Bionano Access™ v1.8.3 Release Notes

DOCUMENT NUMBER:
RNOTE-00023

DOCUMENT REVISION:
A

Effective Date:
2025-Aug-04

bionano™

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Revision History

REVISION	NOTES
A	Initial release.

Bionano Access

This document describes the v1.8.3 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 v1.8.3 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 1.8.3 is compatible with Saphyr® Instrument Control Software (ICS) versions 4.9 and above. Bionano Access is designed to integrate directly with the Bionano Solve® v3.8.3 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.

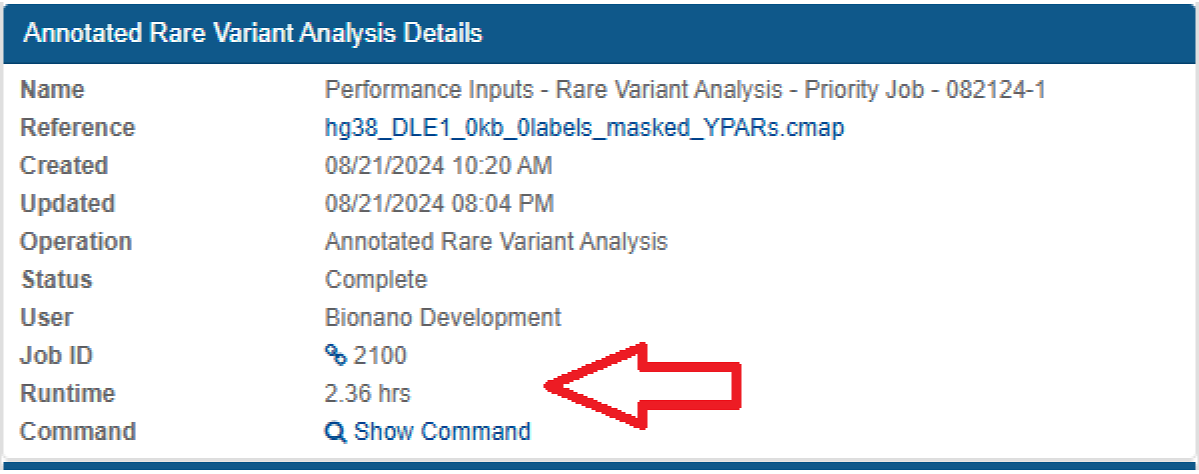
Improvements in Bionano Access 1.8.3

BNX Alignment jobs import rapidly

In previous versions a bug in our obfuscation software caused BNX Alignment jobs to take an exceptionally long time to import. Many customers believed their jobs had failed. The issue revolved around splitting the map files into individual maps for each contig. We worked with the Bioinformatics team to split the files in advance and then import them. BNX Alignment imports are almost immediate now.

Job Runtimes Displayed

The job details window will now show the job runtime. The runtime will update each time a stage completes.

