



Bionano Access™ v1.8.2.1 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 |
| E | Changes for 1.8.2 update |
| F | Changes for 1.8.2.1 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**.

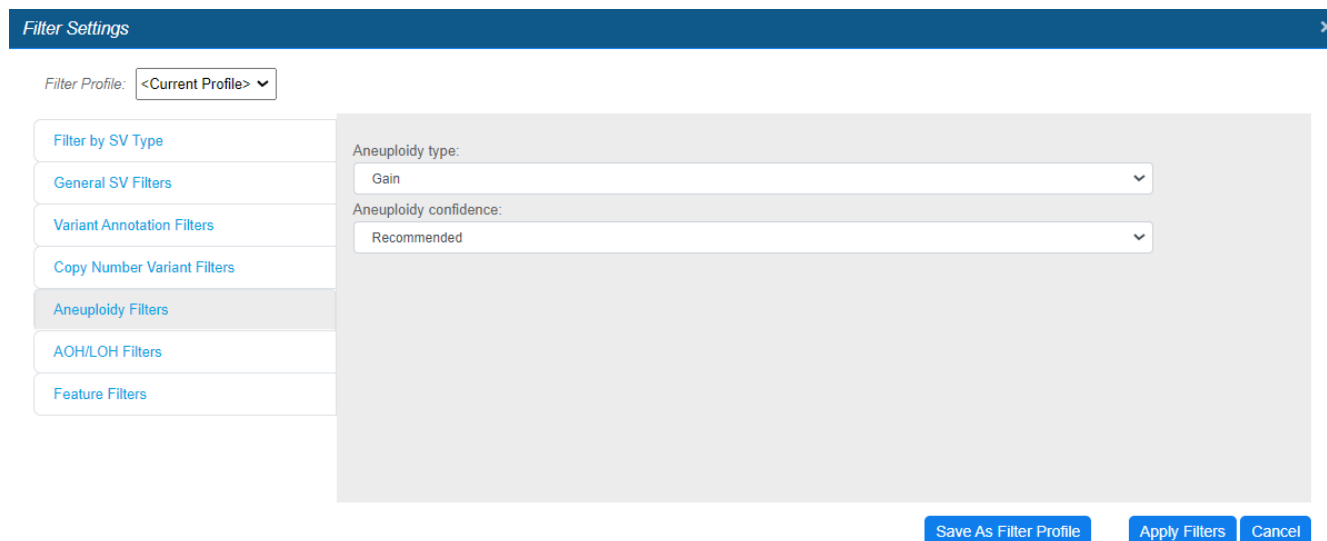


Figure 3. Aneuploidy filter settings.

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.

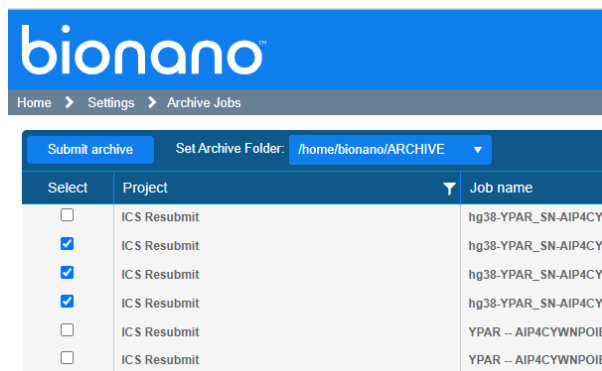


Figure 4. Job archive.

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.

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.

