



Data2Bio's tGBS Technology

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Next Generation Sequencing (NGS) technologies are revolutionizing biology. But analyzing NGS data requires dedicated bioinformatics specialists who are not available in most labs. Data2Bio™ can help you overcome the challenges of analyzing increasingly large and complex NGS data sets. Members of our team were early adopters of NGS technologies and have been analyzing NGS data ever since. We can help you design, conduct and analyze a wide variety of NGS experiments from data generated by Illumina, Roche 454, and Ion Torrent instruments.

NGSeasy™ Services

<p>RNA-Seq</p> <p>RNA-seq experiments to discover differentially expressed genes.</p> <p>Learn more ></p>	<p>ChIP-Seq</p> <p>ChIP-seq experiments to discover protein binding sites in the genome.</p> <p>Learn more ></p>	<p>SNP Discovery</p> <p>Genome resequencing to discover genetic variants (i.e., SNPs).</p> <p>Learn more ></p>	<p>Transcriptome Assembly</p> <p>Assemble paired-end transcripts into contigs.</p> <p>Learn more ></p>
<p>Mapfast</p> <p>Mapfast genotyping-by-sequencing mapping service.</p> <p>Learn more ></p>	<p>Custom & Turn-key Projects</p> <p>Describe your requirements and we will design an experiment.</p> <p>Learn more ></p>	<p>Grant Proposal Consultations</p> <p>Consultations to help you develop a winning design for the NGS components of your grant proposal.</p> <p>Learn more ></p>	<p>NGS Data Deposition/Submission</p> <p>Deposit your NGS data into a public database.</p> <p>Learn more ></p>

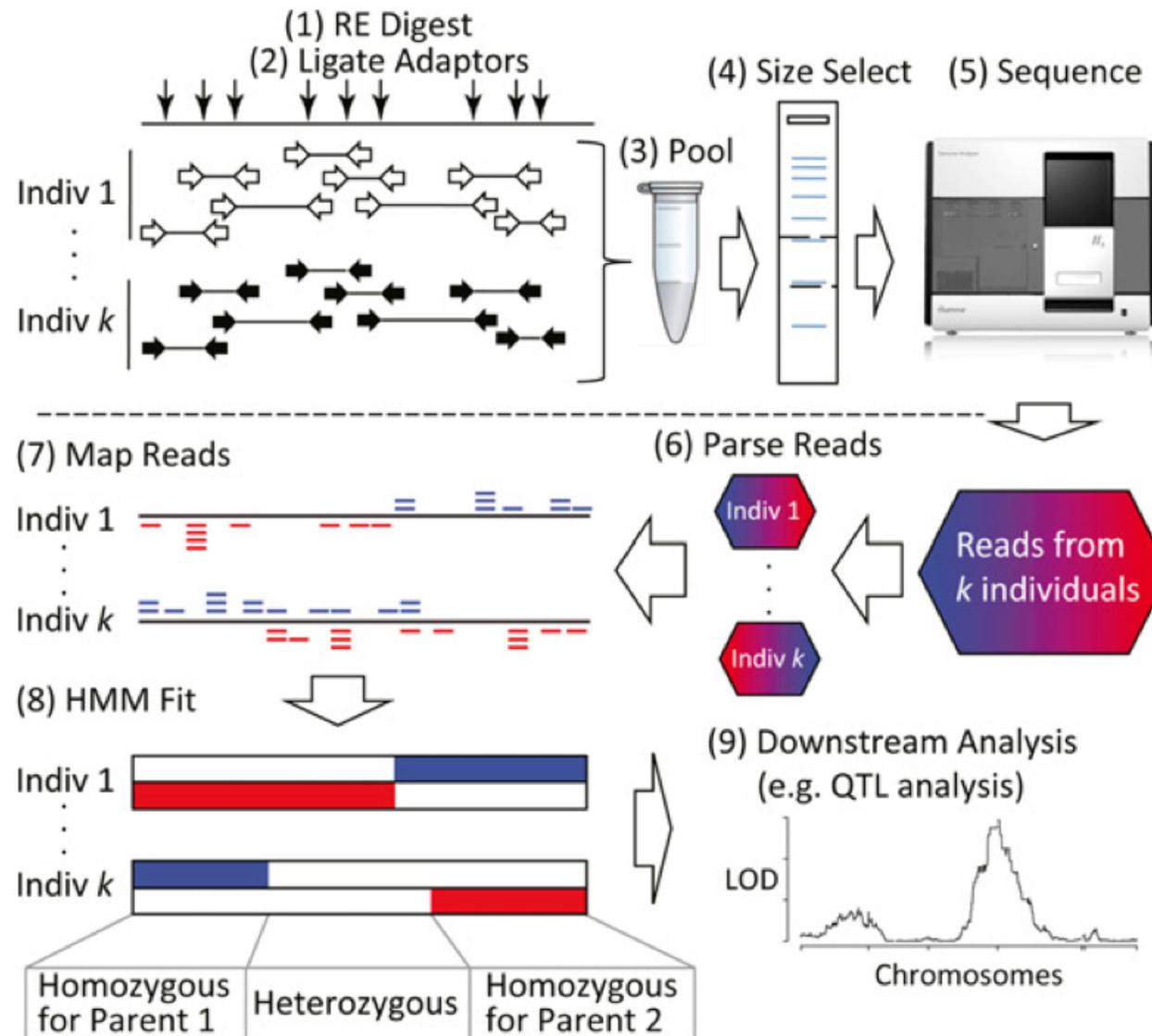
- Founded in 2010, the privately held Data2Bio designs, conducts, analyzes and interprets research projects involving next generation sequencing

