PCR ARRAY HANDBOOK v3.0

The Complete Technical Guide to PCR ARRAYS

Cancer
Cytokines
Biomarkers
ECM & Adhesion
Oxidative Stress
Signal Transduction
Inflammation
Stem Cells
MicroRNA
Epigenetics
Toxicology

NEW 100 Selected Peer-reviewed Publications

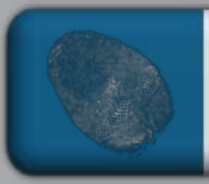
SABiosciences™

Focus on your Pathway™

QUICK REFERENCE

APOPTOSIS page 12

AVAILABLE ARRAYS **27**



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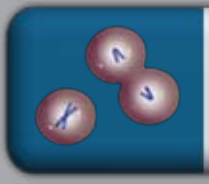
AVAILABLE ARRAYS **22**

CANCER page 12

AVAILABLE ARRAYS **28**



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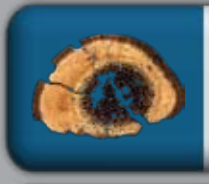
AVAILABLE ARRAYS **23**

CYTOKINES page 13

AVAILABLE ARRAYS **22**



ECM/ADHESION page 13

AVAILABLE ARRAYS **25**

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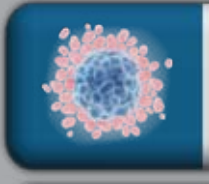


STEM CELL/DEVELOPMENT page 13

AVAILABLE ARRAYS **26**

TOXICOLOGY/DRUG ADME page 13

AVAILABLE ARRAYS **19**

ORDERING INFO

TEL: **301.682.9200**

FAX: **301.682.7300**

www.SABiosciences.com

support@SABiosciences.com

SABiosciences Corporation

6951 Executive Way, Frederick, MD 21703 USA

Compatible Instrument	PCR Array Plate Format
Applied Biosystems (ABI)	
ABI 5700	A
ABI 7000	A
ABI 7300	A
ABI 7500 Standard 96-well Block	A
ABI 7500 FAST 96-well Block	C
ABI 7700	A
ABI 7900HT Standard 96-well Block	A
ABI 7900HT FAST 96-well Block	C
ABI 7900HT 384-well Block	E
ABI StepOnePlus™	C
Bio-Rad	
iCycler	A
iQ5	A
MyiQ	A
CFX96	D
CFX384	E
Chromo4™	A
Opticon 2®	D
Stratagene	
Mx3005p	A
Mx3000p	A
Mx4000	D
Roche	
LightCycler 480 96-well Block	F
LightCycler 480 384-well Block	G
Eppendorf	
Mastercycler ep realplex	A
TaKaRa	
TP-800	A
Fluidigm	
BioMark	H

PCR ARRAY GUARANTEE

PCR ARRAYS have a truly remarkable performance record. SABiosciences is so confident that you will love the sensitivity, reproducibility, & reliability of our PCR ARRAY System that we back up all of our PCR ARRAY products with a 30 day money-back guarantee. If you are dissatisfied with the performance of your PCR ARRAYS within 30 days of purchase, you are eligible for a full refund.*

* Visit for Complete Details: *www.SABiosciences.com/guarantee.php*

Pricing is only valid for customers in the USA. Prices are subject to change. Researchers outside the USA should contact their local SABiosciences' distributor for technical information and pricing. The international distributor list can be found online:

http://www.SABiosciences.com/distributor.php

PCR ARRAY HANDBOOK VERSION 3.0

RT² Profiler™ PCR ARRAYS

The Most Accurate and Sensitive Technology for Pathway Gene Expression Analysis

What Are PCR ARRAYS?

RT² Profiler™ PCR Arrays are the most reliable and sensitive gene expression profiling technology for analyzing focused panels of genes in signal transduction, biological process, or disease-related pathways using real-time PCR.

How Are PCR ARRAYS Utilized?

RT² Profiler PCR Arrays are exceptionally valuable tools for studying cancer, immunology, stem cells, toxicology, biomarker discovery/validation, and phenotypic analysis of cell and tissue samples (fresh, frozen, and fixed).

Why Use RT² Profiler™ PCR ARRAYS?

- ***Simplicity:***
  The simplicity of RT² Profiler PCR Arrays makes routine expression profiling practical in any research laboratory with a real-time instrument.
- ***Performance:***
  RT² Profiler PCR Arrays have the sensitivity, reproducibility, specificity, and reliability to accurately profile multiple genes simultaneously in 96- or 384-well formats.
- ***Relevance:***
  RT² Profiler PCR Arrays focus on profiling the genes relevant to the pathways or disease states important to your research.

Anatomy of a 96-well RT² Profiler PCR ARRAY

Human Inflammatory Cytokines and Receptors PCR Array

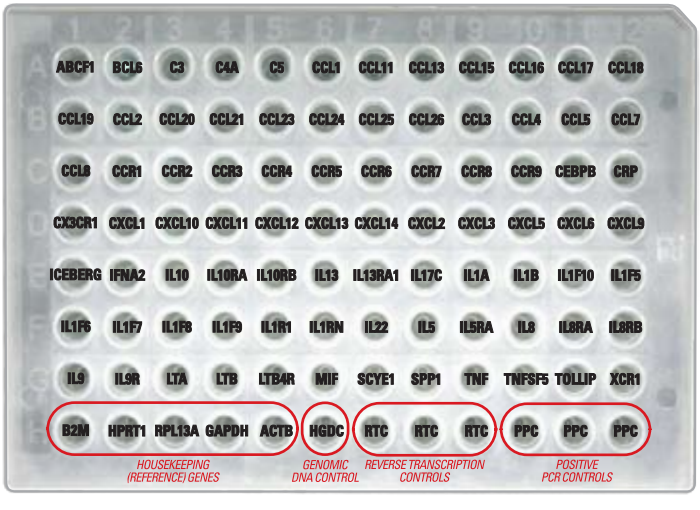
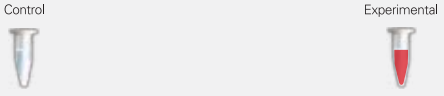


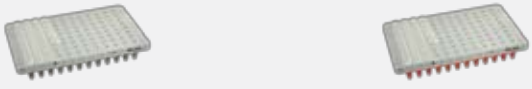
Figure 1: Each Well in a PCR Array Measures the Expression of a Gene Related to a Pathway or Disease State. Each cataloged PCR Array contains a list of the pathway-focused genes as well as five housekeeping (refererence) genes on the array. Wells H6 through H12 contain a panel of proprietary controls to monitor genomic DNA contamination (HGDC) as well as the first strand synthesis (RTC) and real-time PCR efficiency (PPC).

How PCR ARRAYS Work

1. Convert Total RNA to cDNA.



2. Add cDNA to RT² SYBR® Green Master Mix. Aliquot Mixture Across PCR Array.



3. Run in Your Real-Time PCR Instrument.

4. Data Analysis.

SYBR® Green Versus TaqMan® Chemistries

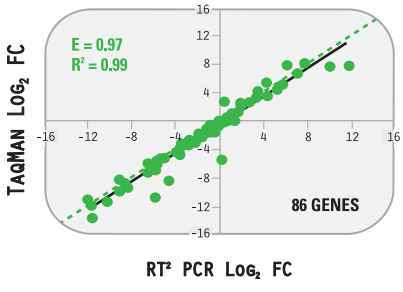


Figure 2: Comparable Biological Results.* Gene expression analysis was compared between RT² Profiler PCR Arrays (SYBR Green-based) and the TaqMan platform. Regression analysis of fold differences, with data normalized against POLR2A, demonstrate that both platforms yield similar biological results.

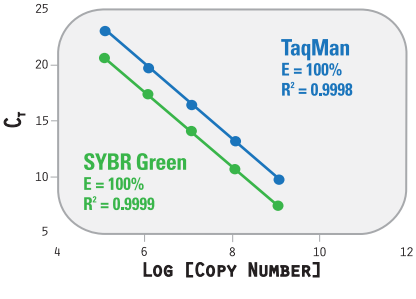


Figure 3: Sensitivity with RT² SYBR Green Versus TaqMan Chemistry.* PCR amplicons detected using the same primer pair with or without TaqMan probes in either SYBR Green or TaqMan chemistry. SYBR green chemistry yields earlier C_Ts for each dilution, demonstrating better sensitivity than TaqMan chemistry.

* **BMC Genomics 2008, 9: 378.**

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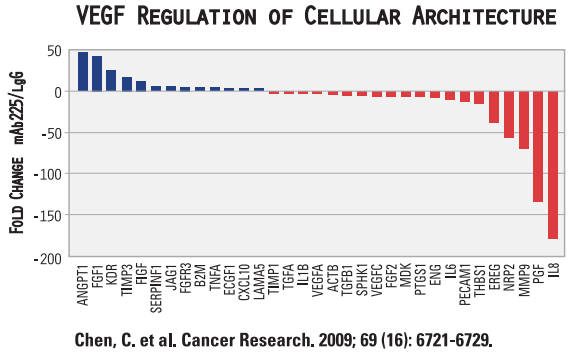
Application: *Angiogenesis*



Chen, C. et al. Cancer Research. 2009; 69 (16): 6721-6729.

Figure 4: Relative Fold Change Between Disorganized and Organized Colonies Using the RT² Profiler Angiogenesis PCR Array. RNA isolated from unorganized T4-2 cells treated with a control antibody (IgG) or reverted to an organized colony by blocking EGFR signaling (mAB225) was reverse transcribed and relative gene expression data was obtained using the Human Angiogenesis PCR Arrays. The expression profile of 84 genes relevant to Angiogenesis as well as 5 housekeeping genes was assayed. Fold change calculations were done using SABiosciences' data analysis software which automatically calculates the fold change in gene expression between the treated and control groups.

Application: *Immune Response*

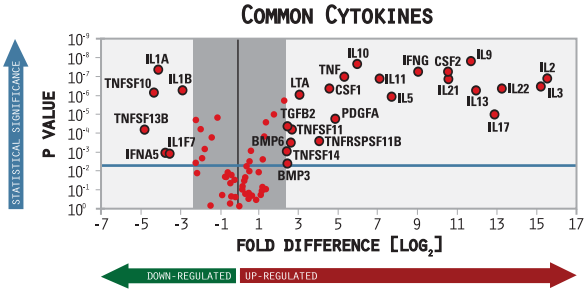


Figure 5: Common Cytokine PCR Array Identified 23 Up-Regulated and 6 Down-Regulated Genes Following PBMC Stimulation. Triplicate total RNA samples from human peripheral blood mononuclear cells (either untreated or stimulated with 50 ng/mL PMA and 1 µg/mL ionomycin for 6 hours) were characterized with the Human Common Cytokine PCR Array. Twenty-three cytokine genes are up-regulated (> 5-fold,p < 0.0005) including interleukins, colony stimulating factors, and TNF ligands after 6 hours of stimulation. Six interleukin and TNF ligand genes are down-regulated under the same conditions.

Application: *Determining Drug Toxicity with PCR ARRAYS*

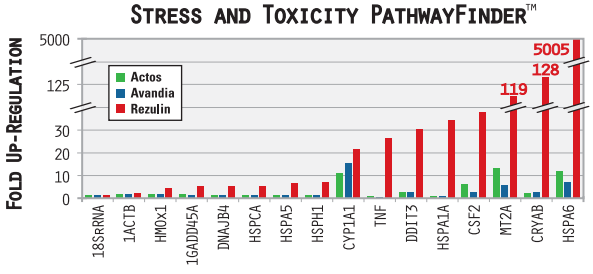


Figure 6: Stress and Toxicity PathwayFinder™ PCR Array Uncovered Distinct Gene Expression Profiles Associated with Liver Toxicity Caused by 3 PPARγ Agonists. RNA from HepG2 cells treated with three different glitazone PPARγ agonists for type 2 diabetes mellitus was characterized, and the results were compared to that of a vehicle (DMSO) control. The drug withdrawn due to idiosyncratic liver toxicity (*Rezulin*), induces very different changes in the expression of stress-related genes than two safer drugs still on the market (*Avandia* and *Actos*).

Application: *ECM PCR ARRAYS for Cancer Biomarker Discovery*

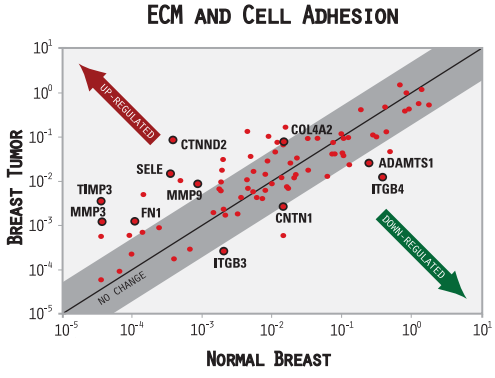


Figure 7: ECM and Cell Adhesion PCR Arrays Revealed Up- and Down-Regulated Genes in Breast Cancer. Total RNA from a normal human breast and a human breast tumor were characterized in technical triplicates, and the relative expression levels for each gene in the two samples are plotted against each other in the Scatter Plot. Genes encoding the matrix metallopeptidases (MMP3 and MMP9) and their inhibitors (TIMP3) are up-regulated, while genes encoding integrins (ITGB3 and ITGB4) are down-regulated, by at least three-fold (outside the silver field) in breast tumors relative to normal tissue.

