Novogene

Human Whole Exome Sequencing Solutions

Exome sequencing provides a cost-effective alternative to whole genome sequencing. 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 solutions.

Our Key Features & Advantages

Reliable & Faster Turnaround Time

The strategic locations of our labs across Asia and our extensive NGS system can provide faster turnaround time.

Real-time Project Management

View and manage your projects on our customer service portal.

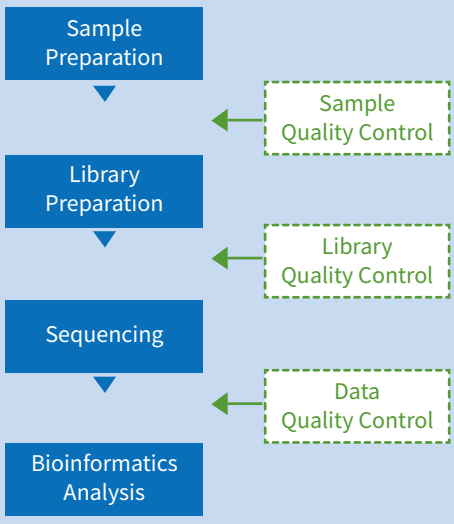
Multiple Choices

We offer multiple library choices (Agilent, Kapa and IDT probe) and a comprehensive data analysis pipelines for your research needs.

Unsurpassed Data Quality

We guarantee that ⩾ 80% of bases have a sequencing quality score ⩾ Q30, exceeding Illumina's official guarantee of ⩾ 75%.

Project Workflow



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Standard Analysis Pipeline

Standard Analysis	Advanced Analysis
Data quality control	Tumor evolution analysis (Cancer)
Alignment with reference genome, statistics of sequencing depth and coverage	Tumor neoantigen identification (Cancer)
SNP/InDel/SV/CNV calling, annotation and statistics	Candidate variant identification (Disease)
Somatic SNP/InDel/SV/CNV calling, annotation and statistics (paired tumor samples)	Linkage analysis (Disease)
	Xenograft tumor analysis (PDX)

Standard Analysis Content

Platform	Illumina Novaseq 6000
Read Length	Paired-end 150
Recommended Sequencing Depth	For Mendelian disorder/rare disease: effective sequencing depth above 100× (12G) For tumor samples: effective sequencing depth above 200× (24G)
Data Quality	Guarantee Q30 ≥ 80%
Turnaround Time	Approximately 4 weeks from verification of sample quality to data delivery (<24 samples)

Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity
DNA Library (Human Exome)	Genomic DNA	≥ 400 ng	≥ 20 ng/μL	≥ 20 ng/μL	OD260/280=1.8~2.0 No degradation, no contamination
	FFPE Genomic DNA	≥ 800 ng	-	-	Fragments should be longer than 1000 bp

Publications

Listed below are some publications that were supported by Novogene solutions.

Journal	IF	Title
International Journal of Cancer	5.229	Preliminary exploration of potential molecular therapeutic targets in recurrent and metastatic parathyroid carcinomas.
Eur Respir J	7.877	Germline BMP9 mutation causes idiopathic pulmonary arterial hypertension.

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