Capture-Seq

Finding needles in the genomic haystack

Capture-Seq is the most comprehensive targeted genotyping system for:

- Allele mining: pre-breeding marker discovery
- SNP genotyping and haplotyping
- QTL mapping and candidate gene identification
- Genetic fingerprinting
- Polyploid genomic selection
- Resistance gene sequencing (RenSeq)
- Pan-genome construction and mapping

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About Capture-Seq

Capture-Seq is a targeted next generation sequencing (NGS) solution for characterising hundreds of thousands genomic targets in any species (including complex polyploids). These results can be flexibly applied towards pre-breeding marker discovery, including diversity analysis, and high-throughput genotyping for breeding. Rapid Genomics offers an extensive library of optimised Capture-Seq genotyping panels for a wide range of plants and animals, as well as the option to design customised panels for novel commercial or research solutions.

Capture-Seq's flexibility, both in scope and application, provides a superior option to alternative NGS solutions. Capture-Seq results are more compatible with complex genomes than array (SNP chip) technology. Legacy data from any platform can be incorporated into Capture-Seq panels, ensuring consistency with prior datasets in any agricultural programme. Additionally, Capture-Seq panels can reliably recover similar genomic targets across closely related species.

Capture-Seq solutions are available for both high and low volume applications. There is no minimum sample number required to utilise an existing Capture-Seq panel or for custom Capture-Seq panel design.

Full-service Capture-Seq solutions, including custom panel designs, are delivered at Rapid Genomics starting from tissue/DNA to FASTQ data, SNP calls or additional bioinformatic data analyses.

Capture-Seq projects follow 3 easy steps:

1 Contact us

- Project scope
- Research goals and timelines
- Species/group and sample volume

2 Sample processing

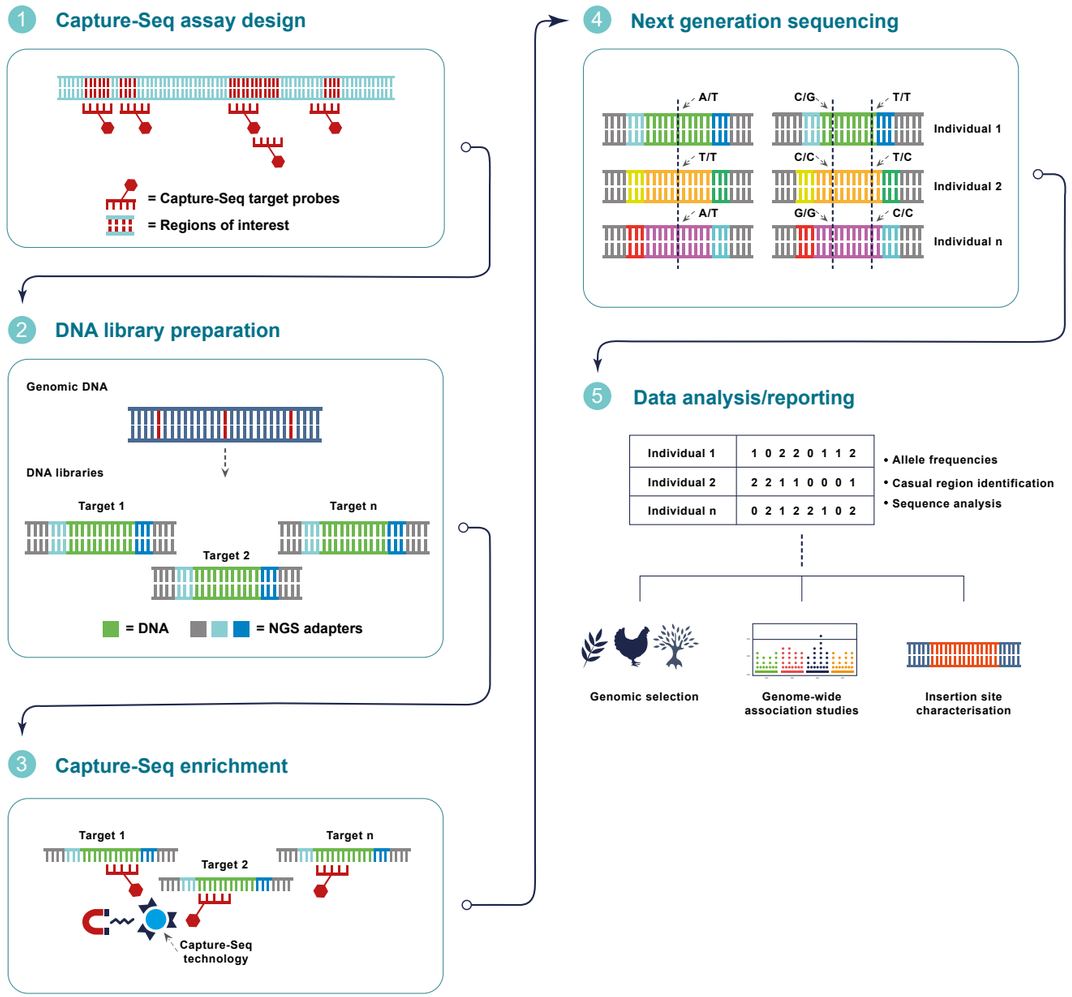
- Capture-Seq probe synthesis
- Predesigned or custom
- Batch submissions or all-at-once

3 Receive results

- FASTQ data or assembled loci

Species	Genotyping objective	# Capture-Seq targets	# SNPs detected	Missing data %
Maize	Fine mapping resistance genes (R-genes)	5,000	4,623	0.15
Sugarcane	Genomic selection and genetic mapping	10,000	37,976	0.1
Loblolly pine	Genomic selection	20,000	67,525	0.002
Blueberry	Genomic selection and genetic mapping	31,000	205,057	0.03

Capture-Seq workflow and technology



Capture-Seq solutions begin with bioinformatically designing Capture-Seq probes (for custom panels) to target genomic regions of interest **(1)**. Once finalised, samples are processed to NGS DNA libraries **(2)** and Capture-Seq enrichment selectively recovers the targeted regions while removing other, undesirable DNA sequences **(3)**. After Capture-Seq enrichment, libraries are sequenced via NGS **(4)** and processed to identify markers for additional data analyses and applications **(5)**.

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