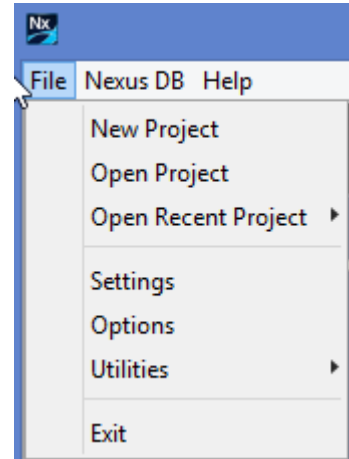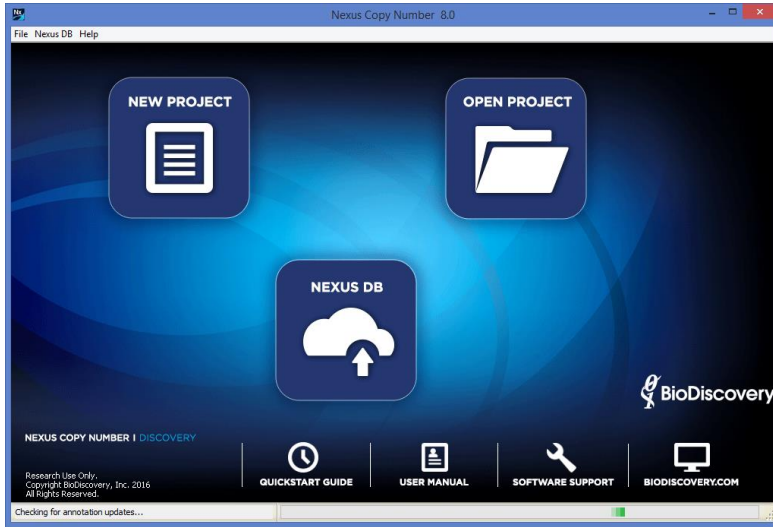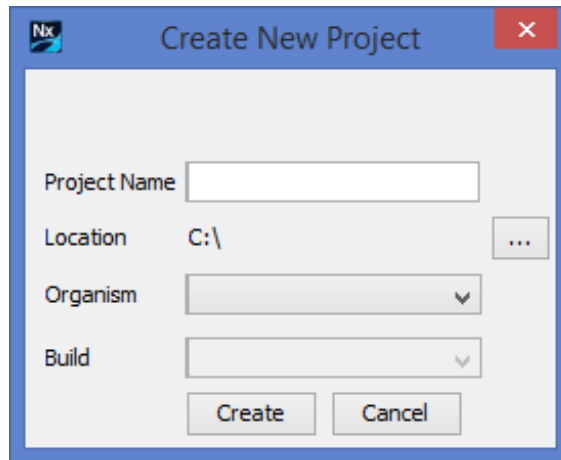## How to Load Affymetrix OncoScan Data:

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 to load your data.
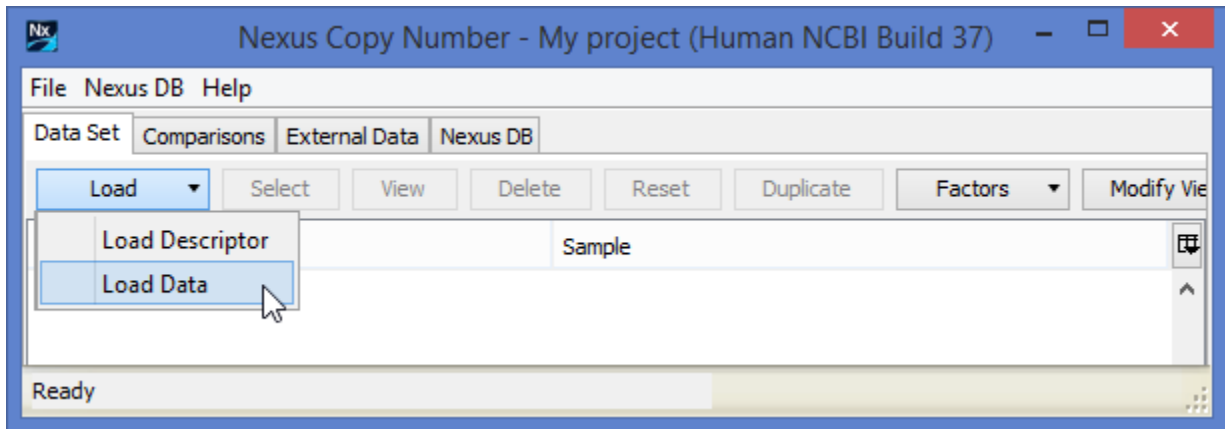

