

stGBS – simplified, targeted genotyping by sequencing kits and services for high-throughput AgBio applications

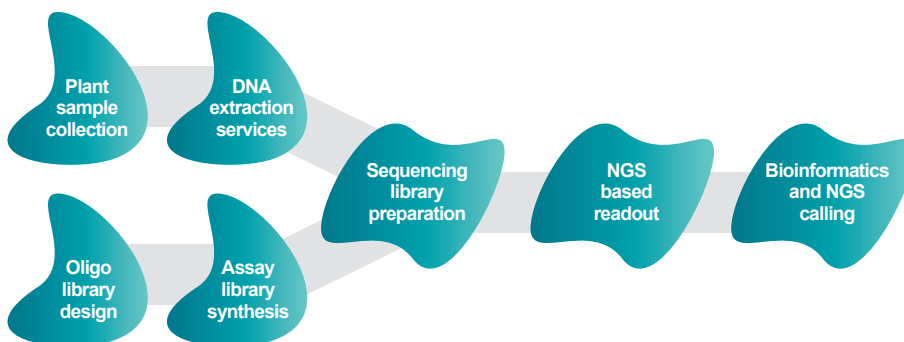
Key features

- Based on an economical massively parallel PCR amplification of up to thousands of targets, across thousands of samples.
- Optional bioinformatic analysis available which include read filtering and trimming, mapping to reference genome, and variant calling with FreeBayes.
- Available as laboratory service and custom dispensed kits depending on your needs.

What is included?	stGBS kits	stGBS service
Oligo library design and synthesis	✓	✓
Library preparation reagents	✓	✓
Sample collection kits (optional)		✓
DNA extraction service (optional)		✓
Library preparation service (optional)		✓
Next generation sequencing		✓
Data analysis* (optional)	✓	✓

* includes read filtering and trimming, mapping and variant calling

Lab service project workflow



Technical specifications

- SNPs: 500-5000 amplicons per panel
- Genome sizes: 500 Mbp-16 Gbp
- Sample type: leaf punch, seed, purified gDNA
- Sequencing performance: >90% on-target (aligned reads)*
- Coverage: >90% coverage uniformity (at >20% of mean depth)*
- Design coverage: >90% of requested bases typical*
- Default service turnaround time (sample delivery to data delivery): 2 weeks (10 business days)
- Total service time (from project initiation to first data): 6-8 weeks
- Data security: all sequencing data and analysis kept in our in-house network
- Data delivery: physical delivery by encrypted hard drive or online via Amazon S3 or Citrix ShareFile

*actual performance may be affected by genomic complexity, ploidy, and other considerations

Service deliverables

Raw and trimmed read data (*.fastq.gz); mapping data for each sample (*.BAM format); variant caller output (*.VCF) and clean genotype data in machine readable form (*.CSV) along with sequencing and mapping quality control metrics (*.PDF)

Contact information

For any queries about stGBS, please contact your sales representative.

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