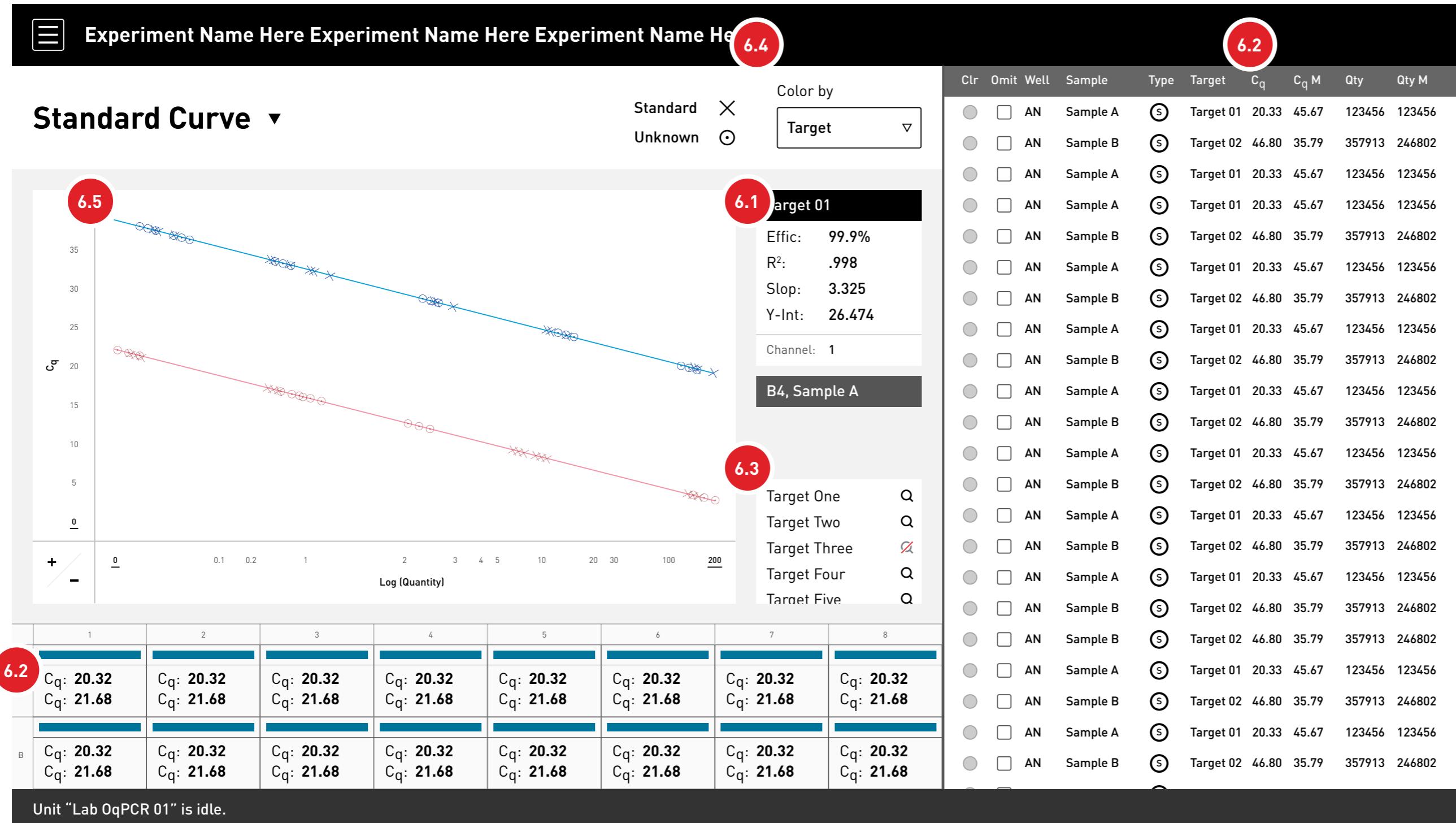


[US-REVA-6]

