Bionano Access™ Software User Guide

DOCUMENT NUMBER:
CG-30142

DOCUMENT REVISION:
R

Effective Date:
2025-Aug-04

Table of Contents

Revision History

REVISION	NOTES
N	Update for Bionano Access 1.7 1) Removed references to Irys line of products. 2) Updated various legacy terms and associated procedures to conform with Saphyr terms. 3) Updated Jobs Menu 4) Included EnFocus™ Fragile X Analysis Options to menu. 5) Added NxClinical Bundle Download feature. 6) Added Chips Metrics Dashboard feature. 7) Added Perform Duo and Trio Analysis execution steps. 8) Enhanced explanation of the following features a. Circos Plot visualization b. Enhanced Whole Genome visualization. c. Curated Variant List 9) Added Visualization Reporting functionality. 10) Updated View option settings Updated Settings section to reflect Access 1.7 updates
O	Updated for Bionano Access 1.8 1) Revised section formatting for conciseness and clarity without changing meaning. 2) Changed listing of Terms and Definitions to table format. 3) Reworded redundant information or deleted altogether. 4) Created table for reference documents table. 5) Put “Job Options” and “Job Operations” text into tabular form.
P	Updated for Bionano Access 1.8.1 1) Added Guided Assembly section.
Q	Updated to include information on Stratys™ and Stratys™ Compute
R	Updated for v1.8.3

References

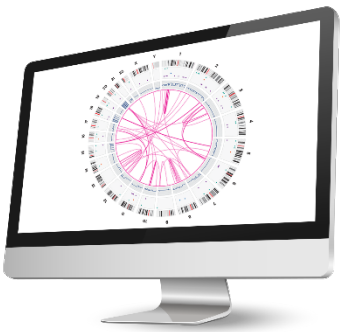
Table 1. References

Document Number	Reference Title
CG-00045	*OGM File Format Specification Sheet*
CG-30073	*Bionano Solve Theory of Operation: Hybrid Scaffolding*
CG-30110	*Bionano Solve Theory of Operation: Structural Variant Calling*
CG-30170	*Bionano Access Installation Guide*
CG-30173	*Data Collection Guidelines*
CG-30190	*Bionano Solve Theory of Operation: Variant Annotation Pipeline*
CG-30223	*Molecule Quality Report Guidelines*
CG-30304	*Bionano Access Dashboard Guidelines*
CG-30321	*Bionano Solve Theory of Operation: Bionano EnFocus™ FSHD Analysis*
CG-30377	*How to enable HTTPS in Bionano Access*
CG-30457	*Solve Theory of Operation: Bionano EnFocus™ Fragile-X Analysis*

Glossary

Table 1. Bionano Access Terms

Term	Definition
Cluster	Multiple compute servers can be organized into units, or clusters, which can be combined and scaled to user computing requirements.
Compute On Demand (COD)	A cloud-based computing platform, optimized for Bionano pipelines to perform bioinformatics analyses. The pipelines can work on custom clusters with custom configurations.
Job	Also known as Objects in version 1.6.1 or earlier - a distinctive set of output files that depend on a chosen operation. Examples include molecule data, map alignments, assemblies, hybrid scaffold results, and variant annotations.
Prep	Also known as a Molecule Set, this is the experiment setup consisting of the sample, reference, and enzyme in one flow cell.
Cohort	The number of subgroups that each scan is divided into for real-time analysis. One scan contains multiple cohorts, and run metrics are generated for each cohort.
Consensus Character MAP (CMAP)	The Bionano CMAP file is a raw data file which provides location information for label sites within a genome map or an i*n silico* digestion of reference or sequence data. CMAPs may refer to a reference as well as a query (sample consensus map). The CMAP is a tab-delimited text-based file. See *OGM File Format Specification Sheet* (CG-00045) for more details.
Board Neutral Exchange (BNX)	The Bionano BNX file is a raw data view of molecule and label information, and quality scores per channel identified during a run. BNX v1.3 supports one or two label channels, or colors. See *OGM File Format Specification Sheet* (CG-00045) for more details.
GUID	A Global Unique Identifier or GUID is a system generated serial numbers used to track unique items such as samples and or chip runs.
OGM	Optical Genome Mapping



Introduction

The Bionano Access™ Software enables users to remotely manage chip runs on the instrument, launch bioinformatic analysis jobs, explore genomic data, and characterize structural variants. One instance of Bionano Access can support multiple instruments including both Saphyr® and Stratys™ systems.

Bionano Access orchestrates a large portion of the OGM workflow (see **Figure 1**). First, in Access users can define the sample prep that will be loaded into a chip cartridge for scanning. Then Access monitors and collects the molecule data from the chip run. After the chip run, Access can launch jobs to align the molecules and identify structural variants. Access monitors the analysis jobs and collections the results. Users can then visualize those results using the rich set of visualization tools that Access contains.

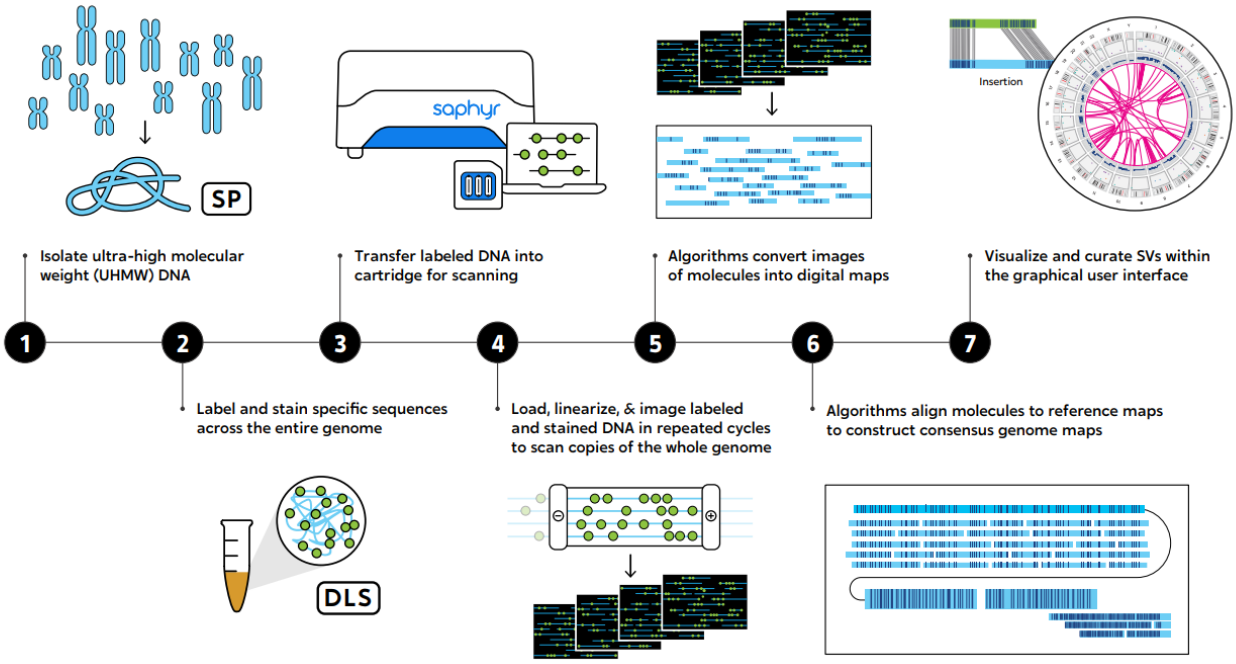


Figure 1. Optical Genome Mapping workflow

This guide will familiarize users with how to use Access to perform this workflow. First, this guide will cover how to access the system and then will cover chip setup and chip run dashboards. Next, how to launch and manage analysis jobs will be reviewed and then how to use the visualization tools. Lastly, various administrative options and settings will be discussed.

Installation

Bionano Access is a web application. It is installed on a single centralized web server and accessed by workstations on the same network using an Internet browser. To set up an instance of Bionano Access follow the instructions in the *Bionano Access Installation Guide* (CG-30170). Once the instance of Bionano Access has been created, the user will know the URL for the local Binano Access web application.

Login Screen

When connecting with Bionano Access via a browser, the login page will be displayed first (**Figure 2**). Provide credentials on the login screen to enter the application. If logging in for the first time, the user will be prompted to create a new password to replace the initial temporary password on the account. That way only the user will know their own password. If the system has email enabled there will be a **Forgot Password** option on the **Login** page in case a password is forgotten.

Administrators who set up the system control password complexity, session controls, password expiration, and password retention. Depending on how the system is configured, the passwords provided may be subject to different criteria. It will also affect how often a new password is necessary.

Bionano Access has a bookmarking feature. If the user requests any **Bionano Access** page but does not have an active session, the system will bookmark the URL and then redirect to the login page. After providing valid credentials, the system will load the bookmarked URL initially requested. After login in, if there is no bookmark, the system will load the **Home** page. After logging in, the session may expire if inactive for too long. If the session expires the user will be returned to the **login** screen. The bookmarking feature works in this case also. After logging in to refresh the session, the system will return to the page last viewed.

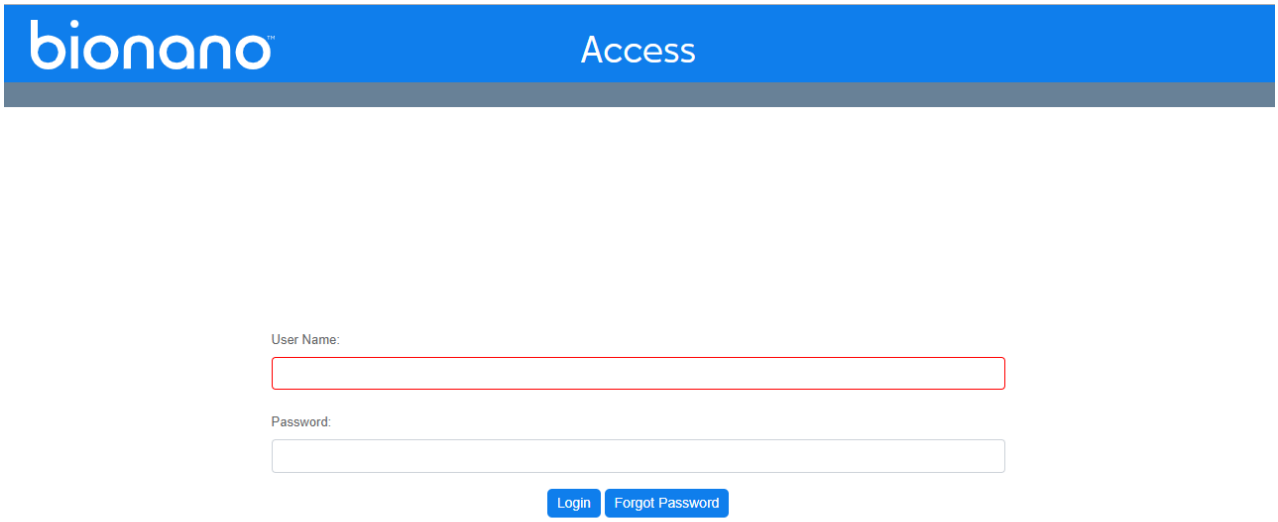


Figure 2. Login Screen

Home Page

The **Bionano Access Home Page** is the default landing page after logging in. From the home page the user can chose which system module they want to access. The modules available may vary depending on how the system is configured or the current user's permissions. The home page also displays the current status of various system services.

Table 1. Bionano Access modules

Module	Description	Availability	Note
Analysis	Users create, view, edit, and manage projects. Users can also import and export data.	All user roles.	Name changed from "Projects" to "Analysis" in Access 1.7
Chips	Users can set up and manage Saphyr or Stratys experiments, view templates, and track chip run progress.	Only for systems integrated with an Instrument. (Not available for Read-Only)	Name changed from "Experiments" to "Chip" in Access 1.7
Settings	Users can manage user accounts, shared resources, system settings, and system services. Users can also run the in silico digestion tool to generate new references.	Only available to "Administrator" and "Project Lead" user roles.	

Module	Description	Availability	Note
Compute On Demand	Users can manage tokens, redeem vouchers, and track Compute On Demand jobs.	Only available for systems enabled with Compute On Demand.	

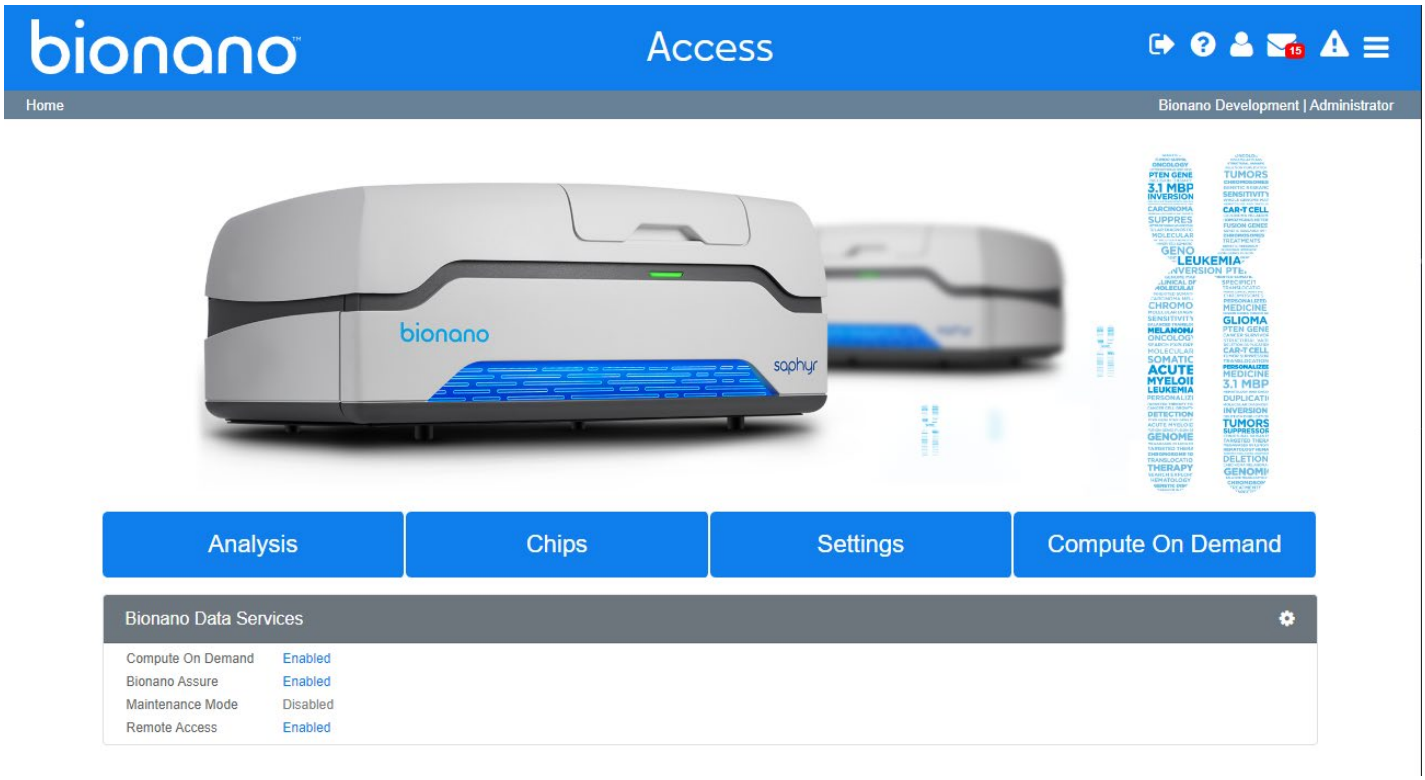


Figure 3. Access software Home Screen

Page Header

On most pages there is a header at the top of the screen. We do not show the header in the viewer screens to give maximum screen space to examine genomic data. Below the header there is a grey navigation bar. On the left side the navigation bar displays breadcrumbs, and on the right, it displays the active user's name and role. The header includes some icons in the upper right corner that are links to helpful functions. Mouse hovering over any of these icons will display a hint. The icons available may change from page to page depending on the context. In this section we describe the common icons typically seen on most screens.

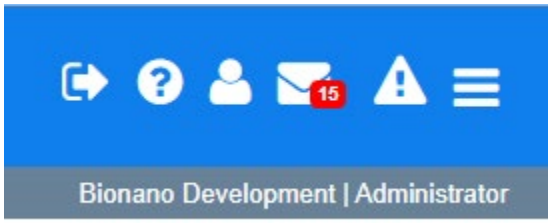


Figure 4: Header icons

Logout

Clicking the logout icon will terminate the session and return to the **login** page. It is good practice to logout when leaving a shared system or will not be using the application again in the near future.

Help

Users can click the **Help** icon to access the **Help** page in Access. Software version information for Access and Solve, Compute On Demand version information for Bionano Tools and Solve, if enabled, video tutorials, security patch information and support contact information are all available here as well.

User Profile

Click the **User Profile** icon to see account settings. The user can change the user's email address, password, and/or enable email notifications.

Message Center

Click the **Message Center** icon to read and delete messages. Messages can be deleted after they have been read. The icon will indicate in red the number of unread messages. Bionano Access is capable of sending email notifications which it is configured to do by default. The Message Center was created for sites where the instrument and associated computer systems have been isolated and it cannot transmit email messages. Whenever the system might potentially send an email it also creates a message in the message center. This way the user is certain to be notified when background processes such as jobs or imports are completed.

Alerts

Bionano Access sends alerts to notify system administrators of errors or system conditions that require attention. This is the foundation of proactive system diagnostics where the system can monitor itself and alert those responsible when action is needed. This feature works similarly to the messaging and message center, where notifications are sent to specific users regarding job status and other system events. Alerts are broadcast to all users in the Administrator role. The **Alerts** icon will appear in the header of Bionano Access next to the existing

Message Center Icon. The system will also post alerts that pertain to a chip run on the dashboard sent by the instrument. The alert icon will display the number of unread alerts in red just like the message icon.

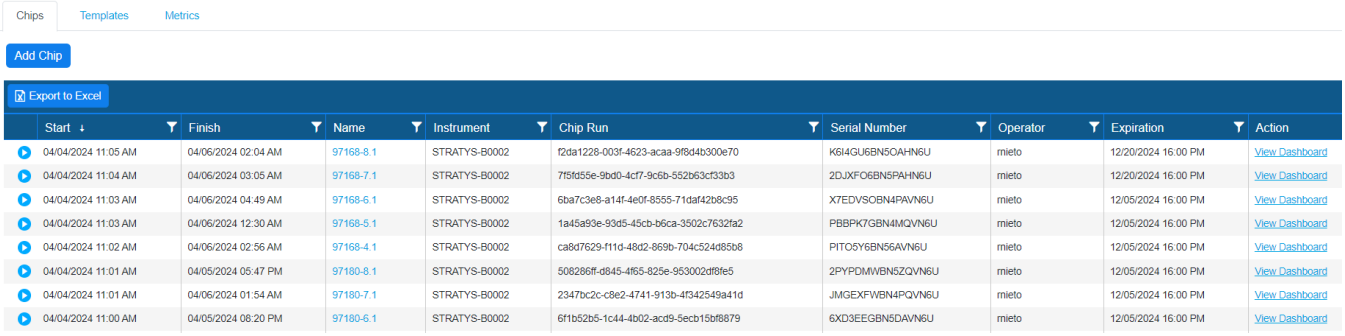
Menu

The menu provides a convenient way to jump between system modules without having to return to the home page. The menu also has a **Job ID Search** feature. In the **Job Search ID** field, the user can enter a job number and the system will go to that job.

Chip Module

When the chips module is selected the system will display the chip list. You can sort the chip list by clicking on the column header you want to sort. The first click on a column header will sort the list in ascending order by the value in the selected column. The second click on the column header will sort the list in descending order. A third click on the column header will remove the sort on that column. The chip list can only be sorted on one column at a time. If you click to add a sort on another column it will replace any sort you had. It is possible to filter the list by clicking on the filter icon for the column header that corresponds to the values you want to filter. You can filter on multiple columns. To clear a filter, click the filter icon again then click the 'Clear' button.

Chips go through two stages. When they are first created a chip is just the chip setup. A chip setup defines the sample prep loaded into each flowcell. Once that chip setup becomes associated with a physical chip and loaded into the instrument it becomes a chip run. You can change the chip setup, but you cannot change a chip run. Once a chip has started in the instrument the chip setup will become locked. In the chip list, chips that have a 'View Dashboard' link are chip runs. To edit a chip, click the chip name value. If the chip has already started, the chip setup forms will be locked. Click the carrot icon in the leftmost column to see the flowcells for that chip.



Start	Finish	Name	Instrument	Chip Run	Serial Number	Operator	Expiration	Action
04/04/2024 11:05 AM	04/06/2024 02:04 AM	97168-8.1	STRATYS-B0002	f2da1228-003f-4623-acaa-9f8d4b300e70	K6I4GU6BN5OAHN6U	mieto	12/20/2024 16:00 PM	View Dashboard
04/04/2024 11:04 AM	04/06/2024 03:05 AM	97168-7.1	STRATYS-B0002	7f5fd55e-9bd0-4cf7-9c6b-552b63cf33b3	2DJXFO6BN5PAHN6U	mieto	12/20/2024 16:00 PM	View Dashboard
04/04/2024 11:03 AM	04/06/2024 04:49 AM	97168-6.1	STRATYS-B0002	6ba7c3e8-a14f-4e0f-8555-71daf42b8c95	X7EDVSOBN4PAVN6U	mieto	12/05/2024 16:00 PM	View Dashboard
04/04/2024 11:03 AM	04/06/2024 12:30 AM	97168-5.1	STRATYS-B0002	1a45a93e-93d5-45cb-b6ca-3502c7632fa2	PBBPK7GBN4MQVN6U	mieto	12/05/2024 16:00 PM	View Dashboard
04/04/2024 11:02 AM	04/06/2024 02:56 AM	97168-4.1	STRATYS-B0002	ca8d7629-f11d-48d2-869b-704c524d85b8	PITO5Y6BN56AVN6U	mieto	12/05/2024 16:00 PM	View Dashboard
04/04/2024 11:01 AM	04/05/2024 05:47 PM	97180-8.1	STRATYS-B0002	508286ff-d845-4f65-825e-953002df8fe5	2PYPDMWBN5ZQVN6U	mieto	12/05/2024 16:00 PM	View Dashboard
04/04/2024 11:01 AM	04/06/2024 01:54 AM	97180-7.1	STRATYS-B0002	2347bc2c-c8e2-4741-913b-4f342549a41d	JMGEXFWBN4PQVN6U	mieto	12/05/2024 16:00 PM	View Dashboard
04/04/2024 11:00 AM	04/05/2024 08:20 PM	97180-6.1	STRATYS-B0002	6f1b52b5-1c44-4b02-acd9-5ecb15bf8879	6XD3EEGBN5DAVN6U	mieto	12/05/2024 16:00 PM	View Dashboard

Figure 5: Chip List

At the top of the chip list screen there are three tabs. Initially you will be on the Chips tab, but there are two other tabs: Templates and Metrics. Any chip setup can be made into a chip template. A chip template allows you to quickly make a chip setup. A chip template saves all the settings from a selected chip setup except the sample. When you start a chip setup from template you just select the sample(s). The rest of the chip setup will be auto populated from your template. Chip templates are part number specific. You can sort and filter the chip template list just like the chip list. You can also delete chip templates if you have sufficient permissions.

The Metrics tab will display a dashboard of chip run metrics. It will plot total DNA, N50, Average Label Density, Map Rate, DNA per scan, and Longest Molecule. By default, it will plot chip runs for the last 30 days, but you can also choose to see the plots for 60 or 90 days. Each plot data point is clickable. If you click on a data point it will display the dashboard for the chip run corresponding to that data point. If you have more than one instrument each instrument will be plotted in a different color.

