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Bionano Access® v1.8.1 Release Notes

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Revision History

REVISION	NOTES
A	Initial release.
B	Revision.
C	Changes for 1.8.1 update
D	Added tickets to known issues

Bionano Access

This document describes the v1.8.1 release of Bionano Access® and will provide an overview of what is changing with this release so that users may better understand the impact of moving to this version. Should there be any questions please contact support@bionano.com.

Introduction

Bionano Access v1.8 is a new release of the Bionano Access product. Bionano Access supports installation on Windows and Linux systems. Data between users is shared using Projects, and performance is much improved through rendering optimizations and graphics acceleration. This application is designed for installation on a single centralized server that can be shared across an organization. For information about system requirements and installation please refer to the *Bionano Access Installation Guide* (CG-30170).

Compatibility

Bionano Access 1.8.1 is compatible with Saphyr Instrument Control Software (ICS) versions 4.9 and above. Bionano Access is designed to integrate directly with the Bionano Solve® v3.8.1 pipeline running on Saphyr Compute and Bionano Compute servers and on Bionano Compute on Demand (COD). Compute configurations which are not directly compatible will continue to be supported from the command line, with a manual import of results into Bionano Access.

Mac Support

Installing Bionano Access locally on a Mac system is no longer supported. Bionano will not be offering mac installers for Bionano Access version 1.8.1. Mac is still supported as a client to interact with a Bionano Access server running on either Windows or Linux through a standard browser.

Improvements for Bionano Access 1.8.1

ADD SUPPORT TO LAUNCH GUIDED ASSEMBLY OPERATIONS

The new **Guided Assembly** operation has been added to the **Project Browser** (**Figure 1**). For details on this operation, refer to *Bionano Solve Theory of Operation: Structural Variant Calling* (CG-30110).

Figure 1. Guided Assembly window

ADDED SUPPORT FOR AUTO GUIDED ASSEMBLY LAUNCH WHEN SETTING UP A CHIP

When setting up a chip, there is an option to auto-launch **Guided Assembly** with the resulting BNX file (**Figure 2**).


Figure 2. Guided Assembly auto-launch checkbox.

Improvements for Bionano Access 1.8

Below is a brief description of new features that have been added with this release. For more detailed information on these new features please refer to Bionano user manuals and video tutorials.

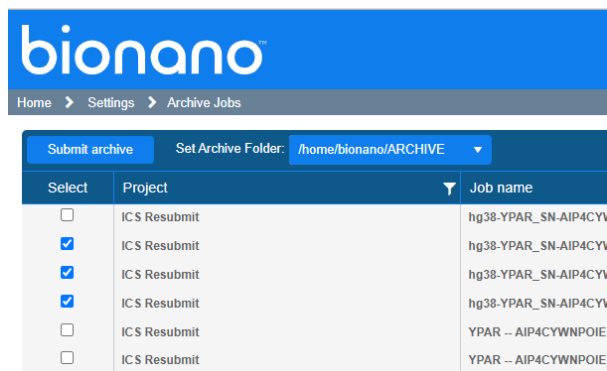**USER CAN NOW FILTER ANEUPLOIDY EVENTS IN THE VIEWER**

The **Filter Settings** dialog in the viewer now supports the filtering of Aneuploidy events by type or confidence, as seen in **Figure 3**.
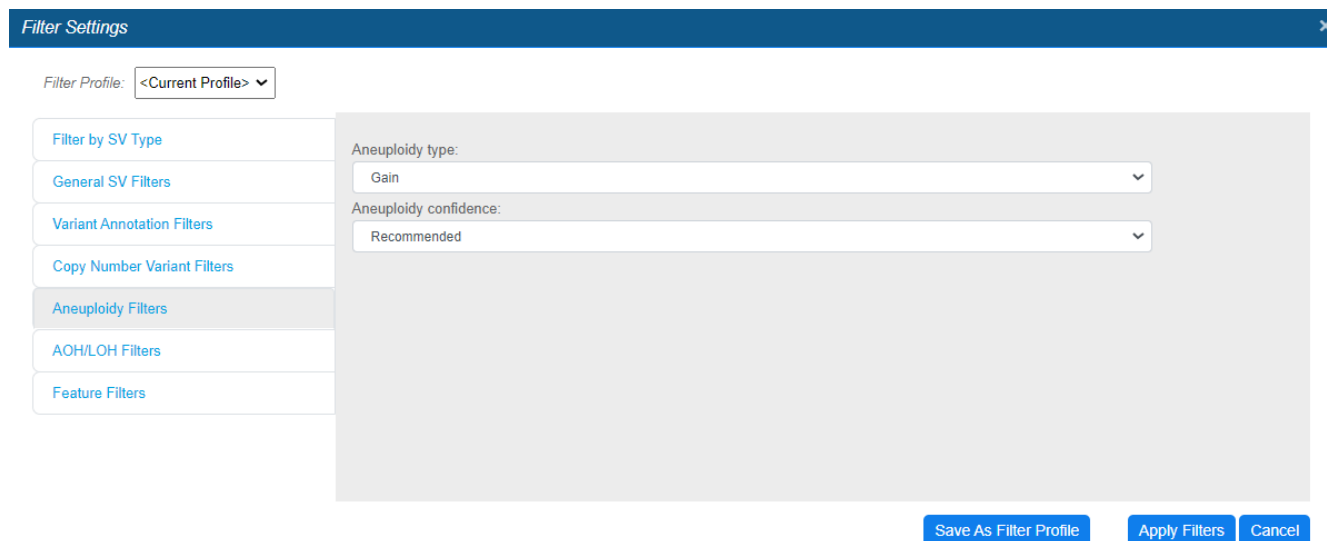
Figure 3. Aneuploidy filter settings.

