IMPROVE THE EFFICIENCY OF CANNABIS BREEDING

MARKER ASSISTED BREEDING (MAB) | MARKER ASSISTED SELECTION (MAS)

For research use only. Not for use in diagnostic procedures.

Automated Cannabis Testing Solutions

PerkinElmer
For the Better
Marker Assisted Breeding (MAB), a technique commonly used in agricultural industries, can be used by Cannabis breeders to associate regions of genetic variation (locus/loci) with a specific phenotypic trait. Marker Assisted Selection (MAS), a selection process used in MAB where a trait of interest is selected based on a specific genetic marker, allows Cannabis breeders to select for specific characteristics such as yield, potency, vigor, disease resistance; potentially strengthening strains and enhancing crops through traditional breeding techniques.

Using low-pass Whole Genome Sequencing (WGS) provides an accurate and cost-effective solution to measure genome-wide genetic variation in Cannabis without having to invest in the time and labor required to grow the seedlings to maturity prior to phenotypic analysis. Low-pass WGS provides an order of magnitude more data, greater statistical power, and enhanced variant discovery capabilities outperforming other techniques, such as microarrays for MAS.

Use of MAS in Cannabis Breeding

NEW CANNABIS STRAINS

Germplasm Resources
Cultivators, Breeding Lines,
Wild Relatives, etc.

Screening & Selection

Population development
Recombination or segregation

Screening & Selection
Adaptable & Scalable Solutions for Varying Throughput
PerkinElmer’s end-to-end solutions allow Cannabis breeders to minimize errors, reduce hands-on time, and increase throughput and reproducibility. Flexible instrumentation modules, based on your testing and throughput requirements, can be added to meet your needs. Contact your PerkinElmer sales representative for more information.

Versatile Library Prep Automation
With flexibility in throughput, capacity and dynamic volume range, high quality manufacturing standards, and outstanding customer service and support, PerkinElmer offers automated liquid handling solutions optimized to meet your laboratory’s needs.

Optimized Library Prep
The NEXTFLEX® Rapid XP DNA-seq Pre-Plated automation kit and pre-plated NEXTFLEX® Unique Dual Index barcodes eliminate the need for plate set-up, offering plug-and-play library construction on the Sciclone® G3 NGS/NGSx workstations and increase the sensitivity, flexibility and speed of library prep making them ideal for low-pass WGS.

High-throughput Analysis of Specific Cannabis Markers
With the ability to multiplex up to 384 samples at a time and a simplified sample preparation protocol, targeted re-sequencing with NEXTFLEX® amplicon panels is ideal for screening a large number of Cannabis plants for specific markers. With a completely automated workflow, the custom NEXTFLEX® amplicon panels provide a simple and robust method for high-throughput, targeted Cannabis re-sequencing applications including:

- Marker-assisted selection for Cannabis breeding
- Confirmation of on-target and off-target CRISPR gene editing experiments

LOW-PASS WHOLE GENOME SEQUENCING WORKFLOW

PerkinElmer’s complete automated workflow for low-pass WGS allows Cannabis breeders to efficiently identify genetic differences controlling desired phenotypes allowing for the identification of important phenotypes such as THC, CBD, terpenes, and disease resistance allowing breeders to predict the future commercial viability of each seedling.

Nucleic Acid Quality Control
VICTOR Nivo® Plate Reader

Library Prep Automation*
Sciclone® G3 NGSx / NGSx iQ™ Workstation with NEXTFLEX® Rapid XP DNA-Seq Kit

Library Quality Control
LabChip® GX Touch™ HT Nucleic Acid Analyzer

Sequencing
External

Data Analysis

perkinelmer-appliedgenomics.com/cannabis
Improve the efficiency of your cannabis breeding with PerkinElmer's complete workflow solutions: perkinelmer-appliedgenomics.com/cannabis

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