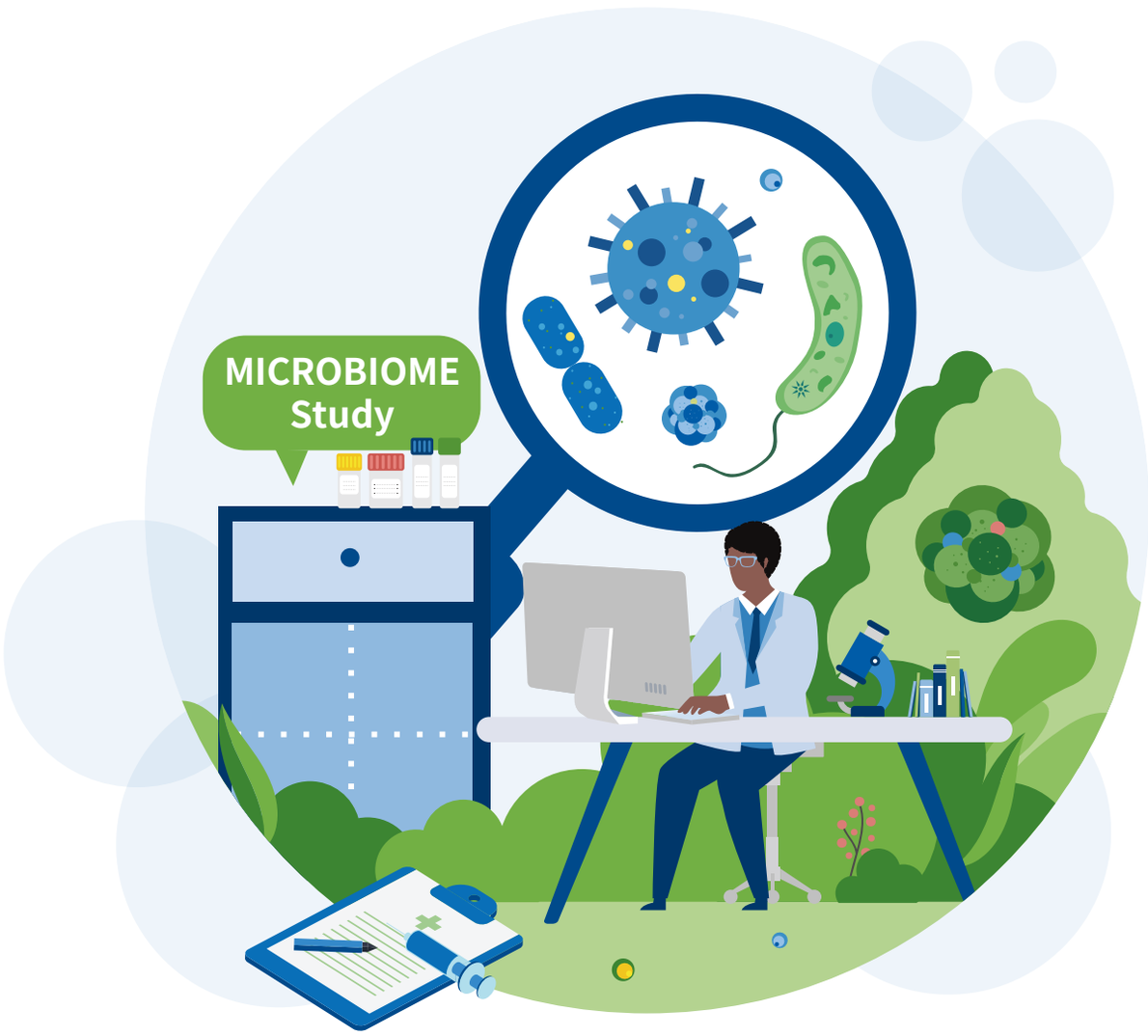
Novogene



Your One-stop MICROBIOME Study

Our sequencing expertise and comprehensive analysis equip you to unlock the microbiome.

