



Bionano Access™ v1.8.2 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
E	Changes for 1.8.2 update

Bionano Access

This document describes the v1.8.2 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 v1.8.2 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 1.8.2 is compatible with Saphyr® Instrument Control Software (ICS) versions 4.9 and above. Bionano Access is designed to integrate directly with the Bionano Solve® v3.8.2 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 1.8.2. 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

ADDED 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).

Guided Assembly

Guided Assembly Name: test - Guided Assembly

Operation Type: Low Allelic Fraction
 Constitutional

Estimated Genome Size (Gbp): 4

Tags (optional): Add a tag

Description (optional):

Selected BNX: BIOIN-2894 input

Reference: hg38_DLE1_0kb_0labels.cmap

Organism: Human

VIA Setting: GuidedAssemblyTest OGM BAM (default)

Advanced Guided Assembly Options

Advanced Variant Annotation Pipeline Settings

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**).

Isolation Kit Lot Number: optional

Labeling Kit Lot Number: optional

Auto De Novo Assembly:

Auto Guided Assembly: 

Auto Rare Variant Analysis:

Auto EnFocus FSHD:

Auto EnFocus Fragile-X:

Add to Flowcell 1 Add to Flowcell 2

Back Save Chip Save as Template Cancel

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**.

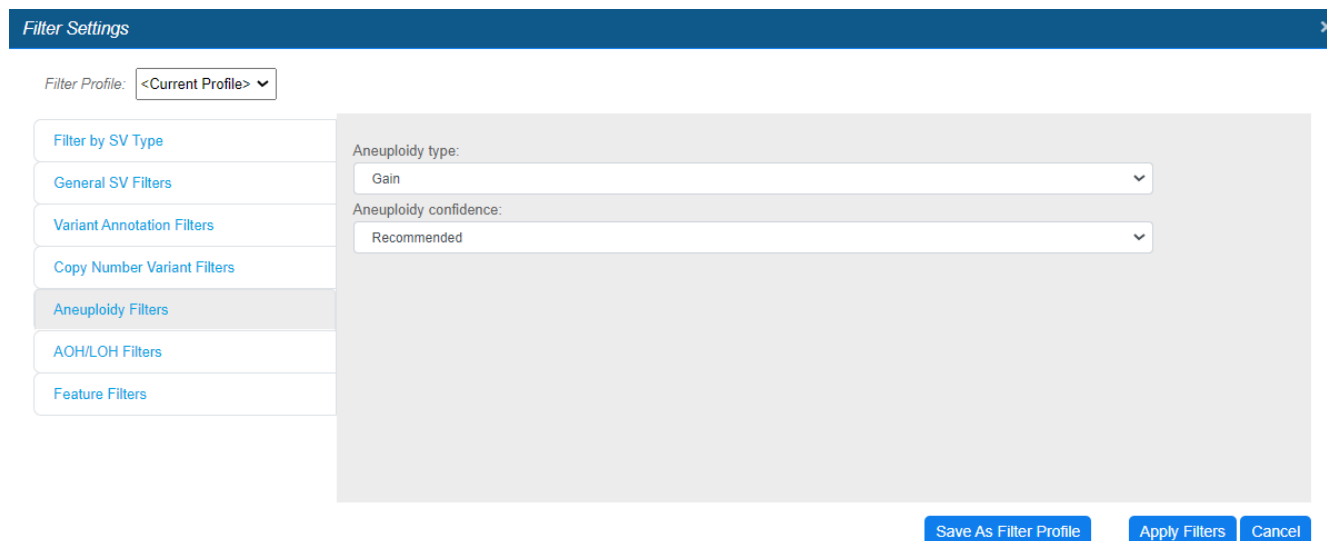


Figure 3. Aneuploidy filter settings.

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.

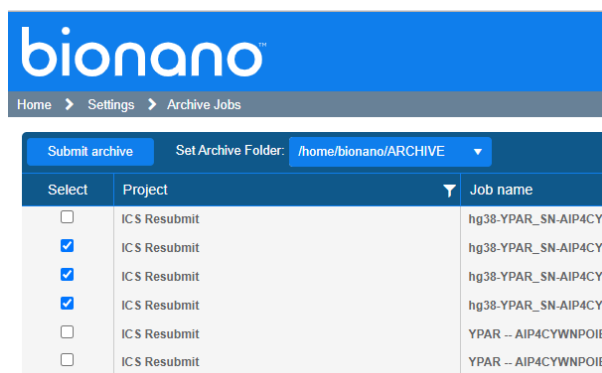


Figure 4. Job archive.