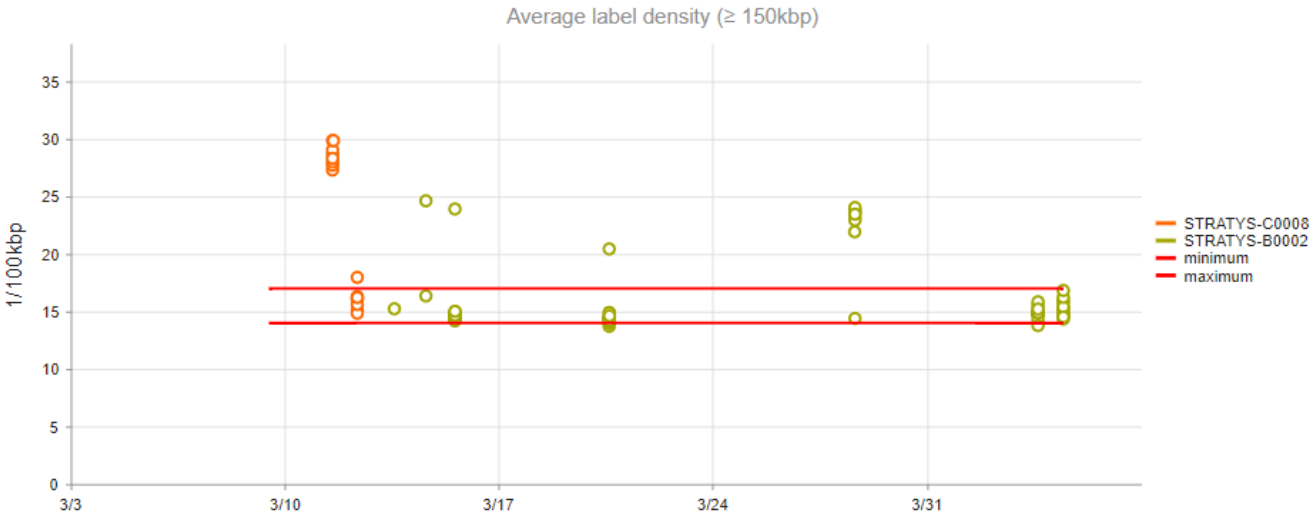


Figure 6: The Average Label Density plot from the Metrics Page

Creating a Chip Setup

To create a new chip, click the ‘Add Chip’ button on the chip list. A chip setup tells the instrument what to expect in each flowcell and how to process the chip. This is why it is not possible to change the setup after the chip run has started. There are two steps to creating a chip setup. The first step collects information about the chip. The first step will require the user to provide a chip name and select the part number. The user can also provide an optional description, enter the serial number, and/ or select a chip template. We will discuss chip templates in more detail in the following sections. If the serial number is provided up front, the instrument will automatically match the chip to the chip setup when starting a chip run on the instrument. If the serial number was not provided the instrument will prompt the use to select a pending experiment that matches the part number of the chip being run. Provide the information requested and click next to proceed to the second step.

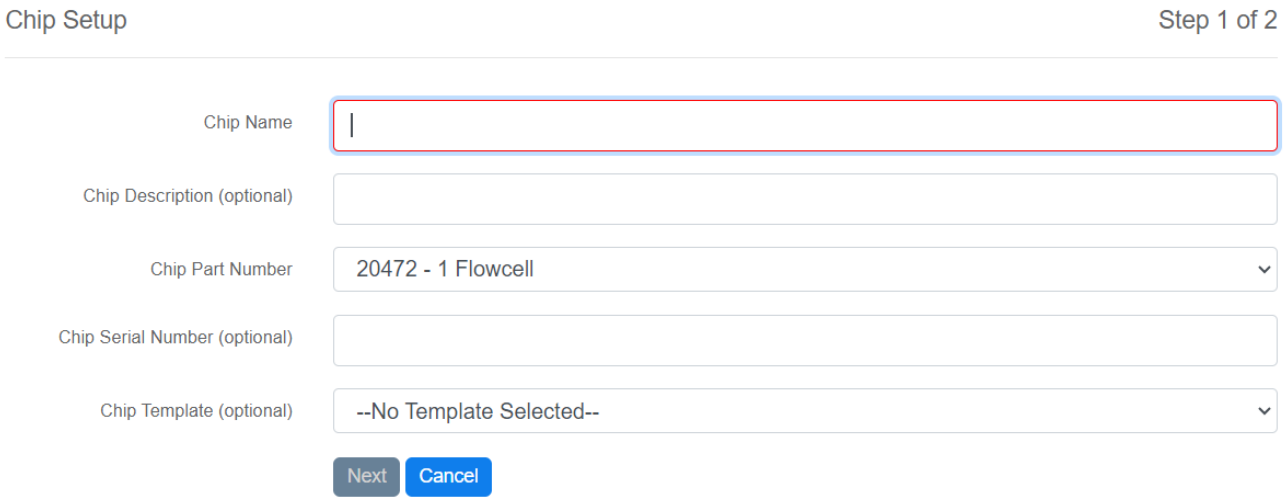


Figure 7: Chip Setup Step 1

In the first step information about the chip was collected. In the second step the user will define the setup for each flowcell. The screen is divided roughly in half. Use the form on the left to define a sample preparation or 'Molecule Set.' Then you can click the 'Add to Flowcell' buttons at the bottom to add the molecule set to the selected flowcell. The 'Add to Flow cell' buttons will be disabled until you have defined a valid molecule set. If you want to change the molecule set in a flow cell just click the remove link in the flow cell then redefine the molecule set. Remember these screens will be locked if the chip run has already started. Next, we will describe the inputs to compose a molecule set.

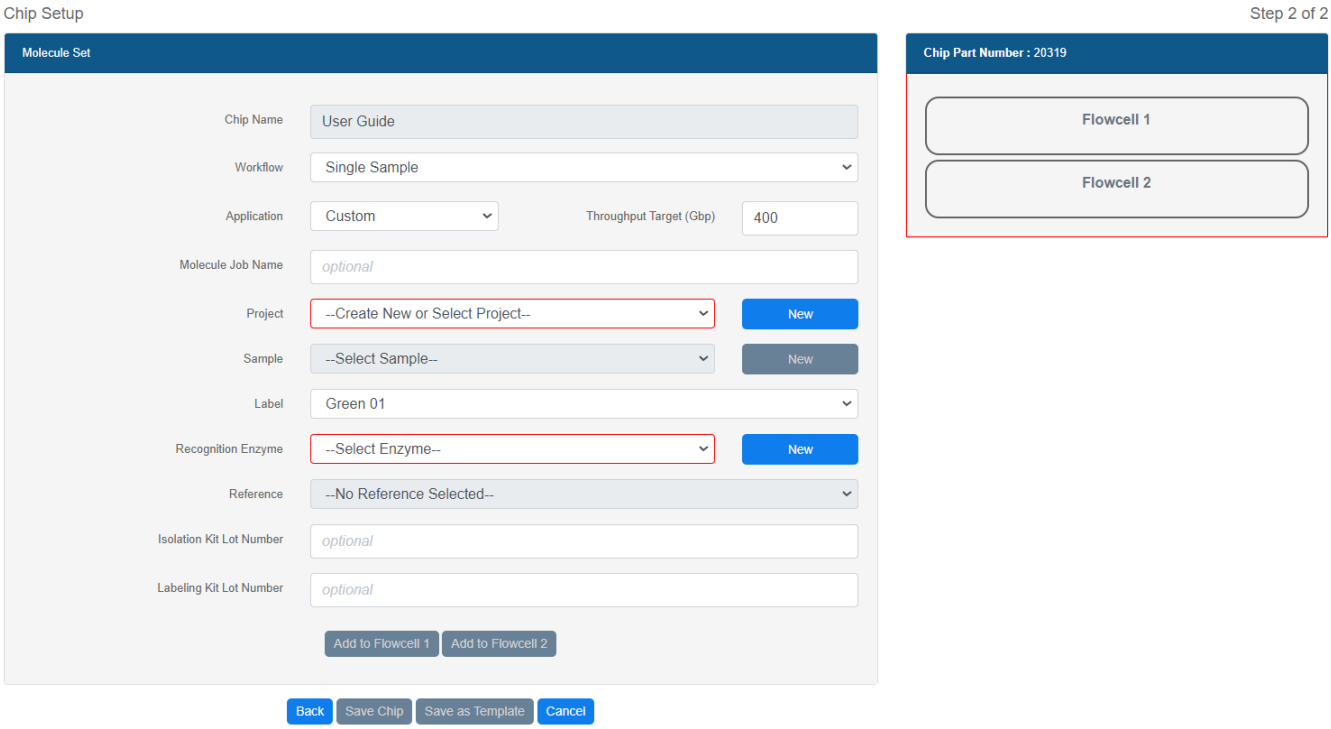


Figure 8: Single Sample Chip Setup Step 2

Workflow

Bionano Access supports three flow cell workflows, Single Sample, Multiplex, and Dual Labeled. Systems that are equipped with a single laser for detection will only run the Single Sample workflow and the workflow selection will not be disabled. The Multiplex and Dual Labeled workflows require both green and red lasers. The single sample workflow will generate a single molecule (BNX) file as a result. The multiplex workflow will generate two molecule files, one for green and one for red. The Dual Labeled workflow will generate a single BNX file that has both green and red labels. The molecule set form will change based on the workflow selected.

Flowcells

The number of flowcells to populate will depend on the chip part number that was selected on the first screen. Once you have defined your molecule set you can click the Add to flowcell button(s). To modify a molecule set you have already added to a flowcell, click the remove link in the flowcell panel on the right and then define the updated molecule set then add it to the flowcell. The figure above shows a chip that has two flowcells.

Throughput Target

The default throughput target is 400Gbp. This means the instrument will collect this much DNA then stop. The application selection here will change the throughput target to a recommended amount based on the type of analysis. It is also possible to enter a custom amount. There is a throughput limit based on the chip part number you selected in step 1.

Molecule Job Name

The system will give each molecules file (BNX) a name automatically based on the chip serial number, flow cell index, and time stamp. You can provide a name if you want the result file to have a specific name.

Project

Data in Bionano Access is organized into projects. Projects serve as a mechanism to group sample analysis results. Project can also be used to control what data users can see. How to logically organize data into projects is entirely up to the user. Select the project where the resulting molecules file should appear. Click the 'New' button to create a new project if needed.

Sample

All analysis and chip runs are associated with a sample. One sample may have many chip runs and analysis jobs. Samples are also project specific so the samples available for selection will depend on the project selected. Click the 'New' button to create a new sample if needed.

Label

The label selection is only visible if you are running the Single Sample workflow on an instrument with both red and green lasers. In this case you can choose if you will be using Red or Green labels.

Recognition Enzyme

In this drop down select the recognition enzyme used in the sample preparation. Typically, most customers will use the DLE-1, but the chip setup does support other known and custom enzymes.

Reference

Selecting a reference is optional. If you do not select a reference, the system will not provide any mapping metrics for the chip run and resulting molecules file. The reference selections will change depending on what recognition enzyme you selected. It is possible to create and use custom references. We will cover how to do that later in the user guide. If the wrong reference was selected or it is necessary to change the reference, it is possible to modify the molecules file in the analysis module after the chip run has completed.

Lot Numbers

For quality control purposes it is always a good idea to track the lot numbers used in your sample preparation. The Isolation Kit and Labeling Kit lot numbers are optional inputs.

Auto Operations

If the chip setup defined is for a human sample using a Bionano provided reference, the system will offer the option to launch auto analysis operations using default settings. The selected operation(s) will begin when the chip run has completed. The Auto Guided Assembly will run as a Low Allelic Fraction operation since that is the

default. To run these operations with customer or modified settings, launch them manually from the project browser outlined in the Analysis module later in this document.

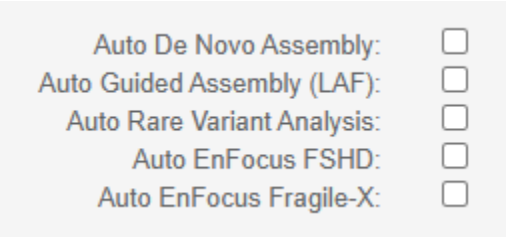


Figure 9: Auto Operations during Step 2 of Chip Setup

Saving your Chip Setup

Once each flow cell has been populated, click the 'Save Chip' button to complete the chip setup. You will be returned to the chip list. Clicking the Cancel button on step one or step two will abort the chip setup creation or edit and return the user to the chip list.

Chip Templates

There are many inputs to create a chip setup. The user must provide the project, sample, recognition enzyme, label, reference, etc. for each flow cell. When running the instrument, the operator will often use the same protocol for processing samples. The only thing that is changing between chip runs is typically the sample. You can save all the settings for a chip run as a chip template.

In step 2 of the chip setup creation screens there is a 'Save as Template' button to create a chip template. Bionano Access ships with several default chip templates for things such as Enforces FSHD Analysis. When you create a chip template the system will determine the unique number of samples used and prompt the user to name each sample slot.

When a chip template is selected in step 1 the system will prompt the user to select the sample for each sample slot in the template. When the 'Next' button is clicked step 2 will be auto populated with the samples selected and the settings from the chip template. The user only needs to review the chip setup and click 'Save Chip' to complete the creation of the chip setup.

Users cannot edit chip templates. To change a chip template, delete the template from the chip template list and create it again via the chip setup screens.

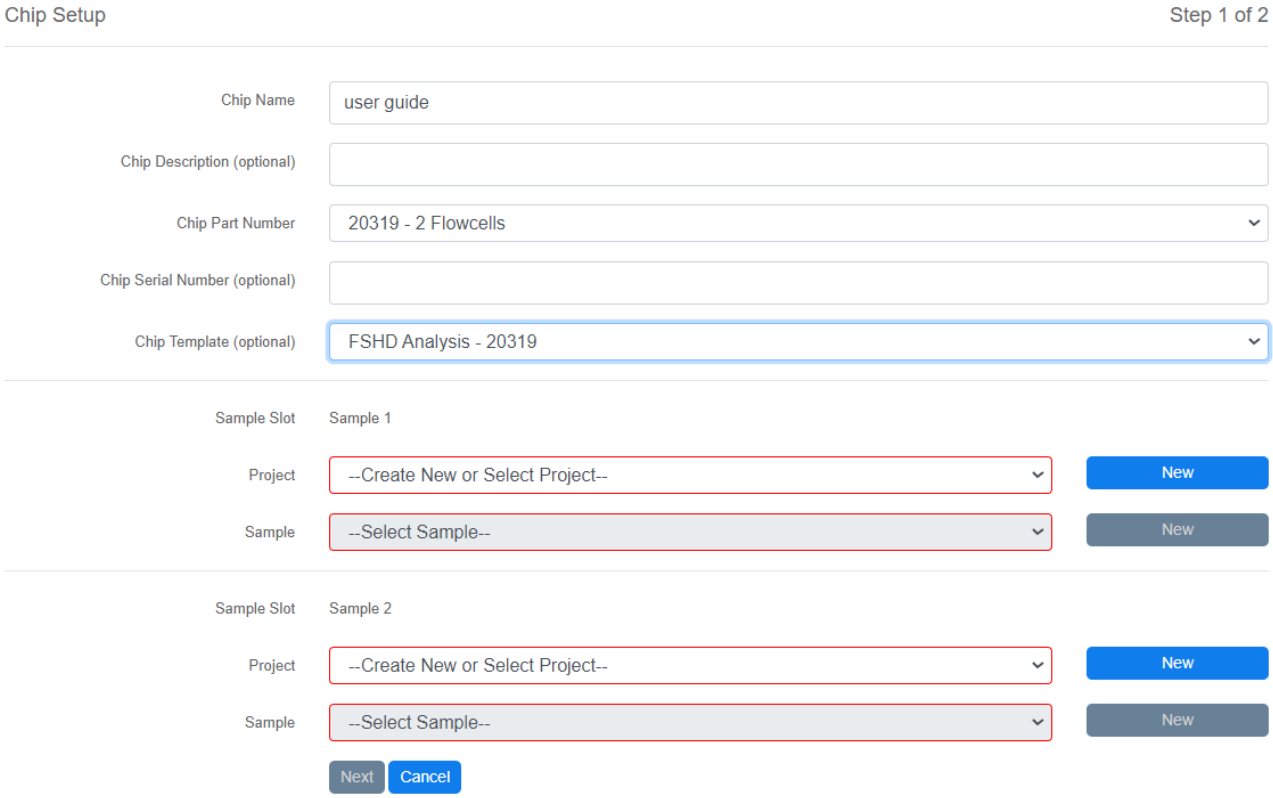


Figure 10: Chip Template Selection

Chip Dashboards

Once a chip run has started you can click on the 'View Dashboard' hyperlink in the chip list. The chip dashboard will allow you to monitor the chip run remotely. The top of the dashboard provides metadata about the chip run so that it is clear which chip run is being displayed. Below the dashboard will plot the DNA collected per Scan and the Map Rate (provided a reference was selected in the chip setup). Click on either plot to enlarge it. Click on it a second time to return it to normal size. At the bottom of the dashboard there is a table that displays summary information for each flow cell.

The Plot column in the summary table includes a color tile and a checkbox. The dashboard will plot metrics for each sample in each flow cell. The color tile in the plot column helps the user know which line is which sample in the graphs. The user can toggle the checkbox in the plot column to turn the corresponding line in the graph on or off.

The first row of the summary table breaks the data into two sections. The section on the left pertains to the current chip run. The right-hand section shows the cumulative metrics for the chip which would include any chip runs for that chip.

When a chip run is completed a molecules file (BNX) will be generated for each sample in each flowcell. Those resulting molecule files will be accessible in the Analysis module in the project that was selected. You can click the project name for a prep to jump to that project. You can also click on the icon in the Result column to navigate directly to that molecules file. The result icon will not be visible until the molecules file is available.

Figure 11: Chip Dashboard

Analysis Module

In the **Analysis** module Project Leads can create projects and control who can access them. Inside the projects they are authorized to use, users can launch analysis jobs and review results. This section describes the functions that can be performed in the **Analysis** module.

Projects

Data in Bionano Access is organized into projects. Projects serve as a mechanism to group sample analysis results. Project can also be used to control what data users can see. How to logically organize data into projects is flexible. Job and sample names must be unique within a given project.

Project List

When selecting the Analysis Module, the initial screen displayed is the Project List. It will list the projects the user is authorized to access. If the user is a Project Lead or Administrator, they will see all the projects. If a user or read-only user, they will only see the projects authorized to access. In the screenshot below all columns to the right of the Date Created column are visible only to Project Leads and Administrators. Users can sort the list by clicking on the column headers and add or remove filters by clicking the filter icons in the corresponding column header.

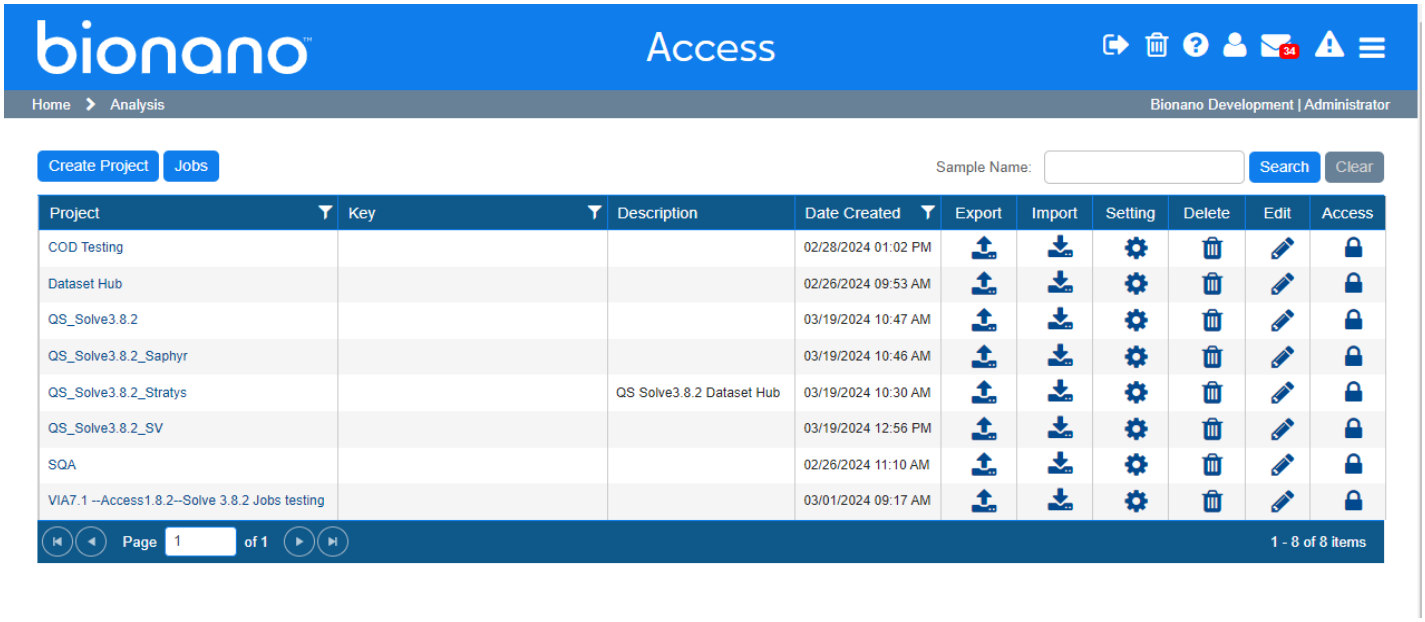


Figure 12: Project List

Users in the Project Lead or Administrator role can create Projects on the Project List screen by clicking the 'Create Project' button. The system will prompt the user for the project name, key, and description. The key field is useful if the site uses project codes or identifiers.

Sample Search

At larger sites there may be a lot of projects. If you are looking for a particular sample, but don't know which project it is in you can use the sample name search field at the top of the Project List screen. Input the sample name desired and click the 'Search' button. The list of projects will change to include any project that has a sample whose name includes the search string you submitted. If there are no matching projects the list will be empty. To reset the list click the 'Clear' button. The 'Clear' button will only be active if search criteria is active.