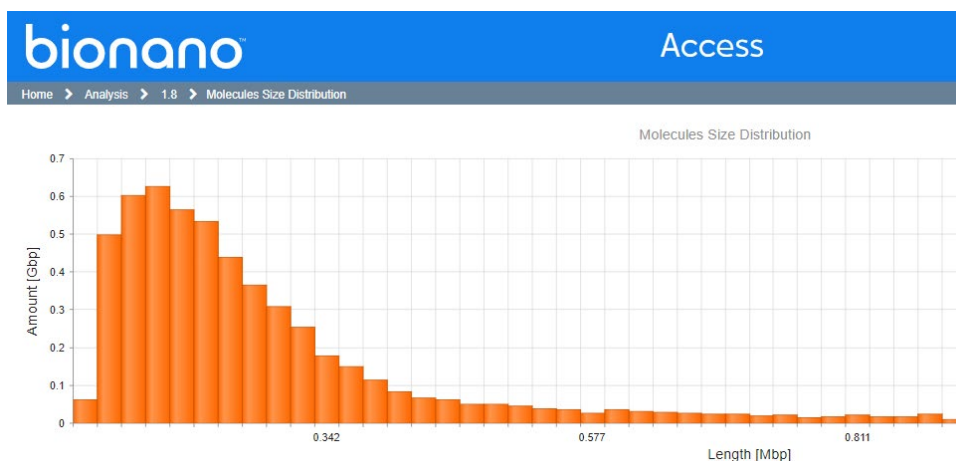


Figure 7. Molecule Size Distribution graph.

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.

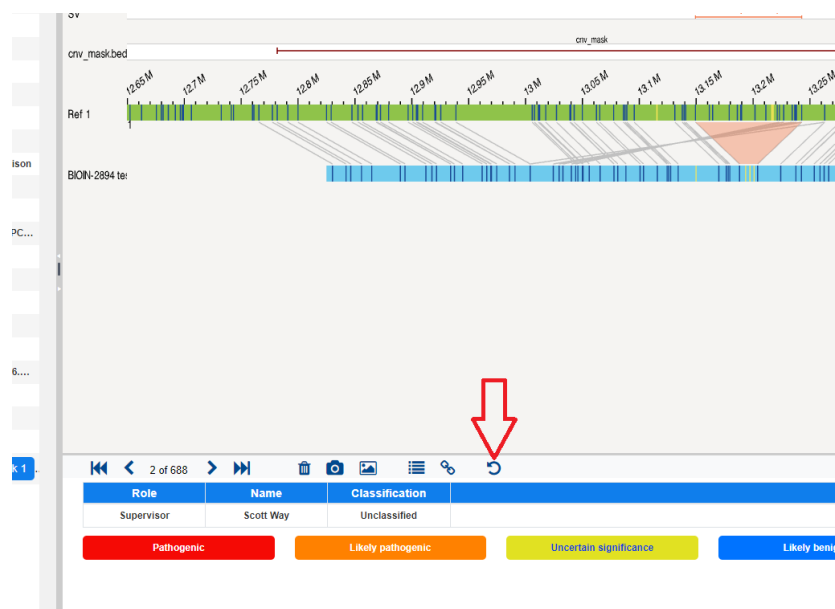


Figure 8. Refresh Display icon.

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**.

