



Bionano Access® v1.8 Release Notes

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Revision History

REVISION	NOTES
A	Initial release.
B	Revision.

Bionano Access

This document describes the v1.8 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 Windows, Mac, 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 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 pipeline running on Saphyr Compute and Bionano Compute servers and on Bionano Compute on Demand. 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.

Improvements

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 1**.

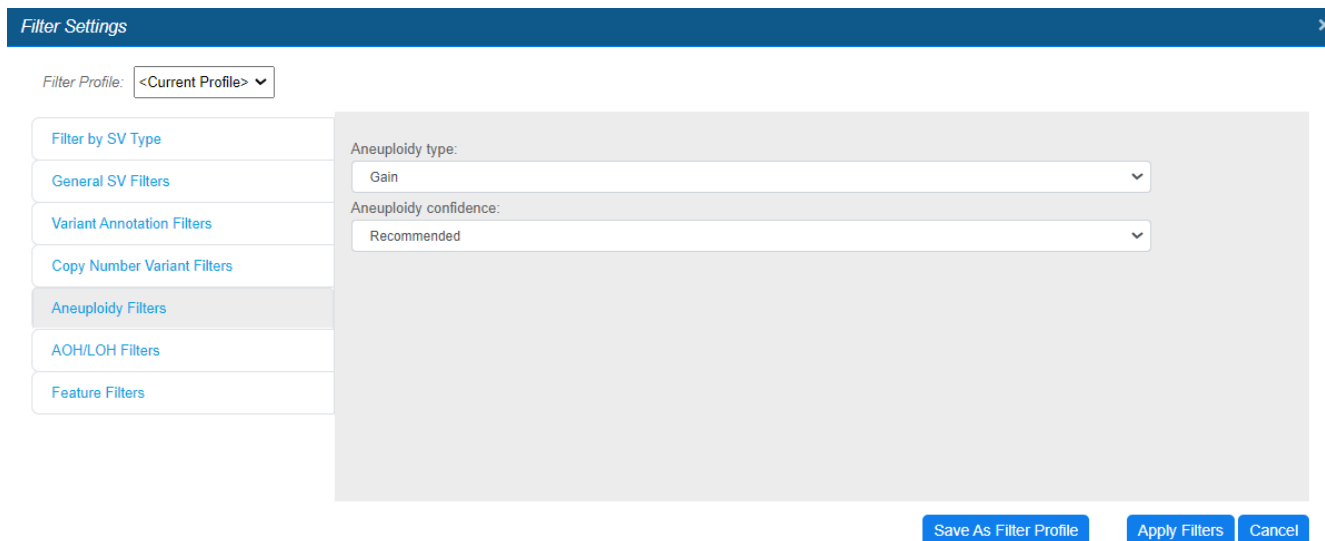


Figure 1. Aneuploidy filter settings.

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 2**. 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.

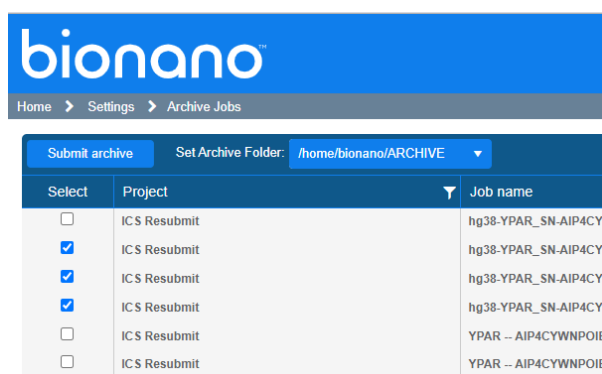


Figure 2. Job archive.

USER CAN FILTER BNX BASED ON SCAN NUMBER

The **BNX Filter** operation now allows users to filter BNX files by scan number (see **Figure 3**). 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.

