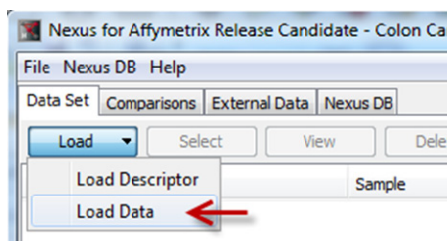


Nexus Express Quick Reference Card

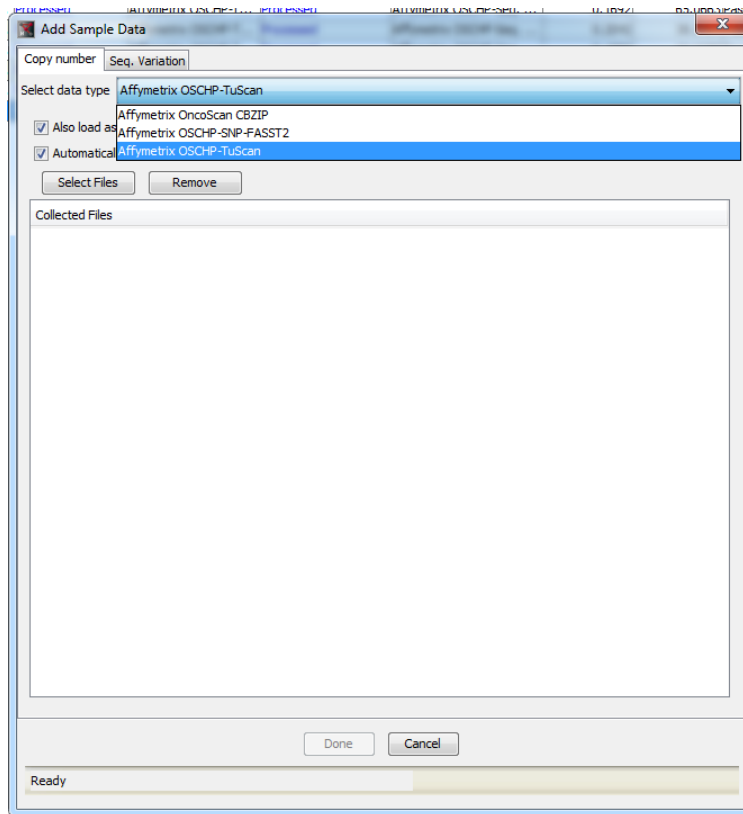
1. Open an existing project or create a new project from the start page or the File menu.



2. When creating a new project, Click the **Load → Load Data** button to add data to the project.



In the “Copy number” tab, select “Affymetrix-OSCHP - TuScan” as the data type for OncoScan™ FFPE Assay Kit copy number data. If you would like to also view Somatic Mutations within your OncoScan™ data, please select the top check box “Also load associated Seq View data”. If you would like to have the data process immediately after loading your OSCHP files, check the box “Automatically Start Processing After Data Loading”. Click on the “Select Files” button and an explorer window will appear. Navigate to your OSCHP files, select the files you would like to view and click “Done”.



3. Review your analysis parameters

In the Dataset Tab, if you did not select the option “Automatically Start Processing” above, please click the “View” button to process your OSCHP files. Click on “Processed” in the “Status” column for a given sample to have the “Settings” dialog box appear. Under “Analysis” you can see the algorithm used to process the data. Affymetrix’s TuScan algorithm is the recommended default algorithm for OncoScan™ data. The alternative algorithm is SNPFAST2 from BioDiscovery. If analyzing the OncoScan™ data with SNPFAST2, please go to page 14 of this QRC.

