

Protocol Sheet


Roche® LightCycler® 480 instrument setup instructions for qBiomarker Copy Number PCR Arrays

Important points before starting

- Please read the handbook supplied with the qBiomarker Copy Number PCR Array, paying careful attention to the “Safety Information” and “Important Notes” sections, before beginning this procedure.
- Make sure the real-time PCR instrument is working properly. Refer to the manufacturer’s Installation and Maintenance manual if needed.
- Make sure the correct thermal block cycler (384-well block format for G plate or 96-well for F plate) is in place.
- Turn on the LightCycler 480 instrument; the main switch is located at the back of the instrument. Turn on the computer linked to the instrument and log on to Windows® XP.

Procedure

Creation of PCR protocol template

1. Start LightCycler 480 software 1.5.0 SP4.
2. Enter Username and Password when the Login dialog box appears and click the  button to proceed with the login. The “Overview” window will appear.
3. Wait for the initiation of the instrument to finish and the two status LEDs on the front of the instrument to become stable. The left LED should become a steady green while the right LED should be a steady orange.
4. In the “Overview” window (Figure 1), click the “New Experiment” button on the right-hand side of the window to launch the “Run” module.



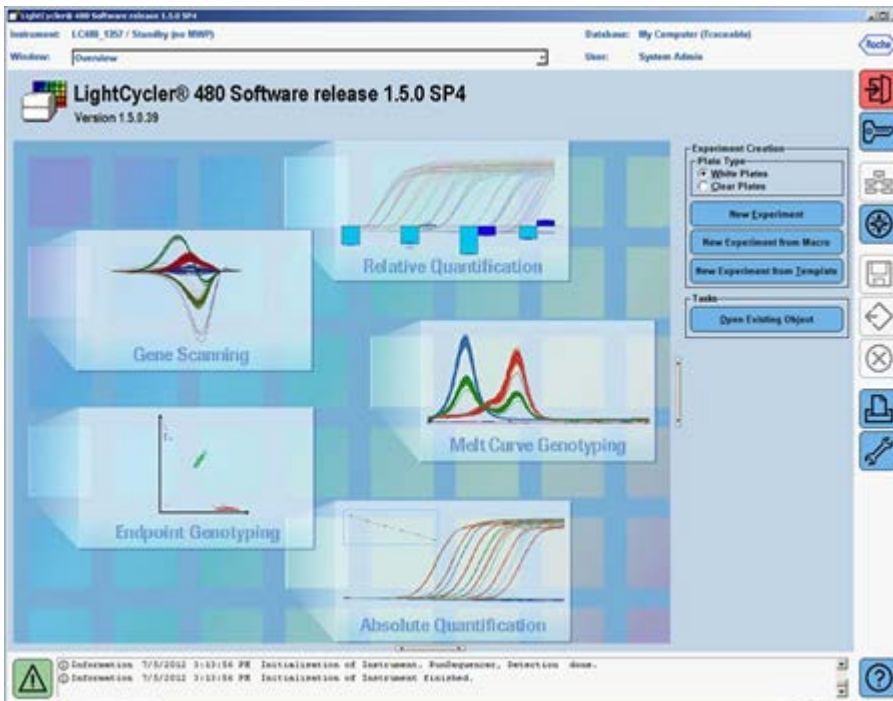


Figure 1. "Overview" window.

5. In the "Setup" area at the top of the "Run Protocol" tab (Figure 2), specify the following setup parameters:
 - "Detection Format": SYBR® Green 1
 - "Block Type": should show the correct block format (384 or 96)
 - "Plate ID": this field is optional
 - "Reaction Volume": 10 μ l for G plate or 25 μ l for F plate

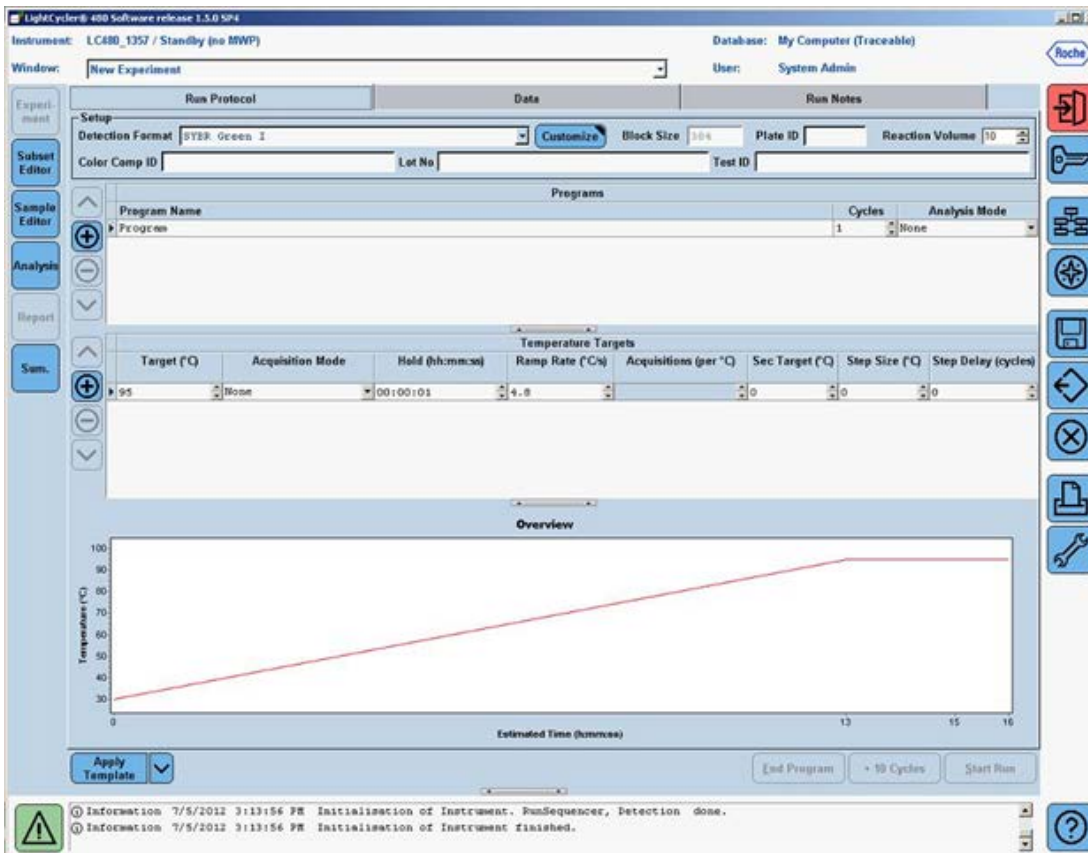



Figure 2. Initial run protocol window.