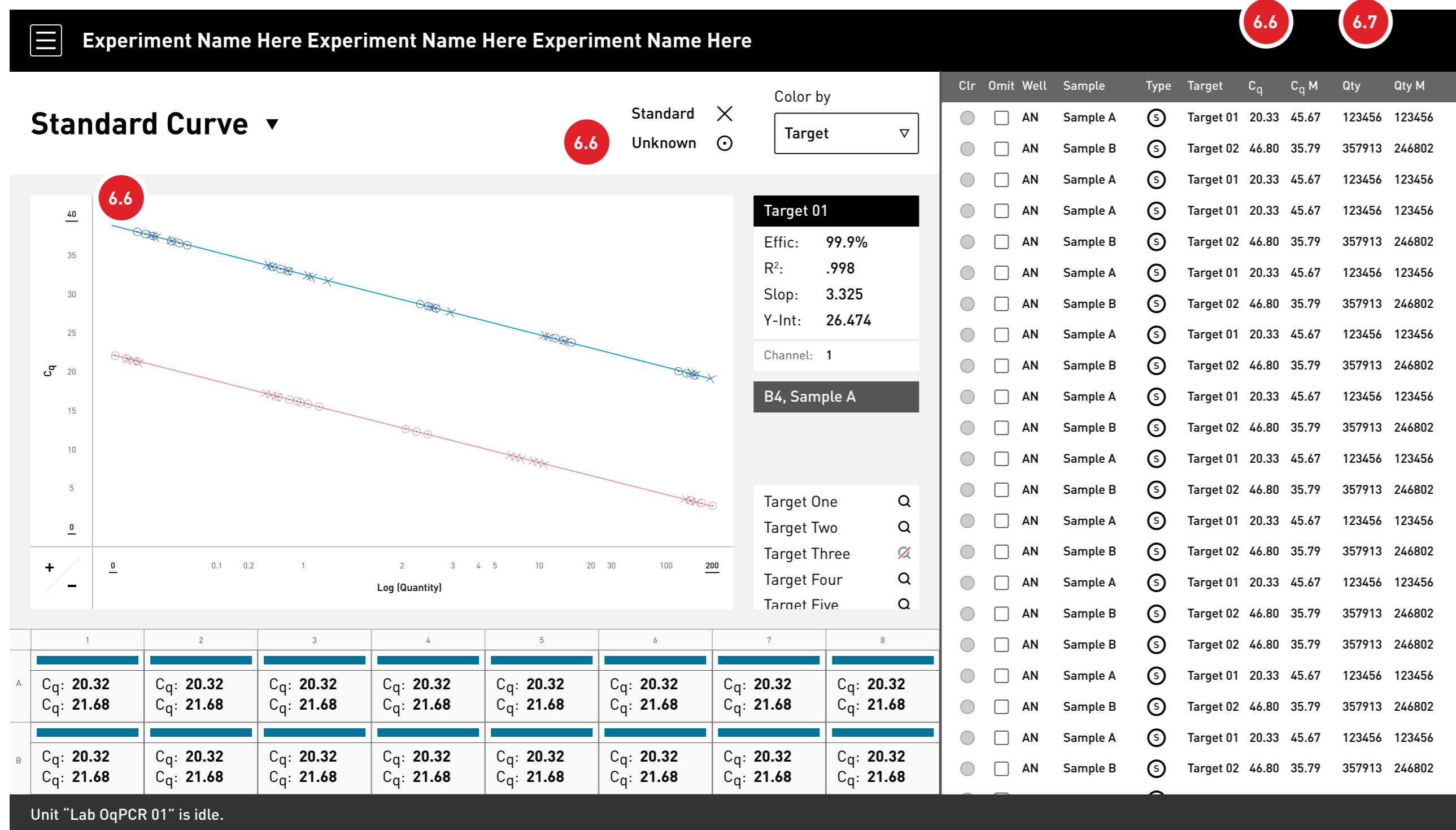
Standard Curve Output - Basic features

[US-REVA-6] Standard Curve Output - Basic features



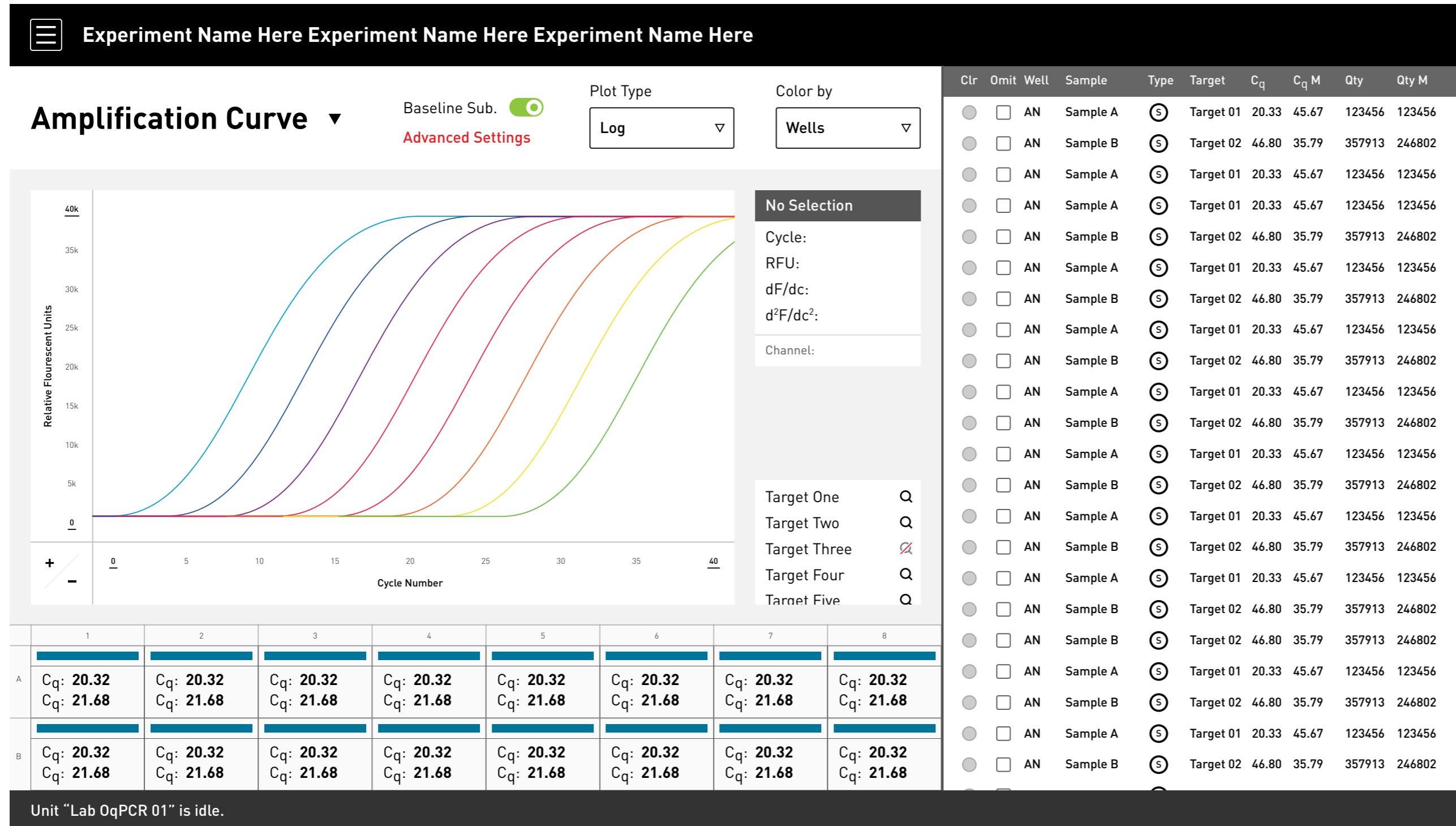
- 6.1. The following should be displayed for each curve:
 - a. Efficiency to 2 decimals (e.g. 102.50%), b. R2 to 3 decimals (e.g. 0.999), c. Slope to 3 decimals (e.g. -3.477), and d. Y-intercept to 2 decimals (e.g. 40.63)
 - 6.2. For each data point (per-target, per-well): a. The Cq should be displayed to 2 decimals (e.g. 20.32) and b. The quantity should be displayed to 6 digits of precision
 - 6.3. For standard curve and amplification curve plots, it should be possible to plot all targets, or just selected targets.
 - 6.4. For standard curve and amplification curve plots, it should be possible to color by sample, target, or well
 - 6.5. For each target which standards are defined within an experiment, the software shall interpolate and plot a standard curve. - a. The standard curve shall be plotted with a minimum of 2 data points of differing concentration, b. If there are more data points, all data points shall be used to interpolate a more accurate curve, and c. The curve equation, PCR efficiency, and R2 values shall be displayed to the user

[US-REVA-6] Standard Curve Output - Basic features



- 6.6. On a per-target basis, Unknown samples should be plotted on the standard curve, and the calculated concentration displayed, a. Calculated concentrations should be displayed both for each well, and for each replicate group.
- 6.7. For each replicate (per-target, per-sample): a. The Cq mean and Cq standard deviation should be displayed to 2 and 3 decimals respectively (e.g. 28.24 for mean, 0.074 for SD), and b. The quantity mean and standard deviation should be displayed to 6 digits of precision
- Data tables on the amplification and standard curve screens should be updated per design.
 - Amp Screen Follows*

[US-REVA-6] Standard Curve Output - Basic features



- Data tables on the amplification and standard curve screens should be updated per design.
 - *Amp Screen illustrates Data Table*

[US-REVA-17]

New plate layout - Basic features

[US-REVA-17]: New plate layout - Basic features

Experiment Name Here Experiment Name Here Experiment Name Here

Plate Layout

Using Standards from 112117 Sports Genome Silva

	1	2	3	4	5	6	7	8
A	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Positive Control + FAMHEXD
B	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Negative Control - FAMHEXD

17.4 Sample
Sample Alpha ▾

17.2 Ch.1 Target
Target Alpha ▾

Type
S U + -

Quantity
1,000,000 10×10^6

17.2 Ch.2 Target
Target Beta ▾

Type
S U + -

Quantity
1,000,000 10×10^6

Clear...
Choose ▾

Unit "Lab 0qPCR 01" is idle.

- The basic features for new plate layout will be implemented in this user story and the requirements are as follows:
- 17.1. The user shall be able to assign names to targets.
 - The current user flow calls for creating and editing Targets + Samples on the dedicated screen of the same name.
 - The user then edits additional attributes and assigns those existing Targets + Samples on the Plate Layout Screen
 - Target + Sample Screen on next page
- 17.2. On a per-well, per channel basis, the user can assign: a. Type (NTC, Positive Control, Standard, Unknown), b. Target and c. Concentration, if type is standard.
- 17.3. The user shall be able to assign names to samples.
 - See note above, next page
- 17.4. On a per-well basis, the user can assign a sample. Assigning the same sample to multiple wells indicates replicates.

[US-REVA-17]: New plate layout - 17.1 on T+S Screen

The screenshot shows the 'Experiment Name Here' screen with two main sections: 'Samples' and 'Targets'. Both sections have tables with columns for Name, Ch., and Color, and include an 'Add Sample' or 'Add Targets' button.

Samples		
Name	Ch.	Color
17.3 Default Sample, Appears on Empty State	1	■ Delete

Targets		
Name	Ch.	Color
17.1 Default Sample, Appears on Empty State	1	■ Delete

△ USE CASE:
Starting State/Clean Slate

Unit "Lab OqPCR 01" is idle.

- 17.1. The user shall be able to assign names to targets.
 - *The current user flow calls for creating and editing Targets + Samples on the dedicated screen of the same name.*
- The user then edits additional attributes and assigns those existing Targets + Samples on the Plate Layout Screen
- *Target + Sample Screen here*
- 17.3. The user shall be able to assign names to samples.
 - *See note above*

[US-REVA-18]

New plate layout - Advanced features

[US-REVA-18] New plate layout - Advanced features

Experiment Name Here Experiment Name Here Experiment Name Here

Plate Layout

Using Standards from 112117 Sports Genome Silva

	1	2	3	4	5	6	7	8
A	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Positive Control + FAMHEXD
B	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here S Abcdefghijk 4.9×10^{10} S GAPDH67890 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U Abcdefghijk 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Sample Name Here U GAPDH67890 4.9×10^{10}	Negative Control - FAMHEXD

Sample

Sample Alpha	Ch.1 Target Target Alpha	Type S U + -	Quantity 1,000,000 10×10^6	Clear... Choose
	Ch.2 Target Target Beta	Type S U + -	Quantity 1,000,000 10×10^6	

Unit "Lab 0qPCR 01" is idle.