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.

The screenshot shows the Bionano Access web interface for the BNX Filter. The interface includes a header with the Bionano logo and 'Access' text. Below the header is a breadcrumb trail: Home > Analysis > Access 1.8 Testing > BNX Filter. The main content area is divided into several sections:

- Filtered Molecule Name:** A text input field containing 'test - Molecule Filter'.
- Channel Information:** A text input field containing '1 - CTTAAG - (DLE-1) , Reference: hg38_DLE1_0kb_0labels.cmap'.
- Reference:** A dropdown menu showing 'hg38_DLE1_0kb_0labels.cmap'.
- Tags (optional):** A text input field containing 'Add a tag'.
- Description (optional):** A large text area for additional information.
- Filter Settings:** A section with various checkboxes and input fields:
 - Swap channel color:**
 - Label Count:**
 - Length (kbp):** Minimum: 100, Maximum: 5000
 - Total DNA (Gbp):** Total DNA: 300
 - Sampling:** Random (dropdown), Random Seed: 17
 - Scan number:** Start: (dropdown), End: (dropdown) - This row is highlighted with a red box.

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

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**.

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

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.

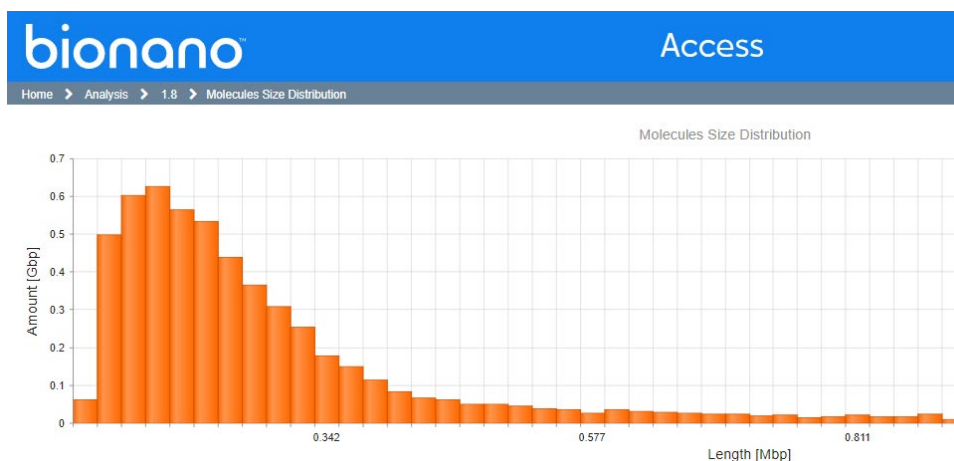


Figure 7. Molecule Size Distribution graph.

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 employ 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**.

