

Release Notes

Agilent CytoGenomics v5.3

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Product Number

G1662AA – “CytoGenomics Client 1 year named” license (including Feature Extraction). This license supports installation of one client and server (to host the CytoGenomics database) on one machine. For additional client only installations, which connect to the same database on the central server, additional copies of this license are needed.

Overview

CytoGenomics is a cytogenetics research software tool designed to streamline your workflow for processing, analyzing and reporting of cytogenetic measurements. This includes copy number changes and copy neutral Loss of Heterozygosity and Uniparental Disomy data, generated with human samples on Agilent SurePrint G3 CGH-only and CGH+SNP microarray platforms. As of CytoGenomics 5.3 we offer an even more streamlined workflow with a highly sophisticated user interface.

CytoGenomics is designed to: (1) import raw TIFF images generated from the Agilent microarray scanner as well as some non-Agilent scanners and (2) run Feature Extraction and perform analysis using customizable workflows. Utilizing the built-in database, CytoGenomics allows the user to store and query samples and aberrations by classification information or location information. In addition, users can connect from aberration annotations to OMIM, DGV, and Entrez public databases to analyze sample aberrations. During sample review, multiple users can annotate, edit and classify aberrations with full record traceability and generate signed-off reports on processed samples.

CytoGenomics supports an enterprise server/client model for concurrent usage and collaboration. With strong analysis algorithms, data visualization, data management and reporting functionality, CytoGenomics software extends the Agilent microarray based product offerings into a complete cytogenetic clinical research solution.

Key new features of CytoGenomics 5.3

- Support for the new HT microarray multipack formats (16x and 24x), including all new Feature Extraction protocols and QC metric sets
- Updated set of preloaded tracks with updated annotation information for all supported genome builds (hg17, hg18, hg19, and hg38)
- An expanded Overlaid view setting in Triage View that displays overlaid data in all panes of the Genome View, Chromosome View, and Gene View
- Option to include columns in the Triage View CGH Probes table that display the red and green signal values measured for each CGH probe in all samples open in Triage View

- Ability to adjust the zoom level in the Chromosome View, Gene View and Tracks View using the mouse scroll wheel.
- Option to disable the SureFISH web links in the Interval Table
- Option to enable the classification "Count" column in the Interval Table in all sessions of Triage View
- Ability to copy to the Clipboard one or more rows in the Tab View table in Triage View, allowing for pasting of the content into another program
- Update to Cyto Report PDFs in which the Genes section includes active hyperlinks to the OMIM website for OMIM and OMIM-Morbid genes
- Addition of color rendering options when plotting the Moving Average in Triage View
- Option to enable the plotting of Aberration Bar Legends in the Genomic Viewer and PDF Cyto reports, which better show the locations of aberrations when CGH Probes scatter plots are included in the display.
- Secured communication between the LDAP server and CytoGenomics client machine during user authentication.

Installation Instructions

New Installation

- Refer to the installation guide available at:
<http://www.agilent.com/cs/library/usermanuals/public/G1662-90069.pdf>

System Requirements for Agilent CytoGenomics

Requirements for Windows systems

- Operating system: 64-bit Windows 11 Enterprise or Professional, Windows 10 Enterprise or Professional, or Windows Server 2019
(Note: For all of these operating systems, the regional setting must be set to English)
- Programs: Any program that enables you to open PDF files (for example, Adobe Reader)
- Processor: > 2 GHz (> 3 GHz recommended)
- Working memory (RAM): 8 GB (12 GB recommended)
- Hard disk space: 500 GB
- Display Resolution 1280 x 768 or higher

Requirements for Macintosh systems

- Operating System: Macintosh OS Monterey (v12.6) and BigSur (v11.7)
- Any program that enables you to open PDF files (for example, Adobe Reader)
- Processor: Apple M1 chip with 8-core CPU and 8-core GPU
- Working memory (RAM): 8 GB (16 GB unified memory recommended)
- Hard disk space: 40 GB (For analysis of large datasets, more space is required)
- Display resolution 1280 x 768 or higher

In an effort to improve the performance and overall user experience with CytoGenomics, as of version 4.0.3, CytoGenomics is no longer supported on 32-bit machines.