ADMINISTRATORS CAN ARCHIVE RESULTS FROM ACCESS TO DISK

With Bionano Access v1.8, users with the Administrator role can archive jobs, as shown in **Figure 4** This operation allows for offloading results to enterprise storage so that disk space for additional analysis jobs can be reclaimed and/or to declutter projects. These jobs can be restored later, if needed. The system will verify the files being restored to ensure they match the original files. It is also possible to extend the storage capacity of the Bionano Access server with enterprise storage. Contact support@bionano.com for details on how to mount enterprise storage for job archival or additional storage.

Figure 4. Job archive.

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USER CAN FILTER BNX BASED ON SCAN NUMBER

The **BNX Filter** operation now allows users to filter BNX files by scan number (see **Figure 5)**. Users can specify a **Start** value, **End** value, or both to create a range that will be retained. The scan number specified will be included in the results.

Figure 5. Filtering BNX files by scan number.

ADD OVERLAPPING FEATURES TO STRUCTURAL VARIANT (SV) REPORT

When generating an SV report, the system will automatically list any overlapping features visible in the viewer for each variant.

ADD IMAGES TO SV REPORT

The SV Report has been modified to include snap shots of the Ideogram and Whole Genome views in addition to the Circos plot.

ALLOW USER TO FILTER THE CLASSIFICATION REPORT BY CLASSIFICATION

When generating an SV report, users can choose which variants to include in the output based on their classification (e.g., Pathogenic, Benign). The system will offer a checkbox for each American College of Medical Genetics (ACMG) classification, as seen in **Figure 6**.

Figure 6. SV Report classifications filter.

MOLECULE SIZE DISTRIBUTION NOW AVAILABLE

An option to view a **Molecule Size Distribution** graph (**Figure 7**) for molecule jobs in the **Project Browser** has been added. The system will need to load and read the molecules file. These files can be large, so it may take several minutes for the results to appear.
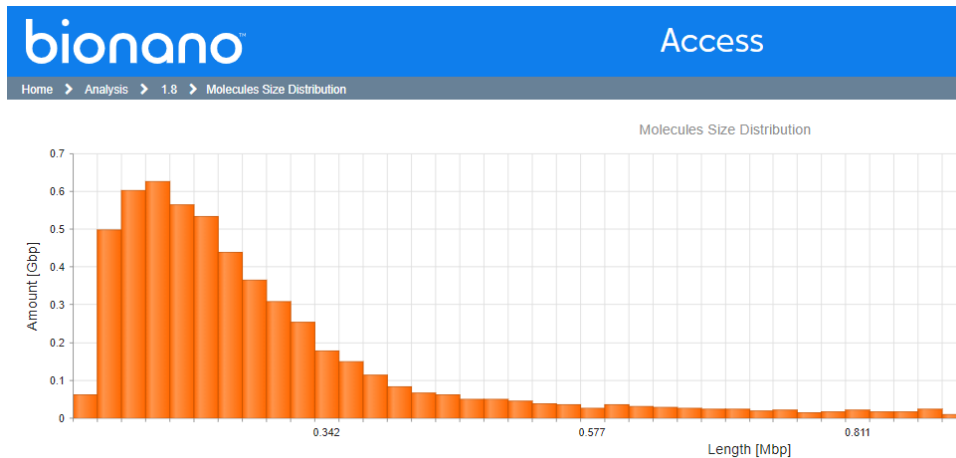
Figure 7. Molecule Size Distribution graph.