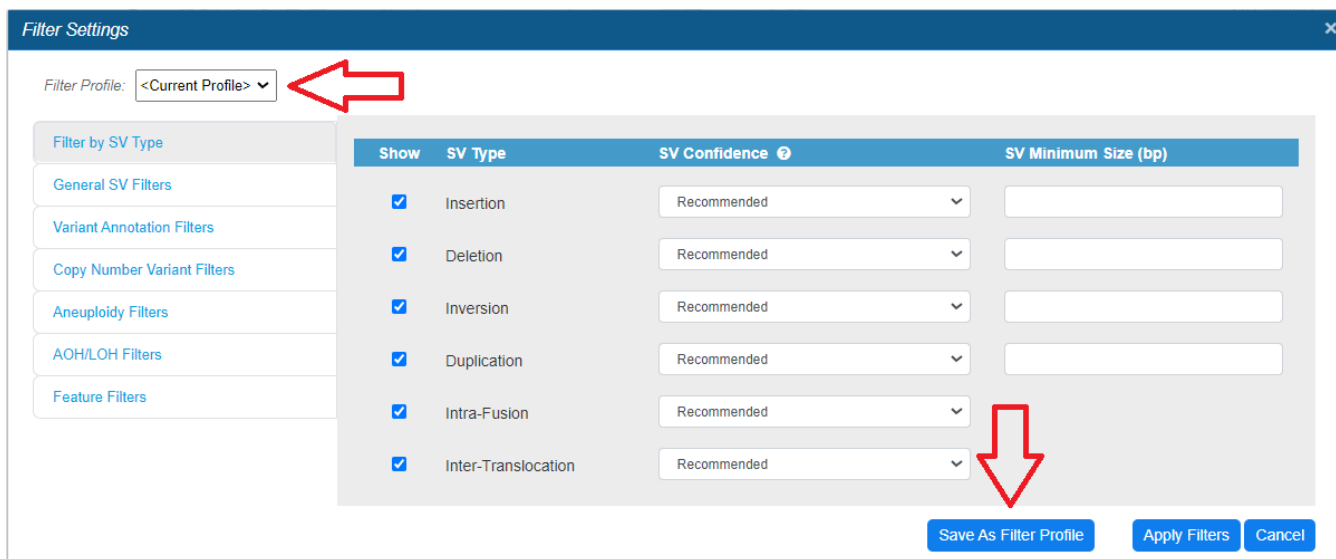


Figure 9. Selecting (top left) and saving (bottom right) **Filter Profiles**.

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**).

Curated Variant List						
Reconcile records Review complete Remove records Remove all records						
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 11. Sorting the curation list.

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.

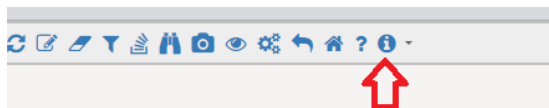


Figure 12. Tour Icon.

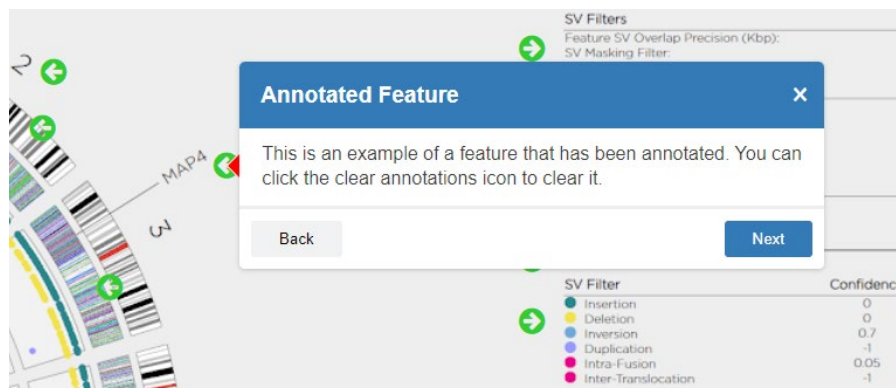


Figure 13. Tour screen with component explanation.

AUTOMATE TRANSFER DATA TO VIA

To facilitate the migration of data to Bionano’s VIA™ software 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 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).

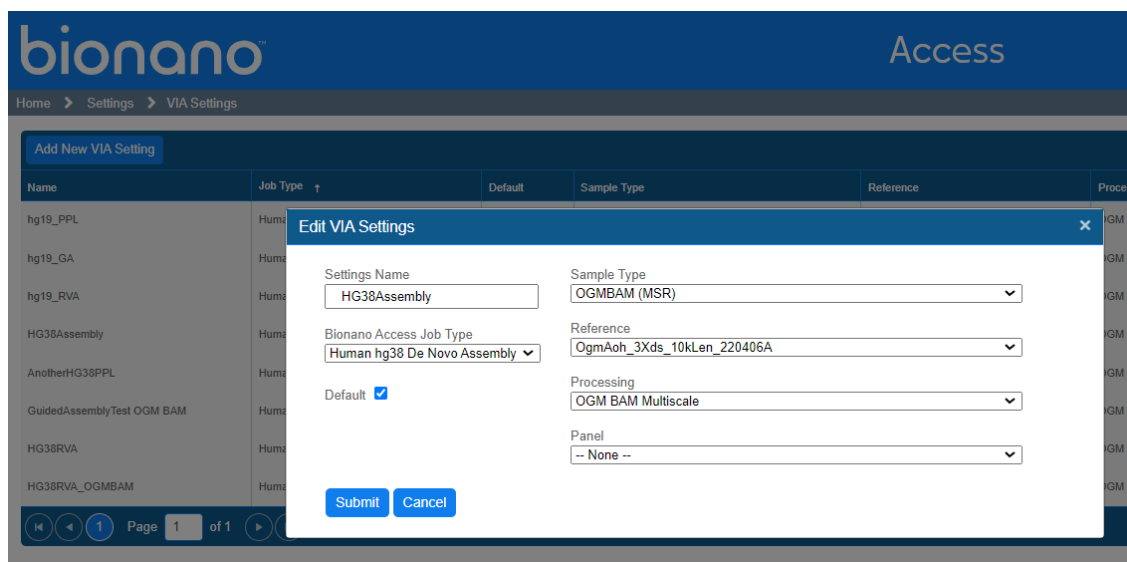


Figure 14. Editing VIA settings.

