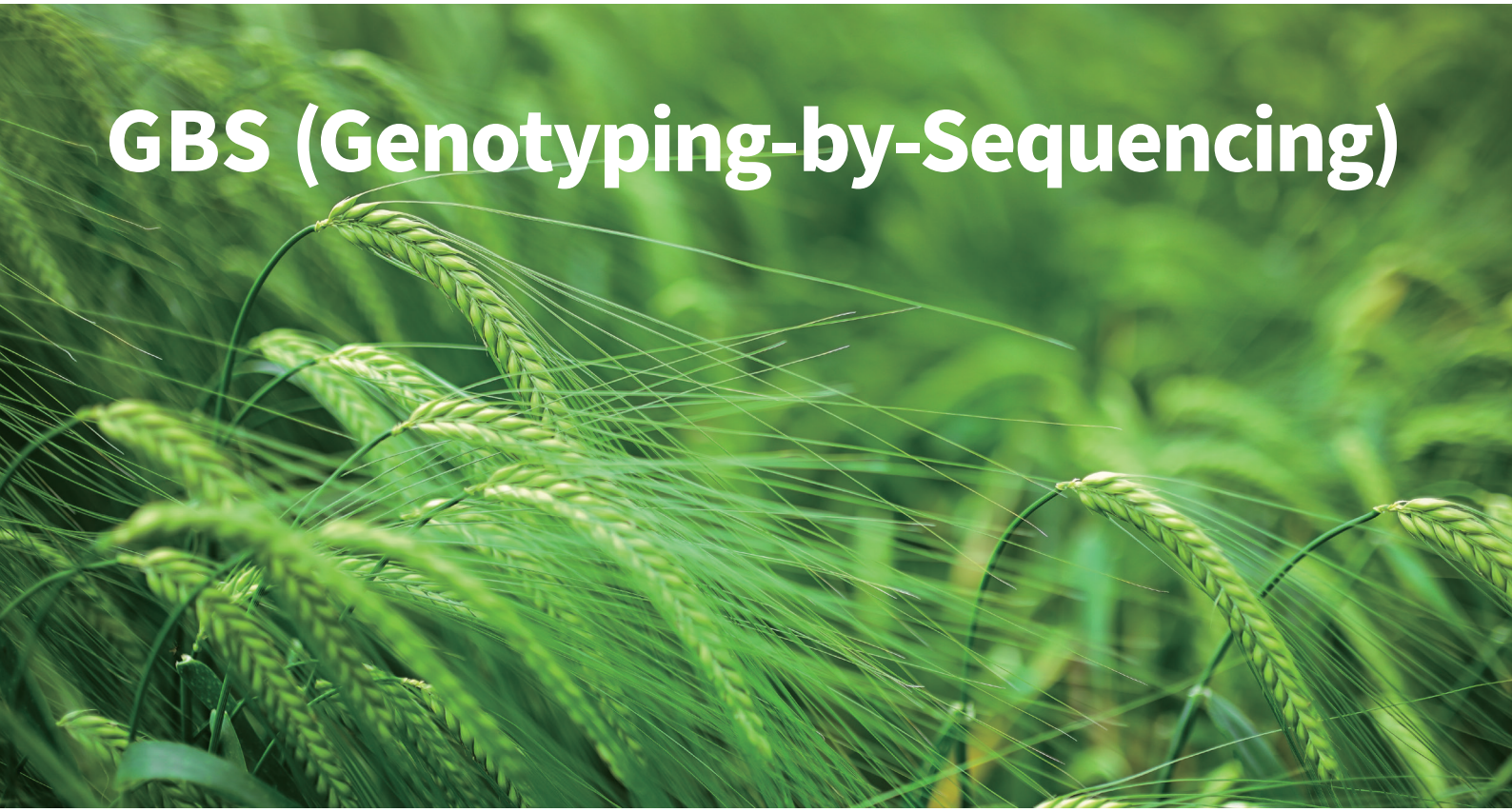
Novogene

GBS (Genotyping-by-Sequencing)



GBS (Genotyping-by-Sequencing) is a common Reduced-Representation Genome Sequencing technique in which genomic DNA is enzymatically digested, and then the ends of the fragment are sequencing in high throughput.

GBS technology can flexibly adjust the number of tags required to capture the restriction sites for varied research purposes, thus controlling the range of the capture sequence. The GBS can reduce the complexity of the genome with lower data amount, simplify the operation and save the cost, which is especially suitable for large amounts of samples.

Our Key Features & Advantages

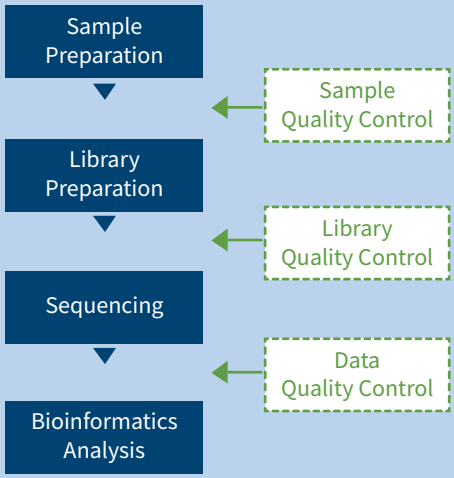
Comprehensive Analysis
High-confidence SNP markers for downstream trait loci and population evolution analysis.

Versatile Conditions
Feasible for samples with and without reference genome.

Extensive Experience
Completed numerous genotyping sequencing projects for our customers and published highlighted journal articles.

Real-time Project Management
Our Customer Service System (CSS) online platform allows for real-time project tracking 24/7, collaboration with your team and other helpful information.

Project Workflow



Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity (Qubit/Agarose Gel)
Genotyping by Sequencing (GBS)	Genomic DNA	⩾ 0.6 μg	⩾ 15 μL	⩾ 20 ng/μL	OD260/280 = 1.8-2.0 No degradation or RNA contamination

Standard Analysis Content

Standard Analysis (With Reference)	Standard Analysis (Without Reference)
Data quality control: filtering reads containing adapter or with low quality	**Data quality control:** filtering reads containing adapter or with low quality
Mapping: Alignment with reference genome, statistics of sequencing depth and coverage	Merge paired-end reads as reference
SNP/Indel calling, annotation and statistics	**Mapping:** Alignment with reference, statistics of sequencing depth and coverage
SNP genotyping analysis	SNP/Indel calling, annotation and statistics
Tags statistics	SNP genotyping analysis
	Tags statistics

Publications

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

Journal	IF	Title
Front Plant Sci	5.753	Identification and Functional Verification of Cold Tolerance Genes in Spring Maize Seedlings Based on a Genome-Wide Association Study and Quantitative Trait Locus Mapping
Front Plant Sci	5.753	Construction of a SNP-Based High-Density Genetic Map Using Genotyping by Sequencing (GBS) and QTL Analysis of Nut Traits in Chinese Chestnut (Castanea mollissima Blume)
Front Plant Sci	5.753	Dissection of the Genetic Basis of Yield-Related Traits in the Chinese Peanut Mini-Core Collection Through Genome-Wide Association Studies
BMC Genomics	3.969	Development of a high-density linkage map and mapping of the three-pistil gene (Pis1) in wheat using GBS markers
Euphytica	1.895	Construction of a high-density genetic map using genotyping by sequencing (GBS) for quantitative trait loci (QTL) analysis of three plant morphological traits in upland cotton (Gossypium hirsutum L.)

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