

Chromosome Analysis Suite (ChAS) Software: Single Sample Analysis

Analyze CEL file data: make CYCHP files containing CN/LCSH/Mosaicism results for displaying in browser

In Single Sample Analysis, you compare the values in one or many selected CEL files serially with the values in a previously created Reference Model File. One reference file is provided with ChAS.

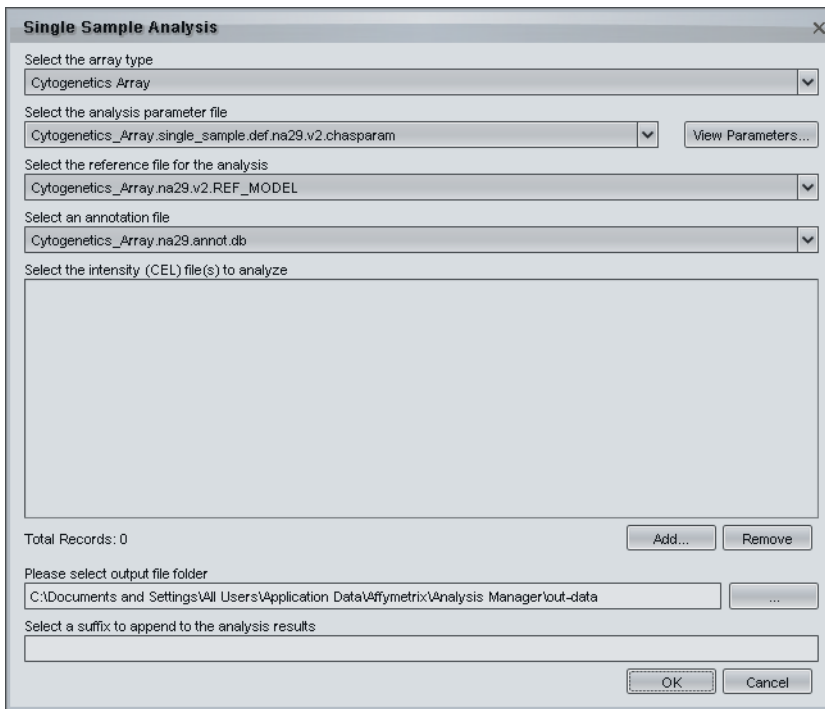
During the analysis, ChAS generates CYCHP files with Graph data for each probe and Segment data describing Copy Number, Long Contiguous Stretches of Homozygosity, and Mosaicism events.

These CYCHP files can be loaded into ChAS for viewing and study.

To perform Single Sample Analysis:

1. From the Analysis menu, select **Single Sample Analysis...**

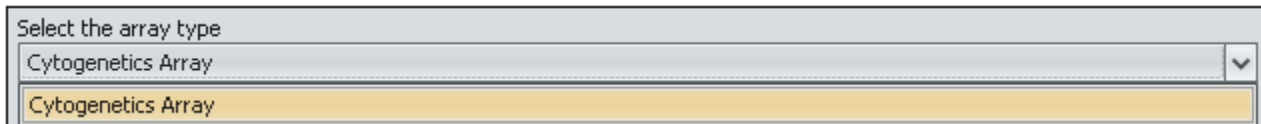
The Single Sample Analysis dialog box opens.



The dialog box titled "Single Sample Analysis" contains the following fields and controls:

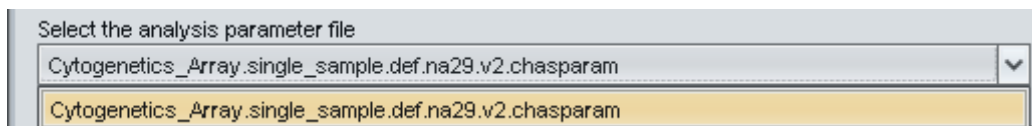
- Select the array type:** A dropdown menu with "Cytogenetics Array" selected.
- Select the analysis parameter file:** A dropdown menu with "Cytogenetics_Array.single_sample.def.na29.v2.chasparam" selected, and a "View Parameters..." button to its right.
- Select the reference file for the analysis:** A dropdown menu with "Cytogenetics_Array.na29.v2.REF_MODEL" selected.
- Select an annotation file:** A dropdown menu with "Cytogenetics_Array.na29.annot.db" selected.
- Select the intensity (CEL) file(s) to analyze:** A large empty text area.
- Total Records:** A label "Total Records: 0" with "Add..." and "Remove" buttons.
- Please select output file folder:** A text field containing "C:\Documents and Settings\All Users\Application Data\Affymetrix\Analysis Manager\out-data" and a browse button "...".
- Select a suffix to append to the analysis results:** An empty text field.
- Buttons:** "OK" and "Cancel" buttons at the bottom.