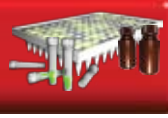
Popular Pathway-Focused PCR ARRAYS	
Angiogenesis	Inflammatory Cytokines & Receptors
Apoptosis	NFκB Signaling Pathway
Cancer PathwayFinder™	Oxidative Stress & Antioxidant Defense
Cell Cycle	Signal Transduction PathwayFinder™
Chemokines and Receptors	Stem Cell
Common Cytokines	Stress and Toxicity PathwayFinder™
DNA Damage Signaling Pathway	TGFβ / BMP Signaling Pathway
Endothelial Cell Biology	Th1-Th2-Th3
Epithelial to Mesenchymal Transition	Toll-Like Receptor Signaling Pathway
Extracellular Matrix and Adhesion	Wnt Signaling Pathway
Custom PCR Arrays *(Detailed Information on Page 8)*	Gene Expression Analysis Services *(Detailed Information on Page 17)*

Complete the RT² Profiler PCR ARRAY System	
Plate Format	Pack Size
96-well Plate	2 Arrays
96-well Plate	12 Arrays
96-well Plate	24 Arrays
384-well Plate	4 Arrays
Add up to 4 Genes to any PCR Array	

PCR ARRAY Accessories	Pack Size	Catalog #
RT² First Strand cDNA Synthesis Kit	12 Samples	C-03
RT² Nano PreAMP cDNA Synthesis Kit	12 Samples	C-06
RT² FFPE PreAMP cDNA Synthesis Kit	12 Samples	C-07
RT² Nano PreAMP cDNA Synthesis Primer Mixes	12 Samples	Various
SYBR Green w/ ROX Master Mix	2 Arrays	PA-012
SYBR Green w/ Fluorescein Master Mix	2 Arrays	PA-011
SYBR Green Only Master Mix	2 Arrays	PA-010
FREE PCR Array Data Analysis Software		

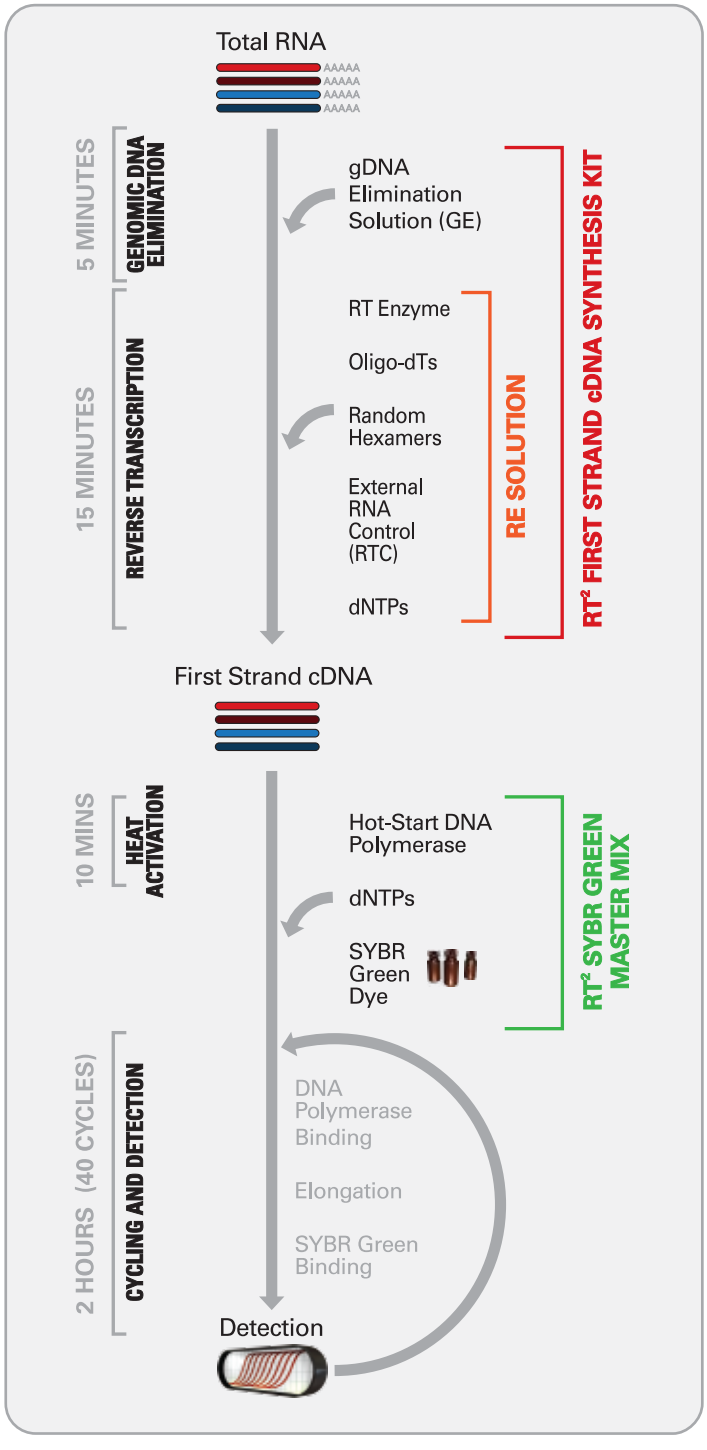
RT² PROFILER PCR ARRAY SYSTEM

A Complete & Reliable Solution for Gene Expression Analysis



How The PCR ARRAY System Works

SABiosciences RT² Profiler PCR Arrays are a complete system for Pathway-Focused Gene Expression Analysis. From Sample Preparation to Data Analysis, the PCR Array system includes four components that GUARANTEE high-quality, reproducible, and reliable gene expression data.



Integral to the performance of the PCR Array system is a proprietary set of control elements that enhance the reliability of your data and serve as a guarantee for performance over time. These elements allow researchers to quickly assess the quality of their data by determining if samples were contaminated with genomic DNA (gDNA), the quality of the reverse transcription reaction, and real-time PCR efficiency. Each component of the RT² Profiler system contributes to these quality control elements by incorporating an interlocked system for comprehensive monitoring of each step of the PCR Array process.

- ***RT² Profiler PCR ARRAYS***
  Each pathway-focused PCR Array includes 89-wet bench validated qPCR Primers Assays (including 5 housekeeping genes) and a proprietary control panel.
- ***RT² SYBR Green qPCR Master Mixes***
  A unique formulation of buffers (GE) that co-evolved with the primer design algorithm provides high amplification efficiencies. Available with reference dyes (ROX, Fluorescein or without).
- ***RT² First Strand cDNA Synthesis Kit***
  An External RNA Control detected by the PCR Array tests the quality of input RNA. It also features a proprietary genomic DNA elimination buffer essential for eliminating residual gDNA, ensuring specific detection of mRNA.

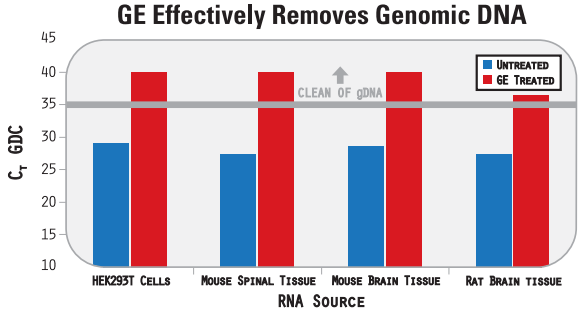


Figure 1: Elimination of Genomic DNA Contamination. RNA from HEK 293T cells, mouse spinal tissue, mouse brain tissue, or rat brain tissue was characterized on SYBR Green PCR Arrays before (blue bars) and after (red bars) treatment with gDNA Elimination Buffer from the RT² First Strand Kit.

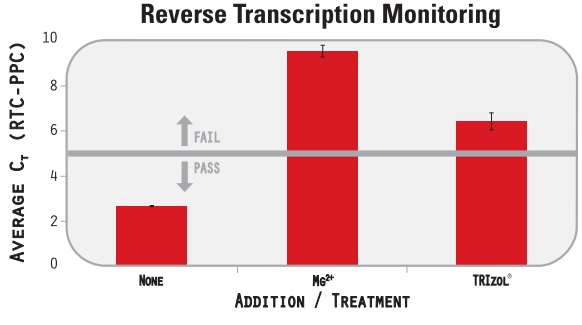


Figure 2: Monitoring Inhibition in Reverse Transcription. Human universal RNA was added with magnesium salt to simulate RNA degradation or added with TRIzol® reagent to simulate contamination that inhibits enzyme activity. RT² First Strand Kit was used for cDNA synthesis.

- ***FREE Data Analysis Software***
  The power of the PCR Array to assess the expression of a pathway-focused set of genes over a wide range of detection yields an abundance of data. With our FREE PCR Array Data Analysis tool, go from raw C_t values to fold change results displayed in a variety of formats (Scatter Plots, Volcano Plots, Clustergram) in a MATTER OF MINUTES.

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RT² Profiler PCR Array Performance

Reliable and Reproducible Pathway-focused Gene Expression Analysis

RT² Profiler PCR Arrays are used and trusted by thousands of research scientists for pathway-focused gene expression analysis. Several factors, including the RT² Primer Assay design algorithm, the proprietary control panel, and the strict manufacturing and quality control procedures, ensure the outstanding performance and reliability of our PCR Arrays. Each PCR Array and every qPCR Primer Assay is wet-bench validated to guarantee their performance, with results demonstrating several performance parameters demonstrated here.

Distinct Specificity

The complete PCR Array System , with high quality input RNA, is guaranteed to yield single bands without primer dimers or other secondary products. The proprietary primer design algorithm incorporates more than ten thermodynamic and sequence alignment criteria, and our wet-bench validation provides confidence that every real-time qPCR Assay accurately represents the expression of the queried gene. Over 20,000 gene-specific RT² PCR Primer Assays have been designed and shipped to satisfied customers.

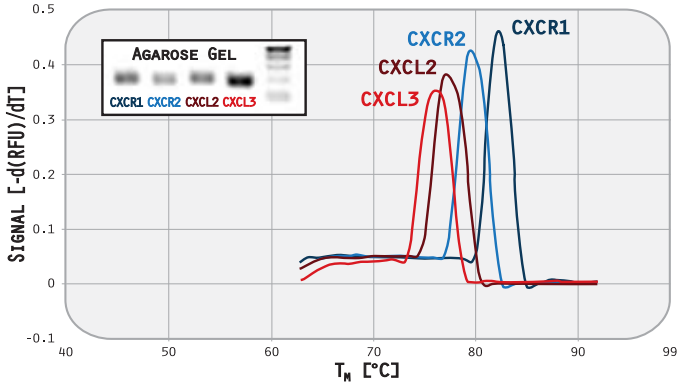

Figure 1: PCR Arrays Amplify A Single Gene-Specific Product in Every Reaction. Universal total RNA was characterized for four chemokine and chemokine receptors using RT² Primer Assays, followed by a dissociation (melt) curve analysis. PCR Arrays specifically detect individual genes despite the expression of related gene family members in the same RNA sample.

High Sensitivity and Wide Dynamic Range

A key benefit of using pathway-focused PCR Arrays for gene expression analysis is that genes that are over expressed can be measured as reliably as those that are under expressed. The complete PCR Array System yields > 85% positive call with 25 ng - 5 µg RNA or >90% with as a little as 1 ng PreAMP RNA. The 8-log wide dynamic range provided by real-time PCR is unparalleled when comparing a pathway-focused gene panel of varying expression levels across a variety of samples.

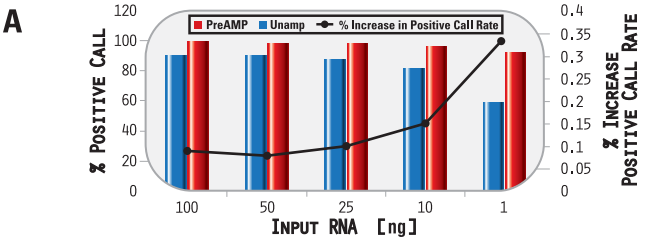

Figure 2: PCR Arrays Detect as Little as 1 ng RNA. Different amounts of universal total RNA were characterized using the Human Inflammatory Cytokines and Receptors PCR Array (PAHS-011) with or without PreAMP. The percentage of detectable genes was calculated for each RNA amount, with 1ng RNA analysis enabled with the new PreAMP technology.

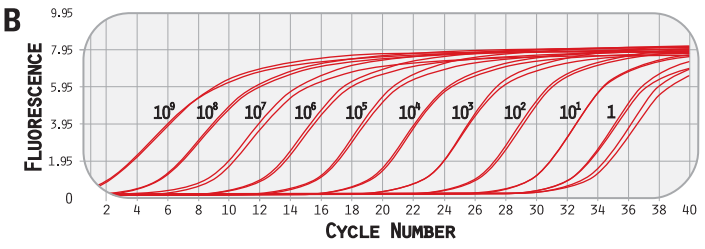

Figure 3: PCR Arrays Detect RNA Across a Wide Dynamic Range. Ten-fold serial dilutions of Human CHRNA5 were characterized with the respective RT² qPCR Primer Assay.

Uniform PCR Amplification Efficiency

One prerequisite for PCR Array technology is that the amount of template product doubles with every cycle. The more the assays deviate from this ideal, the error in the fold change calculation (ΔC_t) increases exponentially. Only with consistently high amplification efficiencies can PCR Arrays yield meaningful comparison of gene expression levels of all genes simultaneously. The unique combination of SABiosciences' proprietary primer design algorithm and rigorous testing of every primer assay by hand guarantees the high performance of every primer assay on the PCR Arrays.

Superb Reproducibility

Regardless of user or instrument used, the complete PCR Array System demonstrates strong correlations across technical replicates, lots, and instruments with average correlation coefficients > 0.99 insuring reliable detection of differences in expression between biological samples.

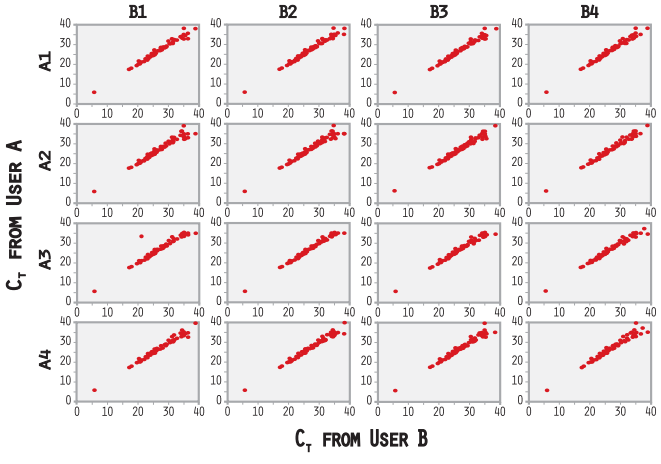

Figure 4: PCR Arrays Yield Highly Reproducible Results. Four replicate sets of raw threshold data (1-4) obtained by two different scientists (A & B) at two different times on Human Drug Metabolism RT² Profiler PCR Arrays are directly compared. The results demonstrate a high degree of correlation ($R^2 > 0.990$).

RT² Profiler PCR Arrays: A Trusted & Reliable System

PCR Arrays have been used by thousands of researchers who have successfully submitted and published their PCR Array results in very high impact journals, including Science, PNAS, Cancer Research, the Nature & Cell family of journals, and others (See Pages 18-23).

RT² Nano PreAMP™ cDNA Synthesis Kit

Enabling the Analysis of 1 Nanogram of RNA with RT² Profiler™ PCR ARRAYS

What Is the RT² Nano PreAMP™ cDNA Synthesis Kit?

RT² Nano PreAMP cDNA Synthesis Kit and Primer Mixes are a breakthrough technology enabling expression analysis starting from as little as 1 ng of total RNA. It employs a proprietary preamplification process to faithfully increase the amount of targeted cDNA for PCR Array analysis. This technology empowers RT² Profiler PCR Arrays to accurately analyze **nanogram** levels of total RNA.

Samples that can NOW be characterized with real-time PCR Arrays include:

- ***Laser Captured Microdissection Samples (LCM)***
- ***Fine Needle Aspiration Biopsies (FNAB)***
- ***Stem Cell Clusters or Embryoid Bodies***
- ***Flow Cytometry / Fluorescent-Activated Cell Sorting (FACS)***

Combined with PCR Arrays, the RT² Nano PreAMP cDNA Synthesis Kit and Primer Mixes extends the PCR Array System to accurately analyze a pathway-focused set of genes with as little as 1 ng of total RNA.