6. In the "Programs" section, click the  button twice to add two more program lines.
7. Click to change the "Program Name" of the first program to "Heat Activation." Leave the number of "Cycles" at "1", and leave the "Analysis Mode" as "None." In the "Program Temperature Targets" section, enter the values for the following parameters (see Figure 3):

Target (°C)	Acquisition mode	Hold (hh:mm:ss)	Ramp rate (°C/s)	Acquisition (per °C)	Sec target (°C)	Step size (°C)	Step delay (cycles)
95	None	00:10:00	4.8*		0	0	0

*This is the default ramp rate for 384-well block. The default ramp rate for 96-well block is 4.4°C/s.

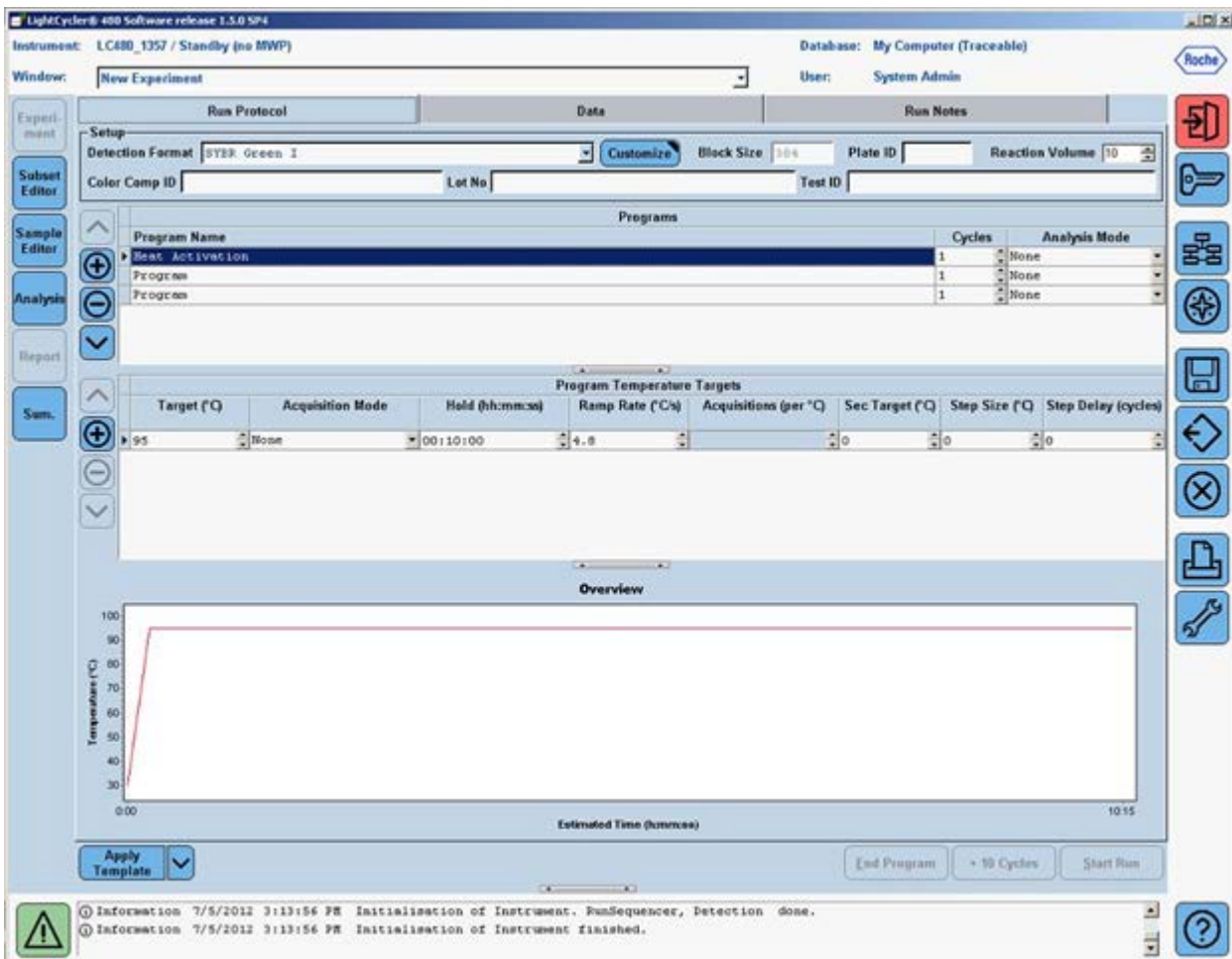



Figure 3. Setup of the first program — “Heat Activation.”

8. Click to change the “Program Name” of the second program to “PCR Cycling”. Change the number of cycles to “45”** and change the “Analysis Mode” to “Quantification”. In the “Program Temperature Targets” section, click the  button to add one more temperature target line. Enter the values for the following parameters (Figure 4):

Target (°C)	Acquisition mode	Hold (hh:mm:ss)	Ramp rate (°C/s)	Acquisition (per °C)	Sec target (°C)	Step size (°C)	Step delay (cycles)
95	None	00:00:15	1.0		0	0	0
70	Single	00:01:00	1.0		0	0	0

** The PCR is run for extra five cycles (i.e. 45 cycles) rather than the typical 40 cycles indicated in the handbook as this will allow the use of the Second Derivative Maximum method available with the LightCycler 480 software for data analysis. See Data Analysis section for further details.

