

# Automated Dicentric Chromosome Identifier

## *Version 6.1, Centromere Candidates Selection and Telomere Location*

The graphical user interface (GUI) of the ADCI software is aimed to provide an easy and friendly control interface for its users to evaluate the algorithm we designed and, more importantly, to collect information that could help us improve our algorithm. The objective of this document is to provide important instructions on the usage of ADCI GUI v6.1.

Image loading, ranking, and processing steps are the same as earlier versions. A major update in version 6.1 is that the main window with the full metaphase image is used only for viewing, and the new Chromosome Editor window becomes the interface of all chromosomes manipulations. However, most control widgets in previous versions are kept in version 6.1. To avoid unnecessary operations, please follow the step-by-step instructions in this document.

## Main Window Overview and Sample Loading

To start ADCI, double click the file **Automated\_Dicentric\_Chromosome\_Identifier.exe**. Users will see two windows: *Automated Dicentric Chromosome Identifier* (main window) and *Debug Window* (figure 1).

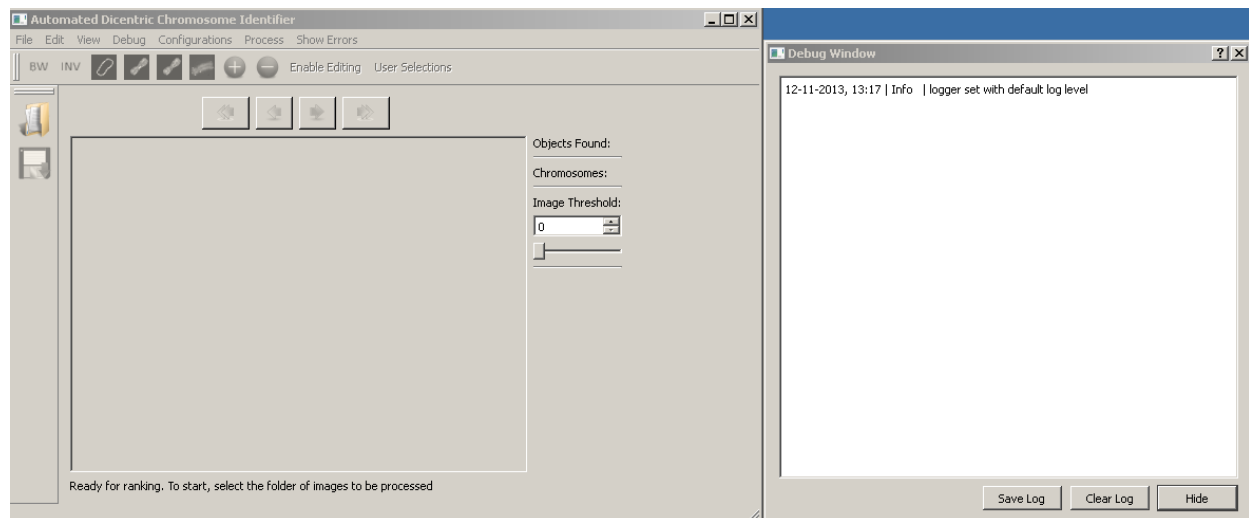


Figure 1, main window and debug window

The *Debug window* is designed for developers. Users do not have to deal with it normally. Figure 2 shows the components of the main window. To load a sample, click the folder icon in left tool bar or the *Open Single Sample* option in the *file* menu. Users can also load multiple samples by choose the *Open Multiple Samples* in the *file* menu. Select the folder containing all images in a sample, and ADCI will pop-up the *Image Ranking* window.

