Saphyr® System User Guide

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Chapter 1: Overview

Introduction

The Saphyr® System (Saphyr Instrument, Bionano Compute and Saphyr Compute that are integrated via a web server) provides rapid, high-throughput, long-range genome mapping capabilities for *de novo* assembly, hybrid scaffold, and structural variation analysis.

Features

- **Easy load-and-go workflow**—The adaptive loading feature in the Instrument Control Software (ICS) makes the necessary adjustments during the run to ensure the optimal conditions for DNA molecule loading are maintained throughout the scanning. The automated loading process takes only 3 minutes to set up.
- **Convenient setup and flow**—Bionano Access™ lets users design experiments, track run performance, perform automatic downstream analysis, and share data.
- **Real-time analysis**—Bionano Access enables users to view real-time data and performance metrics from any internet browser with connection to your Access Server as the run progresses.
- **Structural variation analysis**—Bionano Access provides visualization of all structural variation (SV) types, including homozygous and heterozygous SV analysis and results from trio analyses.
- **Hybrid scaffolding**—Bionano Solve provides enhanced capabilities for merging Bionano maps to generate hybrid scaffolding. The Bionano Solve tool automatically resolves conflicts, displays those conflicts graphically, and lets users edit those assemblies to further improve the scaffold quality.

Workflow

To perform a run on the Saphyr, use the following workflow example as a guide:

1. Perform DNA extraction and nicking, labeling, repairing, staining (NLRS) of samples for the run.
2. Set up an experiment and specify run parameters on Bionano Access.
3. Load sample on Saphyr Chip™ and attach the Saphyr clip to the chip.
4. Turn the Saphyr instrument on and log on to the Instrument Control Software (ICS).
5. Insert the Saphyr chip into the instrument.
6. Set up run.
7. Track run performance and analyze data on Bionano Access.

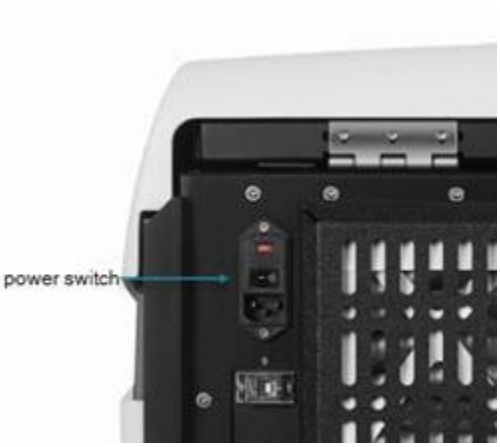
Prepare Sample

For details on DNA extraction and NLRS of samples, visit the Bionano Support page.

Chapter 2: Getting Started

Start the Saphyr Instrument

1. Locate the power switch on the back of the instrument.
2. Press the power switch to turn the instrument on.



3. Proceed to log on the Saphyr Instrument Control Software.

Red Light on Instrument

CAUTION: Before lifting the sample door to insert or remove the Saphyr chip, ensure the front LED panel is illuminating blue. If the front LED panel light is red as shown in Figure 1, do not open the sample door. Contact Bionano Genomics Support for assistance. Users may be at risk for laser radiation exposure if the sample door is open.

Figure 1: Front LED Panel is Red

Instrument Status on the Front Panel

The LED light on the front panel below the sample door indicates the following:

Color	Description
Light off	The instrument is powered off.
Flashing blue	The instrument door is open.
Flashing yellow	The instrument is initializing.

Color	Description
Green	The instrument is ready to scan.
Flashing green	The instrument is scanning.
Red	The instrument encountered an error.

Log On to the Saphyr Instrument Control Software

1. Launch the Instrument Control Software (ICS) using the shortcut icon on the desktop. When the software is launched and initializes the Saphyr instrument, the status icon is blue  .

   The icon is at the top-right corner of the screen.

2. Enter the user name and password.
3. Click **Logon**.

ICS Menu Options

The following menu appears on the Main Menu.

Option	Description
Insert Chip	Lets users insert the Saphyr chip into the Saphyr instrument.
Create New Scan	Lets users set up a run.
Data Administration	Lets users manage data on the Saphyr Instrument Controller, such as managing disk space, viewing run status, and deleting runs.
Remove Chip	This option is available when a run is successfully completed or when a run is cancelled. Lets users remove the chip from the Saphyr instrument.
Resubmit Run to Access	Lets users reanalyze existing run data. Refer to Appendix C for detailed instructions.

Instrument Control Software (ICS) Icons

The icons are at the top right-corner of the ICS screen.

Saphyr Instrument Status

The Saphyr instrument icon indicates the status of the Saphyr instrument.

Icon	Color	Description
	Blue	The instrument is working normally.
	Flashing Green	The instrument is initializing.

Icon	Color	Description
	Flashing Red	The instrument encountered an error. Click the icon to view more details.
	Flashing Bright Blue	The instrument door is open or the laser interlock switch is open.
	Amber	The instrument is not receiving power.
	Purple	The instrument hardware is not correctly configured. Contact Bionano Genomics Support for assistance.

Data Service Status

The data service icon indicates that the Saphyr instrument is scanning normally and is sending data to the Instrument Controller.

Icon	Color	Description
	Blue	The data service is working normally.
	Flashing Green	The data service is sending data to Bionano Access.
	Red	The data service is unable to connect to Bionano Access. Click the icon to view more details.