4. In the **Add Sample Data** window, select **Affymetrix-OSCHP-TuScan** from the **Select data type** drop down in the **Copy Number** tab. This will process samples using Affymetrix's TuScan algorithm for segmentation. You can also use BioDiscovery's SNP-FASST2 algorithm for segmentation – just select the data type **Affymetrix-OSCHP-SNP-FASST2** instead.
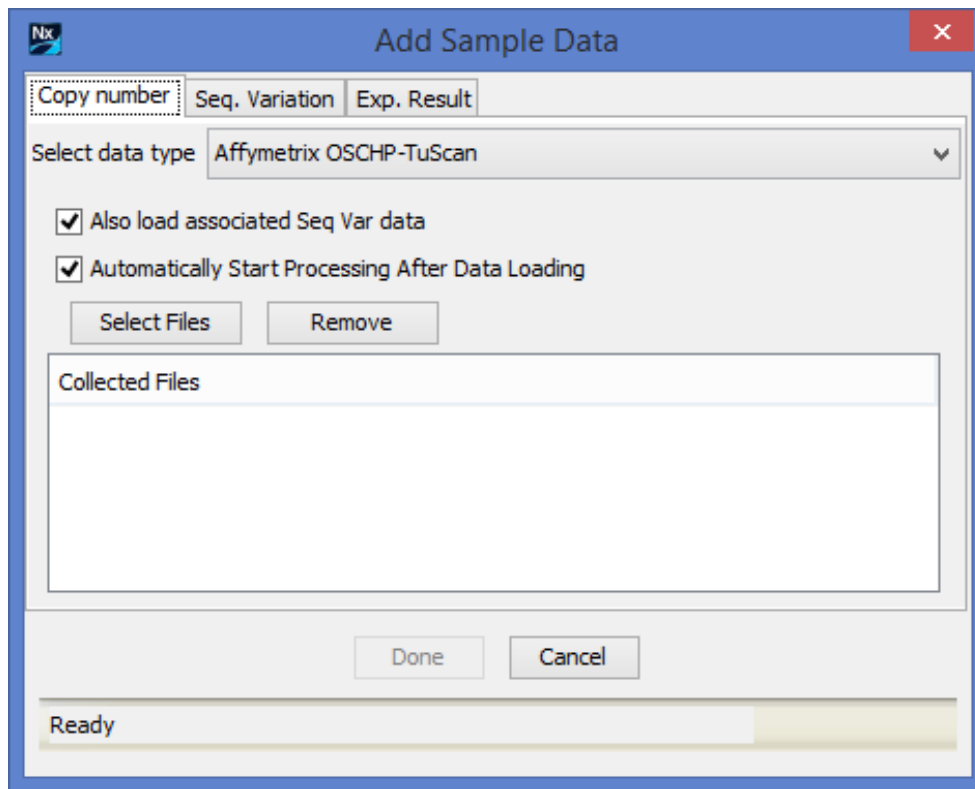

  a. To load the somatic mutation data in addition to the copy number data select the check box **Also load associated Seq Var Data**, if applicable.

b. The option **Automatically start processing after data loading** 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**.