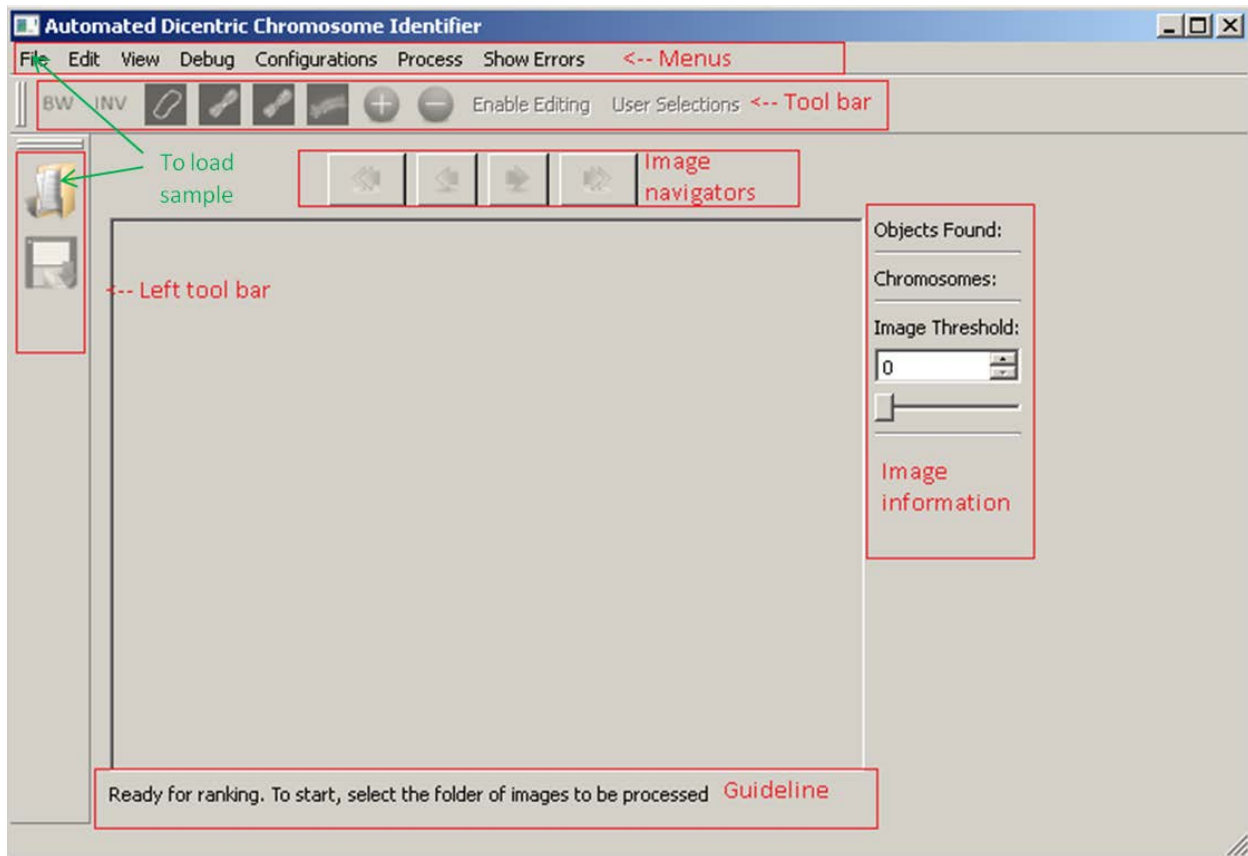


Figure 2, layout of main window

## Image Ranking

Figure 3 shows the *Image Ranking* window. Users only need to click *Start Ranking*. When ranking process is finished, users will be able to select a certain number of top images. There are other controlling widgets in the *Image Ranking* window, but users do not have to deal with them now.