SV REFRESH-FOCUS ADDED TO CLASSIFICATION SCREEN

As users page through variants on the **Variant Classifier** page, the system will load the selected variant to the viewer. While making an evaluation, users may zoom or scroll around. The display of the variant can be reset by clicking the **Refresh Display** icon on the **Classifier** toolbar, seen in **Figure 8**.
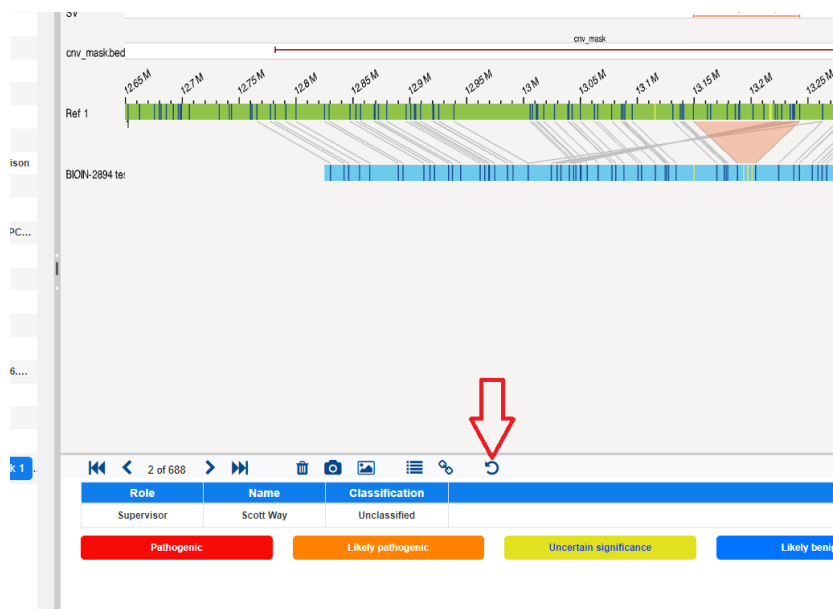
Figure 8. Refresh Display icon.

USER CAN CREATE AND SAVE NAMED FILTER PROFILES IN THE VIEWER

In the **Filter Settings** dialog, current filter settings can be saved as a **Filter Profile**. When the **Filter Profile** is created it can be shared so other users can use it. To use an existing Filter Profile, select the desired profile in the drop-down box in the upper lefthand corner, as seen in **Figure 9**.
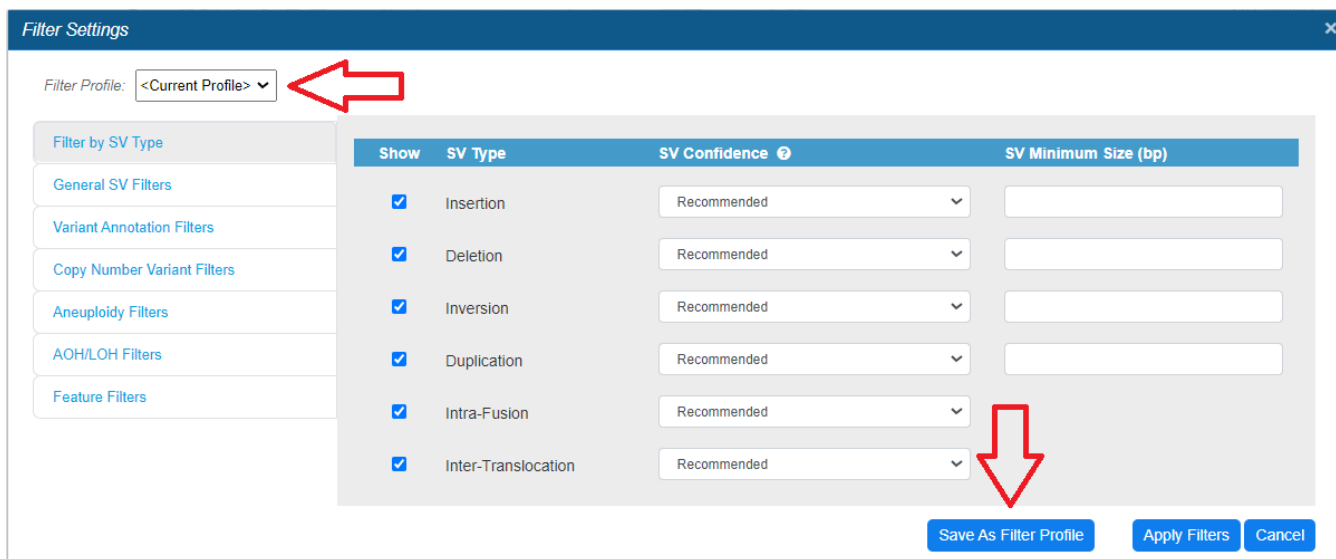
Figure 9. Selecting (top left) and saving (bottom right) Filter Profiles.

