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biosystems**

Chromosome Analysis Suite (ChAS) v4.5.1

New features and improvements

ChAS 4.5.1

- Support Auto CEL Analysis for CytoScan750K Accel array.

- ChAS 4.5.1 includes the features listed below from ChAS 4.5

ChAS 4.5:

- Automatic upload of CytoScan and OncoScan data files from scanner to ChAS and Franklin™ by Genoox™

- Support Auto CEL Analysis for CytoScan HD Accel array.

- Enhanced cybersecurity protection with ChAS DB administrator password change.

- Option to display OMIM Gene with a phenotype map key of 3 only.

- New arrow bars in the Detail View for easier scrolling up and downstream in the genome.

Changes and updates

1. ChAS v4.5.1 does not support upgrades from ChAS v4.5 (or earlier). Before installing ChAS v4.5.1, you must use the Windows® **Add/Remove Program** feature to remove any previous version of ChAS. After the uninstall is complete, double-click on the ChAS v4.5.1 installer, then follow the installation prompts.

2. While uninstalling ChAS v4.5 (or earlier), the installer automatically archives all previous ChAS library files into the following folder: C:\Affymetrix\ChAS\Library\Archived_ChAS_Lib_Files

3. ChASCelUploader tool included to provide automatic upload of CEL files from the scanner workstation to network drive.
   Note: If you are using the CytoScan750K Accel array, please contact your local FAS on how to update the configuration file to support this array type.

4. When using the ChASCelUploader tool for Oncoscan and Oncoscan_CNV arrays, the CEL file naming convention follows the same rule as the Auto CEL Analysis. For more information, please refer to the user guide, page 502-503.

5. To use Franklin by Genoox for advanced interpretation analysis, please contact your local sales representative for information on ChAS AIR tokens for Franklin.

6. Auto CEL Analysis now supports CytoScanHD Accel Array in ChAS 4.5 or above.

7. Auto CEL Analysis now supports CytoScan750K Accel Array in ChAS 4.5.1 or above.

8. ChAS DB administrator password needs to be changed when launching from ChAS 4.5 or above first time after installation.

   - **Attention: Changing of the ChAS DB administrator password is new for ChAS 4.5 or above. <u>There isn't a way to reset it if you do not remember the password.</u>**

   - **Best Practices for ChAS Database Password Change**

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- o Please remember the new password after changing the ChAS DB administrator password.
- o In Addition, create another administrator user (as a backup to the admin user)
- o Backup the ChAS database regularly, especially after you modified the database. If the password is forgotten, locate the last database backup.
  - Uninstall ChAS
  - Reinstall ChAS
  - The ChAS DB administrator password will be restored to the default and then can be changed
  - Restore the latest database backup
    (Note: any data that was not backed up will not be restored. You will need to publish that data again. It is highly recommended to backup your database after data is published.)

9. Customizing QC settings option in Analysis Workflow Suite is available on ChAS 4.5.

10. Support to display the OMIM Gene with a map key of 3 only.

11. Add the left-right scroll button in the detail view of ChAS browser.

12. BACs, FISH clones and Old OMIM are removed from the available set of segment table columns in ChAS 4.5 or above.

13. There are no new Library file packages updates for ChAS 4.5. For ChAS 4.5.1, the CytoScan750K Accel library file package is available.
    The quarterly updated NAGA files (NetAffxGenomicAnnotations.Homo_sapiens.hg19.na20250201 and NetAffxGenomicAnnotations.Homo_sapiens.hg38.na20250201) are available for downloading from within ChAS and product website.

Recommended and minimum requirements

Table 1 Software

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 10 or Windows 11 Internet Explorer 11.0 (or above) or Windows Edge	Windows 10 or Windows 11 Internet Explorer 11.0 (or above) or Windows Edge
Available Disk Space	250 GB HD + data storage	150 GB HD + data storage
Free Disk Space Required at Installation	$\geq$ 5 GB	$\geq$ 5 GB
RAM	32 GB	16 GB

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Library file packages

Table 2 Available Library file packages

Array name	hg19	hg38
CytoScan HD	CytoScanHD_Array_Analysis_Files_hg19_NA33.r10.zip	CytoScanHD_Array_Analysis_Files_hg38_NA36.r7.zip
CytoScanHD Accel	CytoScanHD_Accel_Analysis_Files_hg19_NA33.r1.zip	CytoScanHD_Accel_Analysis_Files_hg38_NA36.r1.zip
CytoScan 750K	CytoScan750K_Array_Analysis_Files_hg19_NA33.r10.zip	CytoScan750K_Array_Analysis_Files_hg38_NA36.r7.zip
CytoScan750K Accel	CytoScan750K Accel_Array_Analysis_Files_hg19_NA33.r1.zip	CytoScan750K Accel_Array_Analysis_Files_hg38_NA36.r1.zip
CytoScan Optima	CytoScanOptima_Array_Analysis_Files_hg_19_NA33.r10.zip	CytoScanOptima_Array_Analysis_Files_hg_38_NA36.r7.zip
CytoScan XON	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	OncoScan_Array_Analysis_Files_hg19_NA33.r9.zip	OncoScan_Array_Analysis_Files_hg38_NA36.r7.zip
OncoScan CNV	OncoScan_CNV_Analysis_Files_hg19_NA33.r7.zip	OncoScan_CNV_Analysis_Files_hg38_NA36.r7.zip
CytoScan HTCMA	CytoScan_HTCMA_96_ChAS_Files_hg19.r3.zip	CytoScan_HTCMA_96_ChAS_Files_hg38.r3.zip

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Known issues in v4.5

- After installing the ChASCelUploader tool, you may need to reboot your system before the tool will start.