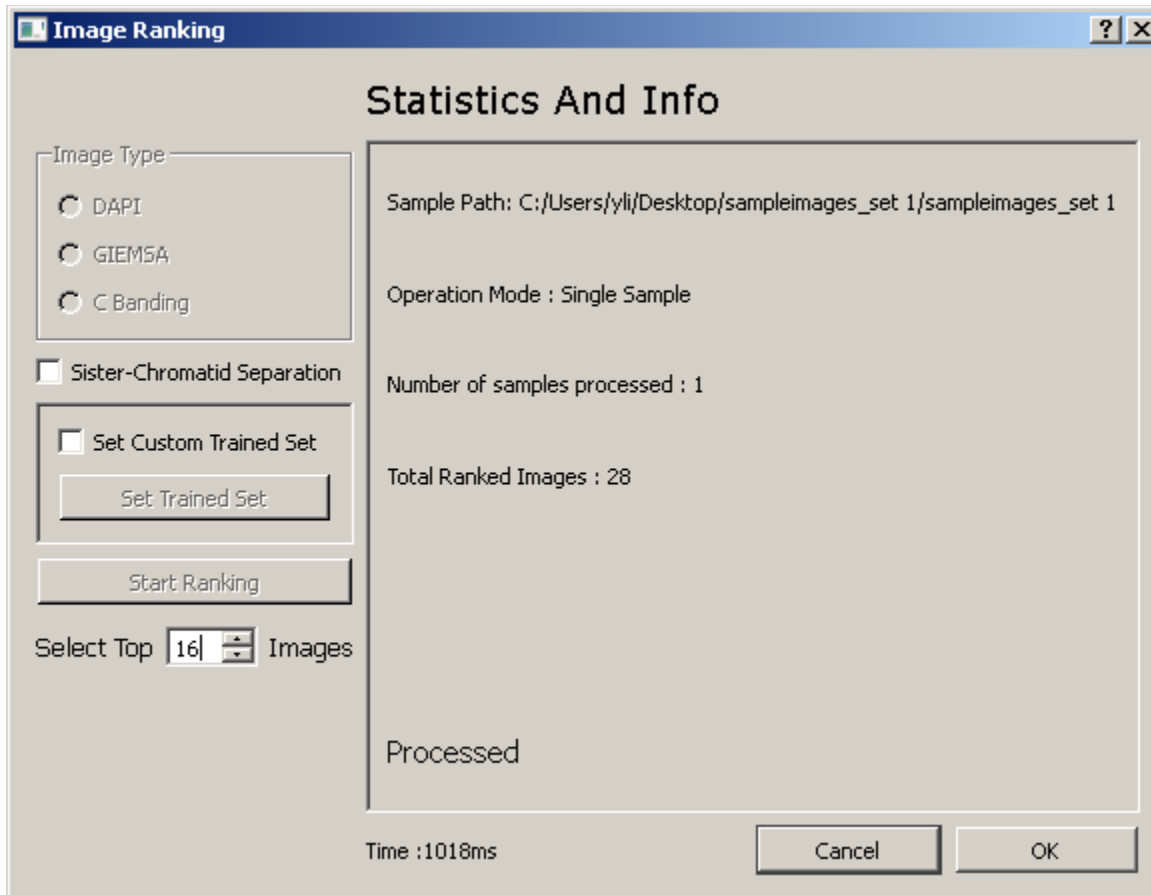


Figure 3, Image Ranking window after Ranking of 28 images with 16 top images to be selected

## Image Viewing, Adjusting Segmentation and Processing

After select how many top images to process in the Image Ranking window, users will see the selected images in the middle area of the main window. To view the next or previous image, use the image navigator buttons. The tool bar provides two buttons to view the binary image and inverted image of current metaphase image.

From the binary image, users can see how ADCI segment chromosomes in current metaphase. If users think some chromosomes are visually separate but ADCI segment them to one blob in the binary image, users can try adjusting threshold to separate them, most likely increasing threshold. Changes of segmentation will be displayed in the binary image. High threshold can separate some clustered chromosomes but also may break other chromosomes. Please adjust the threshold to a good balance. If adjusting threshold is done before processing, user can process the current image or the whole sample. If adjusting threshold happens after current image has been processed, users need to re-process the image.

Figure 4 shows the image before processing and threshold controlling widget. The buttons of increasing and decreasing threshold by 1 in the tool bar are legacy of previous versions. Users should use the spin

box and slide at the right side of image to control threshold. Figure 5, 6, 7 show how threshold changes the segmentation. Figure 5 shows the default dynamic threshold in which some chromosomes are not well separated. In figure 6, threshold is carefully increased to separate the two touching chromosomes. Figure 7 shows a threshold too high that breaks chromosomes.



