

Cost-effective and scalable content for EDV assessment and other maize breeding applications.

- **Comprehensive Solution for EDV Testing**
High-discrimination coverage with 3047 evenly spaced markers designed for EDV assessment
- **Add-On Content for Multiple Applications**
Customizable to support varietal identification, genetic purity testing, marker-assisted selection, and other applications
- **Affordable, Standard Platform**
Single platform for various maize applications reduces costs and eliminates manual processing errors
- **Unrivaled Call Rates and Accuracy**
> 99% average call rates and > 99.9% reproducibility

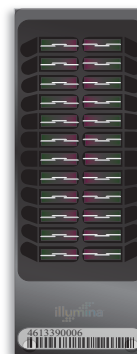


Figure 1: MaizeLD BeadChip—Designed for EDV assessment, the MaizeLD BeadChip features 3047 evenly spaced SNPs.

Maize (*Zea mays* L. ssp. *mays*) was domesticated from the grass teosinte in Central America¹ over the last ~10,000 years, resulting in dramatic expansion of the maize genome through proliferation of long terminal repeat retrotransposons.² It is an important model organism for fundamental research into gene inheritance and function,³ and a staple crop.

In 2009, researchers completed an improved draft sequence of the 2.3-gigabase genome of the B73 maize line.⁴ This assembly was used to compare sequence data of other key maize lines. From these efforts, over 1 million SNPs have been identified.⁵

Maize exhibits high levels of both phenotypic and genetic diversity and has been subject to high selective breeding pressure for yield improvement, particularly among large companies supporting growers with regionally appropriate seed. To create standards for recognizing varietal development efforts, the International Union for the Protection of New Varieties of Plants outlined definitions for essentially derived varieties (EDV) in 1991.⁶ EDVs are obtained, either directly or indirectly, from an initial variety (by selection of a natural or induced mutant), a somaclonal variant, a selection of variant plants from the initial variety, backcrossing, or transformation by genetic engineering. If they fulfill these conditions, EDVs are eligible for plant breeders' rights.

Under the guidance of the International Seed Federation, the American Seed Trade Association and the French Breeders Association identified SNPs that are equivalent to the simple sequence repeat (SSR) markers traditionally used to determine EDV status.⁷ To provide the seed industry with a standard tool for EDV assessment, the MaizeLD BeadChip (Figure 1) contains 3047 internationally recognized EDV markers based on genetic and physical maps. This array also offers the capability to add custom markers, enabling other maize breeding applications to be run on the same platform.

SNP selection was based on a comparison of pairwise distance data for inbred maize lines generated using SNP markers from the MaizeSNP50 BeadChip and SSR markers previously shown to discern EDV status.⁷ In a collaboration between Illumina, Syngenta, and Pioneer, the markers were initially selected based on quality assurance analysis criteria from genotyping of US and European public and commercially relevant samples. SNP data were eliminated from subsequent analyses if they exceeded the following thresholds:

- > 10% of missing SNPs per genotype
- > 10% of missing genotypes per SNP
- > 5% heterozygous SNPs per genotype
- > 10% heterozygous genotypes per SNP

After discarding 43 SNPs with insufficient data quality or vulnerability to ascertainment bias, final comparisons were made using 26,874 SNPs. Also, 3047 SNPs were selected to provide even genomic coverage to facilitate SNP-based breeding applications.

The MaizeLD BeadChip offers a comprehensive genotyping solution for EDV testing in maize, providing the high discrimination necessary to assess EDV status. Compared to traditional SSR markers, SNP genotyping offers higher throughput, resolution, and reproducibility, resulting in high accuracy. Many agricultural researchers today are transitioning from SSR analysis to SNP genotyping. With the MaizeLD BeadChip, researchers can assess all EDV markers at the same time across many samples rather than running separate assays for each gene of interest.

For Research Use Only. Not for use in diagnostic procedures.

