Vericheck QX700™ ddPCR™ Replication Competent Lentivirus Kit

User Guide

Catalog #	Description
12025890	**Vericheck QX700 ddPCR Replication Competent Lentivirus Kit,** 96 reactions, includes assay, supermix, positive control, negative control, and internal control

Product Description

Replication competent viruses (RCVs) are virus particles that can infect cells and replicate to produce additional infectious viral particles. These may be generated after the introduction of a lentiviral vector into the target cells by homologous or nonhomologous recombination. Samples are collected during different stages of the viral production workflow to test for replication competence.

The Vericheck QX700 ddPCR Replication Competent Lentivirus (RCL) Kit can be used to confirm the presence or absence of replication competent lentivirus during the production of cell and gene therapy drug products. The kit accomplishes this by detecting residual vesicular stomatitis virus G glycoprotein (*VSV-G*) gene contamination.

Kit Contents

See Table 1 for kit contents. The kit contains reagents for 96 reactions. Store kit components at -20°C.

Table 1. Kit contents.

Product	Product Cap Color	Tubes/Kit	Volume/Tube, µL
QX700 ddPCR RDQ Supermix (5x)	Gray	2	100
QX700 ddPCR RCL Assay (20x)	Green	1	60
ddPCR Internal Control	Pink	1	900
ddPCR RCL Positive Control	Clear	1	80
Nuclease-free water	Clear	1	1,500

Required Equipment, Reagents, and Consumables

See Table 2 for required materials that are not included in the kit.

Table 2. Additional required materials.

Droplet Digital™ PCR (ddPCR) System	Consumables and Reagents
• QX700 E Droplet Digital PCR System* (Bio-Rad Laboratories, Inc., #17011036), or • QX700 S Droplet Digital PCR System* (Bio-Rad, #17010638), or • QX700 HT Droplet Digital PCR System* (Bio-Rad, #17010628)	• RDG16 Cartridges (Bio-Rad, #12025252) • RDG16 Cartridge Holder (Bio-Rad, #12025262) • Staticide SW12 Anti-Static Wipes (ACL, Inc.) • Kimtech Science Precision Wipes (Kimberly Clark, #05511)

Optional: The Vericheck QX700 ddPCR RCL Kit is compatible with MseI restriction enzyme.

Overview of Sample and Control Types

A QX700 plate consists of up to three 16-well cartridges for 48 total wells. Positive Control, Negative Control, Negative Workflow Control (NWC), and sample(s) should be included on every plate. A brief description of each reaction type is provided below. Positive Control and the Negative Control should be tested in duplicate. Samples and the NWC can be tested using 2–4 replicates. For unknown samples, it is recommended to use four replicates to maximize sensitivity.

- **Positive Control:** Positive Control is provided as a component of the kit and is positive for the RCL target. Positive Control reactions are prepared by directly combining Positive Control with a master mix that contains Internal Control. The final reaction should be positive for RCL (FAM) and positive for Internal Control (HEX)
- **Negative Control:** Negative Control reactions are prepared by directly combining nuclease-free water with a master mix that contains Internal Control. This reaction should be negative for RCL (FAM) and positive for Internal Control (HEX)

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- **Negative Workflow Control (NWC):** The NWC is a nuclease-free water sample that has been processed with the same workflow as the samples. Internal Control is added to the NWC at the start of the sample preparation workflow. NWC reactions are prepared by directly combining NWC with a master mix that does not contain Internal Control. This reaction should be negative for RCL (FAM) and positive for Internal Control (HEX)
- **Sample:** Internal Control is added to each sample at the start of the sample preparation workflow. Sample reactions are prepared by directly combining the sample with a master mix that does not contain Internal Control. This reaction should be positive for Internal Control (HEX)

Sample Preparation

Perform DNA extraction for each sample with the QIAGEN QIAamp DNA Mini Kit following the Protocol for Crude Cell Lysates and Other Samples or with a user-preferred extraction method. For optimal performance, samples extracted with the QIAamp Kit should be eluted in 200 µL.

The ddPCR Internal Control can be spiked into the sample prior to extraction and used to estimate percent recovery of extracted samples. **To use:** Ensure the Internal Control tube is fully thawed to room temperature, then vortex at maximum speed for 15 sec. For a 200 µL elution volume, add 14.3 µL of Internal Control to the sample prior to extraction.

It is recommended to run an NWC with each round of extractions to ensure no contamination is introduced during the extraction process. **To use:** Begin with nuclease-free water instead of the sample, add 14.3 µL of Internal Control, and carry it through the entire extraction workflow, eluting in 200 µL.

Note: Most extracted samples will not require dilution and can be added directly to the ddPCR reaction.