Figure 4, main window before processing image

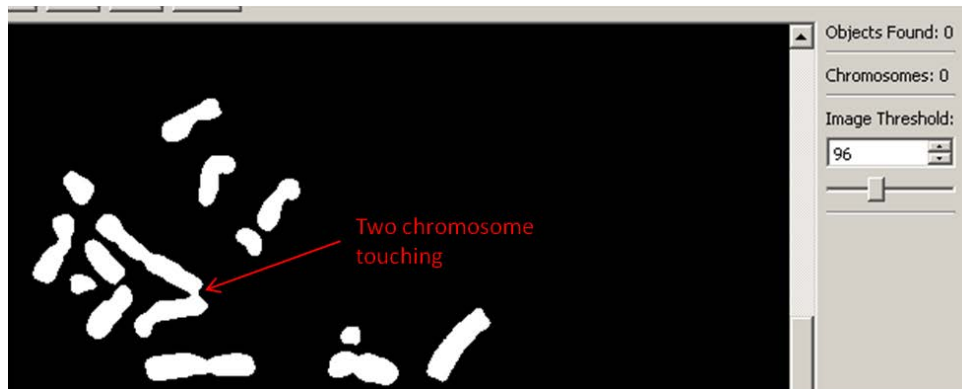


Figure 5, binary image with default threshold (96), two chromosomes touching

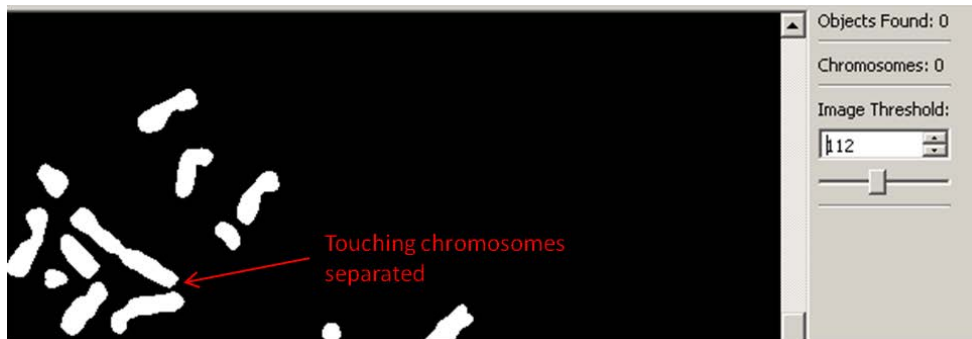


Figure 6, carefully increased threshold (112) to separate touch chromosomes

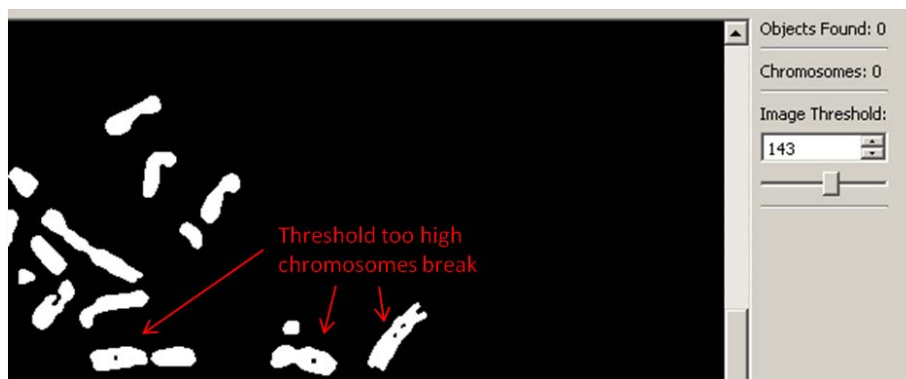


Figure 7, threshold too high (143) that breaks chromosomes

To process images, click the *Process* menu. Users can let ADCI process all selected image by choosing *Process Samples* or only current image by choosing *Process Current Image*. When it is processing images, ADCI may be not-responding for a few seconds. User can also see the progress bar at the bottom of the main window. Just wait for the complete of processing.

ADCI provides four buttons to control the features viewing of a processed image: displaying contour, centerline, centromere candidates and telomere marking points. Only valid chromosomes will be highlighted with these features. See figure 8. As the full image is only for viewing, please ignore the *Enable Editing* button and *User Selections* button. They are legacy of previous versions. Figure 9 is a processed image with contours displayed.

