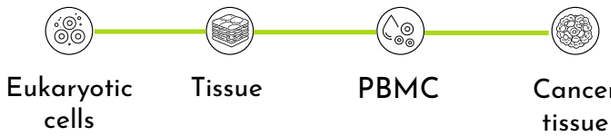
Total RNA / Small RNA–enriched RNA

miRNA-seq: 50 ng – 500 ng
mRNA-seq: 100 ng – 500 ng

RNA Integrity (RIN)

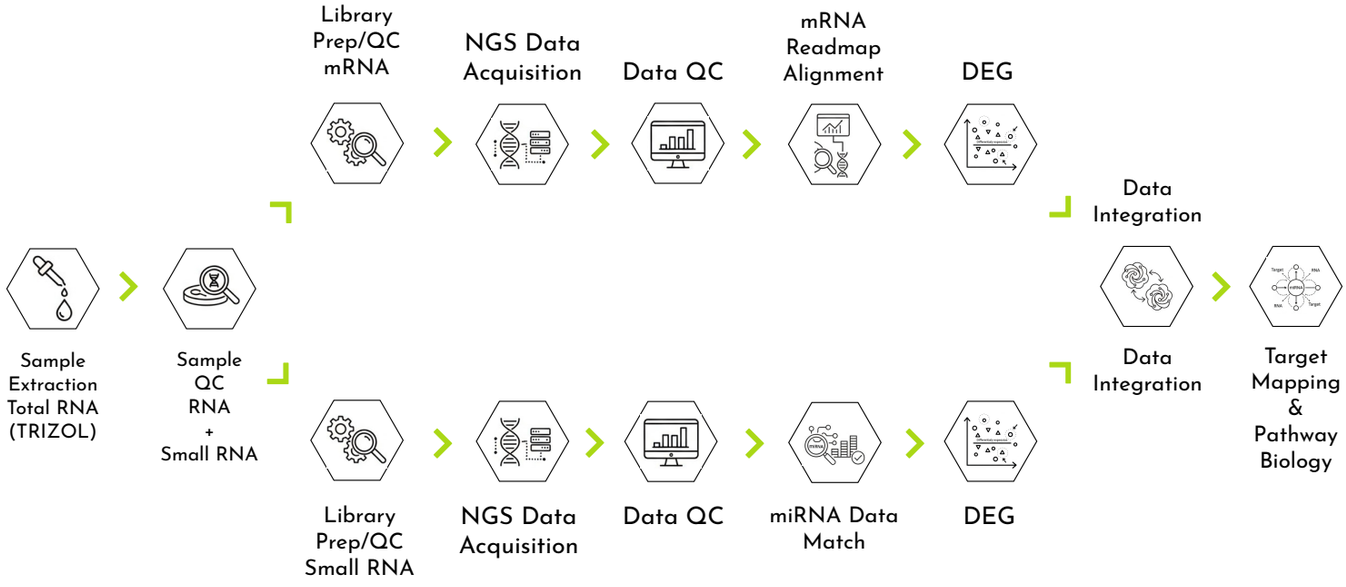


Sample Types



Platform Illumina platforms | 50 × 1 or 75 × 1
10M miRNA | 30-35M Total RNA

Process Map



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