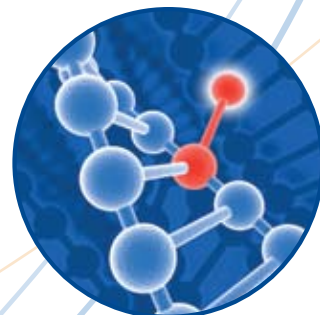


MassARRAY®

Quantitative Methylation Analysis

High Resolution Profiling.
Simplified with EpiTYPER®.



SEQUENOM®

MassARRAY[®]

Quantitative Methylation Analysis

Overview

Unprecedented Levels of Performance

The EpiTYPER assay is based on proven bisulfite-conversion biochemistry followed by PCR and a proprietary base-specific cleavage process.

The resulting cleavage pattern depends on the presence of methylated cytosine in the original genomic DNA.

The cleavage products are automatically and quantitatively analyzed by MALDI-TOF mass spectrometry.

This combination creates a highly accurate, sensitive, and high-throughput method for the quantitative analysis of DNA methylation.

MassARRAY EpiTYPER is scalable and allows you to analyze multiple CpGs without compromising accuracy, sensitivity, or reproducibility. The EpiTYPER software provides convenient solutions for data analysis and export.

Testimonial

“We are successfully using Sequenom’s EpiTYPER for quantitative DNA methylation analysis in our comprehensive cancer center research programs. This product enables us to analyze multiple CpGs in one amplicon and to reliably compare their methylation status between individual samples. Unlike classic methods for assessing methylation events at individual sites in the genome, EpiTYPER quantitatively assesses methylation ratios simultaneously across multiple CpG sites over multiple samples dramatically increasing the scope and throughput of analysis.”

Norma J. Nowak, Ph.D.,

Associate Professor, Director, Scientific Planning
RPCI and University at Buffalo, NY

The EpiTYPER Assay

MassARRAY EpiTYPER is the method of choice for the quantitative analysis of DNA methylation and identification of differentially methylated CpG sites in any genomic region or candidate gene.

Efficiency

- Bisulfite treated DNA to data in 8 hours
- Covers multiple CpGs in amplicons of up to 600 bp
- Compatible with formalin-fixed paraffin-embedded tissue samples

Precise & Accurate

- High precision (5% CV)
- High inter-laboratory reproducibility

Sensitive

- Detects down to 5% change in methylation levels

Cost Effective

- 96 and 384 well microplates formats available
- Multiple CpGs analyzed in one simple reaction and from one amplicon

Simple Workflow

- No need to design CpG-specific primers
- No PCR product purification required
- Ideal for investigating a few or several hundred target regions
- Convenient software solutions for comparison between samples

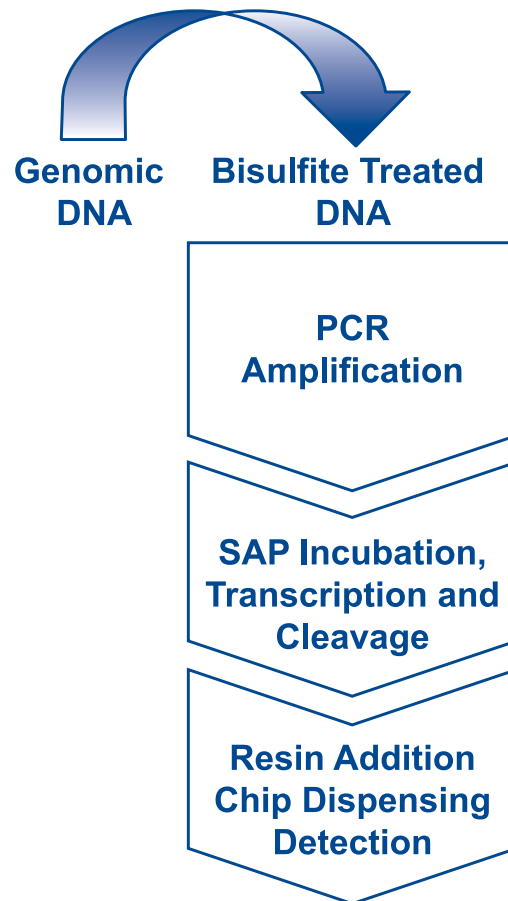
How it Works

Base-specific cleavage with MassCLEAVE – The starting point of the protocol is bisulfite treatment of genomic DNA. This treatment converts non-methylated cytosine into uracil, thus generating methylation dependent sequence changes in the genomic DNA template. PCR, with T7-promotor tagged reverse primers, is used to amplify the template while preserving the induced sequence changes. After SAP treatment *in vitro* transcription is performed, the generated transcript is subjected to an enzymatic base specific cleavage. The resulting fragments differ in size and mass depending on the sequence changes generated through bisulfite treatment. The fragment mass is determined by MALDI-TOF MS and the EpiTYPER software generates a report that contains quantitative information for each analyzed fragment.

