Bionano Access® v1.6 Release Notes

Document Number: 30382

Document Revision: B

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Revision History

Revision	Notes
A	Initial release of document.
B	Revision for Update 1.6.1

Bionano Access

This document describes the v1.6.1 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

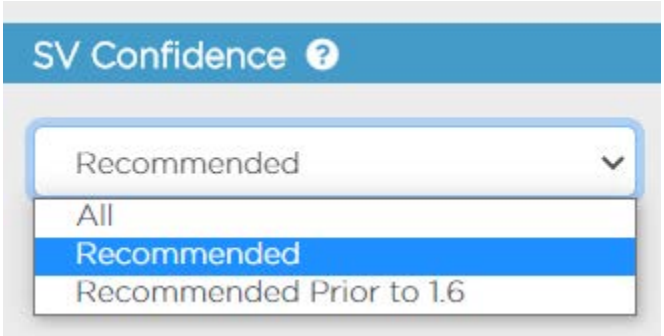
Bionano Access v1.6.1 is a new release of our Bionano Access product. Bionano Access supports Windows, Mac, and Linux systems. Data between users is shared using projects, and performance is much improved through rendering optimizations and graphics acceleration. This application is designed for install 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 1.6.1 is compatible with Saphyr Control Software versions 4.9 and above. Bionano Access is designed to integrate directly with the Bionano Solve® v3.6 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.

Notice

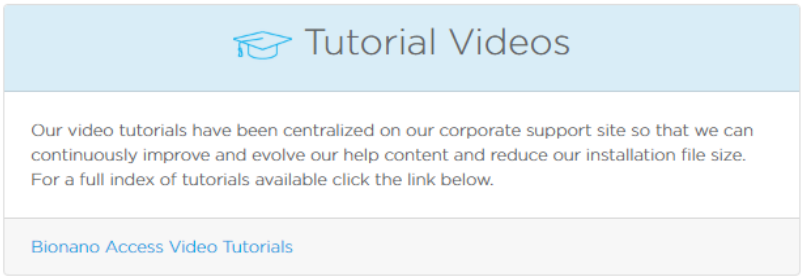
In Bionano Solve 3.6 the confidence model for structural variants was changed. The recommended filters in Access 1.6 were updated to reflect the new model. However, these new recommended levels are not appropriate for datasets generated with previous versions of Bionano Solve. In the Bionano Access 1.6.1 update a new recommended filter for data generated using versions prior to 1.6 (image below) is added. Use the ‘Recommended Prior to 1.6’ for any datasets that were generated before you installed Bionano Access 1.6.

