



A transcriptome is a set of all the transcripts in one cell or one population of cells at certain status. Transcriptome analysis helps to identify genes that are differentially expressed in distinct cell populations. Researchers can also gain a deeper insight into gene boundary identification, variable cleavage, and transcript variation.

RNA sequencing via Illumina platforms, based on SBS (sequencing by synthesis) chemistry, offers a wide range of benefits such as high throughput and high accuracy out of low sample requirements. It is a powerful tool for studying RNA transcriptional activity.

Our Key Features & Advantages



Reliable & Faster Turnaround Time

The strategic locations of our labs across Asia and our extensive NGS system can provide faster turnaround time.



Extensive Experience

We have extensive records of sequencing projects that have been published in journals.



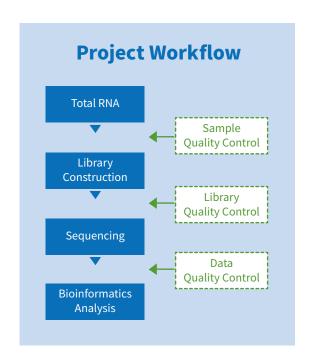
Multiple Choices

We offer multiple library choices and a comprehensive data analysis pipelines for your research needs.



Unsurpassed Data Quality

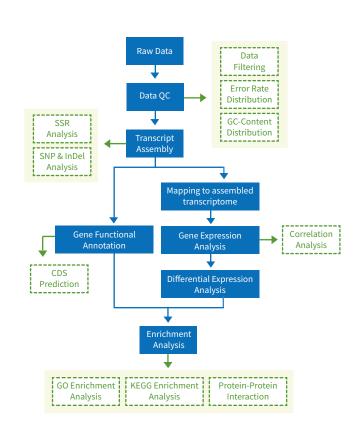
We guarantee that \geq 80% of bases have a sequencing quality score \geq Q30, exceeding Illumina's official guarantee of \geq 75%.



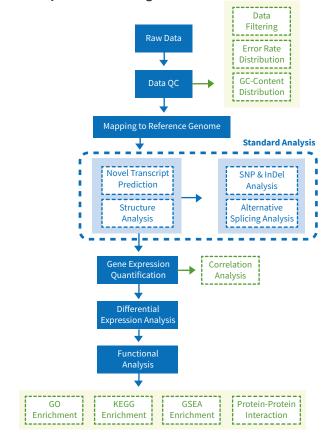


Standard Analysis Pipeline

denovo RNA-seq



RNA-seq with reference genome



Sample Requirements

Library Type	Sample Type	Amount	RIN	Volume	Concentration
Eukaryotic mRNA Library (poly A enrichment)	Total RNA sample (Eukaryotic)	≥ 0.4 µg	≥ 6.3 (animals) ≥ 5.8 (plants & fungi)	≥ 20 µL	≥ 20 ng/µL
Eukaryotic Directional mRNA Library (poly A enrichnment)	Total RNA sample (Eukaryotic)	≥ 0.8 µg	≥ 6.3 (animals) ≥ 5.8 (plants & fungi)	≥ 20 µL	≥ 20 ng/µL

Publications

Listed below are some recent publications that were supported by Novogene solutions. We have successfully sequenced more than 150 species, including rice, Arabidopsis, tomato, peanut, cotton, cucumber, human, rat, etc. Researchers have published many high-tier articles in journals such as Cell Stem Cell, Genome Research, Nature Communications, and more with our RNA sequencing services.

Journal	IF	Title
Cell Host & Microbe	17.87	Drosophila Histone Demethylase KDM5 Regulates Social Behavior through Immune Control and Gut (2019)
Cell	31.40	Targeting Epigenetic Crosstalk as a Therapeutic Strategy for EZH2-Aberrant Solid Tumors (2018)

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