Respiratory Tract Microbiota Profiling Experiments v2

APPLICATION GUIDE

TaqMan™ Assays for respiratory tract microbiota profiling experiments using OpenArray™ Plates

for use with:

TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate

Custom TaqMan™ OpenArray™ Plate

MagMAX™ Viral/Pathogen Ultra Nucleic Acid Isolation Kit

QuantStudio™ 12K Flex Instrument with OpenArray™ block (QuantStudio™ 12K Flex OpenArray™ AccuFill™ System)

Catalog Number A49044

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Revision C

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For descriptions of symbols on product labels or product documents, go to thermofisher.com/symbols-definition.

Revision history: MAN0019506 C (English)

Revision	Date	Description
C	19 September 2024	• Vortex instructions were updated ("Set up the PCR reactions in an OpenArray™ 384-well Sample Plate (OpenArray™ AccuFill™ Software v2.0)" on page 34). • Sealing instructions were updated ("Seal the OpenArray™ Plate" on page 41). • Minor verbiage updates throughout document.
B.0	6 December 2021	• Instructions were added for the OpenArray™ AccuFill™ Software v2.0. • The Biomek™ Seal and Sample Foil Lids were changed to an optional material. • The volumes that are provided for setting up PCR reactions had the 10% overage removed (an overage is still recommended, to be determined and calculated by the user).
A.0	5 January 2021	New document.

The information in this guide is subject to change without notice.

Contents

1 Overview

Product description

TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate (Cat. No. A49044) is an efficient, easy-to-use fixed-content OpenArray™ plate for the characterization of key respiratory tract microbial targets. The plate includes 35 TaqMan™ assays that have been optimized for detection of 32 respiratory tract viral and bacterial nucleic acid, including two assays that target SARS-CoV-2. The plate also includes control assays for TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*), TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control, and the human RNase P RPPH1 gene. For a complete list of assays included in the plate, see "TaqMan™ assays included in the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate" on page 6.

The assays perform well with total nucleic acid that is isolated from nasopharyngeal swab, nasopharyngeal aspirate, and bronchoalveolar lavage (BAL) research samples using the MagMAX™ Viral/Pathogen Ultra Nucleic Acid Isolation Kit.

TaqMan™ assay designs and assay target sequences have undergone rigorous bioinformatics selection and analysis to maximize strain coverage and minimize potential for off-target cross-reactivity. Qualified TaqMan™ assays have undergone performance testing to verify that results are accurate with high levels of sensitivity and specificity.

TaqMan™ assays for respiratory tract microbiota profiling

TaqMan™ assays included in the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate

The following assays are included in the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate.

Note: This format 112 TaqMan™ OpenArray™ Plate contains 35 TaqMan™ assays for 32 microbial targets, and the TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control, plated in triplicate, and assays for the TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*) and human RNase P RPPH1 gene controls plated in duplicate. Each TaqMan™ OpenArray™ Plate can be used for running up to 23 samples and one control sample.

The assays can also be ordered in a Custom TaqMan™ OpenArray™ Plate.

Table 1 Assays for respiratory tract microbiota

Target organism	Assay name	Nucleic acid type	Assay ID
Bacteria			
Bordetella bronchiseptica / parapertussis / pertussis	Bordetella	DNA	Ba06439624_s1
Bordetella pertussis	B.pertussis	DNA	Ba06439623_s1
Chlamydophila pneumoniae	C.pneumoniae	DNA	Ba06439616_s1
Haemophilus influenzae	H.influenzae	DNA	Ba06439625_s1
Klebsiella pneumoniae complex	K. pneumoniae	DNA	Ba04932083_s1
Legionella pneumophila	L.pneumophila	DNA	Ba06439617_s1
Mycoplasma pneumoniae	M.pneumoniae	DNA	Ba06439620_s1
Staphylococcus aureus	S.aureus	DNA	Ba04646259_s1
Streptococcus pneumoniae	S.pneumoniae	DNA	Ba06439619_s1
Virus			
Adenovirus	AdV_1of2	DNA	Vi99990001_po
Adenovirus	AdV_2of2	DNA	Vi99990002_po
Human Coronavirus 229E	CoV_229E	RNA	Vi06439671_s1
Human Coronavirus HKU1	CoV_HKU1	RNA	Vi06439674_s1
Human Coronavirus NL63	CoV_NL63	RNA	Vi06439673_s1
Human Coronavirus OC43	CoV_OC43	RNA	Vi06439646_s1
Human Enterovirus (pan assay)	EV_pan	RNA	Vi06439631_s1
Human Enterovirus D68	EV_D68	RNA	Vi06439669_s1
Human Metapneumovirus (hMPV)	hMPV	RNA	Vi99990004_po
Human Parainfluenza virus 1	hPIV1	RNA	Vi06439642_s1
Human Parainfluenza virus 2	hPIV2	RNA	Vi06439672_s1
Human Parainfluenza virus 3	hPIV3	RNA	Vi06439670_s1
Human Parainfluenza virus 4	hPIV4	RNA	Vi99990005_po
Human Respiratory Syncytial Virus A (RSVA)	RSVA	RNA	Vi99990014_po
Human Respiratory Syncytial Virus B (RSVB)	RSVB	RNA	Vi99990015_po
Human Rhinovirus 1/2	RV_1of2	RNA	Vi99990016_po

Table 1 Assays for respiratory tract microbiota *(continued)*

Target organism	Assay name	Nucleic acid type	Assay ID
Human Rhinovirus 2/2	RV_2of2	RNA	Vi99990017_po
Human herpesvirus 4 (HHV4 – Epstein-Barr Virus)	HHV4	DNA	Vi06439675_s1
Human herpesvirus 5 (HHV5 – Cytomegalovirus)	HHV5	DNA	Vi06439643_s1
Human herpesvirus 6 (HHV6)	HHV6	DNA	Vi06439627_s1
Influenza A	Flu_A_pan	RNA	Vi99990011_po
Influenza A/H1-2009	Flu_A_H1	RNA	Vi99990009_po
Influenza A/H3	Flu_A_H3	RNA	Vi99990010_po
Influenza B	Flu_B_pan	RNA	Vi99990012_po
Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2); S protein gene	SARS-CoV2S	RNA	Vi07918636_s1
Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2); N protein gene	SARS-CoV2N	RNA	Vi07918637_s1

Table 2 Assays for respiratory tract microbiota controls

Control name	Assay name	Nucleic acid type	Assay ID
TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*)	B.atrophaeus	DNA	Ba06596576_s1
TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control	Xeno	RNA	Ac00010014_a1
Human RNase P RPPH1 gene	RPPH1	DNA	Hs04930436_g1

Additional TaqMan™ assays for respiratory tract microbiota profiling

The following TaqMan™ assays are not included in the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate. For respiratory tract microbiota profiling using these assays, use a Custom TaqMan™ OpenArray™ Plate.

Target organism	Assay name	Nucleic acid type	Assay ID
Bacteria			
Bordetella holmesii	B.holmesii	DNA	Ba06439621_s1
Coxiella burnetii	C.burnetii	DNA	Ba06439618_s1
Moraxella catarrhalis	M.catarrhalis	DNA	Ba06439622_s1
Fungus			
Pneumocystis jirovecii	P.jirovecii	DNA	Fn06439626_s1

(continued)

Target organism	Assay name	Nucleic acid type	Assay ID
Virus			
Human Bocavirus	HBoV	DNA	Vi99990003_po
Human herpesvirus 3 (HHV3 – Varicella zoster Virus)	HHV3	DNA	Vi06439647_s1
Human Parechovirus	HPeV	RNA	Vi99990006_po
Measles virus	Measles	RNA	Vi99990013_po
Middle East Respiratory Syndrome coronavirus (MERS)	MERS_CoV	RNA	Vi06439644_s1
Mumps virus	Mumps	RNA	Vi06439657_s1
Severe Acute Respiratory Syndrome coronavirus (SARS)	SARS_CoV	RNA	Vi06439634_s1

TaqMan™ OpenArray™ Plate products and formats

TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate

The TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate (Cat. No. A49044) contains pre-plated, dried down TaqMan™ assays for respiratory tract microbiota profiling. For the complete lists of assays included with the plate, see “TaqMan™ assays included in the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate” on page 6.

Contents and storage

Table 3 TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate (Cat. No. A49044; format 112 assays and up to 24 samples)

Component	Amount	Storage
TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate	1 plate	–25°C to –15°C

Custom TaqMan™ OpenArray™ Plate formats

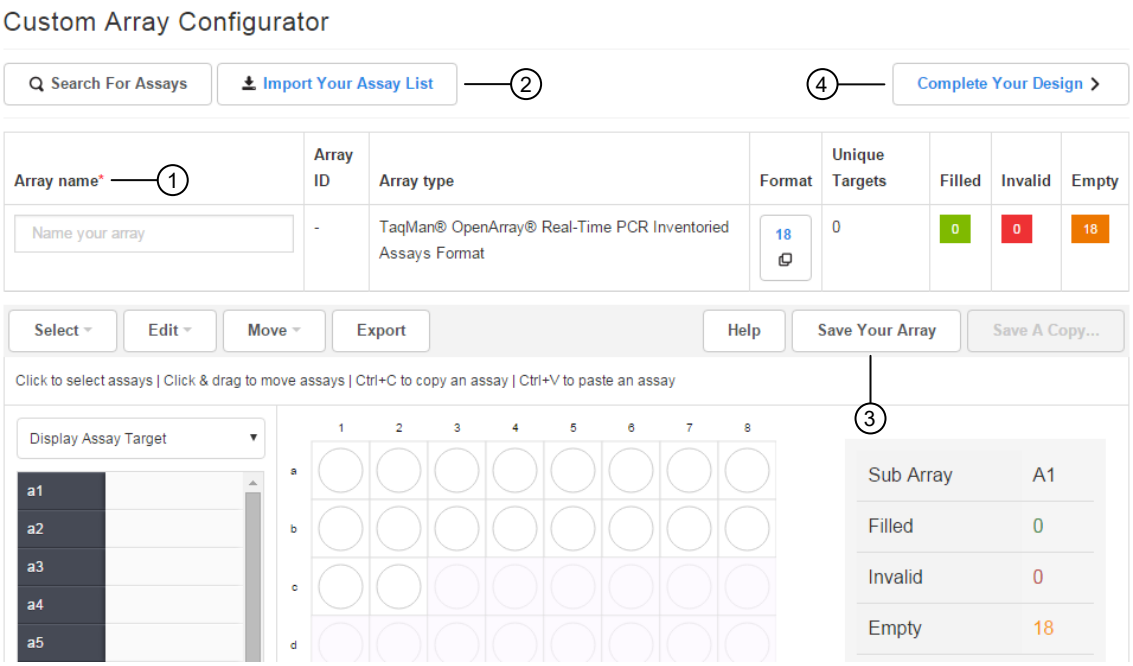
Custom TaqMan™ OpenArray™ Plate contain pre-plated, dried down TaqMan™ assays for respiratory tract microbiota profiling.

Array format	Number of assays	Maximum number of samples
56	56	48
112	112	24
168	168	16

Note: We recommend at least three technical replicates of each reaction.

Configure and order Custom TaqMan™ OpenArray™ Plates

1. Go to **thermofisher.com/order/custom-array**.
2. For array type, select **TaqMan™ OpenArray™ Real-Time PCR Inventoried Assays Format**.
3. *(Optional)* In the table, click **View Layout** to preview the layout of the plate.
4. In the table, click **Select** to configure a plate with the desired array format.
   The **Custom Array Configurator** screen displays.



① **Array name**
② **Import Your Assay List**
③ **Save Your Array**
④ **Complete Your Design**

5. Enter the custom array name in the **Array name** text field.
6. Click **Import Your Assay List**, then upload or copy-paste the assay information:
   - Under **Upload a list of Assay IDs**, click **Choose File**, then select a tab-delimited text file (TXT) containing Assay IDs.

     or
   - Under **Enter a list of Assay IDs**, paste the Assay IDs, then click **Import Entered List**.
7. Follow the on-screen instructions to configure the assays on the plate.

