

Bacterial Whole Genome Sequencing Service (Complete Genome)

Bacterial whole genome sequencing is an important tool for mapping genomes of novel organisms, finishing genomes of known organisms, or comparing genomes across multiple samples. Generating rapid and accurate bacterial genome sequence information is critical for detecting low frequency mutations, finding key deletions and insertions, and discovering other genetic changes among bacterial strains. Genetika Science Indonesia is offering bacterial whole genome sequencing service using Next Generation Sequencing (NGS) with Oxford Nanopore platform.



The advantages from our offering are:

1. 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/ CNV/ SV with great reliability.
2. Oxford Nanopore platform is a NGS technology that analyze DNA sequence in long-read lengths. Long-read sequencing offers easier assembly, ability to span repetitive genomic regions, and ability to identify large structural variation (SV).
3. When DNA extraction is done in Genetika Science's Lab, High Molecular Weight (HMW) DNA extraction is performed in order to fulfill the requirement of long-read sequencing system. Furthermore, bacterial complete genome can be achieved by using Oxford Nanopore long-read platform.
4. Reliable service with reliable results, fast turnaround time, and competitive price.
5. Reliable Bioinformatics analysis for both de novo and re-sequencing (with reference) analysis.

Sample Requirements

If HMW DNA extraction from bacteria culture is required:

Please send the bacteria in plate culture or liquid culture (preferred). Please make sure the culture is pure and single culture. The suggested number of cells required is 5×10^8 – 5×10^9 cells. Liquid culture is preferred due to larger amount of bacteria. When shipping of liquid culture to us is not possible to do, plate culture is still acceptable.

Note

- Please do not send in stab culture due to small amount of bacteria.
- When it is not possible for HMW DNA extraction, the extraction by column method will be done instead (will not get HMW DNA).
- HMW DNA from both gram positive and gram negative bacteria can be extracted well.

If genomic DNA is submitted

Genomic DNA concentration: minimum 50 ng/uL by Nanodrop

Volume: minimum 30 uL

Purity A260/280: 1.80 – 2.00

Workflow



What Will You Get From Genetika Lab?

- Raw data in fastq file.
- Bioinformatics analysis, includes:
 - Sequencing QC.
 - Consensus sequence (FASTA sequence file).
 - Completeness of assembled genomes.
 - Taxonomy check.
 - BLAST analysis of 16S gene.
 - Genome annotation (GO, KEGG, EC, and COG).
 - Variants analysis (SNP, InDel, CNV and SV analysis – for re-sequencing analysis).

For further inquiries, please feel free to contact us at:



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