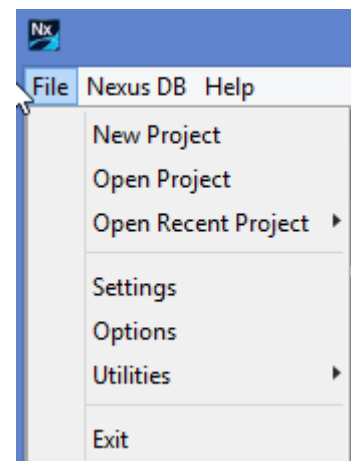
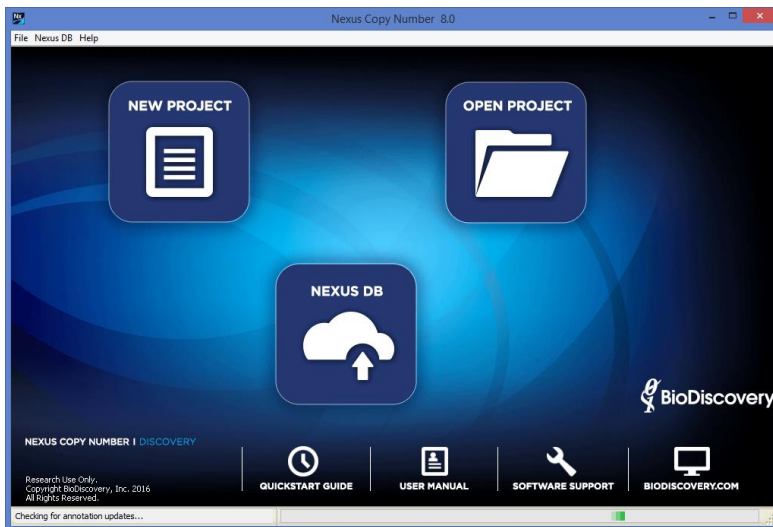


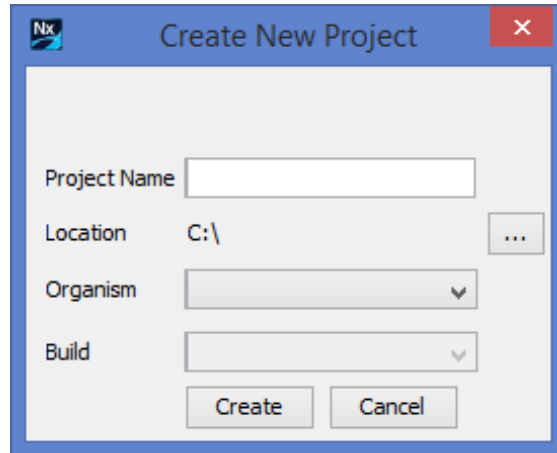
HOW TO LOAD ILLUMINA DATA

1. You need to create **Custom Final Report** files to load Illumina data into Nexus Copy Number. Run GenomeStudio to create the final report files following the steps below.
 - a. Select **Analysis->Reports->Report Wizard**. A dialog box will appear.
 - b. Select **Final Report** and click **Next**.
 - c. On the next two pages select the samples and sample groups you want.
 - d. On the following page (the **Final Report Format** page), select **Standard** for the radio buttons at the top.
 - e. Below the **Custom Report** dropdown is the **Report Settings** panel containing several fields that can be edited. Make sure that either **Sample ID** or **Sample Name** is present in the **Displayed Fields** list, as well as **Chr, Position, Log R Ratio, SNP Name, B Allele Freq,** and **GC Score**. Any other values can be present but they will be ignored by Nexus Copy Number. Click **Save Current** to save these settings so that you don't have to select the columns next time. When creating the final report, make sure that the file is grouped by Sample ID not SNP name (by default, **Sample ID** is checked for **Group By**).

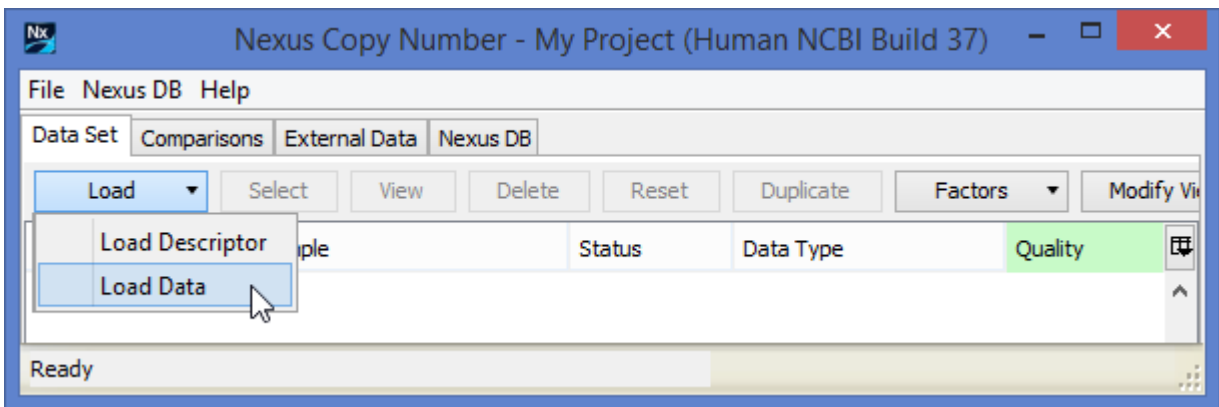
2. Launch Nexus Copy Number. Create a new project or open an existing project from the start page. You can also open and create projects from the **File** menu.




