

Maize 1K Panel

High-throughput genotyping technology is very important for effective crop breeding programs. GBTS technology integrates the advantages of array-based and high throughput sequencing, showing advantages in customized flexibility, high throughput, and low cost. Molbreeding collaborated with Dr. Xu Yunbi's team (CAAS-CIMMYT), has developed a series of GBTS panels, including from 1K – 45K (GenoBaits®). These panels can serve an effective and efficient tool for genotyping and population structure classification, and genome prediction analysis.

Product Highlight

- **Broad selection of polymorphisms:**
The markers on this panel were selected from Hap Map3 which is based on the whole genome sequencing of 1,218 major maize inbreds and improved worldwide cultivar accessions.
- **Supply segment SNP information, rich markers information, increase markers availability**
The inclusion of flank SNPs was implemented to enhance segment polymorphism and augment marker information, in addition to the core SNPs.
- **The liquid chip upgrade offers flexibility for achieving rapid product iteration**
Reinforce product application scenarios by progressively incorporating newly emerged GMO markers and functional markers into the products.
- **Low application cost and high throughput detection**
The application of GBTS technology, characterized by its high efficiency and low cost, can effectively meet the requirements of industrialized breeding.

Application

1. Germplasm classification and Evaluation
2. Heterotic groups division
3. Linkage map construction
4. Marker-trait association
5. Transgenic backcross background selection/Targeted improvement
6. Genome selection



Maize Capture Kit ordering information

Catlog	Product Name	Target Region Number	Target SNP Sites	Total Capture SNP Sites	Marker Type
PHR0093_Ma45K	GenoBaits® Maize 45K Panel	43,670	44,935	264,553	SNP
PHR0093_Ma10K	GenoBaits® Maize 10K Panel	11,156	11,535	53,705	SNP
PHD0093_Ma1K	GenoBaits® Maize 1K Panel	1,354	1,354	4,589	SNP

Service process



Submit sample
for DNA QC



Library construction and
sequence capture



High-throughput
sequencing



Data quality control and
sequence trimming



Automatic Bioinformatics
analysis on cloud

The distribution of 1K markers across the genome

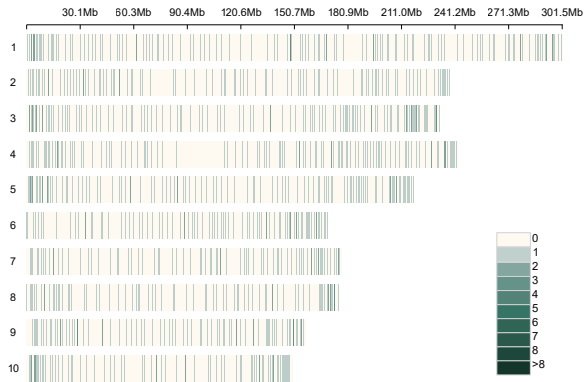


Figure 1 Distribution of SNP numbers on chromosomes

In Figure 1, the 1,354 core regions with 4,589 SNP markers, evenly distributed on 10 maize chromosome.

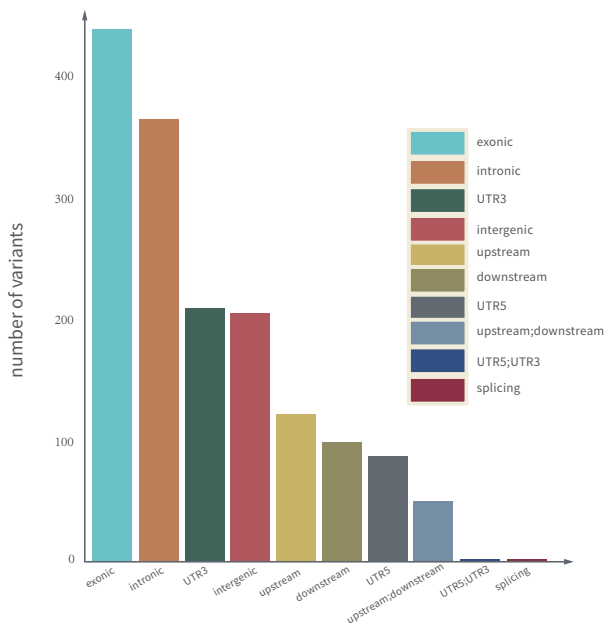


Figure 2 Histogram of MAF Distribution

In Figure 2, the MAF average of 1,354 target SNP markers in GenoBaits® Maize 1K Panel is 0.36.

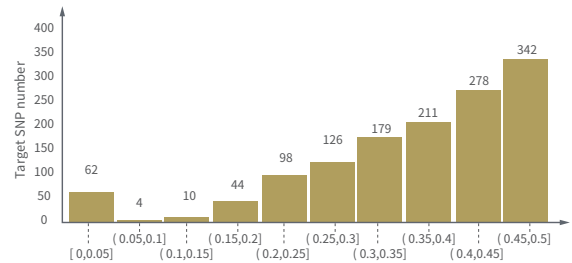


Figure 3 Annotation of SNP

As shown in the figure 3, annotation of 4, 589 SNP markers located in exonic accounted for 23.34%.

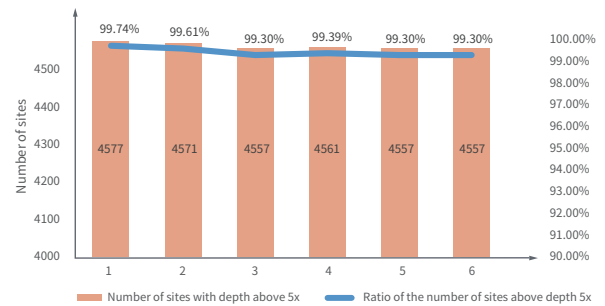


Figure 4 Statistics of core SNP sites with a sequencing depth exceeding 5x

More than 99.7% of the 1,354 core SNP sites had sequencing depths exceeding 5x. The average sequencing depth of each sample reaches over 109x.

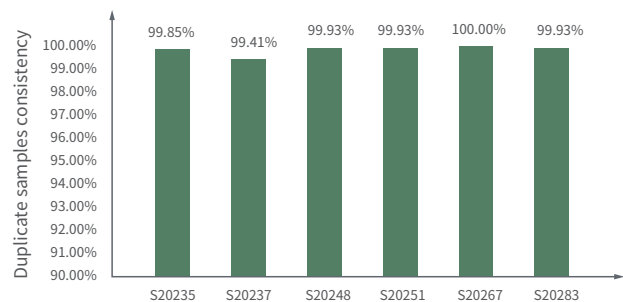


Figure 5 Repetitive consistency of genotypes

The genotypic results of over 99% loci exhibited consistent patterns across repetitions, indicating excellent experimental repeatability.