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USER CAN ENTER COORDINATES FOR WHOLE GENOME VIEW

Coordinates can now be entered in the **Whole Genome** view to zoom to a particular region of interest (see **Figure 10).**

Figure 10. Whole Genome coordinates input field.

USER CAN SORT CURATION LIST SCREEN ON MULTIPLE COLUMNS

In this release, it is possible to sort the curation list based on multiple columns. Each click on the selected column header will toggle the sort direction for that column from ascending to descending, then off. If the choice is to sort more than one column a number will appear to indicate the precedence of each column sort. In **Figure 11**, the list is sorted first by chromosome (**Chr**) and then by variant type (**Type**).

Figure 11. Sorting the curation list.

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VIEWER TOUR FEATURE ADDED

A **Tour** icon (**Figure 12**) has been added to the toolbar in the viewer. When the **Tour** icon is clicked, it will open the **Tour** screen (**Figure 13**). Click the green arrows for an explanation of each viewer component.
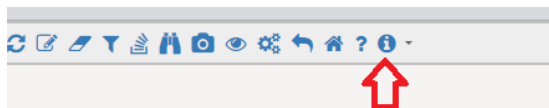
Figure 12. Tour Icon.
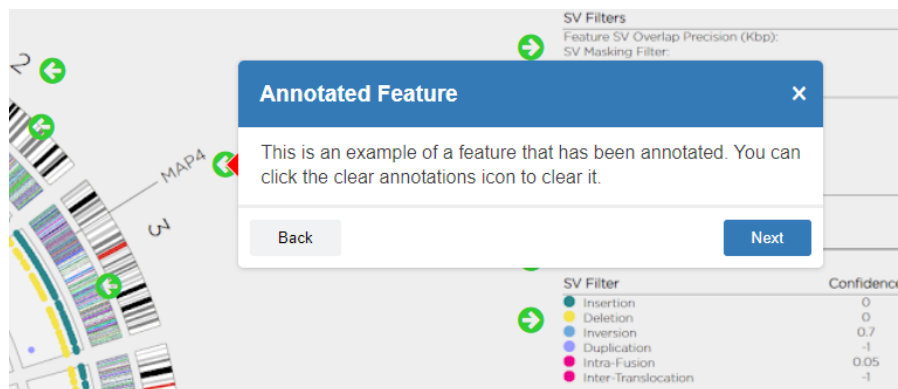
Figure 13. Tour screen with component explanation.