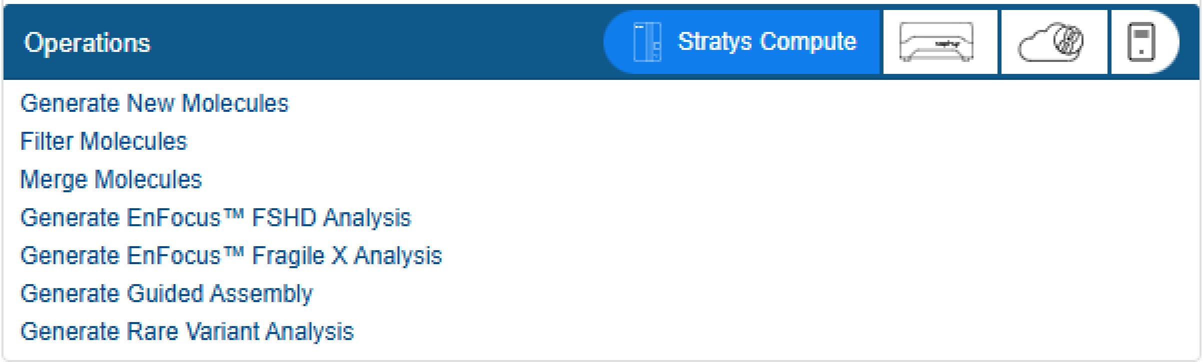


Annotated Rare Variant Analysis Details

Name	Performance Inputs - Rare Variant Analysis - Priority Job - 082124-1
Reference	hg38_DLE1_0kb_0labels_masked_YPARs.cmap
Created	08/21/2024 10:20 AM
Updated	08/21/2024 08:04 PM
Operation	Annotated Rare Variant Analysis
Status	Complete
User	Bionano Development
Job ID	2100
Runtime	2.36 hrs
Command	Show Command

New Stratys Compute Operations

EnFocus, Variant Annotation, and Rare Variant Analysis operations have been enabled for Stratys Compute systems.



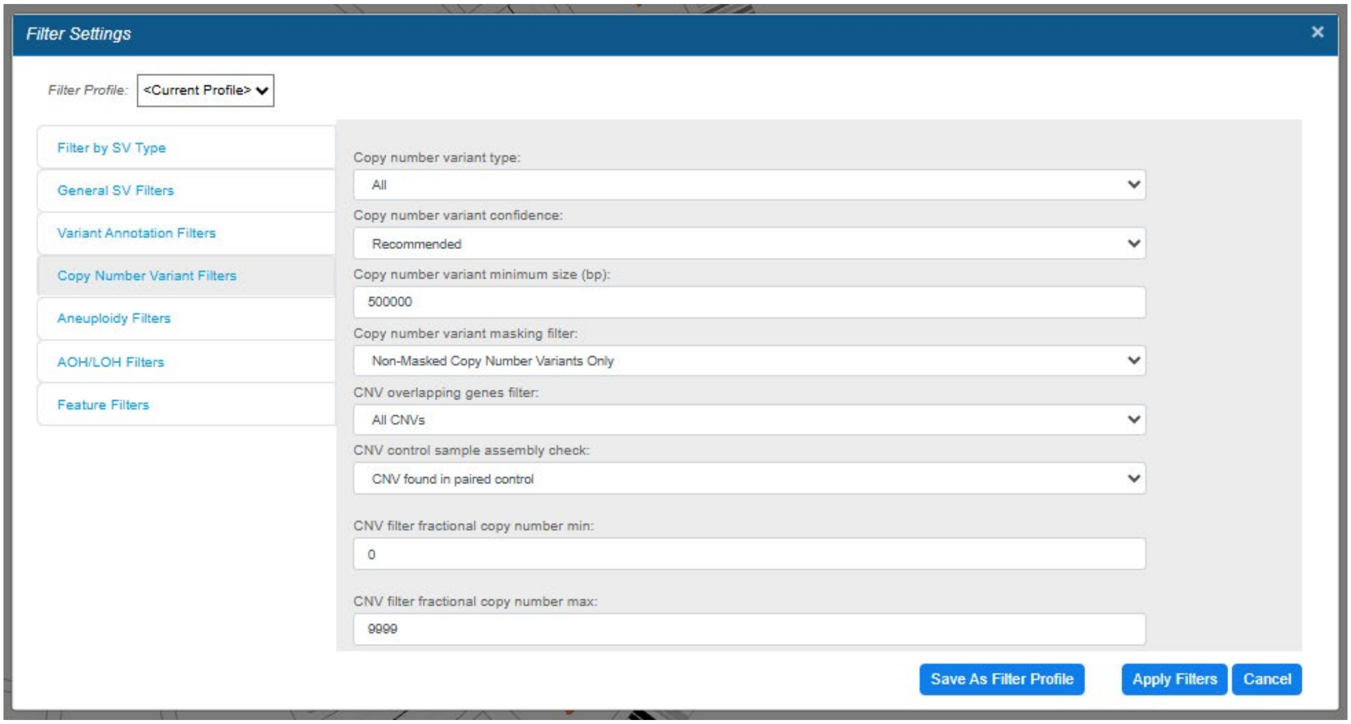
Generate New Molecules
Filter Molecules
Merge Molecules
Generate EnFocus™ FSHD Analysis
Generate EnFocus™ Fragile X Analysis
Generate Guided Assembly
Generate Rare Variant Analysis