8. *(Optional)* Click **Save Your Array** at any time to save the array configuration to your Thermo Fisher Scientific account.

9. When the plate is configured, click **Complete Your Design**, then follow the on-screen instructions to complete the order.

Materials required but not supplied

Unless otherwise indicated, all materials are available through thermofisher.com. "MLS" indicates that the material is available from fisherscientific.com or another major laboratory supplier.

Catalog numbers that appear as links open the web pages for those products.

Materials required for nucleic acid isolation

Nucleic acid isolation kit

Table 4 MagMAX™ Viral/Pathogen Ultra Nucleic Acid Isolation Kit (Cat. No. A42356)

Component	Amount	Storage
Binding Solution	60 mL	15–25°C
Wash Solution	100 mL	
Elution Solution	10 mL	
Nucleic Acid Binding Beads	2 mL	
Proteinase K	1 mL	
Enzyme Mix	5 mL	–25°C to –15°C

Additional materials

Item	Source
Instrument and equipment	
KingFisher™ Flex Magnetic Particle Processor 96DW with deep-well heat block	5400630
Adjustable micropipettors	MLS
Multi-channel micropipettors	MLS
Plastics and consumables	
KingFisher™ 96 Deep-Well Plate	95040450
KingFisher™ 96 KF microplate (200 µL)	97002540
KingFisher™ 96 tip comb for DW magnets	97002534
Conical Tubes (15 mL)	AM12500

(continued)

Item	Source
Conical Tubes (50 mL)	AM12501
Nonstick, RNase-free Microfuge Tubes, 1.5 mL	AM12450
Nonstick, RNase-Free Microfuge Tubes, 2.0 mL	AM12475
MicroAmp™ Clear Adhesive Film	4306311
Filtered micropipettor tips	MLS
Reagent reservoirs	MLS
Reagents	
Ethanol, 100% (molecular biology grade)	MLS
Nuclease-free water	AM9932, or equivalent
Universal Transport Media, for preparation of negative extraction control	Fisher Scientific 22-031-14, or equivalent
(*Optional*) 1X PBS (1X), pH 7.4, for reconstitution of TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*)	10010023

Materials required for preamplification

Item	Source
Instrument and equipment	
Thermal cycler, one of the following (or equivalent): • Veriti™ Thermal Cycler, 96-well standard block • SimpliAmp™ Thermal Cycler • ProFlex™ PCR System	Contact your local sales office
Microcentrifuge	MLS
Vortex mixer	MLS
Micropipettes	MLS
Tubes, plates, and other consumables	
MicroAmp™ Optical 96-Well Reaction Plate	N8010560, or equivalent; see **thermofisher.com/plastics**
MicroAmp™ Clear Adhesive Film	4306311
Aerosol-resistant barrier pipette tips	MLS
Disposable gloves	MLS

(continued)

Item	Source
Reagents	
Genomic DNA/RNA	See page 17
TrueMark™ Respiratory Panel 2.0 PreAmp Primers	A49049
TaqPath™ 1-Step RT-qPCR Master Mix, CG	• A15299 (5 x 1 mL) • A15300 (1 x 10 mL)
Nuclease-free water	AM9937, or equivalent

Materials required for OpenArray™ Plate workflow

Item	Source
Instruments, software, and equipment	
OpenArray™ Sample Tracker Software (Not required for OpenArray™ AccuFill™ Software v2.0)	—[1]
QuantStudio™ 12K Flex OpenArray™ Plate Press 2.0	A24945
QuantStudio™ 12K Flex Real–Time PCR System with OpenArray™ block and QuantStudio™ 12K Flex OpenArray™ AccuFill™ System	4471090
Centrifuge, capable of spinning sample plates at 1,000 × *g*	MLS
Plates and accessories	
OpenArray™ 384-well Sample Plates, black	4482221
(Optional) Biomek™ Seal and Sample Foil Lids (for pre-plating step)	Beckman Coulter™ 538619
OpenArray™ AccuFill™ System Tips	4458107
QuantStudio™ 12K Flex OpenArray™ Accessories Kit[2]	4469576
Forceps	MLS
Reagents	
Preamplified genomic DNA/RNA	See page 21
OpenArray™ Plates with TaqMan™ Assays	• A49044 • Custom ordered[3]

(continued)

Item	Source
TaqMan™ OpenArray™ Real-Time PCR Master Mix	4462164
Ethanol	MLS

[1] Included with the QuantStudio™ 12K Flex Software.

[2] Each kit contains the items needed to assemble up to 10 plates: 12 lids and plugs, 12 immersion fluid syringes, and 2 carriers. Each custom OpenArray™ Plate order is shipped with accessories kits.

[3] See page 9.

Materials required for data analysis

Item	Source
Software, select one of the following:	
Relative Quantification Application (recommended)	apps.thermofisher.com
QuantStudio™ 12K Flex Software	Included with QuantStudio™ 12K Flex Real–Time PCR System

Optional controls

Control	Purpose	How to use	Cat. No.
TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control	Synthetic RNA control for RNA recovery, reverse transcription, preamplification, and PCR	Nucleic acid isolation: Add to samples along with the Binding/Bead Mix	A39179
TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*)	Lyophilized organism control for nucleic acid extraction and purification	Nucleic acid isolation: Stand-alone sample, or add to samples after Enzyme Mix	A39180
TrueMark™ Respiratory Panel 2.0 Amplification Control	DNA plasmid control for real-time PCR	Real-time PCR: Stand-alone sample added directly to the plate	A48101

TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control

TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control is a synthetic RNA control that serves as an exogenous process control for nucleic acid isolation and RNA recovery, reverse transcription, preamplification, and PCR. The control is used with the proprietary TaqMan™ assay for Xeno™ sequences, which is included in the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate.

TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control is supplied at a concentration of 10,000 copies/µL. During nucleic acid isolation, 10 µL of the control can be added to each test sample along with the nucleic acid binding reagents (Binding Solution). When carried through the respiratory tract microbiota workflow, the control is used to monitor nucleic acid recovery, RNA reverse

transcription, cDNA preamplification, and PCR. The control can be used to identify sample-specific amplification inhibition, which reduces the likelihood of false negatives and provides confidence that results are accurate. It is recommended that the control is added to each sample during nucleic acid isolation.

TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*)

TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*), serves as a process control for cell lysis and nucleic acid recovery. The control is used with the proprietary TaqMan™ assay for *Bacillus atrophaeus* sequences.

Like other gram-positive bacteria, *Bacillus atrophaeus* has thick cell walls than can be difficult to lyse. This characteristic makes gram-positive bacteria an ideal control to monitor the efficiency of cell lysis and subsequent nucleic acid recovery.

TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*) is supplied lyophilized with a quantity of 1×10^9 copies/vial, and is reconstituted in 200 µL of 1X PBS (1X), pH 7.4 to a final concentration 5×10^6 copies/µL. During nucleic acid isolation, 10 µL of the control is processed as a stand-alone sample in a background of universal transport media. It can be added to the negative extraction control, and may also be added to one or more test samples at the start of the extraction process. The control is carried through the remainder of the workflow with the test samples. It is recommended that at least one stand-alone control sample is run per extraction plate.

TrueMark™ Respiratory Panel 2.0 Amplification Control

TrueMark™ Respiratory Panel 2.0 Amplification Control contains a linearized multi-target plasmid with target sequences for each respiratory tract microbiota assay on the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate. The plasmid also contains target sequences for TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control, TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*), and the human RNase P RPPH1 gene. It can be included in respiratory tract microbiota profiling experiments as a positive control for panel-specific amplification.

TrueMark™ Respiratory Panel 2.0 Amplification Control is supplied at a concentration of 1×10^5 copies/µL. During real-time PCR, 2.5 µL of the control is used as a stand-alone sample in 2 wells of the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate. The control can be used if needed to verify assay performance and to help with troubleshooting.

Note: The amplification control RV target sequence is a perfect match to the RV_1of2 assay target, and contains a mismatch with the RV_2of2 assay target. Lower Amp Scores and C_q confidence scores can be noted for RV_2of2 versus RV_1of2.

Workflow

Respiratory tract microbiota profiling experiments

Isolate nucleic acid using MagMAX™ Viral/Pathogen Ultra Nucleic Acid Isolation Kit (page 17)

Start with bronchoalveolar lavage, nasopharyngeal swab, or nasopharyngeal aspirate samples

Perform preamplification (page 21)

Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v1.2 (page 24) **OR Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v2.0** (page 32)

Seal and run the OpenArray™ Plates (page 41)

Analyze data (page 46)

2 Isolate nucleic acid using MagMAX™ Viral/Pathogen Ultra Nucleic Acid Isolation Kit

For required materials, see “Materials required for nucleic acid isolation” on page 11.

Procedural guidelines

- Perform all steps at room temperature (20–25°C) unless otherwise noted.
- Ensure that Nucleic Acid Binding Beads remain in a homogeneous suspension while pipetting. Vortex beads before use.

Before first use of the kit

- Download the KingFisher™ Flex script **MVP_Ultra_Flex** from the MagMAX™ Viral/Pathogen Ultra Nucleic Acid Isolation Kit (Cat. No. A42356) product page, then install it on the instrument.

  See the instrument user guide for instructions to install the script.

- Prepare fresh 80% Ethanol using 100% absolute Ethanol and Nuclease-free water, sufficient for 1.5 mL per sample, plus 10% overage.

Set up the KingFisher™ Flex instrument

- Ensure that the KingFisher™ Flex instrument has the appropriate magnetic head and heat block installed.
  - 96 deep-well magnetic head
  - 96 deep-well heat block
- Ensure that the **MVP_Ultra_Flex** script is installed on the instrument.

Reconstitute TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*)

Use of the TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*) is optional.

1. Remove metal fastener from vial using tweezers and place vial on ice.
2. Remove rubber stopper from vial, then add 200 µL 1X PBS (1X), pH 7.4 to the vial.
3. Replace the rubber stopper, then vortex the tube to mix.
4. Transfer reconstituted sample to a 1.5-ml tube, then store on ice or at 4°C.

Note: Store the reconstituted control at 4°C for up to 48 hours. For long term storage, store the reconstituted control at –80°C to –20°C for up to 4 months. Mix well to resuspend before use.

The final concentration of the control is 5×10^6 copies/µL.

Set up the processing plates

Set up the processing plates outside the instrument according to the following table. Cover the plates with a temporary seal, then store at room temperature for up to 1 hour while you set up Sample Plate.

Plate type	Plate position	Plate ID	Reagent	Volume per well
Deep well[1]	2	Wash 1 Plate	Wash Solution	1000 µL
	3	Wash 2 Plate	80% Ethanol	1000 µL
	4	Wash 3 Plate	80% Ethanol	500 µL
	5	Elution Plate	Elution Solution	60 µL[2]
Standard[3]	6	Tip Comb	96DW Tip Comb	—

[1] KingFisher™ 96 Deep-Well Plate
[2] The elution volume can be increased to a maximum of 100 µL.
[3] KingFisher™ 96 KF microplate

Set up Sample Plate, then start processing

(*Optional*) Reconstitute TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*) before use in step 3 (see page 18).

1. Swirl the bottle of Enzyme Mix, then place on ice.
2. Add 50 µL of Enzyme Mix to each well in a KingFisher™ 96 Deep-Well Plate (Sample Plate).

3. Add samples and controls to the appropriate well containing Enzyme Mix.

Sample or control	Instructions
Sample	Add 200–400 µL of sample to a well.
Negative Extraction Control (NEC)	Add 200–400 µL of Universal Transport Media to a well.
(*Optional*) TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*)	• Combine 10 µL of reconstituted control with 390 µL of Universal Transport Media in a well. *or* • Add 10 µL of reconstituted control to one or more sample wells.

4. On the KingFisher™ Flex instrument, select the **MVP_Ultra_Flex** script, then press **Start**.

5. Follow the instrument prompts to load sample and processing plates, then press **Start**.

Proceed immediately to the next step.