Bionano Access Connection Status

The Bionano Access Connection icon indicates that there is a network connection between the Saphyr instruInstrument Controller and Bionano Access.

The instrument network connection must be connected to Bionano Access before it can perform a run. If connection fails while the instrument is scanning, ICS will cache run data locally.

Icon	Color	Description
	Blue	The control software is connected to Bionano Access.
	Amber	The control software is unable to connect to Bionano Access.

Windows Update

The Windows Update icon will only display when an update is available.

Icon	Color	Description
	Red	A Windows update is available and highly recommended that this be done manually by the user before starting a run. ICS does not allow automatic updates in order to prevent interference with instrument operation.

Chapter 3: Configure Analysis Settings

Bionano Access

The Instrument Control Software provides data transfer and subsequent analysis to Bionano Access. Users can track run progress and view results in real time.

For more details on Bionano Access analysis and visualization features, see the *Bionano Access Software User Guide (document # 30142)*.

Logon to Bionano Access

After the installation of the Bionano Access software on the server, a URL will be provided to log on.

1. Navigate to the Bionano Access web page.
2. Enter the user name and password.
3. Click **Login**.

Bionano Access Modules

The following menu appears on the Main Menu.

Module	Description
Projects	This module lets users create, view, edit, and manage their projects. Additionally, users can import and export data.
Experiments	This module lets users set up and manage their experiments, view templates, and track chip run progress.
In Silico Digestion	This module lets users perform *in silico* digestion of reference file, update digestion settings, and view results.
Settings	This module lets users create users, manage user accounts, add references, configure software, and upload masked BED files.

User Roles

There are four unique user roles in Bionano Access. The personnel with administrator privileges can assign roles to users.

Roles	Description
Administrator	The administrator can assign user roles, manage user accounts, and delete projects permanently or restore deleted projects.
Project Lead	The project lead can give users access to view projects and create and manage projects. All project leads can view and edit all projects in the Projects list.
User	The user can view the projects that they have access to and create and edit experiments.
Read Only	This role can view the projects that they have access to.

Add Users

Users must have administrator privileges to perform this task.

All users should have their own user account with a valid email address. Bionano Access notifies users via email when their job is complete.

1. From the Bionano Access main menu, select **Settings**.
2. Select **User Accounts**.
3. Click **New User**.
4. Enter the user information.
5. At the **Role** field, choose one of the following:
   - User
   - Project Lead
   - Administrator
   - Read Only
6. At the **User Status** field, chose one of the following:
   - Active: The account is active and the user can log on to Bionano Access.
   - Disabled: The account is disabled and the user cannot log on to Bionano Access.
7. Click **Submit**.
   The new user account appears on the *User Accounts* screen.

Experiments

In the Experiments module, users can add new experiments, manage experiments, track run performance, and view quality metrics in real time. Users can create multiple experiments for one project. Additionally, users can view and edit templates.

For more details on Bionano Access Experiment Creation features, see the *Bionano Access Software User Guide (document # 30142)*

Create an Experiment

Each Saphyr chip can only be associated to one experiment. Before inserting the chip into the Saphyr instrument, create an experiment to associate with the chip. The run results are posted for the experiment that is associated with the chip.

An experiment created on Bionano Access is in *pending* status until it is associated with a Saphyr chip. Users can modify or delete pending experiments. When an experiment is associated with a scan on the Saphyr, users cannot modify or delete the experiment.

Only users in the Administrator or Project Lead role can create experiments.

1. From the Main Menu, select **Experiments**. The *Experiment Design* window appears.
2. Select **Add Experiment**.
   A dialog box appears.
3. At the **Project** field, select the project that is associated with the experiment from the drop-down list.
4. [Optional] If users do not have a project for this experiment, click **New** to create a project.
5. At the **Experiment Name** field, type the experiment name.

6. [Optional] At the **Experiment Description** field, type in a brief description.
7. [Optional] At the **Experiment Template** field, select a template from the drop-down list.
8. Click Next.

   Note: For Multiplex and Dual Labeled Samples, see the *Bionano Access Software User Guide (document # 30142)* for additional configuration instructions on the next screen.
9. At the Sample field, select a sample from the drop-down list or click New to add a sample.
10. At the **Recognition Enzyme** field, select an enzyme from the drop-down list or click **New** to add an enzyme.
11. [Optional] At the **Reference** field, select a genome reference for the experiment from the drop-down list.

    Note: For supported samples that have a guaranteed throughput, a reference must be supplied in order to generate the required dashboard info with MQR results for flowcell compensation through Bionano Support when guaranteed throughput is not met.
12. [Optional] At the **Comment** field, type in a brief comment.
13. Click **Add to Flowcell 1**.

    To edit information to Flowcell 1, click **Remove** in the *Chip* pane, and then make the changes.
14. Repeat step 9 through step 12 for Flowcell 2.

    Important: Users must populate information for both flowcells.
15. Click **Add to Flowcell 2**.

    To edit information to Flowcell 2, click **Remove** in the *Chip* pane, and then make the changes.
16. Click **Next.**
    A summary of the experiment appears.
17. By default, the **Auto Assemble Human** check box is selected if the reference is a human genome. Users can deselect the check box.

    This option indicates that when there is at least 70X effective coverage, the *de novo* assembly will start using the human haplotype assembly parameters immediately after the molecules file is generated.

    Note: Users without a dedicated assembly server will not be presented with the option to perform auto assembly.
18. Click **Done**.
    The *Experiment List* screen appears.