Calculating Internal Control Amount for Alternate Elution Volumes

The volume of Internal Control added to the sample varies and is based on the final elution volume of the extracted sample. For elution volumes other than 200 µL, use the following equation to calculate the volume of Internal Control to add to the sample:

U = E/14

Where:

U = volume of Internal Control to spike into the sample prior to extraction, µL

E = elution volume, µL

Reaction Setup

1. Determine the plate layout prior to setting up the reaction mix. It is recommended to include at least two replicate wells for all controls and samples. Four replicates will maximize sensitivity. Reactions are set up in pairs of wells to avoid pipetting small volumes (Figure 1).

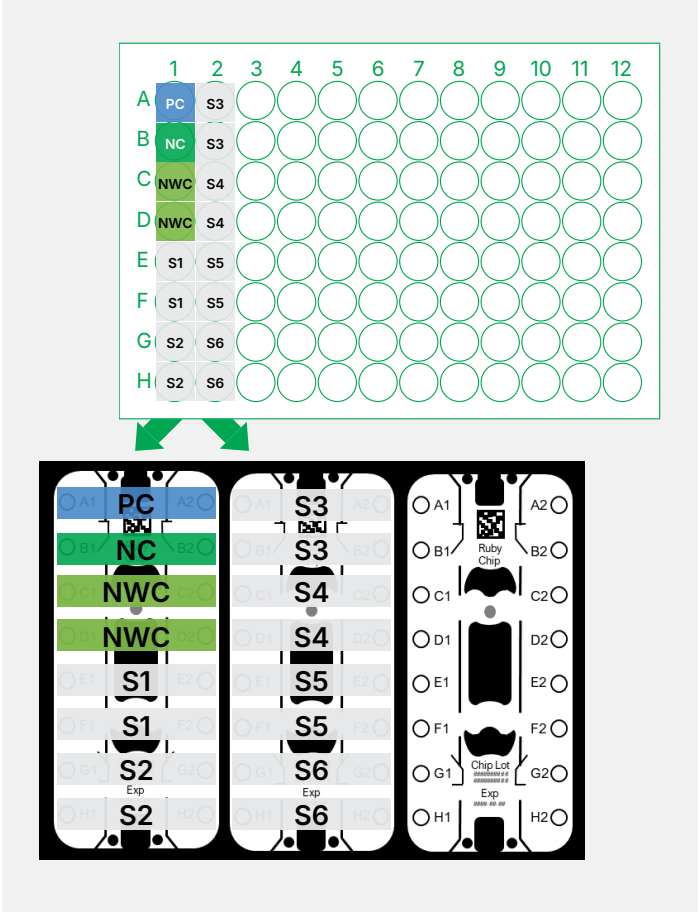


Fig. 1. Protocol schematic. NC, Negative Control; NWC, Negative Workflow Control; PC, Positive Control; S1–S6, samples 1–6.

2. Thaw all kit components to room temperature. Mix all tubes thoroughly by vortexing at maximum speed for 15 sec to ensure homogeneity. Centrifuge briefly to collect contents at the bottom of each tube.

   Tip: Thorough vortexing (maximum speed for 15 sec) of each component at this step is essential for success.

3. For reference, Table 3 provides an overview of the volumes and all components added to each control and sample reaction.

Table 3. Reaction component and volumes overview.

Component	Control or Unextracted Samples (1x), µL	Extracted Sample or NWC (1x), µL
QX700 RDQ Supermix (5x)	1	1
ddPCR RCL Assay (20x)	0.25	0.25
ddPCR Internal Control or water	0.25 Internal Control	0.25 water
DNA sample or Control	3.5 Control	3.5 sample or NWC
Total Volume	**5**	**5**

NWC, Negative Workflow Control.

4. Assemble a premix containing QX700 RDQ Supermix and ddPCR RCL Assay according to Table 4.

Table 4. Premix volumes.

Component	1x Reaction, µL	1 Pair of Wells + Overage, µL	Premix Setup for 1 Cartridge (16 Wells) + Overage, µL
QX700 RDQ Supermix (5x)	1	2.8	32
ddPCR RCL Assay (20x)	0.25	0.7	8
Total Volume*	**1.25**	**3.5**	**40**

*The final 1x QX700 ddPCR reactions have a total volume of 5 µL. The reactions are prepared with overage to account for liquid loss during pipetting steps.

5. **Important:** Mix the premix thoroughly by vortexing the tube at maximum speed for 15 sec. Ensure there are no precipitates.

6. Prepare a master mix for the Positive Control, Negative Control, and any unextracted samples according to Table 5. Mix thoroughly by vortexing.

Table 5. Controls or Unextracted Sample master mix volumes. This master mix contains Internal Control.

Component	1x Reaction, µL	Master Mix Setup for 4 Control Wells + Overage, µL
Premix	1.25	8.75
ddPCR Internal Control	0.25	1.75
Total Volume*	**1.5**	**10.5**

*The final 1x QX700 ddPCR reactions have a total volume of 5 µL. The reactions are prepared with overage to account for liquid loss during pipetting steps.

