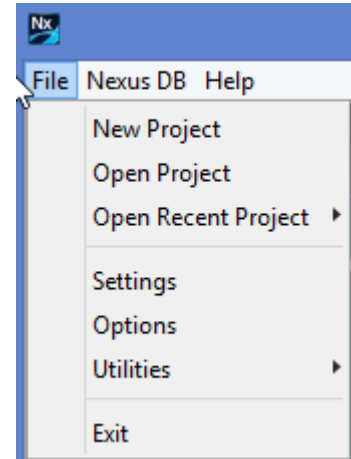
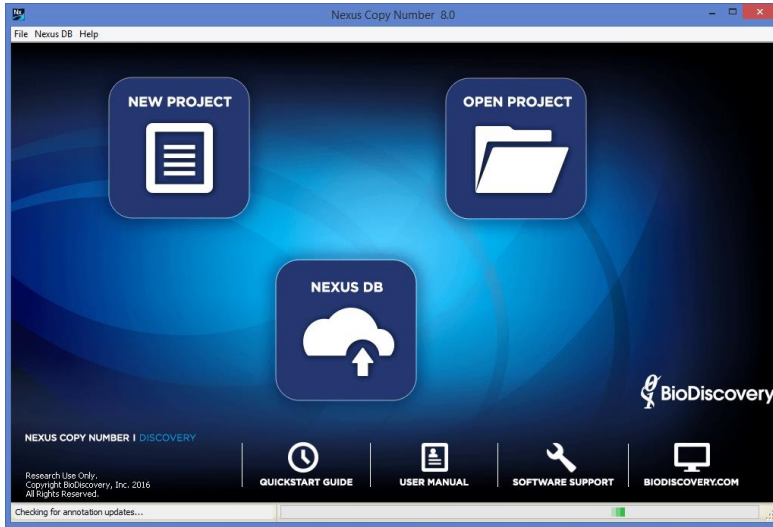
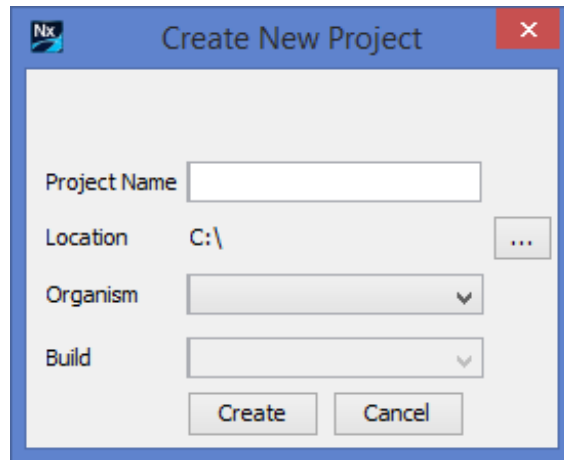


HOW TO LOAD AFFYMETRIX CEL DATA:

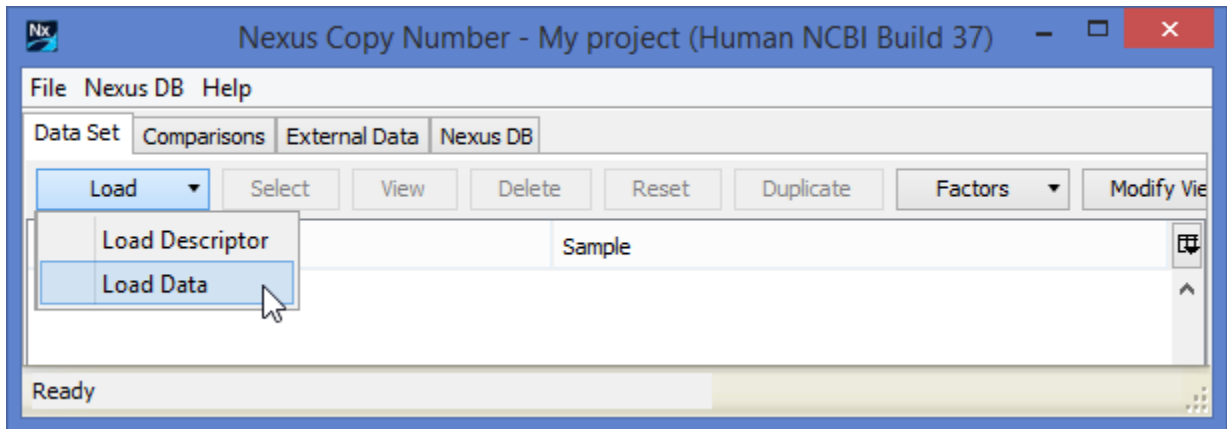
1. Launch Nexus Copy Number. Create a new project or open an existing project from the start page. You can also open and create projects from the **File** menu.