- Once basic features for new plate layout have been implemented, the following advanced features should be implemented as a part of this user story
 - 18.1. On a per-experiment basis, the user shall be able to select a different experiment, from which standards should be used. This allows the user to re-use the same standard curve repeatedly to analyze samples,
 - User can only perform this action on the Target + Sample screen
 - 18.2 If this feature is used, it should not be possible to assign the Standard type to any wells in the experiment
 - Note following screen showing Target + Sample row statuses
 - After an experiment is run, it should be possible to modify anything about the plate layout, or change the experiment from which standards are imported, and results should be re-analyzed with the new settings. This allows the user to correct a mistake in their plate layout after the experiment is run.
 - Refer to "Experiment Run" header + footer in Component Library
 - When selecting experiments to import standards from, it should be possible to sort the experiments by name or ID. The default sort should be by ID descending.
 - See Import Standards Overlay after T + S Screen

[US-REVA-18] New plate layout - Advanced features

112117 Sports Genome Silva

18.2 Samples + Targets are Locked Standards have been imported to x dependent experiments

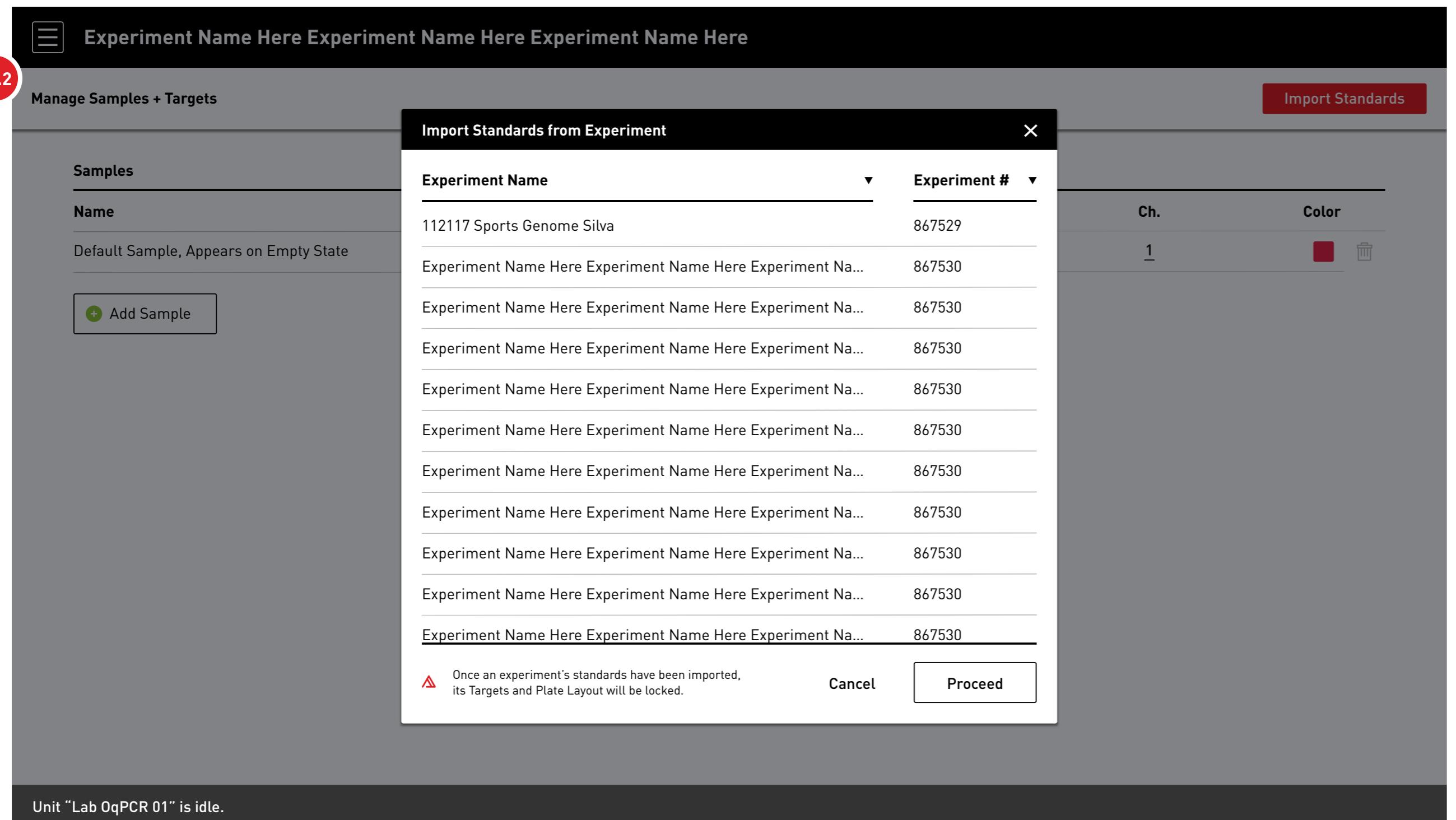
Samples			
Name	Ch.	Color	
Imported, Assigned	1		
Imported, Assigned	1		
Imported, Assigned	1		

Targets			
Name	Ch.	Color	
Imported, Assigned	1		
Imported, Assigned	1		
Imported, Assigned	1		
Imported, Not Assigned	1		

Unit "Lab OqPCR 01" is idle.

- 18.2 If this feature is used, it should not be possible to assign the Standard type to any wells in the experiment
 - Screen shows how Parent Experiment is no longer editable

[US-REVA-18] New plate layout - Advanced features

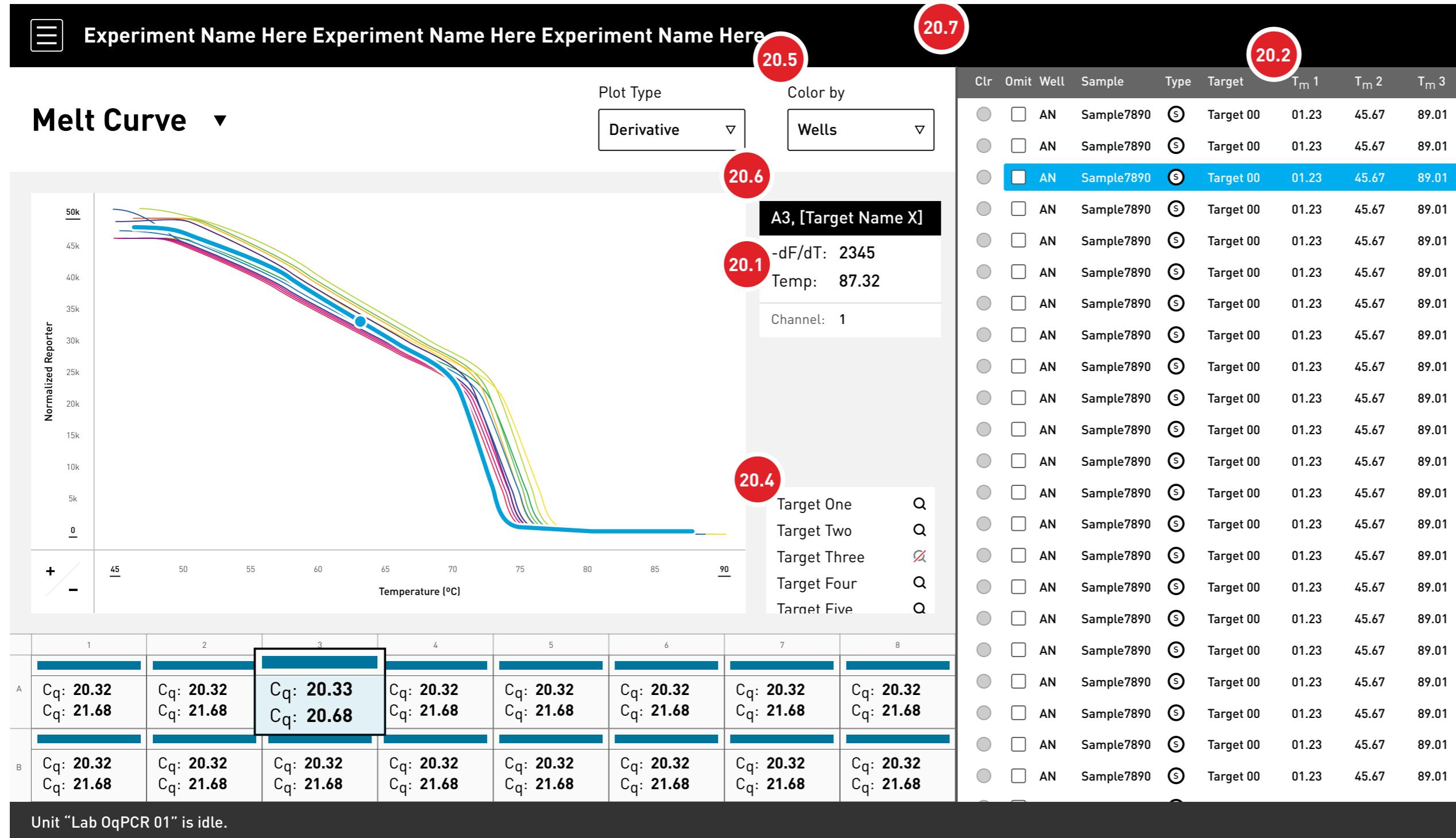


- When selecting experiments to import standards from, it should be possible to sort the experiments by name or ID. The default sort should be by ID descending.
 - *See Import Standards Overlay after T+S Screen*

[US-REVA-20]