Leading Edge Genomic Services & Solutions

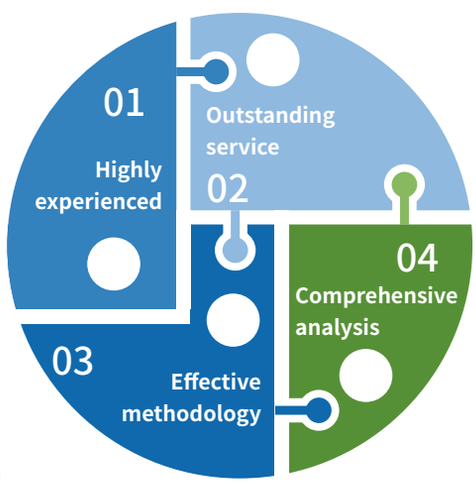
16S/18S/ITS Amplicon Metagenomic Sequencing

16S/18S/ITS amplicon metagenomic sequencing is frequently used to identify and differentiate microbial species. Short (<500 bp) hypervariable regions of conserved genes or intergenic regions, such as 16S of bacteria and archaea or 18S/ITS of fungi, are amplified by PCR and analyzed using NGS technology. The resulting sequences are compared against microbial databases.

Advantages & Highlights

- Sequenced over 170,000 samples,
- resulting in nearly 30 published papers.

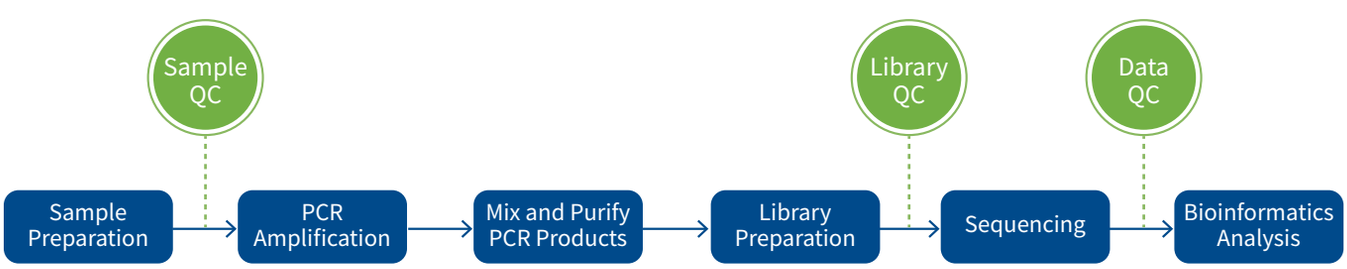
- 200-500bp insert DNA library; Illumina platform PE 250bp;
- 30K/50K/100K reads packages with bioinformatic analysis are available;
- 25 business days from verification of sample quality without data analysis



- Provide high-quality sequencing and efficient standardized workflow
- Fast turnaround times
- Bioinformatic analysis at cost-effective prices

- Provide expert bioinformatic analysis using the latest sequence databases and software
- Generate high-quality, publication-ready data

