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?

<table>
<thead>
<tr>
<th>What is included</th>
<th>stGBS kits</th>
<th>stGBS service</th>
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</thead>
<tbody>
<tr>
<td>Oligo library design and synthesis</td>
<td>✓</td>
<td>✓</td>
</tr>
<tr>
<td>Library preparation reagents</td>
<td>✓</td>
<td>✓</td>
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<tr>
<td>Sample collection kits (optional)</td>
<td></td>
<td>✓</td>
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<tr>
<td>DNA extraction service (optional)</td>
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<td>✓</td>
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<td>Library preparation service (optional)</td>
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<td>Next generation sequencing</td>
<td></td>
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<tr>
<td>Data analysis* (optional)</td>
<td>✓</td>
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</tbody>
</table>

* includes read filtering and trimming, mapping and variant calling

Lab service project workflow

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Plant sample collection
DNA extraction services
Oligo library design
Assay library synthesis
Sequencing library preparation
NGS based readout
Bioinformatics and NGS calling
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.

Integrated tools.
Accelerated science.

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