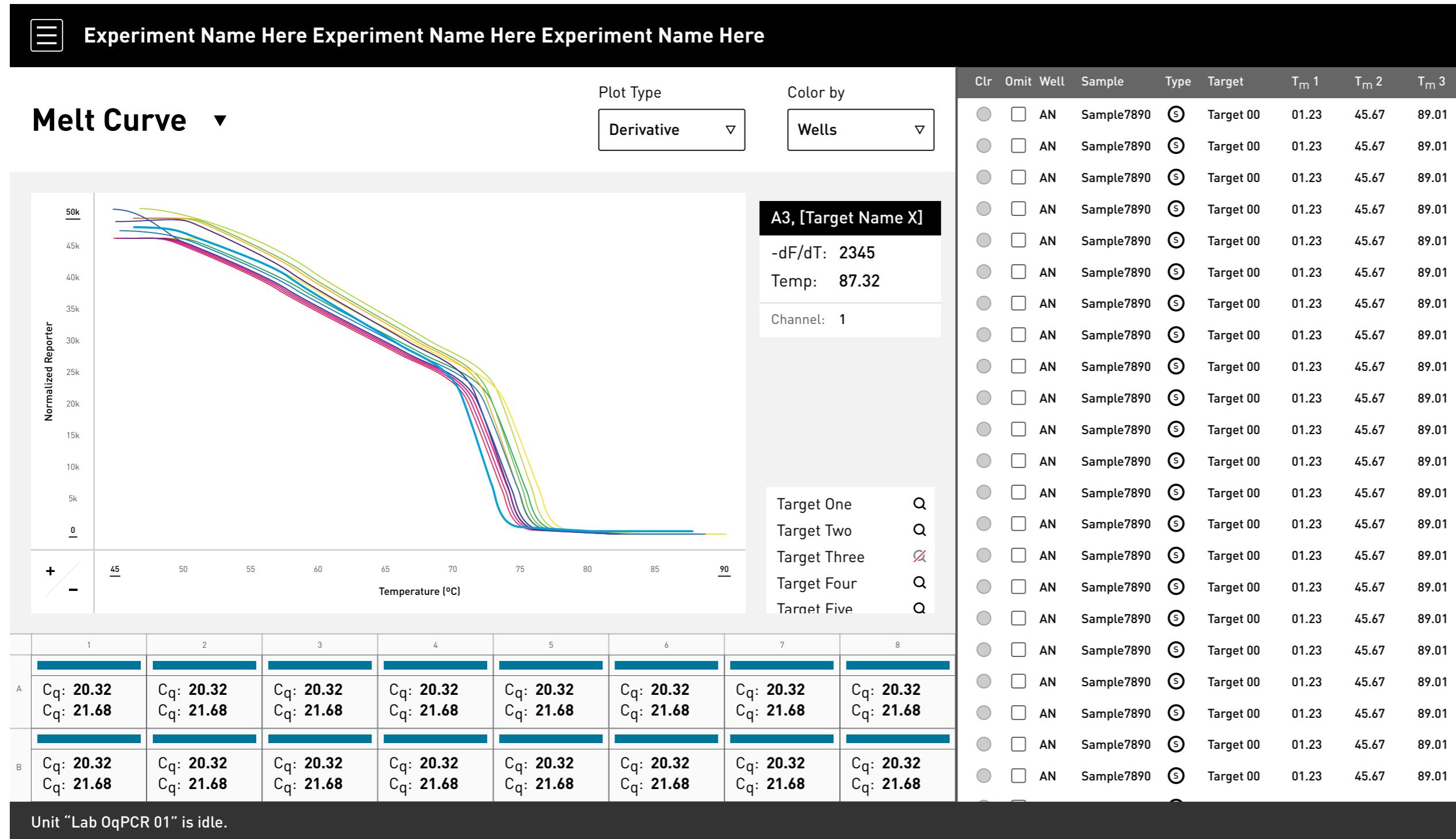
Melt curves should be displayed for both channels, multiple peaks should be called, and updated melt curve hover data box

[US-REVA-20] Melt curves should be displayed for both channels, multiple peaks should be called, and updated melt curve



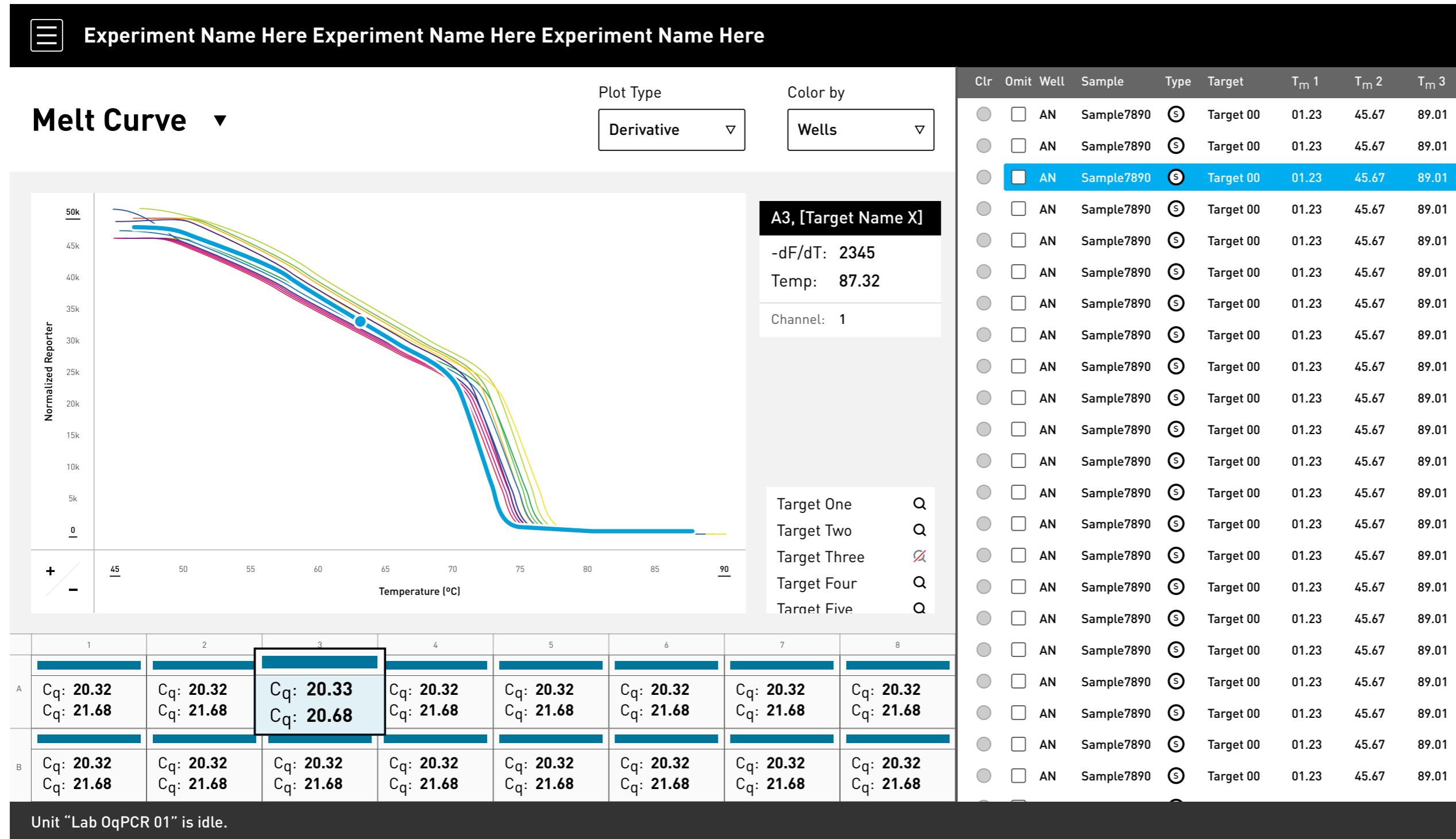
- Requirements:
- 20.1. Melt curves & Tm values should be calculated for all targets
- 20.2. The software should display Tm peaks for all targets
- 20.3. The software should display up to 4 Tm peaks per target per well, depending on how many are detected
 - *Need extra Tm Column?*
- 20.4. The user should be able to select which targets are displayed
- 20.5. The user should be able to color curves by target, well, or sample
- 20.6. The data box shown when the user selects and hovers over melt curves should be updated per the design.
- 20.7. The table shown on melt curve screen should be updated per design

[US-REVA-20] Melt curves should be displayed for both channels, multiple peaks should be called, and updated melt curve



- User has HOVERED over A3, (Light Blue line)
- Selected Box:
 - Title Bar turns Black from Mid-Grey
 - Live-updates as the user HOVERS over any line
- Graph Line States:
 - >>HOVERED Line: 2px, Moves to highest Z-Index

[US-REVA-20] Melt curves should be displayed for both channels, multiple peaks should be called, and updated melt curve