The screenshot shows the 'Access' page in the Bionano web application. The breadcrumb trail is 'Home > Analysis > Access 1.8 Testing > BNX Filter'. The 'Filtered Molecule Name' is 'test - Molecule Filter'. The 'Channel Information' is '1 - CTTAAG - (DLE-1) , Reference: hg38_DLE1_0kb_0labels.cmap'. The 'Reference' is 'hg38_DLE1_0kb_0labels.cmap'. The 'Tags (optional)' field contains 'Add a tag'. The 'Description (optional)' field is empty. The 'Filter Settings' section is highlighted with a red box and contains the following options:

- Swap channel color
- Label Count
- Length (kbp)
 - Minimum: 100
 - Maximum: 5000
- Total DNA (Gbp)
 - Total DNA: 300
 - Sampling: Random
 - Random Seed: 17
- Scan number
 - Start: [dropdown]
 - End: [dropdown]

At the bottom of the filter settings are 'Submit' and 'Cancel' buttons.

Figure 3. 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 4**.

- Pathogenic Variants
- Likely pathogenic Variants
- Uncertain significance Variants
- Likely benign Variants
- Benign Variants
- Unclassified Variants

Figure 4. SV Report classifications filter.

MOLECULE SIZE DISTRIBUTION NOW AVAILABLE

An option to view a **Molecule Size Distribution** graph (**Figure 5**) 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.

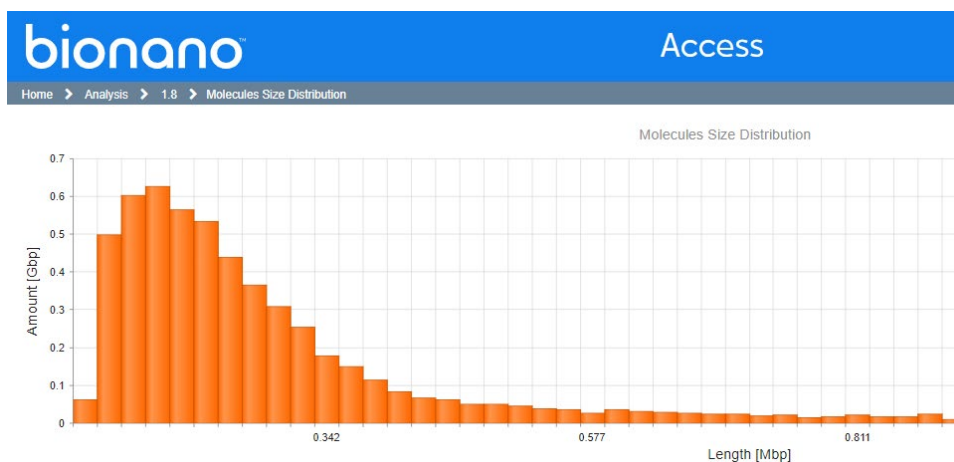


Figure 5. Molecule Size Distribution graph.

SV RE-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 6**.