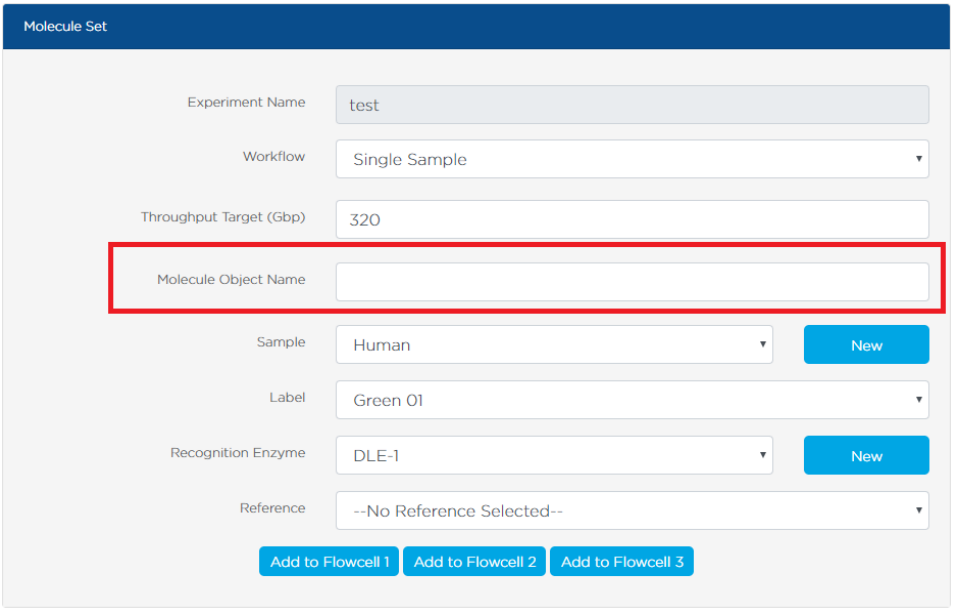


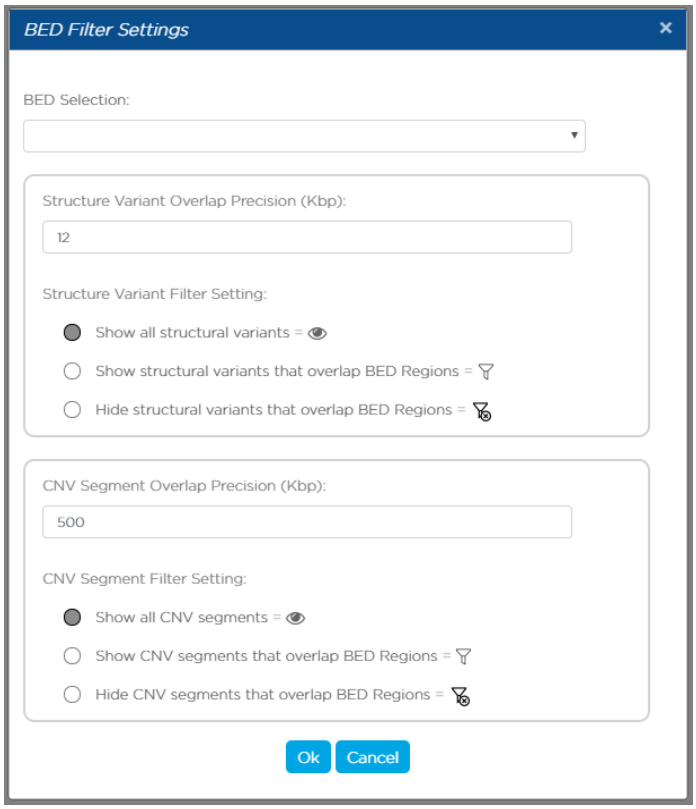
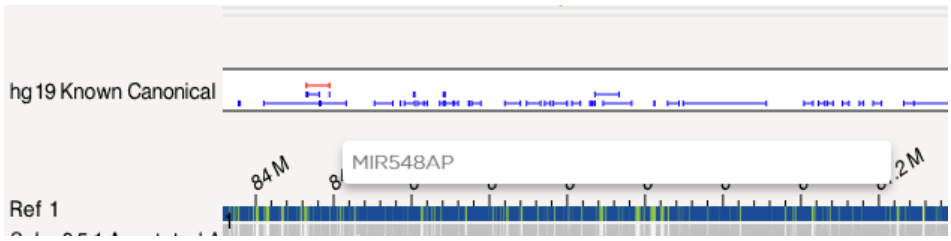
You can find the “Tools versions: 1.6” in the De Novo Assembly Report or the Rare Variant Analysis Report if the SVs were called using Access 1.6/Solve 3.6. If it is not 1.6 you can assume you should use the ‘Recommended Prior to 1.6’ filter instead of the ‘Recommended’ filter. Prior to Access 1.6/Solve 3.6, the recommended confidence cutoff is only validated for SVs called in De Novo Assembly, and we recommended to use the same cutoff for SVs called in Rare Variant Analysis. You are also able to generate your own named filters for use within the Bionano Access system if you have confidence values you would prefer to use. Refer to our video tutorials on named filters for more information.

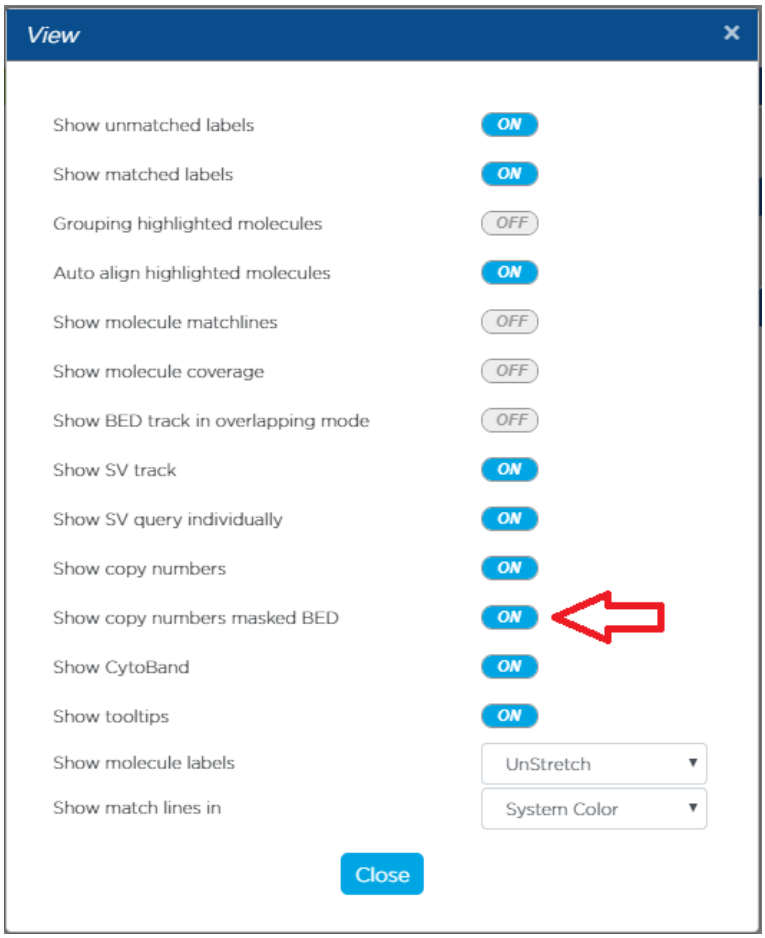
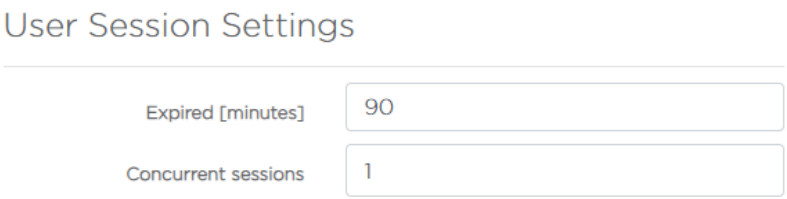
Improvements

