applied biosystems

AccuSEQ™ Real-Time PCR Software v3.1

USER GUIDE

Windows™ 10 Operating System

for use with:
QuantStudio™ 5 Real-Time PCR Instrument
SEQ family of detection kits

Catalog Numbers A48509 and A48592
Publication Number 100094287
Revision G

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Revision history: Pub. No. 100094287

Revision	Date	Description
G	8 August 2022	Update for the ViralSEQ™ Lentivirus Proviral DNA Titer Kit (Cat. No. A53561).
F	16 February 2022	Update for the ViralSEQ™ Lentivirus Physical Titer Kit (Cat. No. A52597).
E	21 September 2021	Update for the resDNASEQ™ Quantitative E1A DNA Fragment Length Kit (Cat. No. A51969) and resDNASEQ™ Quantitative Synthetic Vero DNA Kit (Cat. No. A53242).

Contents

1 Product information

Product description

The Applied Biosystems™ AccuSEQ™ Real-Time PCR Software v3.1 is the software component of an integrated workflow for the SEQ family of analytical detection and quantification assays. These assays are used for analytical testing for impurities and contaminants during the biopharmaceutical manufacturing process. The software has templates for Applied Biosystems™ MycoSEQ™ Mycoplasma Real-Time PCR Detection Kit, the Applied Biosystems™ ProteinSEQ™ protein quantitation systems, and the Applied Biosystems™ resDNASEQ™ Quantitative DNA Kits. It also includes a custom template option to support real-time PCR assays without a pre-defined template, such as the Applied Biosystems™ ViralSEQ™ real-time PCR assays. Security, audit, and e-signature capabilities help enable 21 CFR Part 11 compliance. For more information about the AccuSEQ™ Real-Time PCR Software, see **thermofisher.com/accuseq**.

The AccuSEQ™ Real-Time PCR Software v3.1 is designed to work with the QuantStudio™ 5 Real-Time PCR Instrument using 0.1-mL 96-well plates, with either fast or standard cycling. See the instrument user guide for additional information (*QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. MAN0010407).

Software installation and upgrades should only be performed by authorized and trained Thermo Fisher Scientific personnel.

Note: The AccuSEQ™ Real-Time PCR Software v3.1 is not compatible with the AccuSEQ™ software v2.x that works with the 7500 Fast Real-Time PCR Instrument. Files cannot be shared between systems.

Minimum computer requirements

Component	Requirement
Computer	Intel Core i5 (Quad Core 2.6Hz) or higher processor, with 16GB of RAM and a minimum of 250 GB hard disk space.
Operating system	Windows™ 10 Pro, 64-bit
Browser	Google™ Chrome™ version 74 or higher
Screen resolution	1920 x 1080 (Laptops) 1280 x 1024 (Monitors or laptops)

Assay types supported by the AccuSEQ™ Real-Time PCR Software v3.1

Purpose	Description
MycoSEQ™ assays (page 31)	
Detection of more than 90 species of mycoplasma.	The MycoSEQ™ assay is a real-time PCR assay that utilizes melt curve analysis to determine the presence or absence of more than 90 Mycoplasma species. The assay uses Power SYBR™ Green detection technology, which utilizes multiple parameters, amplification plot (C_t), melting temperature (T_m), and derivative value (D.V.) for interpretation of results. Multiparameter analysis provides highly sensitive and specific detection of fewer than 10 Mycoplasma genome copies per reaction.
ProteinSEQ™ assays (page 65)	
Detection of CHO HCP impurities	The ProteinSEQ™ CHO HCP Quantification Kit is a host cell protein (HCP) protein quantification solution with high sensitivity and a 4-log dynamic range. ProteinSEQ™ (CHO HCP) experiments use a standard curve to determine absolute quantity of the analyte in your sample.
resDNASEQ™ assays (page 46)	
Detection of residual host cell DNA from a variety of expression systems.	resDNASEQ™ assays combine high-recovery PrepSEQ™ sample preparation and TaqMan™ Assay-based quantification of residual DNA. resDNASEQ™ experiments use a standard curve to determine absolute quantity of residual DNA in your sample.
ViralSEQ™ assays (see page 78)	
Detection of residual viral DNA from a variety of sample types.	The ViralSEQ™ assays are highly sensitive TaqMan™ Assay-based detection or quantification kits. The kits detect the presence of viral nucleic acids in cell culture samples during upstream analytical testing as well as for lot release testing (MMV only). ViralSEQ™ kits contain TaqMan™ probes and primers, TaqMan™ master mixes, and negative and positive controls. Assays for MMV, Vesivirus, and Mycoplasma can be set up and run in the same plate.
Custom assays (page 129–156)	
Used to design, run, and analyze your own standard curve or melt curve experiment.	The custom workflow allows you to design your own template and experiments, and is meant for experiments not covered by existing factory default templates, such as the ViralSEQ™ detection or quantitation assays.

Workflow

Create an experiment from a template

See Chapter 7, “Create a custom template” to edit or create a new template.

▼

Assign plate and well attributes

▼

Set up and run the PCR reactions

▼

Load the plate in the instrument

▼

Start the run

▼

Monitor the run

▼

Chapter 9, “Review the results and generate a report”

▼

Export data and print reports

Use security, audit, and e-signature (SAE) functions

The AccuSEQ™ Real-Time PCR Software includes security, audit, and e-signature (SAE) features to help enable 21 CFR Part 11 compliance. These functions are collectively referred to as the SAE module.

Note: Compliance with 21 CFR Part 11 is the sole responsibility of the end user.

Overview of the SAE module components

The Security, Audit, and E-Signature module provides the following SAE functionality in the AccuSEQ™ Software:

- **System security**—Requires users to sign in to the AccuSEQ™ Software and determines user access to functions (permissions).

  If a user account does not have permission to perform a function, the function is grayed out in the software.

  For more information on permissions, see *Security, Audit, and E-Signature (SAE) Administrator Console v1.0.1 User Guide* (Pub. No. MAN0018760).
- **Auditing**—Automatically audits changes to experiments and other information that is accessible only to an administrator.
- **E-signature** —Allows users to provide an electronic signature (user name and password) after reviewing an experiment. For more information, see “E-sign an experiment” on page 171.

  Note: If the **E-Sign** button in the **Results** screen is grayed out, the signed-in user account does not have the e-signature function enabled.
- **Audit & E-Sign Reports**—Allows any user to view the audit and e-signature records for an experiment. For more information, see “View audit and e-sign reports for an experiment” on page 171.

Configuring the SAE module

For information on configuration, see *Security, Audit, and E-Signature (SAE) Administrator Console v1.0.1 User Guide* (Pub. No. MAN0018760).

Network and password security requirements

Network configuration and security

The network configuration and security settings of your laboratory or facility (such as firewalls, anti-virus software, network passwords) are the sole responsibility of your facility administrator, IT, and security personnel. This product does not provide any network or security configuration files, utilities, or instructions.

If external or network drives are connected to the software, it is the responsibility of your IT personnel to ensure that such drives are configured and secured correctly to prevent data corruption or loss. It is the responsibility of your facility administrator, IT, and security personnel to prevent the use of any unsecured ports (such as USB, Ethernet) and ensure that the system security is maintained.

Note: The AccuSEQ™ Software cannot connect to an Active Directory (to use existing domain usernames/passwords).

Password security

Thermo Fisher Scientific strongly recommends that you maintain unique passwords for all accounts in use on this product. All passwords should be reset upon first sign in to the product. Change passwords according to your organization's password policy.

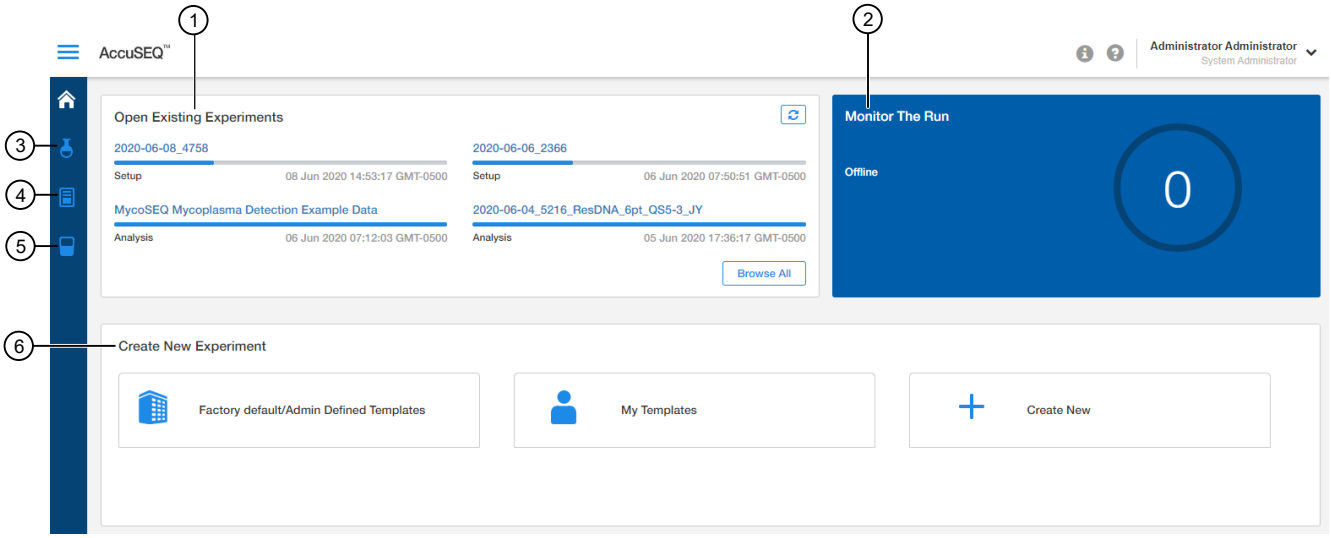
It is the sole responsibility of your IT personnel to develop and enforce secure use of passwords.

Navigate the AccuSEQ™ Real-Time PCR Software

Home screen

Use the **Home** screen to:

- View the last four experiments run
- Monitor a run. See “Monitor the run” on page 38.
- Create a new template. See “Create or open a template” on page 130
- Create an experiment from a template. See “Create an experiment from a template” on page 143
- Create a copy of an existing experiment. See “Create a copy of an existing experiment” on page 144



① **Open Experiment**—View the last 4 experiments run on the instrument. Click **Browse All** to open a full list of experiments.

② **Monitor the Run**—View the time remaining for the run; view the instrument calibration status. For information on instrument calibration, see the *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. A43322).

③ **Experiments** list

④ **Templates** list

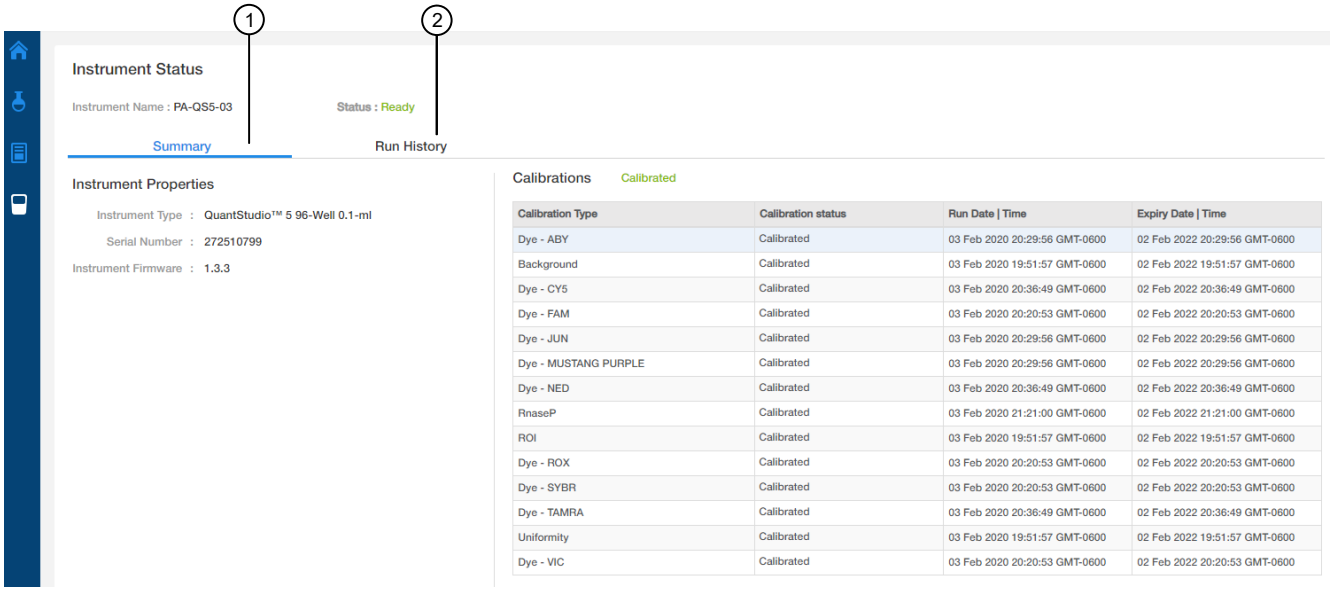
⑤ **Instrument status**

⑥ **Create New Experiment**—Select from existing templates or create a new one.

Instrument status screen

Use the **Instrument status** screen to:

- View the instrument calibration log
- View the instrument Run History



Calibration Type	Calibration status	Run Date | Time	Expiry Date | Time
Dye - ABY	Calibrated	03 Feb 2020 20:29:56 GMT-0600	02 Feb 2022 20:29:56 GMT-0600
Background	Calibrated	03 Feb 2020 19:51:57 GMT-0600	02 Feb 2022 19:51:57 GMT-0600
Dye - CY5	Calibrated	03 Feb 2020 20:36:49 GMT-0600	02 Feb 2022 20:36:49 GMT-0600
Dye - FAM	Calibrated	03 Feb 2020 20:20:53 GMT-0600	02 Feb 2022 20:20:53 GMT-0600
Dye - JUN	Calibrated	03 Feb 2020 20:29:56 GMT-0600	02 Feb 2022 20:29:56 GMT-0600
Dye - MUSTANG PURPLE	Calibrated	03 Feb 2020 20:29:56 GMT-0600	02 Feb 2022 20:29:56 GMT-0600
Dye - NED	Calibrated	03 Feb 2020 20:36:49 GMT-0600	02 Feb 2022 20:36:49 GMT-0600
RnaseP	Calibrated	03 Feb 2020 21:21:00 GMT-0600	02 Feb 2022 21:21:00 GMT-0600
ROI	Calibrated	03 Feb 2020 19:51:57 GMT-0600	02 Feb 2022 19:51:57 GMT-0600
Dye - ROX	Calibrated	03 Feb 2020 20:20:53 GMT-0600	02 Feb 2022 20:20:53 GMT-0600
Dye - SYBR	Calibrated	03 Feb 2020 20:20:53 GMT-0600	02 Feb 2022 20:20:53 GMT-0600
Dye - TAMRA	Calibrated	03 Feb 2020 20:36:49 GMT-0600	02 Feb 2022 20:36:49 GMT-0600
Uniformity	Calibrated	03 Feb 2020 19:51:57 GMT-0600	02 Feb 2022 19:51:57 GMT-0600
Dye - VIC	Calibrated	03 Feb 2020 20:20:53 GMT-0600	02 Feb 2022 20:20:53 GMT-0600

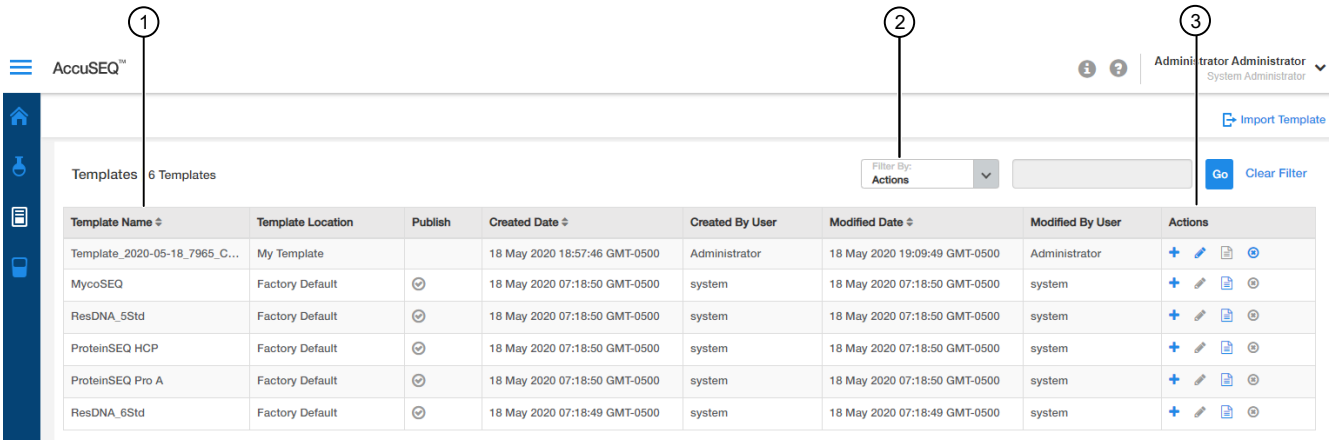
① Summary tab—Contains calibration information.
② Run History tab—Contains a log of instrument events.

Templates screen

Use the Templates screen to:

- View the full list of templates on the instrument (published and unpublished from the user's Default/Admin Defined and My Template lists).
- Create an experiment from a template
- Edit, delete, publish, or unpublish a template.

For information on templates, see Chapter 7, “Create a custom template”.



① **Template Name**—View the published templates available for use. If your user account includes the View Unpublished template permission, unpublished templates are also listed. For information on publishing templates, see “Publish a template” on page 140.

② **Filter by**—Use to filter templates.

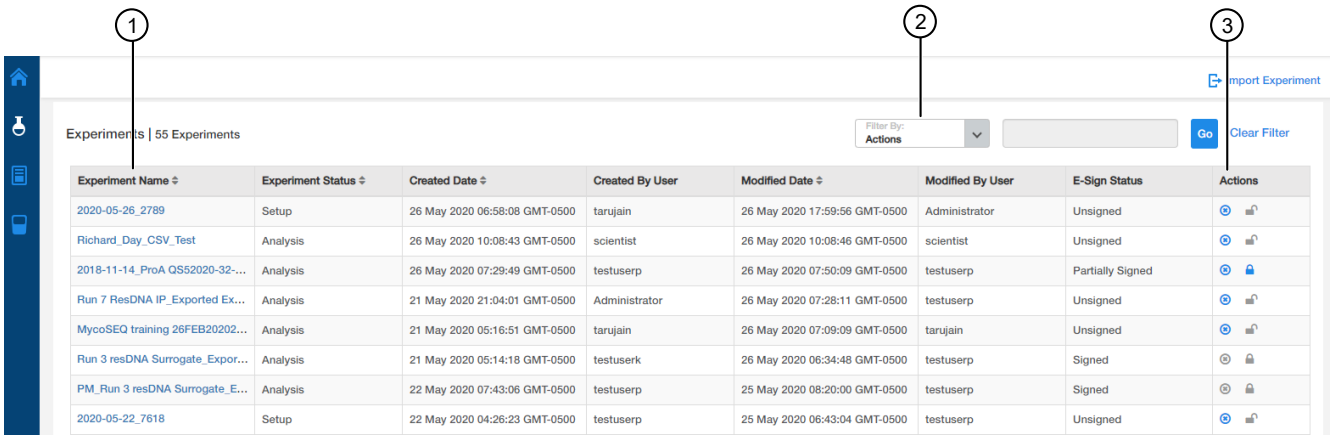
③ **Actions**—Depending on the role of the user that is signed in, the ability to + **Create**, **Edit**, **Publish**, or **Delete** templates.

Experiments screen

Use the Experiments screen to:

- View the full list of experiments
- Filter experiments (by parameters such as Created Date or User)
- Open an experiment
- Delete an experiment
- View if an experiment has an e-signature.

For more information on creating an experiment from an existing experiment, see “Create a copy of an existing experiment” on page 144.



① **Experiment Name**—View a complete list of experiments run on the instrument (most recent first).

② **Filter by**—Use to filter experiments.

③ **Actions**

- ⊗—Delete the experiment; For permissions, see the *AccuSEQ Quantstudio5 Security, Audit, and E-signature (SAE) Administrator Console v1.0 User Guide* (Pub. No. 100084439)
- **(Locked gray icon)**—signed
- **(Unlocked gray icon)**—unsigned
- **(Locked blue icon)**—partially signed; click to go to the E-sign page

Setup screens

Use the **Setup** screen to confirm the properties and methods used in default templates or to create a custom template or experiment. For more information on creating a custom template, see Chapter 7, “Create a custom template”.

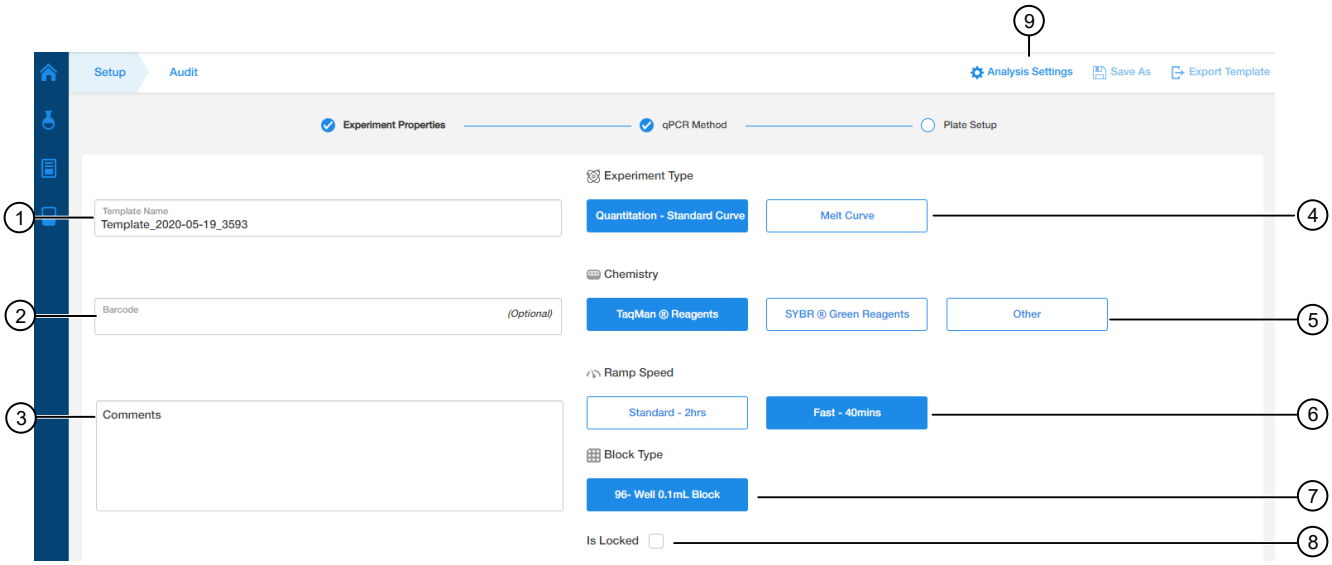


Figure 1 Experiment Properties screen.

For more information, see “Enter template properties” on page 132.

1. **Template Name**—Use the software-generated name, or create a unique name.
2. **Barcode**
3. **Comments**
4. **Experiment Type**
5. **Chemistry**
6. **Ramp Speed**
7. **Block Type**—fixed as a 96-Well 0.1mL block
8. **Is Locked** checkbox—check to lock the template
9. **Analysis Settings**

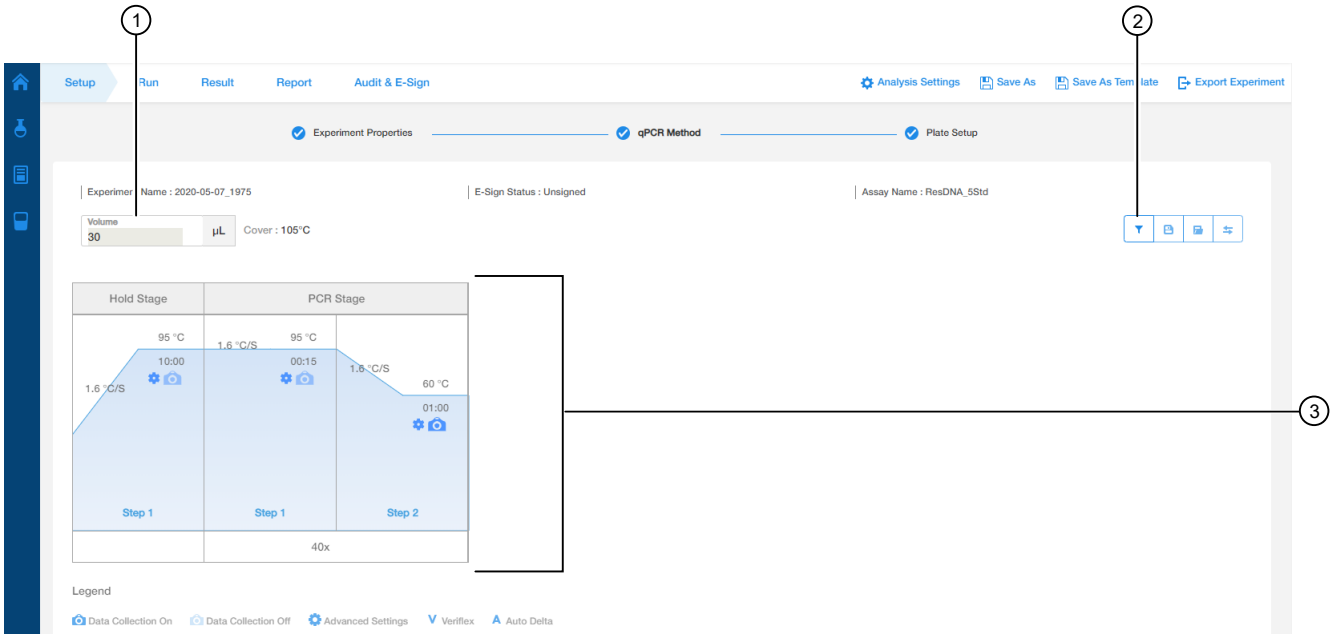


Figure 2 qPCR method screen

For more information, see "Confirm or edit the run method and optical filter selection" on page 133.

① Reaction volume. The volume is fixed in locked templates.
② Optical filters
③ PCR parameters

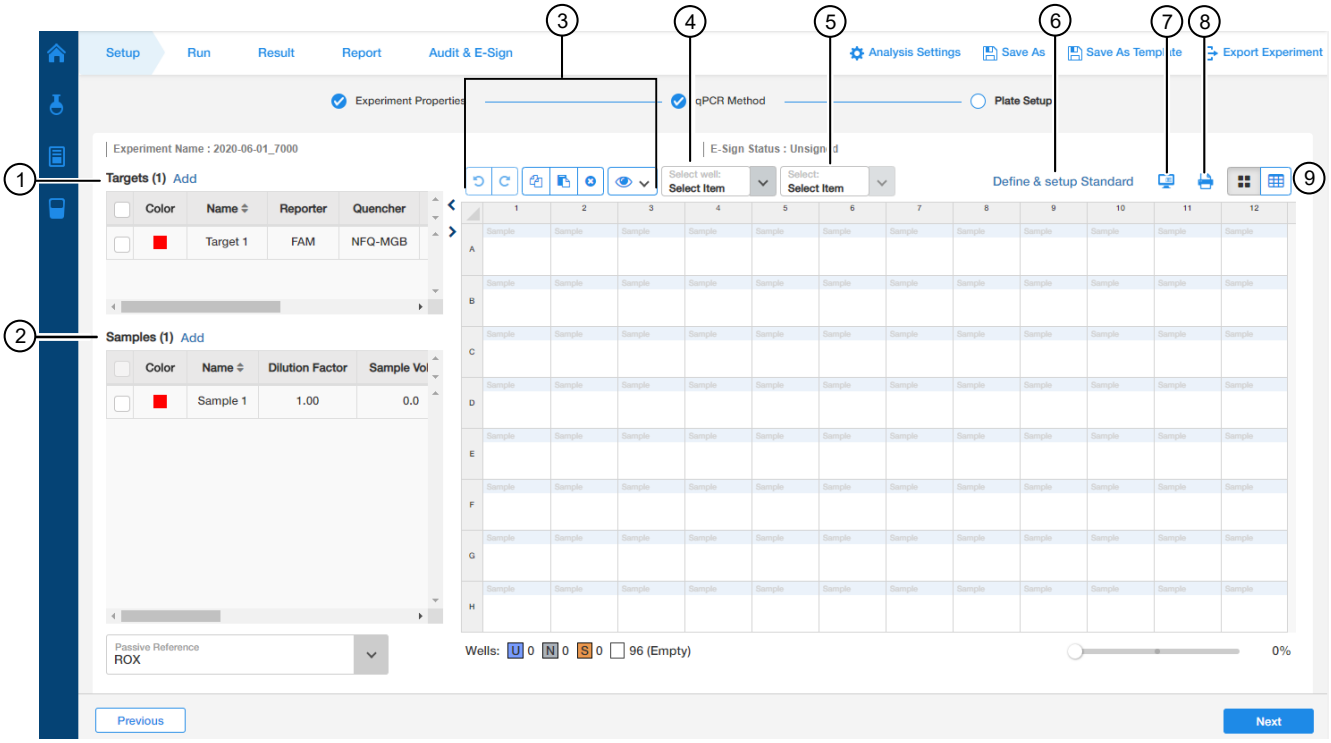


Figure 3 Plate Setup screen

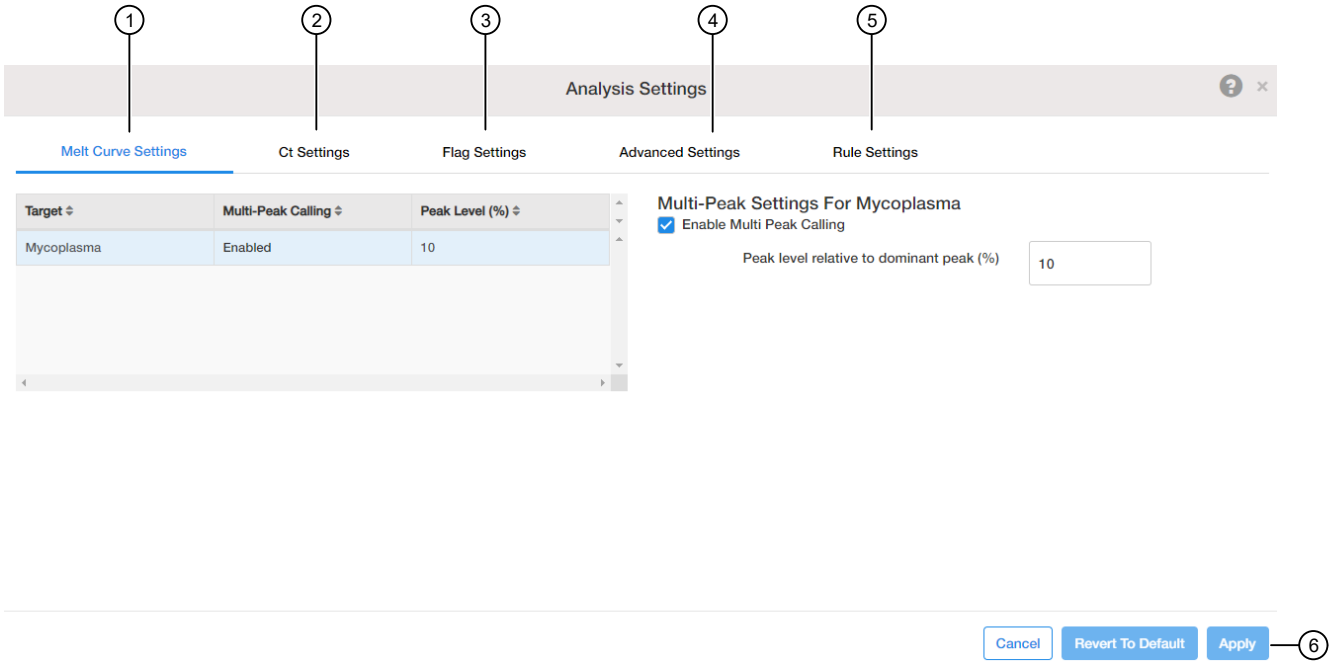
For more information, see "Assign plate and well attributes" on page 134.

① Targets
② Samples
③ Plate setup toolbar
④ Select Item to highlight (Sample, Target, or Task).
⑤ Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
⑥ Define & setup Standard
⑦ (View Legend)
⑧ (Print Preview)
⑨ View (Grid View or Table View)

Analysis settings screen

Use the **Analysis settings** screen to:

- Adjust the **Melt Curve Settings** (MycoSEQ™ experiments only)
- Adjust the **Ct Settings**
- Adjust the **Flag Settings**
- Adjust baseline settings for individual wells (**Advanced Settings**)
- Adjust the **Rule Settings** (MycoSEQ™ experiments only)



① Melt Curve Settings
② Ct Settings
③ Flag Settings
④ Advanced Settings
⑤ Rule Settings
⑥ Actions (Click **Apply** to confirm changes before closing the window.)

Run screen

Use the **Run** screen to:

- View Amplification plot or Melt curve plot (MycoSEQ™ or custom melt curve experiments only)
- View the **Post Run Summary**
- Start a run

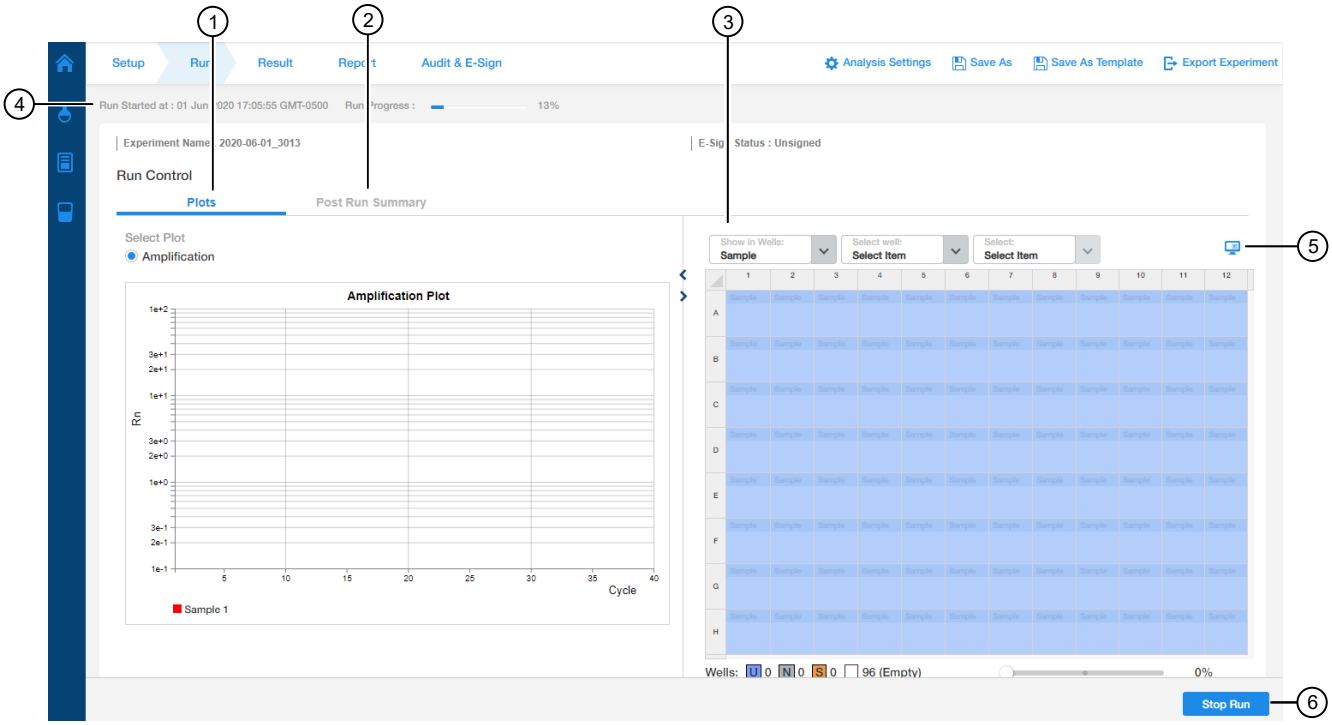


Figure 4 Example: MycoSEQ™ Run Screen

① **Plots**
② **Post Run Summary**
③ **View**—Select a parameter to view in **Plots**
④ Progress bar—Displays percentage of the run that is completed
⑤ View Legend
⑥ **Stop Run**—Stops the run

Results screen

Use the **Results** screen to:

- View the plate call (MycoSEQ™ assays only)
- View the well calls (MycoSEQ™ assays only)
- Omit wells and reanalyze the experiment

Note: The **Analyze** button is disabled if the user does not have permission to both omit wells and analyze data.

- View plots
- E-Sign the experiment

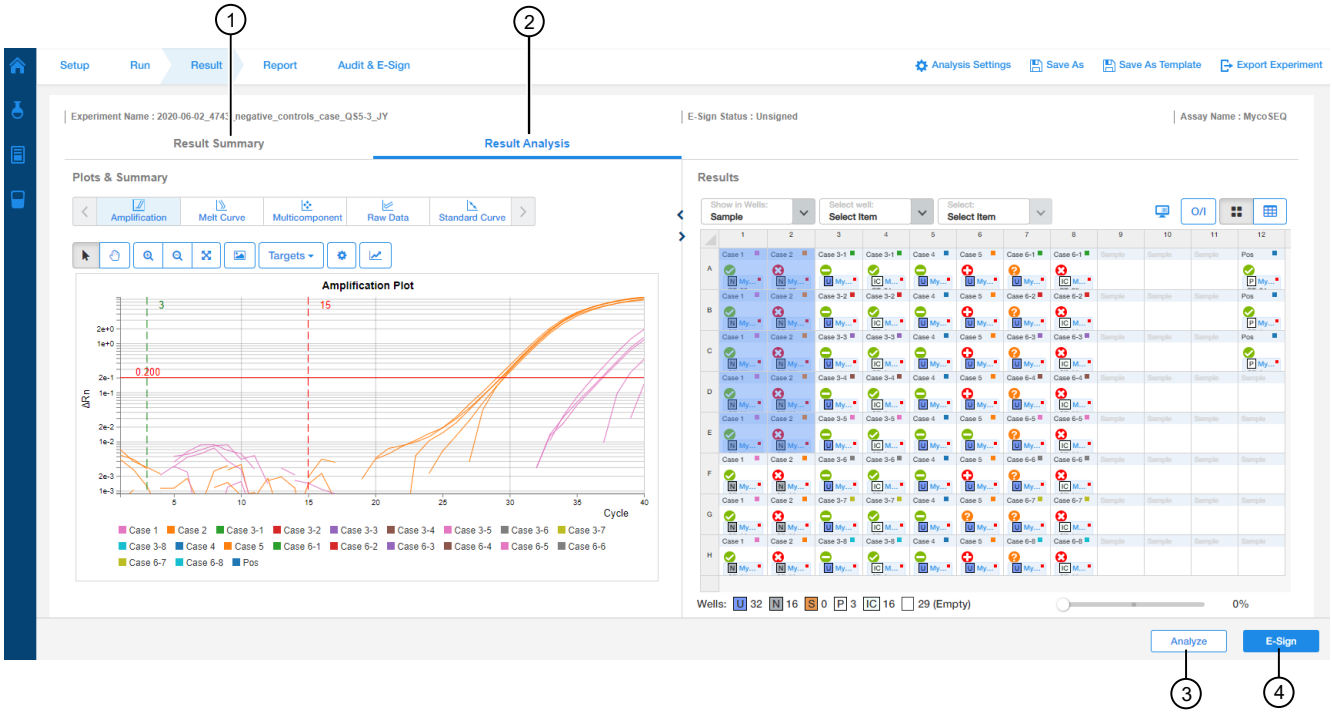


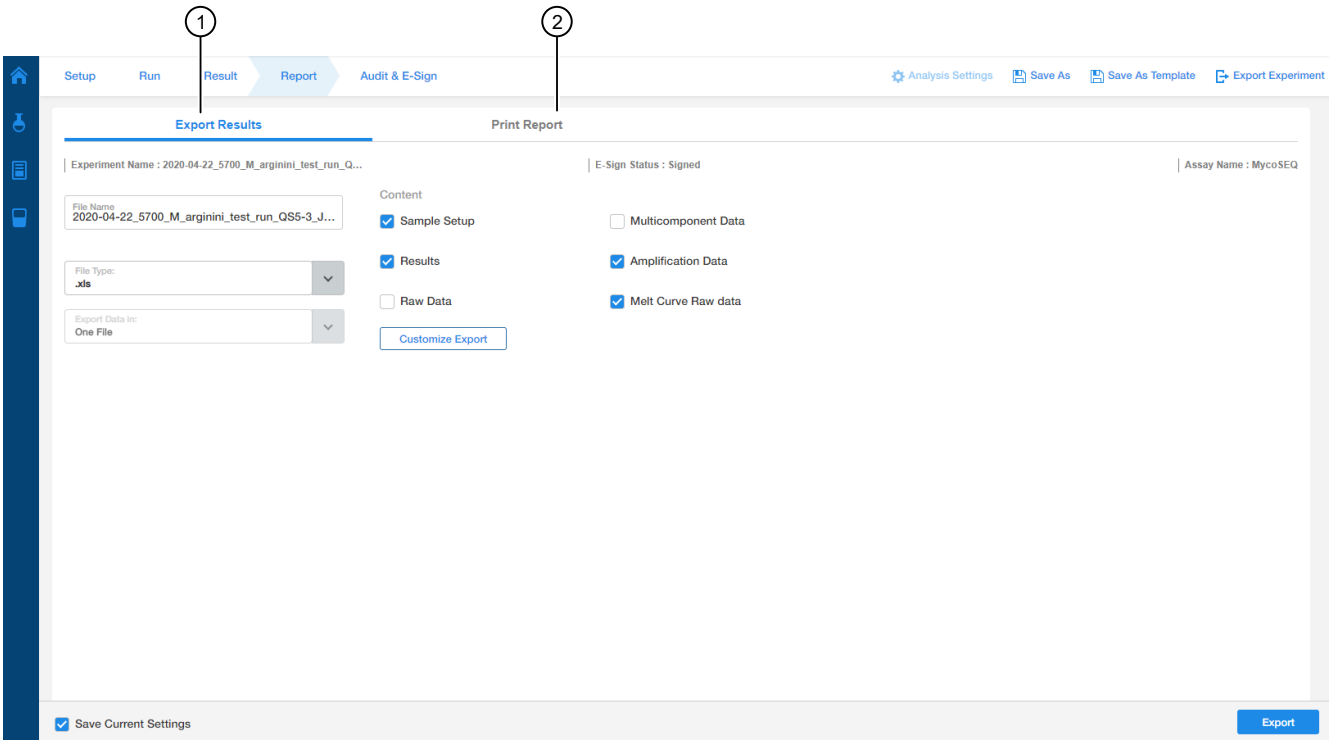
Figure 5 Example of Results screen (MycoSEQ™ assay)

① **Result Summary** pane—only available for MycoSEQ™ assays
② **Result Analysis** pane
③ **Analyze**—Use after omitting wells.
④ **E-Sign**

Report screen

Use the **Report** screen to:

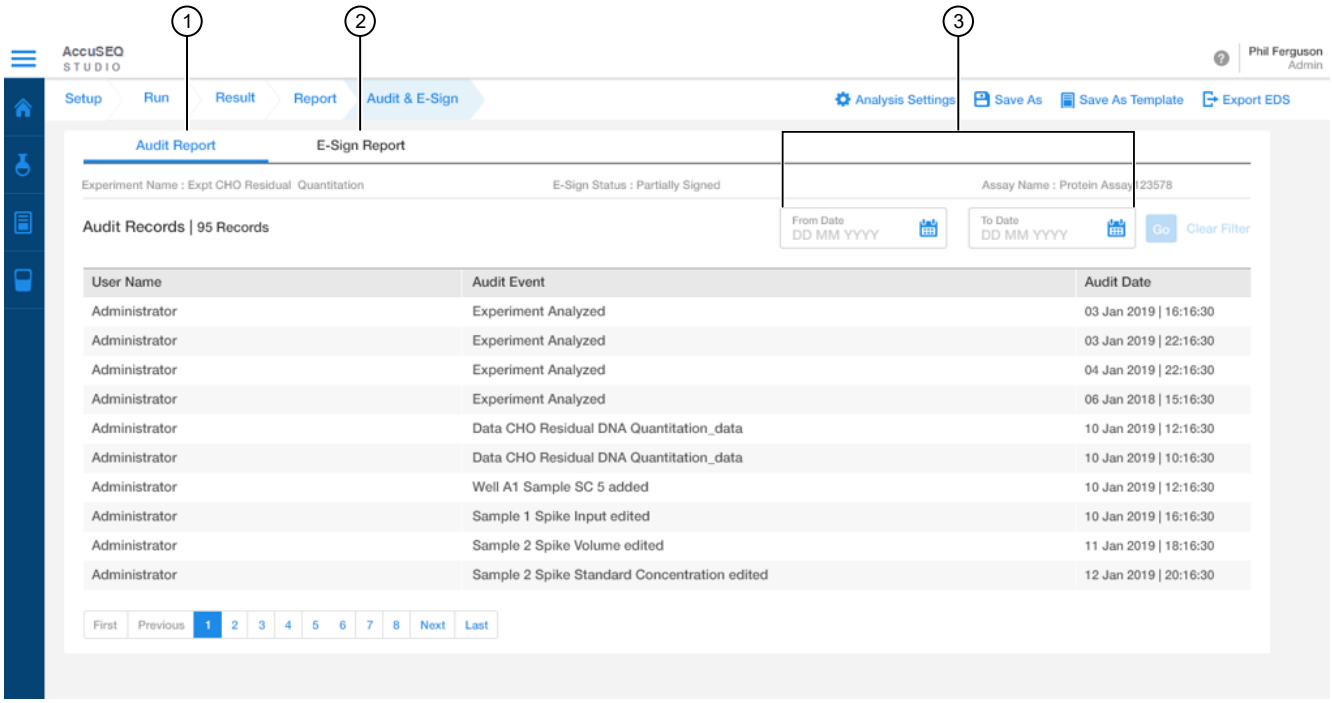
- Export results
- Customize export
- Print a report



① **Export Results**
② **Print Report**

Audit & E-sign screen

Use the **Audit & E-sign** screen to view the audit or e-signature report for an experiment.



① **Audit Report**
② **E-Sign Report**
③ Filter results by date

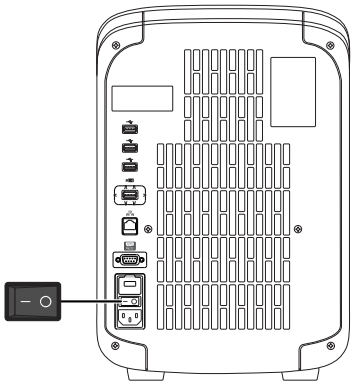
2 General procedures to operate the QuantStudio™ 5 Instrument

Before running experiments with the AccuSEQ™ Real-Time PCR Software, familiarize yourself with the QuantStudio™ 5 Instrument.

Before you begin

Power on the instrument

1. Touch anywhere on the touchscreen to determine if the instrument is in sleep mode. If the home screen is displayed, the instrument is already powered on.
2. If the home screen is not displayed, power on the instrument by pressing the switch on the rear panel.



If left unattended (for about two hours), the instrument automatically enters sleep mode (enabled by default) to conserve power.

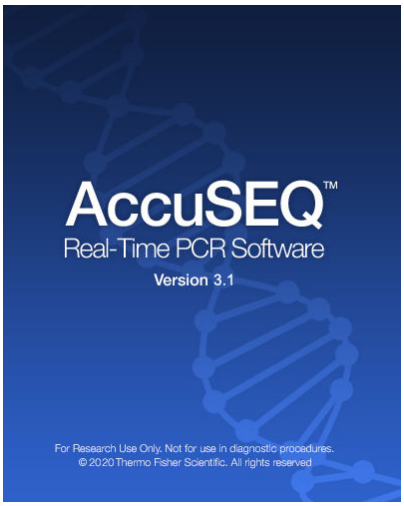
Note: To customize the sleep mode setting, touch ⚙ **(Settings) ▸ Instrument Settings ▸ Sleep Mode**.

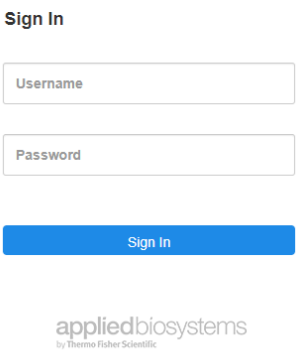
Sign in to the AccuSEQ™ Real-Time PCR Software

Thermo Fisher Scientific recommends configuring the Windows™ 10 screen save feature to require sign in when the screensaver is activated. This prevents other users from accessing the AccuSEQ™ Real-Time PCR Software and making changes.

1. Launch the AccuSEQ™ Real-Time PCR Software by double-clicking the AccuSEQ icon .
2. Enter the **Username**, then **Password**.

   (First login only) The default username is **Administrator** and the default password is **Administrator**.
3. Click **Sign in**.





The following restrictions may be seen in the software:

- Access to functions in the software is based on the permissions associated with the individual user account.
- If a user account does not have permission to perform a function, the function is grayed out in the software.
- If the system is configured for password expiration, you will be periodically prompted to change your password. If the system is configured to monitor failed log in attempts, you will be locked out of the software if you incorrectly enter your user name or password more than a specified number of times.

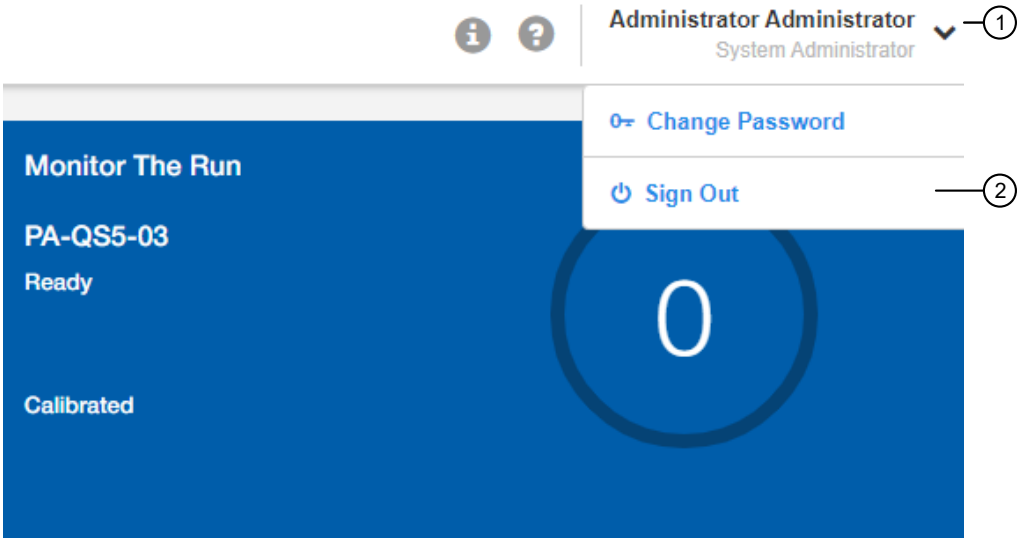
Change your password

When your password is about to expire, a message is displayed when you sign in.

1. Click your user name in the top right of the menu bar.
2. Click **Change Password**.
3. Enter the old password.
4. Enter a new password, confirm the new password, then click **OK**.

Sign out of the AccuSEQ™ Real-Time PCR Software

Click the username in the top right corner of the AccuSEQ™ Real-Time PCR Software home screen, then click **Sign out**.



① Username
② Sign out

Monitor Instrument Status

Basic instrument status is displayed in the **Monitor The Run** pane of the **(Home)** screen.

① Instrument name
② Instrument status (Ready, Running, Offline)
③ Calibration status

- Calibrated—All required calibrations are "Current". Required calibrations include: Background, ROI, Uniformity, and Dyes.
- Not calibrated—None of the required calibrations are complete.
- Requires calibration—One or more dyes are not calibrated.

④ Time lapsed (if a run is in progress)
⑤ Total run time
⑥ Experiment name

1. In the **(Home)** screen, click **(Instrument Status)**.
2. Click **Summary** to display a list of current instrument calibrations and their expiry dates and times. Ensure that the instrument is calibrated. For information on instrument calibration, see the *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. A43322).
3. Click **Run History** to display a complete list of experiments that have been run on the instrument.

3 Set up, run, and review MycoSEQ™ experiments

Overview

The MycoSEQ™ Mycoplasma Detection System integrates real-time PCR and *Power* SYBR™ Green technology, instruments, and software. It is used with the Applied Biosystems™ PrepSEQ™ nucleic acid extraction kits to detect more than 90 species of Mycoplasma.

The MycoSEQ™ template in the AccuSEQ™ Software includes default cycle threshold (Ct), derivative value (DV), and melting temperature (Tm) values to make automated mycoplasma calls (Present, Absent, Review, or Fail).

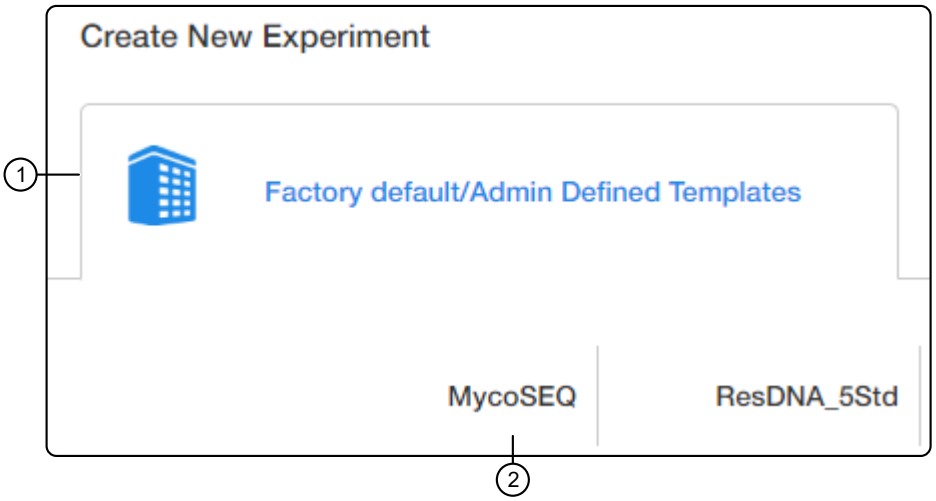
For detailed instructions on running the MycoSEQ™ assay, see the *MycoSEQ™ Mycoplasma Real-Time PCR Detection Kit User Guide* (Pub. No. 4482248).

Create a MycoSEQ™ experiment

1. In the **Home** screen, click the **Factory default/Admin Defined Template** tab, then select **MycoSEQ**.

Note: To create a copy of an existing MycoSEQ™ experiment, see “Create a copy of an existing experiment” on page 144.

To create a custom MycoSEQ™ experiment, see the *MycoSEQ™ Mycoplasma Real-Time PCR Detection Kit User Guide* (Pub. No. 4482248). Custom MycoSEQ™ experiments must be set up as **Quantitation-Standard Curve** type experiments with SYBR™ chemistry.



① **Factory default/Admin Defined Template** tab
② **MycoSEQ** template

2. In the **Experiment Properties** pane of the **Setup** tab:
   a. (*Optional*) Change the system-generated name of the experiment.

   Note: Names must be unique. Deleted experiment names can not be reused.

   b. (*Optional*) Enter the plate **Barcode**, then add **Comments**.

