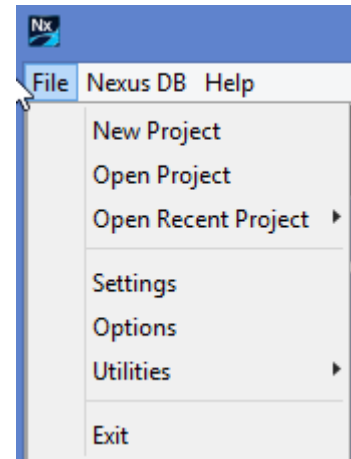
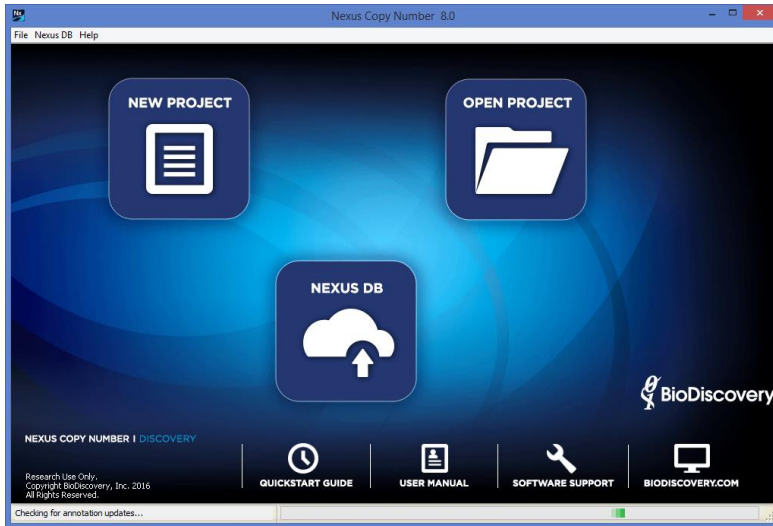


## HOW TO LOAD (MATCHED) NGS DATA:

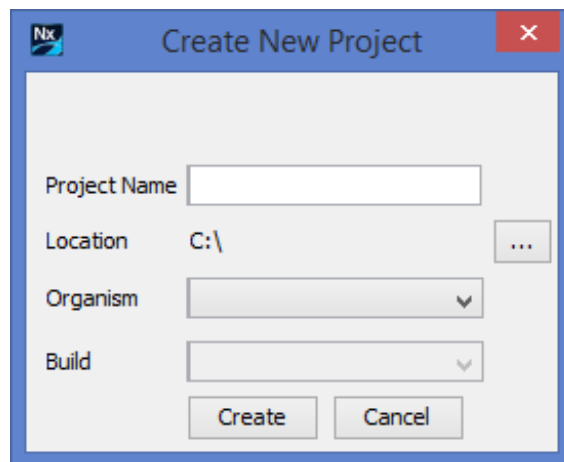
Nexus Copy Number can load and process data from WES, WGS, or targeted panels. The software loads BAM files for matched tumor-normal pairs.

### LOADING AND PROCESSING MATCHED BAM FILES

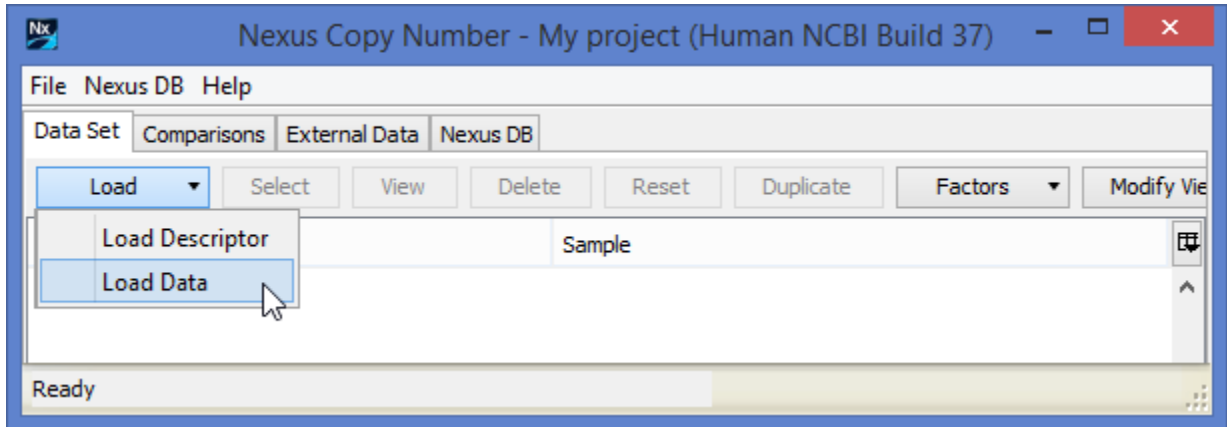
1. Launch Nexus Copy Number. Create a new project or open an existing project from the start page. You can also open and create projects from the **File** menu.