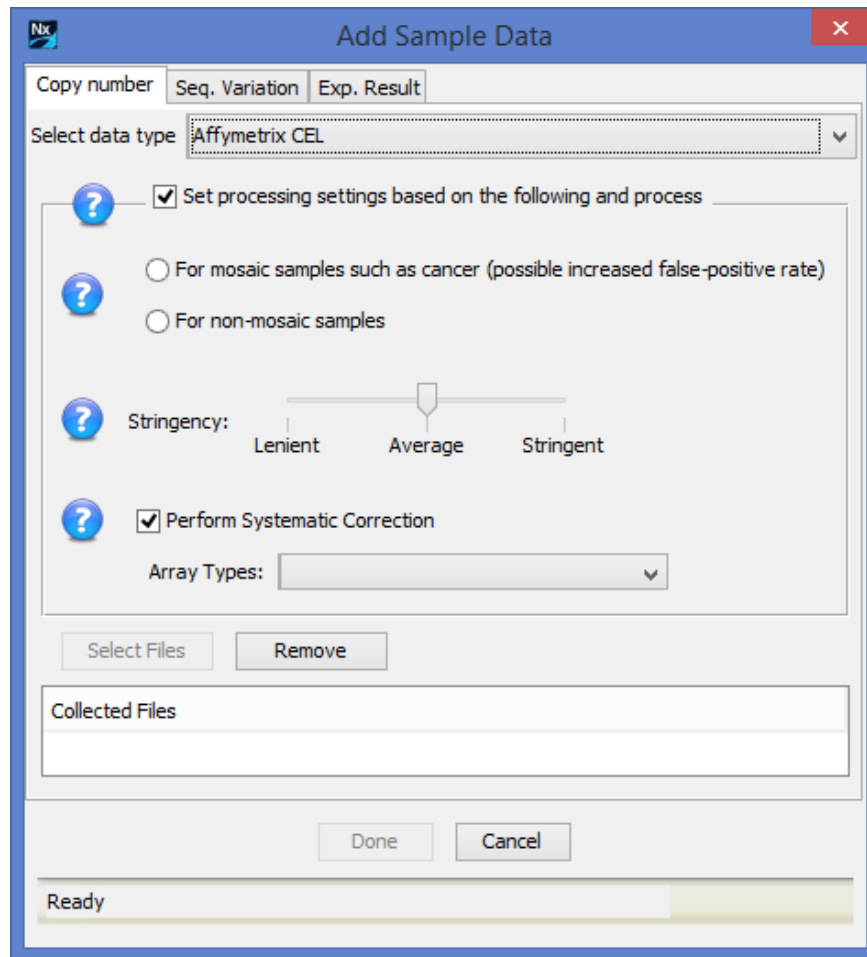
2. Specify a name for your project and a place to save it on your computer. Select the appropriate genome and build, based on the mapping information for your probes.



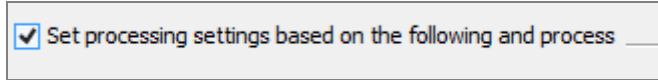
3. Select **Load** -> **Load Data** from the Data Set tab.



4. In the **Add Sample Data** window, select **Affymetrix CEL** from the **Select data type** drop down in the **Copy Number** tab. A number of options will be displayed. Clicking on the  icon will provide more details on the parameters.

