

Automated DNA Quantification, Normalization, and Amplification Setup

USER BULLETIN

for use with:

HID NIMBUS® QNA System

HID NIMBUS® Presto QNA System

Publication Number MAN1000064

Revision A00



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

Revision history: MAN1000064 A00 (English)

Revision	Date	Description
A00	20 March 2024	New document for automated DNA quantification, normalization, and amplification setup on the HID NIMBUS® QNA System and the HID NIMBUS® Presto QNA System.

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

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Product information

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IMPORTANT! Before using this product, read and understand the safety information in the manufacturer's documentation.

IMPORTANT! Before using this product, read and understand the information in the “Safety” appendix in this document.

Product description

The Applied Biosystems™ HID NIMBUS® QNA System and HID NIMBUS® Presto QNA System are automated systems that include optimized scripts and use validated software to support high-throughput workflows for streamlined quantification, normalization, and amplification plate preparation. Unauthorized modifications are not supported.

The HID NIMBUS® QNA System and the HID NIMBUS® Presto QNA System can set up 96 reactions for quantification in <45 minutes, and set up 96 reactions for normalization and amplification in <90 minutes.

The system is available in the following configurations:

Configuration	Description
HID NIMBUS® QNA System (Cat. No. A55771)	- Includes the Microlab® NIMBUS™ Liquid Handler and the Applied Biosystems™ HID NIMBUS® System Software - Supports automated plate setup for DNA quantification, normalization, and amplification
HID NIMBUS® Presto QNA System (Cat. No. A55769) ^[1]	- Includes the Microlab® NIMBUS™ Liquid Handler, the KingFisher™ Presto Purification System, and the Applied Biosystems™ HID NIMBUS® System Software - Supports automated DNA purification, and automated plate setup for DNA quantification, normalization, and amplification

^[1] For information about DNA purification, see the *PrepFiler™ and PrepFiler™ BTA Automated Forensic DNA Extraction Kits: Automated DNA Purification on the HID NIMBUS® Presto Systems User Bulletin* (Pub. No. MAN0019368).

Note: The system is also available as the HID NIMBUS® Presto System (Cat. No. A55395), configured for automated DNA purification only. For information about DNA purification, see the *PrepFiler™ and PrepFiler™ BTA Automated Forensic DNA Extraction Kits: Automated DNA Purification on the HID NIMBUS® Presto Systems User Bulletin* (Pub. No. MAN0019368).

System components

The HID NIMBUS® systems for quantification and amplification include the following components:

- Microlab® NIMBUS™ Liquid Handler
- HID NIMBUS® System Software
- Laptop computer
- (HID NIMBUS® Presto QNA System only) KingFisher™ Presto Purification System
- (Optional) Clean Air Protection (CAP) system, with UV lamps

The Microlab® NIMBUS™ Liquid Handler is an automated liquid handling platform.

The HID NIMBUS® System Software facilitates automated DNA purification, and automated plate setup for DNA quantification, normalization, and amplification. For information about DNA purification, see the *PrepFiler™ and PrepFiler™ BTA Automated Forensic DNA Extraction Kits: Automated DNA Purification on the HID NIMBUS® Presto Systems User Bulletin* (Pub. No. MAN0019368).

Compatible kits

To prepare for quantification runs, the HID NIMBUS® QNA System and the HID NIMBUS® Presto QNA System are equipped to work with the Quantifiler™ Trio Automated DNA Quantification Kit (Cat. No. [A58787](#)). This kit is designed to quantify the total amount of amplifiable human DNA in a sample and includes all the necessary reagents for detection, amplification, and quantification of three human-specific DNA targets. For more information about the Quantifiler™ Trio Automated DNA Quantification Kit, see the *Quantifiler™ Trio Automated DNA Quantification Kit User Guide* (Pub. No. MAN1000066).

To prepare for amplification runs, the HID NIMBUS® QNA System and the HID NIMBUS® Presto QNA System are equipped to work with various short tandem repeat (STR) multiplex assays. Compatible kits include the following:

- GlobalFiler™ PCR Amplification Kit (Cat. No. [4476135](#) and Cat. No. [4482815](#))
- GlobalFiler™ IQC PCR Amplification Kit (Cat. No. [A43565](#))
- VeriFiler™ Plus PCR Amplification Kit (Cat. No. [A35495](#))
- Yfiler™ Plus PCR Amplification Kit (Cat. No. [4484678](#) and Cat. No. [4482730](#))
- NGM Detect™ PCR Amplification Kit (Cat. No. [A31832](#))

Deck layouts

To view the deck layout for quantification, see Figure 5 and Figure 6.

To view the deck layout for amplification, see Figure 12 and Figure 13.

To view the deck layout for purification, see the *PrepFiler™ and PrepFiler™ BTA Automated Forensic DNA Extraction Kits: Automated DNA Purification on the HID NIMBUS® Presto Systems User Bulletin* (Pub. No. MAN0019368).

Note: These layouts are provided for reference. Follow the software prompts for detailed run-specific information about labware locations, reagent positions, and volumes.

IMPORTANT! Use only the input labware that was used at installation for robot axis teaching. If your laboratory wants to change labware, contact Thermo Fisher Scientific Technical Support for more information.

Materials supplied with the HID NIMBUS® systems

Table 1 Deck components

Item	Hamilton Cat. No.
16-Position Sample Tube Carriers	6601693-01
MicroTube Inserts	182238

Table 1 Deck components *(continued)*

Item	Hamilton Cat. No.
Carrier with the following configuration: 4 x NTR Pedestal 4 x 96-Well Microplate Adapter	6604980-01
200-mL Reagent Trough Carrier	6603240-01
Carrier with the following configuration: 2 x FTR Pedestal 6 x 60-mL Reagent Trough Pedestal - NTR Pedestal with Multi-Tube Adapter	6604985-01
Carrier with the following configuration: 2 x FTR Pedestal 2 x Plate Stack Pedestal	6604990-01
CO-RE® Paddles	97021-01
Barcode Reader	97360-01

Required materials not supplied

Unless otherwise indicated, all materials are available through [thermofisher.com](https://www.thermofisher.com). "MLS" indicates that the material is available from [fisherscientific.com](https://www.fisherscientific.com) or another major laboratory supplier. Catalog numbers that appear as links open the web pages for those products.

Table 2 Materials for automated quantification

Item	Source
Tips, Conductive Non-sterile Filter, 50 µL	A58978
MicroAmp™ Optical 96-Well Reaction Plate (recommended)	N8010560
MicroAmp™ Optical Adhesive Film (recommended)	4311971
RNase-Free Microfuge Tube (1.5 mL) (recommended)	AM12450
Quantifiler™ Trio Automated DNA Quantification Kit	A58787

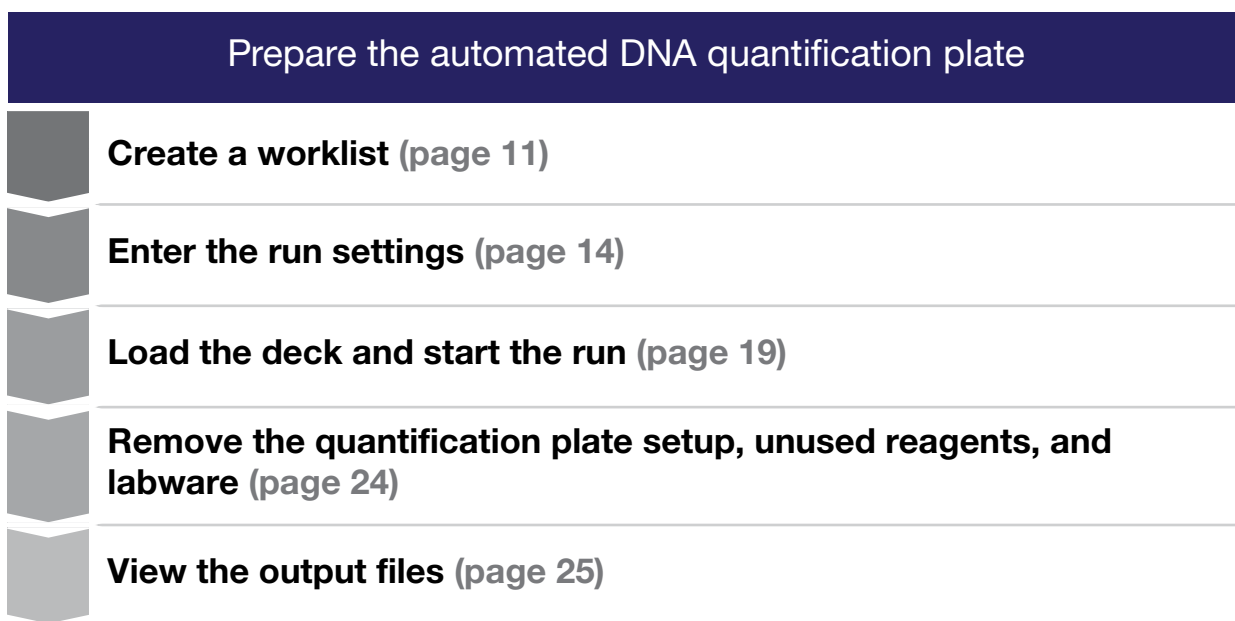
Table 3 Materials for automated amplification

Item	Source
Tips, Conductive Non-sterile Filter, 50 µL	A58978
MicroAmp™ Optical 96-Well Reaction Plate (recommended)	N8010560
RNase-Free Microfuge Tube (1.5 mL) (recommended)	AM12450
60-mL Reagent Reservoir, Self-Standing with Lid	56694-01
TE buffer	12090015
PCR amplification kit, one of the following:	
GlobalFiler™ PCR Amplification Kit	4476135 (200 reactions)
	4482815 (1,000 reactions)
GlobalFiler™ IQC PCR Amplification Kit	A43565
VeriFiler™ Plus PCR Amplification Kit	A35495
Yfiler™ Plus PCR Amplification Kit	4484678 (100 reactions)
	4482730 (500 reactions)
NGM Detect™ PCR Amplification Kit	A31832

2

Perform the automated DNA quantification setup run

Workflow



Guidelines for the automated quantification run

- The Quantifiler™ Trio Automated DNA Quantification Kit is sufficient for ≤ 960 samples, depending on the batch size.
- The HID NIMBUS® QNA System and HID NIMBUS® Presto QNA System are only compatible with 1.5 mL microcentrifuge tubes, 96-well PCR plates, and KingFisher™ 96-well deep-well plates for purified sample input.
- Before loading the instrument deck, remove air bubbles from the surface of reagents and samples. Bubbles can lead to incorrect liquid detection and pipetting errors.
- When loading tubes on the deck, ensure that the tip will not come into contact with any objects, including the tube caps, to prevent false liquid detection. Firmly press down on all labware placed on the instrument deck.

- We do not recommend a reagent or sample volume <35 µL in microcentrifuge tubes. If the eluate volume from purification is <35 µL, use a MicroAmp™ PCR plate as the input labware.
- For information on barcode positioning, see the *NIMBUS HD Operator's Manual* (Pub. No. 98538-01).
- Before the first run of the day, we recommend that you perform daily maintenance. See *NIMBUS HD Operator's Manual* (Pub. No. 98538-01) for instructions.

