Platform of microorganisms Fast Identification and Assembly Evolution

PFI+MGAP Microbial bioinformatics software suite

- PFI built-in microbial database
- Load identification and assembly bioinformatics process
- Equipped with laboratory information management system
- External localized server

Platform of microorganisms Fast Identification and Assembly Evolution

PFI+MGAP Microorganisms analysis platform suite

MGI's Platform of microorganisms Fast Identification and assembly evolution is a one-stop platform developed specifically to simplify the analysis of Microbial MPS genetic data. The system includes three types of bioinformatics analysis software: Microorganisms Fast Identification Software (PFI) , Microbial Genome Analysis Pipeline (MGAP) and metarget-COVID software. The system is also equipped with a professional laboratory information management system ZLIMS, providing a graphical operation interface, ready to use after booting.

Equipped with laboratory information management system: ZLIMS

Graphical interface, easy to use.

Full-process information management from sample entry, library preparation,sequencing, data analysis to the generation of bioinformatics reports.

External localization server

CPU	Intel Xeon Gold 6240*2
Memory	192GB DDR4
Solid state drive	2TB+250GB
Mechanical hard disk	30TB 7200 SATA 3.5 inch

PFI

Able to process metatranscriptomic data analysis, metagenomic data processing. Analyze and identify microbial nucleotide sequence in the original sample, and automatically generate identification results which provides a reference for accurate detection in the field of microorganisms.

MGAP

Contains multiplex analysis modules for pathogenic microorganisms sequencing data of bacteria, fungi, and virus, realizing from the sequencing data to genome assembly, system evolution analysis, and automatic calculation of mutation. The test results are for research reference, and customers can flexibly choose analysis modules according to actual needs.

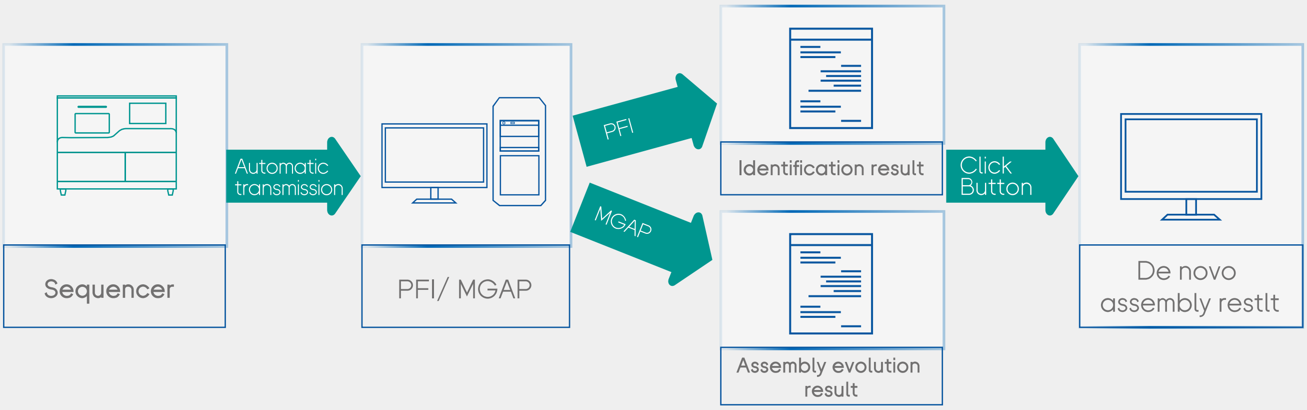
metargetCOVID

MGI 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.