7. Prepare a master mix for extracted samples and the NWC according to Table 6. Mix thoroughly by vortexing.

Table 6. Extracted Sample or NWC master mix volumes. This master mix does not contain Internal Control as it has already been added to the samples.

Component	1x Reaction, µL	Master Mix Setup for 12 Sample or NWC Wells + Overage, µL
Premix	1.25	25
Nuclease-free water	0.25	5
Total Volume*	**1.5**	**30**

NWC, Negative Workflow Control.

*The final 1x QX700 ddPCR reactions have a total volume of 5 µL. The reactions are prepared with overage to account for liquid loss during pipetting steps.

8. Prepare one reaction mix for each set of two wells in the columns of a ddPCR 96-Well Plate or a strip tube as follows:
   a. Dispense 4.2 µL of the appropriate master mix to each well
   b. Add 9.8 µL of sample

9. Seal the ddPCR 96-Well Plate, vortex at maximum speed for 15 sec, and centrifuge at 1,000 rcf for 1 min. Visually verify that all the liquid is at the bottom of the well. If preparing reaction mixes in tubes, vortex each tube at maximum speed for 15 sec and centrifuge briefly to collect the contents at the bottom of each tube.

10. Once reaction mixes are ready, proceed to QX700 plate setup.

QX700 Plate Setup

For detailed instructions and best practices for successful cartridge setup, refer to the QX700 Droplet Digital PCR System Instrument Guide (10000171493).

Anti-Static Treatment

1. Wrap a prewetted anti-static wipe around a finger and thoroughly wipe the underside and all edges of the cartridge with the anti-static wipe.
2. Gently place and drag the cartridge across the Kimtech Precision Wipe to blot any excess anti-static product and return to the cartridge holder.

   Note: The same anti-static wipe can be used for up to three cartridges.

Cartridge Piercing

1. Hold the piercing tool in one hand and hold down the edges of the cartridge with the other hand.
2. Position the piercing tool above one column of wells and in contact with the foil.
3. Press the piercing tool down to pierce the foil.
4. Repeat for both columns of all cartridges.

Manually Loading Reaction Mix

Tip: Depending on the plate layout, reactions can be loaded using single-channel pipetting to load one well at a time or multi-channel pipetting to load an entire column at one time.

1. Load 5 µL of reaction mix into the pipet tip(s).
2. Hold down the edges of the cartridge with the other hand to keep it in place while pipetting.
3. Holding the pipet vertically, insert the tip inside the inlet well until it lightly touches the bottom of the well.
4. Gently lift the pipet tip slightly off the bottom of the inlet well—approximately 1 mm above the bottom—such that the pipet tip remains inside the oil.
5. Continuing to hold the pipet at a 90° angle, eject the reaction mix by pressing the pipet to the first stop in a continuous and rapid motion. Do not lift the pipet out of the inlet well while ejecting the reaction mix.

   Important: To prevent bubbles, do not press the pipet down to the second stop.
6. Repeat for all wells of all cartridges.

Experiment Setup and QX700 Run

The Vericheck QX700 ddPCR RCL Kit is compatible with the QX700 ddPCR System Control Software v1.5 and above.

Experiment setup for each QX700 run requires three files: a protocol file, an assay file, and an experiment file. A premade protocol file and assay file for the Vericheck QX700 ddPCR RCL Kit are available for download from the product page. These two files contain the thermal cycling and acquisition settings specific to the RCL Kit (summarized below). Users must create a new experiment file for each run. If using downloaded protocol and assay files, skip to the Experiment File Setup and Starting Run section. For in-depth instructions on experiment setup, refer to the QX700 Droplet Digital PCR System Instrument Guide (10000171493).

Protocol File Setup

1. Select **QX700 ddPCR Supermix for RDQ** from the Mix Type dropdown menu.
2. Apply the thermal cycling conditions from Table 7.

Table 7. Thermal cycling conditions for the QX700 ddPCR System.

Step	Step Number	Temperature, °C	Time, sec	Number of Cycles	Ramp Rate, °C/sec
Partition for Ruby Chip	Step 1	-	-	-	-
Enzyme activation	Step 2	95	600	1	1
Begin loop for 40 iterations	Step 3	-	-		-
Denaturation	Step 3.1	94	10	40	1
Annealing/ extension	Step 3.2	60	60		1
Release for Ruby Chip	Step 4	-	-	-	-

3. Under the Programs section, select **2. Reading** and define the Reading Program according to Table 8. Ensure FAM (blue), HEX (teal), and Cy5 (red) are toggled to the right, into the **ON** position. All other channels can be toggled **OFF**.

Table 8. Vericheck QX700 ddPCR RCL Kit exposure configuration for the QX700.

Dye Name	Channel	Exposure, ms
FAM	Blue	85
HEX	Teal	273
Cy5	Red	51

Assay File Setup

1. Under the Assay Structure section, ensure that the three channels listed in Table 9 are toggled to the right, into the **ON** position. The RCL Kit targets are detected in the FAM (blue) and HEX (teal) channels, as shown in Table 9.