Priority Samples

On Stratys systems it is now possible to mark chips for priority processing. Those samples will also receive priority processing downstream in Access. Priority processing can only be enabled from ICS, but it can be disabled in Access if priority processing is not needed on additional analysis jobs. Priority jobs will not pause jobs that are already being processed but will jump to the top of the queue ahead of any non-priority jobs. The priority status will appear in the job list, project sample list, and job launch screens (if enabled).

CNV Filtering updated

The Copy Number Variat Filters tab has been updated to include CNV overlapping genes filter, CNV control sample assembly check, and CNV Filter fractional copy number min and max.



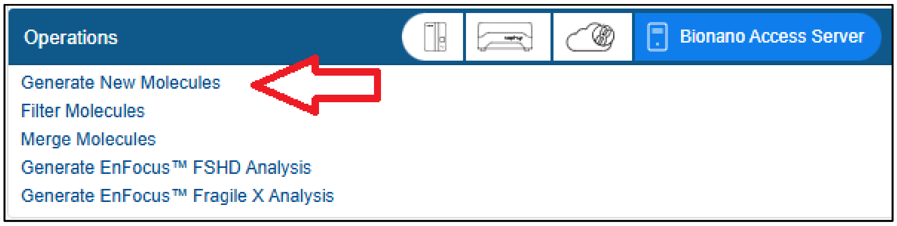
Copy number variant type: All
Copy number variant confidence: Recommended
Copy number variant minimum size (bp): 500000
Copy number variant masking filter: Non-Masked Copy Number Variants Only
CNV overlapping genes filter: All CNVs
CNV control sample assembly check: CNV found in paired control
CNV filter fractional copy number min: 0
CNV filter fractional copy number max: 9999

EnFocus Mode

After enabling EnFocus mode it is possible to run EnFocus operations on the Bionano Access Server. Contact support for instructions how to enable EnFocus mode.

Molecules are Immutable

In previous versions of Bionano Access you could change the reference on a molecules file and generate new molecule metrics. This caused the previous molecule metrics to be deleted. To preserve the metrics associated with molecules we no longer allow this. Instead, there is an operation to 'Generate New Molecules'. You can choose another reference, and it will make a new molecules job with a different name and the original molecules file is preserved.



Tickets

The features released with Bionano Access version 1.8.3 are listed in **Table 1**.

Table 1. Released features in v1.8.3

Summary	Ticket
Add Priority Sample to Sample Chip API	IW-10280
Show run time in status for local jobs	IW-10325
Force Assembly Type for Guided	IW-10334
Remove Display Name from VIA Sync	IW-10417
Add filtering for CNV Found In fields	IW-10420
Make molecule files immutable	IW-10426
Add pipeline queue on Access server	IW-10439
Add VAP operations for Stratys Compute	IW-10447
Add RVP operation for Stratys Compute	IW-10452
Edit Priority Sample Setting	IW-10462
Priority Jobs	IW-10463
Run Solve File Sync on startup	IW-10540
add touch for Stratys file cleanup	IW-10559