Settings

Select data typeAffymetrix OSCHP-TuScan

Parameters

Ratio Column

Log2Ratio

High copy gain threshold

4

Robust Variance Sample QC Calculation

Percent outliers to remove

3.0

Set as Current

Close

Settings

Select data typeAffymetrix OSCHP-Seq. Variant

Parameters

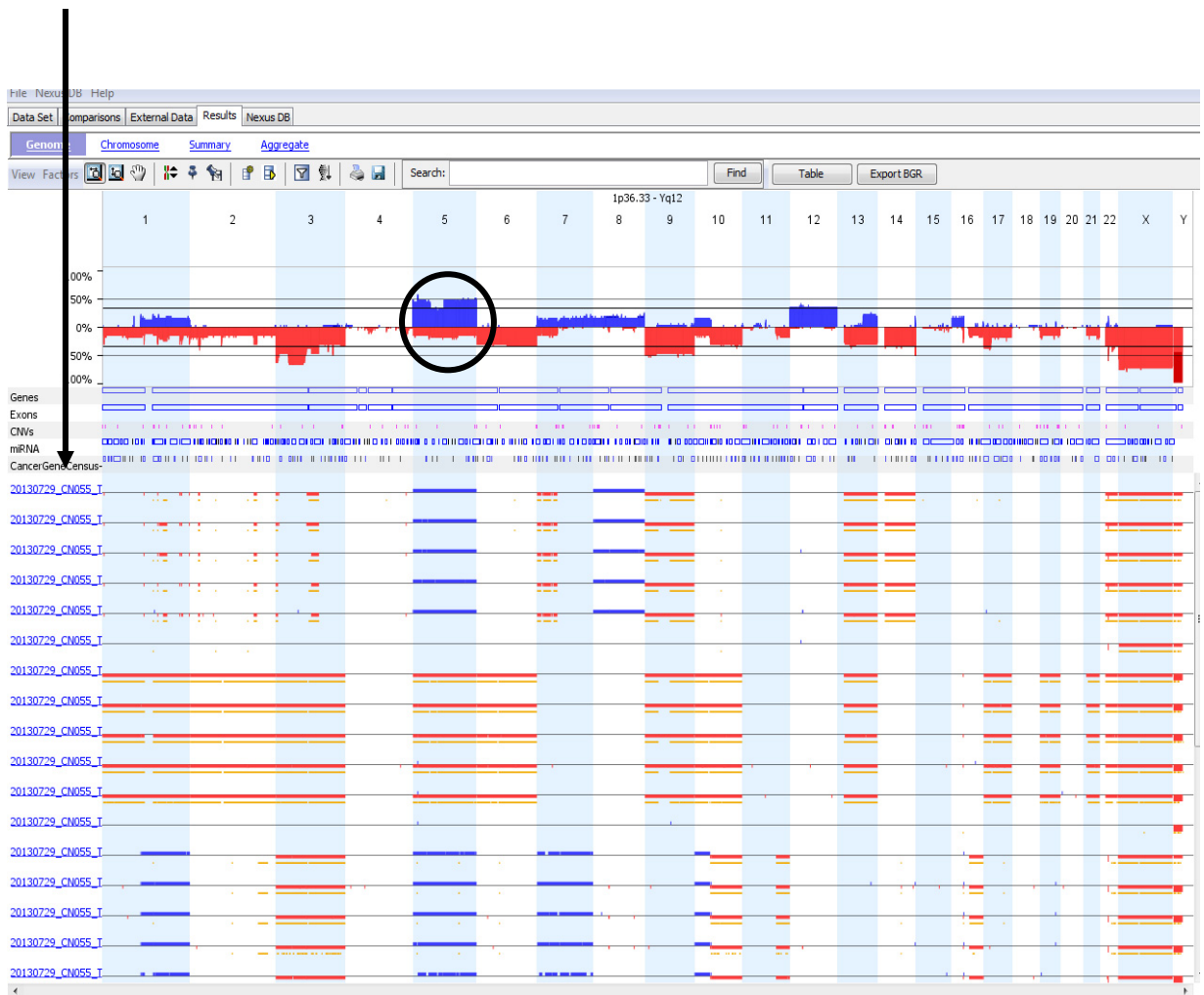
Remove Somatic Mutations with Value(s)