Table 9. Assay structure details. The dyes used in the assay file should match the dyes used in the protocol file.

Dye Name	Channel	Associated Target
FAM	Blue	RCL
HEX	Teal	Internal Control
Cy5	Red	Not used

2. Under the Spill-over compensation matrix section, select **Load compensation matrix from file (.ncm)** to load a previously created compensation matrix. Alternatively, spillover compensation can be adjusted in the result file after the data has been collected.

Experiment File Setup and Starting Run

1. Under the DIGITAL EXPERIMENTS tab, click **New**, then **Start from a blank experiment.**
2. Disable any unused cartridge or unused wells by first clicking **Enable/disable elements**, then clicking the disable button next to each unused cartridge or well.
3. If desired, add cartridge labels or sample names. This can be done manually or by using the tools under Sample Settings in the Details section to load sample information from a CSV file or to apply Automatic Sample naming.
4. Under the Files section, add the previously created or downloaded protocol and assay files.
5. Apply the protocol file by dragging it to each cartridge (Figure 2).

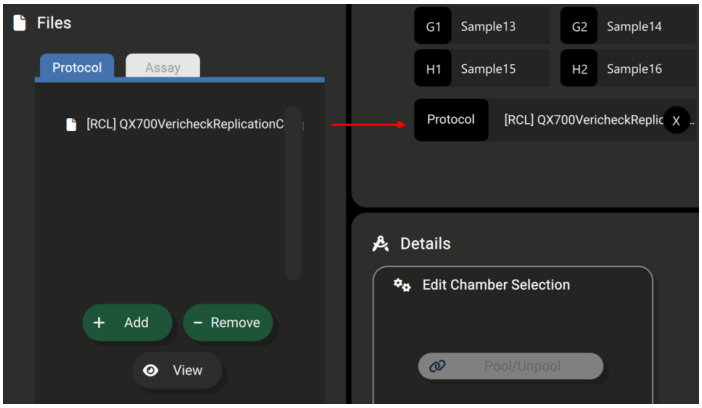


Fig. 2. Applying the protocol file. Drag the desired protocol from the Files section to the protocol box under each cartridge (red arrow).

6. Apply the assay file by selecting all wells and dragging the file to all wells (Figure 3).

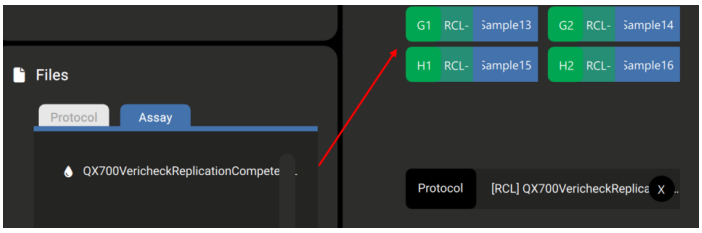


Fig. 3. Applying the assay file. Drag the desired assay from the Files section to the desired well(s) (red arrow). The assay will be assigned to all selected wells.

7. At the top, click **Save As** to save the experiment file.
8. Click **Plan Run** in the bottom right Experiment Summary section to proceed to chip loading.
9. When prompted by the software, gently load the plate into the instrument until the status light begins blinking.
10. Click **Start Run**.
11. Check the Status tab to see the run progress and status. When the run is complete, click on the run and download the result file.

    Note: The user must click **Download Result File** to save the data.

Data Analysis and Result Interpretation

The RCL signal is detected in the FAM (blue) channel, and the Internal Control is detected in the HEX (teal) channel. The Cy5 channel (red) contains no probes. The concentration reported is copies/µL of the final 1x ddPCR reaction. An overview of the data analysis process for the Vericheck QX700 ddPCR RCL Kit is provided below. For more detailed instructions on data analysis, refer to the QX700 ddPCR System Analysis Software User Guide (10000171494).

Quality Check and Thresholding Adjustment

1. Open the data file and navigate to the Quality Control tab. Review the quality flags, chamber images, and droplet counts and exclude problem wells from analysis. Refer to the QX700 ddPCR System Analysis Software User Guide (10000171494) for explanations of quality flags and detailed instructions on performing quality control.
2. Navigate to the Plots & Populations heading under the Analyze Data tab. Examine the control well FAM/HEX 1D and 2D plots for uniformity. See Figure 4 for example Positive Control and Negative Control FAM/HEX 2D plots. The Cy5 channel is not used but will have a background fluorescence signal as seen in Figure 4.

   Tip: Click the gears icon to adjust the 2D plots so the FAM channel is on the vertical axis and the HEX channel is on the horizontal axis.
3. Examine the replicate sample well plots for uniformity and examine any outliers for problems. Do not include any problem wells in the final analysis.
4. Examine the automatically applied FAM and HEX threshold lines in all wells for accuracy. If any clusters are cut off by the thresholds, the threshold lines should be manually adjusted. It is recommended to use the Lines thresholding tool and to apply common thresholds for all control and sample wells.