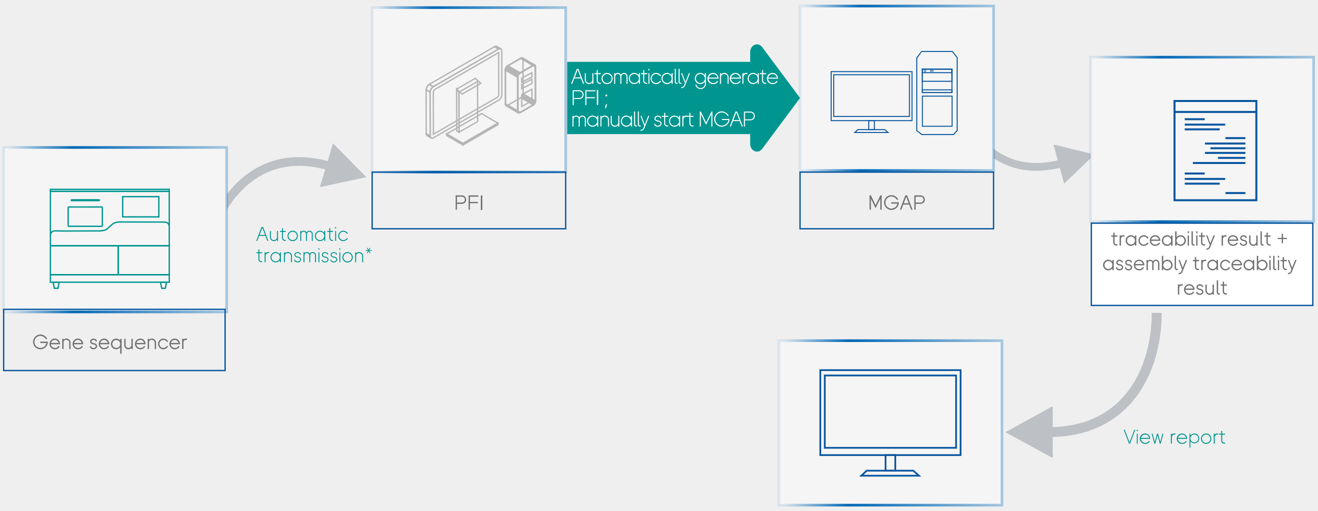
☑ PFI and MGAP operate separately

1.PFI：PFI is used for metagenomic species identification, and use the interest species FASTQ file to de novo assembly

2.MGAP : MGAP is used for assembly and traceability analysis of known pathogen species



☑ PFI for identification, and then select the target species for assembly traceability analysis



☑ MGI metargetCOVID software is an bioinformatics workflow based on Linux operating system, which includes basic data QC, short reads alignment, variants detection，assign the clade and lineage.

One click to complete the virus sequence identification, assembly and Phylogeny analysis

Data QC	Sequence Alignment	Data Processing
• Raw data • Filtered data	SPIKE-IN CONTROL sequence, Human GAPDH Gene as internal reference, and the target virus sequence (SARS-CoV-2 reference: MN908947.3)	• Virus identification • Virus sequence assembly • Mutation detection • Variants detection • Variants annotation • Functional effect prediction • Phylogeny analysis

PFI 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 nCOV-19 sequences, and supports regular updates.

Pathogen database

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

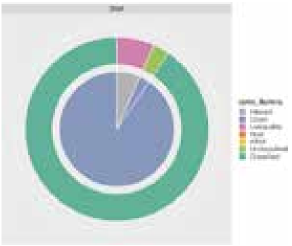
*This function needs to be equipped with a localized high-throughput sequencer. It is recommended to use the DNBSEQ sequencing platform manufactured by MGI.

PFI Processing Pipeline

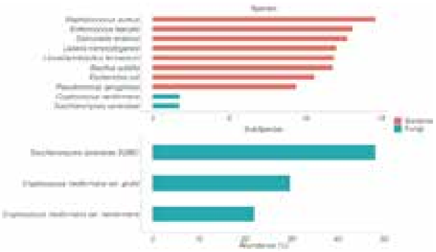
Data processing	Data QC	Remove poor quality reads included adapters and N bases.
	Remove host	Remove host DNA and rRNA*
	Species identification	1. Database comparison, classification 2.Prediction of resistance gene 3.Prediction of virulence gene 4.Activity analysis* Tips: indicates that microorganism 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

