

# Transcriptome Sequencing (RNA-Seq)

**Transcriptome sequencing (RNA-seq)** is the set of genes which are transcribed in any one condition is known as the transcriptome, and the process of determining the genetic codes contained in the transcriptome, and their relative proportions, is known as transcriptome sequencing.

A transcriptome is the full range of messenger RNA, or mRNA, molecules expressed by an organism. The term "transcriptome" can also be used to describe the array of mRNA transcripts produced in a particular cell or tissue type.

## **What can a transcriptome tell us?**

An RNA sequence mirrors the sequence of the DNA from which it was transcribed. Consequently, by analyzing the entire collection of RNA sequences in a cell (the transcriptome) researchers can determine when and where each gene is turned on or off in the cells and tissues of an organism.

**Genetika Science Indonesia is offering RNA-Seq service as one of our portfolio service parts.**

We offers reliable and accurate insights into RNA from extraction to data analysis.

## What sequencing platform Genetika Science is using?

- Illumina NextSeq 2000

## What kind of RNA-Seq services Genetika Science is offering?

- Eukaryotic mRNA sequencing
- Bacterial RNA sequencing
- Whole Transcriptome Sequencing



## Sample Requirement:

### • Raw Samples

- For tissue samples, the samples should be flashfrozen with liquid nitrogen first.
- Then send the samples in liquid nitrogen (preferable) or dry ice.
- Alternatively, send the samples (except for plant samples) in DNA/RNA shield solution at room temperature.

### • Total RNA Samples

- RNA concentration  $\geq 50$  ng/ $\mu$ l with volume of 50  $\mu$ l.
- RNA Purity (OD260/280)  $\geq 2.0$  with no genomic DNA contamination.
- RNA Integrity Number (RIN)  $\geq 5$  with LSU and SSU rRNA still intact.

## What kind of data you will receive from this service?

- Raw data in fastq file format
- Sequencing QC
- Assembly and gene prediction
- Transcript annotation
- When sending more than 2 samples:
  - Transcript quantification
  - Differential Gene Expression (DGE) analysis
  - Gene Ontology analysis
  - Visualization (Volcano plot and Heatmap).



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