



Eukaryotic mRNA Sequencing

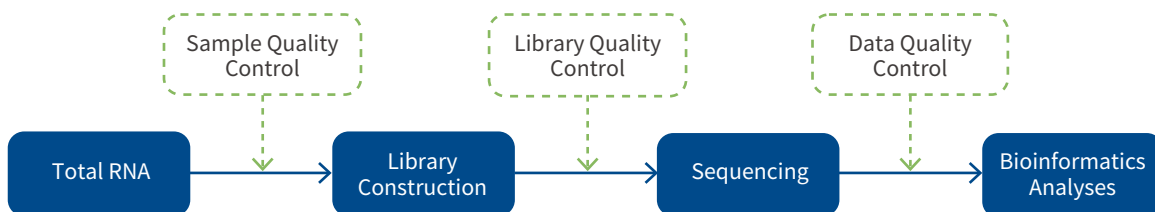


The use of next-generation sequencing (NGS) technology for mRNA-Seq allows researchers to analyze the continuous change of the cellular transcriptome. At Novogene, we use the state-of-the-art Illumina platform for all mRNA-Seq projects. We offer advanced, affordable, and comprehensive solutions for research relating to gene profiling and functions, structural analyses, and more. Our highly experienced bioinformaticians use widely accepted mainstream software and a mature in-house pipeline. Our standard or customized data analysis packages come with publication-ready results to meet virtually any project request.

Novogene Advantages

- More than 200,000 samples successfully sequenced at an industry-leading turnaround time
- Extraordinary NGS intelligent delivery system applied to provide more efficient and reliable services
- Exceptional data quality guarantee (Q30 \geq 80%, exceeding Illumina's benchmarks)
- Free in-house bioinformatics software to visualize data flexibly

Project Workflow



Service Highlights



Sequencing Strategy

NovaSeq 6000 platform, paired-end 150 bp, 250-300 bp insert cDNA library, 6 Gb raw data/sample (recommended)



Sample Requirement

Total RNA as low as 400ng, For a low-input library, please contact us for details



Turnaround Time

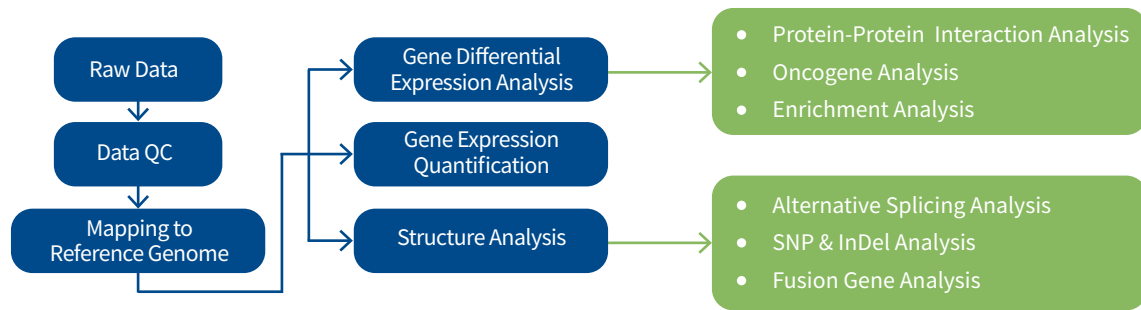
As fast as 10 business days after sample quality verification



Bioinformatics Analysis

Disease-oriented analysis content (fusion gene, oncogene analysis and more) specially catered for human and mouse mRNA sequencing projects

Bioinformatics Analysis Pipeline



Standard analysis process for species of human and mouse.
Customized analysis is also available. Please contact us for details.

Novogene Powered Publications

Year	Journal	Title
2019	<i>Cell Host & Microbe</i>	Drosophila histone demethylase KDM5 regulates social behavior through immune control and gut microbiota maintenance
2019	<i>Nature communications</i>	Hematopoietic PBX-interacting protein mediates cartilage degeneration during the pathogenesis of osteoarthritis
2019	<i>Nature Communications</i>	Therapeutic role of miR-19a/19b in cardiac regeneration and protection from myocardial infarction
2019	<i>Science Advances</i>	The prostate cancer risk variant rs55958994 regulates multiple gene expression through extreme long-range chromatin interaction to control tumor progression
2019	<i>New Phytologist</i>	Diacylglycerol kinase and associated lipid mediators modulate rice root architecture
2019	<i>Environmental Science & Technology</i>	Study of the persistence of the phytotoxicity induced by graphene oxide quantum dots and of the specific molecular mechanisms by integrating omics and regular analyses
2018	<i>Nature communications</i>	Armadillo repeat containing 12 promotes neuroblastoma progression through interaction with retinoblastoma binding protein 4
2018	<i>cell</i>	Targeting epigenetic crosstalk as a therapeutic strategy for EZH2-aberrant solid tumors
2018	<i>Cancer research</i>	E6 protein expressed by high-risk HPV activates super-enhancers of the <i>EGFR</i> and <i>c-MET</i> oncogenes by destabilizing the histone demethylase KDM5C

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Novogene Corporation Inc.

8801 Folsom Blvd #290, Sacramento, CA 95826

916-252-0068-383 inquiry_us@novogene.com en.novogene.com

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