User Bulletin

Applied Biosystems TaqMan® Low Density Array

September 5, 2010

SUBJECT: Running TaqMan® Low Density Arrays on 7900HT Real-Time PCR Systems

In This User Bulletin

This user bulletin describes procedures for using TaqMan Low Density Arrays (TaqMan Arrays) to perform relative quantitation (RQ) of targets using the comparative C_T (ddC_T) method on Applied Biosystems 7900HT Systems.

System Overview

TaqMan Arrays' 384-wells are pre-loaded with TaqMan Gene Expression Assays. Each TaqMan Array evaluates from one to eight cDNA samples generated in a reverse transcription step using random primers on 7900HT Systems.

Required Components

- Applied Biosystems 7900HT Fast Real-Time System or ABI PRISM® 7900HT Sequence Detection System
- Sequence Detection Systems (SDS) Software v2.1 or later
- Sorvall® or Heraeus centrifuge
- 7900HT TaqMan® Low Density Array Hardware Upgrade Kit (PN 4329012)
  - Low Density Array Thermal Cycling Block
  - 7900HT System heated cover
  - Low Density Array Sealer
  - Four centrifuge buckets and adapters (specific to the Sorvall® or Heraeus centrifuge)
- 7900HT TaqMan® Low Density Array Chemical Installation Kit (PN 4340090)
  - Sequence Detection Systems 384-Well Spectral Calibration Kit
  - Sequence Detection Systems 96-Well Spectral Calibration Kit
  - Spectral Calibration Reagents
  - Low Density Array RNase P Installation Kit
  - Calibration Cards (4 cards)

Before You Begin

Before you perform gene quantitation, make sure that:

- You are familiar with the safety guidelines in the "Safety and EMC Compliance" section of the *Applied Biosystems 7900HT Fast Real-Time PCR System Site Preparation and Safety Guide* (PN 4351923)
- SDS software v2.1 or later is installed.
- The Low Density Array Thermal Cycling Block is installed.
- A background run and pure dye runs have been performed and instrument performance has been verified within the last 6 months. For more information, refer to the *SDS Online Help*.

Applied Biosystems

Singleplex Applications

The TaqMan Array is recommended for use with singleplex applications.

Related Products

Product	Applied Biosystems Part Number
TaqMan® Gene Expression Assays	4331182
TaqMan® Universal PCR Master Mix (2×) with UNG	4304437
TaqMan® Universal PCR Master Mix (2×) without UNG	4324018
Endogenous Controls	Applied Biosystems web site (www.appliedbiosystems.com)

Related Documents

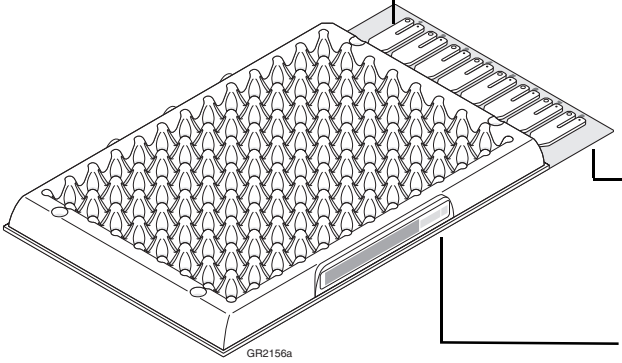
Document	Applied Biosystems Part Number
Applied Biosystems 7900HT Fast Real-Time PCR System Relative Quantitation Using Comparative C_T Getting Started Guide	4364016
Applied Biosystems 7900HT Fast Real-Time PCR System Maintenance and Troubleshooting Guide	4365542
Applied Biosystems Sequence Detection Systems Software Online Help (SDS Online Help)	N/A
Applied Biosystems 7900HT Fast Real-Time PCR System Site Preparation and Safety Guide	4351923
Applied Biosystems 7900HT Fast Real-Time PCR System and SDS Enterprise Database User Guide	4351684
ABI PRISM® 7900HT Sequence Detection System User Guide	4317596
Real-Time PCR Systems Chemistry Guide	4348358
TaqMan® Universal PCR Master Mix Protocol	4351891
TaqMan® Gene Expression Assays Protocol	4364226
High Capacity cDNA Archive Kit Protocol	4322169

Performing Gene Quantitation with TaqMan Arrays

Introduction

About TaqMan Arrays

The TaqMan Array functions as an array of reaction vessels for the PCR step. Typically, the wells of the TaqMan Array contain TaqMan Gene Expression Assays that detect the real-time amplification of user-specified targets. Relative levels of gene expression are determined from the fluorescence data generated during PCR using the ABI PRISM®7900HT Sequence Detection System or Applied Biosystems 7900HT Fast Real-Time PCR System Relative Quantitation software.



Fill Reservoir (1 of 8)
A reservoir for the cDNA sample or control before it is centrifugally transferred into the wells.

Fill consumable
The segment of the TaqMan Array that contains the eight fill reservoirs. After the TaqMan Array is centrifuged and sealed, the fill consumable is trimmed off.

Barcode
Provides coded access to TaqMan Array coded databases.

