

FUNGUS GENOME FINE MAP with a new algorithm

PacBio SMRT Sequencing solves the genomic puzzle

Novogene offers fungus genome fine mapping using both the PacBio and Illumina platforms. Our scientists utilize an optimized combination of short reads and long-range sequencing information to achieve the most comprehensive and cost-effective *de novo* assembly results for your fungal genome.

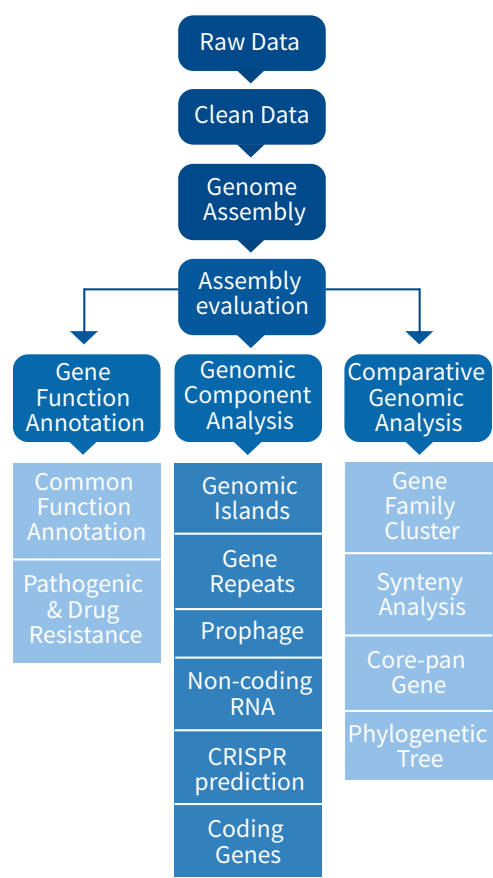
Novogene Advantages

- Largest Sequencing Capacity in the World**
Enables high quality data, fast TAT
- Package Price Offered**
From sample QC to gene annotation
- Extensive Experience**
Over 2,000 microbial sequencing projects
More than 20 publications

Service Highlights

- Optimized Assembly Strategy**
Genome Survey, Illumina short-read sequencing (350bp library, 50X) + PacBio ultra-long reading (20kb SMRT Bell library, 100X)
- Convincing Data Quality**
Guaranteed from Illumina: Q30>80%
- Outstanding Read Length**
Average PacBio polymerase read is more than 20Kbp

Bioinformatics Workflow



Number of contigs and N50 are well performed, from our sophisticated experience		
Number of contigs	N50 of contigs	Gene coverage
25	3.5Mbp	40%

What You Can Expect

Anatomy For Genome Structure And Function

- Non-coding RNA
- Repetitive regions
- Coding area
- Pathogenic & drug resistance
- Flexible annotation for multiple databases: KOG; Pfam; KEGG; TCDB; CAZy; NR; GO

Sample Requirements

DNA Amount	DNA Concentration	Purity
10μg	100ng/μL	No degradation, no contamination

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