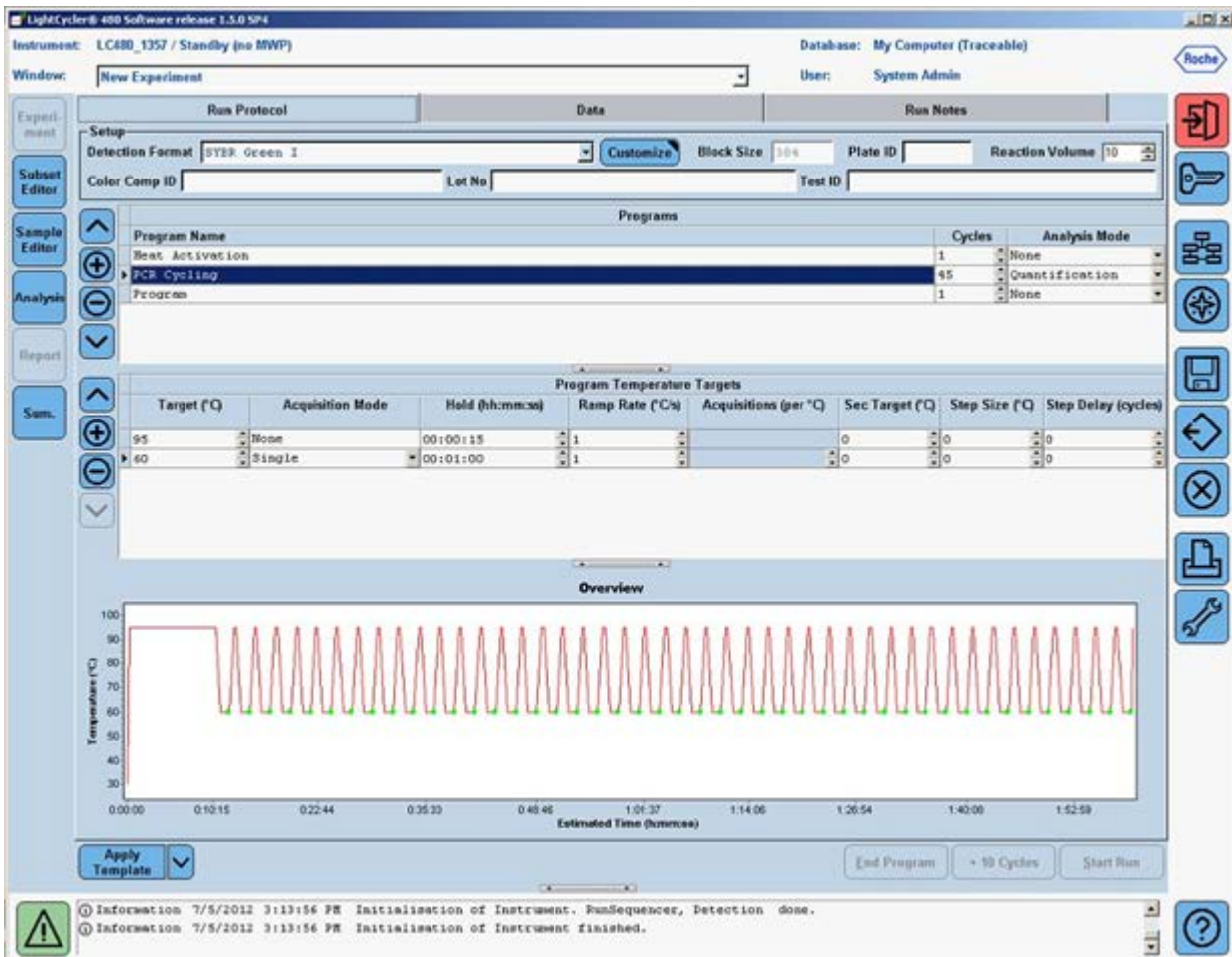



Figure 4. Setup of the second program — “PCR Cycling.”

- Click to change the “Program Name” of the third program to “Melt Curve.” Leave “Cycles” at “1” and change “Analysis Mode” to “Melting Curves.” In the “Temperature Targets” section, click the  button once to add one more temperature target line. Enter the values for the following parameters (Figure 5):

Target (°C)	Acquisition mode	Hold (hh:mm:ss)	Ramp rate (°C/s)	Acquisition (per °C)	Sec target (°C)	Step size (°C)	Step delay (cycles)
60	None	00:00:15	4.8*				
95	Continuous		0.03	20			

* This is the default ramp rate for 384-well block. The default ramp rate for 96-well block is 4.4 °C/s.