absent

Set as Current

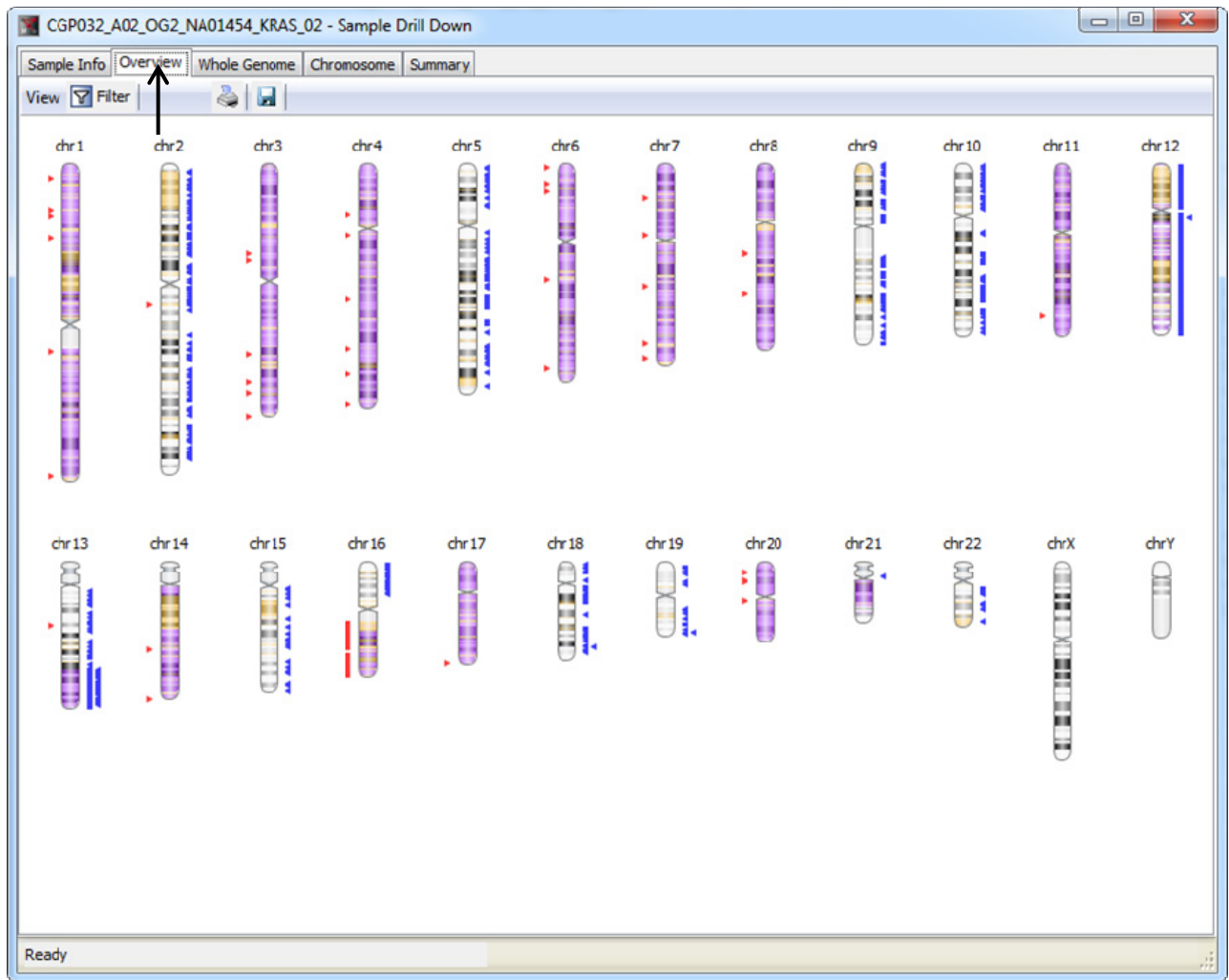
Close

4. In the Dataset tab, you can review the TuScan algorithm metrics for OS-MAPD, OS- ndSNPQC, OS- ndWavinessSd, OS-CellCheckPairStatus, OS-% Aberrant Cell, OS-Ploidy, and OS- Low Diploid Flag. For details descriptions of these metrics, please refer to the OncoScan Console Software User Manual.
5. Once all samples are in a “processed” status, the samples will be displayed in the Results Tab which is a multi-sample view. All the samples in the project (or the ones for which you have selected the check box in the Dataset Tab), will be listed on the left of the Results tab. The top graph allows for viewing common aberrations across the dataset. In the example below, ~50% of the samples have a gain on Chromosome 5 (black circle). To drill down into a specific sample, click on the name of the sample on the left of the screen (arrow).



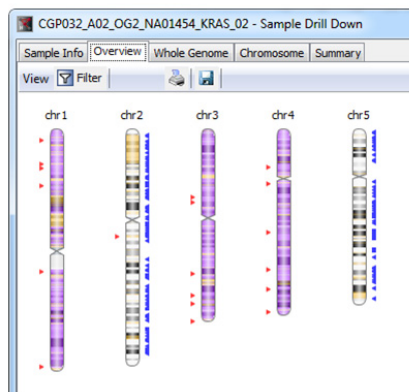
Single Sample Data Analysis/Interpretation:

1. From the Results Tab, click on the OSCHP file name to bring up the individual sample details.
2. First, determine if the sample needs re-centering (adjustment for ploidy).
 - a. In the “Sample Info”, check if “OS Diploid Flag” is “Yes”. This usually indicates Ploidy correction is needed.
 - b. Click the “Overview” tab (arrow) in the sample drill down window.

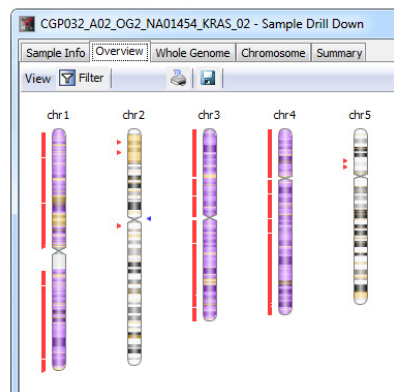


- c. If there are regions of allelic imbalance (indicated by purple shading of the chromosome) that do not have copy number changes associated with them (blue or red bars next to the chromosome) probe centering is likely required. Also, if there are regions of loss (indicated by a red bar to the left of the chromosome) that have no allelic imbalance or LOH, probe centering is likely needed. See the example below:

Requires re-centering

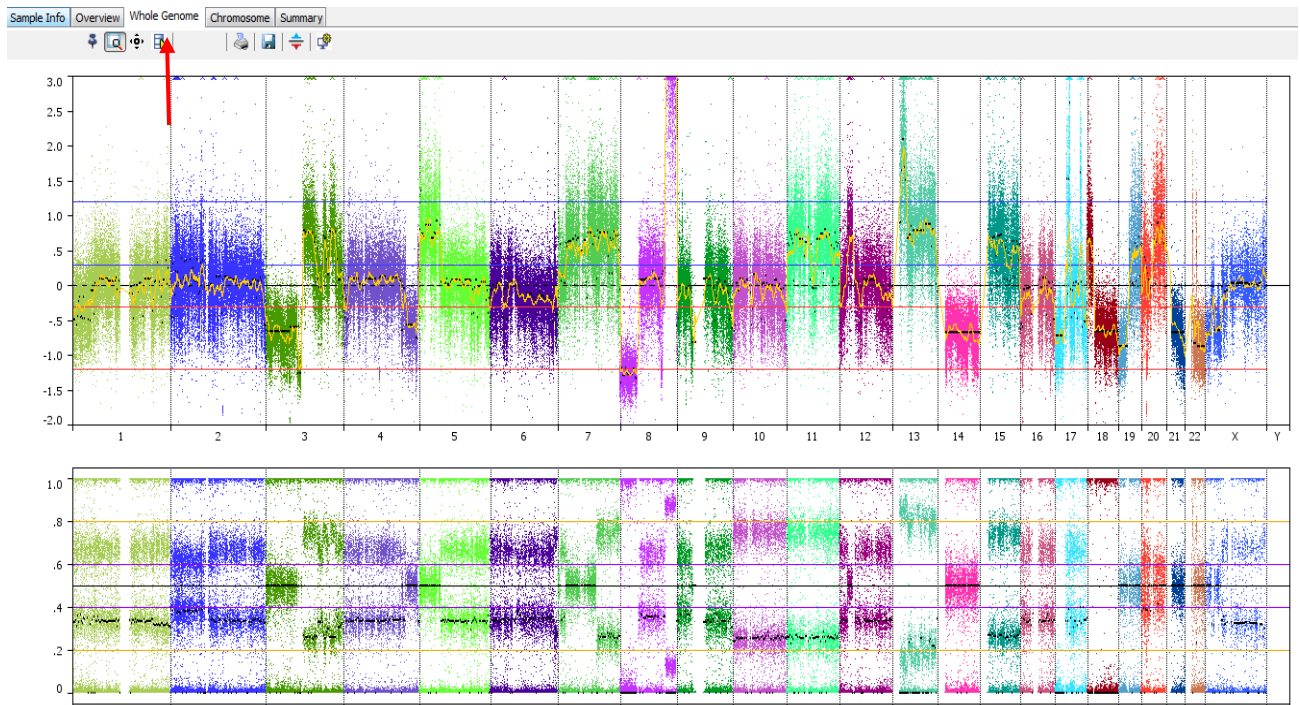


Probably ok



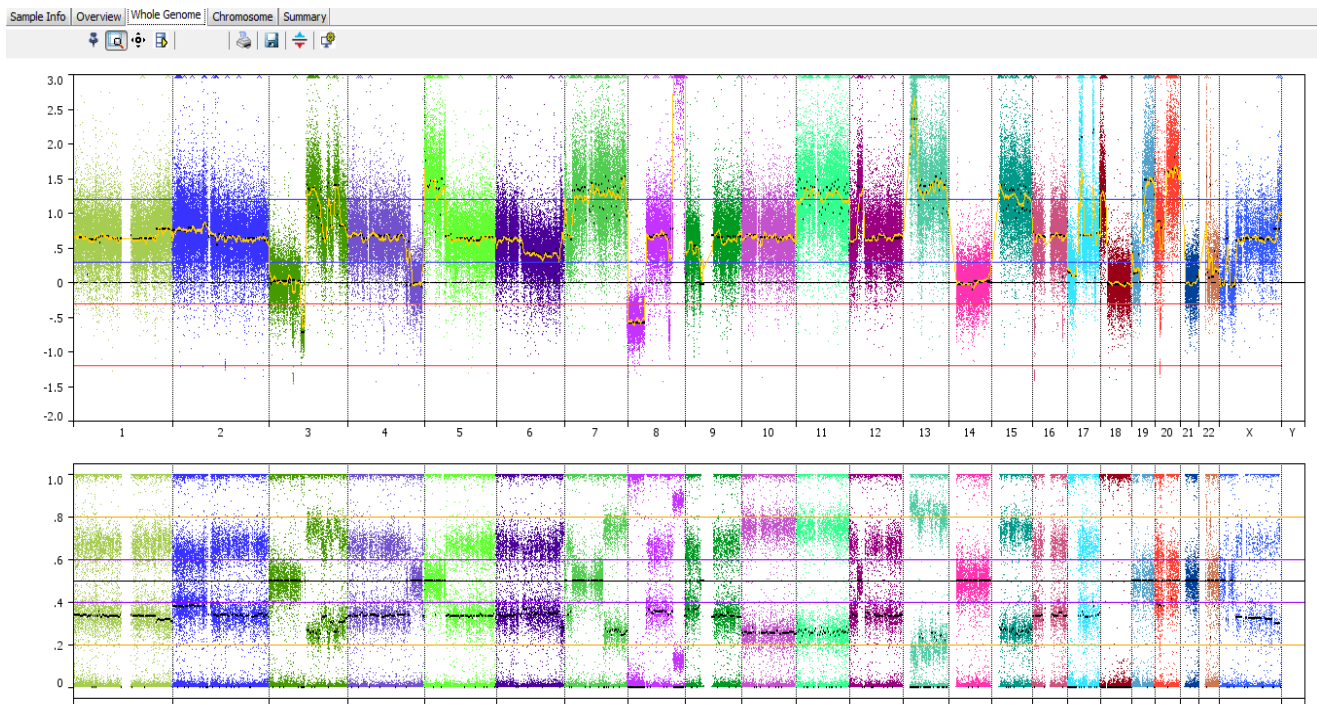
IMPORTANT: The following section on recentering the sample in the software is applicable for the SNPFASST2 algorithm only.

- d. Click on the “Whole Genome” tab (arrow in figure below) in the sample drill down to display the intensity and B-allele frequency information across the whole genome. [NOTE: Another check to see if the sample needs recentered is to examine the autosomal regions with 3 tracks in the BAF graph that are being called as a loss or a gain according to the logR graph. This would also indicate the sample likes needs corrected in terms of ploidy.]. In the sample below, we have already seen that the Overview suggest this sample might need recentered. In looking at the Whole Genome View, the logR graph for Chromosome 3p and 14 indicates a loss, whereas the BAF track has 3 tracks representing at least 2 alleles and therefore indicating this sample needs recentering. [For some samples, one may need to identify regions that have 3 tight bands on the BAF, but in the logR graph are elevated above the 0 (diploid) line.]