- ***RT² Nano PreAMP cDNA Synthesis Kit:*** Proprietary kits include optimized reagents for first strand cDNA synthesis and preamplification from only 1 ng of total RNA.
- ***RT² Nano PreAMP cDNA Synthesis Primer Mixes:*** Ready-to-use primer mixes for amplifying pathway-specific cDNA templates on corresponding RT² Profiler PCR Arrays.

Benefits of RT² Nano PreAMP cDNA Synthesis Technology

- ***Robust Performance on Small Samples:*** Analyze up to 4 different PCR Arrays starting with as little as 1 ng of Total RNA.
- ***Easy Workflow and Designed for Routine Use:*** Simple and quick procedures with minimal hands-on time to preamplify target templates in under 2 hrs.
- ***Superior Sensitivity:*** Maximally enhances the sensitivity of RT² Profiler PCR Arrays to analyze limited amounts of RNA.

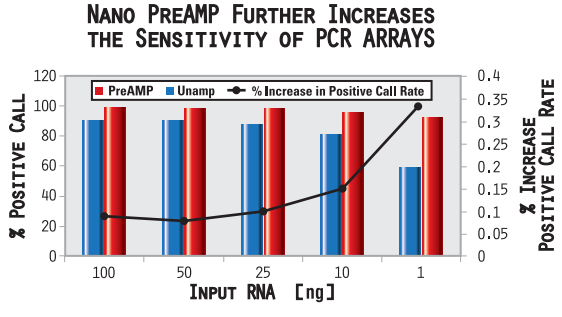

Figure 1. RT² Nano Preamplification Significantly Increases Sensitivity of Detection from 1 ng RNA Samples. Different amounts of human universal RNA were converted to cDNA with (red) or without (blue) RT² Nano preamplification. The unamplified and preamplified samples were then analyzed on the Human Inflammatory Cytokines and Receptors PCR Array (PAHS-011), which contains 84 pathway-specific assays, plus controls, including 5 assays for housekeeping genes. Threshold cycle values (C_t) were obtained and any genes with a $C_t < 35$ were considered to be present. Results indicate that with Nano preamplification, a 33.7% increase in positive call rate is observed in samples with as little as 1 ng RNA.

How RT² Nano PreAMP cDNA Synthesis Kits Work

Two Simple Steps:

1. cDNA First Strand Synthesis

   This kit provides enough reagents for synthesizing first strand cDNA from 12 different samples of as little as 1 ng total RNA.

2. Preamplification of cDNA for Pathway Specific Genes

   Each first strand cDNA synthesis reaction can be amplified by 4 different sets of PCR Array-specific Primer Mixes, allowing gene expression analysis for one sample on as many as 4 different PCR Arrays.

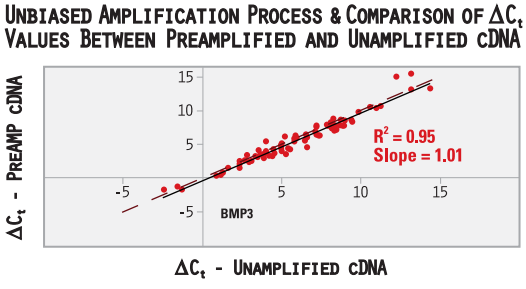

Figure 2. Unbiased Amplification Process - Highly Comparable ΔC_t Values Between Preamplified and Unamplified cDNA from Human Liver Tumor RNA. First strand cDNA was synthesized from 5 ng of human liver tumor RNA. One-quarter of each RT product was used for preamplification with the RT² Nano PreAMP cDNA Master Mix Kit plus the Human Cancer PathwayFinder™ Nano PreAMP Primer Mix. Unamplified cDNA synthesized from 500 ng of the same liver tumor RNA sample was used as the control. PreAMP amplified and unamplified cDNA samples were then analyzed on the Human Cancer PathwayFinder™ PCR Array, and the threshold cycle values (C_t) were obtained. The ΔC_t value for each gene was calculated by subtracting the average C_t value of the five reference genes (B2M, HPRT1, RPL13A, GAPDH, and ACTB) on the PCR Array from the C_t value of each gene of interest. The concordance of the ΔC_t values between preamplified and unamplified samples was evaluated by regression analysis. Data points with $C_t \geq 35$ were considered to be absent genes and were excluded from the analysis. The dashed line represents the ideal slope of 1.0. The solid line shows a linear regression fit with the R^2 and slope indicated. The high correlations between preamplified and unamplified cDNA were also obtained from universal RNA samples *(data not shown)*.

RT² Nano PreAMP cDNA Synthesis Products

Product	Catalog #
RT² Nano PreAMP cDNA Synthesis Kit	C-06
RT² Nano PreAMP cDNA Synthesis Primer Mixes*	
Human Cancer PathwayFinder™	PBH-2033
Human Apoptosis	PBH-7012
Human Angiogenesis	PBH-4024
Human Mesenchymal Stem Cell	PBH-4082
Human Embryonic Stem Cell	PBH-1081
Human Extracellular Matrix and Adhesion Molecules	PBH-0013
Human Inflammatory Cytokines and Receptors	PBH-4011
Mouse Inflammatory Cytokines and Receptors	PBM-9011
Human Toll-like Receptor Signaling Pathway	PBH-5018
Mouse Toll-like Receptor Signaling Pathway	PBM-0018
RT² Nano PreAMP Primer Mixes for All PCR Arrays	PBX-####

* PreAMP Primer Mixes for Custom PCR Arrays available

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RT² FFPE PreAMP™ PCR ARRAY System

Enabling the Analysis of FFPE Samples with PCR ARRAYS

Gene Expression Analysis from FFPE Samples

An innovative solution enabling the accurate qRT-PCR analysis of Formalin-fixed Paraffin-embedded (FFPE) samples. The RT² FFPE PreAMP technology utilizes multiplex tandem PCR to preamplify gene-specific cDNA with minimal bias. This kit is intended for preamplification of first-strand cDNA from fragmented total RNA from FFPE samples for gene expression analysis with RT² Profiler PCR Arrays.

The combination of a simplified **Xylene-Free** RNA extraction and a high-fidelity amplification process maximizes recovery of RNA and microRNA (miRNA). RT² Profiler PCR Arrays facilitate easy and reliable expression analysis of genes associated with a biological pathway or a diseased state from FFPE samples.

Benefits of RT² FFPE PreAMP PCR ARRAY System

- ***Quick and Efficient:*** High quality and high-yield total RNA and miRNA isolation from FFPE samples in 70 minutes
- ***Superior Sensitivity:*** PreAMP protocol significantly enhances qRT-PCR detection sensitivity for FFPE samples
- ***Easy Workflow:*** Simple **Xylene-Free** procedure and robust performance

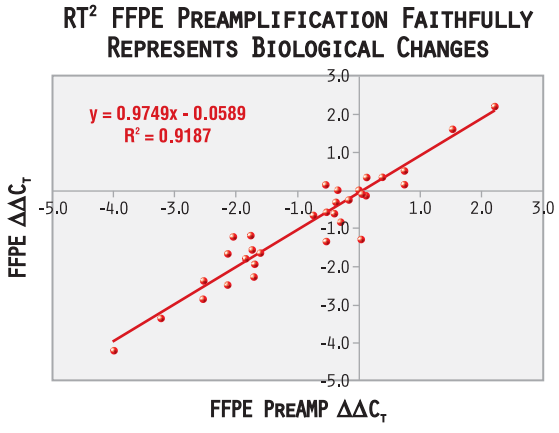
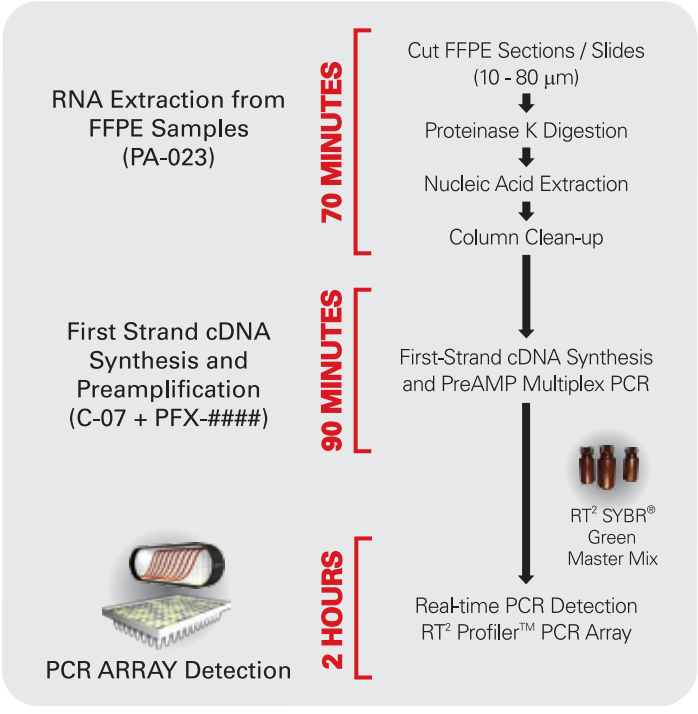


Figure 1. Highly Comparable Gene Expression Fold Change Results between FFPE Preamplified and Unamplified Samples. RNA extracted from FFPE spleen and intestine samples were extracted using the RT² FFPE RNA Extraction Kit and converted to cDNA with and without preamplification. All four cDNAs were analyzed on the Human Cancer PathwayFinder™ PCR Array. The $\Delta\Delta C_t$ comparison and genes with raw C_t values lower than 33 in both unpreamplified spleen and intestine samples are presented.

RT² FFPE PreAMP Performance

- *Increased positive call rate from FFPE samples*
- *Increased detection of genes previously classified as "Absent"*
- *Unbiased amplification of preamplified genes*
- *Faithful conservation of biological changes*

How the RT² FFPE PreAMP PCR System Works



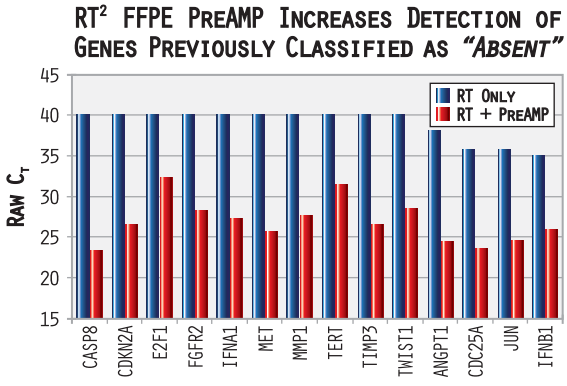


Figure 2. Genes extracted from FFPE samples previously classified as *"Absent"* are now detectable after RT² FFPE Preamplification. RNA was extracted from FFPE spleen sample (human) with the RT² FFPE RNA Extraction Kit and reverse transcribed to cDNA using RT² FFPE preamplification (red bars) and without PreAMP (blue bars). Results of the Human Cancer PathwayFinder PCR Array showed 55% of unpreamplified genes were virtually undetectable with no genes in the 10-20 C_t range. Preamplified genes with C_t values > 30, shift into the reliably quantitative range (C_t = 10-30).

RT² FFPE PreAMP & RNA Extraction Products

Product	Catalog #
RT² FFPE RNA Extraction Kit	PA-023
RT² FFPE PreAMP cDNA Synthesis Kit	C-07
RT² FFPE PreAMP Primer Mixes for All PCR ARRAYS	PFX-####
Custom RT² FFPE PreAMP Primer Mixes for PCR ARRAYS	Inquire
Pathway-Focused RT² Profiler PCR ARRAYS	Inquire
Instrument-Specific SYBR® Green qPCR Master Mixes	Inquire

Custom PCR ARRAYS & Assay Design

Focus on Your Genes with PCR Arrays & Assays Created from Your Gene List

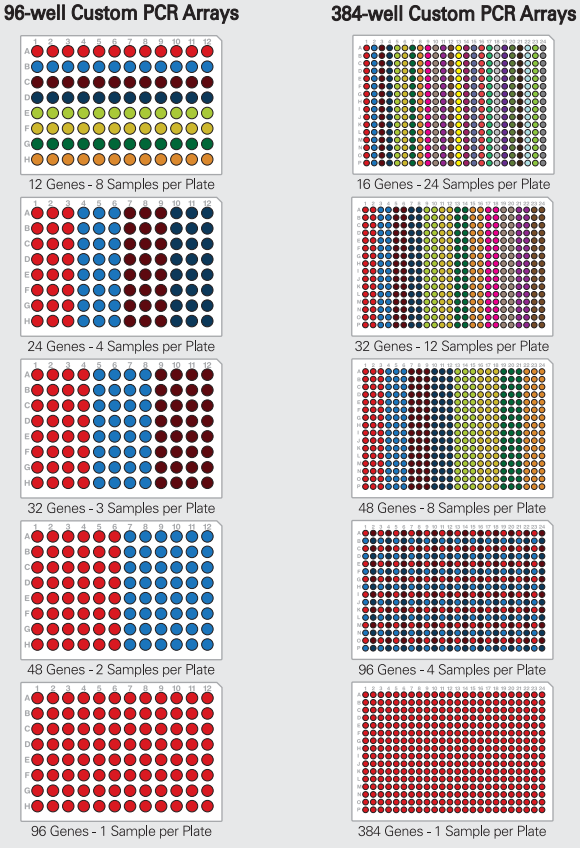
What Are Custom PCR ARRAYS?

Custom RT^2 Profiler™ PCR Arrays are a high-throughput approach for profiling the expression of your genes of interest. Choose from any gene in the human, mouse, rat, Rhesus Macaque or Drosophila genomes (up to 384 different genes). Whether your interests are in biomarker discovery, microarray followup, drug development, disease characterization, or signal transduction mechanisms, Custom RT^2 Profiler PCR Arrays enable focused expression analysis on your genes of interest.

Why Custom PCR ARRAYS from SABiosciences?

- ***Performance:*** Each assay within a Custom RT^2 Profiler PCR Array is designed and wet bench-validated using a set of rigorous parameters to insure the genes in your sample across a wide dynamic range are reproducibly recognized and quantified.
- ***Flexibility:*** Custom RT^2 Profiler PCR Arrays are available in a number of easy-to-use formats for quick sample loading and data analysis.
- ***Turnaround Time:*** Submit your 96- or 384-gene list and receive your Custom PCR Arrays in 2 weeks.

