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

Applications

Method utilizes directional RNA libraries to process poly A+ enriched RNA into NGS libraries. Suitable for profiling changes in gene expression for discovering biology. The project can involve understanding differences in 'control' vs 'treatment, profiling changes in time or development series. Projects often use multiple biologival replicates analyzed to provide precision in inference of changes in gene expression profiling.

Pros

- High sensitivity for mRNA
- Accurate quantification > 98% of mRNA
- Cost-effective
- Ideal for differential expression studies of mRNA for infering gene regultion

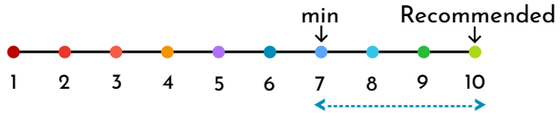
Notes

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

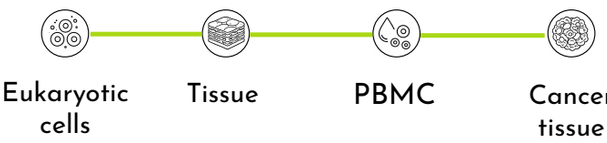
Input

Total-RNA Conc: 100ng - 500ng

RNA Integrity (RIN)



Sample Types



Platform

Illumina platforms | 150 x 2

Process Map

Standard Deliverables

Download Sample Report

- 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.

Pricing

Per sample	Per project
28500₹	120000₹

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RNA-seq (Eukaryotic Poly-A | Non-Model Organism - De Novo/Reference-Guided)

Applications

Strain variations or lack of available nearest reference requires creation of a de-nove transcript assembly. De novo transcriptome improves annotation and mapping of reads, especially for plant/fungal samples where nearest reference has variations limiting suitability of available reference. Suitable for projects where isolate is charecterized for changes in treatment or developmental stage.

Pros

- Suitable for samples with need to create refernce genome
- High sensitivity for poly-adenylated RNA
- Accurate expression quantification after assembly
- Suitable for evolutionary and ecological studies

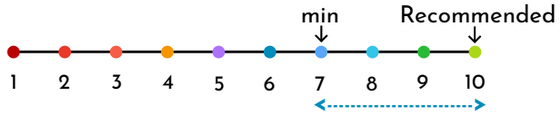
Notes

- Higher computational complexitythen 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 acquistition → Primary Data QC → De-novo Assembly → Annotation → Refmapping → DEG

Standard Deliverables

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- Raw & QC Trimmed data (.fastq files) and QC reports per sample
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RNA-seq (Total RNA | Human / Mouse /Rat)

Applications

Suitable for comprehensive profiling of total RNA, when requirement span non-poly adenylated RNA such as histone RNA, tRNA and other forms of RNA. The method uses ribodepletion, followed by generation of directional RNA libraries for NGS profiling.Total RNA profiling is suitable for partially degraded RNA where RIN does not meet criteria for poly A based RNA profiling.

Pros

- Profiles Total RNA including tRNA, lncRNA etc.
- Suitable for partially degraded RNA
- Broad transcriptome coverage
- Quantification of transcript isoform using reference genome

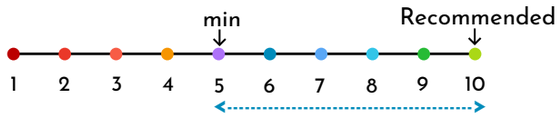
Notes

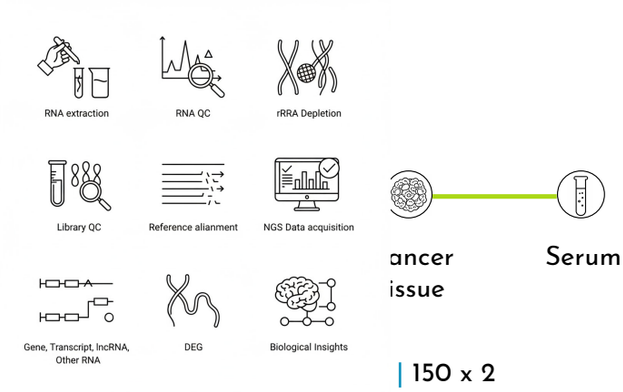
- Increased data complexity and need for sequencing depth
- rRNA depletion efficiency impacts data quality

Input

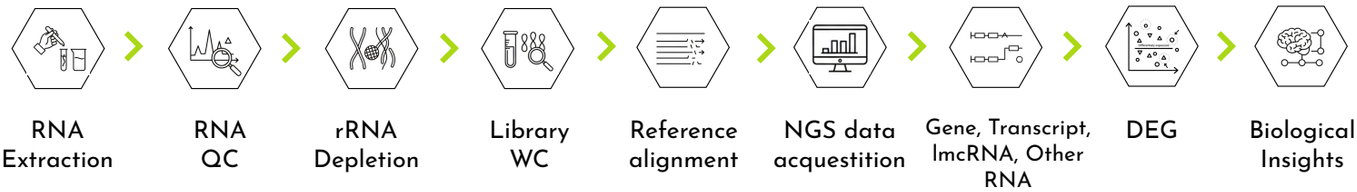
Total-RNA Conc: 100ng - 1 µg

RNA Integrity (RIN)





Process Map



Standard Deliverables

Download Sample Report

- 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

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RNA-seq (bacterial | With Reference Genome)

Applications

bacterial RNA-seq is used to profile gene expression changes upon treatments. RNA-seq allows sensitive profiling of gene expression changes. *Reference based mapping can be variable and may require de novo assembly to discover transcripts for example acquired by horizondal transfer or plasmid/episomal encoded genes. *he process involves microbial ribosomal RNA depletion followed by preparation of directional RNA libraries for NGS.

Pros

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

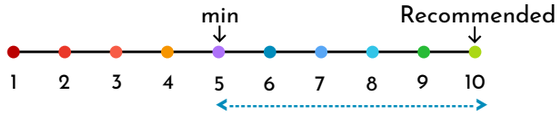
Notes

- Requires high-quality RNA for rRNA depletion
- Reference genome quality impacts mapping
- Not suitable for mixed samples

Input

Total-RNA Conc: 100ng - 1 µg

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 acquistition → Primary Data QC → Reference mapping and annotation → DEG → Biological insights

Standard Deliverables

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- Raw & QC Trimmed data (.fastq files) and QC reports per sample Mapped data (.BAM) files sample and related QC reports
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