

Chromosome Analysis Suite (ChAS)

Software v4.6

Pub. No. MAN1002088 Rev. A

New features and improvements in ChAS v4.6

- Mosaic LOH segmentation.
- Ability to filter segments based on mosaic percentage.
- ISCN 2024 Nomenclature update.
- Annotation addition of the MANE track.
- Ability to perform a Mendelian Error Check between a proband and parents run on different CytoScan™ arrays.
- Ability to hide Chromosome X in the Karyoview Export.
- Ability to select/unselect all chp files in a single action.
- Ability to export the Selected Chromosome View as a PNG image.
- Inclusion of column headers when using the clipboard function in tables.
- Ability to export Microarray Nomenclature for a sample with no segments.
- Cybersecurity updates:
 - ChAS database password storage in Windows™ Credential Manager.
 - Administrator password change after installation.
 - ChAS database tools sign out after 30 minutes of inactivity.
 - Self-signed certificate on installation.
 - https communication with ChAS DB and external DB.
 - Updated backend components to recent versions.
- Standardized Log2 Ratio in Chromosome Summary Data.

Changes and updates

- ChAS v4.6 does not support upgrades from ChAS v4.5.1 (or earlier). Before installing ChAS v4.6, you need to use the Windows™ **Add/Remove Program** feature to remove any previous version of ChAS. After the uninstall is complete, double-click the ChAS v4.6 installer, then follow the installation prompts.
- When uninstalling ChAS v4.5.1 (or earlier), the installer automatically archives all previous ChAS library files into the following folder:
C:\Affymetrix\ChAS\Library\Archived_ChAS_Lib_Files
- In ChAS 4.6, updated library file packages are available for the CytoScan™ HD Array, CytoScan™ HD Accel Array, CytoScan™ 750K Array, and CytoScan™ 750K Accel Array. These updated library files need to be downloaded to use the new features in v4.6.
- ChASCellUploader tool included to provide automatic upload of CEL files from the scanner workstation to network drive.
- When using the ChASCellUploader tool for Oncoscan and Oncoscan_CNV arrays, the CEL file naming convention follows the same rule as the Auto CEL file analysis. For more information, see the “Automatic CEL file analysis” appendix in the *Chromosome Analysis Suite User Guide* (Pub. No. [MAN0027798](#)).
- To use Franklin by QIAGEN™ for advanced interpretation analysis, contact your local sales representative for information about ChAS AIR tokens for Franklin.
- The quarterly updated NAGA files (NetAffxGenomicAnnotations.Homo_sapiens.hg19.na20260601 and NetAffxGenomicAnnotations.Homo_sapiens.hg38.na20260601) are available for downloading from within ChAS and the product website.
- ChAS 4.6 creates its own self-signed certificate on each installation. To set up and use a remote ChAS DB connection, contact Technical Support for instructions.
- Any ChAS DB backup created before ChAS 4.6 needs to be restored and a backup created in ChAS 4.6 (**Database Tools ▶ Database Maintenance**) before remapping or merging. This is due to updating postgres to 18.3 and to ensure compatibility.

Best practices for ChAS database password change

- Ensure that you remember the new password after changing the ChAS DB administrator password.
- In addition, create a second administrator user as a backup to the default administrator user.
- Backup the ChAS database regularly, especially after you modified the database. If the password is forgotten, locate the last database backup.

Change the ChAS DB administrator password

1. Uninstall ChAS Dx.

2. Reinstall ChAS Dx.

The ChAS DB administrator password is restored to the default and can now be changed.

3. Restore the latest database backup.

Note: Any data that was not backed up is not restored. You need to publish that data again. It is highly recommended to backup the database after data are published.

Software requirements

- Windows™ 11 Professional 64-bit operating system.
- Windows™ Server 2022, or Windows™ Server 2025 standard 64-bit operating system.
- Microsoft Edge™ browser.
- Administrative privileges are required to install ChAS Dx.
- Adobe™ Acrobat Reader™ (or an equivalent PDF reader) must be installed on the workstation to view the help file and to save graphs/tables as PDF files.
- Microsoft™ Word to save graphs/tables as DOCX files.

System properties	Recommended system requirements	Minimum system requirements
Processor	3 GHz (or greater) Pentium® Quad Core Processor	3 GHz (or greater) Pentium® Dual Core Processor
64-bit Windows™ operating system and web browser	Windows™ 11 Internet Explorer™ 11.0 browser (or later) or Microsoft Edge™ browser	Windows™ 11 Internet Explorer™ 11.0 browser (or later) or Microsoft Edge™ browser
Available disk space	250 GB HD + data storage	150 GB HD + data storage
Free disk space required at installation	>5 GB	>5 GB
RAM	32 GB	16 GB

Library file packages

Table 1 Available library file packages.

