

## RNA-seq (Total RNA | Human / Mouse /Rat)

TC-S-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.

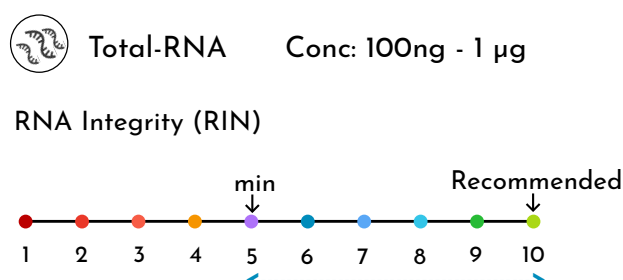
#### Pros

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

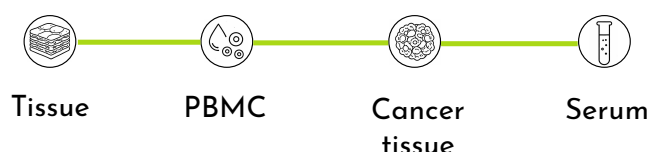
#### Notes

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

### Input

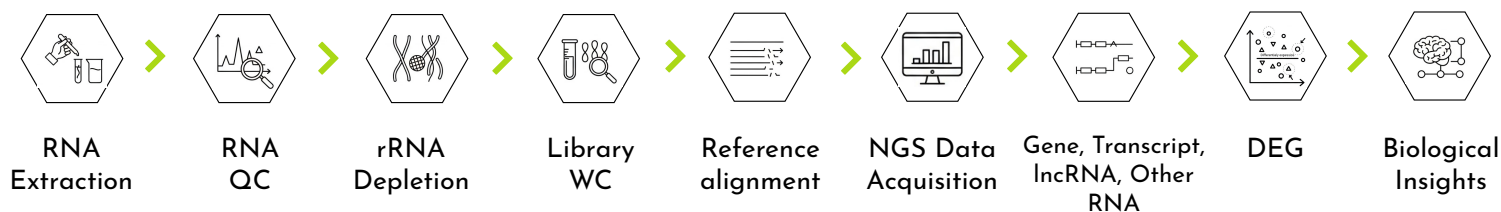


### Sample Types



Platform Illumina platforms | 150 x 2

### Process Map



### Standard Deliverables

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- Raw Data 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 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/Clustering 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.