

Microbial Whole Genome Sequencing



Microbial Whole Genome Sequencing is a powerful tool to identify key variants and genetic changes and their possible application in both pathogenicity and disease outcome.

Unlike conventional Polymerase Chain Reaction (PCR), Next Generation Sequencing (NGS) excels in the way of multiplexing the vast number of samples, providing identifications of SNP/ InDel/ CNV/ SV with greater reliability, faster turnaround time and lower costs.

Our Key Features & Advantages



Comprehensive & Superior Data Analysis

We offer comprehensive analysis on species evolution, population characteristics, selection pressure, etc. Our informatics expertise and sequence processing capacity can deliver superior data and analysis results.



Extensive Experience

We have extensive records of sequencing projects covering a range of research, including pathogenic bacteria, probiotics, edible bacteria, medicinal strains, and industrial strains.



Reliable & Faster Turnaround Time

We provide high-quality sequencing (with Q30 score $\geq 85\%$), an efficient standard workflow, fast turnaround time, and cost-effective bioinformatics analysis.



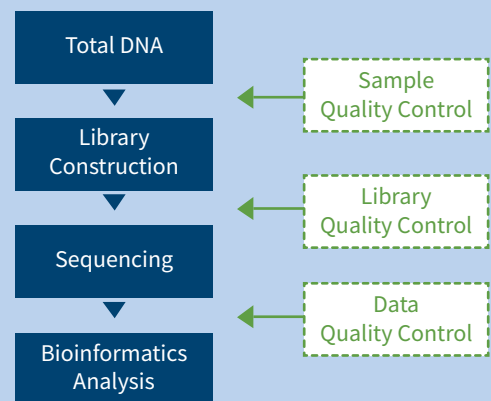
Real-time Project Management

Our Customer Service System (CSS) online platform allows for real-time project tracking 24/7, collaboration with your team and other helpful information.

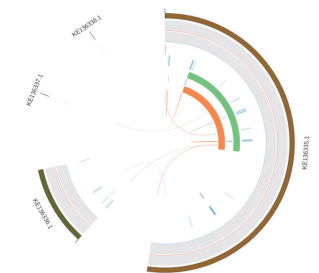
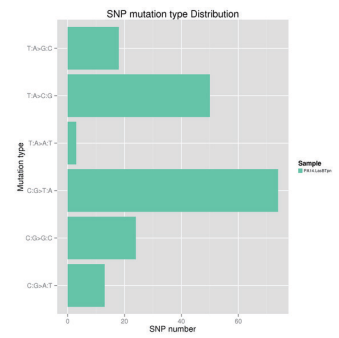
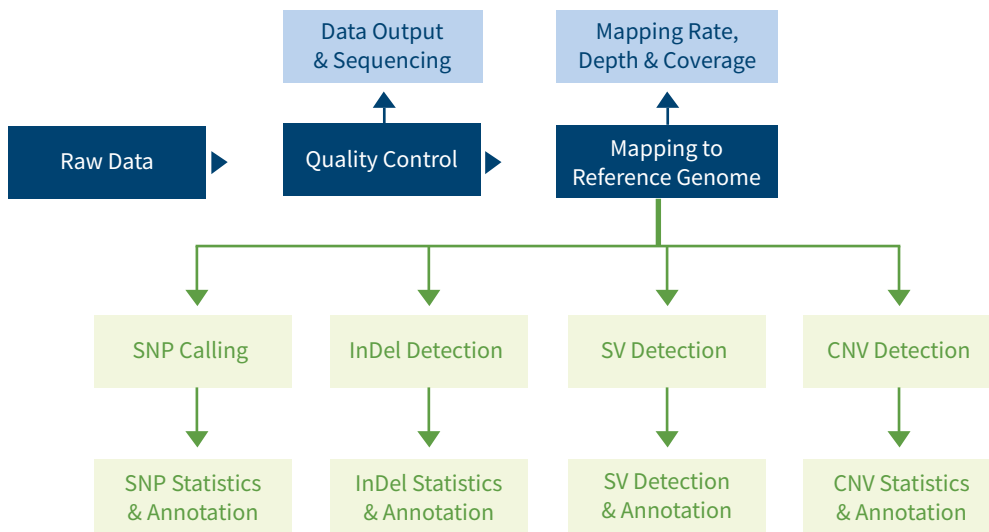
Applications

- Variation detection
- Characterization of difference interpretation
- Large-scale evolution research
- Pre-requisite study of novel species identification

Project Workflow



Standard Analysis Pipeline



Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity
Microbial Whole Genome Library (350bp)	Genomic DNA	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	OD260/280= 1.8-2.0, No degradation, No contamination, no color
Microbial Whole Genome Library (PCR-free 350bp library)	Genomic DNA	≥ 1.2 μg	≥ 20 μL	≥ 10 ng/μL	

Publications

Journal	IF	Title
Environmental Science and Technology	11.357	Multi-Omic Profiling of a Newly Isolated Oxy-PAH Degrading Specialist from PAH-Contaminated Soil Reveals Bacterial Mechanisms to Mitigate the Risk Posed by Polar Transformation Products (2023)
Emerging Microbes & Infections	19.568	Population genomics of emerging Elizabethkingia anophelis pathogens reveals potential outbreak and rapid global dissemination (2022)
mSystems	6.663	Dynamics and Microevolution of Vibrio parahaemolyticus Populations in Shellfish Farms (2021)

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