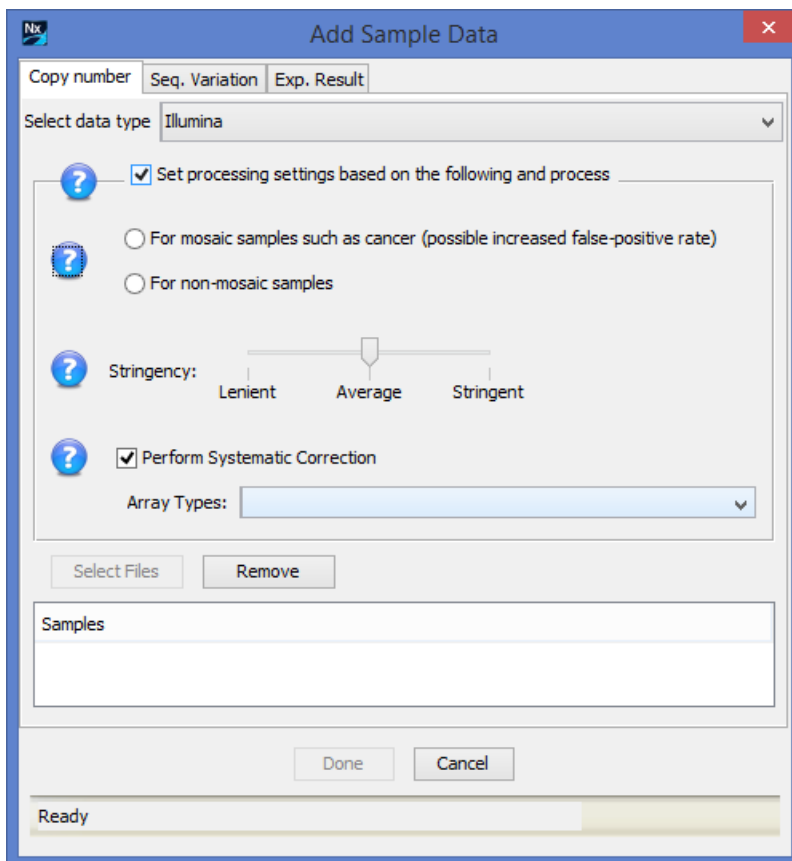
- 3. Specify a name for your project and a place to save it on your computer. Select the appropriate genome and build, based on the mapping information for your probes.



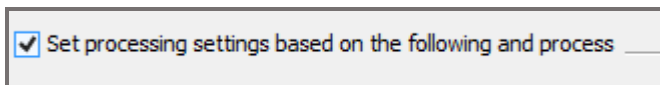
- 4. Select **Load** -> **Load Data** from the Data Set tab to load your data.



- 5. In the **Add Sample Data** window, select **Illumina** 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.

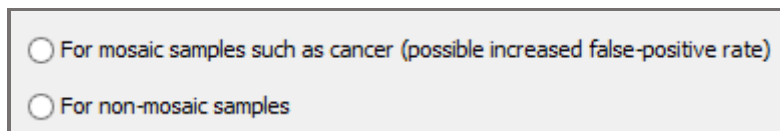


The option **Set processing settings based on the following and process** uses default parameters for the type of data you are loading and immediately begins processing after data loading is complete. To adjust settings from the default parameters, uncheck this box and see the section **Settings** in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

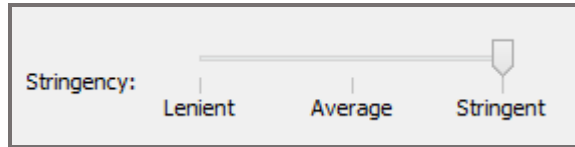


With the box checked, make selections for the rest of the parameters as suggested below:

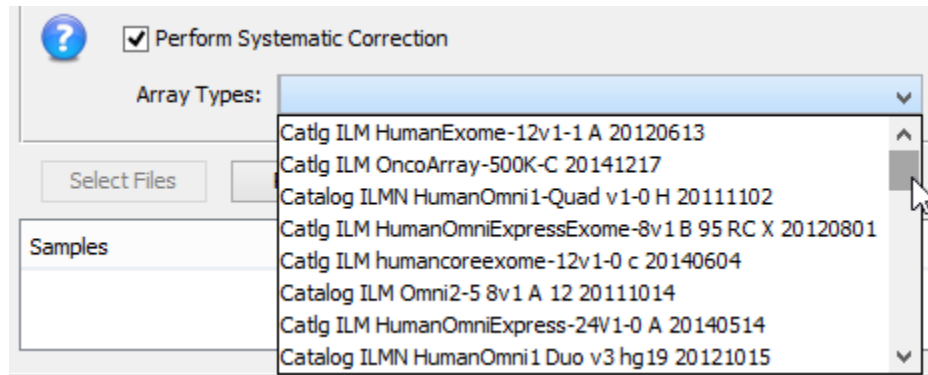
- a. Select one of the radio buttons depending on the type of data you are loading (typically, cancer=mosaic; all others =non-mosaic). The selection here adjusts the thresholds used to make calls (e.g. High Gain, Gain, Loss, Big Loss).



