

# **Metatranscriptomics Sequencing (NGS)**

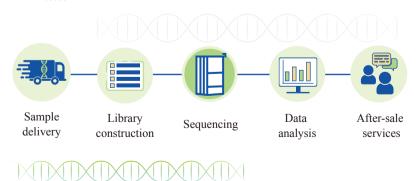
#### Product Introduction ....

Metatranscriptome sequencing identifies gene expression of microbes (both eukaryotes and prokaryotes) within natural en -vironments (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 ....



## Service,Advantages....

# 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.
- 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.

- Full suite of metatranscriptome analysis software to obtain maximum transcriptome information of microbial communities.
- Using the latest version of the gene function database, gene expression information of microbial communities can be annotated and analyzed more accurately
- After-sale services: After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

### Service-Specifications ....

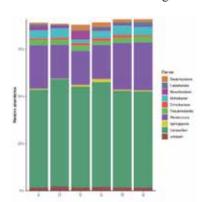
Platform	Sequencing	Recommended data	Turnaround Time
Illumina	PE150	12 G	37

### Sample-Requirements ....

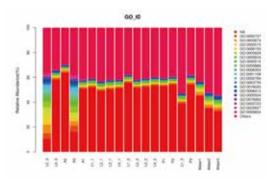
Qubit Conc. (ng/μL)	Amount (µg)	Volume (μL)	OD260/280
50	1.0	20	1.6-2.5

## Demo Results ....

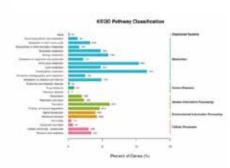
1. Relative abundance histogram



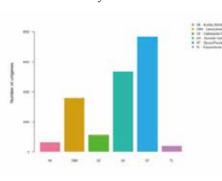
2. GO Annotation



3. KEGG Annotation



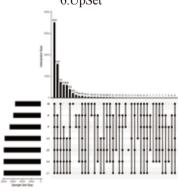
4. CAZy classification



5. LEFse analysis



6.UpSet



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