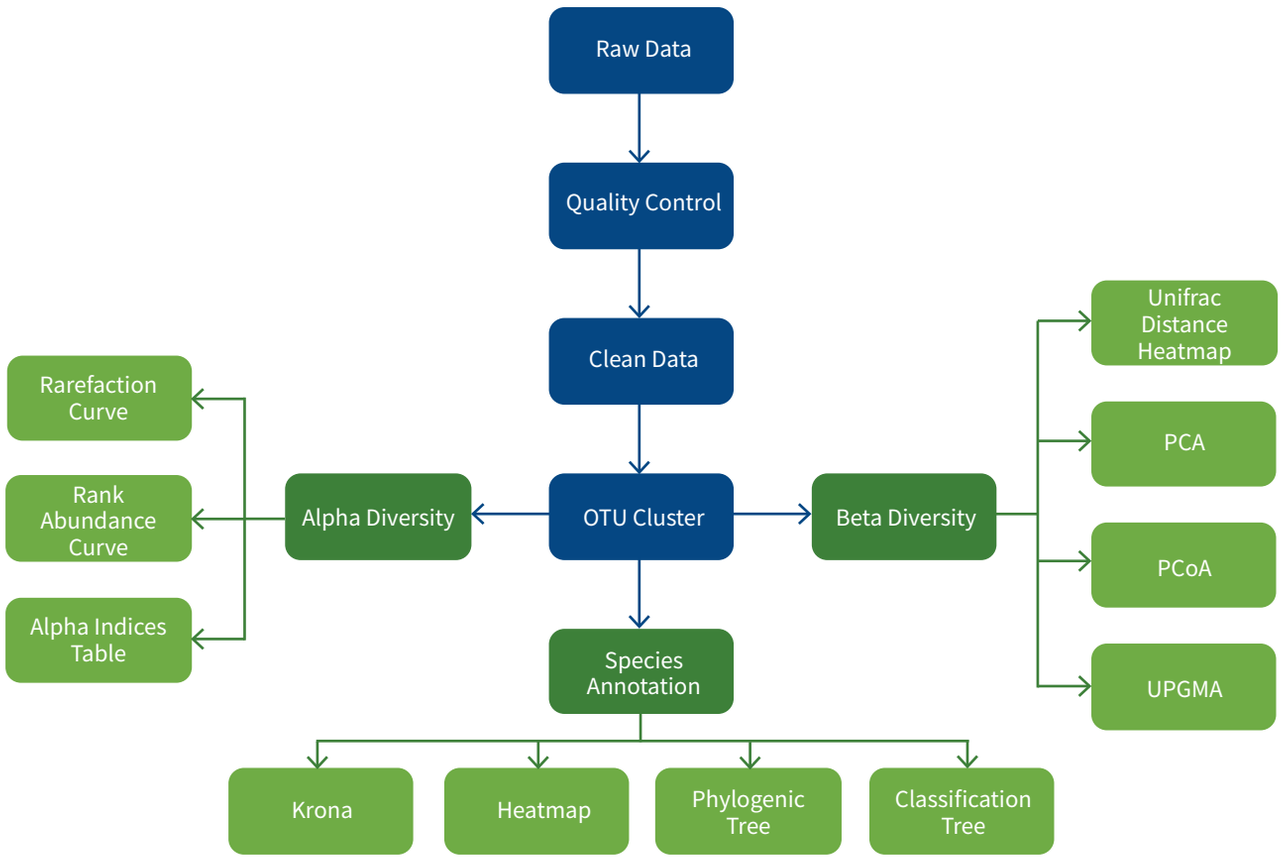
Project Workflow



Sample Requirements

SAMPLE TYPE	AMOUNT	CONCENTRATION	VOLUME	PURITY
Genomic DNA	⩾ 150 ng	⩾5 ng/μL	⩾ 30 μl	OD260/280=1.8-2.0, no degradation or RNA contamination

Analysis Pipeline



Novogene Client Publication

The microbiota maintains homeostasis of liver-resident γδT-17 cells in a lipid antigen/CD1d-dependent manner (Li *et al,* 2017)

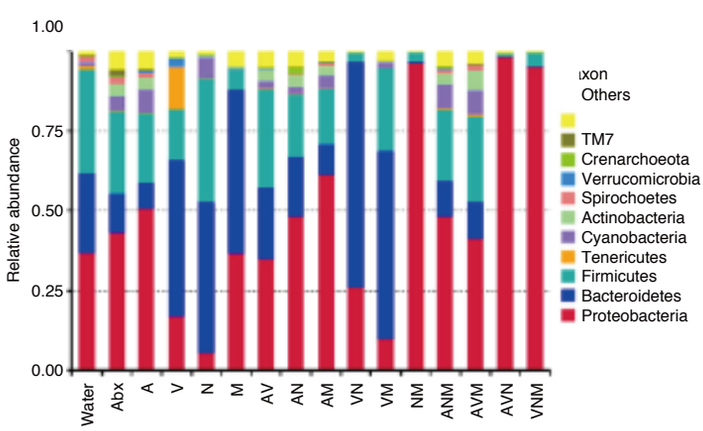
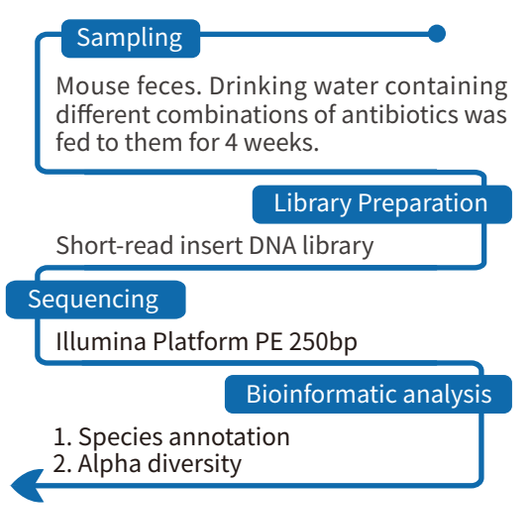


