Novogene

Human Genome Sequencing

hWGS & hWES

Leading Edge Genomic Services & Solutions

Human

Human Whole Genome Sequencing

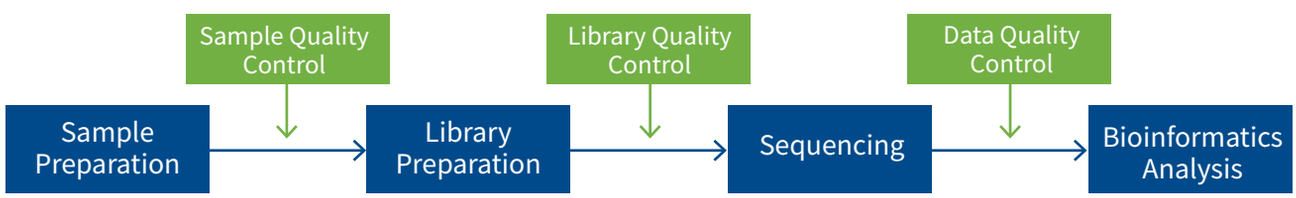
Human whole genome sequencing (hWGS) enables researchers to catalog a genetic constitution of individuals and capture all variants present in a single assay. It is utilized to study cancer and a variety of diseases, as well as human population evolution studies and pharmacogenomics.

Equipped with the powerful Illumina NovaSeq 6000 system, Novogene is capable of sequencing up to 280,000 human genomes per year at the lowest cost per genome. With extensive experience in whole genome sequencing and advanced bioinformatics capabilities, Novogene is able to expertly meet customer needs for delivering large project results with quick turnaround times and the highest quality results.

Novogene Advantage

- Scalable Sequencing Capacity
- Industry-Leading Data Quality Guarantee (Q30 > 80%)
- Competitive Pricing
- Extensive In-House Bioinformatics Expertise

Project Workflow



Sequencing Specifications

Sample Requirements

- DNA Amount: ⩾ 200 ng (gDNA from fresh tissues); ⩾ 0.8 μg (gDNA from FFPE)
- DNA Concentration: ⩾ 10 ng/μL
- Purity: OD 260/280 = 1.8-2.0; no degradation and no contamination (RNA or protein)