Gene Layouts



Customer Data: *Validate Microarray Expression Analyses*

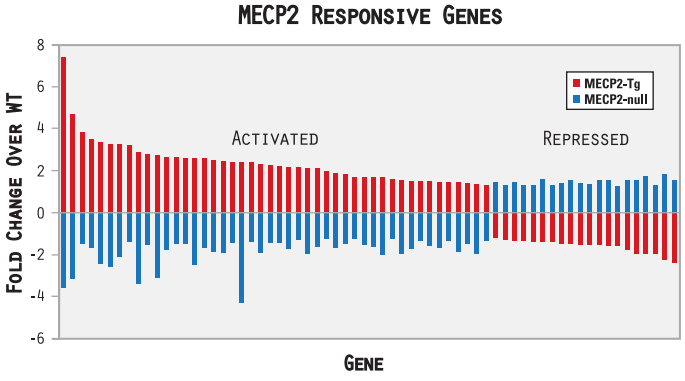


Figure 1: Gene Expression Changes in Hypothalamus of MECP2 Mouse Models. Validation of expression changes for 66 genes by qPCR analysis. Gene expression levels from microarray analyses were validated in four MECP2-Tg males and four Mecp2-null males. Data is plotted as relative up-regulation (red) or down-regulation (blue) over Wild-type ($P < 0.05$, *t* test). Each column represents a single gene, and represents data from four samples for each genotype.

Chahrour, M., et al. Science 2008; 320: 1224-1229.

96-well Custom PCR ARRAYS	
Format	**# of Plates** (minimum)
12 Genes, 8 Samples / Plate	12, 24
24 Genes, 4 Samples / Plate 32 Genes, 3 Samples / Plate 48 Genes, 2 Samples / Plate 96 Genes, 1 Samples / Plate	24
All Formats	>24

384-well Custom PCR ARRAYS	
Format	**# of Plates** (minimum)
16 Genes, 24 Samples / Plate	6, 12
32 Genes, 12 Samples / Plate 48 Genes, 8 Samples / Plate 96 Genes, 4 Samples / Plate	6, 12
Up to 384 Genes, 1 Samples / Plate	24
All Formats	>24

PCR ARRAY Accessories	Pack Size	Catalog #
RT^2 First Strand cDNA Synthesis Kit	12 Samples	CA-03
RT^2 qPCR-Grade RNA Isolation Kit	12 Samples	PA-001
RT^2 Nano PreAMP cDNA Synthesis Kit	12 Samples	C-06
RT^2 FFPE RNA Extraction Kit	12 Samples	PA-023
RT^2 FFPE PreAMP cDNA Synthesis Kit	12 Samples	C-07
Custom RT^2 Nano or FFPE PreAMP Primer Mixes		Inquire
SYBR® Green Master Mixes *(see page 16)*		
FREE PCR Array Data Analysis Software		

Data shown is used with permission of *Science* and respective authors.

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ChampionChIP™ qPCR System

Reliable Chromatin IP with Real-Time PCR Precision Achieved in Only **ONE DAY!**

The ChampionChIP™ System provides the first complete platform for the analysis of *in vivo* protein-DNA interactions using Chromatin Immunoprecipitation (ChIP) and real-time PCR (qPCR) detection. With validated high-quality ChIP-grade antibodies and PCR primers for any genes' promoter region, a simple and robust one-day preparation assay quickly delivers reliable and biologically relevant results. ChIP qPCR is a powerful and versatile method for the analysis of chromatin DNA bound by transcription factors, co-regulators, modified histones, chromatin remodeling proteins, or other nuclear factors from live cells. However, the tedious process and variable results have limited many researchers' ability to adopt this technique to study dynamic protein-DNA interactions in native chromatin environments. The ChampionChIP™ System, yields the most reliable ChIP assay results with qPCR precision in just a single day.

How the ChampionChIP™ System Works

The ChampionChIP One-Day Kit simplifies the usual two- to five-day ChIP protocol down to a manageable six to eight hours. Its crosslink reversal step is much faster and less tedious than conventional methods, and its DNA purification step yields a larger quantity and higher quality ChIP DNA than other one-day kits.

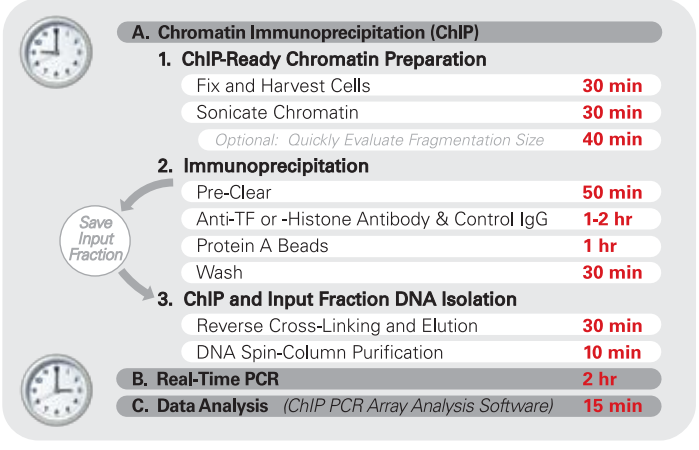


Figure 1: The Entire ChampionChIP System Protocol Can Be Completed in a Single Day. The ChampionChIP System includes a simplified high-performance One-Day ChIP Kit, ChIP-Grade Antibodies, real-time PCR primers, and a FREE ChIP PCR Array Data Analysis Suite.

High Specificity

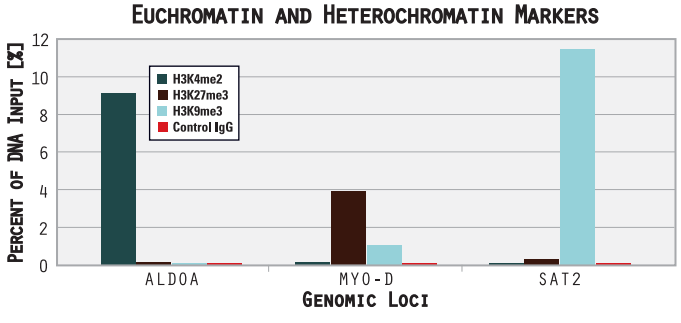


Figure 2. The ChampionChIP System Readily and Correctly Identifies Different Euchromatin and Heterochromatin Loci. ChampionChIP antibodies against modified histones (H3K4me2, H3K27me3, H3K9me3) or control IgG were used for precipitating chromatin from HeLa cells. Each ChIP DNA fraction was analyzed by real-time PCR using primers specific for the ALDOA, MYO-D, and SAT2 loci to calculate percentages of co-precipitating DNA relative to input.

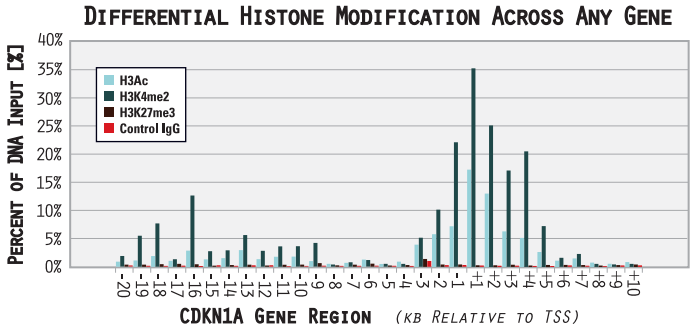


Figure 3: Differential Histone Modification Tiling Across the Sequence of Any Gene. ChampionChIP antibodies for modified histones (H3Ac, H3K4me2, H3K27me3) or control IgG were used for precipitating chromatin from one million HeLa cells. Each ChIP DNA fraction was analyzed with a ChampionChIP Tiling Array representing 30 one-kb tile intervals across the genomic sequence of the CDKN1A gene. The results obtained from three independent experiments are consistent with active transcription of the CDKN1A gene.

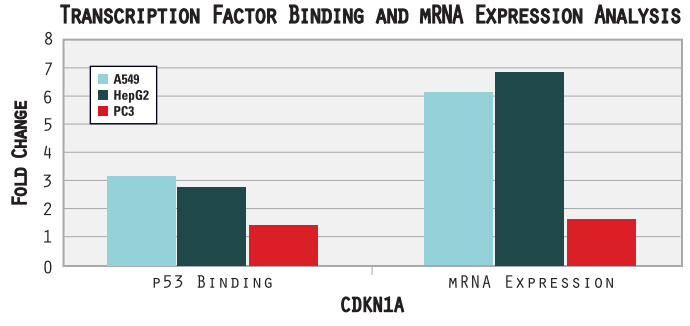


Figure 4: Treatment with 5-Fluorouracil Increases CDKN1A Gene Expression and p53 Binding in Cell Lines Expressing Wild-Type But Not Mutant p53. Triplicate samples from A549, HepG2, and PC3 cells were treated with 5-FU (300 µM, 6 h), and either subjected to ChIP with an anti-p53 antibody followed by qPCR analysis of the CDKN1A-2kb p53 binding site, or harvested for RNA to analyze CDKN1A expression by real-time RT-PCR. The results of both assays are expressed as the fold-increase upon 5-FU treatment.

ChampionChIP qPCR System

Product	Catalog #
ChampionChIP PCR Arrays	
Human Stem Cell Transcription Genes	GH-501
Human Oncogene & Tumor Suppressor Genes	GH-502
Human T Helper Cell Differentiation	GH-503
ChampionChIP One-Day Kit	GA-101
ChampionChIP Antibody Kits *(Antibody + qPCR Controls)* Human RNA Polymerase II, p53 and Histones (H3Ac, H4Ac, H3Kme2, H3K9me3, H3K27me3)	See Website
ChampionChIP qPCR Primers *Any Promoter Region in the Human, Mouse or Rat Genome*	Inquire
Custom ChampionChIP qPCR Array *Transcription Factor Binding Sites or Promoter Tiling*	Inquire
SYBR Green w/ ROX Master Mix	PA-012
SYBR Green w/ Fluorescein Master Mix	PA-011
SYBR Green Only Master Mix	PA-010
FREE ChIP PCR Array Data Analysis Software	

RT² MicroRNA PCR ARRAYS

Simultaneous Detection of Genome-Wide or Pathway-Focused miRNA

What are miRNAs?

MicroRNAs are endogenous single-stranded RNA molecules 19-25 nucleotides in length, synthesized in a regulated manner from larger RNA molecules. Many miRNA sequences have been found in a variety of species [for example, ~700 miRNAs in humans, and ~500 in mice].

Why Use SABiosciences miRNA PCR ARRAYS?

Detecting every miRNA across the entire genome in a specific and sensitive way is a very technologically challenging task. Many miRNA family members and otherwise distinct miRNA species have very similar sequences. Moreover, other RNA species such as snRNA, tRNA, mRNA, and rRNA can cause non-specific amplification, making the specific analysis of mature miRNA even more problematic. SABiosciences' proprietary miRNA detection technologies enable uniformly high PCR amplification efficiencies, allowing simultaneous detection of miRNA under uniform cycling conditions.

The RT² miRNA PCR Array accurately analyzes the expression of up to 96 or 384 microRNA sequences simultaneously on ANY real-time PCR instrument. SABiosciences' patent-pending miRNA technology integrates a universal-tailing and reverse transcription reaction specific for miRNA with accurate expression level measurement of distinct miRNA sequences that may differ by a single nucleotide base. RT² miRNA PCR Arrays are the most specific and sensitive technology for analyzing genome-wide miRNA expression.

- ***Sensitivity:*** As little as 0.5 µg total RNA needed
- ***Multi-Sequence Flexibility:*** Analyze up to 384 sequences simultaneously
- ***Simplicity:*** As easy as a real-time PCR Array experiment

Why Study miRNA?

MicroRNA represents a new layer of regulation in endogenous gene transcription and translation. Since there are ~700 miRNAs in humans, with each miRNA potentially having hundreds of targets, the majority of genes may be subject to regulation by one or more miRNAs. miRNAs are already being considered as cancer biomarkers, and their importance is being realized in a variety of other research areas, such as differentiation, neurobiology and immunology. There are three major ways to start studying miRNA:

1. ***Expression Analysis:***

   The best technology for determining the expression of miRNA is the SABiosciences miRNA PCR Array System.

2. ***Bioinformatic Prediction:***

   Identification of miRNAs that potentially regulate your genes of interest is possible with our powerful yet simple bioinformatic algorithm at:

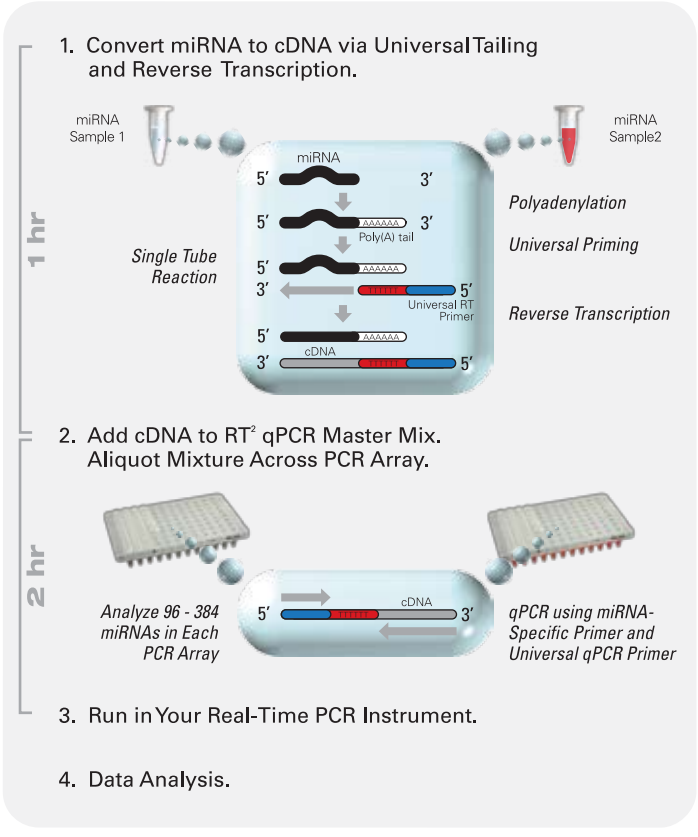
   http://www.SABiosciences.com/miRNAsearch.php

3. ***Functional Studies:***

   The function of individual miRNAs can be identified via miRNA over expression or suppression of miRNA function. [Over 500 miRNAs in their endogenous genomic context are available as expression constructs].

