Bionano Access® v1.5 Release Notes

Document Number: 30314

Document Revision: D

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Legal Notice

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Revision History

Revision	Notes
A	Initial release of document.
B	Added tickets for 1.5.1 update
C	Added ticket IW-5666 to 1.5.1 update
D	Adding tickets for 1.5.2 update

Bionano Access

This document describes the v1.5 release of Bionano Access®. In this document we will provide an overview of what is changing with this release so that you may better understand the impact of moving to this version of our visualization software. Should you have any questions please contact support@bionanogenomics.com.

Introduction

Bionano Access v1.5 is a new release of our 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 install on a single centralized server that can be shared across an organization. For information about system requirements and installation please refer to our Installation Guide (P/N 30170).

Compatibility

Bionano Access is compatible with data generated on both Irys and Saphyr instruments. Existing Irys Data generated via Auto Detect v2.1.4 or IrysSolve v2.1 pipeline can be uploaded into Bionano Access. Bionano Access is compatible with Saphyr Control Software versions 3.1.4, 4.8 and 4.9.

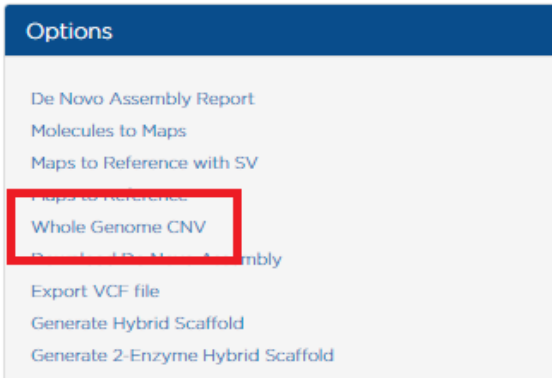
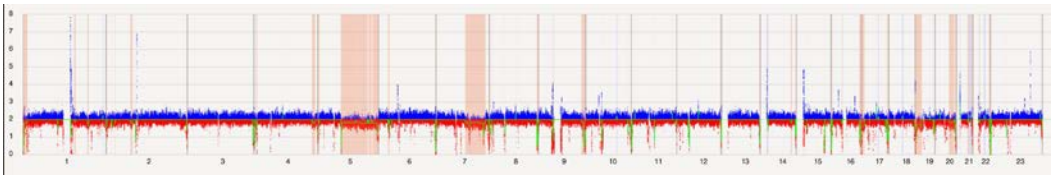
Bionano Access is designed to integrate directly with the Bionano Solve® v3.5 pipeline running on Saphyr Compute and Bionano Compute servers. Compute configurations which are not directly compatible will continue to be supported from the command line, with a manual import of results into Bionano Access.