Figure. 1 16S rDNA sequencing reveals that commensal microbe load positively correlates with hepatic γδT-17 cell numbers



Reference:Li F, Chen Y, Bai L, *et al.* The microbiota maintains homeostasis of liver-resident γδT-17 cells in a lipid antigen/CD1d-dependent manner. *Nature Communication* 8: 13839 (2017)

Shotgun Metagenomic Sequencing

In shotgun metagenomic sequencing, genomes from environmental samples are analyzed without the prior isolation and cultivation of individual species; therefore, it is a powerful technique for studying microbial communities in their natural habitat, with a broad range of applications. At Novogene, our customers can rely on our expertise in Next Generation Sequencing (NGS) to help them explore the rich genetic repertoire of microbial communities, while also benefiting from our bioinformatics expertise to help identify the species, genes, and pathways represented in their samples. Novogene provides metagenomic sequencing service with an Illumina HiSeq platform and an assembly-first strategy. Additionally, our bioinformatics analyses provide gene predictions, functional annotations, and taxonomic annotations. Our standard analysis package includes, mPATH, heatmaps, PCA, cluster analysis, and other programs, generating high-quality, publication-ready data.

Advantages & Highlights

Highly experienced

We have completed over 400 metagenomic sequencing projects for our customers and have published multiple metagenomic papers.

Outstanding service

We provide high-quality sequencing, an efficient standard workflow, and bioinformatics analyses at cost-effective prices.

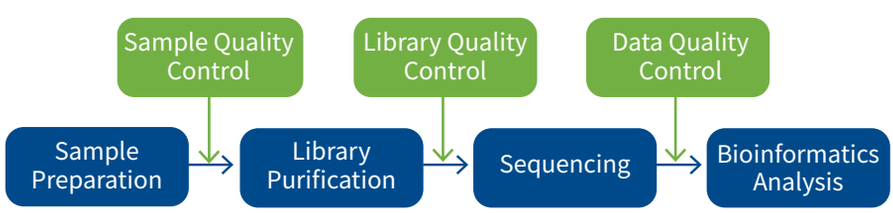
Effective methodology

350bp insert DNA library, Illumina platform PE 150bp. For each sample, 6Gb and 12Gb packages are available, with Q30 ⩾ 80%.

Comprehensive analysis

Expert bioinformatics analyses with three databases (KEGG, eggNOG, and CAZy) provides comprehensive data on annotated genes and metabolic pathways.