Points to note regarding results generated in v5.0 & 5.1 & 5.2 & 5.3 in analyses of tiff images

- With the new gridding algorithm for feature extraction (FE) that was introduced in CytoGenomics 5.0, there may be some minor differences in some QC metric values and aberration calls when compared to earlier versions of CytoGenomics.
To recreate the gridding algorithm used in CytoGenomics 4.0.x, create a new protocol in Feature Extraction for CytoGenomics 5.3.x with 'Use Enhanced Gridding' setting set to False. See the Feature Extraction for CytoGenomics 5.3.x User Guide for instructions.
- In previous versions of FE i.e. in v4.0.x, the Background Peak Shifting algorithm was only applied to Agilent arrays, and was not applied to non-Agilent arrays. This discrepancy was fixed in FE for CytoGenomics 5.0.2. This fix might result in differences in the FE output file for non-Agilent arrays when compared to earlier versions of FE for CytoGenomics. These differences in the FE output file could further result in different QC metric results and aberration calls for the sample.
- The "Multisample" view for viewing workflow results was removed from CytoGenomics starting with version 5.0. CytoGenomics users are advised to use the Triage View to triage multiple samples (up to 24 at a time) with no restriction on the designs and analysis methods used among the samples being triaged.
- For CGH+SNP arrays, CytoGenomics 5.0, 5.1, 5.2 and 5.3 report LOH intervals near the centromere differently from previous versions of CytoGenomics. In version 4.0.3, LOH intervals were reported across p-q arm. In subsequent versions, this issue was corrected, resulting in either reporting the LOH interval as ending at the centromere or not reporting the interval at all if it does not cross the threshold.
- For HT microarray multipack formats (16x and 24x), the feature extraction step will fail if any of the arrays on the slide are empty. Any arrays on the slide that do not contain a sample must be loaded with 1× hybridization buffer. The 4 arrays in the corners of the slide must contain a sample.

Migrating data from the previous version of CytoGenomics

You can migrate your data from version 3.0 or 4.0 to version 5.3.x using the new Migration Utility application. At the completion of installation of CytoGenomics v5.3.x, you are automatically prompted to launch the Migration Utility application, but you can choose to perform the migration at a later time. Please be aware, however, that if you choose to migrate data at a later time, all processed samples in v5.3.x will be lost and have to be reanalyzed again. The migration process copies the data from the previous version of the database into the new database structure. **It is highly recommended that you perform data migration from version 3.0 or 4.0 to 5.3.x immediately upon completion of installation of CytoGenomics v5.3.x**

Migration to v5.3.x is supported from v3.0.x and v4.0.x. The process for migrating your data is described below.

Instructions for migrating from v3.0.x or v4.0.x (if not performed immediately after installation of v5.3.x):

- Launch the 'MigrationUtility.exe' application from the client installation directory.
- Before proceeding with the migration, read the prerequisites on the login screen carefully.
- Login with the installed user.
Note: Installed user needs to have an enabled account with the administrator privileges on the old server to migrate the data.
- Enter the details for the old server.
- Click the "Start Migration" button.
- Confirm pre-requisites have been met to proceed with migration.

Migration from versions prior to v3.0:

- First, upgrade the previous version (v1.0, 1.5, 2.0, 2.5, 2.7, or 2.9) to version 3.0 or 4.0 using CytoGenomics 3.0 installer or CytoGenomics 4.0 installer. Agilent Informatics Support team can provide that CytoGenomics installer upon request.
- Then, follow the steps specified in above section, *Instructions for migrating from v3.0.x or v4.0.x*.