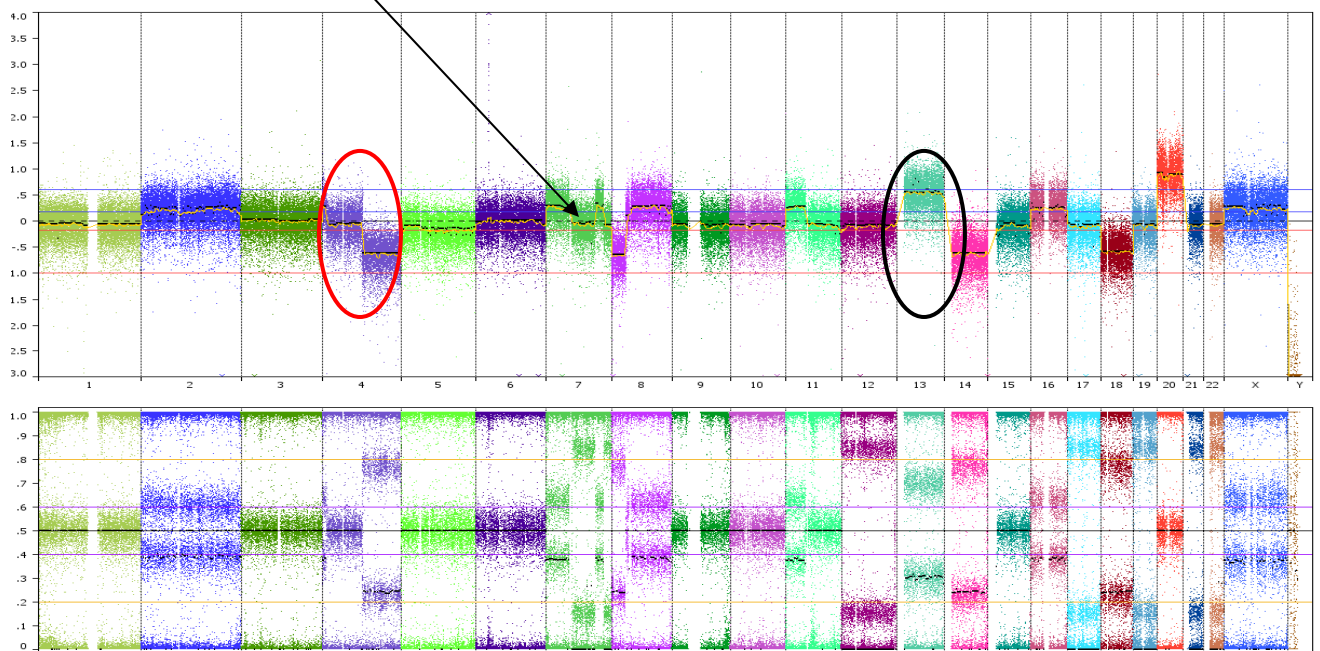


- e. Examine the intensity and B-allele frequency data to identify diploid regions. Zoom into the diploid region using the rectangular zoom tool .
- f. Click the “Set Diploid Regions” button () and then click the “Add Region” button. Add as many diploid regions as necessary and then click “Apply” to initiate reprocessing of the sample setting the identified regions to CN=2.

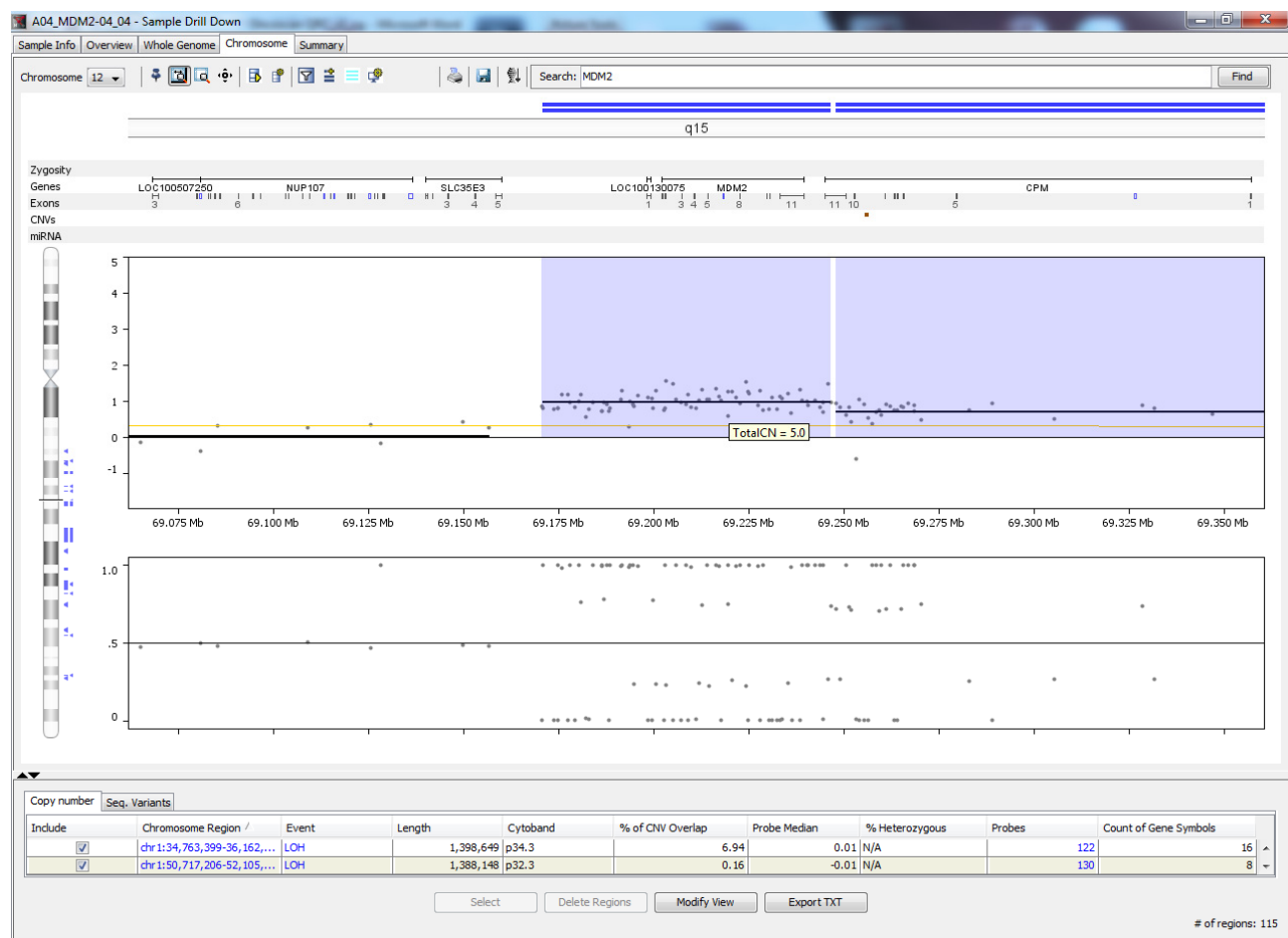
The figure below shows the same sample after recentering using Chromosome 14 as baseline. Those regions with 3 tracks in the BAF now have a logR graph centered at 0 which is a more likely scenario. [Note that in the cases where the ploidy is 4, there may be 3 allele tracks as each chromosome may have duplicate resulting in no allelic imbalance.]



