


Plant and Animal Whole Genome Sequencing (Short Read Sequencing)




Whole genome sequencing is a comprehensive method that enables the detection of all genetic information within individuals or populations. With the availability of a reference genome, whole genome sequencing effectively identifies the mutations, leading to further analysis in various fields such as disease development, and agricultural breeding programs.

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


Our Key Features & Advantages

- 


Extensive Experience

 - 16,000+ SCI articles, 100,000+ accumulative impact factor.
- 

Competitive Turnaround Time

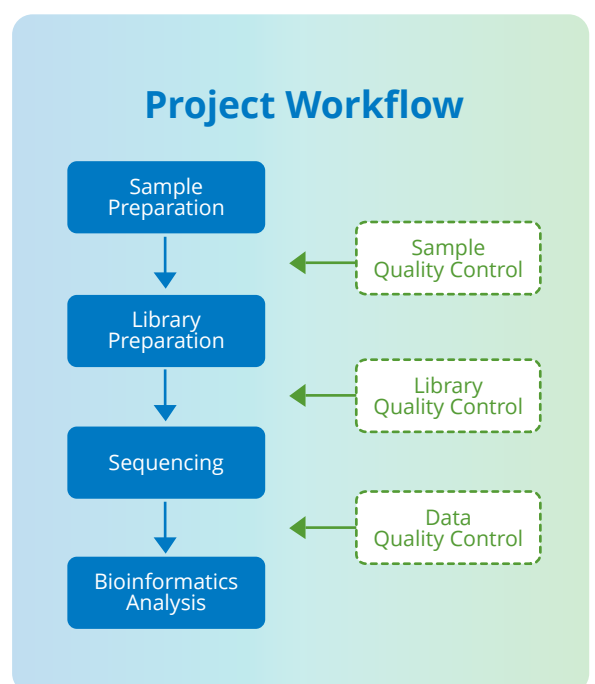
 - 15~22 working days.
- 

Comprehensive Services

 - Multiple sequencing platforms, sequencing strategies and bioinformatics analysis.
- 

Real-Time Project Management

 - 24/7 real-time customer service system (CSS system).



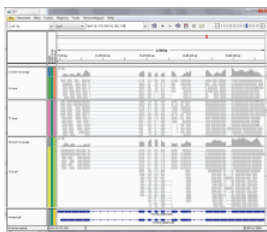
Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity
Plant & Animal Whole Genome Library (350bp)	Genomic DNA	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	OD260/280=1.8~2.0; No degradation, No contamination
Plant & Animal PCR-free Library (350bp)	Genomic DNA	≥ 1.2 μg	≥ 20 μL	≥ 50 ng/μL	

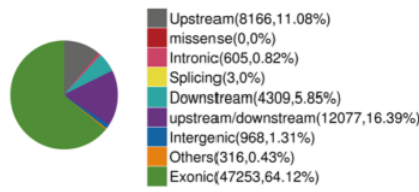
Analysis Content

Standard Analysis	Advanced Analysis	Customized Analysis
<ol style="list-style-type: none"> 1. Data quality control 2. Alignment with reference genome 3. Variant (SNP, InDel) calling, annotation and statistics 	<ol style="list-style-type: none"> 1. Data quality control 2. Alignment with reference genome 3. Variant (SNP, InDel) calling, annotation and statistics 4. SV calling, annotation and statistics 5. CNV calling, annotation and statistics 	<ol style="list-style-type: none"> 1. Genome-wide association study 2. Bulked Segregation Analysis 3. Population Genetics Analysis <p>Contact us for comprehensive information, we are here to provide you with personalized solutions.</p>

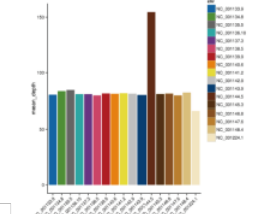
Demo Analysis Result



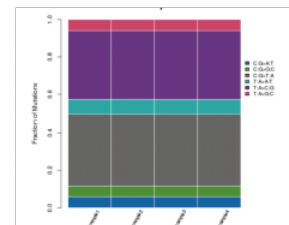
IGV visualization



The number of SNPs in different regions of genome



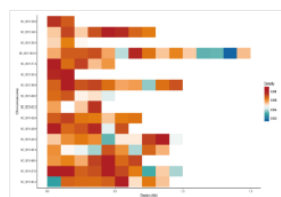
Mapping depth of each chromosome



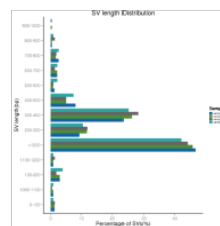
Mutation spectrum



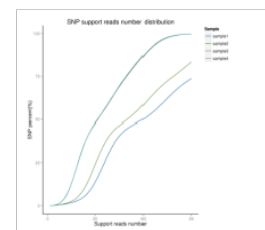
Whole genome variants distribution



Variants density



SV length distribution



Support reads distribution

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 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_PAWGSshortread_V1_2024