Novogene

Bacterial and Fungal Whole Genome Re-sequencing

Leading Edge Genomic Services & Solutions

Service Introduction

Bacterial and fungal whole genome re-sequencing is a critical tool to complete the genomes of known bacterium and fungi, as well as to compare multiple genomes or to map genomes of new organisms. It is of great importance to sequence entire genomes of bacterium and fungi in order to generate accurate reference genomes, to do microbial identification and other comparative genome studies.

Compared with traditional methods like PCR, next generation sequencing (NGS) excels in the way of multiplexing vast number of samples, providing identifications of SNP/InDel/SV with great reliability, turnaround time and cost performance.

Service Specifications

Library preparation and sequencing strategy

- Genomic DNA or PCR product will be fragmented to prepare 350 bp insert library
- Paired-end (PE) 150 bp strategy by using Illumina NovaSeq platform

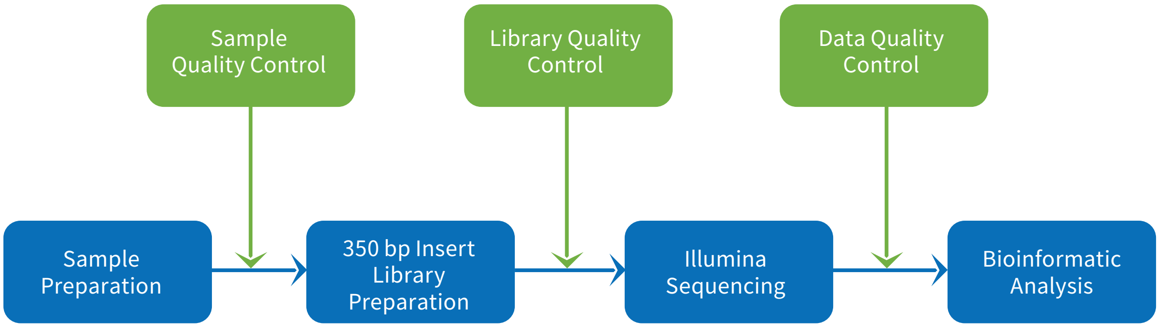
Quality standard and sequencing depth

- No less than 80% of bases with a Q30 (99.9% accuracy) quality score
- Recommend sequencing coverage of ⩾100× for bacterial genomes, ⩾50× for fungal genomes

Turnaround time and analysis options

- Typically 18 business days from confirmation of library preparation to raw data delivery
- Various analysis options from standard bioinformatics package to custom analysis

Project Workflow



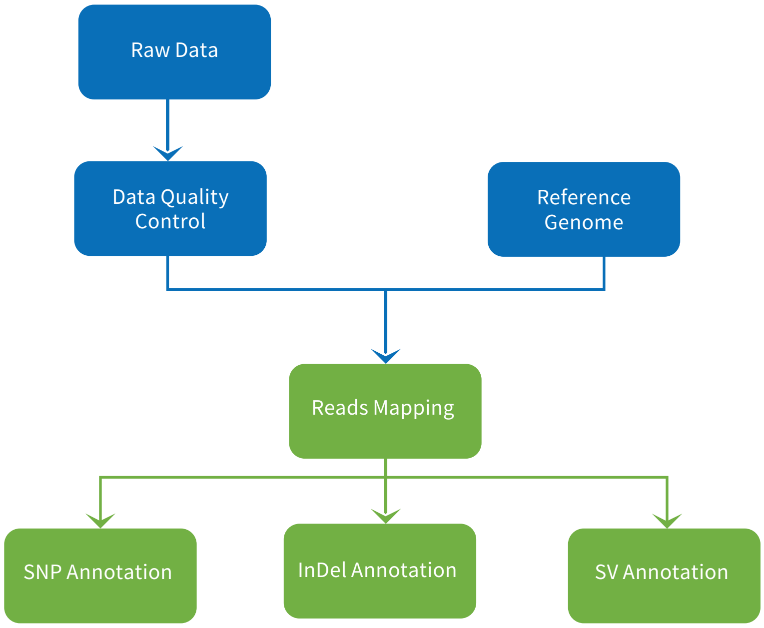
Sample Requirements

Sample Type	Amount	Volume	Concentration	Purity
Genomic DNA	⩾ 300 ng	⩾ 20 μL	⩾ 5 ng/μL	OD260/280=1.8-2.0, No degradation or RNA contamination
PCR Product	⩾ 1.5 μg	⩾ 20 μL	⩾ 20 ng/μL	OD260/280=1.8-2.0, No degradation or RNA contamination

Data Analysis

Besides raw data output, Novogene offers a variety of standard and customized analysis for your bacterial and fungal genome re-sequencing projects.