Sequencing Strategy

- 350 bp insert DNA library
- NovaSeq 6000 platform, PE150

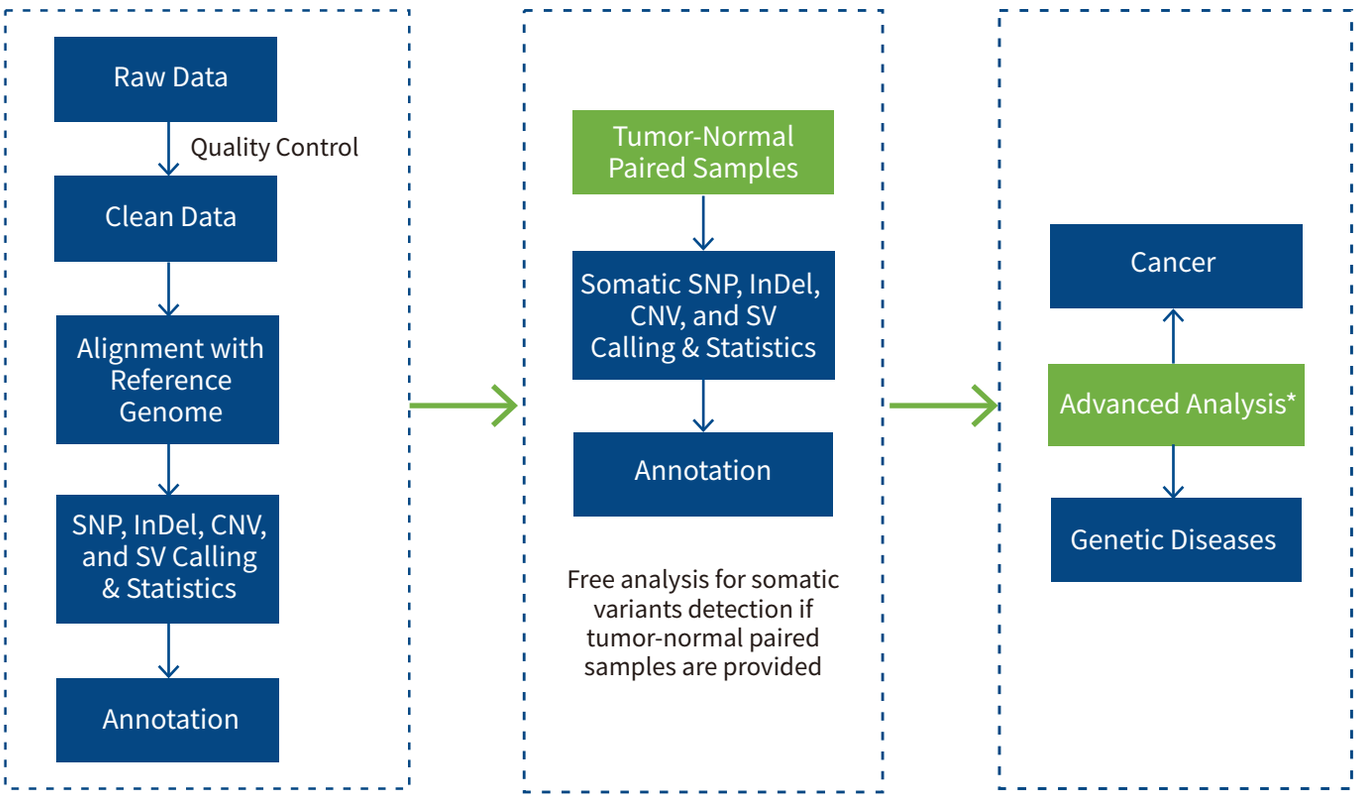
Recommended Sequencing Depth

- For tumor tissues: 50×, adjacent normal tissues and blood 30×
- For rare diseases: 30-50×

Turnaround Time

- 11 working days after verification of sample quality without data analysis (depending on sample size)

Analysis Pipeline



* Detailed items on advanced analysis to suit your project are available. Please contact us for more information.

Novogene Powered Publications

Year	Journal	Title
2020	*Nature*	A genomic and epigenomic atlas of prostate cancer in Asian populations
2020	*Nature Cell Biology*	Chromosomal translocation-derived aberrant Rab22a drives metastasis of osteosarcoma
2020	*Nature Communications*	Somatic *SF3B1* hotspot mutation in prolactinomas
2020	*JAMA Cardiology*	Association of Rare *PTGIS* Variants With Susceptibility and Pulmonary Vascular Response in Patients With Idiopathic Pulmonary Arterial Hypertension
2019	*Nature*	Proteomics identifies new therapeutic targets of early-stage hepatocellular carcinoma
2019	*Journal of Hepatology*	Genomic sequencing identifies WNK2 as a driver in hepatocellular carcinoma and a risk factor for early recurrence
2019	*European Respiratory Journal*	Germline *BMP9* mutation causes idiopathic pulmonary arterial hypertension
2018	*Proceedings of the National Academy of Sciences*	Identification of genetic risk factors in the Chinese population implicates a role of immune system in Alzheimer's disease pathogenesis
2018	*Cell*	Mutational landscape of secondary glioblastoma guides MET-targeted trial in brain tumor

Human Whole Exome Sequencing

Exome sequencing provides a cost-effective alternative to whole genome sequencing, as it targets only the protein coding region of the human genome responsible for a majority of known disease-related variants. Whether you are conducting studies in rare mendelian disorders, complex disease, cancer research, or human population studies, Novogene's comprehensive human whole exome sequencing (hWES) service provides a high-quality, affordable, and convenient solution.

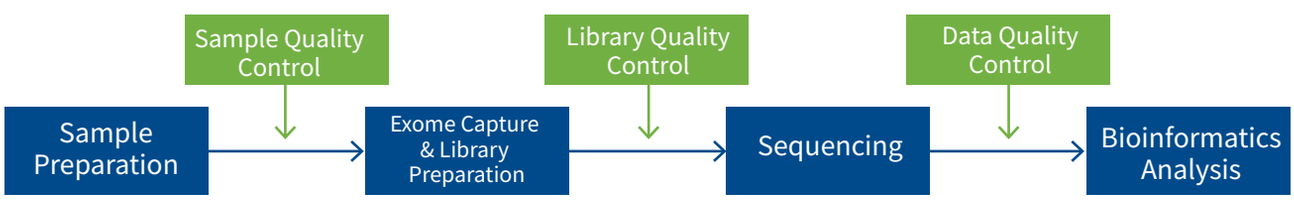
Advantages of hWES

Targeted Protein Coding Region:
by capturing and sequencing protein coding region, hWES is utilized to reveal variants related to protein structure

High Accuracy:
with high sequencing depth, hWES facilitates detection of common variants and rare variants with frequencies lower than 1%

Cost Effective:
hWES yields approximately 85% of human disease mutations from 1% of human genome

Project Workflow



Sequencing Specifications

Exome Capture

- Agilent SureSelect Human All Exon V6 Kit

Sequencing Strategy

- NovaSeq 6000 platform, PE150

Sample Requirements

- DNA Amount: ⩾ 400 ng (gDNA from fresh tissues); ⩾ 0.8 μg (gDNA from FFPE)
- DNA Concentration: ⩾ 20 ng/μL
- Purity: D260/280 = 1.8-2.0; no degradation and no contamination (RNA or protein)