Chapter 4: Prepare Chip

Load Sample on Saphyr Chip

- Equilibrate the samples and Saphyr chip (sealed in pouch) to room temperature for at least 30 minutes prior to use.
- When loading sample, ensure there is no airflow around the chip to avoid sample evaporation.
- Proceed quickly through the following steps to minimize sample evaporation.
- Use gloves (powder free) for this procedure.

Important: Both flowcells need to be loaded with samples. If only one flowcell is loaded with sample, this may cause evaporation and sample contamination to the unused flowcell.

1. Open the pouch containing the Saphyr chip.

   Important: Do not open the pouch containing the Saphyr chip when it is cold. Wait until the pouch is at room temperature before removing the chip. Opening a chip while it is cold may damage the chip and cause performance degradation.

2. Place the chip on a clean and level lab bench.
3. With a 10 µl pipette, press the plunger down and hold at the first stop. Lower the pipette tip into the sample and gently stir the sample with the tip.
4. Position the pipette tip near the middle or bottom of the sample and slowly aspirate 8.5 µl of the sample.
5. Begin loading the sample in the inlet well of flowcell 1.

Align the pipette tip over flowcell 1 inlet well on the right of the chip, and then slowly dispense the sample until the bottom of the inlet well is coated with sample solution. Continue to dispense until the entire volume of 8.5 µl is in the well.

The fluid level in the inlet well should be flat. Always maintain positive pressure on the plunger to avoid bubble formation.

6. Repeat steps 3 through 5 for flowcell 2 inlet well.
7. Set a timer for 2 minutes to allow the sample to wet through the channels.
8. When the timer stops, begin loading the sample into the outlet wells of flowcell 1 and flowcell 2. Apply the same techniques for loading the sample into the inlet wells to the outlet wells.
9. With a 20 µl pipette positioned near the middle or bottom of the sample, slowly aspirate 11 µl of the sample and slowly dispense the sample into the outlet well of flowcell 1. Repeat the step for flowcell 2.
10. Ensure that the fluid level in the inlet and outlet wells is flat.
11. Add the necessary volume of nuclease-free water to the inlet and outlet wells to replace sample solution that has evaporated.

Important: The inlet and outlet wells should be filled with sample solution during the initial load. Do not compensate for lack of sample solution by adding nuclease-free water or buffer. Nuclease-free water should only be added after all wells are loaded to replace volume lost by evaporation.

Proceed to attaching the Saphyr clip on to the Saphyr chip.

Saphyr Clip Care

Always position the Saphyr clip on its back.

Figure 2: Correct Position

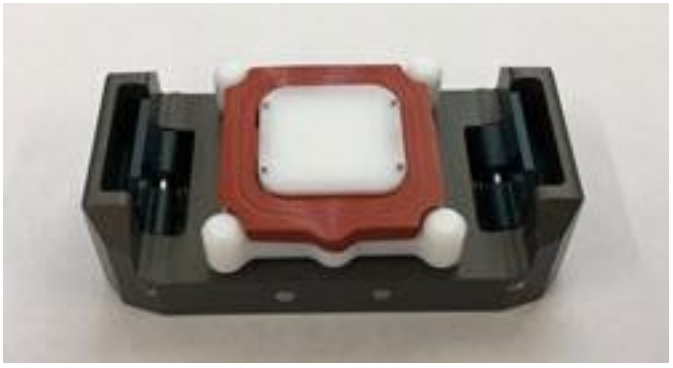


Figure 3: Incorrect Position

Attach Saphyr Clip to Saphyr Chip

Use gloves (powder free) for this procedure.

1. Align the clip on the chip by verifying the appropriate clip orientation.
   Make sure the clip is aligned correctly; putting the clip on backwards may break the chip.
2. Place the clip over the chip.
3. Using both hands, apply an even downward force on the right and left side of the clip to attach. Note: downward pressure should be applied to the clip, not the chip.
   Users will hear a click when the clip is attached. Once the clip is attached to the chip, do not remove it unless necessary. If users remove the clip, then rehydrate the chip inlets and outlets with nuclease-free water to replace any sample solution that has evaporated.
4. The chip can be left out for up to 1 hour at room temperature before starting the run.

Figure 4: Orient Saphyr Clip to Align with Saphyr Chip

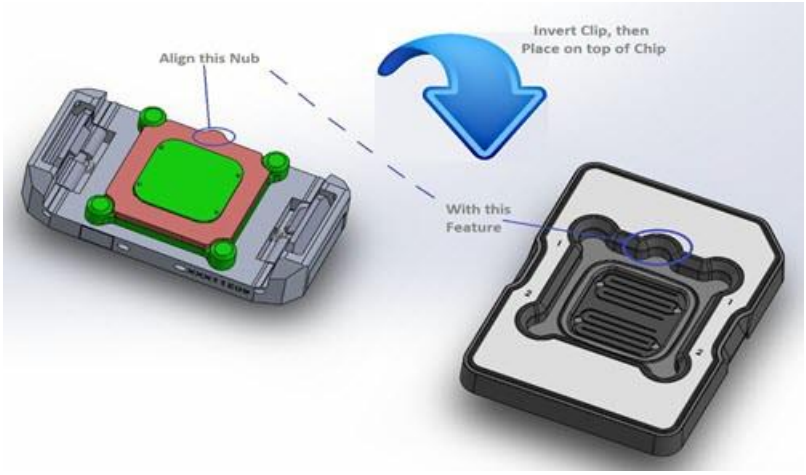


Figure 5: Clip Attached to Chip

Chapter 5: Perform Run

Insert Saphyr Chip

Before inserting the Saphyr chip into the Saphyr instrument, check the underside of the chip for dust or debris. If there is dust or debris, gently wipe the underside of the chip with lens paper. Avoid touching the underside of the chip with anything other than lens paper.