Continue processing to bind, wash, and elute the nucleic acid

1. During the enzyme treatment incubation on the instrument, prepare the Binding/Bead Mix.
   a. Vortex the tube of Nucleic Acid Binding Beads to fully resuspend the beads.
   b. Combine the following components for the required number of samples, plus 10% overage.

   IMPORTANT! Binding Solution is viscous. Pipet slowly to avoid bubbles and to ensure that the correct volume is delivered.

Component	Volume per sample
Binding Solution	530 µL
Nucleic Acid Binding Beads	20 µL
(*Optional*) TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control	10 µL
Total	**550 µL** or **560 µL**

2. Gently invert the Binding/Bead Mix 5 times to mix, then store at room temperature until the next step.

3. When prompted by the instrument (approximately 20 minutes after the start of the script), remove the Sample Plate from the instrument.

4. Add 10 µL of Proteinase K to each sample in the Sample Plate.

   Note: Add the Proteinase K to the sample separately from and before the Binding/Bead Mix. Combining the reagents, or adding in a different order can affect nucleic acid recovery.

5. Gently invert the Binding/Bead Mix 5 times to mix, then use a manual pipet (single or multi-channel) to dispense the appropriate volume to each sample and control well in the Sample Plate.
   - 550 µL: Binding/Bead Mix only *or*
   - 560 µL: Binding/Bead Mix + TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control

   IMPORTANT! Binding/Bead Mix is viscous. Pipet slowly to avoid bubbles and to ensure that the correct volume is delivered. Invert the Binding/Bead Mix regularly to avoid bead settling.

6. Return Sample Plate to the instrument, then press **Start** to resume the script.

7. When processing is complete (~30 minutes after adding Binding/Bead Mix), remove Elution Plate from instrument.
   The purified nucleic acid is in Elution Plate.

8. Transfer the nucleic acid samples to a 96-well storage plate or seal Elution Plate.

Store nucleic acid samples on ice for immediate use or at –20°C for longer-term storage.

3 Perform preamplification

For required materials, see “Materials required for preamplification” on page 12.

Good laboratory practices for PCR and RT-PCR

- Wear clean gloves and a clean lab coat.
  - Do not wear the same gloves and lab coat that you have previously used when handling amplified products or preparing samples.
- Change gloves if you suspect that they are contaminated.
- Maintain separate areas and dedicated equipment and supplies for:
  - Sample preparation and reaction setup.
  - Amplification and analysis of products.
- Do not bring amplified products into the reaction setup area.
- Open and close all sample tubes carefully. Avoid splashing or spraying samples.
- Keep reactions and components capped as much as possible.
- Use a positive-displacement pipettor or aerosol-resistant barrier pipette tips.
- Clean lab benches and equipment periodically with 10% bleach solution or DNA decontamination solution.

Perform preamplification

Note: Preamplification of the TrueMark™ Respiratory Panel 2.0 Amplification Control is not recommended.

1. Prepare the PreAmp Reaction Mix: Combine the following components for the number of required reactions plus 10% overage, then mix thoroughly by pipetting up and down.

Component	Volume per reaction
TaqPath™ 1-Step RT-qPCR Master Mix, CG	2.5 µL
TrueMark™ Respiratory Panel 2.0 PreAmp Primers[1]	2.5 µL

[1] The TrueMark™ Respiratory Panel 2.0 PreAmp Primers contains primers for all respiratory tract microbiota assays plus the TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control and the RNase P RPPH1 gene, but does not contain primers for the TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*).

2. Distribute the PreAmp Reaction Mix, then nuclease-free water or sample nucleic acid to the appropriate wells of a 96-well plate.

Component	Sample reaction	No-template control (NTC) reaction
PreAmp Reaction Mix	5 µL	5 µL
Sample DNA or NEC	5 µL	—
Nuclease-free water	—	5 µL
Total volume per reaction	**10 µL**	**10 µL**

3. Seal the plate with adhesive film.

4. Gently vortex the plate for 10 seconds to mix, then briefly centrifuge to bring contents to the bottom of the wells.

5. Place the plate in a thermal cycler that is programmed with the following thermal cycling conditions, then start the run.

Stage	Step	Temperature	Time
Hold	UNG incubation[1]	25°C	2 minutes
Hold	Reverse transcription	50°C	30 minutes
Hold	Activation	95°C	2 minutes
Cycling (14 cycles)	Denaturation	95°C	15 seconds
	Annealing/Extension	60°C	2 minutes
Hold	Inactivation	99.9°C	10 minutes
Hold	—	4°C	Hold

[1] Heat-labile UNG is completely inactivated during the initial ramp to 95°C.

6. Store the plate on ice until dilution for PCR (see "Dilute the preamplified sample" on page 22).

Dilute the preamplified sample

To determine dilution volumes, first determine the total volume of diluted preamplified sample that is required for PCR (see Chapter 4, "Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v1.2" or Chapter 5, "Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v2.0"). We recommend that you prepare only the volume of diluted preamplified sample that is required for your experiment. The undiluted preamplified sample can be stored at –20°C long term.

1. Vortex, then briefly centrifuge the plate that contains the completed preamplification sample reactions.

2. Remove the adhesive film from the plate.

3. Prepare a 1:10 dilution of the preamplified samples in a new 96-well plate.
   a. Transfer the desired volume of the preamplified samples to a new 96-well plate (for example, 2 µL).
   b. Add the appropriate volume of nuclease-free water to each sample and control well (for example, 18 µL).
4. Seal the plate with new adhesive film.
5. Vortex the plate for 10 seconds, then briefly centrifuge.
6. Proceed directly to prepare the OpenArray™ Plates (see Chapter 4, “Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v1.2” or Chapter 5, “Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v2.0”).

Seal the plate that contains the unused portion of the undiluted preamplified samples, then store at –20°C.

4 Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v1.2

For required materials, see “Materials required for OpenArray™ Plate workflow” on page 13.

For instructions for OpenArray™ AccuFill™ Software v2.0, see Chapter 5, “Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v2.0”.

This chapter contains brief procedures. For detailed procedures, see the following documentation.

Document	Pub. No.
QuantStudio™ 12K Flex Real–Time PCR System: OpenArray™ Experiments User Guide	4470935
OpenArray™ Sample Tracker Software Quick Reference	4460657
OpenArray™ AccuFill™ System User Guide	4456986

Workflow

Microbiota profiling experiments with OpenArray™ plates

Generate 384-well sample plate layouts in the OpenArray™ Sample Tracker Software (page 27)

Set up the PCR reactions in an OpenArray™ 384-well Sample Plate (OpenArray™ AccuFill™ Software v1.2) (page 28)

Set up the OpenArray™ AccuFill™ Instrument and the OpenArray™ AccuFill™ Software (page 29)

Transfer reactions to the OpenArray™ Plate using the OpenArray™ AccuFill™ Instrument (page 30)

Seal the OpenArray™ Plate (page 41)

Run the OpenArray™ Plate on the QuantStudio™ 12K Flex Instrument (page 44)

Check the quality–control images (page 45)

One-time procedures

Set up default folders and software preferences

This procedure simplifies the file locations used in the OpenArray™ AccuFill™ Software.

Set up the default file locations and preferences before using the QuantStudio™ 12K Flex OpenArray™ AccuFill™ System for the first time.

1. Create the following four folders in a convenient location on the same computer drive as the OpenArray™ AccuFill™ Software:
   - `TPF Files`
   - `Sample Tracker 96-well Input`
   - `Sample Tracker 384-well CSV Files`
   - `Loaded TPF Files`

2. *(Optional)* Copy a template file into the OpenArray™ Sample Tracker Software folder.
   - Navigate to this folder on your computer: `<drive>:\Program Files (x86)\Applied Biosystems\OpenArray Sample Tracker\examples`.
   - Copy the `96-Well Sample Plate 1.csv` template file, which is provided with the OpenArray™ Sample Tracker Software.
   - Paste the template file into the `Sample Tracker 96-well Input` folder.

3. In the OpenArray™ Sample Tracker Software, select **View** ▸ **Preferences**, then enter the following preferences:

Field	Selection
Experiment Type	**Gene Expression**
OpenArray™ Plate	Select the OpenArray™ format that will be run most often, such as **Gene Expression – 112.**
Pipettor	**Fixed** or **Adjustable** tip spacing
Import Data Directory	**Sample Tracker 96-well Input**
Export Data Directory	**Sample Tracker 384-well CSV Files**

4. In the OpenArray™ AccuFill™ Software, select **Instrument** ▸ **Edit Preferences** ▸ **Require Sample Integration**, then select the folders indicated in this table:

OpenArray™ AccuFill™ Software folder	Default folder	Folder contents
`OpenArray Plate File Input Folder`	`TPF Files`	TPF files for the OpenArray™ Plates, with assay name and location
`Sample Plate File Folder`	`Sample Tracker 384-well CSV Files`	CSV 384-well sample plate layout files
`Loaded OpenArray Plate File Folder`	`Loaded TPF Files`	Integrated TPF files generated during processing with the OpenArray™ AccuFill™ Software.

5. In the QuantStudio™ 12K Flex Software, select **Tools** ▸ **Preferences** ▸ **OpenArray**, then select the **Loaded TPF Files** folder for the software **Setup Folder**.

Note: If the QuantStudio™ 12K Flex Software is not on the same computer as the OpenArray™ AccuFill™ Software, transfer the loaded TPF files to the computer running the QuantStudio™ 12K Flex Software.

Obtain TPF files

Go to **thermofisher.com/OA-platefiles** to obtain the TPF files for the TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate.

Set up the optimized folder locations and software preferences before downloading TPF files to your computer. See “Set up default folders and software preferences” on page 25.

Generate 384-well sample plate layouts in the OpenArray™ Sample Tracker Software

Before generating 384-well sample plate layouts, see “One-time procedures” on page 25 to complete the following tasks:

- Set up optimized folder locations and software preferences.
- Download the TPF files for the OpenArray™ Plates into the TPF Files folder.

1. Using a spreadsheet program, create a 96-well sample CSV file.
   a. Navigate to the following folder, then open the `96-Well Sample Plate 1.csv` template that is provided with the OpenArray™ Sample Tracker Software.

      <drive>`:\Program Files (x86)\Applied Biosystems\OpenArray Sample Tracker\examples`

   b. **Save As** the template as a new 96-well sample CSV file. Save your 96-well sample CSV file in the **Sample Tracker 96-well Input** folder.

   c. Enter or copy the sample names into your 96-well sample CSV file.
2. Open the OpenArray™ Sample Tracker Software.
3. In the **Properties** screen, select **Gene Expression** for **Experiment Type**, then select the appropriate settings for **OpenArray™ Plate** and **Pipettor**.
4. In the **Samples** screen, click  **Import**, then select and import your 96-well sample CSV file that you created in step 1.
5. In the **Sample Mapping** screen, confirm that the samples for a single OpenArray™ Plate are assigned to one color.

   Note: If necessary, correct the **OpenArray™ Plate** and **Pipettor** settings in the **Properties** screen.
6. In the **Sample Mapping** screen, click the **384-Well Plate** tab, then click **Export** ▸ **Export *.csv**.
7. Select **384-Well Plate (for AccuFill)**, enter a file name, then save the exported file.

Plate layouts for the 384-well sample plates are saved to individual CSV files in the **Sample Tracker 384-well CSV Files** folder.

Set up the PCR reactions in an OpenArray™ 384-well Sample Plate (OpenArray™ AccuFill™ Software v1.2)

IMPORTANT! The 4 × 12 area(s) of the OpenArray™ 384-well Sample Plate being filled must match the area(s) designated in the OpenArray™ Sample Tracker Software for that set of samples.

1. Remove an OpenArray™ Plate from the freezer and set it aside. Allow it to come to room temperature in its unopened sleeve (~15 minutes).

   The OpenArray™ Plate must be completely thawed before transferring reactions to it from the OpenArray™ 384-well Sample Plate created in this section.

2. Gently swirl the contents of the TaqMan™ OpenArray™ Real-Time PCR Master Mix to thoroughly mix. Do not invert the bottle.