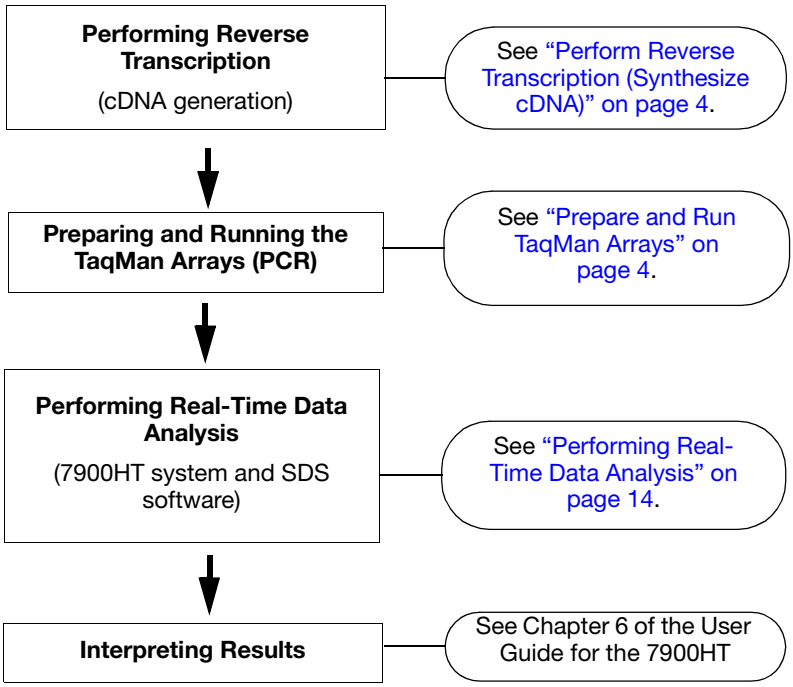
About the Comparative C_T Method for Relative Quantitation

The TaqMan Array is designed for two-step RT-PCR. In the reverse-transcription (RT) step, cDNA is reverse transcribed from total RNA samples using random primers from the High Capacity cDNA Archive Kit. For more information about the RT-PCR process, see the *High Capacity cDNA Archive Kit Protocol* (P/N 4322169).

In the PCR step, PCR products are amplified from cDNA samples using the TaqMan® Universal PCR Master Mix and TaqMan® Gene Expression Assays. The TaqMan assays are pre-loaded in each reaction well of the TaqMan Array. For more information on TaqMan Gene Expression Assays, see the *Real-Time PCR Systems Chemistry Guide* (P/N 4348358).

Overview

Performing gene quantitation involves:



Perform Reverse Transcription (Synthesize cDNA)

Synthesize DNA from total RNA samples using the High Capacity cDNA Archive Kit (PN 4322171). This is the first step in the two-step RT-PCR gene expression quantitation experiment. Use only total RNA samples and random primers to generate cDNA. For more information about synthesizing cDNA, see the *High Capacity cDNA Archive Kit Protocol* (P/N 4322169). Use only total RNA samples and random primers to generate cDNA for use with the TaqMan Array.

Store all cDNA samples at -15 to -25 °C. To minimize repeated freeze-thaw cycles of cDNA, Applied Biosystems recommends that you store your cDNA samples in aliquots.

Prepare and Run TaqMan Arrays

For safety and biohazard guidelines, refer to the "Safety" section in the *TaqMan® Universal PCR Master Mix Protocol* (PN 4351891). For all chemicals in **bold** type, read the MSDS and follow the handling instructions. Wear appropriate protective eyewear, clothing, and gloves.

Amplify cDNA. Amplifying cDNA is the second step in the two-step RT-PCR experiment. In this step, the sample-specific PCR mix is loaded into a TaqMan Array which is pre-loaded with TaqMan® Gene Expression Assays. The TaqMan Array is then run on the 7900HT system for quantitative real-time PCR analysis.

Preparing the sample-specific PCR mix

Note: For details on setting up the reactions, see the *TaqMan® Universal PCR Master Mix Protocol* (PN 4351891).

1. For each sample, label 1.5-mL centrifuge tube.
2. Remove each cDNA sample from the freezer. Thaw the samples by rolling them between your fingers.
3. Gently vortex the samples, then centrifuge the tubes.
4. For each sample, add the following components to the labeled 1.5-mL microcentrifuge tubes:

Component	Volume (µL) per Fill Reservoir
cDNA sample (30 to 1000 ng‡) + RNase-free water	50.0
TaqMan® Universal PCR Master Mix (2×)	50.0
Total Volume	**100.0**

‡ Each sample-specific PCR mix should contain 30 to 1000ng of total RNA converted to cDNA. The amount of cDNA to add depends upon the abundance of the specific gene transcript. The cDNA sample volume, with added water (RNase/DNase-free) should be 50 µL.

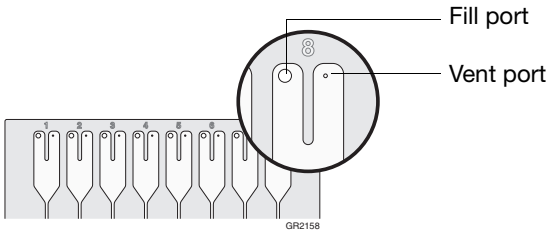
5. Cap the microcentrifuge tubes and thoroughly mix the solution by gently vortexing.
6. Centrifuge the tubes to eliminate air bubbles from the mixtures.
7. Continue with loading the TaqMan Arrays as described below.

