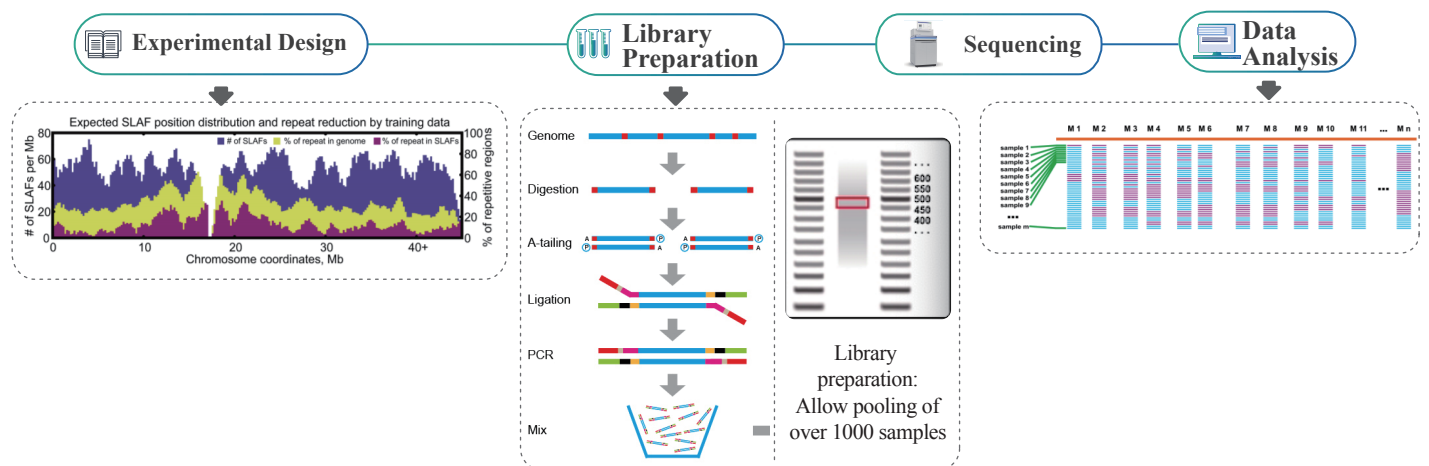


Specific-Locus Amplified Fragment Sequencing (SLAF-Seq)

Reduced Representation Genome Sequencing (RRGS)

High-throughput genotyping through reduced representation genome sequencing (RRGS) is a cost-effective alternative to whole genome sequencing (WGS). It involves extracting restriction fragments to create a reduced representation library (RRL), enabling efficient genetic marker discovery. Specific-locus amplified fragment sequencing (SLAF-Seq) is a self-developed strategy for SNP genotyping with or without a reference genome.



Service Workflow



Bioinformatics

- Raw data quality control**
- Reference genome alignment**
 - SLAF tag identification
 - SNP identification
 - SNP annotation (With reference genome)
 - InDel identification and annotation (With reference genome)

Service Advantages

- SLAF technology with high-throughput sequencing can generate hundreds of thousands of markers in a single run, suiting scientific research requirements.
- Bioinformatics pre-design enables personalized experimental scheme with suitable enzyme combinations for different species and research objectives.
- Self-developed bioinformatics workflow ensures high-quality analysis for the SLAF-seq.
- Even distribution of SLAF Tags with an average of 1 SLAF/4 kb and less than 5% of repetitive sequences in SLAF data.
- Extensive experience in hundreds of species covering plants, mammals, birds, insects, aqua organism, etc.

Service Specifications

Genome Size	Recommended SLAF Tags	Applications	Recommended Population Scale	Sequencing strategy and depth	
				Depth	Tag Number
< 500 Mb	100 K or WGS	GWAS	Sample number ≥ 200	10X	According to genome size
500 Mb-1 Gb	100 K			10X	
1 Gb-2 Gb	200 K	Genetic Evolution	Individuals of each subgroup ≥ 10 ; total samples ≥ 30	10X	According to genome size
Giant or complex genomes	300-400 K			10X	

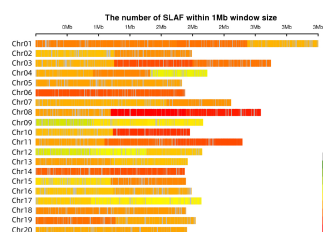
Sample Requirements

Sample Requirements

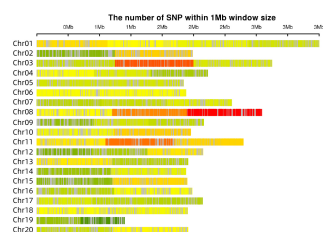
Sample	Conc.(ng/μl)	Amount(μg)	Purity	
DNA extracts	>35	>1.6 (Volume>15 μl)	OD260/280: 1.6-2.5	Limited degradation and contamination

Note: Three samples, each with three enzyme schemes, will be performed for pre-experimentation.

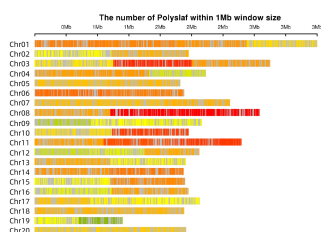
Demo Results



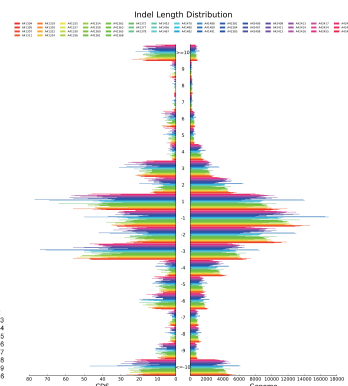
Poly-SLAF Distribution



SNP Distribution



SLAF Distribution



InDel Length Distribution

Featured Publications

Year	Journal	Article	Applications
2023	Journal of Integrative Agriculture	SLAF marker based QTL mapping of fruit-related traits revealed a major-effect candidate locus ff2.1 for flesh firmness in melon	Genetic Map
2023	Research Square	Genome-wide association analysis of resistance to frogeye leaf spot China race 7 in soybean based on high-throughput sequencing	GWAS
2023	Forests	Insight into the Complex Genetic Relationship of Chinese Fir (Cunninghamia lanceolata (Lamb.) Hook.) Advanced Parent Trees Based on SSR and SNP Datasets	Evolutionary Genetics
2023	Agriculture	QTL Mapping for Fiber Quality Based on Introgression Lines Population from <i>G. hirsutum</i> × <i>G. tomentosum</i>	Marker Development



Biomarker Technologies (BMKGene) GmbH

 BioZ, Johann-Krane Weg
 42, 48149 Münster, Germany
  tech@bmkgene.com
 www.bmkgene.com

Copyright©2009-2023 Biomarker Technologies (BMK) GmbH.
 All Rights Reserved. Information and specifications are subject
 to change at any time without notice.