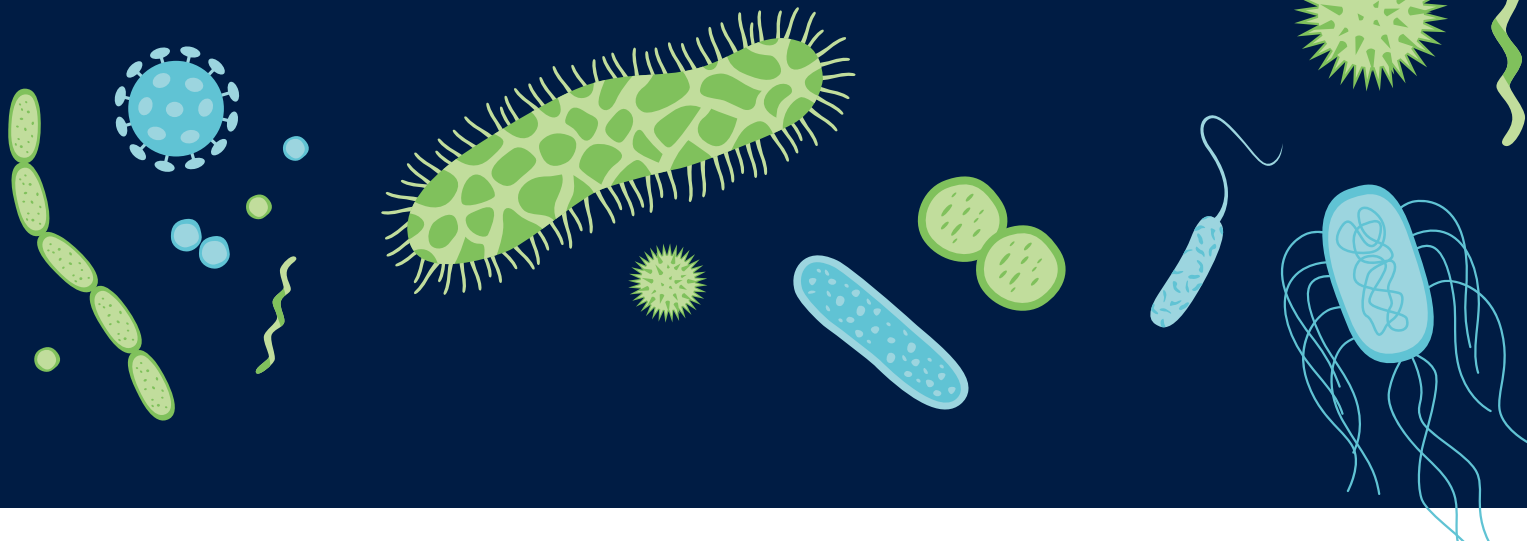


# Microbial Whole Genome Sequencing



**Microbial Whole Genome Sequencing** is a powerful tool to finish the genome of known bacteria and fungi, and map genomes of new organisms.

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/ SNV/ SV with greater reliability, faster turnaround time and lower cost.

## 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.



### Real-time Project Management

View and manage your projects on our customer service portal.



### 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.



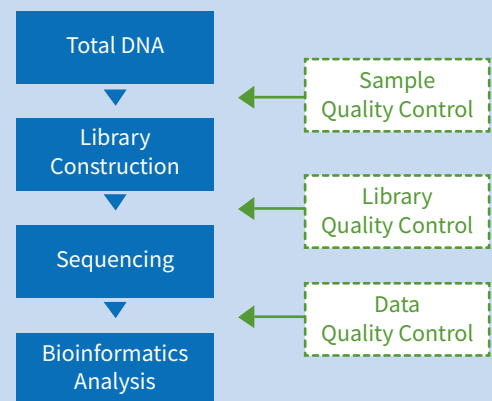
### Reliable & Faster Turnaround Time

The strategic locations of our labs across Asia and our extensive NGS system can provide faster turnaround time.