How miRNA PCR ARRAYS Work

As Easy as a Real-time PCR Experiment



Specificity

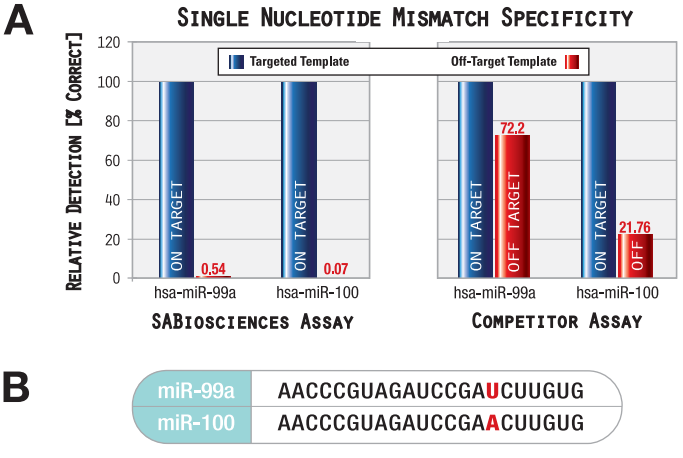


Figure 1: miRNA qPCR Assays Distinguish Single Nucleotide Mismatches. RT² miRNA PCR Assays and a competitor's assays for miR-99a and miR-100 were used to detect both corresponding synthetic templates, whose sequences differ by only one nucleotide (B). Relative detection of the off-target template is calculated as a percentage of the correct template detection (A). RT² miRNA PCR Assays' proprietary primer design specifically discriminates closely related sequences better than competing assays.

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Sensitivity and Dynamic Range

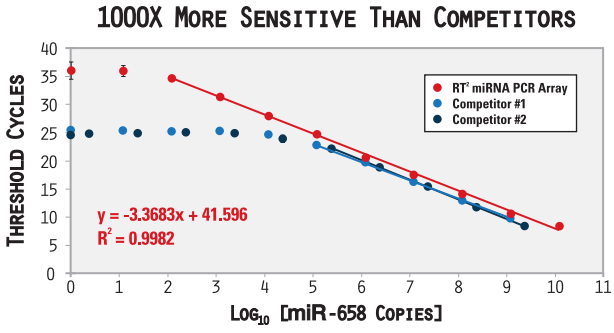

Figure 2: 1000-Fold Higher Sensitivity Than Our Competitors. Samples containing serially diluted synthetic miR-658 template spiked into a constant amount of small RNA that lacks miR-658, were analyzed with miR-658-specific RT² miRNA qPCR Assays and other commercial assays. The resulting threshold cycle values are plotted versus the amount of synthetic template used. RT² miRNA PCR Assays' proprietary reaction formulation detects 1000-fold lower concentrations of miR-658 with a wider linear dynamic range than competing assays.

Accuracy

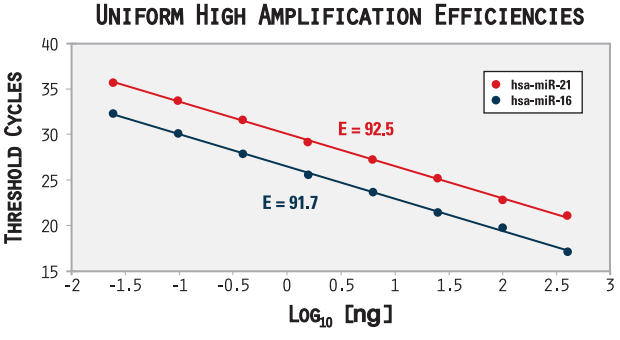

Figure 3: miRNA PCR Assays Yield the Most Accurate Results. Threshold cycle values from miR-16 and miR-21 specific RT² miRNA qPCR Assays are plotted versus the amount of HEK293 small RNA in a serial dilution series. Serial dilutions of pooled synthetic cDNA templates were similarly used to calculate the amplification efficiencies of 468 assays (average efficiency of 95.37% ± 6.19%). Consistently high amplification efficiencies and sensitivity enable miRNA PCR Arrays to accurately analyze multiple sequences simultaneously using the $\Delta\Delta C_t$ method.

Reproducibility

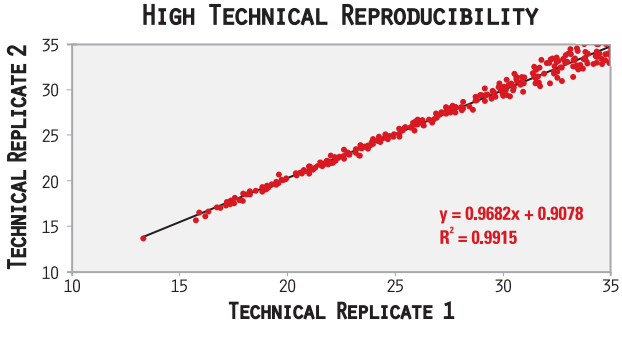

Figure 4: miRNA PCR Arrays Yield Highly Reproducible Results. Duplicate samples of human brain small RNA were characterized with the Human Genome RT² miRNA PCR Array, and the raw threshold cycle values from each array were plotted against each other. The linear fit of the data with a strong correlation factor ($RT^2 > 0.99$) indicates that miRNA PCR Array results can be reliably compared between plates, runs, biological replicates, and samples.

Application: *Cancer Research - Colon Cancer Biomarkers*

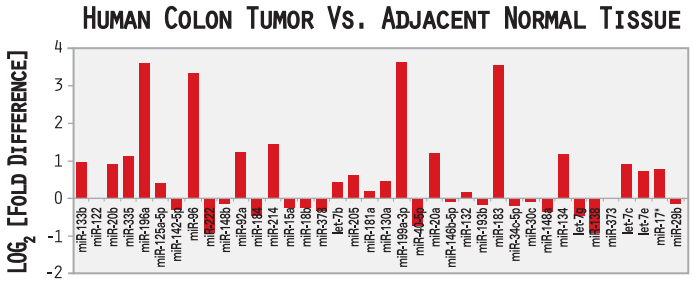

Figure 5: RT² Human Cancer miRNA PCR Array Identifies Potential Colon Cancer Biomarkers. Small RNA isolated from human color tumor and matched adjacent normal tissue (Biochain) were characterized with PCR Arrays containing assays specific for 88 cancer-related human miRNA sequences. Fold-differences are calculated from raw C_t values normalized to a panel of housekeeping small nuclear RNA. Several miRNA biomarkers are up-regulated in colon cancer.

Application: *Stem Cell Research - Osteogenic miRNA Markers*

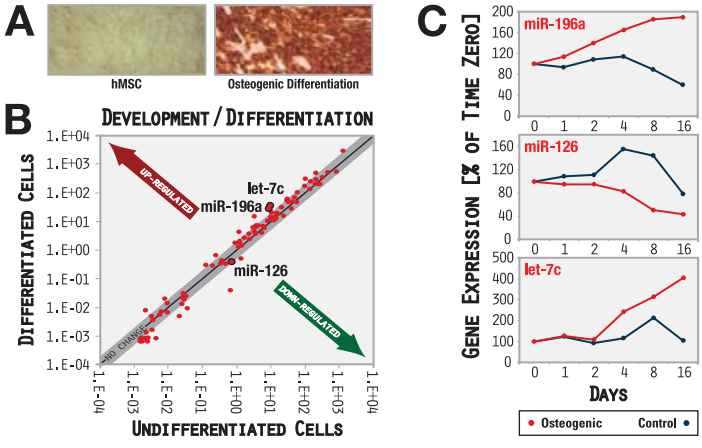

Figure 6: Cell Differentiation and Development miRNA PCR Arrays Identify Sequences Potentially Regulating Osteogenesis. Human adipose tissue-derived mesenchymal stem cells (hMSC) grown in normal or osteogenic differentiation medium for 16 days were stained with Alizarin Red (A) and isolated for relative miRNA expression profiling. The results are shown in the scatter plot (B). Many miRNA sequences exhibit unique time-dependent changes in expression compared to undifferentiated controls (C).

RT² miRNA PCR ARRAYS		
Product	Human	Mouse
Genome, 384-well	MAH-3100	MAM-3100
Cancer	MAH-102	MAM-102
Cell Differentiation / Development	MAH-103	MAM-103
miFinder™	MAH-001	MAM-001
Custom RT² miRNA PCR Array	Inquire	Inquire

miRNA PCR ARRAY Accessories	Pack Size	Catalog #
RT² qPCR-Grade miRNA Isolation Kit	12 Samples	MA-01
RT² miRNA First Strand Kit	12 Samples	MA-03
SYBR® Green w/ ROX® Master Mix	2 Arrays	PA-012
SYBR® Green w/ Fluorescein Master Mix	2 Arrays	PA-011
SYBR® Green Only Master Mix	2 Arrays	PA-010
FREE miRNA PCR Array Data Analysis Software		

SABiosciences™
PATHWAY-POWERED

RT² PROFILER™ PCR ARRAYS

- Technology Overview *(page 2)*
- Over 100 Pathways Available *(page 24)*
- Start With as Little as 1 ng of RNA *(page 6)*
- Analyze FFPE Samples with PCR Arrays *(page 7)*
- Over 600 Peer-reviewed Publications
- Custom PCR Arrays Available for Human, Mouse, Rat, Rhesus Macaque and Drosophila
- To Learn More, Please Visit the PCR Product Web Page:

www.SABiosciences.com/RTPCR.php

APOPTOSIS	BIOMARKERS	CANCER	CELL CYCLE
Angiogenesis	Breast Cancer and Estrogen Receptor Signaling	Angiogenesis	Angiogenesis
Apoptosis	Cell Surface Markers	Angiogenic Growth Factors & Angiogenesis Inhibitors	Apoptosis
Autophagy	Dendritic and Antigen Presenting Cell	Apoptosis	Autophagy
Cancer PathwayFinder™	Epigenetic Chromatin Modification Enzymes*	Autophagy	Cancer PathwayFinder
Cell Cycle	Epigenetic Chromatin Remodeling Factors*	Breast Cancer and Estrogen Receptor Signaling	Cell Cycle
DNA Damage Signaling Pathway	Epithelial to Mesenchymal Transition *(EMT)**	Cancer Drug Resistance and Metabolism	DNA Damage Signaling Pathway
Drug Metabolism: Phase II Enzymes	Extracellular Matrix and Adhesion Molecules	Cancer PathwayFinder	Epithelial to Mesenchymal Transition *(EMT)**
Endothelial Cell Biology	Hematopoietic Stem Cells and Hematopoiesis	Cell Cycle	MAP Kinase Signaling Pathway
Heat Shock Proteins	Homeobox *(HOX)* Genes	Chemokines & Receptors	Neurogenesis and Neural Stem Cell
MAP Kinase Signaling Pathway	Mesenchymal Stem Cell	DNA Damage Signaling Pathway	NFκB Signaling Pathway
NFκB Signaling Pathway	Stem Cell	Epithelial to Mesenchymal Transition *(EMT)**	p53 Signaling Pathway
Oxidative Stress and Antioxidant Defense	T-cell and B-cell Activation	EGF / PDGF Signaling Pathway	PI3K-AKT Signaling Pathway
p53 Signaling Pathway	Th_1-Th_2-Th_3	MAP Kinase Signaling Pathway	Signal Transduction PathwayFinder
PI3K-AKT Signaling Pathway		Oxidative Stress and Antioxidant Defense	Transcription Factors
Signal Transduction PathwayFinder		p53 Signaling Pathway	
Stress and Toxicity PathwayFinder		Protein Phosphatases*	
TNF Ligand and Receptor		PI3K-AKT Signaling Pathway	
Unfolded Protein Response*		TGFβ BMP Signaling Pathway	
		Tumor Metastasis	
		Wnt Signaling Pathway	

RT² MicroRNA PCR ARRAYS

- Regulation of Gene Transcription and Translation *(page 10)*

Cancer	Cancer	Cancer	Cancer
Cell Differentiation and Development	Cell Differentiation and Development	miFinder™	Cell Differentiation and Development
miFinder™	miFinder™	Whole Genome	miFinder™
Whole Genome	Whole Genome		Whole Genome

Methyl-Profiler™ PCR ARRAYS

- Accurate Detection of DNA Methylation at CpG Islands Without Bisulfite *(page 12)*

Breast Cancer	Breast Cancer	Breast Cancer	Breast Cancer
Gastric Cancer	Gastric Cancer	Gastric Cancer	Gastric Cancer
Liver Cancer	Liver Cancer	Liver Cancer	Liver Cancer
Lung Cancer	Lung Cancer	Lung Cancer	Lung Cancer
Prostate Cancer	Prostate Cancer	Prostate Cancer	Prostate Cancer

* **NEW** PCR Array

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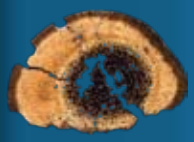
CYTOKINES / INFLAMMATION

- Chemokines & Receptors
- Common Cytokine
- Inflammatory Cytokines and Receptors
- Inflammatory Response and Autoimmunity
- Interferon and Receptor
- Interferon α, β Response
- JAK / STAT Signaling Pathway
- NFκB Signaling Pathway
- T Cell Anergy & Immune Tolerance
- T-cell and B-cell Activation
- TGFβ BMP Signaling Pathway
- Th_{17} for Autoimmunity and Inflammation
- Th_1-Th_2-Th_3
- Toll-Like Receptor Signaling Pathway
- TNF Ligand and Receptor
- Unfolded Protein Response*

- miFinder™
- Whole Genome

- Inflammatory Response
- T Cell Activation
- Cytokine Production

ECM / ADHESION



- Angiogenesis
- Angiogenic Growth Factors & Angiogenesis Inhibitors
- Atherosclerosis
- Chemokines and Receptors
- Common Cytokine
- Embryonic Stem Cells
- Endothelial Cell Biology
- Extracellular Matrix and Adhesion Molecules
- Growth Factors
- Inflammatory Cytokines and Receptors
- MAP Kinase Signaling Pathway
- Mesenchymal Stem Cell
- NFκB Signaling Pathway
- Osteogenesis
- TGFβ BMP Signaling Pathway
- Tumor Metastasis
- TNF Ligand and Receptor

- Cancer
- miFinder™
- Whole Genome

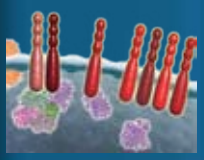
- Breast Cancer
- Gastric Cancer
- Liver Cancer
- Lung Cancer
- Prostate Cancer

NEUROSCIENCE

- Alzheimer's Disease
- Apoptosis
- cAMP / Ca^{2+} Signaling PathwayFinder
- Drug Transporters
- Embryonic Stem Cells
- GPCR Signaling PathwayFinder
- Heat Shock Proteins
- Hedgehog Signaling Pathway
- Hypoxia Signaling Pathway
- Mesenchymal Stem Cell
- Neurogenesis and Neural Stem Cell
- Neuroscience Ion Channels and Transporters
- Neurotransmitter Receptors and Regulators
- Neurotrophin and Receptors
- Nitric Oxide Signaling Pathway
- Notch Signaling Pathway
- Oxidative Stress and Antioxidant Defense
- Stem Cell

