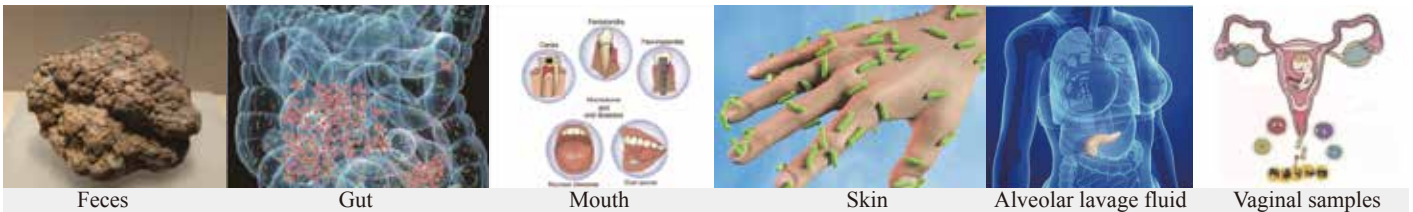


# Metatranscriptomics Sequencing (NGS)

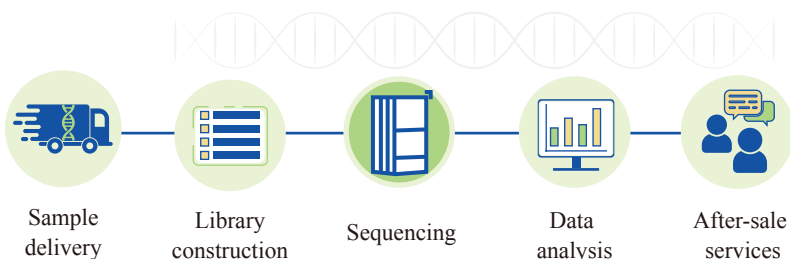
## Product Introduction

Metatranscriptome sequencing identifies gene expression of microbes (both eukaryotes and prokaryotes) within natural environments (i.e. soil, water, sea, feces, and gut.). Specifically, this service allows obtaining whole gene expression profiling of complex microbial communities, taxonomic analysis of species, functional enrichment analysis of differently expressed genes, and more.

## Application



## Service Workflow



## Bioinformation List

- Transcript assembly;
- Integrated the assembled transcripts of all samples;
- Taxonomy annotation: Alpha diversity and beta diversity analysis;
- Function annotation: GO, KEGG, eggNOG, CAZy, CARD, PHI, VFDB, etc.;
- Statistics and differential analysis.

## Service Advantages

- To study the changes of complex microbial communities at the transcriptional level and explore potential new genes.
- Helps to explain microbial community interactions with the host or environment.