Project Import / Export

To transfer data between projects on the same Bionano Access Server use the copy button in the Project Browser (detailed below). To transfer data between different Bionano Access Servers use the project export and import feature from the project list. Results for an individual job can be downloaded from the Project Browser directly in the browser. Project Export files can be considerable in size because they include multiple jobs and thus are not transferable through the browser. The export files are written to the file system on the Bionano Access Server instead. To use the Project Export and Import features effectively you must have access to the file system on the Bionano Access Server. The file location for export and import files can be configured but the default location is ~/access/share/exports and ~/access/share/imports.
After clicking the project export icon in the Project List the user will be prompted for the export name and which jobs to export. The selected jobs will be written to a single export file which is a specialized zip file. It will take time to generate the export file. When the export launch screen is submitted the export process will run in the

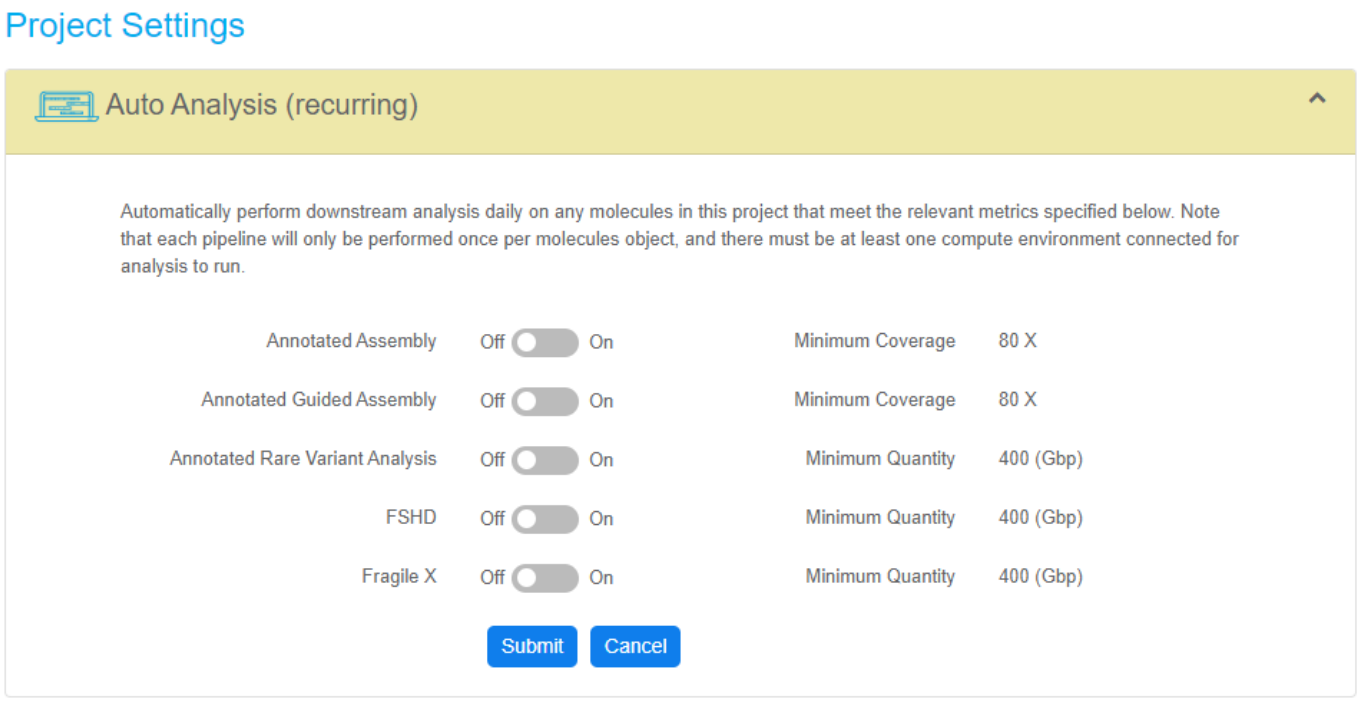
background and the system will notify the user via email and the message center when the export file is completed. Because the export files can get large, we recommend not exporting more than 10 jobs at a time.

After an export file has been generated, a system administrator with file access can move the file from the source Bionano Access Server to the target Bionano Access Server and place it in the ~/access/share/imports folder. When the Project Import icon is clicked on the Project List the system will prompt the user which file they want to import from the ~/access/share/imports folder. The user can also choose which jobs from that import file they want to import. The jobs from the import file will be imported into the selected project. The system will send a notification after each job is imported.

To prevent overloading the system the system will only process one project export and or import at a time. If multiple exports or imports are submitted they will be processed serially to insure the performance of the system is not impacted.

Project Settings (Auto Analysis)

1. Users with the Project Lead or the Administrator role can edit project settings to enable auto analysis operations. Auto analysis will automatically perform downstream analysis daily on any molecules in this project that meet the relevant metrics specified below. Note that each pipeline will only be performed once per molecules object, and there must be at least one compute environment connected for analysis to run.Go to **Bionano Access** main menu, select **Analysis**. The **Projects** window appears.
2. Click the **Settings** icon of the project. The **Project Settings** window appears.
3. Under the **Auto Analysis (recurring)** panel, switch on auto-analysis for the desired operations.
4. Click **Submit**.



Remove Project

To protect against the accidental deletion of data, deleting projects is intentionally difficult. You can only permanently delete projects that are empty. To delete a project there must be no chip data, and you must have deleted a jobs that project contains. To remove a project, click the trash can icon corresponding to the project you want to remove in the Project List. Only Project Leads and Administrators can remove projects. When you remove a project it is moved to the trash, but it is not permanently deleted. Only users with Administrator role can permanently delete a project and as noted it must be empty. Administrators can access the list of deleted projects by clicking on the trash can icon in the header on the Project List as shown in the image below. Administrators also have the option to restore removed projects from the trash if desired.

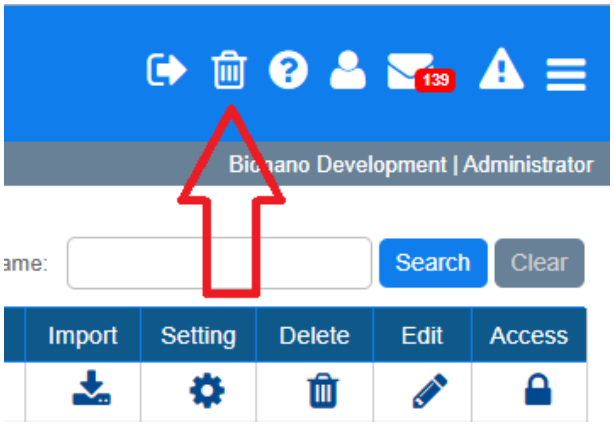


Figure 13. Trash can icon to access deleted project list

Edit Project

Users with the Project Lead or Administrator role can edit projects to change the name, key or description by clicking the pencil icon in the project list corresponding to the project they want to change.

Give Users Access to View Projects

Project Leads and Administrators can control which User and Read-Only users can access a selected project. Click the lock icon in the Project List corresponding to the Project to modify who can access it. The system will bring up the Project Access Control screen. Use the 'Grant Access' and 'Remove Access' buttons to shift selected users from the left (all users) to the right (users with access) to adjust who can access the project. Click the 'Close' button to return to the Project List.

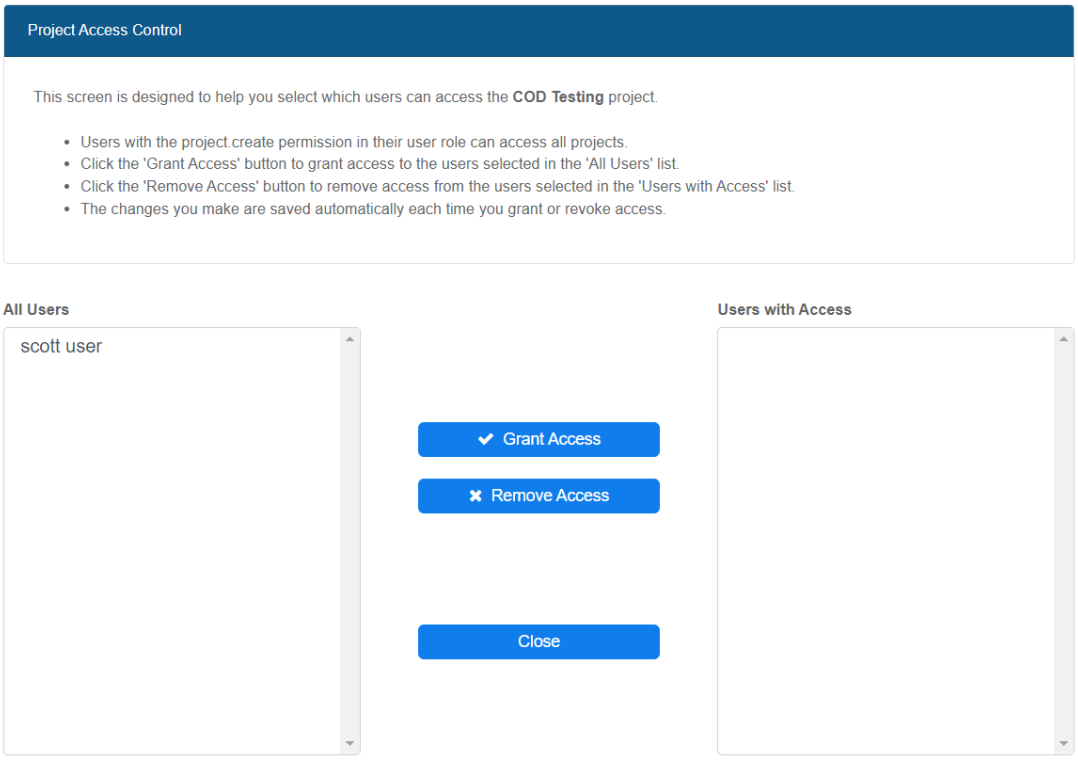


Figure 14: Project Access Screen

Project Browser

Projects contain jobs. Each job holds the results of a Bioinformatic analysis operation. After a project is selected from the Project List the system will display the Project Browser (image below). The Project Browser screen is split into two tables with buttons along the top. The table on the left shows jobs in the selected project. The panels in the table on the right are contextual. They will display information and options based on the job selected in the table on the left.

The jobs can be sorted by clicking on the column headers. The first click on the header will sort the column in ascending order. The second click will sort the column in descending order. The third click on a column header will remove the sort. It is possible to sort on multiple columns. A number indicator in the column header will indicate the order in which the column sort will be applied. Click on the filter icon in the column header to apply a filter to the table on the values in that column. Note: In some cases when you clear your cookies or remove jobs from the list your table settings may be reset back to the defaults.

On the right side of the Project Browser there are a series of panels aligned vertically. From top to bottom they are Sample Details, Job Details, Options, and Operations. The sample panel shows information about the sample associated with the selected job. The Job Details panel shows information about the selected job. The header on the Job Details panel will reflect the type of job. In the example image below, it says ‘Molecule Details,’ because the job selected is a Molecules job. Next is the Options panel. The Options panel will list hyperlinks for things you can do with the selected job. Last is the Operations panel. The Operations panel will list hyperlinks to launch Bioinformatic analysis jobs with the selected job as input. Remember these panels are contextual so the links and information available will vary depending on the type of job you have selected. The links available may also be different based the user role of the active account. Read-Only users cannot launch any jobs on the Operations Panel.

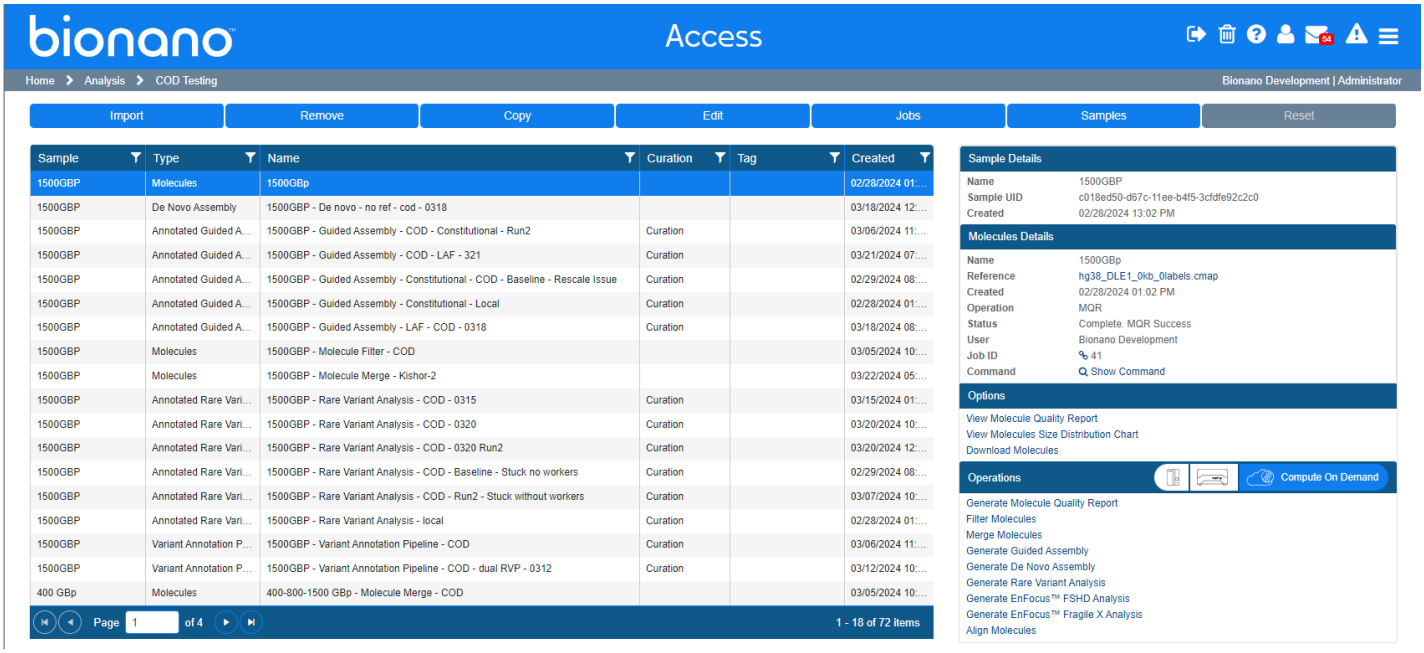


Figure 15. Project Browser

Sample Panel

Each job is associated with a sample. Multiple jobs may share the same sample. When a job is selected on the project browser the sample panel will display the metadata available for the related sample. If a given sample

property is blank, it simply will not be displayed in the panel. The system generates a Global Unique Identifier (GUID) for each sample automatically. The Sample UID value is the system generated GUID.

Job Details Panel

The job details panel displays high level information about the selected job such as when the job was launched, who launched the job, what is the status of the job, what type of operation was launched, and the job's identifier. If there is a reference, it will be displayed as a hyperlink. If you click on the reference hyperlink, the system will download the reference file to your workstation. Next to the job ID there is a chain icon. If you click the chain icon, it will copy the hyperlink to that job to your clipboard. You can share the link with other users. They must have access to the selected project of course for it to work. Many of our Bioinformatic operations require complex inputs that Access simplifies for the user. Click the show command link in the details panel to see the raw command Access complied to launch the job. This can be useful to verify the parameters used.

Options Panel

The options panel displays functions you can perform with the selected job. This panel will typically include a link to the quality report or informatics summary. Most bioinformatic analysis jobs will generate a report. A dialog will display the report when this link is clicked. Most reports are in JSON format and can be downloaded from the dialog. We also provide an API where these reports can be retrieved if you need to incorporate the QC data into a LIMS system. Refer to our API guide for more information.

The options panel also typically will include an option to download the results. The results of a selected job are typically bundled into a zip file. The download option will download the zip file to the local workstation. Unpack the zip file locally to review or retrieve specific files. Some result files can be large. Depending on the network speed it may take some time for result files to download.

Many operations will include an option to view the results, maps, or alignments. These links will open the viewer and allow the exploration of the genomic data that was generated. The viewer offers a complex and comprehensive set of features and is discussed in greater detail later in this document.

Operations Panel

The operations panel allows the user to launch Bioinformatics analysis jobs using the selected job as input. The operations available will vary depending on the type of job and compute platform selected. If the system has more than one type of compute platform available there will be a selector on the top of the panel (figure below). Select the compute platform to target before clicking the link to launch an operation. The operation selections will vary depending on what type of compute platforms are configured. If you only have a single compute platform enabled the selection will not appear. When you click on any operation link, the system will prompt you for the inputs

necessary to launch that type of job. If you have no compute resources configured the operation links will be disabled or will not appear at all. When you submit the launch form, the job will be created and will run in the background. You will receive a notification when the job has completed. Each type of job is described in greater detail later in this document.

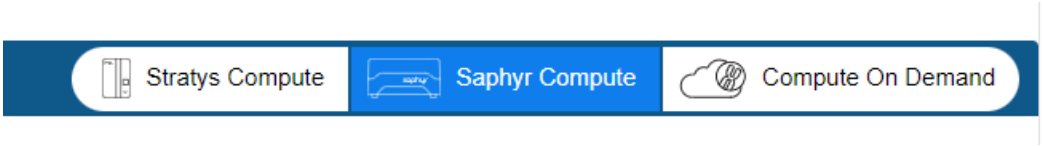


Figure 16: Example compute selection on operations panel

Project Browser Buttons

The buttons across the top of the Project Browser provide various useful functions for the selected project described in this section.

Import

Each Bioinformatics job may generate thousands of output files. These result files are packaged into a single zip file for convenience. The zip file for a job can be downloaded from one Bionano Access server and imported into another. After clicking the import button, the system will prompt for the type of job being imported. The system will prompt for different information based on the type of job selected. Most jobs will require the single zip result file as input, but there are some exceptions such as alignment, molecules, features, or FASTA jobs. Alignment import jobs will require the input of three files: the reference CMAP, the query CMAP, and the alignment XMAP file. Molecule files will require a BNX file in compressed or uncompressed format. FASTA jobs will require FASTA files. Feature import jobs will accept BED or GTF files.

There are some common inputs that jobs will require. First, every job must have a unique name. Second, every job must be associated with a sample. The import dialog will give the option to create a new sample if needed. Click the ‘New’ button next to the sample field to create a new sample. Tags and or a description can optionally be added as well.

Tags provide a useful way of cataloging jobs using keywords. The tag input is a comma separated list of keywords. You can filter the jobs in the project browser using a keyword to find any jobs whose tag field contains that keyword. For example, in a selected project a filter could find all jobs that have the keyword ‘cancer’ in the tag field.

After clicking the submit button on the import form, the results file will be uploaded to the server. A progress bar will indicate the progress of the upload. Do not close or refresh this page until the file is fully uploaded or the

import will fail. The speed of the upload will depend on the network speed between the browser and the Bionano Access web server.

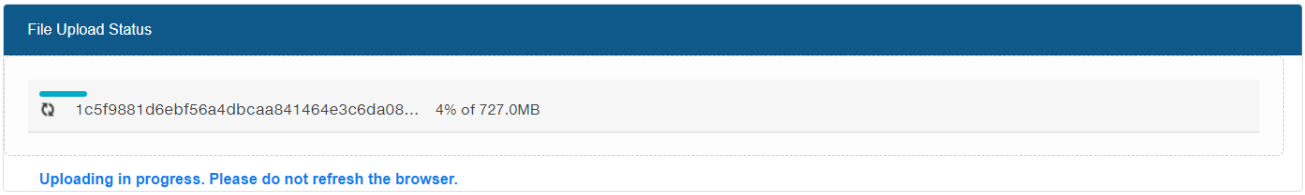


Figure 17: Import progress bar

After the file has uploaded, the system will indicate the file will be processed in the background and a notification will be sent once the import has completed. You can close the browser or navigate away at this point. Each import is considered a job. The email notification will include a hyperlink to the completed import job.

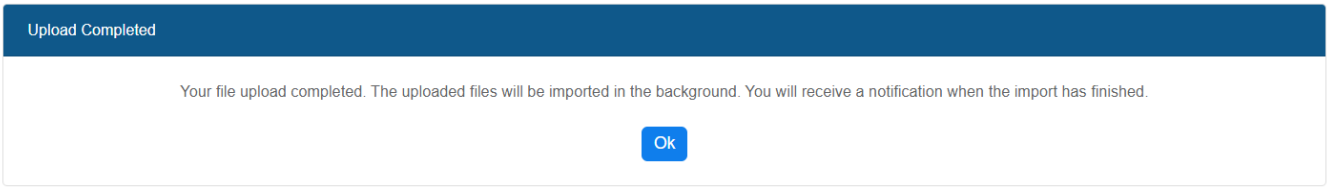


Figure 18: Import confirmation

Remove Job

Users can remove jobs from a project. If the selected job was copied to another project, removing it will not affect the copy. To remove a job simply select the job you want to remove in the job list and click the remove button. When you remove a job, you will be prompted to confirm you want to remove the selected job. After confirmation, the selected job will be moved to the trash. Administrators can access deleted jobs by clicking on the trash can icon in header on the Project Browser screen. Administrators can restore jobs from the trash or delete them permanently.

Copy Job

Users can copy a job to another project. To copy a job, select the job in the job list on the Project Browser and click the copy button. The system will prompt the user to select the target project. The list of projects available will only reflect the projects the user is able to access. Jobs must have unique names. The copy will fail if the target project contains a job with the same name already. When you copy a job, the system will not duplicate the result files where possible to conserve disk space.

Edit Job

Users can modify job metadata by selecting the job in the job list on the Project Browser and clicking the Edit button. They will have the option to change information such as the job name, sample, description, and tags. In some cases, the reference can also be changed. Some ASCII characters are not allowed in job names. The system will warn you if that is an issue.

Sample Button

The sample button will navigate you to the Sample List. The sample list offers a different view of jobs in the project where they are grouped by sample.

Job Button

The job button will navigate you to the Job List. This is different than the job list on the project browser. The project browser only shows jobs for the selected project. The Job List shows all jobs (filtered by the user's project permissions). It is useful to see current job activity or to locate a specific job.

Reset

The reset button will clear any filters that have been set in the column headers of the job list table. The button will be disabled (greyed out) if there are no active filters.

Analysis Operations

Bionano Access can perform many different operations. In this section we will provide an overview of each operation. This user guide will outline how to launch each operation and what features each operation offers. For more details on the algorithms behind these operations or their clinical relevance please refer to other guides and tutorial materials.

Molecule Quality Report (MQR)

Whenever a molecules file is introduced to Bionano Access either from a chip run or import, the system will automatically run a Molecule Quality Report. The MQR will provide two types of quality metrics on the molecules file. It will provide molecule metrics and mapping metrics. The mapping metrics will depend on the reference selected. If no reference was associated with the molecules file there will be no mapping metrics. Generally, it is not necessary to run an MQR because they are run automatically. If the reference is changed on a molecules file, it will delete the existing MQR, and the user will need to generate another report. This is because the mapping metrics are based on the reference used so it needs to be re-generated if the reference is changed. To generate a Molecule Quality Report first select the molecules file of interest in the project browser. Then click the 'Generate Molecule Quality Report' link in the operations panel.

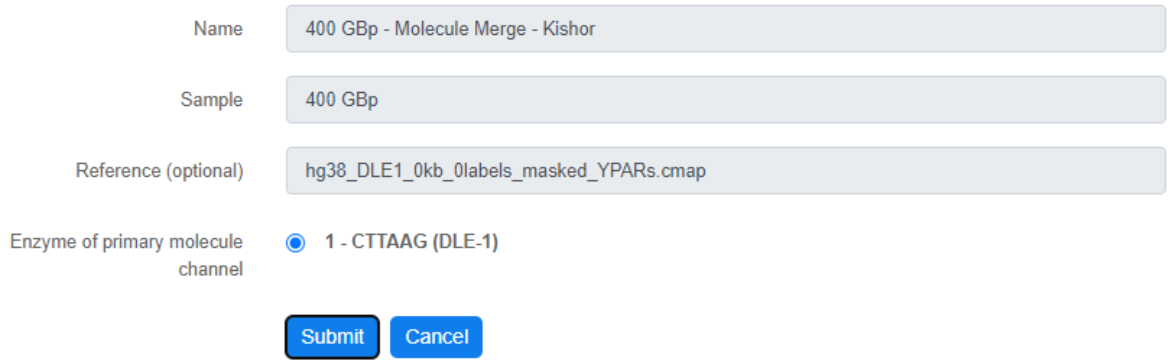


Figure 19: MQR Launch Screen

The MQR operation launched from the project browser will only generate metrics on a single channel (or color). If it is a dual labeled molecules file that has both red and green the user will need to select which channel should be used for the report. On the MQR launch screen just click the 'Submit' button to launch the MQR. The MQR operation will run in the background after it has been launched. The user will be returned to the project browser after the operation has been submitted. The system will provide a notification to the user once the operation has competed.

To view the report, select the molecules file of interest then click the 'View Molecule Quality Report' link in the options panel. A dialog will appear with the report. The system will allow the user to copy, download, and or print the report from the dialog window.

Filter Molecules

Different applications of OGM technology recommend different amounts of DNA. In some cases, it is helpful to reduce the size of the molecules file or filter out unwanted aspects it may contain. The Filter operation will allow the user to filter a molecules file on the following:

Channel	Channels can be swapped or removed if you have a Dual Labeled Sample.
Label Count	Molecules with below the minimum label count will be removed.
Length	Molecules below the minimum or above the maximum will be removed.
Total DNA	Molecules will be reduced until the specified amount of DNA is reached. The system can remove molecules randomly or by size.
Scan Number	Molecules before the start scan or above the end scan will be removed.