c. Click **Select Files** to select your **Affymetrix OSCHP** files to load into Nexus Copy Number. You can select any number of files but they must all be Affymetrix OSCHP 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:
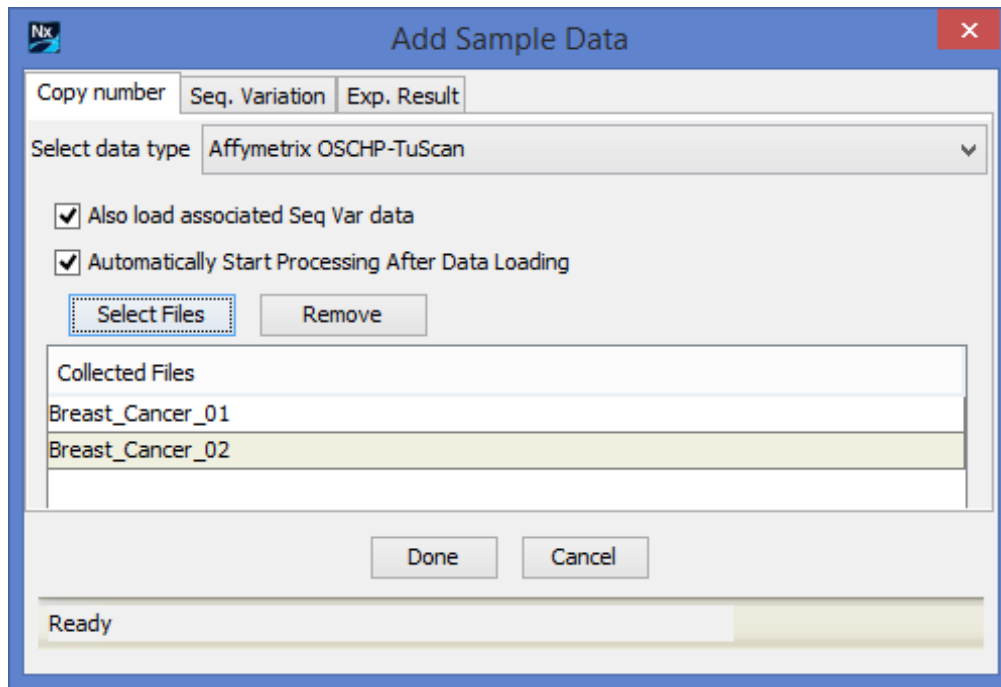
Click **Done** after you have selected all your files.

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.
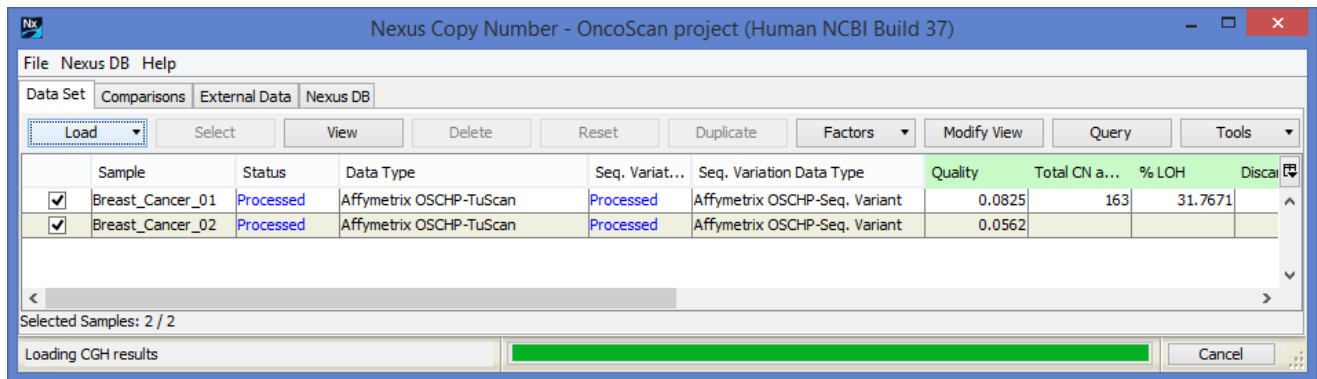
Once processing is complete, results will be displayed in the window.