Agilent CytoGenomics 2.9

Product Overview Guide

For Research Use Only. Not for use in diagnostic procedures.

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What is Agilent CytoGenomics?

Cytogenetic research labs are increasingly turning to array CGH to improve detection of copy number changes and increase sample throughput. Alongside Agilent’s gold standard CGH+SNP and CGH microarrays, Agilent CytoGenomics software completes Agilent’s array-based cytogenetic research solution. Agilent CytoGenomics provides a statistically and visually powerful tool to streamline the day-to-day cytogenetic sample analysis research workflow. It offers full support for efficient analysis of cytogenetic samples and easy report generation, based on information from both external databases and an internal database. Key automation features enable a seamless flow through the experimental process, starting with full automation of data upload and analysis, and ending with customized report generation.

With Agilent CytoGenomics, cytogenetic research labs can analyze a normal, constitutional sample in less than five minutes. This increases efficiency and throughput, while enabling cytogenetic researchers to better detect copy number and copy-neutral aberrations across the genome.

Agilent CytoGenomics supports CGH analysis for both constitutional and tumor samples from either fresh or FFPE sample sources. The SNP-based LOH (Loss or Lack of Heterozygosity) and UPD (Uniparental Disomy) analysis is supported for both constitutional and liquid tumor samples from fresh sample sources only.

Agilent CytoGenomics provides cytogenetic laboratories security data access through three types of user roles: Technician, Scientist, and Administrator. Each of the three user roles has unique permissions to access a selected set of features and data in the software. (See Table 1.)

An Agilent CytoGenomics workflow (Figure 1) automatically feature extracts images generated by a microarray scanner. The extracted data is then filtered and analyzed, and aberrant intervals are identified. You can edit, suppress, add, or classify identified aberration calls during sample triage. A set of reports is generated at the end of the workflow, including a customizable cyto report. Audit trails of changes are available to display or export.
Agilent CytoGenomics Workflow — from image to result

Question about cytogenetics sample

Auto-Processing Workflow

Manual Workflow

Scanned images in auto-processing workflow input folder

Images or extracted files are selected

Extract “features” from images (Feature Extraction in background)

Filter data that does not pass standards (Metric Evaluation)

Analyze extracted data for aberrations (Analysis)

Agilent CytoGenomics Workflow

Results ready for display & review

Figure 1 Agilent CytoGenomics Workflow — from image to result
Getting Help

To get help within Agilent CytoGenomics 2.9

Agilent CytoGenomics 2.9 has an online help system that provides detailed instructions on using the software and descriptions of the user interface. To open the help, click Help near the top right corner of the program window.

Help videos are also available from within the Agilent CytoGenomics program. These short videos give you instructions for doing basic tasks within the program. You can access the videos from the CytoGenomics Home screen.

To contact Agilent Technical Support

Technical support is available by phone and/or e-mail.

<table>
<thead>
<tr>
<th>Resource</th>
<th>To find technical support contact information</th>
</tr>
</thead>
</table>
| Contact Agilent Technical Support by telephone or e-mail message (United States and Canada) | Telephone: (800-227-9770)  
E-mail message: informatics_support@agilent.com |
| Contact Agilent Technical Support by telephone or e-mail message (for your country) | 1 Go to http://www.agilent.com/genomics/contactus.  
2 Under Worldwide Sales, Support and Distributors click to select a country. Complete e-mail message and telephone contact information for your country is displayed. |

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Key Features

This section provides an overview of the features and capabilities available in Agilent CytoGenomics 2.9. The “tabs” at the top of the program window provide access to related tasks and commands. Users see only the tabs for which they have access, according to their assigned user role. (See “User Roles and Capabilities” on page 8.)

The Home tab - getting started with CytoGenomics

Capabilities within the Home tab include:
• Entering your user license for the software
• Watching help videos for CytoGenomics
• Accessing the full set of Auto-Processing functions
• Opening links to other Agilent Genomics software programs

The Analysis Workflow tab – selecting samples and running analyses

Capabilities within the Analysis Workflow tab include:
• Running manual workflows
• Adding sample information
• Importing design files
• Viewing array images by launching the Feature Extraction program
The Sample Review tab – reviewing analyses

Capabilities within the Sample Review tab include:

- Monitoring workflow jobs
- Displaying Cyto reports and aberration results
- Triaging samples:
  - Check in/out samples
  - Add sample and interval notes
  - Modify, add, or suppress calls
  - Add/change intervals classifications
  - Review SNP fit and change copy number peak assignments
  - Search database for similar classified intervals
  - Sign off samples and generate sign off reports
- Reanalyzing samples
- Viewing results from multiple samples side-by-side using Multisample View
- Transferring results to Cartagenia BENCH

The Configure Settings tab – setting up system defaults and analysis methods

Capabilities within the Configure Settings tab include:

- Setting up analysis method parameters
- Creating customized Cyto report templates
- Configuring system preferences, including
  - Dynamic and static tracks
  - Default view preferences
  - Default input/output folders
  - Default genome build
  - Auto-Processing workflow settings
  - Standard notes and classifications
  - Cartagenia BENCH data transfer settings
- Entering your account information for Cartagenia BENCH and Agilent eArray
The Supporting Files tab – managing samples, designs, gene lists, tracks, and other supporting files

Capabilities within the Supporting Files tab include:
• Viewing sample attributes and data
• Downloading new builds of a design from eArray
• Exporting sample attribute files
• Importing design files
• Importing genotype reference files
• Importing and exporting probe ID lists
• Importing and exporting tracks
• Opening the workflow log
• Displaying list of samples in the database, organized by design/build

The Admin tab – managing users and database

Capabilities within the Admin tab include:
• Adding new users and assign roles
• Changing roles for existing users
• Enabling/disabling user access to the program
• Displaying or changing database connection parameters for the client computer
• Backing up the CytoGenomics database
**User Roles and Capabilities**

The following table lists the capabilities allowed for the three different user roles within Agilent CytoGenomics 2.9.

**Table 1  User roles and capabilities**

<table>
<thead>
<tr>
<th>Role</th>
<th>Tasks and capabilities</th>
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</thead>
<tbody>
<tr>
<td>Technician</td>
<td>• Run manual or auto-processing workflows</td>
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<tr>
<td></td>
<td>• Add sample information</td>
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<tr>
<td></td>
<td>• Monitor workflow jobs</td>
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<tr>
<td></td>
<td>• Display reports and aberration results</td>
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<td></td>
<td>• Triage samples</td>
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<tr>
<td></td>
<td>• Check in/out samples</td>
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<td></td>
<td>• Add notes</td>
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<tr>
<td></td>
<td>• Add or suppress calls</td>
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<tr>
<td></td>
<td>• Add/change interval classifications</td>
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<tr>
<td></td>
<td>• Review and change SNP peak assignment</td>
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<td></td>
<td>• Transfer results to Cartagenia BENCH</td>
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<tr>
<td></td>
<td>• Display auto-processing logs</td>
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<tr>
<td></td>
<td>(Technicians cannot sign off samples.)</td>
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<tr>
<td>Scientist</td>
<td>Technician tasks, plus:</td>
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<tr>
<td></td>
<td>• Configure system preferences, including</td>
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<tr>
<td></td>
<td>• Default input/output folders</td>
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<tr>
<td></td>
<td>• Auto-processing workflow settings</td>
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<tr>
<td></td>
<td>• Default view preferences</td>
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<tr>
<td></td>
<td>• Default genome build</td>
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<tr>
<td></td>
<td>• Standard notes, classifications, and queries</td>
</tr>
<tr>
<td></td>
<td>• Dynamic and static tracks</td>
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<tr>
<td></td>
<td>• Cartagenia BENCH data transfer settings</td>
</tr>
<tr>
<td></td>
<td>• Set analysis and workflow settings</td>
</tr>
<tr>
<td></td>
<td>• Create standard notes, classifications, and queries</td>
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<td></td>
<td>• Create customized cyto report templates</td>
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<td></td>
<td>• Manage samples</td>
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<td></td>
<td>• Evaluate and chart QC trends</td>
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<tr>
<td></td>
<td>• Sign off results</td>
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<tr>
<td>Administrator</td>
<td>Complete system access, including all Technician and Scientist tasks, plus</td>
</tr>
<tr>
<td></td>
<td>• Add users and roles</td>
</tr>
<tr>
<td></td>
<td>• Change database connection settings for client systems</td>
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</tbody>
</table>
In this book

This book provides an overview of Agilent CytoGenomics. It shows the overall design of the program and how different users can work with it to fulfill their roles in the laboratory.