Create a worklist

For a quantification run, we recommend using a worklist for the samples in XLS, XLSX, or CSV format. Templates are installed on the provided laptop computer.

Alternatively, use the worklist generated from the run-tracking report of the purification workflow. For more information about the purification workflow, see *PrepFiler™ and PrepFiler™ BTA Automated Forensic DNA Extraction Kits: Automated DNA Purification on the HID NIMBUS® Presto Systems User Bulletin* (Pub. No. MAN0019368).

1. Before each run, navigate to the **ExampleWorklists** folder on the system computer:

```
C:\Program Files (x86)\Hamilton\HID Nimbus  
System\QuantNormAmp\Resources\Example Worklists
```

Note: If you cannot find the worklist templates on the computer, contact your local Thermo Fisher Scientific representative.

2. Copy the required template, then save it with a new file name.
3. In the saved copy, enter information for each sample, as shown in Table 4, Figure 1, and Figure 2.

IMPORTANT! The worklist must include the required information shown in Table 4. Do not change the column headings or leave cells blank. The system only reads XLS, XLSX, and CSV formats.

Table 4 Worklist information for each sample

Required column order	Required column heading	Action
1	Sample ID	Enter the sample name or ID associated with the sample. The sample ID must be unique. The following characters are valid in the worklist: • 0–9 • a–z (uppercase and lowercase) • _ (underscore) • - (hyphen) We recommend that you do not use the period character because it causes issues in the overall target adjustment in the amplification workflow.
2	Eluate Position	For tubes, use numeric values. For plates, use alphanumeric values. Note: The eluate position on the instrument deck refers to the loading position, regardless of your choice to remove samples from the run during quantification or amplification.
3	Eluate Barcode	If you are using barcodes, enter the expected eluate barcode for each sample lysate tube or for the MicroAmp™ PCR plate or KingFisher™ deep-well plate. • Tubes—Each tube has a unique barcode. • Plates—All sample wells of the plate have the same barcode.

IMPORTANT! To proceed with plate setup, ensure the barcode information on the worklist matches the barcodes loaded on the instrument in the same positions. You must include barcode information in all sample lines. If barcode information is absent in one or more sample lines, you will receive a read error on import. For plates, use the same barcode for each sample. If barcodes are not used, fill the input and eluate barcode cells with **No Barcode**.

Sample ID	Eluate Position	Eluate Barcode
Sample 1	1	No Barcode
Sample 2	2	No Barcode
Sample 3	3	No Barcode
Sample 4	4	No Barcode
Sample 5	5	No Barcode
Sample 6	6	No Barcode
Sample 7	7	No Barcode
Sample 8	8	No Barcode
Sample 9	9	No Barcode
Sample 10	10	No Barcode
Sample 11	11	No Barcode
Sample 12	12	No Barcode
Sample 13	13	No Barcode
Sample 14	14	No Barcode
Sample 15	15	No Barcode
Sample 16	16	No Barcode
Sample 17	17	No Barcode
Sample 18	18	No Barcode
Sample 19	19	No Barcode
Sample 20	20	No Barcode

Figure 1 Quantification worklist example for tubes

Sample ID	Eluate Position	Eluate Barcode
Sample 1	A1	No Barcode
Sample 2	B1	No Barcode
Sample 3	C1	No Barcode
Sample 4	D1	No Barcode
Sample 5	E1	No Barcode
Sample 6	F1	No Barcode
Sample 7	G1	No Barcode
Sample 8	H1	No Barcode
Sample 9	A2	No Barcode
Sample 10	B2	No Barcode
Sample 11	C2	No Barcode
Sample 12	D2	No Barcode
Sample 13	E2	No Barcode
Sample 14	F2	No Barcode
Sample 15	G2	No Barcode
Sample 16	H2	No Barcode
Sample 17	A3	No Barcode
Sample 18	B3	No Barcode
Sample 19	C3	No Barcode
Sample 20	D3	No Barcode

Figure 2 Quantification worklist example for plates

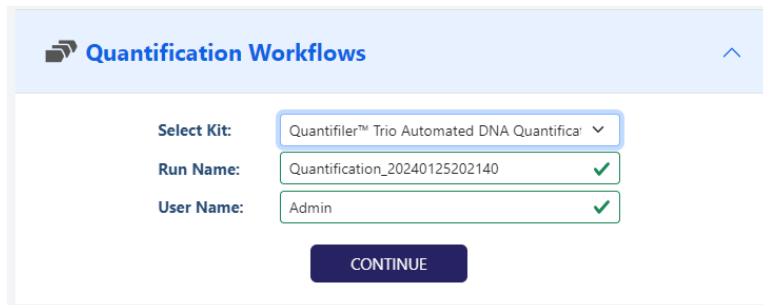
Enter the run settings

1. On the desktop, click  **Applied Biosystems HID NIMBUS System Software**.

Note: If the shortcut is not present on the desktop, navigate to C:\Program Files (x86)\Hamilton\HID Nimbus System\Application

2. (Optional) Expand the **Input Catalog Number** pane, then scan or type the Quantifiler™ Trio Automated DNA Quantification Kit catalog number.

3. Expand the **Quantification Workflows** pane, then enter the workflow information.



The screenshot shows a software window titled "Quantification Workflows" with a blue header bar. Below the header, there are three input fields: "Select Kit:" with a dropdown menu showing "Quantifiler™ Trio Automated DNA Quantifica...", "Run Name:" with a text box containing "Quantification_20240125202140" and a green checkmark, and "User Name:" with a text box containing "Admin" and a green checkmark. At the bottom of the form is a dark blue button labeled "CONTINUE".

- a. Use the **Select Kit** dropdown list to select a kit.
- b. (If needed) Change the run name, then enter a user name.

IMPORTANT!

- The run name and user name fields cannot include special characters other than - (hyphen) and _ (underscore).
 - The run name and user name must be 1–30 characters in length.
-

Note: The run name is prepopulated with the workflow type, followed by the date and time (format: Quantification_YYYYMMDDhhmmss). The input run name determines the folder where the run tracking and instrument import files are saved. Use the run name field to organize files across purification, quantification, and amplification workflow runs on the HID NIMBUS® systems.

4. Click **CONTINUE**.
The settings window is displayed.

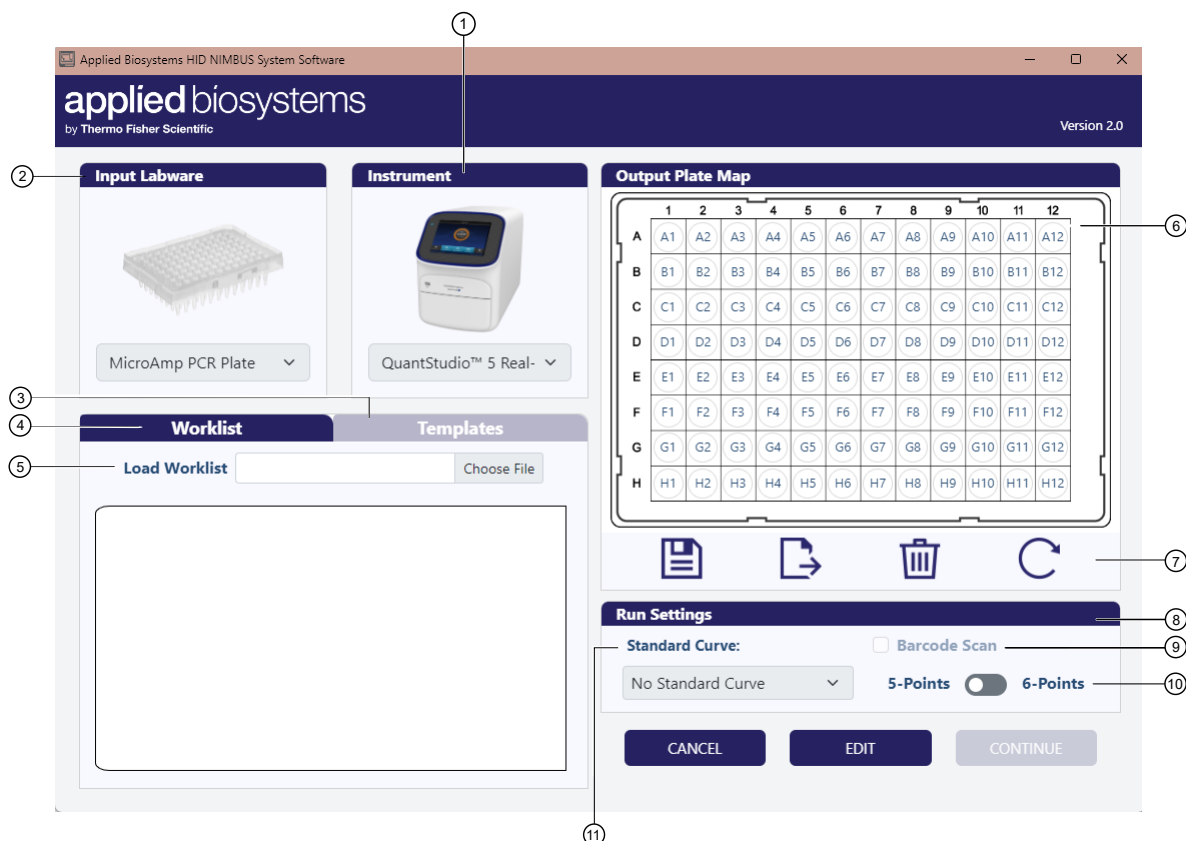


Figure 3 Settings window

- | | |
|----------------------------|--------------------------------------|
| ① Select an instrument | ⑦ Plate map tools |
| ② Select the input labware | ⑧ Run Settings pane |
| ③ Select a template | ⑨ Enable or disable barcode scanning |
| ④ Worklist tab | ⑩ Points toggle |
| ⑤ Import a worklist | ⑪ Select a standard curve option |
| ⑥ Plate map | |

5. Select the input labware and the instrument for the quantification experiment.
 - a. Click **EDIT** to unlock the user input interface.
 - b. In the **Parameter Modification** window, click **CONTINUE**.
 - c. Use the dropdown list in the **Input Labware** pane to select an option.
 - **MicroAmp PCR plate**
 - **Microcentrifuge Tubes**
 - **KingFisher Deep Well Plate**
 - d. Use the dropdown list in the **Instrument** pane to select an option.
 - **QuantStudio™ 5 Real-Time PCR System**
 - **7500 Real-Time PCR System**

- e. Click **SAVE** to confirm the selection.

Anytime that you edit the parameters, the edits are tracked in the GUI log file, located at C:\Program Files (x86)\Hamilton\LogFiles

6. In the **Worklist** tab, import a worklist.

- a. In the **Worklist** pane, click **Choose File**, or click within the blank file upload field.
- b. Select the prepared worklist or select purification run tracking file.

Note: Before uploading, ensure that the worklist matches the input labware. For example, if you are using a MicroAmp™ PCR plate, ensure that the worklist is not intended for 1.5-mL microcentrifuge tubes.

- c. (Optional) To change a worklist after it has been uploaded, click **Choose File**, or click within the blank file upload field. In the **Changing Worklist** window, click **CONTINUE**.

