RAPID GENOMICS

GD-SEQ

Addition By Subtraction

About GD-Seq

Genome Depletion Sequencing (GD-Seq) is a proprietary genotyping solution focused on eliminating repetitive DNA elements which are characteristic of many plant & animal genomes.

GD-Seq's ability to remove repetitive genome elements, yields datasets with improved sequencing depth in low copy number regions when compared to whole-genome sequencing results. Using equivalent sequencing efforts, GD-Seq is up to 500% more effective while still recovering up to 90% of all known exons (maize). Evaluating GD-Seq's efficacy in any species is simple and straightforward.

These unique technical advantages make GD-Seq the ideal alternative to traditional untargeted sequencing for many industries & applications.

For commercial applications, GD-Seq can be used to "skim" the genome at shallow depth, identifying markers or haplotypes which can be imputed to larger datasets for powerful breeding or phylogenetic solutions. Any sequencing depth in any species can be targeted.

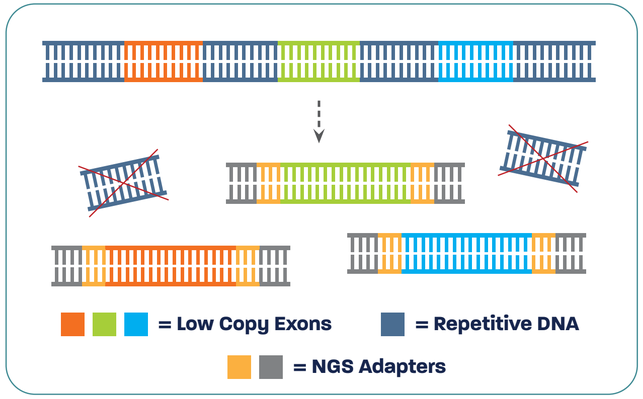
Full-service GD-Seq solutions are offered at Rapid Genomics starting from tissue or DNA to FASTQ data, SNP calls or additional bioinformatic data analyses.

Key Features:

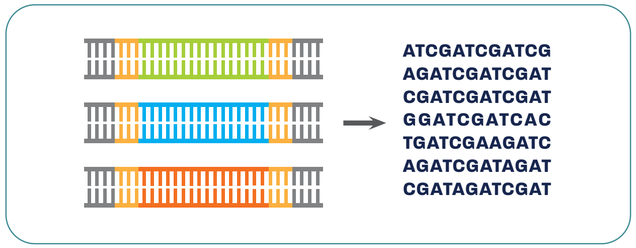
- Enhanced discovery
- Identify markers in large, repetitive genomes where WGS won't work
- Improved efficiency
- Lower costs for genome skimming vs WGS
- Commercially scaled
- Use GD-Seq for high-throughput genome skimming & imputation

GD-Seq Workflow & Technology

1 **Convert Genomic DNA into Sequencing-Ready Libraries while Removing Repetitive Elements**

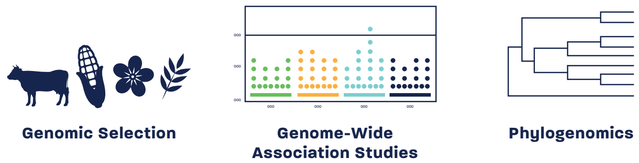


2 **Sequence GD-Seq Libraries Via NGS and Identify Markers**



3 **Analyze Data for Marker Identification and Additional Reporting**

Individual 1	1 0 2 2 0 1 1 2
Individual 2	2 2 1 1 0 0 0 1
Individual n	0 2 1 2 2 1 0 2



Genomic Selection | Genome-Wide Association Studies | Phylogenomics

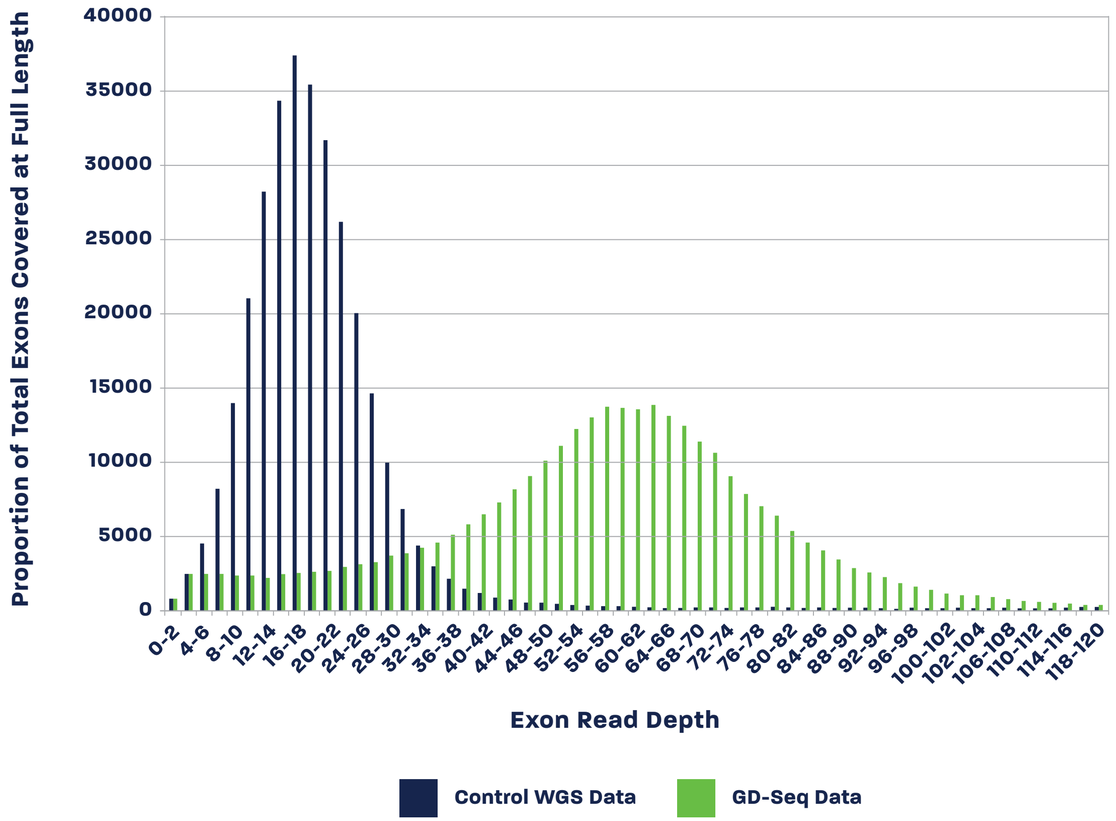
Use GD-Seq for:

- Marker discovery & imputation
- Up to 500% more effective than whole-genome sequencing
- Haplotype phasing
- Loci mapping: QTL, gene & causal variant analysis

GD-Seq vs WGS: Maize

Maize samples were processed, sequenced and analyzed using GD-Seq and traditional whole-genome sequencing protocols. Each dataset was generated using equivalent sequencing read quantities and analyzed for read depth in all exons of the B73 reference genome. GD-Seq results recovered 90% of all exons and sequencing depth improved by 300% – 500%, demonstrating suitability for discovery and genome skimming applications.

GD-Seq: Number of Total Exons Covered at Full Length at Depth X



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.

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