Amplification: Precision Melt Analysis Software

The Power of Precision

Precision Melt Analysis Software is a convenient, easy-to-use application that imports and analyzes data files generated from the CFX Opus 96, CFX96 Touch, CFX96, CFX Opus Deepwell, CFX96 Touch Deep Well, CFX Opus 384, CFX384 Touch, CFX384, CFX Duet, or CFX Connect Real-Time PCR System to genotype samples based on the thermal denaturation properties of double-stranded DNA. The software can be used for a variety of genotyping applications, including scanning for new gene variants, screening DNA samples for single nucleotide polymorphisms (SNPs), identifying insertions/deletions or other unknown mutations, and determining the percentage of methylated DNA in unknown samples.

Precision Melt Analysis Software makes it easy for you to:

- Streamline your data analysis using the customizable default analysis settings
- Tailor the software to the appropriate analysis by using multiple data view options to manually assign sample genotypes
- Examine results from a number of melt files, without having to export data, using the Melt Study module
- Analyze multiple experiments from a single plate using the Well Groups feature
- Publish your data in several formats by easily exporting data and images

Visit bio-rad.com/PrecisionMeltAnalysisSoftware for more information.
Efficient and Effective Analysis

Precision Melt Analysis Software saves analysis time by assigning sample genotypes automatically based on cluster analysis, or allowing manual use of multiple data view options to tailor the software to the appropriate analysis. Use the normalized melt curves plot feature to generate a basic representation of the different clusters based on curve shifting (for homozygotes) and curve shape change (for heterozygotes). Difference curve plots of a sample fluorescence versus a selected control at each temperature transition provide a convenient visual aid to interpret the data.

Precision Melt Analysis Software enables data comparison between multiple file runs by combining data into a single Melt Study. Develop a standard library of melt curve runs to analyze an unlimited number of melt experiments without having to export data.

A representative difference curve plot generated from data normalized to a mutant sample. Data from homozygous wild-type (■), mutant (■), and heterozygote (■) samples are shown. RFU, relative fluorescence units.

SNP genotyping by Precision Melt Analysis Software using data generated by the CFX384 Real-Time PCR System. Discrimination of human hemochromatosis S65C SNP genotypes (A to T substitution). Data from homozygous wild-type (■), mutant (■), and heterozygote (■) samples are shown on a normalized melt curve plot. RFU, relative fluorescence units.

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