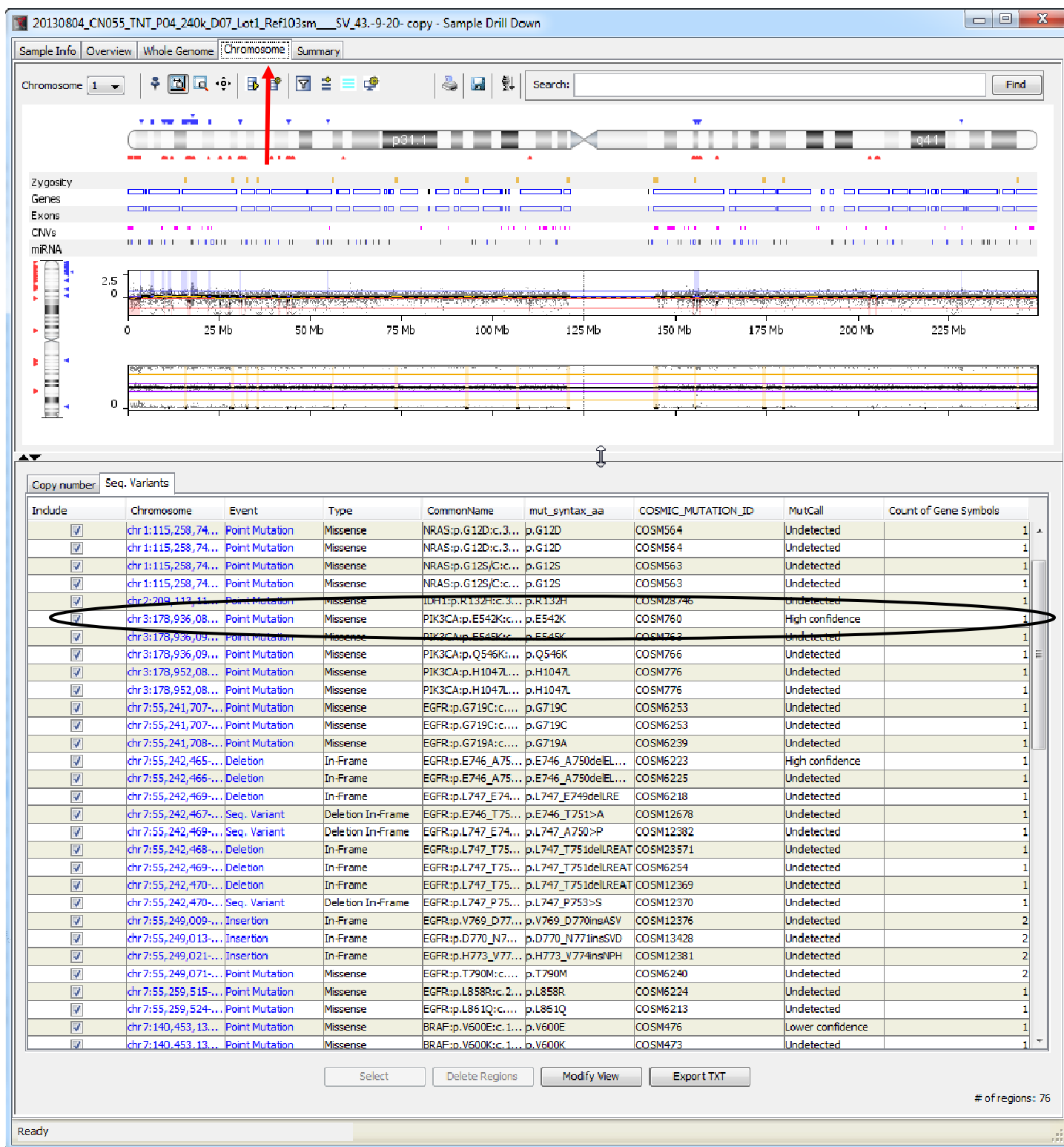
- Use the Whole Genome View to identify gains, losses, LOH and copy neutral LOH, by reviewing the logR and the BAF tracks together. In the example below, Chromosome 4 shows diploid on the p arm (logR at 0 and 3 BAF tracks), while the q arm shows a loss (downward shift of the logR data and 4 BAF tracks, red oval). Chromosome 13 is an example of a gain (upward shift of the logR data and 4 BAF tracks, black oval). The interstitial region of Chromosome 7 shows copy neutral LOH (logR data at 0 and 4 BAF tracks, arrow).



4. Use the Chromosome view to zoom to probe level, and to view copy number aberrations. To view copy number in a gene of interest, type “the gene name” in the search box and click **Find**. The software will zoom into that gene. You can mouse over the aberration to get linear copy number call. For example, screen shot of an aberration with a linear copy number of 5.0 for the MDM2 gene is shown below.



5. To view the Somatic Mutation data for each sample, click on the Seq Variants tab located under the graphs on the Chromosome tab (red arrow) . This table lists somatic mutation annotation information as well as provides a call for each mutation in the assay in the MutCal column. In the figure below, the oval outlines a somatic mutation with a high confidence call for that particular mutation.



- To view samples that contain aberrations in a list of genes, go to the "Dataset" tab, click on the **Query** button (located in the red circle in the image below). Type your list of genes or load a tab delimited text file with the gene names, click **Run**. You can quickly identify the samples in the project that have aberrations in your genes of interest.

