

Metatranscriptome Sequencing Solutions

A large, glowing blue DNA double helix structure that curves across the top half of the page, set against a dark blue background with bokeh light effects.

Metatranscriptome refers to the total content of gene transcripts (RNA copies of the genes) in a nature community (i.e., soil, water, sea, feces, and gut). It is considered a unique entity at a specific moment of sampling, and it changes with time and environmental variation.

Metatranscriptome sequencing can now be applied to obtain the whole expression profile in a community and follow the dynamics of gene expression patterns over time or environmental parameters. It can help improve our understanding of the structure, function, and adaptive mechanisms in complex communities.

It identifies gene expression of microbes, both eukaryotes, and prokaryotes, within natural environments. Specifically, this service allows you to obtain whole gene expression profiling of complex microbial communities, taxonomic analysis of species, functional enrichment analysis of differently expressed genes, and more.

Our Key Features & Advantages



Extensive Experience

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



Comprehensive Analysis

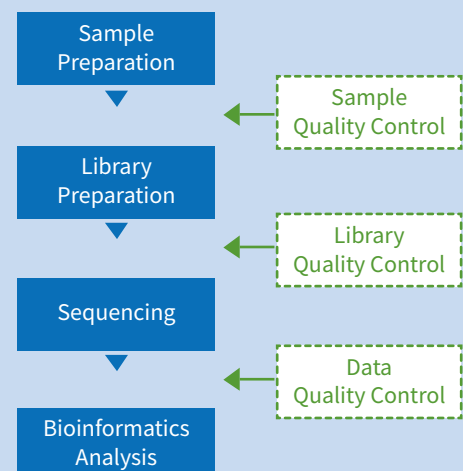
Utilizing mainstream software and mature in-house pipeline to meet multiple bioinformatic requests.



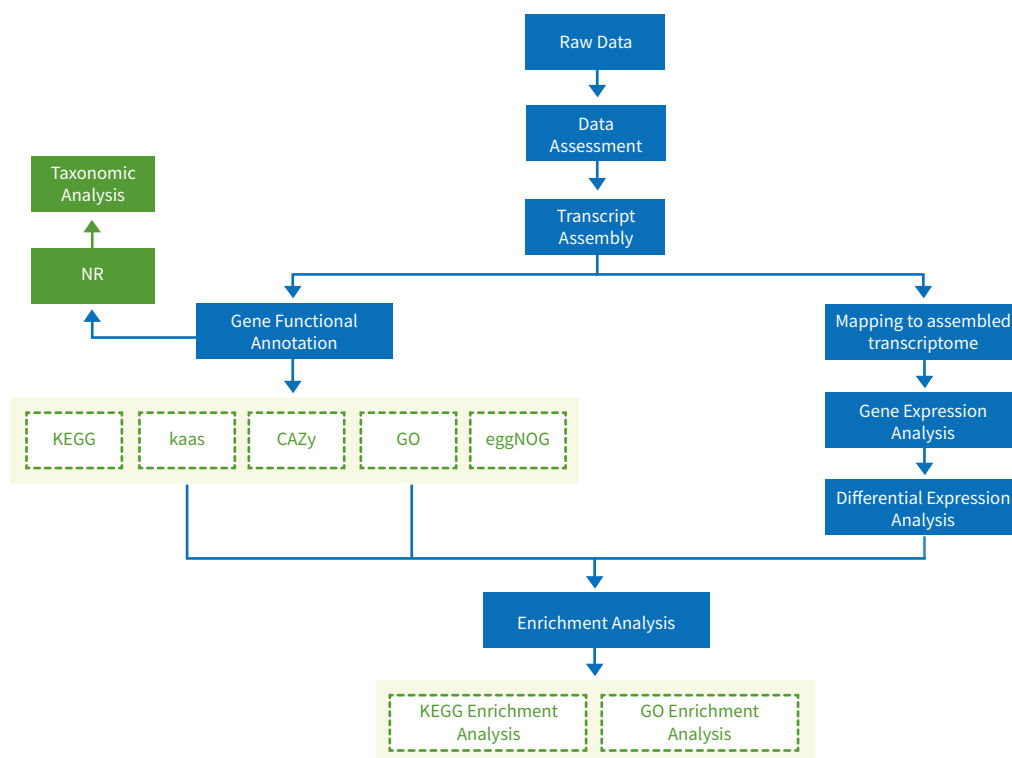
Unsurpassed Data Quality

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

Project Workflow



Standard Analysis Pipeline



Sample Requirements

Library Type	Sample Type	Amount	RNA Integrity Number (Agilent 2100)	Purity NanoDrop
Meta-transcriptome Library	Total RNA	≥ 2 µg	≥ 6.5, smooth baseline	OD260/280 = 1.8-2.2; OD260/230 ≥ 1.8;

Publications

Listed below are some publications that were supported by Novogene solutions.

Journal	IF	Title
PNAs	9.35	Cryptophyte farming by symbiotic ciliate host detected in situ (2016.07)
Journal of Clinical Investigation	12.8	HECTD3 mediates TRAF3 polyubiquitination and type I interferon induction during bacterial infection[J]. Journal of Clinical Investigation (2018)

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NovogeneAIT Genomics Singapore Pte. Ltd.
(Joint Venture & Sequencing Centre)

Novogene International Pte. Ltd.
25 Pandan Crescent #05-15 TIC Tech Centre, Singapore 128477

T: +65-8823-3182
e: marketing_amea@novogeneait.sg

en.novogene.com