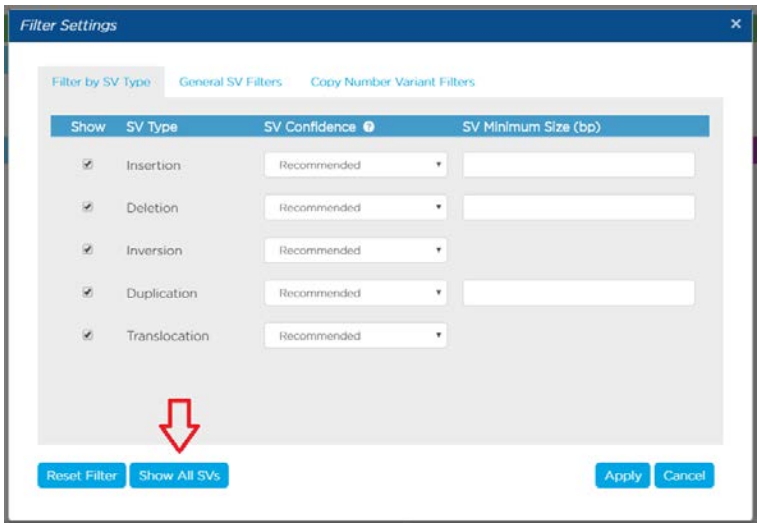
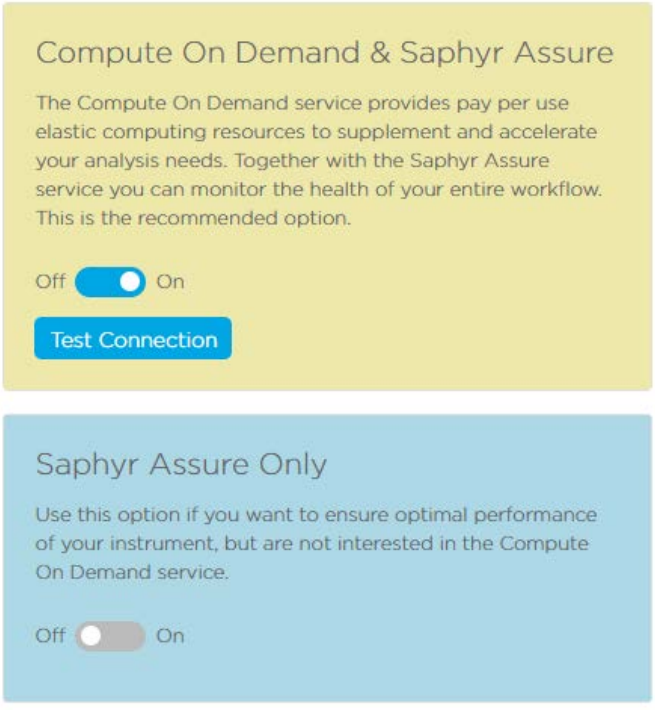
Below is a brief description of new features that have been added with this release. For more detailed information on these new features please refer to our user manuals and video tutorials.

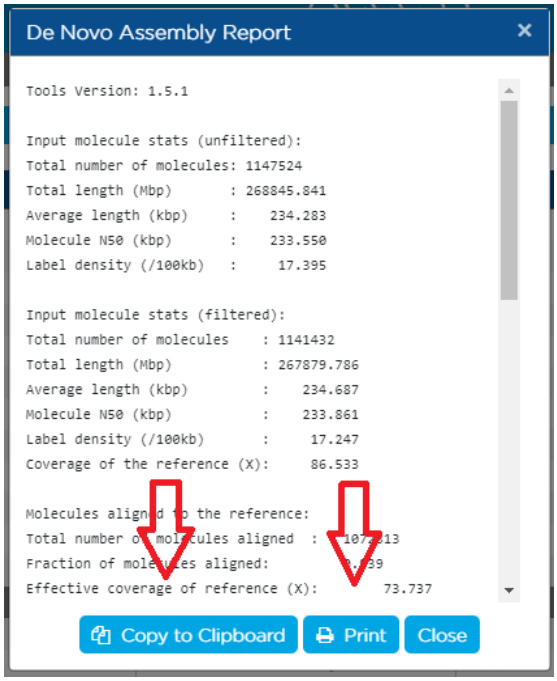
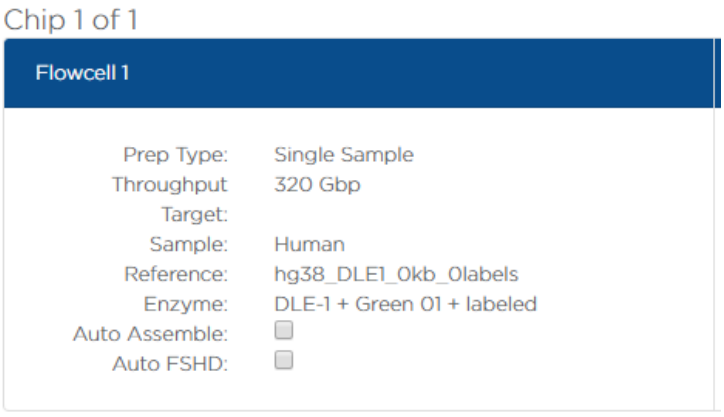
Improvement	Description
Centralize Tutorials	The help page within Bionano Access contains a variety of video tutorials. These tutorials are still accessible from the help page, but they have been moved to a centralized storage location (requires Internet access). This reduces our installer file size and allows us to deliver updates easily when new content becomes available. 