   Note: Names and comments are not editable post analysis.

   c. Click **Next**.

   Note: Experiment names cannot be changed after this step.

3. In the **qPCR Method** pane of the **Setup** tab, view the default volume and cycling conditions (cannot be changed).

Note: This assay is run with a **Standard** ramp speed (2hrs).

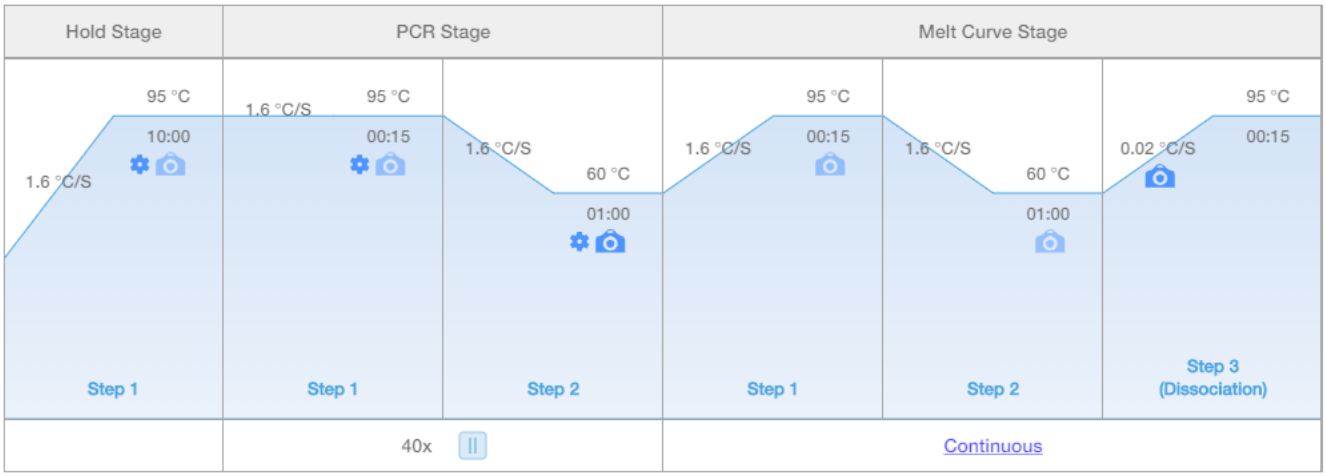


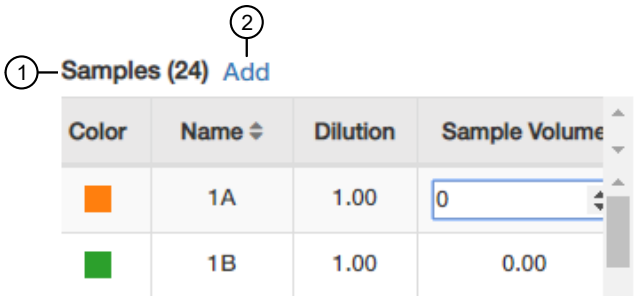
Figure 6 MycoSEQ™ template default cycling conditions

4. Click **Next**.

5. In the **Samples** pane of the **Setup** tab, enter the sample **Name**. Add additional **Samples** if needed.

Note: Only the sample **Name** is necessary for experiments run from the factory default **MycoSEQ** template.

IMPORTANT! Do not change the **Targets**.



① **Samples** pane
② **Add**—adds additional samples

For more information on plate setup, see “Assign plate and well attributes” on page 134.

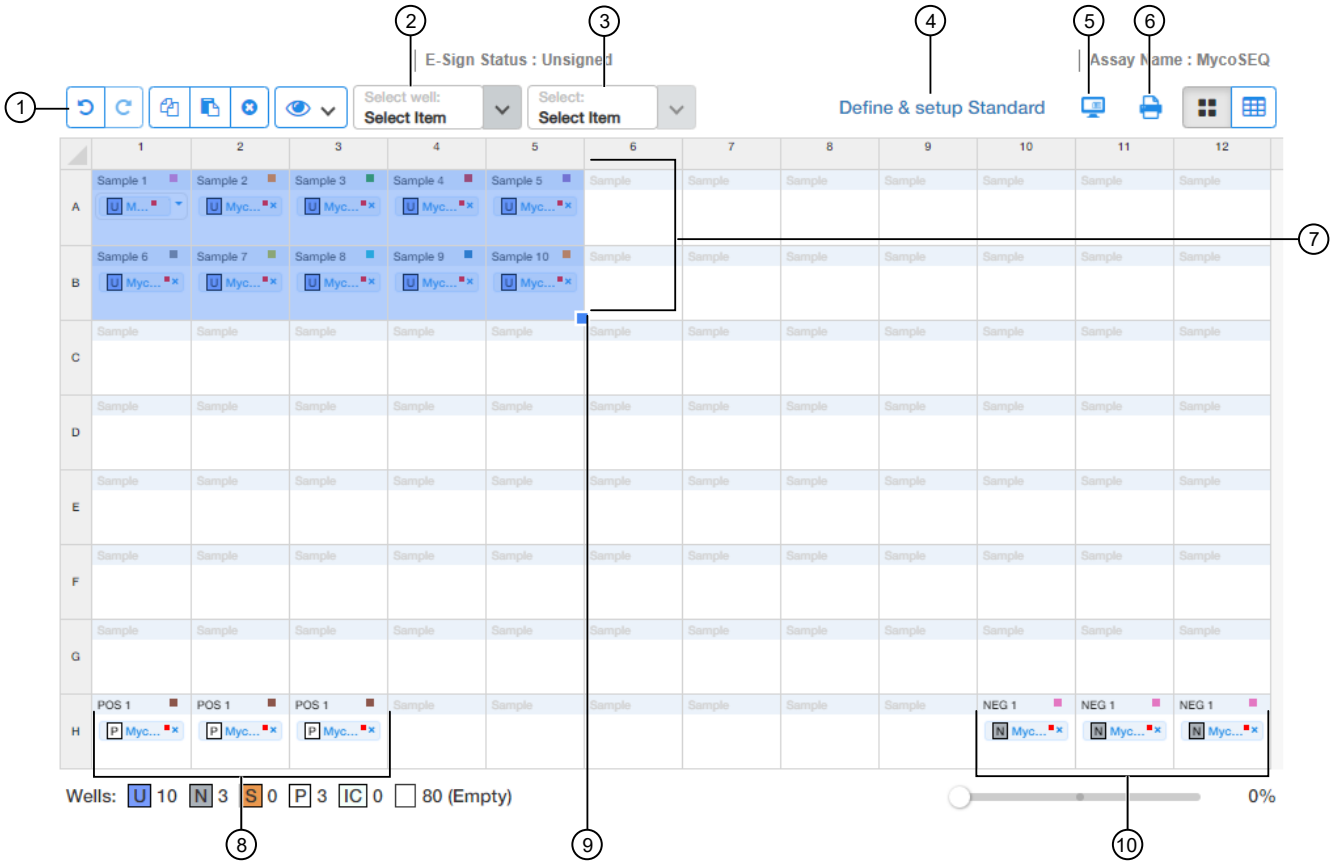


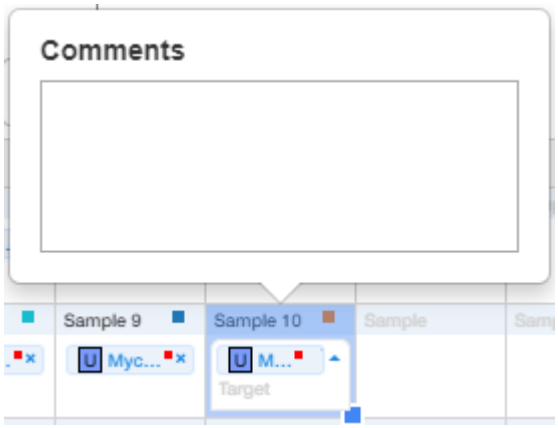
Figure 7 MycoSEQ™ template default sample plate layout

① Toolbar (in order: Undo, Redo, Copy, Paste, Delete, View)
② Select Item to highlight (Sample, Target, or Task).

Note: If additional samples are added, the **Target** displays as an **S** in the wells (experiment type–**Quantitation**).

③ Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
④ Define & setup Standard
⑤ (View Legend)
⑥ (Print Preview)
⑦ 5 default **Samples** with and without an inhibition control (IC)
⑧ Positive control (P) in triplicate
⑨ Selected samples. Click-drag to add additional samples.
⑩ No template control (N) in triplicate

6. (*Optional*) Double-click wells to add **Comments**. Comments can also be added post-analysis.



7. Click **Next**.
   The **Run** tab is displayed.

8. Experiments are auto-saved in the software. To save, exit the experiment. The software prompts you to save changes. Click **Yes**.

   Note: Clicking **Save As** will create a copy of the experiment.

9. Assemble the PCR reactions following the manufacturer's instructions for the reagents and following the plate layout set up in the template. See *MycoSEQ™ Mycoplasma Real-Time PCR Detection Kit User Guide* (Pub. No. 4465874).

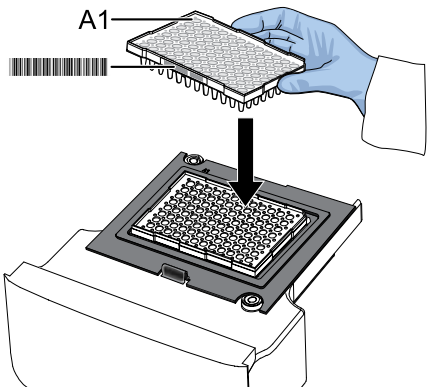
Immediately proceed to “Load the plate in the instrument” on page 36.

Load the plate in the instrument

CAUTION! Use optical flat caps for tubes. Rounded caps can damage the heated cover.

Load the plate.

1. Touch ⏏ to eject the instrument drawer.
2. Load the plate onto the plate adapter so that:
   - Well A1 of the plate is in the top-left corner of the plate adapter.
   - The barcode faces the front of the instrument.



IMPORTANT! The instrument should be used by trained operators who have been warned of the moving parts hazard.

Note: Do not remove the black plate adapter before loading a plate or tube strips. If used, tube strips can fit loosely in the adapter, but the heated cover applies the appropriate pressure to seat the tube strips securely in the adapter.

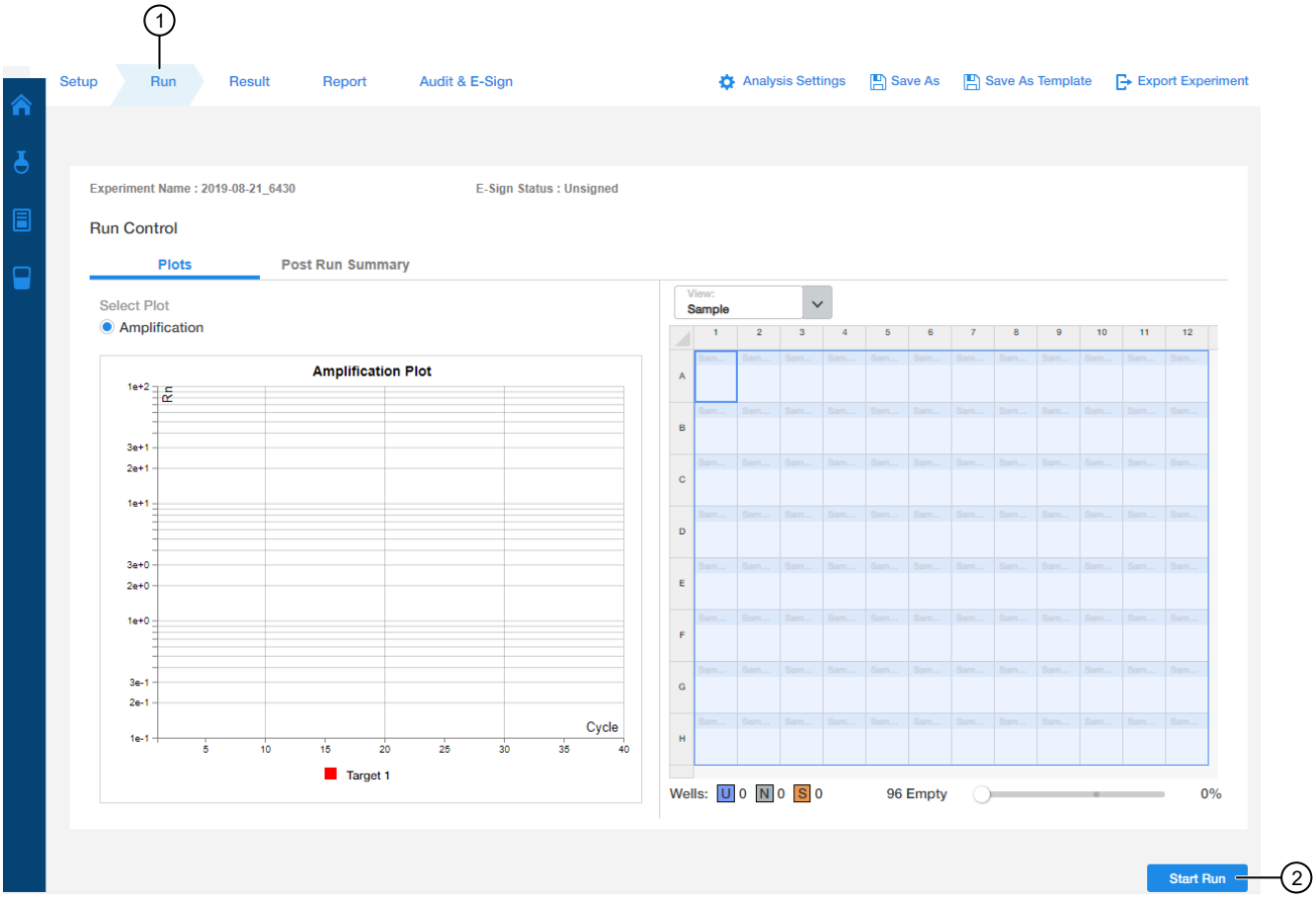
CAUTION! PHYSICAL INJURY HAZARD. During instrument operation, the plate temperature can reach 100°C. Allow it to cool to room temperature before handling.

3. Touch ⏏ to close the instrument drawer.

Start the run

Start the run in the AccuSEQ™ Software.

Option	Description
If the experiment is open	Click **Start Run**.
If the experiment is closed	1. Open the experiment. See “Open an experiment” on page 145. 2. Click the **Run** tab. 3. Click **Start Run**.



1 **Run** tab
2 **Start Run** button

A message stating **Run has been started successfully** is displayed when the run has started.

Monitor the run

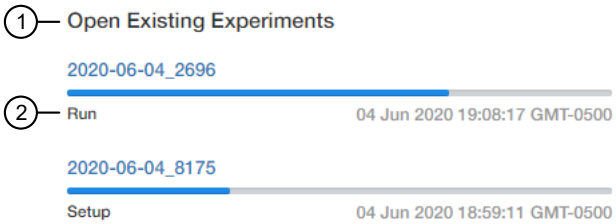
Monitor the run from one of the following places:

- On the instrument touchscreen. See the *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. A43322).
- In the **Monitor the Run** pane of the AccuSEQ™ Software **(Home)** screen.

1. Instrument name
2. Instrument status (Ready, Running, Offline)
3. Calibration status
   - Calibrated—All required calibrations are "Current". Required calibrations include: Background, ROI/Uniformity, and Dyes.
   - Not calibrated—None of the required calibrations are complete.
   - Requires calibration—One or more dyes are not calibrated.
4. Time lapsed (if a run is in progress)
5. Total run time
6. Experiment name

- In the **Open Existing Experiments** pane of the AccuSEQ™ Software **(Home)** screen. The experiment being run is the first experiment listed. Status is **Run**.

Note: When the run is complete, the status changes to **Analysis** and the bar changes to completely blue.



1. **Open Existing Experiments** pane
2. Experiment status

- In the **Run** tab of the AccuSEQ™ Real-Time PCR Software.

You can perform the following actions.

- Select wells in the plate layout to highlight respective curves in the plot.
- Hover over curves in the plot for well information.
- (*Optional*) Change what is displayed in the table wells of the plate layout, by selecting from the dropdown lists.

For more information, see “Run screen” on page 23.

On run completion, the **Post Run Summary** displays the run length, user and instrument information, and a list of any errors that occurred.

When the run is complete, unload the plate from the instrument.

Review results

Workflow: Review MycoSEQ™ experiments

“View the Result Summary” on page 40

▼

“Evaluate results in the Amplification Plot” on page 161

▼

“View and evaluate the Melt Curve Plot” on page 43

▼

Review data for outliers and *(optional)* “Omit outliers from analysis” on page 165

▼

(Optional) “Review the dye signal profile using the Multicomponent Plot” on page 167

▼

(Optional) “Review the signal profile using the Raw Data Plot” on page 169

▼

(Optional) “Review the flags in the QC Summary” on page 170)

▼

(Optional) “View and configure the analysis settings” on page 152

IMPORTANT! If you omit wells or configure the analysis settings, click **Analyze** to reanalyze the data. See “Results screen” on page 24.

View the Result Summary

If the experiment is not open, see “Open an experiment” on page 145.

The **Result** tab is populated when the run is complete.

Calls are made based on the **Rule Settings** in the **Analysis Settings** for MycoSEQ™ experiments. See “Configure analysis settings” on page 152 and “Rule settings overview (MycoSEQ™ experiments only)” on page 154 for more information.

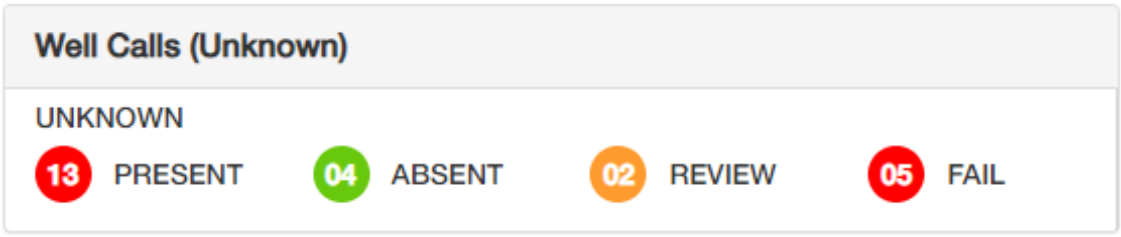
1. View the **Plate Call**.
   a. View the calls for the positive controls (POS).
   b. View the calls for the no template controls (NTC).

   The number inside the circle indicates the number of samples that passed or failed. The overall **Plate Status** (VALID or INVALID) is determined by the POS and NTC calls.

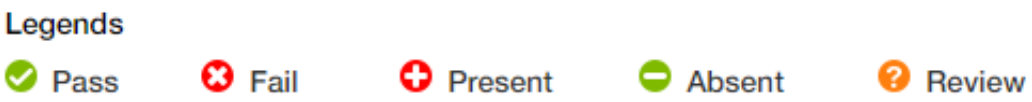
   Note: One passing POS and NTC call are required for a **Plate Status** to be VALID. This requirement is not editable.

1. Plate Call
2. Positive controls (POS)
3. Plate Status
4. No Template Controls (NTC)

2. View the **Well Calls (Unknown)**.
   a. View the total number of wells for each call—Present, Absent, Review, or Fail.



   b. Use the **Legends** to view the calls in the plate



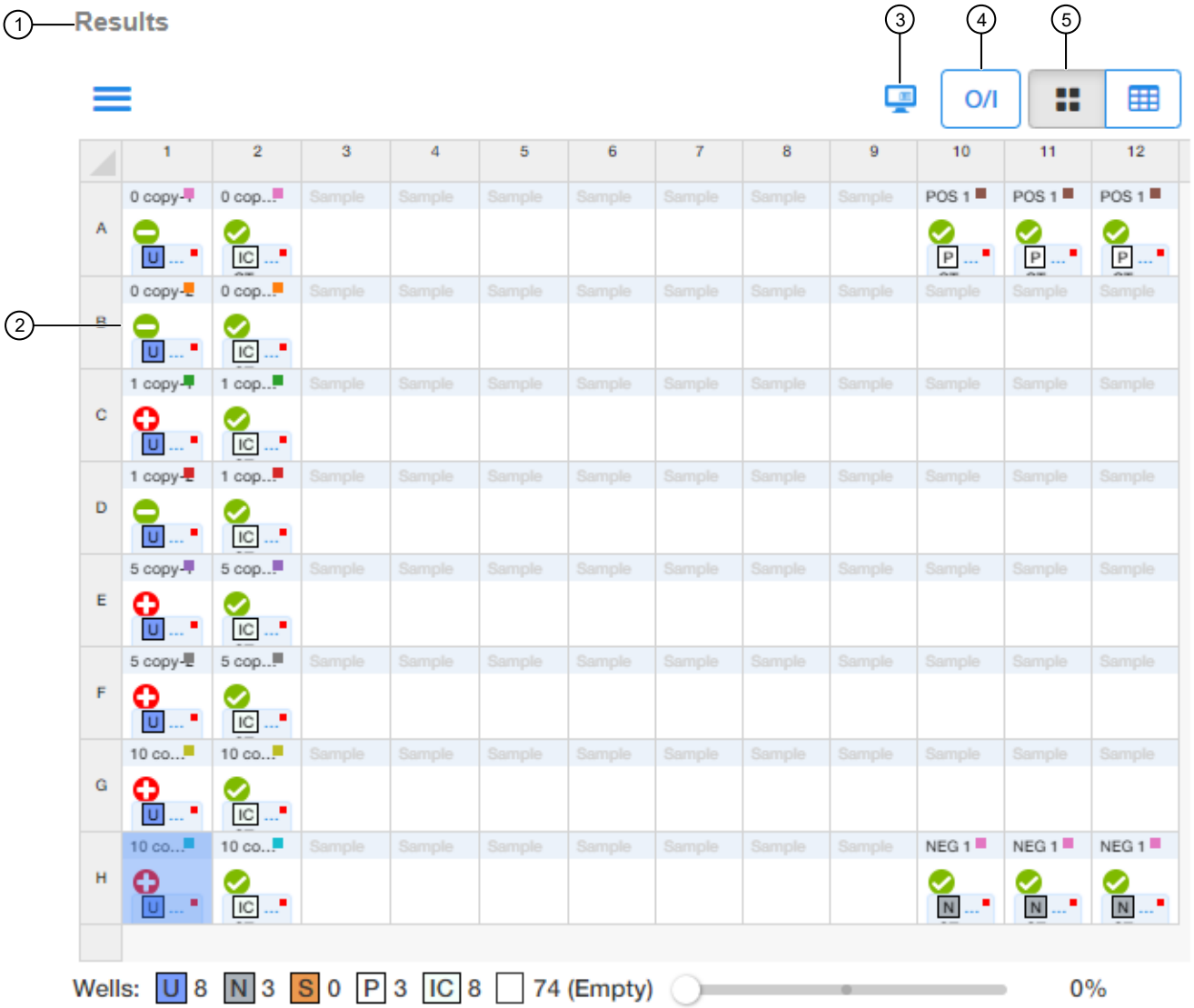


Figure 8 Example MycoSEQ™ Results (Grid View)

① **Results** pane
② Well call
③ View Legend—explains the symbols and letters in the wells. See "Flags" on page 174 for information on the flags.
④ Omit/ Include wells
⑤ Grid View

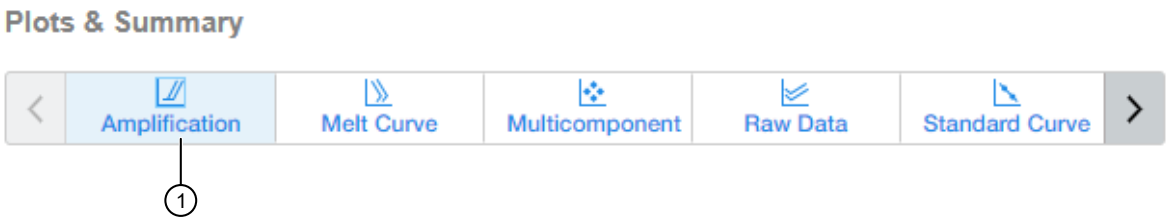
Evaluate the overall shape of the Amplification Plot curves

You can evaluate the overall shape of the **Amplification** curves in the **Result** tab. Evaluating the shape in wells with a **Review** call can help determine if the sample should be rerun, or whether to edit the call to **Present** or **Absent**.

Ensure that the experiment is open in the AccuSEQ™ Software. See "Open an experiment" on page 145.

1. In the **Results Analysis** pane of the **Result** tab, click **Amplification** in the horizontal scroll bar.

   Note: If no data are displayed in the **Result Analysis** pane, then click **Analyze**. See "Results screen" on page 24.

   ① Amplification Plot

   The **Amplification Plot** is displayed for the selected wells in the **(Grid View)** .

2. (*Optional*) Click **(Settings)** , then make the following selections:
   - **Plot Type**: **ΔRn, Rn, or C_T**
   - **Graph Type**: **Log or Linear**
   - **Show**: **Legend**, **Cq Mark** (the cycle at which the curvature of the amplification curve is maximal), or **Unselected**
   - **Plot Color**: **Target**, **Sample**, **Well**, or **Flag_Status**
   - **Threshold**: Select **Auto** or specify a threshold, then decide whether to **Show Threshold**.
   - **Baseline**: Decide whether to **Show Baseline**.

3. (*Optional*) Adjust the **(Plot Properties)**.
   a. (*Optional*) In the **General** tab, add a **Plot Title**, adjust the **Font** and **Color**, then click **Apply**.

   b. In the **X Axis** or **Y Axis** tabs, you can:
      - Add a **Label**
      - Select whether you want **Tick Marks**
      - Select **Auto-adjust range** or enter minimum and maximum values

      Note: The minimum value must be greater than 0.

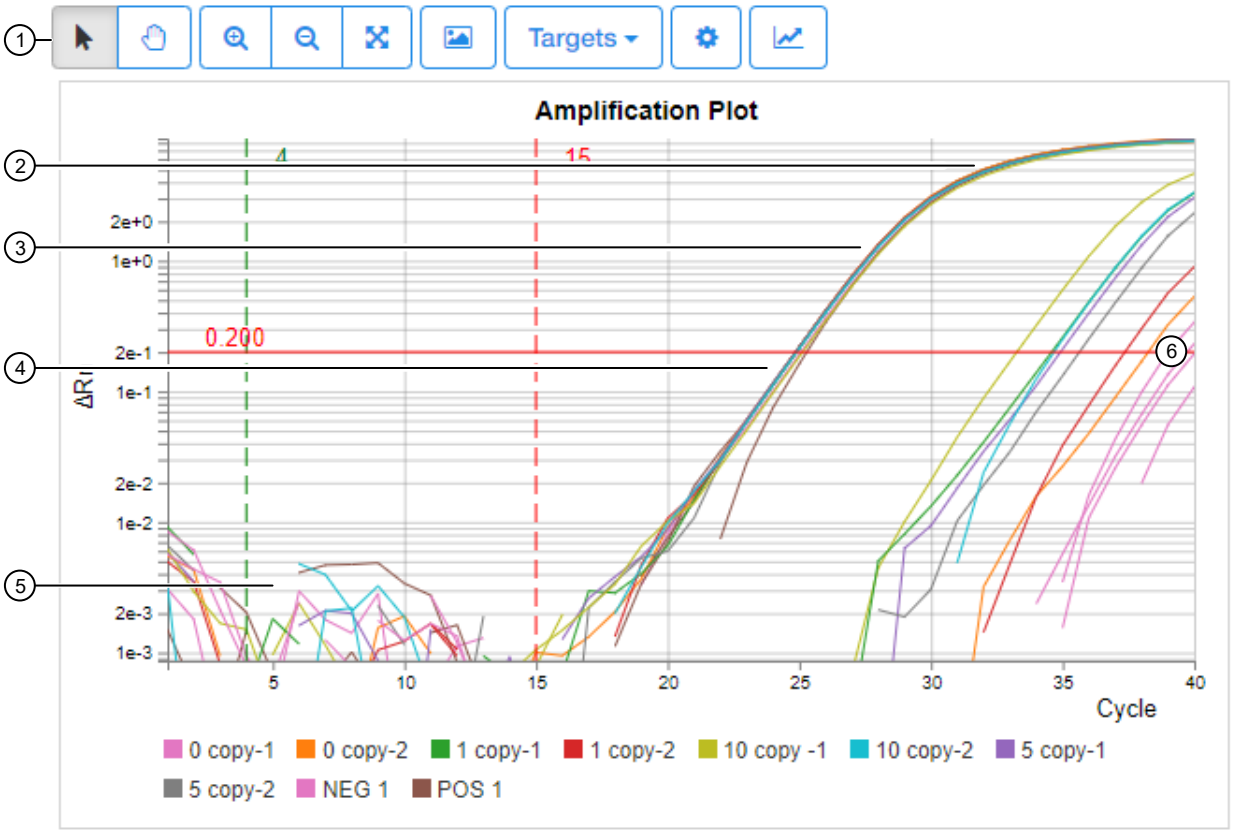
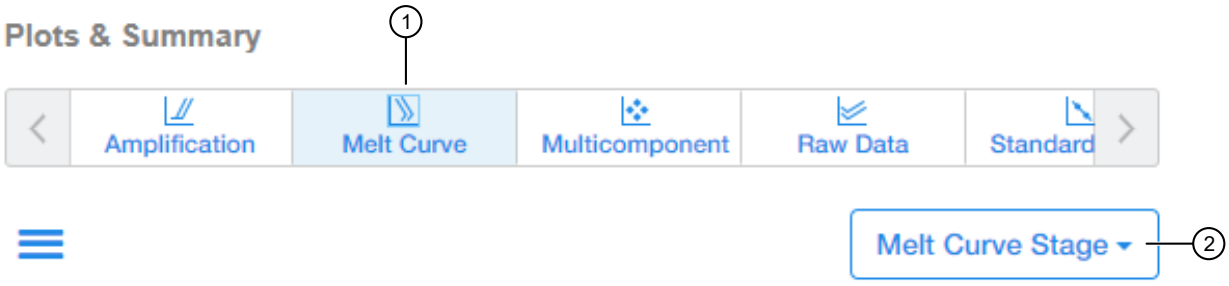


Figure 9 Typical Amplification Plot (4 phases)

① Amplification Plot tools
② Plateau phase
③ Linear phase
④ Exponential (geometric) phase
⑤ Baseline phase
⑥ Threshold

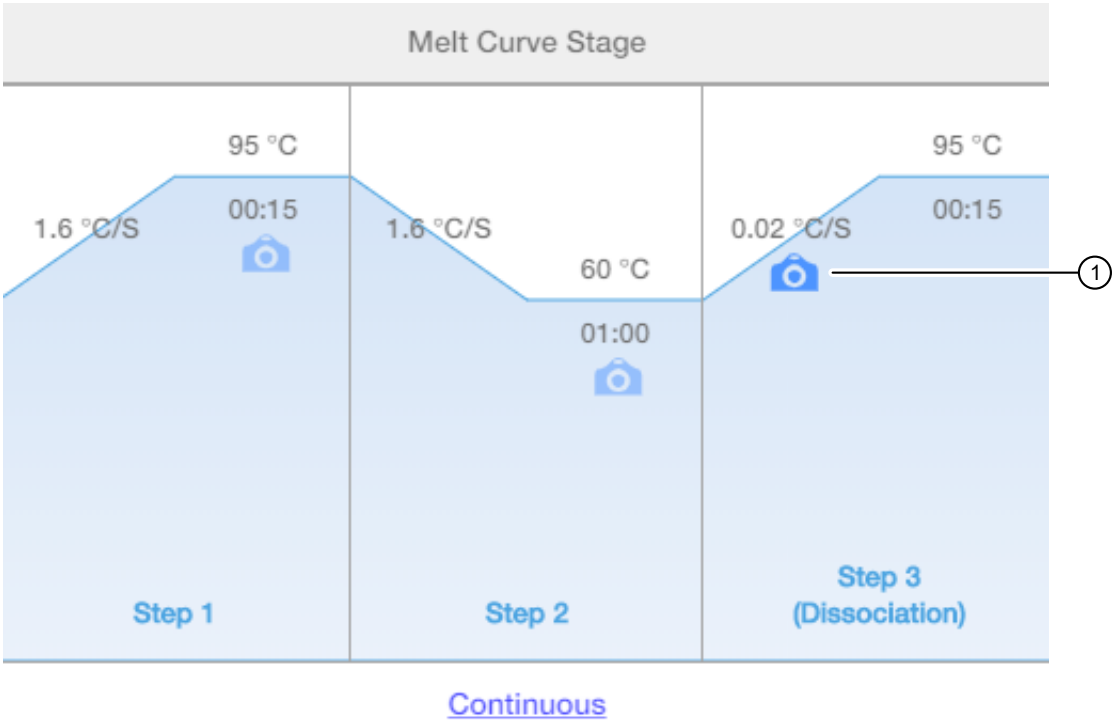
View and evaluate the Melt Curve Plot

You can view and evaluate the **Melt Curve** Plot in the **Result Analysis** window in the **Result** tab.



① **Melt Curve** plot
② **Melt Curve Stage** dropdown

1. In the **Result Analysis** window, select **Melt Curve** Plot from the horizontal scroll bar.
2. Keep the default **Melt Curve Stage**.



① Stage 3 data collection point

3. Click ☰ to configure the plot, then make the following selections:
   - **Targets**: Select Mycoplasma.
   - **Plot Settings**: Select the **Plot Type** and **Plot Color**.
   - **Plot Properties**: Edit **Plot Title**, change fonts, colors, and labels.
   - **Save Image**: Save the image (JPG, PNG, or SVG).
   - Use the select, pan, and zoom options to interact with the plot.

   The **Melt Curve Plot** is displayed for data points that are selected in the plot settings. The data points for selected wells in the **Grid View** or **Table View** are highlighted in the plot (see Figure 10).
4. (*Optional*) View the default **Melt Curve Stage**.
5. Confirm that amplification in the no template control and IC control wells is as expected. Use one of the following options:
   - Select control wells in the **Grid View** or **Table View**, then confirm the location of the data points in the **Melt Curve** Plot.
   - View the amplification plots for the no template controls.

6. In the **Melt Curve** Plot, view the signal intensity and calls for the unknown samples.

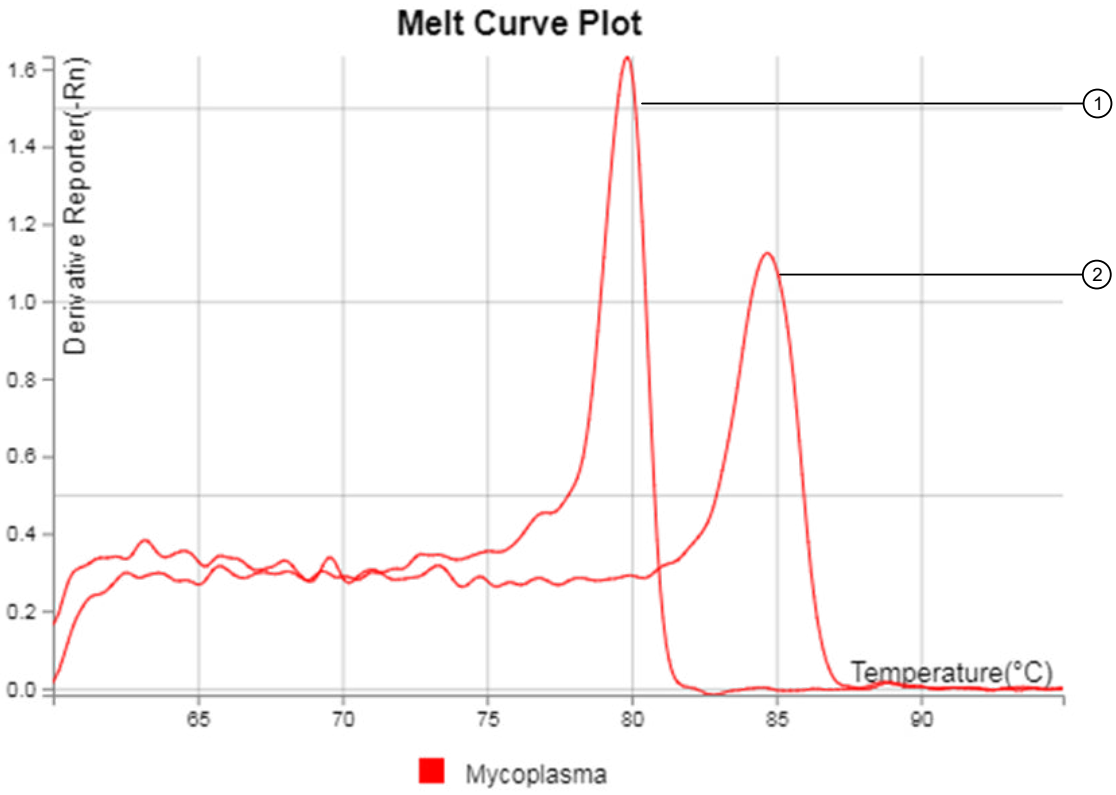


Figure 10 Example Melt Curve Plot

① Melting temperature (Mycoplasma)
② Melting temperature (positive control)

Proceed to one of the following sections.

If	Then
The plate status is VALID and there were no FAIL or REVIEW calls in the wells	Proceed to "Export data and print reports" on page 172
The plate status was INVALID	Rerun the experiment
The plate status is VALID, but there are FAIL or REVIEW calls in the wells	Proceed to Chapter 9, "Review the results and generate a report" and follow the more comprehensive instructions for reviewing the data. Data can be reanalyzed after omitting wells or changing the **Analysis Settings**.

4 Set up, run, and review resDNASEQ™ experiments

Overview

The resDNASEQ™ Quantitative DNA Kits are used to quantify residual host-cell genomic DNA from CHO, *E. coli*, E1A, HEK293, Human, MDCK, NS0, *Pichia*, Sf9 and Baculovirus, and Vero cell lines or from residual plasmid DNA (KanR, the kanamycin resistance gene), which are used for production of biopharmaceutical products.

The software performs the following tasks in resDNASEQ™ experiments.

1. The software measures amplification of the target in a standard dilution series and in test samples.
2. The software generates a standard curve using data from the standard dilution series.
3. The software uses the standard curve to interpolate the absolute quantity of target in the samples.

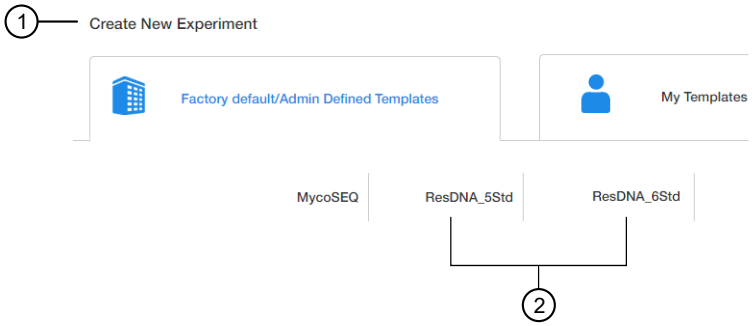
For detailed instructions on running the resDNASEQ™ assay, see the *resDNASEQ™ Quantitative DNA Kits User Guide* (Pub. No. 4469836) or *resDNASEQ™ Quantitative E1A DNA Fragment Length Kit User Guide* (Pub. No. MAN0025643).

Create a resDNASEQ™ experiment (Genomic DNA quantitation)

Note: Do not use default templates for the resDNASEQ™ Quantitative E1A DNA Fragment Length Kit (Cat. No. A51969). Follow the instructions on creating a template and running an experiment in the *resDNASEQ™ Quantitative E1A DNA Fragment Length Kit User Guide* (Pub. No. MAN0025643).

1. In the **Home** screen, click the **Factory default/Admin Defined Template** tab, then select a **resDNASEQ** template.

   Note: To create an experiment from an existing resDNASEQ™ experiment, see "Create a copy of an existing experiment" on page 144.



① **Factory default/Admin Defined Template** tab
② **resDNASEQ** template (ResDNA_5Std or ResDNA_6Std)

Template	Assays
5 standards (_5Std)	*E. coli*, HEK293, Human, *Pichia*, and Sf9 and Baculovirus
6 standards (_6Std)	CHO, Vero, synthetic Vero, MDCK, NS0

2. In the **Experiment Properties** pane of the **Setup** tab:
   a. (*Optional*) Change the system-generated name of the experiment.

      Note: Names must be unique. Deleted experiment names can not be reused.

   b. (*Optional*) Enter the plate **Barcode**, then add **Comments**.

      Note: Comments are not editable post analysis.

      Default resDNASEQ™ settings (cannot be changed)

      - **Experiment Type** is **Quantitation-Standard Curve**
      - **Chemistry** is **TaqMan™ Reagents**
      - **Ramp Speed** is **Standard - 2hrs**

   c. Click **Next**.

      Note: Experiment names cannot be changed after this step.

3. In the **qPCR Method** pane of the **Setup** tab, view the default volume and cycling conditions (cannot be changed).

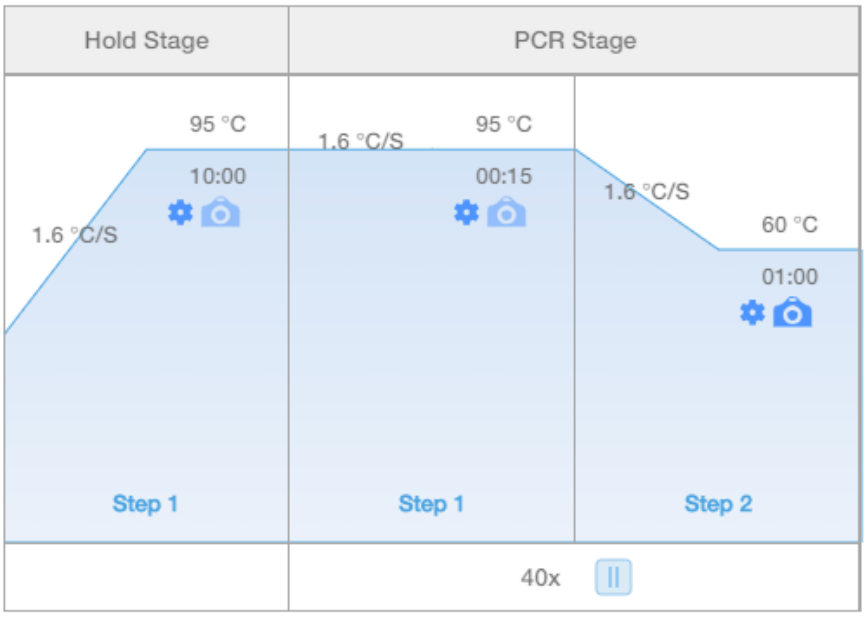
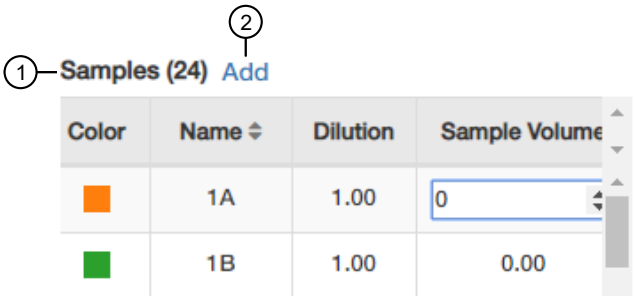


Figure 11 resDNASEQ™ template default cycling conditions

4. Click **Next**.

5. In the **Samples** pane of the **Setup** tab, enter the sample **Name** and **Dilution**. **Sample Volume** is not applicable. Add additional **Samples** if needed.

IMPORTANT! Do not change the **Targets**.



① **Samples** pane
② **Add**—adds additional samples

6. In the **Samples** pane of the **Setup** tab, scroll to the right, then enter the spike information.

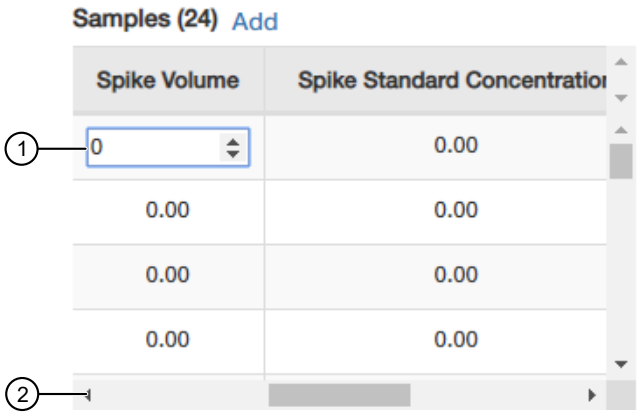
   For more information on plate setup, see “Assign plate and well attributes” on page 134.

   - **Sample Volume**—not applicable; leave as default (0).
   - **Spike Volume**—volume of DNA added to the PCR (set to 10).
   - **Spike Standard Concentration**—expected spike amount per reaction (for example, 10pg).
   - **Reference**—the non-spiked sample; the mean quantity of reference is subtracted during % recovery calculation.

- **Spike Input**—automatically calculated (double check if correct).

  Note: If incorrect, be sure **Spike Volume** is set to 10 and **Spike Standard Concentration** is the expected pg spike per PCR reaction.

- (Optional) **Comments**
- **Protein Concentration**—Drug substance protein concentration (if Total DNA in pg DNA/mg Protein is required).



① Textbox—type in the value, or use the up and down arrows
② Scroll bar—scroll to find the spike parameter

For more information on plate setup, see “Assign plate and well attributes” on page 134.

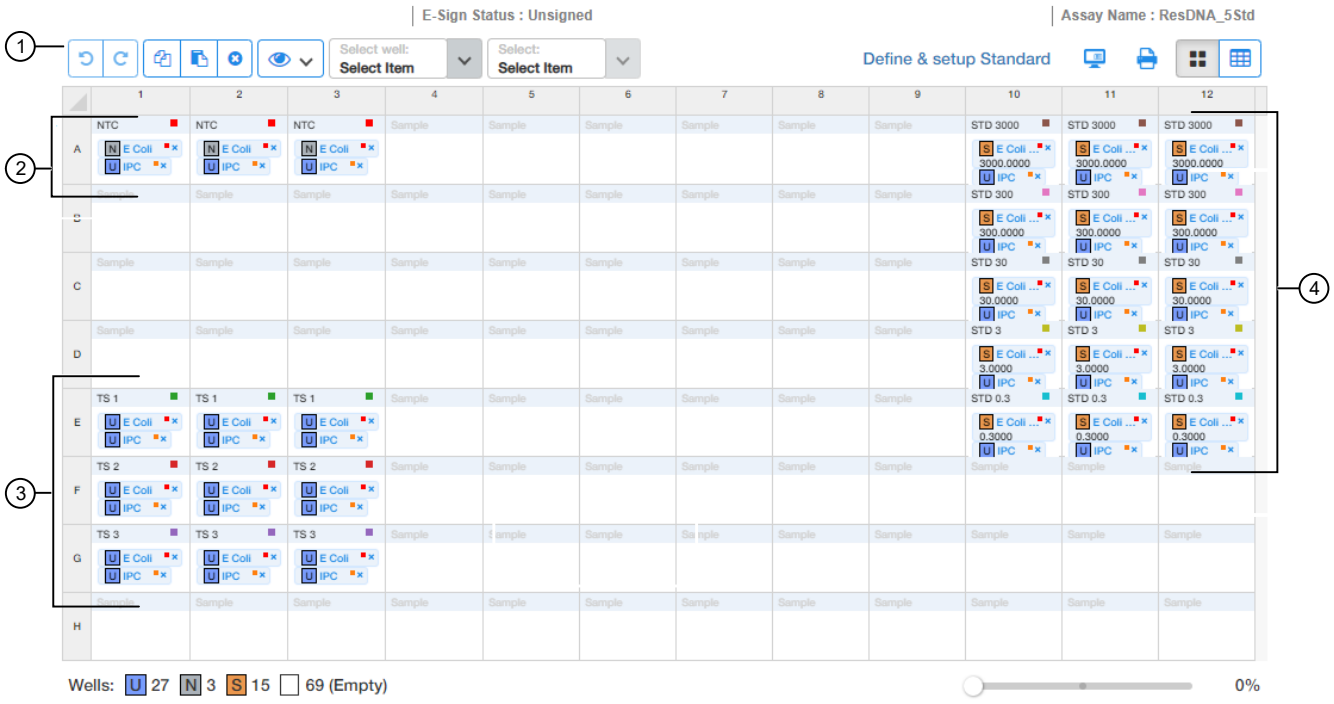


Figure 12 resDNASEQ™_5Std template default sample plate layout

① Toolbar (in order: Undo, Redo, Copy, Paste, Delete, View)
② 3 No Template Control (NTC) samples
③ 3 default **Samples**
④ Standard curve dilutions (S) in triplicate

7. Click **Next**.
   The **Run** tab is displayed.

8. Experiments are auto-saved in the software. To save, exit the experiment. The software prompts you to save changes. Click **Yes**.

   Note: Clicking **Save As** will create a copy of the experiment.

9. Assemble the PCR reactions following the manufacturer's instructions for the reagents and following the plate layout set up in the template. See *resDNASEQ™ Quantitative DNA Kits User Guide* (Pub. No. 4469836).

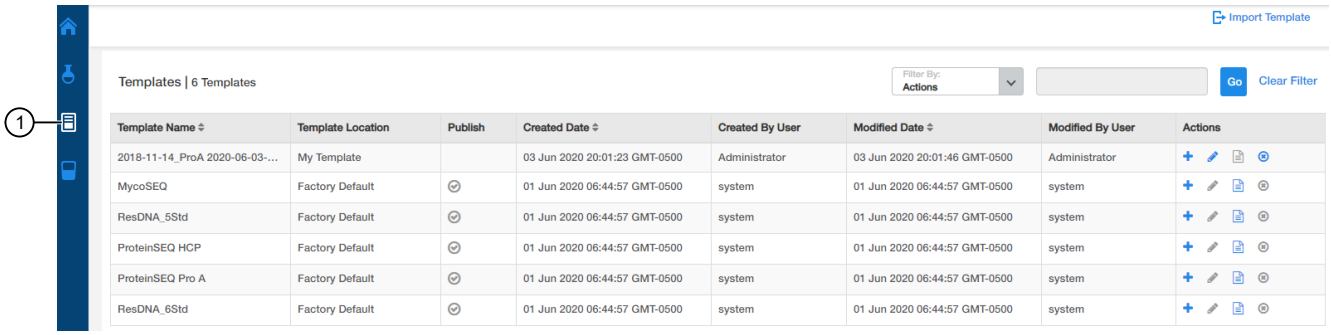
Immediately proceed to “Load the plate in the instrument” on page 36.

Create a resDNASEQ™ template (Plasmid DNA quantitation)

resDNASEQ™ assays quantifying residual plasmid DNA do not use a **Factory default/Admin Defined Template**. Create a new template before the first use of these assays.

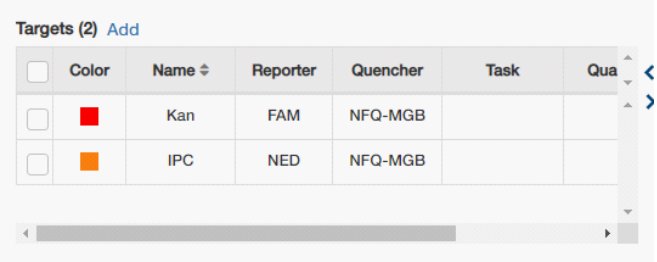
Note: For synthetic Vero assays, follow the instructions for the 6 standard template in "Create a resDNASEQ™ experiment (Genomic DNA quantitation)" on page 47.

1. In the **Home** screen, click **Templates** in the left navigation pane.



1 **Templates** icon

2. Click **Create New** next to the **ResDNA_5Std** factory default template.
3. Click **Next** to move to the **qPCR Method** screen.
4. Click **Next** to move to the **Plate Setup** screen.
5. In the **Plate Setup** screen, add the **Targets** and **Reporters**.



For the resDNASEQ™ Quantitative Plasmid DNA - Kanamycin Resistance Gene Kit, this is the FAM™ dye for the kanamycin (Kan) target and the NED™ dye for the IPC.

6. Click **Save as Template**.
7. Enter a **Template Name** and description, then select **Admin Defined** and **Locked**. Click **Save**.
   The template is saved, and can be accessed from **Templates** in the **Home** screen.
8. Click **Templates** in the **Home** screen, then open the new template.

   Note: The template must be saved prior to editing the **Analysis Settings**

9. Click **Analysis Settings**, then deselect **Default Settings**.

10. Enter new thresholds for the targets.

Table 1 resDNASEQ™ Quantitative Plasmid DNA - Kanamycin Resistance Gene Kit

Target	Threshold
Kanamycin	0.04
IPC	0.02

11. Click Apply, then close the template.

12. In the **Home** screen, click **Templates** in the left navigation pane, then **Publish** the template.
See "Publish a template" on page 140.
The template is listed in the **Factory default/Admin Defined Templates**.

Create a resDNASEQ™ experiment (Plasmid DNA quantitation)

resDNASEQ™ assays quantifying residual plasmid DNA do not use a **Factory default/Admin Defined Template**. Create a new template before the first use of these assays.

1. In the **Home** screen, click **Factory default/Admin Defined Templates**, then select the custom plasmid DNA **resDNASEQ** template created in "Create a resDNASEQ™ template (Plasmid DNA quantitation)" on page 51.

Note: To create an experiment from an existing resDNASEQ™ experiment, see "Create a copy of an existing experiment" on page 144.

2. In the **Experiment Properties** pane of the **Setup** tab:
   a. (*Optional*) Change the system-generated name of the experiment.

   Note: Names must be unique. Deleted experiment names can not be reused.

   b. (*Optional*) Enter the plate **Barcode**, then add **Comments**.

   Note: Comments are not editable post analysis.

   Default resDNASEQ™ settings (cannot be changed)
   - **Experiment Type** is **Quantitation-Standard Curve**
   - **Chemistry** is **TaqMan™ Reagents**
   - **Ramp Speed** is **Standard - 2hrs**

   c. Click **Next**.

   Note: Experiment names cannot be changed after this step.

3. In the **qPCR Method** pane of the **Setup** tab, view the default volume and cycling conditions (cannot be changed).

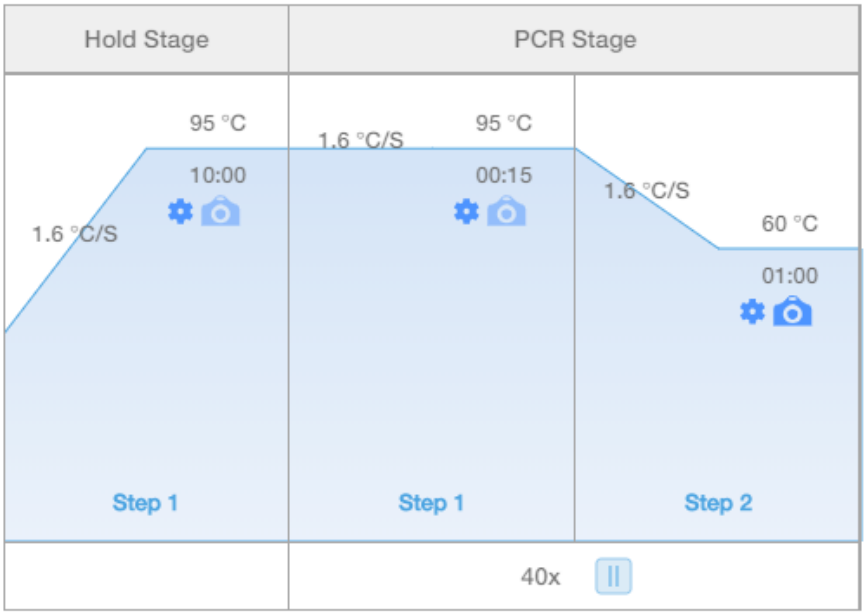
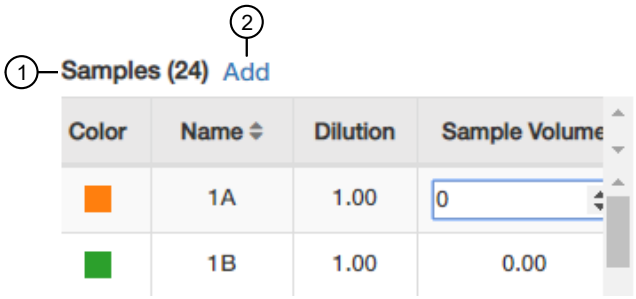


Figure 13 resDNASEQ™ template default cycling conditions

4. Click **Next**.

5. In the **Samples** pane of the **Setup** tab, enter the sample **Name** and **Dilution**. **Sample Volume** is not applicable. Add additional **Samples** if needed.