   Tip: If any wells have significant tilt or if droplets are cut off by the y-axis, the spillover compensation can be adjusted to correct this issue. Go to the Compensate Spillover section of the Setup tab and adjust the Spillover Compensation values for FAM and/or HEX. The resulting compensation matrix file can be saved and applied to future runs, if desired. See the QX700 ddPCR System Analysis Software User Guide (10000171494) for detailed instructions.

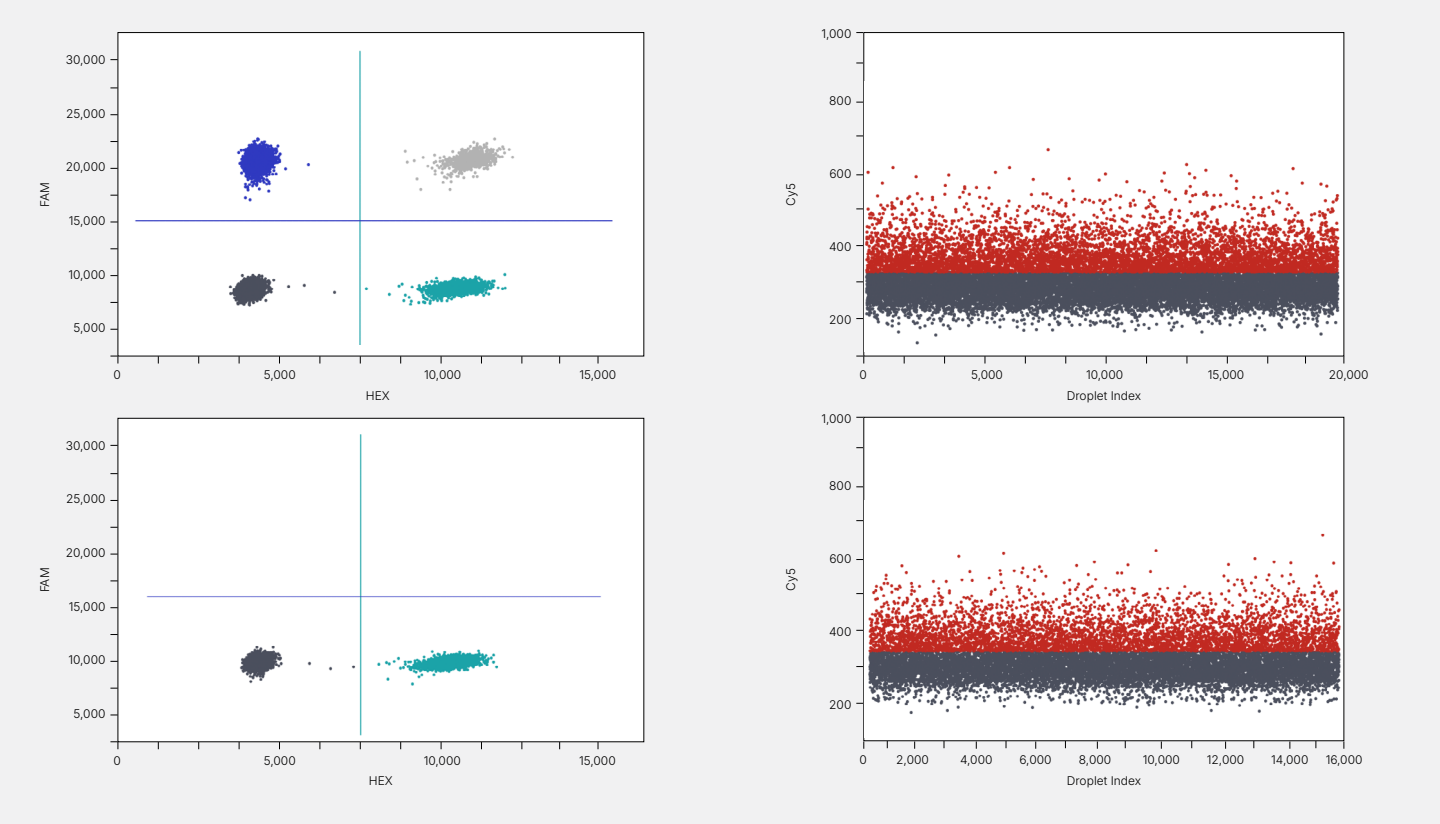


Fig. 4. Example FAM/HEX 2D plots (left) for Positive Control (top) wells and Negative Control (bottom) wells. Corresponding 1D plots for the Cy5 channel (right) show the expected background fluorescence and auto-thresholds for the Cy5 channel. Negative Workflow Control wells are expected to have a similar phenotype to the Negative Control shown above.