Please Note

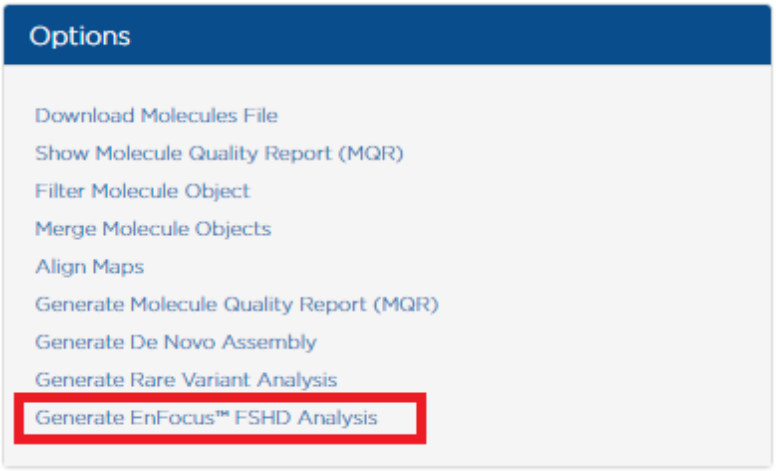
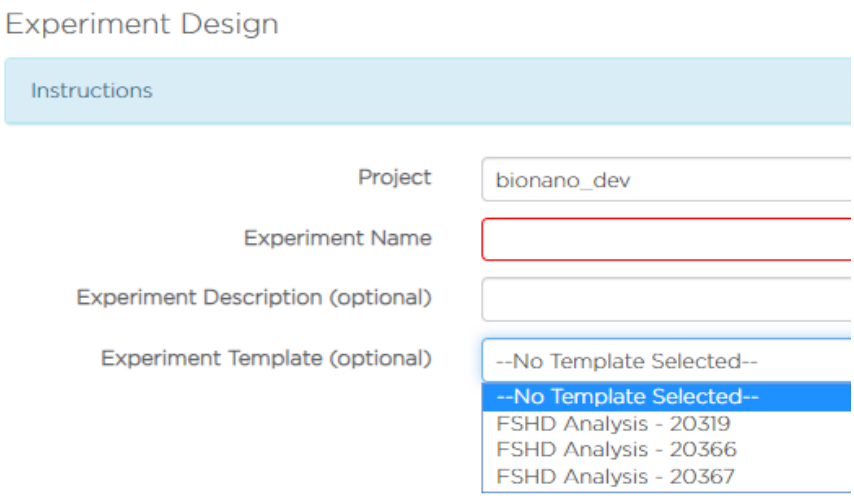
Bionano Access version 1.5.2 has been modified to facilitate 5 Tbp chip runs for selected part numbers. The increased volume is to support 1% allelic fraction detection using the Rare Variant Analysis operation. Please consider carefully how much data you collect and process for other operations. *De novo* assembly has been validated with human data up to 5 Tbp, where automatic down sampling is applied. Non-human de novo assembly has been validated up to 2.2 Tbp on Bionano compute servers. Larger and more complex genomes may require additional memory to process than what is available on standard Bionano compute servers. Bionano is working to insure these data can be processed through the Compute On Demand service in the near future.

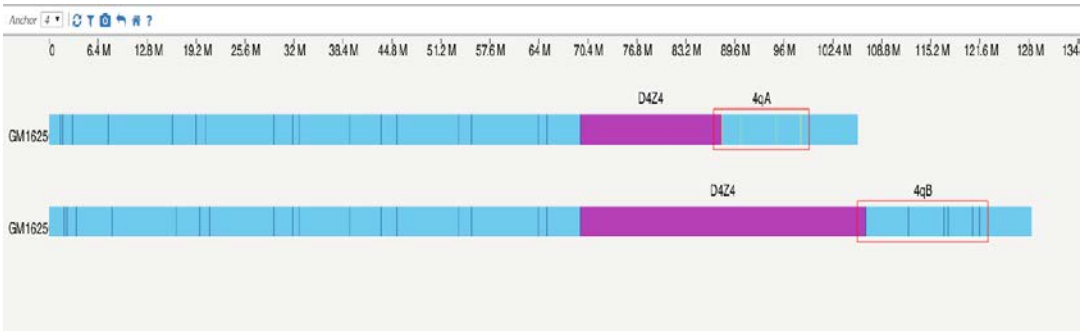
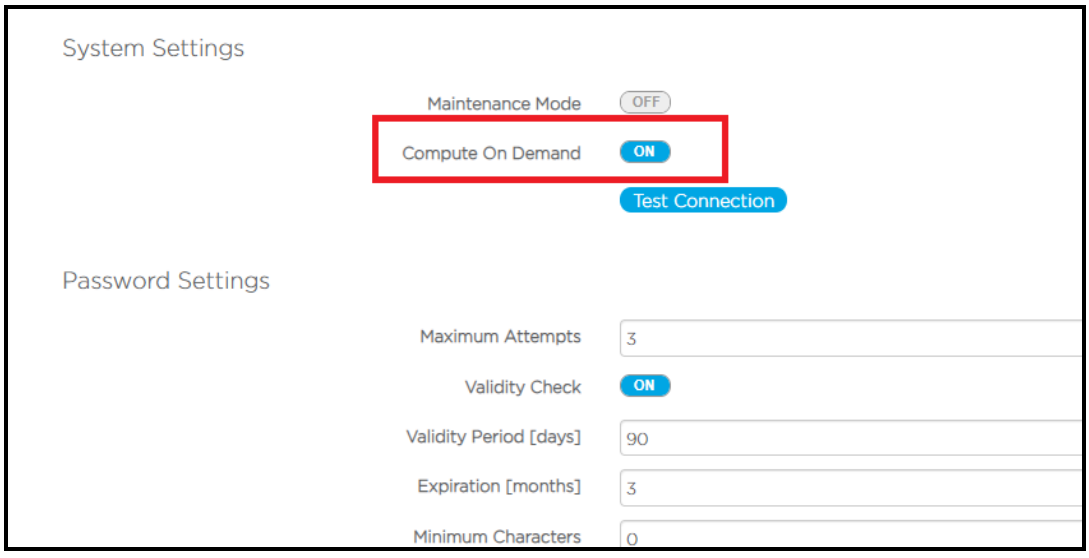
Improvements