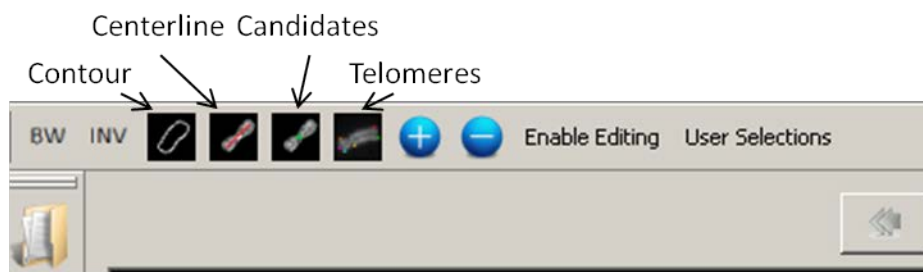


Figure 8, buttons controlling the display of chromosome features in full image

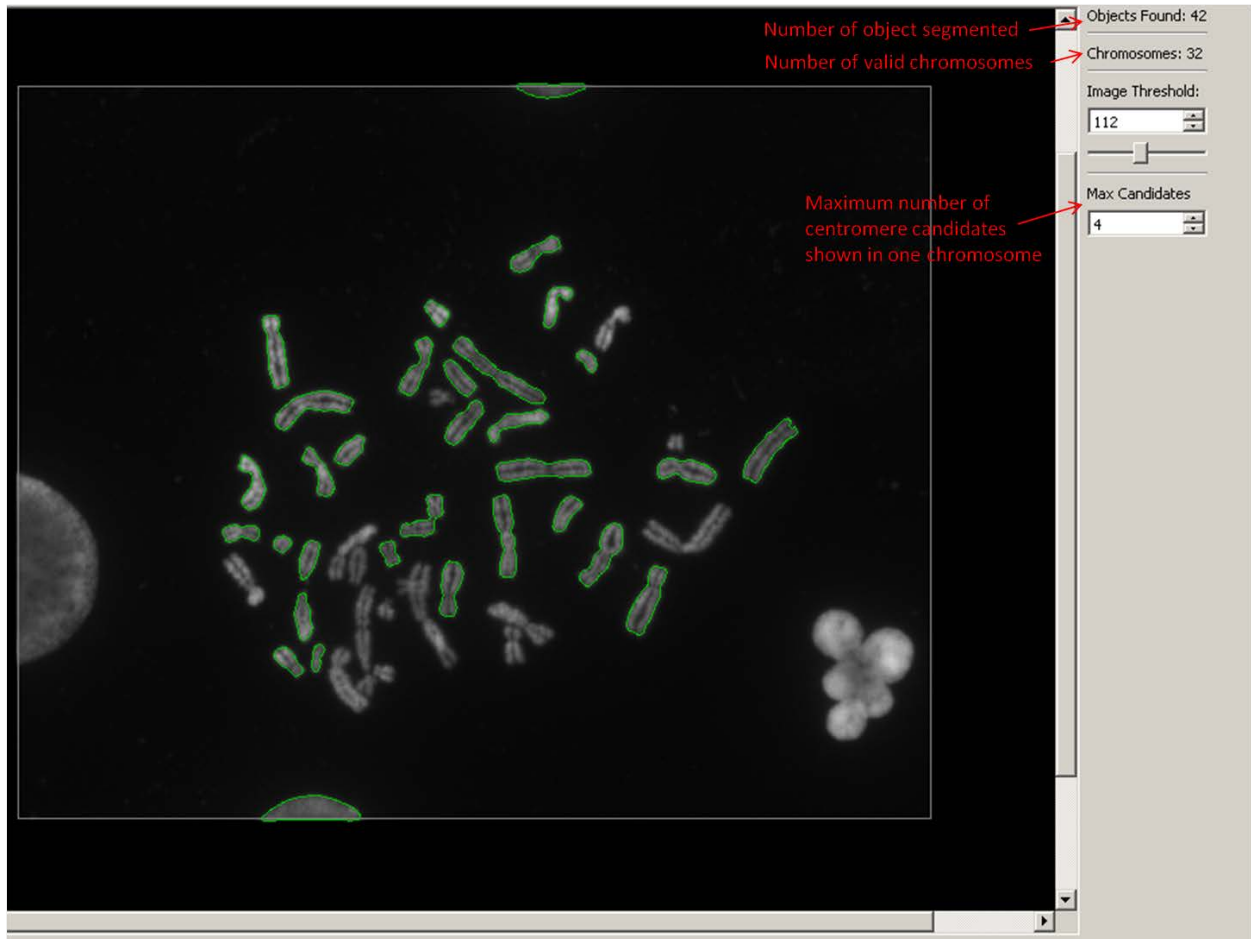


Figure 9, processed image with contour displayed and image information at the right side

To edit a chromosome: marking centromere candidates, telomere combinations etc. left click a valid chromosome in the full image of the main window.

## Chromosome Editing

When a valid chromosome is left clicked, users will see the *Chromosome Editor* window. *Chromosome Editor* consists of two tabs: centromere panel and telomere panel. Figure 10 is the centromere panel. In the enlarged image of the selected chromosome, contour is displayed as dark green dotted line, undefined (initial state) centromere candidates blue dots, accepted candidates light green dots, rejected candidates red dots and manual selection are shown as yellow dots. Users can use the checkboxes of display options at the top of the image to control which features they want to see in the enlarged image. To accept a candidate as a correct centromere, make sure the checkbox *Input As Manual Selection* is unchecked and click the candidate to be accepted in the image. To manually add a correct centromere, make sure the checkbox *Input As Manual Selection* is checked and click the centromere location in the image. Clicking the same location again will set the accepted candidate back to an undefined candidate or will erase the manually added centromere.