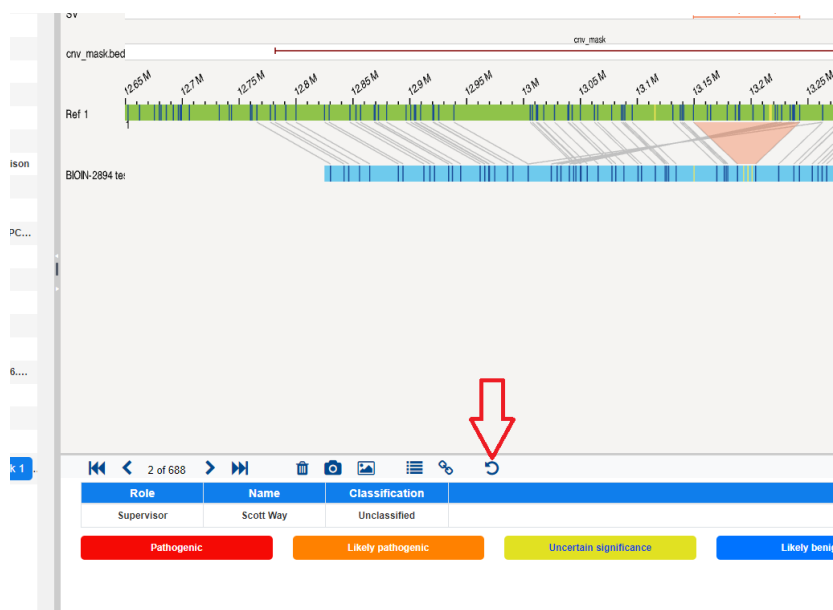


Figure 6. Refresh Display icon.

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 7**.

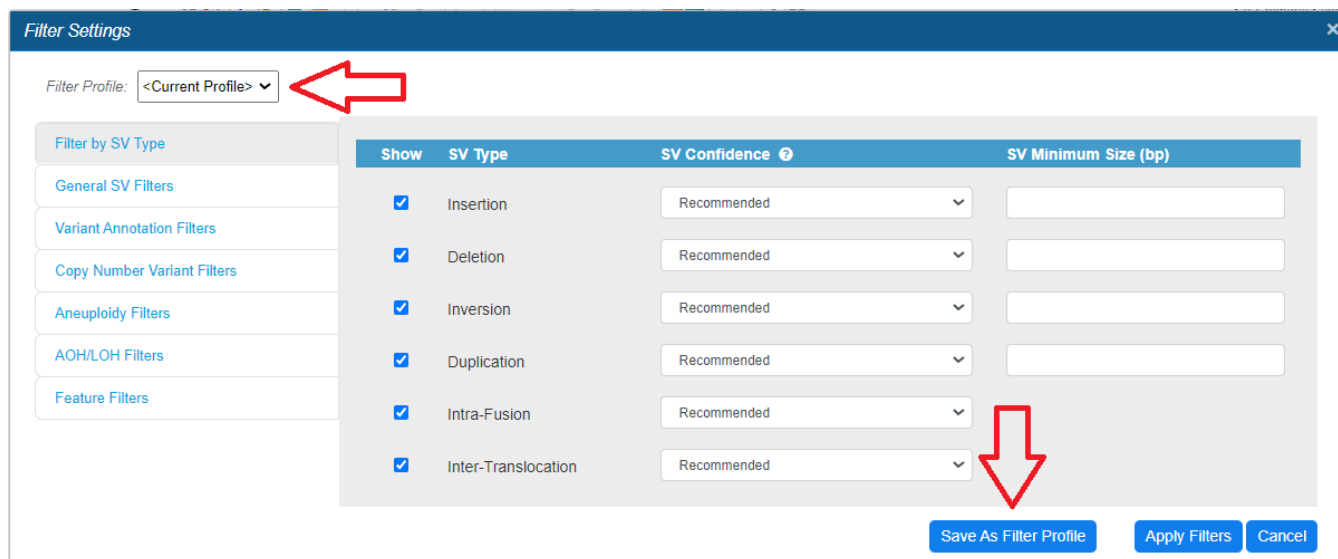


Figure 7. Selecting (top left) and saving (bottom right) Filter Profiles.

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 8**).



Figure 8. 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 9**, the list is sorted first by chromosome (Chr) and then by variant type (Type).

classifica...	Notes	Type ↑ 2	Chr ↑ 1	RefStartPo...	RefEn
Unclassified		deletion	1	404,457	717,796
Unclassified		deletion	1	5,999,446	6,006,9
Unclassified		deletion	1	9,535,154	9,547,1
Unclassified		deletion	1	13,161,545	13,276,;
Unclassified		deletion	1	3,294,886	3,314,1

Figure 9. Sorting the curation list.

VIEWER TOUR FEATURE ADDED

A **Tour** icon (**Figure 10**) has been added to the toolbar in the viewer. When the **Tour** icon is clicked, it will open the **Tour** screen (**Figure 11**). Click the green arrows for an explanation of each viewer component.