Upgrade from CytoGenomics 5.0.x or 5.1.x or 5.2.x to CytoGenomics 5.3.x using Windows CytoGenomics installer:

If you are using CytoGenomics 5.0.x or 5.1.x or 5.2.x and want to upgrade to CytoGenomics 5.3.x, you need to upgrade the CytoGenomics client as well as server application.

- Download Agilent CytoGenomics 5.3.x from the Agilent website and check the system requirements.
- Double-click the Agilent CytoGenomics 5.3.x application file that you downloaded from Agilent. The InstallAnywhere dialog box opens, then the installation wizard opens to the Introduction screen.
- Click Next.
- Click OK in the message box that notifies you to uninstall the client. The uninstaller for CytoGenomics 5.0.x or 5.1.x or 5.2.x launches.
- Click Next in the uninstaller.
- Choose "Uninstall Specific Features" and click Next.
- Select 'Client' and click Uninstall.
- Click Yes in the confirmation message box to confirm that you want to uninstall the CytoGenomics 5.0.x or 5.1.x or 5.2.x client. At the completion of the uninstallation, the installation wizard for CytoGenomics 5.3.x reopens.
- In the installation wizard, select 'Both Client and Server' on the Choose Install Set screen and click Next.
- Continue the installation wizard to finish the client installation for v5.3.x

Upgrade from Cloud on Windows (An internet connection is required):

Note: Cloud update to CytoGenomics 5.3.0 is only supported from CytoGenomics 5.2.1.4 on Windows OS only. Cloud upgrade on Mac OS is not supported. Also, make sure that the 'Check for software update at application startup' check box is selected on the Configure settings > Settings > Local Settings screen. If CytoGenomics 5.2.1.4 is installed on a machine that is behind a proxy server, make sure required proxy credentials are provided on the Admin > Partners > Set Proxy Settings screen.

To automatically download these software updates:

1. Launch CytoGenomics 5.2.1.4 and make sure you have an internet connection. The Updates Available pop-up notification opens.
2. Mark the 'Software update' check box in the notification. The Download button becomes available.
3. Click Download. The Confirm message box opens asking you to confirm that you want to start downloading software update files.
4. Click OK to start the download process. A Progress Status bar is shown. The application is unavailable for use during the software update download.
5. Once the download is complete, the 'Download Successful and CytoGenomics will Restart' message opens. Application restarts automatically, opening to the Login screen.
6. Login to CytoGenomics 5.3 with appropriate username and password.
7. Upon logging in, a notification opens with the message 'Agilent CytoGenomics Client and Server application upgraded successfully'. Click OK to launch CytoGenomics 5.3.

Upgrade from CytoGenomics 5.2.x to CytoGenomics 5.3.x using Macintosh CytoGenomics installer:

If you are using CytoGenomics version 5.2.x on MacOS BigSur (v11.x) and want to upgrade to CytoGenomics 5.3.x, you need to upgrade the CytoGenomics client and server features. The CytoGenomics v5.3 installer is able to detect that the v5.2 server is already installed and in the installation wizard you need to select 'Both Client and Server' on the Choose Install Set screen and click Next.

For all other upgrade cases, users is requested to contact tech support.

Default and preloaded content

Agilent recommends logging in to your SureDesign account at <https://earray.chem.agilent.com/suredesign/index.htm> to download the most up-to-date catalog CGH and CGH+SNP designs

Frequently used external tracks such as CNV_DGV, Multi-Transcripts for Genes, OMIM, etc. are provided upon installation.

Agilent recommended Feature Extraction protocols for CGH microarrays (CytoCGH_0500_1x_Nov17, CytoCGH_0500_2x_Nov17, CytoCGH_0500_4x_Nov17 and CytoCGH_0500_8x_Nov17, CytoCGH_0500_SingleCell_Nov17, CytoCGH_0530_16x_Oct22, CytoCGH_0530_24x_Oct22) and QC metric sets for CGH microarrays (CytoCGH_QCMT_1x_Nov17, CytoCGH_QCMT_2x_Nov17, CytoCGH_QCMT_4x_Nov17, CytoCGH_QCMT_8x_Nov17, CytoCGH_QCMT_SingleCell_Nov17, CytoCGH_QCMT_16x_Oct22, CytoCGH_QCMT_24x_Oct22) are provided as default.