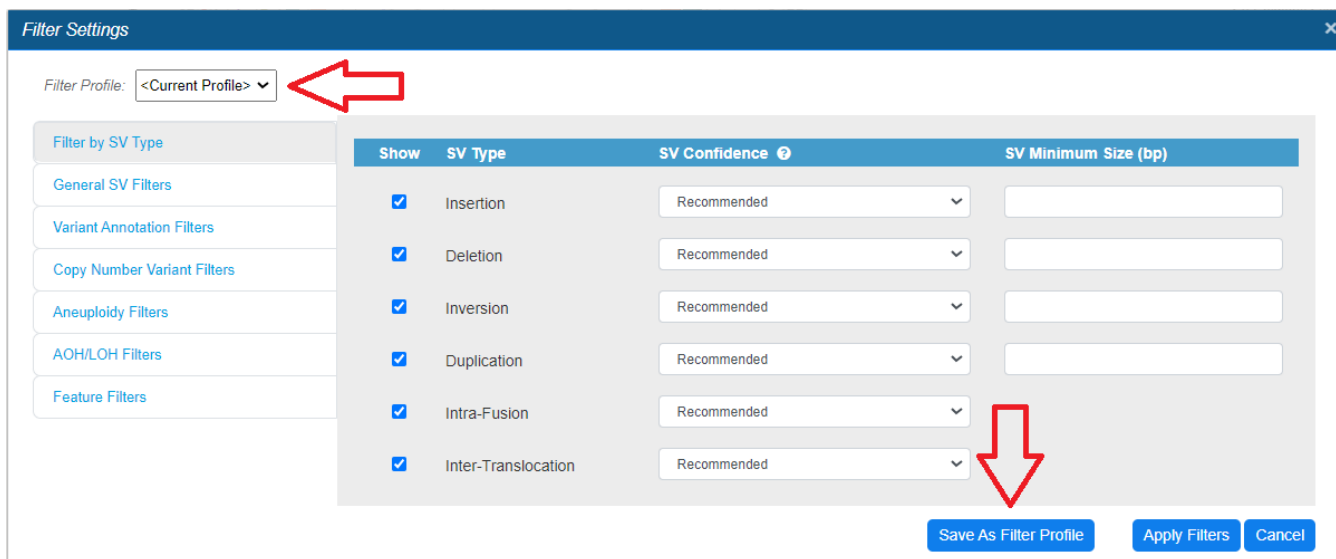


Figure 9. Selecting (top left) and saving (bottom right) **Filter Profiles**.

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**).

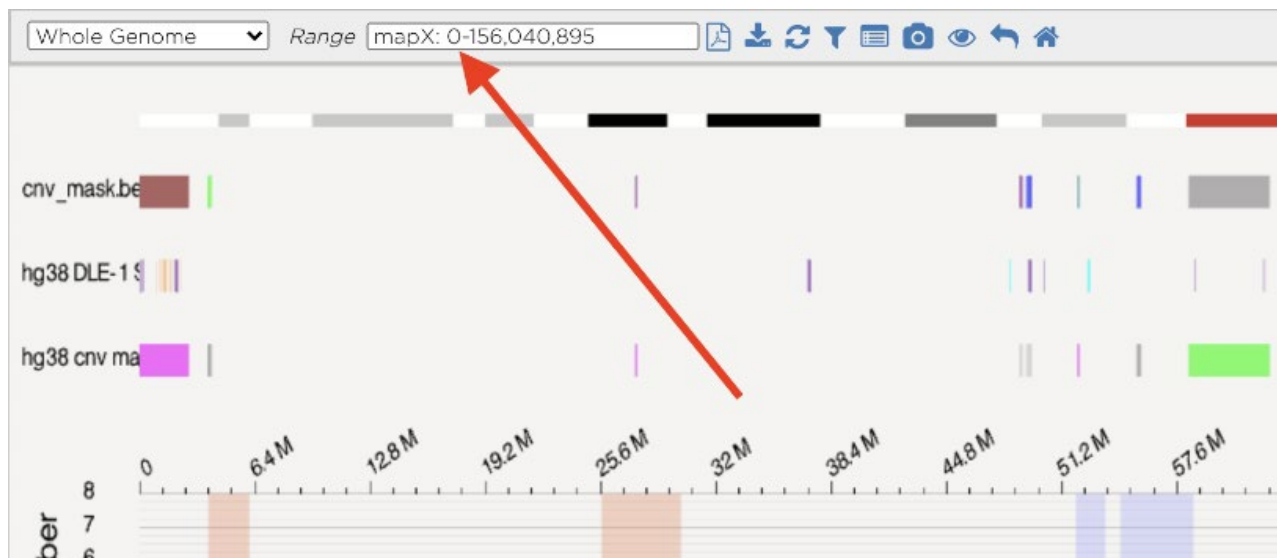


Figure 10. Whole Genome coordinates input field.

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.

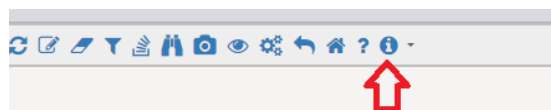


Figure 12. Tour Icon.