1. From the Main Menu, click **Insert Chip**.

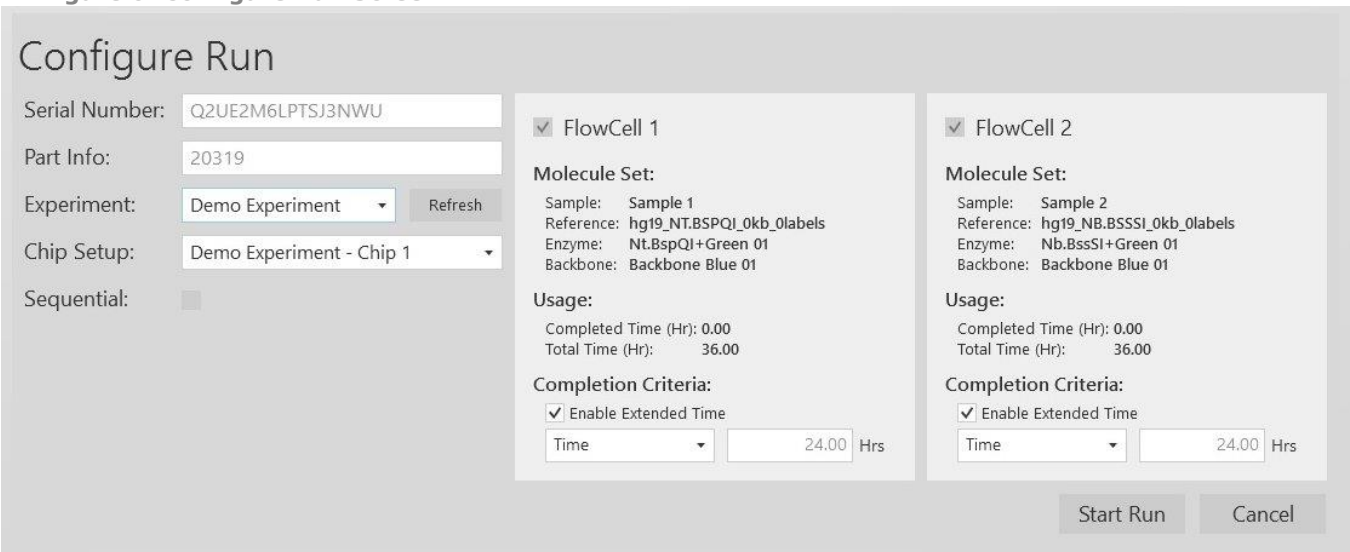
   Users will hear the stage moving outward, which can take about 10 seconds. When the stage has reached the proper position to allow for insertion of the chip, the **Chip is Inserted** option will activate on the screen.
2. Manually lift the sample door of the instrument.
3. Manually lift the bundle arm.
4. Insert the chip onto the stage with the cartridge centered on the stage pins. Make sure that flowcell 1 is farthest from the bundle arm.
5. Gently lower the bundle arm onto the Saphyr clip, and then close the sample door.
6. In the Main Menu, click **Chip is Inserted**.
   The instrument starts registering the chip.
7. If the instrument is unable to identify the chip bar code, then the *Failed to Read Barcode* dialog box appears. Choose one of these options:
   - Click **Retry Barcode Scan**.
   - At the **Serial Number** field, type the serial number that is located on the chip pouch.
   - [Optional] Click **Cancel**. Users can remove the chip and reinsert it again.
   - Click **Apply.**

Proceed to creating a new scan in the Instrument Control Software.

Configure Run Parameters

Use these guidelines when creating a new scan on the Saphyr Instrument Control Software.

Figure 6: Configure Run Screen



Parameter Field	Action
Serial Number—The serial number associated with the chip.	No action; the control software pulls this data from the Saphyr chip.
Part Info— The part number associated with the chip.	No action; the control software pulls this data from the Saphyr chip.
Experiment—The experiment to associate with the chip.	If this is a new chip, select the experiment from the drop-down list. Click **Refresh** if the experiment was recently modified.

Parameter Field	Action
Chip Setup—The chip to use for scanning.	Select the Saphyr chip from the drop-down list.
Sequential—The laser activation sequence.	Only used for multicolor samples. Recommend not be selected without consultation with Bionano FAS. See 30193 Guidelines for Running Red Labeled Samples for more info.
Molecule Set (Flowcell 1 and Flowcell 2) • Sample—The selected sample. • Reference—The selected reference map. • Enzyme—The selected enzyme. • Backbone—The applied label for the backbone.	No action; the control software pulls this data from the selected experiment in Bionano Access.
Usage • Completed Time (Hr)—The number of hours that the instrument has completed scanning for Flowcell 1 or for Flowcell 2. • Total Time (Hr)—The number of scanning hours remaining for both flowcells. This number includes the extended scanning hours.	No action; the control software pulls this data from the Saphyr chip.
Completion Criteria Enable Extended Time—Allow instrument to scan additional hours.	Select the **Enable Extended Time** check box to allow the Saphyr instrument to continue scanning the chip if the minimum throughput is not acquired. The instrument can continue scanning for up to 12 hours. Click the drop-down list to select one of the following: • Time—The instrument scans the chip for the remaining amount of time. The default time is displayed. • Throughput—The instrument scans the chip until the desired throughput is acquired. Enter the desired throughput value, which can be up to 320 Gbp per flowcell.