The filter operation will preserve the original molecules file and create a new one. To filter a molecules file, select the molecules file of interest in the project browser. Then select the 'Filter Molecules' link in the operations panel. The system will prompt the user for the input parameters. There is a checkbox to enable or disable each possible filter parameter. By default, the length and total DNA parameters will be enabled. Select the checkbox to enable the desired parameters, set the filter values, and click the 'Submit' button to launch the operation.

When the operation is submitted the user will be returned to the project browser. The filter operation will run in the background and the system will notify the user once the operation has completed.

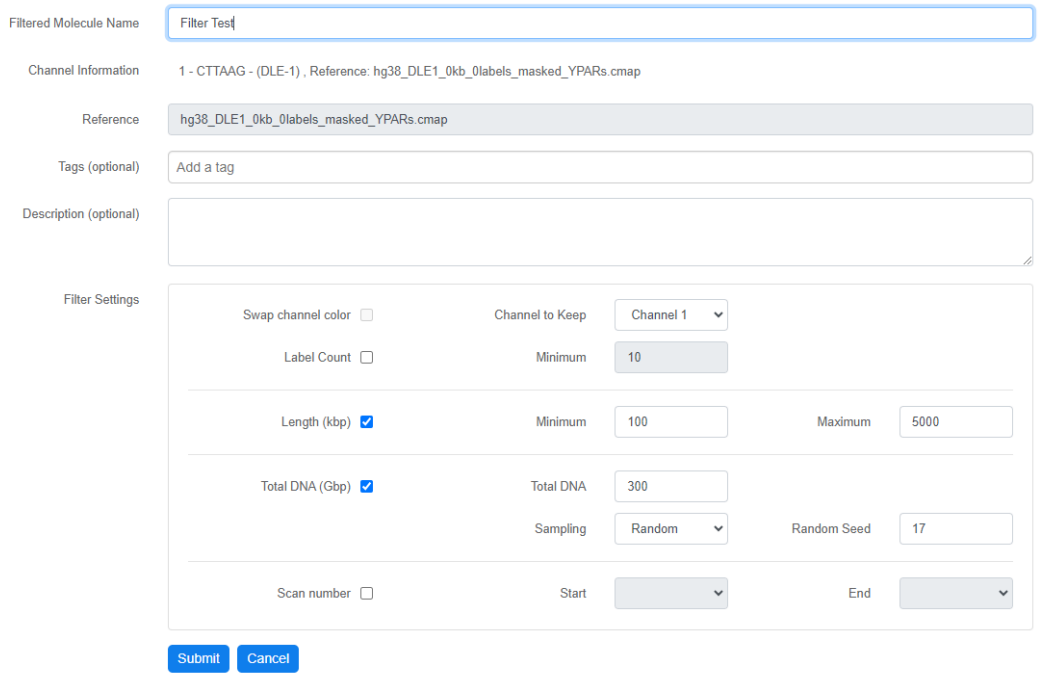


Figure 20: Filter Molecules Launch Screen

Merge Molecules

In some cases, it is necessary to combine molecules files to obtain sufficient DNA for your target application. The Merge Molecules operation allows you to merge molecule files together to create a new molecules file. It is important to note that the molecules you combine should be from the same sample and of similar quality. Merging disparate datasets together will create questionable results downstream when it is used as an input for other operations.

To merge molecules first select one of the molecule files you want to include. Then click the ‘Merge Molecules’ link in the operations panel. The system will be prompt for standard job information such as name, tags, and description. The sample drop down will associate the new molecules file with the selected sample. After the files have been merged the system will automatically generate a Molecule Quality Report on the new molecules file. The mapping metrics for the MQR will be generated using the selected reference. The system will automatically select molecules in the same project that appear to be a good match for the molecules file that was input. If there is not a good match only the input molecules file will be selected like in the example below. In the ‘All Molecules’ table select which molecule files you want merged then click the ‘Submit’ button to launch the operation. The operation will run in the background and notify the user when it has completed.

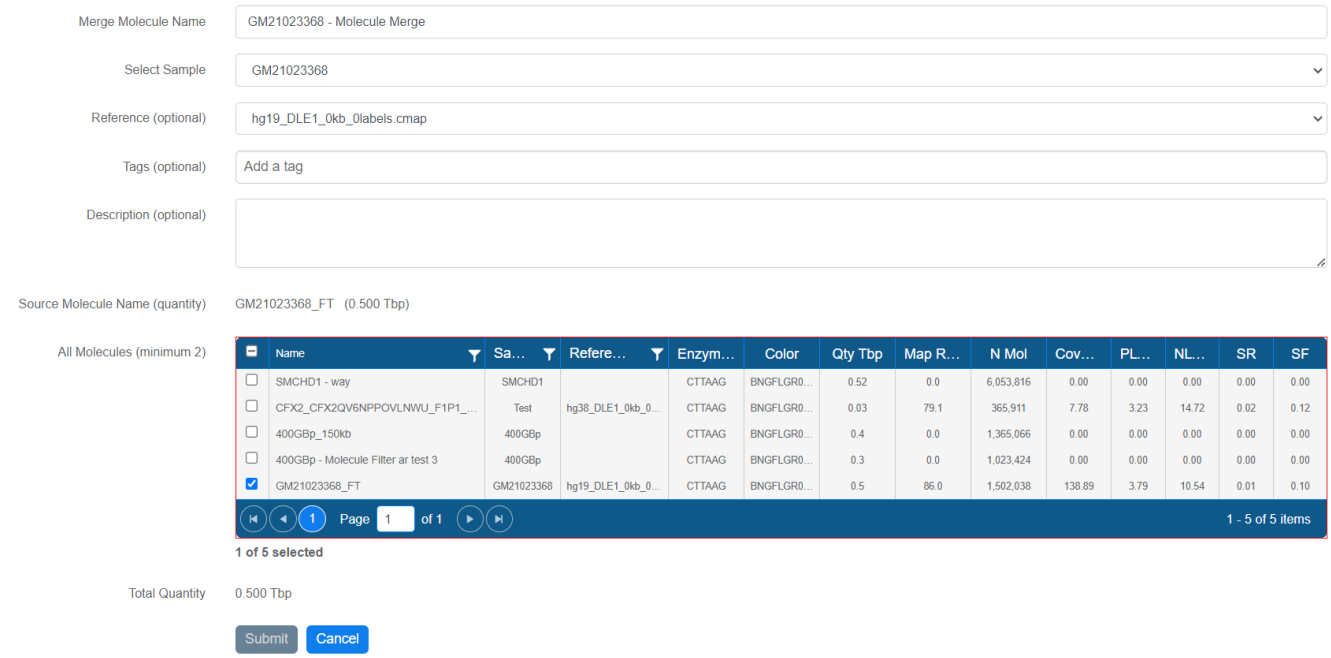


Figure 21: Merge Molecules Launch Screen

Alignment Jobs

There are two types of alignment jobs. It is possible to align molecules directly to a map or align two maps to each other. If you start with a molecules file as the input the system will perform a molecules alignment. If you start with a map or job that contains maps such as a de Novo Assembly, the system will perform a map(s) to map alignment. Beyond the standard job inputs the system will prompt for the target map to be selected. The target map list will include any map file in the project or any reference. The system will also require the selection of which RefAligner configuration file to use for the alignment. For map alignments you will also have the option to click checkboxes for ‘Output Best Alignment’ and ‘Swap Anchor Query.’ The ‘Best Alignment Option’ will only output the best alignment per map, instead of outputting all alignments above the p-value threshold. In our alignments the map is either an anchor or a query. Generally, the reference is the anchor, but in some cases, you may want to reverse that. The ‘Swap Anchor Query’ option allows the user to do that.

De novo Assembly

The system can generate a de novo assembly from a molecules file. For details about the de novo assembly algorithm refer to the Bionano Solve Theory of Operation: Structural Variant Calling document. The de novo assembly operation will align the molecules into consensus maps which are then aligned to the reference. The algorithm will also identify and annotate both structural and copy number variants. To start a de novo assembly, select the input molecules file then click the ‘Generate De Novo Assembly’ link in the operations panel.

The De Novo Assembly launch form is broken into three sections. The first section collects general information about the job. The second and third sections are collapsed by default. If the job is launched without expanding these sections to it will run with the default recommended settings.

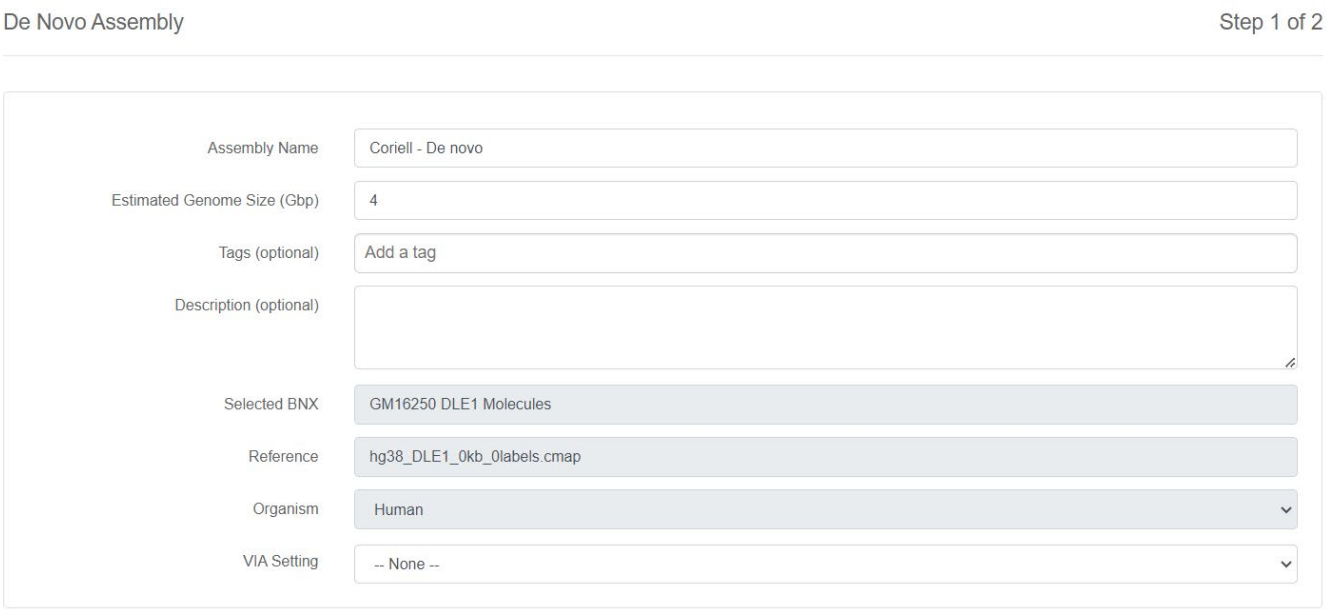


Figure 22: De Novo Assembly Launch Form

The name of the job will default to the sample name plus the operation name, but it can be modified as desired. If the reference for the molecules file selected is human the system will populate the 'Estimated Genome Size' automatically. If the VIA Sync is configured, and you are running a human sample, you can choose to push the results of this job to VIA automatically when the job completes. In the VIA Settings field select the setting you want used for the transfer. There will be a default selection in the VIA Settings field if you have marked a VIA Setting as the default for that type of job. Once you have completed this first section you can click Next to proceed with the recommended settings.

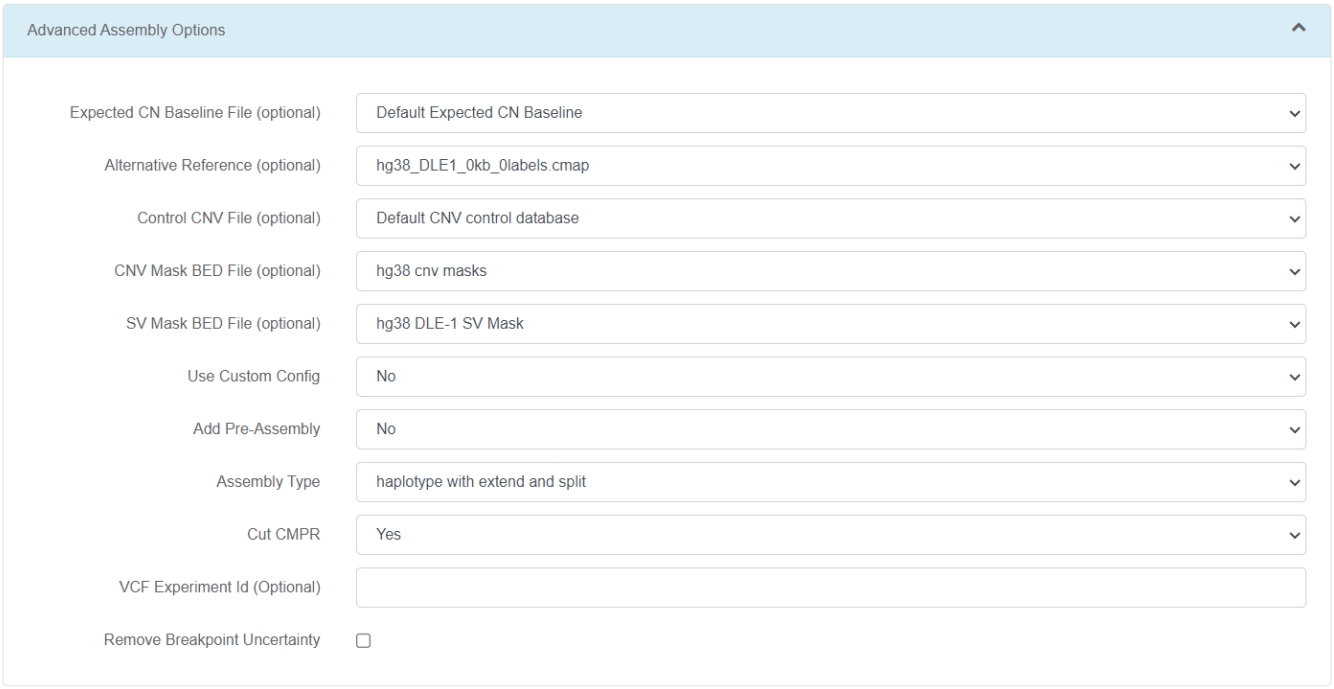


Figure 23: De Novo Assembly Advanced Options

To run a de novo assembly with custom settings, click the carrot on the right side of the Advanced Assembly Options panel to expand the advanced options section. This section will explain each of the settings available.

Expected CN Baseline File:
It specifies a file that describes the expected copy numbers for each chromosome. It is possible to upload custom ECBN Files in the system settings under control databases. It is recommended for human that you use the default control database as shown. This option will not be visible if the sample is not human.

Alternative Reference:
The de novo assembly operation will default to use the reference associated with the input molecules. However, it is possible with human operations to change the reference for the job. This option will not be visible if the sample is not human.

Control CNV File:
This file provides fractional copy number data for the pipeline. This file can be generated by the Bionano Solve package by following the Pre-process custom control data described in the Theory of Operations document.

CNV Mask BED File:
This should be a BED File that defines regions where CNV variants should be ignored. It is possible to use Bionano Solve scripts to generate this file. Refer to the Theory of Operations document regarding Pre-process custom control data. CNV Mask files can be added to the system for selection in the Settings Module under System Features.

SV Mask BED File:

The system includes BED files for annotating insertion and deletion calls overlapping N-base gaps in the reference and putative FP translocation breakpoint calls so that they can be filtered in Access. The former would be annotated with a suffix "_nbase" in the SV type. Insertion and deletion calls in Nbase regions may simply be due to mis-sizing of the N-base gaps in the reference and not genuine SVs. The latter would be annotated with a suffix "_common" or "_segdupe" in the SV type, depending on whether they overlap with common FP calls in control samples or annotated segmental duplication regions, respectively. For example, it includes selected sub-centromeric and sub-telomeric regions that are prone to generating putative FP translocation breakpoint calls. We provide BED files for the de novo assembly pipeline and RVP, separately. Details on custom BED generation are described in the Theory of Operation for Structure Variant Calling document.

Use Custom Config:

The de novo assembly operation takes an optional argument (opt arg) configuration file. Despite the name this file is not optional. This file controls over 400 possible settings used by the pipeline to generate results. The software ships with several system provided opt args and it will automatically determine which file is best to use. Toggle the 'Use Custom Config' input to override the system opt arg selection and manually chose the opt arg file desired. Custom Opt Arg files can be uploaded from the Settings module. It is also possible to make limited changes to the system provided opt arg files and save them as a new opt arg selection. We do not recommend tweaking opt arg files are creating your own without an in depth knowledge of our pipeline or input from Bionano Support.

Add Pre-Assembly:

The 'Add Pre-Assembly' option is for genome assembly or finishing. You would not use this option with a standard human sample. When this option is enabled a preliminary assembly is constructed first, and this assembly is used as the reference for estimating noise parameters in the molecules in subsequent assembly steps. Enabling this option will increase the run time for the operation for the additional initial steps.

Cut CMPR:

During assembly, large non-unique regions (which we call complex multi-path regions, or CMPRs) in the genome maps are recognized and marked. These regions, often associated with large segmental duplications in the genome, create ambiguity in the assembly graph and are prone to mis-assembly. They are detected in a de novo fashion - assembled maps are aligned with each other, and maps that share significant stretches of sequence but are otherwise divergent are identified. If the CMPR, or the shared sequence, is at least 140 kbp, and if the option to split CMPRs is enabled, the maps are split (Figure 1) in order to avoid mis-assembly. The labels encompassing the CMPR would be marked in the Mask column in the CMAP output (see CMAP File Format Specification Sheet; PN 30039) and highlighted in Bionano Access. CMP is enabled by default but can be changed in the 'Advanced Assembly Opitons' section.

VCF Experiment ID:

This operation will output variants in VCF formant for consumption by tertiary analysis products such as VIA. To be compliant with this output format each variant must have an experiment id. Bionao Solve will output a default value but using the 'VCF Exeperiment ID' you can override that value.

Remove Breakpoint Uncertainty:

The system will automatically estimate breakpoint uncertainty. To disable these estimates, toggle the ‘Remove Breakpoint Uncertainty’ setting.

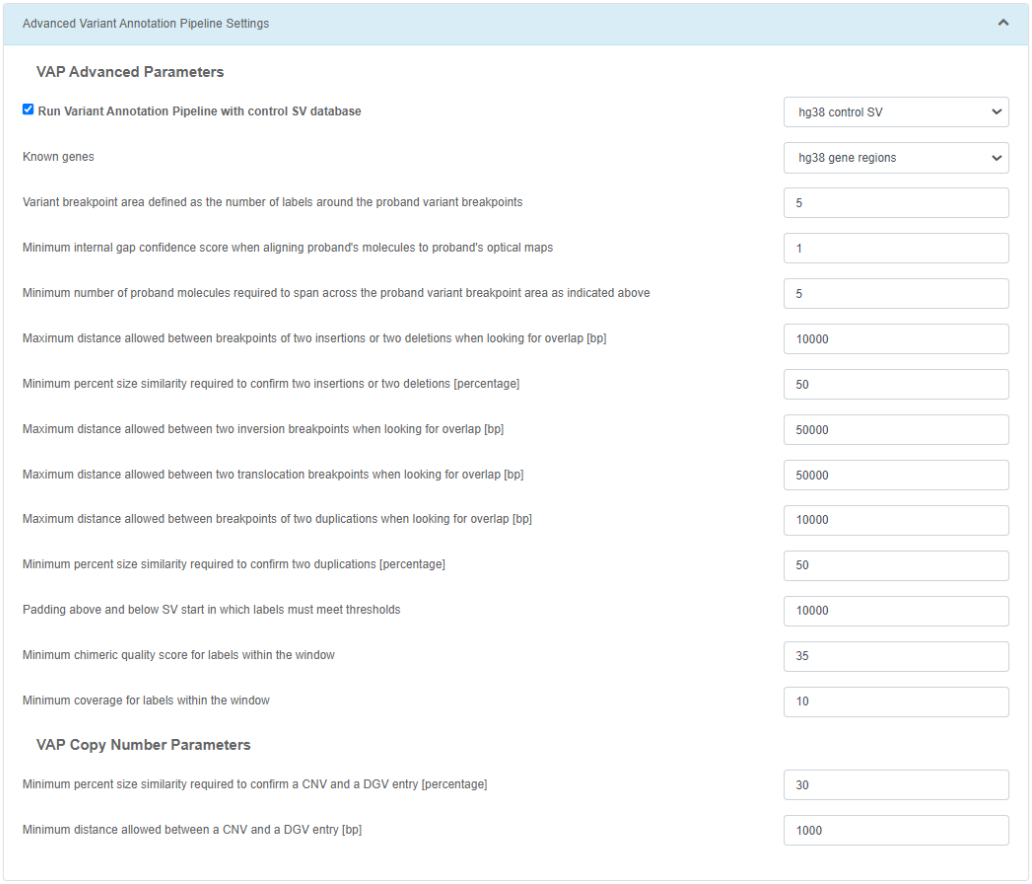


Figure 24: Advanced Variant Annotation Pipeline Settings

By default, the system will automatically annotate the variants in the assembly results when the sample is human. To change how annotation is performed click the carrot in the ‘Advanced Variant Annotation Pipeline Settings’ section header. To disable or prevent annotation uncheck the ‘Run Variant Annotation Pipeline with control SV database’ checkbox. The SV control database and list of genes used for annotation can be modified with the first two drop down inputs. The rest of the inputs have verbose labels and are self-explanatory. For more details on these inputs refer to the Bionano Solve Theory of Operation: Structural Variant Calling document.

Click the ‘Submit’ button to launch your job. You will be returned to the project browser where your new job will be selected. The job will run in the background and send a notification upon completion with a link to the results.

Generate Guided Assembly

The launch screens for the Guided Assembly operation are very similar to the de novo Assembly launch screens but there are a few differences. There are two types of Guided Assembly: constitutional and low allele fraction. The second input ‘Operation Type’ allows you to select which type of Guided Assembly you want to run. The

default is low allele fraction. When you change the operation type it will automatically change the Assembly Type and SV Mask BED file in the Advanced Guided Assembly Options section to the appropriate default selection.