After the worklist is imported, the samples and controls appear in the **Worklist** pane.

7. In the **Run Settings** pane, use the **Standard Curve** dropdown list to select an option.

- **Create New Standard Curve**
- **Use Existing Standard Curve**
- **No Standard Curve**

Note: If a template was applied, a standard curve option is preselected. To remove the standard curve, in the **Run Settings** pane, use the **Standard Curve** dropdown list to select **No Standard Curve**. Do not drag-and-drop standards to  (**Remove Target**).

8. In the **Run Settings** pane, use the toggle to select **5-Points** or **6-Points**.

IMPORTANT! If a template was applied and you select standard curve points that differ from the template, the standards are removed from the plate map. For example, if you select the **Default - 5 Point Duplicates** template but manually change the number of points to **6-Points**, the standards are removed from the plate map.

9. (Optional) Enable barcode scanning.

- a. Click **EDIT** to unlock the user input interface.
- b. In the **Run Settings** pane, select the **Barcode Scan** checkbox.
- c. Click **SAVE** to confirm the selection.

Note: When barcode scanning is on, you are prompted to manually scan the barcodes of the labware and carriers. Your worklist must contain the relevant barcode information to avoid scanning errors.

10. Select an action to set up the plate map.

- Drag-and-drop each sample from the **Worklist** tab to the desired location of the **Output Plate Map**.

Note: The positive control and no template control samples dragged onto the **Output Plate Map** are ignored when importing the quantification data file in the amplification workflow.

- In the **Templates** tab, use the arrows to scroll, select the desired template, then click **APPLY**.

Note: Samples in the worklist that are not included in the plate map blink red in the worklist tab. Click  (**Export Worklist**) to export a worklist for the remaining samples. The file is saved and exported to C:\Program Files (x86)\Hamilton\Local Outputs\Run Name, where the run name is the input selected in step 3.

11. (Optional) Create and save a template.

- Drag-and-drop samples, standards, and controls from the **Worklist** tab to the desired location of the **Output Plate Map**.
- Click  (**Save Plate Map**).
- In the **Save Current Plate Map** window, enter a template name.
- Use the **Template ID** dropdown list to select **Create a new template**.
- Click **SUBMIT**.

12. (Optional) To reset the plate map, click (**Restart Plate Map**).

13. (Optional) To remove a sample or control from the plate map, drag-and-drop a desired target to (**Remove Target**).

The target is immediately removed from a plate map. To add a target back, drag-and-drop the desired target from the **Worklist** tab onto the **Output Plate Map**.

Note: To remove the standard curve, in the **Run Settings** pane, use the **Standard Curve** dropdown list to select **No Standard Curve**. Do not drag-and-drop standards to  (**Remove Target**).

14. Click **CONTINUE**.

The method calculates the required number of tips and reagent volumes according to the number of samples to be processed and the information you provided in the settings.

Load the deck and start the run

IMPORTANT! Due to reagent stability at room temperature, load the deck and start the run within 3 hours.

1. Place all reagents according to the diagram in the deck summary screen (see Figure 5 and Figure 6).
 - a. Prepare the master mix off-deck, then place the quantification reagents on the deck with the specified volumes.

Note: If the master mix requirement is >1,500 µL, we recommend that you prepare the master mix in a single tube, then equally split the master mix into two 1.5 mL microcentrifuge tubes (Cat. No. [AM12450](#)) before placing the tubes on the deck. Click the **Master Mix** row to view a diagram of the tubes and their contents.

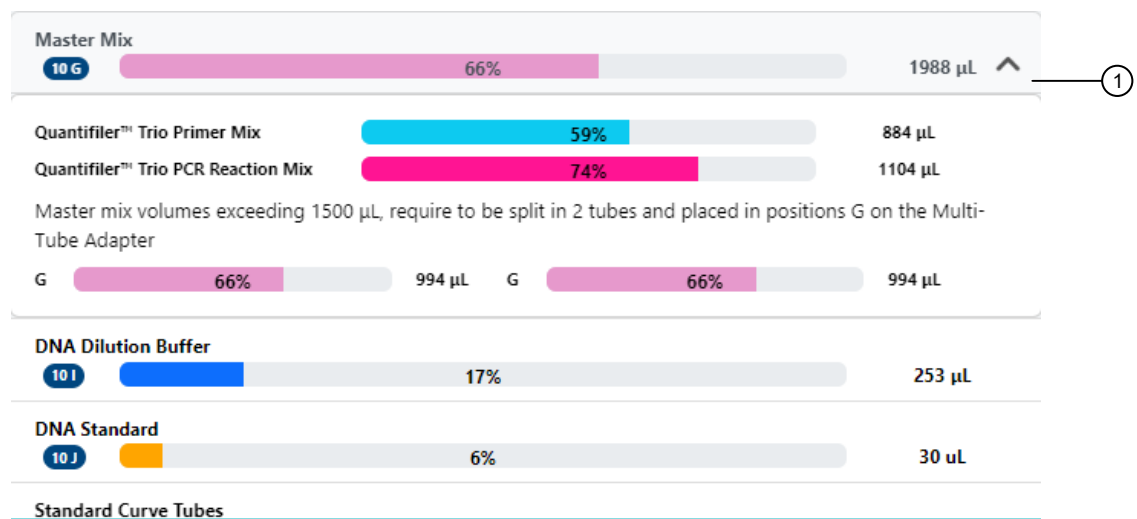


Figure 4 Reagent volumes

① Master Mix row (expanded)

Note: Reagent percentages are calculated based on the labware on the deck.

- b. Place the pointer over each position number on the deck layout to show tips with instructions.
- c. (Optional) Click **Guidance Mode** to follow prompts for how to set up the deck. Click **NEXT** to navigate through the videos. Click **FINISH** to close **Guidance Mode**.

Note: Due to the unavailability of videos for all scenarios, the positions shown in the guidance mode videos are not specific to every use case. To help ensure appropriate guidance for each deck position, read the instructions provided below each video.

- d. Follow the color-coding and letters to load the labware into the correct carriers and positions. When loading the labware, start from the carriers at the back.

IMPORTANT! To avoid a potential collision hazard with the instrument arm and channels, do not leave any objects on the instrument deck that are not specifically called out in the deck loading instructions. This includes de-capping tubes before clicking **CONTINUE**.

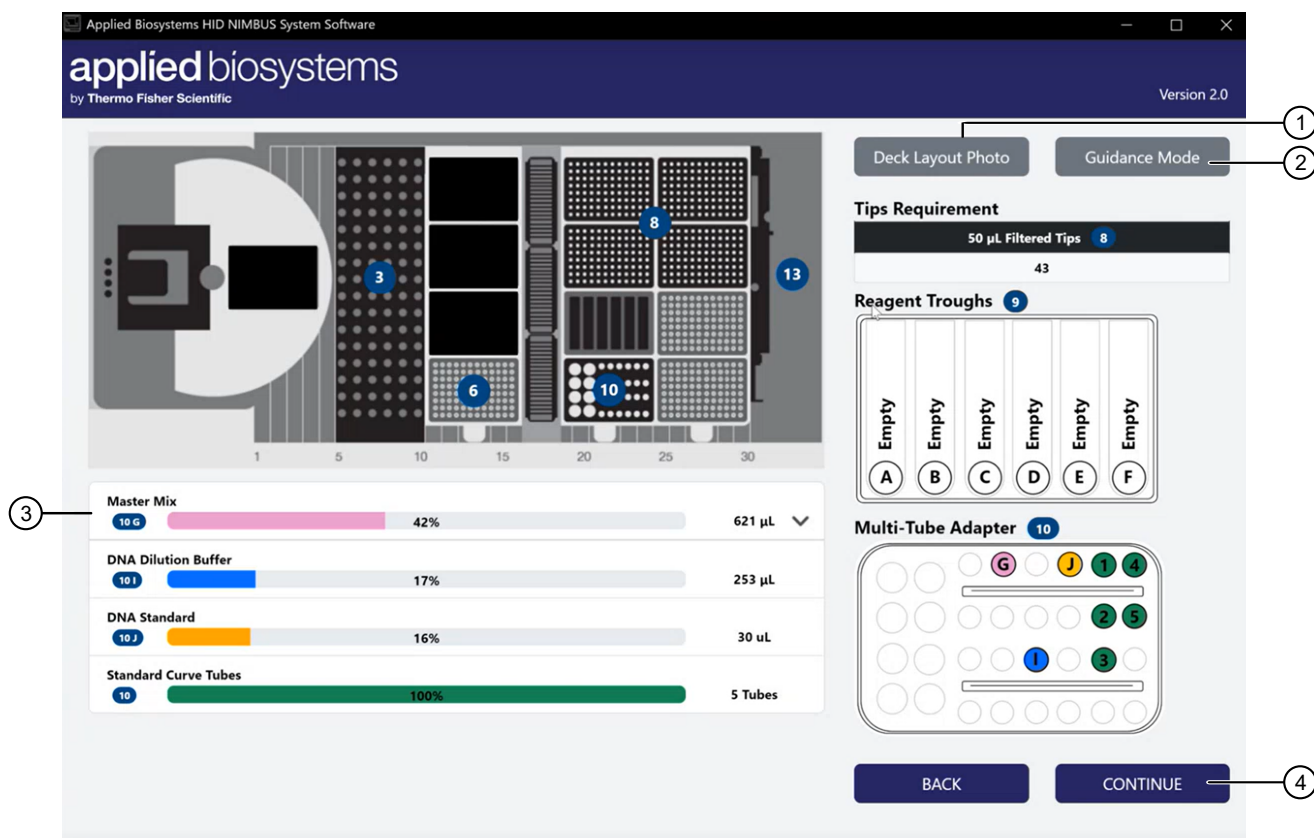


Figure 5 Example quantification deck layout with tubes as the input labware

- ① Change the deck layout image
- ② Access instructional videos
- ③ **Master Mix** row (expandable)
- ④ Continue to the next screen