- miFinder™
- Whole Genome

SIGNAL TRANSDUCTION

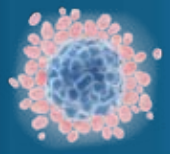


- cAMP / Ca^{2+} Signaling PathwayFinder™
- EGF / PDGF Signaling Pathway
- GPCR Signaling PathwayFinder™
- Hedgehog Signaling Pathway
- Insulin Signaling Pathway
- JAK / STAT Signaling Pathway
- Lipoprotein Signaling and Cholesterol Metabolism
- MAP Kinase Signaling Pathway
- NFκB Signaling Pathway
- Notch Signaling Pathway
- Nuclear Receptors and Coregulators
- PI3K-AKT Signaling Pathway
- Signal Transduction PathwayFinder
- TGFβ BMP Signaling Pathway
- Toll-Like Receptor Signaling Pathway
- Transcription Factors
- Ubiquitination Pathway
- Wnt Signaling Pathway

- Cancer
- Cell Differentiation and Development
- miFinder™
- Whole Genome

- Breast Cancer
- Gastric Cancer
- Liver Cancer
- Lung Cancer
- Prostate Cancer

STEM CELL / DEVELOPMENT



- Cell Cycle
- Dendritic and Antigen Presenting Cell
- Embryonic Stem Cells
- Extracellular Matrix and Adhesion Molecules
- GPCR Signaling PathwayFinder
- Hedgehog Signaling Pathway
- Hematopoietic Stem Cells and Hematopoiesis
- Homeobox *(HOX)* Genes
- Lipoprotein Signaling and Cholesterol Metabolism
- Mesenchymal Stem Cell
- Neurogenesis and Neural Stem Cell
- Neurotrophin & Receptors
- Notch Signaling Pathway
- Osteogenesis
- Stem Cell
- T-cell and B-cell Activation
- TGFβ BMP Signaling Pathway
- Toll-Like Receptor Signaling Pathway
- Transcription Factors
- Wnt Signaling Pathway

- Cancer
- Cell Differentiation and Development
- miFinder™
- Whole Genome

- Stem Cell Transcription Factors

TOXICOLOGY / DRUG ADME

- Apoptosis
- Autophagy
- Cancer Drug Resistance and Metabolism
- Cancer PathwayFinder™
- Cell Cycle
- DNA Damage Signaling Pathway
- Drug Metabolism
- Drug Metabolism: Phase I Enzymes
- Drug Metabolism: Phase II Enzymes
- Drug Transporters
- GPCR Signaling PathwayFinder
- Lipoprotein Signaling & Cholesterol Metabolism
- Mitochondria
- Oxidative Stress and Antioxidant Defense
- p53 Signaling Pathway
- PI3K-AKT Signaling Pathway
- Stress and Toxicity PathwayFinder

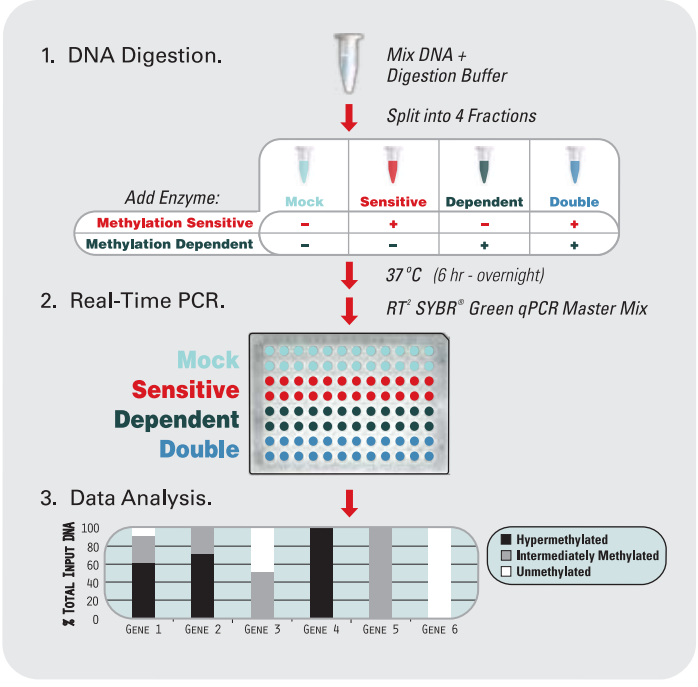
- miFinder™
- Whole Genome

METHYL-PROFILER™ PCR ARRAY SYSTEM

Simple, Fast and Reliable DNA Methylation Analysis **WITHOUT BISULFITE!**

The Methyl-Profiler™ DNA Methylation PCR Array System is an innovative technology enabling fast and accurate detection of DNA methylation status at CpG islands. This technology replaces the tedious and inefficient bisulfite-based methods with simple and simultaneous selective restriction digests of either methylated or unmethylated DNA, and takes advantage of the quantitative power of real-time PCR. The PCR Array format reveals the DNA methylation status of gene panels related to diseases or pathways. The individual primer pairs allow analysis of the DNA methylation status of any human or mouse gene. The reliability and simplicity of the procedure makes this technology ideal for profiling DNA methylation and biomarkers of stem cell growth and differentiation, cancer, and other human diseases.

How DNA Methylation PCR ARRAYS Work



The human genome contains many long hypermethylated stretches of CpG dinucleotide-rich sequences. In this sea of CpG methylation, unmethylated CpG-rich sequences, known as "CpG islands", are found in the promoters of most transcriptionally active genes. These normal patterns of DNA methylation are perturbed in cancer cells, where specific tumor suppressor genes (TSG) become hypermethylated, causing their expression to be silenced. Since every tumor type has a unique "methylation profile", or panel of hypermethylated genes, the analysis of TSG hypermethylation has become very important for basic cancer research, clinical diagnostics, and therapeutic applications.

The Methyl-Profiler PCR Array System fulfills the need to rapidly and simultaneously determine the methylation status of more genes in more samples in a higher-throughput fashion. The current time- and labor-intensive methodologies require bisulfite conversion of unmethylated cytosines to uracil followed by either sequence analysis or PCR using primers sensitive to the resulting base conversion. Bisulfite conversion is not only tedious but is also inefficient and damages DNA. The resulting low yields of DNA make bisulfite-based methods unsuitable for the analysis of small samples.

Why Use the Methyl-Profiler™ PCR ARRAY System?

- ***Simple, Fast and Reliable:***
  No bisulfite conversion and ready-to-use.
- ***Disease- or Pathway-Focused Gene Sets:***
  Simultaneously detect DNA methylation of 24 or 96 genes.
- ***Genome-wide Coverage:***
  Primers to detect methylation of your favorite genes.

The Methyl-Profiler PCR Array System relies on the differential cleavage of target sequences by two different restriction endonucleases whose activities require either the presence or absence of methylated cytosines in their respective recognition sequences. As real-time PCR quantifies the relative amount of intact DNA remaining after each enzyme digestion, the methylation status of individual genes and the methylation profile across a gene panel are reliably and easily calculated. The high yield of DNA from the restriction digests and PCR amplification allow the analysis of smaller, more heterogeneous samples.

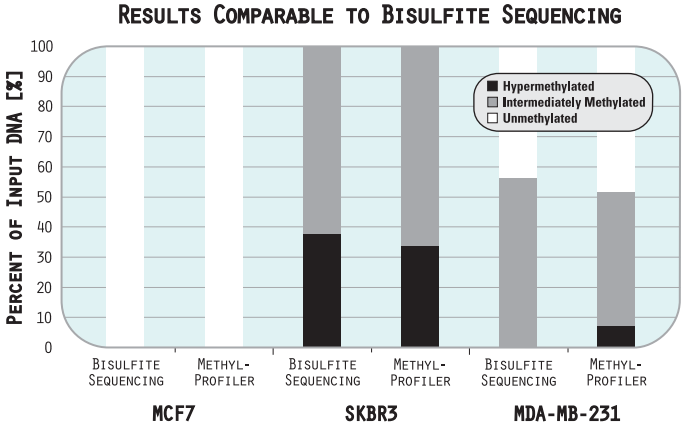


Figure 1: Methyl-Profiler PCR Assays Yield Results Consistent with Bisulfite Sequencing. The methylation status of the cadherin 1 gene (CDH1) was determined using bisulfite sequencing and Methyl-Profiler PCR Assays in three breast cancer cell lines known to have very different CDH1 methylation patterns.

To validate the accuracy of the Methyl-Profiler PCR Array System, its results were compared with those generated by bisulfite sequencing, the gold standard for DNA methylation analysis. The methylation status for both the CDH1 (Figure 1) and CDH13 *(data not shown)* genes observed in three different breast cancer cell lines by the two methods match very closely. Real-time PCR characterization of methylation-dependent and methylation-sensitive restriction enzyme digestions directly quantifies unmethylated and hypermethylated genomic DNA, respectively. The results indicate that the sensitivity and specificity of the Methyl-Profiler PCR Array System rivals bisulfite sequencing, suggesting that it can readily replace more tedious bisulfite PCR validation methods.

Make your DNA Methylation analysis as quick and painless as possible with the Methyl-Profiler DNA Methylation PCR System and EXCEL-based data analysis.

Download our **FREE** *EXCEL* Data Analysis Software:

http://www.SABiosciences.com/dna_methylation.php

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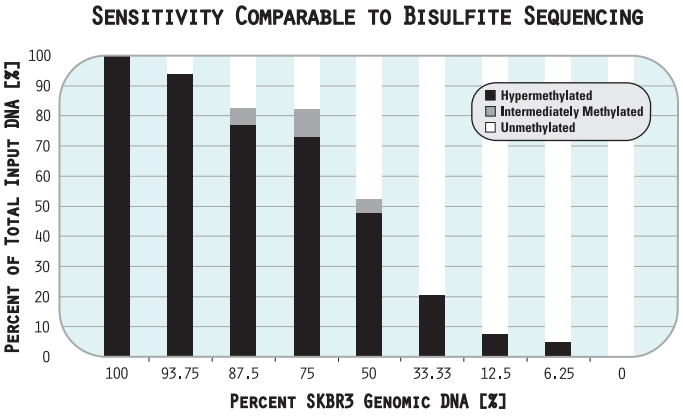


Figure 2: Methyl-Profiler PCR Assays Detect Hypermethylation in Heterogeneous Samples Containing As Little As Five Percent Tumor DNA. SKBR3 breast cancer cell line and normal blood genomic DNA (encoding hypermethylated and unmethylated HIC1, respectively) were mixed in different ratios. Using Human HIC1 Methyl-Profiler qPCR Primers, the percentage of hypermethylated HIC1 relative to total promoter DNA in each mixture was detectable down to five percent.

Primary tumors are typically very heterogeneous, containing a mixture of both cancerous and noncancerous cells. Therefore, reliable tumor characterization requires detecting smaller amounts of hypermethylated DNA diluted in an unmethylated background. Methyl-Profiler PCR Assays have the sensitivity required to detect hypermethylated DNA from breast cancer cells even when they represent only five percent of the total cell population (Figure 2).

Applications

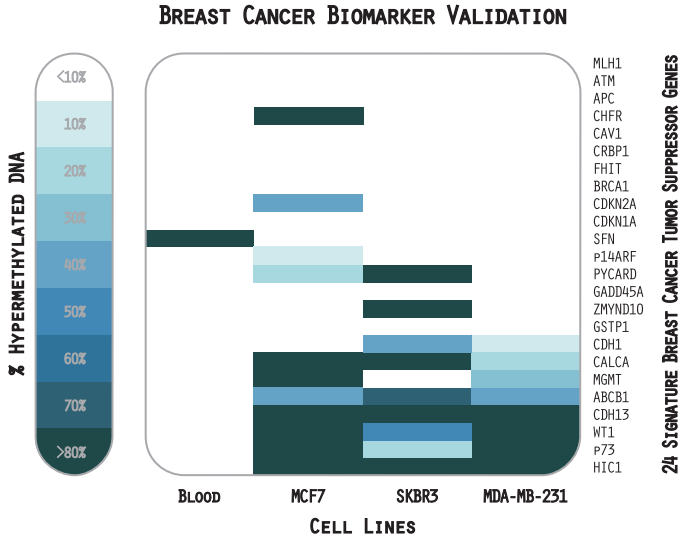


Figure 3: Methyl-Profiler PCR Arrays Validate Breast Cancer Gene Methylation Status in Breast Cancer Cell Lines. Heat map comparison of the hypermethylation status of 24 genes in the genomic DNA of three breast cancer cell lines and blood genomic DNA as determined by Human Breast Cancer Signature Panel DNA Methylation PCR Arrays.

To demonstrate that Methyl-Profiler PCR Arrays can validate methylation biomarkers, we first scanned published results to design a cataloged PCR Array representing a signature panel of the 24 most frequently methylated genes in human breast tumors. We then analyzed the methylation profile of this gene panel in three different breast cancer cell lines (Figure 3). The results further strengthen the correlation of these biomarkers with breast cancer.

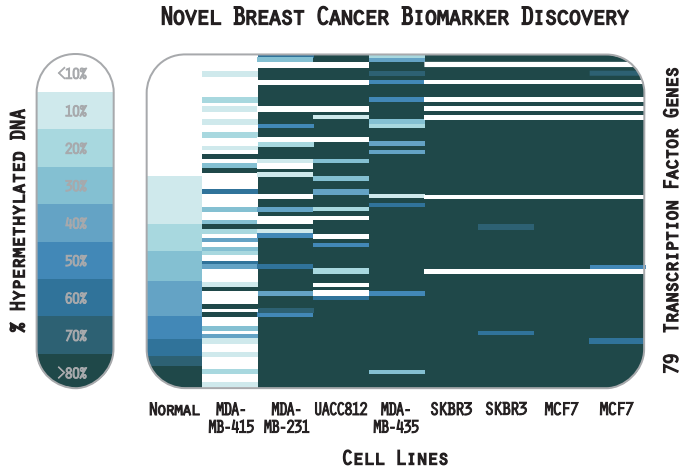


Figure 4: Methyl-Profiler PCR Arrays Discover New Candidate Breast Cancer DNA Methylation Biomarkers. Heat map comparison of the hypermethylation status of a panel of 79 transcription factor genes in six breast cancer cell lines and a normal epithelial cell line as determined with Custom DNA Methylation PCR Arrays.

To demonstrate that Methyl-Profiler PCR Arrays can also discover new biomarkers, we arranged a custom array containing a panel of candidate transcription factor genes, whose methylation status had not been previously associated with breast cancer (Figure 4). We found that breast cancer cell lines also hypermethylate this gene panel, potentially providing a new discovery source for cancer biomarkers.

The Methyl-Profiler DNA Methylation PCR Array System is ideally suited to genomic DNA hypermethylation analysis for both basic research applications and clinical biomarker development. The simple two-step procedure is considerably faster and easier than current bisulfite sequencing and bisulfite PCR methods, and yields closely matching results with equivalent sensitivity.

