

WHITE PAPER

Advancements in Maize Genetics: An Introduction to MolBreeding GenoBaits Maize Panels

Summary

This white paper presents the development of MolBreeding's Maize (*Zea mays*) Panel Series, a comprehensive genomic resource designed to support and accelerate modern maize breeding programs.

Drawing on 83 million SNPs from the global maize HapMap3 Project and validated across 647 elite inbred maize lines, we compile robust genome-wide markers into a single, high-performance 45K marker panel. The panel leverages MolBreeding's innovative multiple-SNP (mSNP) technology, which captures multiple polymorphic sites per target region to substantially increase marker density and genetic resolution without a proportional increase in cost. In addition, a subset of markers is annotated with known functional genes and their controlled key traits, providing practical guidance for applications such as heterotic group classification, QTL mapping, and marker-assisted selection.

The MolBreeding Maize Panel Series empowers researchers and breeders to conduct reliable association analyses (e.g., GWAS), identify favorable alleles, and uncover the genetic architecture of diverse germplasm. These panels also accelerate maize breeding cycles by enabling fast, data-driven decisions across critical applications, including genomic selection, heterotic group classification, hybrid prediction, trait pyramiding, and backcross breeding program design.

Introduction

Zea mays (commonly known as maize or corn), one of the world's most important cereal crops, serves as a staple food, feed, and industrial raw material. Its global cultivation spans diverse climates and regions, making it a cornerstone of food security and agricultural economies. Maize adaptability, yield potential, and economic importance boost active maize breeding research in modern agriculture.

Since the early 21st century, crop breeding has entered the genomic era, where high-throughput genotyping has become a key tool enabling breeders to tackle challenges such as climate change and the need for increased food production. In maize, this is especially important: its complex genome brings both opportunities and challenges for breeders. Its genome is large (~2.3 Gb) and highly diverse, repetitive, with extensive structural variation; transposable elements; and rapid linkage disequilibrium decay - particularly in tropical accessions. This genetic complexity underlies maize's remarkable phenotypic diversity but also makes traditional breeding and marker development technically challenging. As a result, high-density, low-cost genotyping tools capable of revealing genome-wide variation are crucial for exploring its genetic structure and supporting large-scale breeding programs.

Leveraging public maize genomic resources, MolBreeding, in collaboration with the Institute of Crop Science, Chinese Academy of Agricultural Sciences (CAAS), developed the MolBreeding Maize GBTS Panel with 45K core SNPs (targets), followed by derivative subset panels at the marker density of 20K and 10K developed to suit different breeding scenarios.



The GenoBaits® Maize Panels utilize liquid-phase capture technology, combining the stability of solid-chip platforms with the added flexibility of dynamic modification of probe targets, while retaining the cost efficiency of reduced-representation sequencing approaches such as GBS. Each GenoBaits® probe targets a core SNP within a single amplicon and simultaneously captures multiple flanking variants (average 6 SNPs) —thereby generating enriched multi-variant information per locus through this so-called multiple-SNP (mSNP) strategy. Using the GenoBaits® Maize 45K Panel, approximately 250K high-quality SNPs and more than 690K derived haplotypes can be generated. This integrated SNP and haplotype marker system provides enhanced power for both validation and discovery of trait loci. In particular, haplotypes derived from mSNPs capture specific combinations of linked SNPs, summarizing their joint effects and more effectively tagging underlying causal variants. This increases the ability to detect minor-effect QTLs that may be overlooked when analyzing individual SNPs.

Together, these advantages enable breeders to efficiently track favorable alleles, dissect complex traits, and accelerate new maize variety development in a cost-effective and scalable way.

SNP Selection & Probe Design

SNP Calling & Filtration

A total of 1,218 diverse maize accessions from the HapMap3 Project (Bukowski et al., 2018) are used for initial SNP discovery, encompassing global germplasm including temperate, tropical, and subtropical inbred lines (Table 1). From these accessions, a total of 83 million SNP loci are called out and mapped to the B73 reference genome (RefGen_v3).

Germplasm Group	Origin	Representative Lines	Approx. Count
Temperate	USA, China	<i>B73, Mo17, Chang7-2</i>	~400
Tropical/Subtropical	CIMMYT, Africa, Asia	<i>CML lines, Suwan lines</i>	~500
Sweet Corn	Global	<i>sh2/su1 lines</i>	~200
Genetic Stocks	Global	<i>Mutants, founders</i>	~118
Total			1,218

Table 1 Overview of Zea mays lines used for the development of maize panels.