2. Select the array type from the Array Type dropdown. The Cytogenetics Whole Genome 2.7M Cytogenetics Array (Cytogenetics Array) is shown in this example.



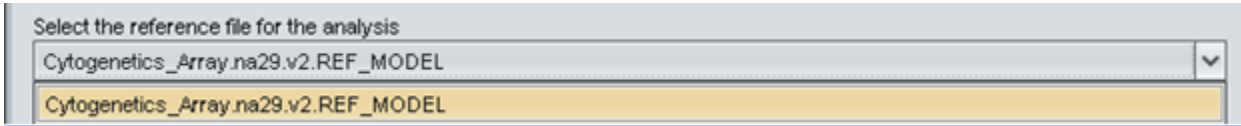
A close-up of the "Select the array type" dropdown menu. The dropdown is open, showing a list with "Cytogenetics Array" selected and highlighted in yellow.

3. Select the Analysis Parameter (*.chasparam) file to use for the analysis.

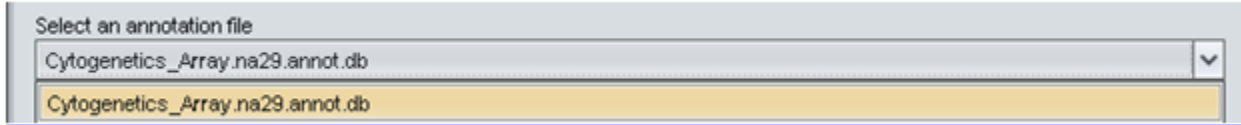


A close-up of the "Select the analysis parameter file" dropdown menu. The dropdown is open, showing a list with "Cytogenetics_Array.single_sample.def.na29.v2.chasparam" selected and highlighted in yellow.

4. Select the Reference Model File from the Reference File drop-down list.



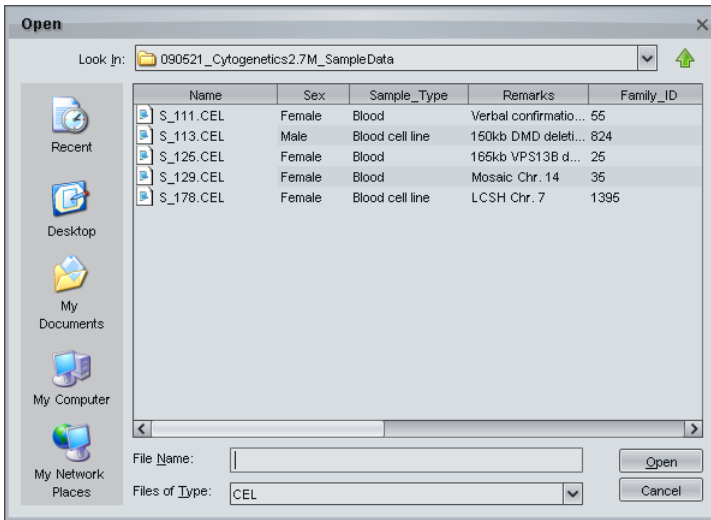
5. Select an annotation file from the Annotation File drop-down list.



6. Select the CEL files for analysis. Each CEL file is analyzed against the Reference individually, there is no minimum number. Affymetrix recommends that you perform analysis operations with all files stored locally.

A. Click **Add**.

The Open dialog box opens.

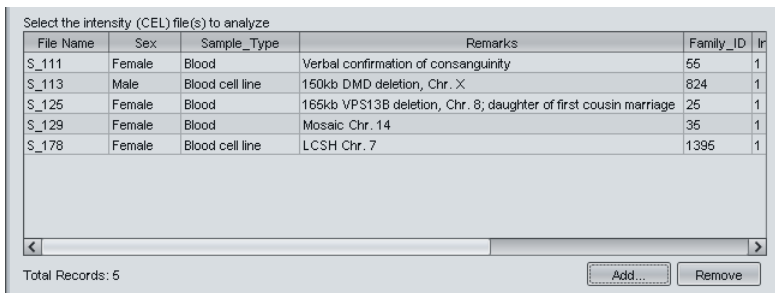


- B.** Navigate to the folder with the CEL files using the navigation controls.