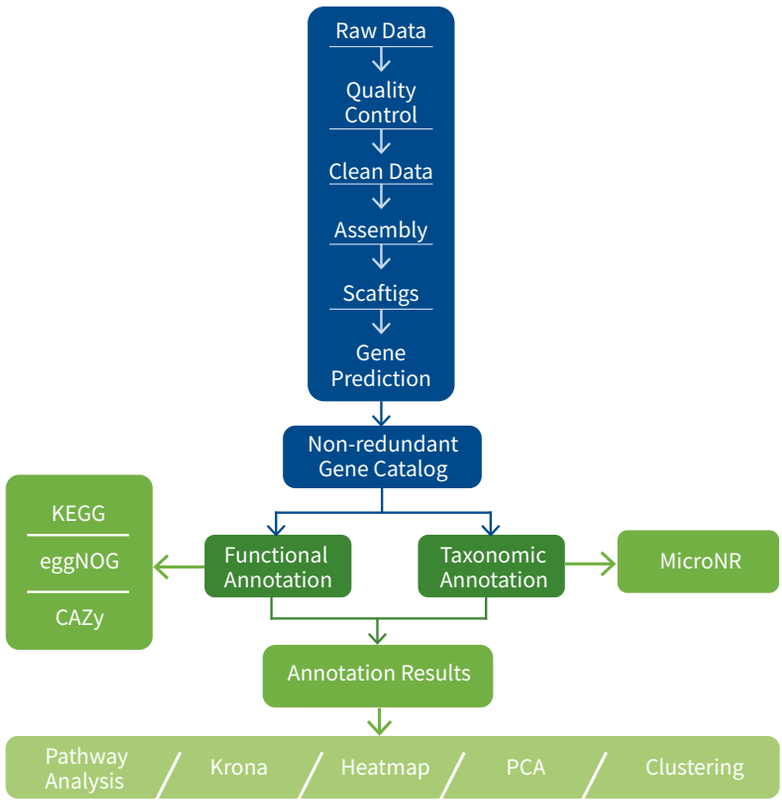
Project Workflow



Sample Requirements

Sample Type	Amount	Concentration	Volume	Purity
Genomic DNA	⩾ 300ng	⩾ 5ng/μL	⩾ 20μl	OD 260/280=1.8-2.0, no degradation or RNA contamination

Analysis Pipeline



Novogene Client Publication

Hypoxia induces senescence of bone marrow mesenchymal stem cells via altered gut microbiota(Xing *et al,* 2018)

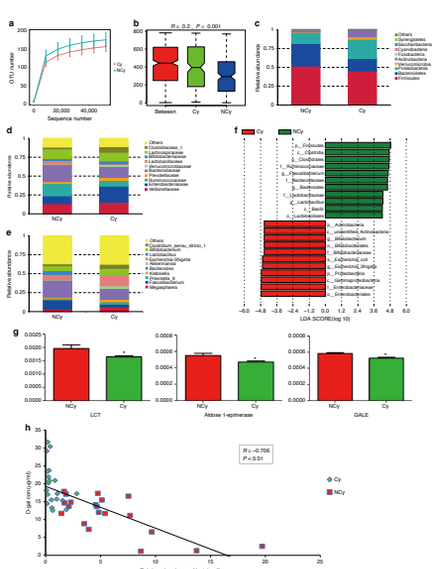


Figure.2 Deep hypoxia leads to intestinal microflora imbalance

Sampling

90 children with congenital heart disease (age over 6 months, no diarrhea, no antibiotics or hormones, no extracardiac abnormalities, no chromosomal abnormalities) were divided into cyanotic (Cy) and non-cyanotic (NCy) groups.

Library Preparation

Short-read insert DNA library

Sequencing

Illumina platform PE 150bp

Bioinformatic analysis

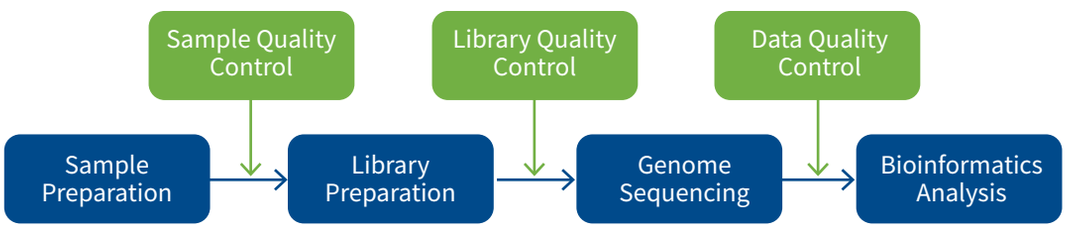
1. Species annotation
2. Differential species analysis
3. Functional analysis

Reference: Xing J , Ying Y , Mao C , *et al.*Hypoxia induces senescence of bone marrow mesenchymal stem cells via altered gut microbiota[J]. *Nature Communication*, 2018, 9(1):2020.