Analysis and Result Interpretation

1. For added sensitivity and ease of analysis, multiple replicate wells may be pooled in the software to form a single aggregated well. Navigate to the Setup tab. Under the Edit Experiment heading, pool replicate wells together by selecting multiple wells with CTRL + click and clicking the Pool button. Do not include wells failing quality checks.
2. Navigate to the View Results tab. Under the Result Table heading, check the concentration of the Positive Control and Negative Control wells. The expected concentrations are summarized in Table 10.

Table 10. Expected Positive Control and Negative Control well concentrations based on reaction type.

Well Type	Expected FAM Range	Expected HEX Range
Positive Control	459-3407 cp/µL	700–1,300 cp/µL
Negative Control	<2 positive droplets	700–1,300 cp/µL

Expected concentration ranges are based on a sample input of 3.5 µL per 5 µL well. cp, copies.

3. Examine the FAM concentration of each sample well to determine if the sample is RCL positive. Table 11 can be used as a guide to interpret results. See Appendix B for samples with FAM concentrations close to the RCL positive cutoff.

Table 11. Unknown Sample result interpretation guide.

Status	FAM Result	Expected HEX Result	Interpretation
Negative	<2 positive droplets	>0 cp/µL	*VSV-G* not detected
Positive	≥2 positive droplets	>0 cp/µL	*VSV-G* detected

cp, copies.

4. Examine the HEX concentration of each sample as well as the Negative Control. The following formula can be used to determine the percent recovery of each extracted sample:

   R = (S/C) x 100%

   Where:

   R = percent recovery
   S = sample well HEX concentration, copies/µL
   C = Negative Control well HEX concentration, copies/µL

   The equation assumes that both Negative Control and sample are added at the same volume, 3.5 µL per 5 µL well. If less sample was used, the equation should be adjusted accordingly.
5. To export the data as a CSV, navigate to the Export tab and select the desired file types to export.

See Appendices A–C for additional performance information, result interpretation, and troubleshooting guidance.

Appendix A. Performance Characteristics

Analytical performance characteristics are summarized in Appendix Table A1. The dynamic range and limit of detection (LOD) were determined using a DNA plasmid sample serially diluted in TE buffer with carrier. The kit is linear throughout the dynamic range. LOD is set as the lowest concentration sample detected in ≥95% of tests. The kit was tested with nuclease-free water (Negative Control), and 1 false-positive droplet was observed at the 95th percentile of tests, supporting a limit of blank (LOB) of 1 positive droplet. Specificity was tested using genomic DNA at 1,000 target copies/µL. The maximum allowable concentrations of common inhibitors in the final 1x ddPCR reaction are listed in Appendix Table A2.

Appendix Table A1. Analytical performance summary.

Dynamic range	10–25,000 copies/well
Linearity	Slope = 0.99, R^2 = 1.00
LOD	<7 copies/well
LOB	1 positive droplet
Specificity	No detection of CHO, HEK293, human, *E. coli*, or *Mycoplasma* DNA at >99.99% specificity

LOB, limit of blank; LOD, limit of detection.

Appendix Table A2. Inhibitor tolerance. Maximum allowable concentrations of inhibitor in the final 1x ddPCR reaction.

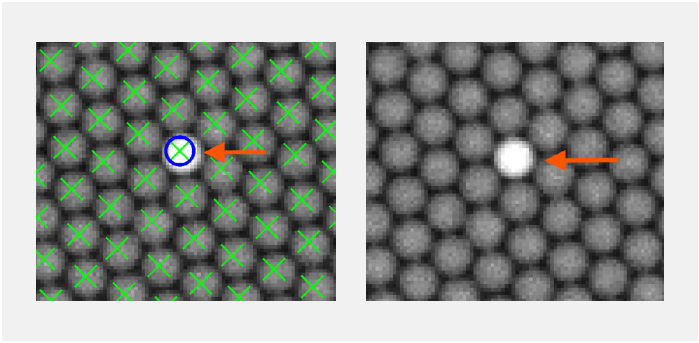
Inhibitor	Allowable Concentration in Final Well
EMEM complete media	10%
Cell lysate	0.1%
DMSO	5%
EDTA	2 mM
SDS	0.01%

DMSO, dimethyl sulfoxide; EDTA, ethylenediaminetetraacetic acid, EMEM, Eagle's Minimum Essential Medium; SDS, sodium dodecyl sulfate.

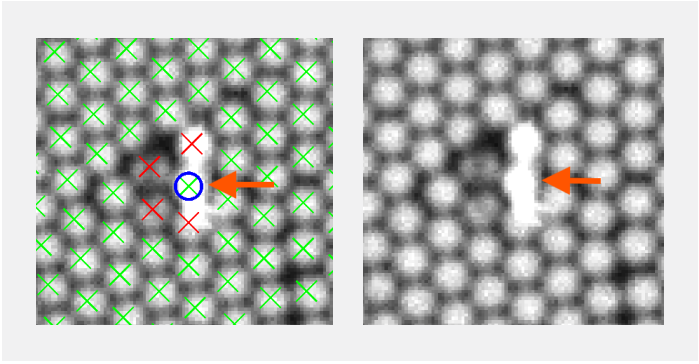
Appendix B. Evaluating Low-Concentration Positive Wells and Droplet Exclusion

For low-concentration FAM-positive wells, evaluate the chamber image to confirm that the droplets counted as positive are true positive droplets and not artifacts such as dust or lint.

