

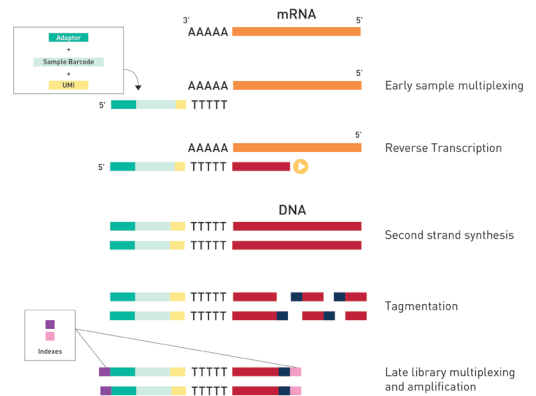


Innovating Epigenetics Solutions

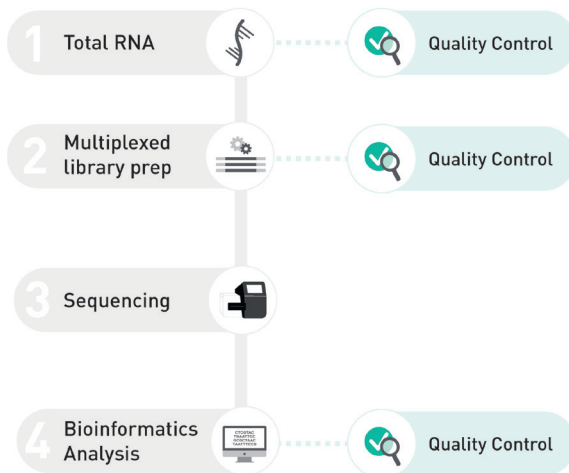
High-throughput 3'mRNA-seq

Scalable and affordable RNA-seq to examine differential gene expression analysis

High throughput 3'mRNA-seq is an attractive solution to perform comparative gene expression analysis on a large number of samples. It enables reliable gene expression quantification for large investigational studies. This approach is optimal for assessing multiple conditions of interest or increasing statistical power underlying any differential expression analysis with larger sets of replicates.



Innovative approach using early sample multiplexing



Affordable end-to-end RNA-seq service

Our Epigenomics Profiling Services assure a fully integrated service-workflow for generation of 3'mRNA-seq libraries, multiplexed sequencing and data analysis. Serviced library preparation uses early sample multiplexing to produce Illumina compatible libraries of sequences close to the 3' end of polyadenylated RNA.

BENEFITS OF HIGH-THROUGHPUT 3'mRNA-Seq

- ✔ Reliable alternative for gene expression analysis
- ✔ Working with very low quality RNA samples
- ✔ Fast turnaround time (from 4 to 6 weeks)
- ✔ Handling large number of samples simultaneously
- ✔ High performance in detecting differentially expressed genes

RNA-seq Profiling Services

High-throughput 3'mRNA analysis

- Reliable gene expression quantification
- Accurate comparison of gene expression levels
- Handling large number of samples simultaneously
- Affordable, attractive solution

mRNA analysis

- Recognition of protein-coding RNAs with specific poly A selection
- Superior complexity and high transcript coverage
- Accurate comparison of gene expression levels
- Detection of novel transcripts and alternative splicing events

Small non-coding RNA including miRNA analysis

- Realistic representation of all small non-coding RNAs
- Detection of novel transcripts and differentially-expressed small RNAs
- Investigation of post-transcriptional regulation of gene expression
- Leveraging the D-Plex technology

Whole transcriptome including long non-coding RNA analysis

- Detection of both coding and non-coding RNAs with optional rRNA depletion
- Recognition of long non-coding RNAs involved in chromatin remodeling and transcriptional/post-transcriptional regulation
- Investigation of the structure of genes, their splicing patterns and other post transcriptional modifications

Bioinformatics analysis

- Standard analysis including read filtering and trimming, read mapping to the genome or transcriptome, gene and transcript quantification
- Advanced analysis including differential expression analysis, gene ontology terms analysis, and pathway analysis
- Data mining and machine learning