AUTOMATE TRANSFER DATA TO VIA

To facilitate the migration of data to VIA, Bionano Access now provides automation to synchronize data. Users with the Administrator role can create custom VIA sync settings. Bionano Access is preconfigured with several default settings for common operations, as seen in **Figure 14**. Users can choose the VIA sync settings to use when launching a job or to push an existing job. Sync settings are tied to the job reference and operation. For more details on syncing data with VIA, refer to *Bionano Access Software User Guide* (CG-30142).
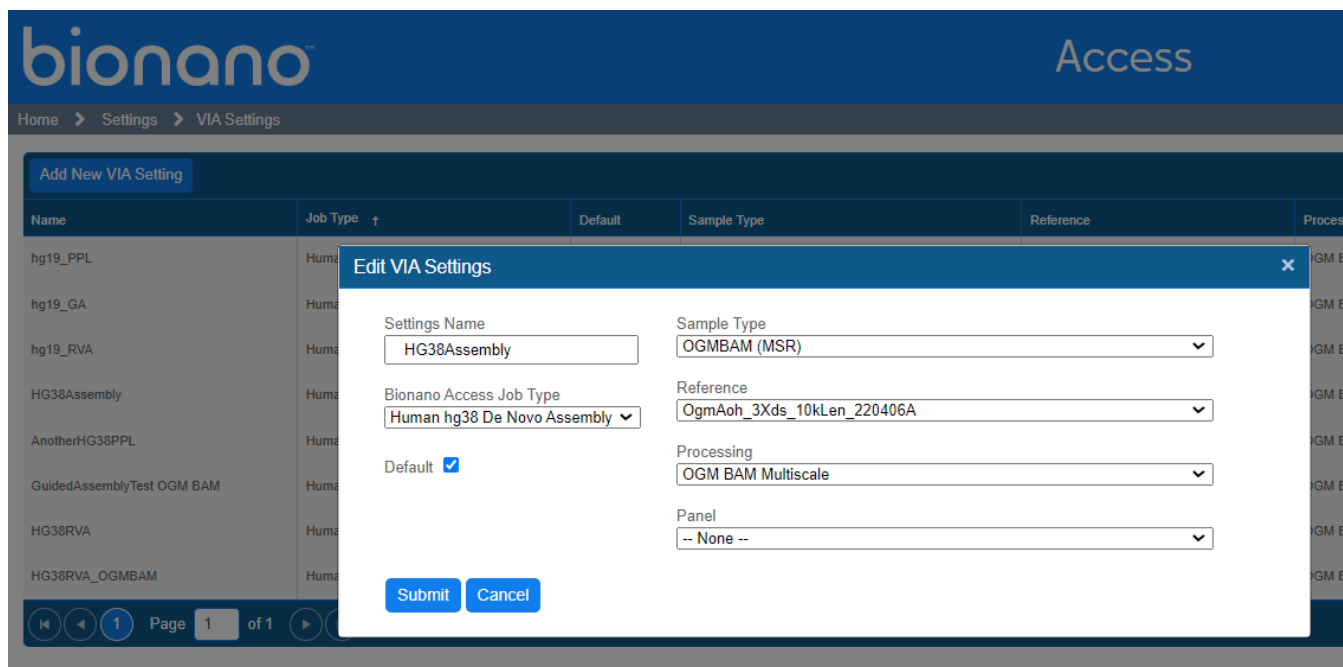
Figure 14. Editing VIA settings.

ON JOB COMPLETION, AUTO-TRANSFER *de novo* **AND RVA DATA TO VIA**

When launching a job, if there are matching VIA sync settings for the reference and operation the user can select which sync setting to use. The results will automatically be transferred to VIA upon completion of the job. The default sync setting will be selected initially, but it can be changed as needed (see **Figure 15**).

Figure 15. VIA sync settings.

ADD AN OPTION LINK IN THE PROJECT BROWSER TO MANUALLY TRANSFER A SELECTED JOB TO VIA

It is also possible to manually transfer existing jobs to VIA. Click the **Upload to VIA** option in the **Project Browser** for the targeted job. The **VIA Upload** dialog will appear (**Figure 16**). Complete the form and click **Submit** to initiate an immediate sync to VIA for that job. If the job already exists in VIA, but a user wants to upload it again, choose the **Overwrite** option.

Figure 16. VIA Upload dialog.

SHOW THE TRANSFER STATUS OF EACH JOB

If a sync has been launched, the job details will now show the status of the data transfer to VIA, seen in **Figure 17.**

Figure 17. Job transfer status

ADD DOWNLOAD LINKS FOR BAM, BAI, AND VCF FILES

Bionano Solve now generates BAM, BAI, and VCF files for use with VIA or other visualization software. Links have been provided for each job where appropriate to download these files.

AUTOMATION TO LAUNCH OPERATION TYPE FOR EACH SAMPLE IN A SELECTED PROJECT

Projects can be configured to automatically generate various operations for each sample (see **Figure 18**). The Project Lead role can enable these settings for a project, but the system will not generate a new job for a given sample if a job with that operation already exists for that sample.

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Project Settings

Auto Analysis (recurring)

Annotated Assembly	Off ⬤ On	Minimum Coverage	80 X
Annotated Rare Variant Analysis	Off ⬤ On	Minimum Quantity	400 (Gbp)
FSHD	Off ⬤ On	Minimum Quantity	400 (Gbp)
Fragile X	Off ⬤ On	Minimum Quantity	400 (Gbp)

Submit   Cancel

Figure 18. Configuring automatic operations.

HIGHLIGHT EXPECTED MOLECULE QUALITY REPORT (MQR) QUALITY LEVELS

The MQR will now highlight values that fall below quality thresholds (see **Figure 19**).