1. In the QX700 ddPCR System Analysis Software, navigate to the Quality Control tab and select the well with a low number of positives.
2. Identify the location of each FAM-positive droplet and zoom in to evaluate the droplet. Use the legend to toggle the droplet status indicators on or off to improve visualization. Appendix Figures B1 and B2 provide an example of a true positive droplet and a droplet called positive due to an overlapping artifact.
3. Manually exclude any positive droplets determined to be artifacts. For detailed instructions on manually excluding droplets, refer to the Performing Quality Control section of the QX700 ddPCR System Analysis Software User Guide (10000171494).



Appendix Fig. B1. A true positive droplet with all indicators turned on (left) and all indicators turned off (right).



Appendix Fig. B2. A droplet that was incorrectly called positive due to a nearby artifact with all indicators turned on (left) and all indicators turned off (right). This droplet should be excluded from analysis.

Appendix C. Troubleshooting

High FAM Signal in Negative Controls

Problem: Multiple FAM-positive droplets (≥2) in the Negative Control or NWC.

Possible cause: Contamination during extraction. Contamination during extraction may cause a high FAM signal only in the NWC; the Negative Control will be clean.

Resolution: Ensure clean reagents are used throughout the extraction process. Use high-quality validated extraction kits.

Possible cause: Environmental contamination. Contamination from the laboratory during ddPCR prep may cause a high FAM signal in both the Negative Control and NWC.

Resolution: Wipe down all surfaces with 10% bleach prior to starting experiments. Change gloves often, especially when handling concentrated positive samples. Work in a PCR hood if possible.

Possible cause: Artifacts. Excessive debris or damage to the RDG16 chip may cause inconsistent false positives.

Resolution: Inspect low-positive wells as described in Appendix B. Minimize dust in the environment while preparing chips.

Positive Control Out of Expected Range

Problem: Positive Control is out of the expected 459–3,407 copies/µL range.

Possible cause: Poorly formed ddPCR clusters. Positive Control cannot be easily thresholded.

Resolution: Check thermal cycling and acquisition settings. Ensure reagents have been stored correctly and are not expired.

Possible cause: Pipetting inaccuracy.

Resolution: Check the master mix recipe. All vortex steps should be done for at least 15 seconds.

Internal Control Out of Expected Range

Problem: Internal Control is out of the expected 700–1,300 copies/µL range or not detected for unknown samples.

Possible cause: Poorly formed ddPCR clusters.

Resolution: Wells cannot be easily thresholded. Check thermal cycling and acquisition settings. Ensure reagents have been stored correctly and are not expired.

Possible cause: Inefficient extraction. No HEX copies are detected for an unknown sample; the control was lost during extraction.

Resolution: Use validated extraction workflows.

Possible cause: Pipetting inaccuracy.

Resolution: Ensure Internal Control was added to the samples if needed. All vortex steps should be done for at least 15 seconds.

Low Droplet Counts

Problem: Consistent wells with less than 10,000 droplets.

Possible cause: Inhibitors in the sample.

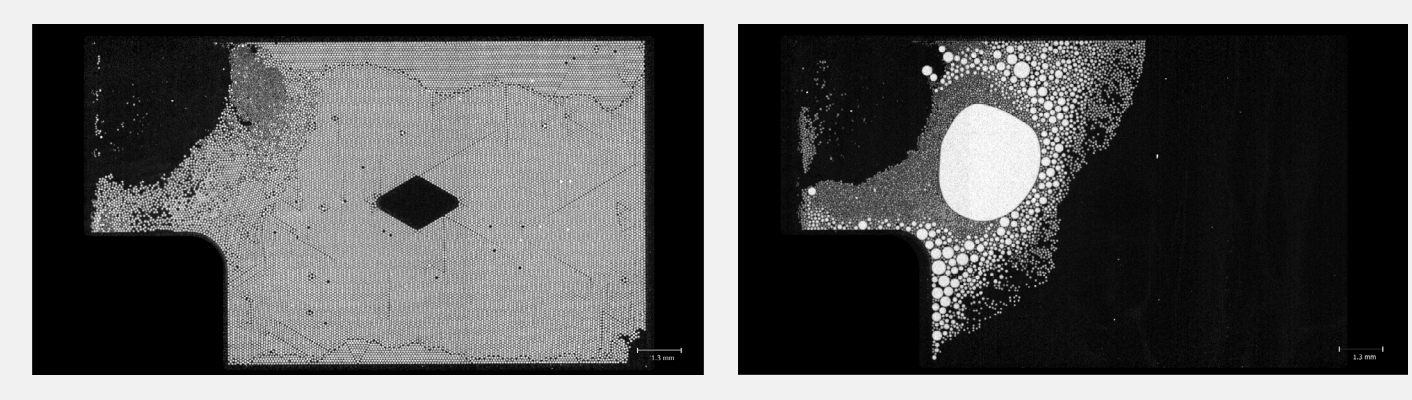
Resolution: In the Quality Control view, numerous large, malformed droplets may be visible, as shown in Appendix Figure C1. Consult Appendix Table A2 and dilute the sample further before testing.