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, as seen in **Figure 17**.

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 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.

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 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.

Project Settings

📄 Auto Analysis (recurring) ^

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

CNV ANNOTATION TAB MODIFIED

The columns on the CNV Annotation Tab in the viewer have been modified to include the 'found in' columns for Parents or Control when a dual or trio variant annotation operation has been performed.

Tickets

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

Table 1. Released features in v1.8

Summary	Ticket
When mousing over a gene in a gene track format (GTF) the system will not display the name and coordinates.	IW-9009
Improved logging when executing command shell operations.	IW-9188

Summary	Ticket
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
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

Summary	Ticket
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
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

Summary	Ticket
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
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 version 1.8 are listed in **Table 2**.

Table 2. Defects Addressed in v1.8.

Summary	Ticket
BNX to CMAP Alignment - no email with link to results is received.	IW-9606

Summary	Ticket
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
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
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
Bnx Alignment Splitting Step is very slow.	IW-10175
Need to improve input validation on BNX Filter operation.	IW-10302
Find map when viewing scaffolds will not find certain maps.	IW-6009
The installer will display an error that the database already exists if users are upgrading.	IW-8011

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 security-related changes, seen in **Table 4**, were implemented.

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
Login form changed to POST data instead of GET	IW-10298
Changed email domain from bionanogenomics.com to bionano.com to prevent DMARC errors	IW-10249
Updated Rescale Command Line Interface (CLI)	IW-10220
Hide Compute On Demand information from Read-Only users	IW-10056
Removed Java 11 Dependency	IW-10055

Bionano Access v1.8.1 Update

This section outlines the changes that were made for Access version 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

Bionano Access v1.8.2 Update

This section outlines the changes that were made for Access version 1.8.2 (**Table 6**):

Table 6. Updates

Summary	Ticket
Updated Annotated CNV outputs to include found in parents / ctrl	IW-10239
Added new environment select for compute options in Project Browser	IW-10028
Cluster load balancing improved	IW-10320 IW-10178
Added application selection for throughput on chip setup	IW-10254
Added job completion source to completion notification email	IW-9997
Changed recommended duplication confidence score filter	IW-10266
Changed recommended confidence filter for Inversions	IW-10213
Sort added to job type on import screen	IW-10172
Added sort to Compute On Demand voucher tab	IW-10151

Summary	Ticket
Redesigned Legend in viewer to conserve space	IW-9492
Modified zoom on Circos to be at mouse location	IW-10285
Removed unnecessary refresh on Circos plot	IW-10290
Made copy number variants clickable in Circos plot	IW-10087
Modified viewer to open in new tab when using Ctrl+Click	IW-10086
Add link to bnx file from chip dashboard	IW-7887
Added new chip part numbers for Stratys Instrument	IW-10216
Add BNX Merge operation for Stratys Compute	IW-10263
Add BNX Filter operation for Stratys Compute	IW-10262
Added Bionano Solve version check for Stratys Compute Servers	IW-10040
Added T2T operations to VIA Sync	IW-9990
Added telomeric gain metrics to VIA Sync	IW-10252
Added Sex / Gender to VIA Sync attributes	IW-9626
Fixed chip setup to auto select new samples when created	IW-10279
Fixed where legend was scaling when you zoom Circos	IW-10268
Fixed where voucher dialog did not appear for Guided Assembly operations	IW-10236
Fixed Variant Annotation links for Guided Assembly operations	IW-10235
Fixed disappearing maps from additional alignment when changing view size	IW-9609
Fixed error on curation reconcile	IW-10286
Fixed curation notations where copy number variant and structural variant have same ID	IW-10212
Fixed where you cannot hide the SV Mask in the viewer	IW-10197
Fixed translocations not appearing correctly in the classifier view	IW-10196

Summary	Ticket
Fixed Exons disappearing when you zoom in	IW-10258
Fixed where curation list only variants was not working in viewer	IW-10158
Prevented 0% for font size	IW-10118
Fixed need to restart Access after enabling Compute On Demand	IW-9941
Removed dependency to install Java 11	IW-10055
Change email domain from bionanogenomics.com to bionano.com	IW-10249

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.

TYPE	CONTACT
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