Methyl-Profiler™ DNA Methylation PCR ARRAYS	
Product*	**Catalog #**
Human Breast Cancer - *Signature Panel*	MeAH-011
Human Gastric Cancer - *Signature Panel*	MeAH-021
Human Liver Cancer - *Signature Panel*	MeAH-031
Human Lung Cancer - *Signature Panel*	MeAH-041
Human Prostate Cancer - *Signature Panel*	MeAH-051
Human Colon Cancer - *Signature Panel*	MeAH-061
Human Stem Cell Transcription Factors - *Signature*	MeAH-511
Human Inflammatory Response - *Signature Panel*	MeAH-521
Human T Cell Activation - *Signature Panel*	MeAH-531
Human Cytokine Production - *Signature Panel*	MeAH-541
Custom Methyl-Profiler PCR Arrays	Inquire

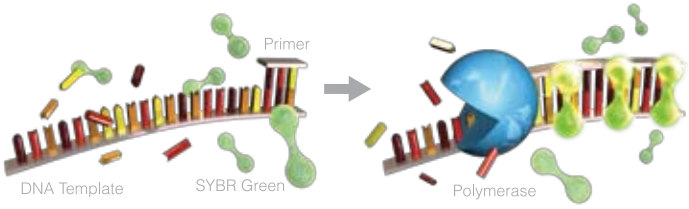
* Methyl-Profiler PCR Arrays are available in Signature Panels (24 genes) & Comprehensive Panels (96 genes).

PCR ARRAY Accessories	Pack Size	Catalog #
Methyl-Profiler qPCR Assays	200 Reactions	Inquire
Methyl-Profiler Enzyme Kit	12 Samples	MeA-03
SYBR Green w/ ROX Master Mix	2 Arrays	PA-012
SYBR Green w/ Fluorescein Master Mix	2 Arrays	PA-011
SYBR Green Only Master Mix	2 Arrays	PA-010
FREE Methyl-Profiler PCR Array Data Analysis Software		

RT² SYBR® Green qPCR Master Mixes

From the Experts in High-Performance SYBR® Green Quantitative PCR

SYBR Green Detection is a popular approach used in quantifying gene expression analysis with RT-PCR. It relies on the preferential binding of the SYBR green dye to double-stranded DNA, resulting in strong fluorescence emission signals, with the signal intensity proportional to the amount of double-stranded DNA present.



High quality PCR reaction components are essential for achieving superior amplification specificity and efficiency. SABiosciences offers a complete solution for using SYBR Green PCR Arrays with the RT² SYBR Green qPCR Master Mixes. Each mix includes a Hot Start Taq DNA polymerase, which provides tighter control over activity, and other proprietary chemical components that significantly minimize primer dimer formation, thereby enhancing amplification efficiencies for even the most difficult-to-amplify genes. The higher SYBR Green signal from our formulations provides greater sensitivity and ensures clean results without sacrificing specificity or amplification efficiency.

Brighter SYBR Green Signal

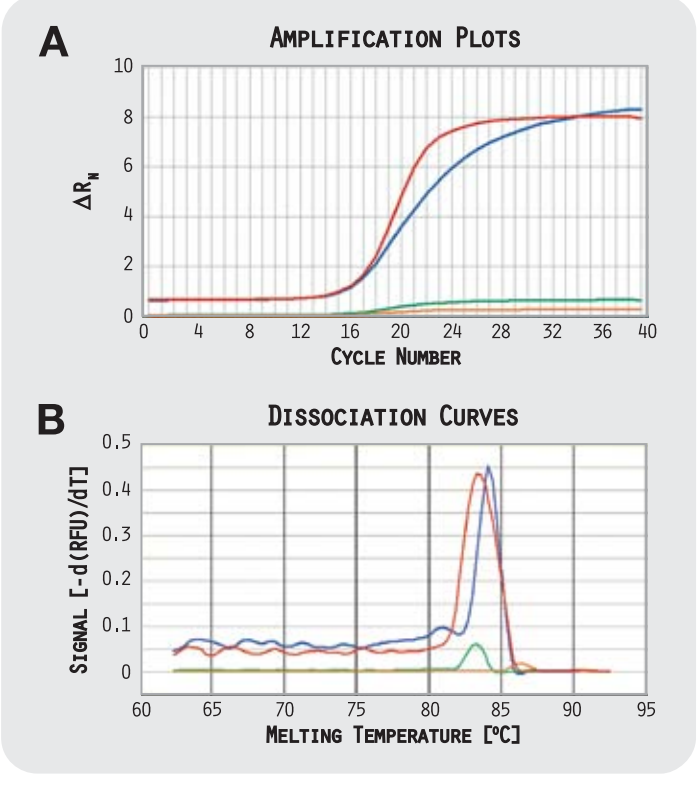


Figure 1: RT² SYBR Green qPCR Master Mixes Provide Greater Sensitivity with a Brighter SYBR Green Signal. Four commercial master mixes were used to detect the expression of human ACTB from the same universal reference RNA. The amplification (A) and the dissociation curves (B) for the master mix from SABiosciences demonstrate a sharper amplification curve and a brighter SYBR Green signal than observed with three competing master mixes.

Greater Sensitivity Without Sacrificing Specificity

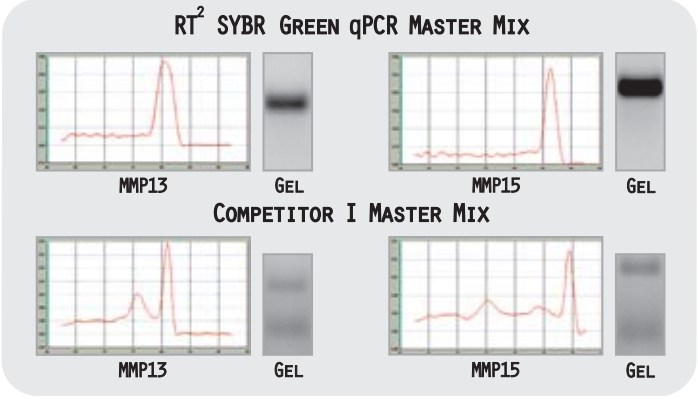


Figure 2: RT² SYBR Green qPCR Master Mixes Provide Greater Sensitivity Without Sacrificing Specificity. RT² SYBR Green qPCR Master Mixes and Competitor I Master Mixes were used in qPCR assays to detect the human MMP13 and MMP15 mRNA in reference RNA. RT² SYBR Green qPCR Master mixes provide detection of the genes at an earlier threshold cycle value (C_t). The real-time dissociation curves and agarose gel electrophoresis characterization reveal the presence of a non-specific secondary product generated with the competitor's master mix which is not amplified by the RT² SYBR Green qPCR Master Mix.

RT² SYBR Green qPCR Master Mix from SABiosciences

- *Proven in > 20,000 Genes & in > 600 Peer-Reviewed Publications*

Compatible PCR Instruments
Applied Biosystems (ABI): *5700, 7000, 7300, 7500, 7500 FAST, 7700, 7900HT, StepOnePlus (96- and 384-well blocks)*
Bio-Rad: *CFX96, CFX384, iCycler, iQ5, MyiQ, Chromo4, Opticon, Opticon 2*
Stratagene: *Mx3000P, Mx3005P, Mx4000*
Roche: *LightCycler 480 (96- and 384-well blocks)*
Eppendorf: *Mastercycler ep realplex*
TaKaRa: *TP800*
Fluidigm: *BioMark*

RT² qPCR Master Mixes

Product	Size	Catalog #
RT² SYBR Green w/ ROX qPCR Master Mix *For All ABI and Stratagene Instruments*	2 Arrays	PA-012
	12 Arrays	PA-012-12
	24 Arrays	PA-012-24
	4 Arrays*	PA-012-8
	25 mL	PA-112
RT² SYBR Green w/ Fluorescein qPCR Master Mix *For Bio-Rad Instruments*	2 Arrays	PA-011
	12 Arrays	PA-011-12
	24 Arrays	PA-011-24
	4 Arrays*	PA-011-8
	25 mL	PA-111
RT² SYBR Green qPCR Master Mix *Without Reference Dye*	2 Arrays	PA-010
	12 Arrays	PA-010-12
	24 Arrays	PA-010-24
	4 Arrays*	PA-010-8
* Plate format is 384-well.	25 mL	PA-110

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Data Analysis
Quick and Easy Software

FREE Web-Based PCR ARRAY Data Analysis Software

This integrated web-based software package for the PCR Array System automatically performs all $\Delta\Delta C_t$ based fold-change calculations from your uploaded raw threshold cycle data. Simply providing the array's catalog number annotates the results to the correct gene list. The web portal delivers results not only in a tabular format but also in scatter, volcano, cluster-gram, and multi-group plots. Perform any pair-wise comparison between groups of experimental replicates by defining your own fold-change and statistical significance thresholds, or compare all of the groups side-by-side. The web portal also helps you correctly interpret the genomic DNA, reverse transcription efficiency, and positive PCR control well data. Make your pathway-focused gene expression analysis quick and painless with the PCR Array System and the PCR Array Data Analysis Suite.

- ***Simple:*** Just upload your data and define your parameters*
- ***Convenient:*** No downloading or installation required
- ***Publication-Ready Output:*** Export all results as FREE *EXCEL* files or PNG image files

* *EXCEL*-based data analysis templates are available from our website.

INSTRUCTIONS

1. Upload your data in a simple *EXCEL* file format.
2. Define your housekeeping genes and experimental groups.
3. Choose an automatically generated data analysis result

Take a test run with pre-loaded sample data set today:
http://www.SABiosciences.com/pcrarraydataanalysis.php

OR

Join our next live webinar entitled: *"PCR Array Data Analysis Tutorial"* at:
http://www.SABiosciences.com/seminarlist.php

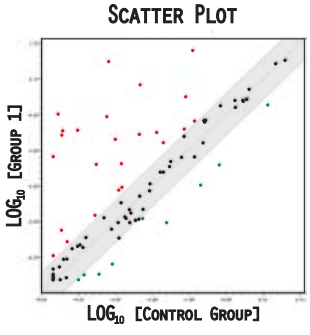

Figure 1: The Scatter Plot Compares Gene Expression Levels Between Two Experimental Conditions. The graph plots the $\log_{10}$ of normalized gene expression levels in a control condition (x-axis) versus an experimental condition (y-axis). Symbols outside the gray area indicate fold-differences larger than a threshold that you can define. The red symbols in the upper-left corner readily identify up-regulated genes, and the green symbols in the lower right corner readily identify down-regulated genes.

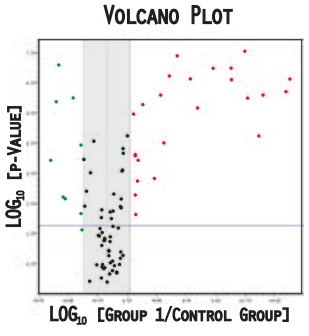

Figure 2: The Volcano Plot Indicates the Statistical Significance of Gene Expression Changes. The x-axis plots the $\log_2$ of the fold-differences, while the y-axis plots their p-values based on student's *t*-test of your replicate raw C_t data. The red and green symbols outside the gray area conveniently have the same meaning as the Scatter Plot. Symbols in the Volcano Plot above the blue line readily identify fold-differences at least as statistically significant as a threshold that you can define.

Service Core
Gene Expression Analysis Services

Service Core for PCR ARRAY Gene Expression Analysis

SABiosciences provides comprehensive PCR Array Gene Expression Analysis Services for all of your real-time PCR-based needs. SABiosciences' Service Team has years of experience in gene expression profiling with quantitative SYBR® Green real-time PCR, as well as RNA isolation of the quantity and quality required by real-time PCR experiments.

Why Use Our Gene Expression Analysis Services?

- No access to a real-time PCR instrument
- Lack the time or manpower to perform the microarray or PCR experiments needed to complete your project
- Prefer to run an optimized pilot project before bringing the technology in-house for a large scale project

Let our in-house experts serve as your "external core facility" to save you time, money, and effort in performing your expression analysis projects. The services are flexible and can be tailored to exactly meet your specific needs. Simply submit experimental samples and receive gene expression profiling results in a matter of days.

Features of the PCR ARRAY Service

- Free consultation on your experimental design to help you take advantage of our expertise
- Confirmation of RNA sample concentration and quality
- Unbiased reverse transcription of RNA into cDNA template, including elimination of genomic DNA contamination
- Detailed and flexible data analysis according to your needs
- Quick results
- Competitive and affordable prices

RNA Isolation Services

- ***Standard:*** Preparation from Cells, Tissue, and Blood
- ***Specialized:*** Preparation from FFPE, LCM, FNAB and Other Samples

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APPLICATION:
CANCER BIOLOGY

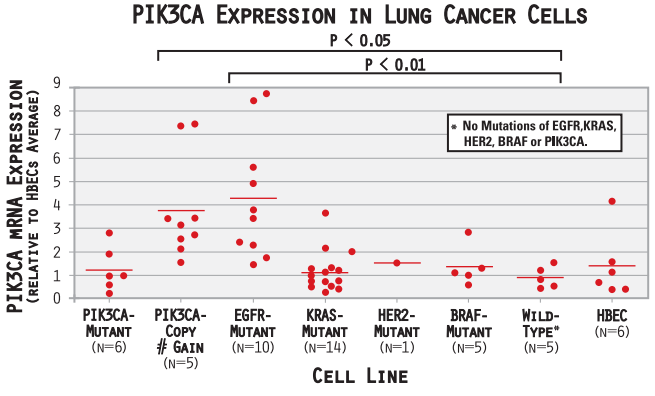

Figure: PIK3CA mRNA Expression in Multiple Lung Cancer Cell Lines. PIK3CA mRNA expression was compared among cell lines having different features, such as PIK3CA alterations or mutations of other genes involved in the EGFR signaling pathway. PIK3CA mRNA expression levels were expressed relative to the mean levels in six HBEC cell lines. PIK3CA mRNA expression in PIK3CA gain or EGFR mutant cell lines were significantly increased compared with that of wild-type cell lines. However, PIK3CA mutant lines do not express increased mRNA levels. Horizontal bars indicate mean values. The Kruskal-Wallis test with Dunn's multiple comparison test was used to determine significance.