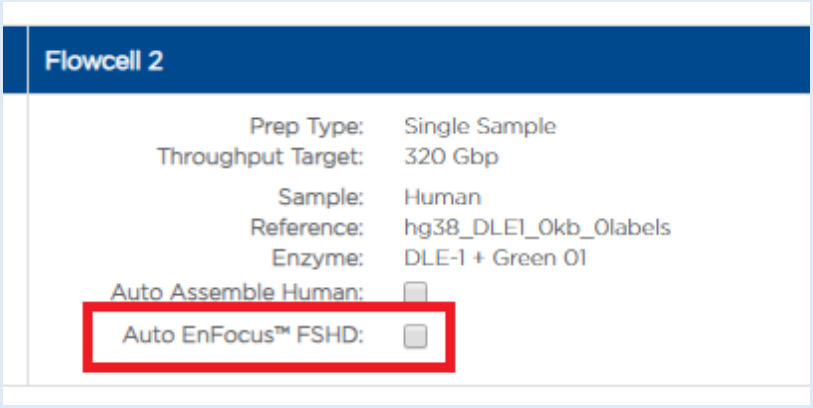
Below is a brief description of new features that have been added with this release. For more detailed information on these new features please refer to our user manuals and video tutorials.

Improvement	Description
Annotate De Novo	When generating a de novo Assembly you can now choose to have the results annotated in a single operation.
Whole Genome Copy Number View	You can now chose to view the copy number track for the whole genome on assemblies. The individual label copy number data points are plotted in blue/red. The smoothed copy number line is in green. The copy number segments identified are shaded. The chromosome numbers are shown across the bottom and the left side shows the number of copies.  
Change MQR launch	A Molecule Quality Report (MQR) is launched automatically when Bnx files are imported into access. Previously you could manually launch a new MQR from the object edit window. Now you can launch a Molecule Quality Report from the options panel instead.

New Circos CNV Track	We have changed the copy number track in our circos plot. We now animate three superimposed lines to help color code the copy number track. Black is the baseline, blue is duplicated, and red is deleted. Here is an example. 
Auto Object Naming	When you generate any object from the project browser it will have a default name based on the sample name and type of operation you are performing. This is a simple convenience designed to save you time.

EnFocus™ FSHD Analysis	Given a molecules file you can perform an analysis for Facioscaphulohumeral Muscular Dystrophy (FSHD). The system will assemble the chromosomes of interest and allow you inspect the results 
FSHD Experiment Template	When creating an experiment we have added experiment templates optimized for EnFocus™ FSHD AnalysisThe templates are named based on the chip you plan to use. 