Reference	hg19_DLE1_0kb_0labels.cmap	Name of the reference genome this sample was aligned to.
Reference Length	3,095,677,412 bp	Total length of reference sequence
Effective coverage	233.51	Total amount of aligned DNA divided by the size of the reference genome.
Map rate	62.2 %	Percentage of molecules that are 150kbp or longer mapped to the reference
Scaling SD	0.01	Linear term in sizing error relative to reference
Site SD	0.11	Constant term in sizing error relative to reference
Relative SD	0.028	Quadratic term in sizing error relative to reference
Base pairs per pixel	420.02	Calculated base pairs per pixel in the alignment by comparing molecules to the reference.
Positive label variance (PLV)	5.17	Percentage of labels absent in reference

Figure 19. Highlighted MQR value.

ADD CSV DOWNLOAD FOR CHIP METRICS

On any chip dashboard there is a new button to **Show Data** (see **Figure 20**). Users can click this button to see the raw data that was collected for the selected chip run. On the **Subsequent Data Points** screen, users can click the **Export to Excel** button to dump all the data points to a spreadsheet.
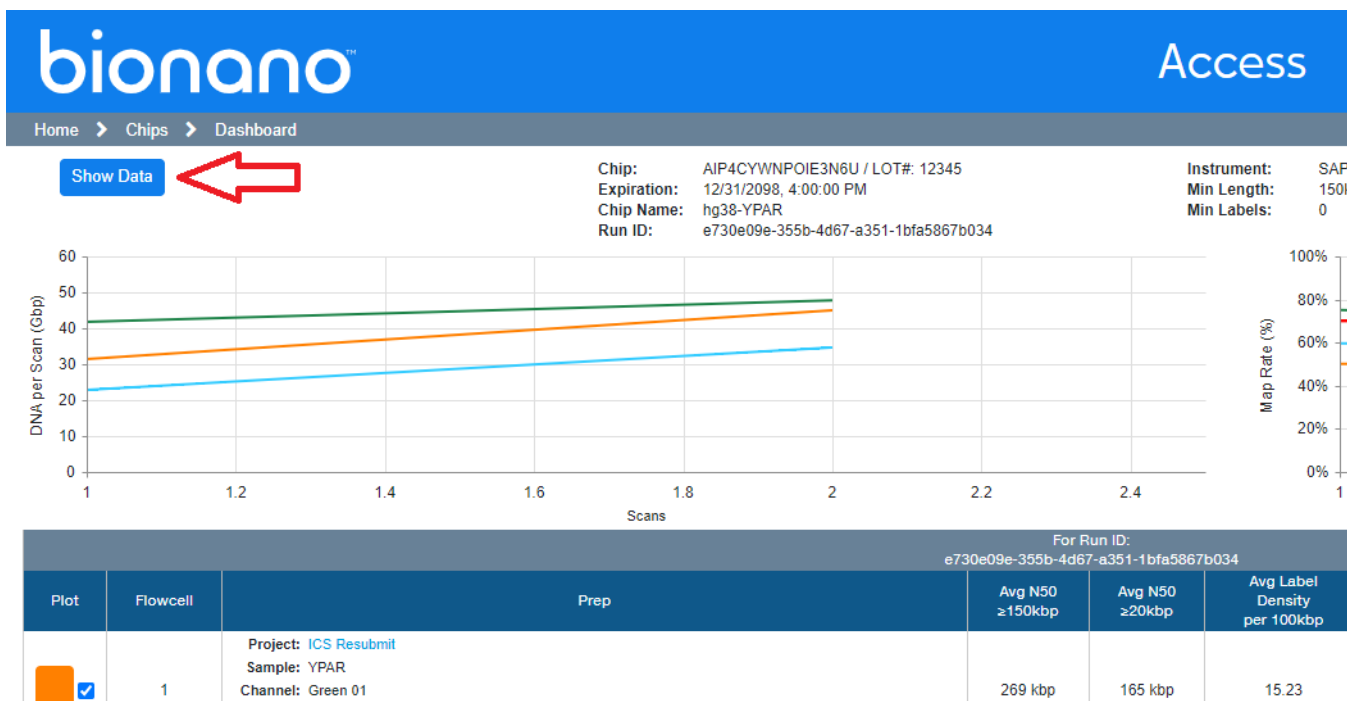
Figure 20. Show Data button.

ADD CHROMOSOME NUMBERS ON WHOLE GENOME VIEW

The **Whole Genome** view has been modified to show the chromosome numbers under the copy number track in addition to the VAF track.

INDICATE ANY BED FILES USED FOR MASKING AS PART OF THE OPERATION

The **SV Summary** legend has been updated to indicate what SV Mask file was used to produce the output, if any.