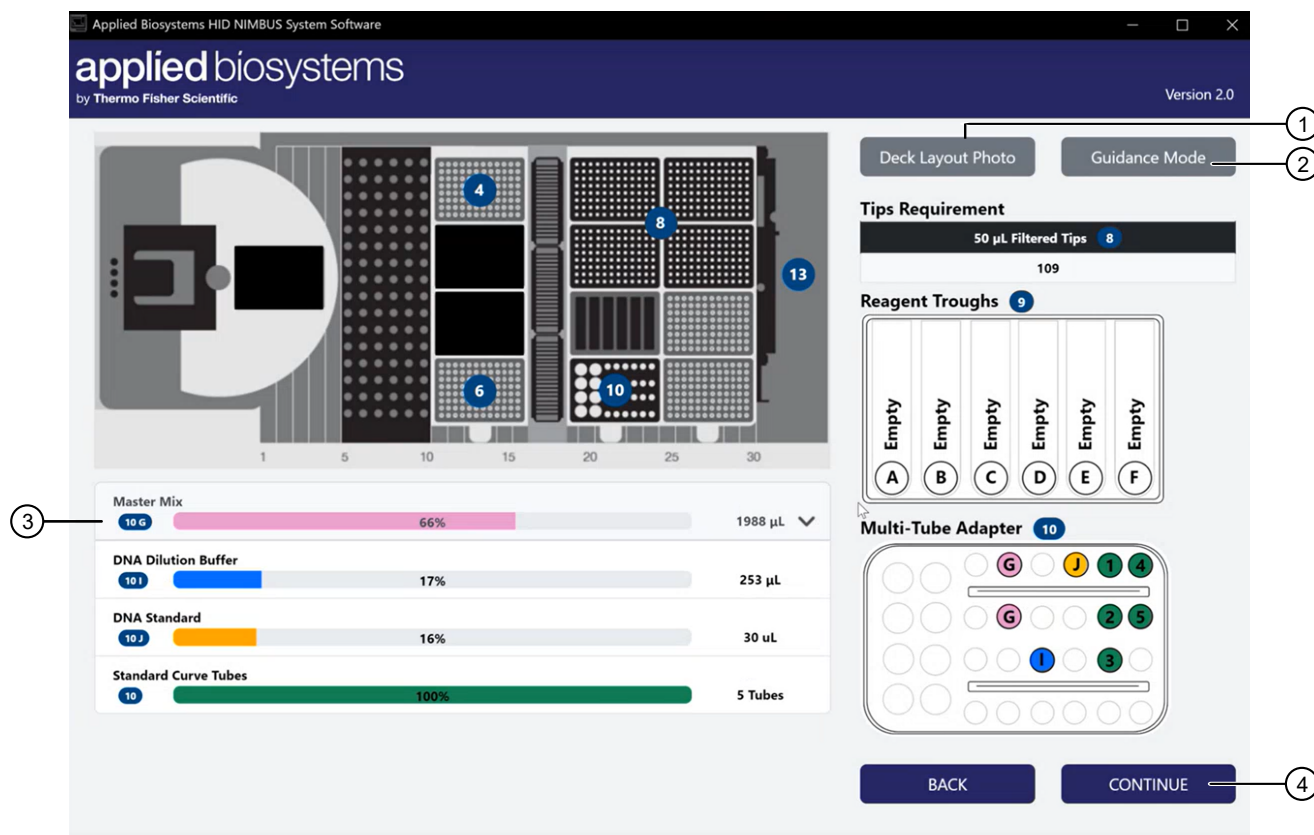


Figure 6 Example quantification deck layout with a plate as the input labware

- ① Change the deck layout image
- ② Access instructional videos
- ③ **Master Mix** row (expandable)
- ④ Continue to the next screen

2. (Optional) If you are using tubes as input labware, load the tubes in the appropriate order: back to front, then left to right, starting with the first carrier at track 5.

3. (Optional) Click **Deck Layout Photo** to change the image format.

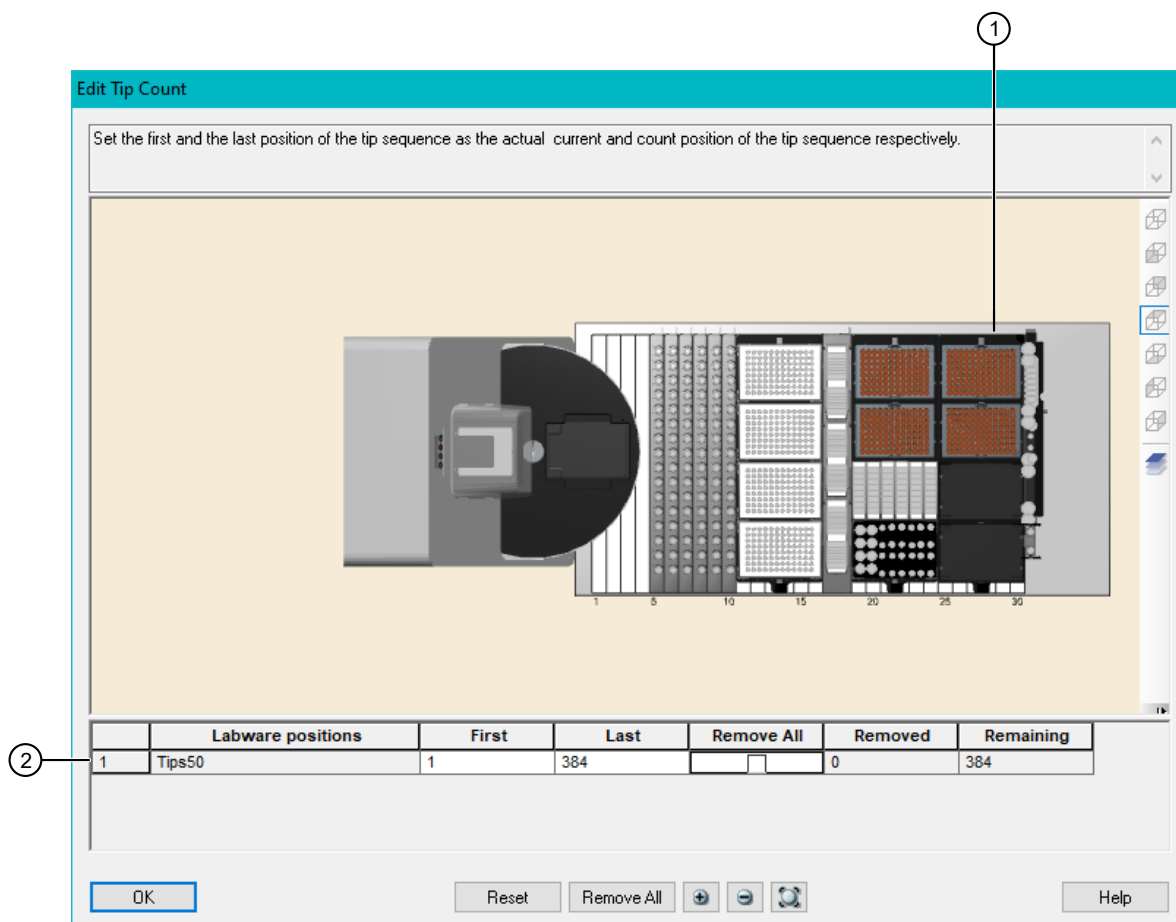
IMPORTANT! Follow the numbered deck layout image when loading the deck. The numbered deck layout image shows deck positions clearly and provides tips with instructions.

4. Click **CONTINUE**.

5. (If needed) Edit the tip counts for the 50 µL tips (position 8) to reflect the number and placement of tips on each rack. Select an action to edit the tip counts.

- Click each position to select/deselect the appropriate wells in the diagram. Gray indicates that the well does not have a tip; orange indicates that the well does have a tip.
- In the **First** and **Last** fields, enter the first and last tip positions.

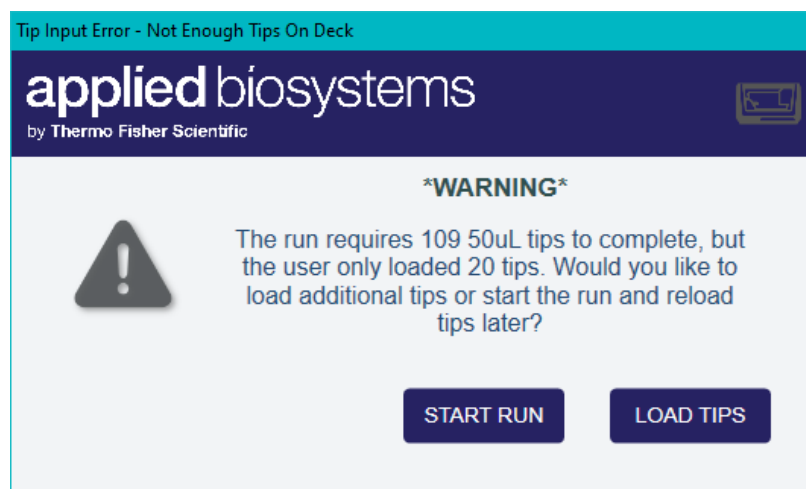
IMPORTANT! The total number of 50 µL tips is 384. The top left rack contains tips 1–96, the bottom left rack contains tips 97–192, the top right rack contains tips 193–288, and the bottom right rack contains tips 289–384. See Figure 5 and Figure 6.



① Diagram

② Text fields

Note: If you do not load enough tips to complete the run, you will be warned to load additional tips or start the run at your own risk. We recommend you click **LOAD TIPS** to complete the run. This will avoid pausing midway through the run to load additional tips.



6. If barcode scanning is on, scan the carrier and labware barcodes.

Note: The carriers should already be loaded in the correct positions on the deck.

- a. At the prompt, slide the specified carrier out of position so that the barcodes can be scanned by the on-deck barcode scanner, then click **Start Scan**.

Note: The scanner reads the carrier and labware barcodes at the same time. You do not need to remove the labware from the carrier.

Carrier Loading

Current Operation

Load carrier sampleTubeCarrier_01 at tracks 5...5

Status

Ignore Current Load

Repeat Carrier Load

Control Panel

Abort Method

Continue

Barcode Values

Select barcode entry to edit value in place

Barcode	Position Mask
STC-E177	STC-****
S0037182	P-01
S0037183	P-02
S0037184	P-03
S0037185	P-04
BAD READ	P-05
BAD READ	P-06
BAD READ	P-07
BAD READ	P-08
BAD READ	P-09
BAD READ	P-10
BAD READ	P-11
BAD READ	P-12
BAD READ	P-13
BAD READ	P-14
BAD READ	P-15
BAD READ	P-16

Update barcode value(s) with manual entry

Figure 7 Barcode scanning in progress

- b. Push the carrier all the way back into position, then click **Finish Scan**.
- c. Repeat substep 6a and substep 6b for each carrier.

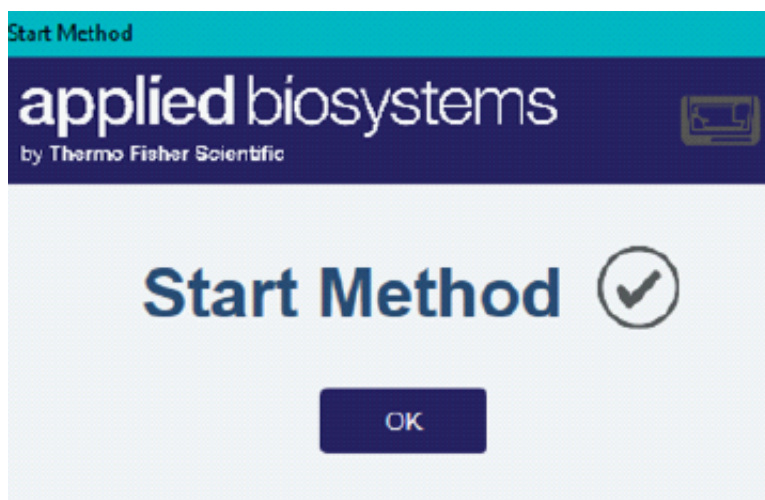
Note: If you are using an input worklist preloaded with barcode information, the system checks that your plates and/or tubes are loaded in the same positions as the worklist. If the loaded positions do not match the worklist, you are prompted to adjust the load positions or abort the run and restart with the correct worklist information.