Nexus for Affymetrix - SampleDataSet (Human NCBI Build 37)

File Nexus DB Help

Data Set Comparisons External Data Results Nexus DB

Load Select View Delete Reset Duplicate Factors Query Tools

Sample	Status	Data Type	Seq. Variation Status	Seq. Variation Data Type	OS-MAPD	OS-ndSNPQC	OS-CellPairCheck Status	OS-ndWavinessSd	OS-% Aberr. Cells	OS-Ploidy	OS-Low Diploid Flag
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1515	68.0620	Pass	0.0476	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1462	64.8833	Pass	0.0456	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1474	63.8122	Pass	0.0490	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0446	NA	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0471	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0688	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0579	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0508	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0495	NA	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0430	NA	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0428	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0624	homogeneous	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0587	NA	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0560	NA	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0518	NA	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0659	NA	2.0000	No
20130729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0469	homogeneous	2.0000	No
20130730_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0606	NA	2.0000	No
20130730_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0527	NA	2.0000	No
20130730_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...			Pass	0.0549	NA	2.0000	No
20130730_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1656	51.1400	Pass	0.0536	NA	2.0000	No
20130730_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1821	47.2093	Pass	0.0587	NA	2.0000	No
20130730_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.2025	42.8262	Pass	0.0558	NA	2.0000	No
20130804_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1653	67.4710	Pass	0.0560	NA	2.0000	No
20130804_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1588	59.6585	Pass	0.0607	NA	2.0000	No
20130804_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1620	57.9069	Pass	0.0557	NA	2.0000	No
20130804_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1563	65.5259	Pass	0.0534	NA	2.0000	No
20130804_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1474	63.7076	Pass	0.0572	NA	2.0000	No
20130804_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1571	58.6815	Pass	0.0496	homogeneous	2.0000	No

Query Panel

Data Type: Genes

MYC
EGFR
FGFR1
ERBB2

☐ Completely covered only

Run Close Load

Query Results: Genes=MYC ...

Sample Aggregate

Select Apply Selection Export TXT Compute Medians Show Classification

Sample	MYC(chr8:128,748,314-128,753,680)	EGFR(chr7:55,086,724-55,275,031)	FGFR1(chr8:38,268,655-38,326,352)	ERBB2(chr17:37,844,392-37,884,915)
20130729_CN055_TNT_P01_240k_C09_Lot2_CX1WANCEF...				CN Loss, LOH
20130729_CN055_TNT_P01_240k_D03_Lot1_D21072XPat0...		CN Gain		
20130729_CN055_TNT_P01_240k_C07_Lot2_CX1WANCEF...				CN Loss, LOH
20130729_CN055_TNT_P01_240k_C08_Lot2_CX1WANCEF...				CN Loss, LOH
20130804_CN055_TNT_P04_240k_B02_Lot2_7ENGXFB7EN...				
20130729_CN055_TNT_P01_240k_A07_Lot2_B5V8RN6SFB...	CN Gain	CN Loss, LOH	CN Gain	
20130729_CN055_TNT_P01_240k_D02_Lot1_D21072XPat0...		CN Gain		
20130730_CN055_TNT_P05_240k_A11_Lot1_WD7135FBPA...				
20130804_CN055_TNT_P04_240k_B01_Lot2_7ENGXFB7EN...				
20130729_CN055_TNT_P01_240k_A11_Lot2_B5V8RN6SFB...	CN Gain	CN Loss, LOH	CN Gain	
20130730_CN055_TNT_P05_240k_A07_Lot1_WD7135FBPA...				
20130730_CN055_TNT_P05_240k_A08_Lot1_WD7135FBPA...				
20130804_CN055_TNT_P04_240k_B04_Lot2_7ENGXFB7EN...				
20130729_CN055_TNT_P01_240k_A10_Lot2_B5V8RN6SFB...	CN Gain	CN Loss, LOH	CN Gain	
20130729_CN055_TNT_P01_240k_D05_Lot1_D21072XPat0...		CN Gain		
20130729_CN055_TNT_P01_240k_C12_Lot2_CX1WANCEF...				
20130730_CN055_TNT_P05_240k_A12_Lot1_WD7135FBPA...				
20130729_CN055_TNT_P01_240k_A12_Lot2_B5V8RN6SFB...				
20130729_CN055_TNT_P01_240k_A09_Lot2_B5V8RN6SFB...	CN Gain	CN Loss, LOH	CN Gain	
20130729_CN055_TNT_P01_240k_A08_Lot2_B5V8RN6SFB...	CN Gain	CN Loss, LOH	CN Gain	
20130730_CN055_TNT_P05_240k_A10_Lot1_WD7135FBPA...				
20130729_CN055_TNT_P01_240k_C11_Lot2_CX1WANCEF...				CN Loss, LOH
20130729_CN055_TNT_P01_240k_D04_Lot1_D21072XPat0...		CN Gain		
20130729_CN055_TNT_P01_240k_D01_Lot1_D21072XPat0...		CN Gain		
20130804_CN055_TNT_P04_240k_B06_Lot2_7ENGXFB7EN...				
20130729_CN055_TNT_P01_240k_D06_Lot1_D21072XPat0...				
20130804_CN055_TNT_P04_240k_B03_Lot2_7ENGXFB7EN...				
20130729_CN055_TNT_P01_240k_C10_Lot2_CX1WANCEF...				CN Loss, LOH
20130729_CN055_TNT_P05_240k_A09_Lot1_WD7135FBPA...				
20130804_CN055_TNT_P04_240k_B05_Lot2_7ENGXFB7EN...				

Ready

7. You can compare copy number data between groups, (e.g., Tumor and Normal) using the comparison analysis functionality.
 - a. In the “Dataset” tab, sample information can be added to the project either by clicking the **Factors** drop down button and then selecting either **Add Factor** to enter the data manually or “Load Factor” to read

data from a tab-delimited text file. Below we are manually adding a “Prognosis” factor. Click **OK** to add a Prognosis Factor column to the dataset.

