Platform of microorganisms Fast Identification

Make Microbial Sequencing Easier
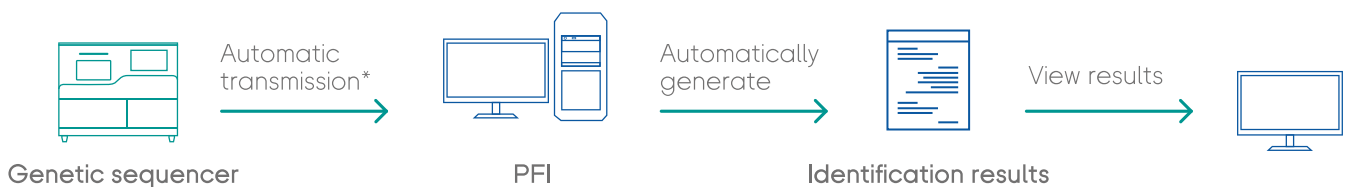
Platform of microorganisms Fast Identification (PFI) is a one-stop platform designed to simplify the analysis of high-throughput genetic sequencing of pathogens. The system includes two types of bioinformatics analysis software: Microorganisms Fast Identification Software (PFI) and metargetCOVID software. The system is also equipped with a professional laboratory information management system ZLIMS, providing a graphical operation interface, ready to use after booting.

Through the automated data processing pipeline on the PFI system, it can perform metatranscriptomic data analysis, metagenomic data, identify the microbial nucleotide sequence in the original sample, and automatically generate identification results. The results could provide a reference for accurate detection in the field of pathogenic microorganisms. The metargetCOVID software can applicable for NGS data analysis of metagenomics sequencing or MGI ATOPlex platform. It has two analysis processes: single strain and mixed strain. The function of single strain process includes mutation detection, mutation annotation, and functional prediction, and is classified using Nextclade and Pangolin software. The function of the mixed strain process includes identification of the composition and abundance of COVID-19 strains in the sample, and identification of the key mutation sites of the strains.

Platform of microorganisms Fast Identification (PFI)

- Built-in species database
- Equipped with information management system
- Load sequencing bioinformatics process
- External localized server

Genetic sequencer → Automatic transmission* → PFI → Automatically generate → Identification results → View results

Built-in Species Database

■ Host database

Includes more than 10 host species, such as humans, pigs, goats, sheep, mice, etc. In addition, the pipeline includes new host species automatically adding function ,customers can add more hosts as needed.

Host database	Includes more than 10 host species

More host species can be customized

■ Pathogen database

Contains more than 20,000 species of microorganisms, including COVID-19 genome and supports updates.

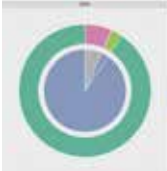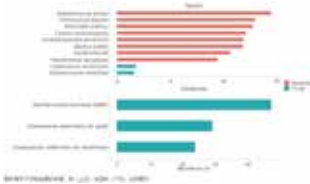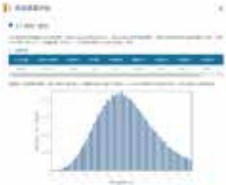| Pathogen database					
Classification of microorganisms	Viruses	Fungi	Bacteria	Archaea	Protozoa +Parasite
Species	8900+	9400+	8000+	300+	600+
Subspecies	3000+	300+	19000+	200+	50+

*This function needs to be equipped with a localized high-throughput sequencer, and the MGI sequencing platform is recommended.

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Workflow

Data processing	Data QC	Remove poor quality reads included adapters and N bases.
	Remove host	Remove host DNA and rRNA
	Species identification	1. Database comparison, classification 2.Prediction of resistance gene 3.Prediction of virulence gene 4.Activity analysis* Tips: indicates that microorganism activity analysis is performed for an analyzed sample only when the sample contains both DNA and RNA data.
	Denovo assembly	Manually start de novo assembly for target species
Identification report	DNA/RNA classification, species	

reads QC Chart

Abundance of species identification

Assembly report	 De novo assembly

MGI metargetCOVID Software

Histograms of Coverage Range

Summary of Result: assemble, variants calling, clade and lineage assign

Lineages distribution of mixed strain
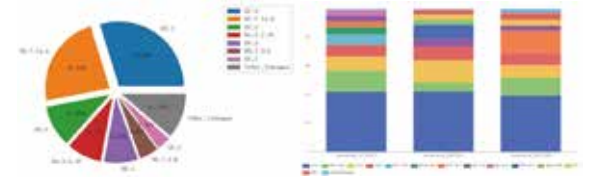
ZLIMS: A MGI laboratory information management software

■ Convenient GUI

■ Whole process management: sample preparation, library preparation, sequencing and data processing

External localization server

CPU	Intel Xeon Gold 6240*2
RAM	192GB DDR4
SSD	2TB+250GB
HDD	30TB 7200 SATA 3.5 inch

Order Information

Product	Part No.
Platform of microorganisms Fast Identification	900-000393-00
metargetCOVID Software Upgrade Package	970-000396-00

CONTACT US

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