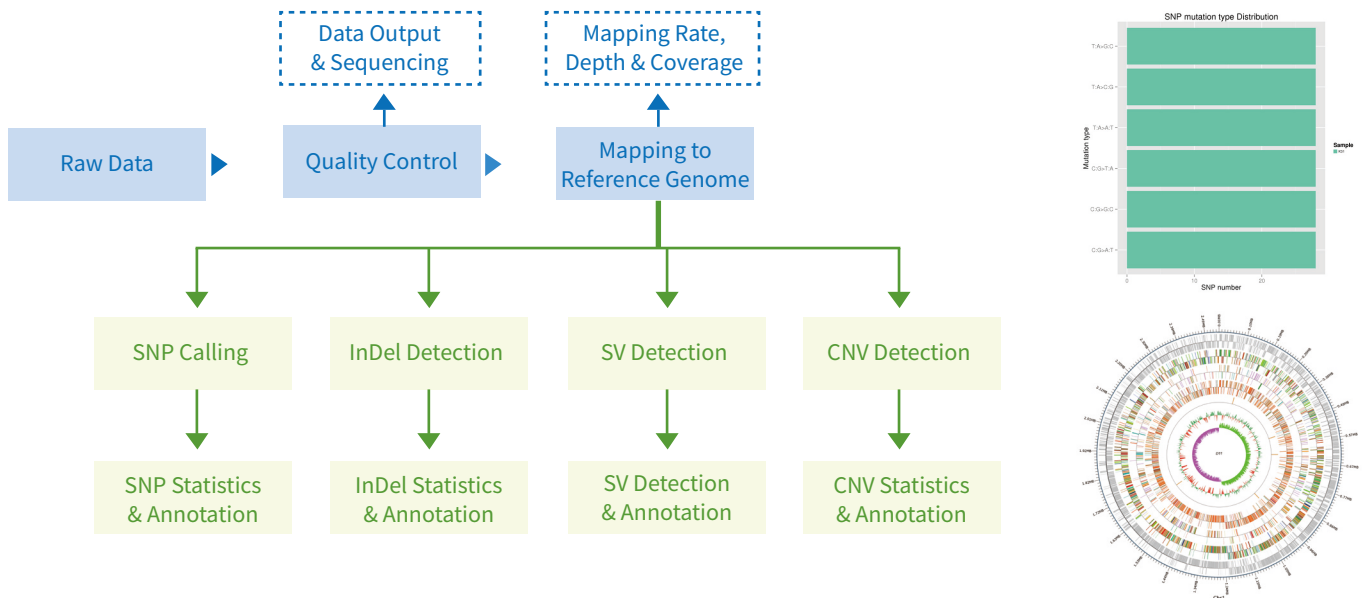
## Applications

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

## Project Workflow



## Standard Analysis Pipeline



## Sequencing Parameters & Analysis Content

<b>Platform Type</b>	Illumina Novaseq 6000
<b>Read Length</b>	Paired-end 150 bp
<b>Recommended Sequencing Depth</b>	100x
<b>Standard Data Analysis</b>	<ul style="list-style-type: none"> <li>• Data quality control: filtering adapter-containing and low quality reads</li> <li>• Alignment with reference genome</li> <li>• SNP/ InDel calling, annotation and statistics</li> <li>• SV/ CNV calling, annotation and statistics</li> </ul>

Note: For detailed information, please contact us for customized data analysis.

## Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity (Qubit/ agarose gel)
Microbial Whole Genome Library (350bp)	Genomic DNA	200 ng	20 µL	10 ng/µL	OD260/280= 1.8-2.0 No degradation No contamination
PCR-free library	Genomic DNA	1.5 µg	20 µL	20 ng/µL	

For Research Use Only. Exclusive for clients in AMEA (Asia Pacific, Middle-East & Africa).

**NovogeneAIT Genomics Singapore Pte. Ltd.**  
(Joint Venture & Sequencing Centre)

**Novogene International Pte. Ltd.**  
25 Pandan Crescent #05-15 TIC Tech Centre, Singapore 128477

T: +65-8823-3182  
e: [marketing\\_amea@novogeneait.sg](mailto:marketing_amea@novogeneait.sg)

[en.novogene.com](http://en.novogene.com)