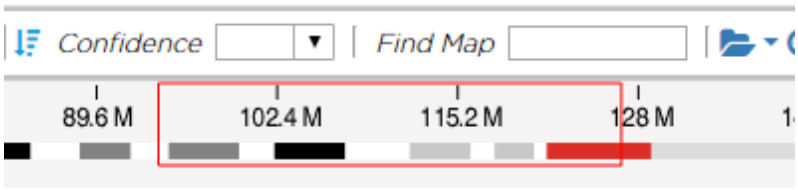
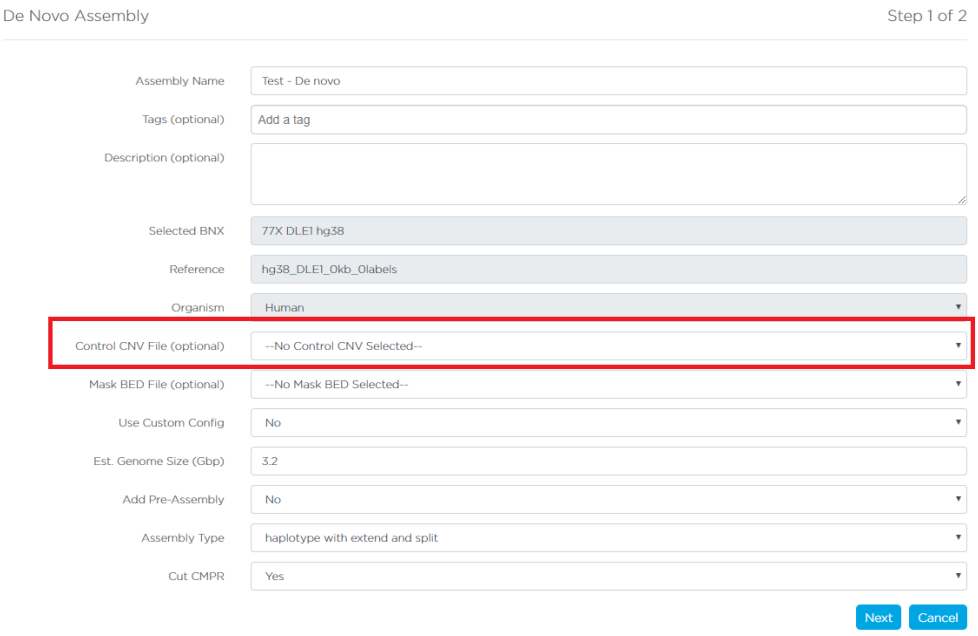
Custom BNX Naming	When defining your experiment, you now have the option to name the molecules object that will be generated. If you leave the name blank the default naming scheme will be used. 

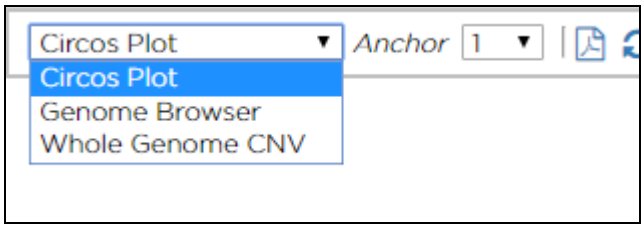
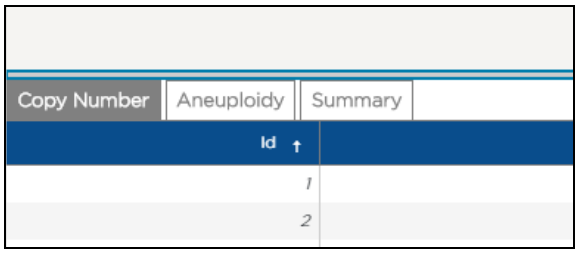
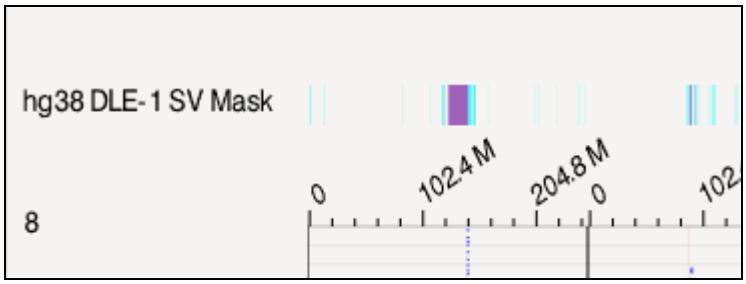
Improved BED filtering	BED Filtering has been expanded to include CNV segments. You can apply a BED filter to structural variants and/or CNV segments. We also relocated the overlap precision field to this dialog and added a separate precision overlap value for CNV segments. 
Overlapping BED regions	The regions in some BED Files overlap. Bionano Access version 1.6 offers a BED track that breaks out overlapping BED regions as shown below. You can toggle the overlap view setting on the BED Track in the viewer settings. 

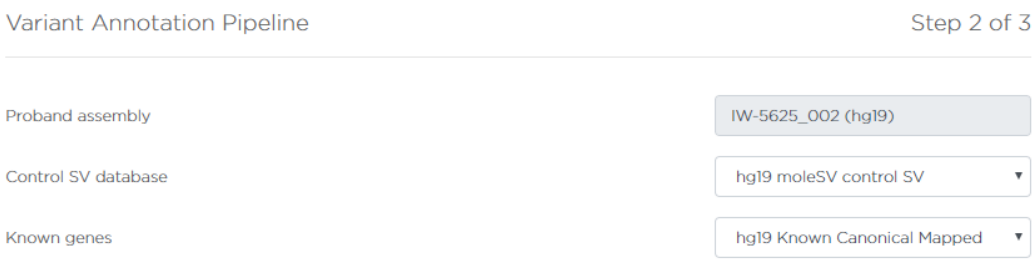
Show CNV suppressed regions	We have added an option to display the copy number masked BED file. This extra visualization can be helpful to understand why copy number variants were not identified in masked regions. 
New Session Settings	Our system settings have been modified to include session expiration and concurrent sessions allowed. This gives administrators greater control to adjust session settings to comply with their local security protocols. 
Deprecate Containers	Variant Annotation operations will now generate Variant Annotation Pipeline objects instead of Containers. Variant Annotation Pipeline objects can be readily imported and exported from the Project Browser. Existing Containers can be converted to Variant Annotation Pipeline objects.