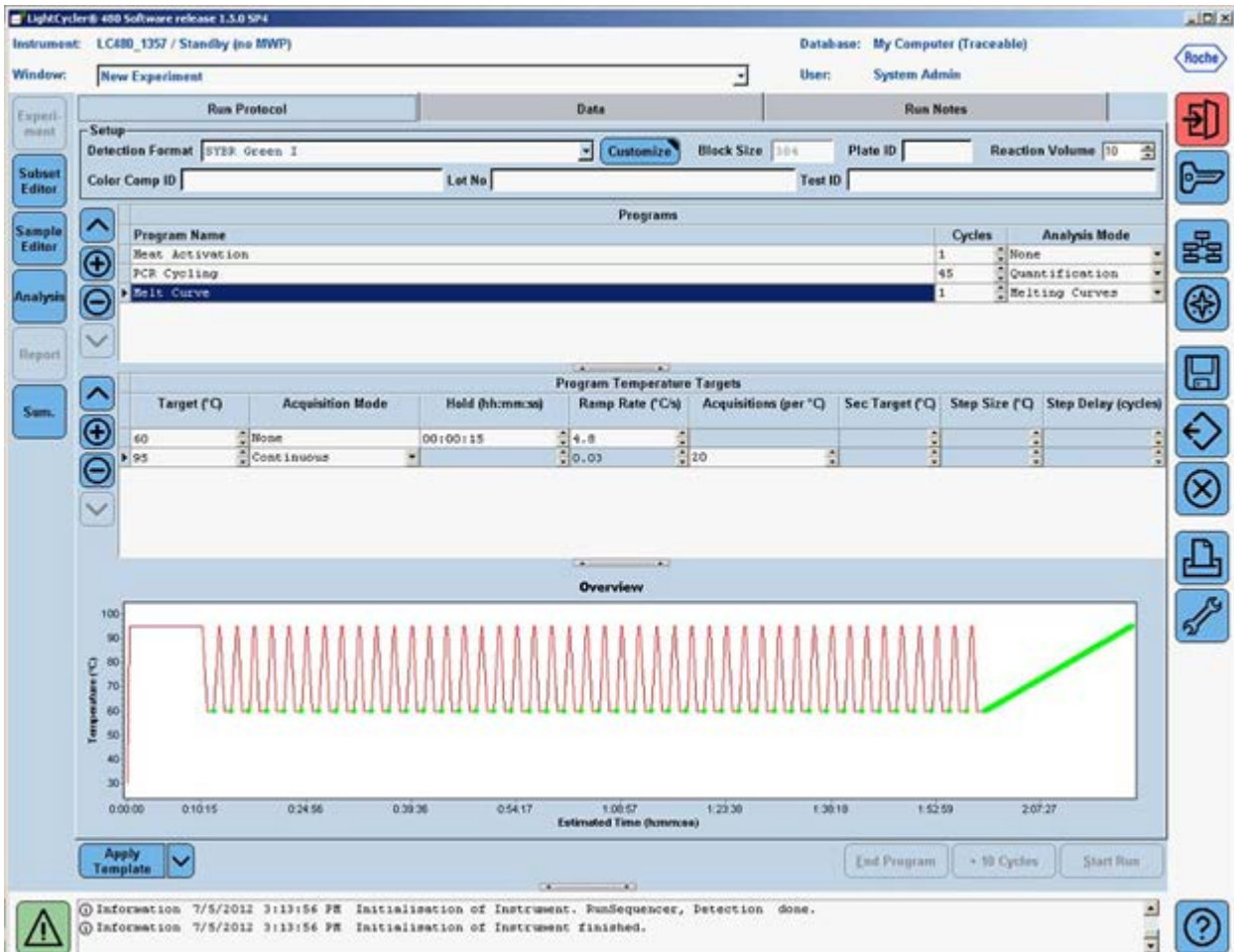


Figure 5. Setup of the third program — “Melt Curve.”

10. Click the down arrow button (▼) right next to the “Apply Template” button on the lower left corner of the screen; select the “Save As Template” button (Figure 6) to save the run template under the filename “CopyNum_PCR_Array_384_LC” if using the 384-well format or “CopyNum_PCR_Array_96_LC” for if using the 96-well format.

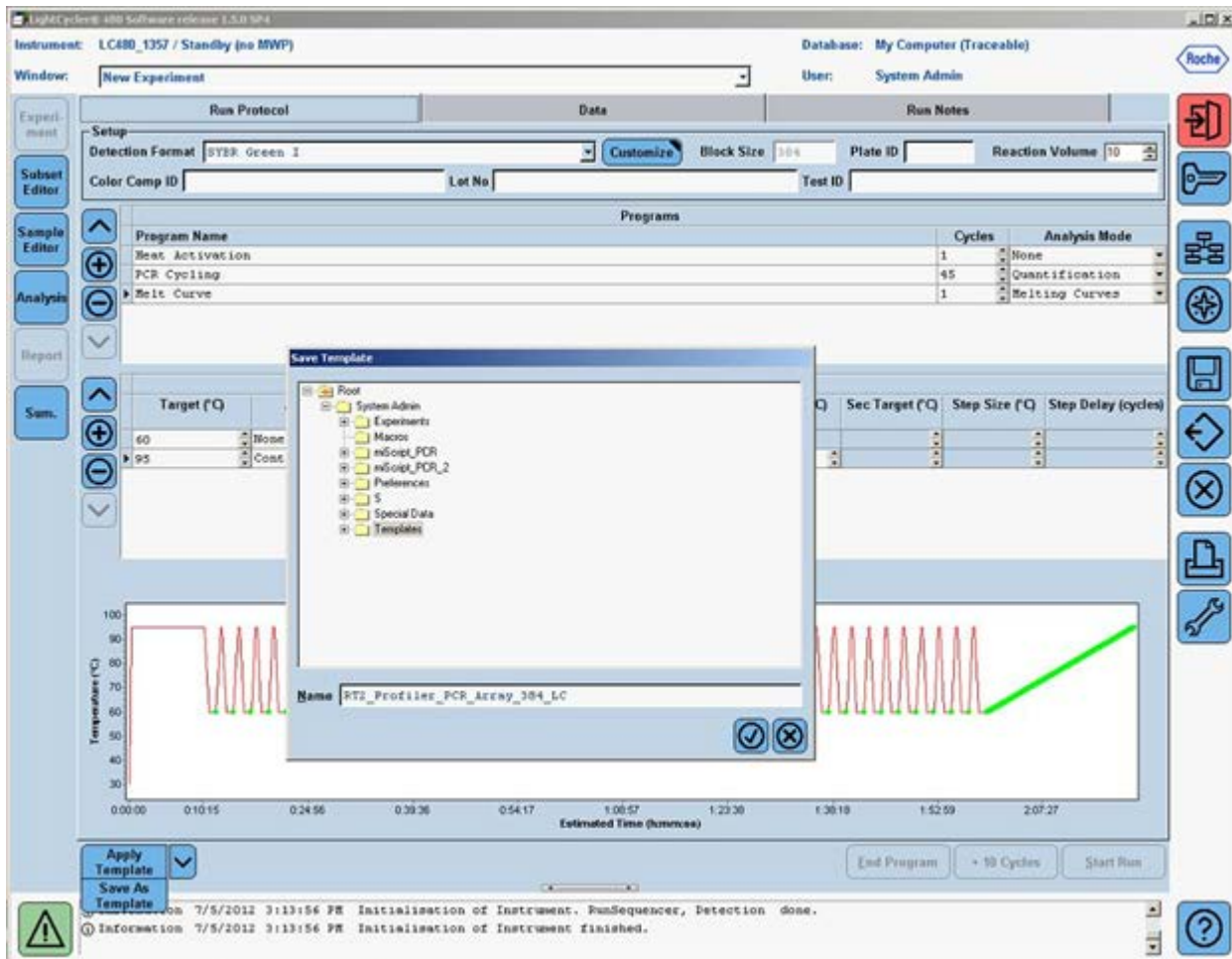


Figure 6. Saving the “Run Template” file.

Performing real-time PCR detection

11. After the PCR array is prepared and centrifuged, bring the plate to the LightCycler 480 instrument to load.
12. Make sure the correct thermal block (384-well block format for G plate or 96-well for F plate) is in place.
13. If the instrument is not on, turn it on using the main switch at the back of the instrument. Turn on the computer linked to the instrument and log on to Windows XP.
14. Start LightCycler 480 software.
15. Enter “Username” and “Password” when the “Login” dialog box pops up and click the button to proceed with the login. The “Overview” window will appear.
16. Wait for the two status LEDs on the front of the instrument to become stable. The left LED should become a steady green while the right LED should be a steady orange.