IMPORTANT! Do not change the **Targets**.



① **Samples** pane
② **Add**—adds additional samples

6. In the **Samples** pane of the **Setup** tab, scroll to the right, then enter the spike information.

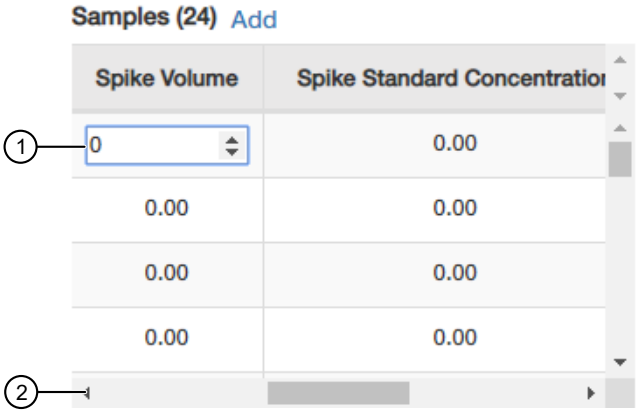
   For more information on plate setup, see “Assign plate and well attributes” on page 134.

   - **Sample Volume**—not applicable; leave as default (0).
   - **Spike Volume**—volume of DNA added to the PCR (set to 10).
   - **Spike Standard Concentration**—expected spike amount per reaction.
   - **Reference**—the non-spiked sample; the mean quantity of reference is subtracted during % recovery calculation.

- **Spike Input**—automatically calculated (double check if correct).

  Note: If incorrect, be sure **Spike Volume** is set to 10 and **Spike Standard Concentration** is the expected pg spike per PCR reaction.

- (Optional) **Comments**
- **Protein Concentration**—Sample protein concentration (if Total DNA in pg DNA/mg Protein is required).



① Textbox—type in the value, or use the up and down arrows

② Scroll bar—scroll to find the spike parameter

For more information on plate setup, see “Assign plate and well attributes” on page 134.

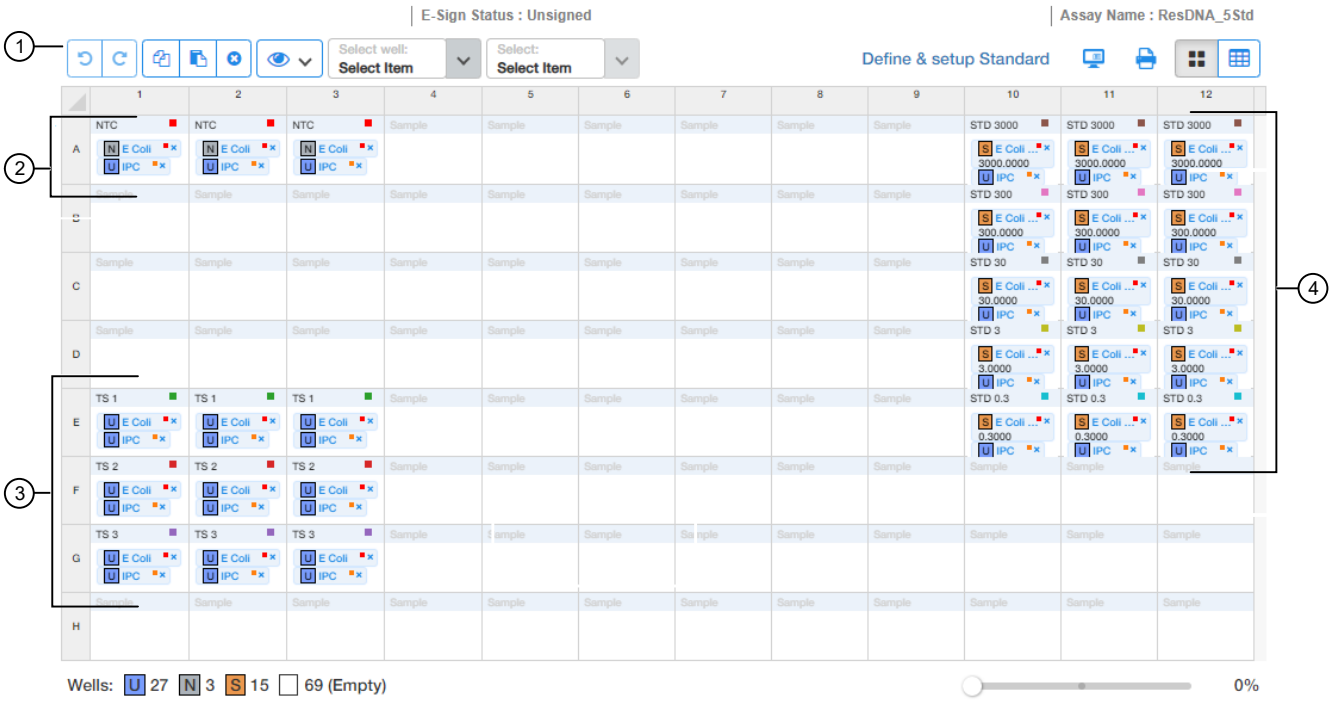


Figure 14 resDNASEQ™_5Std template default sample plate layout

① Toolbar (in order: Undo, Redo, Copy, Paste, Delete, View)
② 3 No Template Control (NTC) samples
③ 3 default **Samples**
④ Standard curve dilutions (S) in triplicate

7. Click **Next**.
   The **Run** tab is displayed.

8. Experiments are auto-saved in the software. To save, exit the experiment. The software prompts you to save changes. Click **Yes**.

   Note: Clicking **Save As** will create a copy of the experiment.

9. Assemble the PCR reactions following the manufacturer's instructions for the reagents and following the plate layout set up in the template. See *resDNASEQ™ Quantitative DNA Kits User Guide* (Pub. No. 4469836).

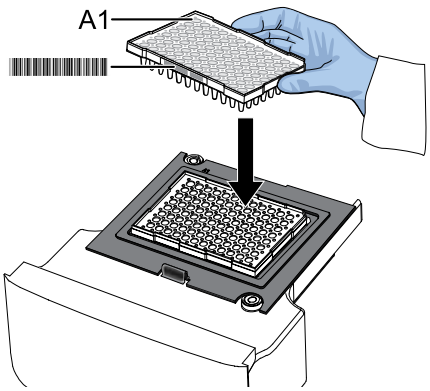
Immediately proceed to “Load the plate in the instrument” on page 36.

Load the plate in the instrument

CAUTION! Use optical flat caps for tubes. Rounded caps can damage the heated cover.

Load the plate.

1. Touch ⏏ to eject the instrument drawer.
2. Load the plate onto the plate adapter so that:
   - Well A1 of the plate is in the top-left corner of the plate adapter.
   - The barcode faces the front of the instrument.



IMPORTANT! The instrument should be used by trained operators who have been warned of the moving parts hazard.

Note: Do not remove the black plate adapter before loading a plate or tube strips. If used, tube strips can fit loosely in the adapter, but the heated cover applies the appropriate pressure to seat the tube strips securely in the adapter.

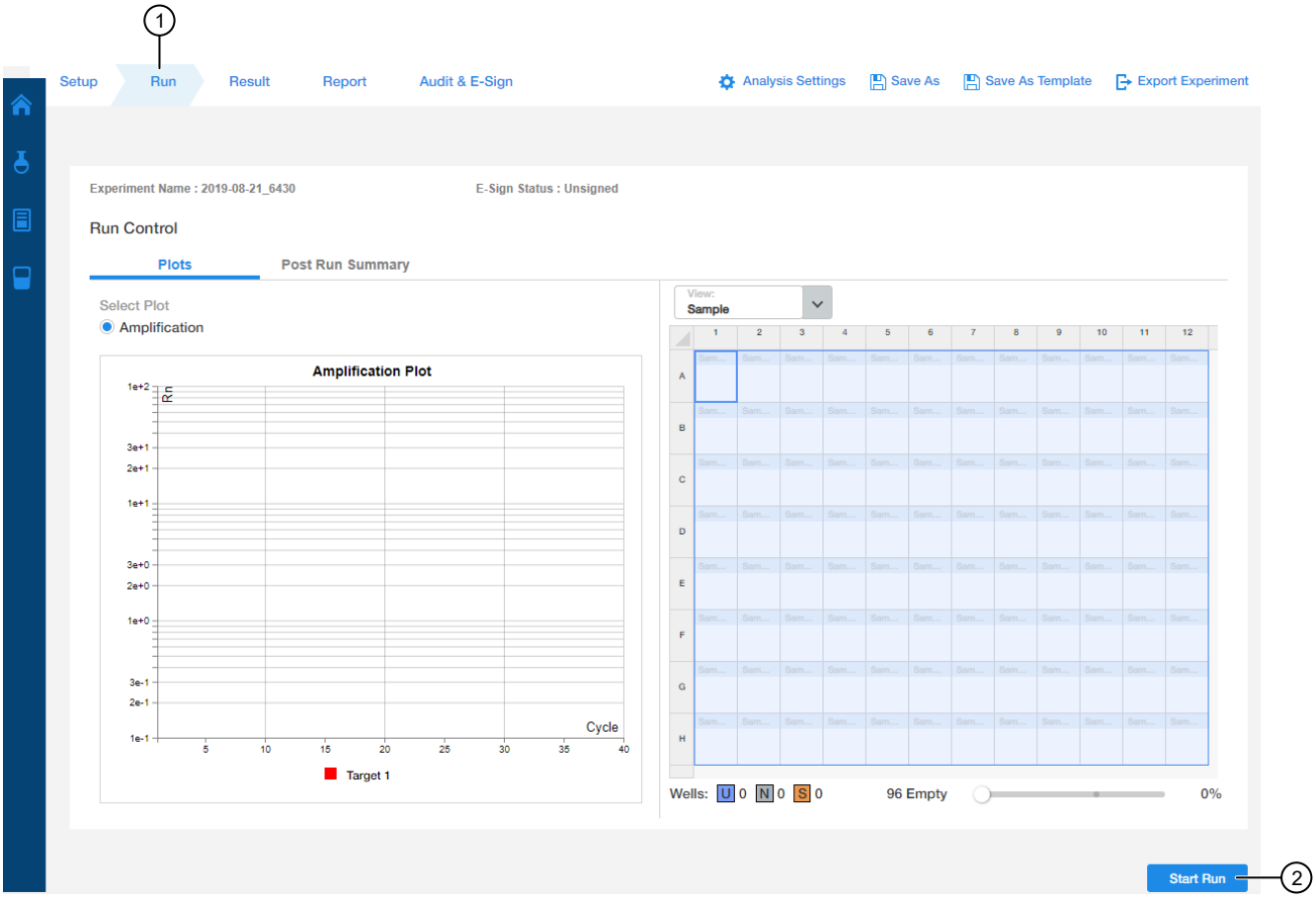
CAUTION! PHYSICAL INJURY HAZARD. During instrument operation, the plate temperature can reach 100°C. Allow it to cool to room temperature before handling.

3. Touch ⏏ to close the instrument drawer.

Start the run

Start the run in the AccuSEQ™ Software.

Option	Description
If the experiment is open	Click **Start Run**.
If the experiment is closed	1. Open the experiment. See “Open an experiment” on page 145. 2. Click the **Run** tab. 3. Click **Start Run**.



1 **Run** tab
2 **Start Run** button

A message stating **Run has been started successfully** is displayed when the run has started.

Monitor the run

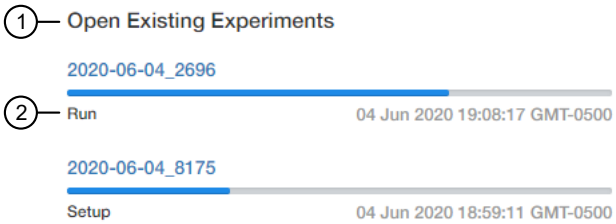
Monitor the run from one of the following places:

- On the instrument touchscreen. See the *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. A43322).
- In the **Monitor the Run** pane of the AccuSEQ™ Software **(Home)** screen.

1. Instrument name
2. Instrument status (Ready, Running, Offline)
3. Calibration status
   - Calibrated—All required calibrations are "Current". Required calibrations include: Background, ROI/Uniformity, and Dyes.
   - Not calibrated—None of the required calibrations are complete.
   - Requires calibration—One or more dyes are not calibrated.
4. Time lapsed (if a run is in progress)
5. Total run time
6. Experiment name

- In the **Open Existing Experiments** pane of the AccuSEQ™ Software **(Home)** screen. The experiment being run is the first experiment listed. Status is **Run**.

Note: When the run is complete, the status changes to **Analysis** and the bar changes to completely blue.



1. **Open Existing Experiments** pane
2. Experiment status

- In the **Run** tab of the AccuSEQ™ Real-Time PCR Software.

You can perform the following actions.

- Select wells in the plate layout to highlight respective curves in the plot.
- Hover over curves in the plot for well information.
- (*Optional*) Change what is displayed in the table wells of the plate layout, by selecting from the dropdown lists.

For more information, see “Run screen” on page 23.

On run completion, the **Post Run Summary** displays the run length, user and instrument information, and a list of any errors that occurred.

When the run is complete, unload the plate from the instrument.

Review results

Workflow: resDNASEQ™ experiments

Evaluate results in the Amplification Plot

▼

View and evaluate the Standard Curve Plot

▼

Review data for outliers and *(optional)* Omit outliers from analysis

▼

(Optional) Review the dye signal profile using the Multicomponent Plot

▼

(Optional) View and evaluate the Raw Data Plot

▼

(Optional) Review the flags in the QC Summary

▼

(Optional) Configure the analysis settings (View and configure the analysis settings)

IMPORTANT! If you omit wells or configure the analysis settings, click **Analyze** to reanalyze the data.

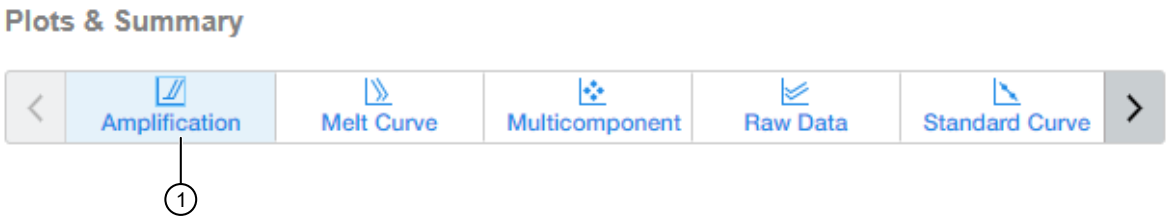
Evaluate the overall shape of the Amplification Plot curves

You can evaluate the overall shape of the **Amplification** curves in the **Result** tab.

Open the experiment in the AccuSEQ™ Software. See "Open an experiment" on page 145.

1. In the **Results Analysis** pane of the **Result** tab, select **Amplification** from the horizontal scroll bar.

   Note: If no data are displayed in the **Result** tab, click **Result Analysis**, then click **Analyze**.



① Amplification Plot

   The **Amplification Plot** is displayed for the selected wells in the **(Grid View)** .

2. Ensure that the **Target** is correct.

3. (*Optional*) Click **(Settings)** , then make the following selections:

   - **Plot Type**: **ΔRn, Rn, or C_T**
   - **Graph Type**: **Log or Linear**
   - **Show**: **Legend**, **Cq Mark** (the cycle at which the curvature of the amplification curve is maximal), or **Unselected**
   - **Plot Color**: **Target**, **Sample**, **Well**, or **Flag_Status**
   - **Threshold**: Select **Auto** or specify a threshold, then decide whether to **Show Threshold**.
   - **Baseline**: Decide whether to **Show Baseline**.

4. (*Optional*) Adjust the **(Plot Properties)**.

   a. In the **General** tab, add a **Plot Title**, adjust the **Font** and **Color**, then click **Apply**.

   b. In the **X Axis** or **Y Axis** tabs, you can:

      - Add a **Label**
      - Select whether you want **Tick Marks**
      - Select **Auto-adjust range** or enter minimum and maximum values

        Note: The minimum value must be greater than 0.

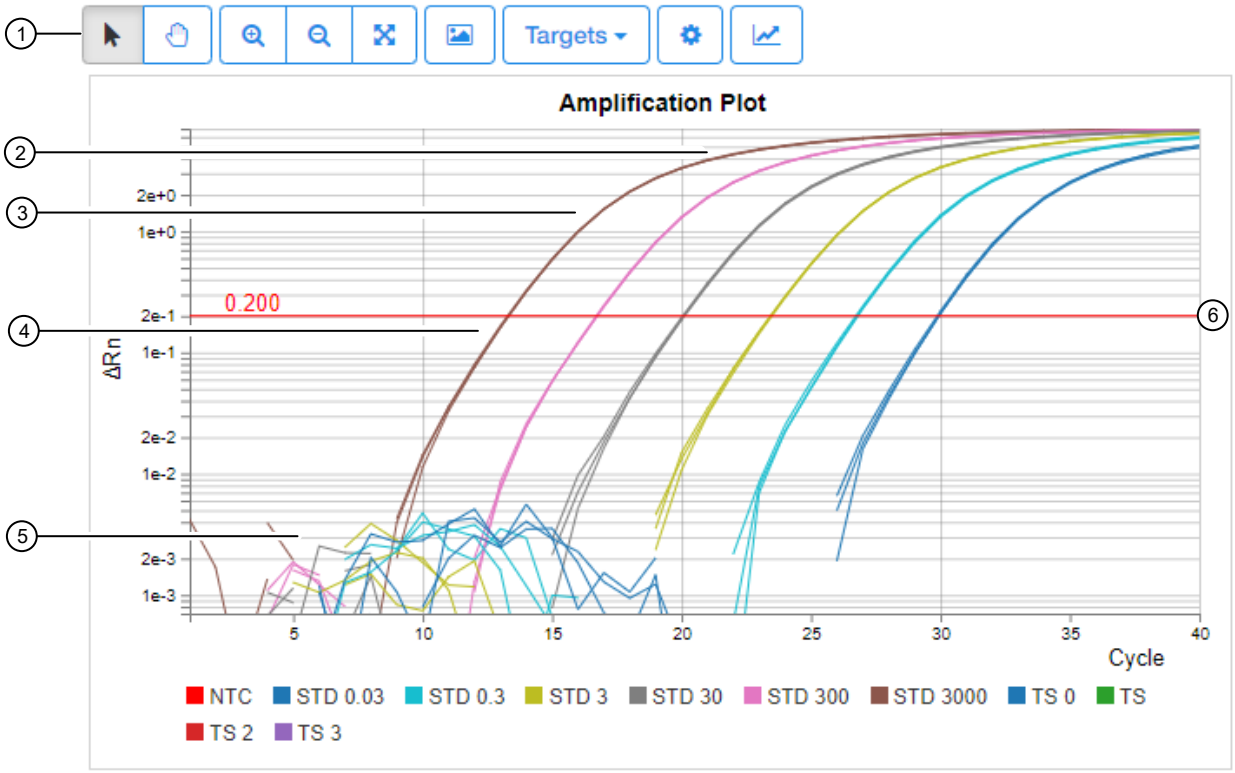


Figure 15 Typical Amplification Plot

① Amplification Plot tools
② Plateau phase
③ Linear phase
④ Exponential (geometric) phase
⑤ Baseline phase
⑥ Threshold. In a multiplex assay, only one threshold is shown per target. Select the desired target to display the threshold line. The threshold line is not displayed if **All** target is selected.

Standard Curve Plot overview

The Standard Curve Plot displays the standard curve for samples that are designated as standards. The software calculates the quantity of an unknown target from the standard curve.

Table 2 Results or metrics to review in the Standard Curve Plot

Results or metrics	Description	Criteria for evaluation
Slope and amplification efficiency	The amplification efficiency is calculated using the slope of the regression line in the standard curve.	A slope close to –3.3 indicates optimal, 100% PCR amplification efficiency. Factors that affect amplification efficiency: • Range of standard quantities—use a broad range of standard quantities, 5 to 6 logs. • Number of standard replicates—include replicates to decrease the effects of pipetting inaccuracies. • PCR inhibitors—PCR inhibitors and contamination in the reaction can reduce amplification efficiency. • Other possible factors: – Inaccurate sample or reagent pipetting – Incorrect plate setup
R^2 value (correlation coefficient)	The R^2 value is a measure of the closeness of fit between the regression line and the individual C_q data points of the standard reactions.	• A value of 1.00 indicates a perfect fit between the regression line and the data points. • An R^2 value > 0.9900 is desirable.
C_t values	The threshold cycle (C_t) is the PCR cycle number at which the fluorescence level meets the threshold.	(Custom assays only) A C_t value > 8 and < 35 is desirable. • C_t value < 8—there may be too much template in the reaction. • C_t value > 35—there may be a low amount of target in the reaction; for C_t values > 35, expect a higher standard deviation.

View and evaluate the Standard Curve Plot

1. In the **Result** tab, select **Standard Curve** in the horizontal scroll bar.

① Standard Curve plot

2. (*Optional*) Click **Table View** to configure the plot, then make the following selections:
   - **Targets**: Select the target of interest
   - **Plot Settings**: Select the **Plot Color Sample**, **Target**, or **Task**
   - **Plot Properties**: Edit **Plot Title**, change fonts, colors, labels, and select whether to auto-adjust or manually enter the range.

     Note: The minimum value must be greater than 0.
   - **Save Image**: Save the image.
   - Use the select, pan, and zoom options to interact with the plot.
3. Select all wells in the **Grid View**
   The Standard Curve Plot is displayed. The slope, R^2 value, amplification efficiency, and error are displayed below the plot.
4. Confirm that the slope, R^2 value, and standard error meet the experimental criteria.
   (Recommended) $R^2 \geq 0.99$.
5. Visually check that all unknown sample values fall within the standard curve range.

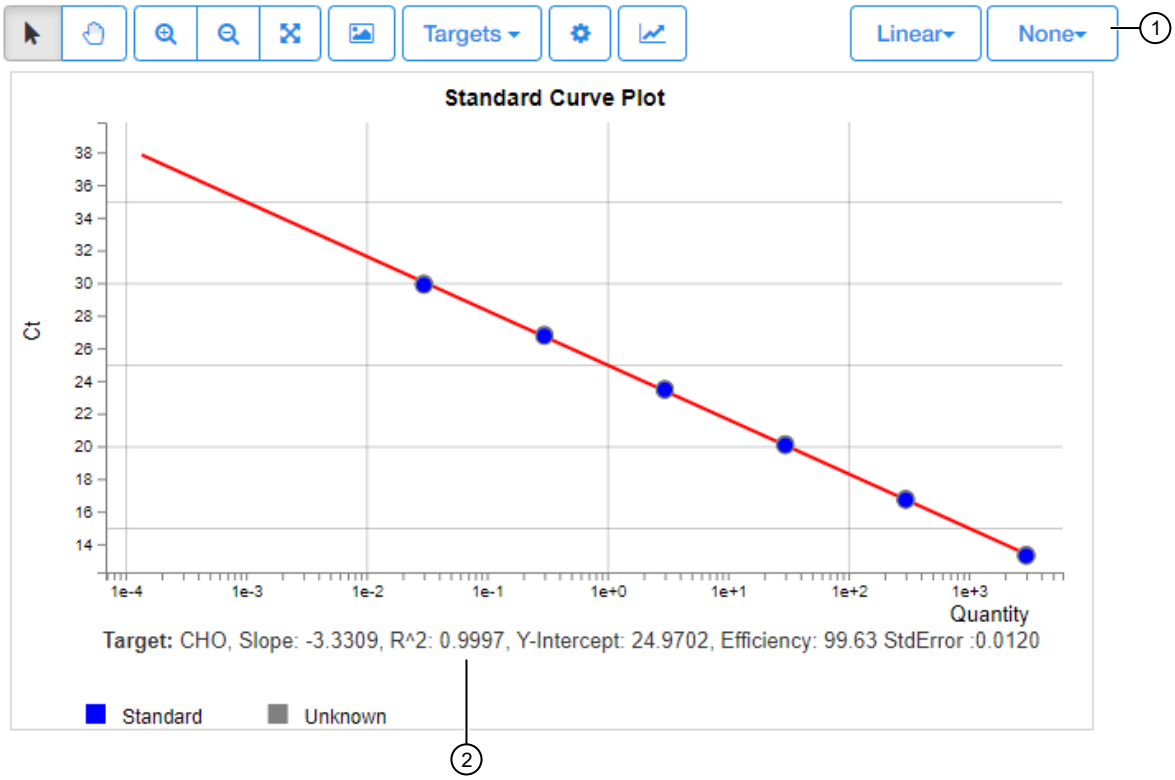


Figure 16 Example Standard Curve Plot

① Default plot settings
② R^2 value

Proceed to one of the following sections.

If	Then
The amplification and standard curve plots were normal and there were no flags in the wells	Proceed to "Export data and print reports" on page 172
The plate had several wells with abnormal amplification or which contained flags	Repeat the experiment, adjusting the template setup and analysis settings to improve results. or Proceed to Chapter 9, "Review the results and generate a report" and follow the more comprehensive instructions for reviewing the data. Data can be reanalyzed after omitting wells or changing the **Analysis Settings**.

5 Set up, run, and review ProteinSEQ™ experiments

Overview

The ProteinSEQ™ Protein Detection System integrates real-time PCR assays, antibodies, instruments, and software to quantify host cell protein contaminants from cell lines.

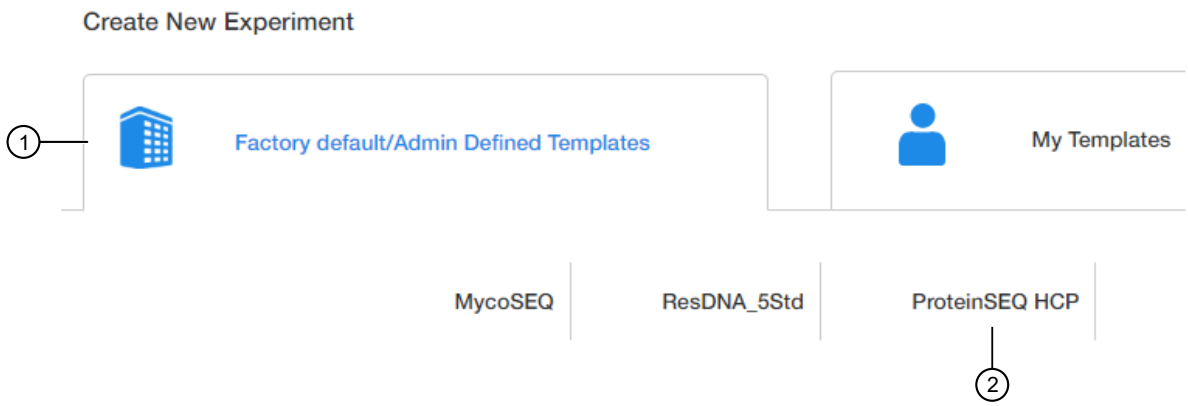
ProteinSEQ™ experiments use a standard curve to determine absolute target quantity in your samples. The software measures amplification of the target in a standard dilution series and in test samples. The software then generates a non-linear standard curve using data from the standard dilution series. The standard curve is used to interpolate the absolute quantity of target in the test samples.

For detailed instructions on running the ProteinSEQ™ assay, see the *ProteinSEQ™ CHO Host Cell Protein Quantification Kit User Guide* (Pub. No. MAN0010806).

Create a ProteinSEQ™ experiment

1. In the **Home** screen, click the **Factory default/Admin Defined Template** tab, then select the **ProteinSEQ HCP** template.

Note: To create a copy of an existing ProteinSEQ™ experiment, see “Create a copy of an existing experiment” on page 144.



① **Factory default/Admin Defined Template** tab
② **ProteinSEQ** template (HCP)

2. In the **Experiment Properties** pane of the **Setup** tab:
   a. (*Optional*) Change the system-generated name of the experiment.

   Note: Names must be unique. Deleted experiment names can not be reused.

   b. (*Optional*) Enter the plate **Barcode**, then add **Comments**.

   Note: Names and comments are not editable post analysis.

   Default ProteinSEQ™ settings (cannot be changed)
   - **Experiment Type—Quantitation-Standard Curve**
   - **Chemistry—TaqMan™ Reagents**
   - **Ramp Speed—Fast - 40mins**

   c. Click **Next**.

   Note: Experiment names cannot be changed after this step.

3. In the **qPCR Method** pane of the **Setup** tab, view the default volume and cycling conditions (cannot be changed).

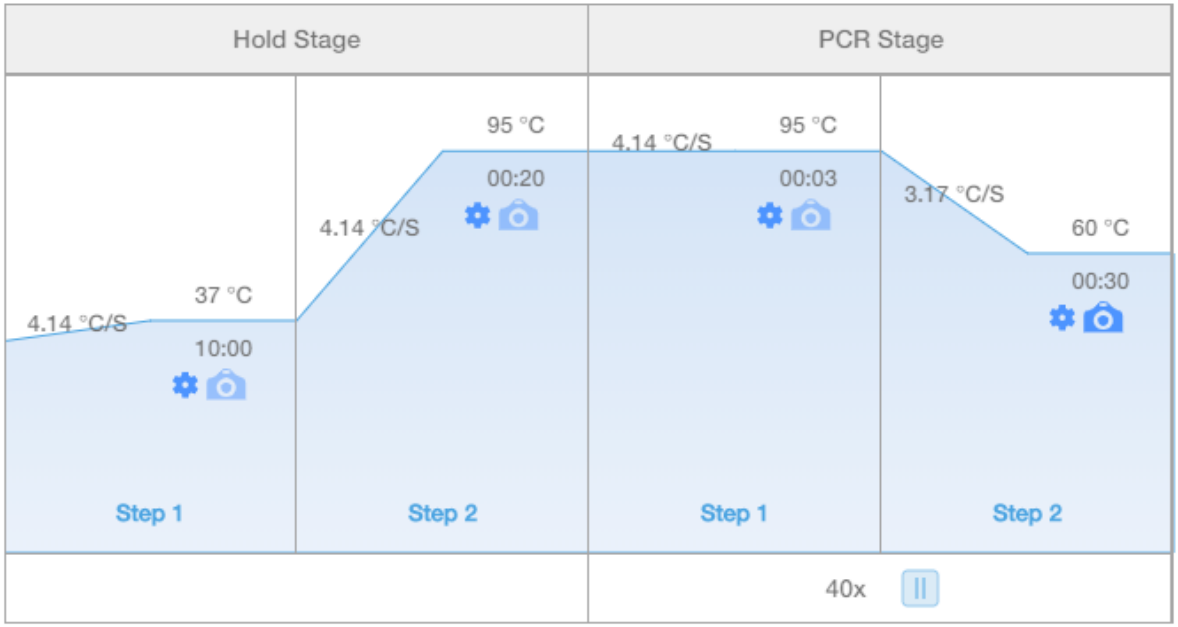
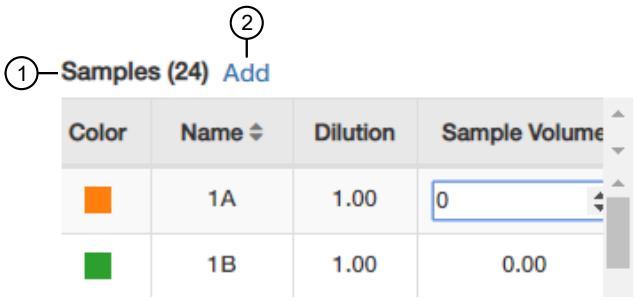


Figure 17 ProteinSEQ™ template default cycling conditions

4. Click **Next**.

5. In the **Samples** pane of the **Setup** tab, enter the sample **Name**, **Dilution**, and **Sample volume**. Add additional **Samples** if needed.

IMPORTANT! Do not change the **Targets**.

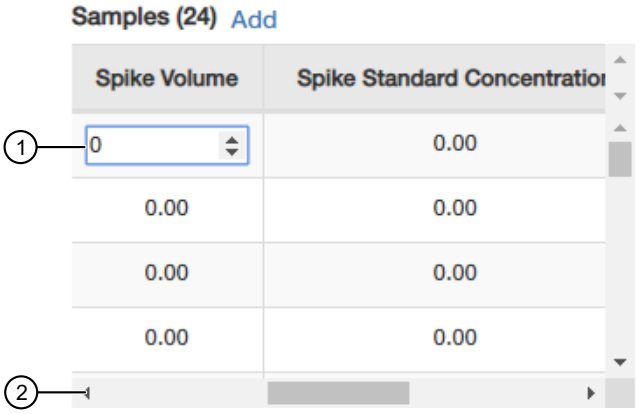


① **Samples** pane
② **Add**—adds additional samples

6. In the **Samples** pane of the **Setup** tab, scroll to the right, then enter the spike information.
   - **Spike Volume**—volume of sample to be spiked (for example, 180 µL).
   - **Spike Standard Concentration**—concentration of standard used in spiking (for example, 625 ng/mL).
   - **Reference**—the non-spiked sample; the mean quantity of reference is subtracted during % recovery calculation.
   - **Spike Input**—automatically calculated (double check that the amount is correct).

     Note: If incorrect, double check entries.

   - (Optional) **Comments**



① Textbox—type in the value, or use the up and down arrows
② Scroll bar—scroll to find the spike parameter

For more information on plate setup, see “Assign plate and well attributes” on page 134.

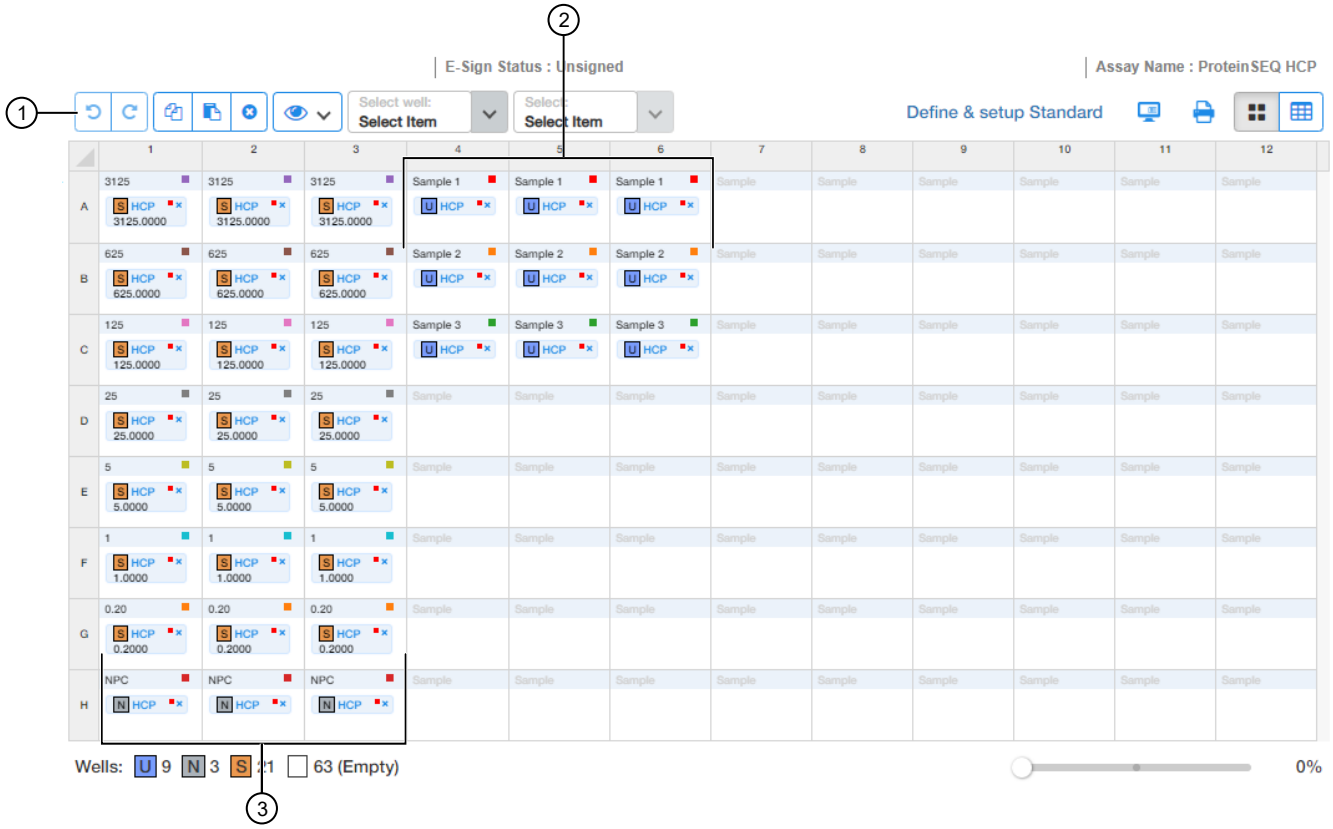


Figure 18 ProteinSEQ™ HCP template default sample plate layout

① Toolbar (in order: Undo, Redo, Copy, Paste, Delete, View)
② 7 standards in triplicate (rows A–G); No Protein Controls (NPCs) in triplicate (row H)
③ 3 default **Samples**

7. Click **Next**.
   The **Run** tab is displayed.

8. Experiments are auto-saved in the software. To save, exit the experiment. The software prompts you to save changes. Click **Yes**.

   Note: Clicking **Save As** will create a copy of the experiment.

9. Assemble the PCR reactions following the manufacturer's instructions for the reagents and following the plate layout set up in the template. See *ProteinSEQ™ CHO Host Cell Protein Quantification Kit User Guide* (Pub. No. MAN0010806).

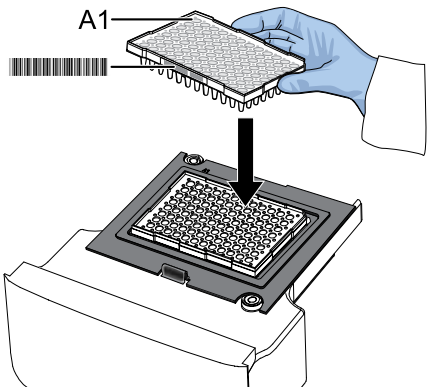
Immediately proceed to "Load the plate in the instrument" on page 36.

Load the plate in the instrument

CAUTION! Use optical flat caps for tubes. Rounded caps can damage the heated cover.

Load the plate.

1. Touch ⏏ to eject the instrument drawer.
2. Load the plate onto the plate adapter so that:
   - Well A1 of the plate is in the top-left corner of the plate adapter.
   - The barcode faces the front of the instrument.



IMPORTANT! The instrument should be used by trained operators who have been warned of the moving parts hazard.

Note: Do not remove the black plate adapter before loading a plate or tube strips. If used, tube strips can fit loosely in the adapter, but the heated cover applies the appropriate pressure to seat the tube strips securely in the adapter.

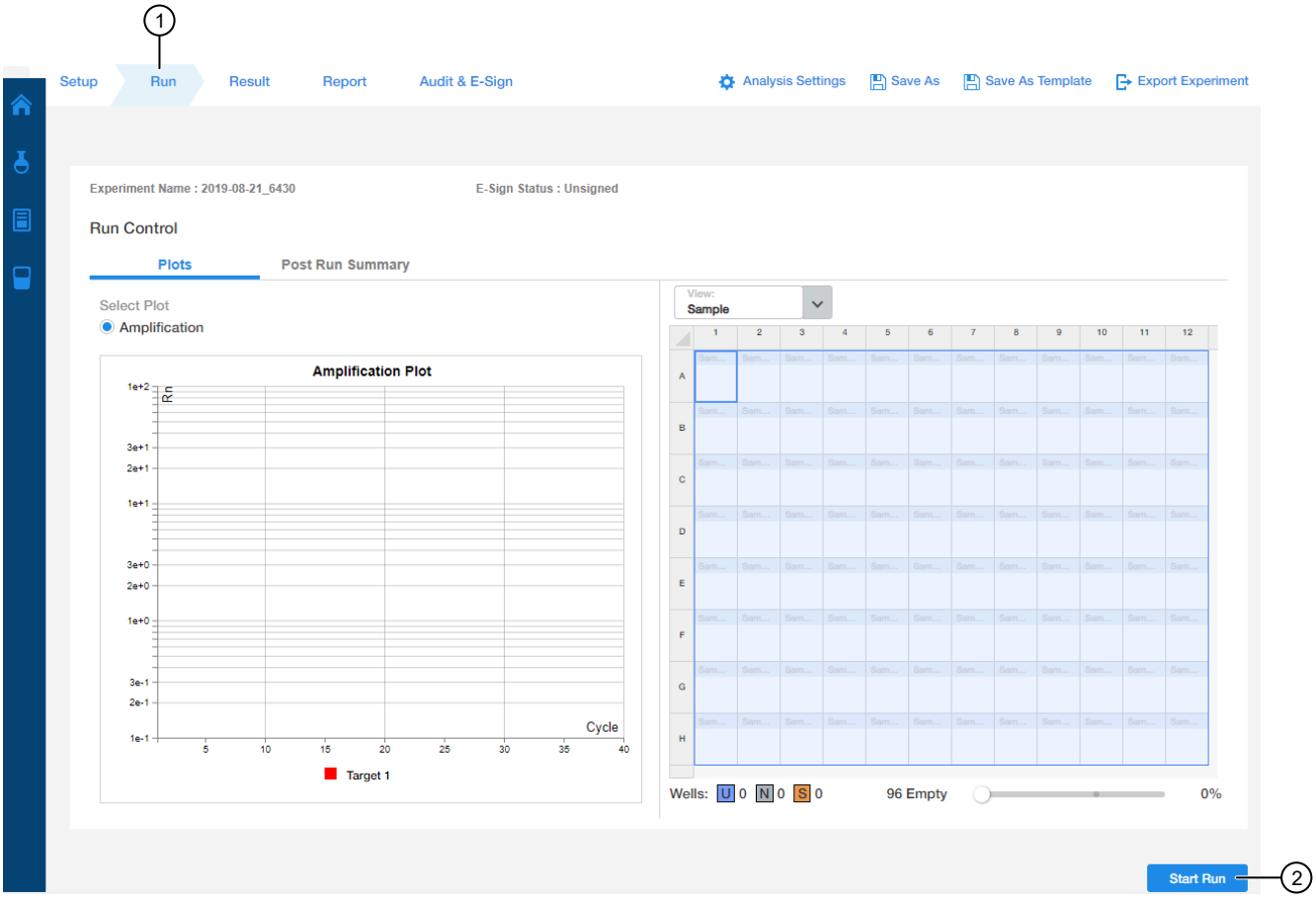
CAUTION! PHYSICAL INJURY HAZARD. During instrument operation, the plate temperature can reach 100°C. Allow it to cool to room temperature before handling.

3. Touch ⏏ to close the instrument drawer.

Start the run

Start the run in the AccuSEQ™ Software.

Option	Description
If the experiment is open	Click **Start Run**.
If the experiment is closed	1. Open the experiment. See “Open an experiment” on page 145. 2. Click the **Run** tab. 3. Click **Start Run**.



1 **Run** tab
2 **Start Run** button

A message stating **Run has been started successfully** is displayed when the run has started.

Monitor the run

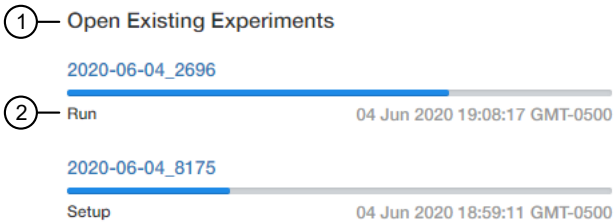
Monitor the run from one of the following places:

- On the instrument touchscreen. See the *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. A43322).
- In the **Monitor the Run** pane of the AccuSEQ™ Software **(Home)** screen.

1. Instrument name
2. Instrument status (Ready, Running, Offline)
3. Calibration status
   - Calibrated—All required calibrations are "Current". Required calibrations include: Background, ROI/Uniformity, and Dyes.
   - Not calibrated—None of the required calibrations are complete.
   - Requires calibration—One or more dyes are not calibrated.
4. Time lapsed (if a run is in progress)
5. Total run time
6. Experiment name

- In the **Open Existing Experiments** pane of the AccuSEQ™ Software **(Home)** screen. The experiment being run is the first experiment listed. Status is **Run**.

Note: When the run is complete, the status changes to **Analysis** and the bar changes to completely blue.



1. **Open Existing Experiments** pane
2. Experiment status

- In the **Run** tab of the AccuSEQ™ Real-Time PCR Software.

You can perform the following actions.

- Select wells in the plate layout to highlight respective curves in the plot.
- Hover over curves in the plot for well information.
- (*Optional*) Change what is displayed in the table wells of the plate layout, by selecting from the dropdown lists.

For more information, see “Run screen” on page 23.

On run completion, the **Post Run Summary** displays the run length, user and instrument information, and a list of any errors that occurred.

When the run is complete, unload the plate from the instrument.

Review results

Workflow: ProteinSEQ™ experiments

“Evaluate the overall shape of the Amplification Plot curves” on page 74

▼

“View and evaluate the Standard Curve Plot” on page 76

▼

Review data for outliers and *(optional)* Omit outliers from analysis

▼

(Optional) Review the dye signal profile using the Multicomponent Plot

▼

(Optional) View and evaluate the Raw Data Plot

▼

(Optional) Review the flags in the QC Summary

▼

(Optional) Configure the analysis settings (View and configure the analysis settings)

IMPORTANT! If you omit wells or configure the analysis settings, click **Analyze** to reanalyze the data.

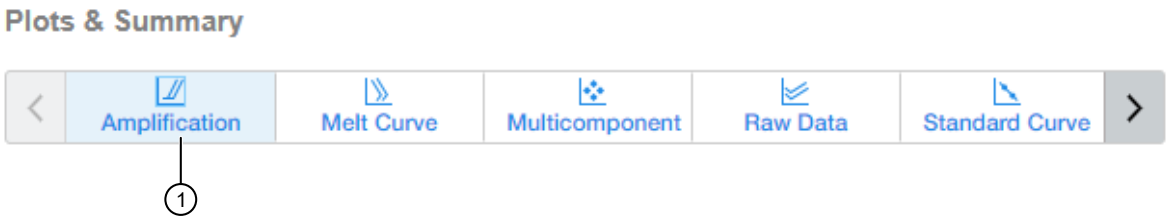
Evaluate the overall shape of the Amplification Plot curves

You can evaluate the overall shape of the **Amplification** curves in the **Result** tab.

Open the experiment in the AccuSEQ™ Software. See "Open an experiment" on page 145.

1. In the **Results Analysis** pane of the **Result** tab, select **Amplification** from the horizontal scroll bar.

   Note: If no data are displayed in the **Result Analysis** pane, then click **Analyze**.

   ① Amplification Plot

   The **Amplification Plot** is displayed for the selected wells in the **(Grid View)** .

2. Ensure that the **Target** is correct.

3. (*Optional*) Click **(Plot Settings)** , then make the following selections:

   - **Plot Type**: **ΔRn, Rn, or C_T**
   - **Graph Type**: **Log or Linear**
   - **Show**: **Legend**, **Cq Mark** (the cycle at which the curvature of the amplification curve is maximal), or **Unselected**
   - **Plot Color**: **Target**, **Sample**, **Well**, or **Flag_Status**
   - **Threshold**: Select **Auto** or specify a threshold, then decide whether to **Show Threshold**.
   - **Baseline**: Decide whether to **Show Baseline**.

4. (*Optional*) Adjust the **(Plot Properties)**.

   a. In the **General** tab, add a **Plot Title**, adjust the **Font** and **Color**, then click **Apply**.

   b. In the **X Axis** or **Y Axis** tabs, you can:

      - Add a **Label**
      - Select whether you want **Tick Marks**
      - Select **Auto-adjust range** or enter minimum and maximum values

        Note: The minimum value must be greater than 0.

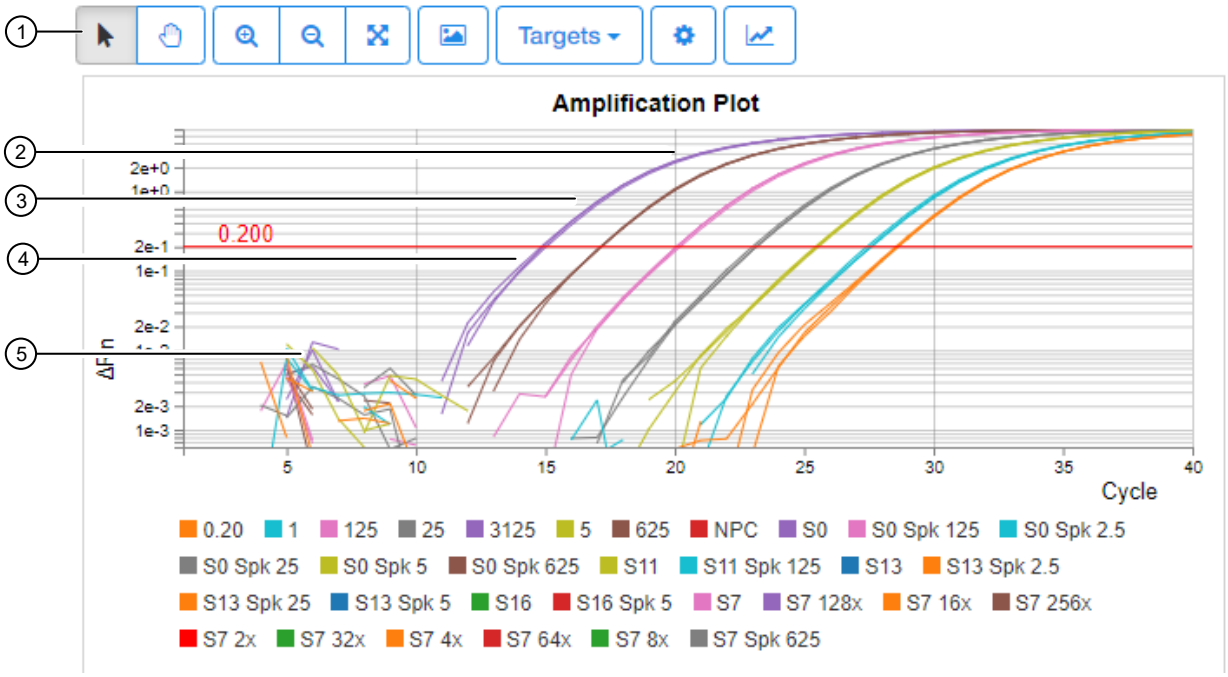


Figure 19 Typical Amplification Plot

① Amplification Plot tools
② Plateau phase
③ Linear phase
④ Exponential (geometric) phase
⑤ Baseline phase

Standard Curve Plot overview

The Standard Curve Plot displays the standard curve for samples that are designated as standards. The software calculates the quantity of an unknown target from the standard curve.

AccuSEQ™ Software v3.1 fits ProteinSEQ™ experiment standards to a standard curve using non-linear method to obtain interpolated values for unknown samples.

- 4PL is commonly used for symmetric curves with asymptotes for both the lower and upper Protein A concentrations.
- 5PL is commonly used if the curve is asymmetric or if either the lower or upper asymptote is not present.
- Apply 1/Y or 1/Y^2 weighting according to your criteria

Evaluate dynamic range using the %CV and the quality of the curve fit.

- R^2 is appropriate for judging linear fits but it is not an appropriate metric for evaluating the quality of a non-linear fit.
- Common acceptance criteria for non-linear curve fits are back-calculation values of 80-120% throughout the curve and 75-125% at the Lower Limit of Quantification (LLOQ).
- Common acceptance criteria for precision are %CV ≤20% throughout the curve and ≤25% at the LLOQ.

View and evaluate the Standard Curve Plot

1. In the **Result** tab, select **Standard Curve** in the horizontal scroll bar.

① Standard Curve plot

2. (*Optional*) Click **Table View** to configure the plot, then make the following selections:
   - **Targets**: Select the target of interest
   - **Plot Settings**: Select the **Plot Color Sample**, **Target**, or **Task**
   - **Plot Properties**: Edit **Plot Title**, change fonts, colors, labels, and select whether to auto-adjust or manually enter the range.

     Note: The minimum value must be greater than 0.
   - **Save Image**: Save the image.
   - Use the select, pan, and zoom options to interact with the plot.

3. Select all wells in the **Grid View**
   The Standard Curve Plot is displayed.

4. Select **4PL** and **None** for plot settings.
   The equation and **Target** are displayed below the plot.

5. Confirm that the back-calculation values meet the experimental criteria.

6. Visually check that all unknown sample values fall within the standard curve range.

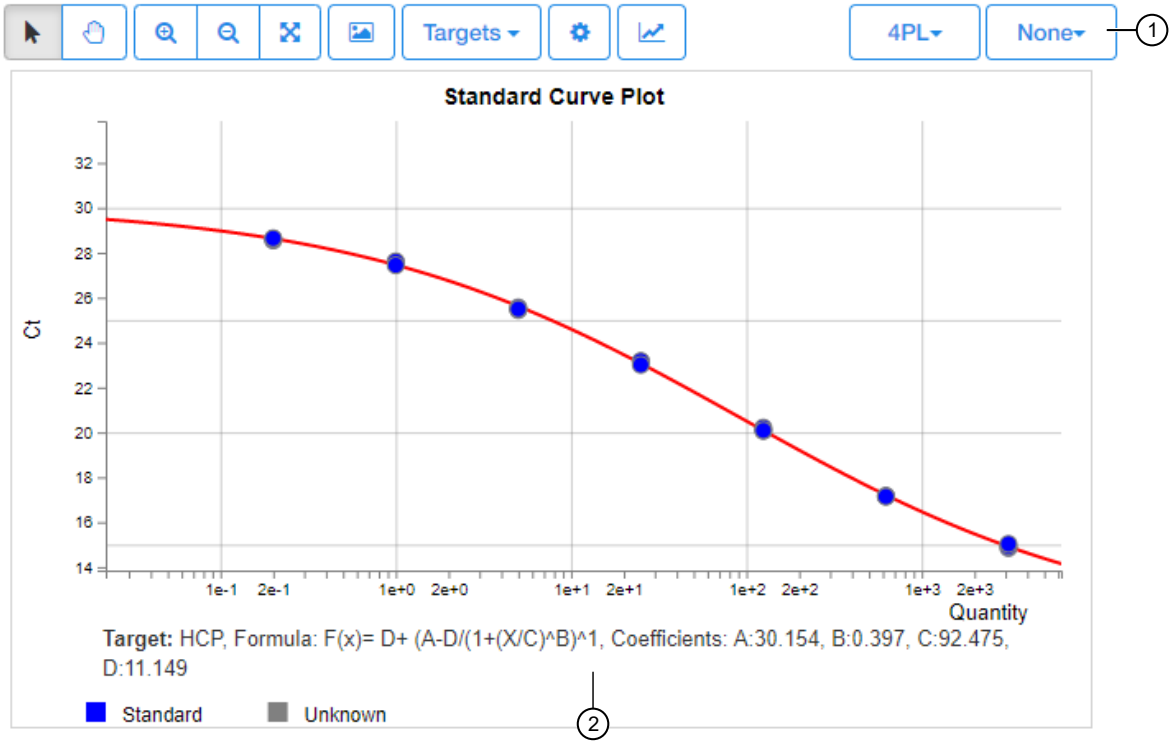


Figure 20 Example Standard Curve Plot

① Default plot settings

② Target, plot, and slope information:

- F(x) is the final protein concentration.
- A—Minimum asymptote. In a standard curve assay, this is the response value at 0 standard concentration.
- B—Hill's slope; refers to the steepness of the curve; should be positive or negative.
- C—Concentration at the inflection point; where the curvature changes direction or signs.
- D—Maximum asymptote. In a standard curve assay, this is the response value for infinite standard concentration.

