



Human Genome Sequencing hWGS & hWES

Leading Edge Genomic Services & Solutions

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



For rare diseases: 30-50×

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	<i>Nature Communications</i>	Somatic <i>SF3B1</i> hotspot mutation in prolactinomas
2020	JAMA Cardiology	Association of Rare <i>PTGIS</i> 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 <i>BMP9</i> 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



Project Workflow



Sequencing Specifications

Exome Capture

- Agilent SureSelect Human All Exon V6 Kit

Sequencing Strategy

- NovaSeq 6000 platform, PE150

Sample Requirements

- DNA Amount: \geq 400 ng (gDNA from fresh tissues); \geq 0.8 µg (gDNA from FFPE)
- DNA Concentration: \geq 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 imes
- For tumor samples: effective sequencing depth above 100×

Turnaround Time

 Within 22 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	<i>Annals of the Rheumatic Diseases</i>	Germline genetic patterns underlying familial rheumatoid arthritis, systemic lupus erythematosus and primary Sjögren's syndrome highlight T cell-initiated autoimmunity
2020	JAMA Cardiology	Association of Rare <i>PTGIS</i> Variants With Susceptibility and Pulmonary Vascular Response in Patients With Idiopathic Pulmonary Arterial Hypertension
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 <i>BMP9</i> 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	<i>Nature Communications</i>	Whole-exome sequencing reveals the origin and evolution of hepato-cholangiocarcinoma



Novogene Corporation Inc.

• 8801 Folsom Blvd #290, Sacramento, CA 95826

🕾 916-252-0068-383 🛛 🗷 inquiry_us@novogene.com 🖉 en.novogene.com

For Research Use Only. Exclusive for Clients in North and South America.

Copyright©2011-2021 Novogene Corporation. All Rights Reserved. Information and specifications are subject to change at any time without notice: Please contact your Novogene representative.

