theraCUES
SIGNALS FOR LIFE

Whole Genome Sequencing – Fungal (De novo) TC-S-AG-WGF-DNV

Applications

Method utilizes shotgun whole-genome sequencing to generate a de novo assembly of fungal genomes without reliance on a reference sequence. This enables comprehensive characterization of fungal genomes, including novel species or strains, complex gene families, repetitive regions, and secondary metabolite biosynthetic clusters. De novo assembly supports studies in fungal biology, pathogenicity, industrial strain development, and evolutionary genomics.

Pros

- Enables discovery of novel fungal genes
- Captures complex and repetitive genomic regions
- Suitable for poorly characterized fungal species
- Supports functional and evolutionary studies
- Structural variation, Synteny and genome organization
- Repeat/Recombination events
- Haplotype phasing

Notes

- Requires high-quality genomic DNA of high molecular weight
- Assembly quality depends on genome size and complexity
- Long-read sequencing recommended for repeat-rich genomes
- 18S strain purity testing recommended

Input

Genomic DNA

- Short-read sequencing: ≥ 200 ng
- Long-read sequencing (recommended): ≥ 1 µg
- DIN/Gel analysis for high molecular weight DNA

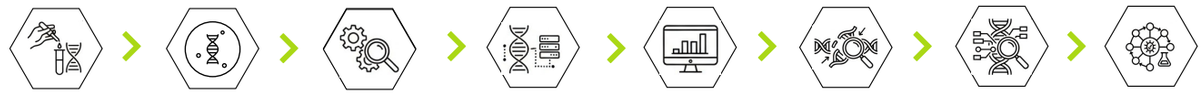
Sample Types

Fungal isolates | Clinical fungal isolates | Environmental fungal isolates | Industrial and agricultural fungal strains

Platform

Long-read sequencing platforms | 50-70X Long read | ~ 2-10 GB | Based on genome/ploidy estimates

Process Map



Standard Deliverables

[Download Sample Report]

- Sample QC, Library QC, and Summary of Methods
- Data QC, Data Trimming, and Pre-processing
- Genome Assembly Summary, Gene Detection, Genome Annotation
- SNP/Allele identification
- Haplotype information from long read parsing
- GFF3 File, Gene List, Repeat Elements, SINE/LINES, Pathway assignment, Secondary metabolite coding genes
- When multiple Strain/Strain matching scoped - Syntany and comparitive genome mapping

References

- Estaki M et al. Curr Protoc Bioinformatics. 2020; PMID:32343490.
- Licata AG et al. Microbiol Spectr. 2025; doi:10.1128/spectrum.01673-25.