A first-round SNP selection is conducted on the 83 million SNPs using the following criteria:

1. Minor allele frequency (MAF > 0.05): Ensure broad applicability that selected SNPs are polymorphic across diverse maize germplasm.
2. Call rate ≥ 95%: retains SNPs with high-quality, reliably genotyped data across all accessions.
3. Target-rich regions (2–15 SNPs per 100 bp): prioritizes genomic windows with multiple SNPs to enable multi-SNP (mSNP) capture within a single probe.
4. Genic enrichment: favors SNPs in functional regions—exons > introns > UTRs > intergenic—resulting in 36.2% of final markers located in genes (Figure 1).
5. Repetitive sequence exclusion: removes SNPs in high-repeat regions, paralogous sequences, or areas with uncertain alignments to ensure probe specificity and accuracy.

Following these filters, 83,916 candidate target regions are selected to proceed to preliminary probe design.

Probe Further Selection and Verification

Probes for the 83K candidate SNPs are initially designed using the GenoBaits® Probe Designer with a length of 110 bp, GC content of 30–70%, and avoidance of SSRs or ambiguous bases. The preliminary panel of 83,916 probes is validated in the wet lab on 647 elite maize inbred lines representing nine major

heterotic groups (Reid, Lancaster, Iodent, PB, PA, SPT, LRC, Tropical, and Sweet corn). Key probe performance metrics included:

- Capture uniformity: ratio of sequencing depth at the target region to average depth
- On-target rate: proportion of useful reads mapping to target regions
- Missing rate: proportion of failed genotype calls
- Genotype accuracy: concordance between biological replicates

Candidate SNPs are removed if they meet any of the following criteria:

- Average missing rate > 20%
- Average sequencing depth < 50x
- Heterozygosity > 50% in inbred lines (indicative of alignment errors from repeats or paralogs)
- Minor allele frequency < 5% in the test population
- Excessive depth variation between samples

After probe optimization and rigorous SNP selection, calling rates for the 45K target regions range from 94.5% to 98.8% across diverse samples, with 99.3% genotype concordance between biological replicates. Target regions are prioritized for high genotyping uniformity, strong polymorphism (high PIC values), stable capture efficiency, and even chromosomal distribution (average marker spacing ~45 kb) (Figure 1).

The final panel includes 44,935 core SNPs covering 43,670 highly polymorphic regions, commercialized as MolBreeding's GenoBaits® Maize 45K Panel.

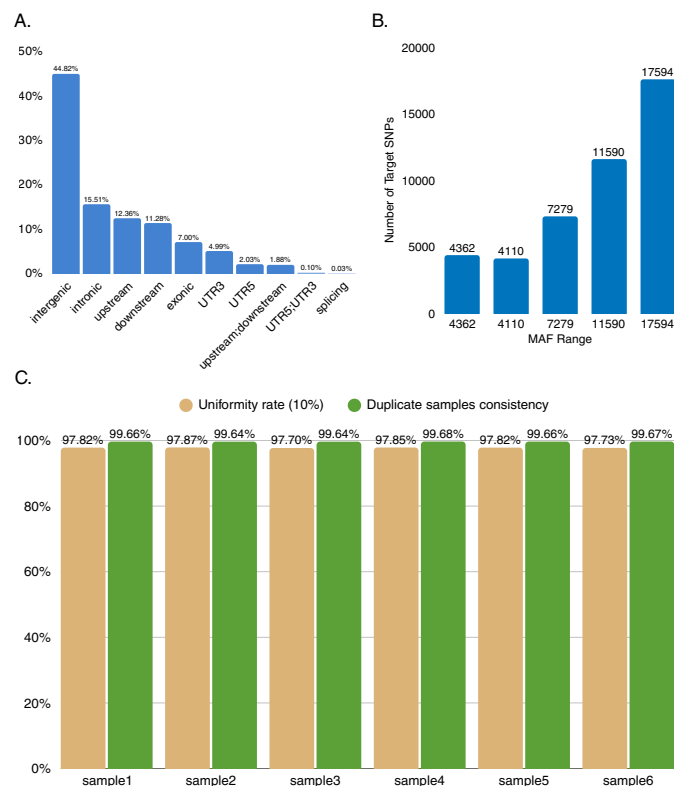


Figure 1 Overview of SNP quality Metrics: A. Genic/Intergenic annotation, B. MAF distribution, C. Uniformity and Genotype consistency analysis.