FSHD Visualization	The genome browser has been customized for FSHD results. It will automatically focus on the areas of interest on either chromosome 4 or 10. The traits of interest in the view have also labeled for you. Here is an example: 
FSHD Report	From the Project Browser you can generate an FSHD report in PDF format. The output report will be downloaded to your workstation upon completion.
Compute On Demand Activation	With the Administrator user role you can now activate Bionano Compute On Demand features from the System Settings Page. Just toggle the on/off button for Compute On Demand and respond to the opt in prompt. Internet access is required to connect to the Bionano Compute On Demand solution. You can test the connection from the System Settings page by clicking the 'Test Connection' button after enabling the service. 

Auto FSHD	When defining an experiment if your sample is human, you are using the DLE-1 enzyme, and you selected our hg38 reference you can choose to automatically start an EnFocus™ FSHD Analysis upon completion of your chip run. The EnFocus™ FSHD Analysis will only start if you collect more than 400Gbp with a map rate of 70% or more and an N50 value over 200. 
Disable Additional Information Section on FSHD Report	You can disable the additional information section on the EnFocus™ FSHD Analysis Report by adding the following to your access configuration file and restarting the access service. Don't forget to add a comma to the previous line to maintain the proper JSON formatting. **`FSHDShowAdditionalDataInformation: false`**

Tickets

Updates

Version	Summary	Ticket
1.5.1	Update Opt Args for Rare Variant Analysis	IW-5588
1.5.1	Wrong error message when opt arg file not found	IW-5582
1.5.1	SV Merge missing token cost	IW-5589
1.5.1	Auto Assembly looking for tar.gz instead of zip file	IW-5666
1.5.2	Error on Password Update	IW-5680
1.5.2	Add experiment support for 5Tbp per flowcell	IW-5634
1.5.2	Add version to token estimate requests	IW-5636
1.5.2	Add limits to local operations	IW-5635
1.5.2	StartAccess.sh being overwritten during install	IW-5730

User Stories

Summary	Ticket
[Import] Import an annotated de novo assembly	IW-4048
[Copy Number] While genome CNV view	IW-4421
[FSHD] Add throughput to experiment template	IW-4778
[FSHD] Auto Object Naming	IW-4789
[FSHD] Initiate FSHD test	IW-4790
[FSHD] Import FSHD result	IW-4792
[FSHD] Make FSHD experiment template	IW-4794
[FSHD] parse new repeat file format	IW-4805
[FSHD] FSHD genome browser visualization	IW-4827 IW-4942
[FSHD] Output Report	IW-4847
[Project Browser] Change MQR operation	IW-4891
[General] Add Versions File	IW-4899
[FSHD] Download JSON	IW-4906
[FSHD] highlight FSHD labels	IW-4928
[FSHD] Display region label	IW-4940
[Compute on Demand] Show selected region on Compute on Demand page	IW-4967
[Compute on Demand] Simplify activation	IW-5023
[FSHD] Download Report in JSON format	IW-5105
[FSHD] pass json object for job identification	IW-5110
[Compute on Demand] support proxy use	IW-5115
[Compute on Demand] support FSHD Analysis	IW-5158
[Copy Number] Add whole copy number view for Rare Variant Pipeline	IW-5228
[Security] Add proxy support for Compute on Demand	IW-5229
[FSHD] Auto FSHD on experiment	IW-5257
[FSHD] Video Tutorial	IW-5261
[FSHD] Provide link to input molecule object	IW-5383

[FSHD] Add merged bnx warning	IW-5385
[FSHD] Add check for merged bnx files	IW-5386
[FSHD] Add whole genome copy number view for FSHD	IW-5436
[FSHD] Add setting to disable additional information on FSHD report	IW-5458

