

Release Notes

Agilent CytoGenomics v5.4

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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 5.4 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 5.4

- Updated software licensing terms to associate each software license with a specific software version.
- Support for microarrays that use a loop design analysis methodology.
- Option to receive alerts on CytoGenomics news and updates.
- New QC metric AOH/cnLOH that measures the percentage of the entire genome (based on genome build) that contains an LOH interval.
- Ability to import design files directly from connected SureDesign account.
- Fast and secured communication between the LDAP server and client machine during user authentication.
- Ability to customize the default size of the flanking regions when displaying an aberration interval in the Gene View of the Triage View window.
- Option to suppress or un-suppress aberration intervals based on inclusion in a dynamic track.
- Track source information for all tracks populated from external sources.

Installation Instructions

New Installation

- Refer to the installation guide available at <http://www.agilent.com/cs/library/usermanuals/public/G1662-90073.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 2022
(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 Ventura (v13.5) or Sonoma (v14.4.1)
- 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 & 5.4 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 5.4.x with 'Use Enhanced Gridding' setting set to False. See the Feature Extraction for CytoGenomics 5.4.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 for the samples being triaged.
- For CGH+SNP arrays, CytoGenomics 5.0, 5.1, 5.2, 5.3 and 5.4 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 5.4.x using the Migration Utility application. At the completion of installation of CytoGenomics v5.4.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 v5.4.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 5.4.x immediately upon completion of installation of CytoGenomics v5.4.x**

Migration to v5.4.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 v5.4.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 or 5.3.x to CytoGenomics 5.4.x using Windows CytoGenomics installer:

If you are using CytoGenomics 5.0.x or 5.1.x or 5.2.x or 5.3.x and want to upgrade to CytoGenomics 5.4.x, you need to upgrade the CytoGenomics client as well as server application.

- Download Agilent CytoGenomics 5.4.x from the Agilent website and check the system requirements.
- Double-click the Agilent CytoGenomics 5.4.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 or 5.3.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 or 5.3.x client. At the completion of the uninstallation, the installation wizard for CytoGenomics 5.4.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 v5.4.x.

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

Note: Cloud upgrade to v5.4 is not supported from the CytoGenomics v5.3.

Upgrade from CytoGenomics 5.3.x to CytoGenomics 5.4.x using Macintosh CytoGenomics installer:

If you are using CytoGenomics version 5.3 on MacOS Ventura (v13.5) and want to upgrade to CytoGenomics 5.4.x, you need to upgrade the CytoGenomics client and server features. The CytoGenomics v5.4 installer is able to detect that the v5.3 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, contact Agilent Technical 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 5.4

- In Triage View, when data from the Gene View is sent to the UCSC Genome Browser, if the region includes overlapping intervals, only the interval coordinates of parent interval are exported. (CYTO-1645)
- In Triage View, for aberrations with multiple overlapping probes in the region, the table on the CGH Probes tab may not highlight all interval region probes. (CYTO-2016)
- On Macintosh systems, sometimes design file download from Sure Design fails with unknown error. (CYTO-1798)
- Application cannot open reports folders that include special characters in the folder name. (CYTO-2111)
- In Triage View, a standard note cannot be added to a sample record if that record previously had a standard note deleted. (CYTO-2020)
- In Triage View, the Genome View cannot render aberrations of very small sizes when in horizontal display mode. (CYTO-2100)
- When searching for records from Sample Review screen, the order of searched records which are in running or waiting status differs from the order of those records as listed in the table on the Sample Review tab. (CYTO-1705)

Known Issues for CytoGenomics 5.4

- On Macintosh systems, the application installation log sometimes reports 'Installation completed with some warning' even though the installation was successful. (CYTO-1750)
- On Macintosh systems, the application may freeze 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)
- 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)
- During CytoGenomics installation, in some rare cases, 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)
- On systems in which CytoGenomics was installed as an upgrade or multiple versions of CytoGenomics coexist, in some cases, feature extraction fails due to the presence of two ODBC installations. (CYTO-2137)
- When over 2100 samples are submitted for analysis, some samples may get stuck in Running status. (CYTO-1596)
- Sometimes installation of CytoGenomics on Windows PC fails with error `java.lang.StackOverflowError`. (CYTO-1842)

PR7001-2680