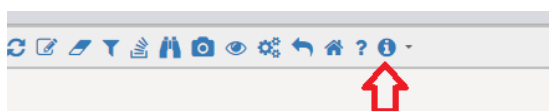


Figure 10. Tour Icon.

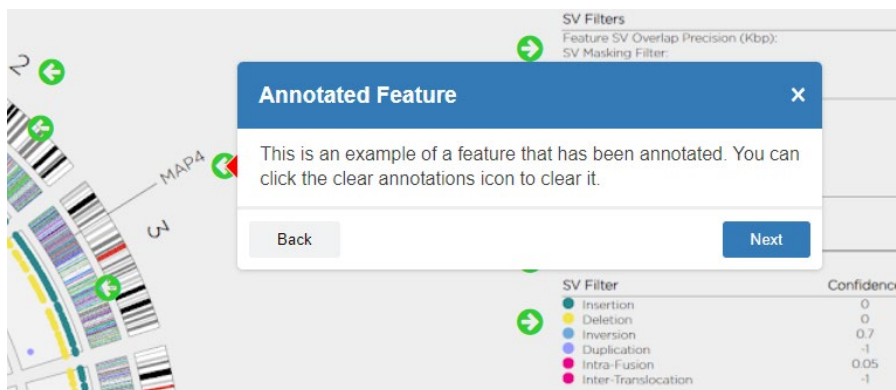


Figure 10. Tour screen with component explanation.

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 11**. 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)*.

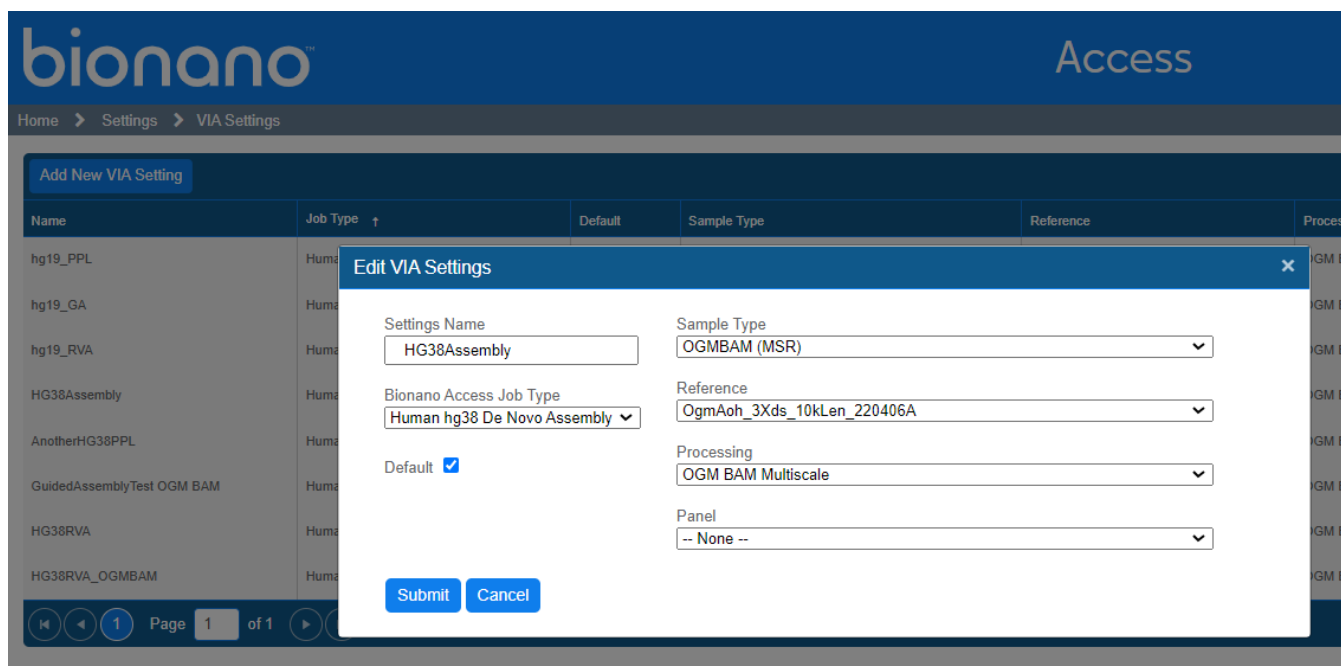


Figure 11. VIA settings.