Create a New Scan

After inserting the Saphyr chip in the Saphyr instrument, the next step is to create a new scan.

1. Navigate to the Instrument Control Software on the desktop.
2. From the Main Menu, click **Create New Scan**.
   The *Configure Run* screen appears. For details, see the above table on run configurations.
3. At the **Experiment** field, select the experiment to associate with the chip from the drop-down list.
   [Optional] Click **Refresh** to update the list.
4. At the **Chip Setup** field, select the chip to run from the drop-down list.
5. Review the run parameters for Flowcell 1 and Flowcell 2.
6. Click **Start Run**.
7. Saphyr starts the following process:
   a) Chip Registration

   Note: If registration fails, click **Retry Registration** and/or refer to Appendix A.

b) DNA Loading Optimization
c) Scanning

When the run is complete, the following message appears: `Run Complete`. Users will receive an email notification that the run is complete.

8. Click the **Home** icon to return to the main menu.

Insufficient Disk Space

When clicking **Start Run** in the *Configure Run* screen, if there is not enough disk space to run the Saphyr chip, ICS displays an error message:

```
Insufficient Disk Space for sample run.
Available:[number] GB
Required:[number] GB

Use the Data Administration screen to delete run data.
```

Follow these steps:

1. Click **OK**.
2. At the *Configure Run* screen, click **Cancel**.
3. From the Main Menu, click **Data Administration**.

   See Appendix B for instructions on deleting runs.

Remove Chip

Users can remove the Saphyr chip from the Saphyr instrument when the run is successfully complete or when the run is stopped.

1. From the Main Menu, click **Remove Chip**.
2. Manually lift the sample door of the instrument.
3. Manually lift the bundle arm.
4. Remove the chip with clip attached.
5. Lower the bundle arm and close the sample door after removing the chip.
6. From the Main Menu, click **Chip is Removed**.
7. Close the Instrument Control Software program.
8. [Optional] Turn off the instrument.
   The instrument can stay on. To set up another chip run, repeat these tasks:
   - *Create an Experiment*
   - *Insert Saphyr Chip*
   - *Create New Scan*

After removing the chip, detach and clean the Saphyr clip as soon as possible. See the *Maintenance* section for details.

Chapter 6: Analyze Data

Data Transfer for Analysis

After the instrument scans the chip for about 15 to 20 minutes, users can monitor the run progress and view quality metrics in real time on Bionano Access.

Following the completion of a run, users can perform the following analyses:

Analysis	Description
Molecules Merge	Merge two or more molecules objects into a single molecules object.
de novo Assembly	Assemble single molecules into consensus maps for SV Detection and Hybrid Scaffold applications.
Hybrid Scaffold	Merge Bionano maps with sequence assemblies to produce long hybrid scaffolds that represent the chromosome structure for analysis.
2-Enzyme Hybrid Scaffolds	Combine two sets of Bionano maps and a sequence assembly to generate two-enzyme hybrid scaffolds, which increases specificity and resolution.
Alignments	Compare two different maps by aligning them to each other.
Structural Variation (SV) Merge	Merge SV calls obtained by using two different enzyme assemblies (e.g. Nt.BspQI and Nb.BssSI) of the same sample. This analysis increases specificity of SVs size, location, and accuracy.
Variant Annotation Pipeline	Identify rare and potential *de novo* SVs for trio (mother, father, and proband) or for cancer research.

For more details on Bionano Access analysis and visualization features, see the *Bionano Access Software User Guide (document # 30142)*.

Chapter 7: Maintenance

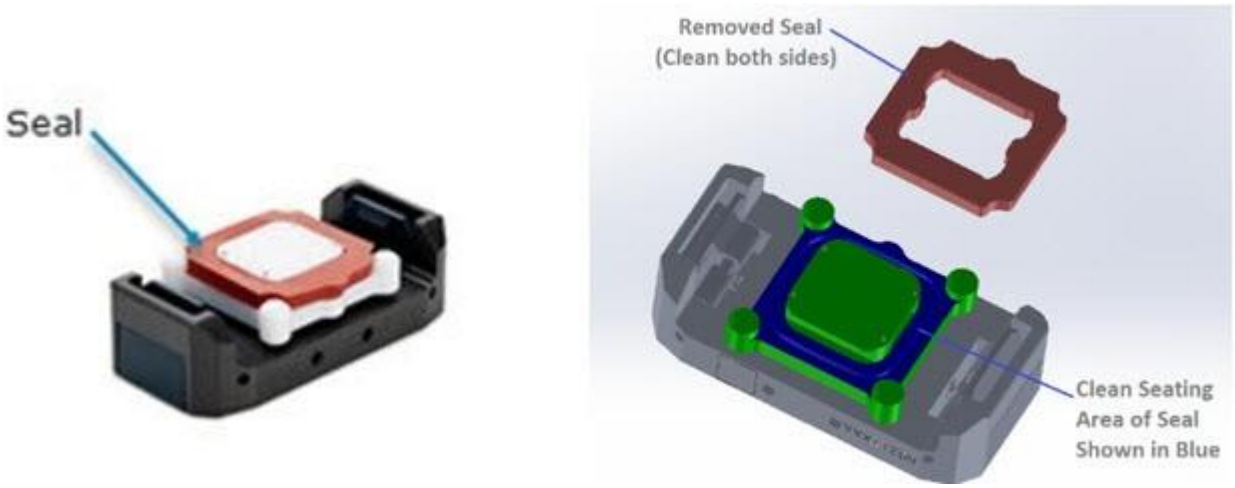
Clean Saphyr Clip and Seal

Clean the clip and seal every time you do the following:

- Remove the Saphyr chip from the Saphyr instrument after a successful run.
- Take the clip out of storage for use.

