Allegro® Targeted Genotyping V2.

PRODUCT SHEET

Efficient and cost-effective SNP interrogation

Allegro Targeted Genotyping V2 provides a fast, scalable, cost-effective approach to perform targeted genotyping on a wide variety of organisms using next generation sequencing.

Using the patented SPET (Single Primer Enrichment Technology) approach to specifically target SNPs of interest, the system provides information-rich sequencing data that cannot be achieved by hybridization pulldown methods. For every on-target sequencing read, a SNP-specific data point is obtained. The result is unparalleled sequencing efficiency, leading to rapid scalability and the lowest cost per data point available.

Why use Allegro Targeted Genotyping?

Allegro provide solutions for these challenges:

- Costly and time-consuming phenotypic assessment
- Fixed, inflexible content with custom genotyping microarrays
- NGS using selection by hybridization requires extensive paired-end sequencing

Allegro offers several unique features:

1. Interrogation of over 100,000 SNPs per sample in a single assay.
2. Complete customization to targeted SNPs, with rapid turnaround and flexibility to add new markers.
3. Use of patented SPET targeting approach for optimal efficiency.
4. Highly scalable multi-plexing to enable large-scale genotyping.
5. Reduced sequencing cost by using single end reads.

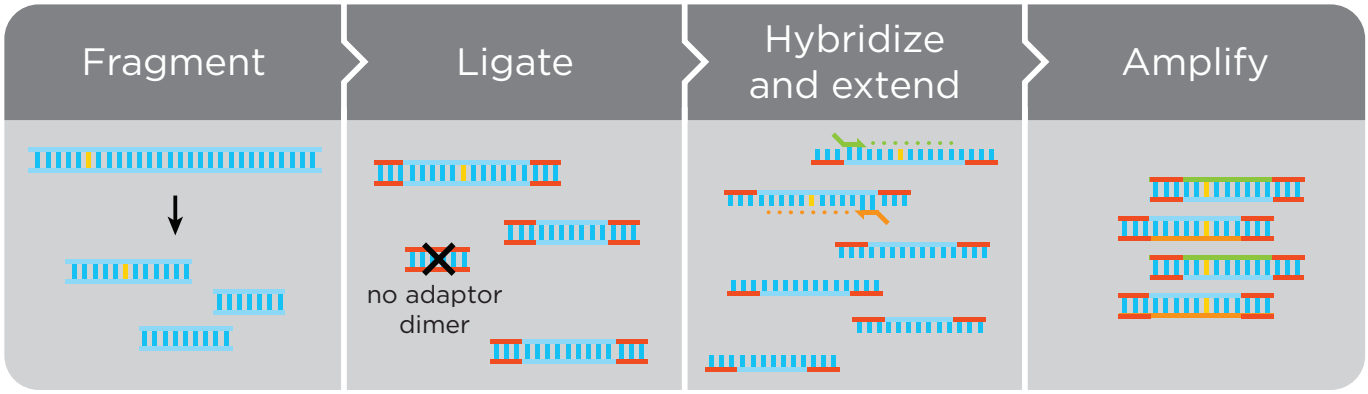

Figure 1: Allegro Targeted Genotyping V2 is a complete end-to-end solution for targeted genotyping, with a simple easy to follow workflow.

Features

- 500 to > 100,000 SNPs in a single design
- Low input of 10–100 ng of DNA
- Simple 24-hour protocol from DNA to library
- Integrated enzymatic fragmentation
- Scalable multiplexing of thousands of samples per sequencing run
- Short, single-end reads capture a SNP in each on-target read
- Highly flexible design process to easily add new content
- Automation-friendly

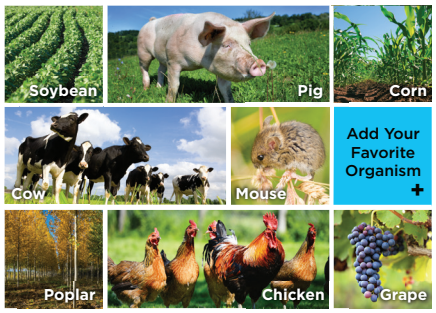

Figure 3: Our experts have designed custom panels for > 60 species. Expert scientists work with you to generate an optimal design.