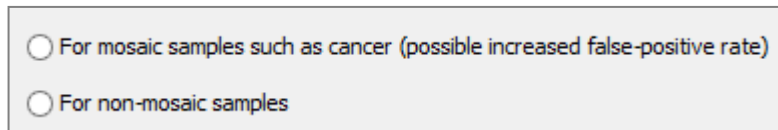


The option **Set processing settings based on the following and process** uses default parameters for the type of data you are loading and immediately begins processing after data loading is complete. To adjust settings from the default parameters, uncheck this box and see the section **Settings** in the **User Manual** for more details.

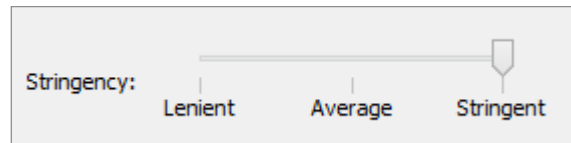


With the box checked, make selections for the rest of the parameters as suggested below:

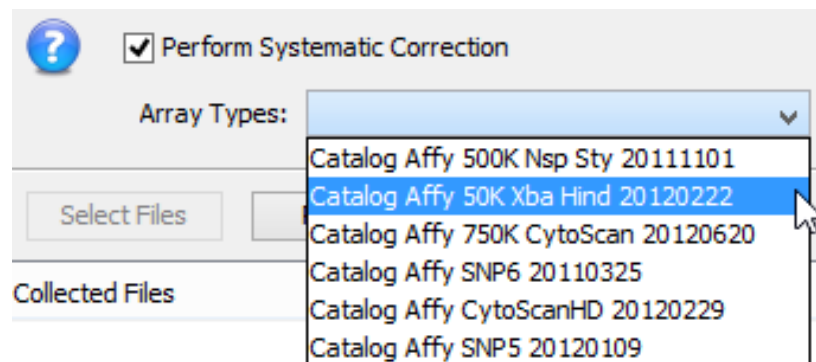
- a. Select one of the options depending on the type of data you are loading (typically, cancer = mosaic; all others = non-mosaic). The selection here adjusts the thresholds used to make calls (e.g. High Gain, Gain, Loss, Big Loss).



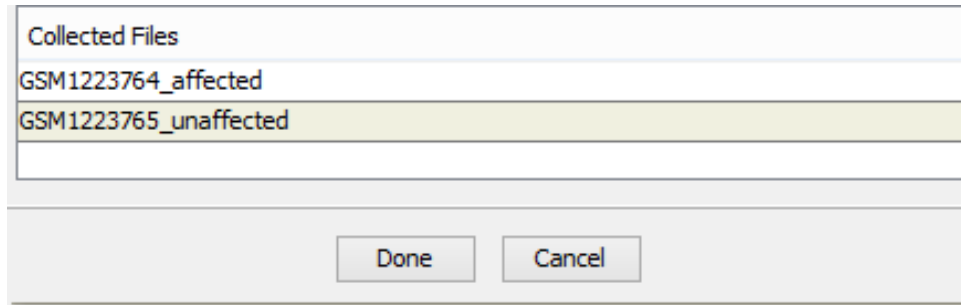
- b. The **Stringency** slider adjusts the sensitivity of the algorithm in making calls. **Lenient** will generate more calls and **Stringent**, fewer calls (more specificity). Adjust the **Stringency** slider and move to **Stringent** for more specificity – you can reprocess later with a different setting if needed.



- c. **Perform Systematic Correction** corrects the wavy pattern often present in the probe distribution. Since the correction is based on probes used, the specific array is needed. Select the array from the **Array Types** dropdown menu. If your array type is not listed in the dropdown, please contact BioDiscovery Support (support@biodiscovery.com) to obtain the necessary files. You can continue to process without performing the correction; just uncheck the box. You can reprocess the samples with systematic correction later.



- d. Click **Select Files** to select your **Affymetrix CEL** files to load into Nexus Copy Number. You can select any number of files but they must all be Affymetrix CEL files. Once you have finished selecting files via the File Chooser, click **Open** and the sample file names will be listed in the **Collected Files** section:



Click **Done** after you have selected all your files.

- 5. Samples will now be loaded and processed. The Data Set tab will be displayed with a progress bar at the bottom showing the loading/processing status of the samples. The **Status** column of the table will also change from **Unprocessed** to **Processed** upon sample processing completion. Once processing is complete, results will be displayed in the window.