17. Press the \leftrightarrow open/close button on the front of the instrument (located next to the instrument status LEDs). The plate loading arm will slide out of the right side of the instrument. Place the PCR array plate into the frame of the loading arm with the flat edge of the array closest to the instrument and the edge with a beveled corner pointing away from the instrument.
18. Press the \leftrightarrow open/close button again to retract the loading arm. Wait for both of the status LEDs to turn steady green.
19. In the "Overview" window, click the "New Experiment" button on the right-hand side of the screen.
20. In the "Run Protocol" tab, click the "Apply Template" button on the lower left corner of the screen. Select and double click to open the appropriate previously saved "CopyNum_PCR_Array_384_LC" or "CopyNum_PCR_Array_96_LC" run template file.
21. Press the "Start Run" button on the lower right corner of the screen to initiate the run. When prompted, save the file under a new filename after which the run will begin.

Data analysis

1. In the "Navigator" window (Figure 7), find and open the run file to be analyzed.

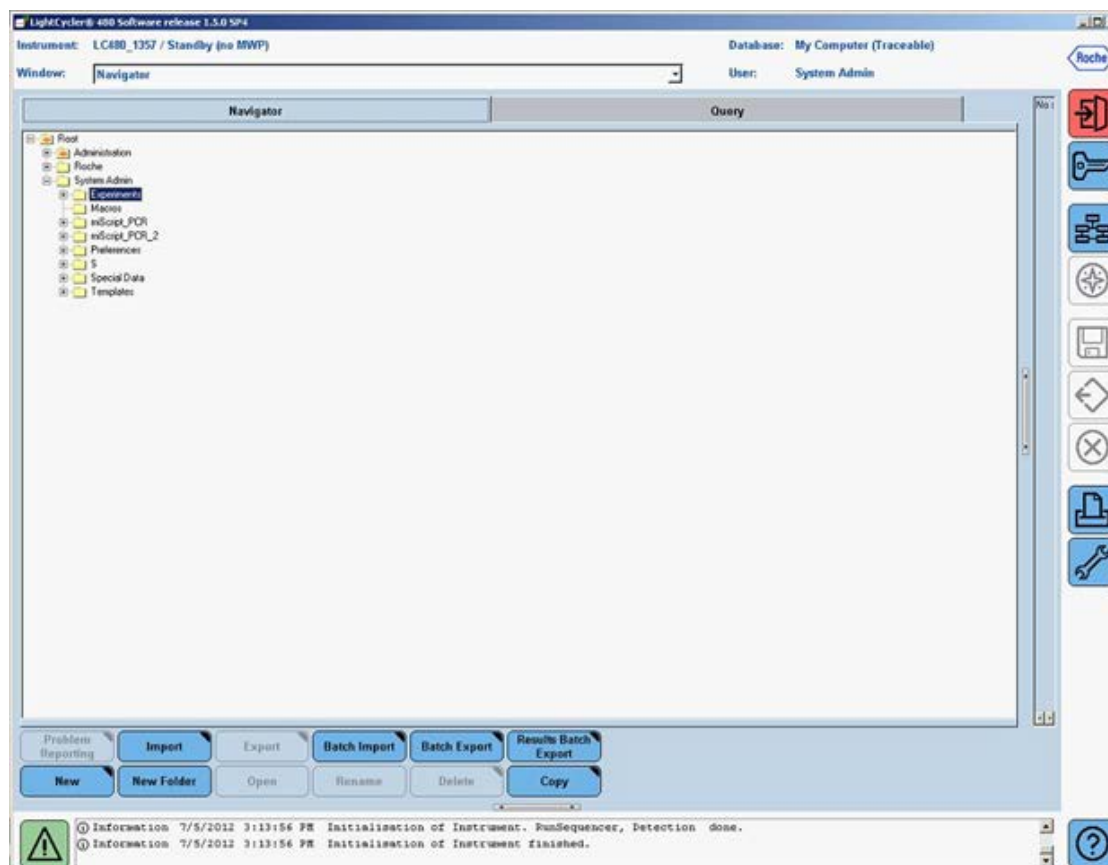



Figure 7. Opening a completed run file.

2. For data analysis using the LightCycler 480, use of the “Second Derivative Maximum” analysis method available in this software is highly recommended. This is an algorithm based on the kinetics of a PCR reaction. This method identifies the crossing point (Cp) of a PCR reaction as the point where the reaction’s fluorescence reaches the maximum of the second derivative of the amplification curve, which corresponds to the point where the acceleration of the fluorescence signal is at its maximum. Hence, this crossing point should always be located in the middle of the log-linear portion of the PCR amplification plot. The advantage of this analysis method is that it requires little user input and produces consistent results.
3. Obtaining the crossing point (Cp) cycle values: Once the selected run file is open, click the “Analysis” button on the left-hand side of the window. In the “Create new analysis” list, double-click to select “Abs Quant/2nd Derivative Max”. In the “Create new analysis” window that opens, make sure the Analysis Type is “Abs Quant/2nd Derivative Max” (Figure 8). Click  to confirm the selection.