Key Traits in *Zea mays*

Maize (*Zea mays* L.) possesses one of the most complex and dynamic genomes among major cereal crops. The maize genome is approximately 2.3 Gb in size and is composed of nearly 85% repetitive sequences, primarily transposable elements. Although modern maize behaves as a diploid species ($2n = 20$), its genome reflects an ancient allopolyploid origin. Following divergence from sorghum approximately 12–16 million years ago, the maize lineage underwent a whole-genome duplication event. Subsequent diploidization involved extensive gene loss (fractionation), subfunctionalization of duplicated genes, and large-scale structural rearrangements.

This complex evolutionary history has contributed to:

- High levels of genetic diversity
- Extensive structural variation
- Complex gene regulation networks
- Strong heterotic patterns between germplasm pools

Over the past two decades, advances in genome sequencing, QTL mapping, GWAS, and functional genomics have enabled the identification of numerous genes underlying key agronomic traits. Well-characterized genes such as *liguleless 1* (leaf architecture), *Vgt1* (flowering time regulation), *ZmCCT* (photoperiod response; response to Gibberella stalk rot), *DREB* family genes (abiotic stress tolerance), and multiple QTLs/genes unlock the genetic basis of trait variation in maize. These discoveries have established a strong foundation for marker-assisted breeding and genomic selection.

To maximize the practical utility of MolBreeding's Maize Panels

Resistance Traits	Genes	# Associated Markers
Cold tolerance	<i>CBF3</i>	7
Northern leaf blight resistance (<i>Exserohilum turcicum</i>)	<i>ZmWAK-RLK1</i>	2
	<i>ZmREM6.3</i>	11
Southern leaf blight resistance (<i>Bipolaris maydis</i>)	<i>ZmCCoAOMT2</i>	11
Banded leaf and sheath blight resistance (<i>Rhizoctonia solani</i>)	<i>ZmFBL41</i>	3
Maize dwarf mosaic virus resistance	<i>ZmABP1</i>	18
Common rust resistance (<i>Puccinia sorghi</i>)	<i>Rp1-D</i>	7
	<i>Rp3</i>	4
Fusarium ear rot resistance (<i>F. verticillioides</i> ; <i>F. proliferatum</i>)	<i>ZmLOX3</i>	5
Gibberella stalk rot resistance (<i>F. graminearum</i>)	<i>ZmCCT</i>	6
Head smut resistance (<i>Sporisorium reilianum</i>)	<i>ZmWAK</i>	2

Table 2 Key resistance traits in *Zea mays*.

for breeding and genetic analysis, we conducted a systematic review of hundreds of well-characterized maize genes reported to be associated with agronomic traits, yield components, abiotic stress tolerance, biotic resistance, and grain quality. Based on curated literature and validated functional studies, SNPs from 45K panel located within functional gene regions, as well as within ± 7 kb flanking regions, are annotated as trait-associated markers. The following Table 2, Table 3 list trait-controlling genes for which physically associated SNPs are included in the 45K panel.

These markers capture genotypic variation within and near genes of interest, providing valuable guidance for downstream association analyses and molecular breeding applications. While their genomic positions suggest potential functional relevance, they do not imply direct causation.



Agronomic Traits	Genes	# Associated Markers
Flowering	<i>ZCN7</i>	7
	<i>ZCN8</i>	4
	<i>ZmMADS1</i>	6
	<i>ZMM31</i>	5
Kernel row number	<i>KRN4</i>	1
Kernel number per row	<i>KNR6</i>	8
Ear branching	<i>ub3</i>	10
Plant height	<i>D8</i>	1
	<i>D9</i>	7
Root growth	<i>br2</i>	5
Leaf architecture	<i>Liguleless1 (LG1)</i>	3
Anthocyanin pigmentation	<i>pericarp color 1 (P1)</i>	12
Starch content	<i>Sh2</i>	2
	<i>Bt2</i>	2
Phytic acid content	<i>lpa1</i>	13
Lysine content	<i>Opaque2</i>	20

Table 3 Key agronomic traits in *Zea mays*.

The functional significance of individual markers should be evaluated in combination with user-generated phenotypic data.

This design strategy ensures that the panel not only delivers robust genome-wide background coverage, but also enriches informative loci aligned with practical breeding objectives.