Defects

Summary	Ticket
[General] Verify submit form layout consistency	IW-4408
[General] Error dialog is too wide	IW-4413
[Compute on Demand] Molecule object disabled if MQR cancelled	IW-4511
[Bnx Merge] Change default Bnx file selections	IW-4549
[Project Browser] Bounced to page one in object list after removing object	IW-4552
[Security] Update form validation for password expiration settings	IW-4694
[Rare Variant] Disable chimeric filter for Rare Variant Analysis	IW-4716
[Rare Variant] Project export for Rare Variant Analysis	IW-4742
[Circos] Improve CVN Visualization	IW-4776
[Alerts] Rare Variant Analysis notification missing link	IW-4804
[Rare Variant] Missing back button on second page of workflow	IW-4808
[Rare Variant] Tags not saved after Rare Variant Analysis launch	IW-4809
[MQR] Sample name and job id blank when running MQR on Compute on Demand	IW-4811
[Project Browser] Error message missing on duplicate copy operation	IW-4814
[Compute on Demand] de novo Assembly back button not working	IW-4828
[Compute on Demand] New MQR on object with existing MQR fails	IW-4830
[Scaffold] molecules missing in Maps to NGS with conflicts	IW-4835
[Viewer[Floating labels after changing stretch settings	IW-4839
[Assembly] Download VCF link is disabled	IW-4844
[Security] double email on password reset	IW-4848
[Project Browser] fix Completed job filter on job list	IW-4871
[Viewer] SV Report fails if no variants selected	IW-4874
[MQR] Cannot run MQR with only Bionano Access Server	IW-4876
[Alerts] Double email on Bnx Merge operations	IW-4879
[Compute on Demand] VAP job failed to upload	IW-4914
[Compute on Demand] VAP options not visible	IW-4918
[Compute on Demand] Scaffold options not active	IW-4919
[Compute on Demand] Molecule options not visible	IW-4920
[Bnx Workflow] fix Chip Stats for multiplexed chips	IW-4922
[Rare Variant] Rare Variant Analysis not showing BED or Reference	IW-4923
[Exp Design] ‘Primary’ label not in correct position	IW-4924
[SV Report] Font size changed to be consistent	IW-4926
[Bnx Merge] Empty mergebnx.tar.gz imported for job that failed	IW-4945
[Compute on Demand] Add assembly check for matching enzymes	IW-4951
[Project Browser] Send cancel command to all assembly servers	IW-4961

[Security] Can't change email without also changing password	IW-4968
[General] User email setting not populated in user profile	IW-4969
[Rare Variant] Restrict Rare Variant Analysis to DLE-1 only	IW-4972
[Import] Bnx import failing on large dual labeled sample	IW-4975
[Viewer] Cytoband missing in genome browser	IW-4976
[Security] Force new password on first login	IW-4992
[General] Modify GetWebHostIP to exclude 111.111.111.1 address	IW-5008
[Bnx Workflow] Avoid scp to self on Bionano Access Server after mergeRun	IW-5019
[Bnx Workflow] Heartbeat won't detect completed mergeRun jobs	IW-5022
[Bnx Workflow] Duplicate imports for multiplex flowcell	IW-5037
[Compute on Demand] Change job status to failed for upload failures	IW-5075
[Variant Annotation] Not all filter criteria displayed in circos legend	IW-5093 IW-5108
[Compute on Demand] Overrun notice missing server	IW-5090
[Copy Number] Hide masked cnv segments in copy number track	IW-5142
[General] Update Opt Arg files from Bionano Solve	IW-5160
[Compute on Demand] Add COD pipeline version to help page	IW-5196
[Compute on Demand] Make COD online check version specific	IW-5197
[Assembly] Change the assembly SV mask bed file used for Bspql	IW-5201
[Exp Design] Project names not in order when creating new experiment	IW-5208
[Exp Design] Allow user role to create experiments	IW-5209
[Variant Annotation] SV chirmeric score not applied to SV Anntotation Tab	IW-5213
[Security] Cannot filter user table by user role	IW-5417
[Import] Force cmap suffix to always be lower case	IW-5220
[Viewer] Chimeric Score Filter not working properly	IW-5259
[Project Browser] Tags not saved on some operations	IW-5274
[Scaffold] Wrong config selected for DLE-1	IW-5283
[FSHD] Add hyperlink to email notification	IW-5286
[Variant Annotation] Hide pie chart	IW-5363
[Security] User table not changing after updates	IW-5427
[Help] versions missing	IW-5457

Technical Assistance

For technical assistance, contact Bionano Genomics 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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