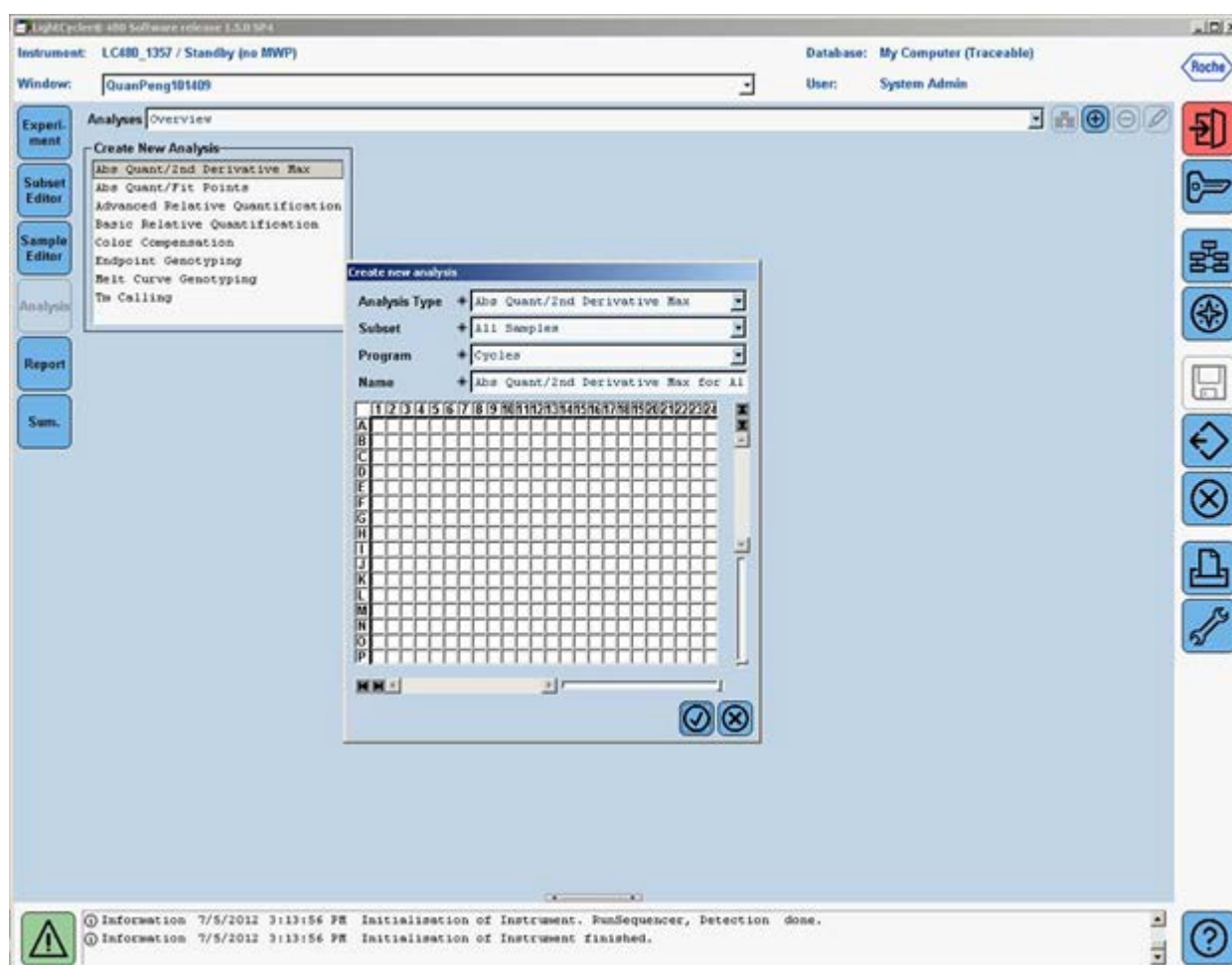


Figure 8. Setting up the analysis for the second derivative maximum.

- The "Analysis Window" with the amplification curves will appear (Figure 9). To proceed, click the down arrow button (▼) on the lower right corner of the screen to set the analysis to "High Confidence." Next, click the "Calculate" button to generate Cp values. The calculation may take a few minutes.

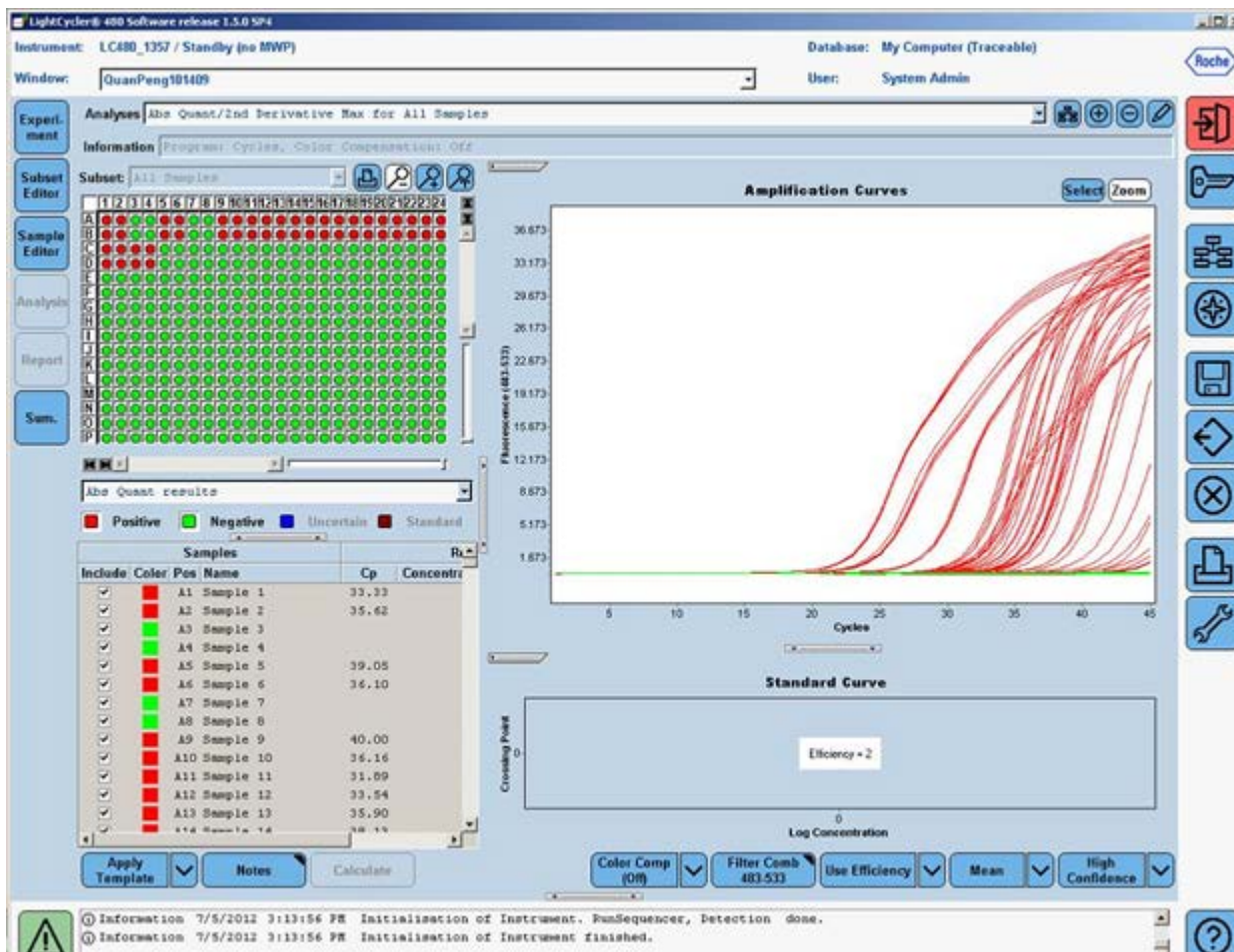



Figure 9. Obtaining the crossing point (Cp) cycle values at the second derivative maximum.

