Release Notes

Agilent CytoGenomics v5.2.1

Agilent CytoGenomics v5.2.1.4

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. With CytoGenomics 5.2 we now 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 5.2

- New layouts for the Triage View data that set the orientation and arrangement of the views while still allowing you to customize and adjust the display
- New Triage View toggle buttons and menus that simplify customization of the display, including undocking views into separate windows and switching between overlaid and stacked data views for triage of multiple samples
- Support for combining aberration tracks from different genome builds using the UCSC LiftOver tool
- Option to allow suppressed calls to be included in dynamic tracks
- New Enhanced Spot Finding algorithm option for feature extraction that helps to more accurately define the center location of the features when using a customized CGH protocol

- New database link for viewing regions of called aberration intervals in the genome browser website DECIPHER, which specializes in tools for interpreting the biological significance of genomic variants in the hg38 genome
- Updated reports that include the ArrayID sample attribute as part of the Analysis Settings information for improved sample traceability
- Option to make Cyto report PDFs editable, which allows for copying text and images from the report and adding comments
- Automatic retention of your selections in the Tracks View so that the same tracks are displayed when Triage View is reopened

Key new features of CytoGenomics v5.2.1

- The CytoGenomics application was updated to use the latest version of Apache's Log4j2 software library in order to take advantage of the enhanced security features that the latest version has to offer. Please note that previous versions of CytoGenomics are not affected by the log4j2 vulnerabilities first reported in December of 2021. By updating CytoGenomics with the latest version of the Log4j2 software library, Agilent is taking a proactive step in safeguarding CytoGenomics users from the possibility of future security threats. Follow these Log4j2 vulnerability reports for additional information on the subject: CVE-2021-44228, CVE-2021-45046, CVE-2021-4104.

Installation Instructions

New Installation

- Refer to the installation guide available at Refer to the installation guide available at http://www.agilent.com/cs/library/usermanuals/public/G1662-90065.pdf

System Requirements for Agilent CytoGenomics

Requirements for Windows systems

- Operating system: 64-bit 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 Catalina (v10.15) or Macintosh OS Mojave (v10.14)
- Any program that enables you to open PDF files (for example, Adobe Reader)
- Processor: 3 GHz Intel Core 2 Duo CPU or better
- Working memory (RAM): 8 GB (12 GB 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 & 5.2.1 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 5.2.x with 'Use Enhanced Gridding' setting set to False. See the Feature Extraction for CytoGenomics 5.2.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 5.2.1 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.

Migrating data from the previous version of CytoGenomics

You can migrate your data from version 3.0 or 4.0 to version 5.2.x using the new Migration Utility application. At the completion of installation of CytoGenomics v5.2.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 newly processed samples in v5.2.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 5.2.x immediately upon completion of installation of CytoGenomics v5.2.x**

Migration to v5.2.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 v5.2.x)

- Launch the 'MigrationUtility.exe' application from the client installation directory.
- Before proceeding with the migration, read the pre-requisites 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 to CytoGenomics 5.2.x using Windows CytoGenomics installer:

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

- Download Agilent CytoGenomics 5.2.x from the Agilent website and check the system requirements.
- Double-click the Agilent CytoGenomics 5.2.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 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 client. At the completion of the uninstallation, the installation wizard for CytoGenomics 5.2.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 v5.2.x

Upgrade from CytoGenomics 5.2.0 to CytoGenomics 5.2.1 using Windows CytoGenomics installer:

If you are using CytoGenomics version 5.2.0 and want to upgrade to CytoGenomics 5.2.1, you only need to upgrade the CytoGenomics client as there are no changes to the server software. When initiating installation of v5.2.1, the uninstaller for the CytoGenomics v5.2.0 client will automatically open as part of the installation process for v5.2.1. The CytoGenomics v5.2.1 installer is able to detect that the latest server is already installed and will notify you that only the CytoGenomics v5.2.1 client will be installed.

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

Versions of CytoGenomics prior to version 5.2.x are not compatible with the macOS Catalina operating system. You must upgrade CytoGenomics to v5.2.x in the current macOS before upgrading your machine to macOS Catalina.