Show All Button	The Filter Settings dialogue now includes a Show All SVs button. 
Down Sampling	When launching Compute On Demand de novo assembly jobs on human samples, the system will automatically prompt you to down sample to save computing time and token cost.
Saphyr Assure	Administrators can enable the Saphyr Assure service from the setting screen in this release. We offer combined Compute On Demand and Saphyr Assure (recommended) and Saphyr Assure Only options only when signing up. 

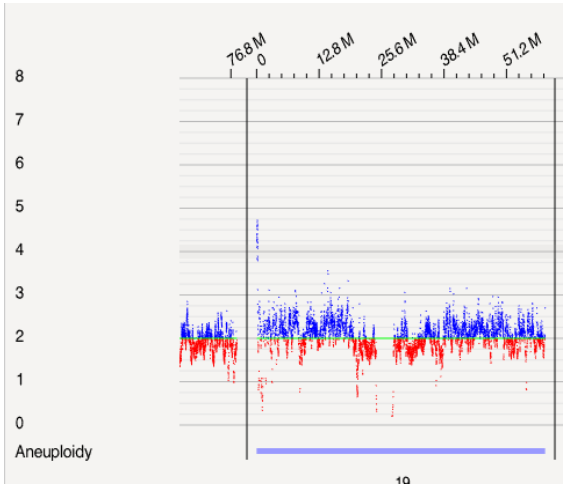
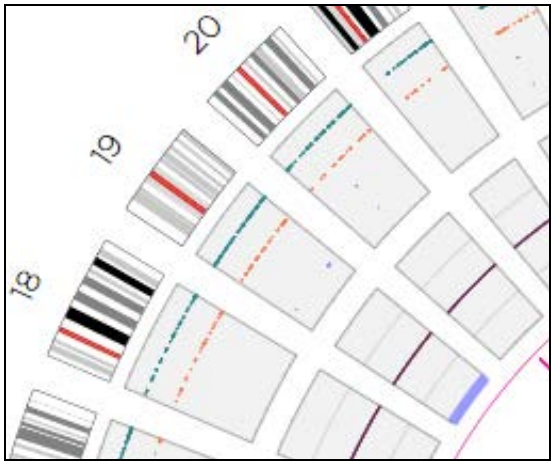
Report Print Buttons	Copy to Clipboard and Print buttons have been added to all dialogs where we are displaying output reports from Bionano Solve for your convenience. 
Auto FSHD	When defining experiments, you can now choose to run Auto FSHD if you are running a human sample. When you select Auto FSHD, an FSHD job will be launched automatically when the chip run completes. 

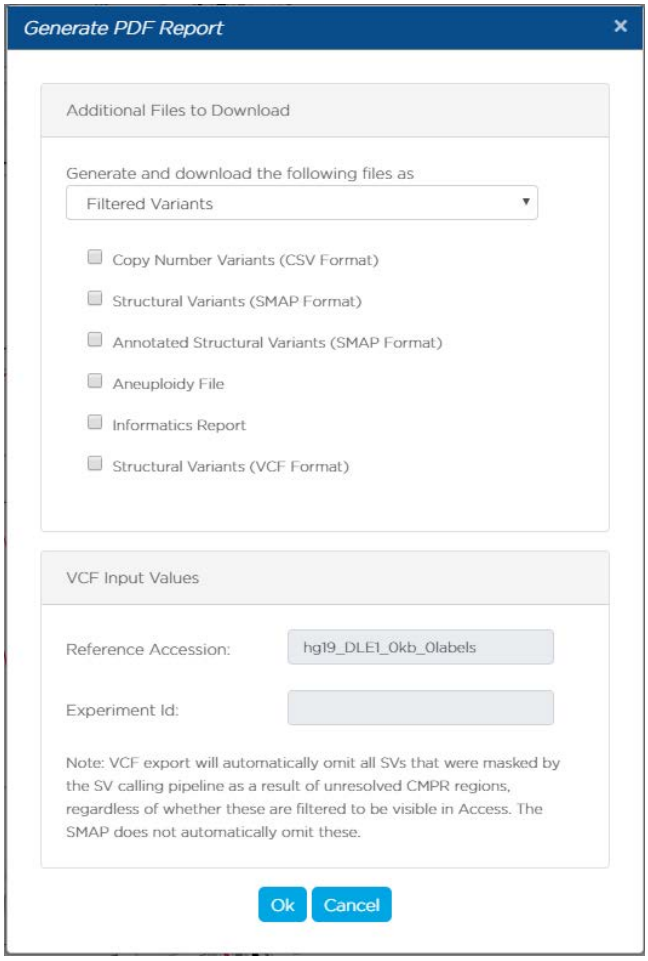
Cytoband Modified	The cytoband no longer zooms when you zoom on the maps. The cytoband track does not stay at full resolution like the ruler. We extended the indicator of your current view to include both the ruler and the cytoband track. 
Non-Human CNV	When launching operations with CNV computations included you can now select the control database you want to use. Project Leads can upload custom control databases in the system settings. You can also omit a selection to skip CNV. For more information on how to create a control file refer to the Introduction to Copy Number Analysis document. 

