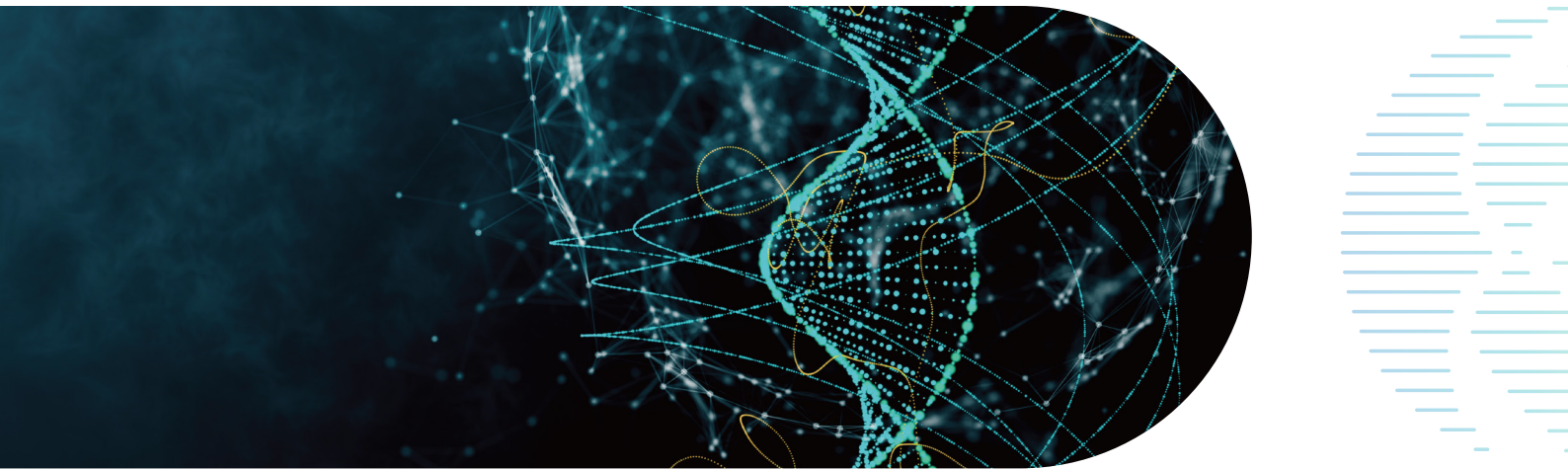


# Human Whole Genome Sequencing

## (Short Read Sequencing)



Human whole genome sequencing enables researchers to catalog the genetic constitution of individuals and capture all the variants present within the genome. This variant identification is typically utilized in studies of various diseases, especially in cancer development, human population, and pharmacogenomics.

At Novogene, a diverse range of sequencing platforms and strategies is available to meet your needs. Our cutting-edge options include the Illumina NovaSeq X Plus/6000 platforms, PacBio Revio/Sequel II systems, and the Nanopore PromethION system.

### Our Key Features & Advantages



#### Comprehensive Services

- Multiple sequencing platforms, sequencing strategies and bioinformatics analyses.



#### Competitive Turnaround Time

- 15-22 working days.



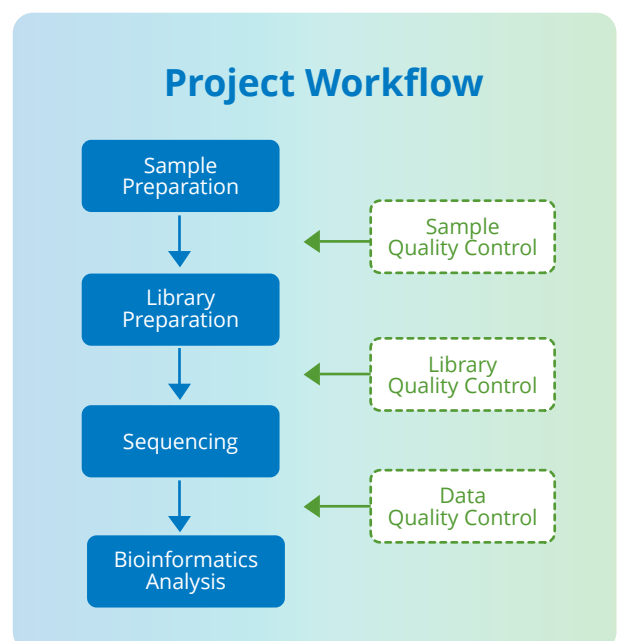
#### DNA Extraction Services

- Tissue, Blood, Plasma, PBMC, etc.



#### Real-Time Project Management

- 24/7 real-time Customer Service System (CSS).



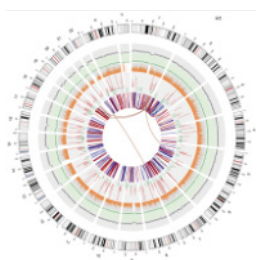
## Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity
Human 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
	FFPE* DNA	≥ 400 ng	≥ 20 µL	≥ 15 ng/µL	Fragments longer than 1,000bp
Human PCR-free Library (350bp)	Genomic DNA	≥ 1.2 µg	≥ 20 µL	≥ 50 ng/µL	OD260/280= 1.8-2.0; No degradation, No contamination, No color

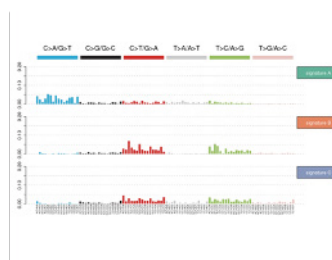
## Analysis Content

Standard Analysis	Advanced Analysis
<ol style="list-style-type: none"> <li>1. Data quality control</li> <li>2. Alignment with reference genome</li> <li>3. SNP/InDel/SV/CNV calling, annotation and statistics</li> <li>4. Somatic SNP/InDel/ SV/ CNV calling, annotation, and statistics (for paired tumor samples only)</li> </ol>	<ol style="list-style-type: none"> <li>1. Tumor Mutation Burden Analysis ( Cancer)</li> <li>2. Identification of Driver Mutations in Noncoding Regions (Cancer)</li> <li>3. Candidate Variant Filtration (Disease)</li> <li>4. ACMG Classification for Variants (Disease)</li> <li>5. HLA Typing (Personalized)</li> <li>6. CRISPR/Cas9 Off-target Analysis (Personalized)</li> </ol>

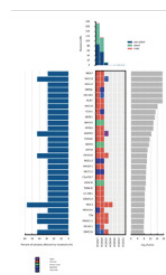
## Demo Analysis Result



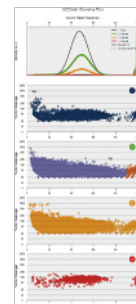
Circos visualizing genetic variants



Mutational Spectrum & Mutational Signature Analyses



Significantly Mutated Gene & Pathway Landscape Analysis



Intra-tumor Heterogeneity Analysis

If you are interested to explore long read sequencing possibilities with PacBio and Nanopore platforms, please contact us for more details.

### Novogene AMEA (Asia Pacific, Middle-East & Africa)

[novogene.com/amea-en](https://novogene.com/amea-en)    [marketing\\_amea@novogeneait.sg](mailto:marketing_amea@novogeneait.sg)

[NovogeneAIT](#)    [NovogeneAMEA](#)

© 2024 Novogene Co., Ltd. All Rights Reserved.

Information and specifications are subject to change at any time without notice. Please contact your Novogene representative.

AMEA\_hWGS\_v1\_2024