3. Following the plate layout designated in the OpenArray™ Sample Tracker Software, add master mix, then DNA samples, to the wells of an OpenArray™ 384-well Sample Plate.

   (Optional) Use the TrueMark™ Respiratory Panel 2.0 Amplification Control in place of diluted preamplified sample, as a positive amplification control sample.

Component	Volume per well	Volume per sample
TaqMan™ OpenArray™ Real-Time PCR Master Mix	2.5 µL	5.0 µL
Diluted preamplified sample	2.5 µL	5.0 µL
Total reaction volume	**5.0 µL**	**10.0 µL**

   Note: An overage is recommended when preparing the components.

4. Thoroughly mix each PCR reaction by pipetting up and down or by using the "mix" function on a multi-channel pipette.

5. Seal the OpenArray™ 384-well Sample Plate with an aluminum foil seal, remove the foil flap, then mark the edges of the filled 4 × 12 area with a pen.

6. Centrifuge the plate at 1,200 × *g* for 1 minute.

7. Score the foil along the lines that were marked before centrifuging.

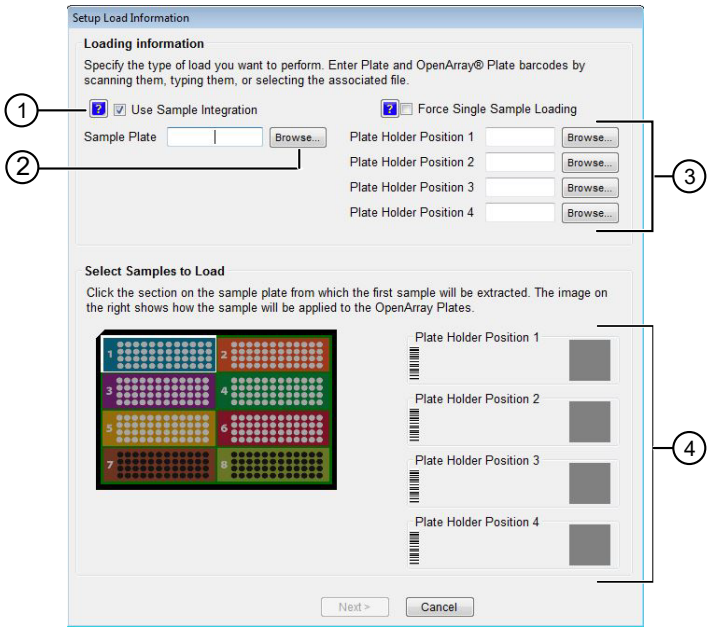
   Do not remove the foil from the scored area at this time.

If you make a sample layout error before the AccuFill™ procedure – Repeat “Generate 384-well sample plate layouts in the OpenArray™ Sample Tracker Software” on page 27 with a corrected 96-well sample CSV file.

Set up the OpenArray™ AccuFill™ Instrument and the OpenArray™ AccuFill™ Software

IMPORTANT! Do not use OpenArray™ AccuFill™ System Tips that exceed the expiration date (shown on the outer box that contains the tip trays).

1. In the OpenArray™ AccuFill™ Software, click **Setup and Load**.
   The **Setup Load Information** window appears.



① **Use Sample Integration** checkbox; select to integrate TPF files and the 384-well sample plate CSV file.

② **Browse** button; click to locate and select the 384-well sample plate CSV file. The button is displayed only if **Use Sample Integration** is selected.

③ **Browse** buttons; click to locate and select the TPF files for the OpenArray™ Plates that will be placed in the corresponding **Plate Holder Position** on the deck of the OpenArray™ AccuFill™ Instrument. The buttons are displayed only if **Use Sample Integration** is selected.

④ **Plate Holder Position** corresponding to the position of the OpenArray™ Plate on the deck of the instrument.

2. Configure the **Loading Information** pane for sample integration using the 384-well sample plate CSV file and TPF files.
   a. In the **Loading Information** pane (top section of the window), ensure that the **Use Sample Integration** checkbox is selected.

   b. Click **Browse** to the right of the **Sample Plate** field, then select the 384-well sample plate CSV file that you generated with the OpenArray™ Sample Tracker Software in the Sample Tracker 384-well CSV Files folder.

   c. Click **Browse** to the right of the **Plate Holder Position** of the OpenArray™ Plate, then select the TPF file for the OpenArray™ Plate in the TPF Files folder.

3. In the **Select Samples to Load** pane (bottom section of the window), click the corresponding 4 × 12 area of the 384-well sample plate image, then click **Next**.
   The **Setup Deck** window is displayed.

4. In the OpenArray™ AccuFill™ Instrument, ensure that:
   - Tip boxes and tips are loaded as shown in the **Setup Deck** window.
   - The lids are removed from the tip boxes.
   - The waste bin in the instrument is emptied.

5. In the **Setup Deck** window, confirm that the deck is ready:
   - Select **The tips are configured as shown above**.
   - Select **The Waste Bin is empty**.

Transfer reactions to the OpenArray™ Plate using the OpenArray™ AccuFill™ Instrument

IMPORTANT! Ensure that the OpenArray™ Plate is thawed and that the entire plate is at room temperature.

1. Prepare the items needed to seal the loaded OpenArray™ Plate (next section).

   Note: The OpenArray™ Plate must be sealed promptly after being loaded with the reactions, as described here.

   - Ensure that the QuantStudio™ 12K Flex OpenArray™ Plate Press 2.0 is ready.
   - Gather and remove from their packaging the following: an OpenArray™ Lid, plug, syringe with OpenArray™ Immersion Fluid, and syringe tip.
   - Attach the syringe tip to the syringe, carefully push some of the fluid through the tip to remove air bubbles, then lay the syringe aside.

2. Load the OpenArray™ Plate and the OpenArray™ 384-well Sample Plate into the OpenArray™ AccuFill™ Instrument.
   - **OpenArray™ Plate**—Remove the plate from its sleeve, then place the plate in the appropriate plate holder position in the instrument.
     Ensure that the barcode on the OpenArray™ Plate is facing left and the serial number is facing right.
   - **OpenArray™ 384-well Sample Plate**—Place the 384-well sample plate onto the deck of the instrument, then use forceps to peel the foil from the filled area of the plate.

3. Close the door of the instrument.

4. In the OpenArray™ AccuFill™ Software **Setup Deck** window, select the following confirmations:
   - **The OpenArray Plate is in the Plate Holder**
   - **Remove foil from the highlighted section of the Sample Plate**

5. Click **Load**.

6. As soon as the **Remove OpenArray Plate** window appears, open the instrument door and remove the loaded OpenArray™ Plate.

7. Proceed immediately to seal the OpenArray™ Plate.
   See “Seal the OpenArray™ Plate” on page 41.

Note: For best results, seal the OpenArray™ Plate within 90 seconds of completion of loading to prevent evaporation.

---

5 Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v2.0

For required materials, see “Materials required for OpenArray™ Plate workflow” on page 13.

For instructions for OpenArray™ AccuFill™ Software v1.2, see Chapter 4, “Prepare the OpenArray™ Plates with OpenArray™ AccuFill™ Software v1.2”.

This chapter describes the full run workflow. For other workflow options, see the following documentation.

This chapter contains brief procedures. For detailed procedures, see the following documentation.

Document	Pub. No.
QuantStudio™ 12K Flex Real–Time PCR System: OpenArray™ Experiments User Guide	4470935
QuantStudio™ 12K Flex OpenArray™ AccuFill™ System User Guide	MAN0025669
OpenArray™ AccuFill™ Software v2.0 Quick Run Workflow Without Sample Information Quick Reference	MAN0025835
OpenArray™ AccuFill™ Software v2.0 Full Run Workflow Quick Reference	MAN0025836

Download TPF files

The TPF files are downloaded directly from **thermofisher.com/OA-platefiles** based on an order.

The computer with the OpenArray™ AccuFill™ Software v2.0 must be connected to the internet.

1. In the **TPF/SPF** screen, select the **Download** radio button.
2. Select the product.
   - **TaqMan OpenArray Custom**
   - **TaqMan OpenArray Inventoried**

3. Enter the following information.

Product	Information
TaqMan OpenArray Custom	a. Enter the ***Lot number*** or ***Batch number***. b. Enter one ***Serial number*** from the lot. **Note:** Only one serial number is required. The serial number is used to confirm the lot number or batch number. All of the files in the lot or batch are downloaded.
TaqMan OpenArray Inventoried	Enter the list of ***Serial numbers*** or ***Barcodes***. Separate more than one serial number or barcode with a comma or a line break. **Note:** The serial number or barcode entered corresponds to the file that is downloaded. Enter a serial number or barcode for each file to download.

Note: The fields that are displayed depend on the product selected in step 2.

4. *(Custom Gene Expression plates only)* Select one of the following options:
   - **With microbial target names**
   - **Without microbial target names**

Note: The microbial target name selection is not displayed if inventoried products are selected.

5. Click **Download**.

The location of the files is displayed at the top of the screen. The location of the downloaded files is set in the **Preferences** menu, in the **OpenArray plate file folder** field. See *QuantStudio™ 12K Flex OpenArray™ AccuFill™ System User Guide* (Pub. No. MAN0025669) for more information about setting the preferences.

The files are in a compressed ZIP folder.

Click **Open folder** to access the files or click ✕ **(Close)** to close the message.

Extract the files from the compressed ZIP folder.

Set up the PCR reactions in an OpenArray™ 384-well Sample Plate (OpenArray™ AccuFill™ Software v2.0)

IMPORTANT! The 4 × 12 area(s) of the OpenArray™ 384-well Sample Plate being filled must match the area(s) designated in the OpenArray™ AccuFill™ Software for that set of samples.

1. Remove an OpenArray™ plate from the freezer and set it aside. Allow it to come to room temperature in its unopened sleeve (~15 minutes).

   The OpenArray™ plate must be completely thawed before transferring reactions to it from the OpenArray™ 384-well Sample Plate created in this section.

2. Gently swirl the contents of the TaqMan™ OpenArray™ Real-Time PCR Master Mix to thoroughly mix. Do not vortex the bottle.

3. Following the designated sample plate layout, add master mix, then DNA samples, to the wells of an OpenArray™ 384-well Sample Plate.

   (Optional) Use the TrueMark™ Respiratory Panel 2.0 Amplification Control in place of diluted preamplified sample, as a positive amplification control sample.

Component	Volume per well	Volume per sample
TaqMan™ OpenArray™ Real-Time PCR Master Mix	2.5 µL	5.0 µL
Diluted preamplified sample	2.5 µL	5.0 µL
Total reaction volume	**5.0 µL**	**10.0 µL**

   Note: An overage is recommended when preparing the components.

4. Thoroughly mix each PCR reaction by pipetting up and down or by using the "mix" function on a multi-channel pipette. Alternatively, vortex the OpenArray™ 384-well Sample Plate for 10–15 seconds after sealing with aluminum foil in step 5.

5. Seal the OpenArray™ 384-well Sample Plate with an aluminum foil seal, remove the foil flap, then mark the edges of the filled 4 × 12 area with a pen.

6. Centrifuge the plate at 1,200 × *g* for 1 minute.

7. Score the foil along the lines that were marked before centrifuging.

   Do not remove the foil from the scored area at this time.

If you make a sample layout error, it is possible to correct this in the OpenArray™ AccuFill™ Software using the plate rotation feature. For more information, see *QuantStudio™ 12K Flex OpenArray™ AccuFill™ System User Guide* (Pub. No. MAN0025669).

Before you begin—full run workflow

- Prepare samples in an OpenArray™ 384-well plate (see "Set up the PCR reactions in an OpenArray™ 384-well Sample Plate (OpenArray™ AccuFill™ Software v2.0)" on page 34).
- Place the sample plate in the sample plate holder on the AccuFill™ instrument deck, with the notch to the left.

  Do not stack sample plates.
- Load the tip boxes, then remove the tip box covers.

  Do not stack the tip boxes.
- Place the OpenArray™ Plates in the plate holders.
- Clear the instrument deck, empty and replace the waste bin, then close the instrument door.
- Allow the instrument to perform a self-test if the run is being started after the software is launched.
- Prepare the QuantStudio™ 12K Flex OpenArray™ Accessories Kit materials prior to uncovering tip boxes and removing OpenArray™ plates from packaging.