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**
[Installer] Hide error when database exists	IW-8011
[Viewer] [Whole Genome] No tick marks in the range 0-50K	IW-9885
Input validation not updated when replacing configuration file	IW-10162
Bnx Alignment import is very slow	IW-10175
Improve BNX filter input validation	IW-10302
Coding regions and Exons visually indistinguishable	IW-10304
BNX Filter max size validation improved	IW-10326
Variant Annotation does not exclude cancelled jobs	IW-10351
Duplicate molecule object created after chip run	IW-10364
[Curated Variant List] Double click does not work on first render	IW-10366
Analyst's Curation pane does not show Supervisor's notes	IW-10370
Supervisor classification not shown for Analyst	IW-10373
[Variant Classifier] Remove record icon not visibly disabled	IW-10376
Project Access description does not always load	IW-10383
[Security] Able to bypass expired password change screen	IW-10384
Project Browser Grid visually cut off	IW-10389
[Exp Design] minimum not plotted on Metrics tab	IW-10400
Confirm use of YPARS with auto operations	IW-10403
Rename cnv vaf column to cnfoldchange	IW-10410
Auto launch job naming not consistent	IW-10411
CNV drawn incorrectly on whole genome view	IW-10415
No error message when no annotations to export	IW-10423

Customer created cod organization name with single quote	IW-10424
sample name allows tab	IW-10425
change python commands to python3	IW-10428
features dialog not working correctly on circos	IW-10429
filter and merge operations fail when BAS is selected and there is no local compute	IW-10434
Can't pull token estimate for Variant Annotation if job name is not unique	IW-10442
Filtering by scan causes refaligner to fail	IW-10445
Annotated CNV download is empty	IW-10446
[Installer] file not found errors	IW-10453
[Installer] npm audit warnings	IW-10454
Link from classifier not zooming to variant in genome browser	IW-10455
[Viewer] Optimize GTF files for display in Circos Plot	IW-10458
[Viewer] update CNV graph for new CNV Filters	IW-10459
[Viewer] Legend not reflecting updated job name	IW-10460
Add priority removal warning	IW-10468
Show runtime always	IW-10469
Legend SV Count is messed up after switching views	IW-10475
Report Generation Failed	IW-10476
Remove sample from SVvtooltip	IW-10477
Overlap precision is missing in dialog	IW-10482
Fix translocation line on ideogram	IW-10483
Details button on curation list not working for copy number variants	IW-10484
Remove Irys Opt Arg Files	IW-10487

Feature file hyperlink not working	IW-10488
Add spinner for password update	IW-10489
Switch to using VIA Sample Type API call that only returns OGM	IW-10501
Launch selections for dual vap launch are missing for HG38 YPARS	IW-10502
Control database wrong for dual variant annotation	IW-10504
System warning not working	IW-10505
Login banner is showing on user profile screen.	IW-10507
Inconsistency in Nav Menu	IW-10515
Download VCF API is failing	IW-10516
Maintenance Mode not working	IW-10518
Cannot change sample name for de novo via upload	IW-10519
Classification button not updating after classification made	IW-10521
Cannot download curated variants	IW-10525
CNV metrics missing from informatics report	IW-10526
Search in Genome Browser for a gene does not always zoom	IW-10531
Runtime not showing for completed COD jobs	IW-10535
Target Maps for Alignment jobs are not sorted by name by default	IW-10536
Unusual property repeats in informatics report	IW-10537
jobid in informatics report showing as date	IW-10541
Job details missing items for BNX Alignment	IW-10542
Gene labels not showing on 2nd gene track for translocations	IW-10543
Cannot view curated list in Circos plot.	IW-10544
[Circos Plot] does not consume the "Show tooltip" view option	IW-10552

Not getting export completion emails	IW-10554
ICSN not showing on generate variant report dialog after review completed	IW-10555
Do not allow spaces in the export file name	IW-10557
Gender not transferred to VIA	IW-10558
Allow -1 for VAF min and max values when filtering	IW-10560
Whole Genome View failing for FHSD	IW-10566
Auto Analysis does not set vap_params needed to run annotation	IW-10569
RVA link not showing for non-human samples	IW-10573
Auto Analysis detecting jobs in other projects	IW-10574

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
[Security] Smartmatch library deprecated	IW-10382
[Security] Offline logout	IW-6202
[Security] In Silico Digestion not limited to Project Leads	IW-10490
[Security] Could not log in after setting new password	IW-10485
[Security] Database password exposed in knexfile.js	IW-10438
[Security] Database password appears in install script	IW-10405

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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Email	support@bionano.com
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