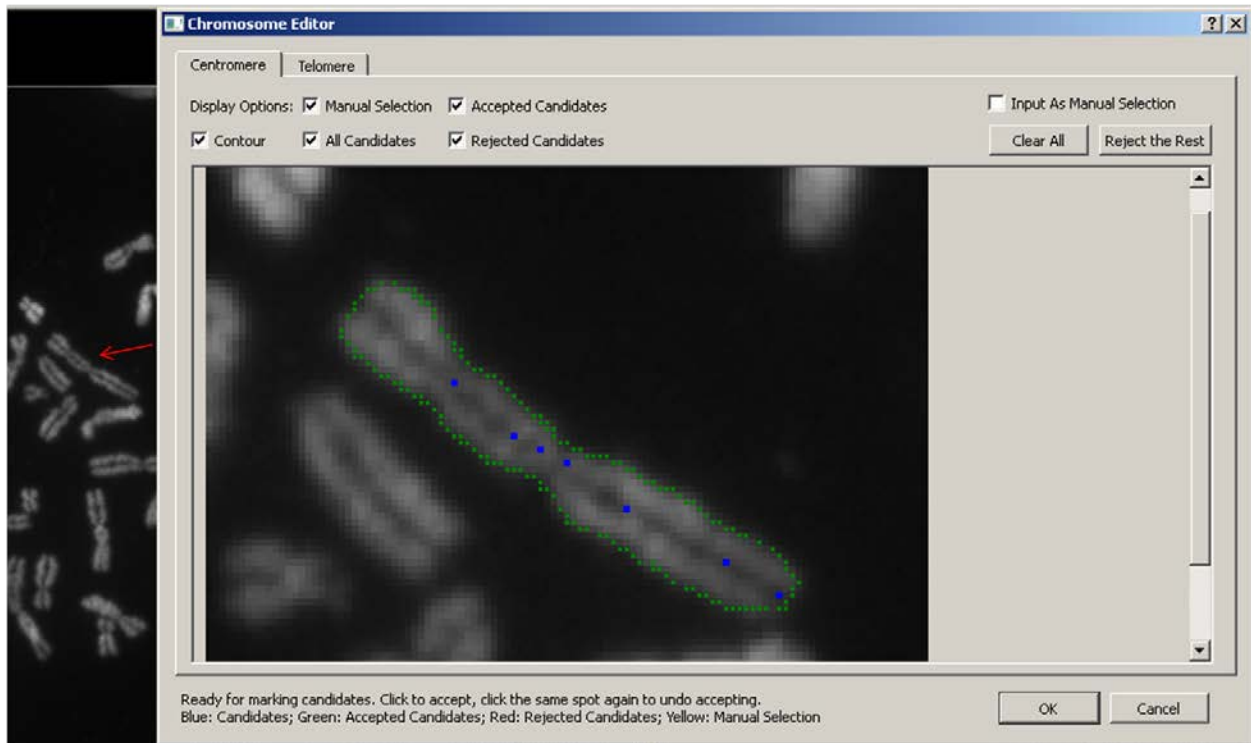


Figure 10, Centromere panel in Chromosome Editor, initial state

To reject all undefined (initial state, not being accepted) candidates, click the button *Reject the Rest*. To clear what have been done and go back to initial state, click the button *Clear All*. Figure 11 shows the same chromosome in figure 10 with two accepted centromere candidates (light green) and the rest rejected (red). Figure 12 shows a chromosome with one manually added centromere (yellow) and all rejected candidates.

Figure 13 shows the telomere panel of the *Chromosome Editor*. For each chromosome, there are 12 combinations defining the telomere of the chromosome. The green dot and red dot in one blue ellipse define one telomere. Two telomere definitions (ellipses) make a combination. Users should check the checkbox under the correct telomere combination. Users can select two or more combinations, but this should only happen when there are more than one best combinations which should be rare.

Edited chromosomes will have red contour in the full image instead of green one. If chromosome clusters are recognized by ADCI as a valid chromosome, users should ignore them without any editing.