- Core strengths are bioinformatics, genomics and breeding

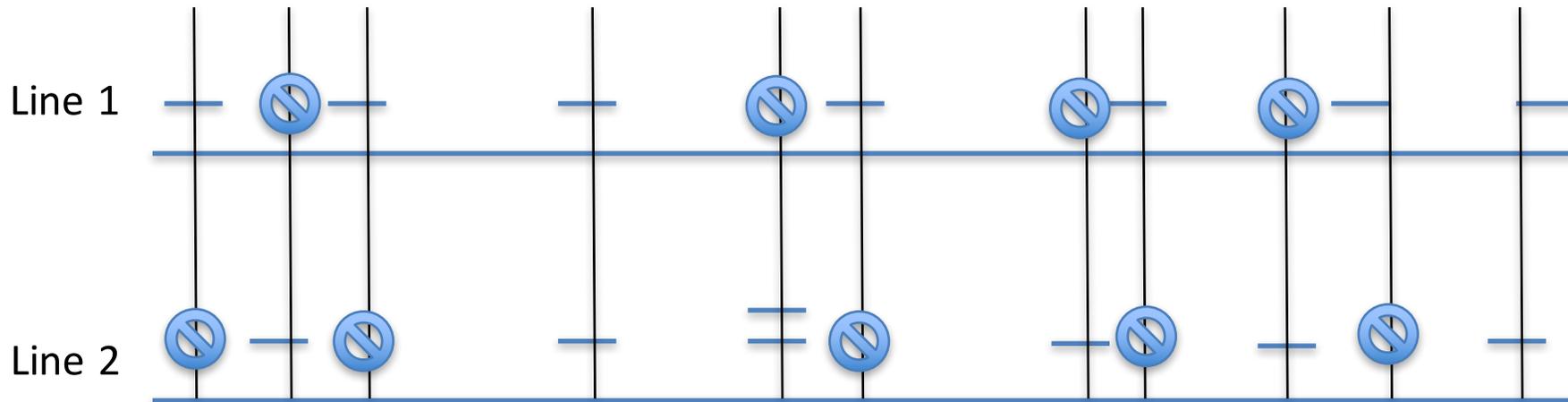
- Offices in the US and China; Academic and private-sector customers on all continents except Africa and Antarctica

- Proprietary genomic technologies associated with DNA barcoding, genotyping-by-sequencing (tGBS) and genome sequencing (BAC-Seq) as well as proprietary bioinformatic pipelines

An Example of “Conventional” GBS



Conventional GBS



Up to 1M sites, i.e., more than is required for most applications

SNP calls based on few reads (increasing error rate)

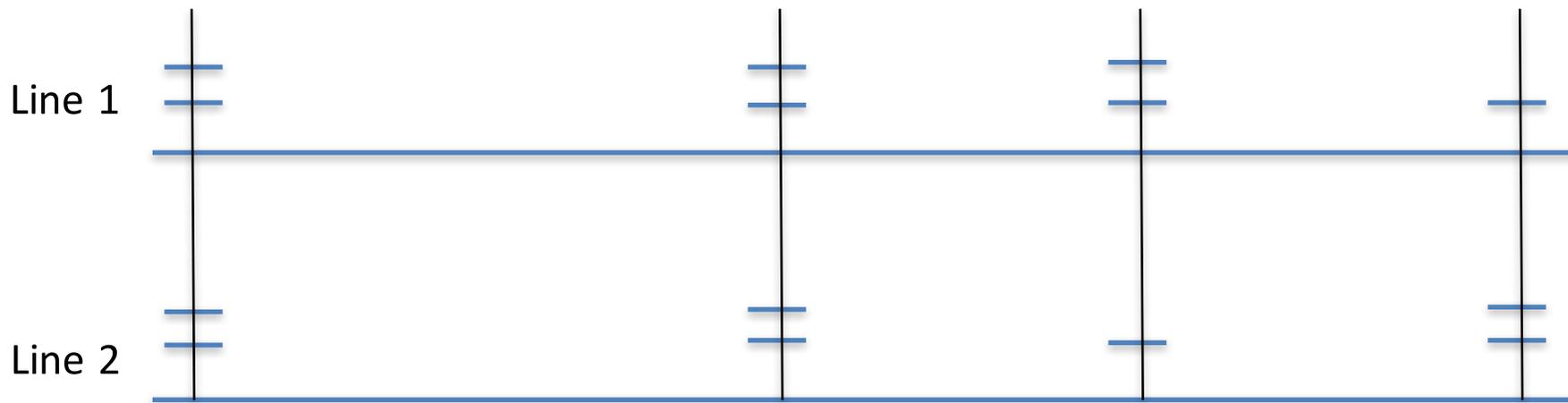
Can not call heterozygotes and rare alleles

Limited overlap of sites among lines -> missing data across lines

Requires *imputation* (heavy-duty bioinformatics)

-> difficult in species without a reference genome

Tunable GBS (tGBS)



tGBS more stringently controls fraction of genome that is sequenced and genotyped (“read selection”). Given same number of reads/sample, reads are clustered at fewer sites, increasing read depth:

- 1,000s to tens of thousands of SNPs (“tunable”) -> adequate for most applications
- *Less missing data* across lines; more repeatability
- *High confidence SNP calls-even for rare or minor frequency alleles*
- *Can confidently genotype heterozygous loci*