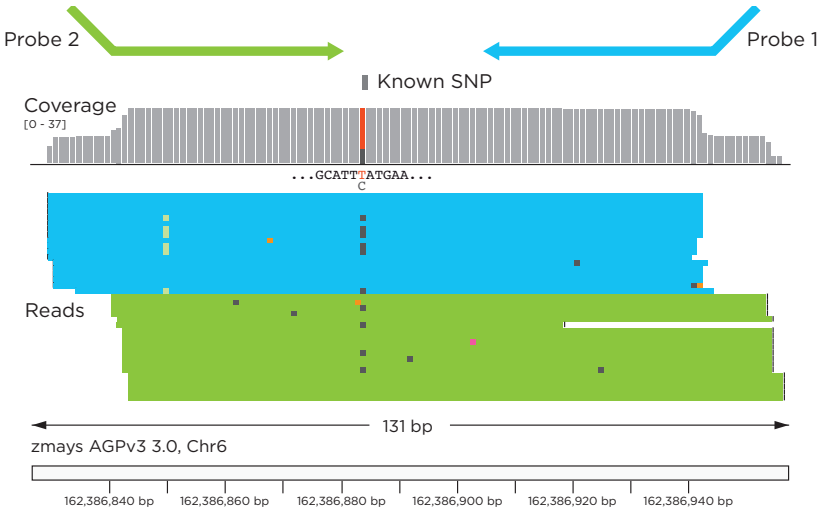

Figure 2: *Zea mays* custom panel designed with two probes for every SNP captures information from every read. Reads from both probes independently capture and confirm the presence of a SNP. Custom targeted panels enable high accuracy SNP-based genotyping.

Sample	Input	Fraction aligned AVG (SD)	Fraction on-SNP AVG (SD)	Probes detected AVG (SD)	Total reads AVG
HD701	100 ng	0.975 (0.001)	0.930 (0.001)	0.982 (0.002)	446592
	10 ng	0.972 (0.001)	0.926 (0.001)	0.968 (0.001)	287747

Table 1: Allegro yields sequecing libraries with specific, informative and complete genotyping results across a range of inputs.

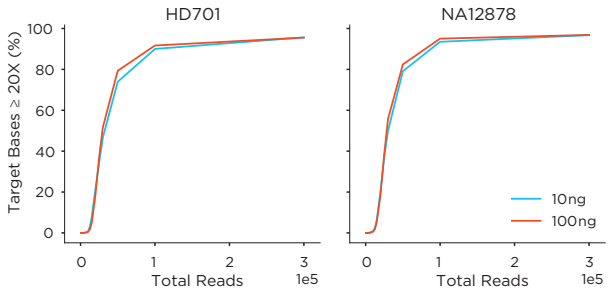

Figure 4: Sequencing Depth vs Coverage. Reads from 8 HD701 and 16 NA12878 Allegro libraries were pooled and down-sampled to determine the effect of read depth on target coverage. Allegro enables accurate calls for greater than 95% of targeted SNPs with 300K total reads on the validation panel.

Ordering information

Product Name	~# SNPs	Part no.	No. of reactions
Allegro Targeted Genotyping V2, <5,000 Probes	<2,500	10050	192, 384 and 768
Allegro Targeted Genotyping V2, 5,000-10,000 Probes	2,500-5,000	10051	192, 384 and 768
Allegro Targeted Genotyping V2, 10,000-50,000 Probes	5,000-25,000	10052	192, 384 and 768
Allegro Targeted Genotyping V2, 50,000-100,000 Probes	25,000-50,000	10053	192, 384 and 768
Allegro Targeted Genotyping V2, >100,000 Probes	>50,000	Ask your account executive.	

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401002 V 1.0, 2019-06