De novo Sequencing

Using *de novo* sequencing to obtain the genomic information of microbes provides a fresh start for exploring the genetic structure and functions, studying the evolutionary origin of microbial populations, as well as developing potential applications of these abundant microbes in medicine, disease, agriculture, and environment. For the microbial genome, Novogene offers *de novo* sequencing service using both PacBio and Illumina platforms. We provide multifaceted sequencing services including genome survey, frame map, complete map, and fine map tailored to different research needs. For each project, our scientists will design the best sequencing strategy utilizing an optimal combination of short reads and long-range sequencing information to achieve the most comprehensive *de novo* assembly results for your genome of interest.

Project Workflow



Sequencing Strategy & Data Quality Guarantee

GENOME CHARACTERISTICS	SEQUENCING PLATFORM	SEQUENCING STRATEGY	DELIVERED DATA PARAMETERS	APPLICATION	TURNAROUND TIME (TAT)
Microbial genome frame map	Illumina PE150	350 bp insert DNA library ⩾ 100X	—	Large scale of samples, fast scanning	Start from 30 business days
Bacteria complete map	PacBio Sequel I	⩾ 100X PacBio reads	1 Scaffold, 0 gap	Small number of bacteria samples, fine mapping	Start from 45 business days
Fungus fine map (with free survey)	PacBio Sequel I& Illumina PE150	⩾ 50X Illumina reads + ⩾ 100X PacBio reads	Contig N50 ⩾ 1Mb (genome size < 100 Mb) Contig N50 > 500Kb (genome size ⩾ 500 Kb)	Small number of fungus samples, fine mapping	Start from 45 business days