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CANCER PATHWAYFINDER™

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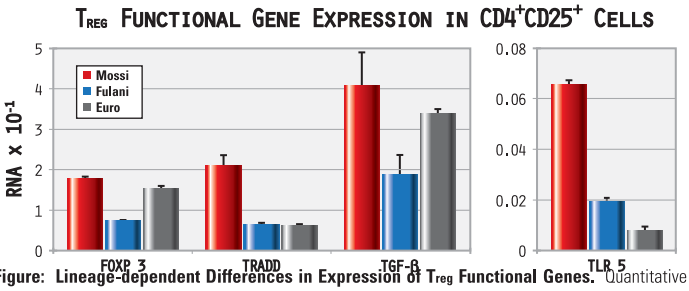

Figure: Lineage-dependent Differences in Expression of T_{reg} Functional Genes. Quantitative PCR analysis of selected genes related to T_{reg} function in $CD4^+CD25^+$ cells from Mossi, Fulani, and European donors infected with *Plasmodium falciparum* (malaria). $CD4^+CD25^+$ cells were isolated from 12 Mossi (red bars) and 12 Fulani (blue bars) donors included in the study and 10 European donors (gray bars), and lysed to obtain total RNA. Equal amounts of RNA (50 ng) from each donor were reverse-transcribed and amplified in duplicate in RT² Custom PCR Arrays to simultaneously examine the mRNA levels of nine selected genes related to T_{reg} activity using PPIA, GAPDH, and ACTB as housekeeping genes (HKG). Data was normalized to the mean values of the HKG, and a relative amount of RNA was calculated using the $2^{-\Delta C_t}$ method.

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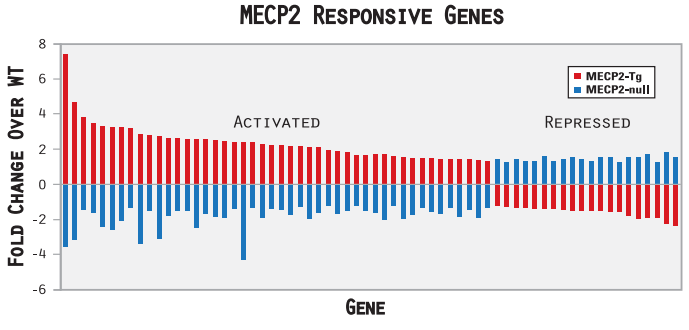

Figure: Gene Expression Changes in Hypothalamus of MECP2 Mouse Models. Validation of expression changes for 66 genes by qPCR analysis. Gene expression levels from microarray analyses were validated in four MECP2-Tg males and four MECP2-null males. Data is plotted as relative up-regulation (red) or down-regulation (blue) over WT ($P < 0.05$, *t* test). Each row represents a single gene, and each column represents data for four samples from each genotype.

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COMPLETE PCR ARRAY PRODUCT CATALOG

RT² Profiler PCR ARRAYS*	Human	Mouse	Rat
Alzheimer's Disease	PAHS-057	PAMM-057	
Angiogenesis	PAHS-024	PAMM-024	PARN-024
Angiogenic Growth Factors and Inhibitors	PAHS-072	PAMM-072	PARN-072
Apoptosis	PAHS-012	PAMM-012	
Atherosclerosis	PAHS-038	PAMM-038	
Autophagy	PAHS-084	PAMM-084	
Breast Cancer and Estrogen Receptor Signaling	PAHS-005	PAMM-005	PARN-005
cAMP / Calcium Signaling PathwayFinder™	PAHS-066	PAMM-066	
Cancer Drug Resistance and Metabolism	PAHS-004	PAMM-004	
Cancer PathwayFinder™	PAHS-033	PAMM-033	PARN-033
Cell Cycle	PAHS-020	PAMM-020	PARN-020
Cell Surface Markers	PAHS-055		
Chemokines and Receptors	PAHS-022	PAMM-022	PARN-022
Common Cytokines	PAHS-021	PAMM-021	PARN-021
Dendritic and Antigen Presenting Cell	PAHS-406		
Diabetes	PAHS-023	PAMM-023	PARN-023
DNA Damage Signaling Pathway	PAHS-029	PAMM-029	PARN-029
Drug Metabolism	PAHS-002	PAMM-002	PARN-002
Drug Metabolism: Phase I Enzymes	PAHS-068		PARN-068
Drug Metabolism: Phase II Enzymes	PAHS-069		PARN-069
Drug Transporters	PAHS-070		PARN-070
EGF / PDGF Signaling Pathway	PAHS-040		PARN-040
Embryonic Stem Cells	PAHS-081	PAMM-081	
Endothelial Cell Biology	PAHS-015	PAMM-015	PARN-015
Extracellular Matrix and Adhesion Molecules	PAHS-013	PAMM-013	PARN-013
GPCR Signaling PathwayFinder™	PAHS-071		PARN-071
Growth Factors	PAHS-041	PAMM-041	PARN-041
Heat Shock Proteins	PAHS-076	PAMM-076	
Hedgehog Signaling Pathway	PAHS-078	PAMM-078	
Hematopoietic Stem Cells and Hematopoesis	PAHS-054		
HIV Infection and Host Response	PAHS-051		
Homeobox *(HOX)* Genes	PAHS-083	PAMM-083	
Housekeeping Genes	PAHS-000	PAMM-000	PARN-000
Hypoxia Signaling Pathway	PAHS-032	PAMM-032	PARN-032
Inflammatory Cytokines and Receptors	PAHS-011	PAMM-011	PARN-011
Inflammatory Response and Autoimmunity	PAHS-077		
Innate and Adaptive Immune Responses	PAHS-052	PAMM-052	
Insulin Signaling Pathway	PAHS-030	PAMM-030	PARN-030
Interferon α,β Response	PAHS-016	PAMM-016	
Interferons and Receptors	PAHS-064	PAMM-064	
JAK / STAT Signaling Pathway	PAHS-039	PAMM-039	PARN-039
Lipoprotein Signaling and Cholesterol Metabolism	PAHS-080	PAMM-080	PARN-080
MAP Kinase Signaling Pathway	PAHS-061	PAMM-061	PARN-061
Mesenchymal Stem Cells	PAHS-082	PAMM-082	
Neurogenesis and Neural Stem Cell	PAHS-404	PAMM-404	
Neuroscience Ion Channels and Transporters	PAHS-036	PAMM-036	PARN-036
Neurotransmitter Receptors and Regulators	PAHS-060	PAMM-060	PARN-060
Neurotrophins and Receptors	PAHS-031	PAMM-031	PARN-031
NFκB Signaling Pathway	PAHS-025	PAMM-025	PARN-025
Nitric Oxide Signaling Pathway	PAHS-062	PAMM-062	PARN-062
Notch Signaling Pathway	PAHS-059	PAMM-059	
Nuclear Receptors and Coregulators	PAHS-056	PAMM-056	PARN-056
Obesity		PAMM-017	PARN-017
Osteogenesis	PAHS-026	PAMM-026	PARN-026
Oxidative Stress and Antioxidant Defense	PAHS-065	PAMM-065	PARN-065
p53 Signaling Pathway	PAHS-027	PAMM-027	PARN-027
PI3K-AKT Signaling Pathway	PAHS-058		
Signal Transduction PathwayFinder™	PAHS-014	PAMM-014	PARN-014
Stem Cell	PAHS-405	PAMM-405	PARN-405
Stress and Toxicity PathwayFinder™	PAHS-003	PAMM-003	PARN-003
Stress Response to Cellular Damage		PAMM-019	
T-Cell and B-Cell Activation	PAHS-053	PAMM-053	
T Cell Anergy and Immune Tolerance		PAMM-074	
TGFβ / BMP Signaling Pathway	PAHS-035	PAMM-035	PARN-035
Th1-Th2-Th3	PAHS-034	PAMM-034	PARN-034
Th17 for Autoimmunity and Inflammation	PAHS-073	PAMM-073	
TNF Ligands and Receptors	PAHS-063	PAMM-063	
Toll-Like Receptor Signaling Pathway	PAHS-018	PAMM-018	PARN-018
Transcription Factors	PAHS-075		
Tumor Metastasis	PAHS-028	PAMM-028	
Ubiquitination *(Ubiquitinylation)*	PAHS-079	PAMM-079	
Wnt Signaling Pathway	PAHS-043	PAMM-043	PARN-043

PCR ARRAYS	Size
96-well	2 Arrays
96-well	12 Arrays
96-well	24 Arrays
384-well	4 Arrays
Add up to 4 Genes to any PCR Array	

Compatible Instrument	Plate
Applied Biosystems (ABI)	
ABI 7000	A
ABI 7300	A
ABI 7500 Standard 96-well Block	A
ABI 7500 FAST 96-well Block	C
ABI 7900HT Standard 96-well Block	A
ABI 7500HT FAST 96-well Block	C
ABI 7500HT 384-well Block	E
ABI 5700 *(Perkin Elmer)*	A
ABI 7700 *(Perkin Elmer)*	A
ABI StepOnePlus	C
Bio-Rad	
iCycler	A
iQ5	A
MyiQ	A
CFX96	D
Chromo4 *(MJ Research)*	A
Opticon (2) *(MJ Research)*	D
Stratagene	
Mx3005p	A
Mx3000p	A
Mx4000	D
Roche	
LightCycler 480 96-well Block	F
LightCycler 480 384-well Block	G
Eppendorf	
Mastercycler ep realplex	A

Master Mix	Catalog #
RT² SYBR® Green w/ ROX®	
2 Arrays *(96-well)*	PA-012
12 Arrays *(96-well)*	PA-012-12
24 Arrays *(96-well)*	PA-012-24
4 Arrays *(384-well)*	PA-012-8
25 mL	PA-112
RT² SYBR® Green w/ Fluorescein	
2 Arrays *(96-well)*	PA-011
12 Array *(96-well)*	PA-011-12
24 Arrays *(96-well)*	PA-011-24
4 Arrays *(384-well)*	PA-011-8
25 mL	PA-111
RT² SYBR® Green Only	
2 Arrays *(96-well)*	PA-010
12 Arrays *(96-well)*	PA-010-12
24 Arrays *(96-well)*	PA-010-24
4 Arrays *(384-well)*	PA-010-8
25 mL	PA-110

PCR Accessories	Catalog #
First Strand Kit	C-03
RNA Isolation Kit	PA-001
Nano PreAMP Kit	C-06
Nano PreAMP Primer Mixes	Various
FFPE RNA Extraction Kit	PA-023
FFPE PreAMP Kit	C-07
FFPE PreAMP Primer Mixes	Various
Primer Assays	Various

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RT² miRNA PCR ARRAYS	Human	Mouse	Size
Whole Genome (96-well)	MAH-100	MAM-100	8 Plates
Whole Genome (384-well)	MAH-3100	MAM-3100	2, 12, 24 Plates
Cancer (96-well)	MAH-102	MAM-102	2, 12, 24 Plates
Cancer (384-well)	MAH-102-E,G	MAM-102-E,G	4 Plates
Cell Differentiation/Development (96-well)	MAH-103	MAM-103	2, 12, 24 Plates
Cell Differentiation/Development (384-well)	MAH-103-E,G	MAM-103-E,G	4 Plates
miFinder™ (96-well)	MAH-001	MAM-001	2, 12, 24 Plates
miFinder (384-well)	MAH-001-E,G	MAM-001-E,G	4 Plates
RT² qPCR-Grade miRNA Isolation Kit	MA-01	MA-01	12 Samples
RT² miRNA First Strand Kit	MA-03	MA-03	12 Samples
RT² miRNA qPCR Assays	Various	Various	200 Reactions

Methyl-Profiler™ DNA Methylation PCR ARRAYS	Signature Panel*	Complete Panel*
Human Breast Cancer	MeAH-011	MeAH-8010
Human Gastric Cancer	MeAH-021	MeAH-8020
Human Liver Cancer	MeAH-031	MeAH-8030
Human Lung Cancer	MeAH-041	MeAH-8040
Human Prostate Cancer	MeAH-051	MeAH-8050
Human Colon Cancer	MeAH-061	MeAH-8060
Human Stem Cell Transcription Factor	MeAH-511	
Human Inflammatory Response	MeAH-521	
Human T Cell Activation	MeAH-531	
Human Cytokine Production	MeAH-541	
Methyl-Profiler DNA Methylation Enzyme Kit *(12 samples)*	MeA-03	MeA-03
Human qPCR Primers for Promoter CpG Islands *(200 reactions)*	Inquire	Inquire
Custom Methyl-Profiler PCR Array	Inquire	Inquire

** Methyl-Profiler Signature Panels profile the promoter methylation status of 24 genes and Complete Panels profile 96 genes.*

ChampionChIP™ PCR ARRAYS	Size	Catalog #
ChampionChIP PCR Arrays		
Human Stem Cell Transcription Factors	4, 12, 24 Plates	GH-501
Human Oncogene & Tumor Suppressor Genes	4, 12, 24 Plates	GH-502
Human T Helper Cell Differentitation	4, 12, 24 Plates	GH-503
ChampionChIP One-Day Kit	12 samples	GA-101
ChampionChIP Antibody Kits *(antibody and qPCR controls)*		
Human RNA Polymerase II	12 Samples	GA-111
Human p53	12 Samples	GA-112
Human Histone H3Ac	12 Samples	GAH-7201
Human Histone H4Ac	12 Samples	GAH-5207, GAH-3203, GAH-8208
Human Histone H3K4me1, H3K4me2, H3K4me3	12 Samples	GAH-3203
Human Histone H3K9me1, H3K9me2, H3K9me3	12 Samples	GAH-5210, GAH-8211, GAH-6204
Human Histone H3K27me3	12 Samples	GAH-9205
ChampionChIP qPCR Primers - *Whole Genome*	200 Reactions	Various
Custom ChampionChIP qPCR Arrays	Inquire	Inquire

FREE Data Analysis Software	Web Page
Web-based Data Analysis Software	
RT² Profiler PCR Arrays	www.SABiosciences.com/pcrarraydataanalysis.php
RT² miRNA PCR Arrays	www.SABiosciences.com/mirnaArrayDataAnalysis.php
EXCEL-based Data Analysis Software	
Methyl-Profiler PCR Arrays	www.SABiosciences.com/dna_methylation_data_analysis.php
ChampionChIP qPCR System	www.SABiosciences.com/chipqpcr.php

Service Core for Gene Expression Analysis	Web Page
Quantitative PCR Services	
RT² Profiler PCR Array - *Focus on Pathways or Diseases*	www.SABiosciences.com/PCRArrayService.php
RT² Real-Time PCR - *Analyze Individual Genes and Verify Array Data*	www.SABiosciences.com/RT2PCRService.php
RNA Isolation Services	
Standard - *Preparation from Cells, Tissue, Blood and Other Samples*	www.SABiosciences.com/RNAIsolationService.php
Specialized - *Preparation from FFPE, LCM, FNAB and Other Samples*	www.SABiosciences.com/RNAIsolationService.php
Complete Service Solutions for FFPE, LCM, FNAB and Other Small Samples	
Formalin-Fixed Paraffin-Embedded	www.SABiosciences.com/FFPEService.php
Laser Capture Microdissection	www.SABiosciences.com/LCMFNABService.php
Fine Needle Aspiration Biopsies and Other Small Samples	www.SABiosciences.com/LCMFNABService.php
Illumina Gene Expression Analysis Services	
Genotyping and Copy Number Variation (CNV)	www.SABiosciences.com/illuminagenotyping.php
Whole- Genome Expression BeadChips	www.SABiosciences.com/illuminageneexp.php

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