Loading the sample-specific PCR Reaction mix into fill reservoirs

1. When the original packaging (plastic tubs) has reached room temperature and you are ready to load PCR reaction mix, carefully remove a TaqMan Array from its packaging.
2. Place the TaqMan Array on a lab bench, with the foil side down.
3. Load 100 µL of the desired sample-specific PCR reaction mix into a 100µL micropipette.

4. Hold the micropipette in an angled position and place the tip in the fill port.

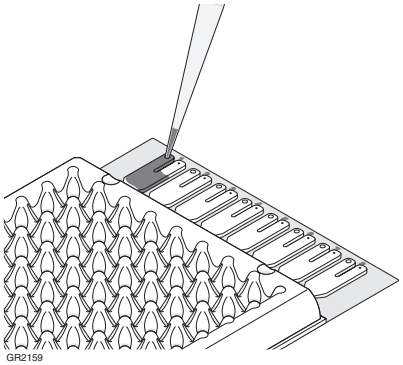
   Note: There is a fill port on the left arm of each fill reservoir; it is the larger of the two holes.



   IMPORTANT! Do not allow the tip to contact and possibly damage the coated foil beneath the fill port.

5. Dispense the sample-specific PCR reaction mix so that it sweeps in and around the fill reservoir toward the vent port.

   IMPORTANT! Pipette the entire 100 µL into the fill reservoir. Do not allow the tip to contact and possibly damage the coated foil beneath the fill port. Be careful when pushing the micropipette plunger to its second stop position (to expel the sample-specific PCR reaction mix from the tip). If a large amount of air is released, it can push the reaction mix out of the fill reservoir via the vent port or introduce bubbles into the fill reservoir.



Centrifuging the TaqMan Array

After the fill reservoirs have been loaded with cDNA samples, the arrays are centrifuged to distribute the cDNA samples to the reaction wells.

1. Place TaqMan Arrays into Buckets.

   IMPORTANT! The Sorvall/Heraeus buckets and array holders required for the TaqMan Arrays are custom-made. Do not use any other bucket/array holder system for this procedure.

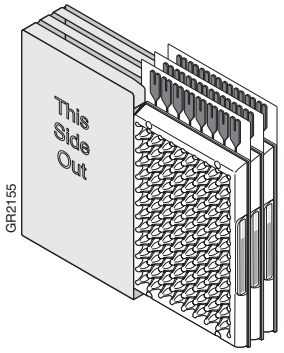
   a. Obtain an empty Sorvall/Heraeus Custom Bucket and array holder. The centrifuge holds four Sorvall/Heraeus buckets. Each bucket holds up to three TaqMan Arrays (loaded and/or blank balance arrays) in the array holder. The array holder supports the TaqMan Array during centrifugation.

   b. Place the bucket on a lab bench, with the label facing you.

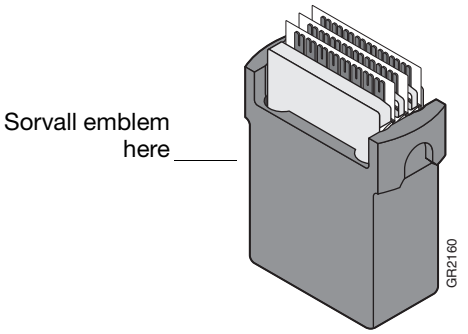
   c. Insert TaqMan Arrays into the array holder, making sure that:

– The fill reservoirs project upwards out of the array holder
– The reaction wells face the same direction as the “This Side Out” label.

IMPORTANT! Use blank balance arrays to fill any remaining positions in the array holder. Failing to do so will impair the sample loading. Use the blank balance arrays provided with the installation kits.

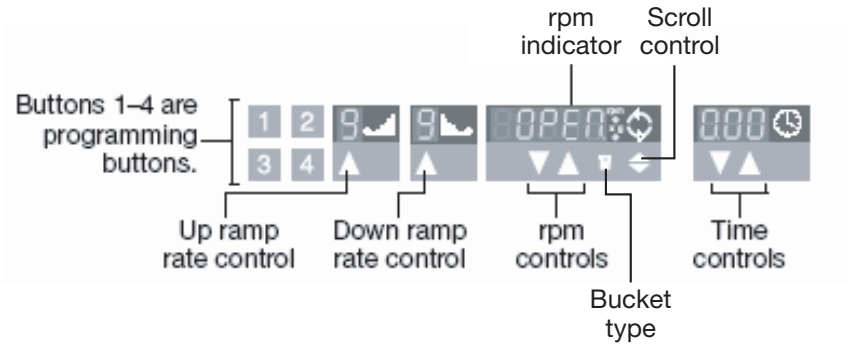


d. Place a filled array holder in the bucket so that the “This Side Out” label faces the front of the bucket, which may have the Sorvall emblem on it.



2. Set the Centrifuge settings.
   a. Power on the centrifuge.
   b. Use the front panel controls on the centrifuge to set the bucket type to **15679** for both the Sorvall and Heraeus centrifuge. See your centrifuge operator’s manual for information about your particular centrifuge.

