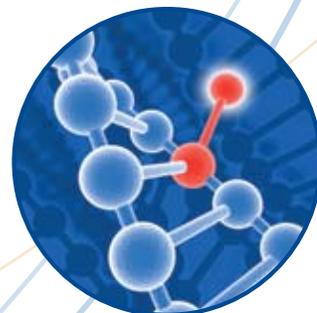


MassARRAY®

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

MassARRAY[®]

Genetic Analysis System

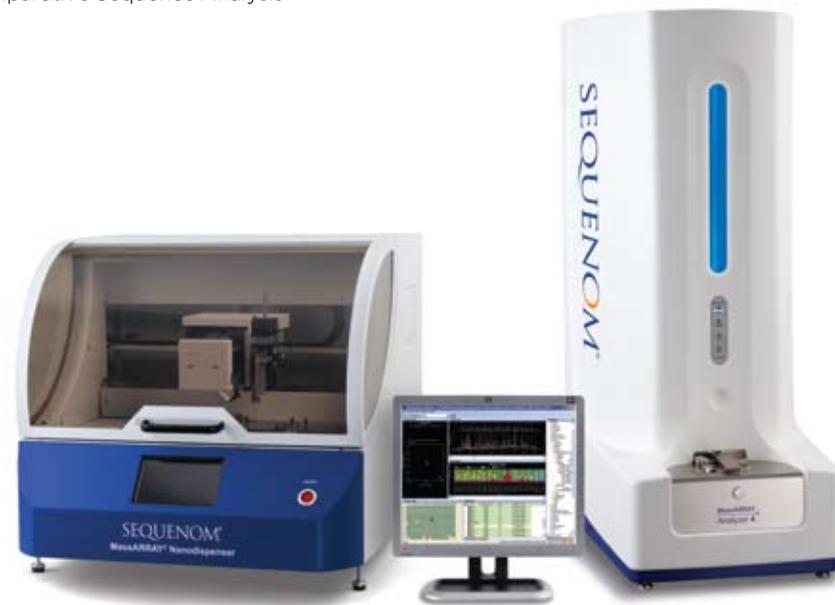
MassARRAY Analyzer 4 System

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
TCGAAGCCGATGATCGACCAGTATGCGCATGAATGATCGAAGCCGATGATCGACCAGT
AAGTATGCGCATTATGCGCATGATGATCGAAGATCGAAGTATGCGCATTATGCGCATGATGAG
AGTATGGCGCATTATGCGCGCATGATGATCGA GACCAGTATGGCGCATTATGCGCGCATGATGCAGTATGGCGCAT
GAAGTAGTATCATGATGATCGAAGCCGATGAGATCGAAGTAGTATCATGATGATCGAAGCCGACGAAGTAGTATCATGA
CGATGATCGACCAGTATGCGCATGATGATCGAAGTATGCGCATTATGCGCATGATGATCGAAGCCGATGATCGACCAGTA
CGCATTATGCGCATGATGATCGAAGCCGATGATCGACCAGTATGCGCATGATGATCGAAGTATGCGCATTATGCGCATGA
CGCATTATGCGCGCATGATGATCGAAGTATCATGATGATCGAAGCCGATGATCGACCAGTATGGCGCATTATGCGCGCAT
TATCATGATGATCGAAGCCGATGAGTATCATGATGATCGAAGCCGATGATGATGATCGAAGTATCATGATGATCGAA
GATCGAAGTATGCGCATTATGCGCATGATGATCGAAGCCGATGATCGACCAGTATGCGCATGATGATCGAAGTATGCGCA
CGATGATCGACCA TATGCGCATGATGATCGAAGTATGCGCATTATGCGCATGATGATCGAAGCCGATGATCGACCAGTA
GTATCATGATGATCGAAGCCGATGATCGACCAGTATGGCGCATTATGCGCGCATGATGATCGAAGTATCATGATGATCGA

Publications

- Coolen MW, Stirzaker C, Song JZ, et al. Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional activity. *Nat Cell Biol.* 2010;12:235-246.
- Docherty SJ, Davis OSP, Haworth CMA, Plomin R, Mill J. DNA methylation profiling using bisulfite-based epityping of pooled genomic DNA. *Methods.* 2010;52(3):255-8.
- Khoury H, Suarez-Saiz F, Wu S, Minden MD. An upstream insulator regulates DLK1 imprinting in AML. *Blood* 2010;115(11): 2260-2263.
- Nygren AOH, Dean J, Jensen TJ, et al. Quantification of fetal DNA by use of methylation-based DNA discrimination. *Clin Chem.* 2010;56:1627-1635.
- Tobi EW, Lumey LH, Talens RP, et al. DNA methylation differences after exposure to prenatal famine are common and timing- and sex-specific. *Hum Mol Genetics.* 2009;18(21):4046-4053.
- van den Boom D, Ehrlich M. Mass spectrometric analysis of cytosine methylation by base-specific cleavage and primer extension methods. *DNA Methylation: Methods and Protocols.* Vol. 507, 2nd ed. 2008:207-227. doi:10.1007/978-1-59745-522-0_16.
- Wong CCY, Caspi A, Williams, B, et al. A longitudinal study of epigenetic variation in twins. *Epigenetics.* 2010;5(6):1-11.
- Wu H, Coskun V, Tao J, et al. Dnmt3a-dependent nonpromoter DNA methylation facilitates transcription of neurogenic genes. *Science.* 2010;329(5990):444-448.

For more information please contact your area Sequenom office.

NORTH AMERICA: +1 (877) 443-6663

EUROPE: +49 4089 967640

ASIA-PACIFIC: +61 7 3845 369

www.sequenom.com

CHINA: +86 10 8048 07 37

sequenom.china@sequenom.com

JAPAN: +81- 3-6802-5590

sequenom.japan@sequenom.com

SEQUENOM®

The MassARRAY Analyzer 4 System (also referred to as MALDI-TOF), EpiTYPER Assay and EpiTYPER software are for research use only. Not for use in diagnostic procedures. ©2011 Sequenom, Inc. All rights reserved. Sequenom, MassARRAY, EpiTYPER, and SpectroCHIP are registered trademarks of Sequenom, Inc., and MassCLEAVE is a trademark used by Sequenom, Inc. Products and/or processes are covered by one or more claims of United States Patent Nos. 6,569,385; 6,300,076; 6,258,538 and foreign equivalents. Other U.S. and foreign patents pending.

#sq189_methyl_v4(0113-2011)