The HID NIMBUS® System Software performs the following functions:

- **For the microcentrifuge tubes input labware**—Cross-references the scanned barcodes against the expected barcodes supplied in the worklist.
- **For the plate input labware**—Cross-references the scanned barcode against the expected barcode supplied in the worklist.

7. Close the instrument door.

The **Start Method** dialog box is displayed.



8. Click **OK**.

The door automatically locks and the run starts.

Remove the quantification plate setup, unused reagents, and labware

1. Open the instrument door.
2. Remove the plate that contains the quantification plate setup, seal it with an optical adhesive film, then proceed to setting up the real-time PCR instrument.

Note: The import file for the real-time instrument is generated by the HID NIMBUS® System Software. To locate the import file, navigate to:

C:\Program Files (x86)\Hamilton\Local Outputs\Quantification_YYYYMMDDHHMMSS

3. Cap and store the remaining Quantifiler™ THP DNA Dilution Buffer.
4. If the **Create New Standard Curve** option was selected, cap and store the remaining Quantifiler™ THP DNA Standard.
5. Store the low-binding tubes containing the serial dilutions of the standard curve if still within the usable range (14 days stored at 2–8°C).

6. Properly dispose of any unused master mix in the microcentrifuge tubes.

IMPORTANT! Do not reuse the leftover master mix. Dispose of any unused volumes.

7. Empty the waste container that contains used tips.

IMPORTANT! To properly dispose of all used reagents and labware, see Appendix B, “Safety”.



WARNING! Do not use cleaning or disinfecting solutions which contain hypochlorite, such as bleach, on the instrument.

Clean the HID NIMBUS® QNA systems after each use. For detailed instructions, see the *NIMBUS HD Operator's Manual* (Pub. No. 98538-01).

View the output files

The output files for each run include a run-tracking report and a log file. Both files are given software-generated unique identifiers.

On the HID NIMBUS® QNA system or HID NIMBUS® Presto QNA system computer, open the output file of interest, based on the run date.

Output file	File name and location	Description
Run-tracking report	QuantificationRunTracking_Quantification_Run Name.xls, located at C:\Program Files (x86)\Hamilton\Local Outputs\Run Name	An Excel™ file that includes the following information: • Run Information • Lot Tracking • Run Status List • Worklist • Final Sample List • Pipette Tracking • Pipette Error Report
Real-time PCR import file	Quantification_Run Name_RT.txt, located at C:\Program Files (x86)\Hamilton\Local Outputs\Run Name	A TXT file that includes detailed information and is used as an input for the real-time PCR instrument software.
Log file	<unique identifier>_Trace.trc, located at C:\Program Files (x86)\Hamilton\LogFiles	A TRC file that includes detailed information for each robotic step that was performed during the run.
	Quantification_Run Name_GUILog.txt, located at C:\Program Files (x86)\Hamilton\LogFiles	A TXT file that includes information for each instance the edit function is used to modify parameters.

3

Perform the automated DNA normalization and amplification setup run

Workflow

Prepare the automated DNA amplification plate	
	Create a worklist (page 27)
	Enter the run settings (page 30)
	Load the deck and start the run (page 35)
	Remove unused reagents and labware (page 41)
	View the output files (page 42)

Guidelines for the automated amplification run

- The HID NIMBUS® QNA System and HID NIMBUS® Presto QNA System are only compatible with 1.5 mL tubes and 96-well PCR and deep-well plates.
- Before loading the deck, remove air bubbles from the surface of reagents and samples, as bubbles can lead to liquid sensing and pipetting errors.
- When loading tubes on the deck, ensure that the tip will not come into contact with any objects, including the tube caps, to prevent false liquid sensing.
- The instrument does not dispense an allelic ladder. The positions of the ladders within the plate layout are provided for traceability purposes. These plate positions are empty for CE plate setup.
- To prevent tip collisions, firmly press down all labware when loading the instrument deck.

- For information on barcode positioning, see the *NIMBUS HD Operator's Manual* (Pub. No. 98538-01).
- Before the first run of the day, we recommended that you perform daily maintenance. See *NIMBUS HD Operator's Manual* (Pub. No. 98538-01) for instructions.

Create a worklist

For an amplification run, we recommend using a worklist for the samples in XLS, XLSX, or CSV format. Templates are installed on the provided laptop computer.

Alternatively, use the worklist generated from the run-tracking report of the purification workflow. For more information about the purification workflow, see *PrepFiler™ and PrepFiler™ BTA Automated Forensic DNA Extraction Kits: Automated DNA Purification on the HID NIMBUS® Presto Systems User Bulletin* (Pub. No. MAN0019368).

1. Before each run, navigate to the **ExampleWorklists** folder on the system computer:

```
C:\Program Files (x86)\Hamilton\HID Nimbus  
System\QuantNormAmp\Resources\Example Worklists
```

Note: If you cannot find the worklist templates on the computer, contact your local Thermo Fisher Scientific representative.

2. Copy the required template, then save it with a new file name.
3. In the saved copy, enter information for each sample, as shown in Figure 8 and Figure 9.

IMPORTANT! The worklist must include the required information shown in Table 5. Do not change the column headings or leave cells blank. The system only reads XLS, XLSX, or CSV formats.

Table 5 Worklist information for each sample

Required column order	Required column heading	Action
1	Sample ID	Enter the sample name or ID associated with the sample. The sample ID must be unique. The following characters are valid in the worklist: • 0–9 • a–z (uppercase and lowercase) • _ (underscore) • - (hyphen) We recommend that you do not use the period character because it causes issues in the overall target adjustment in the amplification workflow.
2	Eluate Position	For tubes, use numeric values. For plates, use alphanumeric values.
3	Eluate Barcode	If you are using barcodes, enter the expected eluate barcode for each sample lysate tube or for the MicroAmp™ PCR plate or KingFisher™ deep-well plate. • Tubes—Each tube has a unique barcode. • Plates—All sample wells of the plate have the same barcode.
4	(Optional) Concentration	Add quantitation data if a separate quantitation data file is not uploaded.

IMPORTANT! To proceed with plate setup, ensure the barcode information on the worklist matches the barcodes loaded on the instrument in the same positions. You must include barcode information in all sample lines. If barcode information is absent in one or more sample lines, you will receive a read error on import. For plates, use the same barcode for each sample. If barcodes are not used, fill the input and eluate barcode cells with **No Barcode**.

Sample ID	Eluate Position	Eluate Barcode
Sample 1	1	No Barcode
Sample 2	2	No Barcode
Sample 3	3	No Barcode
Sample 4	4	No Barcode
Sample 5	5	No Barcode
Sample 6	6	No Barcode
Sample 7	7	No Barcode
Sample 8	8	No Barcode
Sample 9	9	No Barcode
Sample 10	10	No Barcode
Sample 11	11	No Barcode
Sample 12	12	No Barcode
Sample 13	13	No Barcode
Sample 14	14	No Barcode
Sample 15	15	No Barcode
Sample 16	16	No Barcode
Sample 17	17	No Barcode
Sample 18	18	No Barcode
Sample 19	19	No Barcode
Sample 20	20	No Barcode

Figure 8 Amplification worklist example for tubes

Sample ID	Eluate Position	Eluate Barcode
Sample 1	A1	No Barcode
Sample 2	B1	No Barcode
Sample 3	C1	No Barcode
Sample 4	D1	No Barcode
Sample 5	E1	No Barcode
Sample 6	F1	No Barcode
Sample 7	G1	No Barcode
Sample 8	H1	No Barcode
Sample 9	A2	No Barcode
Sample 10	B2	No Barcode
Sample 11	C2	No Barcode
Sample 12	D2	No Barcode
Sample 13	E2	No Barcode
Sample 14	F2	No Barcode
Sample 15	G2	No Barcode
Sample 16	H2	No Barcode
Sample 17	A3	No Barcode
Sample 18	B3	No Barcode
Sample 19	C3	No Barcode
Sample 20	D3	No Barcode

Figure 9 Amplification workflow example for plates

Enter the run settings

1. On the desktop, click  **Applied Biosystems HID Nimbus System Software**.

Note: If the shortcut is not present on the desktop, navigate to C:\Program Files (x86)\Hamilton\HID Nimbus System\Application

2. (Optional) Expand the **Input Catalog Number** pane, then scan or type the STR amplification kit package number.
3. Expand the **Amplification Workflows** pane, then enter the workflow information.

 **Amplification Workflows**

Select Kit:
GlobalFiler™ PCR Amplification Kit

Run Name:
Amplification_20231205115902

User Name:
Admin

CONTINUE

- a. Use the **Select Kit** dropdown list to select a kit.

- b. Change the run name, if needed, then enter a user name.

IMPORTANT!

- The run name and user name fields cannot include special characters other than - (hyphen) and _ (underscore).
- The run name and user name must be 1–30 characters in length.

Note: The run name is prepopulated with a string in the format of the kit name, followed by the date and time (format: Amplification_YYYYMMDDhhmmss). The input run name determines the folder where the run tracking and instrument import files are saved. Use the run name field to organize files across purification, quantification, and amplification workflow runs on the HID NIMBUS® systems.

4. Click **CONTINUE**.

The settings window is displayed.

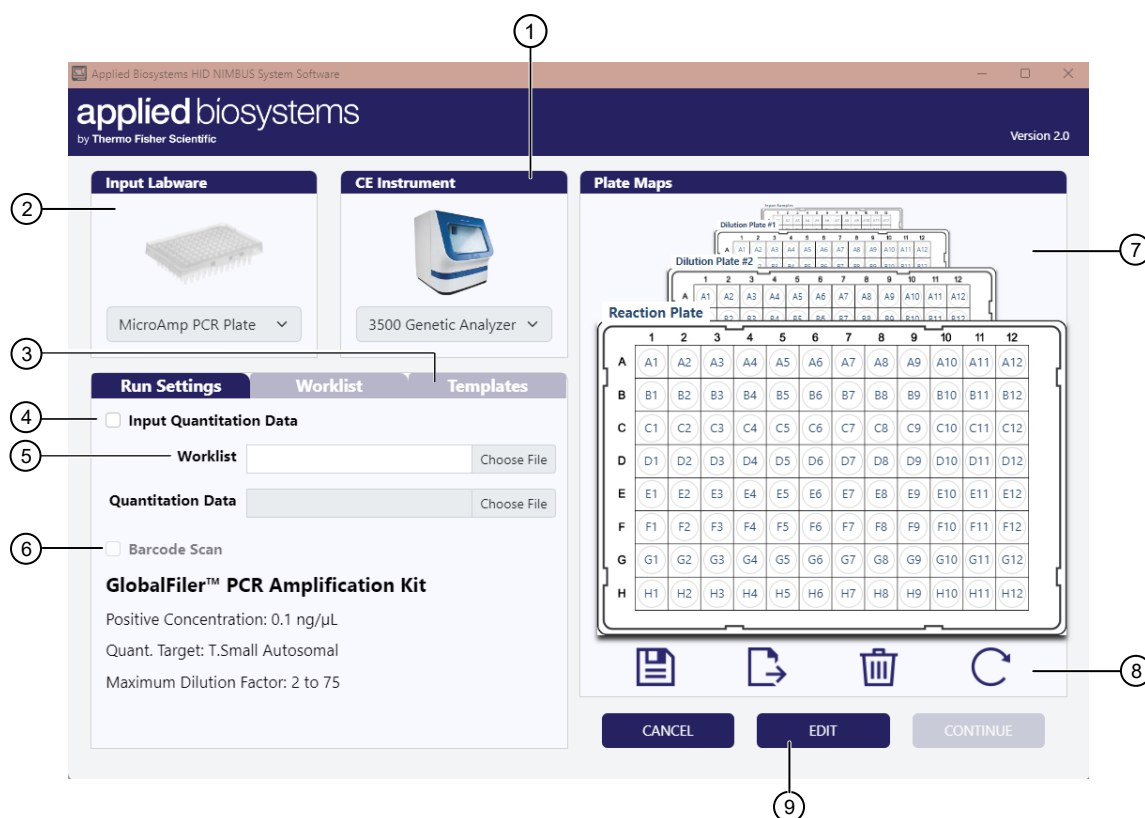


Figure 10 Settings window

- ① Select an instrument
 - ② Select the input labware
 - ③ Select a template
 - ④ **Input Quantitation Data** checkbox
 - ⑤ Import a workload
 - ⑥ Enable or disable barcode scanning
 - ⑦ Plate maps
 - ⑧ Plate map tools
 - ⑨ Enable selection of input labware, instrument, and target concentration
5. Select the input labware and the instrument for the capillary electrophoresis run.
 - a. Click **EDIT** to unlock the user input interface.