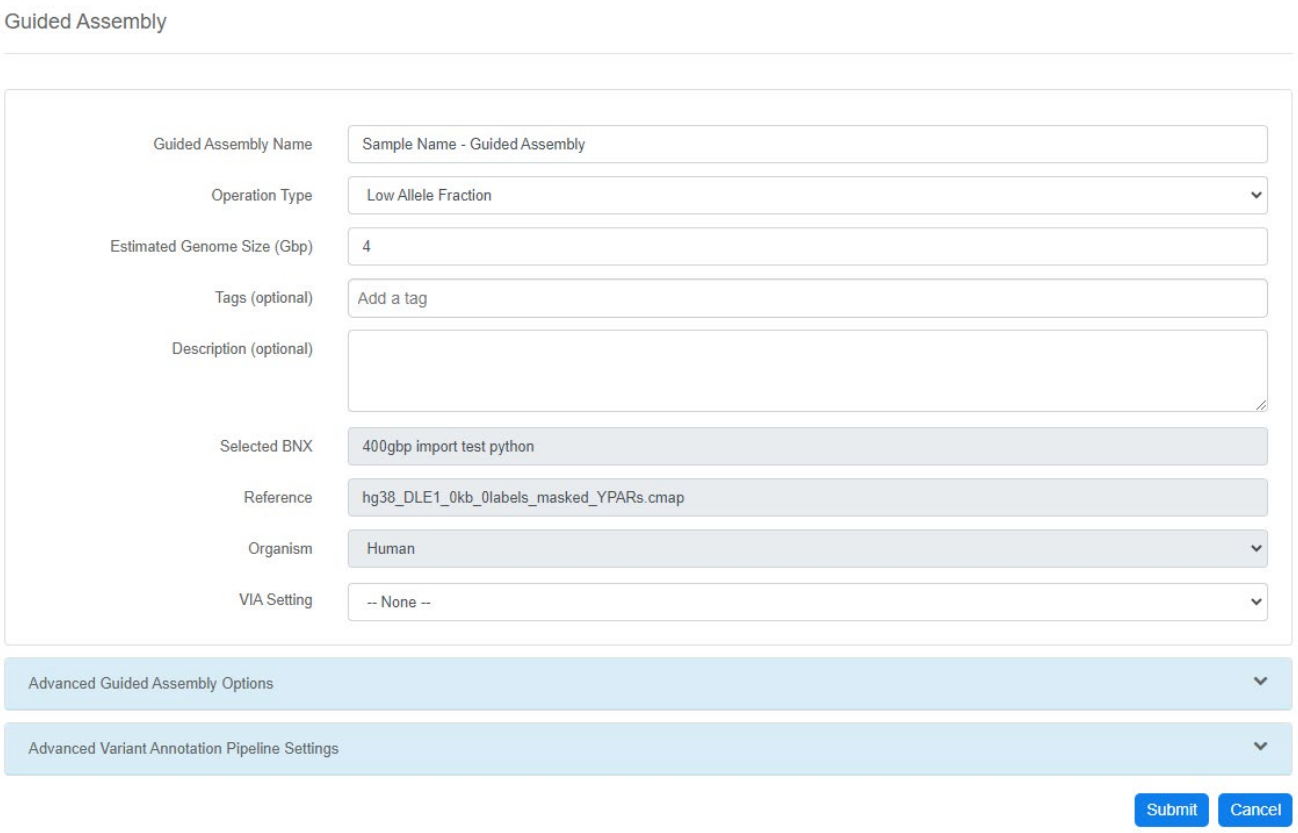


Figure 25: Guided Assembly Launch Screen

Rare Variant Analysis

Like Guided Assembly the launch screens for the Rare Variant Analysis operation are also very similar. While the de novo Assembly operation can be used for non-human purposes both the Guided Assembly and Rare Variant Analysis operations are intended for human use only. The links to launch these operations will be disabled if the molecules job selected does not have a human reference.

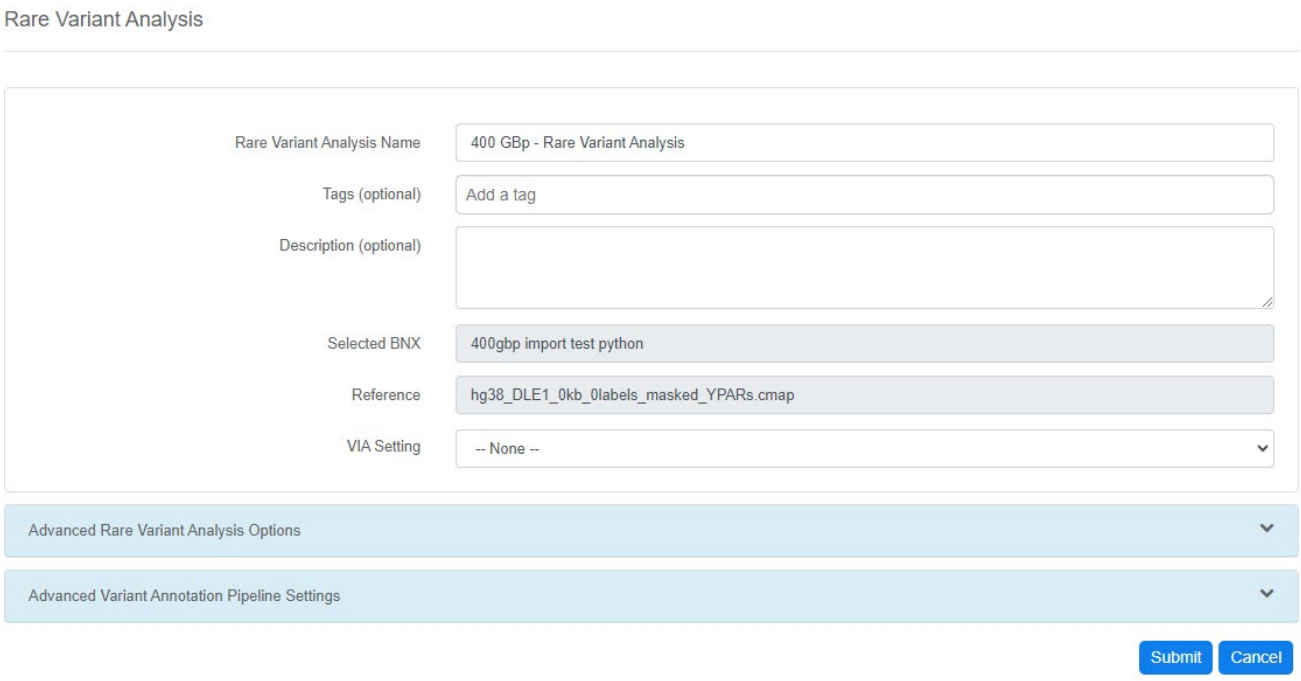


Figure 26: Rare Variant Analysis Launch Screen

EnFocus FSHD Analysis

The EnFocus FSHD Analysis operation is only available for human samples. If your dataset does not meet the expected quality standards, you will receive a warning when you attempt to launch the operation. You can choose to proceed or cancel the operation. Also be aware you cannot use merged BNX files as input. The system checks for this and will fail your job if a merged BNX file is detected. The Enfocus FSHD Analysis operation is very controlled. The only inputs you can modify when you launch an EnFocus FSHD Analysis operation is the job name, description, and tags. All the parameters for the algorithm are locked down. For more information about the EnFocus FSHD Analysis operation refer to the Bionano Solve Theory of Operation: Bionano EnFocus FSHD Analysis document (30321).

EnFocus Fragile-X Analysis

The EnFocus Fragile-X Analysis operation is only available for human samples. If your dataset does not meet the expected quality standards, you will receive a warning when you attempt to launch the operation. You can choose to proceed or cancel the operation. Also be aware you cannot use merged BNX files as input. The system checks for this and will fail your job if a merged BNX file is detected. The Enfocus Fragile-X Analysis operation is very controlled. The only inputs you can modify when you launch an EnFocus Fragile-X Analysis operation is the job name, description, and tags. All the parameters for the algorithm are locked down. For more information about the EnFocus Fragile-X Analysis operation refer to the Bionano Solve Theory of Operation: Bionano EnFocus Fragile-X Analysis document (30457).

Variant Annotation

There are three annotation operations. They are single, dual, and trio. When the variant annotation operation was first released it was only available as a separate operation. To annotate the results of a de novo assembly first a de novo assembly would be generated and subsequently a single annotation job would be submitted. Nowadays the de novo assembly, rare variant analysis, and guided assembly operations are all annotated by default. The only reason to run a single is typically to rerun the annotation with different parameters.

The dual and trio annotation operations allow you to compare annotations between datasets. The dual will allow you to compare a case vs control while the trio will allow you to compare a subject vs parents. With the filtering available you can determine which variants are unique to a given subject or shared with the control or parents. For more information about the Variant Annotation operation refer to the Bionano Solve Theory of Operations: Variant Annotation Pipeline document (30190).

The Variant Annotation Pipeline launch screen will prompt for the name, tags, and description for the job. The dataset selected to launch the operation will be the subject. You will be prompted to select the results of additional jobs depending on the type of annotation selected. For example, in the screen shot below the system is prompting for mother and father assemblies because a trio operation was selected. The selections for control, mother, or father will be limited to match the same type of operation that was selected as the subject.

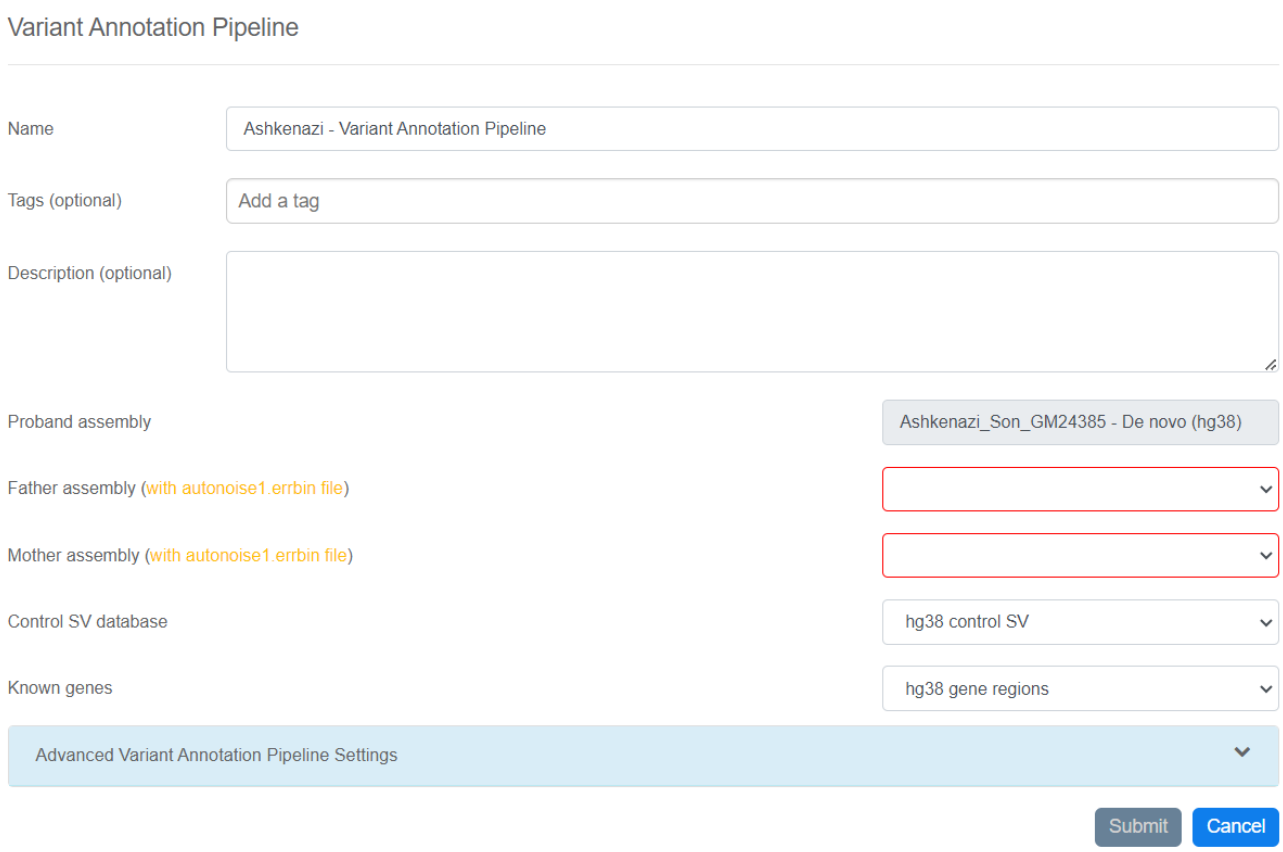


Table 2. Bioinformatics operations supported:

Operation	Description
***In silico* digestion of data sequences**	Perform *in silico* digestion by transforming a FASTA file into a Bionano CMAP file format. Calculates the estimated label density of FASTA file.
Merge molecule data sets	Merge two or more molecule jobs into a single molecule job.
Filter molecule jobs	Filter molecules jobs by length and total amount with random selection or enrich for longest molecules.
Generate *de novo* assemblies	Assemble single molecules into consensus maps for structural variant (SV) detection and hybrid scaffold applications.
Generate guided assembly	An optimized assembly operation tuned for human samples.
Perform rare variant analysis	Detect structural variants at low allelic fraction.
Generate EnFocus™ FSHD analysis	Analyze regions relevant to facioscapulohumeral muscular dystrophy (FSHD).
Generate EnFocus™ Fragile X syndrome analysis	Analyze regions relevant to Fragile X syndrome
Align maps	Compare two different maps or molecules to maps by aligning them to each other.
Build hybrid scaffolds	Merge maps with sequence assemblies to produce contiguous hybrid scaffolds that represent the chromosome structure.
Annotate structural variants	Provide variant annotation for downstream filtering and prioritization of SVs based on Bionano internal human database or custom control database. Perform dual or trio comparisons.

Visualization Features

Once an analysis operation finishes the results can be visualized. Click the 'View Results' hyperlink in the options panel to view the results of the selected job. If you are not familiar with the Project Browser or the options panel, please read the previous Analysis section. Not all jobs will have a 'View Results' option. When you click the 'View Results' link the viewer will be loaded. It may take a moment for the screen to render depending on how much data is involved. The Viewer has six screens, the Circos Plot, Genome Browser, Whole Genome View, Ideogram, Curated Variant List, and the Classifier. The circos plot view will load by default if the sample is human. If the sample is not human, the Genome Browser will be the default view. The Curated Variant List and Classifier screens will only be available if the data set has been annotated.

The Toolbar

There is a toolbar at the top of the screen for all views. The options and or icons on the toolbar will vary depending on which screen you are on. The Classifier screen will not have the same options as the Circos Plot. Figure X above depicts the toolbar for the circos plot. In the table below we have provided an explanation of what each toolbar icon does. Each option will also display a text hint when the mouse hovers over the icon.

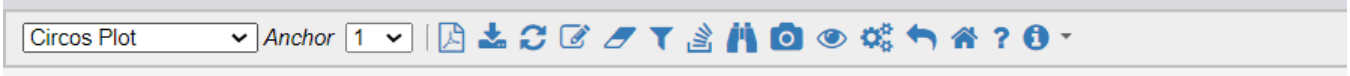
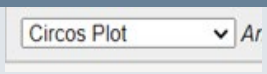
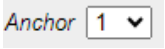
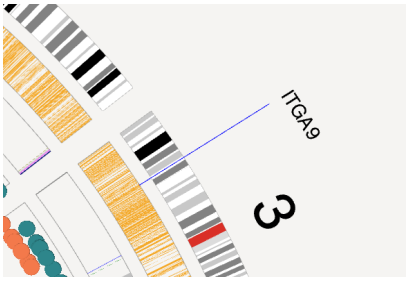


Figure 27: Circos Toolbar

Table 3: Viewer Toolbar Options

Option	Description	Views
 View selector	Use the view selector to select which view to display. The options may be different whether or not the selected dataset is annotated.	All
 Anchor	The anchor value is the chromosome. The genome browser is designed to show one chromosome at a time. If you select a value in the anchor drop down that chromosome will be displayed in the Genome Browser view.	Circos Genome Browser
 Generate Report	Generate a PDF report of the selected variants. You can choose to output the variants that meet the active filter criteria or the variants in the curation list.	All
 Download Files	When you download a result from the Project Browser you will get the entire results set. Bionano Access offers the option to download a subset of the variant data directly from the viewer. Clicking this option will give you the option to download selected copy number variants, structural variants, the aneuploidy file, and or the informatics report.	All
 Refresh	The volume and nature of data the viewer must render is complex. Sometimes when you manipulate the view extensively it can be helpful to reset the view. The Refresh icon will redraw the view resetting it to default render.	Circos Genome Browser Whole Genome Ideogram Classifier
 Annotate Features	The Circos plot can display tracks that show the regions defined in feature (BED) files. Using annotate feature option will put a text label on a selected region from a feature file or a selected cytoband. This can be useful when making a screen shot of results. Here is an example of an annotated feature: 	Circos

Clear Annotations	The clear annotations icon will clear any annotations that were added to the view with the annotation features option.	Circos
Filter Settings	The filter settings option will open the filter dialog. The viewer offers extensive options to filter variants. The filter dialog will be outlined later in this document.	Circos Genome Browser
Add to Curated List	Variants that meet established filter criteria can be added to the curation list. Variants in the curation list can be classified	
Search Genomic Features	If you know the name of a selected feature, but are having difficulty locating it in the view, click the search genomic features option.	Circos Genome Browser
Export to JPG	The Export to JPG will take a screenshot of the viewer and save to a file that will download to the browser.	Circos Genome Browser Whole Genome Ideogram
View Options	The view options icon will open the view options dialog. The view options dialog allows you to toggle various view options. The options available in the view options dialog will vary depending on the active view. Some settings will affect multiple views. The view option dialog and each option in it are detailed later in the document.	Circos Genome Browser Whole Genome
View Settings	The view settings icon will open the view settings dialog. These are settings that affect how the visualization is rendered. Some settings will affect multiple views. The view settings dialog is discussed later in this document.	Circos Genome Browser Whole Genome View
Return to Project Browser	Clicking this icon will return you to the project browser with the current dataset selected.	All
Home	Clicking this icon will return you to the Bionano Access home screen.	All
Shortcuts	There are many keystrokes and mouse shortcuts that can be used to interact with the view. Clicking the shortcut icon opens a dialog that lists all the keystroke and mouse shortcuts. These are powerful and useful options you should review if you are not familiar with them.	All
Tour	Clicking the tour icon will open the tour view. There is a drop-down carrot next to the tour icon you can use to select which view to tour. When the tour icon the system will display a static image of the view selected with green icons you can click on to get an explanation of each feature on the screen. You can click the 'Next' button in the hint window to move to the next hint.	Circos

The Circos Plot View

The Circos Plot screen is divided into three areas, the toolbar, the legend, and the plot. The toolbar is across the top of all viewer screens. On the circos plot screen the plot is on the left and the legend is on the right. The Circos plot is displayed by default for human assemblies, rare variant analysis, and variant annotations. Click and drag the plot to move it and use the mouse wheel to zoom in and out.

The circos plot has tracks or rings that are broken into segments. Each segment represents a chromosome. The large number or letter next to each segment is the chromosome identifier. Each track or ring on the circos plot depicts different data. The summary tab on the legend lists what the track. In the image below the outer most ring is the cytoband track. The red mark indicates the centromere. When you hover over the segments in the cytoband it will highlight the segment and give you the name and position. You can use the annotate feature to add a label to a cytoband segment of interest.

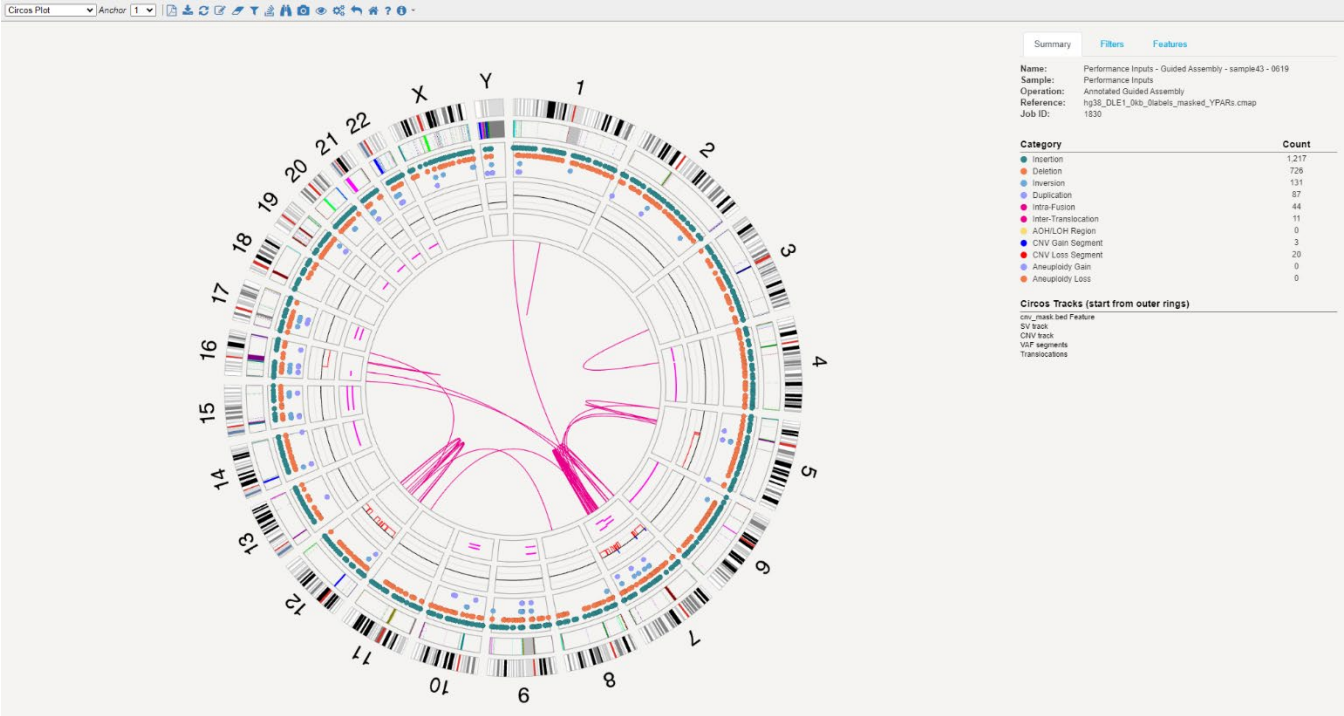


Figure 27: Typical Circos Plot

Inside of the cytoband track is a feature track. In this case it is displaying the cnv mask. The number of feature tracks will vary depending on what features you have selected. In the view options you can choose to see the SV or CNV mask that was used. You can also select additional features on the 'Features' tab of the legend. Adding features and using them as filters will be discussed later in this document. When you hover over a region on a feature track it will display a hint with the name and position of that region. The system will not display a hint when a name has not been defined in the BED File for that region.

Inside the feature tracks is the SV track. This track shows a dot where each SV is located. The color of the dot depends on the type of SV. The summary tab on the legend shows what type of SV corresponds to each color. You can hover over an SV to get details on that variant. If you click on an SV the system will open the Genome Browser and zoom to the selected SV. The size of the dots in the SV track can be adjusted in the view settings by changing the Circos Plot SV size setting. The dot that represents the SV is not relative to the size of the SV. At the elevation of the Circos plot, if the dot was relative to the actual size of the SV it would not be visible. It is also possible to change the colors used for each type of variant in the View Settings if you prefer a different color scheme.

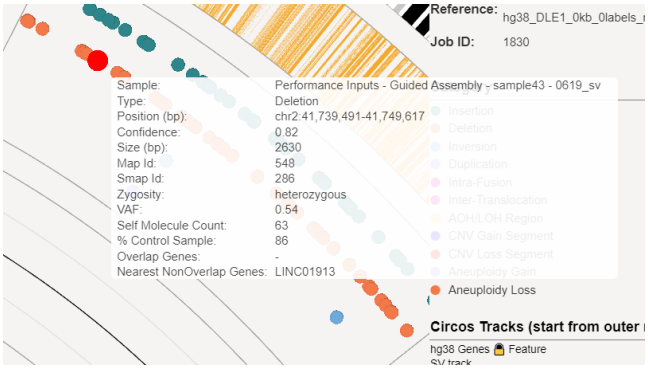


Figure 28: SV hint from Circos Plot

Inside of the SV track is the copy number track. The horizontal scaling lines indicate the copy number value. The black line represents 0. The blue segments represent copy number gain while the red sections represent copy number loss. The thick line at the bottom of the copy number track is present when an aneuploidy is detected on that chromosome. The gain, loss, and aneuploidy colors can be changed in the View Settings. The maximum copy number track height can also be set in the View Settings.