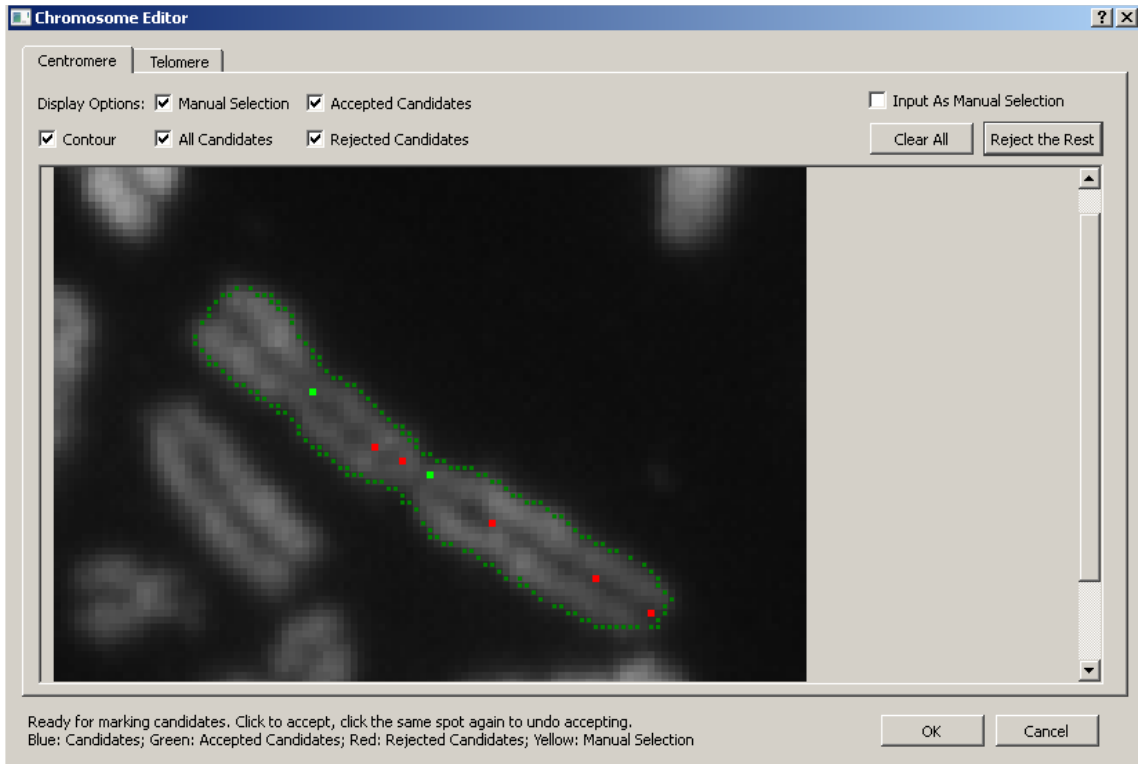


Figure 11, two centromere candidates accepted, the rest rejected

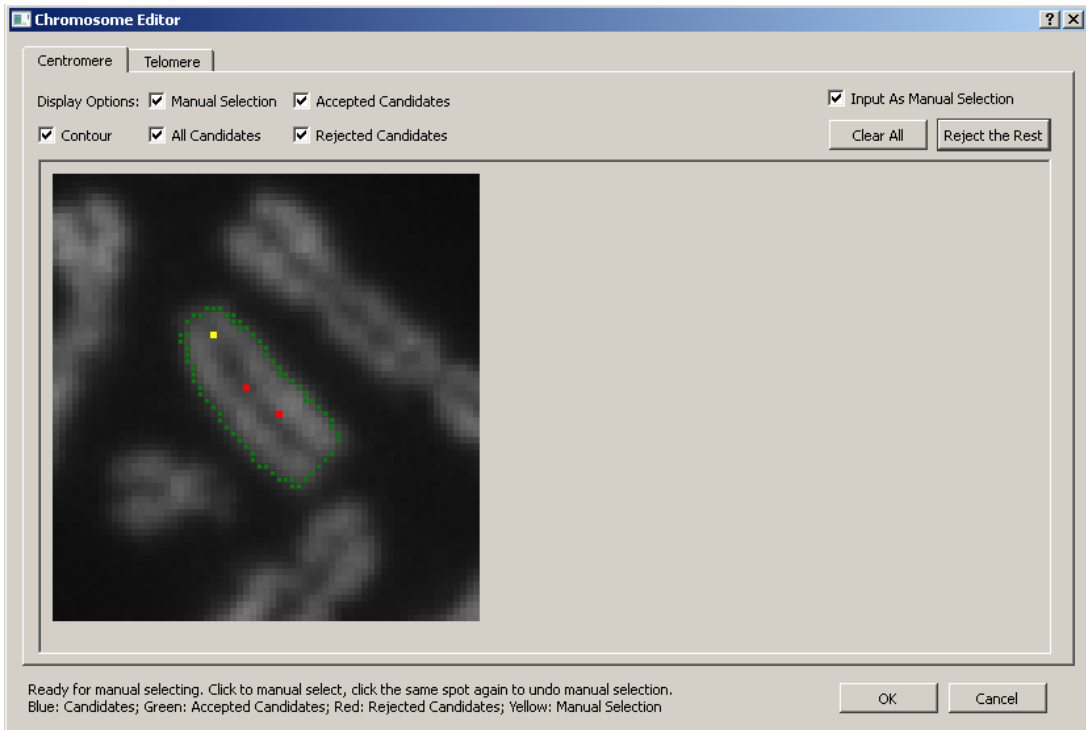


Figure 12, manually selected centromere when candidates miss the correct centromere, candidates rejected