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Tickets

The features released with Bionano Access 1.8 are listed in **Table 1**.

Table 1. Released Features in 1.8

Summary	Ticket
When mousing over a gene in a gene track (GTF format) the system will not display the name and coordinates.	IW-9009
Improved logging when executing command shell operations.	IW-9188
Added system mm39 references.	IW-8881
Added stable region assessment value to VIA sync.	IW-9236
User can now filter aneuploidy events in the viewer.	IW-7278
BED and GTF files have been updated to harmonize with VIA.	IW-9493
Added YPARS references.	IW-9094
Administrators can archive results from Access to disk.	IW-9322
Auto-noise BNX only extracted from zip when required for VAP to save disk space.	IW-7492
User can swap colors on two color BNX files.	IW-8000
User can filter BNX based on scan number.	IW-4697
User can remove one color from two color BNX file.	IW-4698
System will notify operator when job auto-launch criteria not met.	IW-7830
System will now track chip expiration date.	IW-8221
Added number of CNV and aneuploidy calls to informatics report.	IW-9392
160x down sample option added for assembly operations.	IW-7894
Map ID added to variant hover in viewer.	IW-6687
T2T references added to the system.	IW-7485

Summary	Ticket
Added chip template for mosaic *de novo* 800gbp.	IW-7968
Added control to set N-base gap size of hybrid assembly.	IW-7835
Added overlapping features to SV Report.	IW-6772
Added operation type to legend in the viewer.	IW-7555
Allow user to filter the classification report by classification (ex. pathogenic, benign, etc.).	IW-7721
Changed region input in viewer to accept map to be consistent with UCSC browser.	IW-7046
Classifications are now sorted by severity instead of alphabetically.	IW-7640
Molecule size distribution now available.	IW-1307
SV Re-Focus added to classification screen.	IW-7309
User can create and save named filter profiles in the viewer.	IW-6747
User can enter coordinates for whole genome view.	IW-6710
User can swap hg19 and hg38 references when launching assemblies.	IW-7093
A confirmation dialog has been added when adding variants to curation list.	IW-8384
User can sort curation list screen on multiple columns.	IW-7641
User can now select the view they want to review from the **Tour** screen.	IW-8318
Viewer tour feature added.	IW-7674
Automate transfer data to VIA.	IW-8554
Add system settings for VIA Connection Settings.	IW-8312
On job completion auto-transfer *de novo* and RVA data to VIA.	IW-8623
Automation to launch operation type for each sample in a selected project.	IW-8175

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Summary	Ticket
Allow user to select VIA sync settings for each job.	IW-8316
Show the transfer status of each job.	IW-8551
Check existing VIA sync settings are valid.	IW-8549
Add an option link in the project browser to manually transfer a selected job to VIA.	IW-8464
Create a log file for the content of the zip file.	IW-6041
Add API calls to download informatic reports in JSON format.	IW-8218
Provide API to download VCF files for select jobs.	IW-5554
Highlight expected MQR Quality Levels.	IW-8243
Add Ideogram image to SV Report.	IW-6713
Add jobs link to the slide out menu.	IW-7988
Add whole genome image to SV Report.	IW-7585
Add csv download for chip metrics.	IW-7181
Add option to download feature files from settings.	IW-7848
Show raw datapoints for chip dashboard.	IW-2944
Export chip list to csv.	IW-1901
Prevent upload of duplicate references.	IW-7395
Add Enzyme to informatic reports.	IW-8343
Add download links for bam, bai and vcf files.	IW-9062
Add setting to filter all reference lists to show only human.	IW-9279
Add link to jobs list on **Project List** screen.	IW-7696

Summary	Ticket
Make the reference in the job details a hyperlink.	IW-7831
Check node version on startup of access.	IW-8026
Add default attribute mapping for VIA sync transfers.	IW-9516
Add Chromosome numbers on Whole Genome View.	IW-7851
Indicate any bed files used for masking as part of the operation.	IW-7982
Add setting to limit SV track size.	IW-7521

The defects that have been addressed in Bionano Access 1.8 are listed in **Table 2**.

Table 2. Defects Addressed in 1.8.

