

## Metatranscriptome Sequencing

### 1. Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	*RIN (Agilent 2100™)	Purity (NanoDrop™)
Meta-transcriptome Library	Total RNA	≥ 1 µg	≥ 20 µL	≥ 50 ng/µL	≥ 6.5, smooth base line	OD260/280 ≥ 2.0, OD260/230 ≥ 2.0, no degradation, no contamination

\*RIN: RNA Integrity Number

### 2. Sequencing Parameters

Platform	Illumina Novaseq 6000
Read length	Paired-end 150
Recommended sequencing depth	≥ 40 million read pair per sample for the species with reference genome
Data quality	Guaranteed ≥ 85% bases with Q30 or higher
**Turnaround time	Within 4~5 weeks from library construction verification to data releasing without bioinformatic analysis

\*\*Turnaround time varies depending on the project volume.

### 3. Data Analysis Contents

Standard analysis
Data filtering
De novo Assembly
Gene Functional Annotation
rRNA& mRNA Taxonomic Analysis
Gene expression quantification & Differential expressed genes profiling & Enrichment analysis
Comparative Analysis between Various Samples