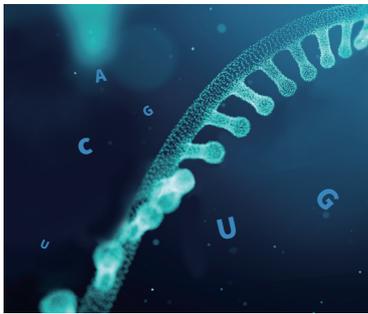


Eukaryotic mRNA Sequencing



mRNA-Seq uses next-generation sequencing (NGS) to reveal the presence and quantity of messenger RNA in a biological sample at a given moment, analyzing the continuously changing cellular transcriptome. Novogene's mRNA-Seq, based on state-of-the-art Illumina NovaSeq platforms with paired-end 150 bp sequencing strategy, offers complete solutions for gene expression quantification and differential gene expression analysis among groups of samples, as well as for identification of novel transcripts, alternative splicing, and gene fusion events, etc. Our experienced bioinformaticians work closely with customers to provide standard and customized data analysis and publication ready results for species with and without a reference genome.



Extensive experience with over 30,000 samples

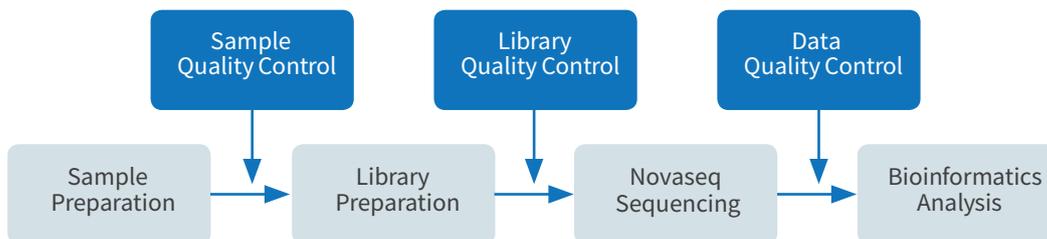


Data quality exceeds Illumina's official guarantee



In house pipeline to meet different analysis requirement

Project workflow



Sequencing parameter

Platform	Illumina NovaSeq 6000	
Read length	Pair-end 150	
Recommended Sequencing Depth	Recommended: 15G for animals and plants 3G for fungi	Minimum: 6G for animals and plants 2G for fungi
Data quality	Guaranteed Q30 \geq 80%, exceeding Illumina's official benchmark of \geq 75%	
Turnaround time	Express service: 15 working days from sample delivery to data delivery (<24 samples)	

Samples requirement

Library Type	Sample Type	Amount Required	Volume	Concentration	RNA Integrity Number (Agilent 2100)	Purity (NanoDrop™)
Eukaryotic RNA-Seq (cDNA library)	Total RNA	\geq 0.4 μ g	\geq 20 μ L	\geq 20 ng/ μ L	\geq 6.8 (Animal), smooth base line \geq 6.3 (Plant and Fungus), smooth base line	OD260/280 \geq 2.0, OD260/230 \geq 2.0, No degradation, No contamination

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