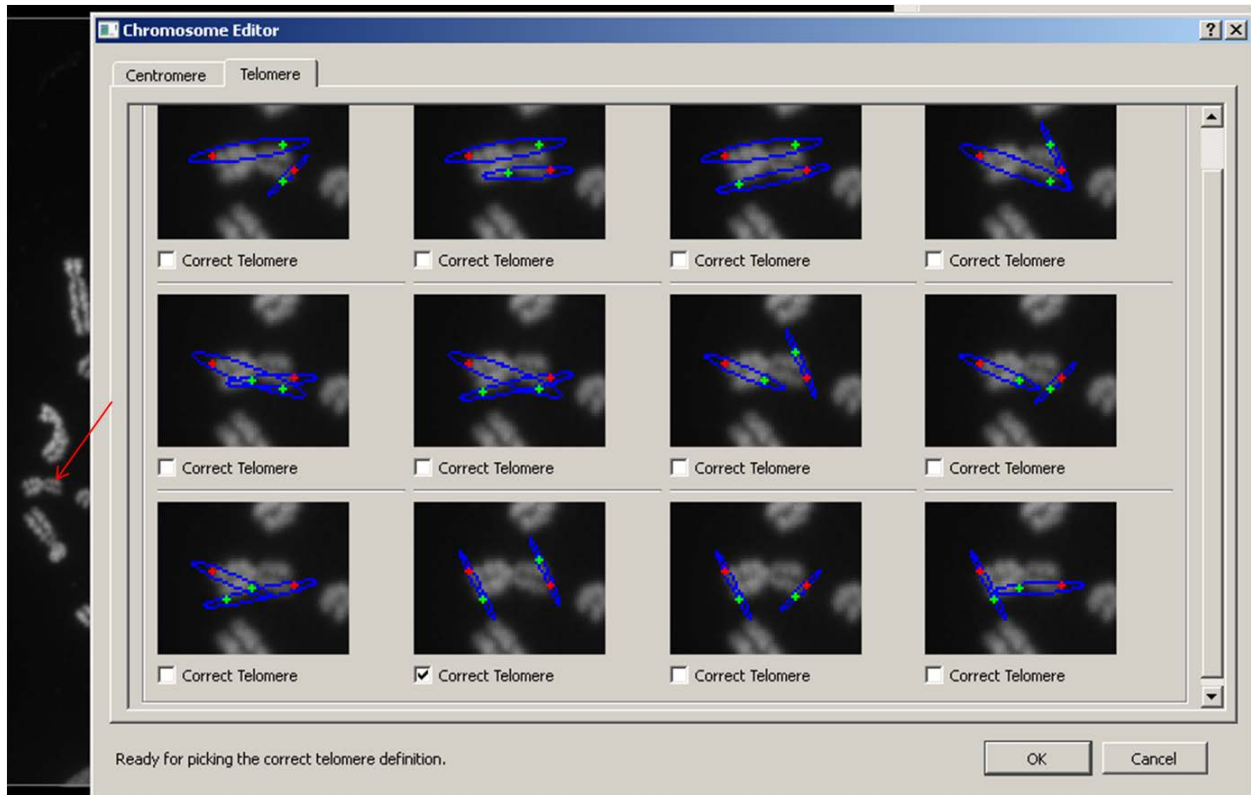


Figure 13, telomere panel in Chromosome Editor, the second combination at row 3 is selected as correct telomere

## Save Chromosome Data

When having done the editing, users can save the edited data of the whole sample or the current image. These data are vital to the improvement of ADCI. To save chromosome data, click the *file* menu, go to *Save Chromosome Data* and choose *Current Sample* or *Current Image*, figure 14. ADCI will save chromosome data as a .mat file, and it will ask users to provide the name for this file. Please use a filename which contains some information of the sample or the image that can help differentiate it from other samples. For example, the chromosome data of sample set A can be saved as A.mat and the chromosome data of image 001 in sample set A can be saved as A-001.mat. This makes analysis of the data generated by users easier.



Figure 14, saving chromosome data

## Known problems

In rare cases, ADCI may crash. Please save the data in time. A recommended way is dealing with one sample at one time, and saving chromosome data when the editing of one sample is done.