- Once the Cp values are generated, move the mouse over to the "Samples" window and click to highlight the samples result table. Right click the table and select "Export" button to export the data. A "Save table data" dialog box will appear (Figure 10). Enter a filename to save the data as a text file. Then click the  button on the right panel to save the second derivative maximum analysis and the Cp values as part of the run file.

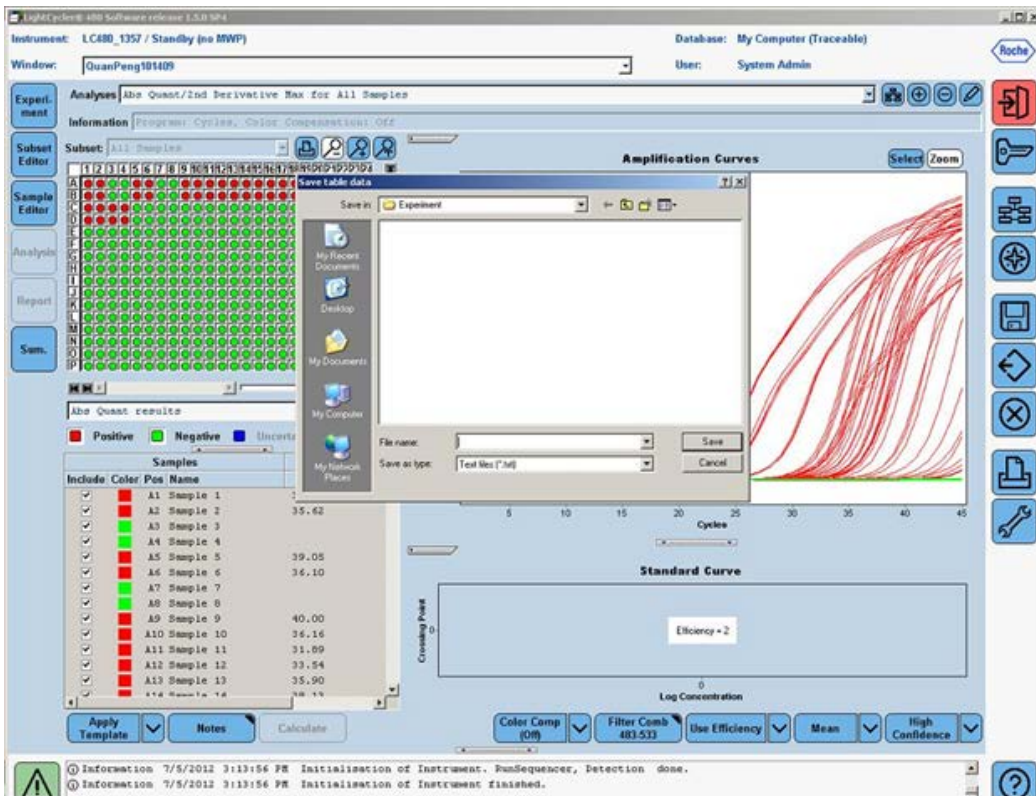




Figure 10. Exporting the Cp values.

- To proceed with the melt curve analysis, click the  button located on the right of the Analyses line at the top of the window. The Create new analysis dialog box will open (Figure 11). Select the "Tm calling" for the Analysis Type. Then click  to confirm the selection.