Array	hg19	hg38
CytoScan™ HD Array	CytoScanHD_Array_Analysis_Files_hg19_NA33.r11.zip	CytoScanHD_Array_Analysis_Files_hg38_NA36.r8.zip
CytoScan™ HD Accel Array	CytoScanHD_Accel_Analysis_Files_hg19_NA33.r2.zip	CytoScanHD_Accel_Analysis_Files_hg38_NA36.r2.zip
CytoScan™ 750K Array	CytoScan750K_Array_Analysis_Files_hg19_NA33.r11.zip	CytoScan750K_Array_Analysis_Files_hg38_NA36.r8.zip
CytoScan™ 750K Accel Array	CytoScan750K_Accel_Array_Analysis_Files_hg19_NA33.r2.zip	CytoScan750K_Accel_Array_Analysis_Files_hg38_NA36.r2.zip
CytoScan™ Optima Array	CytoScanOptima_Array_Analysis_Files_hg_19_NA33.r10.zip	CytoScanOptima_Array_Analysis_Files_hg_38_NA36.r7.zip
CytoScan™ XON Array	CytoScan_XON_Array_Analysis_files_hg19_NA33.r8-Part1.zip CytoScan_XON_Array_Analysis_files_hg19_NA33.r8-Part2.zip	CytoScan_XON_Array_Analysis_Files_hg38_NA36.r8-Part1.zip CytoScan_XON_Array_Analysis_Files_hg38_NA36.r8-Part2.zip
OncoScan™ CNV Plus Array	OncoScan_Array_Analysis_Files_hg19_NA33.r9.zip	OncoScan_Array_Analysis_Files_hg38_NA36.r7.zip
OncoScan™ CNV Array	OncoScan_CNV_Analysis_Files_hg19_NA33.r7.zip	OncoScan_CNV_Analysis_Files_hg38_NA36.r7.zip
CytoScan™ HT-CMA Array Plate	CytoScan_HTCMA_96_ChAS_Files_hg19.r3.zip	CytoScan_HTCMA_96_ChAS_Files_hg38.r3.zip

Known issues in v4.6

- macas-3484 – Annotation tracks (for example, OMIM Phenotype) may display colored annotations in a different order when collapsed. For accurate viewing, expand the track.
- After installing the ChASCellUploader tool, you may need to reboot the system before the tool will start.
- If you uninstall ChASCellUploader tool, sometimes the desktop shortcut does is not removed. You need to manually delete the desktop shortcut and the ChASCellUploader folder under C:\ProgramData

Known ChAS issues not addressed in v4.6

- When upgrading a user profile from a previous version of ChAS, the link out to the DECIPHER website uses the old url and returns an error message. To correct the problem, you can create a new user profile or contact your FAS to obtain a Default Hyperlinks file to import into ChAS to update the DECIPHER link to their new url. See chapter 20 the *Chromosome Analysis Suite User Guide* (Pub. No. [MAN0027798](#)) for details on importing a Hyperlinks file.
- On a rare occasion, an error can occur if you copy and paste a directory path to a file path name. The alternative is to browse to the path location.
- More than 5 GB of hard drive space is required for installation. The computer must be restarted after clearing space on the hard drive in order for the installer to recognize there is >5GB.
- When publishing data, merging data, or restoring/backing up a database, do not interrupt the process. Let the database process complete, otherwise, the database becomes unusable.
- If you are running the AutoCelAnalysis feature with folders on a server and lose internet connection, the **Retry** option sometimes does not work. To continue on, stop the application, restart ChAS, then relaunch the AutoCelAnalysis.
- When using the AutoCelAnalysis feature, it is a best practice to not use any spaces in the input, output and archive folders.
- When using Automatic Cel Analysis the Input folders cannot be named any of the following array names: Cyto750K, CytoHD, CytoOptima, CytoXON, OncoScan and OncoScanPlus.
- If you run into small icons or small fonts on a monitor display with high DPI, run in compatibility mode for the ChAS.exe properties icon. See “Run ChAS in compatibility mode” on page 5.
- In Task Manager, the ChAS 4.x icon does not display when ChAS is running. Instead it is showing ChAS as “OpenJDK Platform Binary”.
- It can take up to 30 minutes to remap a database containing ~150,000 segments.
- After a secure connection between the ChAS Browser and the ChAS Server is established, the message “This site is not secure” may appear when opening the **DatabaseTools** page. If this message appears, refresh the window, then try again. Contact technical support for information about using a self-signed certificate when communicating with the ChAS DB.