Sample Requirements

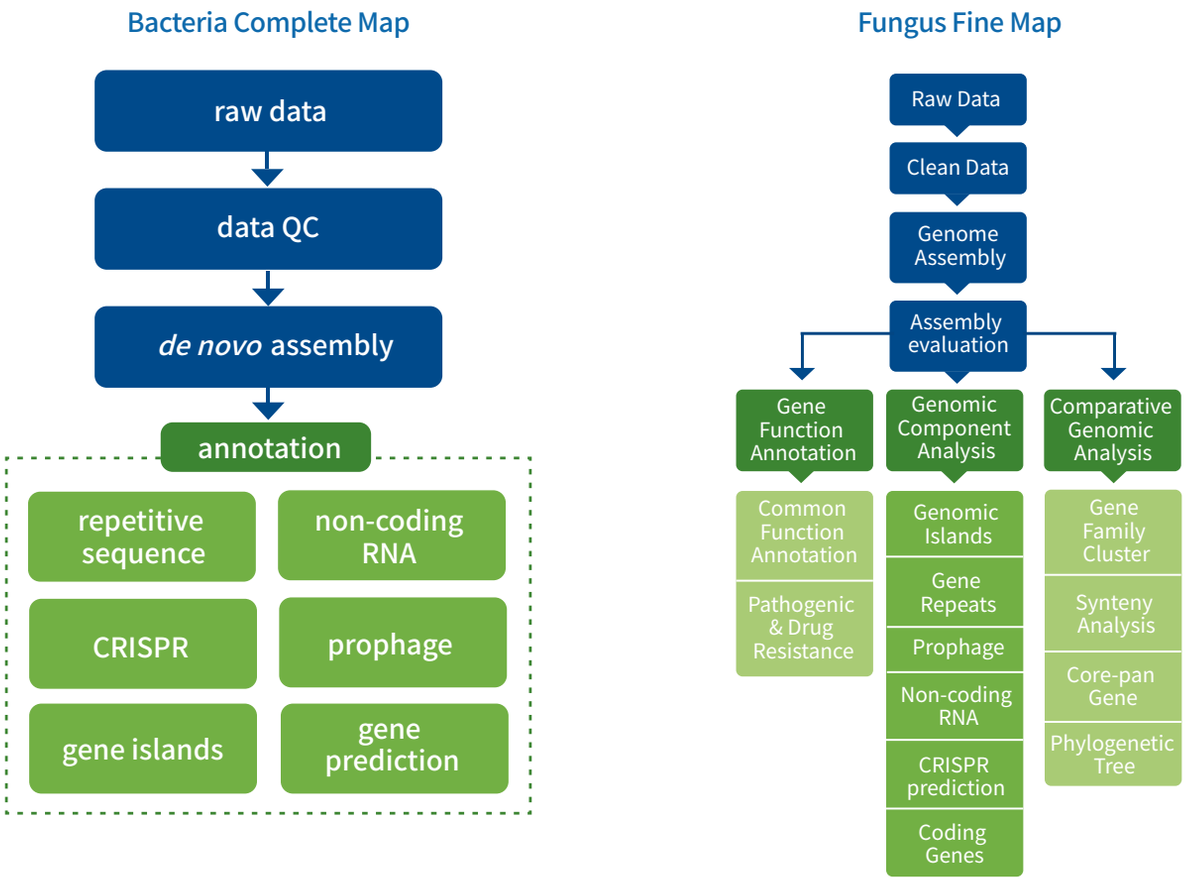
DNA amount for survey: ⩾ 1 μg

DNA amount for genome *de novo* sequencing per library: ⩾ 1 μg (for Illumina sequencing) and ⩾ 10 μg (for PacBio sequencing)

DNA concentration: ⩾ 20 ng/μL (for Illumina sequencing) and ⩾ 100 ng/μL (for PacBio sequencing)

Purity: No degradation, no DNA contamination

Analysis Pipeline



Novogene Client Publication

Comparative genomics identifies the *Magnaporthe oryzae* avirulence effector *AvrPi9* that triggers *Pi9*-mediated blast resistance in rice(Wu *et al,* 2015)

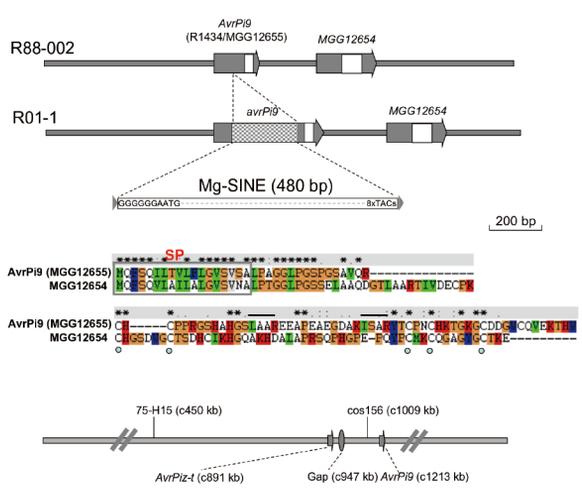


Figure. 3 Through comparative genomic analysis of *R01-1* and *B88-002* strains, a Mg-SINE insertion sequence of *AvrPi9* gene was found in *R01-1,* which affected the *AvrPi9* gene and inhibited the resistance mechanism mediated by *Pi9* gene in rice.

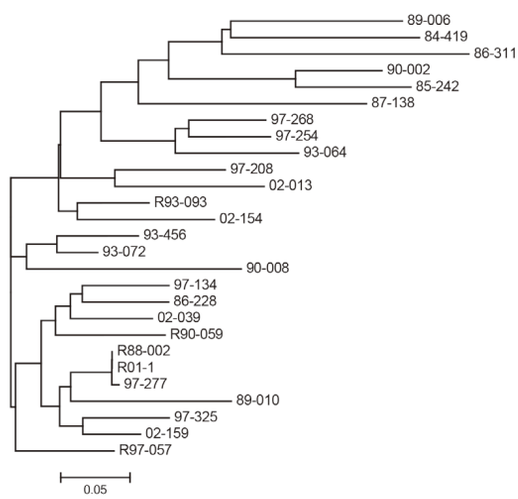


Figure. 4 Statistics of *de novo* assembly and annotation results of *R01-1* and *R88-002*

Sampling: *R01-1* (ancestral strain) and *B88-022* (closely related non-toxic strain)

Library Preparation: 350bp insert DNA library

Sequencing: Illumina platform PE 150bp

Bioinformatic Analysis: *De novo* assembly, Evolutionary analysis based on amplification products, Genome assembly annotation, Comparative genomic analysis

Reference: Wu J, Kou Y, Bao J, *et al*. Comparative genomics identifies the *Magnaporthe oryzae* avirulence effector *AvrPi9* that triggers *Pi9*-mediated blast resistance in rice[J]. *New phytologist* , 2015, 206(4): 1463-1475.

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