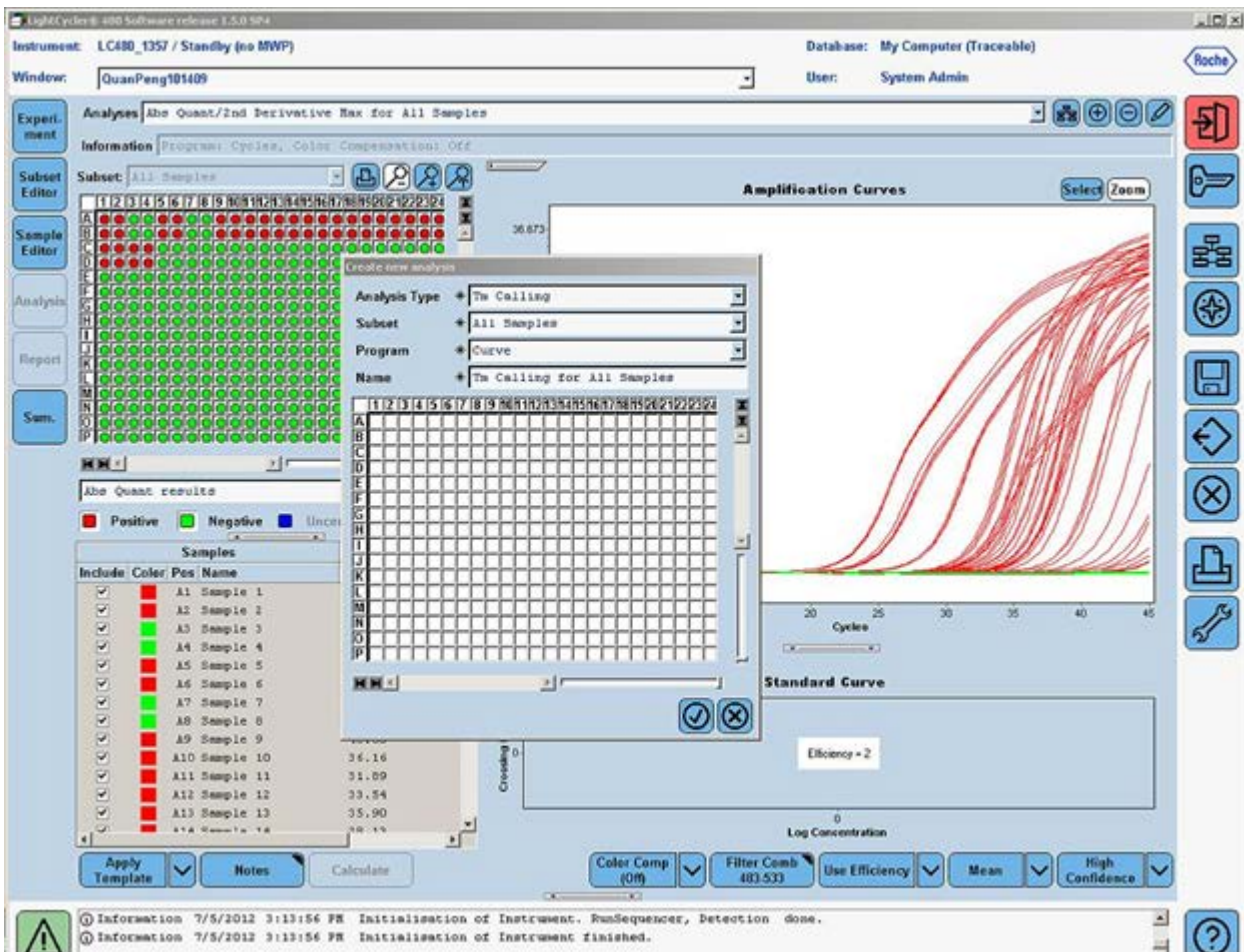


Figure 11. Setting up the melt-curve analysis.

7. The Analysis window with the raw melt curves will appear (Figure 12). To proceed, click the down arrow button (▼) on the lower right corner of the screen to set the analysis to "SYBR Green I Format". Next click the "Calculate" button. The calculation may take several minutes. Once the melting peaks and T_m values appear, check the specificity of each assay by ensuring the presence of a single melt peak in each well. Then click the (📄) button on the right panel to save the melt curve analysis as part of the run file.

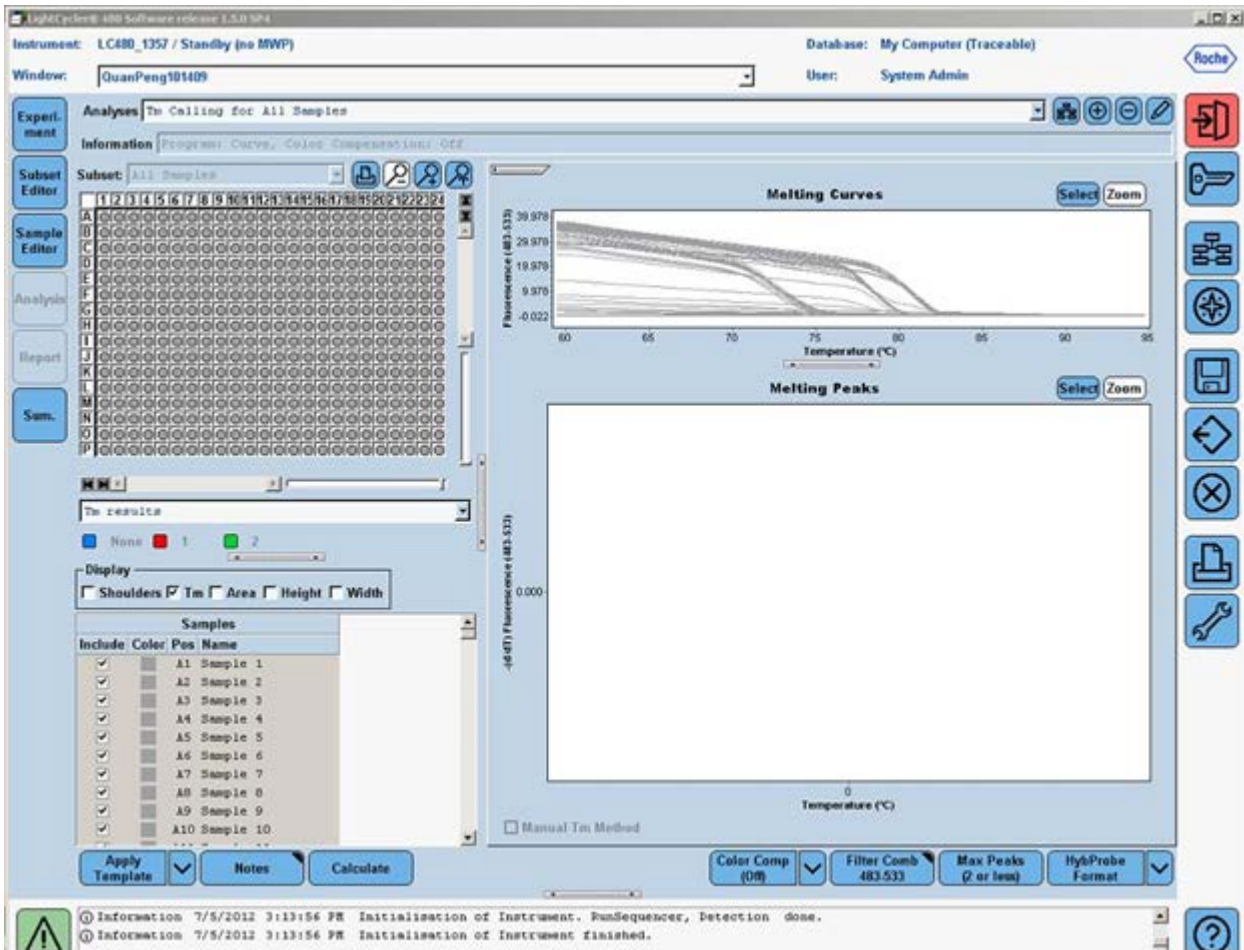


Figure 12. Generating melt-curve analysis.

- To save the melt peak values: Move the mouse over to the "Samples" window and click to highlight the result table. Right click the "Export" button to export the data. A "Save table data" dialog box will appear (Figure 13). Enter a filename to save the data as a text file.



Figure 13. Exporting the melt curve data.

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