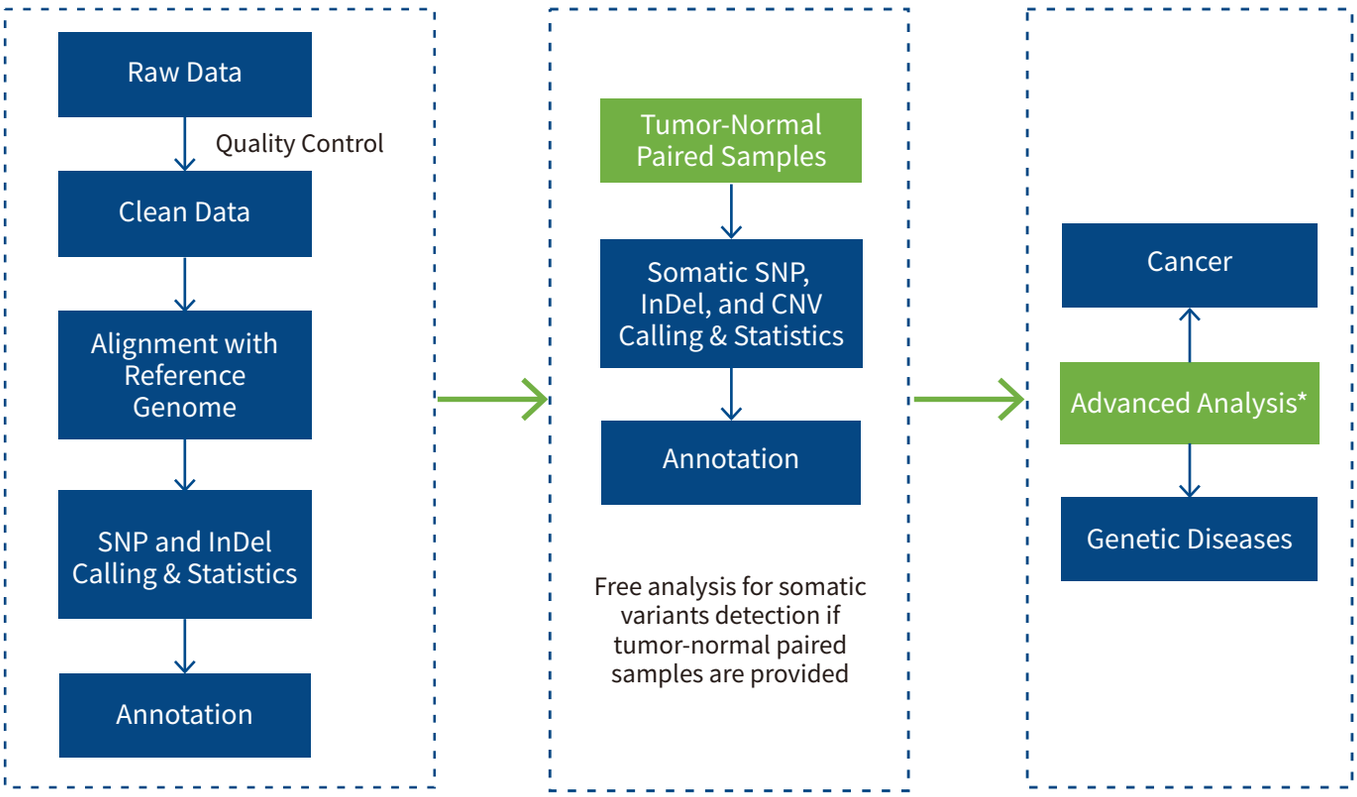
Recommended Sequencing Depth

- For Mendelian disorders/rare diseases: effective sequencing depth above 50×
- For tumor samples: effective sequencing depth above 100×

Turnaround Time

- Within 13 working days after verification of sample quality without data analysis (depending on sample size)

Analysis Pipeline



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2019	*Gut*	Integrated multiomic analysis reveals comprehensive tumour heterogeneity and novel immunophenotypic classification in hepatocellular carcinomas
2019	*Journal of Hepatology*	Genomic sequencing identifies WNK2 as a driver in hepatocellular carcinoma and a risk factor for early recurrence
2019	*European Respiratory Journal*	Germline *BMP9* mutation causes idiopathic pulmonary arterial hypertension
2019	*Cancer Research*	Multiregion Sequencing Reveals the Genetic Heterogeneity and Evolutionary History of Osteosarcoma and Matched
2018	*Cell*	Mutational landscape of secondary glioblastoma guides MET-targeted trial in brain tumor
2018	*Nature Communications*	Whole-exome sequencing reveals the origin and evolution of hepato-cholangiocarcinoma

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