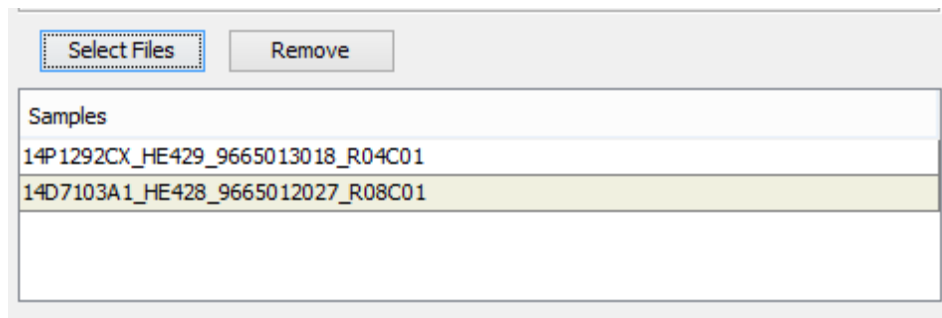
- b. The **Stringency** slider adjusts the sensitivity of the algorithm in making calls. **Lenient** will generate more calls and **Stringent**, fewer calls (more specificity). Adjust the **Stringency** slider and move to **Stringent** for more specificity – you can reprocess later with a different setting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

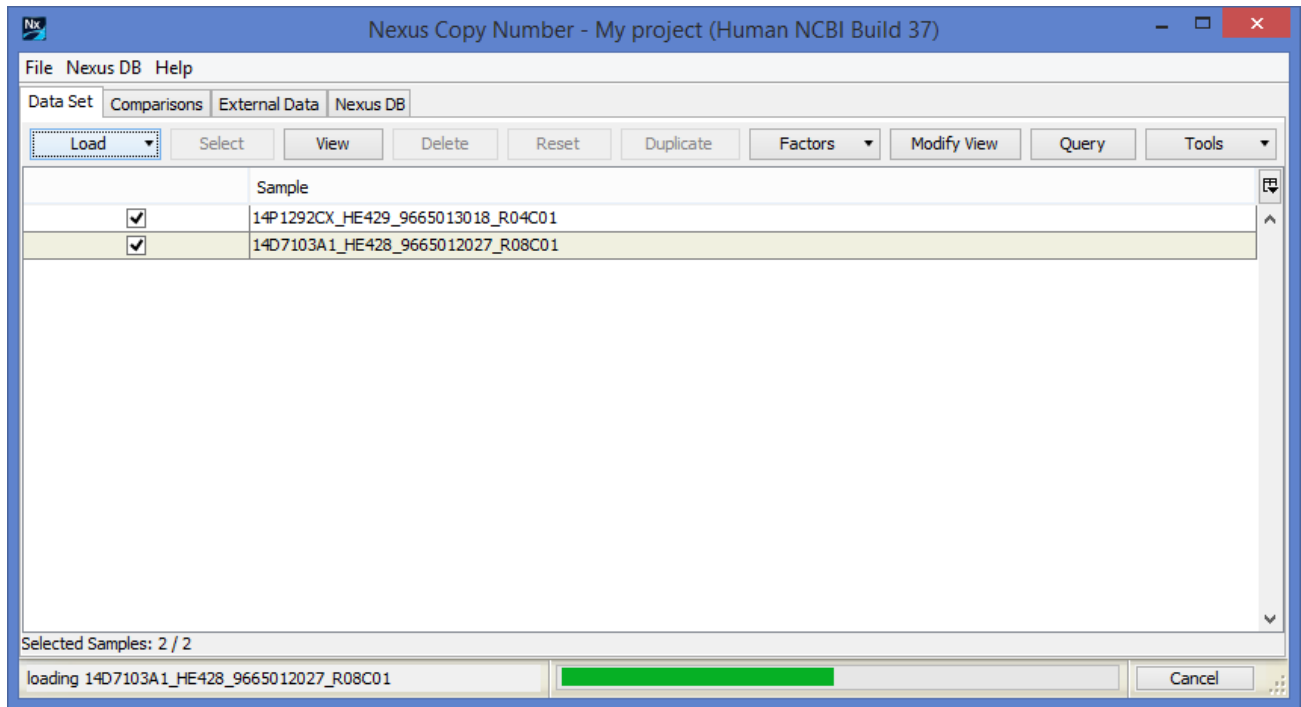


- d. Click **Select Files** to select your **Illumina Final Report** files to load into Nexus Copy Number. You can select any number of files but they must all be Illumina Final Report files. Once you have finished selecting files via the File Chooser, click **Open** and the file sample names will be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



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

- 6. 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.