Agilent recommended CGH analysis settings (Default Analysis Method - CGH v2); CGH+SNP analysis settings (Default Analysis Method – CGH + SNP v2); Mosaic analysis settings (Mosaic Analysis Method) and Single cell analysis settings (Single Cell Small Aberration Analysis Method, Single Cell Long Low Aberration Analysis Method, and Single Cell Recommended Analysis method) are provided as default.

Agilent Feature Extraction for CytoGenomics

Agilent Feature Extraction (FE) for CytoGenomics is a component within CytoGenomics. FE performs TIFF image processing, background subtraction and normalization of microarray data. You have the option of using this component as part of a CytoGenomics workflow or as a standalone tool.

Issues Fixed in CytoGenomics 5.3

- In Triage View, the Add Call command does not work when the Gene View, including SNP pane, is not displayed. (TT ID #296451)
- When opening multiple samples in Triage View, the order of the sample tabs differs from the order in which the records were selected on the Sample Review screen. (TT ID #296543)
- In Triage View, when the start and/or stop positions of an aberration are edited, the Cytoband location listed in the interval table is not updated accordingly. (TT ID #296589)
- In Triage View, the intermediate Cyto Report will not open if the sample does not have any aberration calls. (TT ID #296591)
- In the ISCN Nomenclature report, the ISCN interval values are sometimes missing or out of order after a call is assigned a classification. (TT ID #296709)
- On Macintosh systems, logging in to CytoGenomics as a local user erroneously fails. (TT ID #296369)

- In some cases, when the CGH & SNP Plots window is accessed from Triage View, the Add Peak dialog box fails to populate the Log Ratio drop-down list. (TT ID #296386)
- In the QC Metrics window, when graphs are plotted in "Frequency Distribution (Pie Chart)" view, the Export Graphs command may fail to display the graph correctly in the generated PDF. (TT ID #296565)
- The Search Records tool is not working properly when searching for records by Classification. (TT ID #296604)
- When generating a Cyto Report with a custom template in which the Chromosome View is set to show 4 images per report page, the PDF report is missing the Chromosome View images. (TT ID #296278)
- When generating a Cyto Report with a custom template in which optional sample attributes are selected for display, the generated PDF may be damaged if those sample attributes are unassigned for the sample. (TT ID #296860)
- On the Sample Review screen, when records are sorted by the Array Set column, the application temporarily freezes. (TT ID #296920)
- In some cases, when an Auto-Processing workflow is in-progress, the Sample Review screen may display incorrect sample attribute information. (TT ID #296932)
- In the Triage View Interval Table, when attempting to view the genomic location of a CNV call in the DGV external database, the DGV link may open to the hg19 genome build even if the sample was analyzed with a hg38 design. (TT ID #296766)
- In the Triage View Gene View, the gene names are not clearly visible when the viewing preferences are set to apply a log ratio range of 4 or higher. (TT ID #296738)
- In Triage View, when an aberration track containing >60,000 intervals is displayed in Tracks View, the application response time slows. (CYTO-1712)
- In the viewing preferences, the Gene name font size option does not work as expected. (TT ID #297007)
- In Triage View, the moving average plot line is not always clearly visible behind the scatter plot data. (CYTO-1348)
- When a custom track gets renamed, the name may sometimes revert back to the original. (CYTO-1367)
- In Triage View, when the Interval Table is filtered to only display aberrations of a certain type, the Suppress/Unsuppress Intervals tool is not applied to the filtered-out intervals. (TT ID #296601)
- After signing off a sample in Triage View, the software does not open a prompt for accessing the output folder containing the reports. (CYTO-1439)
- The Search Records tool is not working properly when searching records for intervals on the X or Y chromosome. (CYTO-1479)
- The Single Cell Triage View is slow to refresh after changes are made to the view preferences. (TT ID #279272)
- When trying to use the Filter Aberrations tool for an aberration track displayed in the Triage View Tracks View, the tool displays an error message if the same attribute is added to the filter conditions more than once. (TT ID #282443)
- When a design filter is not applied to an analysis workflow, the signal intensities for non-unique probes are not included in the Signal Intensity pane when the sample is first opened in Triage View. (CYTO-1778)
- Updated Apache Commons Text library v1.10 to address reported vulnerability CVE-2022-42889. (CYTO-1774)
- Cytoband images have formatting and scaling issues in PDF Cyto Report. (CYTODX-282 and CYTODX-409)
- The ISCN report can sometimes fail to indicate the presence of aberrations on non-autosomal chromosomes. (CYTODX-283)
- In Triage View, the tooltips for the SNP Probe data shows an incorrect value for the log ratio. (CYTO-1779)

