SERVICE OVERVIEW

Long-read Human Whole Genome Resequencing

Service Description

Structural variants (SVs), including deletions, insertions, duplications, and inversions, account for most base pairs variations in an individual human genome.

Long-read sequencing can precisely position in SV, as well as solving complex SV structures. Long-read sequencing can effectively solve some of the insurmountable problems in short-read sequencing, and greatly improve the detection rate of large structural variation sites by constructing ultra-long fragment libraries.

The advent of new long-read sequencing technology has led to a revolution in genome sequencing, where long reads up to 100 Kb can be sequenced in a single run without PCR amplification. Long-read sequencing approaches provide the opportunity to more accurately and reliably detect SNP, InDel, SV and CNV at a much higher resolution.

Sequencing Service Specification

Our long-read sequencing services are performed with long-read platforms and standard bioinformatics pipelines for superior data quality and analysis results.

Sample Preparation and Services

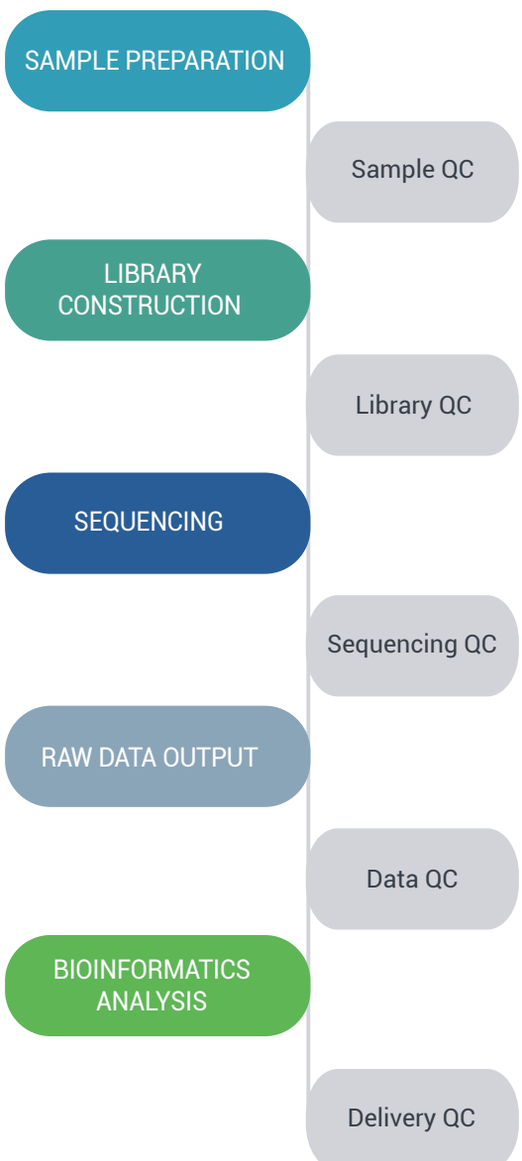
- PacBio Revio & Nanopore platforms are available
- 3-6 ml fresh blood samples are recommended.
- Appropriate sequencing strategies are recommended according to different data

Turnaround Time

- Nanopore（normal library）: Typical 30 working days from sample QC acceptance to data analysis report availability
- PacBio: Typical 30 working days from sample QC acceptance to data analysis report availability
- Expedited services are available; contact our specialist for details

Project Workflow

We care for your samples from the start through to the result reporting. Highly experienced laboratory professionals follow strict quality procedures to ensure the integrity of your results.



Quality Data Fast TAT Cost Effective

Sequencing Technology

Our long-read sequencing services are performed with the PacBio Revio platform and the Nanopore platform.

Data Analysis

Beside long-read data output, we offer a range of standard and customized bioinformatics pipelines for your project. Reports and output data flies are delivered in these file formats: FASTQ, BAM, VCF, JSON and TXT.

STANDARD BIOINFORMATICS ANALYSIS

1 Data filtering: filter the low quality reads
2 Data alignment: long reads were aligned to the human reference sequences by alignment software
3 Data statistics: statistical sequencing depth and coverage
4 SNP calling and annotation
5 InDel calling and annotation
6 SV calling and annotation
7 CNV calling and annotation

CUSTOM ANALYSIS

Further customization of bioinformatics analysis to suit your unique project is available:
Please contact our technical representative.

Sample Requirements

Sample Type	Library Type	Amount	OD	Sample Purity
Genomic DNA	PacBio HiFi CCS	m≥15μg, c≥80ng/μL	OD260/280：1.6-2.2 OD260/230：1.6-2.5	No contamination with RNA, protein or salt ions; colorless and transparent; non-sticky.
Genomic DNA	Normal Nanopore library	m≥9μg, c≥90ng/μL	OD260/280=1.8-2.2 OD260/230=1.8-2.2	
Genomic DNA	Nanopore Ultra long library	m≥16μg, c≥153ng/μL	OD260/280=1.6-2.5 OD260/230=1.6-2.5	

To Learn more

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

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