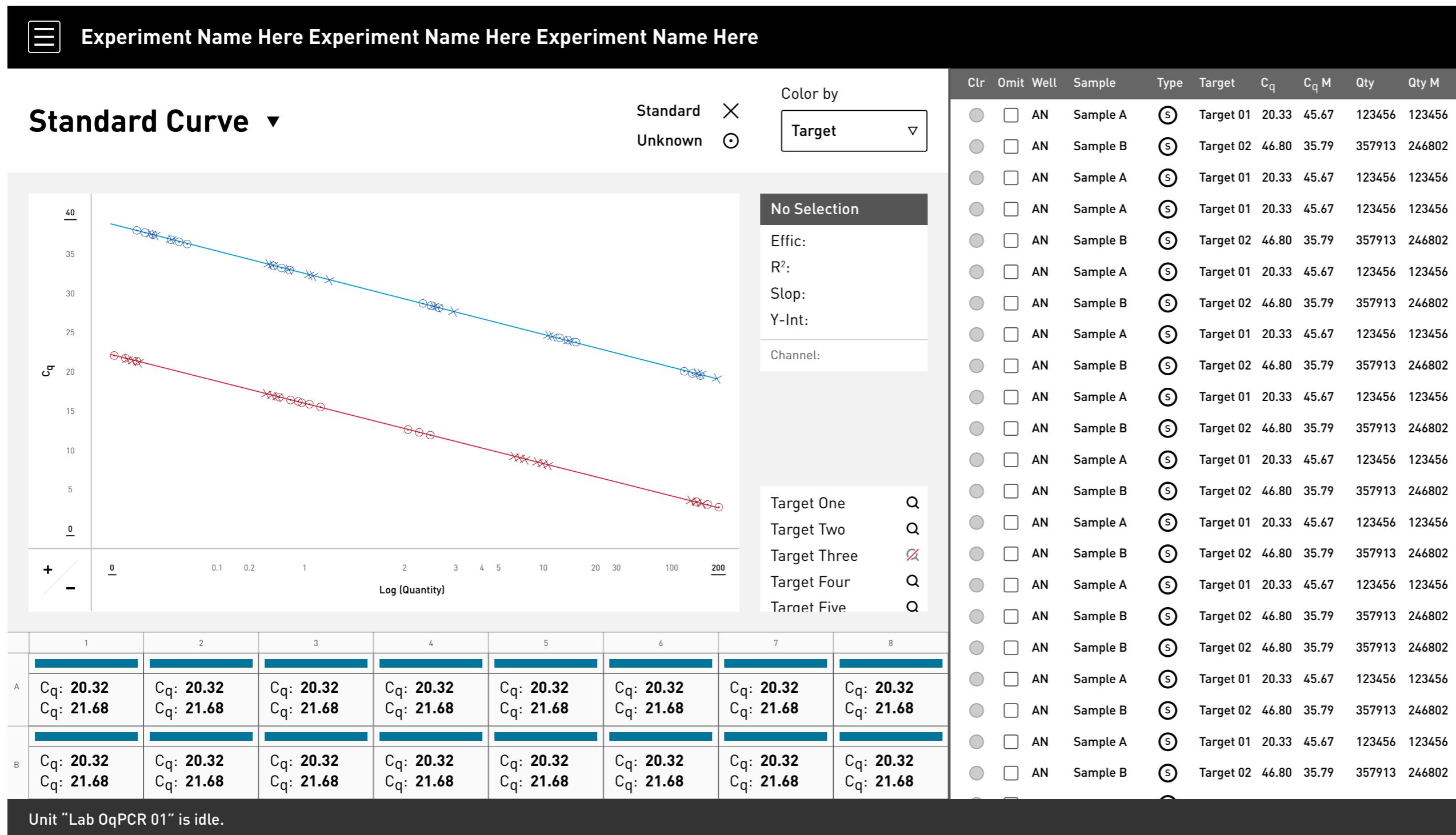


- User has SELECTED A3
- Selected Box:
 - Title Bar remains Black
 - Live-updates to the X + Y coordinates along the line even if they don't follow the line directly
 - Line stays SELECTED until the user clicks off
- Graph Line States:
 - >>SELECTED:
 - Line: 8px line weight, additional 2px white border, moves up to higher point of Z-index so it rests “above” all other graph lines
 - Dot: 10px, additional 2px white border, highest Z-index so it rests “above” SELECTED Line
- Table:
 - A3 shows SELECTED State: Highlights row, associated Line is in SELECTED state
 - Note: A User Clicking a Row triggers the same action as Clicking on a Line

[US-REVA-21]

Design for Standard Curve Output &
Display Melt Curves

[US-REVA-21] Design for Standard Curve Output



- General Standard Curve Notes

[US-REVA-21] Design for Display Melt Curves

- General Melt Curve Notes

[US-REVA-23]

Add data table screen and update nav
menu design

[US-REVA-23] Add data table screen and update nav menu design

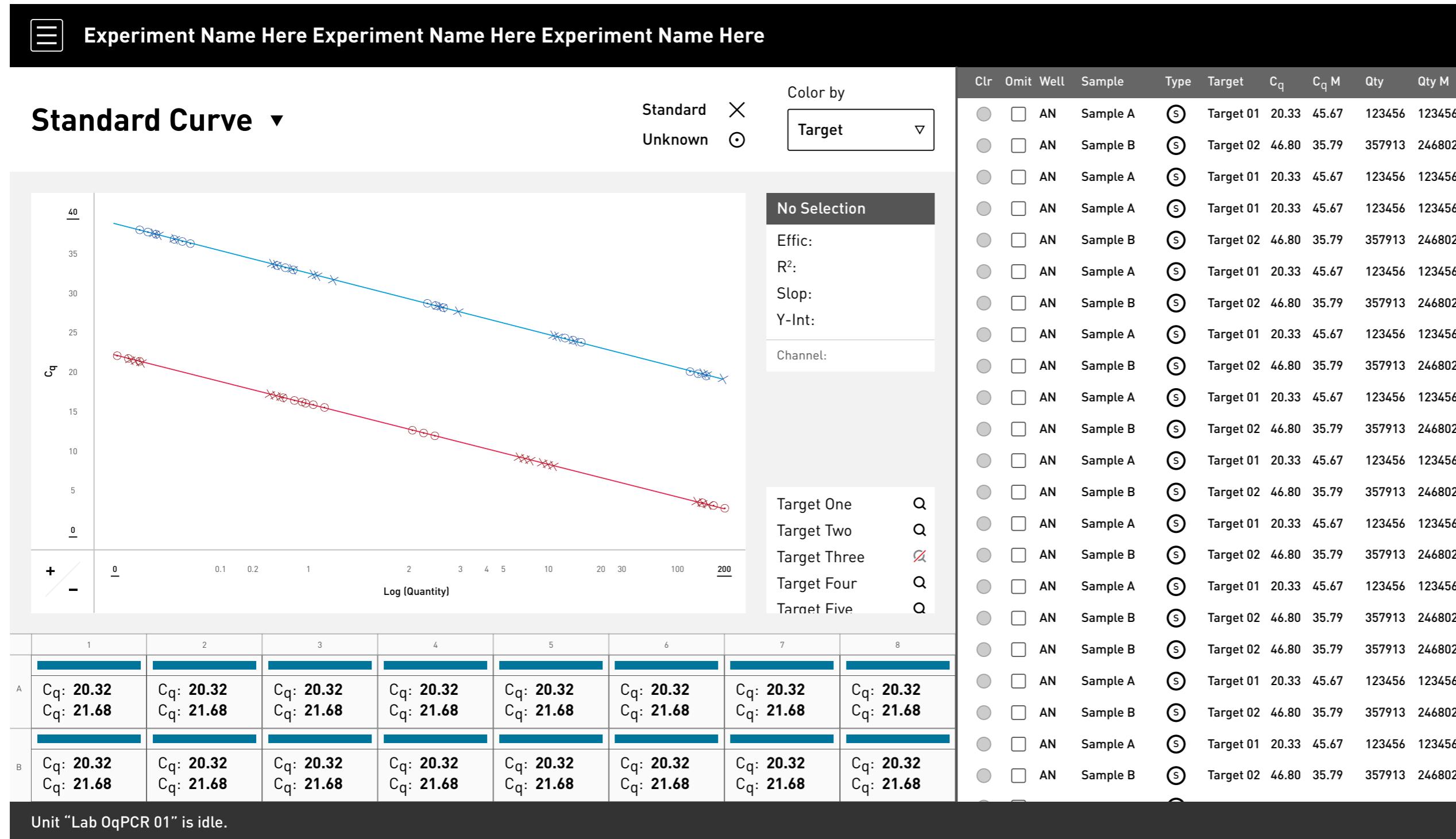
- Add a new data table screen, which will show additional tabular information we don't have room to show on the amplification, standard curve, and melt curve screens.
 -
 - Acceptance Criteria & Demos:
 - 1. User should be able to navigate to data table screen per design
 - 2. Data table screen formatted per design and displays experimental information accurately
 - 3. Nav menu should be updated to include slight design updates