- In Triage View, when the Configure Scales settings have been customized in the View Settings, those custom changes are removed if the Layout Settings are reset to the default layout. (CYTODX-361)
- In Triage View, when multiple CGH+SNP samples are open and then additional CGH+SNP samples are opened from within Triage View, the Genotype column in the SNP Probes table does not show the values for the newly added records. (CYTO-1675)
- If a custom record attribute is created and is only made editable after running an analysis in which that record attribute was assigned, the value for that attribute fails to be displayed in the Sample Review screen. (CYTO-1583)
- When a design includes replicate SNP probes, the software may fail to detect all LOH intervals in the sample. (CYTO-1819)
- For hg19 samples, Triage View does not offer a link for accessing the Decipher browser. (CYTO-1800)
- On several of the Configure Settings screens (Classification, Notes, and Customized Links), moving the 'Disable' column in the table causes the software to freeze. (CYTODX-499)
- Auto Processing fails for all workflows on the server if any of the Tiff Image Input Folders defined on the client systems is found to not exist. (CYTODX-505)
- In the Cyto Report, the image of the Chromosome View may differ slightly from than displayed in the Triage View. (CYTODX-567)

Known Issues for CytoGenomics 5.3

- Order of searched records which are in running or waiting state is not the same as listed in the Sample Review tab (CYTO-1705)
- Application installation log on Macintosh systems reports, 'Installation completed with some warning'; although these can be ignored. (CYTO-1750)
- Sometimes on Macintosh systems, CytoGenomics hangs/crashes while generating Cyto Report Gene View images if the 'Load Track' option is selected in the report template and the track has a large number of annotations. (TT ID #292709)
- In Triage View, tooltips are not displayed completely in the Gene View and Track View when those views are in floating mode and panel size is reduced. (TT ID #296079)
- On Macintosh systems, sometimes downloading a design from SureDesign fails as the downloaded zip file cannot be read by application. (CYTO-1798)
- In Triage View, double-clicking the Chromosome View title bar causes the Genome View to become a floating window rather than converting the Chromosome View to a floating window. (CYTO-1790)
- In rare cases, while installing CytoGenomics the installer may display a message reading "Insert New Media." The installation must be cancelled, and the installer must be closed and restarted. (CYTO-1857)

Known issues for Feature Extraction for CytoGenomics 5.3

- When in grid mode, changing the color scale from "All Channels" to either "Red Channel" or "Green Channel" does not work properly. (TT ID #085513)
- When viewing a microarray image in high fidelity, opening the Scan Image Properties window may cause the image to appear distorted. (TT ID #063425)
- On some Windows PCs, the Microsoft Visual C++ 2008 Redistributable Package may need to be reinstalled if license registration or extraction does not proceed.

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