IMPORTANT! Be sure to set the correct bucket type. This will ensure that the maximum rotational speed stays within the manufacturer’s specified limits.



a. Using the front panel controls (EASYSet touchpad is shown above), set the following operations parameters:

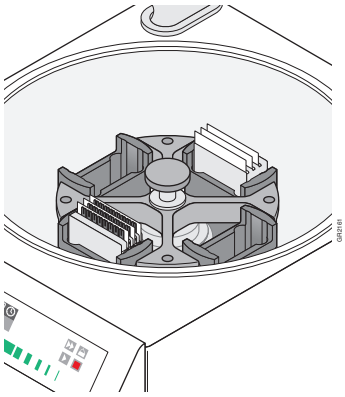
Parameter	EASYSet (touchpad)	QUIKSet (knob-operated)
Up Ramp rate	9	3
Down Ramp rate	9	N/A
Rotational speed	1,200 rpm (331 × g)	1200 rpm
Centrifugation time	2 × 1 min	2 × 1 min

1. Place the Buckets into the centrifuge.
   a. Press the **Open** button on the centrifuge to open the centrifuge cover.

   b. Place a loaded bucket onto an open rotor arm of the centrifuge. Make sure the bucket can swing easily within its slotted position on the rotor arm.

c. Place the remaining buckets onto the rotor arms, per step b.

CAUTION The manufacturer recommends running the centrifuge with all four buckets, even if only two buckets contain arrays. Make sure the buckets and their contents are balanced. Opposing buckets should have matching weights. If the buckets are not fully loaded with arrays containing the sample-specific PCR reaction mix, place blank balance arrays and array holders into the buckets.



d. Close the centrifuge cover.

2. Start the centrifuge.

a. Press the **Start** button.

The centrifuge starts, then automatically stops after 1 min, per the programmed sequence.

b. Repeat step a so that the TaqMan Arrays are centrifuged for a total of two consecutive, 1-min spins to ensure complete distribution of the sample-specific PCR reaction mix.

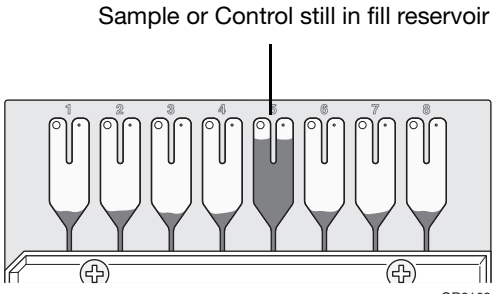
c. Open the centrifuge cover by pressing the **Open** button.

d. When the cover has fully opened, remove the buckets from the centrifuge, then remove the array holders from the buckets.

e. Remove all TaqMan Arrays from the buckets by gently lifting them by their carrier sides.

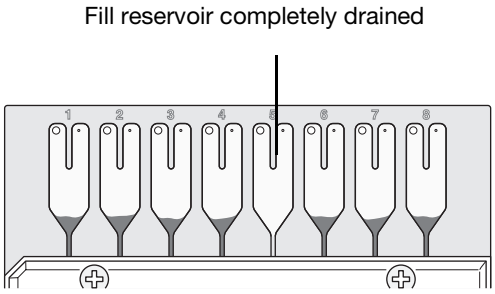
f. Examine the TaqMan Arrays to determine whether filling is complete. The amount of cDNA sample or control remaining in the fill reservoirs should be uniform and consistent from reservoir to reservoir.

– If there is excess cDNA sample or control remaining in a fill reservoir (as shown below), filling is incomplete (or not uniform). Centrifuge the TaqMan Array again for 1 additional minute. Note that if the reservoir filling is still not complete after the additional centrifuge cycle, use another TaqMan Array. If you choose to process the TaqMan Array further you should void the results for the affected fill reservoir (sample).



IMPORTANT! Do not exceed 1200 rpm or accumulated centrifugation times of more than 3 minutes. Excessive centrifugation speeds and times may deform the array.

– If a fill reservoir is completely drained (as shown below), it is possible that some wells were not filled properly. The TaqMan Array should not be processed further. Use another TaqMan Array. If you choose to process the TaqMan Array further you should void the results for the affected fill reservoir (sample).

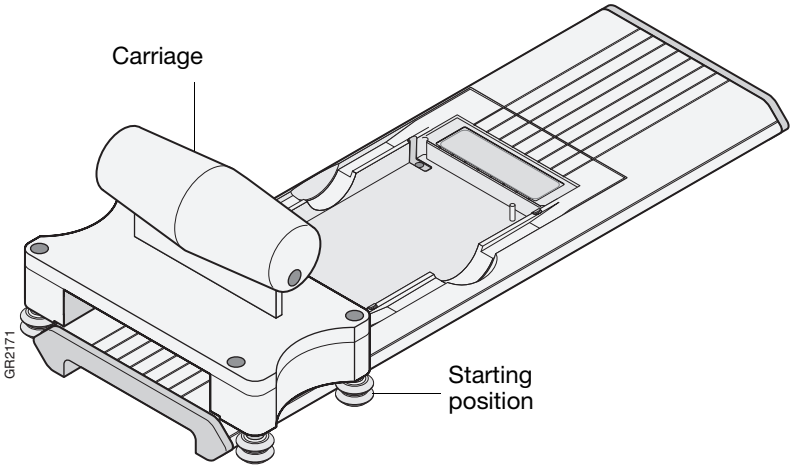


Sealing the TaqMan Array

The sealer isolates the wells of a TaqMan Array after it is loaded with cDNA samples and master mix. The sealer uses a precision stylus assembly (carriage) to seal the main fluid distribution channels of the array.

Proper operation of the sealer using a slow, steady and deliberate motion is critical to the successful use of the TaqMan Array card.

