

TO PROCESS ROCHE NIMBLEGEN DATA:

1. You need to create a sample descriptor file (a tab delimited text file) to load data into Nexus. Navigate to the **Templates** folder in the Nexus installation directory. Here you will find several arrays types that Nexus is able to process. Open the folder titled **Nimblegen**. Here you will find different template files and you will select one of these depending on your input data. If you have raw normalized data that is not segmented (*_normalized_segMNT.txt files), then open **NimblegenNormalized-Template.txt**. If you have data that has already been segmented (*_segtable_segMNT.txt), then open **NimblegenSegtable-Template.txt**. It may be easiest to edit this file by opening it in a spreadsheet application such as Excel. Please note that if you want to load both normalized and segtable data for the same samples into the same project then the sample names have to be different in the sample descriptor files; e.g. add **_Seg** to the segtable sample descriptor names (i.e. **5614202** for Normalized and **5614202_Seg** for the Segtable sample name. Otherwise you will be overwriting the data for the same sample.
2. In the first column, **Sample Name**, specify a unique name for each sample that you are loading. In the second column, **File**, specify the location of your input data file. You can use either the full path (e.g. C:\Program Files\BioDiscovery\Nexus\My Projects\sample1_normalized.txt) or a relative path (relative to where you will save this sample descriptor file). Those are the only required columns. You can add an unlimited number of additional columns to specify Factors (clinical data annotations) for each sample. The column header is **Factor:** followed by a name for the Factor. Save this file with a new name and make sure to save it as a tab-delimited text file.
3. Run Nexus and click the **Create a New Project** or **Open Existing Project** button. If creating a new project, in the resulting dialog, specify a name for your project and choose a genome and then the appropriate genome build based on the mapping information for your probes. If adding additional samples to an existing project, select your project folder in the resulting dialog.
4. On the next screen, click the **Load Descriptor** button and choose the sample descriptor file you saved in step 3 above. You will see all your samples loaded into Nexus. You can click **View** to process the data and see the results.

Example sample descriptor file for Nimblegen normalized data:

Data Type:	Nimblegen Normalized		
Sample Name	File	Factor:Gender	Factor:Tumor Type
sample 1	C:\Nexus Projects\Brain Tumor\sample1_normalized_segMNT.txt	M	GBM
sample 2	C:\Nexus Projects\Brain Tumor\sample2_normalized_segMNT.txt	M	GBM
sample 3	C:\Nexus Projects\Brain Tumor\sample3_normalized_segMNT.txt	F	AOA
sample 4	C:\Nexus Projects\Brain Tumor\sample4_normalized_segMNT.txt	M	AO

Example sample descriptor for Nimblegen segmented data:

Data Type:	Nimblegen Segtable		
Sample Name	File	Factor:Gender	Factor:Tumor Type
sample 1 seg	C:\Nexus Projects\Brain Tumor\sample1_segtable_segMNT.txt	M	GBM
sample 2 seg	C:\Nexus Projects\Brain Tumor\sample2_segtable_segMNT.txt	M	GBM
sample 3 seg	C:\Nexus Projects\Brain Tumor\sample3_segtable_segMNT.txt	F	AOA
sample 4 seg	C:\Nexus Projects\Brain Tumor\sample4_segtable_segMNT.txt	M	AO