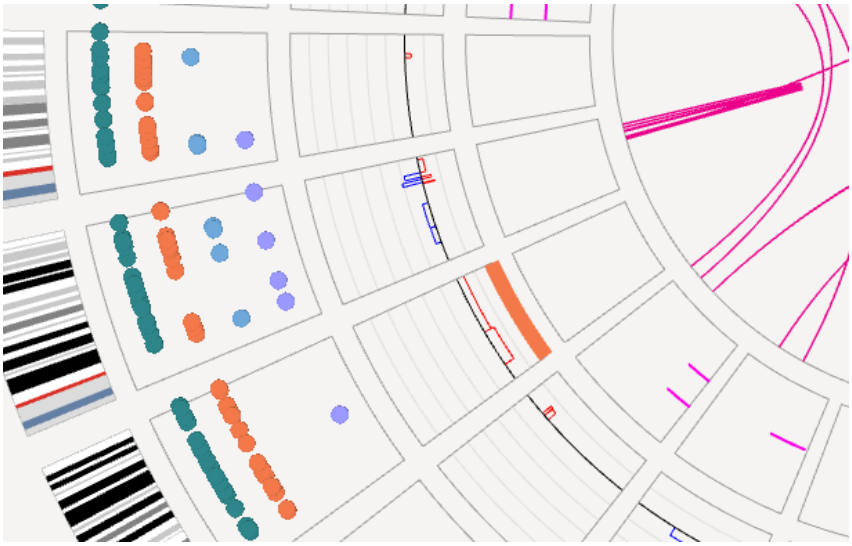


Figure 29: Copy Number Track

The next track shows Variant Allele Fraction (VAF) segments. The segmentation smooth line helps distinguish changes in the VAF pattern across the genome. By default, the VAF smooth lines will only display in *de novo* results. For RVA results, the VAF track is not displayed by default. Users can change this setting in **View Options** for the Circos Plot.

The pink lines across the center of the plot depict translocations. The line points to the break points on each chromosome. Clicking on translocation in the circos plot will zoom to that translocation in the genome browser view.

The Genome Browser

The genome browser is our original and most detailed viewer. Where the Circos plot is good to get a quick overall perspective of the genome, the genome browser is designed to explore alignments and variants in detail. These views complement each other. The genome browser will show one chromosome at a time or one map at a time if you are viewing an alignment operation. Use the anchor drop down field in the toolbar to select which map or chromosome you want to view. If you clicked a variant in another view it will open in the Genome Browser automatically. In that case, the system will automatically display the correct anchor.

Zoom

It is possible to zoom in and out on the genome browser several ways. To zoom to precise coordinates, use the 'Range' input field on the toolbar. Below the toolbar there is a ruler and the cytoband track. The ruler will show a red box around the portion of the anchor that is being displayed. If you are zoomed in significantly the red box on the ruler may just be a line. Click on a region in the cytoband track and the viewer will zoom to that region. Click and drag a box on the ruler to designate the area to display. It is possible to manually zoom the view by using the mouse wheel. You can click and drag individual tracks left or right. If you click in an open space, you can click and drag the entire view left or right.

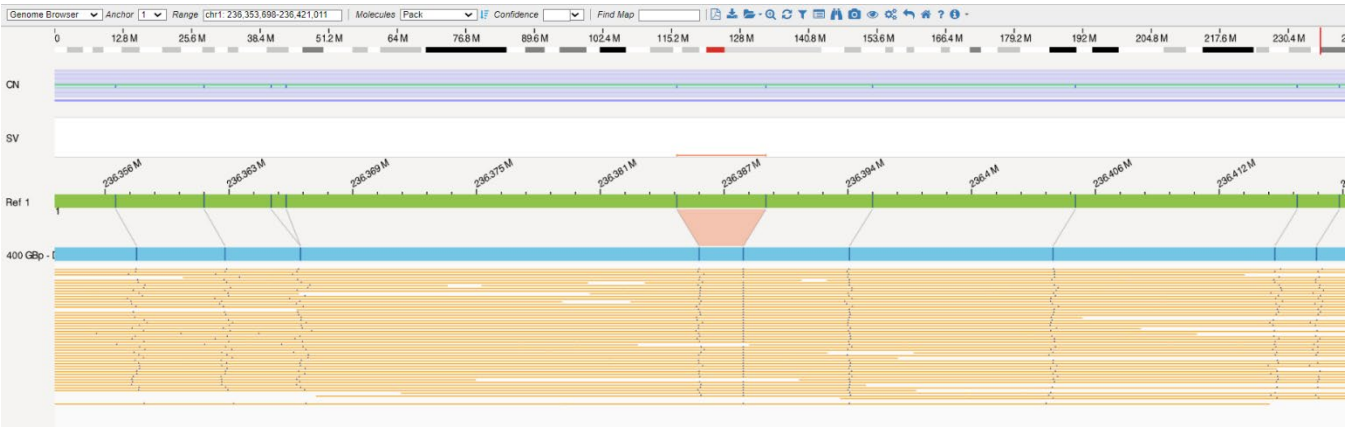


Figure 30: Genome Browser View

Maps

There are three levels to the map data in the Genome Browser. The top level is the anchor or reference. In the image above the reference track is labeled ref 1 and the reference map is green. The second level is the consensus maps. These are the blue maps in the image above. There are generally multiple tracks of consensus map. The system will generate enough tracks that consensus maps will not overlap. The third level is the induvial molecules. These are the yellow lines. The molecules are not visible by default. Right click on any consensus map and choose show molecules to see the molecules that compose that consensus map. If the molecules have not been visualized previously, it may take a moment for them to load. The map data is driven by

cmap files produced by Bionano Solve. The consensus maps are color coded to the recognition enzyme used so you can view alignments of different recognition enzymes and easily distinguish them. The colors for all maps can be changed in the view settings. The image above shows the default color scheme for the DLE1 recognition enzyme. Every map has an ID. The map ID is visible in the mouse hover hint. If you know the ID of the map you want to view you can enter it into the 'Find Map' input in the toolbar. If a corresponding map is found the viewer will zoom to that map.

Molecules

Molecules by default will display in pack format. Meaning they will be compacted into the tightest formation possible under the consensus map. You can choose to arrange them in other ways such as by start or by size. on the toolbar by using the 'Molecules' dropdown selection. Some arrangements may cause the molecules to extend past the bottom of the screen. It is possible to extend or compress the height of the molecules. Hover your mouse over the molecules, click and hold the Alt button, then use your mouse wheel to change the height. This can be useful to squish them down, but can also be helpful to make them bigger so the labels are more visible. It is also possible to scroll the molecules up and down so you can see past the bottom of the screen. Hover your mouse over the molecules, click and hold the Ctrl button, then use your mouse wheel to scroll.

Alignments

So how are the maps aligned? First you will notice that the maps have lines on them. These are the recognition sites where the selected recognition enzyme identified a site known as a label. Then there are lines that connect the labels from the anchor to the consensus map(s). The alignment data is driven by xmap files generated by Bionano Solve. When you hover over any label a hint will appear with detailed information about that label. The system will also highlight the alignment lines for the selected label in red. By default, we do not show alignment lines for molecules; it clutters the view. However, if you select a label with molecules visible the system will indicate which molecules for that consensus map support the selected label. The molecules will also snap their alignment to the selected label so it easier to interpret. In Figure x below you can see the blue molecules support the selected label and they are all aligned on the selected label. In the View Options you can enable molecule alignment lines. In View Settings you can also change alignment highlight colors.

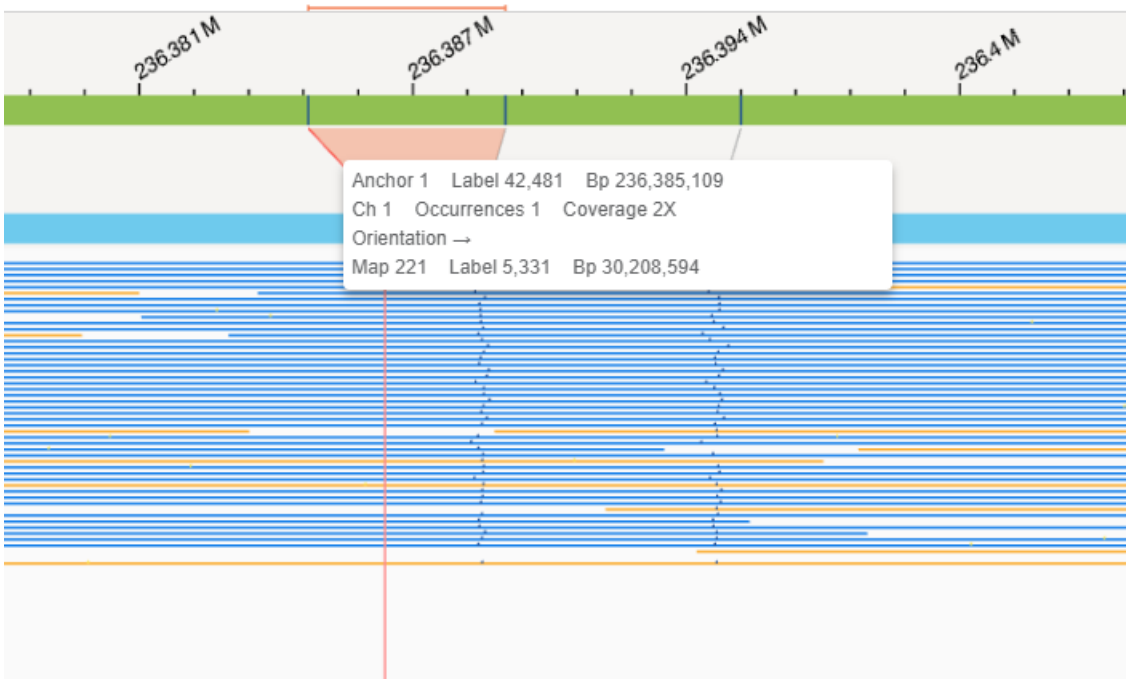


Figure 31: Supporting Molecules

Some labels may be a different color and have no alignment lines. These are unmatched labels. That means the recognition enzyme identified a site, but that site could not be aligned to the reference. In the View Options you can hide unmatched labels. In the View Settings you can change the color of unmatched labels. Bionano Access will show unmatched labels by default.

Variants

Examining variants to determine their significance is the primary use of the Genome Browser. Across the bottom of the screen there will be a series of tabs. Apart from the Match groups tab these tabs list different types of variants. The tabs may also be different depending on whether your job was annotated. Annotated datasets will have extra columns in the SV Annotation and CNV Annotation tabs. The tabs at the bottom of the screen can be sorted and filtered. If you click the ellipse in a column header, you can also select which columns are visible on that tab. If you click on a row in the SV or CNV tabs the viewer will automatically display the selected variant.

When the system displays a selected variant, it will show the consensus maps affected and will hide all other maps to avoid cluttering the view. To see other maps, click the Show All button (magnifying glass with plus sign) in the toolbar. It is possible to view more than one variant at a time by checking the checkbox in the tab corresponding to the desired variants. Keep in mind that variants can be small and if two variants are selected that are far apart, they may be difficult to see. You may need to zoom out to see them both at the same time.

Variants are color coded by their type. You can adjust the colors for each type of variant including insertions, deletions, translocations, inversions, gains, losses, etc. The colors selected in the View Settings will also affect the dots on the SV ring in the Circos Plot.

The Genome Browser also has an SV track. It will draw a line to indicate where variants are detected. The lines will be color coded based on the type of variant. A hint will be displayed for the variant when the cursor is on the variant line. If a variant line in the SV track is clicked the system will display that variant.

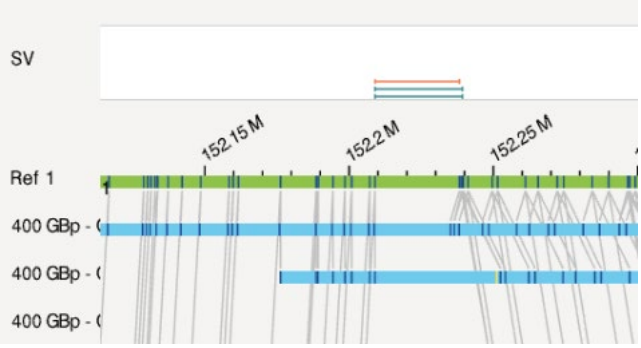


Figure 32: SV Track

Variant Context

Understanding the context of a variant is important to determine its significance. At the top of the genome browser there are various tracks that can be used to better discern the context of a given variant. From the View Options dialog you can turn tracks on or off to show the copy number track, the copy number mask regions, the SV track, the SV mask regions, the AOH/LOH track, and the Cytoband Track. Each of these tracks can provide context when evaluating a variant.

Beyond the tracks you can enable from the View Options you can also chose to show feature tracks by right clicking on the anchor map and choosing 'Show Feature'. Feature files are great for showing genes or other regions of interest. There are two types of feature files. There are BED files which will show a basic color-coded region and GTF files which will depict genes complete with direction, exons, transcripts, etc.

Figure 33: Example of gene from a GTF based Feature File

If your dataset is annotated, the tabs at the bottom of the genome browser will also indicate other helpful contextual information such as overlapping genes, nearest gene, and presence in control samples.

Structural Variant Examples

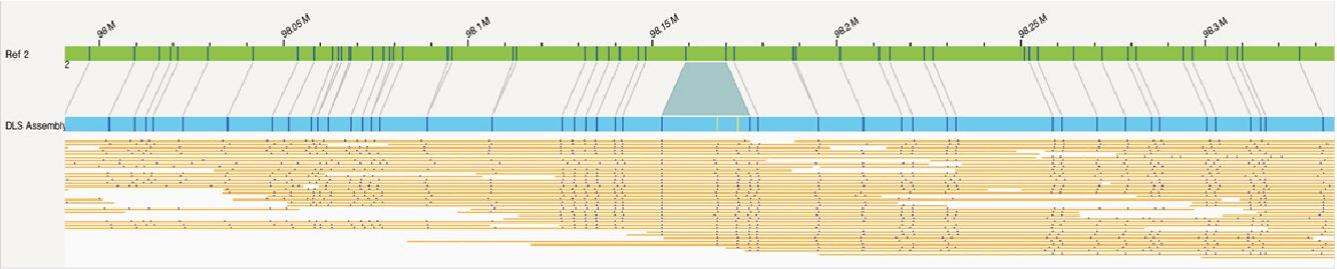


Figure 34. Insertion

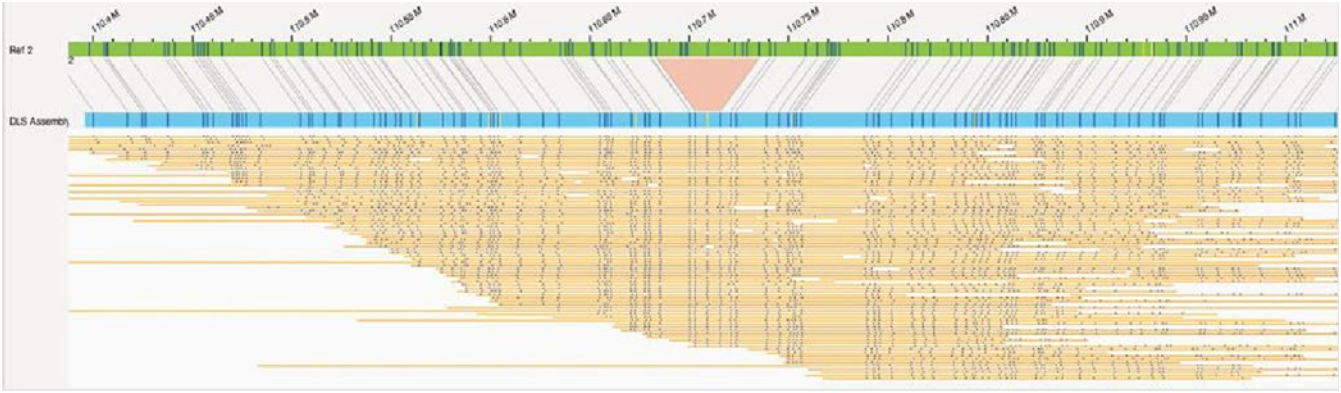


Figure 35. Deletion

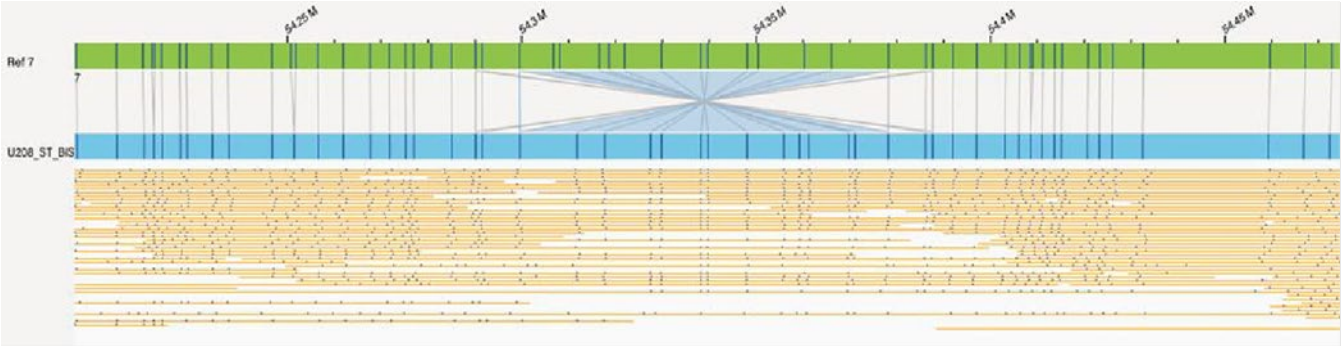


Figure 36. Inversion

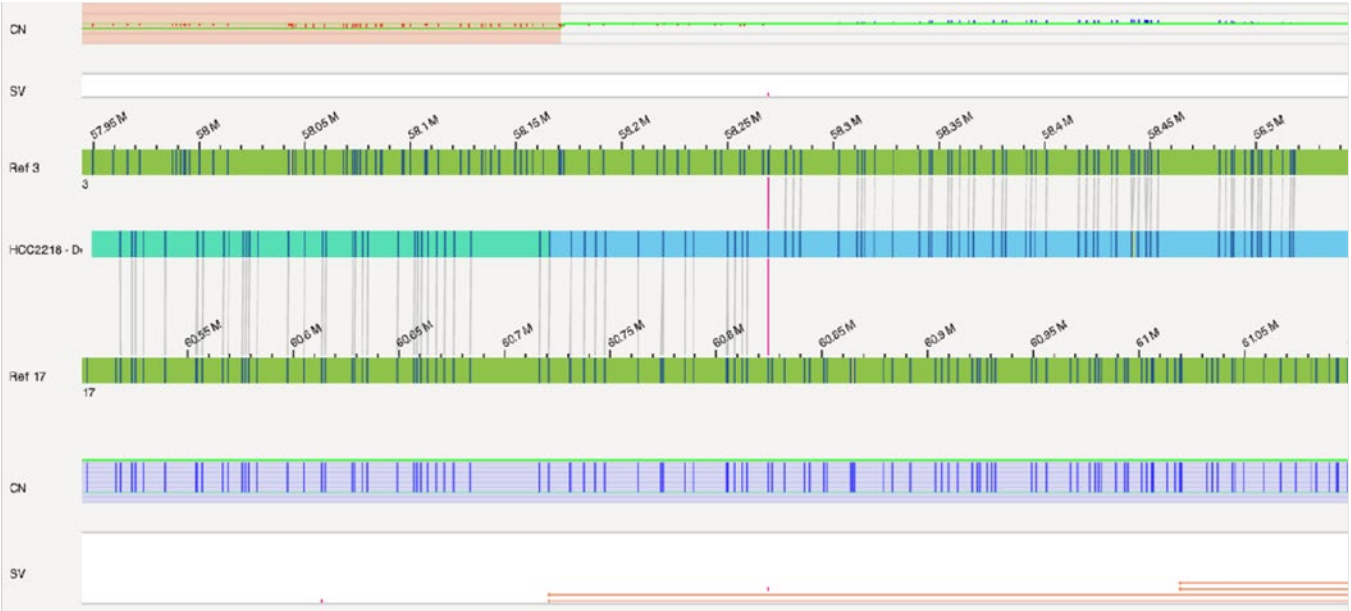


Figure 37. Translocation

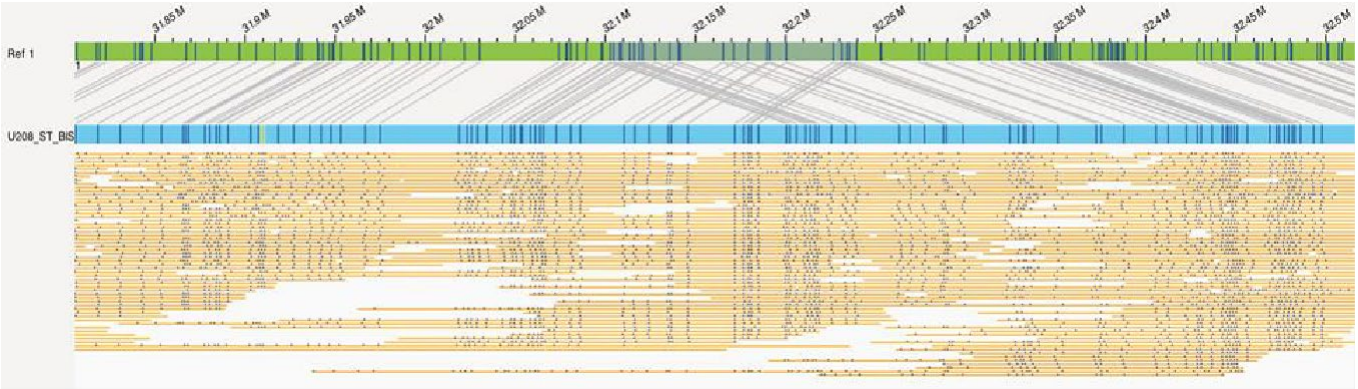


Figure 38. Duplication

FSHD VISUALIZATION

The genome browser has been customized for FSHD results. It will automatically focus on the areas of interest on either chromosome 4 or 10. The consensus maps are shown in blue. The repeat region of interest, labeled as D4Z4, is in purple, and the haplotype-specific regions, labeled as either 4qA or 4qB, are highlighted. Below is an example:

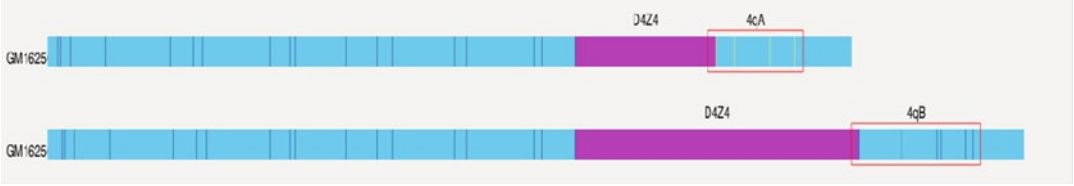


Figure 39. FSHD Visualization example

COMPLEX MULTI-PATH REGION VISUALIZATION

The genome browser view highlights Complex Multi-Path Regions (CMPR). For CMPR detail information, refer to *Bionano Solve Theory of Operation: Structural Variant Calling* (CG-30110) for more details. By default, it is shown in mint green on the assembled map, as below (**Figure 14**):

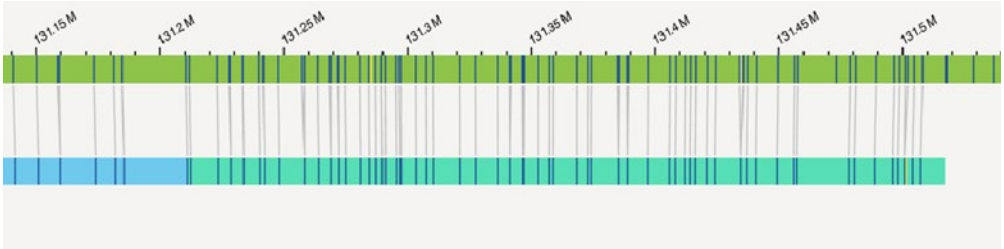


Figure 40. Complex Multi-Path Visualization example

The Whole Genome View

The Whole Genome View displays the Copy Number, AOH/LOH, and VAF tracks for the entire genome, but in greater detail than the Circos Plot. Clicking on an event in the Whole Genome View will drill down to that variant in the Genome Browser where it can be viewed in detail. The view can be zoomed using the mouse wheel and dragged left or right.