[US-REVA-23] Add data table screen and update nav menu design

- Navigating to the Uber Table via the Experiment Menu

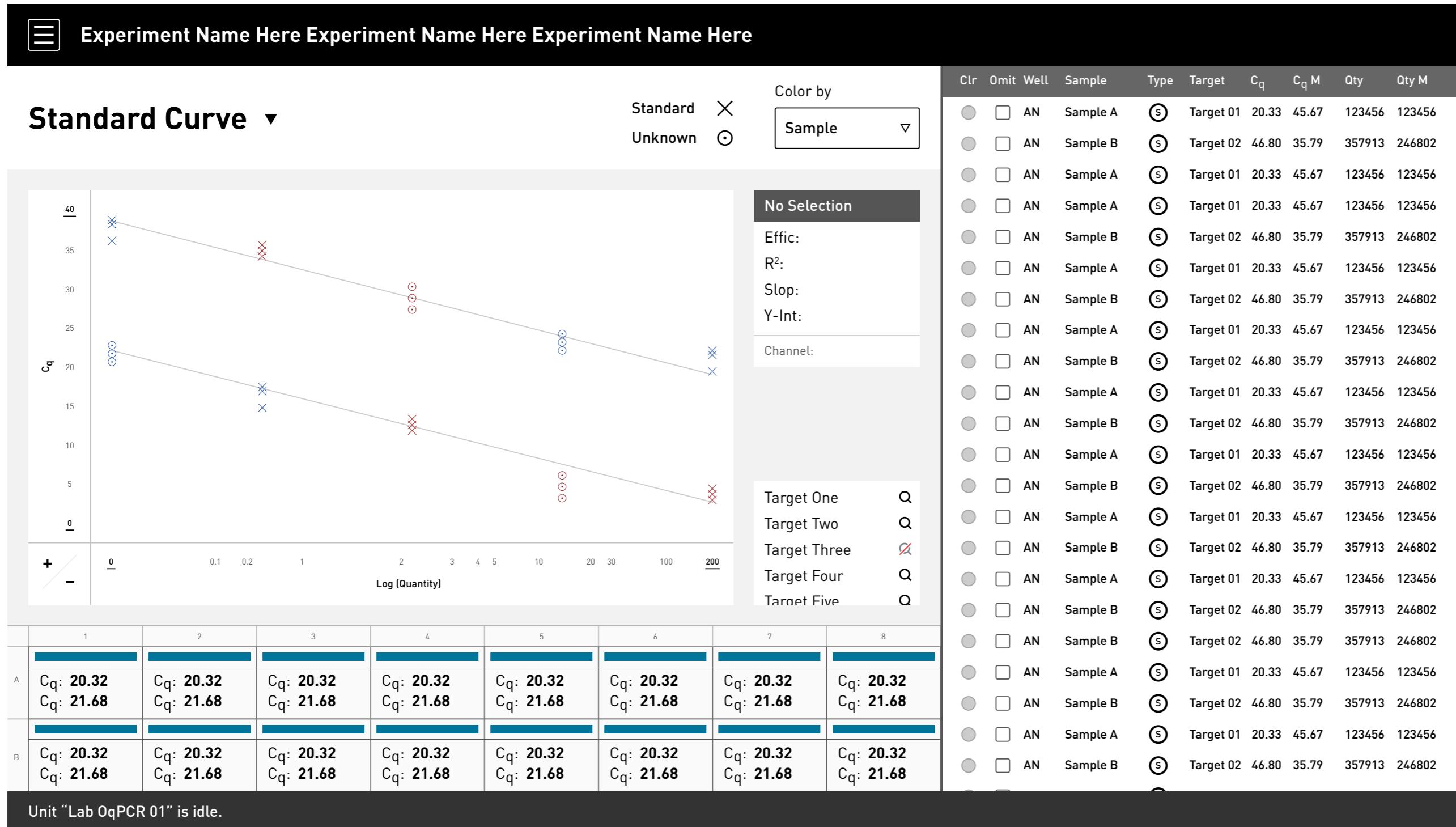
**[US-REVA-24] Standard Curve Output -
Curve Display**

[US-REVA-24] Standard Curve Output - Curve Display



- Standard curves should be displayed showing both the data points and the resulting line for all targets, including imported targets/standards.
-
- Acceptance criteria:
- 1. Demo plot of standard curve from 5 point experiment and display of line equation info
- 2. Demo plotting unknown data points and displaying calculated quantities
- 3. Demo experiments consisting of multiple targets in different wells, and thus multiple standard curves
- 4. Demo experiments consisting of multiple targets in the same wells, and thus multiple standard curves

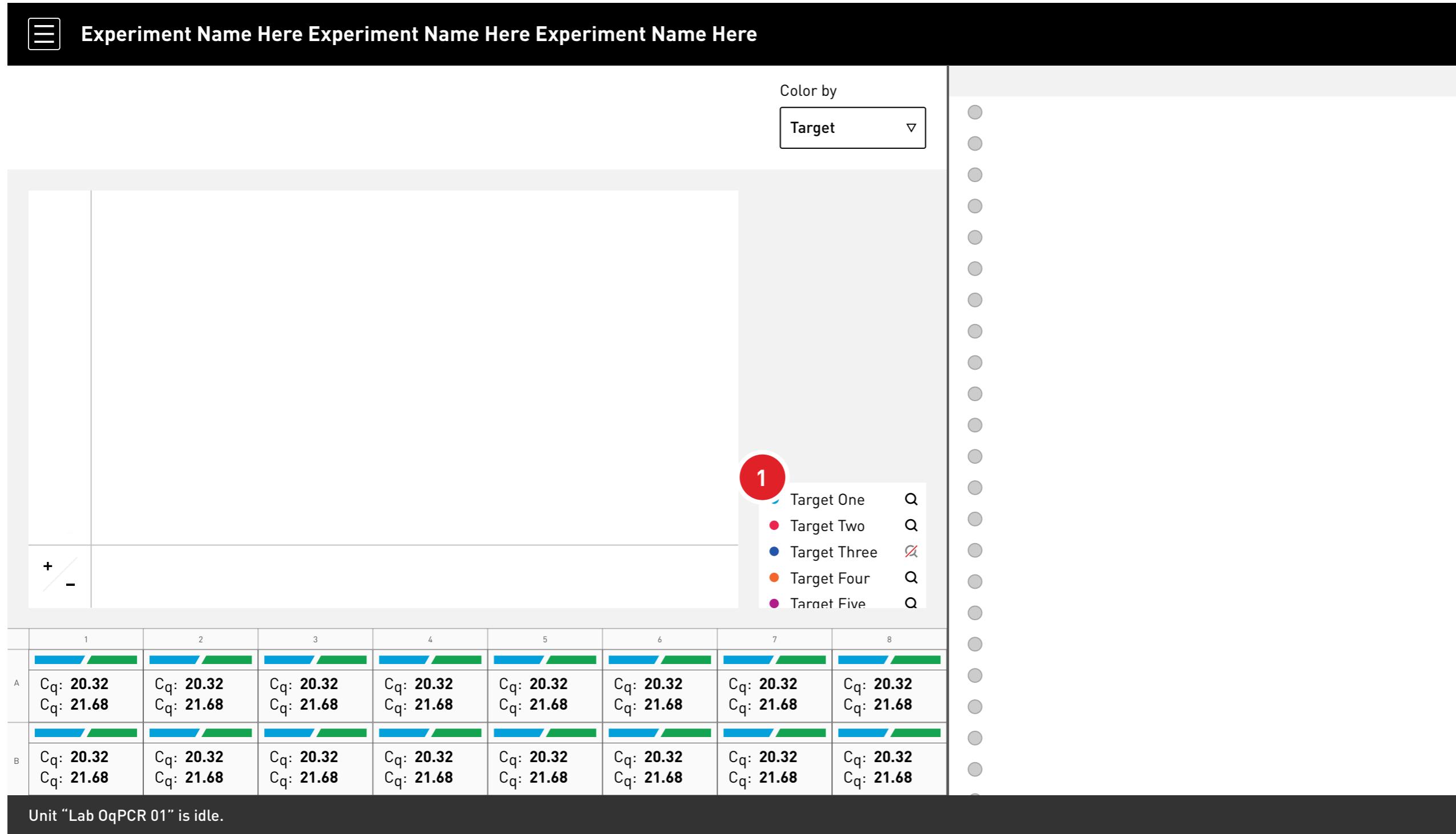
[US-REVA-24] Standard Curve Output - Curve Display



- Standard curves should be displayed showing both the data points and the resulting line for all targets, including imported targets/standards.
 -
 - Acceptance criteria:
 - 1. Demo plot of standard curve from 5 point experiment and display of line equation info
 - 2. Demo plotting unknown data points and displaying calculated quantities
 - 3. Demo experiments consisting of multiple targets in different wells, and thus multiple standard curves
 - 4. Demo experiments consisting of multiple targets in the same wells, and thus multiple standard curves

