

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

TC-S-BT-EPA-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.

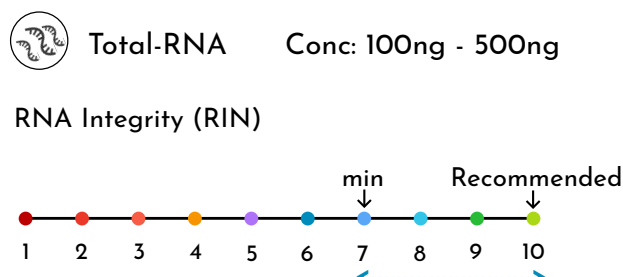
Pros

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

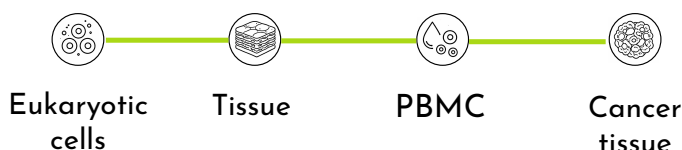
Notes

- 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

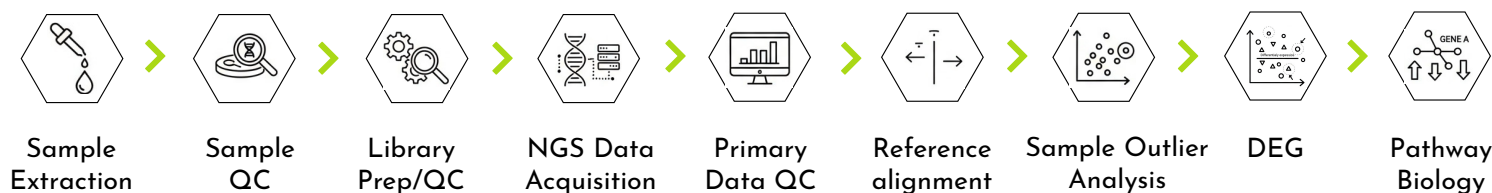


Sample Types



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 pathway 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.