  These materials are used to seal the OpenArray™ Plates.

  IMPORTANT! OpenArray™ Plates must be sealed immediately after loading.

Configure the experiment design for the full run workflow

A TPF file *is* required for this workflow.

Navigate to the **Full Run** screen.

1. In the **Configure design** pane, in the **Experiment type** section, select **Gene expression**.
2. In the **Plate format** section, select a format.

   The values in the **Plate format** section depend on the experiment type that was selected in step 1.
3. If the **Pipettor** section is displayed, select a type of pipette.
   - **Fixed**
   - **Adjustable**
4. In the **Add your OpenArray Plate serial numbers** section, click **Choose File**, navigate to the location of the TPF file, then select the file.

   Repeat for each TPF file.
5. In the **Add your sample plates - optional** section, click **Choose File**, navigate to the location of the CSV file, then select the file.

   The format of the sample plate file is validated. For information about the required format, see the *QuantStudio™ 12K Flex OpenArray™ AccuFill™ System User Guide* (Pub. No. MAN0025669).

   The name of the file is displayed in the **Select file** field.

6. Repeat step 5 for each CSV file.
7. Click **Next**.

The **Map plates** pane is displayed.

Proceed to "Add or edit sample names" on page 36.

Add or edit sample names

If needed, navigate to the **Map plates** pane in the **Full Run** screen.

If a sample plate file was imported, the sample names are displayed. The sample plate layout defined in the sample plate file can be edited.

If the sample plate file was not imported, the samples must be added manually.

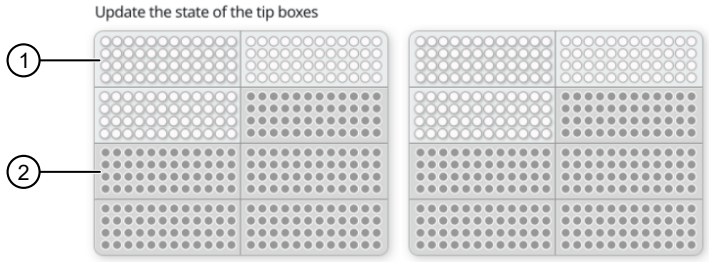
1. Add or edit the sample name.
2. Click **Next**.

Proceed to "Verify the run setup and start the run" on page 36.

Verify the run setup and start the run

1. Click each tip box section so that the status on the **Verify and start run** pane matches the physical tip box in the instrument.

   We recommend starting the run with full tip boxes. The instrument does not start the run if there are not enough tips on the deck.



① Section of the tip box that is full.
② Section of the tip box that is empty.

2. *(Optional)* Click **Auto-fill tip boxes**.

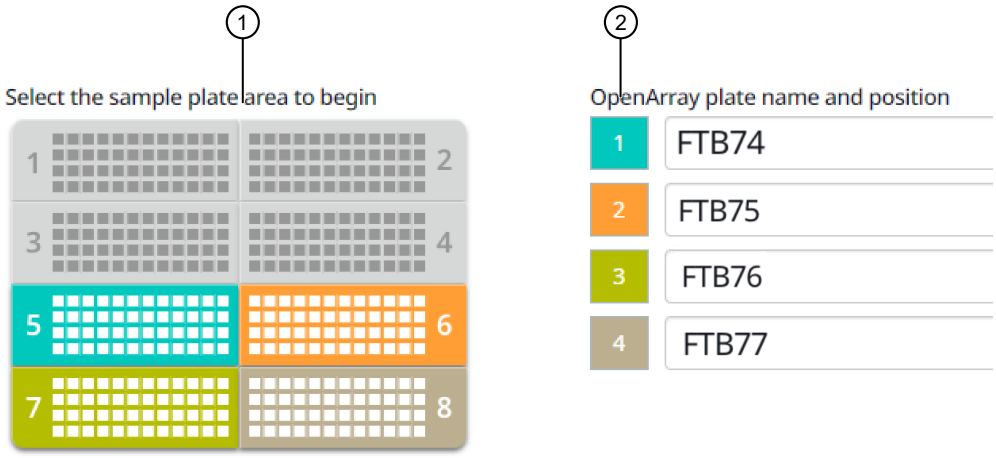
   The status of all sections of the tips boxes is set to full.

3. Select the first section of the sample plate to be used to fill the OpenArray™ Plate.

   Select the first section of the sample plate if multiple plates are filled during a run. The software selects the total number of sections that correspond with the total number of plates.

In the following example, section 5 was selected. The group of sections 5, 6, 7, and 8 is highlighted by the software because four plates are being filled.

The position box displays the color that corresponds to the section of the sample plate.



① Sample plate section (section 5, 6, 7, and 8 are highlighted).
② Corresponding plates.

4. Remove the foil from the appropriate sections of the sample plate, then click the checkbox to confirm.

   Remove the foil only from the sections of the sample plate that are used to load a single OpenArray™ Plate.

   Note: Do not remove the foil from all the sections of the sample plate at once.

5. Close the instrument door.

6. Click **Start Run**.

   The run does not begin under any of these conditions.

   - The waste bin is not in position.
   - The sample plate is not in position.
   - The plates are not in position.
   - There are more plates on the instrument deck than are defined in the experiment setup.

The **Deck** screen is displayed.

For a description of the run progress, see *QuantStudio™ 12K Flex OpenArray™ AccuFill™ System User Guide* (Pub. No. MAN0025669).

IMPORTANT! Each OpenArray™ Plate must be prepared for PCR immediately after it is filled (see “Remove the OpenArray™ Plate from the OpenArray™ AccuFill™ Instrument” on page 38).

Remove the OpenArray™ Plate from the OpenArray™ AccuFill™ Instrument

After an OpenArray™ Plate is filled, the **Remove plate and foil** dialog box is displayed (see Figure 1).

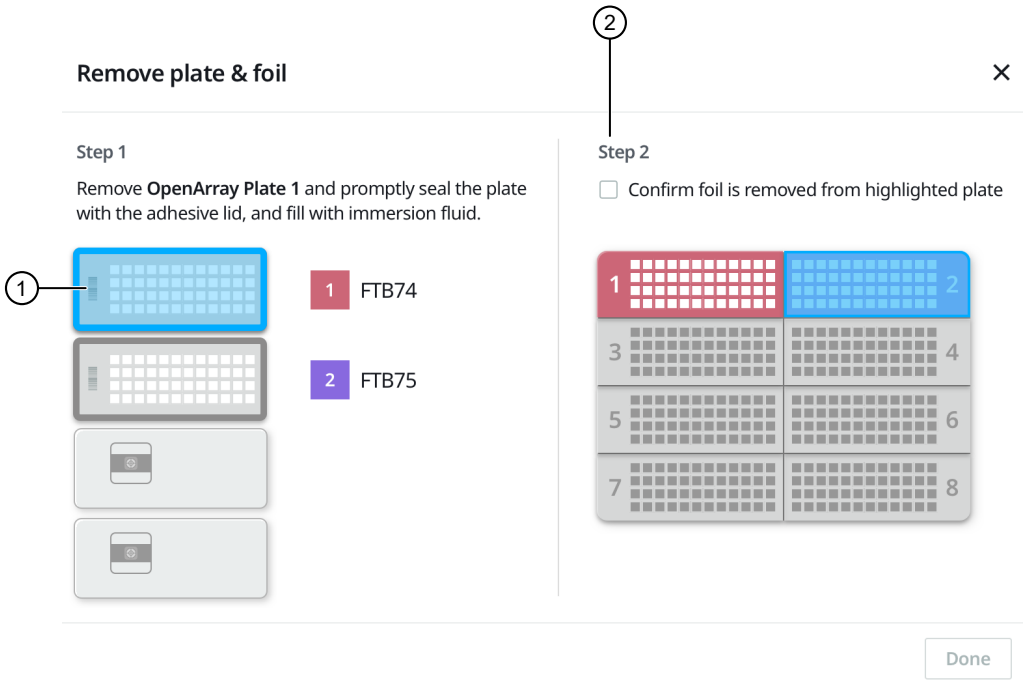


Figure 1 Remove plate and foil dialog box.

① OpenArray™ Plate to remove from the instrument.
② **Confirm foil is removed from highlighted plate section** checkbox.

Remove each OpenArray™ Plate *immediately* after it has been filled, even if the run was set up to fill multiple plates.

After the last OpenArray™ Plate in the run is filled, the **Remove plate** dialog box is displayed (see Figure 2).

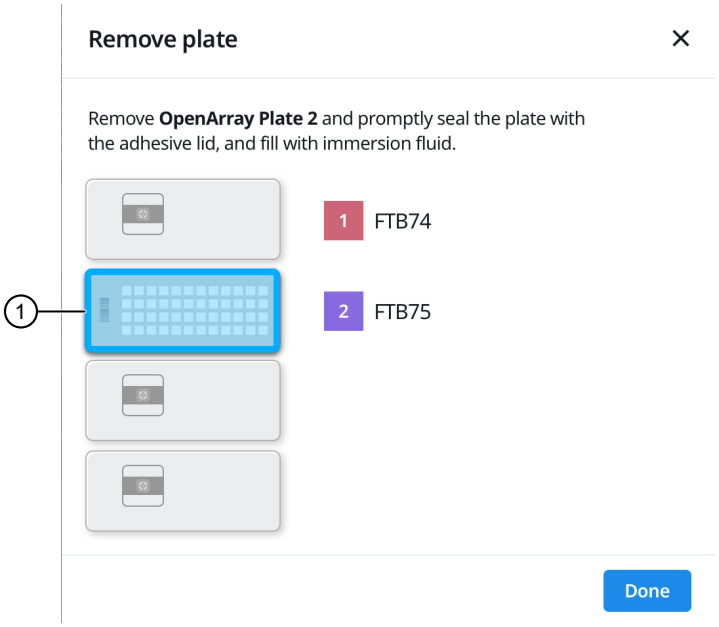


Figure 2 Remove plate dialog box

① OpenArray™ Plate to remove from the instrument

1. Open the instrument door and remove the OpenArray™ Plate that is indicated by the blue box in the dialog box.

   IMPORTANT! Remove the OpenArray™ Plate immediately, to avoid evaporation within the plate.

   One of the following dialog boxes is displayed:

   - The **Remove plate and foil** dialog box.
   - The **Remove plate** dialog box (after the last OpenArray™ Plate is filled).

2. Seal the case and fill the OpenArray™ Plate with immersion fluid.

   See “Seal the OpenArray™ Plate” on page 41.

3. *(For **Remove plate and foil** dialog box only)* Remove the foil seal from the next section of the sample plate, then select the checkbox to confirm that the foil is removed from the section of the plate that is highlighted.

   Note: Remove the foil only from the next section of the sample plate. Do not remove the foil from all sections of the sample plate.

4. Close the instrument door.

5. Click **Done**.

   The run does not proceed under any of the following conditions:

   - The waste bin is not in position
   - The sample plate is not in position
   - The plates are not in position
   - There are more plates on the instrument deck than are defined in the experiment setup

   The instrument proceeds to load the next OpenArray™ Plate.

6. Repeat step 1 to step 5 for each OpenArray™ Plate to be loaded.

After all of the plates have been loaded, the **Deck** screen displays **Run completed successfully. Empty the waste bin before performing another run.**

A loaded TPF is generated for each OpenArray™ Plate. The loaded TPF file corresponds to the original TPF file that was imported for the run. The files are exported to the folder that was designed in the **Preferences**.

Note: Some workflows might not generate a loaded TPF file. For more information about the workflows available for the OpenArray™ AccuFill™ Software v2.0, see *QuantStudio™ 12K Flex OpenArray™ AccuFill™ System User Guide* (Pub. No. MAN0025669).

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6 Seal and run the OpenArray™ Plates

Seal the OpenArray™ Plate

IMPORTANT! Throughout this procedure, handle the OpenArray™ Plate and the OpenArray™ Case only by the edges.