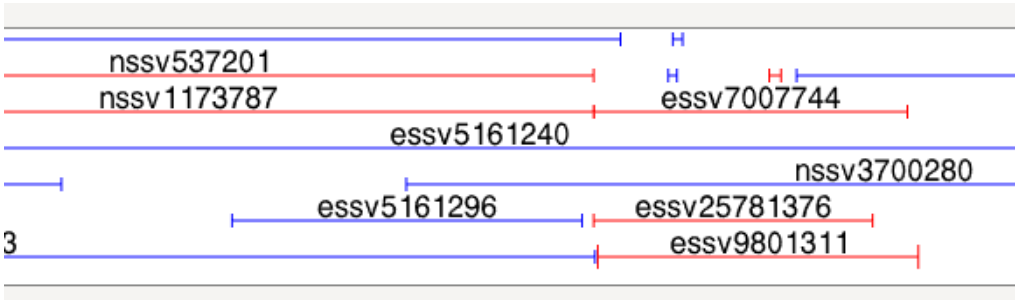
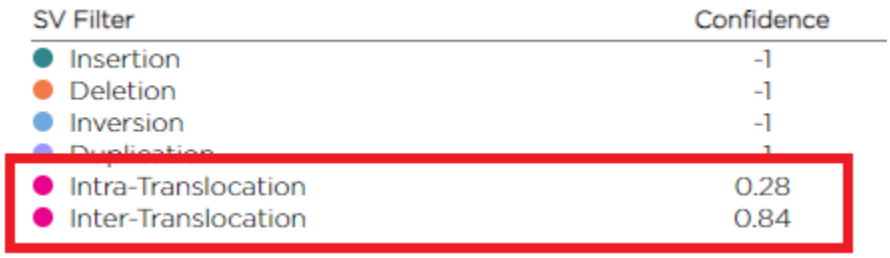
Whole Genome CNV Improvements	The whole genome copy number view has been integrated in the drop-down along with the circos plot and the genome browser viewer. Now you can switch between views using the drop-down in the toolbar (image below).  The whole genome copy number view now also includes data tabs along the bottom.  Ruler marks have been added to the whole genome copy number track and we added BED Tracks. Right click on the copy number track to add or remove BED Tracks. BED files selected in other views will appear in the whole genome copy number view automatically. The ruler marks reset at each chromosome. 

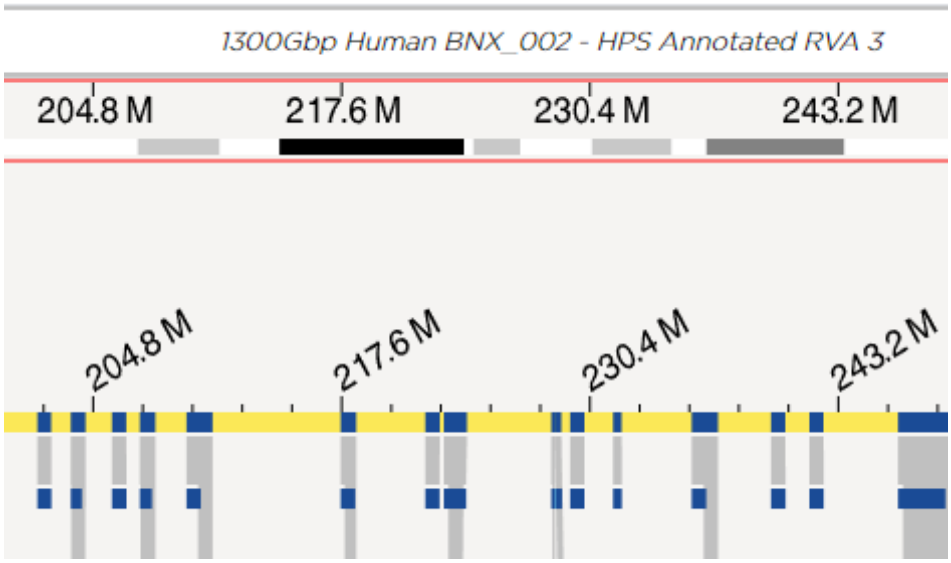
<table>
<tr><td>Non-Human Annotation</td><td>When you launch an annotation operation you can now choose the control structure variant database and known gene list to be used. This facilitates annotation of non-human species. The system will default the selection for you automatically when you are using an hg19 or hg38 reference. Users with the Project Lead role or greater can upload control databases and gene lists for selection in the system settings. Refer to the Bionano Solve Theory of Operation Variant Annotation Pipeline document on additional information regarding how to create control databases and gene lists for upload.
 
</td></tr>
<tr><td>Add annotation to auto assembly</td><td>In release 1.5 we added the ability add annotation to a de novo assembly operation. In this release we added annotation to all auto assemblies by default. No extra steps are required.</td></tr>
<tr><td>Add non-human references</td><td>In this release we added several common non-human references including the following:

<table>
<tr><th>Genome build</th><th>Common name</th><th>Latin name</th></tr>
<tr><td>mm10</td><td>House mouse</td><td>Mus musculus</td></tr>
<tr><td>TAIR10</td><td>Thale cress</td><td>Arabidopsis thaliana</td></tr>
<tr><td>GRCg6a</td><td>Chicken</td><td>Gallus gallus</td></tr>
<tr><td>Glycine_max_v2.1</td><td>Soybean</td><td>Glycine max</td></tr>
<tr><td>IRGSP-1.0</td><td>Japanese rice</td><td>Oryza sativa Japonica Group</td></tr>
<tr><td>Rnor_6.0</td><td>Norway rat</td><td>Rattus norvegicus</td></tr>
<tr><td>Sorghum_Bicolor_NCBIv3</td><td>Sorghum</td><td>Sorghum bicolor</td></tr>
<tr><td>b73_refgen_v4</td><td>Maize</td><td>Zea mays</td></tr>
<tr><td>BDGP6.28</td><td>Common fruit fly</td><td>Drosophila melanogaster</td></tr>
<tr><td>GRCz11</td><td>Zebrafish</td><td>Danio rerio</td></tr>
</table></td></tr>
</table>

Aneuploidy visualization	We have added an aneuploidy visualization to the copy number track. It appears in all three views. The aneuploidy indicator appears in purple below. You can change the color of the aneuploidy indicator by changing the SV duplication or deletion color in the view settings.  