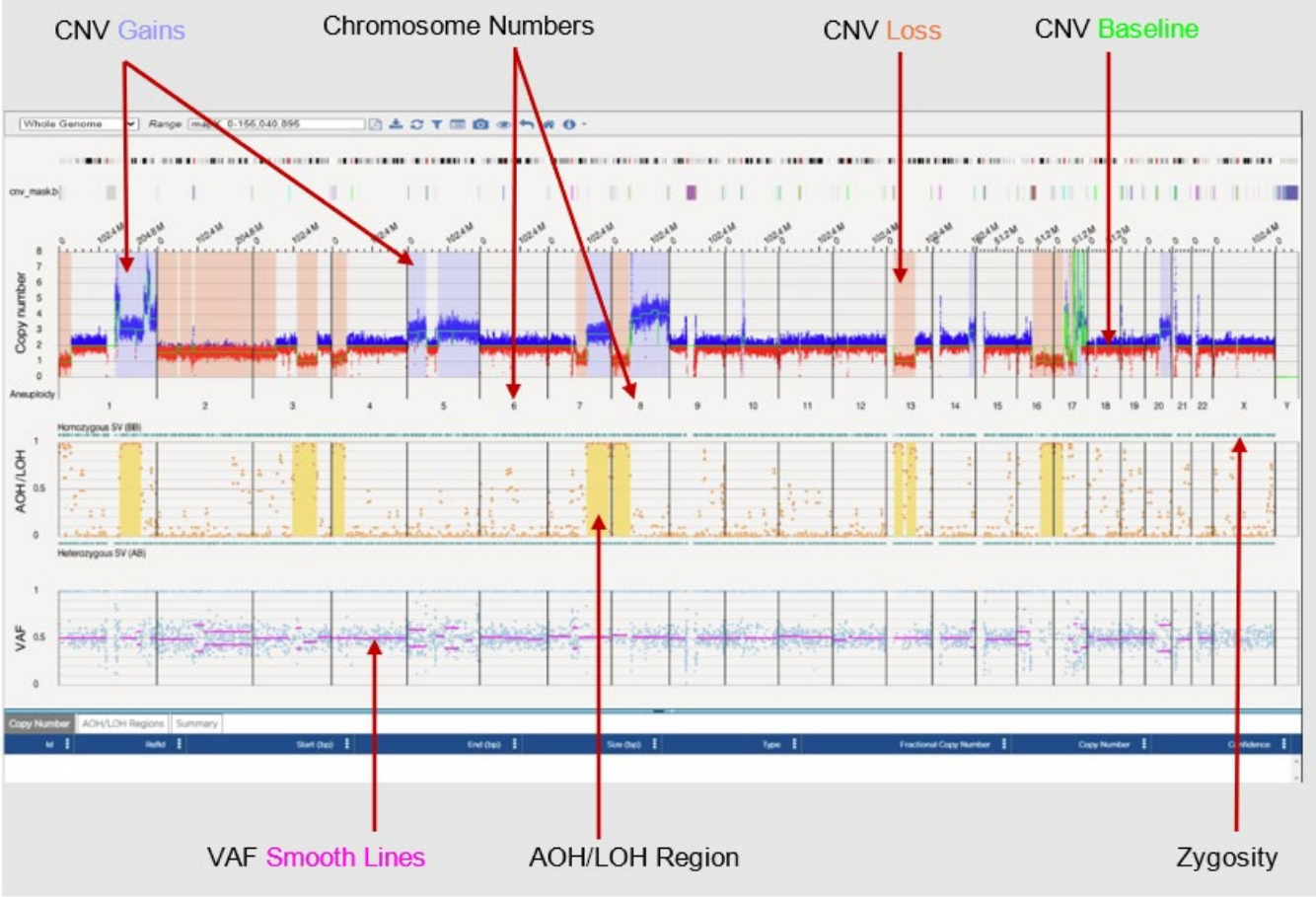


Figure 41. Whole Genome visualization example.

The **Copy Number** plot represents the CNV profiles across the chromosomes. The Y axis shows copy number for each of the chromosomes plotted on the X axis. Molecules showing regions with increased copy number from the calculated baseline (green) are shown in blue and regions with decreased copy number are shown in red.

The **AOH/LOH** graph represents regions of AOH/LOH calculated for structural variants identified in the *de novo* workflow. The X axis represents chromosomes, and the Y axis represents the range of zygosity for these genomic locations. The teal dots represent zygosity of the variant. Users can also plot the probability of the SV to be present in the LOH/AOH region (orange dot). The regions of the genome that have a consistently high AOH/LOH calls will be indicated with a yellow-colored block. The AOH/LOH graph is only available on the *de novo* Assembly result.

The **Variant Allele Fraction (VAF)** plot represents the fraction of copies that are of a particular allele in a defined population. The VAF track provides a visual illustration of this difference with a scatter plot of allele frequencies for a given variant. The Y axis represents the range of the allelic frequency across the different chromosomes plotted on the X axis. The mean of the frequency rests around .5 for diploid genome and is color-coded magenta. If the data show fluctuations in the ploidy, the mean value changes and is visualized by more than one magenta line across the region of the genome that shows polyploidy. The Variant Allele frequency is calculated for all SVs detected in the SV detection pipelines. Users can choose to filter variants based on their allelic frequency.

Ideogram View

Ideograms provide a schematic representation of chromosomes familiar to cytogeneticists. They are used to show the relative size of the chromosomes and their characteristic banding patterns. Bionano Access 1.7 now has an interactive viewer to show the location of the structural variants, copy number variants and loss of heterozygosity on human chromosomes. SVs, CNVs, AOH/LOH can be chosen to display on chromosomes. All chromosomes and cytobands can be viewed via Ideogram.

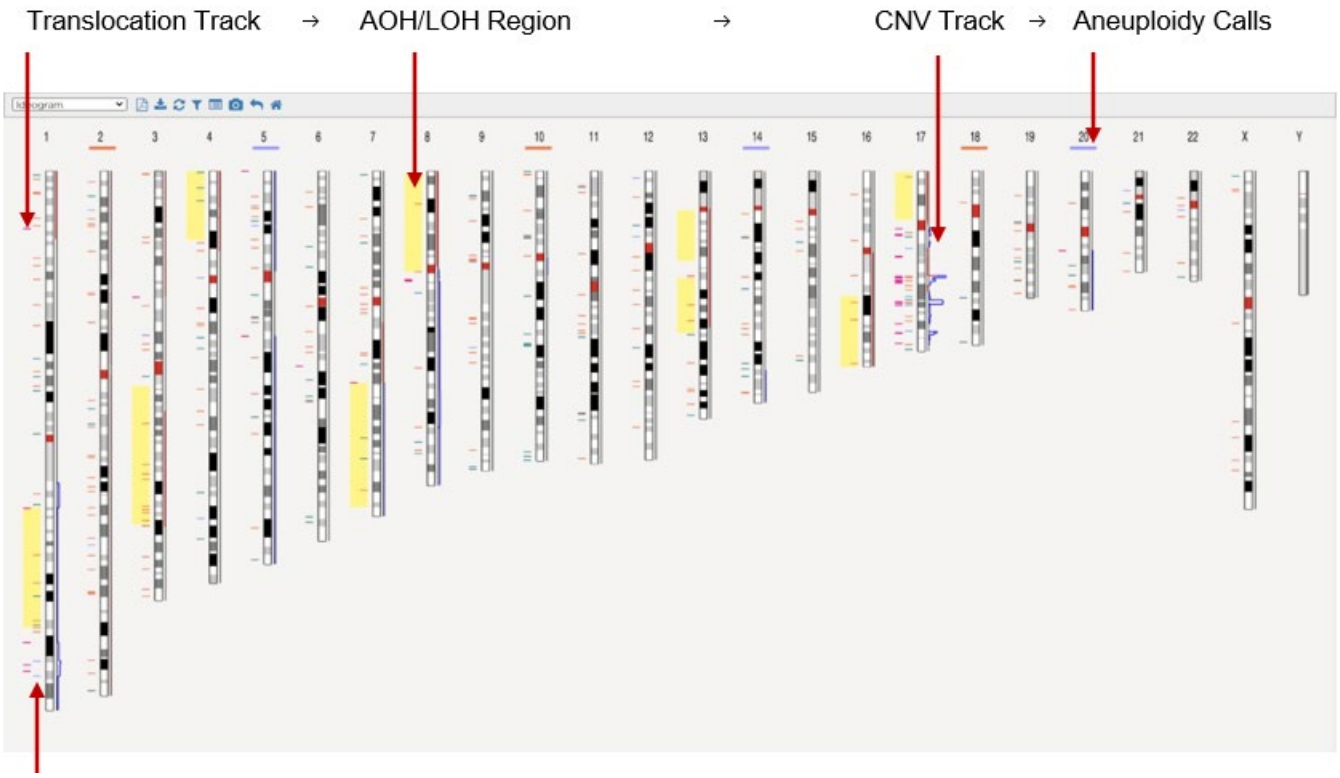


Figure 42. Ideogram view example.

The Cytoband information is shown in the black-and-white banding pattern with centromere in red. The SV track is on the left and the CNV track is on the right of each chromosome. Aneuploidy information is also marked on the top under the chromosome number as a blue band for a gained copy of a chromosome and a red band for a lost copy of a chromosome. The yellow blocks in the SV track represent the AOH/LOH regions. When the mouse is hovered over any variant the system will display a hint with details about the selected variant. When the mouse is hovered on a translocation the system will draw a line to connect the other break point of the translocation.

The Curated Variant List

The Add to Curated Variant List button on the Circos view will append all variants that meet the active filter criteria to the Curated Variant List. When you select the Curated Variant List view the variants that were selected

will be listed. This list can be sorted and filtered by using the column headers on the table. The Curated Variant List provides summary information about the selected variants. The Curated Variant list was intended to be used like an index to order and select where to start classification. If you double click on any variant in the table, the Classification view will open and will jump to the selected variant. The Classification view displays all data available on the selected variant to facilitate informed decisions when classifying a variant.

You can remove individual variants from the list by selecting them and clicking the 'Remove records' button. The list can be cleared by clicking the 'Remove all records' button. The system will be prompt for confirmation before removing any records.

While the Classifier view is intended for the classification of data you can select classifications in the list as well in the left most column. Classifications are color coded to help visually identify the severity of the variant. As we noted this view provides cursory information for indexing purposes, but you can click on the icon in the details column to get the full details on any given variant.

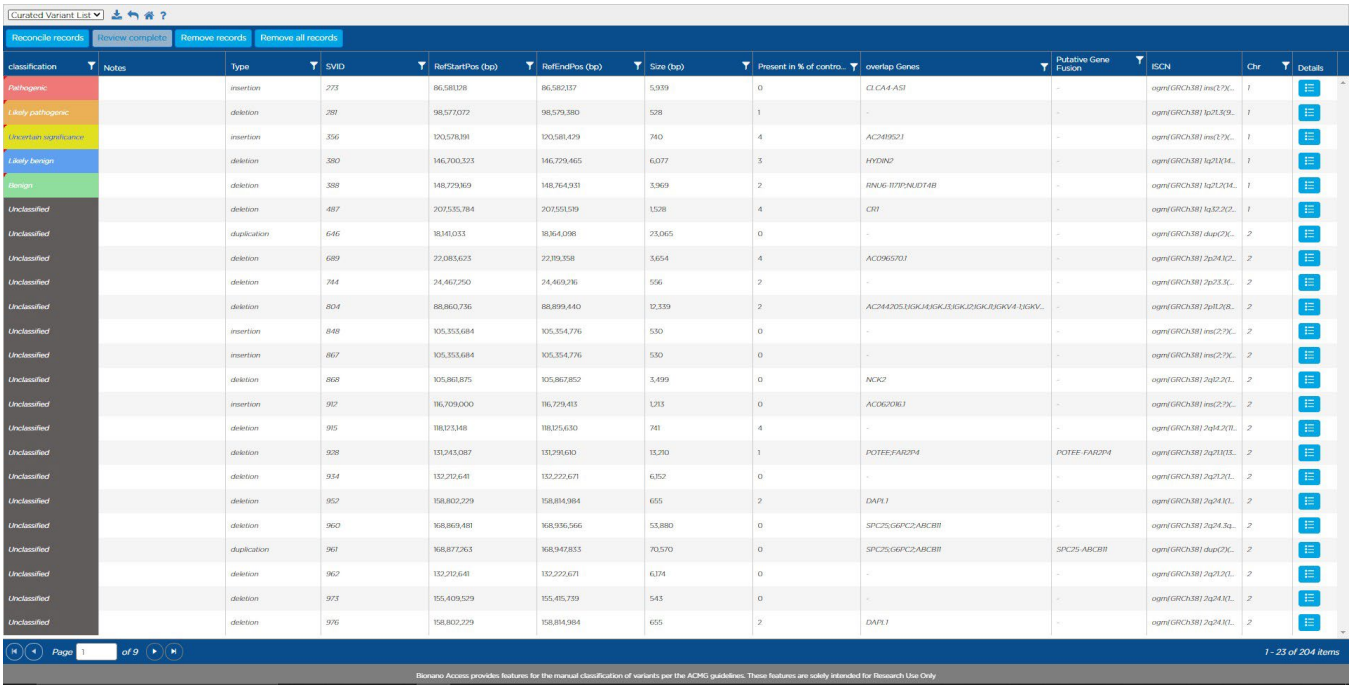


Figure 43. Curated Variant list example.

Variant Classifier

The variant classifier view is an interactive view that allows users to curate and visualize one variant in the curated variant list at a time. Bionano Access provides features for the manual classification of variants per the ACMG guidelines (see **Figure 8** through **Figure 12**). These features are solely intended for Research Use Only.

1. In Bionano Access, navigate to the **Viewer** screen of the job to analyze.
2. Select **Variant Classifier** from the drop-down list.
3. **Variant Classifier** view shows up.
4. Secondarily, users can double-click on a variant in the **Curated Variant** list which will also lead to the **Variant Classifier** beginning with the selected variant.

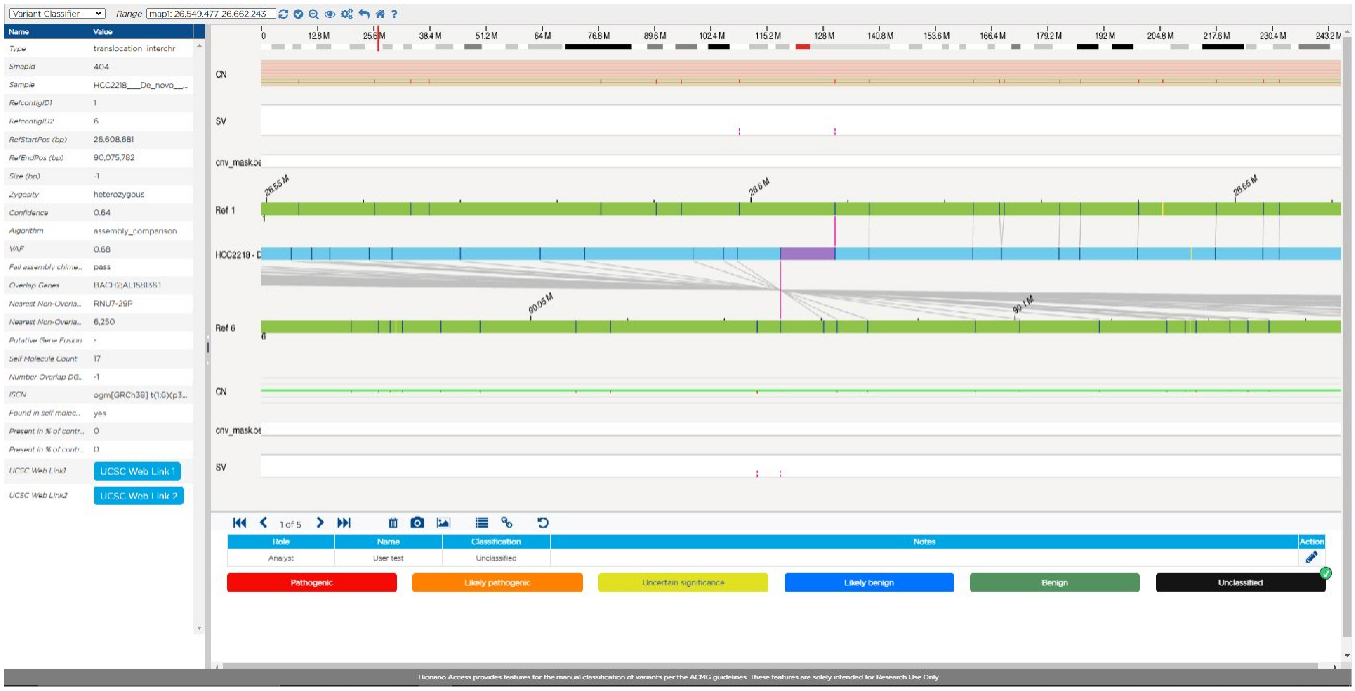
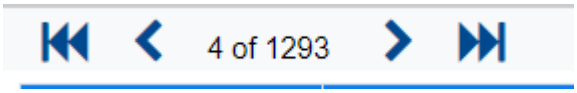


Figure 44. Variant Classifier visualization example.

The classifier view is broken into three areas. The leftmost panel will display all the properties for the selected variant. The properties displayed may vary depending on what data is available or the type of variant selected (structural variant vs copy number variant). The top right panel will show the selected variant in a view that should be very similar to the Genome Browser view. Refer to the Genome Browser view for more details on how to interact with this panel. The bottom right panel has the controls for variant classification. Across the top of the classification panel there is a tool bar.

Toolbar Icon	**Purpose**
	This portion of the tool bar indicates how many variants are in the Curated Variant list and allows you to move to the next variant in the list or to the ends of the list.

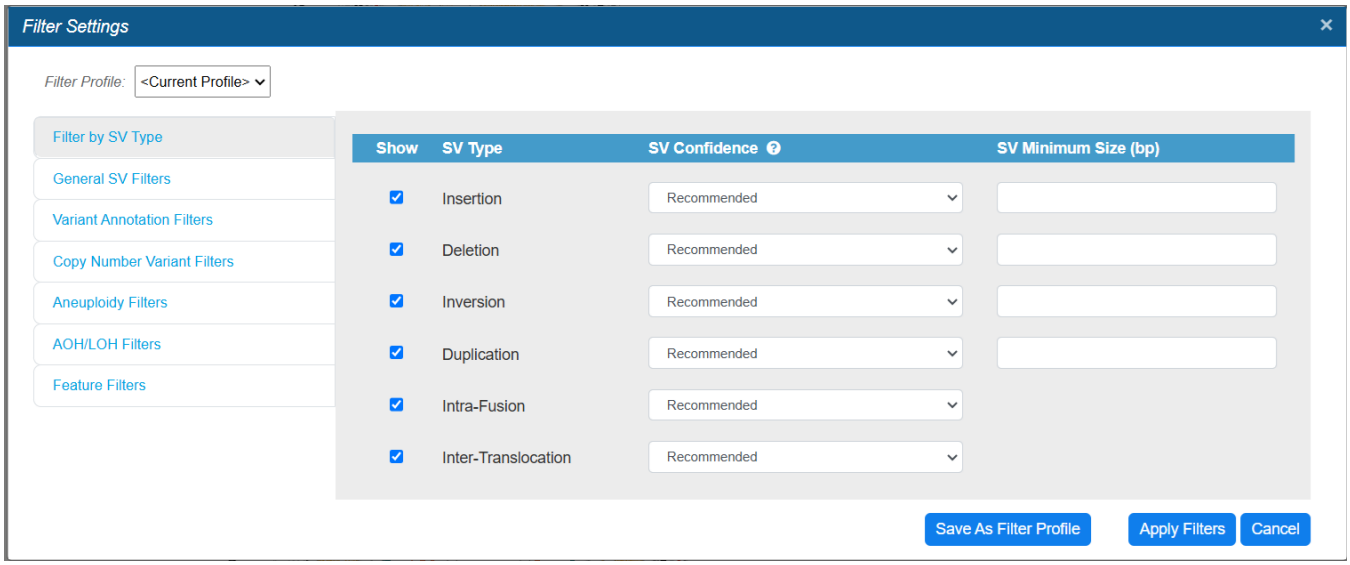
	This button will remove the current variant from the Curated Variant List.
	This button will capture an image of the genome browser panel in its current state. This image will be included in the Variant Report.
	This button will show the image currently saved for the selected variant.
	This button will take you back to the Curated Variant list. The current variant in the Classifier view will be selected when you return to the Curated Variant list.
	The genome browser panel in the Classifier view has a subset of the functionality of the actual Genome Browser view. The chain icon will jump to the Genome Browser view and zoom to the selected variant.
	This button will refresh the view. This can be helpful if you manipulated the genome browser panel and it needs to be reset.

Below the toolbar there is a grid that shows any classifications that have been made. If you are curating as an Analyst, you will only see the classifications that you have made. If you are reviewing classifications, a supervisor, you will see all classifications that have been made. Comments can be added to your classification by clicking on the pencil icon in the classification grid.

Below the classification grid there is a button group with one button for each possible classification. If the variant has already been classified a checkmark will appear on the button that corresponds to the classification that was made. To support rapid classification, when you click on any classification button that classification will be assigned to the current variant, and the classifier view will automatically move to the next variant in the Curated Variant list. So, if you intend to add a comment, be sure to do that before clicking on a classification button because it will move you to the next record.

Variant Filtering

Our analysis algorithms can detect numerous variants. It is common practice to filter the variants to identify those of interest. There are a few ways to do this. One way is to click on the filter icon in the toolbar to open the filter dialog. The filter dialog allows you to filter variants based on various properties. The filter dialog has multiple tabs along the left side to break up the filter criteria into logical groups. The filters you apply are applied to all views. So, as you switch between views you should be seeing the same set of variants based on your active filter criteria. You can see the active filter criteria in the legend which appears on the circos plot or by clicking on the SV Summary icon in the toolbar in the whole genome, ideogram, and genome browser views.



In the filter dialog you can filter variants based on their confidence score. The scale for each SV Type is different. To simplify things Bionano Access provides a recommended filter setting. In the Settings module it is possible to create other named confidence fitter settings you can select. It does require Project Lead access to create named filters for confidence scores.

Filter settings can be saved as a profile by clicking the ‘Save As Filter Profile’ button and then providing a name. You can then select the saved profile from the drop down in the upper left corner of the filter dialog. The filter profile drop down also includes selections to reset to recommended defaults and show all.

The other way to filter variants is based on their location. On the circos plot click on the Features tab in the legend. Here you can add features to the view. When you add a feature, you can choose to see only variants that overlap regions in the selected file. It is also possible to use a feature file as a mask and filter out variants that overlap regions in the selected file. If you are working with a particular disease or set of genes you can create a feature file and show only variants that affect those regions.