The number of trait-associated markers and the breadth of trait categories covered across the three panels are under continuous development. Detailed trait-associated marker lists for the three maize panels are available upon request by contacting cs@molbreeding.com or your project manager. Updated annotations and expanded trait coverage will be incorporated into future versions of this white paper.

Ready-to-Use Maize GBTS Panels

Three GenoBaits maize panels—45K, 10K, and 1K marker densities—have been developed based on the Zea mays B73 reference genome (RefGen_v3). Each panel integrates:

- Genome-wide background SNPs for population structure, diversity, and background selection
- Trait-associated “foreground” SNPs curated and annotated through comprehensive literature review

In the GenoBaits® Maize 45K panel, SNPs are evenly distributed across the genome at an average spacing of approximately 45 kb (~0.045Mb), ensuring robust and uniform genome-wide coverage (Table 4; Figure 2). As expected in maize, noticeable marker gaps occur in highly repetitive (peri)centromeric and heterochromatic regions, where suppressed recombination and low gene density limit effective target selection.

Technology	Product name	Core SNP	Total SNPs (Core SNP + mSNPs)	Trait Marker
GenoBaits®	GenoBaits® Maize 45K Panel (PHR0093)	44,935	~264,553	Included
GenoBaits®	GenoBaits® Maize 10K Panel	11,535	~53,705	Included
GenoBaits®	GenoBaits® Maize 1K Panel (PHD0093 V2.0)	1,354	~4,589	Included

Reference Genome: *Zea_mays_AGPv3*

Table 4 Overview of three ready-to-use GenoBaits broccoli panels

Performance of the GenoBaits® Maize 45K Panel

GenoBaits Maize 45K panel delivers the highest-density genome-wide coverage, capturing validated target regions with <5% missing data. Its performance has been validated across thousands of maize samples in the past projects.

Key performance average metrics include:

- Alignment Rate: >91%
- Coverage Uniformity ($\geq 20\%$ depth threshold): >94%
- Mean Sequencing Depth: ~70× (adjustable depending on sequencing strategy)
- Target SNP Call Rate: >97%

These metrics demonstrate the panel's stability, reproducibility, and applicability across genetically diverse breeding materials.