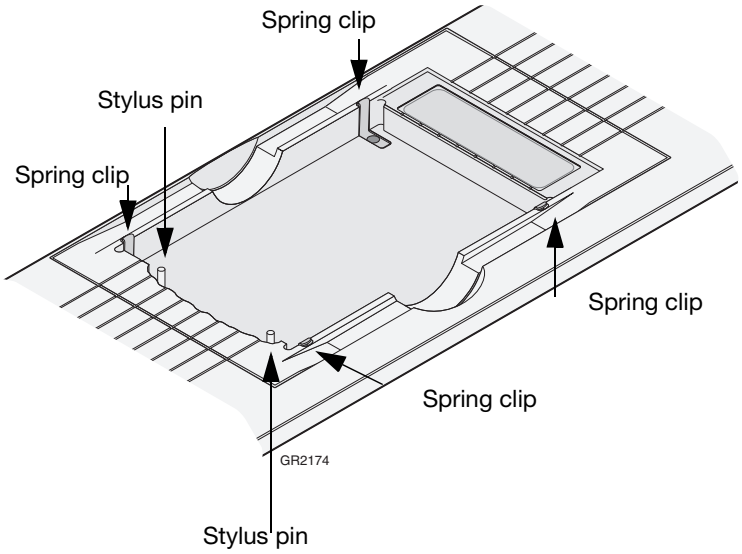
1. Position the sealer.
    a. Place the sealer on a sturdy lab bench, approximately waist high so that it can be easily used.
    b. Turn the sealer so that the front end ("starting position" as shown below) is closest to you and the back end is farthest from you. In the correct position, the arrows on the sealer are pointing away from you.



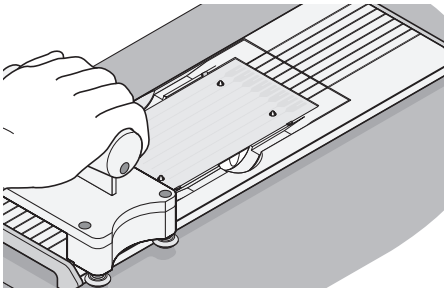
    c. Place the sealer's carriage in its starting position.

    IMPORTANT! Never insert a TaqMan Array into the sealer if the carriage is not in its starting position. The TaqMan Array will be irreparably damaged if the carriage is moved across it toward its starting position.

2. Insert a TaqMan Array into the sealer:
    a. Orient the TaqMan Array in the proper direction over the sealer's insert plate. The TaqMan Array's fill reservoir end should be the end closest to the arrows etched in the base of the sealer.
    b. Line up the Array's rear pin groves, foil side up, to the stylus pins on the sealer.



a. Gently place the Array on top of the insert plate and ensure that the front end of the array is held securely in place by the spring clips.

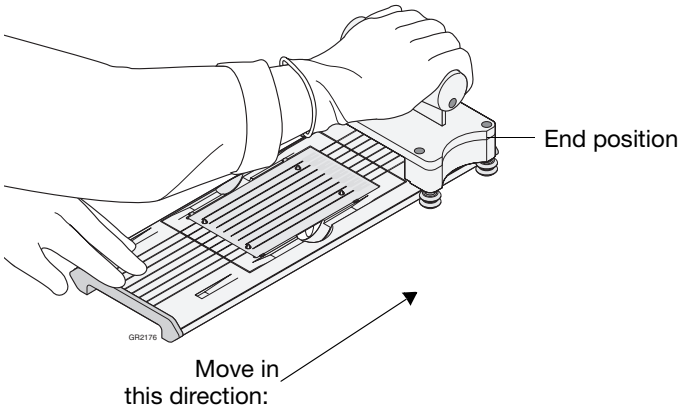


1. Gently push the TaqMan Array until it is seated securely in the insert plate.

   Note: When properly seated, the TaqMan Array's foil surface should be level with the base of the sealer. The four spring clips ensure that the TaqMan Array is held in the proper position.

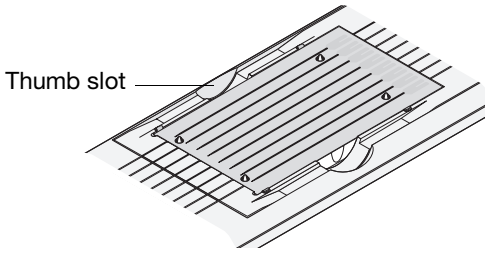
2. Push the carriage across the base of the sealer in the direction of the arrows. Use a slow, steady, and deliberate motion to push the carriage across the entire length of the card until the carriage reaches the mechanical stops. It is important to avoid moving the carriage rapidly across the card.

   CAUTION The sealer has mechanical stops at both ends to prevent the carriage from coming off. Therefore, do not use excessive force or speed when pushing the carriage.



IMPORTANT! Do not move the carriage back before removing the TaqMan Array.

3. Remove the sealed TaqMan Array by grasping its sides and lifting it off the sealer's insert plate. In the middle of the sealer's insert plate, there is a thumb slot to help you easily access one side of the TaqMan Array.