Proceed to one of the following sections.

If	Then
The amplification and standard curve plots were normal and there were no flags in the wells	Proceed to "Export data and print reports" on page 172
The plate had several wells with abnormal amplification or which contained flags	Repeat the experiment, adjusting the template setup and analysis settings to improve results. or Proceed to Chapter 9, "Review the results and generate a report" and follow the more comprehensive instructions for reviewing the data. Data can be reanalyzed after omitting wells or changing the **Analysis Settings**.

6 Set up, run, and review ViralSEQ™ experiments

Overview

The ViralSEQ™ Detection Assays are used to detect or quantitate nucleic acids (DNA and RNA) from adventitious viruses or from viral vectors used in biopharmaceutical manufacturing.

ViralSEQ™ Detection Kits detect the presence of virus in cell culture samples, while ViralSEQ™ Quantitative Kits quantify the amount of virus in cell culture samples.

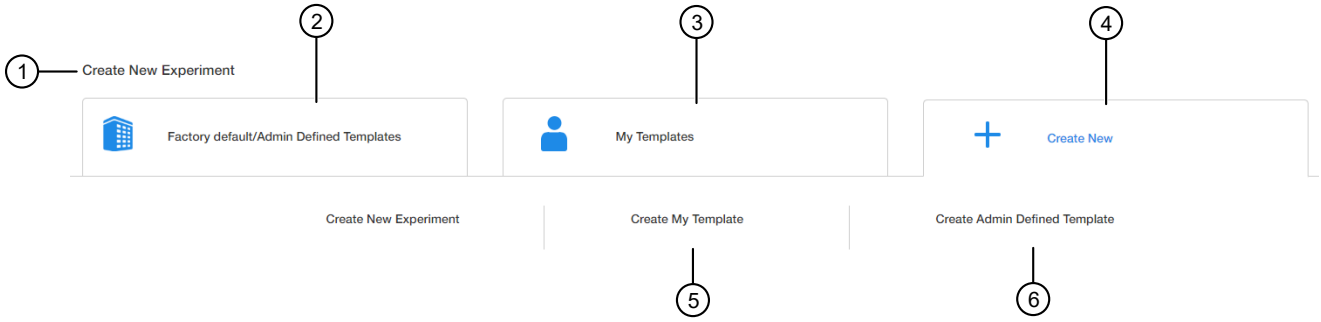
For detailed instructions on running the ViralSEQ™ assays, see the relevant ViralSEQ™ assay user guide.

Set up ViralSEQ™ Mouse Minute Virus (MMV) Real-Time PCR Detection Kit experiments

Create a ViralSEQ™ template

Create a new template in the **(Home)** screen of the AccuSEQ™ Real-Time PCR Software v3.1.

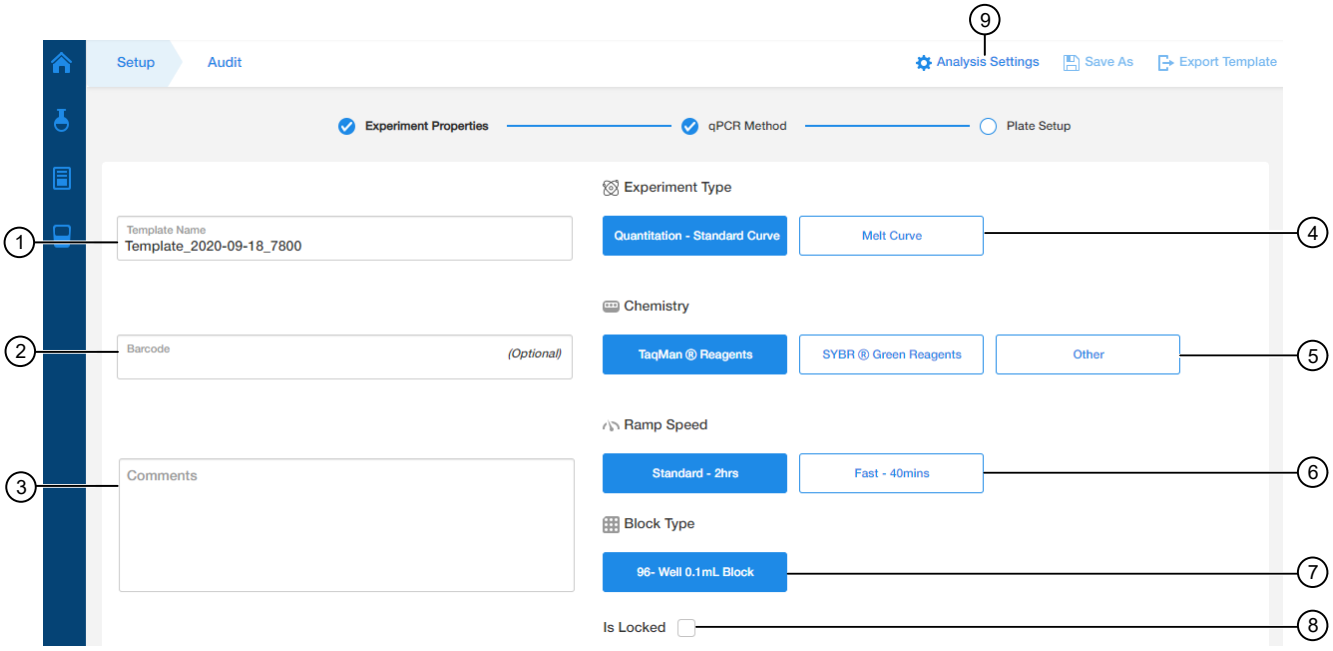
1. Click **Create New** on the home screen.



① **Create New Experiment** pane
② **Factory default/Admin Defined Templates**—List of existing default or Admin Defined templates. These templates can be used as templates for new experiments.
③ **My Templates**—List of templates available to the user that is signed in. These templates can be used as templates for new experiments.
④ **Create New**—Used to create an experiment or template with no pre-existing settings.
⑤ **Create My Template**—Used to create a new template (stored locally in **My Templates**).
⑥ **Create Admin Defined Template**—Used to create a new template (Administrator only).

2. Select **Create My Template** or **Create Admin Defined Template**.

3. Edit the **Experiment Properties** as required.



① Software-generated **Template Name**
② **Barcode** field
③ **Comments** field
④ **Experiment Type**
⑤ **Chemistry**
⑥ **Ramp Speed**
⑦ **Block Type** (fixed as a 96-Well 0.1mL block).
⑧ **Is Locked** checkbox (Only Administrators can create locked **Admin Defined Templates**).
⑨ **Analysis Settings**

a. In the **Template Name** field, specify the template name.

b. (*Optional*) Enter information in the **Comments** field.

c. In the **Setup** tab, select:

- **Experiment Type—Quantitation-Standard Curve**
- **Chemistry—TaqMan Reagents**
- **Ramp Speed—Standard-2hrs**
- **Block Type—96-Well 0.1mL Block**

d. (*Optional*) Select **Is Locked** to lock the template. If locked, users are unable to edit the template.

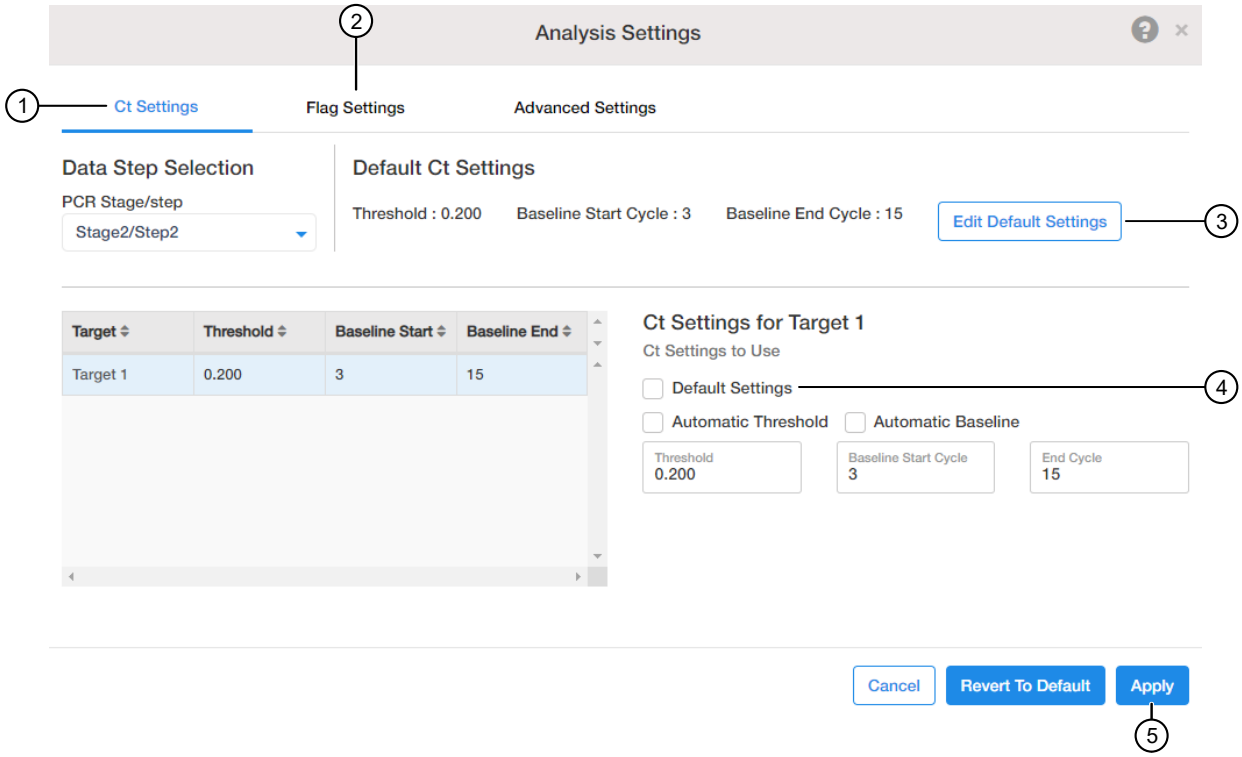
4. Click **Analysis settings** to change the default C_t Settings and Flag Settings.

a. In the **C_t Settings** tab, click **Edit Default Settings**.

b. Deselect **Automatic Threshold**, then deselect **Automatic Baseline**.

c. Click **Save Changes**.

d. Deselect **Default Settings**, then click **Apply** to save any changes before closing the window.



① **C_t Settings**
② **Flag Settings**
③ **Edit Default Settings** button
④ **Default Settings** checkbox
⑤ **Apply** button

e. In the **Flag Settings** tab, deselect the following flags.

- **CQCONF**—Low Cq confidence
- **EXPFAIL**—Exponential algorithm failed
- **NOAMP**—No amplification
- **NOSIGNAL**—No signal in well

Note: Use the scrollbar on the right to scroll down the list of flags.

f. Click **Apply** to save any changes before closing the window.

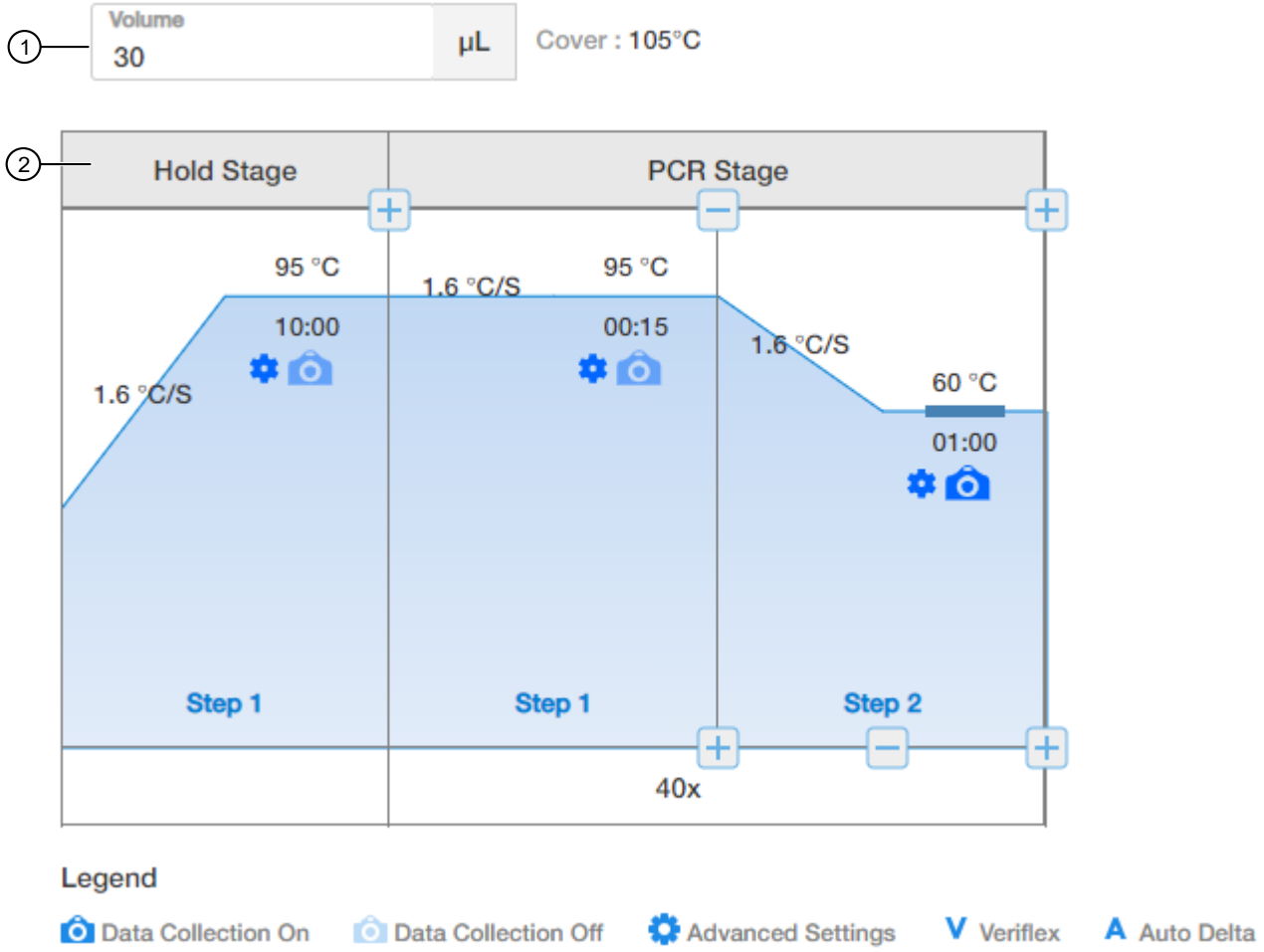
5. Click **Next**.

Template name cannot be changed after this step.

The qPCR Method screen is displayed.

Edit the run method and optical filter selection

Note: This section provides general procedures to edit the run method and optical filter selection in the qPCR Method.

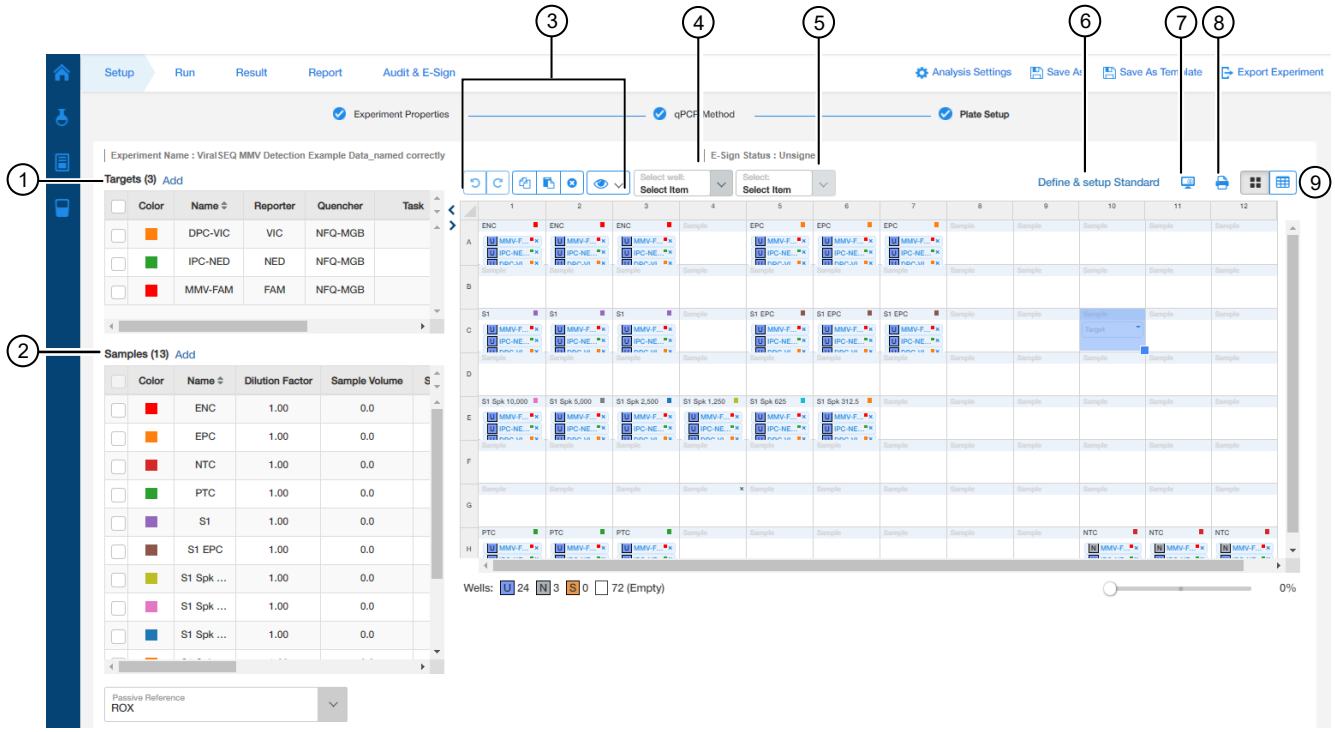


① Reaction volume. The volume is fixed in locked templates. The default for custom templates is 30 µl.
② Hold Stage

1. Delete **Step 1** of the **Hold Stage** in the default run method (thermal protocol).
2. (*Optional*) Click **(Optical Filter Settings)** to view the default filter settings.
   - The default optical filter selection is suitable for the ViralSEQ™ Mouse Minute Virus (MMV) Real-Time PCR Detection Kit.
   - The ViralSEQ™ Mouse Minute Virus (MMV) Real-Time PCR Detection Kit requires the QuantStudio™ 5 System to be calibrated for FAM™, VIC™, and NED™.
   - For more information about system dyes and their calibration and optical filter selection, see *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. MAN0010407).
3. Click **Next**.

Assign plate and well attributes

Note: This section provides general procedures to set up the plate.
For specific instructions for each assay type, see the corresponding chapter in this guide. Do not change **Targets** for default assay templates.



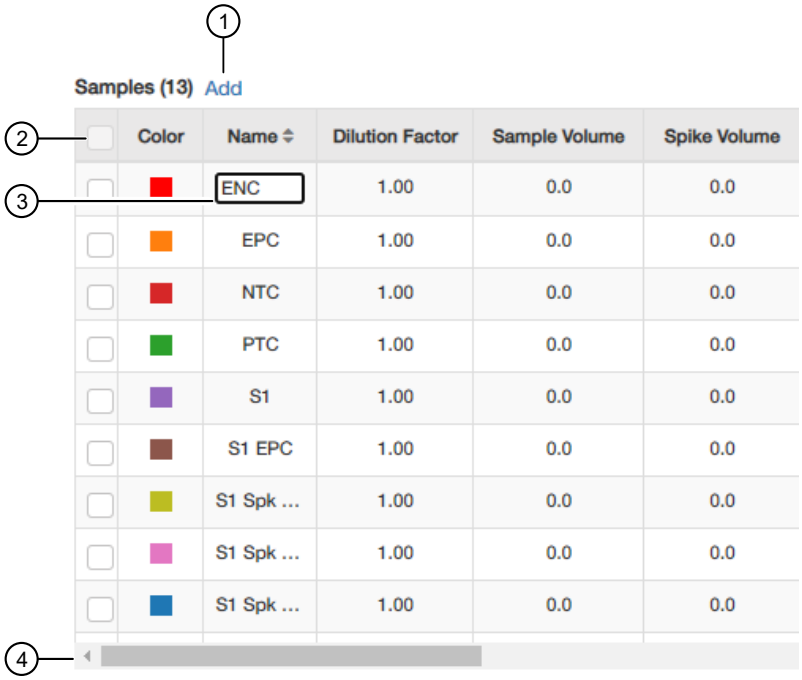
1. Targets
2. Samples
3. Plate setup toolbar
4. Select Item to highlight (Sample, Target, or Task).
5. Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
6. Define & setup Standard
7. (View Legend)
8. (Print Preview)
9. View (Grid View or Table View)

1. In **Plate Setup** screen, click or click-drag to select plate wells in the **(Grid View)** of the plate.

2. Assign the well attributes for the selected wells. Reporters should be FAM™ dye for MMV, NED™ dye for IPC, and VIC™ dye for DPC.

   - To add new **Samples** or **Targets**, click **Add** in the appropriate column on the left of the screen, then edit the new Name and other properties as required. The new sample or target is then selectable within the wells of the plate.

     Note: To change sample names, click the name in the Name column, then type the new name. To change Reporters and Quenchers, click the dye, then select from the dropdown list.



① **Add** button
② Checkbox—Select **Targets** and **Samples** to go in the selected well.
③ Textbox—Click the name to edit.
④ Scrollbar—Use to scroll to additional properties.

When a **Sample** or **Target** name are edited, two entries are added to the Audit trail (one for Delete, and another for Create).

- Use the plate setup toolbar (above the plate) to make edits to the plate.
  - Click **View** to show/hide the Sample Name, Sample Color, or Target from the view.
- To add consecutive samples (with the same **Target**), select a well, then click-drag the dark blue box to the right.

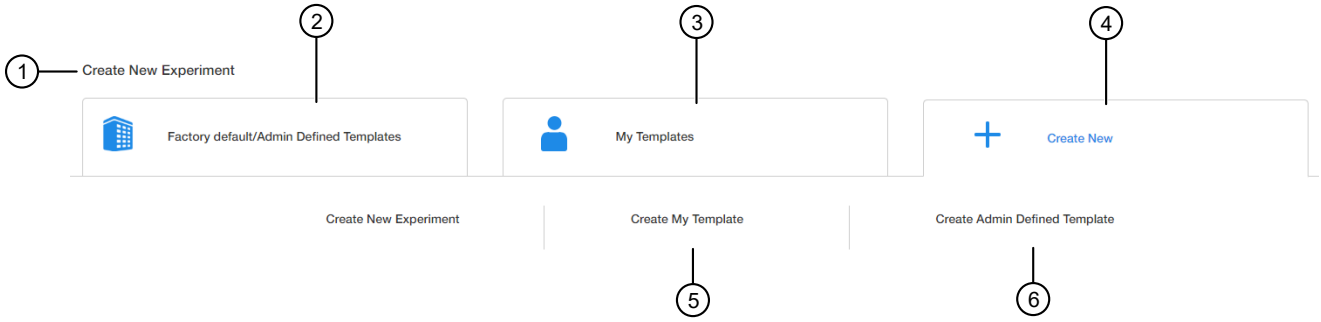
3. (*Optional*) Double-click a well to enter comments for the selected well.
4. Select ROX™ dye from the **Passive Reference** drop-down list (bottom left of screen).
5. Click **Save** to save the template.
   This template can then be used to create experiments.

Set up ViralSEQ™ Vesivirus Real-Time PCR Detection Kit experiments

Create a ViralSEQ™ template

Create a new template in the **(Home)** screen of the AccuSEQ™ Real-Time PCR Software v3.1.

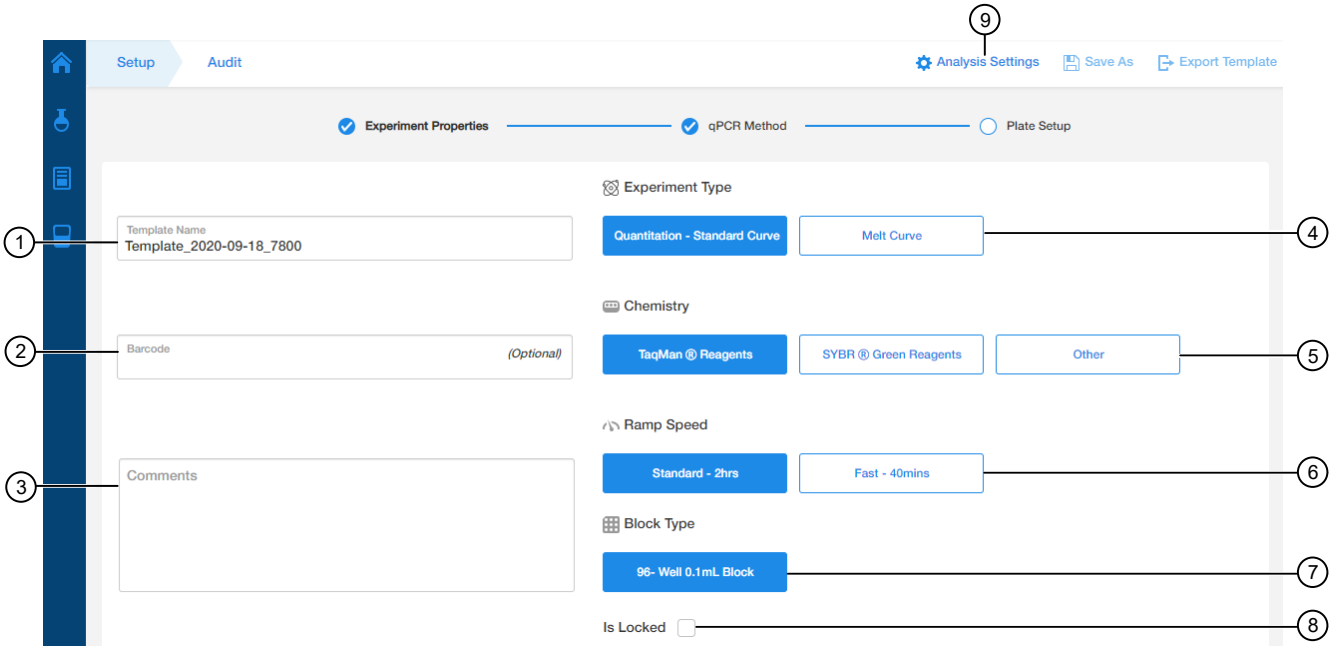
1. Click + **Create New** on the home screen.



① **Create New Experiment** pane
② **Factory default/Admin Defined Templates**—List of existing default or Admin Defined templates. These templates can be used as templates for new experiments.
③ **My Templates**—List of templates available to the user that is signed in. These templates can be used as templates for new experiments.
④ **Create New**—Used to create an experiment or template with no pre-existing settings.
⑤ **Create My Template**—Used to create a new template (stored locally in **My Templates**).
⑥ **Create Admin Defined Template**—Used to create a new template (Administrator only).

2. Select **Create My Template** or **Create Admin Defined Template**.

3. Edit the **Experiment Properties** as required.



① Software-generated **Template Name**
② **Barcode** field
③ **Comments** field
④ **Experiment Type**
⑤ **Chemistry**
⑥ **Ramp Speed**
⑦ **Block Type** (fixed as a 96-Well 0.1mL block).
⑧ **Is Locked** checkbox (Only Administrators can create locked **Admin Defined Templates**).
⑨ **Analysis Settings**

   a. In the **Template Name** field, specify the template name.

   b. (*Optional*) Enter information in the **Comments** field.

   c. In the **Setup** tab, select:
      - **Experiment Type—Quantitation-Standard Curve**
      - **Chemistry—TaqMan Reagents**
      - **Ramp Speed—Standard-2hrs**
      - **Block Type—96-Well 0.1mL Block**

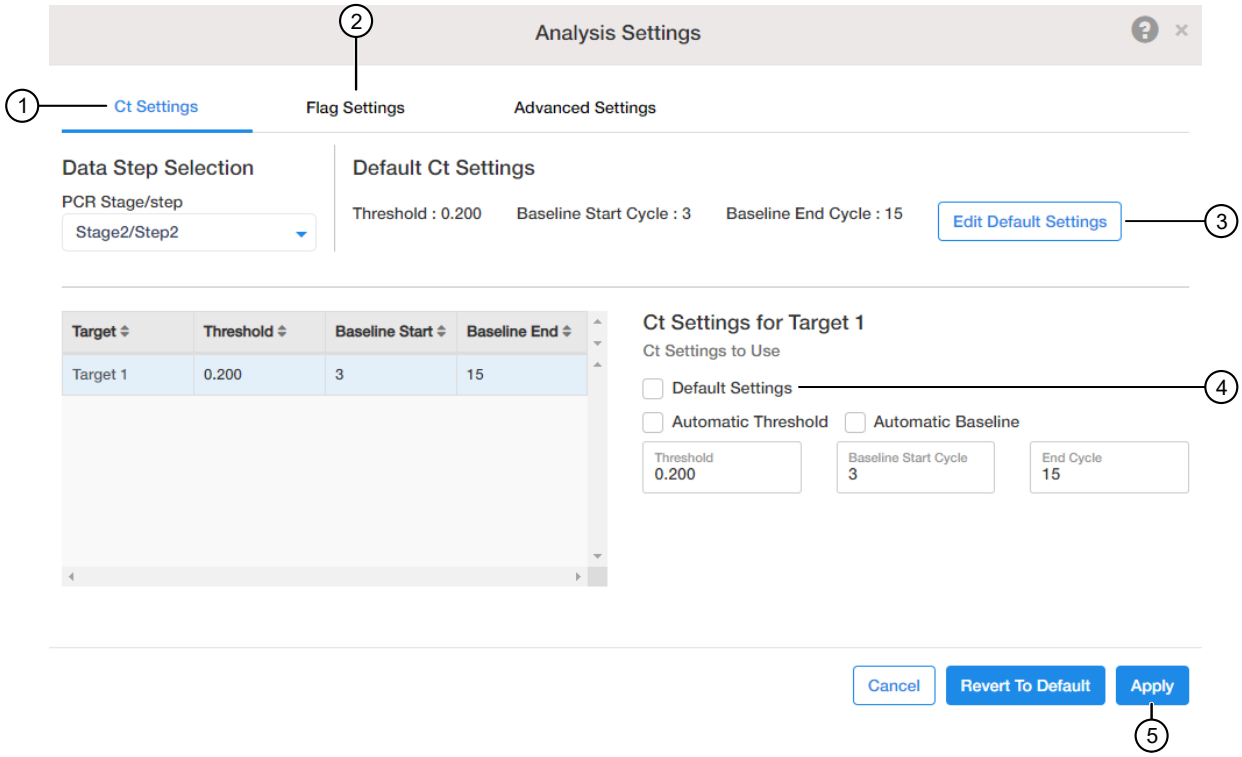
   d. (*Optional*) Select **Is Locked** to lock the template. If locked, users are unable to edit the template.

4. Click **Analysis settings** to change the default C_t Settings and Flag Settings.
   a. In the **C_t Settings** tab, click **Edit Default Settings**.

   b. Deselect **Automatic Threshold**, then deselect **Automatic Baseline**.

   c. Click **Save Changes**.

d. Deselect **Default Settings**, then click **Apply** to save any changes before closing the window.



① **C_t Settings**
② **Flag Settings**
③ **Edit Default Settings** button
④ **Default Settings** checkbox
⑤ **Apply** button

e. In the **Flag Settings** tab, deselect the following flags.

- **CQCONF**—Low Cq confidence
- **EXPFAIL**—Exponential algorithm failed
- **NOAMP**—No amplification
- **NOSIGNAL**—No signal in well

Note: Use the scrollbar on the right to scroll down the list of flags.

f. Click **Apply** to save any changes before closing the window.

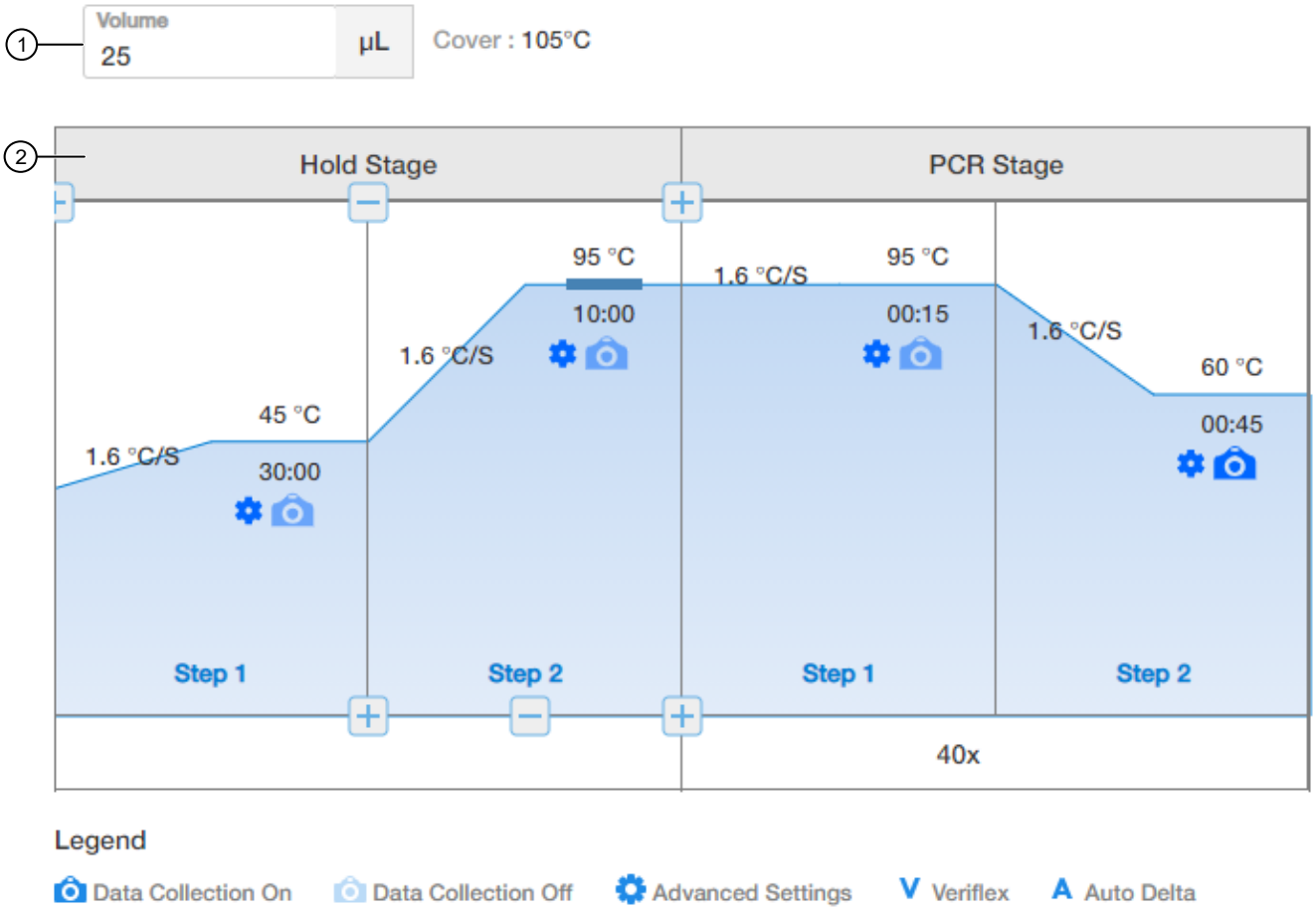
5. Click **Next**.

Template name cannot be changed after this step.

The qPCR Method screen is displayed.

Edit the run method and optical filter selection

Note: This section provides general procedures to edit the run method and optical filter selection in the qPCR Method.



① Reaction volume
② Hold Stage

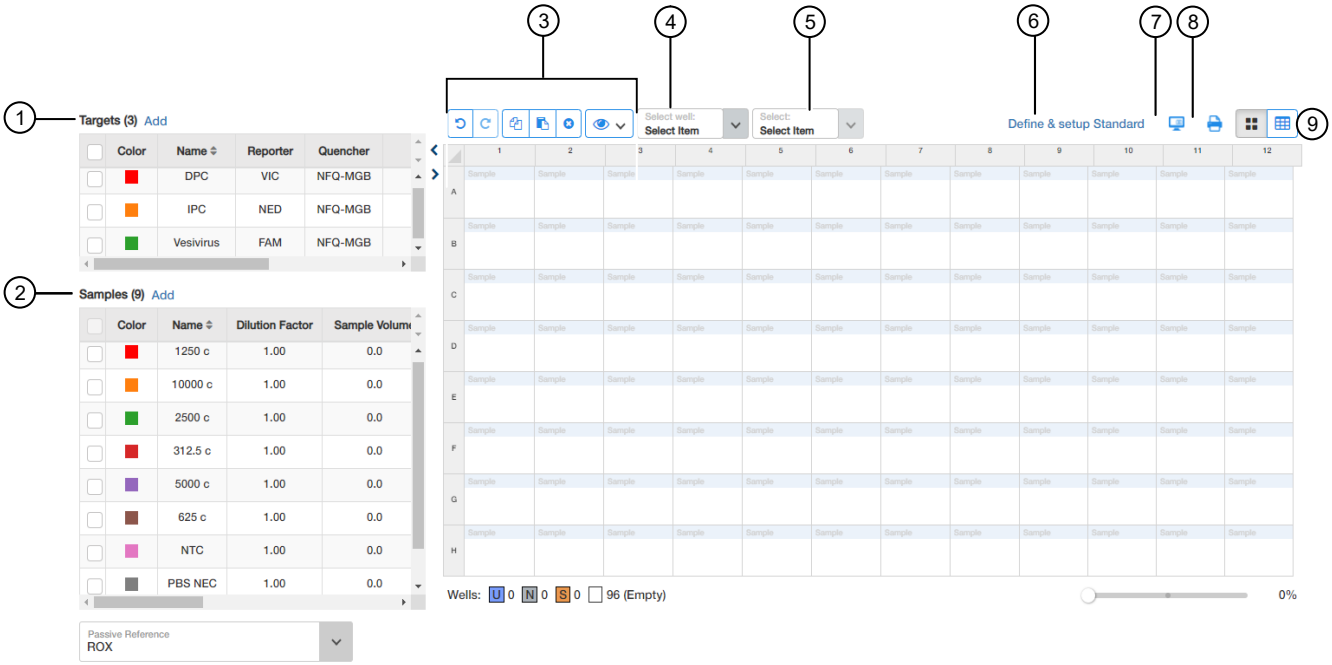
1. Ensure that the reaction volume is set to 25 µl.
2. Change **Step 1** of the **Hold Stage** in the default run method (thermal protocol) to 45°C for 30 minutes.
3. Change **Step 2** of the **PCR Stage** to 60°C for 45 seconds.

4. (*Optional*) Click **(Optical Filter Settings)** to view or edit the default filter settings.
   - The default optical filter selection is suitable for the ViralSEQ™ Vesivirus Real-Time PCR Detection Kit.
   - The ViralSEQ™ Vesivirus Real-Time PCR Detection Kit requires the QuantStudio™ 5 System to be calibrated for FAM™, VIC™, and NED™ dyes.
   - For more information about system dyes and their calibration and optical filter selection, see *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. MAN0010407).

5. Click **Next**.

Assign plate and well attributes

Note: This section provides general procedures to set up the plate.
For specific instructions for each assay type, see the corresponding chapter in this guide. Do not change **Targets** for default assay templates.



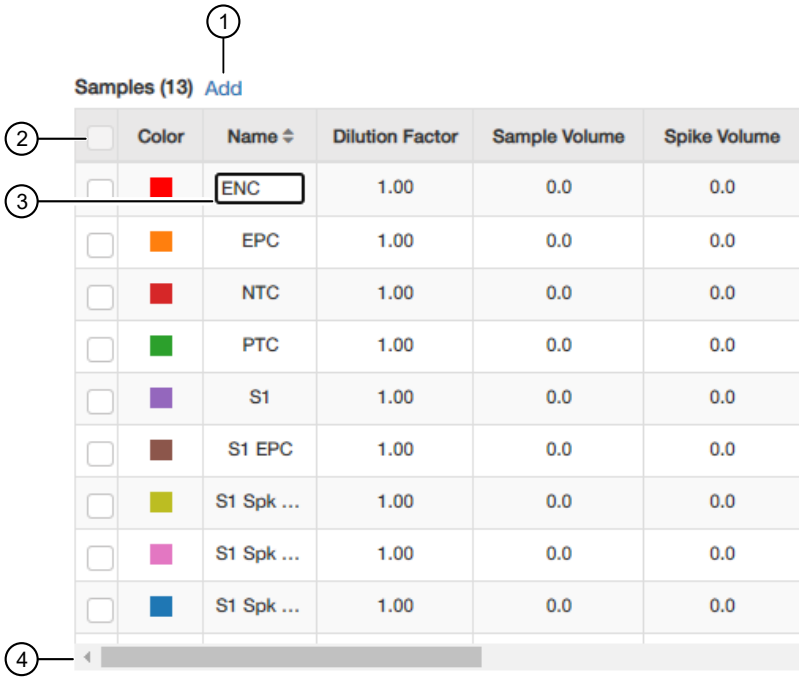
1. Targets
2. Samples
3. Plate setup toolbar
4. Select Item to highlight (Sample, Target, or Task).
5. Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
6. Define & setup Standard
7. (View Legend)
8. (Print Preview)
9. View (Grid View or Table View)

1. In **Plate Setup** screen, click or click-drag to select plate wells in the **(Grid View)** of the plate.

2. Assign the well attributes for the selected wells.

   - To add new **Samples** or **Targets**, click **Add** in the appropriate column on the left of the screen, then edit the new Name and other properties as required. The new sample or target is then selectable within the wells of the plate.

     Note: To change sample names, click the name in the Name column, then type the new name. To change Reporters and Quenchers, click the dye, then select from the dropdown list.



     ① **Add** button
     ② Checkbox—Select **Targets** and **Samples** to go in the selected well.
     ③ Textbox—Click the name to edit.
     ④ Scrollbar—Use to scroll to additional properties.

     When a **Sample** or **Target** name are edited, two entries are added to the Audit trail (one for Delete, and another for Create).

   - Use the plate setup toolbar (above the plate) to make edits to the plate.
     - Click **View** to show/hide the Sample Name, Sample Color, or Target from the view.
   - To add consecutive samples (with the same **Target**), select a well, then click-drag the dark blue box to the right.

3. (*Optional*) Double-click a well to enter comments for the selected well.

4. Select ROX™ dye from the **Passive Reference** dropdown list (bottom left of screen).

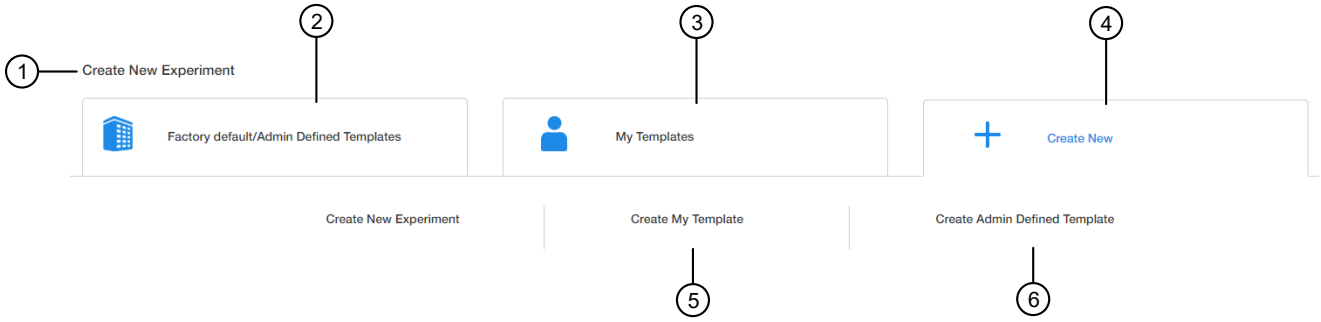
5. Click **Save** to save the template.
   This template can then be used to create experiments.

Set up ViralSEQ™ Quantitative Sf-rhabdovirus Kit experiments

Create a Sf-rhabdovirus ViralSEQ™ template

Create a new template in the **(Home)** screen of the AccuSEQ™ Real-Time PCR Software v3.1.

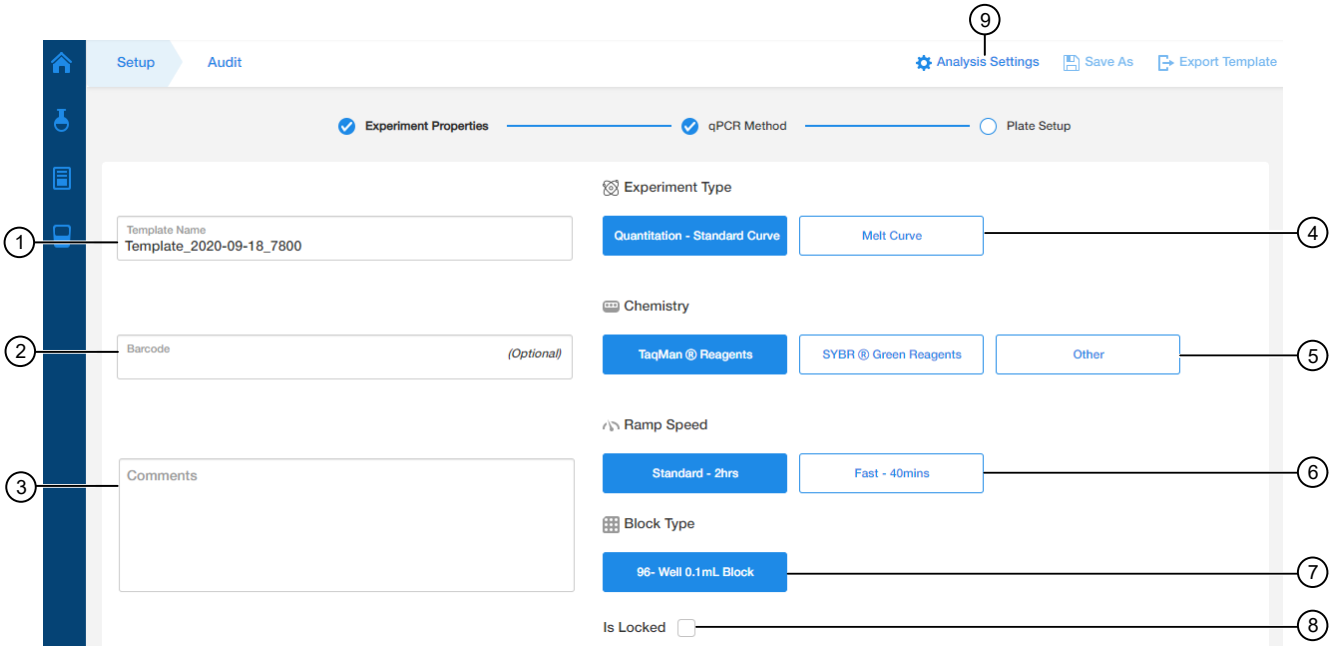
1. Click **Create New** on the home screen.



1. **Create New Experiment** pane
2. **Factory default/Admin Defined Templates**—List of existing default or Admin Defined templates. These templates can be used as templates for new experiments.
3. **My Templates**—List of templates available to the user that is signed in. These templates can be used as templates for new experiments.
4. **Create New**—Used to create an experiment or template with no pre-existing settings.
5. **Create My Template**—Used to create a new template (stored locally in **My Templates**).
6. **Create Admin Defined Template**—Used to create a new template (Administrator only).

2. Select **Create My Template** or **Create Admin Defined Template**.

3. Edit the **Experiment Properties** as required.



① Software-generated **Template Name**
② **Barcode** field
③ **Comments** field
④ **Experiment Type**
⑤ **Chemistry**
⑥ **Ramp Speed**
⑦ **Block Type** (fixed as a 96-Well 0.1mL block).
⑧ **Is Locked** checkbox (Only Administrators can create locked **Admin Defined Templates**).
⑨ **Analysis Settings**

   a. In the **Template Name** field, modify the template name. For example, Sf-Rhabdovirus template.

   b. (*Optional*) Enter information in the **Comments** field.

   c. In the **Setup** tab, select:
      - **Experiment Type—Quantitation-Standard Curve**
      - **Chemistry—TaqMan Reagents**
      - **Ramp Speed—Standard-2hrs**
      - **Block Type—96-Well 0.1mL Block**

   d. (*Optional*) Select **Is Locked** to lock the template. If locked, users are unable to edit the template.

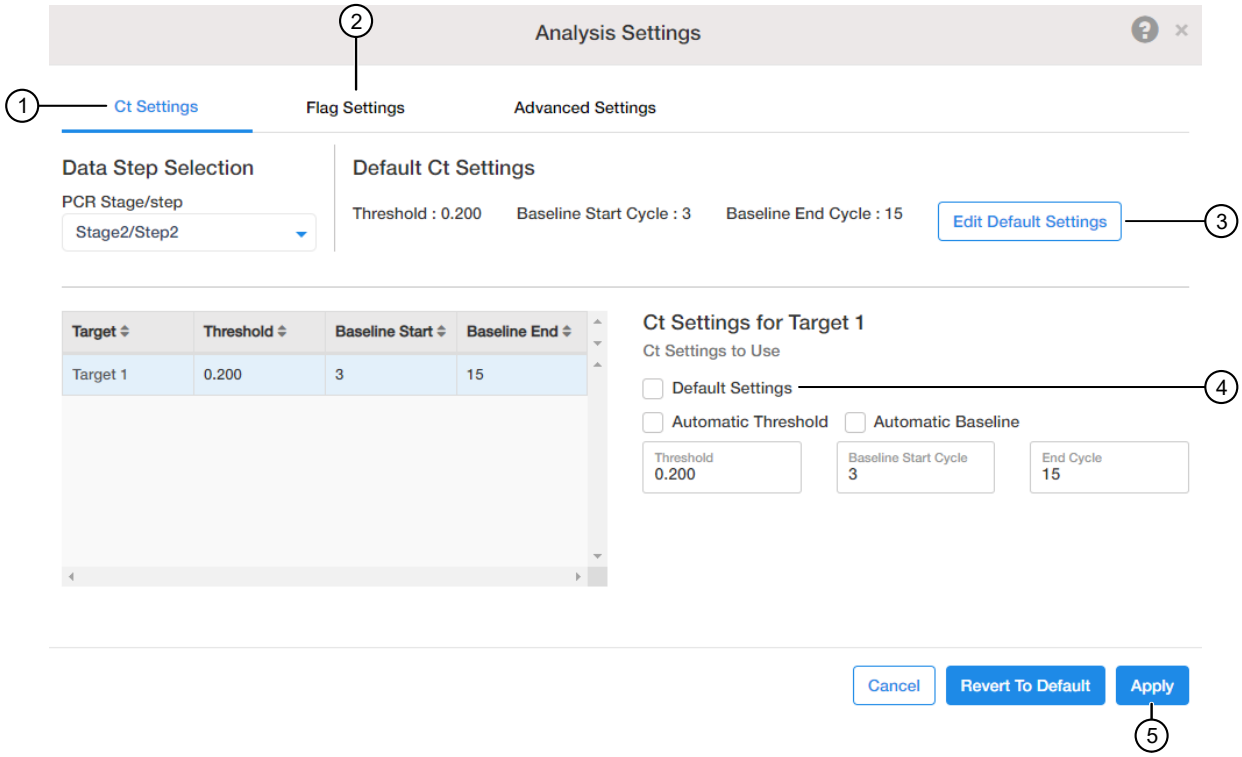
4. Click **Analysis settings** to change the default C_t Settings and Flag Settings.
   a. In the **C_t Settings** tab, click **Edit Default Settings**.

   b. Deselect **Automatic Threshold**, then enter 0.200.

   c. Ensure that **Automatic Baseline** is selected.

   d. Click **Save Changes**.

e. Deselect **Default Settings**, then click **Apply** to save any changes before closing the window.



① **C_t Settings**
② **Flag Settings**
③ **Edit Default Settings** button
④ **Default Settings** checkbox
⑤ **Apply** button

f. In the **Flag Settings** tab, deselect the following flags.

- **CQCONF**—Low Cq confidence
- **EXPFAIL**—Exponential algorithm failed
- **NOAMP**—No amplification
- **NOSIGNAL**—No signal in well

Note: Use the scrollbar on the right to scroll down the list of flags.

g. Click **Apply** to save any changes before closing the window.

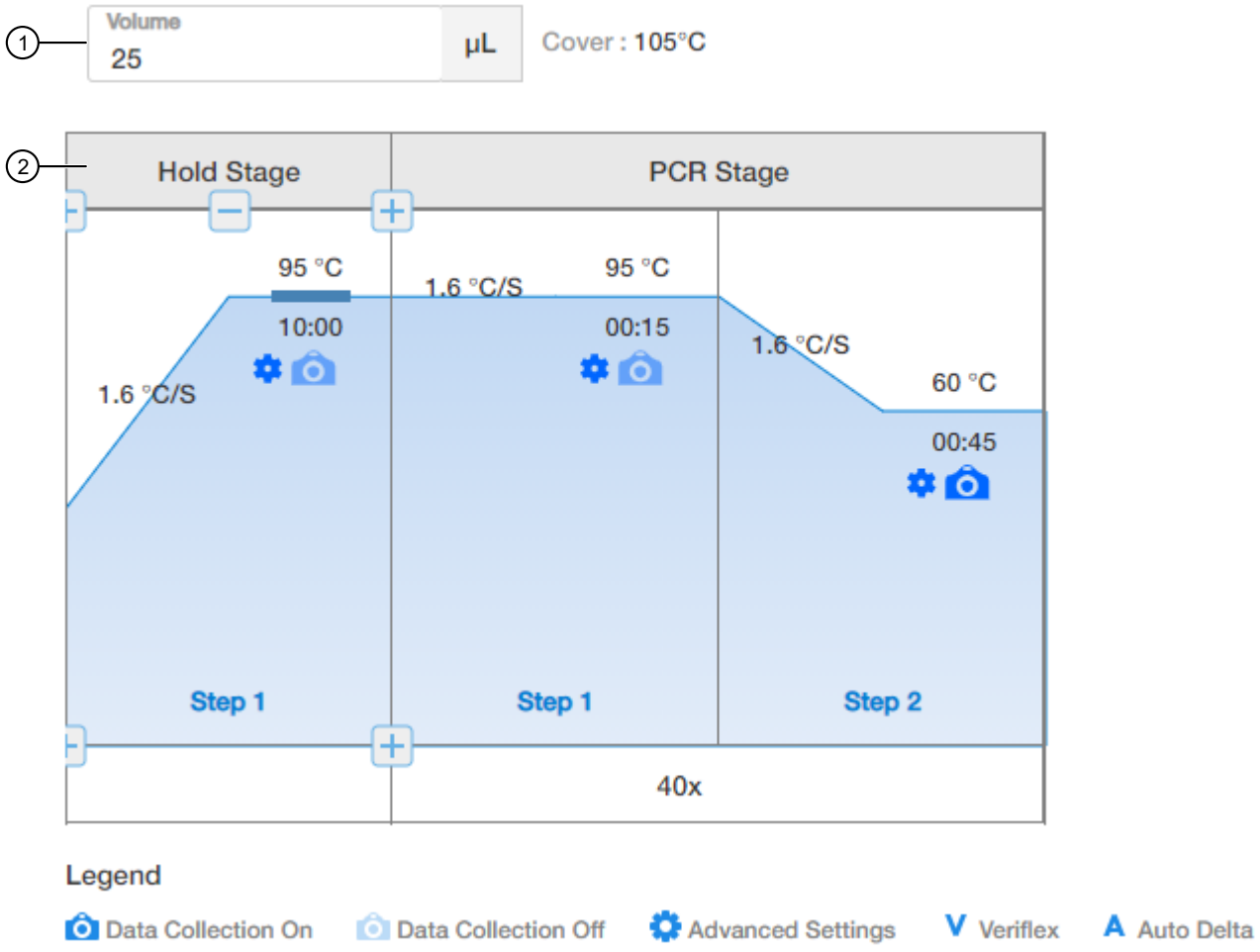
5. Click **Next**.