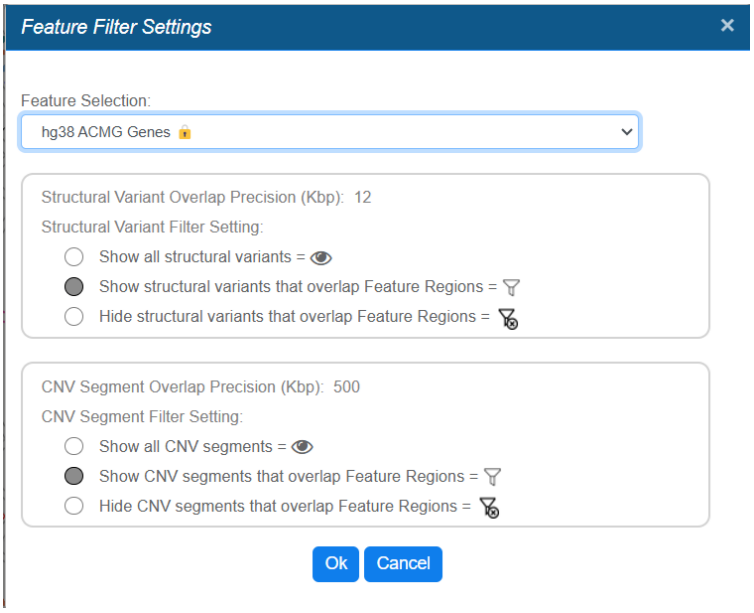


Figure 45: Filtering using Feature Files

Settings

Figure 46. Bionano Access settings

Resource Files

Access the settings module by clicking the ‘Settings’ button on the home page or by clicking the ‘Settings’ option in the menu. The options in the setting module will vary depending on the active user’s role. From the Settings module you can manage various resource files. In the Analysis module data is scoped into projects. Project data is only visible within that given project. Resource files are shared data files that are available across all projects. Resource files include References, System Features, Control Database, and Configurations. The settings module includes options to manage each of these types of resource files. Some default resource files are marked as system files. System provided resource files cannot be modified. Additional user resource files can be added, edited, and even deleted if certain conditions are met.

Banners

The system will allow Administrators to add banners to the login screen and file downloads. This allows organizations to add their policy statements to the system to instruct users related to the intended use of the system within their environment.

System Warnings

The system will allow Administrators to add a warning that appears in the header on every page. The intent of this feature is to allow Administrators to post a message when the system will be offline for service or if there is a known outage that is being addressed.

In silico Digestion

The references used for alignment by Bionano Solve are in CMAP file format. Bionano Access ships with several common references for human, and other popular species. The silico Digestion tool allows conversion of FASTA files for other organisms to CMAP format so they can be used as a reference. The system will prompt for a FASTA file and recognition enzyme. After a short wait, the system will return a CMAP file, QC metrics, and other useful output files. The CAMP file can then be added to the system references if desired. The tool includes management options to control the recognition enzymes available for selection and FASTA files that have been uploaded. If a duplicate digestion is submitted the system will direct the user to the existing results to save time and processing.

System Account Settings

The System Account Settings page allows an administrator to adjust various security controls related to user accounts. This page allows the administrator to change the following:

- Password complexity
- Previous password retention
- Password expiration
- Disable inactive accounts
- Concurrent session limit
- Session expiration
- Maximum login attempts

User Accounts

The user accounts page allows administrators to manage user accounts. From this page Administrators can create new user accounts, disable accounts, unlock accounts, and modify existing accounts. Bionano Access ships with the BionanoAdmin default user account. It is recommended that you make local accounts needed to manage and use the system and then disable this account. Do not use shared accounts for the lab. Each individual should have their own account. This ensures that the proper individuals get notifications when their jobs complete, and is in compliance with most standard data protection regulations. User accounts that have been used to generate data cannot be deleted, but they can be disabled.

Named Filters

In the viewer it is possible to filter each variant type by confidence score. The scale for confidence scores for each type of variant is different so it can become confusing. From this setting screen named filters with specific confidence thresholds can be created and modified. This helps to provide a more user-friendly approach to filtering by confidence score. For example, a named filter can be "High Confidence" instead of set of numbers that are different for each variant type. The system provided named filters cannot be modified to ensure the recommended values are maintained and adjusted for each release. User created named filters can be created, modified, and deleted.

Archive Jobs

Bionano Access Servers ship with storage capacity for sufficient for several years. Bionano does not provide tools to warn you about storage utilization. Data can be archived and moved to other systems to prolong the storage on the system. Contact your IT group to mount external storage to the Bionano Access Server. Jobs can then be selected via this screen and archived to the external file location. These archive files can later be restored when and if desired via the Settings module.

System Services Settings

Bionano Access can be integrated with various other Bionano software products including Bionano Solve, Compute On Demand, VIA, and Bionano Assure. Bionano Solve integration is controlled via the access configuration file, but the other services noted can be enabled via this page. Enabling these services may require accepting terms and conditions related to their use. Connectivity to these services can be tested once enabled. Other sections of this document will describe how to leverage these services.

VIA Software Settings

Users with the Administrator role can create custom VIA sync settings. Bionano Access is preconfigured with default settings for common operations, which users can select from when launching a job or uploading an existing job. For instructions on how to create or edit VIA sync settings, see the "VIA Software" section.

Compute On Demand

Enable Compute On Demand

The Compute On Demand service allows you to run jobs on compute servers in the cloud. The Compute On Demand service is a pay per use service that requires tokens. Tokens can be purchased from orders@bionano.com. You will be sent a voucher that when redeemed on your local Bionano Access server will grant tokens.

To enable the Compute On Demand service login as an administrator. Go to the Settings module and click on the button System Services Settings button. On the Services page click the toggle to turn on the Compute On Demand Service. When you enable the service for the first time you will be prompted for a few things:

- Organization Name – All jobs launched on the Compute On Demand platform will be tagged with this organization name. We recommend setting this value to the domain name in your email address. This name cannot include special characters including spaces.

- Region – Our compute resources are regionalized to assist with General Data Protection Regulation (GDPR) compliance. Select the region where your Bionano Access server resides. You will not be able to change this value later so make your selection carefully.

- Terms and Conditions – To enable the Compute On Demand service you must accept the terms and conditions. If the Terms and Conditions change you will be asked to accept them again.

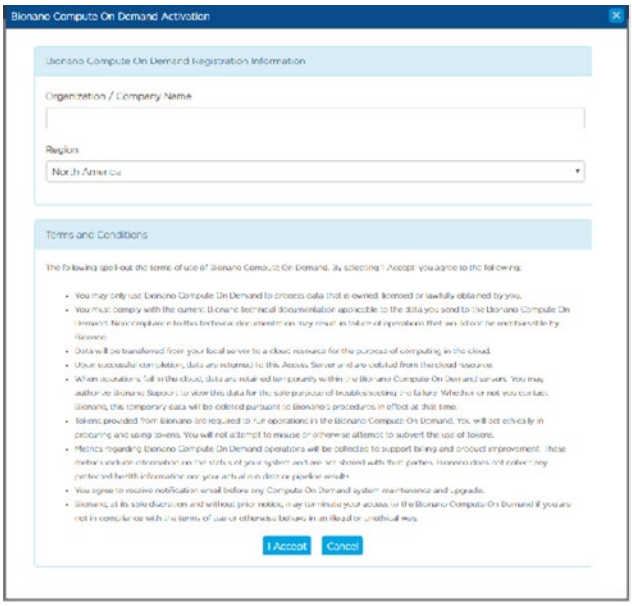
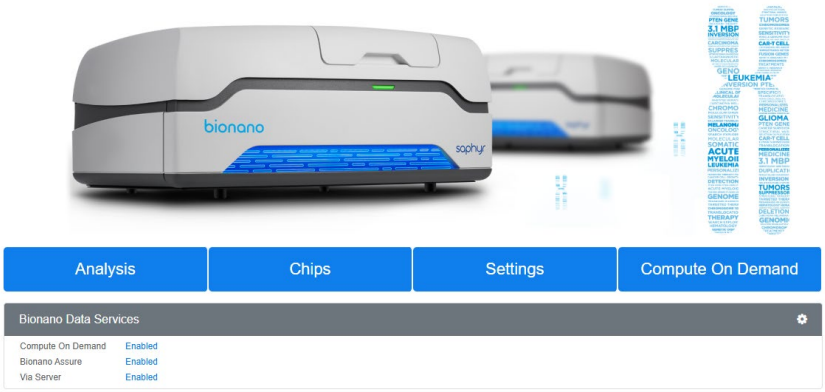


Figure 47. Bionano Compute On Demand Activation window

After the service has been enabled the Compute On Demand panel on the services page will show a 'Test Connection' button you can use to verify connectivity to the service.



After the service has been enabled the Compute On Demand module button on the home page will be enabled. In the Compute On Demand module, you can redeem vouchers, transfer tokens, and track token usage. To redeem a voucher, select the 'Redeem Vouchers' tab in the Compute On Demand module. Then paste the

voucher code into the Voucher code field. You can redeem multiple vouchers at once by putting them in the Voucher Codes field one per line. Click the 'Redeem Vouchers' button to consume the voucher. The Current Token Balance field should update to reflect your updated token balance. Vouchers are region specific so when you order tokens be sure to order them for the region you are using. The tokens will be granted to the active user account used to redeem the voucher.

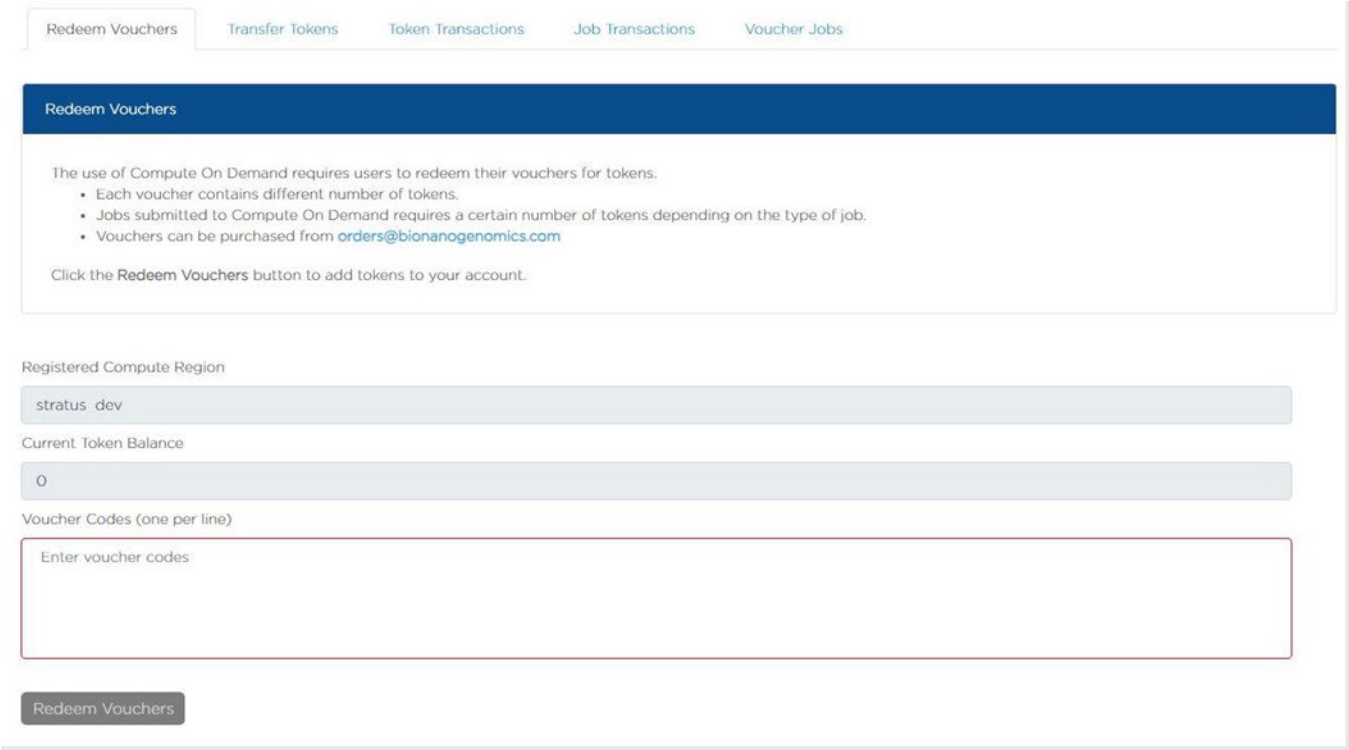


Figure 48. Redeem Vouchers

Users can transfer tokens to other users. Tokens can only be given. They cannot be taken away from other users. To transfer tokens, select the Transfer Tokens tab in the Compute on Demand module, enter the token about to transfer, select the user to receive those tokens and then click the 'Transfer' button. After clicking the 'Transfer' button the token balances will update.

The other tabs will allow you to track token usage. It will provide data on token transfers, compute on demand jobs, and voucher token balances.

Compute On Demand Operations

After enabling the Compute On Demand service users can launch jobs on the Compute On Demand in the Analysis Module. In the Project Browser in the Operations panel select the Compute On Demand environment (Figure 20) to launch jobs using the Compute On Demand Service.

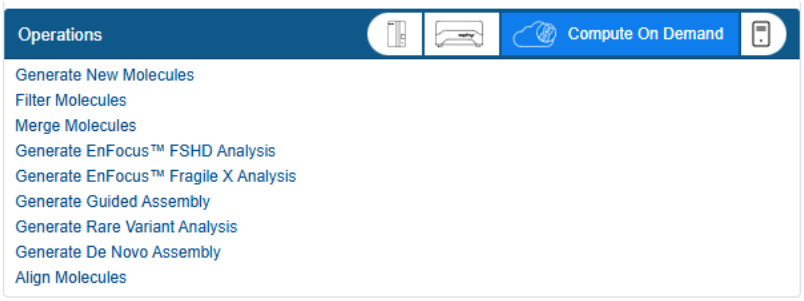


Figure 49. Compute On Demand Drop-Down Toggle

The workflow to launch operations on the Compute On Demand service is the same as running jobs against a local compute server with one exception. The system will provide a token estimate for the job (Figure 21). The runtime and cost for any given job can vary based on the region, quality of data, quantity of data, and availability of compute resources at the time. The estimate provides a minimum and maximum potential cost. Should the cost of the job exceed the maximum quoted you will only be responsible for the maximum token amount. Any difference between the actual cost and the maximum amount will be returned to your account upon completion of the job. Different applications recommend different amounts of DNA be collected and analyzed. Reduce the amount of DNA when possible, depending on what application you are performing to reduce your Compute On Demand token costs.

Figure 50. Token Cost Message Example

VIA Software

VIA is a powerful tertiary analysis software for classifying variants and generating reports. Access can be configured to transfer OGM data directly to an instance of VIA. Jobs in Bionano Access are transferred to VIA as samples. Jobs be transferred to VIA on demand or projects can be configured to transfer jobs automatically. VIA only supports human samples and is not intended for non-human samples.

To transfer data to VIA there are three things that must be configured. First, Access uses a utility program called the VIA Sample Importer to transfer data into VIA. Contact Bionano Technical Support (support@bionano.com) for assistance setting up the VIA Sample Importer. The Bionano Access configuration file

(/home/bionano/access/web/Server/Config/access.txt) file should include the key for viaExe to indicate where the VIA Sample Importer is installed. For example, the viaExe entry line in the access.text file could look like this - "viaExe":"/home/bionano/VIASampleImporter/VIASampleImporter". VIASampleImporter appears twice in this example because the first is the directory and the second is the executable. Be sure to restart the Bionano Access service whenever changing the access configuration file.

Next, setup the connection to the VIA Server. As an Administrator go into the Settings Module. Select the Services Settings page and then provide the connection information to the VIA Server. You can click the test connection button to verify your settings. The VIA Server connection settings will not be visible on the Service Settings page if the VIA Sample Importer has not been configured.

VIA is a highly configurable product. To transfer a given Access job to VIA you must know what Sample Type, processing, reference, panels, etc. should be used. Create VIA Settings in the Settings module to define these mappings between Access job types and VIA sample settings. The VIA Settings page allows you to define and name the sample type, reference, processing, and panel to be used for a given type of job in Access. If you choose to make a VIA setting the default it will be the default selection made when you attempt to transfer that type of job to VIA.

Now that you have the VIA Sample Importer, VIA Server Connection, and VIA settings configured you can begin to transfer jobs to VIA. There are two ways to accomplish this. First, when you launch new jobs for any job types that have VIA settings the VIA setting selection will be available when you launch the job (Figure 22). If there was a default VIA setting for that job type it will appear as the default selection. If you make a VIA setting selection the job will automatically be transferred to VIA upon completion.

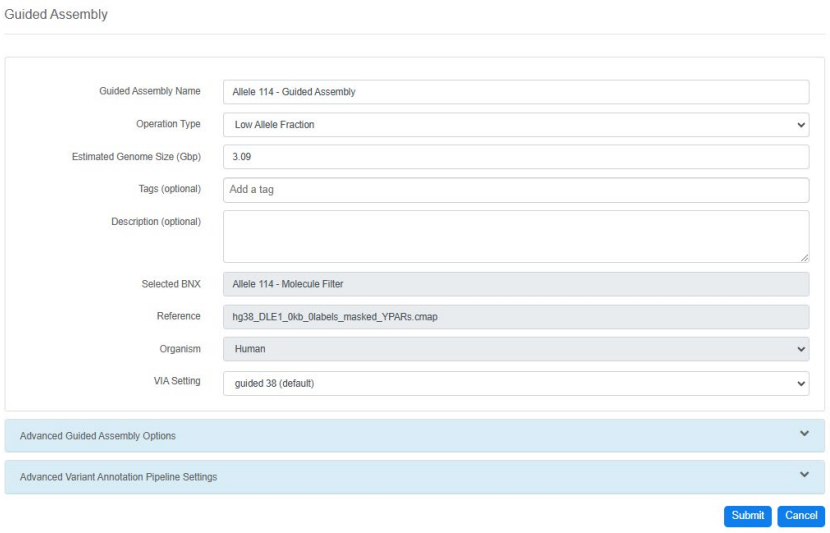


Figure 51 – Launch Screen for Guided Assembly

Second, if you have a job that has already completed, choose the Upload to VIA option in the options panel (Figure 23). You will be prompted to choose the VIA settings to use. It will also allow you to change the sample name and choose to overwrite an existing sample if it already exists in VIA (Figure 24).

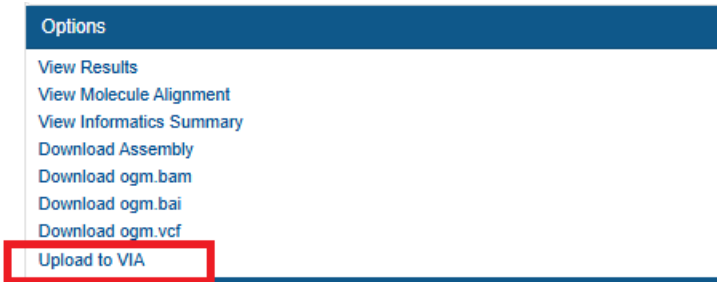


Figure 52

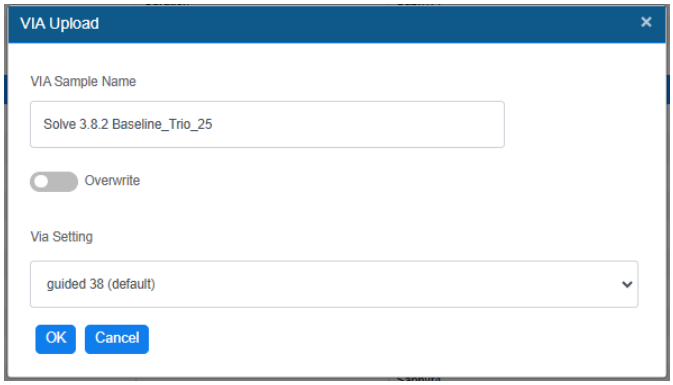


Figure 53

Appendix

Red-Labeled Sample Experiment

Bionano Access supports experiments that use the red laser (if applicable) in the Saphyr instrument. These workflows are disabled by default. To enable this operation, users need to contact *Bionano Technical Support* (support@bionanogenomics.com).

RED-ONLY WORKFLOW

If the capability of running red labeled sample has been enabled, when users open the Single Sample workflow, they will have the choice of selecting green or red. If red-labeled sample setup has not been enabled, the system will only generate experiments using green laser.

DUAL-LABELED WORKFLOW

If red is enabled, the **Dual-Labeled workflow** in the experiment design module will be available. The **Dual-Labeled workflow** is designed to process a single sample with motifs in the DNA labeled using either green or red colors. The system will generate label-related metrics on the dashboard for each color. Users can provide separate references for each color, but only one reference will be associated with the finally merged BNX file. The user is prompted to select which label (the primary) would retain its reference. The **Dual-Labeled workflow** will generate a single BNX file that contains both green and red labels information.

When users import a dual-labeled BNX file, the reference will automatically be associated with channel 1, as specified in the header or the BNX file. Users can select the **Edit** option to designate either channel for the reference. When users run an assembly using a dual labeled BNX file, they will be prompted to select labels from which channel they want to use for assembly. After the assembly is done, when users choose to show molecules in the viewer, the viewer system will show labels for both labeled motifs.

MULTIPLEX WORKFLOW

If red is enabled, the **Sample Multiplex** workflow will be enabled in the **Experiment Design** module. This workflow is designed to process one sample using green and a second sample using red in the same flowcell. This workflow will generate separate dashboard metrics for each color. This workflow will also generate a separate BNX file for each color. It is possible to use the same sample for both red and green, but the molecules loaded should be labeled with only red or green, but not both.

ISCN Symbols and Abbreviated Terms

Symbols and abbreviated terms used in the description of chromosomes and chromosomal abnormalities are listed below (**Table 25**). For a detailed discussion of ISCN notation produced by the Solve pipeline, please refer to *Bionano Solve Theory of Operation Variant Annotation Pipeline* (CG-30190). Consider the following when searching for chromosomal abnormalities:

Table 2. ISCN Symbols and Abbreviated Terms

Symbol/abbreviation	Description
amp	amplification of interval where copy number is greater than 4.
approximate sign (~)	denotes intervals and boundaries of a chromosome segment or number of chromosomes, fragments, or markers; denotes a range of number of copies of a chromosomal region when the exact number cannot be determined.
brackets, square ([ ])	surround number of cells or genome build.
dup	Duplication.
fus	fusion between regions of the same chromosome.
ins	Insertion.
inv	Inversion.
ogm	Optical genome mapping data.
p	Short arm of chromosome.
parentheses ( )	Surround structurally altered chromosomes and breakpoints; surround chromosome numbers, X, and Y in normal and abnormal results; surround coordinates (or nucleotide positions) in abnormal result.
q	Long arm of chromosome.
question mark (?)	Insertion of unknown sequence.
t	Translocation.
x	Copy number.

Technical Assistance

For technical assistance, contact Bionano Technical Support.

Retrieve documentation on Bionano products, SDS's, certificates of analysis, frequently asked questions, and other related documents from the Support website or by request through e-mail and telephone.

TYPE	CONTACT
Email	support@bionano.com
Phone	Hours of Operation: Monday through Friday, 9:00 a.m. to 5:00 p.m., PST US: +1 (858) 888-7663 Monday through Friday, 9:00 a.m. to 5:00 p.m., CET UK: +44 115 654 8660 France: +33 5 37 10 00 77 Belgium: +32 10 39 71 00
Website	www.bionano.com/support
Address	Bionano, Inc. 9540 Towne Centre Drive, Suite 100 San Diego, CA 92121

Legal Notice

For Research Use Only. Not for use in diagnostic procedures.

Patents

Products of Bionano Genomics® may be covered by one or more U.S. or foreign patents.

Trademarks

The Bionano logo and names of Bionano products or services are registered trademarks or trademarks owned by Bionano Genomics, Inc. (“Bionano”) in the United States and certain other countries.

Bionano™, Bionano Genomics®, Saphyr®, Saphyr Chip®, Bionano Access™, Stratys™, Stratys™ Compute, Stratys™ Chip, VIA™, and Bionano EnFocus™ are trademarks of Bionano Genomics, Inc. All other trademarks are the sole property of their respective owners.

No license to use any trademarks of Bionano is given or implied. Users are not permitted to use these trademarks without the prior written consent of Bionano. The use of these trademarks or any other materials, except as permitted herein, is expressly prohibited and may be in violation of federal or other applicable laws.