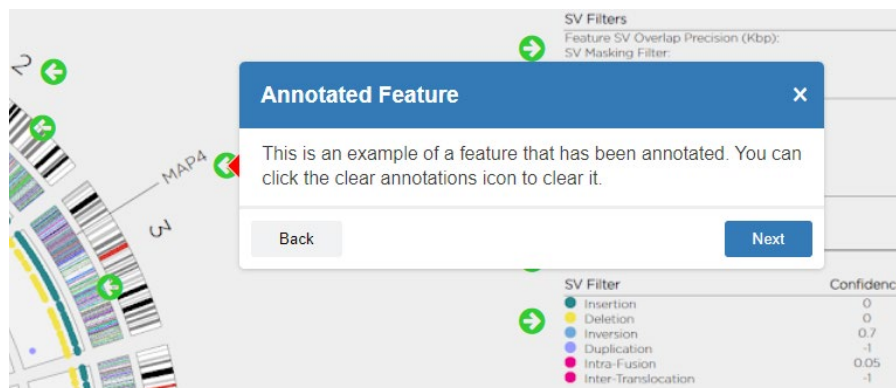


Figure 13. Tour screen with component explanation.

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).

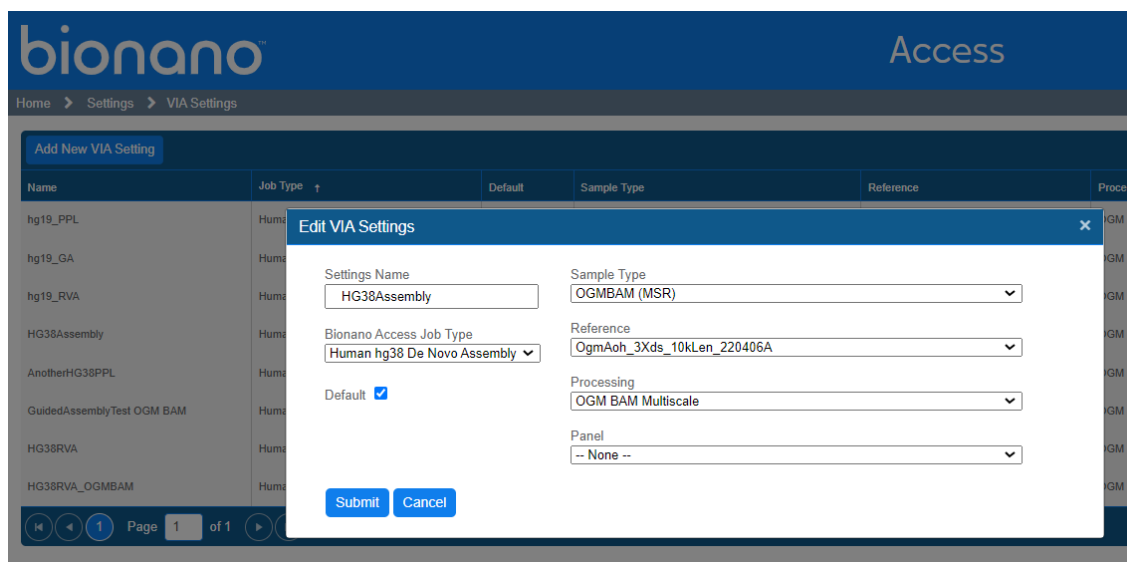


Figure 14. Editing VIA settings.

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) |
| FSHD | 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 |

Bionano Access v1.8.2.1 Update

This section outlines the changes that were made for Access version 1.8.2.1 (Table 7):

Table 7. Updates.

| Summary | Ticket |
|---|----------|
| Enable EnFocus Operations to run on Bionano Access Server | IW-10440 |
| Viewer fails to generate PDF Report for filtered variants | IW-10449 |
| Cannot add molecule set to existing chip | IW-10444 |

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 |
|---------|--|
| Email | support@bionano.com |
| Phone | <p>Hours of Operation: Monday through Friday, 9:00 a.m. to 5:00 p.m., PST US: +1 (858) 888-7663</p> <p>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</p> |
| Website | www.bionano.com/support |
| Address | <p>Bionano, Inc. 9540 Towne Centre Drive, Suite 100 San Diego, CA 92121</p> |

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