Template name cannot be changed after this step.

The qPCR Method screen is displayed.

Edit the run method and optical filter selection

Note: This section provides general procedures to edit the run method and optical filter selection in the qPCR Method.



① Reaction volume
② Hold Stage

1. Ensure that the reaction volume is set to 25 µL.
2. Delete **Step 1** of the **Hold Stage** in the default run method (thermal protocol).
3. Change **Step 2** of the **PCR Stage** to 60℃ for 45 seconds.

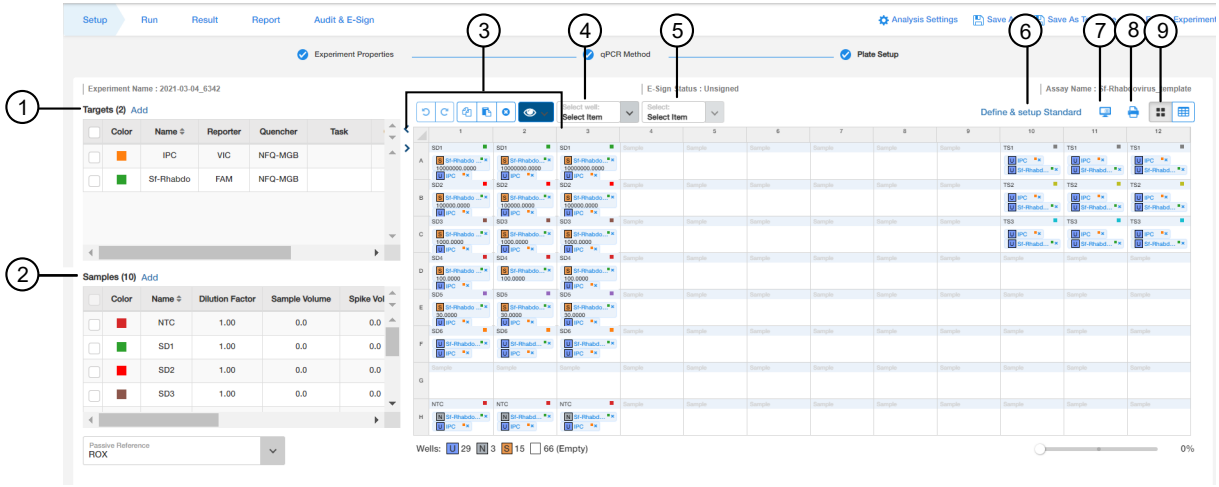
4. (*Optional*) Click **(Optical Filter Settings)** to view or edit the default filter settings.
   - The default optical filter selection is suitable for the ViralSEQ™ Quantitative Sf-rhabdovirus Kit.
   - The ViralSEQ™ Quantitative Sf-rhabdovirus Kit requires the QuantStudio™ 5 System to be calibrated for FAM™ and VIC™ dyes.
   - For more information about system dyes and their calibration and optical filter selection, see *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. MAN0010407).

5. Click **Next**.

Assign plate and well attributes

Note: This section provides general procedures to set up the plate.
For specific instructions for each assay type, see the corresponding chapter in this guide. Do not change **Targets** for default assay templates.

1. In **Plate Setup** screen, click or click-drag to select plate wells in the **(Grid View)** of the plate.

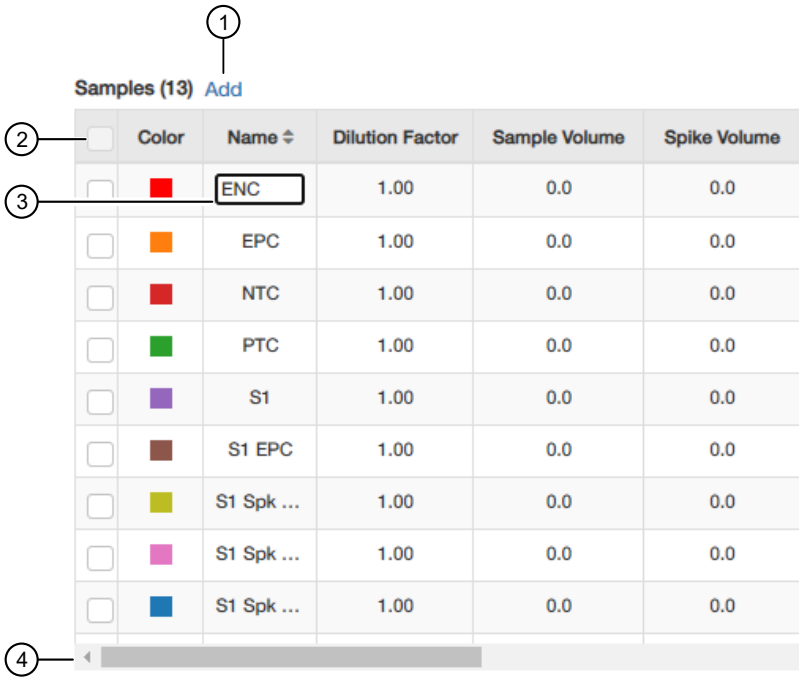


① Targets
② Samples
③ Plate setup toolbar
④ Select Item to highlight (Sample, Target, or Task).
⑤ Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
⑥ Define & setup Standard
⑦ (View Legend)
⑧ (Print Preview)
⑨ View (Grid View or Table View)

2. Assign the well attributes for the selected wells.

   - To add new **Samples** or **Targets**, click **Add** in the appropriate column on the left of the screen, then edit the new Name and other properties as required. The new sample or target is then selectable within the wells of the plate.

     Note: To change sample names, click the name in the Name column, then type the new name. To change Reporters and Quenchers, click the dye, then select from the dropdown list. Select **FAM™** dye as the **Reporter** for Sf-Rhabdovirus and **VIC™** dye as the **Reporter** for IPC. Select **NFQ-MGB** dye for the **Quencher**.



     ① **Add** button
     ② Checkbox—Select **Targets** and **Samples** to go in the selected well.
     ③ Textbox—Click the name to edit.
     ④ Scrollbar—Use to scroll to additional properties.

     When a **Sample** or **Target** name are edited, two entries are added to the Audit trail (one for Delete, and another for Create).

   - Use the plate setup toolbar (above the plate) to make edits to the plate.
     – Click **View** to show/hide the Sample Name, Sample Color, or Target from the view.
   - To add consecutive samples (with the same **Target**), select a well, then click-drag the dark blue box to the right.

3. (*Optional*) Double-click a well to enter comments for the selected well.

4. Select ROX™ dye from the **Passive Reference** dropdown list (bottom left of screen).

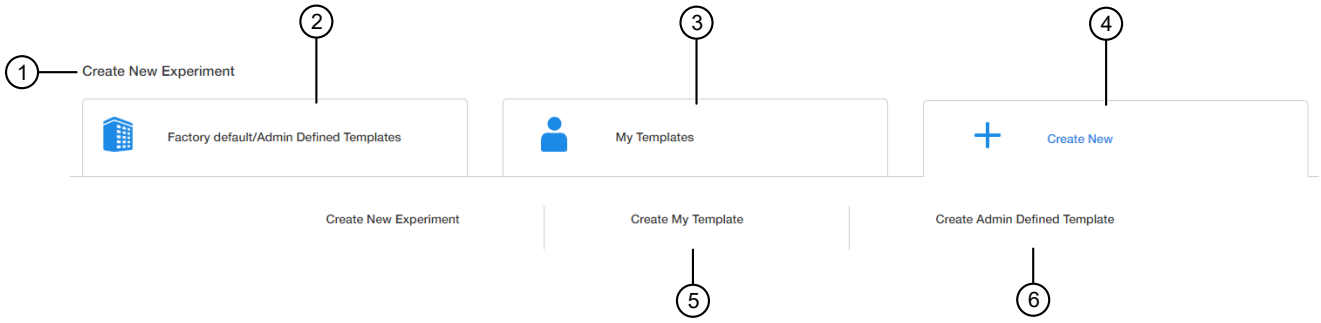
5. Click **Save** to save the template.
   This template can then be used to create experiments.

Set up ViralSEQ™ Lentivirus Physical Titer Kit experiments

Create a ViralSEQ™ template

Create a new template in the **(Home)** screen of the AccuSEQ™ Real-Time PCR Software v3.1.

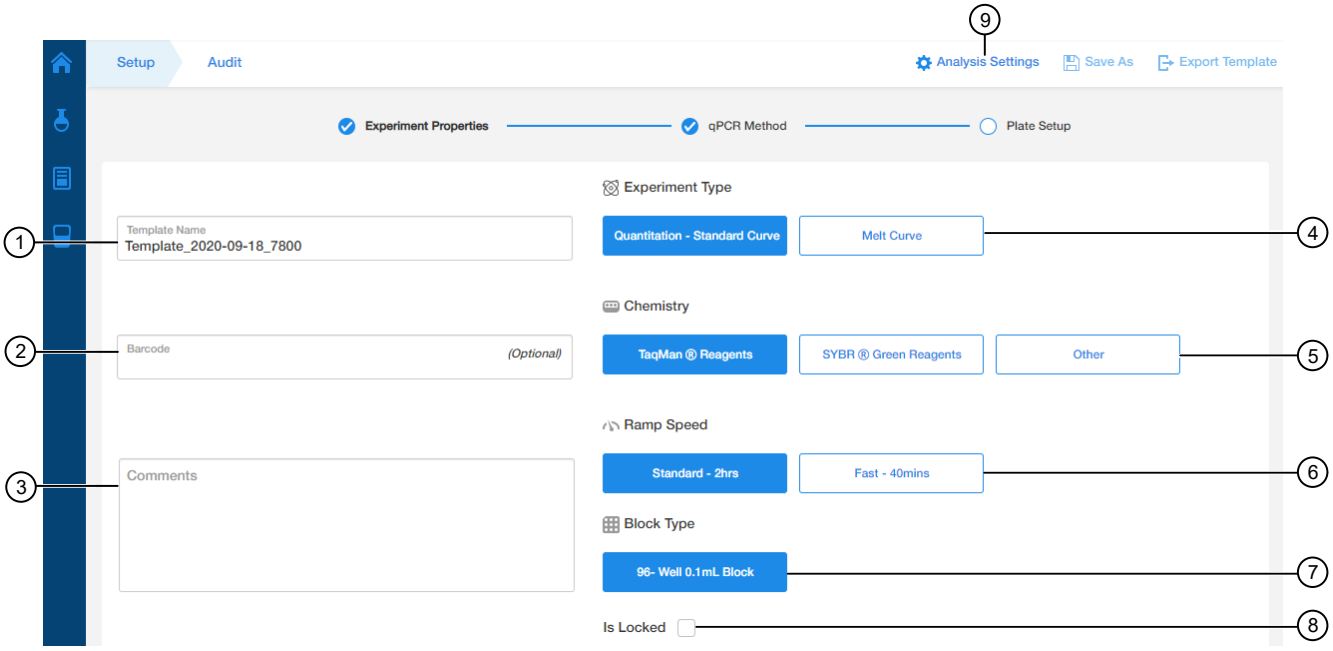
1. Click **Create New** on the home screen.



1. **Create New Experiment** pane
2. **Factory default/Admin Defined Templates**—List of existing default or Admin Defined templates. These templates can be used as templates for new experiments.
3. **My Templates**—List of templates available to the user that is signed in. These templates can be used as templates for new experiments.
4. **Create New**—Used to create an experiment or template with no pre-existing settings.
5. **Create My Template**—Used to create a new template (stored locally in **My Templates**).
6. **Create Admin Defined Template**—Used to create a new template (Administrator only).

2. Select **Create My Template** or **Create Admin Defined Template**.

3. Edit the **Experiment Properties** as required.



① Software-generated **Template Name**
② **Barcode** field
③ **Comments** field
④ **Experiment Type**
⑤ **Chemistry**
⑥ **Ramp Speed**
⑦ **Block Type** (fixed as a 96-Well 0.1mL block).
⑧ **Is Locked** checkbox (Only Administrators can create locked **Admin Defined Templates**).
⑨ **Analysis Settings**

   a. In the **Template Name** field, modify the template name. For example, LV Titer template.

   b. (*Optional*) Enter information in the **Comments** field.

   c. In the **Setup** tab, select:
      - **Experiment Type—Quantitation-Standard Curve**
      - **Chemistry—TaqMan ® Reagents**
      - **Ramp Speed—Standard-2hrs**
      - **Block Type—96-Well 0.1mL Block**

   d. (*Optional*) Select **Is Locked** to lock the template. If locked, users are unable to edit the template.

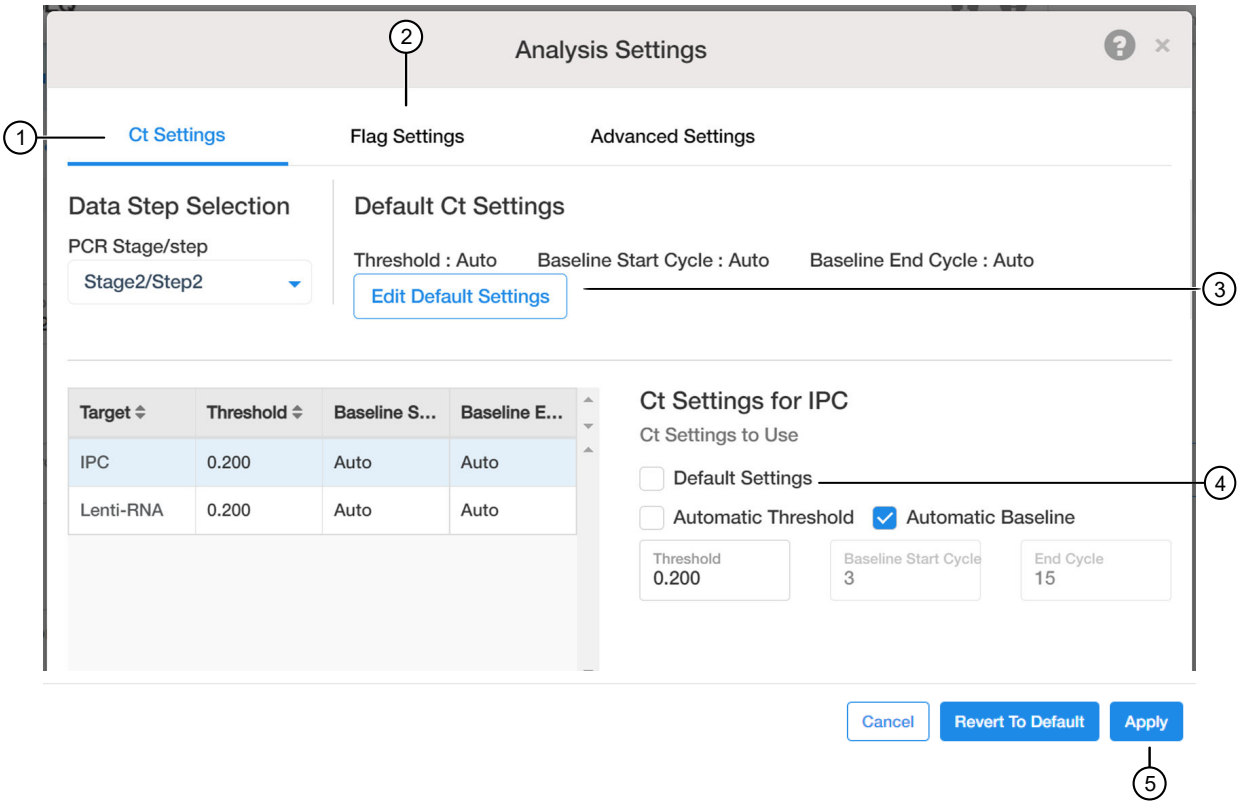
4. Click **Analysis settings** to change the default C_t Settings and Flag Settings.
   a. In the **C_t Settings** tab, click **Edit Default Settings**.

   b. Deselect **Automatic Threshold**, then enter **0.200**.

   c. Ensure that **Automatic Baseline** is selected.

   d. Click **Save Changes**.

e. Deselect **Default Settings**, then click **Apply** to save any changes before closing the window.



① **C_t Settings**
② **Flag Settings**
③ **Edit Default Settings** button
④ **Default Settings** checkbox
⑤ **Apply** button

f. In the **Flag Settings** tab, deselect the following flags.

- **CQCONF**—Low Cq confidence
- **EXPFAIL**—Exponential algorithm failed
- **NOAMP**—No amplification
- **NOSIGNAL**—No signal in well

Note: Use the scrollbar on the right to scroll down the list of flags.

g. Click **Apply** to save any changes before closing the window.

5. Click **Next**.
   Template name cannot be changed after this step.
   The qPCR Method screen is displayed.

Edit the run method and optical filter selection

This section provides general procedures to edit the run method and optical filter selection in the qPCR Method. To edit the default run method, see the *AccuSEQ™ Real-Time PCR Software v3.1 User Guide* (Pub. No. 100094287).

1. Set the reaction volume to **25 µL**.
2. Edit **Step 1** of the **Hold Stage** to 45℃ for 30 minutes.
3. Set **Step 2** of the **Hold Stage** to 95℃ for 10 minutes.
4. Set **Step 1** of the **PCR Stage** to 95℃ for 15 seconds.
5. Edit **Step 2** of the **PCR Stage** to 60℃ for 45 seconds.
6. Set the cycle number to **40**.
7. Ensure that **Data Collection** occurs after **Step 2**.

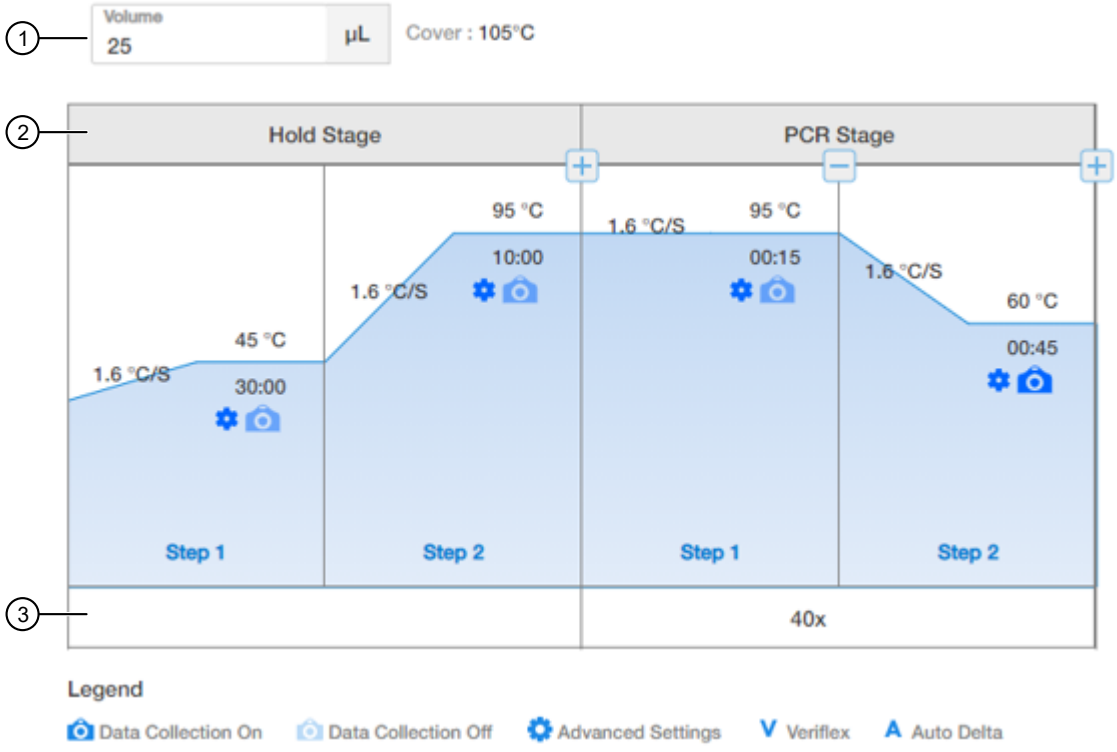


Figure 21 Lentivirus Physical Titer Run Method

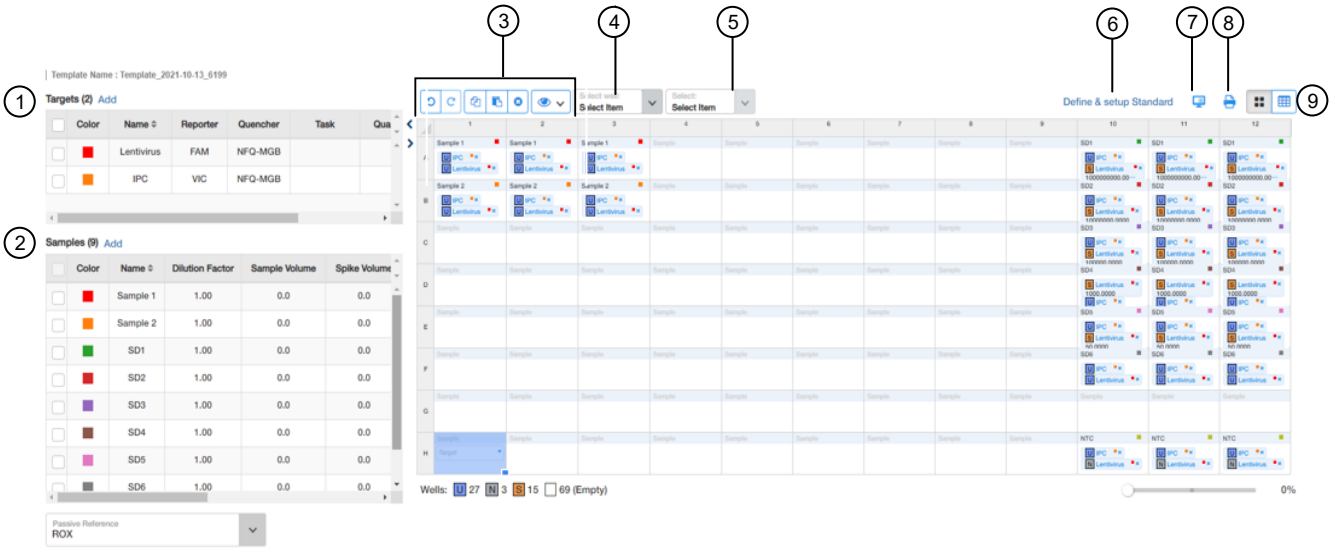
① Reaction volume- set to 25µL
② Stage
③ Cycle number- set to 40 cycles

8. (*Optional*) Click **(Optical Filter Settings)** to view the default filter settings.
   - The default optical filter selection is suitable for the ViralSEQ™ Lentivirus Physical Titer Kit.
   - The ViralSEQ™ Lentivirus Physical Titer Kit requires the QuantStudio™ 5 System to be calibrated for FAM™, VIC™, and ROX™.
   - For more information about system dyes and their calibration and optical filter selection, see *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. MAN0010407).

9. Click **Next**.

Assign plate and well attributes

Note: This section provides general procedures to set up the plate.
For specific instructions for each assay type, see the corresponding chapter in this guide. Do not change **Targets** for default assay templates.



1. Targets
2. Samples
3. Plate setup toolbar
4. Select Item to highlight (Sample, Target, or Task).
5. Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
6. Define & setup Standard
7. (View Legend)
8. (Print Preview)
9. View (Grid View or Table View)

1. In **Plate Setup** screen, click or click-drag to select plate wells in the **(Grid View)** of the plate.

2. Assign the well attributes for the selected wells. Each well should have a Sample Name under **Samples**, as well as the appropriate Targets under **Targets**. Reporters should be **FAM™** dye for Lentivirus Physical Titer, and **VIC™** dye for internal positive control (IPC).

   a. To add new **Samples** or **Targets**, click **Add** in the appropriate column on the left of the screen, then edit the new Name and other properties as required. The new sample or target is then selectable within the wells of the plate.

   b. For each sample (e.g. DNase-treated lentivirus sample, standard curve dilution, or NTC), two targets should be included.
      - Select the **FAM™** dye reporter for Lentivirus Physical Titer detection.
      - Select the **VIC™** dye for IPC detection.

   c. Select **NFQ-MGB** as the quencher for both targets.

   d. For standard curve dilution samples (SD1 to SD5), the **Task** for Lentivirus Physical Titer target should be indicated as "**S**" for Standard, with the appropriate copy number written under **Quantity**. For instance, the quantity for SD1 is 1E9 copies. Change the **Task** by clicking on the field and using the drop-down menu. Copy numbers can be indicated using scientific notation (e.g. "1E9") and the program will convert it to numerical format.

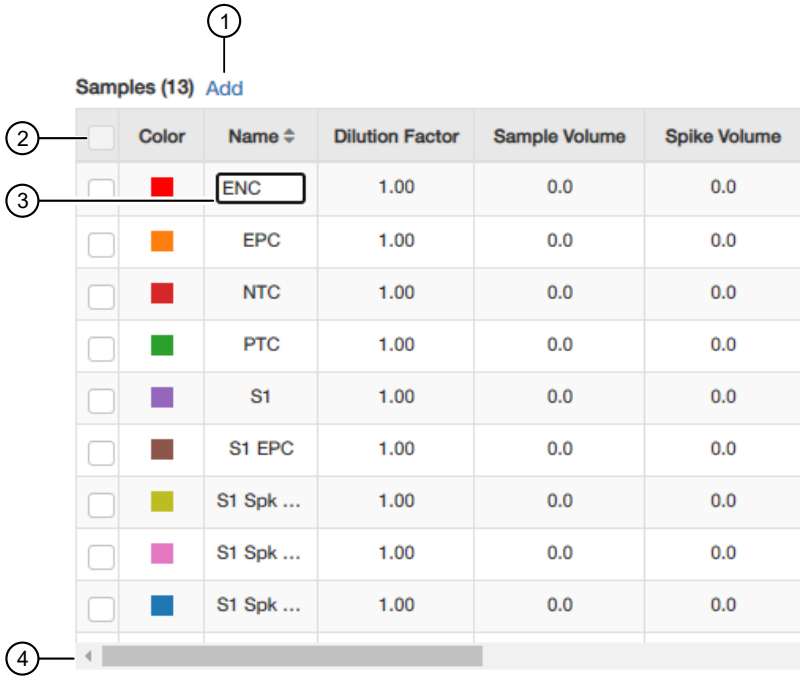
   e. For DNase-treated samples and SD6, set the **Task** for Lentivirus Physical Titer target to **U** for Unknown.

   f. For NTC wells, set the **Task** for Lentivirus Physical Titer target to **N** for NTC.

   g. For IPC wells, set the **Task** for Lentivirus Physical Titer target to **U** for Unknown.

h. To change sample names, click the name in the Name column, then type the new name. To change Reporters and Quenchers, click the dye, then select from the dropdown list.

When a **Sample** or **Target** name are edited, two entries are added to the Audit trail (one for Delete, and another for Create).



① **Add** button
② Checkbox—Select **Targets** and **Samples** to go in the selected well.
③ Textbox—Click the name to edit.
④ Scrollbar—Use to scroll to additional properties.

- Use the plate setup toolbar (above the plate) to make edits to the plate.
  - Click **View** to show/hide the Sample Name, Sample Color, or Target from the view.
- To add consecutive samples (with the same **Target**), select a well, then click-drag the dark blue box to the right.

3. (*Optional*) Double-click a well to enter comments for the selected well.

4. Select ROX™ dye from the **Passive Reference** drop-down list (bottom left of screen).

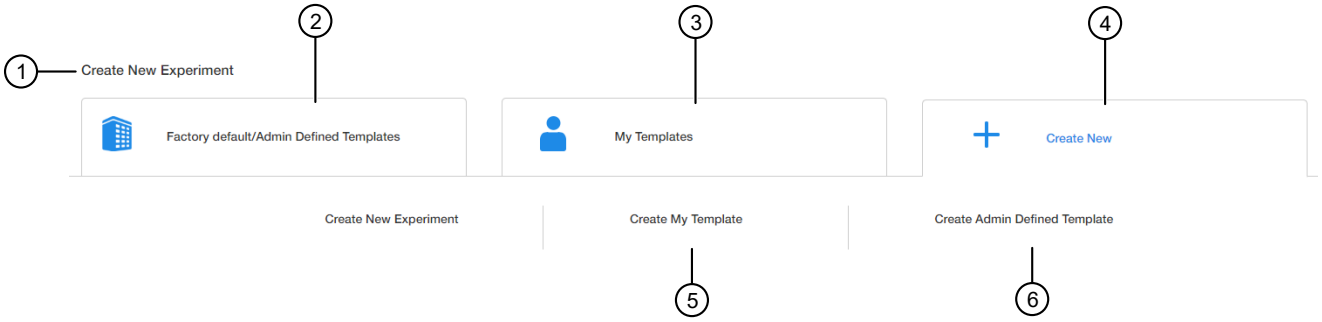
5. Click **Save** to save the template.
   This template can then be used to create experiments.

Set up ViralSEQ™ Lentivirus Proviral DNA Titer Kit experiments

Create a ViralSEQ™ template

Create a new template in the **(Home)** screen of the AccuSEQ™ Real-Time PCR Software v3.1.

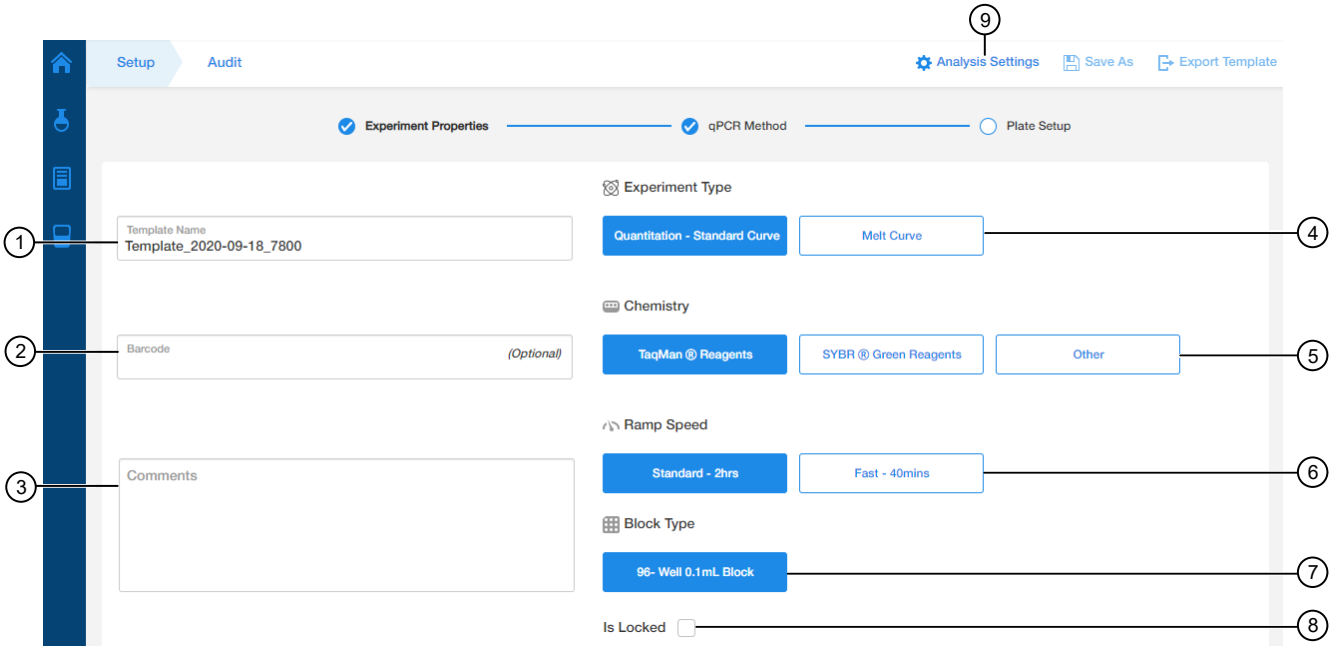
1. Click **Create New** on the home screen.



① **Create New Experiment** pane
② **Factory default/Admin Defined Templates**—List of existing default or Admin Defined templates. These templates can be used as templates for new experiments.
③ **My Templates**—List of templates available to the user that is signed in. These templates can be used as templates for new experiments.
④ **Create New**—Used to create an experiment or template with no pre-existing settings.
⑤ **Create My Template**—Used to create a new template (stored locally in **My Templates**).
⑥ **Create Admin Defined Template**—Used to create a new template (Administrator only).

2. Select **Create My Template** or **Create Admin Defined Template**.

3. Edit the **Experiment Properties** as required.



① Software-generated **Template Name**
② **Barcode** field
③ **Comments** field
④ **Experiment Type**
⑤ **Chemistry**
⑥ **Ramp Speed**
⑦ **Block Type** (fixed as a 96-Well 0.1mL block).
⑧ **Is Locked** checkbox (Only Administrators can create locked **Admin Defined Templates**).
⑨ **Analysis Settings**

a. In the **Template Name** field, modify the template name. For example, LV Titer template.

b. (*Optional*) Enter information in the **Comments** field.

c. In the **Setup** tab, select:
   - **Experiment Type—Quantitation-Standard Curve**
   - **Chemistry—TaqMan Reagents**
   - **Ramp Speed—Standard-2hrs**
   - **Block Type—96-Well 0.1mL Block**

d. (*Optional*) Select **Is Locked** to lock the template. If locked, users are unable to edit the template.

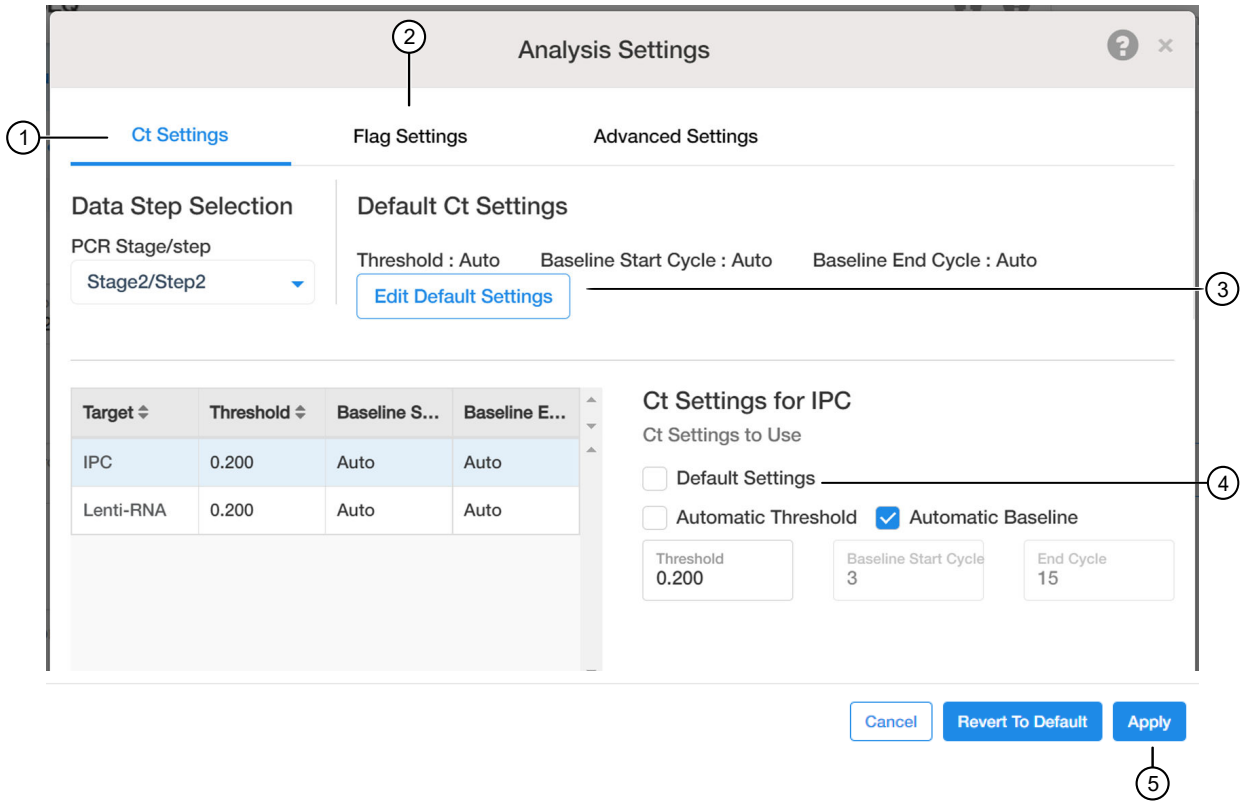
4. Click **Analysis settings** to change the default C_t Settings and Flag Settings.
   a. In the **C_t Settings** tab, click **Edit Default Settings**.

   b. Deselect **Automatic Threshold**, then enter **0.200**.

   c. Ensure that **Automatic Baseline** is selected.

   d. Click **Save Changes**.

e. Deselect **Default Settings**, then click **Apply** to save any changes before closing the window.



① **C_t Settings**
② **Flag Settings**
③ **Edit Default Settings** button
④ **Default Settings** checkbox
⑤ **Apply** button

f. In the **Flag Settings** tab, deselect the following flags.

- **CQCONF**—Low Cq confidence
- **EXPFAIL**—Exponential algorithm failed
- **NOAMP**—No amplification
- **NOSIGNAL**—No signal in well

Note: Use the scrollbar on the right to scroll down the list of flags.

g. Click **Apply** to save any changes before closing the window.

5. Click **Next**.
   Template name cannot be changed after this step.
   The qPCR Method screen is displayed.

Edit the run method and optical filter selection

This section provides general procedures to edit the run method and optical filter selection in the qPCR Method. To edit the default run method, see the *AccuSEQ™ Real-Time PCR Software v3.1 User Guide* (Pub. No. 100094287).

1. Set the reaction volume to **30 µL**.
2. Set **Step 1** of the **Hold Stage** to 95°C for 10 minutes.
3. Set **Step 1** of the **PCR Stage** to 95°C for 15 seconds.
4. Edit **Step 2** of the **PCR Stage** to 60°C for 1 minute.
5. Set the cycle number to **40**.
6. Ensure that **Data Collection** occurs after **Step 2**.

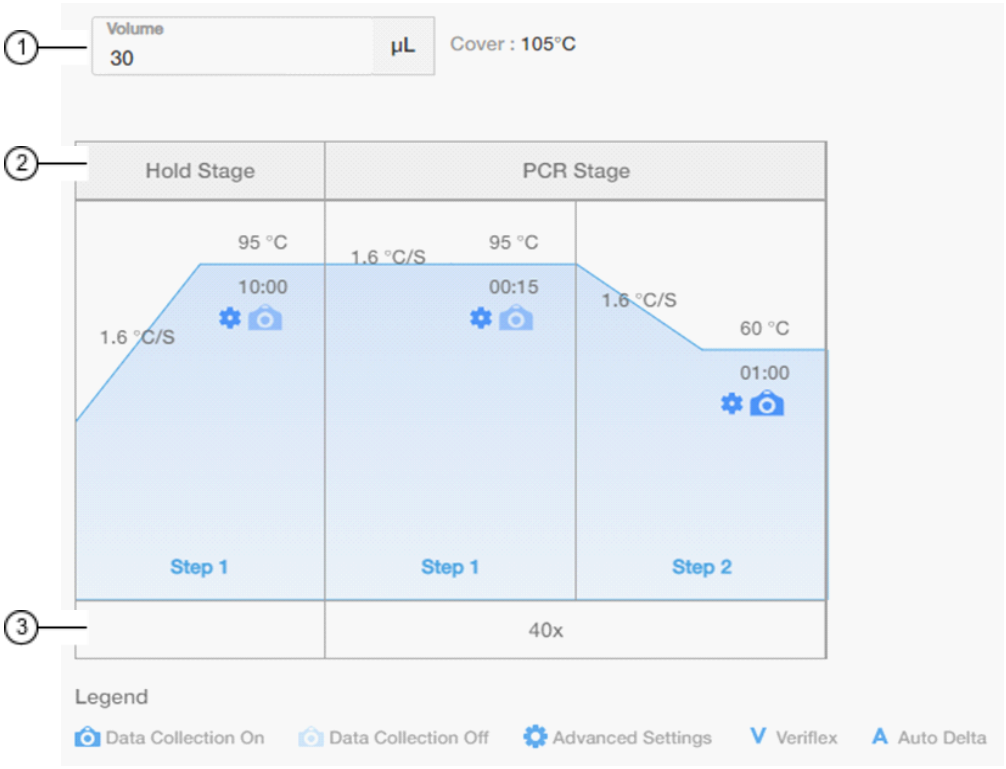


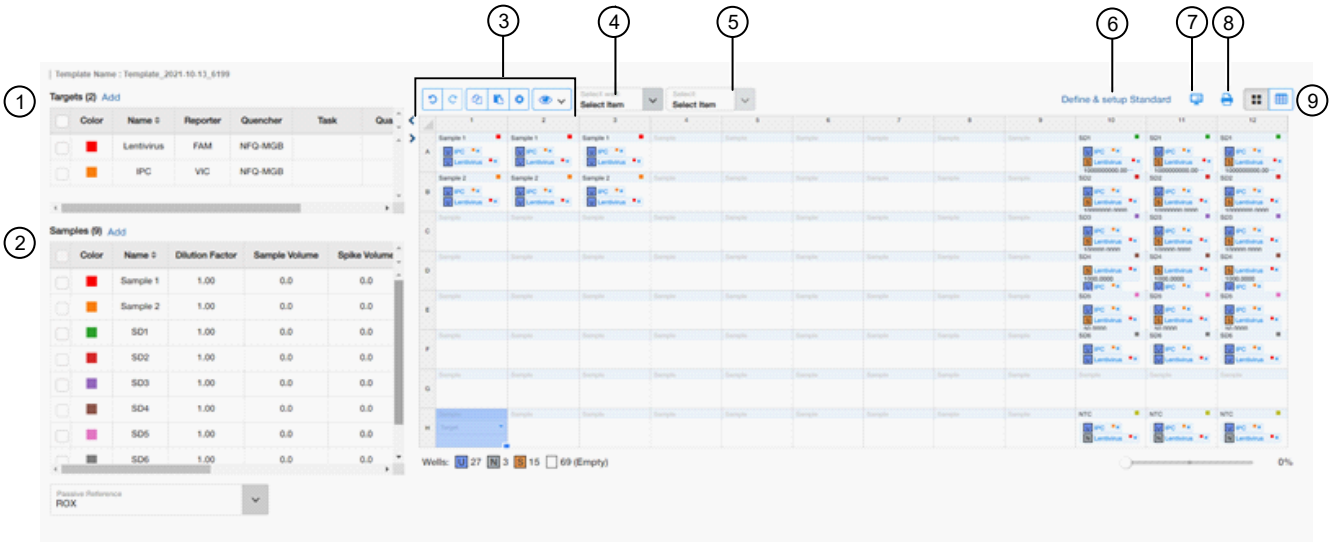
Figure 22 Lentivirus Proviral Titer Run Method

① Reaction volume- set to 30µL
② Stage
③ Cycle number- set to 40 cycles

7. (*Optional*) Click **(Optical Filter Settings)** to view the default filter settings.
   - The default optical filter selection is suitable for the ViralSEQ™ Lentivirus Proviral DNA Titer Kit.
   - The ViralSEQ™ Lentivirus Proviral DNA Titer Kit requires the QuantStudio™ 5 System to be calibrated for FAM™, VIC™, and ROX™.
   - For more information about system dyes and their calibration and optical filter selection, see *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. MAN0010407).
8. Click **Next**.

Assign plate and well attributes

Note: This section provides general procedures to set up the plate.
For specific instructions for each assay type, see the corresponding chapter in this guide. Do not change **Targets** for default assay templates.



① Targets
② Samples
③ Plate setup toolbar
④ Select Item to highlight (Sample, Target, or Task).
⑤ Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
⑥ Define & setup Standard
⑦ (View Legend)
⑧ (Print Preview)
⑨ View (Grid View or Table View)

1. In **Plate Setup** screen, click or click-drag to select plate wells in the **(Grid View)** of the plate.

2. Assign the well attributes for the selected wells. Each well should have a Sample Name under **Samples**, as well as the appropriate Targets under **Targets**. Reporters should be **FAM™** dye for Lentivirus Proviral Titer, and **VIC™** dye for internal positive control (IPC).

   a. To add new **Samples** or **Targets**, click **Add** in the appropriate column on the left of the screen, then edit the new Name and other properties as required. The new sample or target is then selectable within the wells of the plate.

   b. For each sample (e.g. DNase-treated lentivirus sample, standard curve dilution, or NTC), two targets should be included.
      - Select the **FAM™** dye reporter for Lentivirus Proviral Titer detection.
      - Select the **VIC™** dye for IPC detection.

   c. Select **NFQ-MGB** as the quencher for both targets.

   d. For standard curve dilution samples (SD1 to SD5), the **Task** for Lentivirus Proviral Titer target should be indicated as "**S**" for Standard, with the appropriate copy number written under **Quantity**. For instance, the quantity for SD1 is 1E7 copies. Change the **Task** by clicking on the field and using the drop-down menu. Copy numbers can be indicated using scientific notation (e.g. "1E7") and the program will convert it to numerical format.

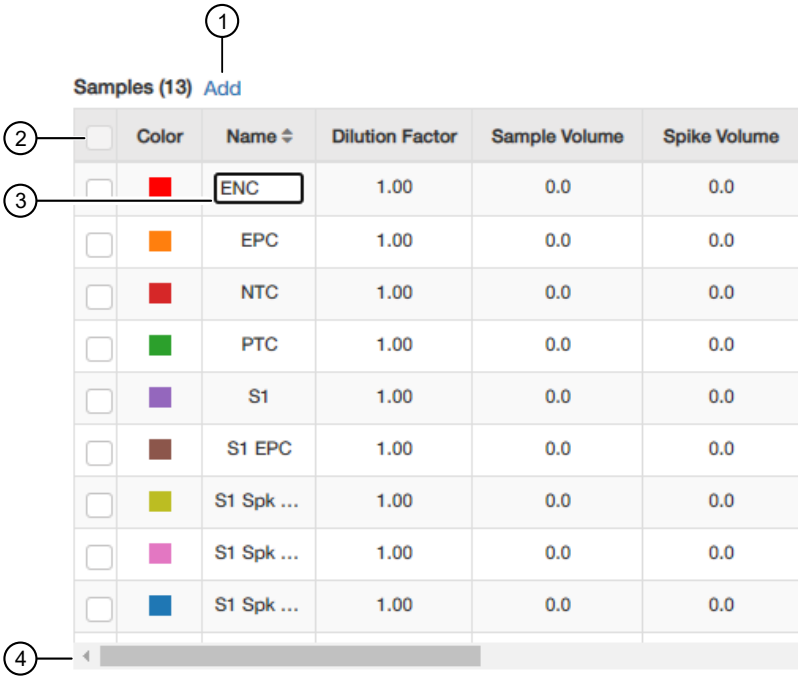
   e. For unknown or test samples and SD6, set the **Task** for Lentivirus Proviral Titer target to **U** for Unknown.

   f. For NTC wells, set the **Task** for Lentivirus Proviral Titer target to **N** for NTC.

   g. For IPC wells, set the **Task** to **U** for all samples.

h. To change sample names, click the name in the Name column, then type the new name. To change Reporters and Quenchers, click the dye, then select from the dropdown list.

When a **Sample** or **Target** name are edited, two entries are added to the Audit trail (one for Delete, and another for Create).



① **Add** button
② Checkbox—Select **Targets** and **Samples** to go in the selected well.
③ Textbox—Click the name to edit.
④ Scrollbar—Use to scroll to additional properties.

- Use the plate setup toolbar (above the plate) to make edits to the plate.
  - Click **View** to show/hide the Sample Name, Sample Color, or Target from the view.
- To add consecutive samples (with the same **Target**), select a well, then click-drag the dark blue box to the right.

3. (*Optional*) Double-click a well to enter comments for the selected well.

4. Select ROX™ dye from the **Passive Reference** drop-down list (bottom left of screen).

5. Click **Save** to save the template.
   This template can then be used to create experiments.

Set up and run the PCR reactions

1. Assemble the PCR reactions. Follow the manufacturer's instructions for the reagents, then follow the plate layout set up in the software. See the appropriate kit user guide for more information.

2. Load the reaction plate into the instrument (see “Load the plate in the instrument” on page 36), then start the run (see “Monitor the run” on page 38).

Note: Thermo Fisher Scientific recommends locking the computer screen during experiment runs to prevent edits/actions by other users. Press **Ctrl+Alt+Delete** ▸ **Lock**.

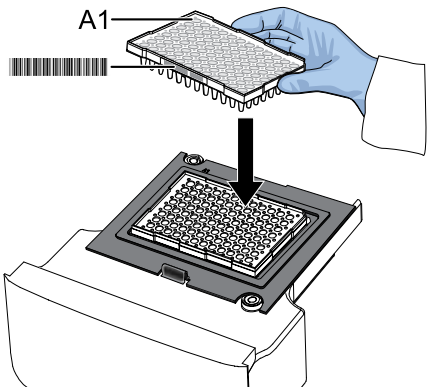
If a run is interrupted, and the AccuSEQ™ Software does not receive the data from the instrument, the **Experiment Status** changes to **Error**.

Load the plate in the instrument

CAUTION! Use optical flat caps for tubes. Rounded caps can damage the heated cover.

Load the plate.

1. Touch ⏏ to eject the instrument drawer.
2. Load the plate onto the plate adapter so that:
   - Well A1 of the plate is in the top-left corner of the plate adapter.
   - The barcode faces the front of the instrument.



IMPORTANT! The instrument should be used by trained operators who have been warned of the moving parts hazard.

Note: Do not remove the black plate adapter before loading a plate or tube strips. If used, tube strips can fit loosely in the adapter, but the heated cover applies the appropriate pressure to seat the tube strips securely in the adapter.

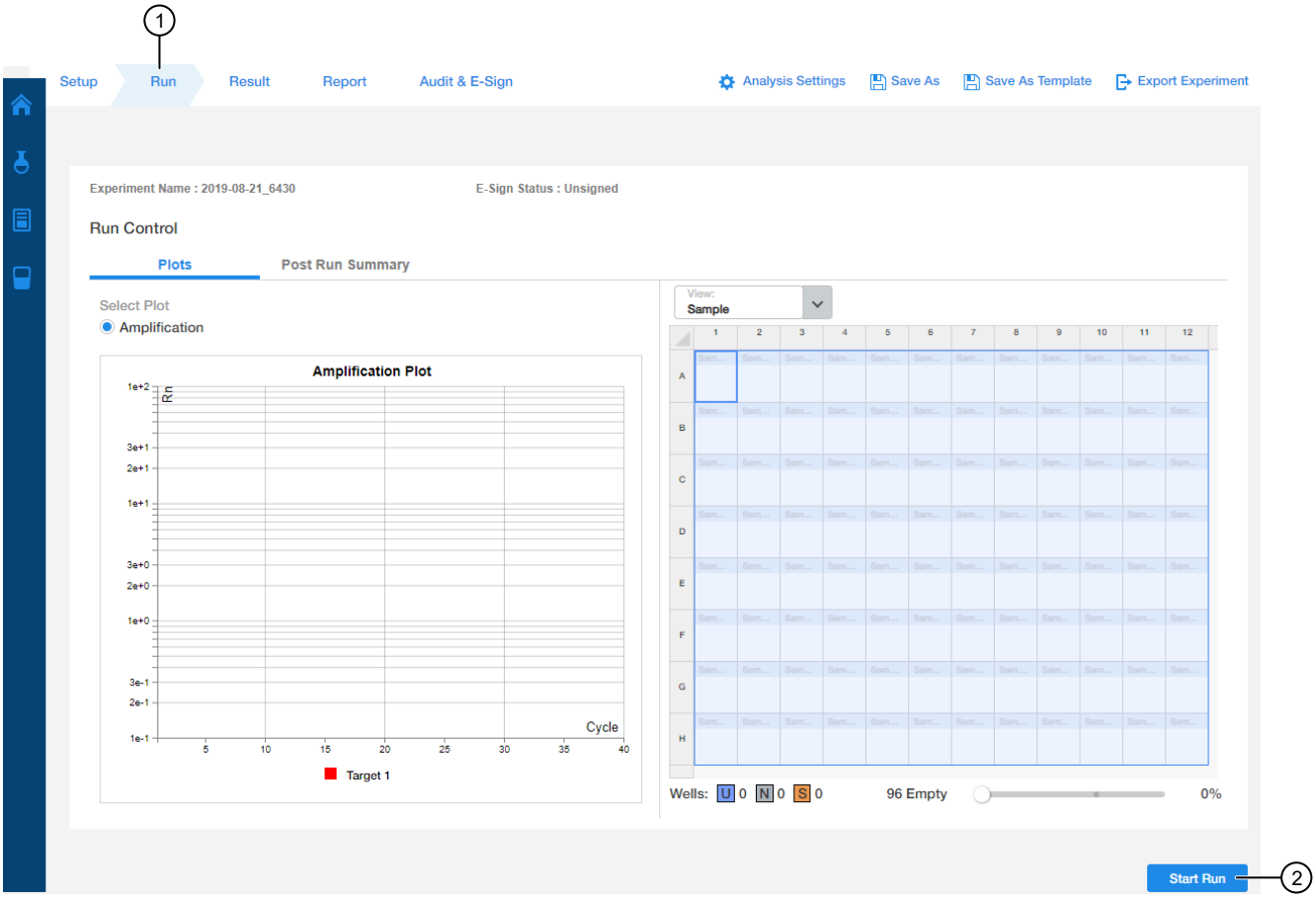
CAUTION! PHYSICAL INJURY HAZARD. During instrument operation, the plate temperature can reach 100°C. Allow it to cool to room temperature before handling.

3. Touch ⏏ to close the instrument drawer.

Start the run

Start the run in the AccuSEQ™ Software.

Option	Description
If the experiment is open	Click **Start Run**.
If the experiment is closed	1. Open the experiment. See “Open an experiment” on page 145. 2. Click the **Run** tab. 3. Click **Start Run**.



1 **Run** tab
2 **Start Run** button

A message stating **Run has been started successfully** is displayed when the run has started.

Monitor the run

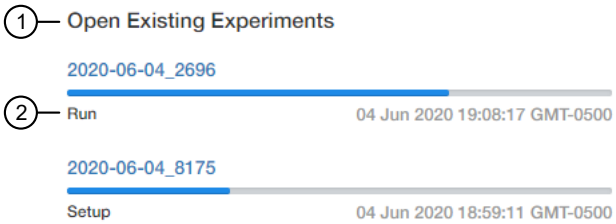
Monitor the run from one of the following places:

- On the instrument touchscreen. See the *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. A43322).
- In the **Monitor the Run** pane of the AccuSEQ™ Software **(Home)** screen.