Summary	Ticket
BNX to CMAP Alignment - no email with link to results is received.	IW-9606
Some BED files are not marked as system files.	IW-8515
SV PDF Report missing Command for RVP operations run on COD.	IW-8378
There is a typo in the Add Configuration dialog.	IW-8326
There is a jitter in the screen when navigating to the **Deleted Jobs** list.	IW-8325
The **Terms and Conditions** text box from the **System Services Settings** page jumps oddly with the first attempt to move it.	IW-7574
Some jobs cannot be deleted from the trash.	IW-7054

Known issues are listed in **Table 3**.

Table 3. Known issues.

Summary	Ticket
When using **Ctrl + mouse** scroll on FSHD results one map track may disappear.	IW-9609
The **SV Summary** legend in the viewer too large for some displays.	IW-9492
The hint when users hover on an SV between the Ideogram, Whole Genome, and Circos views are not consistent.	IW-9446
Some table customizations are not saved after refresh.	IW-9187
When viewer is refreshed additional alignment selections are not retained.	IW-9006
Resizing one column on fixed width grids can cause other columns to become difficult to use.	IW-8958
Some grids cannot scroll horizontally if the viewport is too small.	IW-8879
Due to sub-sampling, there can be discrepancies between the dashboard and final MQR.	IW-8812
The SV Report may have several blank pages in some cases.	IW-7920
Bnx Alignment Splitting Step is very slow	IW-10175
Show Variants from Curation List only is not working in the Genome Browser	IW-10158

Security Improvements

Bionano continues to be a security focused organization. Within each release it is a priority to address security concerns and to enhance the security controls the software provides. Within this release the following security-related changes were implemented.

Security improvements are listed in **Table 4**.

Table 4. Security Related Improvements.

Summary	Ticket
Read-Only users can copy jobs to other projects.	IW-9674
Headers modified for safe char set, framing protection, and sniffing protection	IW-5512 IW-8673
Headers modified to comply with OWASP regulations section 14.4	IW-7694
Updated NPM packages to address 1.7 NPM audit report	IW-7995
Download banner not appearing for all job types	IW-8876
Bcrypt work factor increased to be compliant with OWASP regulations section 2.4.4	IW-7689
Cookies attributes changed to secure and sameSite = strict	IW-7691
Made password reset tokens Access Server specific	IW-8471
Cannot activate account that has been disabled due to inactivity	IW-9012
Check for correct version of nodejs on startup	IW-8026
Fixed SQL injection vulnerabilities where pgknex.raw not used with parameters	IW-9363 IW-9370

Bionano Access v1.8.1 Update

This section outlines the changes that were made for Access 1.8.1 (**Table 5**):

Table 5. Updates.

Summary	Ticket
A message was added to the viewer for when there are no alignments in the results	IW-9709
The last page loaded is bookmarked so if user session expires the system will be returned to the same page after login	IW-8832
Default email credentials were hidden for security reasons	IW-9908
Access will now generate a marker on the compute server when job results have been downloaded	IW-10049
Operation links were modified to only show supported operations when using Stratys compute servers	IW-9992
Enable Guided Assembly Operation	IW-9989
Add Varant Annotation Support for Guided Assembly	IW-9884
Add stable regions to Rare Variant Analysis informatics report	IW-9909
Imported FSHD file name is now obfuscated after upload	IW-8843
[Fixed] Select All checkbox on the **Project Export** screen ignores active filters in grid	IW-9586
Added support for Stratys Compute servers	IW-10003
[Fixed] Auto Sync to VIA was using only Sample Name in some cases	IW-9876
Option to edit scaffold manual cuts was missing	IW-9930
Default location for VIA Sample Importer added to access configuration file	IW-9966
[Fixed] References missing on import	IW-9967
[Fixed] CNVs not added to classification list on second list update	IW-10033
Default Annotation settings changed for Rare Variant Analysis	IW-10053
Viewer optimized to render faster	IW-10085
Update SSH library to work with RedHat	IW-10081

[Fixed] Cannot export Hybrid Scaffold with conflict resolution results	IW-9565
Added Solve Version selection for Import Jobs	IW-9706
[Fixed] Close button not working on Software License Agreement Dialog	IW-9806
[Fixed] Screen capture on circos plot not working	IW-9891
Show Molecule Stats section in Rare Variant Analysis Informatics Report	IW-10026
[Fixed] Chimeric Score not shown in label hint when value is 0	IW-9841
Added Import/Export support for Guided Assembly.	IW-5752
Added support for auto Guided Assembly launch when setting up a chip	IW-8174
Support Guided Assembly operation on Compute on Demand	IW-5768
Add support to launch Guided Assembly operations	IW-5751

Technical Assistance

For technical assistance, contact Bionano Technical Support.

You can 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.

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