Updated SV Report export options	Please note the export options have been updated when you generate an SV Report. Some options have been added and some have been removed (image below). 

Linux Patching Status	In this release we have added a security link on the help page. The link leads to our security page where we share Linux security patching status and offer a sign up for security updates. **Bionano Genomics Security Newsletter** Stay abreast with the latest security recommendations. Fill out the information below to be added to the mailing list. First Name * Last Name * Email * Institution * Job Title * I agree to the Bionano Genomics website terms of use and privacy policy. * Yes Submit
BED Labels	By default the system will now show BED Labels when you are zoomed in sufficiently. You can also always see the BED Label by hovering the mouse over the BED region. You can turn the BED labels on or off in the viewer options. 
Translocations separated	You can now filter for Intra-Translocation and Inter-Translocation variants with different confidence values and we show the count for each separately in the Circos legend. 

Object Name on Toolbar	The name of the object being viewed now appears in the toolbar right justified. 
References added to project export	Previously references associated with objects were not transferred as part of the project export/import process. Now they are transferred automatically if they are not already existing on the target system.
SVG Capture	The SVG screen capture is no longer functional. Our viewer presents too much data to be rendered in an SVG image through a standard browser. The screen capture does not produce a vector graphic anymore until we can find a resolution. You can get jpg screen images only in this release.

Improve Informatics Report	Access will inject the sample name, operator name, server name, and the job date to the de novo Assembly and Rare Variant Analysis informatics reports when viewed in Access. This change was intended to help with chain of custody tracing. Additional improvements are planned in upcoming releases.
	
	`Sample name : My Sample`
	`Operator name : John Doe`
	`Server name : 192.168.48.224`
	`Date of analysis : Thu Oct 01 2020 17:00:04 GMT-0700 (Pacific Daylight Time)`
	`Tools Version : 1.5`
	
	`Input molecule stats (unfiltered):`
	`Total number of molecules: 1147524`
	`Total length (Mbp) : 268845.841`
	`Average length (kbp) : 234.283`
	`Molecule N50 (kbp) : 233.550`
	`Label density (/100kb) : 17.395`

Known Existing Issues

These are known issues that will be addressed in future releases.

Issue	Workaround
Alignments that are moved between systems will always be treated as molecule alignments.	If you need alignment migrated to another system as a map alignment, please use the import feature in the project browser.
In some cases the variant image will not appear on the SV Report. This can happen if the image save was interrupted.	Go to the selected SV tab in the Genome View and click the camera icon to take a fresh image for that variant. You can preview the image by clicking the photo icon.
In some cases the system will not generate the FSHD PDF. This can happen due to disk latency or heavy file I/O.	Click the generate report link again. The report will typically generate properly on the next attempt.

Updates

These are issues that were addressed as part of an update to Bionano Access 1.6.

Version	Summary	Ticket
1.6.1	Replace hg19 SV control file	IW-6666
1.6.1	Add recommended filter for previous versions	IW-6664
1.6.1	Cannot download RVP	IW-6663
1.6.1	Chimeric score filter not hidden for VAP on RVP	IW-6654
1.6.1	VAP Conversion not working on older datasets	IW-6634
1.6.1	Update Compute On Demand Terms and Conditions	IW-6668
1.6.1	Provide link to view Compute On Demand / Saphyr Assure T&C	IW-6672
1.6.1	Incorrect Compute On Demand estimate for Single Annotation	IW-6635
1.6.1	Update Version	IW-6679
1.6.1	Translocations not showing for RVP in some cases	IW-6738
1.6.1	Variant Annotation objects blank after import	IW-6726
1.6.1	Container conversion link active after being clicked	IW-2734
1.6.1	SV Report has blank page	IW-6704

Tickets

These are the features that were released with Bionano Access 1.6.

Summary	Ticket
[Import] Add references to project import / export	IW-1748
[Scaffold] Retain files required for manual cuts	IW-2066
[Project Browser] Make job list a separate screen	IW-3681
[Help] Move tutorials to centralized site	IW-3959
[Export] Add VCF Conversion to variant operations	IW-4467
[Experiment] Custom BNX naming	IW-4608
[Viewer] Move BED overlap to Add BED dialog	IW-4686
[Project Browser] Show input objects in object details	IW-4799