MGAP: Microbial Genome Analysis Pipeline

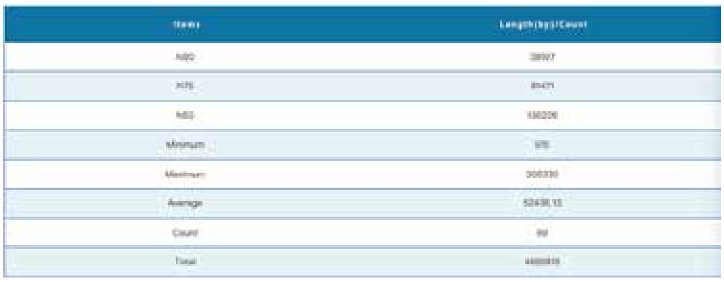
Assembly

Can choose to assemble with or without parameters

Assembly and Annotation

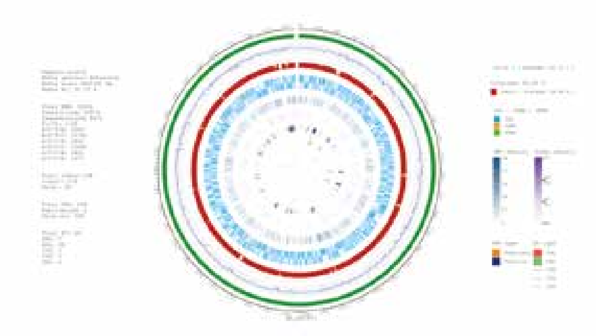
Assembly summary

Genome Assemble is the process of putting nucleotide sequence into the correct order, including *De novo* and Reference guides.



Items	Length(bp)/Count
N50	38997
N75	81471
N90	136226
Minimum	976
Maximum	306330
Average	52436.13
Count	92
Total	4480819

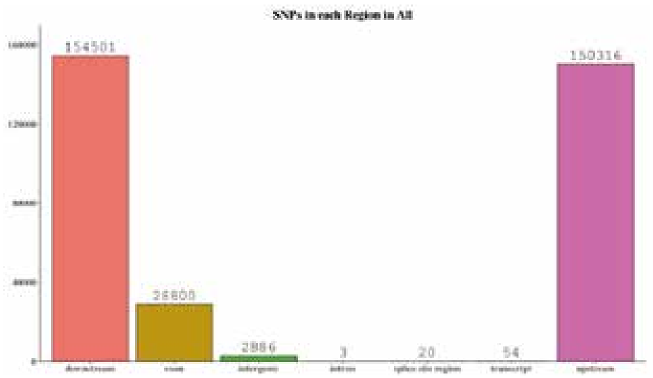
Comparison of assembly results with reference genome



Evolutionary analysis

Species tree analysis based on genome-wide SNPs

Mutation detection



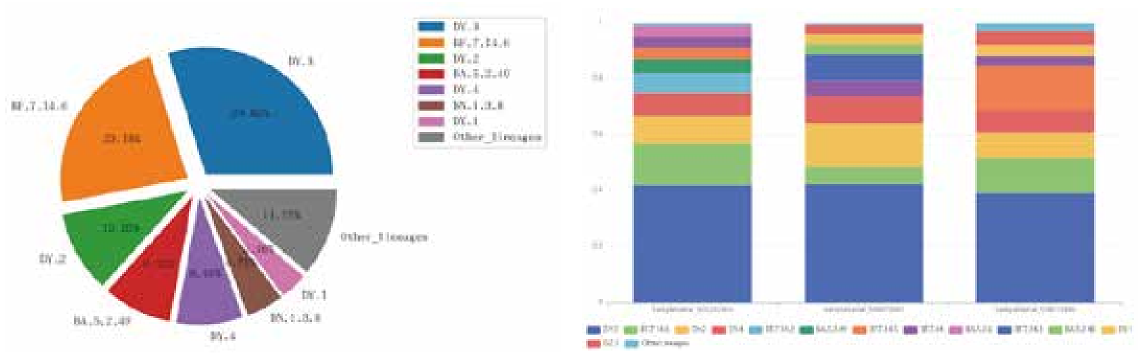
MGI metargetCOVID Software

Histograms of Coverage Range

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

Assemble Size(bp)	Num Ns	Num SNPs	Num INSs	Num DELs	Clade ID	Lineage ID
29890	75	43	0	3	21A (Delta)	AY.4

Lineages distribution of mixed strain



Ordering Information

Product	Part No.
Platform of microorganisms Fast Identification and assembly evolution	900-000399-00
metargetCOVID Software Upgrade Package	970-000396-00

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