2b-RAD Sequencing

Your Gateway to High-Density SNP Genotyping

Reduced-representation sequencing (RRS) refers to the strategic use of appropriate restriction enzymes to digest target genomes, thereby reducing genome complexity and sequencing volume. This approach offers a cost-effective means to develop high-density SNP profiles, boasting simplicity in operation and independence from reference genomes. Key RRS techniques include RAD, GBS, 2b-RAD, and dd-RAD, each offering unique advantages tailored to specific research needs. CD Genomics licensed sequencing-based SNP genotyping technologies (**Genotyping by sequencing, 2b-RAD sequencing and ddRAD-seq)** use restriction digests and molecular identifiers (MIDs) to reduce subsequent sequencing library and processing steps, speeding up your genotyping projects.

Why Choose Our 2b-RAD Sequencing?

Versatility 2b-RAD accepts degraded DNA samples, making it the top choice for challenging samples. Say goodbye to DNA quality concerns and hello to seamless library construction and sequencing.

High Accuracy SNP Genotyping Uniform tag lengths prevent PCR amplification biases, resulting in uniform sequencing depths and highly accurate SNP genotyping. Bid farewell to variability and embrace precise results.

Uniform Tag Distribution Enjoy evenly distributed tags throughout the genome, offering unparalleled coverage and enhancing SNP discovery efficiency.

Flexible Tag Density Control Tailor tag density according to your needs by selecting different combinations of IIB-type restriction enzymes. Increase density for comprehensive coverage or decrease it for enhanced sequencing depth with selective adapters.

Minimal DNA Requirement With 2b-RAD, even tiny DNA samples (1-10 ng) can yield successful results, offering unprecedented opportunities for experimentation with limited samples.

Diverse Marker Development While primarily focused on SNP marker development, 2b-RAD technology can also address large-scale marker deficiencies in reference species, offering a comprehensive solution for diverse projects.

Exceptional Reproducibility Our technology utilizes IIB-type restriction enzymes for single-enzyme digestion, ensuring uniform fragment lengths and eliminating batch effects. Experience consistent results across experiments, enabling seamless data integration.

Workflow of 2b-RAD Sequencing

Enzymatic Cleavage

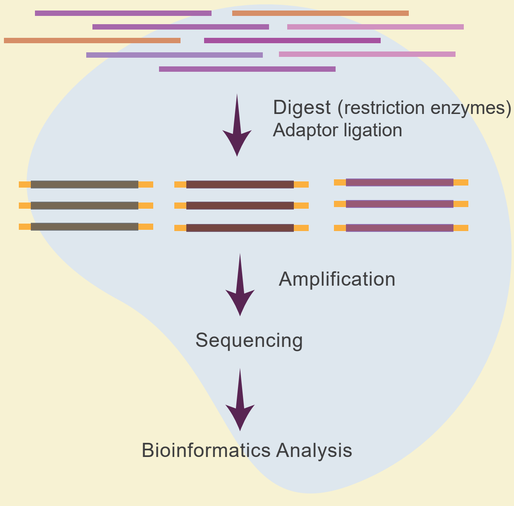
Employ IIB-type restriction enzymes (e.g., BsaXI) to cleave genomic DNA, generating uniform 33 bp tags flanking recognition sites.

Tag Enrichment

Enrich the generated tags for high-throughput sequencing, laying the foundation for comprehensive SNP screening and genotyping across the entire genome.

Bioinformatics Analysis

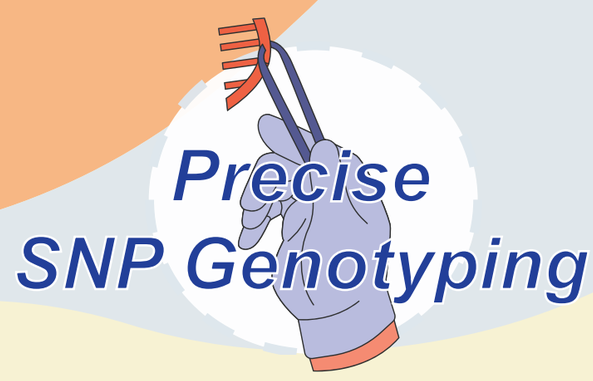
Leverage advanced bioinformatics tools to analyze sequencing data, unraveling the genetic landscape with high-throughput SNP discovery and genotyping.



CD Genomics
The Genomics Services Company

Revolutionizing Genetic Exploration with 2b-RAD Sequencing

Embark on a journey of scientific breakthroughs as our 2b-RAD sequencing service takes your projects and research to new heights. Unleash the power of genomics with advanced technology designed to enhance the efficiency, precision, and scope of your genetic studies.



Bid farewell to inaccuracies. 2b-RAD's uniform tag lengths and high sequencing depth ensure accurate SNP genotyping, providing a solid foundation for your genetic analyses.

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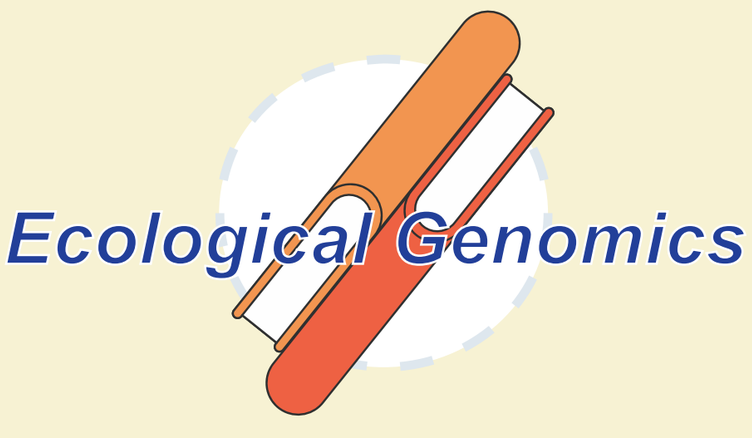
Support wildlife conservation efforts by elucidating genetic diversity, population structure, and migration patterns. Inform conservation strategies, mitigate genetic risks, and preserve biodiversity for future generations.

Unravel the genetic basis of disease resistance in plants and animals using 2b-RAD sequencing. Identify genetic markers associated with resistance traits, facilitating the development of disease-resistant varieties and breeds.



Explore the intricate relationship between genes and the environment with 2b-RAD sequencing. Investigate adaptive genetic variation, ecological interactions, and evolutionary responses to environmental changes.

Traditional amplicon sequencing methods are plagued by amplification biases, off-target amplification, and low resolution. Moreover, they cannot simultaneously detect bacteria, fungi, and archaea. While shotgun metagenomic sequencing offers solutions, it demands high-quality DNA samples and faces cost constraints when dealing with large-scale clinical samples. Additionally, it's unsuitable for samples containing substantial host DNA, such as paraffin-embedded tissues and tumor samples.

With CD Genomics' 2b-RAD sequencing service, embark on a journey of discovery, innovation, and scientific excellence. Elevate your research projects, unlock genetic insights, and pave the way for groundbreaking discoveries that shape the future of genetics and beyond.

Contact CD Genomics for more inspiration and service content.

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