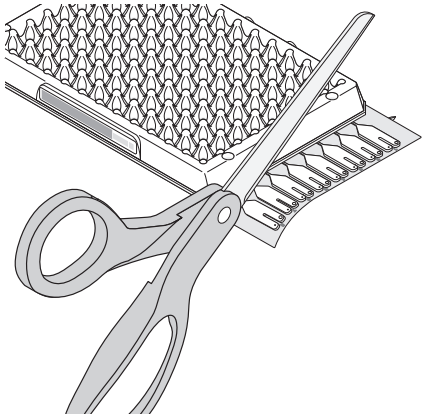


4. Inspect the TaqMan Array for proper sealing. The indentations from the stylus assembly should match up with the TaqMan Array's main channels. If the indentations do not match up or if the foil is in any way damaged, do not use the TaqMan Array.
5. Return the carriage to its starting position on the base of the sealer.

Trimming off the fill reservoirs

Using scissors, trim the fill reservoirs from the TaqMan Array. Use the edge of the TaqMan Array's carrier as a guide.

CAUTION **PHYSICAL INJURY HAZARD**. Take care when trimming off the fill reservoirs. Use scissors rather than razor blades or other unprotected cutting devices.



The TaqMan Array is now ready to be run on the 7900HT instrument.

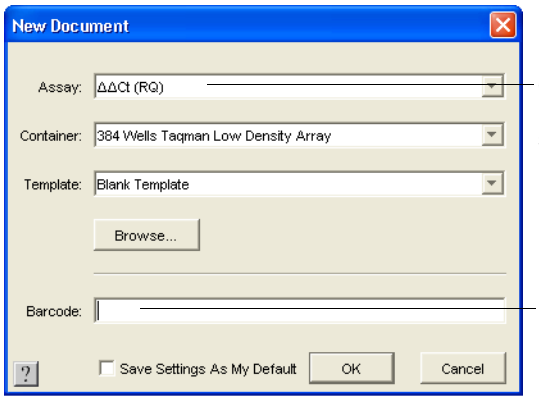
Performing Real-Time Data Analysis

SDS Software Plate Documents

SDS plate documents store data collected from a run including sample names and detectors. TaqMan Arrays are shipped with an Array Information CD which contains an Assay Information File (AIF), SDS Setup file, readme.txt file, and 2 Array map files. The SDS setup file contains information specific to your TaqMan Array. The SDS software uses this setup file to configure the plate document plate grid and setup table. For more information about AIFs and Array map files, see Appendix A.

1. Double-click (SDS v2.1 or later) on the computer desktop. At startup, the software establishes communication with the 7900HT instrument. If the connection is successful, the software displays Connected to 'PlateName' in the status bar when a plate document is open.
2. Import the setup file into a new plate document:
   a. In the SDS software, click (or select **File > New**).
   b. Complete the New Document dialog box using the following settings, then click **OK**.

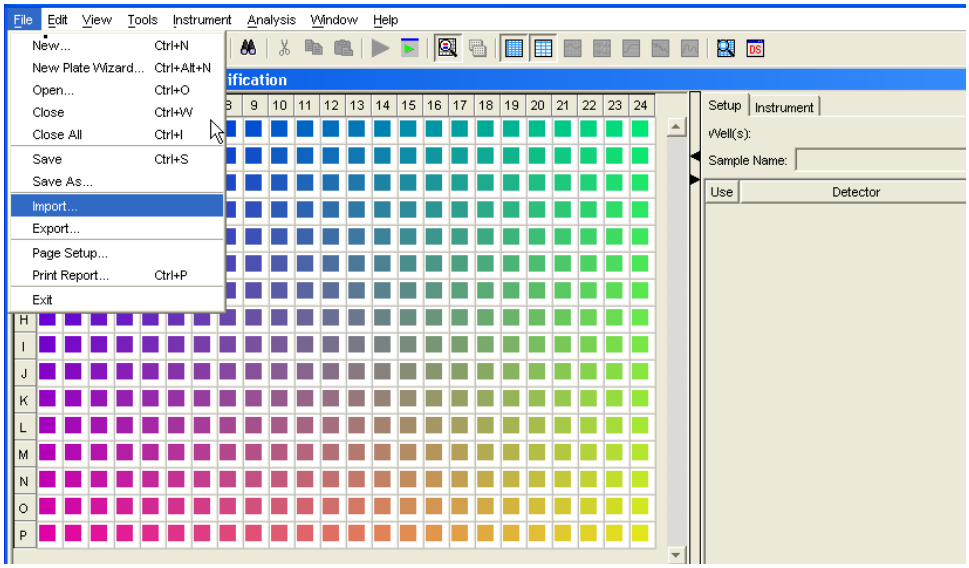
   Note: If you are not using SDS Relative Quantitation software for data analysis, set the Assay type to Standard Curve, AQ, or Absolute Quantitation depending upon your version of SDS software.



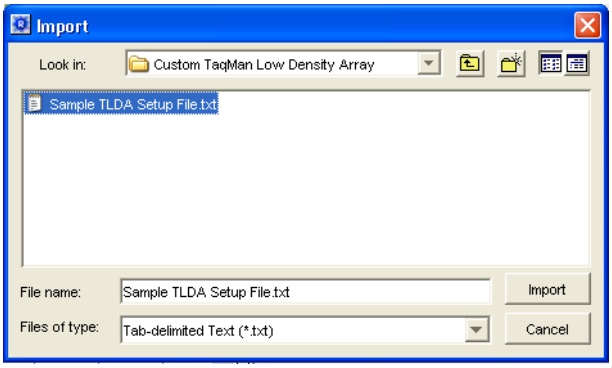
Note that the Assay type may be called "Relative Quantification" depending upon your version of SDS software.