Use gloves when cleaning clips and seals.

Figure 7: Saphyr Clip and Seal



1. Remove the seal from the clip.
2. Use a lint-free wipe saturated with 70% alcohol to remove any visible dirt or debris on both sides of the seal and the surface of the clip and the seal seating area.
3. Place the seal back on the clip. Ensure the seal is in the correct orientation, and then push all corners of the seal down. Ensure the corners of the seal are not sticking up.
4. Use a lint-free wipe saturated with 70% alcohol to remove any visible dirt or debris along the upper side of the seal and center of the clip where the four electrodes are protruding from, as well as the electrodes themselves.

5. Air dry the clip before using it again.
6. Store the clip in a clean case with a cover when not in use.
   The case is not included with the clip.

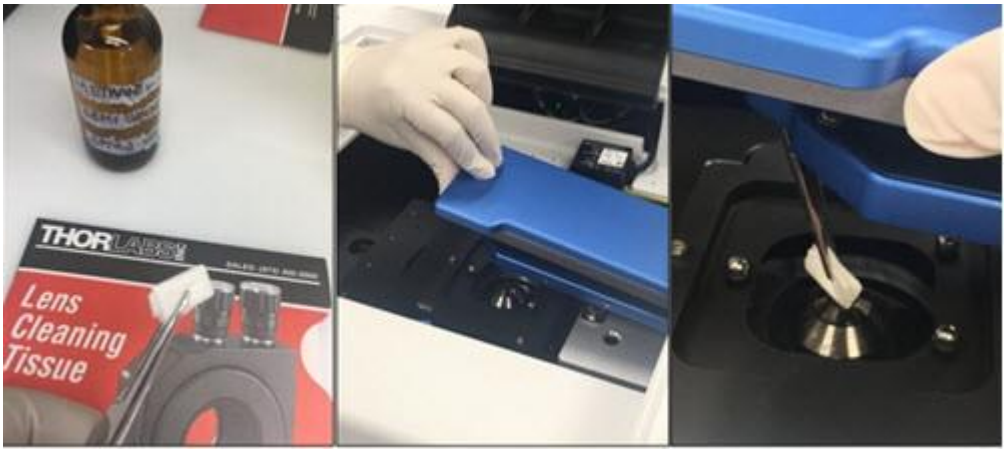
Clean Instrument

Use a lint-free cloth to clean the surface and sides of the instrument.

Clean the Objective Lens

We recommend that users clean the objective lens every 3 months.

Figure 8: Cleaning the Objective Lens



1. Launch the Instrument Control Software.

   Important: A new session of ICS must be started in order to move the stage to the correct position. If ICS is open, please close and restart.

2. Wait until the instrument has finished the initialization process so that the stage reaches the home position, and then close the software.
3. Disconnect the main power connectors from the instrument.
4. Manually lift the sample door.

   Users may need to apply some force to lift the sample door.

5. Fold a lens tissue into four.
6. Clamp the tissue with a flat hemostat or flat forcep, and then add 2 to 3 drops of 98% methanol on the tissue.
7. Lift the bundle arm with one hand, and hold the hemostat with the other hand to clean the surface of the objective lens. Move the tissue in a circular motion.

   Note: The bundle arm does not lift up all the way.

Replace Air Filter

We recommend that users replace the air filter every 3 months. The air filters are included in the Accessory Kit that came with the Saphyr instrument.

1. Turn off the instrument.
2. On the back of the instrument, pull the air filter cover firmly away from the instrument to release the magnets that hold the cover in place.

3. Remove the air filter from its cover.
4. Insert a new air filter. Make sure the Air Flow arrow symbols are facing up (air flows into instrument).

5. Attach the cover with the new air filter to the instrument.

To order additional filters, send a request to orders@bionanogenomics.com. The catalog number is RP-51535.

Appendix A

Troubleshooting

Problem	Possible Cause	Recommended Action
The software did not initialize.	The software was unable to connect to the hardware devices.	Restart the instrument.
• The run does not start due to electrical contact failure • Loading fails during scanning	There is insufficient liquid in the wells because: The chip could be cracked. OR There is evaporation in the flowcell.	Stop the run; remove the chip; examine underneath the chip for liquid. If there is liquid, then the chip is cracked. If there is no liquid, remove the clip from the chip, rehydrate the chip with nuclease-free water, attach the clip to the chip, and reinsert the chip in the instrument, restart the run.
The Saphyr chip does not align during the initial phase of the run.	The chip is not inserted correctly in the instrument.	Stop the run, remove the chip, reinsert the chip on the stage correctly, and restart the run.
The Bionano Access dashboard stops generating data but the instrument is still running.	There is a network outage. When there is a network outage, the instrument continues to image the chip and stores the data on the Instrument Controller.	1. Check the network connections. 2. If there is a network outage, restore connection.
The run is normal based on throughput specifications and labels per 100 kpb, but the map rate is zero.	The reference genome input during setup is incorrect. The enzyme input during setup is incorrect.	Verify that the reference genome and the enzyme is correct. Follow these steps if the reference genome or enzyme is incorrect: 1. Do not stop the run. Wait for the run to complete. 2. In Bionano Access, download the molecules file from the *Project* page. 3. Re-upload the molecules files to Bionano Access; select the correct reference or enzyme during setup. The Molecule Quality Report (MQR) tool will automatically display the correct run results.