- No message is displayed when exporting BAF to IGV for a CYCHP file (processed before ChAS v3.2) and therefore does not include BAF information.
- In the Analysis Workflow, when exporting OncoScan CNV Plus somatic mutations, the start and stop column values are identical. This is different from the start and stop values in the Variants Table in ChAS in which they are offset by 1 bp.
- The message “A connection attempt failed because the connected part did not properly respond after a period of time, or established connection failed because connected host has failed to respond” may appear when you are connecting to a network drive. If this message appears, check the network connection or contact your IT department for assistance.
- PDF exports are updated so that certain columns that can span multiple pages in tables are truncated into a single page. For example, when exporting the **Genes** column from the Segments Table (for a large segment), its cell can span several pages. The PDF writer truncates the information in that cell into a single page. If you want the full list of contents from that column, it is recommended that you export the Segments Table in 'Paragraph Style'.
- In some cases, .NET framework may not be installed on the system. If it is not, it must be installed manually.
- If creating a custom reference model file (specifically on Spanish and Chinese Windows™ operating systems), the computer must be rebooted to use these custom reference model file.
- The following error message may appear after setting the input path:
“The current type, Affymetrix.AnalysisApplication.Infrastructure.IAnalysisDta, is an interface and cannot be constructed. Are you missing a type mapping? ”. Click **OK** to continue. These paths are saved and the software continues.
- An unexpected error message is displayed if the user selects **This PC** or **Network** to save an exported DOCX/PDF report. Ensure that you save the report in a valid path location.
- If using Microsoft Edge™ browser, a message “Don't let this page create more messages” appears. The alternative for this is to close the Microsoft Edge™ browser and relogin to the **Database Tool** page.
- After installing and launching ChAS, an error message “ChAS database cannot be contacted. Server at “<server name>” did not respond” may appear. Click **OK** to acknowledge this message. To resolve this:
 - a. Close ChAS, then right-click the ChAS desktop icon.
 - b. From the shortcut menu, select **Properties**.
 - c. Click the **Compatibility** tab, then go to the **Privilege Level** section.
 - d. Select the **Run this program as an administrator** checkbox, then click **OK**.
 - e. Double-click the ChAS desktop icon to restart.
- If a database has been opened for an extended period, the error code 500 may appear. If this error code appears, close, then relaunch ChAS.
- When submitting an analysis with special characters in the file name, the analysis fails. Ensure that only valid characters are used in the file name.
- When 2 users publish the same sample to the database, a warning message notifies the second user that the file already exists in the database. The user can choose to cancel or override the existing sample. There is no mechanism to revert to an older stat in this software version. In this case, a method to avoid unintentional reanalysis of the same sample/segment is recommended.
- The Analysis Workflow cannot create a CYCHP file if the file name contains a single quote ('), therefore do not use single (') in ChAS filenames.
- In the **Process Pipeline ▶ Edits ▶ Details ▶ Log** tab, **Materially Modified Time** and **By** values are not cleared out of their respective fields when you revert changes.
- An export of large amounts of data to a TXT file from ChAS may include quantities of characters in a single field that the Microsoft Excel™ application cannot process. This is a limitation of the Excel™ application, but should be noted when exporting annotation columns with very large segments.
- Not all user-editable AED file fields can be edited from within the AED Editor. Some basic values (**Start, Stop, Type**) cannot be edited in the AED Editor table directly. You need to use **View/Edit Annotation Properties...** for editing those fields in the annotation of interest.
- In extremely rare cases, an OMIM gene or disease is not present in the OMIM track of the ChAS Browser. This can be because OMIM data have been updated since NetAffx™ Analysis Center last downloaded data used to create the browser tracks. Always ensure that any interpretations of data with the most current information available from the UCSC Browser or the OMIM database by linking out to these resources from within ChAS. Another possibility can be because the gene or region of interest maps to a special region of the genome that is not able to be displayed in the ChAS Browser. Other instances why regions cannot be displayed in the ChAS Browser are:
 - When several genomic segments are known to be a part of a particular chromosome, but have not been formally assigned to a position on the genome.
 - When 4 alternate haplotypes (for regions on Chromosome 5, 6, and 22) are not part of the reference build of the genome.

Run ChAS in compatibility mode

1. Open the ChAS application.
2. Open Windows™ Task Manager.
3. Right-click the OpenJDK Platform binary application, then select **Properties**.
4. Click the **Compatibility** tab, then click **Change high DPI settings**.
5. Select the checkbox under **High DPI scaling override** and ensure that **Scaling performed by** is set to **System**.
6. Click **OK**, then **OK** again to save the settings.
7. Close, then reopen ChAS.

Limited product warranty

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For descriptions of symbols on product labels or product documents, go to thermofisher.com/symbols-definition.

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Revision	Date	Description
A	15 June 2026	Initial release.

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