- b. In the **Parameter Modification** window, click **CONTINUE**.
 - c. Use the dropdown list in the **Input Labware** pane to select an option.
 - **MicroAmp PCR plate**
 - **Microcentrifuge Tubes**
 - **KingFisher Deep Well Plate**
 - d. Use the dropdown list in the **Instrument** pane to select an option.
 - **3500 Genetic Analyzer**
 - **3500xL Genetic Analyzer**
 - **SeqStudio Genetic Analyzer**
 - **SeqStudio 8-Flex Genetic Analyzer**
 - **SeqStudio 24-Flex Genetic Analyzer**
 - e. Click **SAVE** to confirm the selections.
6. In the **Run Settings** tab, select an action to enter sample information.
- **Worklist**—Click **Choose File** or click within the **Worklist** file upload field. Select either the prepared worklist or select purification run tracking file.
 - *(Optional)* **Quantitation Data**—Select the **Input Quantitation Data** checkbox, then click **Choose File** or click within the blank file upload field, located to the right of **Quantitation Data**.

IMPORTANT! If a quantitation data file is not uploaded, a column for quantitation must be present in the worklist.

Note: Quantitation data are exported from the HID Real-Time PCR Analysis Software. For information about exporting quantitation data, see the *Quantifiler™ Trio Automated DNA Quantification Kit User Guide* (Pub. No. MAN1000066).

7. *(Optional)* Enable barcode scanning.
- a. Click **EDIT** to unlock the user input interface.
 - b. In the **Run Settings** pane, select the **Barcode Scan** checkbox.
 - c. Click **SAVE** to confirm the selection.

Note: When barcode scanning is on, you will be prompted to manually scan the barcodes of the labware and carriers.

8. *(Optional)* In the **Worklist** tab, adjust the overall target concentration.
- a. Click **EDIT** to unlock the user input interface.

b. Select an action to adjust the concentration.

- To adjust the target concentration for all samples, use the **Overall Target Concentration** slider scale to adjust the target concentration.
- To adjust the target concentration for individual samples, click the concentration value in the **Conc. Target** column for your sample. In the **Modify Target Concentration** window, enter a new concentration between 0.1 ng and 4.0 ng, and then click submit. Do not include units.

Note: The concentration only displays one decimal. For instance, 0.1 ng and 0.125 ng appear the same, but the calculations for the sample and diluent are different.

Note: If the sample concentration is adjusted after the samples are displayed on the plate map, you must drag-and-drop the sample from the **Reaction Plate** plate map to  (**Remove**), then drag-and-drop the sample from the **Worklist** tab to the **Reaction Plate** plate map. If the overall target concentration is adjusted, you must reapply the template to adjust all the samples. Any individual sample concentrations adjusted previously are reset.

c. Click **SAVE** to confirm the selection.

9. In the **Plate Maps** pane, select an action to set up the reaction plate.

- From the **Worklist** tab, drag-and-drop each sample, control, and ladder to the desired location in the reaction plate.
- In the **Templates** tab, use the arrows to scroll, select the desired template, then click **APPLY**.

Note:

- Templates can be created and saved. For more information, see step 11.
 - If a sample concentration is less than 0.001 ng, it is displayed as zero in the software.
 - The instrument is not capable of dispensing an allelic ladder. The positions of the ladders within the plate layout are only provided for traceability purposes.
 - When a low sample concentration is detected,  (**Low sample concentration**) is displayed to the left of the sample number in the **Worklist** tab. The sample position also appears orange in the **Worklist** tab and in the plate maps.
-

10. (Optional) To remove a sample, ladder, or control from the plate map, drag-and-drop a desired target to (**Remove**).

The target is immediately removed from a plate map. To add a target back, drag-and-drop the desired target from the **Worklist** tab to the reaction plate.

11. (Optional) Create and save a template.

a. Drag-and-drop samples and controls from the **Worklist** tab to the **Output Plate Map**.

Note: In the **Worklist** tab, samples that are not included in the reaction plate blink red. Click  (**Export Worklist**) to export a worklist for the samples that are not included. The file is saved and exported to C:\Program Files (x86)\Hamilton\Local Outputs\Run Name.

- b. Click  (**Save Plate Map**).
 - c. In the **Save Current Plate Map** window, enter a template name.
 - d. Use the **Template ID** dropdown list to select **Create a new template**.
 - e. Click **SUBMIT**.
12. (Optional) To reset the plate map, click  (**Restart Plate Map**).
13. In the **Plate Maps** pane, view or adjust the plate maps.
 - **Input Samples**
 - **Dilution Plate #1**
 - **Dilution Plate #2**
 - **Reaction Plate**

Note: Click a plate to bring it to the front of the stacked plate maps.

Note: Place the pointer over each sample number in **Dilution Plate #1** and **Dilution Plate #2** to view the sample and diluent volumes. Place the pointer over each sample number and control in the **Reaction Plate** to view the sample volume, diluent volume, and target concentration.

14. Click **CONTINUE**.

The method calculates the required number of tips and reagent volumes according to the number of samples to be processed and the information you provided in the **Run Settings** window.

Load the deck and start the run

IMPORTANT! Due to reagent stability at room temperature, load the deck and start the run within 4 hours.

1. Place all the reagents on the deck according to the diagram in the **Deck Summary** screen (see Figure 12 and Figure 13).
 - a. Prepare the master mix off-deck, then place the amplification reagents on the deck with the specified volumes.

Note: If prompted to load two master mix tubes, we recommend that you prepare the master mix in a single tube, then split into two 1.5 mL microcentrifuge tubes (Cat. No. [AM12450](#)) before placing the tubes on the deck. Click the **Master Mix** row to view a diagram of the tubes and their contents.

IMPORTANT! Do not overfill the reagent reservoirs.

IMPORTANT! Keep the primer mix and the PCR reaction mix protected from direct exposure to light. Excessive exposure to light can affect the fluorescent probes and/or the passive reference dye.

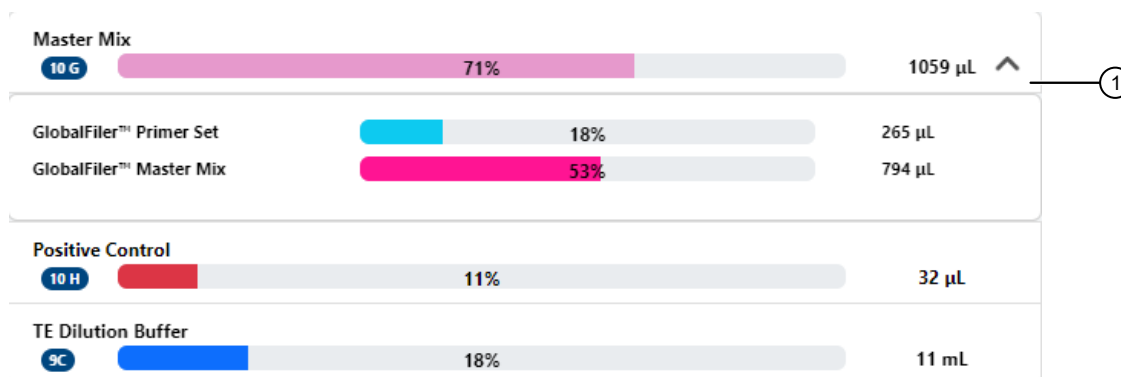


Figure 11 Reagent volumes

① Master Mix row (expanded)

Note: Reagent percentages are calculated based on the labware on the deck.

- b. Fill the 60-mL trough with the specified volume of low TE dilution buffer and place it on deck.
- c. Place the pointer over each position number on the deck layout to show tips with instructions.
- d. (Optional) Click **Guidance Mode** to follow prompts for how to set up the deck. Click **NEXT** to navigate through the videos. Click **FINISH** to close **Guidance Mode**.

Note: Due to the unavailability of videos for all scenarios, the positions shown in the guidance mode videos are not specific to every use case. To help ensure appropriate guidance for each deck position, read the instructions provided below each video.

- e. Follow the color-coding and letters to load the labware into the correct carriers and positions. When loading the labware, start from the carriers at the back.
- f. After all reagents and troughs are filled and placed, click **CONTINUE**.

IMPORTANT! To avoid a potential collision hazard with the instrument arm and channels, do not leave any objects on the instrument deck that are not specifically called out in the deck loading instructions. This includes removing trough lids and de-capping tubes prior to clicking **CONTINUE**.