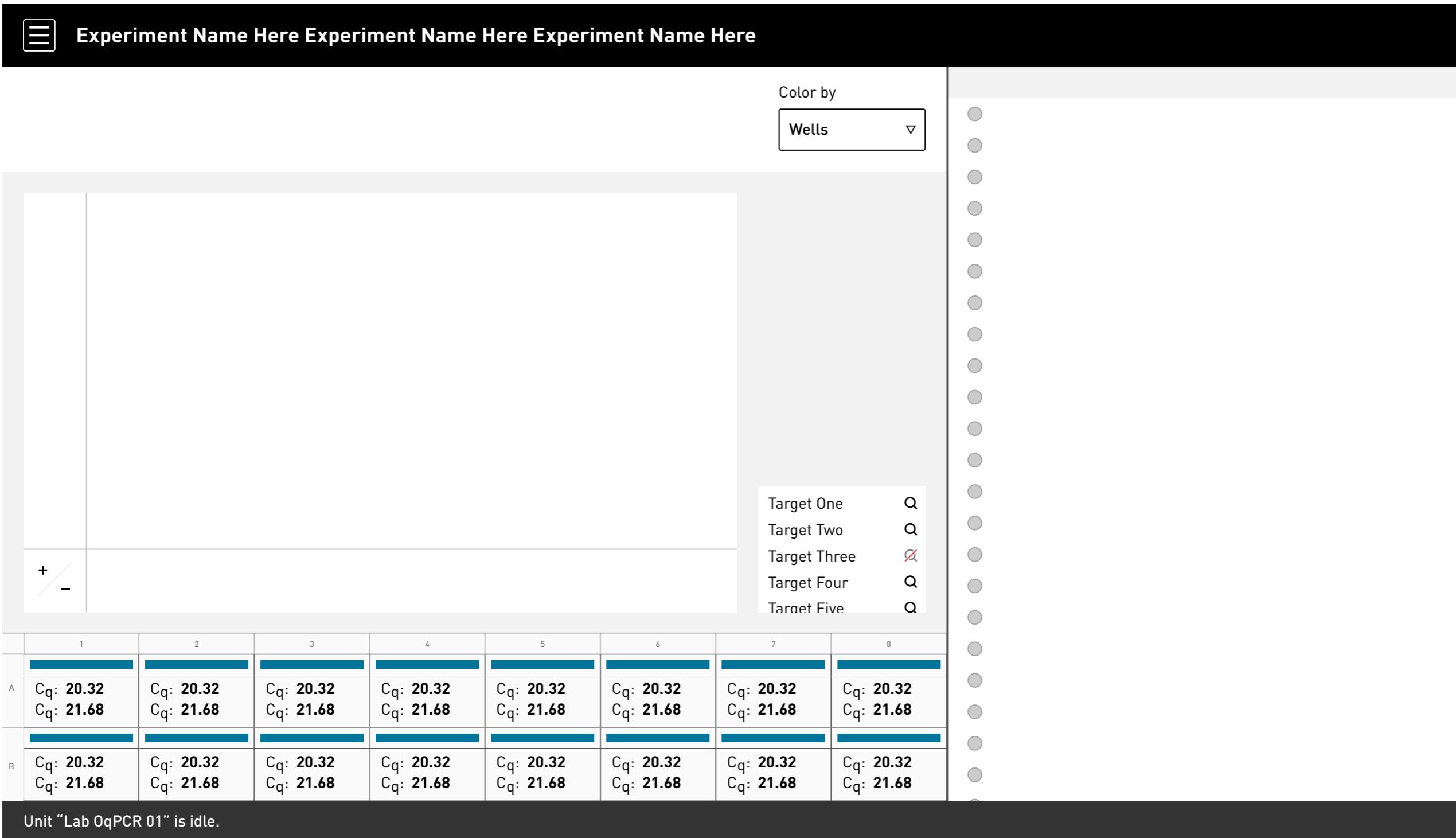
Graph Screen: “Color by” Dropdown Effects

Color by: Target



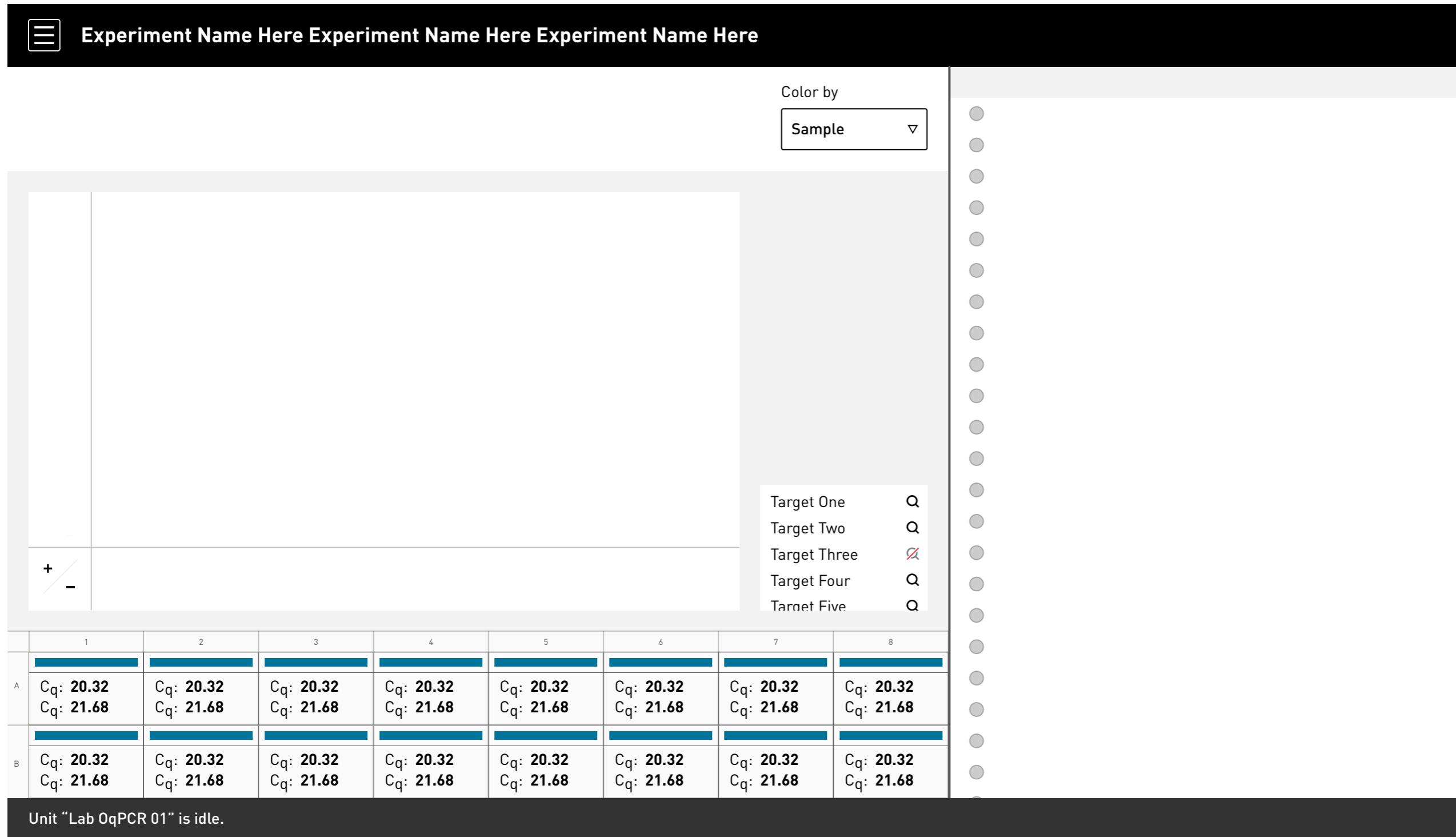
- Target On/Off Box (1)
 - Color Dots: On, Inherits color assigned to Target on "Targets + Samples Screen"
- Well Area
 - Split Color Bar:
 - Left Color: Ch. 1 Target Color (can be shown as empty if no Target assigned to Channel)
 - Right Color: Ch. 2 Target Color (can be shown as empty if no Target assigned to Channel)
- Table View
 - Table Color Dots: Inherits color assigned to Target on "Targets + Samples Screen"

Color by: Wells



- Target On/Off Box
 - Color Dots: Removed on this screen
- Well Area
 - Single Color Bar, Uses existing Well Color Spectrum
A1-8 + B1-8
- Table View
 - Table Color Dots: Uses existing Well Color Spectrum
A1-8 + B1-8

Color by: Sample



- Target On/Off Box
 - Color Dots: Removed on this screen
- Well Area
 - Single Color Bar, Inherits color assigned to Sample on "Targets + Samples Screen"
- Table View
 - Table Color Dots: Inherits color assigned to Sample on "Targets + Samples Screen"

Targets + Samples

Targets + Samples Flow

The screenshot shows the 'Targets + Samples Flow' interface. At the top, there is a dark header bar with three white horizontal bars on the left and the text 'Experiment Name Here Experiment Name Here Experiment Name Here' repeated three times in the center. Below the header is a light gray navigation bar with the text 'Manage Samples + Targets' on the left and 'Import Standards' on the right.

The main area is divided into two sections: 'Samples' on the left and 'Targets' on the right. Both sections have a header with three columns: 'Name', 'Ch.', and 'Color'. Under each section, there is a single row of data:

Name	Ch.	Color
Default Sample, Appears on Empty State	1	

Below each table is a button labeled '+ Add Sample' and '+ Add Targets' respectively.

