miProfile™ Human Colorectal Cancer miRNA qPCR Array

For focused group profiling of human colorectal cancer related miRNA expression

Cat. No. QM006-A (1 x 96-well plate, Format A)
Cat. No. QM006-B (1 x 96-well plate, Format B)
Cat. No. QM006-C (1 x 96-well plate, Format C)
Cat. No. QM006-D (1 x 96-well plate, Format D)
Cat. No. QM006-E (1 x 96-well plate, Format E)

Available as 1 set or 6 sets. Each set contains 84 unique miRNA primers deposited in one 96-well plate.

Introduction

The miProfile human colorectal cancer miRNA qPCR array profiles 84 aberrantly expressed miRNAs which are most relevant to colorectal cancer (CRC). CRC, commonly known as bowel cancer, is a type of cancer from uncontrolled cell growth in the colon, rectum, or appendix, and is considered one of the major causes of cancer death worldwide. At the molecular level, much progress has been made in the last two decades in the identification and characterization of the genetic changes involved in the malignant colorectal transformation process. A number of molecular studies have shown that colorectal carcinogenesis results from an accumulation of epigenetic and genetic alterations, including mutations of APC and TP53 tumor suppressor genes or of DNA repair genes. However, there is mounting evidence suggest that alternative genetic events may occur during colorectal carcinogenesis, sometimes preferentially, sometimes randomly, and sometimes with an overlap. The study of miRNA expression regulation could help to identify miRNA targets associated with different colorectal carcinogenesis pathways and their role as potential biomarkers or therapeutic targets.

- QM006 plate 01: 84 unique miRNA PCR primer pairs

Shipping and storage condition

Shipped at room temperate
Stable for at least 6 months when stored at -20°C

Array format

GeneCopoeia provides five qPCR array formats (A, B, C, D, and E) suitable for use with the following real-time cyclers.

**Important note:** Upon receiving, please check to make sure that the correct array format was ordered to ensure the compatibility with your qPCR instrument.

<table>
<thead>
<tr>
<th>Plate format</th>
<th>Instrument provider</th>
<th>qPCR instrument model</th>
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</thead>
<tbody>
<tr>
<td>A (96-well)</td>
<td>Applied Biosystems</td>
<td>5700, 7000, 7300, 7500, 7700, 7900HT (Standard 96-well block), ViiA™7 (Standard 96-well block)</td>
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<tr>
<td>B (96-well)</td>
<td>Applied Biosystems</td>
<td>7500 (Fast block), 7900HT (Fast block), StepOnePlus™, ViiA™7 (Fast block)</td>
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<td>C (96-well)</td>
<td>Bio-Rad Laboratories</td>
<td>iCycler iQ®, MyiQ™, iQ™5</td>
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<td>D (96-well)</td>
<td>Bio-Rad Laboratories</td>
<td>CFX96™, DNA Engine Opticon™, DNA Engine Opticon 2™, Chromo4™</td>
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<tr>
<td>E (96-well)</td>
<td>Roche Applied Science</td>
<td>LightCycler® 480 (96-well block)</td>
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</table>
Quality control

1. Each miRNA-specific primer in the miProfile miRNA qPCR array has been experimentally validated to yield a single dissociation curve peak and to generate a single amplicon of the correct size for the targeted miRNA.

2. The positive PCR controls (PCR) have been verified to amplify a single amplicon of the correct size with Ct values around $20 \pm 2$.

3. The Spike-in reverse transcription controls (RT) have been verified to amplify a single amplicon of the correct size with Ct values around $20 \pm 3$.

4. $R^2 > 0.99$ was observed for high inter/intra-array reproducibility.

Materials required but not provided

- All-in-One™ miRNA First-Strand cDNA Synthesis Kit
- All-in-One™ qPCR Mix
- Total RNA extraction kit (RNAzol® RT RNA extraction reagent is recommended)
- DNase/RNase free tips, PCR reaction tubes, 1.5 ml microcentrifuge tubes
- 5 ml and 10 ml graduated pipettes, beakers, flasks, and cylinders
- 10 μl to 1,000 μl adjustable single channel micropipettes with disposable tips
- 5 μl to 20 μl adjustable multichannel micropipette, disposable tips, and reservoir
- qPCR instrument, compatible with gene qPCR arrays ordered

Array layout

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<td>HK6</td>
<td>RT</td>
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<td>PCR</td>
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- **miRNA primer pairs**: Wells 1-84 are designated wells for pre-deposited miRNA primer pairs.
- **NC**: Negative controls, which only have the pre-deposited reverse universal primers.
- **HK1-6**: Six pre-deposited housekeeping snRNAs primer pairs, which can be used as endogenous positive controls as well as for array normalization.
- **RT**: Three replicates of spike-in reverse transcription controls, which can be used to monitor the efficiency of the RT reaction. These pre-deposited primer pairs specifically amplify the cDNA template reversed transcribed from the spike-in exogenous RNA in the sample.
- **PCR**: Three replicates of positive PCR controls, which are used to verify the PCR efficiency by amplifying the pre-deposited DNA template with its specific pre-deposited primer pairs.

**miRNA primer list**

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