1. Instrument name
2. Instrument status (Ready, Running, Offline)
3. Calibration status
   - Calibrated—All required calibrations are "Current". Required calibrations include: Background, ROI/Uniformity, and Dyes.
   - Not calibrated—None of the required calibrations are complete.
   - Requires calibration—One or more dyes are not calibrated.
4. Time lapsed (if a run is in progress)
5. Total run time
6. Experiment name

- In the **Open Existing Experiments** pane of the AccuSEQ™ Software **(Home)** screen. The experiment being run is the first experiment listed. Status is **Run**.

Note: When the run is complete, the status changes to **Analysis** and the bar changes to completely blue.



1. **Open Existing Experiments** pane
2. Experiment status

- In the **Run** tab of the AccuSEQ™ Real-Time PCR Software.

You can perform the following actions.

- Select wells in the plate layout to highlight respective curves in the plot.
- Hover over curves in the plot for well information.
- (*Optional*) Change what is displayed in the table wells of the plate layout, by selecting from the dropdown lists.

For more information, see “Run screen” on page 23.

On run completion, the **Post Run Summary** displays the run length, user and instrument information, and a list of any errors that occurred.

When the run is complete, unload the plate from the instrument.

Review ViralSEQ™ results (MMV and vesivirus)

View the amplification plot

1. In the **Result** tab, select **Amplification**.
2. In the **Targets** drop-down list, select the appropriate detectors.

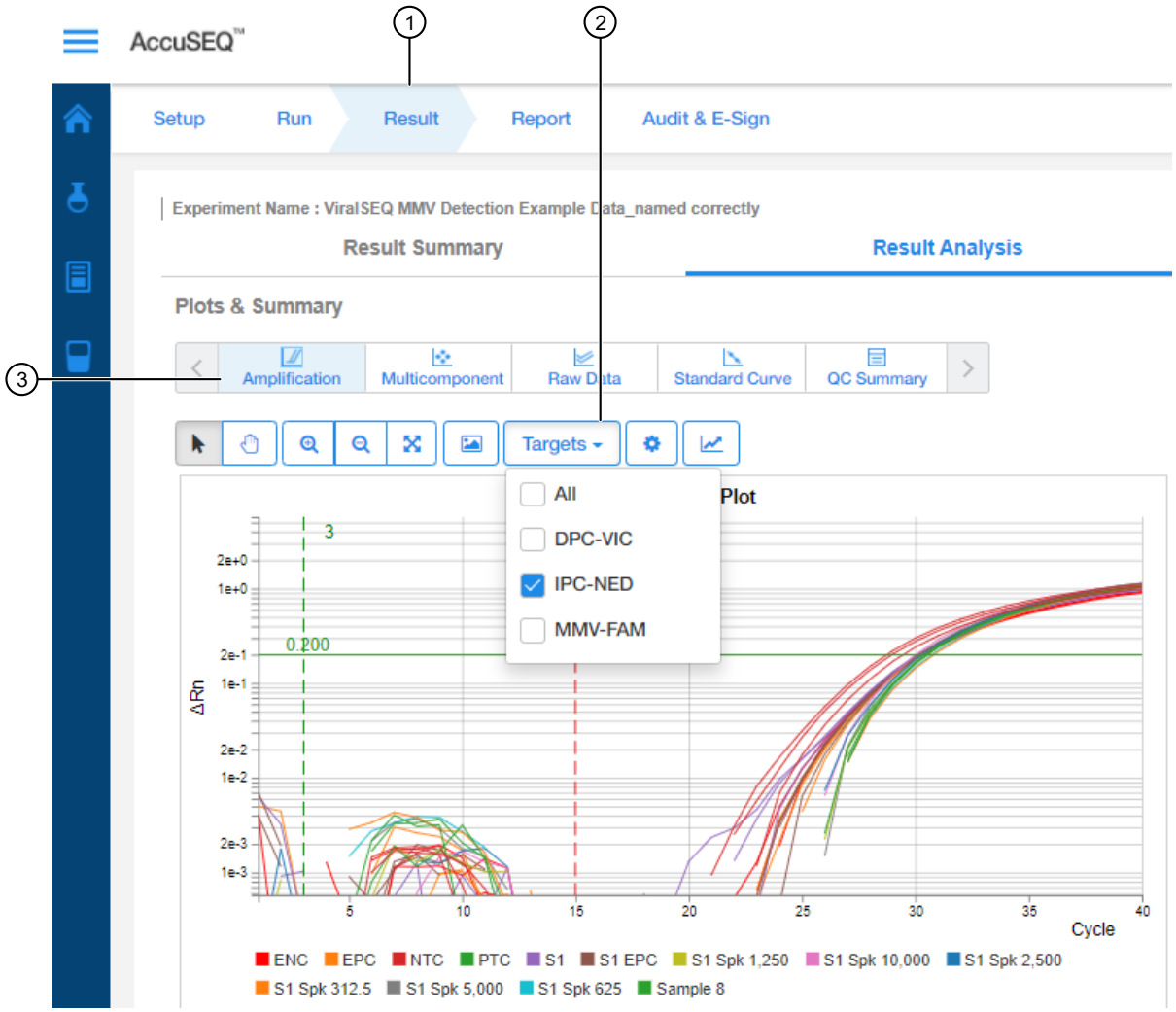


Figure 23 MMV amplification curve

① **Result** tab
② **Targets** drop-down list
③ **Amplification** plot

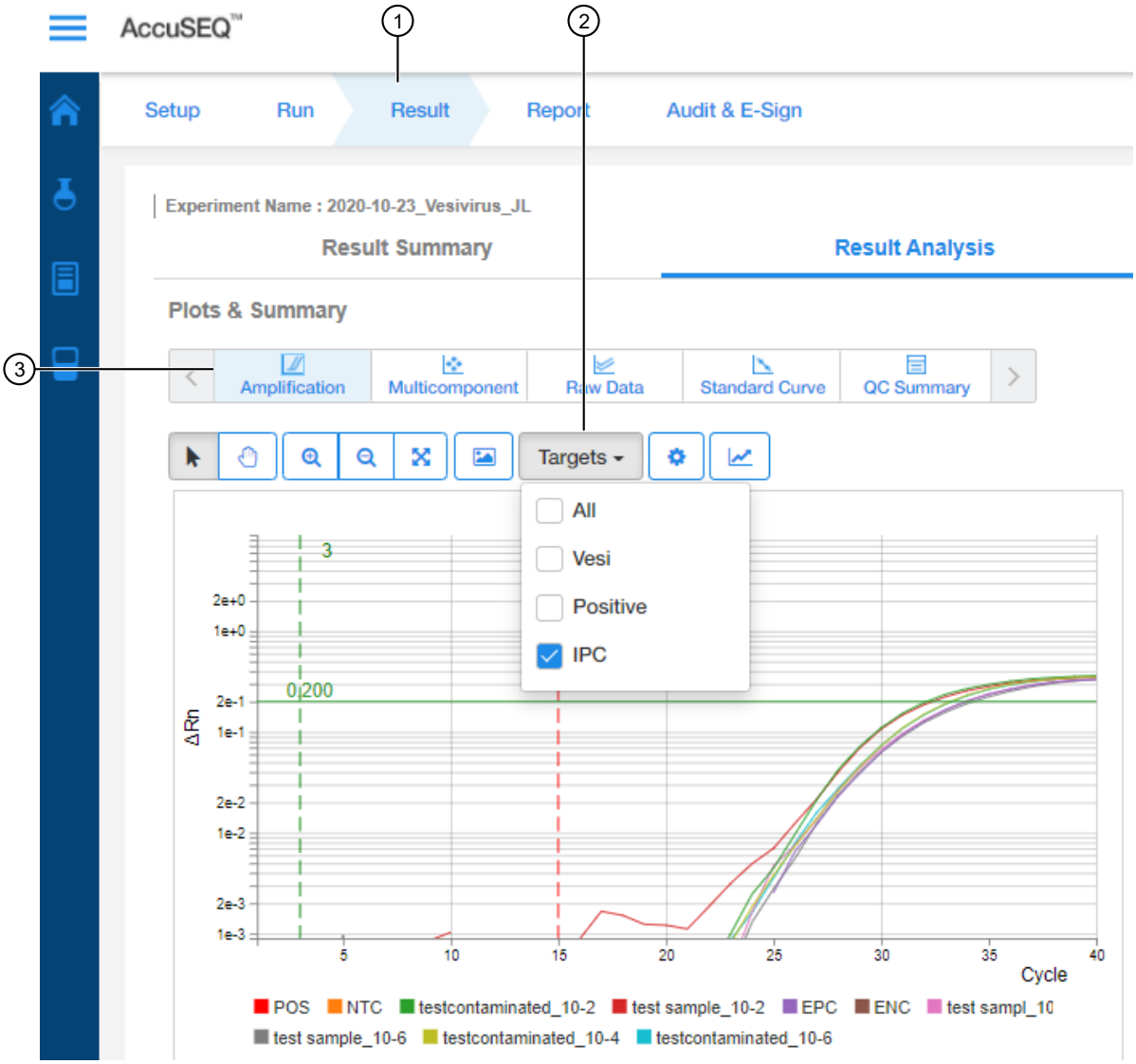


Figure 24 vesivirus amplification curve

① **Result** tab
② **Targets** drop-down list
③ **Amplification** plot

3. Evaluate the results for wells according to Table 3.

Note: The recommended acceptance criteria is subject to your own validation.

Table 3 Recommended acceptance criteria

Sample Type	FAM™ C_t value	VIC™ C_t value	NED™ signal	Call
PCR Negative Control (NTC)	Undetermined	Undetermined	Present	Pass, no control or target DNA detected
PCR Positive Control (PTC) (PTC, 2,000 copies/reaction)	$C_t \leq 32$	$C_t \leq 32$	Present	Pass, positive control DNA detected
Extraction Negative Control (ENC) (Sample DNA extraction)	Undetermined	Undetermined	Present	Pass, no spiked control or target DNA detected
Extraction Positive Control (EPC) (Sample DNA extraction)	$C_t \leq 39.99$	$C_t \leq 39.99$	Present	Pass, spiked positive control DNA detected
Test sample	Undetermined	Undetermined	Present	Negative for virus
Test sample	$C_t \leq 39.99$	Undetermined	Present	Positive for virus

Guidelines to interpret the results (MMV and vesirus)

Examine the wells for these characteristics:

- **IPC signal (NED™ dye)** should be present in all wells.

  If there is a large amount of viral DNA due to competition, the IPC signal can be inhibited or absent in test samples. In a test sample, samples with viral DNA competition show:

  - Low C_t for the target-specific signal (FAM™ dye)
  - C_t > 36 or Undetermined for the IPC signal (NED™ dye)
  - No positive control signal (VIC™ dye)

  If there is viral inhibition and the target-specific signal (FAM™ dye) is present, the IPC signal (NED™ dye) can be ignored and the sample considered positive for the presence of virus.

- **Negative controls:** PCR negative control (NTC) and extraction negative control (ENC)

  Only IPC signal (NED™ dye), should be present in the negative controls. If either VIC™ dye or FAM™ dye is present, the control shows contamination and it is necessary to repeat the experiment with freshly prepared samples and reagents.

- **Positive controls:** PCR positive control (PTC) and extraction positive control (EPC)

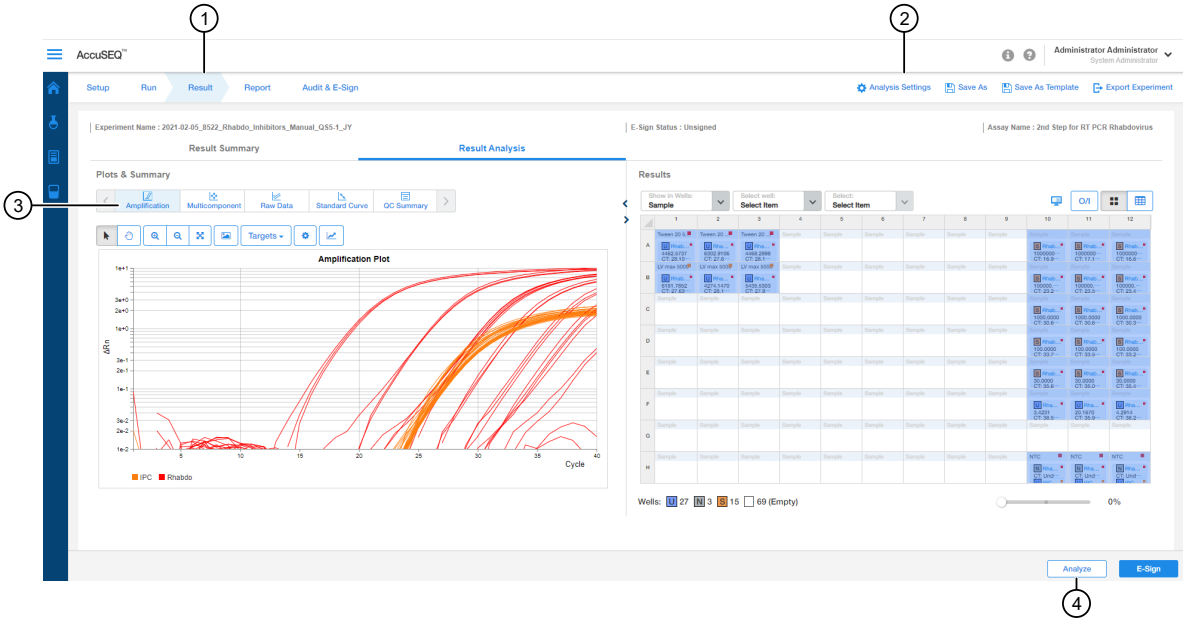
  Target-specific signal (FAM™ dye), positive control signal (VIC™ dye), and IPC signal (NED™ dye) should be present in the positive controls. If they are not, repeat the experiment with freshly prepared samples and reagents.

- **Test samples (Unknowns):** If the only signal detected is IPC (NED™ dye), the test sample is negative for the presence of virus. If both IPC (NED™ dye) and target-specific (FAM™ dye) signals are detected, the test sample is positive for the presence of virus. If positive control signal (VIC™ dye) is present, the test sample shows contamination with the positive control and it is necessary to repeat the experiment with freshly prepared samples and reagents.

Review ViralSEQ™ results (Sf-rhabdovirus)

Review the results

1. In the AccuSEQ™ Real-Time PCR Software, open your experiment, then navigate to the **Result** tab.



1. **Result** tab
2. **Analysis Settings**
3. Plot horizontal scrollbar
4. **Analyze** button

2. In the **Result Analysis** tab, review the Amplification Curve plots for amplification profiles in the controls, samples, and the standard curve. Ensure that threshold is set to 0.200.

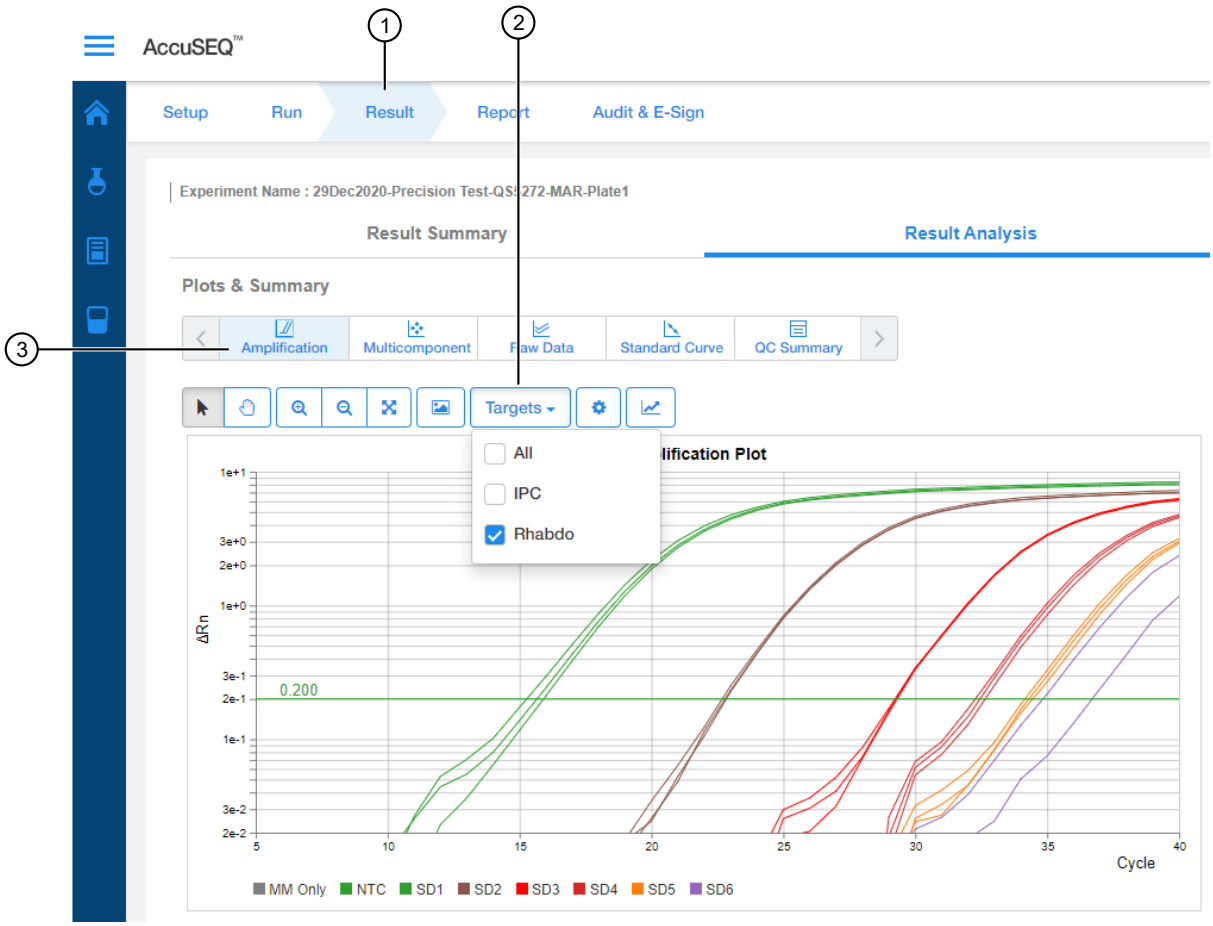


Figure 25

① **Result** tab
② **Targets** drop-down list
③ **Amplification** plot

3. In the **Result Analysis** tab, review the **QC Summary** for any flags in wells.

4. In the **Result Analysis** tab, review the **Standard Curve** plot. Verify the values for the Slope, Y-intercept, R^2, and Efficiency.

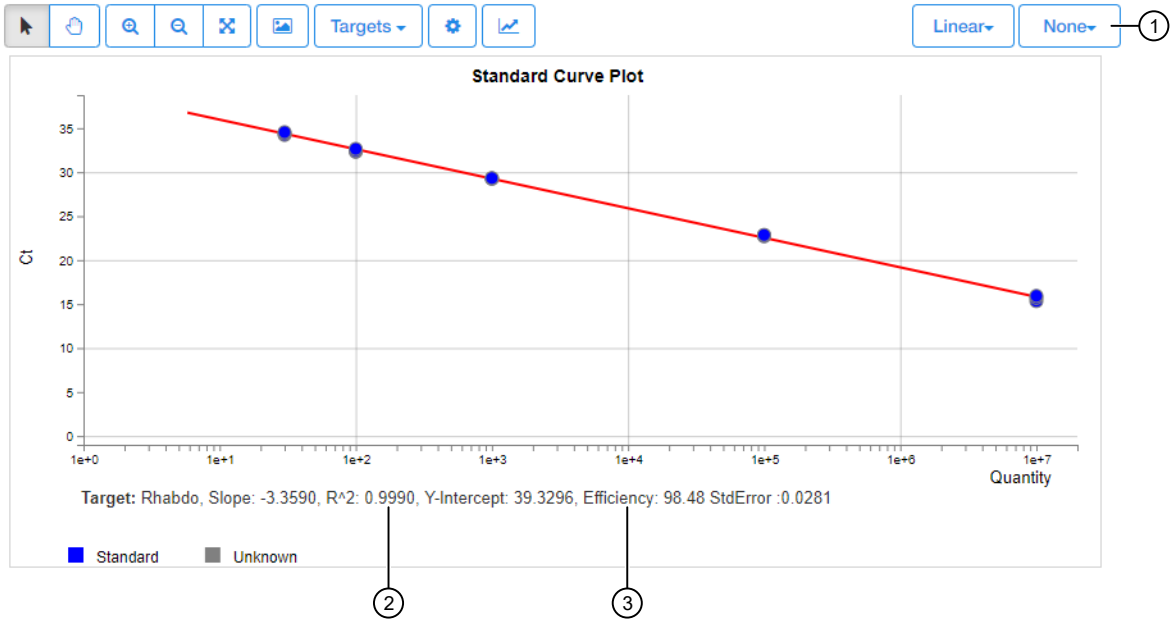


Figure 26 Example Standard Curve Plot

① Default plot settings
② R^2 value
③ PCR efficiency

Note: The **Standard Curve** efficiency should be between 90-110% and the R^2>0.99. If these criteria are not met, up to two points, not in the same triplicate, can be removed from the standard curve data, and the analysis repeated.

---

5. (*Optional*) Navigate to the **Report** tab to generate a report of the experiment, or to export results.

6. (*Optional*) To manually convert the copy number output to a mass measurement, multiply the copy number given by the AccuSEQ™ Real-Time PCR Software to the average molecular weight of the full-length genomic viral RNA (4.348 x 10^6g/mol), then divide by the Avogadro constant.

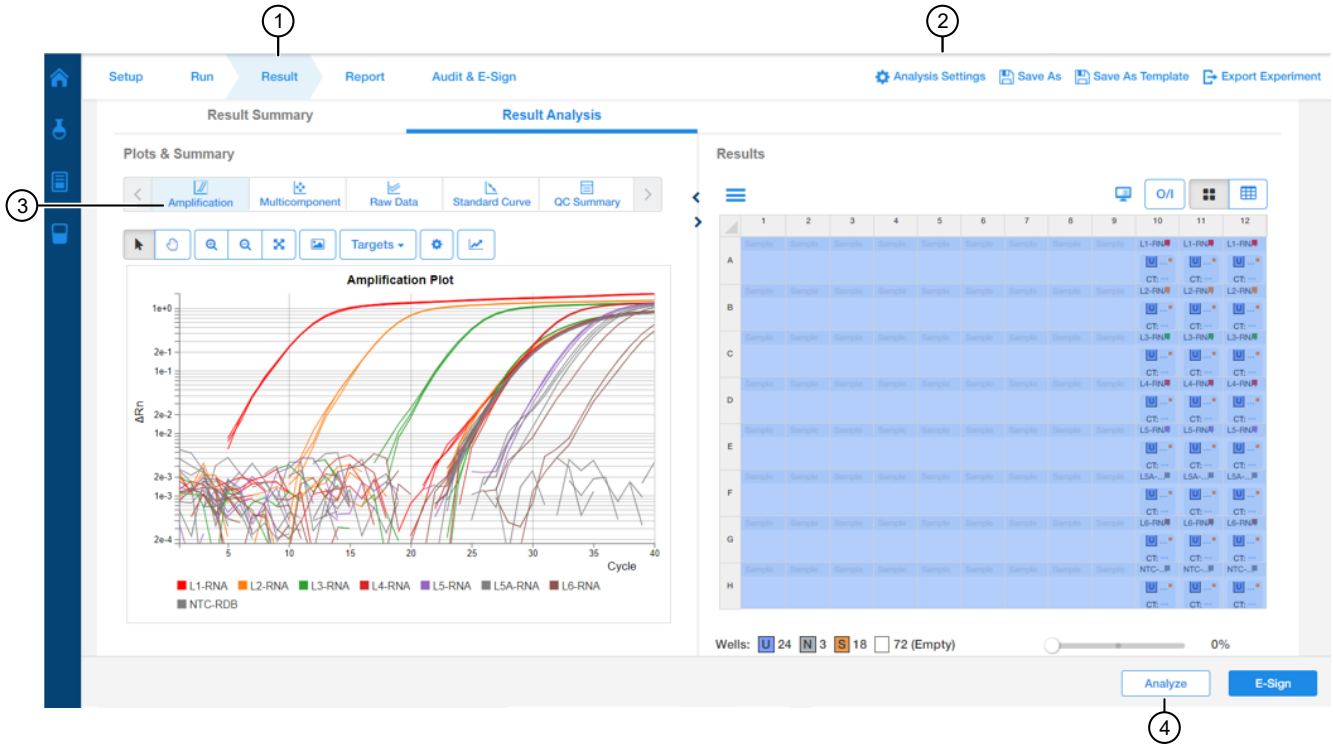
$$Mass\ (g) = \frac{Copy\ number\ x\ Molecular\ weight\ (gmol^{-1})}{6.0221\ X\ 10^{23}\ mol^{-1}}$$

Review ViralSEQ™ results (Lentivirus–Physical)

Review the results

After the qPCR run is finished, use the following general procedure to analyze the results. For more detailed instructions see the *AccuSEQ™ Real-Time PCR Software v3.1 User Guide* (Pub. No. 100094287).

1. In the AccuSEQ™ Real-Time PCR Software, open your experiment, then navigate to the **Result** tab.



1. **Result** tab
2. **Analysis Settings**
3. Plot horizontal scrollbar
4. **Analyze** button

2. In the **Result Analysis** tab, select individual targets, then review the Amplification Curve plots for amplification profiles in the controls, samples, and the standard curve. Ensure that threshold is set to 0.200 with an automatic baseline.

   Note: If any settings are changed, click the **Analyze** button to apply the new settings to the results. Target names and Sample names (under the **Setup** tab) can also be changed after the run is completed.

3. In the **Result Analysis** tab, review the **QC Summary** for any flags in wells.

4. In the **Result Analysis** tab, review the **Standard Curve** plot. Verify the values for the Slope, Y-intercept, R^2, and Efficiency are within acceptable limits.

① Slope, R^2, and Efficiency values

Note: The **Standard Curve** efficiency should be between 90-110% and the R^2>0.99. If these criteria are not met, up to two points, not in the same triplicate, can be removed from the standard curve data, and the analysis repeated.

5. In Table View, ensure that C_t values are within the standard curve range.
   - Samples with C_t values that exceed the upper limit of quantitation (10^9 copies) of the standard curve should be diluted and re-run.
   - Samples with C_t values that exceed the lower limit of detection (LoD of 10 copies) and IPC shows no signs of PCR inhibition, suggests the absence of lentivirus.

6. (*Optional*) Outliers can be excluded from the results. To exclude, select the well, then click **Omit/Include**, then reanalyze by clicking **Analyze**.

7. (*Optional*) Select **File ▸ Print Report** to generate a hard copy of the experiment, or click **Print Preview** to view and save the report as a PDF or HTML file.

8. Export the results.
    a. Navigate to the **Report** tab.
    b. Check all boxes under **Contents**.
    c. Select **Export Data in One File**.
    d. Select the **XLS** format, then click `Export`.

Calculate lentivirus titers from qPCR data

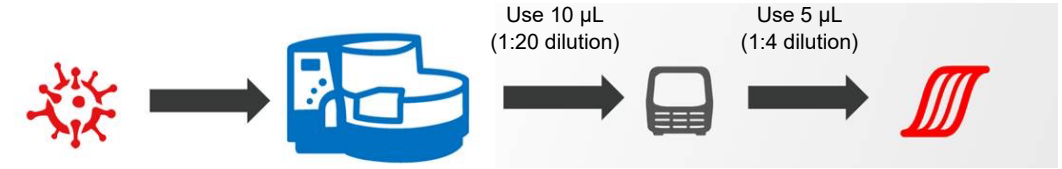
To determine the number of lentivirus RNA copies per mL in the original sample, the copy numbers obtained from the qPCR must be multiplied by the dilution factor of the sample during extraction and DNase I treatment. Since there are 2 copies of RNA/target per lentivirus particle, the number of viral particles per mL (VP/mL) is 0.5x the number of lentivirus RNA copies.

$$\text{Viral particles per mL} = \frac{\text{qPCR copies x sample dilution factor x 0.5}}{\text{Volume of sample used (mL)}}$$

For help in determining the qPCR copy numbers, see the *QuantStudio™ Design and Analysis Desktop Software User Guide* (Pub. No. MAN0010408).

For example, if the following parameters were used,

- 10 µL of lentivirus culture was extracted with the KingFisher™ Flex Purification System with 96 Deep-Well Head and eluted in 200 µL
- 10 µL of this eluate (20x dilution) was treated with DNase I, RNase-free (1 U/µL) in a total volume of 20 µL.
- 5 µL of the DNase-treated sample (4x dilution) was used for the qPCR reaction.



then, the calculation would be:

$$\text{Viral particles per mL} = \frac{\text{qPCR copies x (20x4) x 0.5}}{\text{0.01 (mL)}}$$

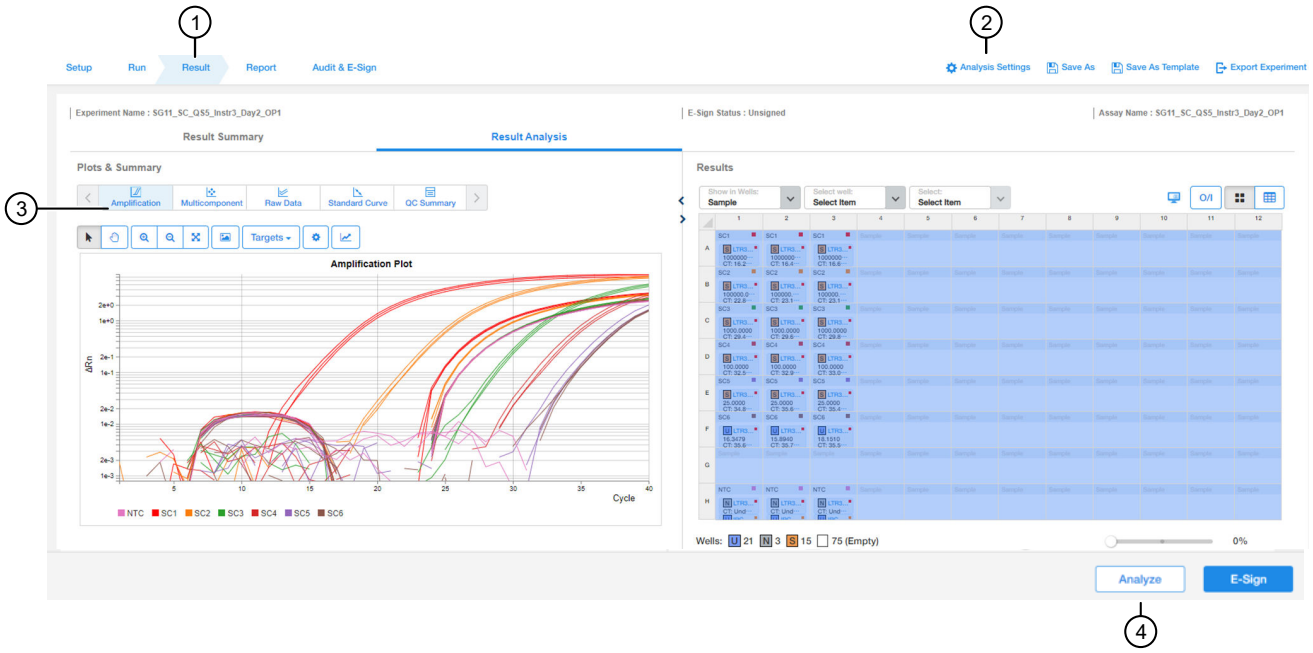
Note: qPCR can only determine the number of physical particles in a virus culture. To determine the numbers of infectious units, cell-based transduction experiments must be carried out. The titers of physical particles are often higher than infectious titers by 10-1000 fold, depending on the purity of the lentivirus preparation and the levels of infectious particles within the culture.

Review ViralSEQ™ results (Lentivirus–Proviral)

Review the results

After the qPCR run is finished, use the following general procedure to analyze the results. For more detailed instructions see the *AccuSEQ™ Real-Time PCR Software v3.1 User Guide* (Pub. No. 100094287).

1. In the AccuSEQ™ Real-Time PCR Software, open your experiment, then navigate to the **Result** tab.



① **Result** tab
② **Analysis Settings**
③ Plot horizontal scrollbar
④ **Analyze** button

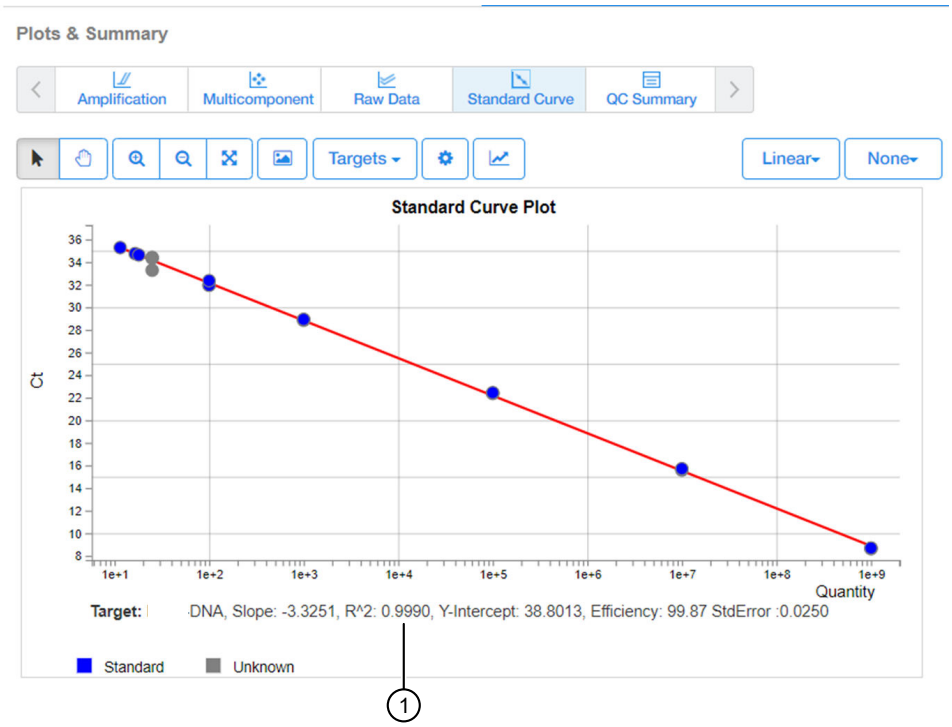
2. In the **Result Analysis** tab, select individual targets, then review the Amplification Curve plots for amplification profiles in the controls, samples, and the standard curve. Ensure that threshold is set to 0.200 with an automatic baseline.

Note: If any settings are changed, click the **Analyze** button to apply the new settings to the results. Target names and Sample names (under the **Setup** tab) can also be changed after the run is completed.

---

3. In the **Result Analysis** tab, review the **QC Summary** for any flags in wells.

4. In the **Result Analysis** tab, review the **Standard Curve** plot. Verify the values for the Slope, Y-intercept, R^2, and Efficiency are within acceptable limits.



① Slope, R^2, and Efficiency values

Note: The **Standard Curve** efficiency should be between 90-110% and the R^2>0.99. If these criteria are not met, up to two points, not in the same triplicate, can be removed from the standard curve data, and the analysis repeated.

---

5. In Table View, ensure that C_t values are within the standard curve range.
   - Samples with C_t values that exceed the upper limit of quantitation (10^7 copies) of the standard curve should be diluted and re-run.
   - Samples with C_t values that exceed the lower limit of detection (LoD of 10 copies) and IPC shows no signs of PCR inhibition, suggests the absence of provirus.

6. (*Optional*) Outliers can be excluded from the results. To exclude, select the well, then click **Omit/Include**, then reanalyze by clicking **Analyze**.

7. (*Optional*) Select **File ▸ Print Report** to generate a hard copy of the experiment, or click **Print Preview** to view and save the report as a PDF or HTML file.

8. Export the results.
   a. Navigate to the **Report** tab.
   b. Check all boxes under **Contents**.
   c. Select **Export Data in One File**.

d. Select the **XLS** format, then click `Export`.

Calculate provirus copies and lentivirus titers from qPCR data

Each provirus has 2 copies of the assay target (LTR).

1. To determine the number of provirus copies in the extracted sample, the copy numbers obtained from the qPCR must be multiplied by 0.5 and then by the dilution factor of the sample during extraction. The concentration of provirus per cell can be calculated based on the number of cells used in the extraction.

$$\text{Provirus copies per cell} = \frac{\text{qPCR copies x sample dilution factor x 0.5}}{\text{Number of harvested cells used for extraction}}$$

For help in determining the qPCR copy numbers, see the *QuantStudio™ Design and Analysis Desktop Software User Guide* (Pub. No. MAN0010408).

For example, if the following parameters were used,

- 10,000 cells were extracted with the KingFisher™ Flex Purification System with 96 Deep-Well Head and eluted in 200 µL.
- 5 µL of this eluate (40x dilution) was used for the qPCR reaction.

then, the calculation would be:

$$\text{Provirus copies per cell} = \frac{\text{qPCR copies x 40 x 0.5}}{\text{10,000}}$$

Note: The number of cells extracted can be determined by the counting of cells or nucleic acid quantity equivalence (1 cell = 6.6 pg for diploid cells). Users should establish the nucleic acid quantity equivalence for cells that are non-diploid.

---

2. To estimate the infectious viral titer (or transduction unit TU/mL), use the volume of lentivirus (mL) that was used to infect the cells seeded for lentivirus transduction and the number of cells seeded for transduction [No. of cells (Day 1)].

$$\text{Infectious viral titer per mL} = \frac{\text{Provirus copies per cell x No. of cells (Day 1)}}{\text{Volume of lentivirus (mL)}}$$

7 Create a custom template

This section describes the general procedures to create a template in the software. To use the default or admin-defined templates in the software, see the following sections:

- Chapter 3, “Set up, run, and review MycoSEQ™ experiments”
- Chapter 5, “Set up, run, and review ProteinSEQ™ experiments”
- Chapter 4, “Set up, run, and review resDNASEQ™ experiments”

Note: For all custom templates, be sure to check all settings, including qPCR method and optical filter selection, for correctness and alignment with your laboratory's standard operating procedures.

Template types

There are three types of templates in the AccuSEQ™ Real-Time PCR Software v3.1.

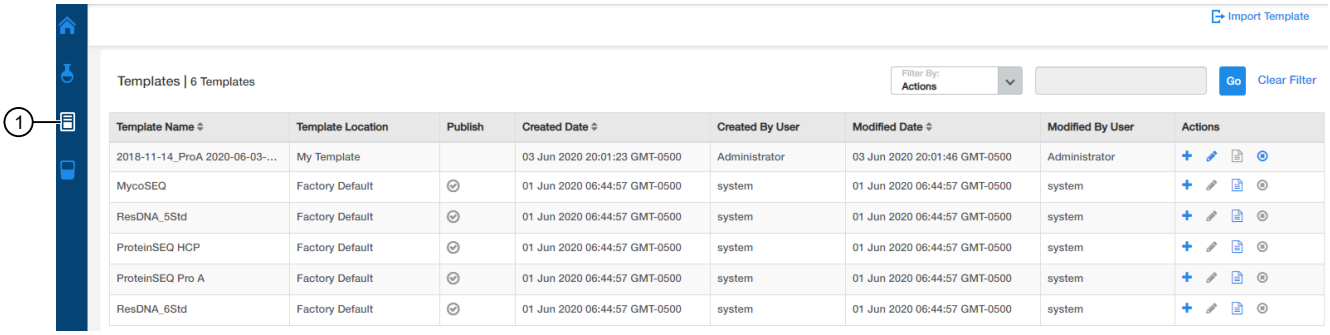
- Factory default Templates—templates supplied with the AccuSEQ™ Real-Time PCR Software v3.1; locked to editing by any user.
- Admin Defined Templates—templates that are created by the Administrator.
- My Templates—templates that are imported or created by the user that is signed in; no other users have permission to view these templates.

Templates can be locked or unlocked. See “Lock a template” on page 140.

Create or open a template

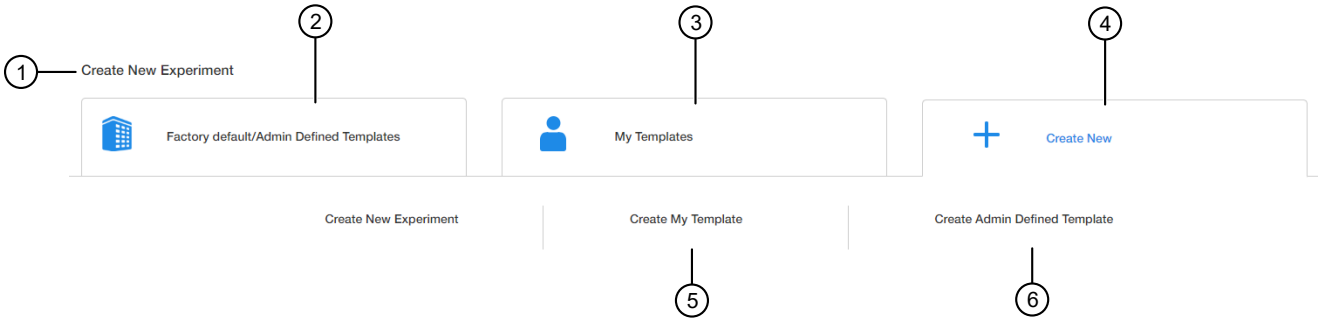
Create a new template or open an existing template in the **(Home)** screen.

- Click **Templates** in the left navigation pane for a full list of templates.



① **Templates** icon

- In the **Create New Experiment** pane, perform one of the following tasks to create a new template.



① **Create New Experiment** pane

② **Factory default/Admin Defined Templates**—List of existing default or Admin Defined templates. These templates can be used as templates for new experiments.

③ **My Templates**—List of templates available to the user that is signed in. These templates can be used as templates for new experiments.

④ **Create New**—Used to create an experiment or template with no pre-existing settings.

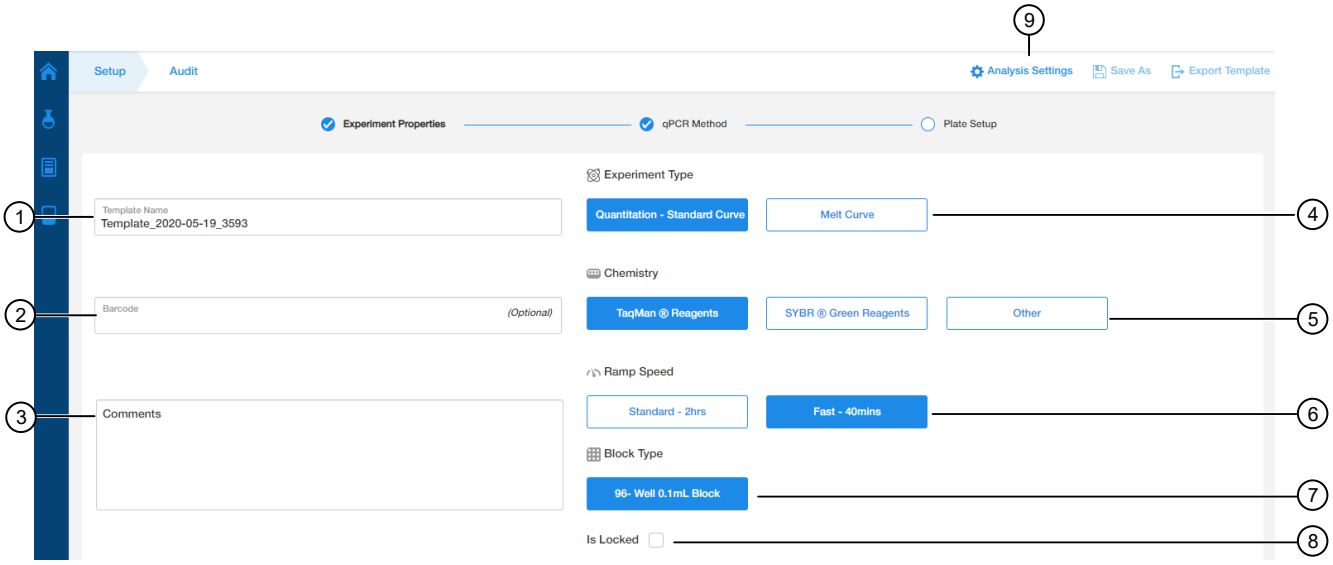
⑤ **Create My Template**—Used to create a new template (stored locally in **My Templates**).

⑥ **Create Admin Defined Template**—Used to create a new template (Administrator only).

Note: Available to other users when **Published**. See “Publish a template” on page 140.

To	Action
Create a template without pre-existing settings	1. Click + **Create New** on the home screen. 2. Select **Create My Template** or **Create Admin Defined Template**. 3. Edit the **Experiment Properties**, **qPCR Method**, and **Plate Setup** as required. 4. Click **Save**.
Create a template from an existing **Factory default** template **Note:** This option must be used when automated presence/absence calling is required for the MycoSEQ assay and when total DNA per Protein Concentration is required for the residual DNA assay.	1. Navigate to **Templates**. 2. Click + **Create New** next to the **Factory default** template. 3. Click **Next**. 4. In the **qPCR Method** screen, click **Save as Template**. 5. Enter the **Template Name** and properties, select if the template **Is Locked** or **Is Admin Defined**, then click **Save**. 6. Navigate to **Templates**, then open the new template. 7. Edit the **Experiment Properties**, **qPCR Method**, and **Plate Setup** as required. 8. Click **Save** in the **Plate Setup** tab to save the changes.
Create a template from an **Admin Defined** template	1. Navigate to **Templates**. 2. Select the desired **Admin Defined** file, then click **Edit**. 3. Click **Save as**. 4. Enter the **Template Name** and properties, select if the template **Is Locked** or **Is Admin Defined**, then click **Save**. 5. Navigate to **Templates**, then open the new template. 6. Edit the **Experiment Properties**, **qPCR Method**, and **Plate Setup** as required. 7. Click **Save** in the **Plate Setup** tab to save the changes.
Create a template from an existing user-created template **Note:** Only templates that are created by the signed-in user are listed under **My Templates**.	1. Navigate to **Templates**. 2. Select the desired **My Templates** file, then click **Edit**. 3. Click **Save as**. 4. Enter the **Template Name** and properties, select if the template **Is Locked** or **Is Admin Defined**, then click **Save**. 5. Navigate to **Templates**, then open the new template. 6. Edit the **Experiment Properties**, **qPCR Method**, and **Plate Setup** as required. 7. Click **Save** in the **Plate Setup** tab to save the changes.

Enter template properties



① Software-generated **Template Name**
② **Barcode** field
③ **Comments** field
④ **Experiment Type**
⑤ **Chemistry**
⑥ **Ramp Speed**
⑦ **Block Type** (fixed as a 96-Well 0.1mL block).
⑧ **Is Locked** checkbox (Only Administrators can create locked **Admin Defined Templates**).
⑨ **Analysis Settings**

1. (*Optional*) In the **Template Name** field, modify the file name.

   Note: Names must be unique. Deleted template names can not be reused. Template names cannot be changed after saving.

2. (*Optional*) Click the **Barcode** field, then enter a plate barcode.

3. (*Optional*) Enter information in the **Comments** field.

   Note: Comments are not editable post analysis.

4. In the **Setup** tab, select, or edit the **Experiment Type**, **Chemistry**, **Ramp Speed**, and **Block Type**. Any edits to the **Chemistry** or **Ramp Speed** clears the entries in **Plate Setup**, **Run Method**, and **Analysis Methods**.

   Note: The experiment type defines the available options for the template setup.

5. (*Optional*) Select **Is Locked** to lock the template. If locked, users are unable to edit the template.

6. (*Optional*) Click **Analysis settings** to change the default C_t Settings, Flag Settings, and Advanced Settings. See “Configure analysis settings” on page 152.

   Note: Click **Apply** to save any changes before closing the window.

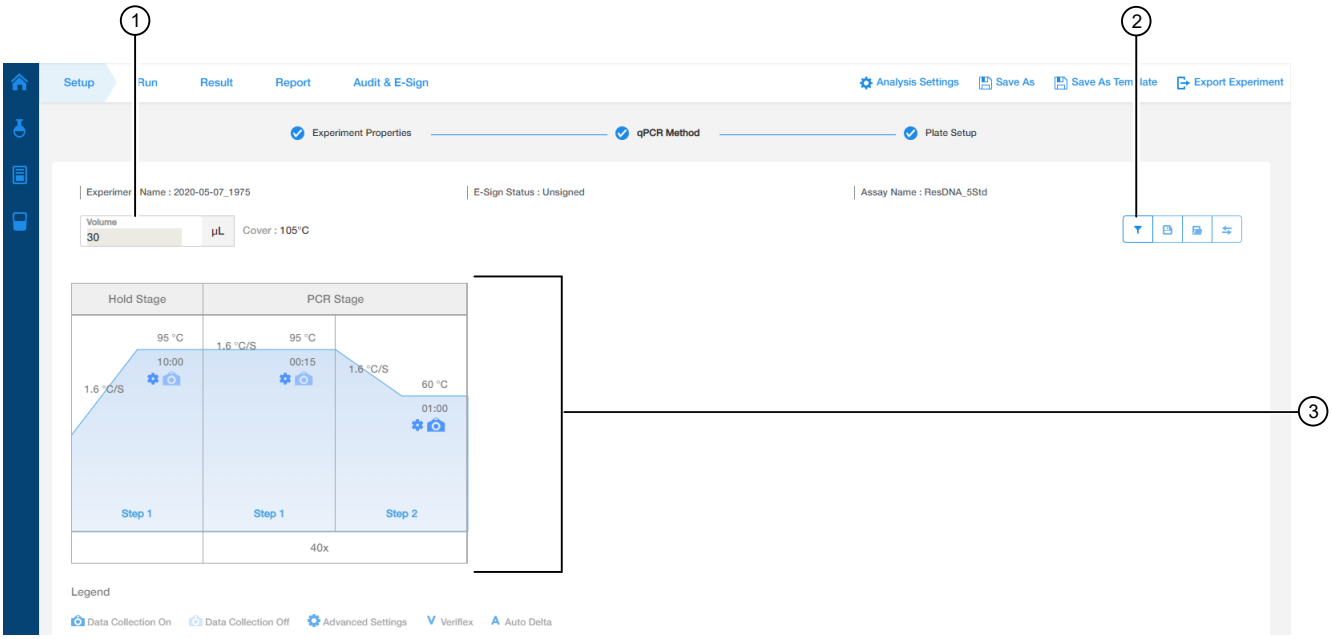
7. Click **Next**.

   Experiment names cannot be changed after this step.

The **qPCR Method** screen is displayed.

Confirm or edit the run method and optical filter selection

Note: This section provides general procedures to edit the run method and optical filter selection in the qPCR Method.
For specific instructions for each assay type, see the corresponding chapter in this guide.



① Reaction volume. The volume is fixed in locked templates. The default for custom templates is 30 µl.
② Optical filters.
③ PCR parameters.

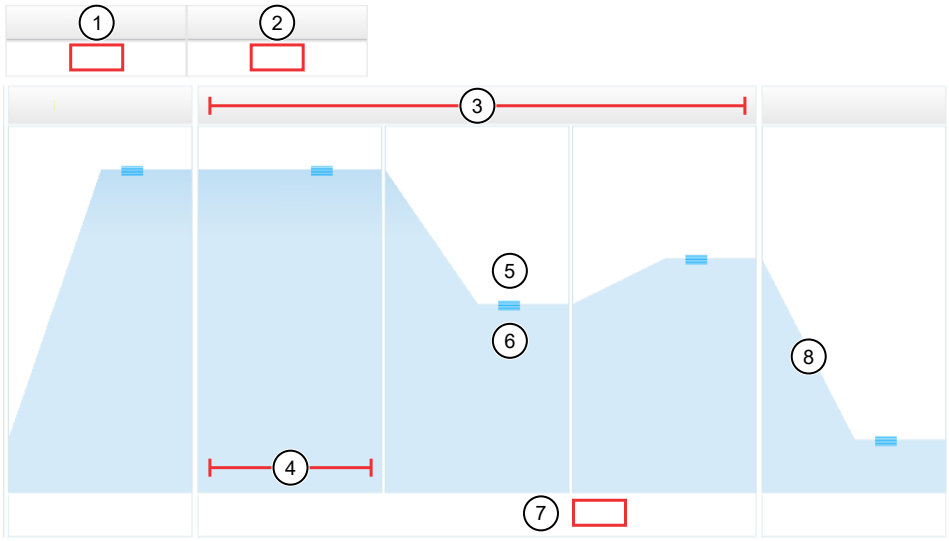
1. (*Optional*) In the **qPCR Method** tab, adjust the reaction volume.

2. (*Optional*) Edit the default run method (thermal protocol).
   - The default run method is optimized for TaqMan™ assays and a broad range of other reagents.
   - To edit the default run method, see “Adjust method parameters” on page 147.

   Note: Auto Delta and Veriflex functionality are not supported by the AccuSEQ™ Software v3.1.

3. (*Optional*) Click **(Optical Filter Settings)** to view or edit the default filter settings.
   - The default optical filter selection is for factory-calibrated (system) dyes.
   - For more information about system dyes and their calibration and optical filter selection, see *QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide* (Pub. No. MAN0010407).
4. Click **Next**.

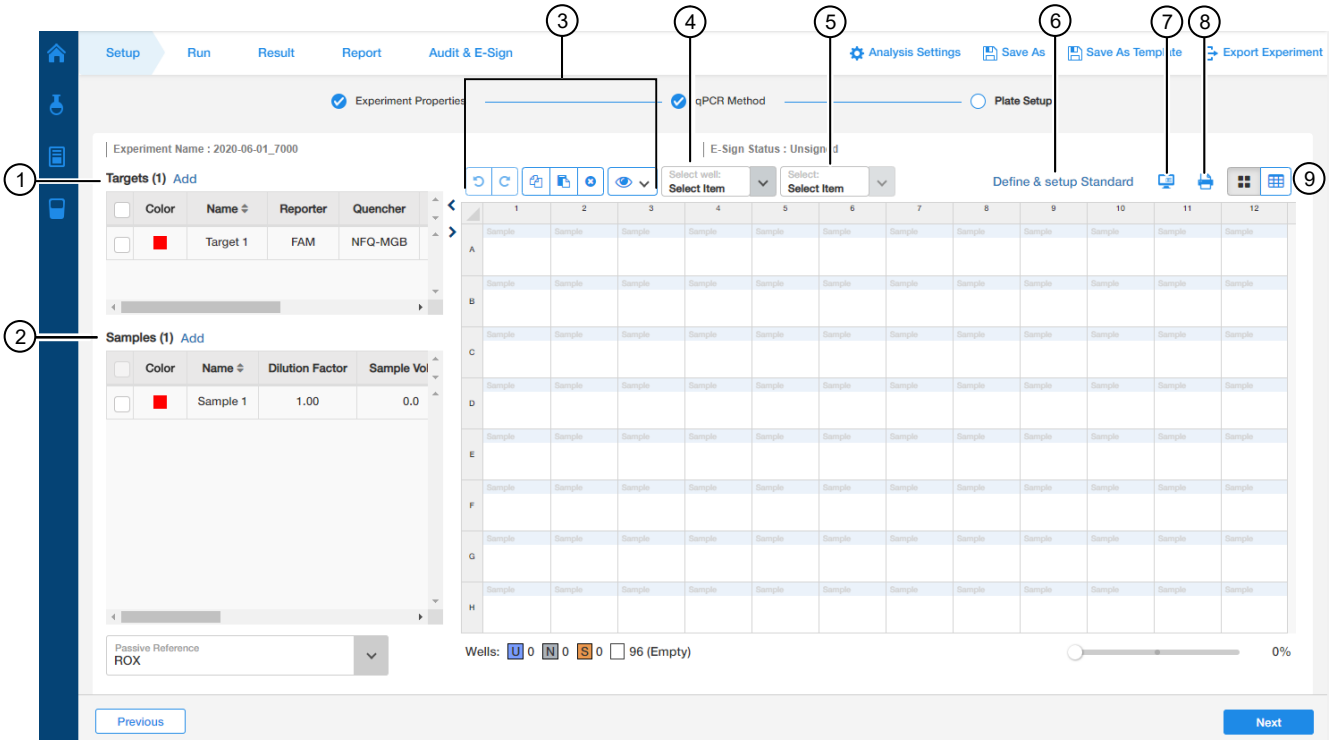
Method elements



1. Reaction volume
2. Heated cover temperature
3. Stage of thermal protocol
4. Step within a stage
5. Step temperature
6. Step hold time
7. Number of cycles
8. Temperature ramp rate

Assign plate and well attributes

Note: This section provides general procedures to set up the plate.
For specific instructions for each assay type, see the corresponding chapter in this guide. Do not change **Targets** for default assay templates.