Stop or End a Run on the Saphyr

Users can stop or end a run at any time while Saphyr is performing these steps: chip registration, DNA load optimization, scanning.

1. From the *ICS Protocol Status* screen, click **Cancel**.
   The button is at the bottom left-side of the screen.
2. Click **Remove Chip**.

View the *Remove Chip* task for more details.

Export Data Configuration

Users can export data configuration to their computer, such as log and calibration data from the instrument, and then send to Bionano Genomics Support for troubleshooting.

1. From the Main Menu, click the **Help** icon at the top-right corner of the screen.
   A dialog box appears.
2. Click **Export Configuration**.
3. [Optional] Select the **Full configuration** checkbox to collect the archived logs.
   This option increases the export file size and the time it takes to compress the files.
4. Click **Compress and Export Configuration**.
5. Type the file name.
6. Select the location to save the ZIP file.
7. Click **Save**.
8. When ICS completes compressing the files, navigate to location of the ZIP file, and then send it to Bionano Genomics Support.

Export Run Diagnostics

Users can export run diagnostic data from a specific run to their computer, and then send to Bionano Genomics Support for troubleshooting.

The run serial number is required for this procedure. Users can obtain the serial number of the run from Bionano Access: **Home** > **Experiments** > **Chip Runs**

1. From the Main Menu, click the **Help** icon at the top-right corner of the screen.
   A dialog box appears.
2. Click **Export Run Diagnostics**.
3. In the text box, paste or type the serial number of the run.
4. Click **Compress and Export Run Diagnostics**.
   The *Browse For Folder* dialog box appears.
5. Select the location to save the `*.SaphyrArchive` file, and then click **OK**.
   If the serial number is not valid or the diagnostic data is no longer available, an error message appears: `Could not find any diagnostic info for serial number [16-digit number]`.

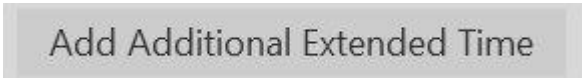
   Click **OK** to return to the *Help* screen.
6. When ICS completes compressing the files, navigate to location of the file, and then send it to Bionano Genomics Support.

Request Additional Run Time

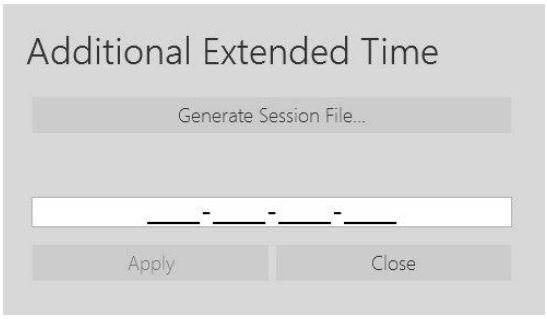
Users can request additional run time for a chip if the target throughput of a good quality sample is not achieved during the standard run time.

Important: Prior to running a chip for additional time the user must remove the chip from the instrument, rehydrate both flowcells with nuclease-free water, and then reinsert the chip.

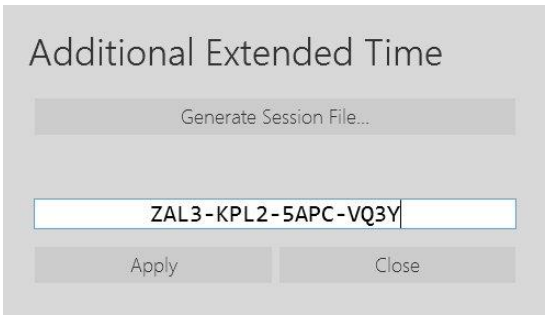
1. Insert the chip as outlined in Chapter 5 and select **Create New Scan**.
2. On the **Configure Run** screen, click on **Add Additional Extended Time**.



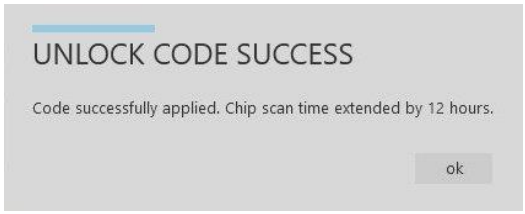
3. Click on **Generate Session File...**



4. The system will generate a **.SaphyrUnlock** file and prompt the user to save the file. Save the file and then send to Bionano Genomics Support.
5. After receiving a 16-digit unlock code from Support, enter the code and click **Apply**.



6. A new window will indicate the duration of the additional scan time added to the chip. Click **OK**.



7. Click **Start Run** to begin scanning the chip.

Note: A new Chip Run ID will be created in Access for the scan.