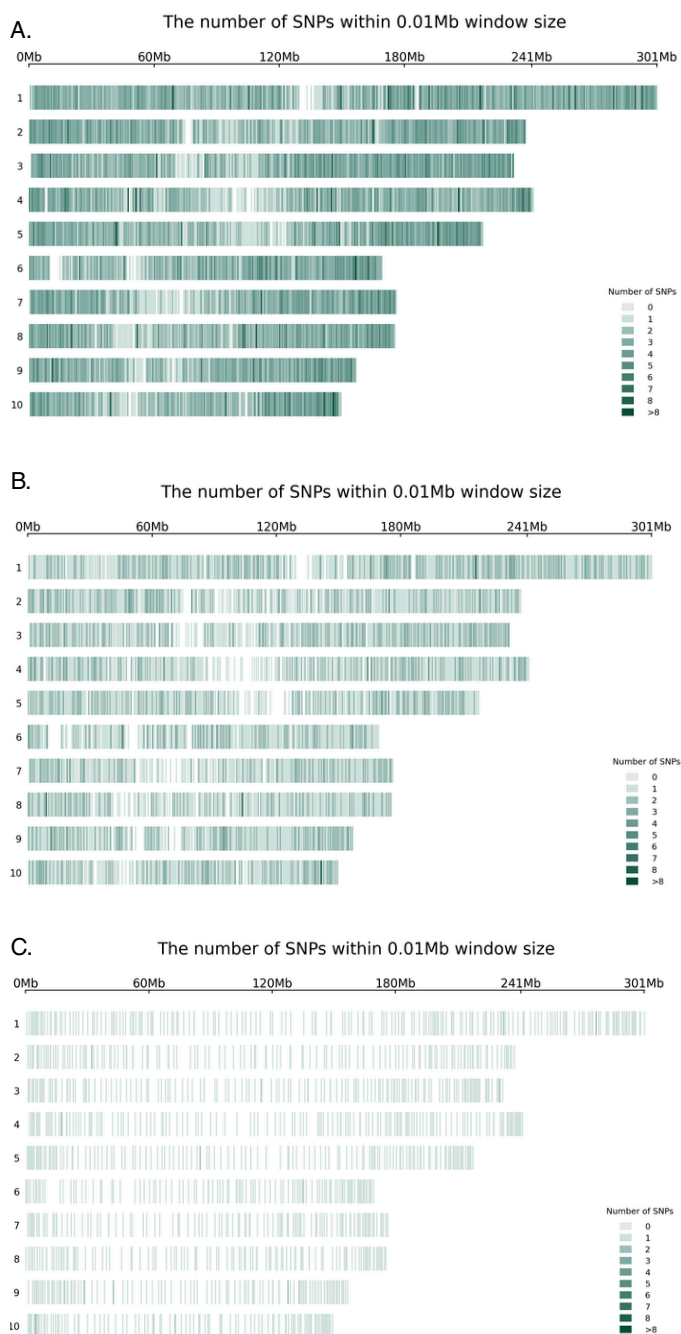


Figure 2 Distribution of SNPs in three maize panels: A. GenoBaits maize 45K, B. 20K, C. 10K panels

Modular Sub-Panels for Scalable Genotyping

Leveraging GenoBaits® liquid-phase capture technology and its flexible modular design, two lower-density sub-panels—GenoBaits® Maize 10K and 1K—have been derived as evenly spaced subsets of the 45K “mother panel”.

The reduced marker densities of the 10K and 1K panels significantly lower sequencing costs, providing a more affordable solution for:

- Early-stage germplasm screening
- Large-scale breeding population genotyping
- Rapid introgression tracking
- Pilot studies or pre-selection programs requiring high sample throughput

These scalable options allow breeding programs to balance resolution and cost efficiency according to project objectives—using the 45K panel for detailed genetic characterization and the 10K or 1K panels for routine, high-volume screening.

Heterotic Group Classification Using the GenoBaits® 45K Maize Panel

Heterotic groups are genetically distinct maize germplasm pools that exhibit strong hybrid vigor (heterosis) when crossed with lines from different groups. Accurate classification of inbred lines into these groups is a fundamental step in maize breeding, guiding parental selection for high-yielding and stable F_1 hybrids.

Classical maize heterotic groups are established through long-term breeding history and extensive testcross evaluation, including groups such as Stiff Stalk (Reid), Non-Stiff Stalk (Lancaster), and Iodent. Breeders historically assessed the combining ability of inbred lines by performing systematic crosses and measuring hybrid performance for key traits such as grain yield, flowering time, and plant architecture. Inbred lines that consistently produce superior hybrids when crossed with lines from a complementary group are classified into the same heterotic group. In practice, certain cross patterns have been widely adopted to develop stable hybrids: the Reid × Lancaster cross represents the classic Corn Belt hybrid pattern, while Reid × Iodent is commonly used in temperate breeding programs. Differences in allele composition between heterotic groups provide complementary genetic potential, contributing to strong heterosis in their F_1 progeny.

To demonstrate the robustness and practical application of the GenoBaits® 45K maize panel, we performed principal component analysis (PCA) on genotyping data from 87 maize inbred lines representing global germplasm. Representative lines from nine major heterotic groups are included as benchmarks for classification (Figure 3). PCA analyses successfully assigned the inbred lines to their respective heterotic groups, with the majority of samples clustering into five clearly distinguishable groups: Stiff Stalk (Reid); Non-Stiff Stalk (Lancaster); Iodent; Tropical; and

Region-specific group from the Huanggai area in China.

These results confirm that the 45K panel captures the key allelic variation underlying heterosis, providing breeders with reliable molecular genetic information. This enables rapid and reproducible classification of germplasm, informs hybrid combination strategies, and supports data-driven breeding decisions to accelerate the development of superior maize hybrids.

