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.

💌 Create New Project 💌	
Project Name	
Location C:\	
Organism 🗸 🗸	
Build	
Create Cancel	

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

NX	Nexu	is Copy Number - My project (Human NCBI Build 37) –	×					
File 1	Nexus DB Help							
Data :	Data Set Comparisons External Data Nexus DB							
	Load Select	t View Delete Reset Duplicate Factors •	Modify Vie					
	Load Descriptor	Sample	₽					
	Load Data		^					
	45							
Ready	у							

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.

Mail Add Sample Data	×					
Copy number Seq. Variation Exp. Result						
Select data type Affymetrix OSCHP-TuScan	*					
✓ Also load associated Seq Var data						
Automatically Start Processing After Data Loading						
Select Files Remove						
Collected Files						
Done Cancel						
Ready						

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:

Add Sample Data						
Copy number Seq. Variation Exp. Result						
Select data type Affymetrix OSCHP-TuScan	~					
✓ Also load associated Seq Var data						
 Automatically Start Processing After Data Loading 						
Select Files Remove						
Collected Files						
Breast_Cancer_01						
Breast_Cancer_02						
Done Cancel						
Ready						

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.

NX			Nexus Copy Num	ber - C	OncoScan pr	oject (Hun	nan NCBI Build	37)			×
File 1	File Nexus DB Help										
Data Set Comparisons External Data Nexus DB											
	Load Select View Delete Reset Duplicate Factors Modify View Query Tools										
	Sample	Status	Data Type		Seq. Variat	Seq. Variation	n Data Type	Quality	Total CN a	% LOH	Discar 🛱
-	Breast_Cancer_01	Processed	Affymetrix OSCHP-TuScan		Processed	Affymetrix OS	CHP-Seq. Variant	0.0825	163	31.7671	^
 Image: A start of the start of	Breast_Cancer_02	Processed	Affymetrix OSCHP-TuScan		Processed	Affymetrix OS	CHP-Seq. Variant	0.0562			
<	· · · · · · · · · · · · · · · · · · ·										
Selected Samples: 2 / 2											
_	ng CGH results									Cance	el .;;

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