Appendix B

Data Administration

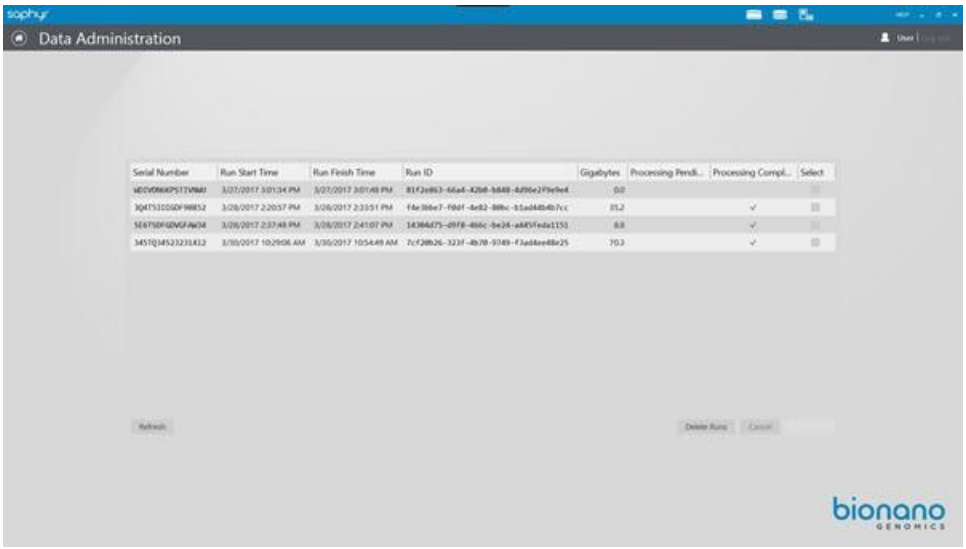
The Data Administration option from the Main Menu allows users to manage run data that are on the Saphyr Instrument Controller.

Delete Runs

After data transfer is complete, delete runs to clear space for a subsequent run. Runs that are currently in progress cannot be deleted.

1. From the Main Menu, select **Data Administration**.

Figure 9: Run Data Info on ICS



Statistic	Description
Serial Number	The chip serial number.
Run Start Time	The run start date and time.
Run Finish Time	The run end date and time.
Run ID	The system-generated run ID.
Gigabytes	The size of the run.
Pending	The check mark indicates the Saphyr Instrument Controller is currently transferring run data to Bionano Access.
Complete	The check mark indicates the Saphyr Instrument Controller has successfully transferred run data to Bionano Access. Users can access all the BNX files for this run.
Select	Select the check box to choose multiple runs for deletion.

[Optional] Click the column heading to sort the information in the column.

2. In the Select column, click the check box of run(s) to delete.

3. Click **Delete Runs**.

   Depending on the data size, this process may take several minutes. Users can view the progress bar in the middle of the screen.

4. [Optional] During the deletion process, click **Cancel** to stop the process.
   The selected run data is restored.
5. When the process is complete, the screen shows the runs that are still on the Saphyr Instrument Controller.
6. Click the **Home**  icon to return to the *Home* page.

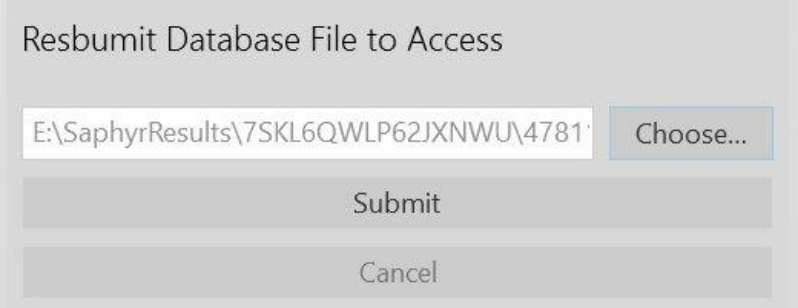
Appendix C

Resubmit Run to Access

The Resubmit Run to Access option from the Main Menu allows users to resubmit a dataset for reanalysis. This may be used if a network connection issue has caused an error in the initial analysis of the run data.

Note: This process can only be completed for full datasets stored locally on the Instrument Controller. If the run has been deleted via **Data Administration**, then resubmission cannot be performed.

1. From the Main Menu, select **Resubmit Run to Access**.
2. Click **Choose…** and select the **.Saphyr** file associated with the dataset you wish to reanalyze.



3. Click **Submit**.
4. The existing Chip Run will be deleted from the Access database, and a new run will be created in Access.

   Note: The Chip Run ID will remain the same.

Appendix D

Instrument Disposal

This label indicates that the instrument meets the 2012/19/EU Directive on waste electrical and electronic equipment (WEEE).

Email support@bionanogenomics.com for instrument disposal.

Figure 10: WEEE Label

Additional Resources

The following documentation is available for download from the Bionano Support page.

Resource	Description
Saphyr System Safety Guide (document # 31044)	Provides information about the instrument safety considerations.
Saphyr Site Prep Guide (document # 30145)	Provides specifications for laboratory space, electrical requirements, and environmental considerations.
Bionano Access Software Guide (document # 30142)	Provides an overview of data analysis.

Technical Assistance

For technical assistance, contact Bionano Genomics Technical Support.

Users can retrieve documentation on Bionano products, Safety Data Sheets (SDS), certificates of analysis, frequently asked questions (FAQs), and other related documents from the Support page or by request through e-mail and telephone.

Type	Contact
Email	support@bionanogenomics.com
Phone	**Hours of Operation:** Monday through Friday, 9:00 a.m. to 5:00 p.m., PST US: +1 (858) 888-7600
Website	www.bionanongenomics.com/support

Bionano Genomics, Inc.
9640 Towne Centre Drive, Suite 100
San Diego, CA 92121
Phone: (858) 888-7600
www.bionanogenomics.com