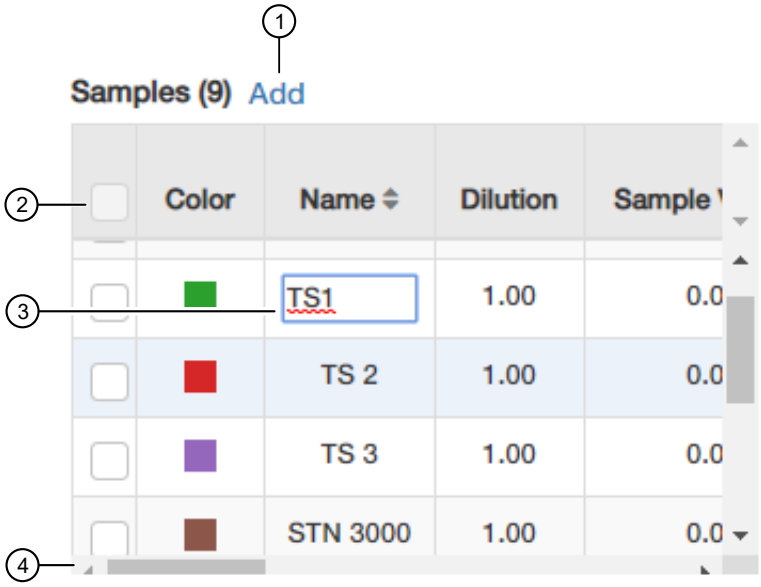
① Targets
② Samples
③ Plate setup toolbar
④ Select Item to highlight (Sample, Target, or Task).
⑤ Select Item. For example, Sample 1. Sample 1 replicates are highlighted.
⑥ Define & setup Standard
⑦ (View Legend)
⑧ (Print Preview)
⑨ View (Grid View or Table View)

1. In **Plate Setup** screen, click or click-drag to select plate wells in the **(Grid View)** of the plate.

2. Assign the well attributes for the selected wells.

   - To add new **Samples** or **Targets**, click **Add** in the appropriate column on the left of the screen, then edit the new Name and other properties as required. The new sample or target is then selectable within the wells of the plate.

     Note: To change sample names, click the name in the Name column, then type the new name. To change Reporters and Quenchers, click the dye, then select from the dropdown list.



① **Add** button
② Checkbox—Select **Targets** and **Samples** to go in the selected well.
③ Textbox—Click the name to edit.
④ Scrollbar—Use to scroll to additional properties.

When a **Sample** or **Target** name are edited, two entries are added to the Audit trail (one for Delete, and another for Create).

- Use the plate setup toolbar (above the plate) to make edits to the plate.
  - Click **View** to show/hide the Sample Name, Sample Color, or Target from the view.
- To add consecutive samples (with the same **Target**), select a well, then click-drag the dark blue box to the right. See “Select plate wells” on page 138 for additional actions.

- (*Optional*) Click **Define & setup Standard** to set up a standard curve.

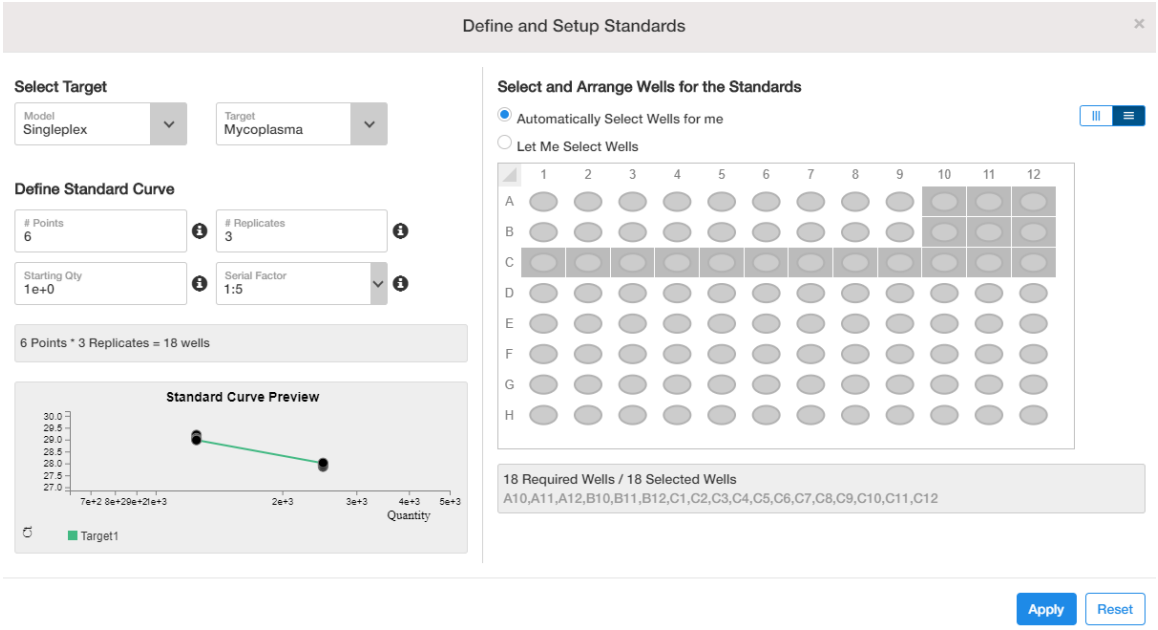
  Note: This option is available, but should not be used, for MycoSEQ™ assays.

  a. Select Singleplex or Multiplex.
  b. Select or type in the Target.
  c. Define the number of points and replicates, the starting quantity, and the serial dilution factor.

     Note: The **Standard Curve Preview** is a representative example only.

  d. (*Optional*) Select **Automatically Select Wells for me** or **Let Me Select Wells** used for the standard curve.
  e. Click **Apply** to save before closing the window.

  Note: Standards can be renamed using the **Sample** tab in the **Plate Setup** pane. For example, SD1, SD2, and SD3.



3. (*Optional*) Double-click a well to enter comments for the selected well.

4. Select a **Passive Reference** from the dropdown list (bottom left of screen).

Select plate wells

- Select plate wells in the **(Grid View)** .

To	Action
Select a single well	Click a well in the plate
Select multiple wells	Click-drag in the plate
Select contiguous wells	Shift+click wells in the plate
Select a column of wells	Click a column header
Select all wells	Click the top-left corner of the plate grid
Select a block of wells	Click a well to define a corner, then shift+click another well on the opposite corner

Note: It is not currently possible to Ctrl+click to add wells in different areas of the plate.

- Select plate wells in the **(Table View)**.

To	Action
Select a single well	Click a row in the table
Select non-contiguous wells	Ctrl+click rows in the table
Deselect a single well	Ctrl+click the selected row

Save the custom template

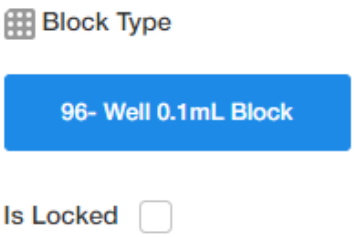
To save the template, do one of the following.

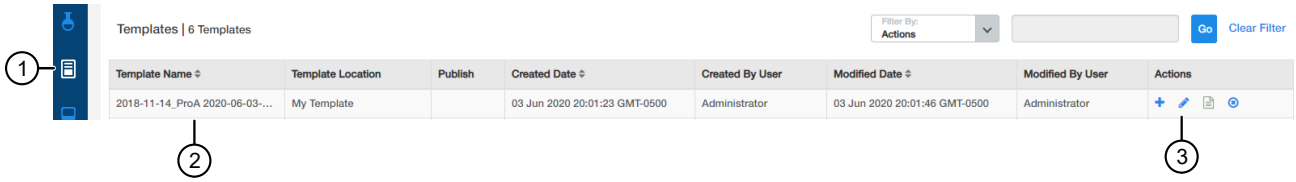
Option	Description
To save a custom template that you created new	Enter the **Experiment Properties**, **qPCR Method** and **Plate Setup** information, then click **Save**. **Template saved successfully** appears.
To save a template from an open Experiment	1. Click **Save As Template** in any tab. 2. Enter a **Template Name**. 3. (*Optional*) Enter a description of the template. 4. Select whether the template **Is Admin Defined** or **Is Locked**. 5. Click **Save**.
To save a template (from an experiment) created from an existing template	1. Open the template that you want to copy. 2. Click **Save As Template** in any tab. 3. Enter a new **Template Name**. 4. (*Optional*) Enter a description of the template. 5. Select whether the template **Is Admin Defined** or **Is Locked**. 6. Click **Save**. Once saved, the new template can be opened and edited if needed.
To save a template from an existing template (excluding factory default templates)	1. Navigate to **Templates**. 2. Click to open the template that you want to copy. 3. Click **Save As** in any tab. 4. Enter a new **Template Name**. 5. (*Optional*) Enter a description of the template. 6. Select whether the template **Is Admin Defined** or **Is Locked**. 7. Click **Save**. Once saved, the new template can be opened and edited if needed.

Lock a template

New templates or unlocked templates can be locked. **Experiment Properties** cannot be edited in locked templates.

Lock the template.

Template type	Action
New	1. Check the **Is Locked** checkbox in the **Experiment Properties** screen of the **Setup** tab.  2. Click **Next** to proceed with locked template creation.
Unlocked template	1. Navigate to the Templates screen. 2. Select the template, then click **Edit**. 3. Check the **Is Locked** checkbox in the **Experiment Properties** screen of the **Setup** tab. 4. Click **Next** to proceed with locked template creation.



① **Templates** list
② **Template Name**
③ **Edit**

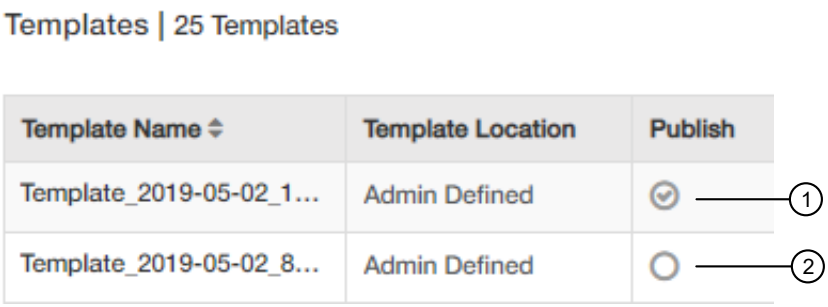
Publish a template

To make a template available for other users, publish the template.

1. Click the **Templates** tab, then select the template of interest.
2. Click **Publish Template** in the **Actions** column.
   Blue icons are active. Gray icons are inactive.

① Create Experiment
② Edit Template
③ Publish Template
④ Delete Template

3. Click **Yes** to verify that you want to publish the template.
   A message is displayed if the template was successfully published, click **OK**.
   Publish is then selected in the templates list.



① Published
② Unpublished

Import template

Import Template is used to import a template created in a different AccuSEQ™ Software v3.1 location.

IMPORTANT! Only EDT files from QuantStudio™ 5 Real-Time PCR Instruments with 0.1-mL blocks are supported for import in the AccuSEQ™ Software v3.1. EDT version 1.3.2 is recommended.

1. In the navigation pane of the **(Home)** screen, click **(Templates)**.
2. Click **Import Template**.
3. Browse to the file of interest, then click **Open**.

   Note: Templates will not import with the same name as an existing template. The software prompts the user for a new name.
   If the AccuSEQ™ Software times out while the import window is open, sign in again, then retry the import.

The template is displayed in the list of templates in the **Templates** pane.

Export a template

Export Template is used to export an experiment to a different AccuSEQ™ Software v3.1 location.

1. In the navigation pane of the **(Home)** screen, click **(Templates)**.
   The **Templates** pane is displayed.
2. Browse to the file of interest, then click **Edit**.
3. In the **Setup** or **Run** tab, click **Export Template**.
4. An EDT file is created, then downloaded.

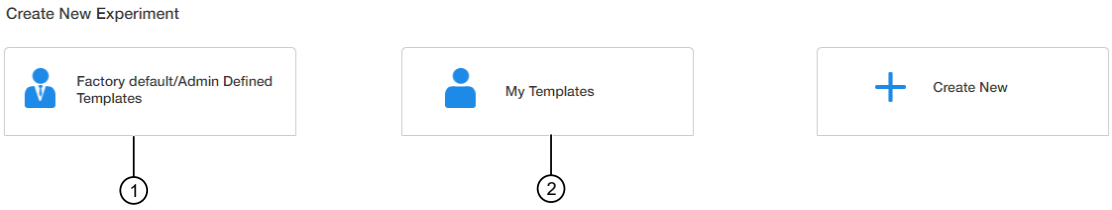
Note: You can change the Chrome™ browser settings to ask where to save each file before downloading.

---

8 General Experiment procedures

Create an experiment from a template

1. Open a template by doing one of the following:
   - In the **Create New Experiment** pane of the **(Home)** screen, select an existing template from the **Factory default/Admin Defined Templates** or **My Templates** tabs.



   ① **Factory default/Admin Defined Templates** tab
   ② **My Templates** tab

   - From the **(Home)** screen, click **(Templates)** for a full list of templates. Select a template, then click **(Create Experiment)**.

2. In the **Experiment Properties** pane of the **Setup** tab:
   a. (*Optional*) Change the system-generated name of the experiment.

   Note: Names must be unique. Deleted experiment names can not be reused. Experiment names cannot be changed after saving.

   b. (*Optional*) Enter the plate **Barcode**.

   c. (*Optional*) Enter **Comments**.

d. Check that the **Experiment Type**, **Chemistry**, and **Ramp Speed** are correct for the assay that you are running.

e. Click **Next**.

3. In the **qPCR Method** pane of the **Setup** tab:
   a. Check that the reaction volume and cycling conditions are correct for the assay that you are running.

   b. Click **Next**.

4. In the **Plate Setup** pane of the **Setup** tab:
   a. Enter **Samples**, **Targets**, and standards.

   b. Click **Next**.

   The **Run** tab opens.

Create a copy of an existing experiment

Usually, experiments are run from existing template files. To create a new template or experiment file, see Chapter 7, “Create a custom template”.

1. Open an existing experiment. See “Open an experiment” on page 145.
   The **Setup** tab opens.

2. In any tab, click **Save As**.

3. Enter the new **Experiment Name**, then click **Save**.

   Note: Names must be unique. Deleted experiment names can not be reused. Experiment names cannot be changed after saving.

4. Navigate to **Experiments**, open the copied experiment, then edit as needed.

5. In the **Experiment Properties** pane of the **Setup** tab:
   a. (*Optional*) Enter the plate barcode.

   b. Ensure that the **Experiment Type**, **Chemistry**, and **Ramp Speed** are correct.

   c. Click **Next**.

6. In the **qPCR Method** pane of the **Setup** tab:
   a. Ensure that the reaction volume and cycling conditions are correct.

   b. Click **Next**.

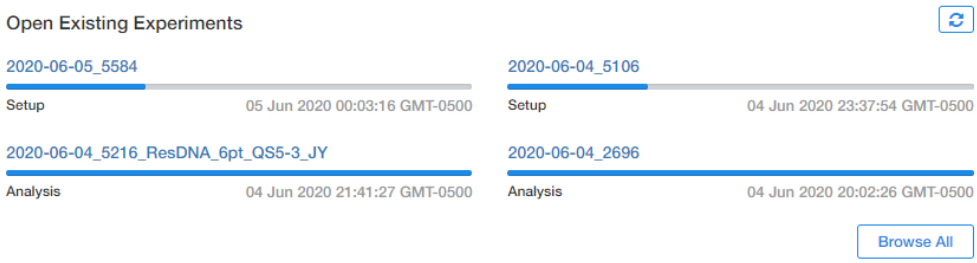
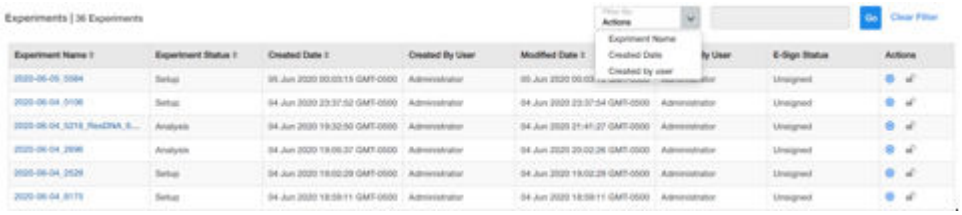
7. In the **Plate Setup** pane of the **Setup** tab:
   a. Enter or edit **Samples**, **Targets**, and standards.
   b. Click **Next**.

   The **Run** tab opens.

8. Click **Start Run**.

Open an experiment

You can open an experiment from 2 locations:

Location	Description
Home screen	To open the most recently run experiments: 1. Click **(Home)**. 2. Click an experiment name, or click **Browse All**. 
Experiments screen	To open previously run experiments: 1. Click **(Experiments)**. 2. If needed, filter, or display the next pages of the list. 3. Click an experiment name. 

Export an experiment

Export Experiment is used to export an experiment that is run on a QuantStudio™ 5 Real-Time PCR Instrument with a 0.1-mL block to a different AccuSEQ™ Software v3.1 location.

1. In the navigation pane of the **(Home)** screen, click **(Experiments)**.
   The **Experiments** pane is displayed.
2. Browse to the file of interest, then click the **Experiment Name** to open.
3. Click **Export Experiment** (top right corner).

   Note: If any data was not analyzed, the user is prompted to analyze the experiment to continue the export.
4. An EDS file is created, then downloaded.

   Note: You can change the Chrome™ browser settings to ask where to save each file before downloading.
   Preferences are not saved following export.

IMPORTANT! Audit records are not exported during **Export Experiment**. To obtain audit records, create a report in the software or from the SAE module. See “Create and print a report” on page 172 or the *AccuSEQ Quantstudio5 Security, Audit, and E-signature (SAE) Administrator Console v1.0 User Guide* (Pub. No. 100084439).

Import an experiment

Import Experiment is used to import an experiment created in a different AccuSEQ™ Software location.

IMPORTANT! Only EDS files from QuantStudio™ 5 Real-Time PCR Instruments with 0.1-mL blocks are supported for import in the AccuSEQ™ Software v3.1. EDS version 1.3.2 is recommended.

1. In the navigation pane of the **(Home)** screen, click **(Experiments)**.
   The **Experiments** pane is displayed.
2. Click **Import Experiment**.
3. Browse to the file of interest, then click **Open**.

   Note: Experiments will not import with the same name as an existing experiment. The software prompts the user for a new name.
   Experiments imported from AccuSEQ™ Software v3.0 will have blank **Run start** and **Run completed** times.
   If the AccuSEQ™ Software times out while the import window is open, sign in again, then retry the import.

The experiment is displayed in the list of experiments in the **Experiments** pane.

Note: The e-signature status of imported experiments is set to **Unsigned**.

Modify a qPCR method

Adjust method parameters

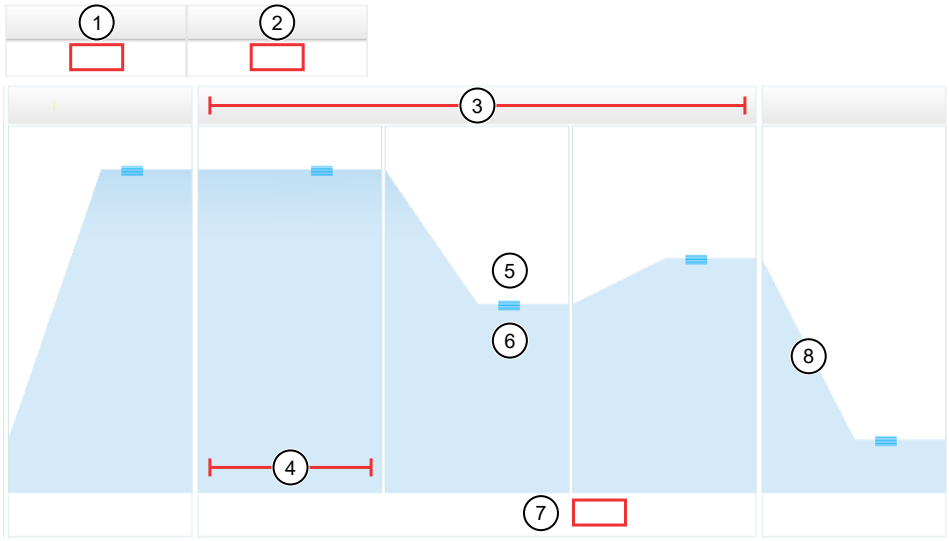
For an overview of the method as it is graphically represented, see “Method elements” on page 148.

- In the **qPCR Method** screen of the **Setup** tab, click a method parameter field to edit the following information:
  - Reaction volume
  - Temperature ramp rate
  - Step temperature
  - Step hold time
  - Number of cycles
- Hover over the temperature, then type in a new temperature to change a step temperature.
- Click to switch data collection on or off at each step.

  Data Collection On enables analysis of data that is collected throughout the PCR, for real-time analysis and troubleshooting.

  Note: If no data collection points are selected, the experiment will run, but the software gives an **Experiment Run Failed** error upon completion.
- Click to configure pause settings.

Method elements



1. Reaction volume
2. Heated cover temperature
3. Stage of thermal protocol
4. Step within a stage
5. Step temperature
6. Step hold time
7. Number of cycles
8. Temperature ramp rate

Add or remove a stage

1. In the **qPCR Method** tab, hover the cursor over the header or footer of a stage to display − and + on the stage borders.

   Note: Hovering within a stage on a step displays the same icons, but they apply to the step only.

2. Add or remove a stage.

Option	Action
Add a stage	1. Click + on the left or right border. 2. Select the type of stage to add.
Remove a stage	1. Click −.

To edit stages, see “Add or remove a step” on page 148.

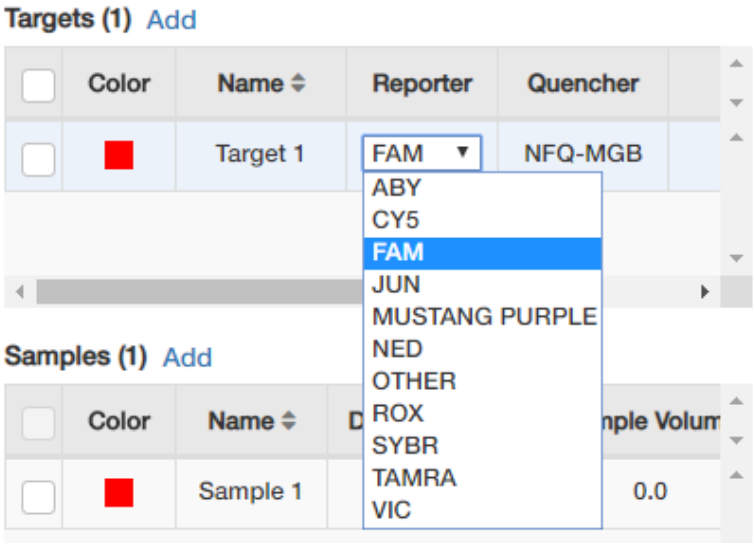
Add or remove a step

1. In the **qPCR Method** tab, hover the cursor over a step to display − and +.
2. Add or remove a step.
   - Click + on the left or right border of a step to add a step before or after, respectively.
   - Click − to remove the step.

Select optical filters

The need to edit optical filter settings is rare, and it is for advanced or custom uses only.

Use the optical filters settings to select a filter set to match the profile of a custom dye reporter (chosen during plate setup).



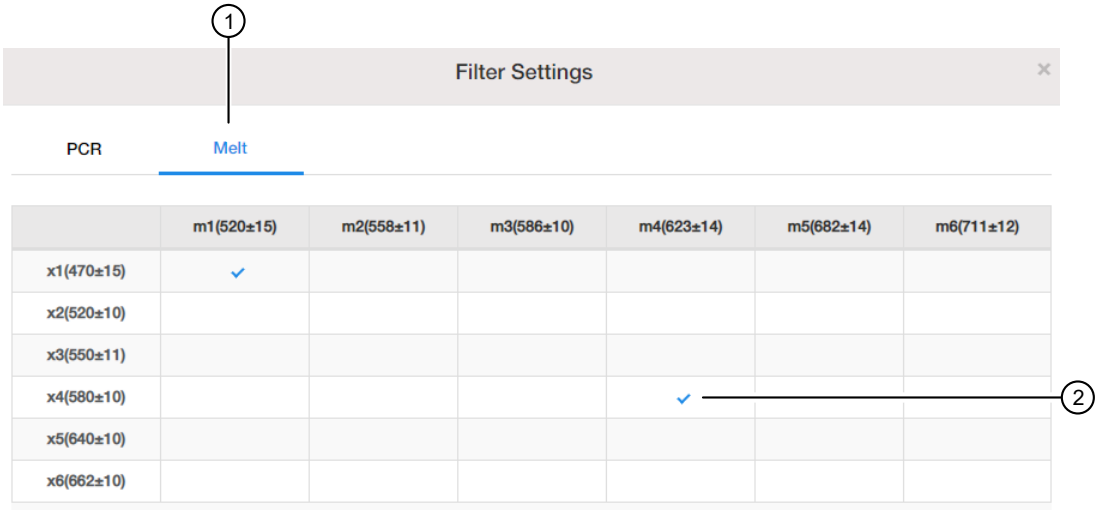
1. In the **qPCR Method** tab, select **(Optical Filter Settings)**.

   The excitation (x) and emission (m) wavelengths that correspond to each filter are shown on the screen.

2. Select the checkboxes to enable or disable filters.

   A **Melt** table is accessible if the method contains a melt curve stage. Otherwise, use the **PCR** table to select optical filters.

   IMPORTANT! Select filter 4 for custom melt curve experiments that use ROX™ dye.



① **Melt** tab
② Filter 4

3. Click **Save** to save changes, or **Cancel** to cancel any changes.

4. (*Optional*) Click ⇆ **Revert to Default** to reset filters.

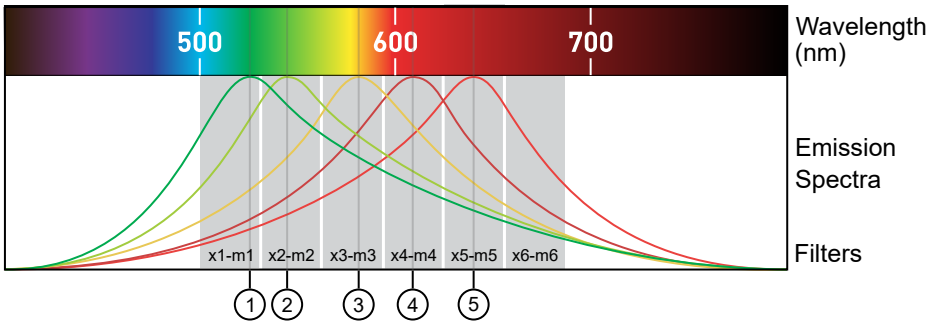
For information on the dyes read by each filter, see "QuantStudio™ 5 Instrument filters and supported dyes" on page 150.

QuantStudio™ 5 Instrument filters and supported dyes

The instrument uses a de-coupled six-color optical filter set that supports the dyes shown in the following table and figure.

Peak filter	Color	Filter wavelength (nm)[1]		Factory-calibrated dyes	Example custom dyes
		Excitation	Emission		
x1-m1	Blue	470 ± 15 nm	520 ± 15 nm	FAM™ dye, SYBR™ Green	SYT09
x2-m2	Green	520 ± 10 nm	558 ± 12 nm	VIC™ dye	JOE™ dye, HEX™ dye, TET™ dye[2]
x3-m3	Yellow	550 ± 10 nm	587 ± 10 nm	NED™ dye, TAMRA™ dye, ABY™ dye	Cy®3
x4-m4	Orange	580 ± 10 nm	623 ± 14 nm	ROX™ dye, JUN™ dye	Texas Red™ dye
x5-m5	Red	640 ± 10 nm	682 ± 14 nm	MUSTANG PURPLE™ dye, Cy™5	LIZ™ dye
x6-m6	Deep-Red	662 ± 10 nm	711 ± 12 nm	None [3]	Cy® 5.5

[1] The central wavelengths are the optimized wavelengths.
[2] The HEX™ and TET™ dyes from Thermo Fisher Scientific fall within the emission wavelength range of the system, therefore they can be added and adapted for use on the instrument.
[3] This filter set currently does not support any dyes supplied by Thermo Fisher Scientific.



① x1-m1 — FAM™ dye, SYBR™ Green
② x2-m2 — VIC™ dye
③ x3-m3 — ABY™ dye, NED™ dye, Cy®3, TAMRA™ dye
④ x4-m4 — JUN™ dye, ROX™ dye, Texas Red™ dye
⑤ x5-m5 — Cy™5, MUSTANG PURPLE™ dye

Edit the ramp increment for the melt curve dissociation step

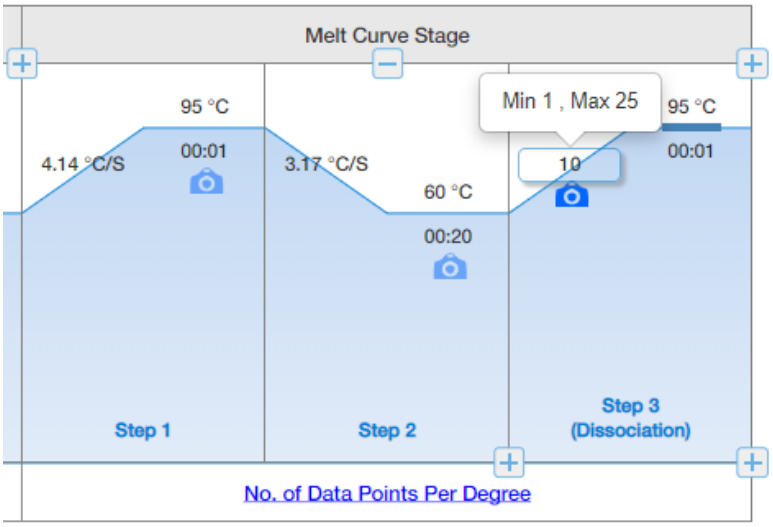
In the **qPCR Method** section of the **Setup** tab, you can perform the following tasks to edit the ramp increment for the melt cure dissociation step.

- Select the ramp increment method for the dissociation step (Click **Continuous** found under the graphical representation of the thermal protocol to change the default).

Option	Description
Continuous (default)	Continuously increases the temperature by the ramp increment (°C/sec).
Step & Hold	Increases the temperature by the ramp increment (°C), then holds at that temperature for the specified time.
No. of Data Points per Degree	Increases the temperature by the ramp increment (°C) and collects the specified number of data points per degree increased.

- (*For all options*) Edit the temperature ramp increment.
  a. Click the ramp increment element in the **Dissociation** step.
  b. Enter a value or use the up/down arrows (default is 0.15°C/s).
- (*Step and Hold only*) Edit the hold time after each temperature increase.
  a. Click the time field under **Step & Hold**.
  b. Enter a value (default is 5 seconds).
- (*No. of Data Points per Degree only*) Edit the number of data points to be collected with each degree increase.
  a. Click the number of data points element in the **Dissociation** step.

b. Enter a value or use the up/down arrows (default is 10 data points).



Configure analysis settings

This section describes the analysis settings that apply to all experiment types, unless otherwise noted.

Guidelines for the analysis settings

- We recommend analyzing the experiment with the default analysis settings.
- If the default analysis settings are not appropriate for the experiment, modify the settings in the **Analysis Settings** dialog box, then reanalyze the experiment.

The default analysis settings are different for each experiment type. The analysis settings determine the following parameters.

- How the baseline, threshold, and threshold cycle (C_t) are calculated
- Which flags are enabled
- Other analysis options that are specific to an experiment type

View and configure the analysis settings

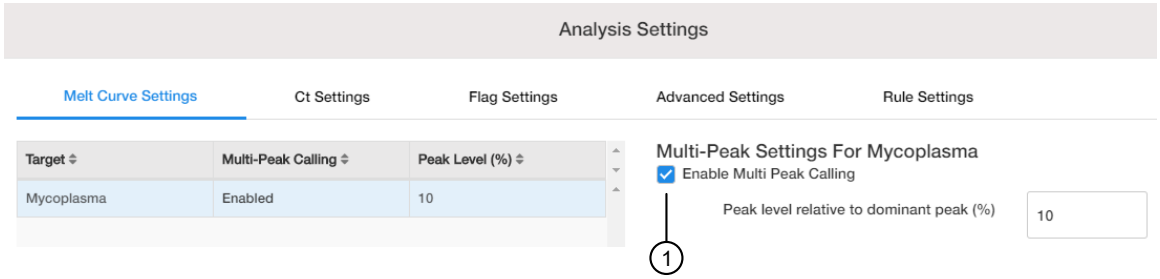
1. In any open **Experiment**, click **Analysis Settings**. To open an experiment see “Open an experiment” on page 145.
2. View and (*optional*) configure the analysis settings.
3. (*Optional*) To return to the default settings, click **Revert to Default**.
4. Click **Apply**.
   Click **Cancel** to discard your changes.
   Data are reanalyzed automatically.

Melt Curve Settings overview

Use the **Melt Curve Settings** to configure melt curve parameters.

- Enable or disable **Multi Peak Calling**.

Note: For a custom MycoSEQ/T_m experiment, uncheck **Enable Multi Peak Calling** in the **Melt Curve Settings** and uncheck the MTP **Use** checkbox in the **Flag Settings** so the QC Summary doesn't report additional peaks and is grayed out.



① Enable Multi Peak Calling

- Adjust the peak level relative to the dominant peak (%).

C_t settings overview

The default C_t settings are appropriate for most applications. Configuration of the settings is an option for analysis of not typical or unexpected run data.

Note: The **C_t Settings** feature is not available for experiments without a PCR stage, such as melt curve experiments.

Table 4 C_t Settings

Setting	Description
Data Step Selection	Determines the stage/step combination for C_t analysis (when there is more than one data collection point in the run method).
Default C_t Setting	Determines how the **Baseline Threshold** Algorithm is set. The **Default C_t Setting** are used for targets unless they have custom settings. **Note:** Use **Edit Default Settings** to edit the default settings for the assay.
C_t Settings for Target	• **Default Settings** selected—The **Default C_t Settings** are used to calculate the C_t values for the target. • **Default Settings** deselected—The software allows manual setting of the baseline or the threshold.

Table 5 Recommendations for manual threshold and baseline settings

Setting	Recommendation
Threshold	Enter a value for the threshold so that the threshold is: • Above the background. • Below the plateau and linear phases of the amplification curve. • Within the exponential phase of the amplification curve. **Note:** If Auto threshold is used, the displayed values are the calculated values. However, the report displays a maximum of 3 decimal places.
Baseline	Select the **Start Cycle** and **End Cycle** values so that the baseline ends before significant fluorescence signal is detected.

Flag settings overview

Use the **Flag Settings** to configure the flag parameters.

- Adjust the sensitivity so that more wells or fewer wells are flagged.
- Change the flags applied by the software for each experiment type.

Advanced settings overview

Use the **Advanced Settings** tab to change baseline settings for individual wells.

Note: The **Advanced Settings** feature is not available for experiments without a PCR stage, such as melt curve experiments.

Rule settings overview (MycoSEQ™ experiments only)

Note: The **Rule Settings** feature is currently only available for MycoSEQ™ experiments.

The default **Rule Settings** are appropriate for most MycoSEQ™ applications. Configuration of the settings is an option for analysis of not typical or unexpected run data. See “View and configure the analysis settings” on page 152.

Table 6 Rule Setting Calls

Setting	Description
Plate Call	Determines whether the plate has passed or failed (by the pass of both the positive and no template controls).
Inhibition Control	Monitors for inhibition in the unknown sample (inhibition in the presence of a positive control).
Well Calls (Unknown)	Determines whether individual wells have passed (called as present or absent), failed, or require review.

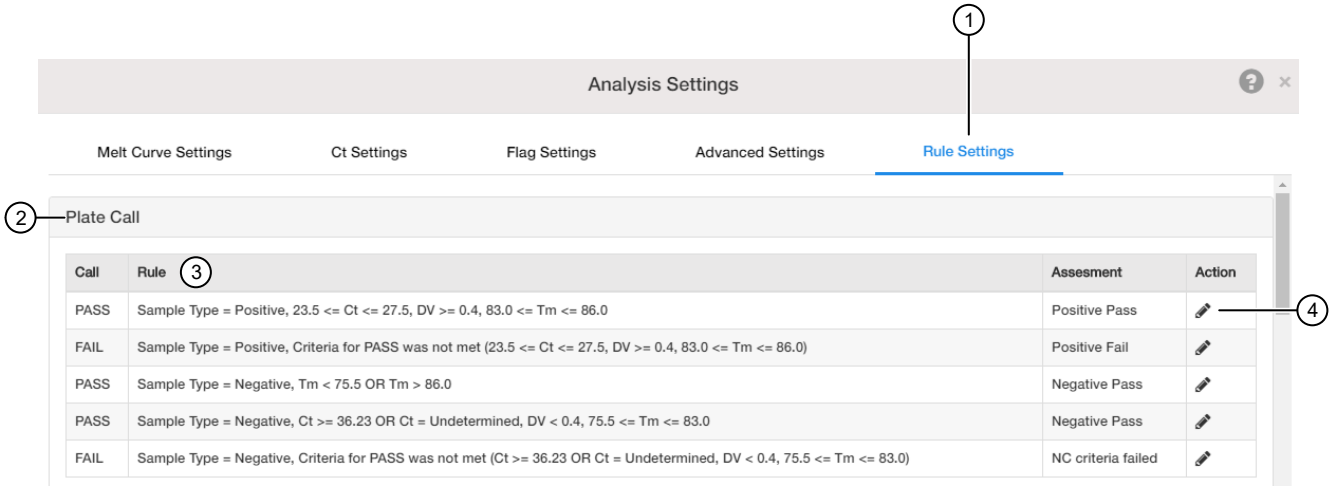


Figure 27 Example Rule Settings (MycoSEQ™ Plate Call)

① **Rule Settings** tab
② **Plate Call** pane
③ **Rule**—Ct, DV, and T_m values for each Sample type call.
④ **Edit**—The Ct, Δ CT (inhibition controls only), DV, and T_m parameters can be adjusted as required after completion of the run.

Note: Rule Settings are editable only after completion of a run.

Set up and run the PCR reactions

1. Assemble the PCR reactions. Follow the manufacturer's instructions for the reagents, then follow the plate layout set up in the software. See the appropriate kit user guide for more information.

2. Load the reaction plate into the instrument (see “Load the plate in the instrument” on page 36), then start the run (see “Monitor the run” on page 38).

   Note: Thermo Fisher Scientific recommends locking the computer screen during experiment runs to prevent edits/actions by other users. Press **Ctrl+Alt+Delete ▸ Lock**.

   If a run is interrupted, and the AccuSEQ™ Software does not receive the data from the instrument, the **Experiment Status** changes to **Error**.

9 Review the results and generate a report

This section includes general information to help in the review and export of the results. For more detailed information about the type of review required for a specific experiment type, see the corresponding chapter in this guide.

Overview of the Result tab

Review and analyze run data in the **Result** tab.

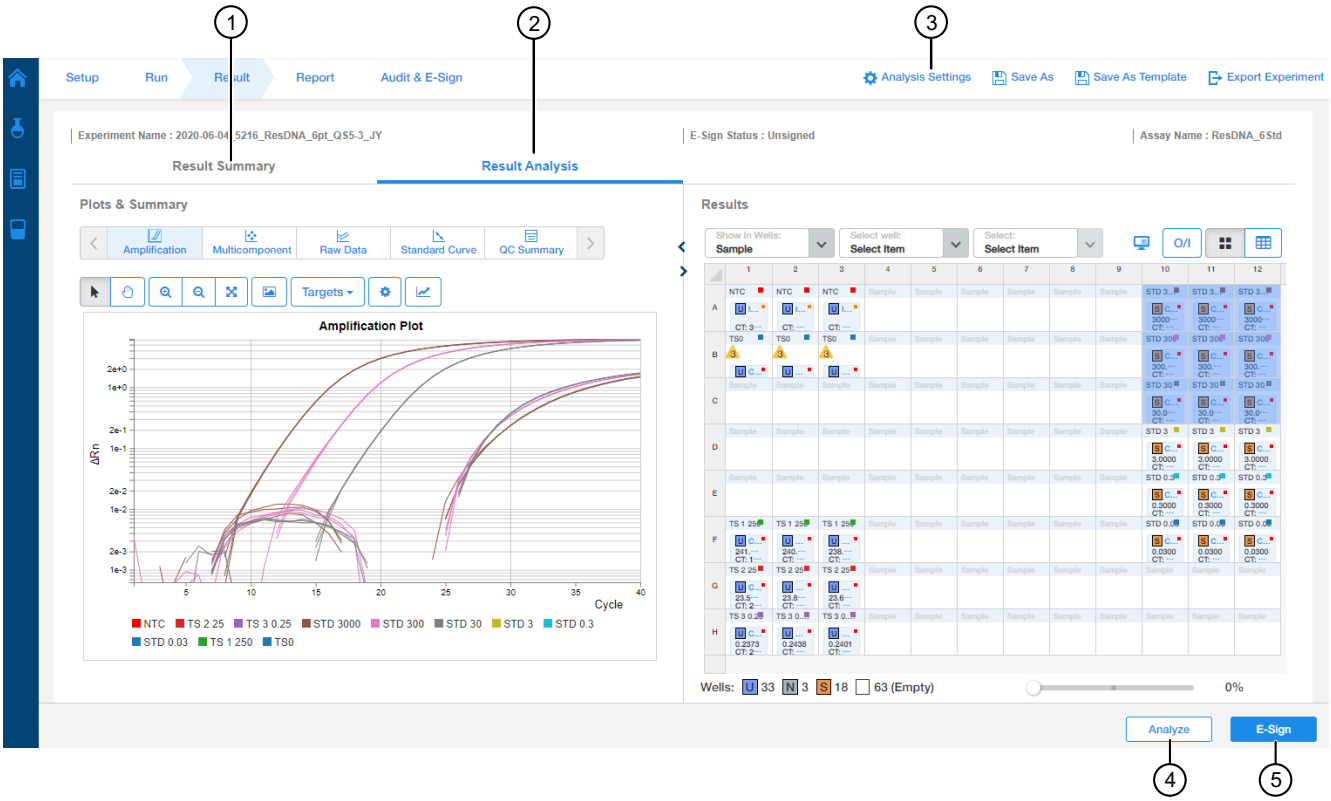


Figure 28 Result tab

① **Result Summary**—Populated for MycoSEQ™ experiments only; displays the overall **Plate Call** and the **Well Call** for individual wells. See Chapter 3, “Set up, run, and review MycoSEQ™ experiments”.

② **Result Analysis**— Displays plots and well information such as sample name and flags.

③ **Analysis Settings**— Click **Analysis Settings** to access analysis settings.

④ **Analyze** button—Click **Analyze** after omitting wells or changing the analysis settings.

⑤ **E-sign** button—Click **E-sign to** to sign the experiment. For information, see “E-sign an experiment” on page 171.

Note: The analysis settings and plots that are available vary by experiment type.

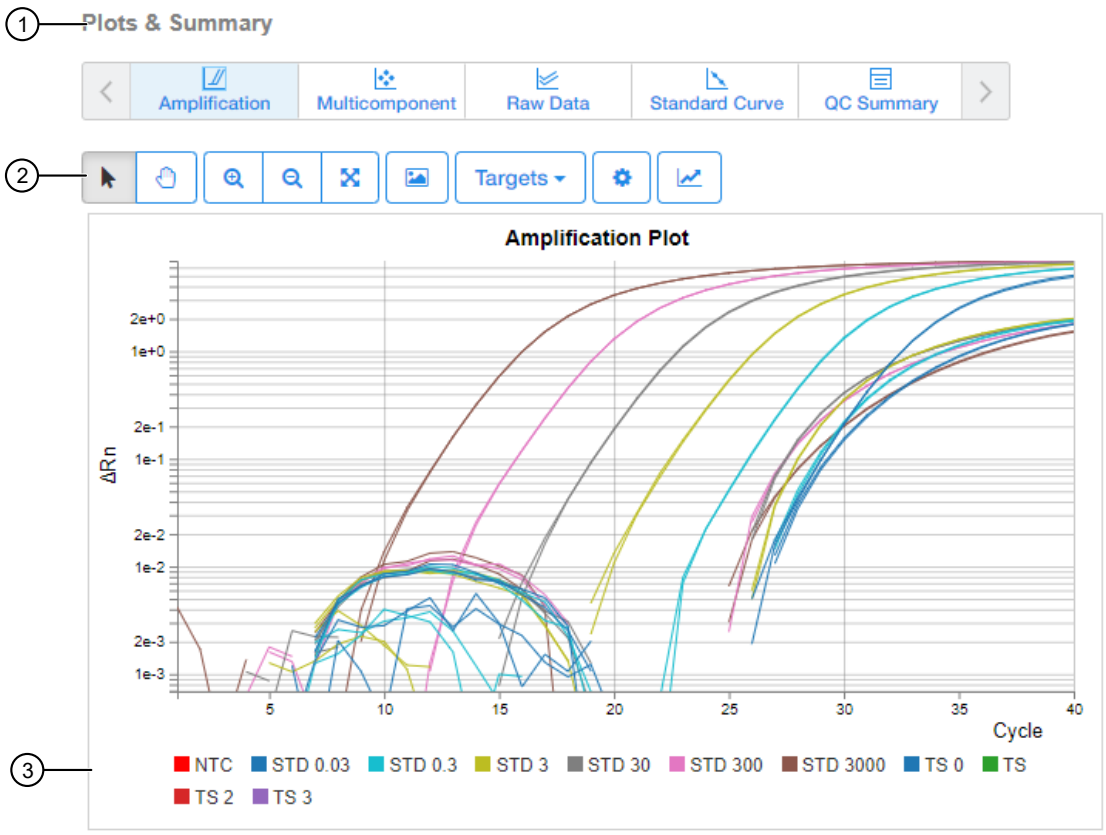


Figure 29 Plots & Summary pane

① Plot horizontal scrollbar
② Plot toolbar
③ Plot legend

The Plot toolbar includes the following options:

- Select and move
- Zoom in and out
- Return to original plot display
- Save plot as image file
- Select targets or dyes
- Configure plot properties
- Show/hide plot legend

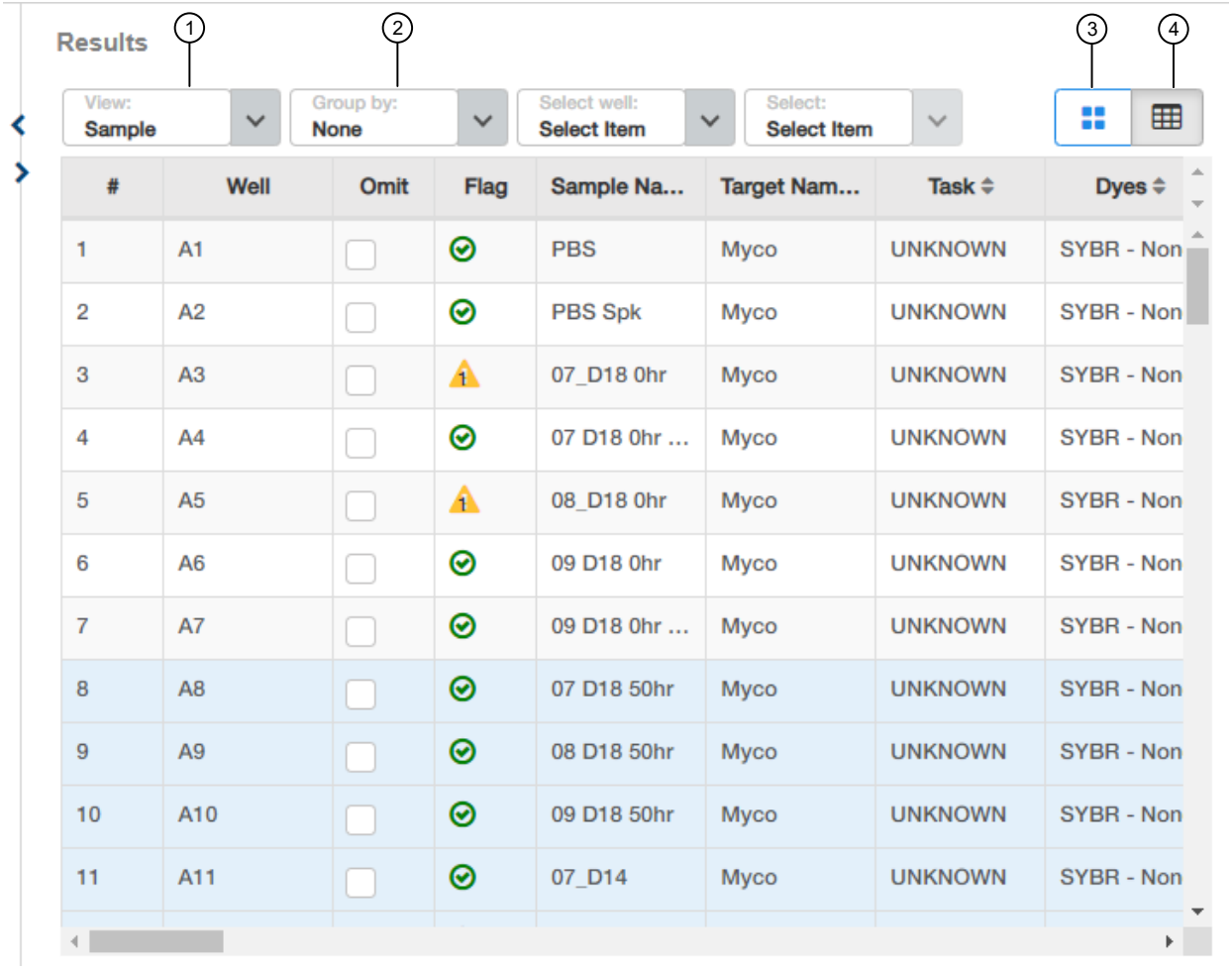


Figure 30 Results pane

① **View**—Select properties to display
② **Group by**—Select a parameter by which to group well rows
③ **Grid View**
④ **Table View** (shown)

Workflow: General procedures to review run results

When a run is complete, the AccuSEQ™ Real-Time PCR Software automatically analyzes the run data using the analysis settings that are specified in the experiment. The software then displays the run results in the **Results** tab.

Evaluate results in the Amplification Plot

▼

Assess the relevant experiment plot for the experiment
(for example, view the **Standard Curve Plot** for resDNASEQ™ experiments)

(see the corresponding chapter in this guide)

▼

Review data for outliers and *(optional)* Omit outliers from analysis

▼

(Optional) Review the dye signal profile using the Multicomponent Plot

▼

(Optional) Review the signal profile using the Raw Data Plot

▼

(Optional) Review the flags in the QC Summary

▼

(Optional) Configure analysis settings

IMPORTANT! If you omit wells or configure the analysis settings, click **Analyze** to reanalyze the data.

Evaluate results in the Amplification Plot

Amplification Plot overview

The **Amplification Plot** displays sample amplification as a function of cycle number or well. You can use the amplification plot to perform the following tasks:

- Confirm or correct baseline and threshold values.
- Identify outliers.
- Identify and examine abnormal amplification. Abnormal amplification can exhibit one of the following characteristics:
  - Increased fluorescence in negative control wells
  - Absence of detectable fluorescence at an expected cycle

Note: If you notice abnormal amplification or a complete absence of fluorescence, see the instrument user guide for troubleshooting information.

Three plots are available. Some plots can be viewed as a linear or $\log_{10}$ graph.

Table 7 Amplification Plot types

Plot type	Description	Use to
ΔRn (Also seen as dRN and Delta RN in the software)	ΔRn is the magnitude of normalized fluorescence signal, relative to the baseline fluorescence, generated by the reporter at each cycle during the PCR amplification.	• Identify and examine irregular amplification. • View threshold values for the run.
Rn	Rn is the fluorescence signal from the reporter dye normalized to the fluorescence signal from the passive reference.	• Identify and examine irregular amplification. • View baseline values for the run.
C_t	C_t is the PCR cycle number at which the fluorescence meets the threshold in the amplification plot.	• Locate outlying amplification (outliers).

Note: C_t vs Well is plotted 0–95, not 1–96.

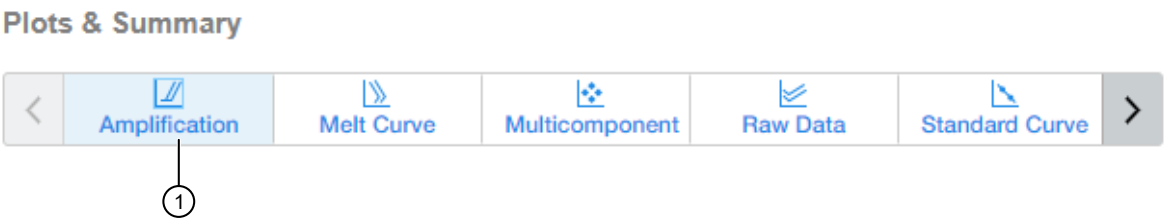
Evaluate the overall shape of the Amplification Plot curves

You can evaluate the overall shape of the **Amplification** curves in the **Result** tab.

Open the experiment in the AccuSEQ™ Software. See “Open an experiment” on page 145.

1. In the **Results Analysis** pane of the **Result** tab, select **Amplification** from the horizontal scroll bar.

Note: If no data are displayed in the **Result** tab, click **Result Analysis**, then click **Analyze**.



① Amplification Plot

The **Amplification Plot** is displayed for the selected wells in the **(Grid View)** .

2. Ensure that the **Target** is correct.

3. (*Optional*) Click **(Settings)** , then make the following selections:
   - **Plot Type**: **ΔRn, Rn, or C_T**
   - **Graph Type**: **Log or Linear**
   - **Show**: **Legend**, **Cq Mark** (the cycle at which the curvature of the amplification curve is maximal), or **Unselected**
   - **Plot Color**: **Target**, **Sample**, **Well**, or **Flag_Status**
   - **Threshold**: Select **Auto** or specify a threshold, then decide whether to **Show Threshold**.
   - **Baseline**: Decide whether to **Show Baseline**.

4. (*Optional*) Adjust the **(Plot Properties)**.
   a. In the **General** tab, add a **Plot Title**, adjust the **Font** and **Color**, then click **Apply**.

   b. In the **X Axis** or **Y Axis** tabs, you can:
      - Add a **Label**
      - Select whether you want **Tick Marks**
      - Select **Auto-adjust range** or enter minimum and maximum values

      Note: The minimum value must be greater than 0.