Possible cause: Improper sample loading. In the Quality Control view, the well may show some well-formed droplets near the injection point, but the chamber is not fully filled.

Resolution: Ensure the full 5 µL is dispensed into each well. Dispense samples approximately 1 mm above the bottom of the well.

Possible cause: Damaged chip. In the Quality Control view, cracks may be visible. Damage may also be visible when inspecting the bottom of the chip.

Resolution: Discard the chip.



Appendix Fig. C1. Example high-quality chamber image (left) and poor-quality chamber image with bubbles caused by excess detergent (right).

Poorly Formed ddPCR Clusters

Problem: ddPCR positive droplets cannot be easily separated from negative droplets, as shown in Appendix Figure C2.

Possible cause: Poor mixing.

Resolution: Proper mixing is critical for the ddPCR workflow. All vortex steps should be done for at least 15 seconds.

Possible cause: Inhibitors in the sample.

Resolution: Consult Appendix Table A2. Dilute the sample further before testing.

Possible cause: Incorrect thermal cycling or acquisition settings.

Resolution: Check protocol settings. If thermal cycling conditions were incorrect, repeat the experiment. If acquisition settings were incorrect, the chip may be reimaged with correct settings.

No Negative Droplets

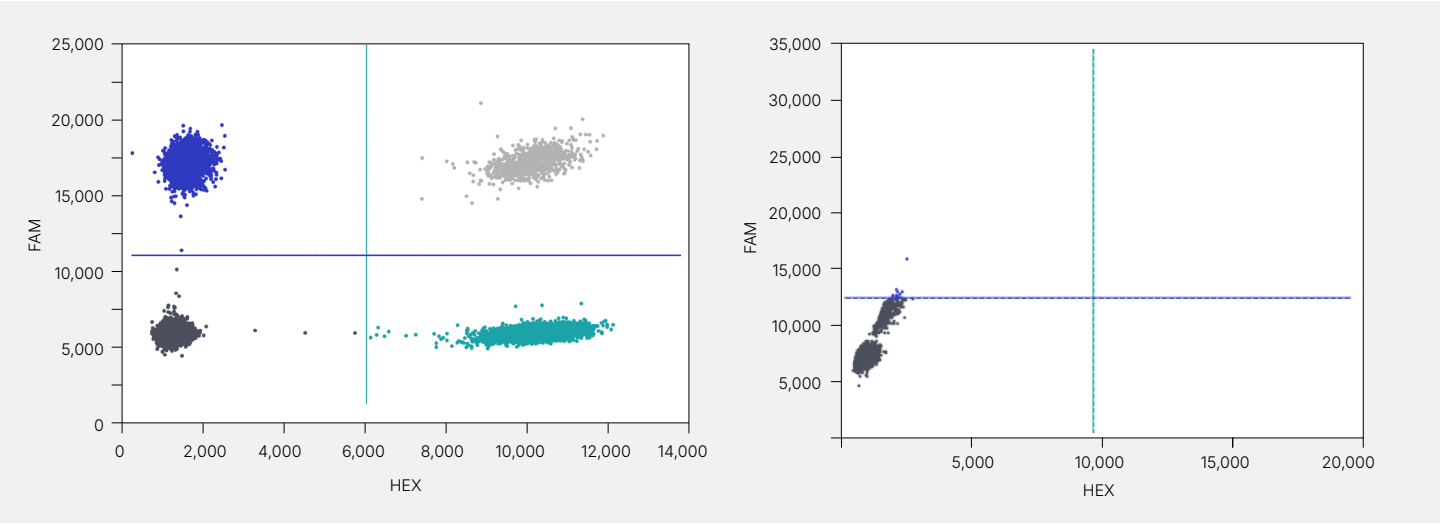
Problem: Sample well has no negative droplets and only high-amplitude clusters are present in the 1D and 2D plots. A concentration value cannot be calculated for the sample, and the result table reports the concentration as “inf”.

Possible cause: The sample is too concentrated and is outside the dynamic range.

Resolution: Dilute the sample further before testing.

Possible cause: Inhibitors in the sample.

Resolution: Consult Appendix Table A2. Dilute the sample further before testing.



Appendix Fig. C2. Expected 2D phenotype (left). Inhibited sample 2D phenotype (right).

Visit **bio-rad.com/QX700VericheckRCLKit** for more information.

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Bio-Rad Laboratories, Inc.

Life Science Group

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