RAPID GENOMICS

CAPTURE-SEQ
EVOLUTIONARY BIOLOGY

Organizing the Tree of Life

Capture-Seq Evolutionary Biology

Predesigned and custom options

- Model & non-model species
- UCEs & orthologous loci
- Full custom design support

Industry-leading experience

- Consistent results: Tens of thousands of samples processed
- Multiple sample types: Fresh, degraded, & environmental DNA

Competitive pricing

- Volume discounting
- Collaborate for even better pricing
- Returning customer & referral discounts

Capture-Seq Evolutionary Biology

Capture-Seq is a targeted next-generation sequencing (NGS) solution for analyzing shared genomic loci between entire taxonomic clades or closely related species, including non-model organisms. Targeted loci often include ultraconserved elements (UCEs), orthologous loci, and other genomic sequences. These regions yield insights for phylogenetics, systematics, population genetics and more. Rapid Genomics specializes in developing and optimizing Capture-Seq tools for plants and animals, including novel assay designs for innovative research questions.

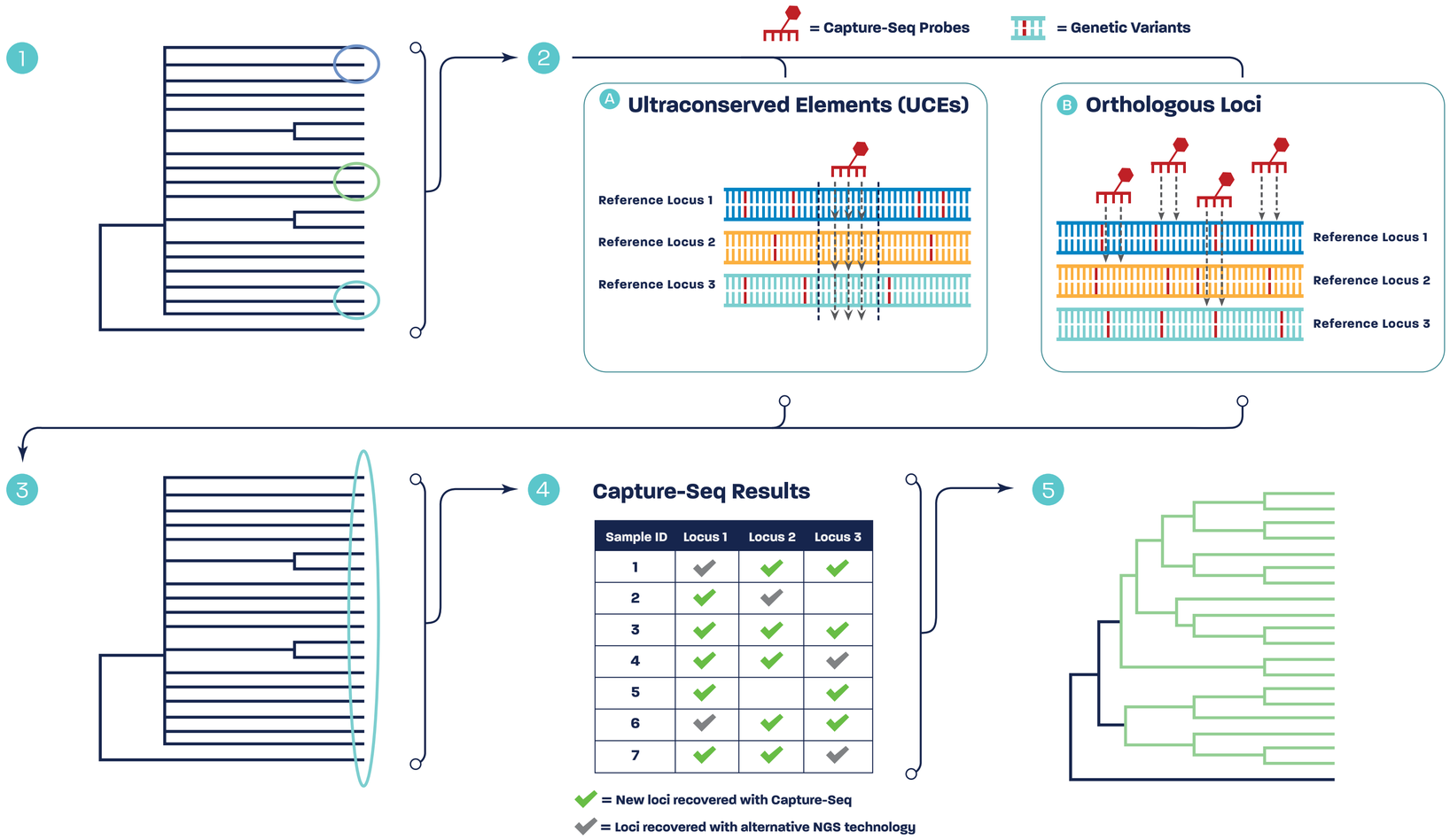
Capture-Seq delivers high-quality results from museum, herbarium, and fresh sample collections. Beyond superior performance with degraded DNA, Capture-Seq yields lower missing data and less bioinformatic complexity than restriction enzyme genotyping-by-sequencing (GBS). Additionally, thousands of loci can be targeted with a single assay, enabling cost and time efficiencies compared to Sanger sequencing. Lastly, Capture-Seq is compatible with complex polyploid genomes and able to differentiate sub-genome information.