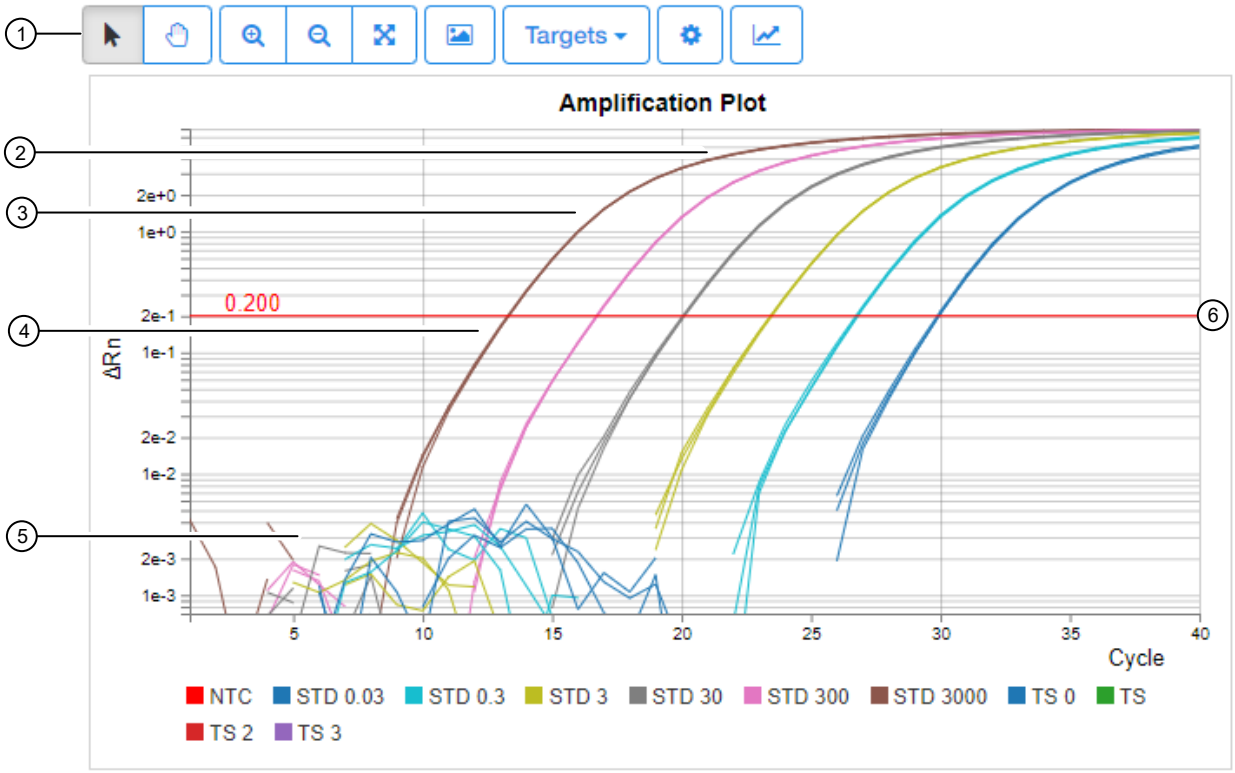


Figure 31 Typical Amplification Plot

① Amplification Plot tools
② Plateau phase
③ Linear phase
④ Exponential (geometric) phase
⑤ Baseline phase
⑥ Threshold. In a multiplex assay, only one threshold is shown per target. Select the desired target to display the threshold line. The threshold line is not displayed if **All** target is selected.

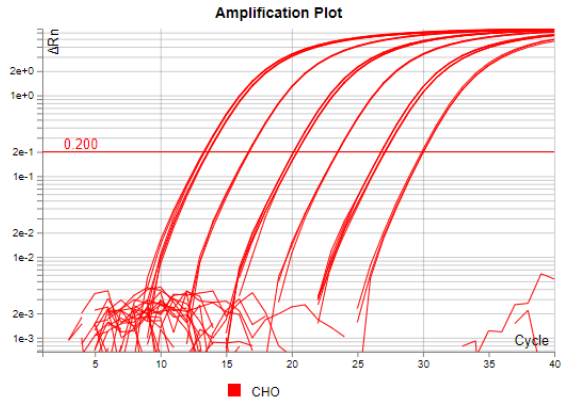
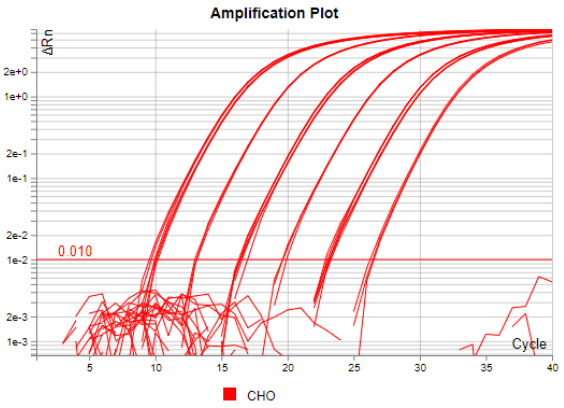
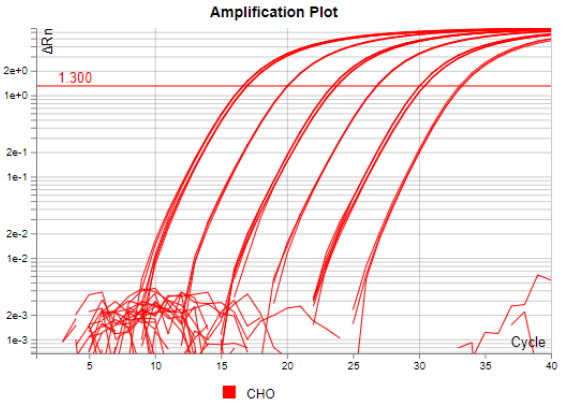
Confirm or correct threshold settings

1. In the **Result** tab, select **Amplification** from the horizontal scroll bar.
   The **Amplification Plot** is displayed for the selected wells in the **(Grid View)** .
2. Click **Targets** to configure what is displayed in the plot.
3. Click **(Settings)** , then make the following selections:
   - **Plot Type**: **ΔRn, Rn, or C_T**
   - **Graph Type**: **Log or Linear**
   - Select what to **Show**: **Legend**, **Cq Mark** (the cycle at which the curvature of the amplification curve is maximal), or **Unselected**
   - **Plot Color**: **Target**, **Sample**, **Well**, or **Flag_Status**
   - **Threshold**: Select **Auto** or specify a threshold, then select whether to **Show Threshold**.
   - **Baseline**: Select **Auto** or specify a threshold, then select whether to **Show Baseline**.

4. (*Optional*) Adjust the threshold.
   - Click-drag the threshold bar into the exponential phase of the curve.
   - Configure the C_t analysis settings (see “Ct settings overview” on page 153).

Table 8 Examples of threshold settings (custom assays only)

Set the threshold in the exponential phase of the amplification curve. A threshold set above or below the optimum can increase the standard deviation of the replicate groups.

Threshold setting evaluation	Example
Threshold set correctly.	
Threshold set too low.	
Threshold set too high.	

Omit outliers from analysis

1. In the **Result** tab, select **Amplification** from the horizontal scroll bar.
   The **Amplification Plot** is displayed for the selected wells in the **(Grid View)** .
2. Click **Targets** to configure what is displayed in the plot.
3. Click **(Settings)** , then make the following selections:
   - **Plot Type**: **ΔRn, Rn, or C_T**
   - **Graph Type**: **Log or Linear**
   - Select what to **Show**: **Legend**, **Cq Mark** (the cycle at which the curvature of the amplification curve is maximal), or **Unselected**
   - **Plot Color**: **Target**, **Sample**, **Well**, or **Flag_Status**
   - **Threshold**: Select **Auto** or specify a threshold, then select whether to **Show Threshold**.

     Note: Threshold must be set at 0.2 for all **Factory default** assays (MycoSEQ™, resDNASEQ™ (except Plasmid DNA - Kanamycin resistance), and ProteinSEQ™ assays. Auto or any other threshold settings are applicable only to custom assays and the resDNASEQ™ Quantitative Plasmid DNA - Kanamycin Resistance Gene Kit.
   - **Baseline**: Select **Auto** or specify a threshold, then select whether to **Show Baseline**.
4. Click **Table View** to look for outliers.
   a. Select **Group by ▸ Replicates**.
   b. Identify outliers in each replicate group.
      Outlier wells typically have one or more QC flags.
5. Omit outliers in the **(Table View)** by selecting **Omit** in outlier rows of the table.

   Note: Blank wells cannot be omitted.
6. Click **Analyze** to reanalyze the run data with any outliers removed.

Optimize display of negative controls in the Amplification Plot

1. In the **Result** tab, select **Amplification** in the horizontal scroll bar.
   The **Amplification Plot** is displayed for the selected wells in the **(Grid View)** .
2. Click **Targets** to configure what is displayed in the plot.
3. Click **(Settings)** , then make the following selections:
   - **Plot Type**: **ΔRn, Rn, or C_T**
   - **Graph Type**: **Log or Linear**
   - Select what to **Show**: **Legend**, **Cq Mark** (the cycle at which the curvature of the amplification curve is maximal), or **Unselected**
   - **Plot Color**: **Target**, **Sample**, **Well**, or **Flag_Status**

- **Threshold**: Select **Auto** or specify a threshold, then select whether to **Show Threshold**.
- **Baseline**: Select **Auto** or specify a threshold, then select whether to **Show Baseline**.

4. In either the **(Grid View)** or **(Table View)**, select the negative control wells (wells that should not have amplification for a particular target).

5. Adjust the display properties for individual wells. To configure the plot properties, select the well or wells of interest, then click **(Plot Properties)**.
   a. (*Optional*) In the **General** tab, add a **Plot Title**, adjust the **Font** and **Color**, then click **Apply**.
   b. In the **X Axis** or **Y Axis** tabs, you can:
      - Add a **Label**
      - Select whether you want **Tick Marks**
      - Select **Auto-adjust range** or enter minimum and maximum values

      Note: The minimum value must be greater than 0.

Evaluate results in the Table View

Table View overview

The **Table View** displays data for each well in the reaction plate. The data that are displayed depend on the specific experiment type and can include the following information:

- Sample name, target name, task, and dyes
- Values that are specific to particular stage of the method
  For example: C_t or melt temperature (T_m)
- Values that are specific to a particular experiment type
  For example: presence/absence calls, or quantities
- Omitted wells
- QC flags
- Comments

Group or sort in Table View

Possible options for grouping or sorting the **(Table View)** are described in the following table. Available grouping categories depend on the specific experiment type and analysis settings.

Note: You can select multiple columns when sorting, but you can only make one selection for grouping rows.

Group category	Description	Notes
Replicates[1,2]	Grouped by replicate	• Examine the C_t or quantity values for each replicate group to evaluate the precision of C_t values.

(continued)

Group category	Description	Notes
Flag	Grouped as flagged and unflagged wells	• A flag indicates that the software found a potential error in the flagged well.
C_t[3]	Grouped by C_t value	• C_t value < 8—there may be too much template in the reaction. • C_t value > 35—there may be a low amount of target in the reaction; for C_t values > 35, expect a higher standard deviation.

[1] For standard curve experiments.
[2] For melt curve experiments.
[3] For genotyping experiments.

Use the **Select** well dropdown list to select a specific **Sample**, **Target**, or **Task**.

Use the **Select** dropdown list to specify the **Sample**, **Target**, or **Task** to highlight in the table.

Review the dye signal profile using the Multicomponent Plot

Multicomponent Plot overview

The **Multicomponent Plot** displays the complete spectral contribution of each dye over the length of the PCR run.

Use the **Multicomponent Plot** to obtain the following information.

- Confirm that the signal from the passive reference dye remains unchanged throughout the run.
- Review reporter dye signal for spikes, dips, and/or sudden changes.
- Confirm that no amplification occurs in the negative control wells.

View and evaluate the Multicomponent Plot

You can view and evaluate the **Multicomponent Plot** in the **Result** tab.

If no data are displayed in the **Result** tab, click **Result Analysis**, then click **Analyze**.

1. In the **Result** tab, select **Multicomponent Plot** in the horizontal scroll bar.
2. Click to configure the plot, then make the following selections:
   - **Plot Color**: **Dye**, **Target**, or **Well**

   The **Multicomponent Plot** is displayed for the selected wells in the **(Grid View)**.

3. In the **(Grid View)**, select wells one at a time, then examine the **Multicomponent Plot** for the following plot characteristics.

Plot characteristic	Description
Passive reference dye	The passive reference dye fluorescence signal should remain relatively constant throughout the PCR process.
Reporter dye	The reporter dye fluorescence signal should display a flat region corresponding to the baseline, followed by a rapid rise in fluorescence as the amplification proceeds.
Irregularities in the signal	Spikes, dips, and/or sudden changes in the fluorescence signal may have an impact on the data.
Negative control wells	The negative control wells should show little or no significant increase in fluorescence signal.

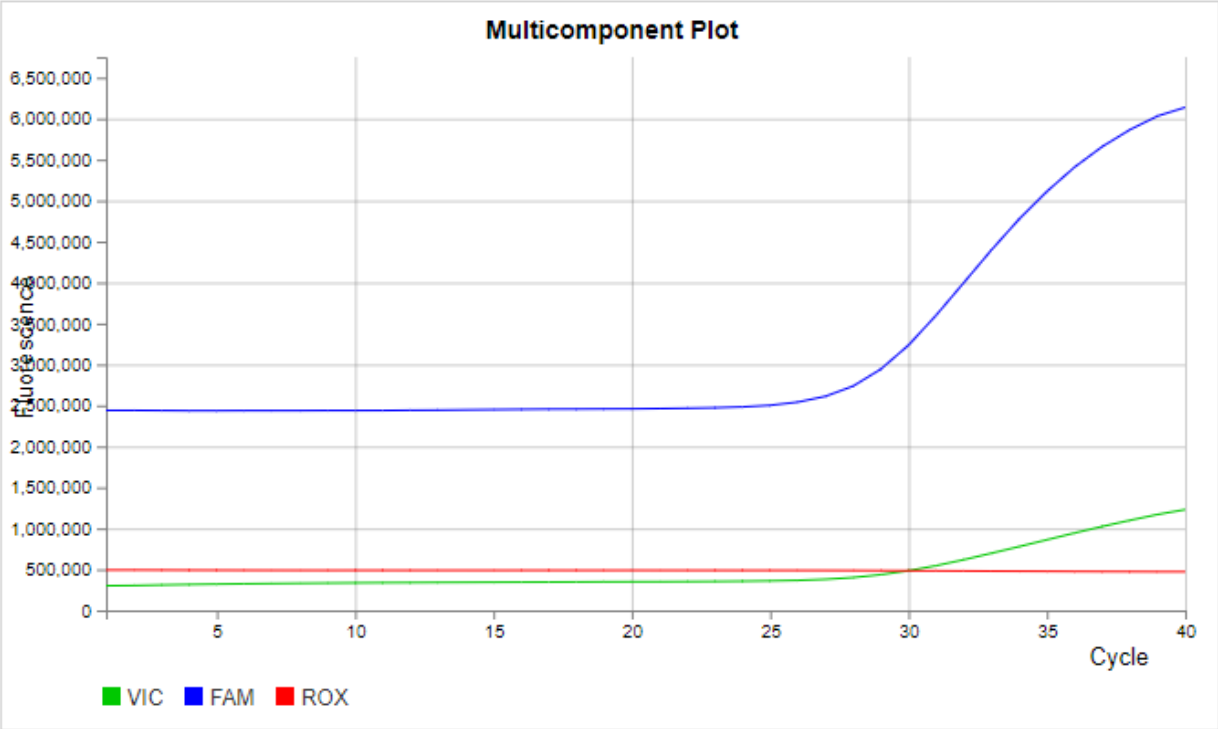


Figure 32 Example Multicomponent Plot (single well; TaqMan™ assays)

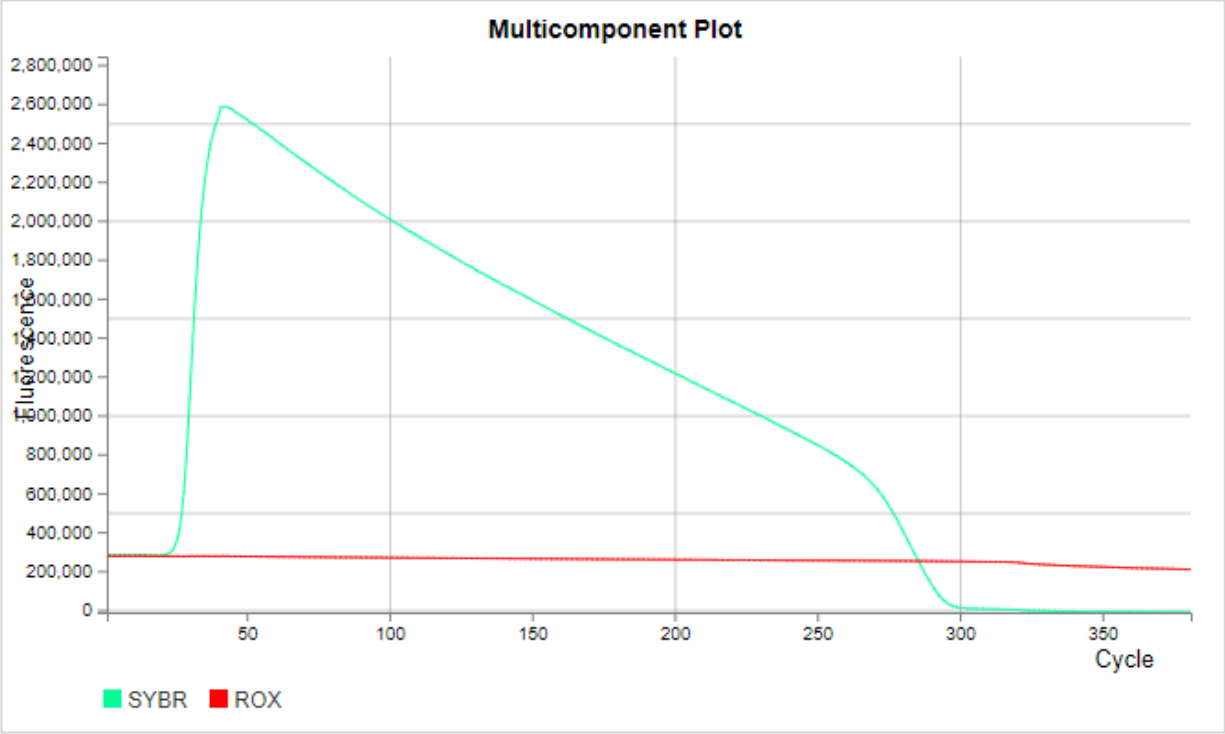


Figure 33 Example Multicomponent Plot (single well; SYBR™- MycoSEQ™ assays)

Review the signal profile using the Raw Data Plot

Raw Data Plot overview

The **Raw Data Plot** displays the raw fluorescence signal (not normalized) for each optical filter during each cycle of the real-time PCR.

View the Raw Data Plot to confirm a stable increase in signal (no abrupt changes or dips) from the appropriate filter.

View and evaluate the Raw Data Plot

You can view and evaluate the **Raw Data Plot** in the **Result** tab.

If no data are displayed in the **Result** tab, click **Analyze**.

1. In the **Result** tab, click **Result Analysis**, then select **Raw Data Plot** in the horizontal scroll bar. The **Raw Data Plot** is displayed for the selected wells in the **(Grid View)**.
2. Click to display the **Legend**.
3. Click-drag the **Show Cycle** pointer from cycle 1 to cycle 40, and confirm that each filter displays the characteristic signal increase.

   For more information on each filter set, see the instrument user guide (see Appendix D, “Documentation and support”).

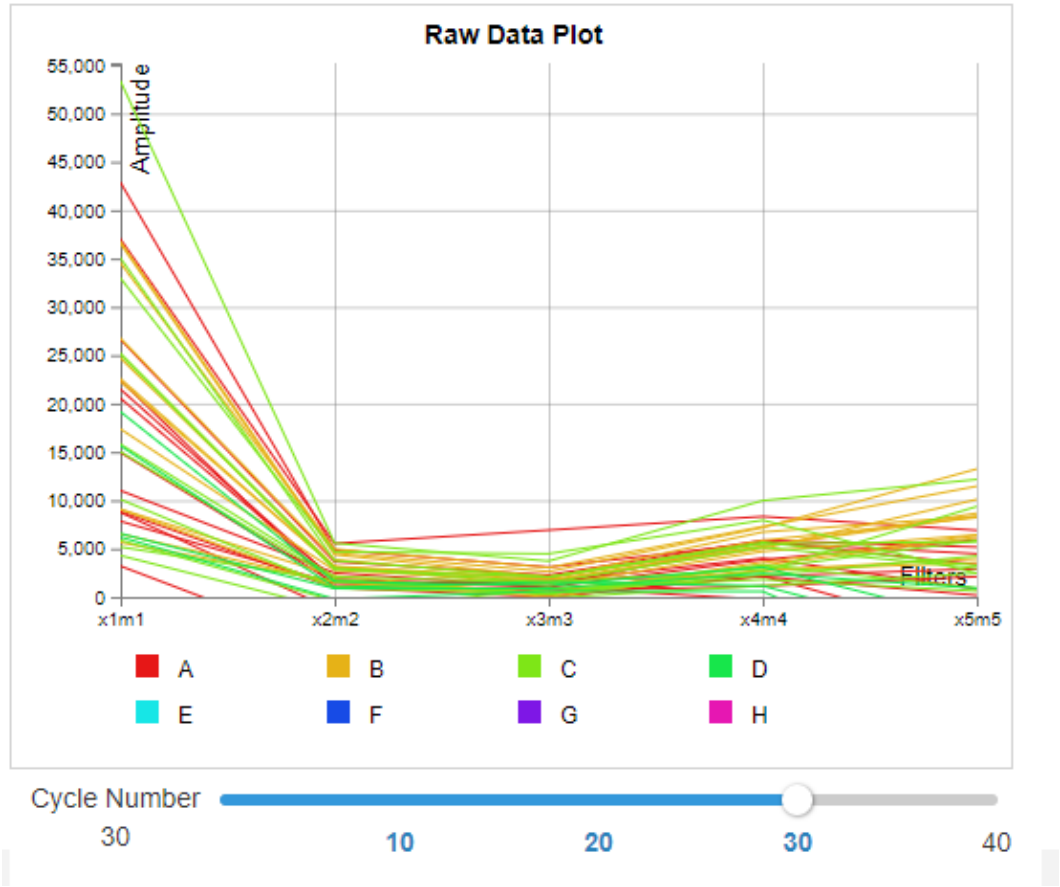


Figure 34 Example Raw Data Plot

Review the flags in the QC Summary

The **QC Summary** in the **Result** tab displays a list of the QC flags, including the flag frequency and location.

If no data are displayed in the **Result** tab, click **Analyze**.

1. In the **Result** tab, click **Result Analysis**, then select **QC Summary** in the horizontal scroll bar.
2. Review the **Flags**.
   The **Wells** column identifies wells that triggered a flag.
3. (*Optional*) Scroll through the flags to see a **Description** of the flag, its **Frequency**, and which **Wells** were flagged. Click the flag of interest for information text about the flag, including the **Flag** name, the **Flag Detail**, the **Flag Criteria**, and the **Flagged Wells**.

E-sign an experiment

1. Open an experiment (see “Open an experiment” on page 145).
2. Click the **Results** tab.
3. Click the **E-Sign** button, then enter your user name and password.

   Note: Users without **E-Signature** permissions will not be allowed to sign.

Table 9 E-signature status

If the experiment is	Icon displayed in Experiments screen[1]
Signed	**(Gray locked icon)**
Partially signed	**(Blue locked icon)**
Unsigned	**(Gray unlocked icon)**

[1] See “Experiments screen” on page 18.

If no additional e-signatures are required, the **E-Signature** status at the top of the screen and in the **Experiments** screen is set to **Signed**.

Revert an e-signature for a partially signed experiment

User accounts that have the **E-Signature** function enabled are allowed to revert the e-signature for partially signed experiments.

Experiments for which e-signature can be reverted have a **(Blue locked icon)** in the **Actions** field on the **Experiments** screen. If the **(Gray locked icon)** is displayed, the e-signature cannot be reverted. See “Experiments screen” on page 18.

1. Navigate to the **Experiments** screen from the **Home** screen.
2. Click the **(Blue locked icon)**.

View audit and e-sign reports for an experiment

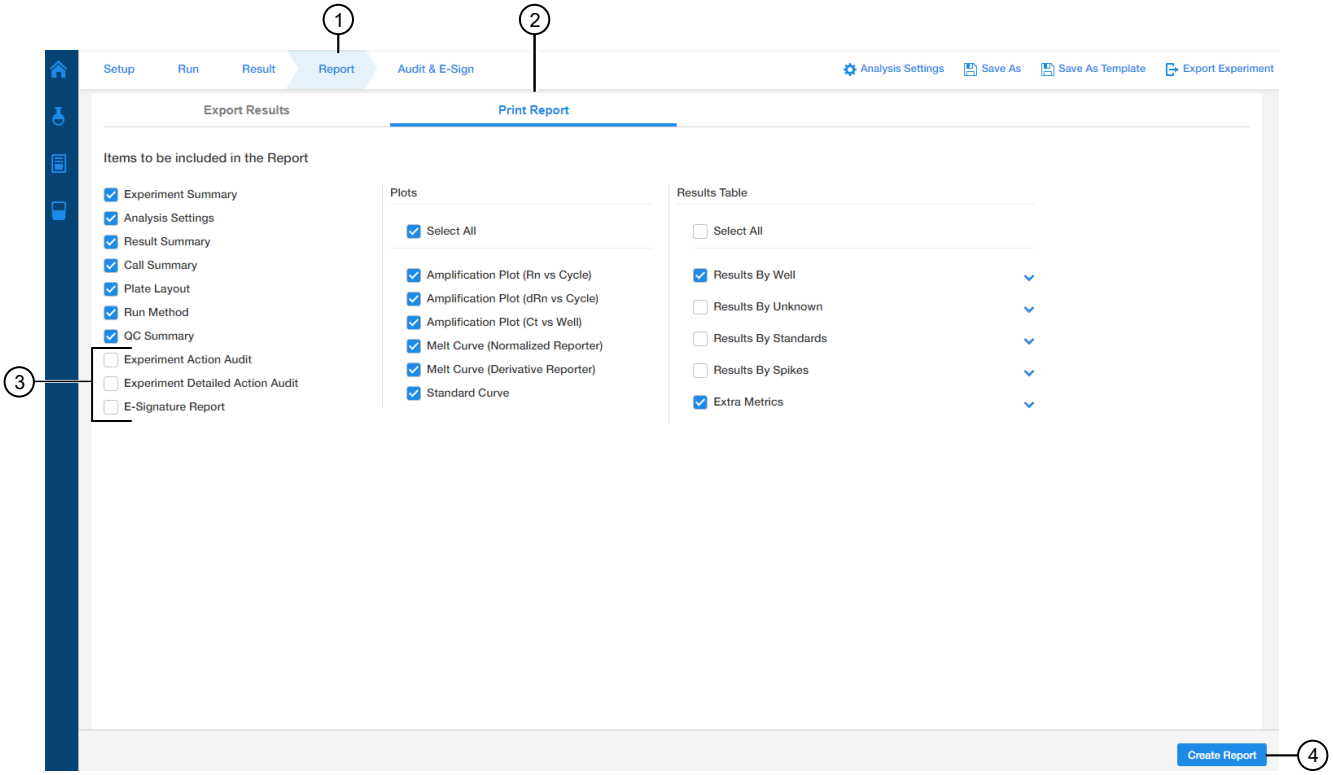
1. Open an experiment (see “Open an experiment” on page 145).
2. Click the **Audit & E-sign** tab at the top of the screen.
3. Click the **Audit Report** tab or the **E-Sign Report** tab to display the report.
4. If needed, enter a date range for the report.

Export data and print reports

Create and print a report

To create a report, an experiment must have a status of **Analysis**.

1. Open the experiment in the AccuSEQ™ Software. See “Open an experiment” on page 145.
2. Navigate to the **Report** tab, then the **Print Report** pane.



1. **Report** tab
2. **Print Report** pane
3. SAE attributes
4. **Create Report** button

3. Select the **Items to be included in the Report**.

Note: Default attributes are preselected when using factory default templates. The order of items in the report varies slightly from what is shown in the software.

IMPORTANT! To select and print SAE attributes, the user must have permission to print.

4. Click **Create Report**, then **View PDF**.

Note: **Run started** and **Run completed** times vary slightly from times listed in **Instrument Status** due to the time delay between the instrument and AccuSEQ™ Software.

The PDF report name differs slightly from the experiment name. Rename the file as required by your laboratory.

5. (*Optional*) Click **Previous** to go back and make different selections for the report.

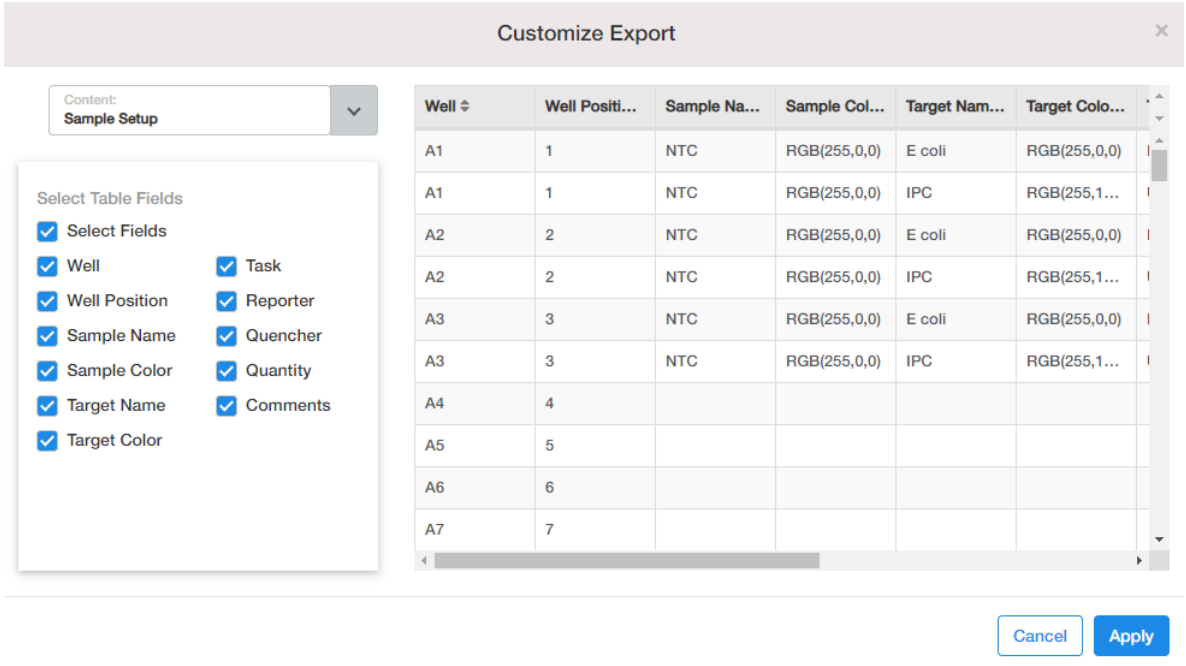
Export results

To export results, an experiment must have a status of **Analysis**.

1. Open the experiment in the AccuSEQ™ Software. See “Open an experiment” on page 145.
2. Navigate to the **Report** tab, then the **Export Results** pane.
3. Enter a **File Name**, then select the File Type (XLS, XLSX, TXT, or CSV).

Note: TXT and CSV files can be exported as combined or separate files.

4. Select the **Content** to export, then click **Export**.
5. (*Optional*) Click **Customize Export** to select additional columns to include in the report.
   a. Select the **Content** to be customized, then **Select Table Fields** to be customized.
   b. Click **Save**.



6. Click **Export**.

Note: The Results are exported to the appropriate location for the file type that is selected.

Flags

QC flags overview

The following flags may be triggered by the run data.

Flag	Description
Pre-processing flags	
BADROX	Bad passive reference signal
OFFSCALE	Fluorescence is off-scale.
NOISE	Noise higher than others in plate
NOSIGNAL	No signal in well
NOAMP	No amplification (not editable)
PRFDROP	Fluorescence signal from the passive reference changes significantly within defined range around the calculated C_q (C_T or C_{RT}) for a given well.
PRFLOW	For the replicate group of a given well, the average passive reference signal is below the percentage of the reference value defined in the analysis settings.
SPIKE	Noise spikes
Primary analysis flags	
BLFAIL	Automatic Baseline Algorithm failed to identify a baseline region for the amplification curve.
CQCONF	Calculated confidence for the C_q (C_T or C_{RT}) value is less than the defined minimum value.
CRTAMPLITUDE	PCR amplification curve amplitude is significantly lower than the other curves generated for the related target.
CRTNOISE	PCR amplification curve exhibits a significant amount of unexplained variability in comparison to the other curves generated for the related target.
CTFAIL	Baseline Threshold Algorithm failed to identify a C_t for the amplification curve.
DRNMIN	Normalized fluorescence (ΔRn) drops below the defined threshold.
EXPFAIL	Baseline Threshold Algorithm failed to identify an exponential region for the amplification curve.
THOLDFAIL	Automatic Threshold Algorithm failed to identify a threshold for the target.
Secondary analysis flags	
MTP	Melt curve analysis shows more than one peak.
AMPNC	Amplification in negative control
HIGHSD	High standard deviation in replicate group

(continued)

Flag	Description
OUTLIERRG	Outlier in replicate group
ZEROPR	Passive reference is zero in at least one cycle

AMPNC flag

AMPNC—Amplification in negative control.

This flag indicates that a sequence in a negative control reaction amplified.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. Ensure that the well corresponds to a negative control well (task = negative control or NTC).
3. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)], and confirm the fluorescence signal increased for the flagged negative control well.
4. If the fluorescence signal did not increase, consider omitting the well from analysis.

Possible Cause	Recommended Action
Contamination in one or more PCR reaction components	• Replace all PCR reaction components with new components, then repeat the experiment. Add water or buffer instead of sample to the well. • Decontaminate the work area and pipettors.
Unstable reaction mix	• Use a hot-start enzyme. • If you are not using a hot-start enzyme, run the reactions as soon as possible after preparation.
Poor primer and/or probe design	• Redesign the primers and/or probe.

BADROX flag

BADROX—Bad passive reference signal.

This flag indicates that the passive reference (usually ROX™ dye) signal is abnormal. The passive reference signal may not be acceptable for normalization of the reporter dye signal.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the multicomponent plot, and review the passive reference signal for abnormalities.
3. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)], and review the data in the C_q region for abnormalities.
4. Examine the reaction plate, and check for condensation and/or inconsistent reaction volumes.

Possible Cause	Recommended Action
Droplets on the sides of the wells	Repeat the experiment. Make sure to centrifuge the plate briefly before loading it into the instrument.
Evaporation resulting from improper sealing or seal leaks	Repeat the reactions. Make sure to seal the plate properly.
Condensation on the reaction plate	
Inconsistent volumes across the plate	Ensure that pipettors are calibrated and functioning properly.
Incorrect concentration of reference dye	Ensure that the master mix is appropriate for the instrument.
Pipetting errors	Calibrate the pipettors, then repeat the experiment.

BLFAIL flag

BLFAIL—Baseline Threshold Algorithm failed to identify a baseline region for the amplification curve.

Note: The BLFAIL flag is only applicable when the Baseline Threshold Algorithm is used to analyze an experiment, though the flag column is always shown in the QC Summary.

This flag indicates that the Automatic Baseline Algorithm failed to identify a baseline region for the amplification curve, and the software cannot calculate the best-fit baseline for the data.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification plot [Rn vs. Cycle (Linear)], and note any late amplification or no amplification.
3. If the amplification is acceptable, set the baseline manually for the well in the analysis settings.
4. Reanalyze the data.
5. Evaluate the results and, if needed, make any additional changes to the baseline.

CQCONF flag

CQCONF—Calculated confidence in the C_q value is low.

This flag indicates that the calculated confidence for the C_q (C_t or C_{rt}) value of the well is less than the minimum value defined in the analysis settings.

Use the CQCONF flag to identify and (*optional*) to omit potentially poor results without manually inspecting every amplification curve. The minimum limit is set during the configuration of the flag settings.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)] and check the shape of the curve.
3. If the curve is not typical, consider omitting the flagged wells from analysis.

CRTAMPLITUDE flag

CRTAMPLITUDE—Low relative amplitude.

Note: This flag is only applicable when the Relative Threshold Algorithm is used to analyze an experiment. The flag does not appear when the Baseline Threshold Algorithm is used.

This flag indicates that the amplitude of the amplification curve (generated from the data set that includes the given well) is significantly lower than the other curves (generated for the related target).

CRTNOISE flag

CRTNOISE—High relative noise.

Note: This flag is only applicable when the Relative Threshold Algorithm is used to analyze an experiment. The flag does not appear when the Baseline Threshold Algorithm is used.

This flag indicates that the amplification curve (generated from the data set that includes the given well) exhibited a significant amount of unexplained variability in comparison to the other curves (generated for the related target).

CTFAIL flag

CTFAIL—Baseline Threshold Algorithm failed to identify a C_t for the amplification curve.

Note: The CTFAIL flag is only applicable when the Baseline Threshold Algorithm is used to analyze an experiment, though the flag column is always shown in the QC Summary.

This flag indicates that the Baseline Threshold Algorithm failed to identify a C_t value for the given well, and the software cannot calculate the threshold cycle (C_t).

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)] and note:
   - Amplification too early
   - Amplification too late
   - Low amplification
   - No amplification
3. If the amplification is acceptable, set the threshold and baseline manually.
4. Reanalyze the data.
5. Evaluate the results. If the adjustments do not produce a valid C_t, consider omitting the well from analysis.

DRNMIN flag

DRNMIN—Detection of minimum ΔRn due to abnormal baseline.

This flag indicates that the normalized fluorescence (ΔRn) for a given well dropped below the threshold defined in the analysis settings.

Use the DRNMIN flag to easily identify and *(optional)* to omit potentially poor results without manually inspecting every amplification curve. The ΔRn threshold value is set during the configuration of the flag settings.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification and multicomponent plots [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)], and review the shape of the curve.
3. If the curve is atypical, consider omitting the flagged wells from analysis.

EXPFAIL flag

EXPFAIL—Baseline Threshold Algorithm failed to identify an exponential region for the amplification curve.

Note: The EXPFAIL flag is applicable if the Baseline Threshold Algorithm is used to analyze an experiment, though the flag column is always shown in the QC Summary.

- It is a common flag for samples that do not amplify (C_t of 'Undetermined').
- The flag is not triggered for wells assigned the NTC task since they are not expected to have an identifiable exponential region.
  NTCs that do amplify will trigger the AMPNC flag to identify unexpected behavior.

Note: This flag indicates that the Baseline Threshold Algorithm failed to identify an exponential region of the amplification plot for the given well. The software set the baseline region to be the full length of the curve.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification plot [Rn vs. Cycle (Linear)], and note:
   - Amplification too early
   - Amplification too late
   - Low amplification
   - No amplification
3. If the amplification is acceptable, set the baseline manually for the well in the analysis settings.

4. Reanalyze the data.

5. Evaluate the results and, if needed, make any additional changes to the baseline in the analysis settings.

HIGHSD flag

HIGHSD—High standard deviation in replicate group.

This flag indicates that the C_q standard deviation for the replicate group exceeds the current flag setting (all replicates in the group are flagged).

If a replicate group is flagged, confirm the results:

1. Select the flagged replicate group in the plate layout or well table.

2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)].
   a. Evaluate whether the signal varies significantly from others in the replicate group.

   b. If the signal varies significantly, consider omitting the outlier wells or omitting the entire replicate group from analysis.

3. If the amplification is acceptable, set the threshold manually.

   Note: Set the threshold manually only for experiments analyzed with the Baseline Threshold Algorithm.

4. Reanalyze the data.

5. Evaluate the results, and, if needed, make any additional changes to the threshold.

Possible Cause	Recommended Action
Droplets on the sides of the wells	Repeat the experiment. Make sure to centrifuge the plate briefly before loading it into the instrument.
Improper sealing or seal leaks	Repeat the reactions. Make sure to seal the plate properly.
Condensation on the reaction plate	
Inconsistent volumes across the plate	
Pipetting errors	Calibrate your pipettors, then repeat the experiment.
Missing reaction component	Repeat the experiment. Make sure to include all reaction components. Do not pipet less than 5 µL of sample when setting up the PCR.
Incorrect reaction setup	Follow the manufacturer's instructions for setting up the reactions.

(continued)

Possible Cause	Recommended Action
Poor DNA template	Repeat the experiment with higher quality DNA template.
Inadequate mixing	Mix the reaction thoroughly by pipetting or using a vortex mixer (medium setting).

MTP flag

MTP—Melt curve analysis shows more than one peak.

Note: The MTP flag is present only in experiments with PCR methods that include a melting curve stage (a temperature ramp configured for data collection).

This flag indicates that the melt curve that is generated from the collected data exhibits multiple peaks. The multiple peaks indicate a possible PCR irregularities such as contamination or nonspecific amplification.

If a replicate group is flagged, confirm the results:

1. View the melt curve plot.
2. Note any peaks in the melt curve which can indicate the melting temperature (T_m) of a target nucleic acid or nonspecific PCR amplification.

NOAMP flag

NOAMP—No amplification.

This flag indicates that the sample did not amplify.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. Ensure that the well does not correspond to a negative-control well.
3. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)], and ensure that the fluorescence signal did not increase in the well.
4. View the multicomponent plot, and note any fluorescence signal higher than the background.

Possible Cause	Recommended Action
Missing template.	• Repeat the experiment. Make sure to include all reaction components.
Target is not expressed in the sample.	• If this occurs in just one sample, it may be correct. • If this occurs in all samples of a particular tissue, search the literature for evidence that the target is expressed in the tissue or sample type of interest.

NOISE flag

NOISE—Noise is higher than other wells in plate.

This flag indicates that the well produced more noise in the amplification plot than the other wells on the same plate.

If a well is flagged, confirm the results:

1. Select the flagged wells and some unflagged unknown wells in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear)] and note any noisy amplification curves in the flagged wells.
3. In the multicomponent plot:
   a. From the dropdown list, select the dye option to color the data according to the dye.
   b. Note any drop in the ROX™ signal relative to the reporter dye, and compare flagged wells with unflagged wells.
   c. If there is a drop in the ROX™ signal relative to the reporter dye, consider omitting the flagged wells from analysis.

NOSIGNAL flag

NOSIGNAL —No signal in well.

This flag indicates that the well produced very low or no fluorescence signal.

If a well is flagged, confirm the results:

1. Select the flagged wells and some unflagged wells in the plate layout or well table.
2. View the multicomponent plot and compare the flagged wells to the unflagged wells:

Observation	Evaluation
The fluorescence signals for all dyes are low and similar to the background signal of the instrument.	The well is empty.
The fluorescence signals are higher than the background signal of the instrument and constant throughout the instrument run.	No amplification occurred.

3. If the flagged well produced no fluorescence signal, consider omitting the well from analysis.
4. On the reaction plate that was run, note the location for each flagged well, and examine each corresponding well in the reaction plate for low reaction volume.

OFFSCALE flag

OFFSCALE —Fluorescence signal is offscale.

This flag indicates that for one or more cycles, the fluorescence signal for one or more dyes in the well exceeds the maximum detectable range of the instrument.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)] or the well table, and note the threshold cycle.
3. View the multicomponent plot:
   a. Review the data for a plateau over one or more cycles.
      A plateau indicates saturation of the instrument detectors.
   b. If the signal plateaus before the threshold cycle, consider omitting the wells from analysis.

Possible Cause	Recommended Action
Too much TaqMan™ probe or SYBR™ Green dye added to the reaction.	Reduce the concentration of reagent added to the reaction.
Fluorescent contaminant on the reaction plate, sample block, or adhesive cover	Perform a background calibration. If fluorescent contamination is detected, clean the block.
Fluorescent contaminant in the reaction	Replace the reagents.

OUTLIERRG flag

OUTLIERRG —Outlier detected in the replicate group.

This flag indicates that the C_q for the well deviates significantly from values in the associated replicate group (only the outlier is flagged).

Outlier removal is based on a modified Grubb's test. For a well to be considered an outlier, it must be identified as an outlier by Grubb's test and its C_q value must be a minimum of 0.25 cycles from the mean.

If a well is flagged, confirm the results:

1. Select the flagged wells and the associated replicate group in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)].
   a. Compare the data from the flagged well to the data from the unflagged replicates.

b. If the C_q or the amplification curve for the flagged well vary significantly, consider omitting the flagged well from analysis.

Possible Cause	Recommended Action
Pipetting errors	Repeat the reactions. Follow these guidelines to reduce pipetting errors: • Prepare enough master reaction mix for the entire replicate group, then transfer aliquots to all appropriate wells in the reaction plate. • Calibrate and service the pipettors regularly. • Pipette larger volumes. • Reduce the number of pipetting steps.
Contamination in that well	• Replace all reagents, then repeat the experiment. • Decontaminate the work area and pipettors.
Improper sealing or seal leaks	Repeat the reactions. Make sure to seal the reaction plate properly.

PRFDROP flag

PRFDROP—Passive reference signal changes significantly near the C_q (C_t or C_{rt}).

This flag indicates that the fluorescence signal from the passive reference changes significantly near the calculated C_q (C_t or C_{rt}) for a given well.

The flag is triggered when the covariance of the passive reference signal near the calculated C_q (C_t or C_{rt}) is above the detection threshold that is set in the flag settings. The algorithm includes up to 5 cycles on either side of the calculated C_q (C_t or C_{rt}) in the passive reference covariance calculation.

Use the PRFDROP flag to identify and optionally to omit potentially poor results without manually inspecting every amplification curve.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)], then review the shape of the curve.
3. If the curve is not typical, consider omitting the flagged wells from analysis.

PRFLOW flag

PRFLOW —Average passive reference signal is below the threshold.

This flag indicates that for the replicate group of a given well, the average passive reference signal is below the percentage of the reference value defined in the analysis settings. The reference value for the PRFLOW flag is computed as a representational example from the set of curves.

Use the PRFLOW flag to easily identify and *(optional)* to omit potentially poor results without manually inspecting every amplification curve. The percentage of the reference value is set during the configuration of the flag settings.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification and multicomponent plots [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)], and review the shape of the curve.
3. If the curve is atypical, consider omitting the flagged wells from analysis.

SPIKE flag

SPIKE—Noise spikes.

This flag indicates that the amplification curve for the given well contains one or more data points inconsistent with the other points in the curve.

If a well is flagged, confirm the results:

1. Select the flagged wells in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)] and evaluate whether the noise spike adversely affects the baseline or C_q.
3. If the baseline is adversely affected, set the baseline and threshold values manually.
4. Reanalyze the data.
5. Evaluate the results.
6. If the changes do not produce a valid C_q, consider omitting the well from analysis.

Possible Cause	Recommended Action
Bubbles in the reaction	Repeat the reactions. Make sure to centrifuge the plate at <1500 rpm for 2 minutes and confirm that the liquid in each well of the plate is at the bottom of the well.
Overall low signal for all dyes in the reaction	Repeat the reactions, pipetting a larger volume into all wells.
ROX™ dye not used as passive reference	Repeat the reactions, using ROX™ dye as the passive reference.
Evaporation due to improper sealing or seal leaks	Repeat the reactions. Make sure to seal the reaction plate properly.
No passive reference included in the experiment	In the analysis settings, reset the default SPIKE threshold value or deselect the use of the SPIKE flag.

THOLDFAIL flag

THOLDFAIL—Automatic Threshold Algorithm failed to identify a threshold for the target.

Note: The THOLDFAIL flag is only applicable when the Threshold Algorithm is used to analyze an experiment. The flag column is always shown in the QC Summary.

This flag indicates that the Automatic Threshold Algorithm failed to identify a threshold for the target. The software cannot calculate the threshold for the given set of wells associated with the target.

If a well is flagged, confirm the results:

1. Select the flagged wells associated with a particular target in the plate layout or well table.
2. View the amplification plot [ΔRn vs. Cycle (Linear) or ΔRn vs. Cycle (Log)], and note:
   - Amplification too early
   - Amplification too late
   - Low amplification
   - No amplification for all wells with this target
3. If the amplifications are acceptable, set the baselines and thresholds manually.
4. Reanalyze the data.
5. Evaluate the results and, if needed, make any additional changes to the threshold or baseline.

A Troubleshooting

Observation	Possible cause	Recommended action
Loss of internet connection during a run	Server malfunction.	Restart the server to reestablish a network connection. **Note:** After a connection is reestablished, the experiment is downloaded automatically by the AccuSEQ™ Software.
Unexpected software shutdown	Power failure or accidental close out.	Restart the software and sign in again.
No connection to instrument	Change in system IP address.	Go to **Application Installation Directory ▸ Applied Biosystems ▸ AccuSEQ ▸ bin ▸ application.properties**. Enter the IP address displayed on the instrument.
Only raw fluorescence readings collected (custom melt curve experiments only)	Optical filter for ROX™ dye is not selected.	Select the optical filter 4 when creating custom melt curve experiments. See "Select optical filters" on page 149.
Inability to **Analyze** data	The user does not have the correct permissions.	Ensure that the user has the ability to **Omit Wells** and **Edit Analysis Settings**. See the *AccuSEQ Quantstudio5 Security, Audit, and E-signature (SAE) Administrator Console v1.0 User Guide* (Pub. No. 100084439).
No values are reported for Amplification Status	An error occurred in the experiment workflow.	Review, then repeat the assay.
No T_m is called in Melt Curve analysis	Two or more wells were selected. T_m is only called for individual wells.	Select one well at a time.
Standard Curve Properties are not visible **Details:** (R^2, Slope, Y-Intercept, Std Error, or 4PL/5PL coefficients)	**Show legends** option has not been selected.	Select **Show legends**.
Print Preview is not working	Web browser adblocker features are preventing report generation.	Disable adblocker features.

B

Decimal places

Decimal place rules in the AccuSEQ™ Software

Decimal places are consistently displayed in the software according to the following rules.

Decimal place displays are not customizable.

Table 10 Decimal place rules

Metric	# of places after the decimal point
C_T	4
C_T Mean	4
C_T SD	4
C_T CV%	2
Quantity	4
Quantity Mean	4
Quantity SD	4
Quantity CV%	2
Dilution Adjusted	4
Reference	4
Reference Adjusted	4
Spike Input	4
% Recovery	2
Back Calculated Value	4
Back Calculated Mean	4
Back Calculated SD	4
Back Calculated %CV	2
Back Calculated % Difference	2
Back Calculated % Difference Mean	4
R2	4

Table 10 Decimal place rules *(continued)*

Metric	# of places after the decimal point
Y-Intercept	4
Slope	4
Efficiency	2
Std Error	4
T_M	2
DV	2
Rn	4
ΔRn	6
Dye Florescence (Melt Curve)	1
Dye Florescence (for assigned dyes under multicomponent data)	1
4PL/5PL coefficients	3
Total DNA per mL	4
Total DNA per Protein Concentration	4
ΔC_T	4

Table 11 Input field restrictions (sample definitions)

Metric	# of places after the decimal point
Sample volume	1
Spike volume	1
Spike standard concentration	2
Quantity	4[1]
Dilution factor	2
Threshold value	3[1]
Protein concentration	4

[1] Input and output fields.

For all input field values, the software rounds output to 4 decimal places and restricts input values to 4 decimal places.

Threshold values

3 decimal places are displayed in the results table, while exporting results, and in reports. Analysis settings show the calculated number of decimal places.

Note: There are no limitations on the number of places before the decimal point.

Auto threshold

The software shows the full calculated value in the following areas:

- The threshold under the **Analysis Settings** window.
- The threshold under **Plot Settings**.
- The threshold line displayed on the **Amplification** plot.

Note: If threshold is changed from Auto to Manual, values are rounded to 3 decimal places.

Manual threshold

The software restricts input to 3 decimal places and displays 3 decimal places in the following areas.

- The threshold under the **Analysis Settings** window.
- The threshold under **Plot Settings**.
- The threshold line displayed on the **Amplification** plot.

Note: If a value with <3 decimal places is entered, the software updates to 3 decimal places. For example, 0.2 becomes 0.200.

C Parts and materials

Kits, consumables, accessories, and reagents

Unless otherwise indicated, all materials are available through **thermofisher.com**.

Store all calibration and RNase P plates at –20°C. All other items can be stored at 15–30°C. Use all materials by the expiration date on the packaging.

Consumables (96-well, 0.1-mL format)

Consumable	Amount	Cat. No.
MicroAmp™ Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL	20 plates	4346906
	200 plates	4366932

Instrument verification or calibration plate	Cat. No.
TaqMan™ RNase P Instrument Verification Plate, Fast 96-Well	4351979
Region of Interest (ROI) and Background Plates, Fast 96-Well 0.1-mL (2 plates) **Note:** For ROI/Uniformity calibrations.	4432426
QuantStudio™ 3/5 Spectral Calibration Plate 1, (FAM™, VIC™, ROX™, and SYBR™ dyes), 96-well, 0.1 mL	A26336
QuantStudio™ 3/5 Spectral Calibration Plate 3 (TAMRA™, NED™ and Cy™5 dyes) 96-well (0.1-mL) plate	A26340

Accessories

Item	Amount	Cat. No.
MicroAmp™ 96-Well Base	10 pieces	N8010531
MicroAmp™ Optical Adhesive Film	25 films	4360954
	100 films	4311971
MicroAmp™ Adhesive Film Applicator	5 applicators	4333183

Documentation and support

Related documents

The following related documents are available:

Document	Publication Number
QuantStudio™ 3 and 5 Real-Time PCR Systems Installation, Use, and Maintenance Guide	MAN0010407
QuantStudio™ 3 and 5 Real-Time PCR Systems Site Preparation Guide	MAN0010405
AccuSEQ™ Real-Time PCR Software v3.1 Quick Reference	100094288
Security, Audit, and E-Signature (SAE) Administrator Console v1.0.1 User Guide	MAN0018760

Assay Document	Publication Number
MycoSEQ™ Mycoplasma Real-Time PCR Detection Kit User Guide	4482248
ProteinSEQ™ CHO Host Cell Protein Quantification Kit User Guide	MAN0010806
resDNASEQ™ Quantitative DNA Kits User Guide	4469836
resDNASEQ™ Quantitative E1A DNA Fragment Length Kit	MAN0025643
ViralSEQ™ Real-Time PCR Kits User Guide	4445235
ViralSEQ™ Lentivirus Titer Kits User Guide	MAN0026126

Note: For additional documentation, see “Customer and technical support” on page 192.

Customer and technical support

Visit **thermofisher.com/support** for the latest service and support information.

- Worldwide contact telephone numbers
- Product support information
  - Product FAQs
  - Software, patches, and updates
  - Training for many applications and instruments
- Order and web support

- Product documentation
  - User guides, manuals, and protocols
  - Certificates of Analysis
  - Safety Data Sheets (SDSs; also known as MSDSs)

  Note: For SDSs for reagents and chemicals from other manufacturers, contact the manufacturer.

Limited product warranty

Life Technologies Corporation and/or its affiliate(s) warrant their products as set forth in the Life Technologies' General Terms and Conditions of Sale at **www.thermofisher.com/us/en/home/global/terms-and-conditions.html**. If you have any questions, please contact Life Technologies at **www.thermofisher.com/support**.

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