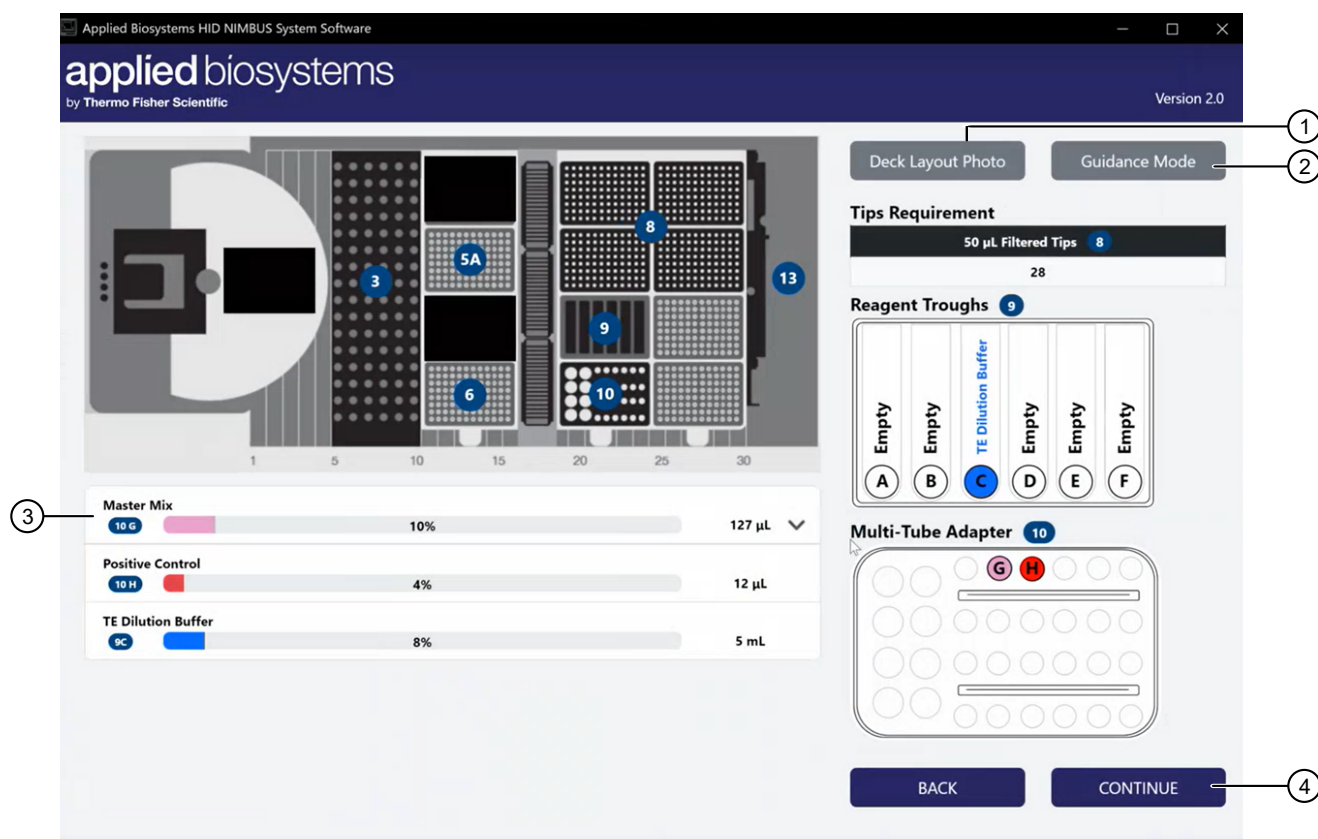


Figure 12 Example amplification deck layout with tubes as the input labware

- ① Change the deck layout image
- ② Access instructional videos
- ③ **Master Mix** row (expandable)
- ④ Continue to the next screen

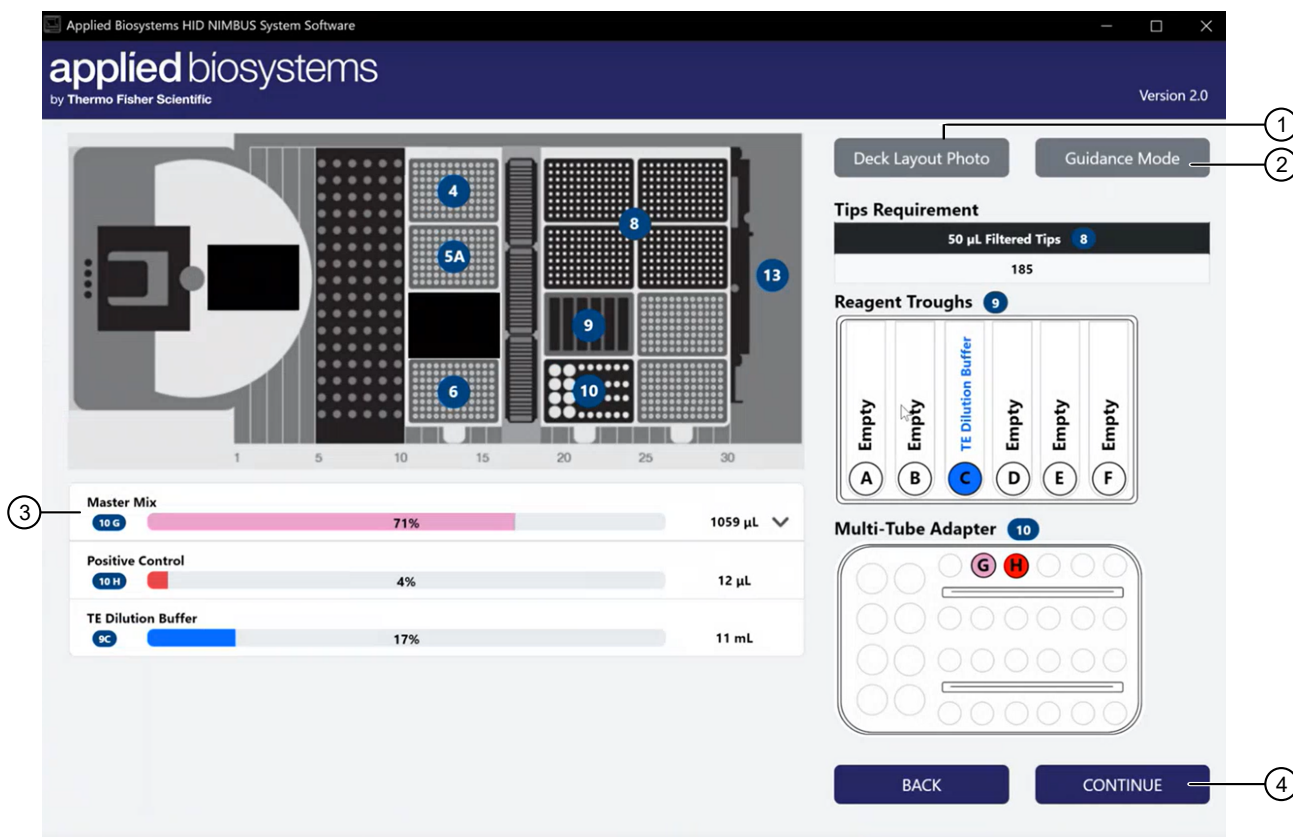


Figure 13 Example amplification deck layout with a plate as the input labware

- ① Change the deck layout image
- ② Access instructional videos
- ③ **Master Mix** row (expandable)
- ④ Continue to the next screen

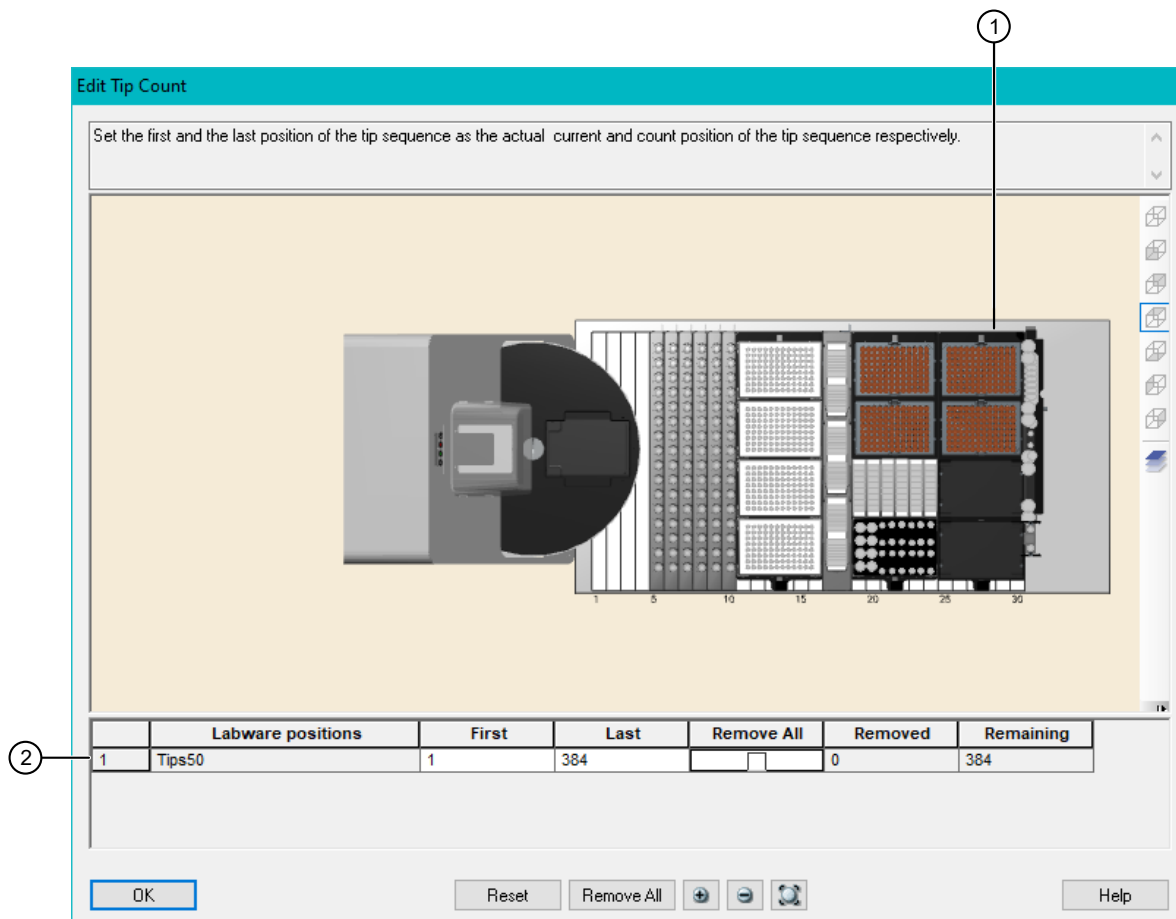
2. (Optional) If you are using tubes as the input labware, load the tubes in the appropriate order: back to front, then left to right, starting with the first carrier at track 5.
3. (Optional) Click **Deck Layout Photo** to change the image format.

IMPORTANT! Follow the numbered deck layout image when loading the deck. The numbered deck layout image shows deck positions clearly and provides tips with instructions.

4. Click **CONTINUE**.

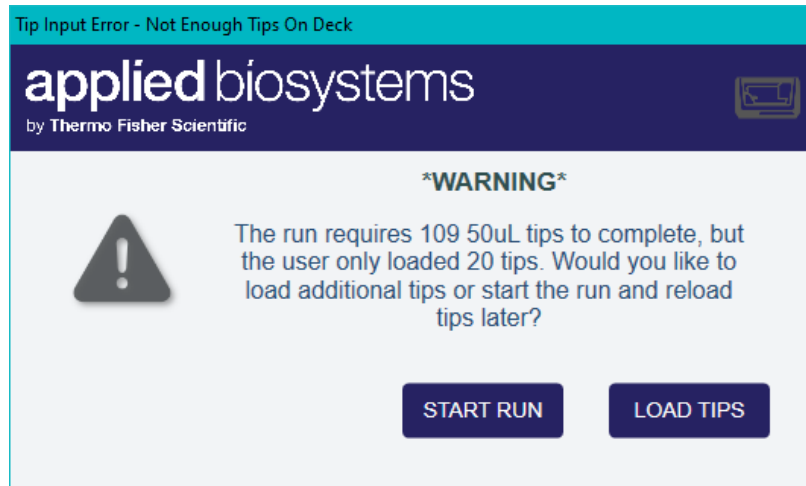
5. (If needed) Edit the tip counts for the 50 μ L tips (position 8) to reflect the number and placement of tips on each rack. Select an action to edit the tip counts.
 - Click each position to select/deselect the appropriate wells in the diagram. Gray indicates that the well does not have a tip; orange indicates that the well does have a tip.
 - In the **First** and **Last** fields, enter the first and last tip positions.