Note: The OpenArray™ Case consists of the sealed OpenArray™ Plate and the OpenArray™ Lid.

1. Place the newly loaded OpenArray™ Plate in the QuantStudio™ 12K Flex OpenArray™ Plate Press 2.0.

   Ensure that the barcode is facing left and the serial number is facing right.

2. From the OpenArray™ Lid, remove the clear protective film from the *inside* of the lid ① and the red adhesive-protective strip ② from around the edge of the lid.

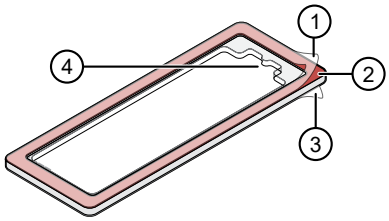
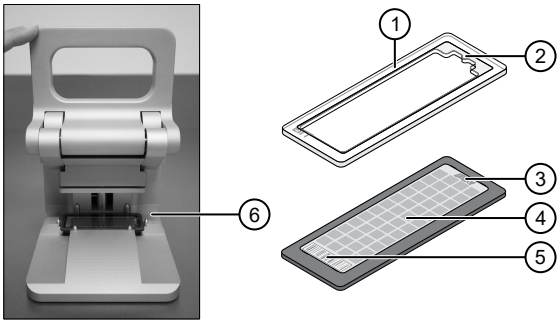


Figure 3 OpenArray™ Lid

① Protective film on inside of the lid (remove before *sealing*)
② Red adhesive-protective strip (remove before *sealing*)
③ Protective film on the outside of the lid (remove before *running*)
④ Notched end (align with serial number on plate)

3. Place the lid in the Plate Press using the alignment pins of the Plate Press for orientation.

IMPORTANT! The notched end of the case lid must be oriented towards the furthest back right-side of the Plate Press.



① OpenArray™ case lid
② Notched end of lid
③ Serial number of plate
④ OpenArray™ Plate
⑤ Barcode of plate
⑥ Alignment pins

4. Seat the lid on the OpenArray™ Plate with the lid adhesive against the plate.

5. Engage the press mechanism until the green flashing light changes to a steady green light (after 20 seconds).

   The status light turns solid green, indicating that the case is sealed.

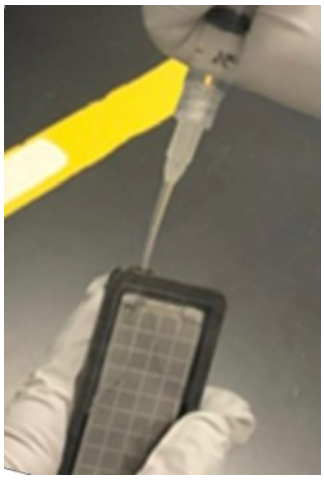
Note: Do not apply additional pressure onto the Plate Press during its actuation.

6. Disengage the press and carefully remove the OpenArray™ Case.

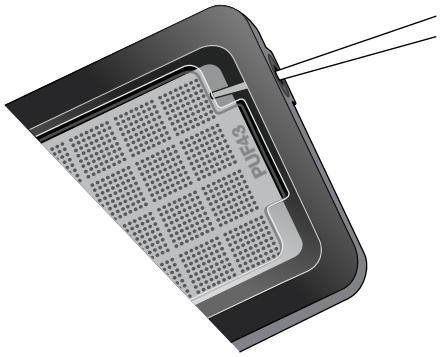
7. Prepare the immersion fluid. Remove the cap, insert the accompanying syringe tip, and prime the syringe by ejecting a small amount of immersion fluid onto a paper towel to ensure no air gap remains in the newly attached pipette tip.

IMPORTANT! If the syringe is not primed, the direct burst of air and fluid can negatively affect the assay(s) at the end of the array.

8. While holding the case upright by its edges at a 15–30 degree angle so that the port is at the highest point of the array, insert the prepared syringe tip into the port in the case.



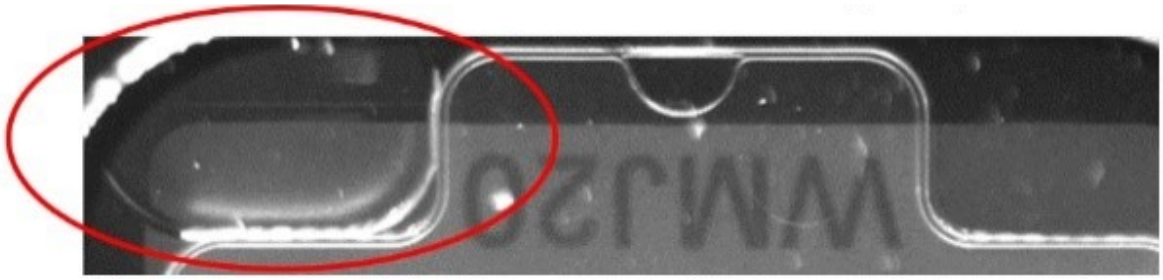
The syringe tip must be in front of the array when filling the case with immersion fluid.



9. Slowly inject the OpenArray™ Immersion Fluid until the case is filled, which should take about 10 seconds to fill. Minimize the creation of additional air bubbles when you dispense the fluid. Leave a small air bubble as shown below.

IMPORTANT! If injected too quickly, the fluid can flush out the samples that are suspended in the through-holes.

Overfilling the array and/or not leaving a small bubble may cause a leak during the PCR run.



10. While holding the case *vertically*, remove the syringe tip, insert the screw end of the OpenArray™ plug into the port of the case, then rotate clockwise until the black handle breaks off.

    Note: Ensure that you are screwing the plug in at the same angle the case base is at. If it is off, it can cause the plug to break off prematurely.

    IMPORTANT! To avoid leaking of immersion fluid, hold the case *vertically* and rotate the plug slowly to avoid cross-threading.

    If the plug handle breaks off prematurely, use a Phillips #0 screwdriver to complete this step. Do not overtighten. If plastic or adhesive remains attached to the screw due to premature breakout of the plug handle, remove it with forceps prior to loading it into the instrument.

11. If needed, clean the case with the lint-free cloth included with the OpenArray™ Plate or a laboratory wipe that has been thoroughly sprayed with ethanol, then dry the case with a clean laboratory wipe.

Run the OpenArray™ Plate on the QuantStudio™ 12K Flex Instrument

You can run up to four OpenArray™ Plates at one time on the QuantStudio™ 12K Flex Instrument.

1. On the QuantStudio™ 12K Flex Instrument touchscreen, touch  to extend the instrument tray arm.
2. Remove the clear protective film from the outside of the OpenArray™ case (sealed plate + lid).
3. Place the OpenArray™ case on the tray arm plate adapter.
   - Support the case from underneath the tray arm to prevent the case from slipping through the adapter.
   - Ensure that the plate barcode and serial number are facing the front of the instrument.
4. Touch  to retract the instrument tray arm.
5. In the  **Home** screen of the QuantStudio™ 12K Flex Software, in the **Run** pane, click **OpenArray**.
6. In the **Select Instrument** pane, select your instrument.
7. Click **Get Plate IDs** to import the barcode of the OpenArray™ Plate.
   Once the OpenArray™ serial number appears, the loaded TPF file corresponding to the plate should appear in the **Setup File** field.
   If the TPF file does not appear, click **Browse**, then select the correct loaded TPF file from the **Loaded TPF** folder.
8. *(Optional)* Click **Browse** to change the **Experiment File Location**.
9. *(Optional)* Change the software-determined **Experiment File Name**.

10. Click **Start Run**.

    Note: The instrument pauses at 41 or 42 seconds prior to the end of the run. Wait for the system to complete the run before opening the EDS file.

11. Transfer the EDS file from the instrument to an accessible location for analysis.

12. Check the QC images for loading issues or leaks.

Check the quality–control images

Check the quality–control (QC) images before analysis. Images can be viewed using ImageJ, an open–source software available from the NIH at **imagej.nih.gov/ig**. For additional information, see Appendix A, “Troubleshooting”.

1. In the QuantStudio™ 12K Flex Software  **Export** screen, click **Browse**, then create a uniquely–named folder for the QC images export.

   IMPORTANT! Create a new folder for images each time. Exporting a second run to the same folder overwrites the images.

2. Click **Export QC Images** at the bottom of the screen.

3. View the following ROX™ image to check for loading quality issues:
   - POST-READ_CHANNEL_4.tiff

4. Check the following spotfinding images for leaks or other displaced sample issues.
   - s02_c001_t03_p0001_m1_x2_e1_cp#_spotfind.tiff
   - s02_c040_t03_p0001_m1_x2_e1_cp#_spotfind.tiff

   Note: The “cp#” in the image file name refers to array positions 1 through 4 within the instrument.

5. If a problem is found, view the following pre-run spotfinding image to determine whether the issue existed before cycling:
   - s00_c001_t01_p0001_m2_x3_e1_cp#_spotfind.tiff

6. View the following FAM™ images to check for fluorescent abnormalities and to confirm any problem seen in the spotfinding images:
   - STAGE2_CYCLE1_CHANNEL_1.tiff
   - STAGE2_CYCLE40_CHANNEL_1.tiff

7. Note any abnormalities found, as well as all other potentially relevant information related to the setup of the run.

7 Analyze data

Select analysis software

Software	Analysis option	
	C_{rt}	QC metrics
Relative Quantification Application (recommended)[1] Access the application at thermofisher.com/connect.	✓	✓
QuantStudio™ 12K Flex Software	✓	✓

[1] To perform data analysis using the application, you must export your data. For detailed instructions about exporting data, see "Export data (if necessary)" on page 46.

Export data (if necessary)

Export your data to review it using the pivot table feature of a spreadsheet program.

1. Open an EDS file in the QuantStudio™ 12K Flex Software.
2. In the **Experiment Menu** pane, click **Export**.
3. Click **Load Export Set** (bottom of the screen), select **GE_export_setting**, then click **OK**.
4. Select **.xlsx** from the **File Type** dropdown list (top-right of the screen).
5. *(Optional)* Perform any of the following actions to customize the file export.
   - Click **Browse** to select a new **Export File Location**.
   - Enter a new file name in the **Export File Name** text field.
   - Click the **Results** tab, then select the content to export.
6. Click **Start Export** (bottom of the screen).
   If **Open file(s) when export is complete** is selected, then the file automatically opens. If the option is not selected, navigate to and open the exported XLSX file.

Review results

Note: These guidelines apply to results from experiments that included three or more technical replicates.

1. In the analysis settings of the software, choose the relative C_{rt} method.

   The relative C_{rt} method is recommended for dried-down assays. Dried-down assays can reconstitute at different rates, causing a dip in the early cycles of the baseline. C_{rt} can correct for a variable baseline.

   - In Relative Quantification Application :
     a. Click **(Analysis Settings)**.
     b. In the **C_q Settings** tab, select **Use C_{rt}**.
     c. Click **Finish**.
   - In QuantStudio™ 12K Flex Software— select **Analysis Settings ▸ Ct Settings ▸ Algorithm Settings ▸ Relative Threshold**.

2. Review amplification curves (in log or linear view), C_{rt} values, and amplification curve QC metrics (Amp Score and C_q Confidence) for each reaction.

QC metric	Description
Amp Score	A value to indicate the quality of the amplification curve.
C_q Confidence	A value to reflect the reliability of the derived C_q.

3. *(Optional)* Filter data in the order indicated in the following table.

Note: We encourage testing and establishing your own C_{rt} cut-off value and amplification curve QC metrics for each assay to achieve high sensitivity and specificity.

Parameter to examine	Consider filtering out sample data using the following cut-off values
C_{rt}	$C_{rt} > 28$
Amp Score	Amp Score < 1.2 The following assays have a cut-off value of < 1.1 • RNase P (RPPH1) • Human Enterovirus (EV_pan)
C_q Confidence	C_q Conf < 0.7 **Note:** The following assays have a cut-off value of < 0.5 • RNase P (RPPH1) • Bordetella holmesii (B. holmesii)

Note:

- We encourage testing and establishing your own C_{rt} cut-off value for each assay to achieve high sensitivity and specificity.
- Through-holes with unexpected C_{rt} values can also be identified by reviewing the Amplification Plot (see "Troubleshoot unexpected Crt values" on page 51).