Instrumentation – Several system options (96- or 384- well) are available depending on your throughput and study requirements. Interrogate 10s to 100s of methylated regions across 10s to 100s of samples.

Software – The EpiTYPER software provides an advanced and convenient solution for the quantitative analysis of CpG Methylation. Numerical and graphic interpretation tools are available and the data are automatically matched to the provided sequence. Basic statistical analysis and confidence ratings are available for built-in quality control.

Superior Performance – MassARRAY EpiTYPER allows you to cost effectively and quantitatively assess the methylation status of multiple CpGs in one or more PCR amplicons. Combined with the data quality and reporting functions, EpiTYPER is an indispensable tool for medium to large scale methylation studies.



The EpiTYPER Software

Data Analyzer Mode

DATA SET SELECTION

- Click on one or both of these buttons to determine which data set is included in tab panes and EpiGram.

SPECTRUM PANE

- Automatically display the mass spectrum for all analyzed amplicons and identifies the selected CpG Site (e.g., see red arrow in spectrum).

METHYLATION TAB PANE

- Obtain customized visual presentation of amplicon data in the most useful format that best suits your needs.



SEQUENCE VIEW PANE

- This display shows the entire forward and reverse nucleotide sequence for the selected amplicon.

Amplicon Display Mode

HIGH DEGREE OF PROGRAM CUSTOMIZATION

- Accessing these menus allows fine-tuning of program parameters, panes to display, and methylation color coding of CpG Sites.

EpiGram TAB PANE

- This pane provides graphical representations of the CpG Sites within the selected amplicon. Each is color-coded representing the degree of methylation shown in the methylation tab pane to provide a quick, reliable comparison between samples and CpG Sites.



MassARRAY[®]

Genetic Analysis System

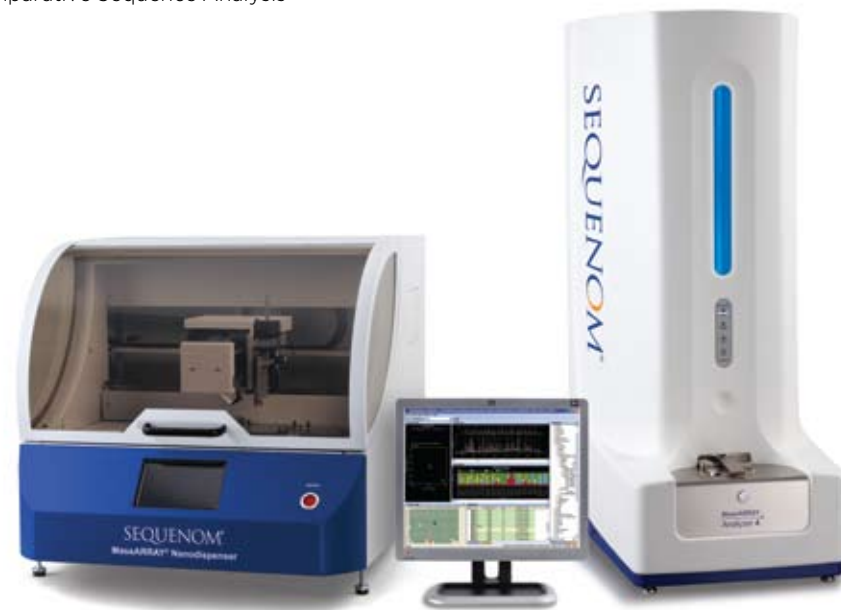
MassARRAY Analyzer 4 System

The MassARRAY technology is used by the leading genetics institutions worldwide. The bench top MassARRAY Analyzer 4 system is a multi-application platform that addresses the following applications:

- Quantitative Methylation Analysis
- SNP Genotyping
- Somatic Mutations
- Quantitative Gene Expression
- Comparative Sequence Analysis

MassARRAY Advantage

MassARRAY genotyping facilitates identification and prioritization of genetic targets within each stage of biomedical research. From targeted discovery utilizing 10s to 100s of multiplexed assays to validation of select markers against 100s to 1000s of samples, the MassARRAY system powers a variety of genomic studies.



**Flexibility of Scale with
Versatility of Application**

ATGATGATCGAAGCCGATGATCGACCAGTATGTATCATGATGATCGAAGC
ATGATCGAAGCCGATGATGATGATCGAAGTACATGATGATCGAAGCCGATGATG
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