- If you uninstall ChASCelUploader tool, sometimes the desktop shortcut does not get removed. You will need to manually delete the desktop shortcut and the ChASCelUploader folder under C:\ProgramData

Known ChAS issues not addressed in v4.5

- When upgrading a user profile from a previous version of ChAS, the link out to the DECPHER website uses the old url and will return an error message. To rectify the issue, 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 the ChAS user guide, Chapter 20 for details on importing a Hyperlinks file.

- On a rare occasion, an error may occur if you copy and paste a directory path to a file path name. Workaround is to browse to the path location.

- More than 5GB 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

- If you are publishing data, merging data, or restoring/backing up a database, please do not interrupt the process. Let the database process complete, otherwise, the database will be 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, and 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, please run in compatibility mode for the ChAS.exe properties icon. To run in compatibility mode, please follow the steps below.
    - Open the ChAS application.
    - Open the Task Manager
    - Right click on the OpenJDK Platform binary application, choose Properties
    - Click on the Compatibility Tab.
    - Click on the Change high DPI settings button.
    - Check the box under High DPI scaling override and ensure that Scaling performed by is set to "System".
    - Click Ok and OK again to save the settings.
    - Close and Reopen ChAS.

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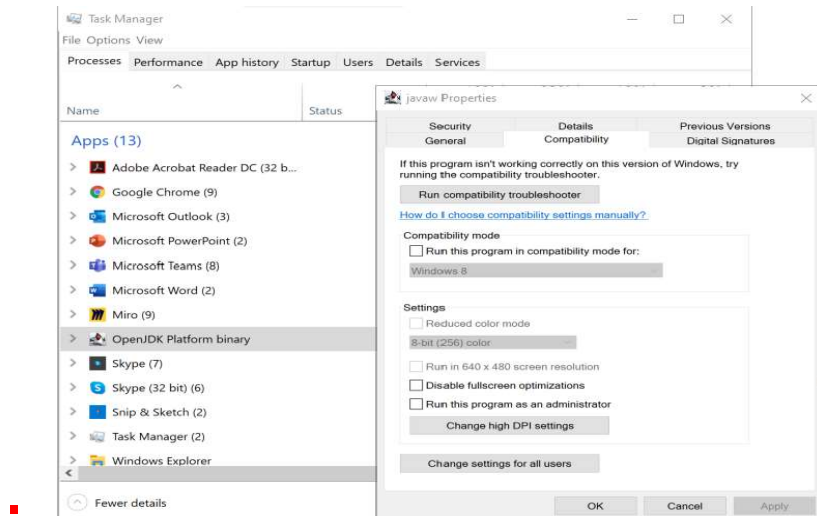
- In the Task Manager, the ChAS 4.x icon does not display when ChAS is running. Instead it is showing ChAS as "OpenJDK Platform Binary"

- It may take up to 30 minutes to remap a database containing ~150,000 segments.

- After a secure connection between ChAS Browser and ChAS Server is established, the message "***This site is not secure***" may appear upon opening the DatabaseTools page. If this message appears, refresh the window, then try again. Contact technical support for information on 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 prior to ChAS v3.2) and therefore will not contain 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 your network connection or contact your IT department for assistance.

- Do not export or save your files to a root drive (example: C:\). Always use a sub- folder(s) (within the root drive) to store your exports or saved files (example: C:\ChAS\My_Exports).

- 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 may 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'.

- On Windows 10 systems, if you select the Database Tools and nothing is displayed, check that your user account control setting is set On.

- In some cases, .NET framework may not be installed on your 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 in order to use these custom reference model file.

- An error message:
  The current type, Affymetrix.AnalaysisApplication.Infrastruction.IAnalysisDta, is an interface and cannot be constructed. Are you missing a type mapping? may appear after setting your input path. Click **OK** and

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continue. These paths will indeed be saved and the software will continue.

- An unexpected error message is displayed if the user selects **This PC** or **Network** to save an exported DOCX/PDF report. Make sure you save your report in a valid path location.

- If using Microsoft Edge, a message *Don't let this page create more messages* appears. The workaround for this is to close Microsoft Edge and re-login to the Database Tool page again.

- 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 on the ChAS Desktop icon.
  b. From its right-click menu, select **Properties**.
  c. Select the **Compatibility** tab, then go to the Privilege Level section.
  d. Check the **Run this program as an administrator** check box, then click **OK**.
  e. Double-click on the ChAS Desktop icon to start ChAS again.

- 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 filename, the analysis will fail. Make sure only valid characters are used in your filename.

- When two users publish the same sample to the database, a warning message alerts 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 re-analysis 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 your 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.

- Export of large amounts of data to TXT file from ChAS may contain quantities of characters in a single field that MS Excel cannot process. This is a limitation of Excel, 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 must use **View/Edit Annotation Properties...** for editing those particular 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 may be because OMIM data has been updated since NetAffx last downloaded data used to create the browser tracks. Always confirm 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 may 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 four alternate haplotypes (for regions on Chromosome 5, 6, and 22) are not part of the reference build of the genome.

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