The auto-uninstaller is not supported on Macintosh systems, which means you will need to first uninstall the CytoGenomics 5.0.x or 5.1.x client before launching the CytoGenomics 5.2.x application file. The instructions for this process are below.

- Launch the uninstaller for Agilent CytoGenomics 5.0.x or 5.1.x Enter the credentials for the administrator.
- Click Next, then click Next again.
- 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 client. At the completion of the uninstallation, click Done to close the uninstaller.
- Download Agilent CytoGenomics 5.2.x from the Agilent website and check the system requirements.
- Double-click the Agilent CytoGenomics 5.2.x application file that you downloaded from Agilent. The InstallAnywhere dialog box opens, then the installation wizard opens to the Introduction screen.
- Click Next.
- Select 'Both Client and Server' and proceed with the installation of v5.2.x

Upgrade from CytoGenomics 5.2.0 to CytoGenomics 5.2.1 using Macintosh CytoGenomics installer:

If you are using CytoGenomics version 5.2.0 and want to upgrade to CytoGenomics 5.2.1, you only need to upgrade the CytoGenomics client as there are no changes to the server software. The CytoGenomics v5.2.1 installer is able to detect that the latest server is already installed and will notify you that only the CytoGenomics v5.2.1 client will be installed.

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) and QC metric sets for CGH microarrays (CytoCGH_QCMT_1x_Nov17, CytoCGH_QCMT_2x_Nov17, CytoCGH_QCMT_4x_Nov17 and CytoCGH_QCMT_8x_Nov17,CytoCGH_QCMT_SingleCell_Nov17) 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 5.2.0

- For sample data that were migrated from a previous version of CytoGenomics, the FE QC reports do not open if the output folder name used an attribute combination. (TT ID #295806)
- When users specify a location to copy all reports, not all signed off reports are copied to that location. (TT ID #292584)
- Single Cell Cyto report does not include chromosomes 17 to 21 in the Genome View image. (TT ID #293522)
- In some cases, when the regional format is not set to English (United States), the Auto-Processing logs do not always display properly in the application. (TT ID #293781)
- Unable to open intermediate or signed off Cyto report PDF when attribute values contained special characters. (TT ID #294368)
- In dynamic tracks based on a classification, errors occur when the classification name is a component within a second classification name. (TT ID #295411)
- CytoGenomics is unable to import designs of the same AMADID generated on same date having different genome builds. (TT ID #294803)
- When using a custom Feature Extraction QC metric set and protocol, the StdDevLR metric is not evaluated according to the range set in the custom metric set. (TT ID #295744)
- Copying console log data at path mentioned in "Copy all Report & Files" (Enhancement) (TT ID #295945)
- Classification column text gets grayed out in the Triage View on sign-off or check-in, making it difficult to read. (Enhancement) (TT ID #290226)

Issues Fixed in CytoGenomics 5.2.1

- For some CGH+SNP custom designs that do not contain SNP probes on all of the chromosomes on which CGH probes are present, CytoGenomics may incorrectly call LOH intervals on chromosomes that do not include SNP data. (TT ID #296590)

Known Issues for CytoGenomics 5.2

- Single Cell Triage View can take a long time to refresh after changes are made to the view preferences. (TT ID #279272)
- In Triage View, filtering the intervals of a track displayed in the Gene View does not work as expected when filter conditions include two of the same attributes. (TT ID #282443)
- Sometimes on Macintosh systems, CytoGenomics hangs/crashes while generating Cyto report Gene View images when 'Load Track' option is selected in the report template and the track has large number of annotations. (TT ID #292709)
- In Triage View, tooltips are not displayed completely in the the Gene View and Track View when those views are in floating mode and panel size is reduced. (TT ID #296079)

Known issues for Feature Extraction for CytoGenomics 5.2

- Changing the color scale does not work while in grid mode. If the user attempts to change color scale from "All Channels" to either "Red Channel" or "Green Channel," the color scale does change. (TT ID #2309)
- Viewing the scan properties can cause the image to appear distorted. Minimizing followed by reopening the image is needed to correct the issue. (TT ID #1959)
- For some Windows PCs, you may need to install the Microsoft Visual C++ 2008 Redistributable Package if license registration or extraction does not proceed.