4. Note replicates with mean $C_{rt} \leq 25$ and a standard deviation > 0.5. The data from these through-holes might require further review.
5. Ensure that at least half of the replicates amplified adequately and pass your review specifications.
6. Use your preferred method to analyze the data.

Considerations for data analysis

Organisms that are covered by more than one assay

- For full strain coverage of adenoviruses or rhinoviruses, two assays are used. A positive result with either or both of the assays indicates a positive result for the organism.
- For SARS-CoV-2 detection, assays to the S-protein and N-protein genes each have high coverage of known strains. A positive with either or both assays indicates a positive result for SARS-CoV-2.

Species-specific assays that are also covered by pan or broad coverage assays

Species-specific assay	Considerations for data analysis
Flu A assays	• The Flu_A_pan assay detects Influenza A H1 and H3, for which there are also strain-specific assays. • Samples that are positive for the Flu_A_H1 or Flu_A_H3 assay typically are positive for the Flu_A_pan assay.
Bordetella assays	• The Bordetella assay detects *B. pertussis*, *B. bronchiseptica*, and *B. parapertussis* strains. Strain-specific assays for *B. pertussis* and *B. holmesii* are also available. • Most samples that are positive for the *B. pertussis* assay are also positive with the Bordetella assay.
RSV assays	• Samples that are positive for the RSVA assay may be detected at a lower efficiency (a difference of several C_{rt} values) by the RSVB assay.
Enterovirus (EV) and rhinovirus (RV) assays	• The RV assays detect both RV and EV strains whereas the EV assays are specific for EV strains. Thus, enterovirus positive samples are detected by both EV and RV assays whereas rhinovirus positive samples are detected only by the RV assays. • The EV_pan assay detects all human enterovirus species except D68, for which there is a strain-specific EV_D68 assay. • Samples that are positive for the EV_D68 assay may be detected at a lower efficiency (a difference of several C_{rt} values) by the EV_pan assay.

(continued)

Species-specific assay	Considerations for data analysis
Bacterial and HHV assays	• It is not unusual to detect *M. catarrhalis*, *H. influenzae*, *K. pneumoniae*, *S. pneumoniae*, and *S. aureus* in respiratory samples as these are commensal or transiently commensal upper respiratory tract microbes. • Due to the high prevalence of human infection with HHV4 (EBV) and HHV6 viruses, these viruses can be detected at low levels in some respiratory samples.

Approximate C_{rt} range for controls

If used as recommended in this guide, the approximate C_{rt} range for control assays are as follows.

Control	Approximate C_{rt} range
TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control	18-20
TaqMan™ Universal Extraction Control Organism (*B. atrophaeus*)	21-23
TrueMark™ Respiratory Panel 2.0 Amplification Control	18-21

Fields for reviewing results with pivot tables

To review results using the pivot table feature of a spreadsheet program, you can use the following settings.

Note: For the "Average of" and "StdDev of" summarizations, use the appropriate source field (**C_{rt}**, **Amp Score**, or **C_q Conf**), then choose the calculation type.

Area of pivot table	Fields to add	
	Target-oriented view	Sample-oriented view
Filters	—	**Sample Name**[1]
Columns	**Sample Name**	—
Rows	**Target Name**	**Target Name**
Values	**Average of C_{rt}**	**Average of C_{rt}**
	StdDev of C_{rt}[2]	**StdDev of C_{rt}**[2]
	Count of C_{rt}	**Count of C_{rt}**

(continued)

Area of pivot table	Fields to add	
	Target-oriented view	Sample-oriented view
Values	—	Average of Amp Score
	—	Average of C_q Conf

[1] To see individual sample results, select the sample from the dropdown list next to the **Sample Name** header.

[2] A **Values** field will automatically appear in the **Column Labels** area.

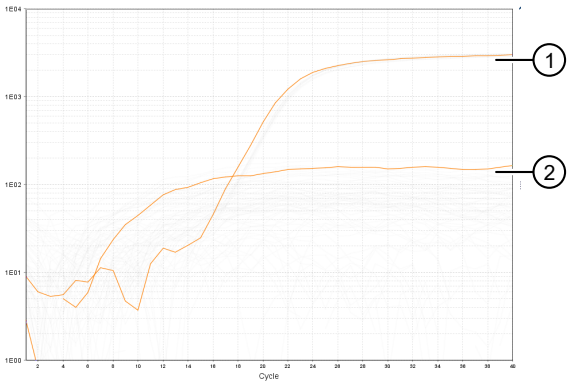
A

Troubleshooting

Troubleshooting: Nucleic Acid Isolation

Observation	Possible cause	Recommended action
Beads remain in sample after elution	Excessive amount of recovered host genomic DNA/RNA is preventing nucleic acid separation from the beads.	Increase elution volume to 100 µL.
		Reduce the input volume of starting sample to 200 µL.
Reduced extraction efficiency of TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control	Proteinase K enzyme was either omitted from the sample or added incorrectly.	Always add Proteinase K enzyme to the sample separately and before adding the Binding/Bead Master mix.
	TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control added at the wrong step.	Ensure that the TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control is added to the Binding/Bead Master mix before dispensing into sample wells.

Troubleshoot unexpected C_{rt} values

Observation	Possible cause	Recommended action
Unexpected C_{rt} values in the amplification plot  ① Expected C_{rt} value (noted in most replicates) ② Unexpected C_{rt} value (too low)	Unexpectedly low C_{rt} values (<10) — Signal variation or noise in early PCR cycles	Review amplification curves, Amp Score, and C_q Confidence values.
		Consider filtering C_{rt} values from analysis.
		Compare replicates, if available.
		Dilute the samples, then repeat the experiment.
	Unexpectedly high C_{rt} values (25–28) — Sporadic amplification	Review amplification curves, Amp Score, and C_q Confidence values.
		Compare replicates, if available.
		Repeat the experiment.

Troubleshoot with cycling and imaging run images (QC images)

Many problems with OpenArray™ results can be diagnosed by examining the quality control (QC) images taken at various points during a cycling/imaging run.

The QC images are fluorescent or reflected light images taken before, during, and after cycling. They may require adjustment to make image features visible. To view the images, we recommend that you install the free software program ImageJ, which allows you to easily manipulate the images in ways that other image viewers cannot.

1. In the QuantStudio™ 12K Flex Software **Export** screen  :
   a. Click **Browse** to select a uniquely-named folder for the QC images export.
   b. Click **Export QC Images** (bottom of screen).

IMPORTANT! Select a new folder for images each time; exporting a second run to the same folder overwrites the images.

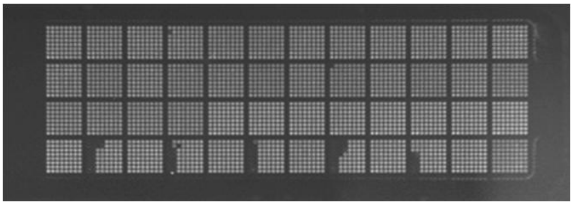
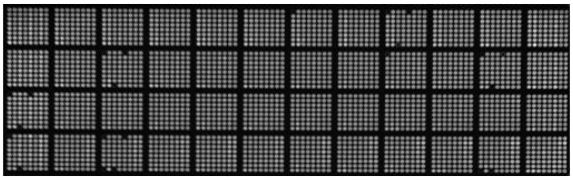
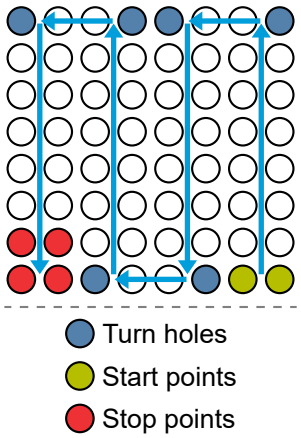
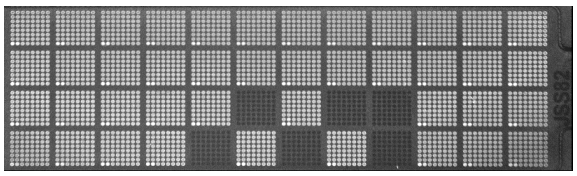
2. Use ImageJ to view the images of interest.

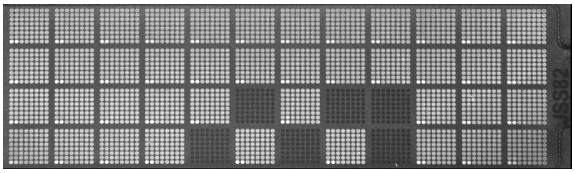
To...	View image...	Image description
Confirm the identity of images within a folder	BARCODE IMAGE.tiff	Reflected light image of the entire OpenArray™ Plate.
Evaluate the loading quality	PRE-READ_CHANNEL_4.tiff POST-READ_CHANNEL_4.tiff	Pre- and post-ROX™ dye images.
Check for existing contamination on the case and/or heated cover	s00_c001_t01_p0001_m2_x3_e1_cp#_spotfind.tiff[1]	Pre-run reflected light spotfinding image (used by the software to determine the location of the holes).
Identify potential leaks or other contamination	s02_c001_t03_p0001_m1_x2_e1_cp#_spotfind.tiff[1]	Mid-run reflected light spotfinding image.
	s02_c040_t03_p0001_m1_x2_e1_cp#_spotfind.tiff[1]	Post-run reflected light spotfinding image.
Look at patterns in the fluorescent data (for example, gradients)	STAGEx_CYCLEy_CHANNEL_1.tiff	FAM™ images at a particular cycle (y) of a particular stage (x) of the run.

[1] The "cp#" in the image file name refers to the array position (1–4) within the QuantStudio™ 12K Flex Real-Time PCR Instrument.

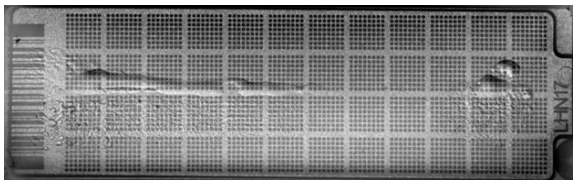
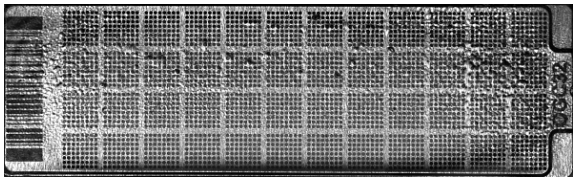
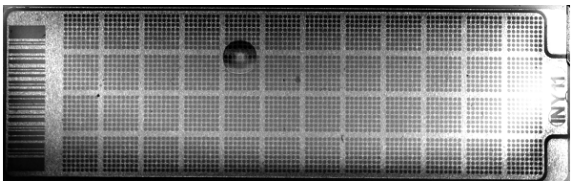
3. *(Optional)* Adjust the images for brightness and/or contrast to make image features visible.
   a. Open the image in ImageJ.
   b. Select **Image ▸ Adjust Brightness/Contrast** (or press **Ctrl+Shift+C**).
   c. Click **Auto** or adjust the sliders until the features of interest in the image are visible.