In the bottom left corner of the main area, there is a light gray box containing a red triangle icon and the text 'USE CASE: Starting State/Clean Slate'.

Unit "Lab OqPCR 01" is idle.

- User visits Targets + Samples for first time
- Default Sample and Target row are populated by default

Targets + Samples Flow

Experiment Name Here Experiment Name Here Experiment Name Here

Manage Samples + Targets Import Standards

Samples		
Name	Ch.	Color
Default Sample, Appears on Empty State	1	 Delete

Targets		
Name	Ch.	Color
Default Sample, Appears on Empty State	1	 Delete

+ Add Sample

+ Add Targets

⚠ USE CASE:
User loads standards

- Same screen as above, Start of Import Standards Flow

Unit "Lab OqPCR 01" is idle.

Targets + Samples Flow

The screenshot shows a software interface for managing samples and targets. At the top, there is a dark header bar with three white horizontal bars on the left and the text "Experiment Name Here Experiment Name Here Experiment Name Here" repeated three times in the center. Below this is a light gray navigation bar with the text "Manage Samples + Targets" on the left and a red "Import Standards" button on the right.

The main area is divided into two sections: "Samples" on the left and "Targets" on the right. Both sections have a header with three columns: "Name", "Ch.", and "Color".

Samples Section:

Name	Ch.	Color
Default Sample, Appears on Empty State	1	

Targets Section:

Name	Ch.	Color
Default Sample, Appears on Empty State	1	

At the bottom of each section is a green-bordered button labeled "+ Add Sample" and "+ Add Targets" respectively.

USE CASE:

Starting State/Clean Slate

Unit "Lab OqPCR 01" is idle.

- User hovers over Import Standards Button (top right of screen)

Targets + Samples Flow

The screenshot shows a software interface for managing samples and targets. At the top, there are three tabs labeled "Experiment Name Here". Below them is a section titled "Manage Samples + Targets" with a "Samples" heading and a "Name" field containing "Default Sample, Appears on Empty State". A button labeled "+ Add Sample" is visible. In the bottom left corner, a box contains the text "⚠ USE CASE: Starting State/Clean Slate". At the bottom, a message states "Unit 'Lab OqPCR 01' is idle." A modal window titled "Import Standards from Experiment" is open in the center. It has two dropdown menus: "Experiment Name" (set to "112117 Sports Genome Silva") and "Experiment #" (set to "867529"). Below these are lists of experiments with their names and IDs. A warning message at the bottom left of the modal says: "⚠ Once an experiment's standards have been imported, its Targets and Plate Layout will be locked." There are "Cancel" and "Proceed" buttons at the bottom right of the modal. To the right of the modal, a table header is visible with columns "Ch." and "Color", showing the first row with "1" and a red square.

- User has clicked Load Standards, sees Previous Experiments modal
- Note: Message at bottom is very important. Once a user loads standards from an existing experiment, that prior experiment becomes a Parent Experiment.
 - Parent Experiments have locked Plate Layouts and [Targets and Samples].
 - This is currently the only warning about this data becoming locked the user will receive.

Targets + Samples Flow

The screenshot shows a software interface for managing samples and targets. At the top, there are three tabs labeled "Experiment Name Here". Below them is a section titled "Manage Samples + Targets" with a "Samples" header. A table lists a single sample named "Sample 01". To the right of the table is a button labeled "+ Add Sample". In the bottom left corner, there is a box containing the text "⚠ USE CASE: Starting State/Clean Slate". At the bottom of the screen, a message states "Unit 'Lab OqPCR 01' is idle." A modal dialog box titled "Import Standards from Experiment" is displayed in the center. It contains two dropdown menus: "Experiment Name" (set to "112117 Sports Genome Silva") and "Experiment #" (set to "867529"). Below these dropdowns is a list of experiment names, with the first item ("112117 Sports Genome Silva") highlighted with a blue background. At the bottom of the dialog, there is a warning message: "⚠ Once an experiment's standards have been imported, its Targets and Plate Layout will be locked." followed by "Cancel" and "Proceed" buttons.

- User has selected Experiment, ready to load

Targets + Samples Flow

☰ 112117 Sports Genome Silva

Samples + Targets are Locked Standards have been imported to x dependent experiments

Samples			
Name	Ch.	Ch.	Color
Imported, Assigned	1	🔒	(A)
Imported, Assigned	1	🔒	(A)
Imported, Assigned	1	🔒	(A)

Targets			
Name	Ch.	Ch.	Color
Imported, Assigned	1	🔒	(A)
Imported, Assigned	1	🔒	(A)
Imported, Assigned	1	🔒	(A)
Imported, Not Assigned	1	🔒	

- NOW-PARENT EXPERIMENT PAGE, NOT DIRECTLY A PART OF THIS FLOW. FOR REFERENCE ONLY
- Top Left: User is told why this screen is now locked
 - Number of experiments using this data is optional for this iteration
- Important: “Add Target/Sample” Buttons are no longer available here
- Symbol Legend:
 - Lock: This row has been imported, cannot be edited or deleted as an individual row
 - A in a Ring: Assigned to a well.
 - Trash: This row can be individually deleted (not applicable on this screen)

⚠ USE CASE:
Starting State/Clean Slate

Unit “Lab QPCR 01” is idle.

Targets + Samples Flow

The screenshot shows the "Manage Samples + Targets" interface. At the top, there is a title bar with three horizontal lines and the text "Experiment Name Here Experiment Name Here Experiment Name Here". Below the title bar, the main area has two sections: "Samples" and "Targets".

Samples

Name	Ch.	Color
Imported, Assigned	1	
Imported, Assigned	1	
Imported, Assigned	1	

Targets

Name	Ch.	Color
Imported, Assigned	1	
Imported, Assigned	1	
Imported, Assigned	1	
Imported, Not Assigned	1	

At the bottom of each section is a button labeled "+ Add Sample" or "+ Add Targets". Above the tables, there is a message "Using Standards from 112117 Sports Genome Silva". To the right of the tables are two buttons: "Clear Imported..." and "Import Standards".

- User has loaded standards from the selected experiment
- “Manage Targets + Samples” Title Bar
 - Shows name of Parent Experiment
 - “Clear Imported...” removes loaded standards from this screen, unmaps them from wells
- “Import Standards” repeats the previous process and **REPLACES** currently loaded standards. Importing a second time does NOT stack data

⚠ USE CASE:
Starting State/Clean Slate

Unit “Lab OqPCR 01” is idle.

Targets + Samples Flow

☰ Experiment Name Here Experiment Name Here Experiment Name Here

Manage Samples + Targets
Using Standards from 112117 Sports Genome Silva
Clear Imported...
Import Standards

Samples		
Name	Ch.	Color
Imported, Assigned	1	🔒 A
Imported, Assigned	1	🔒 A
Imported, Assigned	1	🔒 A

+ Add Sample

Targets		
Name	Ch.	Color
Imported, Assigned	1	🔒 A
Imported, Assigned	1	🔒 A
Imported, Assigned	1	🔒 A
Imported, Not Assigned	1	🔒
Man. Created Target is Assigned	1	A
Manually Created, Ch. Asgnd. by Default	1	A
User is Changing Ch.	1 2	A
Man. Created Target is Assigned	1	A
Man. Created Target is Assigned	2	A
Man. Created Target is Assigned	1	A
Man. Created Target is Assigned	1	A

+ Add Targets

⚠ **USE CASE:**
Starting State/Clean Slate

Unit "Lab QPCR 01" is idle.

- User has manually created Standards in addition to the imported data
- Symbol Legend:
 - Lock: This row has been imported, cannot be edited or deleted as an individual row
 - A in a Ring: Assigned to a well.
 - Trash: This row can be individually deleted
 - If assigned, user must accept warning of Delete Assigned Modal (screen available)

Targets + Samples Flow

☰ Experiment Name Here Experiment Name Here Experiment Name Here

Manage Samples + Targets Using Standards from 112117 Sports Genome Silva Clear Imported... Import Standards

Samples		
Name	Ch.	Color
Imported, Assigned	1	
Imported, Assigned	1	
Imported, Assigned	1	

Add Sample

⚠ USE CASE:
Starting State/Clean Slate

Targets		
Name	Ch.	Color
Imported, Assigned	1	
Imported, Not Assigned	1	
Man. Created Target is Assigned	1	
Manually Created, Ch. Asgnd. by Default	1	
User is Changing Ch.	1 2	
Man. Created Target is Assigned	1	
Man. Created Target is Assigned	2	
Man. Created Target is Assigned	1	
Man. Created Target is Assigned	1	
Man. Created Target is Assigned	2	
Man. Created Target is Assigned	1	
Man. Created Target is Assigned	1	

Add Targets

Unit "Lab OqPCR 01" is idle.

- User has added enough Targets to require scrolling
- As this point is reached, additional rows stack above the “Add Target” button. “ADD SAMPLE/TARGET” BUTTON IS ALWAYS ON-SCREEN WITHOUT NEEDING TO SCROLL