Standard Analysis Pipeline



- Data quality control: e.g. filtering reads containing adapter or with low quality
- Alignment with reference genome, statistics of sequencing depth and coverage
- SNP/InDel/SV calling, annotation and statistics

Custom Analysis Options

A wide range of customized bioinformatics analysis are available, please contact your Novogene representative.

Results Showcase

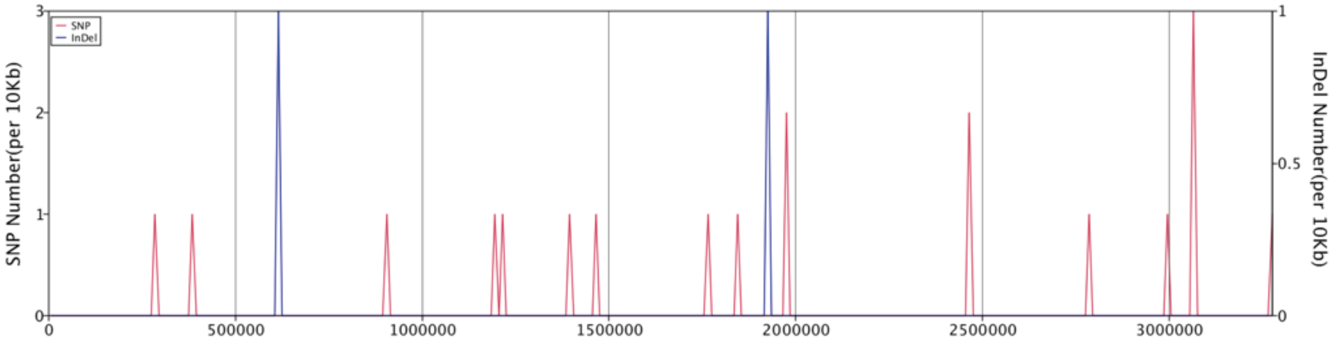


Figure. 1 SNP/InDel distribution. The horizontal axis represents chromosome of reference sequences, the vertical axis represents the number of SNP/InDel per 10 kb region, left ruler for the SNP number, right ruler for the InDel number.

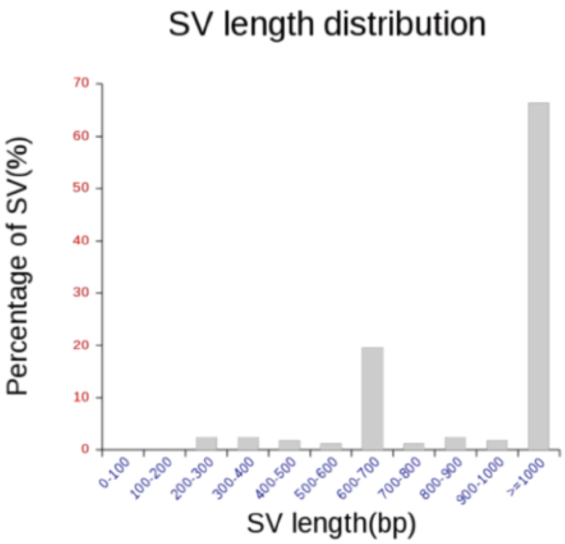


Figure. 2 SV length distribution. The horizontal axis represents the length range of SV, and the vertical axis represents the percentage of SV.

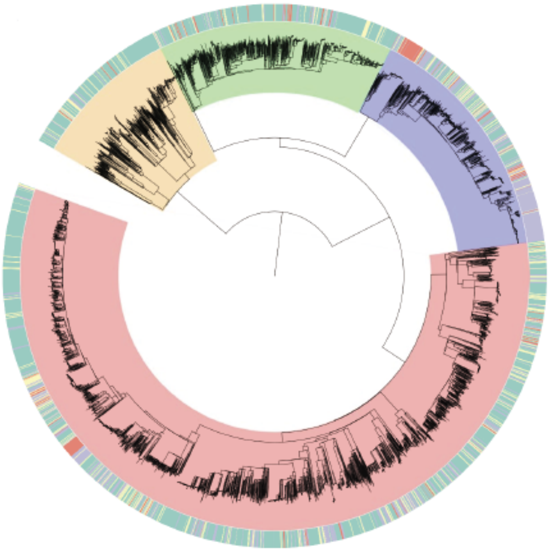


Figure. 3 Whole-genome phylogeny of the 6,465 *Mycobacterium tuberculosis* isolates. Maximum-likelihood phylogenetic tree constructed using 102,160 SNPs and 11,122 InDels spanning the whole genome and rooted on *Mycobacterium canetti*, with isolates color-coded by lineage (inner circle) and drug resistance status (outer circle)[1]

Reference

[1] Coll F, Phelan J, Hill-Cawthorne G A, *et al*. Genome-wide analysis of multi- and extensively drug-resistant *Mycobacterium tuberculosis*. *Nature Genetics*, 2018, 50(2):307-316.

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