



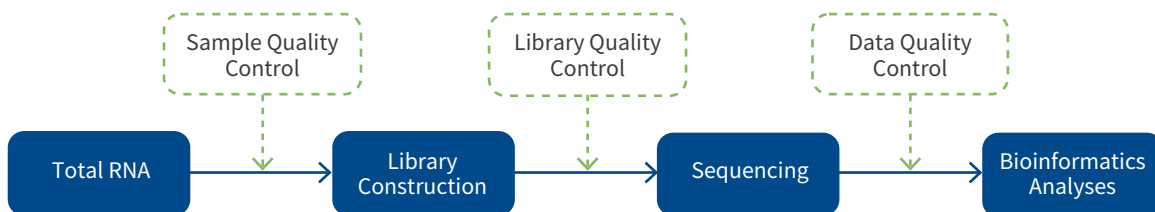
Novogene's Metatranscriptome Sequencing

Metatranscriptome refers to the total content of gene transcripts in a natural community (i.e. soil, water, sea, feces, and gut), considered as a unique entity, at a specific moment of sampling. Metatranscriptome sequencing identifies gene expression of microbes within natural environments. Metatranscriptomics 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. At Novogene, we tailor our metatranscriptomics service based on your research goals to help answer questions that enable you to achieve research objectives.

Novogene Advantages

- More than 200,000 samples successfully sequenced at an industry-leading turnaround time
- An innovative NGS intelligent delivery system applied to save time and increase reproducibility/reliability of results
- 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, 12 Gb raw data/sample (recommended)



Sample Requirement

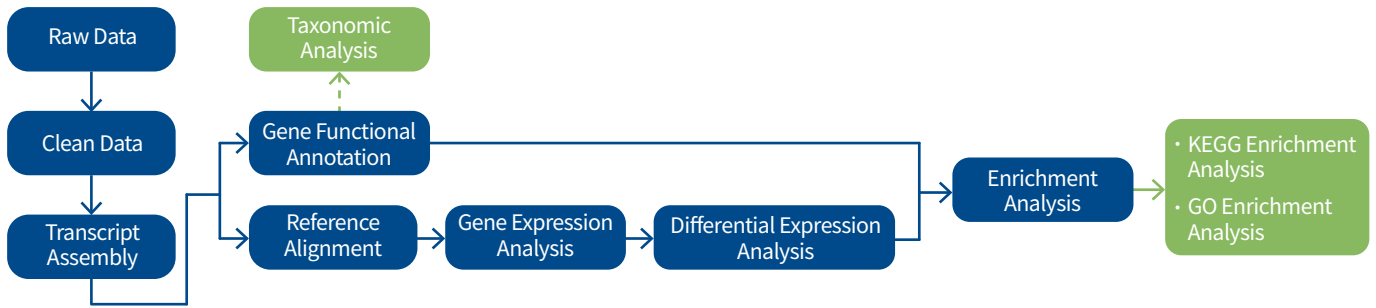
Total RNA 2.5 μ g



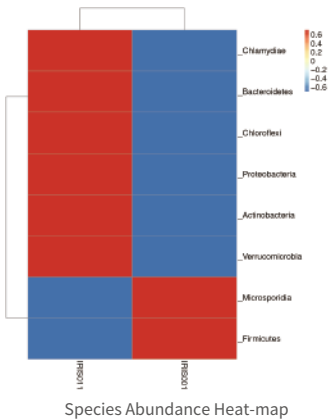
Turnaround Time

15 working days after verification of sample quality without data analysis (depending on sample size)

Bioinformatics Analysis Pipeline



Demo Results

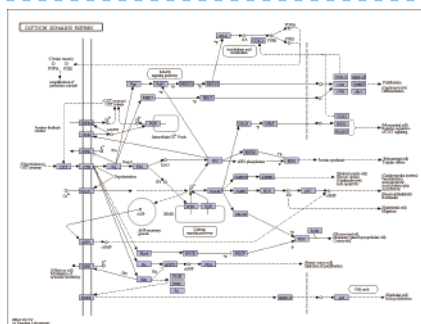


1. Species Analysis

Dominant genera of each sample were selected based on results of species annotation and abundance information, and clustered by its taxonomy information and the inter-sample differences among samples.

2. Differentially Expressed Genes Analysis

Read count value is used as input data to differential expression analysis. Statistically significant differences are represented by red dots (up regulated) and blue dots (down regulated).



3. Functional Enrichment Analysis

In the diagram, if a node contains up-regulated genes, the KO node is labeled in red. If a node contains down-regulated genes, the KO node is labeled in green. If a node contains both up and down-regulated genes, the labeled color is yellow.

Comparative analysis of multiple samples (function comparison, cluster analysis, PCA analysis) to uncover the relationship between samples are also provided, please contact us for details.

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