Legacy data from any platform can be incorporated into Capture-Seq assays, ensuring consistency with prior studies. Mitochondrial and chloroplast data can be obtained as by-products of nuclear Capture-Seq data or by directly targeting either genome.

Capture-Seq is suitable for both high and low volume applications as well as multi-year initiatives. There is no minimum sample number required to utilize an existing Capture-Seq assay or for custom assay design.

Full-service Capture-Seq solutions are available at Rapid Genomics starting from DNA to FASTQ data, locus assemblies and additional bioinformatic data analyses in as few as 6 weeks.

Using Capture-Seq to Understand Evolutionary Relationships & Phylogenetics



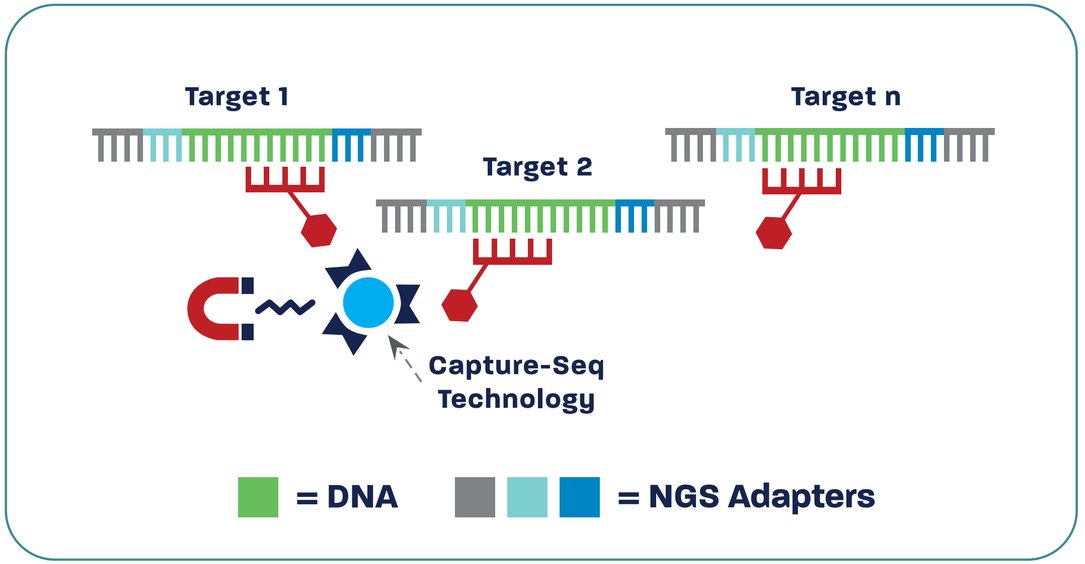
Sample ID	Locus 1	Locus 2	Locus 3
1	✓	✓	✓
2	✓	✓	
3	✓	✓	✓
4	✓	✓	✓
5	✓		✓
6	✓	✓	✓
7	✓	✓	✓

Capture-Seq can resolve phylogenetic relationships without needing direct reference data from all species beforehand.

1. Reference data from representative samples, spanning the evolutionary distance for the taxa of interest, are used to develop a Capture-Seq assay. These resources may be reference genomes, transcriptomes, or newly generated data from Rapid Genomics.
2. Reference data is analyzed and conserved loci are targeted using one of two strategies. For UCE targets, highly conserved regions are selected and targeted, with variants recovered from flanking sequences. For orthologous loci, collections of probes cover all diversity in all taxa for larger target regions, with variants recovered throughout the sequences. UCEs are typically shorter than orthologous loci, but this varies between targets.
3. After developing the targeted assay, taxa of interest are sampled and processed through the Capture-Seq pipeline.
4. Results are aligned against reference data and sequence variation is identified and characterized in a phylogenetic matrix.
5. Using the newly completed matrix, phylogenetic trees and other evolutionary relationships are generated, with improved confidence and resolution compared to alternative, less reliable technologies.

Capture-Seq Enrichment

Capture-Seq utilizes targeted probe hybridization to recover genomic regions of interest. Capture-Seq probes are designed from targeted complementary DNA sequences, synthesized and hybridized to NGS DNA libraries. After hybridization, target regions are selectively recovered while removing surrounding, off-target DNA. Consequently, Capture-Seq provides greater cost-efficiency per target per sample than whole-genome sequencing and GBS.



LEADING A NEW ERA OF GENOMICS

At Rapid Genomics, the key to improving the future is within the secrets of the genome. Our mission is to expand global access to the technologies required for uncovering those secrets with the highest standards of accuracy and reliability. We provide flexible solutions to a range of commercial and research interests focused on agriculture, veterinary genomics, healthcare, and evolutionary biology. Our customers partner with us to advance their goals and, ultimately, strengthen the industries that do everything from producing our food to curing disease.

RAPID GENOMICS

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