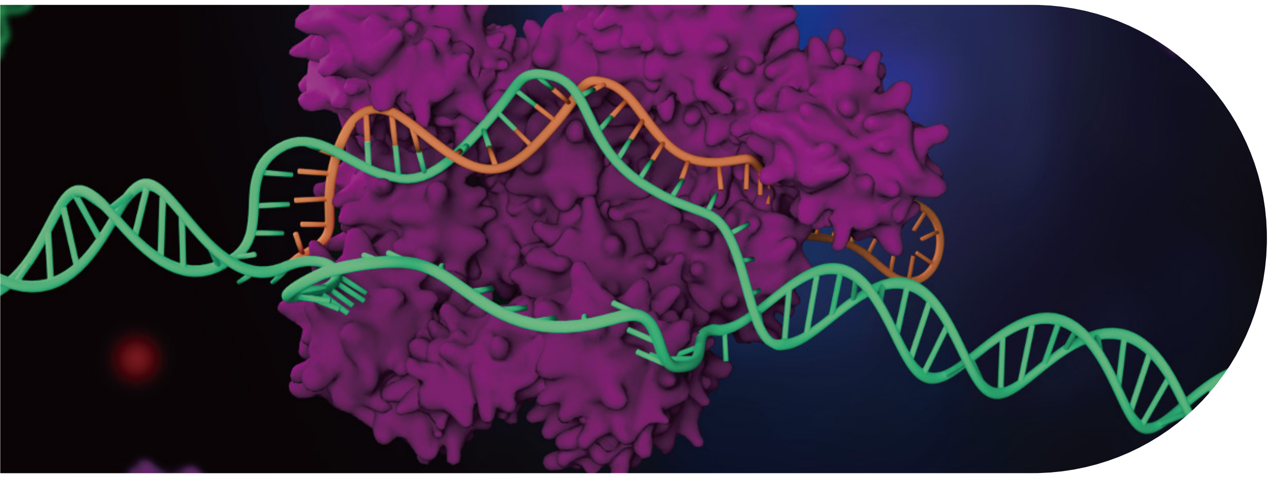
Novogene

mRNA Sequencing

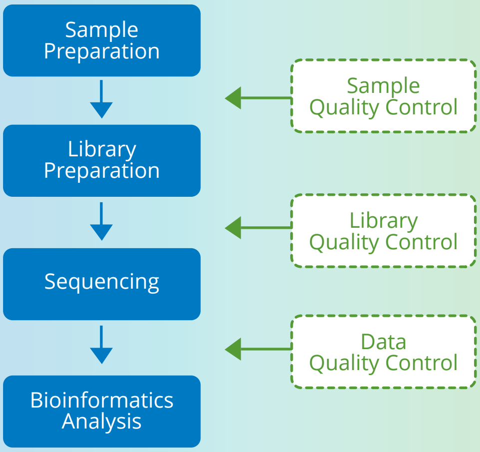


The transcriptome represents the complete set of RNA molecules, including messenger RNAs, that are transcribed from the genome of an organism at a specific point in time. mRNA-seq provides valuable insights into gene expression levels, alternative splicing, isoform diversity, and other aspects of RNA biology. It provides a comprehensive view of the transcriptome and helps uncover the complex regulatory mechanisms underlying gene expression in various biological contexts.

Our Key Features & Advantages

- **Diverse library preparation options**
- **Extensive experience managing various species**
- **Free bioinformatics analysis on our NovoMagic cloud platform**
- **Real-time project management on our Customer Service System**

Project Workflow



Sample Requirements

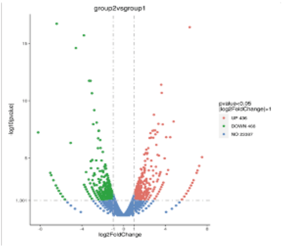
Library Type	Sample Type	Amount	Volume	Concentration	RIN	Purity
Eukaryotic non-directional mRNA Library (poly A enrichment)	Total RNA	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	≥ 4.0, with flat baseline	OD260/280≥2.0; OD260/230≥2.0; No Degradation, No Contamination
Eukaryotic directional mRNA Library (poly A enrichment)	Total RNA	≥ 400 ng	≥ 20 μL	≥ 20 ng/μL	≥5.8, with flat baseline	
Prokaryotic directional RNA library (rRNA depletion)	Total RNA	≥ 500 ng	≥ 20 μL	≥ 25 ng/μL	≥ 6.0, with flat baseline	

Sample requirement of FFPE RNA, Blood RNA (Globin removal), and low input mRNA, please contact marketing_amea@novogeneait.sg.

Analysis Content

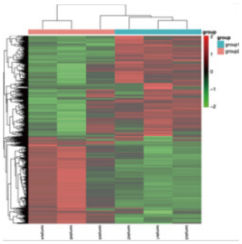
Eukaryotic RNA-seq with reference genome	Eukaryotic RNA-seq without reference genome (*de novo*)
Quantification Analysis (1-6) **Standard Analysis (1-11)** 1. Data quality control 2. Mapping reads to reference genome 3. Gene expression quantification 4. Differential gene expression profiling 5. Functional enrichment analysis: GO/KEGG/GSEA DO/Reactome/DisGeNET (human/mouse only) 6. Protein-Protein Interaction (PPI) analysis	**Standard Analysis** 1. Data quality control 2. De novo transcriptome assembly 3. Gene Functional Annotation Using Seven Databases(NR, NT, KOG, KO, Swiss-Prot, GO and PFAM) 4. CDS Prediction 5. SNP/INDELs calling 6. SSR Analysis 7. Gene Expression Analysis 8. Correlation analysis (for biological replicates only) 9. Differential Expression Analysis (two or more groups of samples) 10. Enrichment Analysis of differentially expressed genes (GO/KEGG) 11. Protein Protein Interaction Analysis
7. Novel transcripts identification 8. SNP & InDel analysis 9. Alternative splicing (AS) analysis 10. Fusion gene analysis 11. Oncogene Functional Annotation (human/mouse only) 12. Fusion Gene Analysis (for tumor and cancer cell line)	

Demo Analysis Results

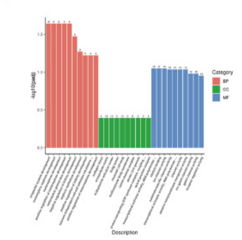


Volcano plot of differential expression genes

Visual identification of genes with large fold changes and statistical significance



Heatmap of differential expression genes



GO enrichment analysis histogram

Different colors represent different functional categories

Novogene AMEA **(Asia Pacific, Middle-East & Africa)**

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