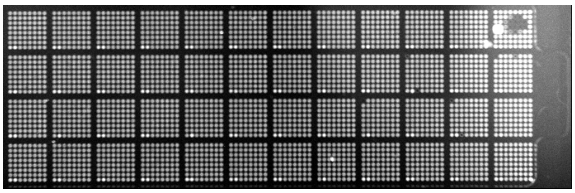
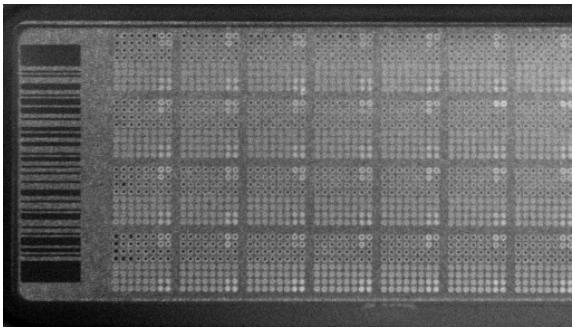
OpenArray™ AccuFill™ Instrument plate loading errors

Observation	Possible cause	Recommended action
There are empty through-holes 	Insufficient sample was added to the 384-well Sample Plate.	Use proper pipetting techniques. Ensure that there are no air bubbles in the pipette tips after sample aspiration.
	Reaction mix (sample + master mix) is not at the bottom of the 384-well Sample Plate.	Centrifuge the plate at 1,200 × *g* for 60 seconds.
Turn-holes are repeatedly missed 	The OpenArray™ AccuFill™ Instrument is aligned too far to the left or to the right. Systematic loading problems can occur with the OpenArray™ AccuFill™ Instrument, which indicates a need for service. For example, when turn-holes are repeatedly missed across multiple subarrays, service is required. Turn-holes are where the instrument changes direction during sample loading. 	Contact your local field service engineer.
Entire subarrays are missing 	The sample/master mix was not added to particular wells in the 384-well Sample Plate.	Visually inspect the plate to ensure that the wells have sample/master mix.
	Stuck tip mandrel on the OpenArray™ AccuFill™ Instrument may need cleaning.	Contact your local field service engineer.

Observation	Possible cause	Recommended action
Entire subarrays are missing  *(continued)*	Pipette tip was not loaded on mandrel.	Contact your local field service engineer for frequent occurrences (infrequent occurrences can be due to a poorly molded tip).

OpenArray™ Plate assembly and handling errors

Observation	Possible cause	Recommended action
Case leaks and bubbles inside the case    Improper sealing of the OpenArray™ Plate in the OpenArray™ Case can lead to immersion fluid leaks or bubble formation inside the case, leading to uneven heating and imaging throughout PCR and to poor quality data. The images above are examples of OpenArray™ Plates that have been affected by immersion fluid leaks. The images show where leaked fluid has condensed on the underside of the heated cover windows and obscured the view of the through-holes. The best image in which to detect leaks is the s02_c001_t03_p0001_m1_x2_e1_cp#_spotfind.tiff image. This image is taken at the start of cycling, which is where most leaks occur. See “Troubleshoot with cycling and imaging run images (QC images)” on page 52.	Plate press was not engaged for at least 20 seconds.	Fully engage the plate press for at least 20 seconds.
	Damaged lid adhesive.	Remove the liner and visually inspect the lid adhesives for defects. Ensure that adhesive is not damaged or warped.
	Damaged fill port screw gasket.	Visually inspect the screw to ensure that the orange gasket is present and not damaged.
	Damaged fill port screw assembly. Breaks off too easily.	The screw may be mis-threaded: unscrew it and use a new screw assembly.
	Oily lid or case from immersion fluid overflow.	Wipe off excess overflow of immersion fluid from the lid, case bottom, and crevices with 70% isopropyl alcohol, using a lint-free cloth (the cloth included with the OpenArray™ Plate is acceptable).
	Immersion fluid was exposed to air for too long.	Do not remove the immersion fluid syringe cap or draw air bubbles into the syringe until you are ready to load.
	Too large of a bubble inside the OpenArray™ Case after sealing.	Minimize the size of the bubble by tilting the OpenArray™ Case so that the fill port is at the highest point. Slowly fill the case with immersion fluid until only a small air bubble remains. Attach the screw and wipe off any excess oil that may have spilled onto the case.
	Damaged plate press, leading to uneven pressure.	Contact your field service engineer if you suspect that your plate press may be damaged.

Observation	Possible cause	Recommended action
Sample blow-out during the addition of immersion fluid 	The reactions in A12 were compromised during the addition of immersion fluid. Injecting the immersion fluid too quickly can purge the sample out of the through-holes near the fill port. Often this is caused by the user not purging the syringe slightly before use.	Dispense a small amount of immersion fluid onto a paper towel before use to ensure smooth operation of the syringe.
Evaporation of reaction mixture in through-holes 	Too much time elapsed before the plate was sealed with lid and immersion fluid. In this example, the top half of each subarray was intentionally left open to the environment to demonstrate the effect of evaporation. “Donuts” are a result of the evaporated fluid in the though-holes.	Add immersion fluid as soon as the case is removed from the plate press to minimize the likelihood of evaporation, then seal the case with the lid.

B

Safety

WARNING! GENERAL SAFETY. Using this product in a manner not specified in the user documentation may result in personal injury or damage to the instrument or device. Ensure that anyone using this product has received instructions in general safety practices for laboratories and the safety information provided in this document.

- Before using an instrument or device, read and understand the safety information provided in the user documentation provided by the manufacturer of the instrument or device.
- Before handling chemicals, read and understand all applicable Safety Data Sheets (SDSs) and use appropriate personal protective equipment (gloves, gowns, eye protection, and so on). To obtain SDSs, see the "Documentation and Support" section in this document.

Chemical safety

WARNING! GENERAL CHEMICAL HANDLING. To minimize hazards, ensure laboratory personnel read and practice the general safety guidelines for chemical usage, storage, and waste provided below. Consult the relevant SDS for specific precautions and instructions:

- Read and understand the Safety Data Sheets (SDSs) provided by the chemical manufacturer before you store, handle, or work with any chemicals or hazardous materials. To obtain SDSs, see the "Documentation and Support" section in this document.
- Minimize contact with chemicals. Wear appropriate personal protective equipment when handling chemicals (for example, safety glasses, gloves, or protective clothing).
- Minimize the inhalation of chemicals. Do not leave chemical containers open. Use only with sufficient ventilation (for example, fume hood).
- Check regularly for chemical leaks or spills. If a leak or spill occurs, follow the manufacturer cleanup procedures as recommended in the SDS.
- Handle chemical wastes in a fume hood.
- Ensure use of primary and secondary waste containers. (A primary waste container holds the immediate waste. A secondary container contains spills or leaks from the primary container. Both containers must be compatible with the waste material and meet federal, state, and local requirements for container storage.)
- After emptying a waste container, seal it with the cap provided.
- Characterize (by analysis if needed) the waste generated by the particular applications, reagents, and substrates used in your laboratory.
- Ensure that the waste is stored, transferred, transported, and disposed of according to all local, state/provincial, and/or national regulations.
- **IMPORTANT!** Radioactive or biohazardous materials may require special handling, and disposal limitations may apply.

AVERTISSEMENT ! **PRÉCAUTIONS GÉNÉRALES EN CAS DE MANIPULATION DE PRODUITS CHIMIQUES.** Pour minimiser les risques, veiller à ce que le personnel du laboratoire lise attentivement et mette en œuvre les consignes de sécurité générales relatives à l'utilisation et au stockage des produits chimiques et à la gestion des déchets qui en découlent, décrites ci-dessous. Consulter également la FDS appropriée pour connaître les précautions et instructions particulières à respecter :

- Lire et comprendre les fiches de données de sécurité (FDS) fournies par le fabricant avant de stocker, de manipuler ou d'utiliser les matériaux dangereux ou les produits chimiques. Pour obtenir les FDS, se reporter à la section « Documentation et support » du présent document.
- Limiter les contacts avec les produits chimiques. Porter des équipements de protection appropriés lors de la manipulation des produits chimiques (par exemple : lunettes de sûreté, gants ou vêtements de protection).
- Limiter l'inhalation des produits chimiques. Ne pas laisser les récipients de produits chimiques ouverts. Ils ne doivent être utilisés qu'avec une ventilation adéquate (par exemple, sorbonne).
- Vérifier régulièrement l'absence de fuite ou d'écoulement des produits chimiques. En cas de fuite ou d'écoulement d'un produit, respecter les directives de nettoyage du fabricant recommandées dans la FDS.
- Manipuler les déchets chimiques dans une sorbonne.

- Veiller à utiliser des récipients à déchets primaire et secondaire. (Le récipient primaire contient les déchets immédiats, le récipient secondaire contient les fuites et les écoulements du récipient primaire. Les deux récipients doivent être compatibles avec les matériaux mis au rebut et conformes aux exigences locales, nationales et communautaires en matière de confinement des récipients.)
- Une fois le récipient à déchets vidé, il doit être refermé hermétiquement avec le couvercle fourni.
- Caractériser (par une analyse si nécessaire) les déchets générés par les applications, les réactifs et les substrats particuliers utilisés dans le laboratoire.
- Vérifier que les déchets sont convenablement stockés, transférés, transportés et éliminés en respectant toutes les réglementations locales, nationales et/ou communautaires en vigueur.
- **IMPORTANT !** Les matériaux représentant un danger biologique ou radioactif exigent parfois une manipulation spéciale, et des limitations peuvent s'appliquer à leur élimination.

WARNING! **HAZARDOUS WASTE (from instruments).** Waste produced by the instrument is potentially hazardous. Follow the guidelines noted in the preceding General Chemical Handling warning.

Biological hazard safety

WARNING! **Potential Biohazard.** Depending on the samples used on this instrument, the surface may be considered a biohazard. Use appropriate decontamination methods when working with biohazards.

WARNING! **BIOHAZARD.** Biological samples such as tissues, body fluids, infectious agents, and blood of humans and other animals have the potential to transmit infectious diseases. Conduct all work in properly equipped facilities with the appropriate safety equipment (for example, physical containment devices). Safety equipment can also include items for personal protection, such as gloves, coats, gowns, shoe covers, boots, respirators, face shields, safety glasses, or goggles. Individuals should be trained according to applicable regulatory and company/ institution requirements before working with potentially biohazardous materials. Follow all applicable local, state/provincial, and/or national regulations. The following references provide general guidelines when handling biological samples in laboratory environment.

- U.S. Department of Health and Human Services, *Biosafety in Microbiological and Biomedical Laboratories (BMBL)*, 6th Edition, HHS Publication No. (CDC) 300859, Revised June 2020
  https://www.cdc.gov/labs/pdf/CDC-BiosafetymicrobiologicalBiomedicalLaboratories-2020-P.pdf
- Laboratory biosafety manual, fourth edition. Geneva: World Health Organization; 2020 (Laboratory biosafety manual, fourth edition and associated monographs)
  www.who.int/publications/i/item/9789240011311

Documentation and support

Related documentation

Document	Publication Number
Isolation of Nucleic Acid for Respiratory Tract Microbiota Profiling Experiments Quick Reference	MAN0018526
Respiratory Tract Microbiota Profiling Experiments v2 using OpenArray™ Plates and OpenArray™ AccuFill™ Software v1.2 Quick Reference	MAN0019509
Respiratory Tract Microbiota Profiling Experiments v2 Using OpenArray™ Plates and OpenArray™ AccuFill™ Software v2.0 Quick Reference	MAN0026009
TrueMark™ Respiratory Panel 2.0, OpenArray™ Plate Product Information Sheet	MAN0019510
TrueMark™ Respiratory Panel 2.0 Amplification Control Product Information Sheet	MAN0019505
TaqMan™ Universal Extraction Control Organism (B. atrophaeus) Product Information Sheet	MAN0018535
TaqMan™ Universal RNA Spike In/Reverse Transcription (Xeno) Control Product Information Sheet	MAN0018534
QuantStudio™ 12K Flex Real–Time PCR System: OpenArray™ Experiments User Guide	4470935
QuantStudio™ 12K Flex Real–Time PCR System Maintenance and Administration Guide	4470689
Thermo Scientific™ KingFisher™ Flex User Manual	MAN0019870
OpenArray™ Sample Tracker Software Quick Reference, for OpenArray™ AccuFill™ Software v1.2	4460657
OpenArray™ AccuFill™ System User Guide, for OpenArray™ AccuFill™ Software v1.2	4456986
QuantStudio™ 12K Flex OpenArray™ AccuFill™ System User Guide, for OpenArray™ AccuFill™ Software v2.0	MAN0025669
TaqPath™ 1-Step RT-qPCR Master Mix, CG User Guide	MAN0007959

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  - Safety Data Sheets (SDSs; also known as MSDSs)

  Note: For SDSs for reagents and chemicals from other manufacturers, contact the manufacturer.

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