

Maize 45K 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.
- Various density designed for different applications**
 Adjunct SNPs are captured with the target SNPs and form multiple SNP clusters, which are essential for haplotype mapping and structure analysis. In this maize 45K SNP panel, Molbreeding designed total of 264,553 multiple SNP clusters, mSNPs. The Maize10K panel has 53,705 mSNP and the 1K SNP has total 4,589 mSNP. Different application can select the appropriate marker density to minimize cost and analysis time.

Application

Applications	40K+	30K	20K	10K	5K	1K	<200
Biological evolution	+++	+++	++	++	+		
Germplasm evaluation	+++	+++	++	++	+	+	
Classification	+++	+++	+++	+++	++	++	
Linkage map construction	+++	+++	+++	++	+	+	
Gene mapping/cloning	+++	+++	+++	+++	++	+	
Marker-trait association	+++	+++	++	+			
Progeny testing	+++	+++	+++	+++	+++	+++	+++
Gene introgression	+++	+++	+++	+++	+++	++	+
Gene pyramiding	+++	+++	+++	+++	++	+	+
Germplasm protection	+++	+++	+++	+++	++	++	+
Quality control	+++	+++	+++	+++	++	++	+
Bioassay	+++	+++	+++	+++	++	+	+

Revised from GUO et al. (2019). More "+" symbols represent the higher levels of suitability.



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
PHD0154_MaFER	GenoBaits® Maize Small Panel	442	442	442	SNP+InDel
PHR0174_Ma20K	GenoBaits® Maize 20K Panel	19,416	20,300	130,498	SNP+GMO

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 45K markers across the genome

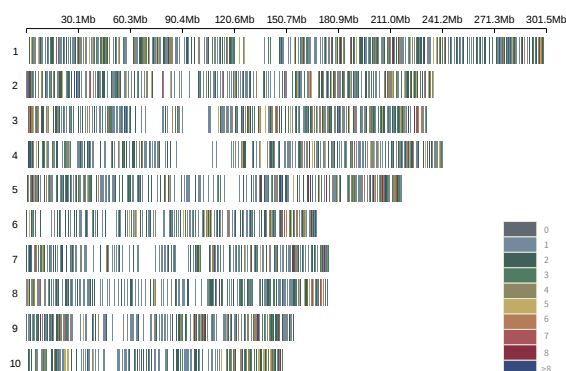


Figure 1 Distribution of SNP numbers on chromosomes

In Figure 1, the 44,935 core regions with 264,553 SNP markers, evenly distributed on 10 maize chromosome.

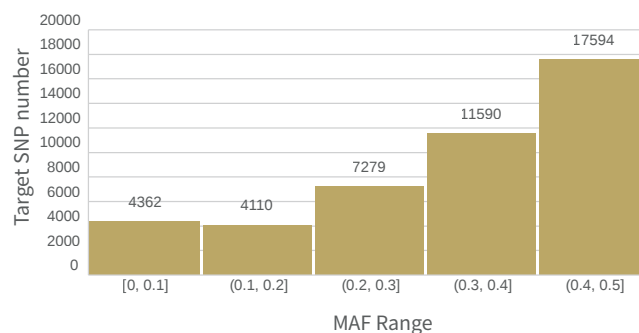


Figure 2 Histogram of MAF Distribution

In Figure 2, the MAF average of 44,935 target SNP markers in GenoBaits® Maize 45K Panel is 0.33.

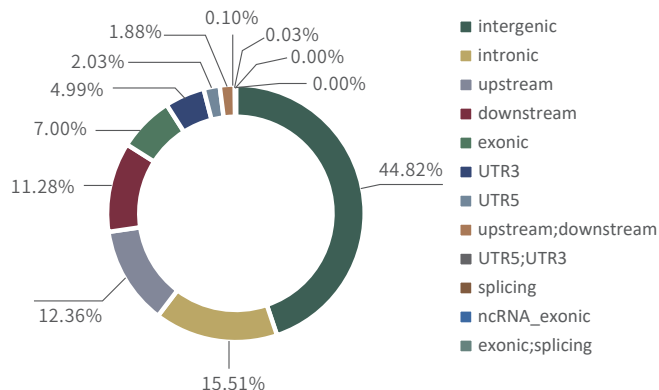


Figure 3 Annotation of SNP

As shown in the figure 3, annotation of all 264,553 SNP markers in GenoBaits® Maize 45K Panel.

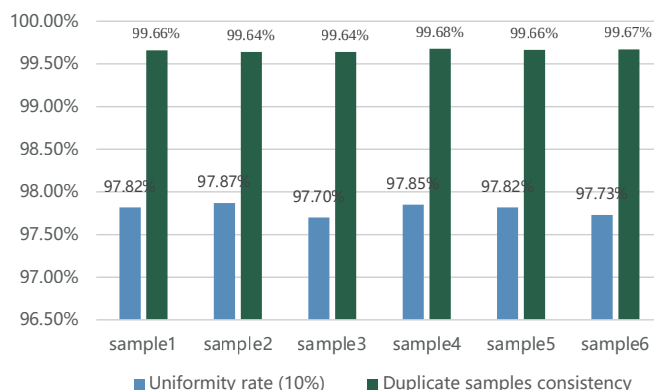


Figure 4 Uniformity_rate10 and duplicate samples consistency of test samples by using GenoBaits® Maize 45K Panel.

As shown in the figure 4, the uniformity_rate10 of test samples were 97.70%-97.87%, duplicate samples consistency not less than 99.64%.

Bioinformatics analysis

GBTS Basic analysis

QC and reference sequence comparison: sequencing data QC, reference sequence comparative analysis, sequencing depth and coverage statistics;
Detection and Annotation of the variation loci include SNP, indel, STR/SSR.

Advanced analysis

Phenotypic analysis;
Population genetic study;
Species identification, Species fingerprint construction;
Genome-wide selection;

Genome-wide association study;
Genetic map construction and QTL mapping;
BSA mixed pool sequencing analysis.

According to customer requirements, customized bioinformatics analysis content can be confirmed in the project stage.