

MassARRAY[®]

Quantitative Gene Expression

Overview

Unprecedented Levels of Precision

MassARRAY Quantitative Gene Expression (QGE) combines Competitive PCR with MALDI-TOF mass spectrometry enabling a highly accurate, sensitive, and high-throughput method for the quantitative analysis of gene expression.

MassARRAY QGE is scalable, allowing you to perform assays without compromising accuracy, sensitivity, or reproducibility. In addition, the method does not use chemiluminescence, fluorescence or other secondary labeling approaches, allowing unambiguous, high-level multiplexing.

Testimonial

“We have successfully tested the MassARRAY system to demonstrate the accuracy, sensitivity and reproducibility of the system. In addition, the methods for measuring relative gene expression differences were demonstrated in a relatively high throughput manner.”

Jiannis Ragoussis, Ph.D.

Genomics Group,
Wellcome Trust Centre for Human Genetics,
University of Oxford.

The QGE Assay

MassARRAY QGE is the method of choice for validation of microarray data, for the investigation of coding and noncoding transcripts – and whenever sensitivity and accuracy are required in transcription analysis.

Flexible Assay Design

- Automated assay design software
- Routine multiplexing at 20-plex level
- No fluorescence label required

Precise & Accurate

- High precision (3% CV) over a wide range of expression levels
- Detects down to 10% change in expression levels

Sensitive

- Limit of detection 1 aM (-3 copies per reaction)
- Low amount of starting material (down to 5 pg) required

Cost Effective

- High level multiplexing in a 384 microplate format
- Ideal for investigating 10-200 genes

Simple Workflow

- Automated, rapid and efficient assay design
- Validated assay panels for data normalization
- Convenient comparison between samples

High Level Multiplexing

How it Works

Competitive PCR – In competitive PCR an internal standard (the competitor) and cDNA are co-amplified in the same reaction. The concentration of the target transcript is calculated from the ratio of the resulting PCR products. MassARRAY QGE determines the ratios through measurement of primer extension product mass signals.

Instrumentation – Several system options are available depending on throughput requirements. SEQUENOM developed the MassARRAY system and its SpectroCHIP® arrays to specifically meet the requirements of moderate to high throughput quantitative genetic analysis.

Software – The software package includes an assay design tool for multiplex primer and competitor design.

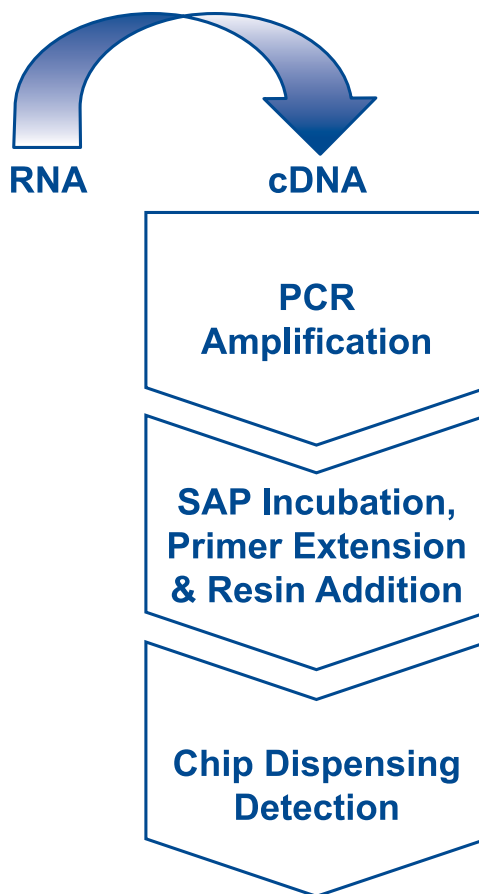
Superior Performance – MassARRAY QGE is an end-point assay and hence independent of PCR kinetics. This makes it possible to compare results from PCR reactions completed at different times, locations and with different reagents.

Multiplexing with MassARRAY QGE results in lower cost and higher throughput than Realtime PCR based methods.

QGE has a higher precision than methods that rely on threshold cycle comparison. Each assay contains an internal standard so that PCR inhibitors or PCR cycle numbers have no effect on quantitation. Less than 3% CV allows the user to measure changes in expression levels down to 10%.