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 12**).

De Novo Assembly Step 1 of 2

Assembly Name:

Estimated Genome Size (Gbp):


Tags (optional):

Description (optional):

Selected BNX:

Reference:

Organism:

VIA Setting: 

Advanced Assembly Options

Advanced Variant Annotation Pipeline Settings

Figure 12. 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 13**). 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.

VIA Upload ✕

VIA Sample Name

Overwrite

VIA Settings

Figure 13. 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 14**.

Sample Details	
Name	test
Sample UID	1affd74e-ef5e-11ed-8a82-3cfdfe92c2c0
Created	05/10/2023 11:11 AM
Annotated Guided Assembly Details	
Name	GA_ With_mol_alignments
Reference	hg38_DLE1_0kb_0labels.cmap
Description	
Created	05/15/2023 02:20 PM
Operation	Import Annotated Guided Assembly
Status	Completed
User	Wilson Rodriguez
Job ID	9266
VIA Status	Complete
VIA Uploaded	05/15/2023 02:21 PM
Options	
View Results	
View Molecule Alignment	
View Informatics Summary	

Sample Details	
Name	77X DLE hg38
Sample UID	c6c4576c-bc41-11ed-8645-3cfdfe92c2c0
Created	03/06/2023 09:10 AM
Annotated de Novo Assembly Details	
Name	77X DLE hg38 - De novo_tools1.8_Solve3.8_348
Reference	hg38_DLE1_0kb_0labels_masked_YPARs.cmap
Description	
Created	07/26/2023 03:37 PM
Operation	Annotated de Novo Assembly
Status	Complete
User	Beverlie Poblete
Job ID	🔗 11119
Command	🔍 Show Command
VIA Status	Complete
VIA Uploaded	07/28/2023 11:57 AM

Figure 14. 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:

Options

- [View Results](#)
- [View Molecule Alignment](#)
- [View Informatics Summary](#)
- [Download Assembly](#)
- [Download ogm.bam](#)
- [Download ogm.bai](#)
- [Download ogm.vcf](#)
- [Upload to VIA](#)

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 15**). 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.

Project Settings

🔧 Auto Analysis (recurring) ^

Annotated Assembly	Off	<input type="checkbox"/>	On	Minimum Coverage	80 X
Annotated Rare Variant Analysis	Off	<input type="checkbox"/>	On	Minimum Quantity	400 (Gbp)
FSHD	Off	<input type="checkbox"/>	On	Minimum Quantity	400 (Gbp)
Fragile X	Off	<input type="checkbox"/>	On	Minimum Quantity	400 (Gbp)

Submit
Cancel

Figure 15. Configuring automatic operations.

HIGHLIGHT EXPECTED MOLECULE QUALITY REPORT (MQR) QUALITY LEVELS

The MQR will now highlight values that fall below quality thresholds (see **Figure 16**).

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 16. Highlighted MQR value.

ADD CSV DOWNLOAD FOR CHIP METRICS

On any chip dashboard there is now a button to **Show Data** (see **Figure 17**). 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 17. 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.

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 <i>de novo</i> 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 <i>De Novo</i> and RVA data to VIA.	IW-8623
Automation to launch operation type for each sample in a selected project.	IW-8175

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 Select All checkbox on the project export screen will ignore any filters and select all jobs.	IW-9586
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
Circos plot can be slow or crash when using large feature files.	IW-9201
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

Security Improvements

Bionano continues to be a security focused organization. Within each release we make it a priority to address security concerns and to enhance the security controls our 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

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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