- C.** Select the CEL files to be analyzed.

- D.** Click **Open** in the Open dialog box.

The files appear in the Intensity file list.



Select a file in the box and click **Remove** to remove it.

The total number of selected files is displayed below the box.

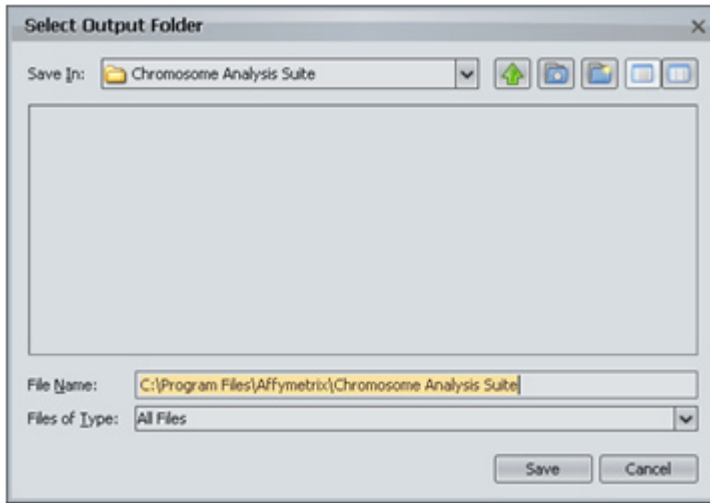
7. Select a folder for the output files.



Enter a path to the file; or

- A.** Click the **Browse** button.

The Select Output Folder dialog box opens.



- B. Navigate to or Create the folder to which you wish to write the resulting CYCHP files using the navigation controls.
- C. Click **Save** in the Select Output Folder dialog box.

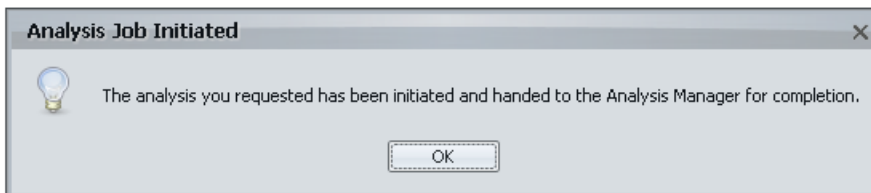
The selected folder appears in the Output File Folder field.

- 8. Optional: Enter a suffix to be added to the output CYCHP file names
This option adds a suffix to the CYCHP files to help you track them.



IMPORTANT: If you have previously run an analysis on the selected CEL files and are saving the new CYCHP files to the same location as the previous files, you need to add a unique suffix to the new files, since otherwise the original CYCHP files will be overwritten.

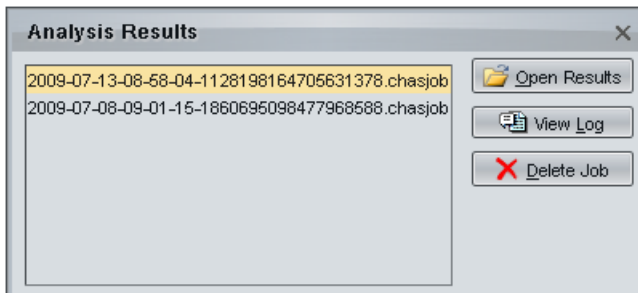
- 9. Click **OK** to begin the analysis. You may be asked to close other applications to free up memory for the analysis; if you close ChAS, it will reopen when the analysis results are ready for viewing in the Browser.



You can track the progress of the analysis in the Analysis Manager.

To track analysis progress, right-click on the Analysis Manager icon  in the status area at the far right of the Windows taskbar, and choose Status. Closing the Analysis Manager status window will not interrupt the Analysis.

When the Analysis job has finished, the Analysis Results dialog box will appear, allowing you to choose the results job and open the results (CYCHP) files in the Browser. The most recently completed jobs are always at the top of the Analysis Results list.



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