The primer extension step subsequent to the competitive PCR provides additional amplification that results in superior sensitivity.

MassARRAY QGE enables studies on trace amounts of material, for example generated in Laser Capture Microdissection as well as measurements of low-abundance RNA species.



QGE Data Analyzer

Data Analysis Mode

PLOT

- Displays the plot of low mass allele vs. high mass allele for the assays selected for analysis

TRAFFIC LIGHT

- Displays a layout of the plate, showing wells that contain reactions and their status in color code

WELL DATA

- Displays detailed assay, calibration ("call"), peak, area, and frequency information related to each assay



SPECTRUM

- Displays the raw spectrum for the data point currently selected, including intensities, resolution and signal-to-noise ratio

Data Summary Mode

CUSTOMER FILTER

- Select your project, then filter down to the specific data of interest contained in the Sample & Assay pane below

SAMPLE & ASSAY

- Drag and drop the data to summarize into the Selection pane, automatically populating the Plot & Histogram panes

SELECTION PANE

- Contains the selected data to summarize

PLOT & HISTOGRAM

- Shows data points, & has several customization options available to create informative data summaries, which can be exported for use in reports



MassARRAY®

Genetic Analysis System

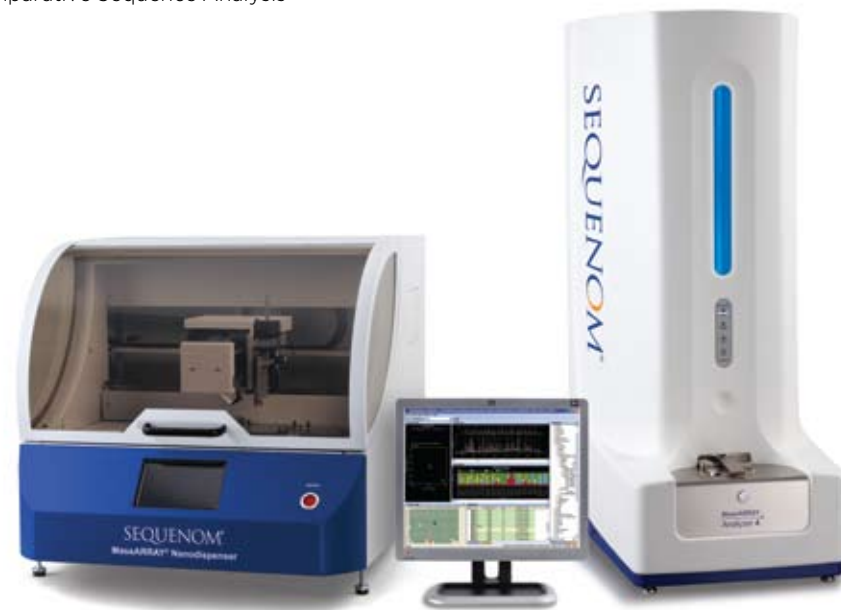
MassARRAY Analyzer 4 System

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
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Publications

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Turakulov, R. et al. (2007) "Ultrasensitive determination of absolute mRNA amounts at attomole levels of nearly identical plant genes with high-throughput mass spectrometry (MassARRAY)." *Plant Cell Physiol* 48 (9): 1379-84.

Opsal, M. A. et al. (2006) "Genomic organization and transcript profiling of the bovine toll-like receptor gene cluster TLR6-TLR1-TLR10." *Gene* 384: 45-50.

Elvidge G.P., Price T.S., Glenny L, Ragoussis J. (2005) "Development and evaluation of real competitive PCR for high-throughput quantitative applications." *Anal Biochem.* 339 (2): 231-41.

Yang, H. et. al. (2005) "Sensitive Detection of human papillomavirus in cervical, head, neck and schistosomiasis-associated bladder malignancies." *Proc Natl Acad Sci USA* 102 (21): 7683-8.

Ding, C. and Cantor, C.R. (2003) "A high-throughput gene expression analysis technique using competitive PCR and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry." *Proc Natl Acad Sci USA* 100 (6): 3059-64.

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