[Viewer] Show only options on toolbar that pertain to current view	IW-4996
[General] Modify startup to verify Solve version on all servers in config	IW-5048
[Security] Inactivity logout setting	IW-5103
[Project Browser] Eliminate object containers	IW-5118
[Compute On Demand] Add token statement to Access	IW-5126
[Viewer] Add show all button to filter dialog	IW-5195
[Compute On Demand] Add option to down sample	IW-5241
[Saphyr Assure] Add option in settings to enable Saphyr Assure Program	IW-5245
[Import] Add references in project export	IW-5321
[Saphyr Assure] Allow users to initiate TeamViewer session from Access	IW-5339
[Project Browser] Add print buttons to bioinformatic reports	IW-5366
[Viewer] Breakout overlapping BED regions	IW-5367
[Experiment] Allow user to filter on chip run guid	IW-5405
[MQR] Add warning when user changes reference	IW-5470
[Experiment] Add Auto FSHD	IW-5500
[Help] Add EULA to help screen	IW-5553
[EnFocus] allow FSHD jobs to process on Bionano Access Server	IW-5555
[Viewer] Remove zoom on cytoband track	IW-5584
[Project Browser] Support non-human CNV	IW-5633 IW-6123 IW-6120 IW-6119 IW-6118
[Viewer] Integrate whole genome CNV view with other views	IW-5638
[Viewer] Filter whole genome CNV view with other views	IW-5639
[Viewer] Add CNV tab to whole genome CNV view	IW-5640
[Viewer] Show BED track on whole genome CNV view	IW-5641
[Annotation] Allow user defined gene lists for annotation	IW-5644
[Viewer] Add fractional copy number lines to CNV view	IW-5645
[Annotation] All user defined control databases for annotation	IW-5646
[Compute On Demand] Add flag to track HPS jobs	IW-5651
[Compute On Demand] Modify job naming for HPS	IW-5652
[Viewer] Show suppressed regions on CNV track	IW-5673
[Compute On Demand] Add page to show voucher token balance	IW-5674
[Compute On Demand] Add page to show jobs by voucher	IW-5675
[Project Browser] Deprecate SV Merge	IW-5677
[Experiment] Add annotation to auto assembly	IW-5708
[Settings] Add mouse and other common non-human references	IW-5737
[Experiment] Add instrument name to chip run list	IW-5764
[Viewer] Extend BED filters to affect CNV segments also	IW-5841
[Security] Disable track / trace requests on web server	IW-5844
[Security] Disable ports 111 and 990 on web server	IW-5845
[Viewer] Add ruler to whole genome CNV view	IW-5855
[Viewer] Add aneuploidy tab to whole genome CNV view	IW-5857

[Viewer] Add BED tab to whole genome CNV view	IW-5858
[Viewer] Add visualization for aneuploidy to CNV track	IW-5889
[SV Report] Update export options	IW-5892 IW-5910 IW-5949
[Compute On Demand] Modify overrun monitoring for HPS	IW-5912
[Viewer] Add a separate BED overlap filter for CNV segments	IW-5956
[Viewer] Show BED track labels	IW-5961
[Security] Add page for Linux security patching status	IW-5982
[Viewer] Add BED track scrolling	IW-5991
[Viewer] Add DGV and exon BED files	IW-6054
[Viewer] Breakout Translocation Filtering by Type	IW-6061 IW-6086
[Viewer] Change default SV size in Circos Plot	IW-6091
[Viewer] Update known canonical bed files	IW-6090
[Viewer] Show ruler on translocation chromosome by default	IW-6092
[Viewer] Show Object Name in Viewer	IW-6137
[Security] Add service indicator to home page	IW-6546
[Security] Inject data into informatics report	IW-6576

These are defects that have been addressed in Bionano Access 1.6.

Summary	Ticket
[Viewer] BED filtering only returned variants where both breakpoints overlapped gene.	IW-6186
[Settings] Editing named filter creates new named filter	IW-6184
[Viewer] Change layout of variant annotation tab in filter dialog	IW-6181
[Viewer] SV Chimeric Score not applied during SV export	IW-6175
[Scaffold] Remove molecule view option	IW-6170
[Viewer] Rulers not displayed correctly in some cases	IW-6149
[Viewer] Found in Self count not matching pie chart	IW-6148
[Project Browser] MQR completion not detected for copied molecule object	IW-6107
[Project Browser] Remove Maps to Reference option	IW-6040
[Compute on Demand] Administrator cannot see all vouchers	IW-6028
[Viewer] Change option sliders	IW-6026
[Viewer] Filtering error for dual and trio variant annotations	IW-5955
[Viewer] Modify vertical axis on whole genome copy number view	IW-5932
[Settings] Change genome label to genome build	IW-5919
[Security] Failed Compute On Demand user registration	IW-5906
[Project Browser] Renaming molecules object deletes MQR	IW-5904

[Viewer] Annotation filters missing for Annotated Rare Variant and Annotated De Novo	IW-5903
[Settings] Cannot disable email in user profile	IW-5896
[Project Browser] Add date created to project list	IW-5890
[SV Report] Add aneuploidy records to SV Report	IW-5885
[FSHD] Report fails to generate if chromosome 10 missing in output json	IW-5882
[Security] Add illegal character warning to inputs	IW-5860 IW-5682
[Project Browser] optarg mapping missing for Saphyr haplotype DLE no extend and split cut seg dupbs human	IW-5838 IW-5583
[Project Browser] Add autofocus on yes / no buttons	IW-5818
[General] Change heartbeat to refresh server connections	IW-5816
[General] Date in grid not sorting as date value	IW-5814 IW-5804 IW-5667
[In Silico] Bad duplicate error when editing enzymes	IW-5794
[Viewer] Too much data to generate SVG	IW-5788
[Import] Too many concurrent imports	IW-5745
[Project Browser] Bnx Merge fails due to nickase string	IW-5738
[Exp Design] Make tabs consistent	IW-5670
[Viewer] Optimize BED Files to handle DGV and exon BED files	IW-5630 IW-3796
[Settings] Unlocking account bounces you to page 1	IW-5613
[Help] Modify how versions are displayed on help index	IW-5591
[Scaffold] Remove aneuploidy tab	IW-5580
[General] Update migration scripts for latest version of knex	IW-5579
[Project Browser] Remove variant annotation pie chart	IW-5363

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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