IMPORTANT! The total number of 50 μ L tips is 384. The top left rack contains tips 1–96, the bottom left rack contains tips 97–192, the top right rack contains tips 193–288, and the bottom right rack contains tips 289–384. See Figure 12 and Figure 13.



- ① Diagram
- ② Text fields

Note: If you do not load enough tips to complete the run, you will be warned to load additional tips or start the run at your own risk. To avoid pausing midway through the run to load additional tips, we recommend that you click **LOAD TIPS**.



6. If barcode scanning is on, scan the carrier and labware barcodes.

Note: The carriers should already be loaded in the correct positions on the deck.

- a. At the prompt, slide the specified carrier out of position so that the barcodes can be scanned by the on-deck barcode scanner, then click **Start Scan**.

Note: The scanner reads the carrier and labware barcodes at the same time. You do not need to remove the labware from the carrier.

Carrier Loading

Current Operation

Load carrier sampleTubeCarrier_01 at tracks 5...5

Status

Ignore Current Load

Repeat Carrier Load

Control Panel

Abort Method

Continue

Barcode Values

Select barcode entry to edit value in place

Barcode	Position Mask
STC-E177	STC-****
S0037182	P-01
S0037183	P-02
S0037184	P-03
S0037185	P-04
BAD READ	P-05
BAD READ	P-06
BAD READ	P-07
BAD READ	P-08
BAD READ	P-09
BAD READ	P-10
BAD READ	P-11
BAD READ	P-12
BAD READ	P-13
BAD READ	P-14
BAD READ	P-15
BAD READ	P-16

Update barcode value(s) with manual entry

Figure 14 Barcode scanning in progress

- b. Push the carrier all the way back into position, then click **Finish Scan**.
- c. Repeat substep 6a and substep 6b for each carrier.

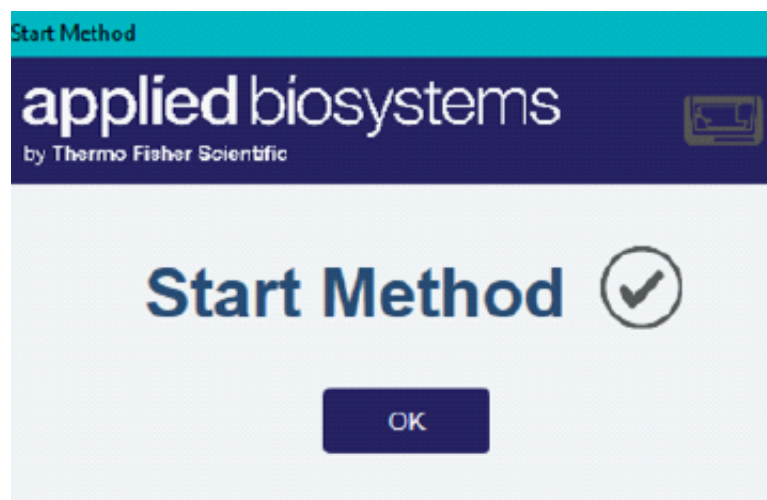
Note: If you are using an input worklist preloaded with barcode information, the system checks that your plates and/or tubes are loaded in the same positions as the worklist. If the loaded positions do not match the worklist, you are prompted to adjust the load positions or abort the run and restart with the correct worklist information.

The HID NIMBUS® System Software performs the following functions:

- **For the microcentrifuge tubes input labware**—Cross-references the scanned barcodes against the expected barcodes supplied in the worklist.
- **For the plate input labware**—Cross-references the scanned barcode against the expected barcode supplied in the worklist.

7. Close the instrument door.

The **Start Method** dialog box is displayed.



8. Click **OK**.

The door automatically locks and the run starts.

Remove unused reagents and labware

1. Open the instrument door.
2. Remove the plate that contains the amplification plate setup, then proceed to set up the CE instrument.

Note: The import file for the capillary electrophoresis instrument is generated by the HID NIMBUS® System Software. To locate the import file, navigate to:

C:\Program Files (x86)\Hamilton\Local Outputs\Run Name

3. Properly dispose of any unused buffer in the reagent troughs.

IMPORTANT! Do not reuse the reagents in the reagent troughs.

4. *(Recommended)* Discard used reagent reservoirs after each run. Use new reservoirs for each run.

5. Properly dispose of any unused master mix in the microcentrifuge tubes.

IMPORTANT! Do not reuse the leftover master mix. Dispose of any unused volumes.

6. Empty the waste container that contains used tips.

IMPORTANT! To properly dispose of all used reagents and labware, see Appendix B, “Safety”.

Clean the HID NIMBUS® systems after each use. For detailed instructions, see the *NIMBUS HD Operator’s Manual* (Pub. No. 98538-01).

View the output files

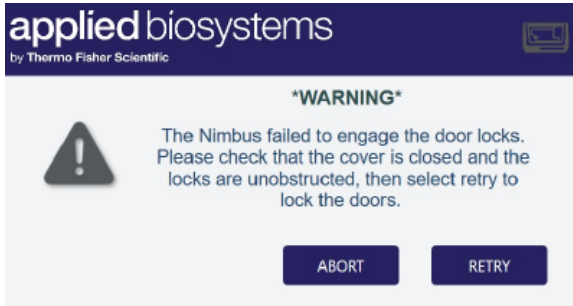
The output files for each run include a run-tracking report and a log file. Both files are given software-generated unique identifiers.

1. On the HID NIMBUS® System Software computer, navigate to C:\Program Files (x86)\Hamilton\Local Outputs\Amplification_YYYYMMDDHHMMSS
2. Open the output file of interest, based on the run date.

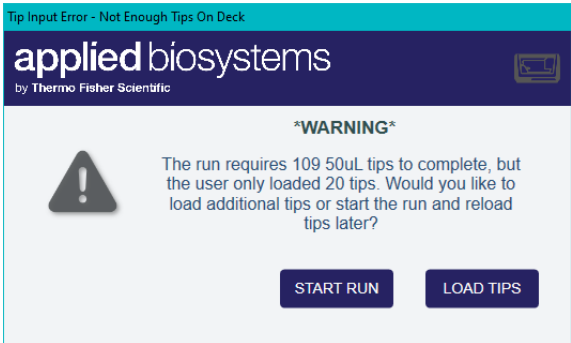
Output file	File name	Description
Run-tracking report	AmplificationRunTracking_Amplification_YYYYMMDDHHMMSS.xls	An Excel™ file that includes the following information: • Run Information • Lot Tracking • Run Status List • Worklist • Final Sample List • Pipette Tracking • Pipette Error Report
	Amplification_YYYYMMDDHHMMSS_CE.csv	A CSV file that includes detailed information and is used as an input for the CE instrument.
Log file	<unique identifier>_Trace.trc, available at C:\Program Files (x86)\Hamilton\LogFiles	A TRC file that includes detailed information for each robotic step that was performed during the run.

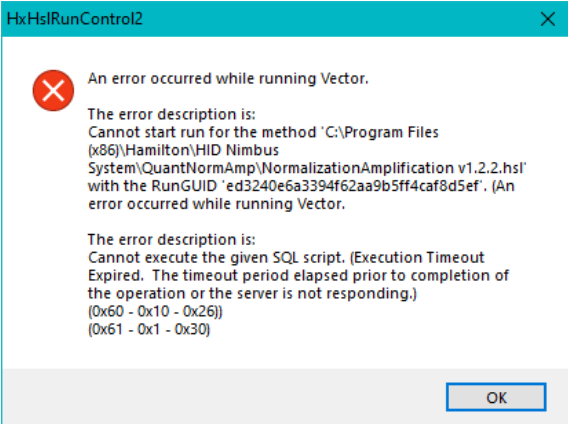


Troubleshooting

Observation	Possible cause	Recommended action
Aspiration is incomplete	The wrong labware was used. Using labware that is different from what is specified in the method and used at installation for axis position teaching may cause the tips to hit the tube bottom or aspirate at an insufficient depth.	Use the labware specified by the method. At installation, the robot axis positions are taught relative to specific plastics. Ensure that the same plastics that were used at installation are used for each step of the process.
A door lock error message is displayed 	The instrument was started with the door unlocked.	1. Close the instrument door. 2. Click RETRY. The system will lock the door.
	The instrument run was paused, then resumed with the door unlocked.	1. Close the instrument door. 2. In the error message, click Launch Control Panel. 3. In the Control Panel dialog box, click Lock Door, then close the dialog box. 4. In the error message, click RETRY to continue the run.

Observation	Possible cause	Recommended action
A clot error message is displayed	A clot was detected during aspiration.	Click the appropriate option in the error message: • Repeat—Retries the step that generated the error. • Cancel—Aborts the run, unless an automatic error recovery has been added to the method. • Abort—Aborts the run and ignores any automatic error recovery options. • Air—Raises the tips to clearance height and aspirates air before continuing the run. • Bottom—Retries aspiration from the bottom of the reagent reservoir, but with the liquid-level detection turned off. • Exclude—Continues the run without using any channel that generated the error in the remaining pipetting steps.

Observation	Possible cause	Recommended action
A liquid-level error message is displayed	The reagent volumes in the reagent reservoirs are too low.	Click the appropriate option in the error message: • Repeat—Retries the step that generated the error. • Air—Raises the tips to clearance height and aspirates air before continuing the run. • Bottom—Retries aspiration from the bottom of the reagent reservoir, but with the liquid-level detection turned off. • Exclude—Continues the run without using any channel that generated the error in the remaining pipetting steps. • Unlock—Unlocks the door so that the operator can correct the problem before continuing.
An insufficient tips error message is displayed 	There are not enough tips to continue the run.	Load additional tips, then fill out the tip counter appropriately to continue. In the error message, click START RUN to continue the run.

Observation	Possible cause	Recommended action
A run control error is displayed 	An attempt to launch a MED file from Venus Run Control.	Use the HID NIMBUS[®] System Software.



Safety

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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, visit [thermofisher.com/support](https://www.thermofisher.com/support).

Safety information for instruments not manufactured by Thermo Fisher Scientific

Some of the accessories provided as part of the instrument system are not designed or built by Thermo Fisher Scientific. Consult the manufacturer's documentation for the information needed for the safe use of these products.

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.



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



WARNING! 4L Reagent and Waste Bottle Safety. Four-liter reagent and waste bottles can crack and leak. Each 4-liter bottle should be secured in a low-density polyethylene safety container with the cover fastened and the handles locked in the upright position.

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
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
<i>PrepFiler™ and PrepFiler™ BTA Automated Forensic DNA Extraction Kits: Automated DNA Purification on the HID NIMBUS® Presto Systems User Bulletin</i>	MAN0019368
<i>HID NIMBUS® Systems Site Preparation Guide</i>	MAN0026468
<i>Quantifiler™ Trio Automated DNA Quantification Kit Product Information Sheet</i>	MAN1000067
<i>Quantifiler™ Trio Automated DNA Quantification Kit User Guide</i>	MAN1000066

Customer and technical support

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