(Optional) Click the Barcode field, then scan or type the bar code.

c. Select **File > Import**.



d. From the Look In field of the Import dialog box, navigate to and select the completed tab-delimited setup table file.



e. Click **Import**. The software imports the setup table information from the text file and automatically configures the plate document plate grid and setup table with detector, detector task, marker, and sample data.

3. Save the plate document. Note that you can save the plate document as an SDS document (*.sds) or SDS template (*.sdt). Saving the plate document as a plate document template is an optional step that is recommended when you want to create duplicate plate documents for a series of plates with identical assay configurations. For more information on document templates, refer to the *SDS Online Help*.

   IMPORTANT! Modifying the contents of the file can corrupt the information on the TaqMan Array.

   a. Click  (or select **File** > **Save As**).

   b. For Files of Type, select **SDS 7900HT Document (*.sds)** or **SDS 7900HT Template Document (*.sdt)** .

   c. Navigate to where you want to save the plate document file.

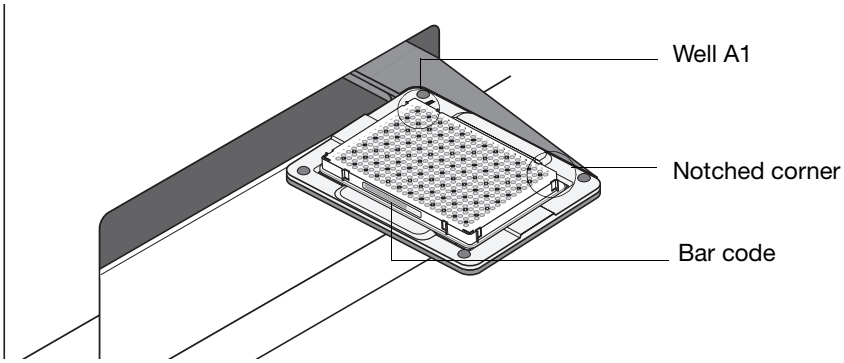
   d. In the File Name field, enter a name for the plate document.

   e. Click **Save**.

Performing the Run

1. Open the plate document in the SDS software.
2. Select the **Instrument** tab of the plate document, then select the **Real-Time** tab.
3. Verify that 

) is displayed in the status bar. If the software is not connected to the instrument, click **Connect to Instrument**.
4. *(Optional)*. If the instrument tray is inside the instrument, click **Open/Close** to rotate the instrument tray to the OUT position.
5. Verify that the TaqMan Array thermal cycling block is installed in the instrument tray. If it is not installed, you must do the following to install the TaqMan Array block:
   - Remove the existing block
   - Install the TaqMan Array block
   - Change the plate adapter
6. Place the prepared array in the instrument tray with:
   - Well A1 at the top left corner of the tray and the notched corner at the top right.
   - The bar code toward the front of the instrument.



7. Click **Start Run**. The instrument tray rotates to the IN position. During the run, the instrument displays real-time status information in the **Instrument > Real-Time** tab and records the fluorescence emissions. Note that you can view the data generated in real-time during the amplification run.
8. When the run is complete and the Run Complete dialog box appears, click **OK** to close the dialog box, click **Open/Close**, then remove the array from the instrument tray.

Running Multiple Arrays.

IMPORTANT! Applied Biosystems recommends running TaqMan Arrays with TaqMan® Universal PCR Master Mix as soon as possible after completing the reaction setup. Therefore, for high-throughput TLDAs you can use the Automation Accessory.

Analyzing Results

For information on analyzing the results, see the SDS Online Help, 7900HT System User Guide, or *Applied Biosystems 7900HT Fast Real-Time PCR System Relative Quantitation Using Comparative C_T Getting Started Guide*.

Ordering

TaqMan® Low Density Array orders can be placed at www.appliedbiosystems.com. A quick guide on ordering arrays can be found on the TaqMan® Low Density Array product page or by going to reference literature (PN 127GU05) on the Literature and Application Notes section. The following table provides a list of available TaqMan Array formats for selected TaqMan® Gene Expression Assays.

P/N	Format	Number of customer selected assays (+ 1 control)	Number of Samples Per Card			
			1 replicate‡	2 replicates	3 replicates	4 replicates
4342247	Format 12	11				8
4346798	Format 16	15			8	
4342249	Format 24	23		8		4
4346799	Format 32	31			4	
4342253	Format 48	27		4		2
4346800	Format 64	63			2	
4342259	Format 96a	95		2		1
4342261	Format 96b	95		2		1
4342265	Format 384	380 + 4 controls	1			

‡ Always run a minimum of two replicates.

Troubleshooting

The following table lists some possible errors, possible causes, and recommended actions.