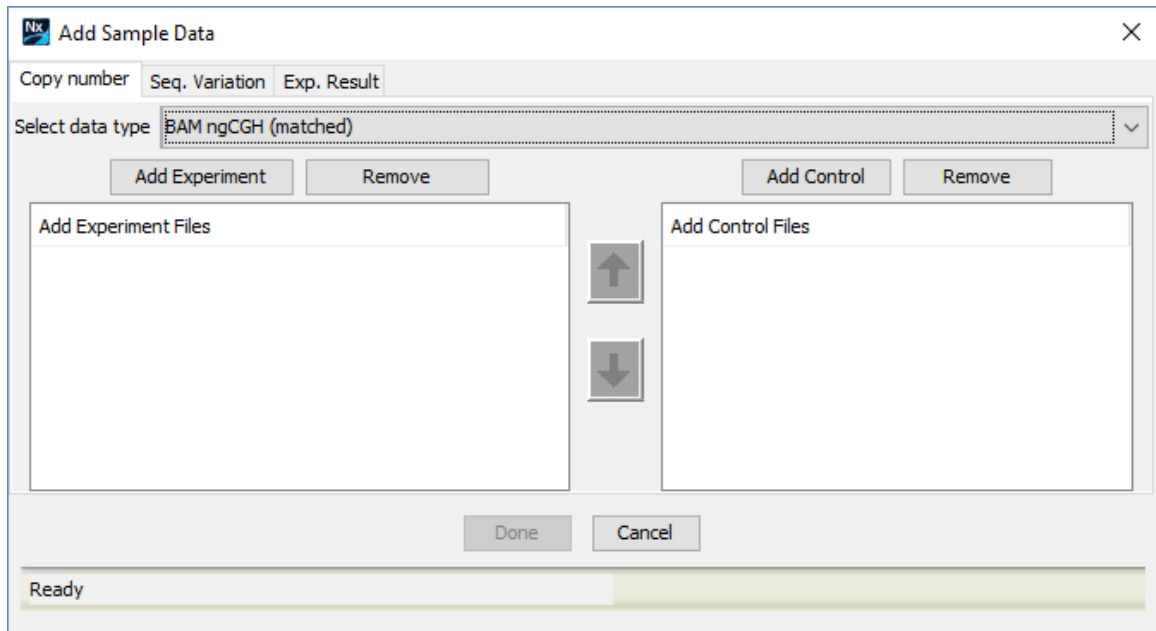
2. Specify a name for your project and a place to save it on your computer. Select the appropriate genome and build, based on the mapping information for your probes.



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

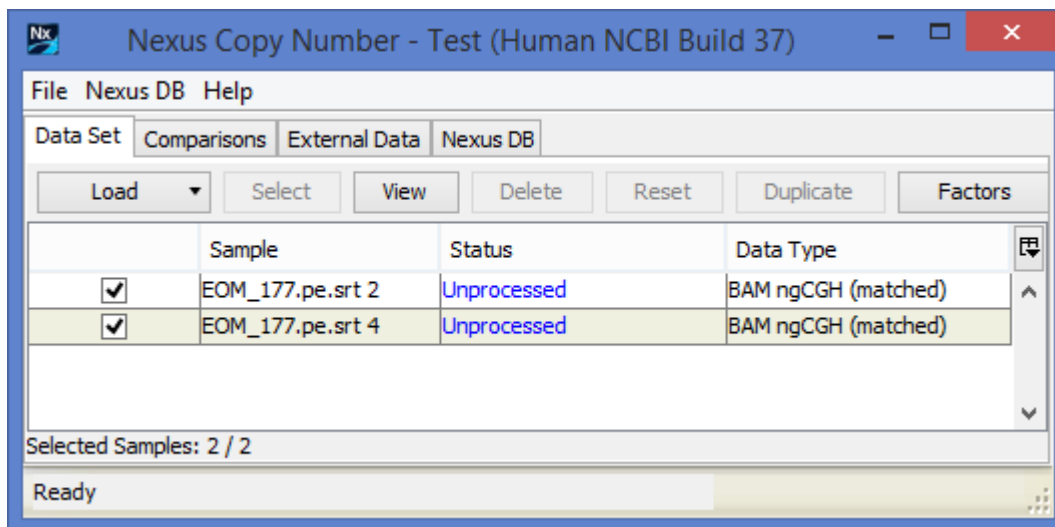


4. In the **Add Sample Data** window, select **BAM ngCGH (matched)** from the **Select data type** drop down in the **Copy Number** tab. You can select any number of files but they must all be BAM files.



- a. Click **Add Experiment** to select your tumor BAM files to load into Nexus Copy Number. Once you have finished selecting tumor files via the File Chooser, click **Open** and the sample file names will be listed in the window. Click **Add Control** to select your normal BAM files to load into Nexus Copy Number. Click **Open** after selecting the normal files and the files will be listed in the window. Highlight file names and use the up and down arrows to align the tumor-normal pairs.
- b. Click **Done** after you have selected and aligned all your files.

Samples will be loaded but not processed and will appear in the Data Set tab with Status as “Unprocessed”.



- Click **View** to process the samples. The Data Set tab will be displayed with a progress bar at the bottom showing the 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.