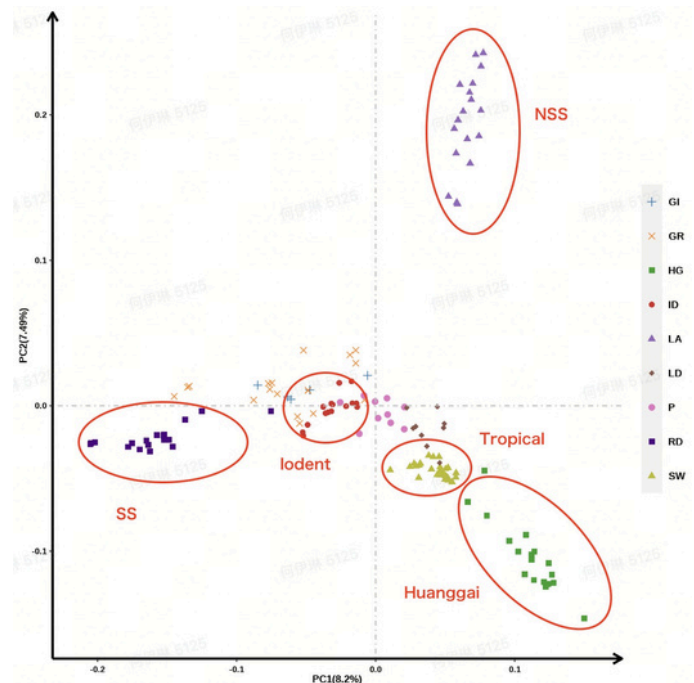


Figure 3 PCA of 87 maize accessions based on the 45K panel markers, showing clustering into nine distinct heterotic lineages:

- GI – Improved Iodent Representative Lines: Tropical or PB (PB/P) heterotic group lines incorporating tropical/subtropical genetic backgrounds. These lines are characterized by strong stress tolerance, high yield potential, and enhanced disease resistance. They serve as key tropical germplasm resources in Chinese maize breeding for improving temperate germplasm and alleviating genetic bottlenecks.
- RD – Reid Representative Lines: Refers to the standard U.S. Reid germplasm group. Compared with locally adapted derivatives, RD lines are closer to the original U.S. germplasm and function primarily as introduced resources in Chinese breeding programs.
- GR – Improved Reid Representative Lines: A heterotic group derived from U.S. Reid germplasm and extensively adapted and improved in China. Representative inbred lines include *Shen5003*, *Tie7922*, and *Ye478*.
- HG – Huanggai Improved Group Representative Lines: Derived from the Chinese landrace *Huangzaosi* and its selected descendants, this group represents one of the core germplasm pools in Chinese maize breeding. Hybrids formed by crossing HG lines with introduced germplasm exhibit strong heterosis. Currently, HG-derived hybrids account for over 60% of the maize cultivation area in China.
- ID – Iodent Representative Lines: Refers to the Iodent heterotic group originating from U.S. Iodent germplasm, which has been widely incorporated into Chinese breeding programs.
- LA – Lancaster Representative Lines: Originating from U.S. Lancaster germplasm. The representative line *Mo17* and its derivatives were widely utilized in Chinese breeding during the 1970s–1980s, resulting in the development of more than 100 hybrids.

- LD – Lushun-Dalian Red Bone Representative Lines: A heterotic group derived from the Chinese landrace *Dan340* and its descendant lines. As a local germplasm group, it has contributed significantly to Chinese maize breeding since the 1990s.
- P – Tropical/Subtropical Representative Lines: A heterotic group developed from the U.S. hybrid P78599. Representative inbred lines selected in China include *Qi319*, *P178*, and *Shen137*. It represents an important introduced tropical heterotic group.
- SW – Suwan Tropical Representative Lines: A synthetic tropical maize germplasm population developed by Kasetsart University (Thailand) through the introduction and evaluation of global maize germplasm. Thirty-six elite materials with superior overall performance were selected and synthetically assembled at Suwan Farm.

- Heterotic group classification and germplasm management (10K-45K)
- Marker-assisted backcrossing and trait introgression (1K-10K)
- Genomic selection (all densities, with imputation from 1K to 45K)

This technology democratizes access to high-density genotyping for breeding programs worldwide, from multinational companies to small-scale operations in developing countries

Conclusion

MolBreeding's Maize GBTS Panels represent a great advancement in maize genotyping technology, combining the mSNP innovation with the GenoBaits® liquid capture platform. By capturing multiple SNPs per amplicon, the 45K panel delivers the genetic resolution equivalent to traditional 250K SNP arrays at a fraction of the cost.

These panels support the full spectrum of modern breeding applications:

- High-resolution GWAS and QTL mapping (45K)

Call to Action

We invite the global maize research and breeding community to collaborate with us in utilizing GenoBaits Maize Panels to accelerate genetic gain and breeding efficiency. Through this collaboration, we aim to unlock the full potential of maize genetic diversity, enabling the development of superior cultivars with enhanced yield, climate resilience, and nutritional quality, contributing to global food security and sustainable agriculture.

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