Observation	Possible Cause	Recommended Action
1. **After removing the TaqMan® Low Density Array from its packaging…**		
Water condenses on the reaction wells (optical side of the TaqMan Array).	The TaqMan Array may not have come to room temperature before being removed from its packaging.	Remove condensation by lightly blowing on the reaction wells. Room temperature pressurized nitrogen or an air blower may be used. **IMPORTANT!** Be sure to remove all water condensation. The exterior surface of the reaction wells (optical side of the TaqMan Array) must be free of water condensation.
2. After pipetting…		
Too little PCR reaction mixture has gone into the fill reservoir.	The PCR mixture was not correctly pipetted into the fill reservoir.	Care must be taken to correctly pipette the entire PCR reaction mixture (100 µL) into the fill reservoir. Add more sample.
Some of the PCR reaction mixture leaks out of the vent port in the fill reservoir.		
Bubbles introduced into fill ports.	Air introduced from pushing the pipette plunger in to its second stop position.	Inspect affected wells after centrifuging and sealing and note any wells that contain bubbles. Delete these from analysis.
3. After Run/Analysis…		
Amplification plots are noisy across portions of TaqMan Array.	Misalignment of TaqMan Array in block.	Check to see if the array feet are crushed. Run test plate (RNaseP or Endogenous Control). Call FAS.
Replicates have poor precision (high standard deviation).	Random PCR or well failure. Assay with steep or noisy baseline	Review multicomponent analysis display for that replicate. Delete the outlier and reanalyze. Set manual baseline with default setting (3–15) for this TaqMan assay (detector) only. Manually set baseline if necessary.
No amplification or poor amplification for specific assay.	Low abundance gene	Review multicomponent analysis display. Use more cDNA.
No amplification or poor precision across many assays.	Non-AB master mix; No Master Mix; No sample.	Use AB Master Mix; Add Master Mix; Add sample.

Appendix A Assay Information and Array Map Files

Assay Information Files (AIFs)

The Assay Information File (AIF) contains gene annotation information for the selected TaqMan Gene Expression Assays on the TaqMan Array. The file is in text format (*AIF_prodNum.txt*, where prodNum is the production number of the array), which can be used by several Applied Biosystems instruments, including the 7900HT System.

Fields in an AIF

All assay information files for TaqMan Arrays contain the fields shown in the table below. The information is provided for each well in the array.

Note: AIFs contain other fields with information which may not apply to TaqMan Arrays. These fields (not included in the table) are marked N/A.

Field Name	Description
Customer Name	Customer organization or institution
Order Number	Customer sales order number
Ship Date	Date the product is packaged for shipment
Delivery Number	Unique number used for shipping
TLDA Format Part Number	Part number of the assays on the card
Product Type	Type of product, as indicated by the product number: for TaqMan® Low Density Arrays, the product type is TaqMan Gene Expression Assays
Assay ID	Unique identifier for the assay
Lot Number	Unique identifier for the manufacturing batch
Plate Type	Container used for the assays (in this case, TaqMan Array)
Well Location	Well location of the assay in the associated bar-coded plate
Assay Mix Concentration	Final concentration of the assay mix
Forward Primer Concentration	Concentration (in µM) of the forward primer
Reverse Primer Concentration	Concentration (in µM) of the reverse primer
Reporter Dye 1	Dye label for the reporter for the assay
Reporter 1 Concentration	Concentration (in µM) of Reporter 1
Reporter 1 Quencher	Quencher used for Reporter 1 of the assay
Context Sequence	25 base nucleotide sequence surrounding the probe

Field Name	Description
Category	Category of the protein based on the PANTHER™ Protein Classification System, Level 1
Category ID	Unique 10-digit ID of the category
Group	Group of the protein based on the PANTHER Protein Classification System, Level 2
Group ID	Unique 10-digit ID of the group
Gene Symbol	LocusLink symbol for the associated gene
Gene Name	LocusLink gene name
Chromosome	Chromosome on which the gene or SNP is found
Species	Organism for which the assay was designed
Target Exons	The two exons (identified by public accession numbers) spanned by the probe
NCBI Gene Reference	NCBI transcript ID detected by the assay
Medline Reference	PubMed references for the gene
Celera ID	Unique assay ID in the Celera Discovery System (CDS)
Cytogenic Band	Chromosomal band location of gene. If not available, the chromosome number is listed instead

Viewing Contents of an AIF

To view the contents of an assay information file in Microsoft Excel as a spreadsheet:

1. 1. Place the TaqMan Array Information CD in the CD drive (typically D: or E:).
2. 2. Launch Microsoft Excel.
3. 3. Open the AIF.
    a. From the File menu, select **Open**.
    b. Navigate to the drive that contains the TaqMan Array Information CD.
    c. Select the *AIF_prodNum.txt* file and click **Open**.

Microsoft Excel displays the contents of the file in a spreadsheet.

Card Map Files

Card maps show the position of the assays on the TaqMan Array. Each card map file contains two color-coded maps. The top map shows the replicate distribution assay gene symbol for each well. The bottom map shows the TaqMan Gene Expression Assay ID numbers.

Card map files also indicate the:

- TaqMan Array configuration and part number.
- Production Number of the card. Each custom TaqMan Array is assigned a unique production number. This number appears as part of the file names of AIF, cardmap, and SDS setup files.

Each TaqMan Array Information CD contains two card map files, one in HTML format, and the other in spreadsheet format.

Card Map Files in HTML Format

The *prodNum_cardmap.html* file contains the card map for your custom TaqMan Array in HTML format. Open the HTML card map when you want to view the map in a browser.

Card Map Files in Spreadsheet Format

The *prodNum_cardmap.xls* contains the card map for your custom TaqMan Array as a Microsoft Excel spreadsheet. Open the card map file as a spreadsheet when you want to print the card map on one page.

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