Nexus for Affymetrix - SampleDataSet (Human NCBI Build 37)

File Nexus DB Help

Data Set Comparisons External Data Results Nexus DB

Load Select View Delete Reset Duplicate Factors Query Tools

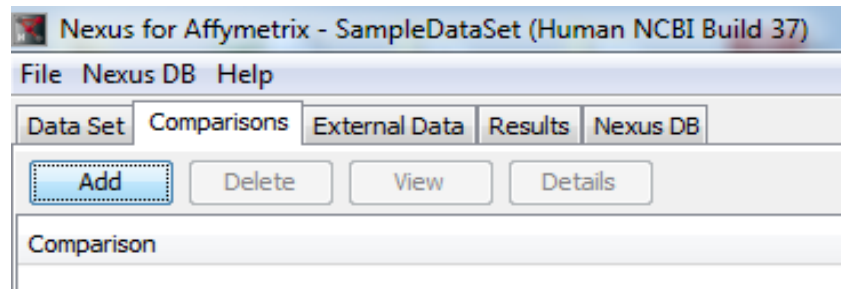
Sample	Status	Data Type	Seq. Variation Status	Seq. Variation Data Type	OS-MAPD	OS-ndSNPQC	OS-CelPairCheck Status	OS-ndWavinessSd	OS-% Aberr. Cells	OS-Ploidy	OS-Low Diploid Flag
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1651	68.0620	Pass	0.0476	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1515	66.2991	Pass	0.0479	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1462	64.8833	Pass	0.0456	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1474	63.8122	Pass	0.0490	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1440	58.7341	Pass	0.0446	NA	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1533	65.0601	Pass	0.0471	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1937	40.8345	Pass	0.0688	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1690	56.5370	Pass	0.0579	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1626	54.5318	Pass	0.0508	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1559	52.2592	Pass	0.0495	NA	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1497	53.7825	Pass	0.0430	NA	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1687	42.8768	Pass	0.0428	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1694	64.9542	Pass	0.0624	homogeneous	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1533	65.6637	Pass	0.0587	NA	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1501	71.4071	Pass	0.0560	NA	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1511	69.4752	Pass	0.0518	NA	2.0000	No
21030729_C...	Processed	Affymetrix O...	Processed	Affymetrix OSCHP-Seq...	0.1532	67.7400	Pass	0.0659	NA	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1653	67.4710	Pass	0.0469	homogeneous	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1588	59.6585	Pass	0.0606	NA	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1515	66.2991	Pass	0.0527	NA	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1474	63.8122	Pass	0.0549	NA	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1440	58.7341	Pass	0.0536	NA	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1563	65.5259	Pass	0.0587	NA	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1474	63.7076	Pass	0.0572	NA	2.0000	No
21030730_C...	Processed	Affymetrix O...	Processed	Affymetrix O...	0.1571	58.6815	Pass	0.0496	homogeneous	2.0000	No

Factor Name
Prognosis
OK Cancel

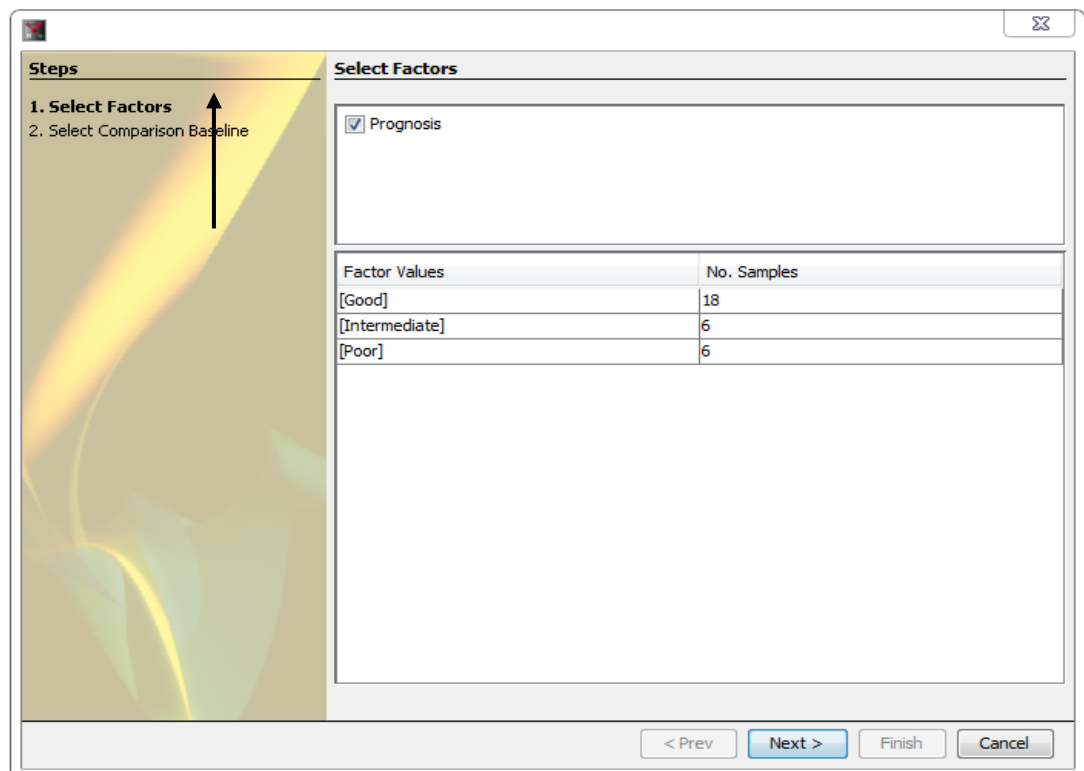
- b. If you are not importing factors from a tab-delimited file, manually enter each Factor field by clicking in the text box for the appropriate samples. The figure below shows the Prognosis for each sample as Good, Intermediate, Poor in the far right column.

Data Set	Comparisons	External Data	Results	Nexus DB							
Load	Select	View	Delete	Reset	Duplicate	Factors	Query	Tools			

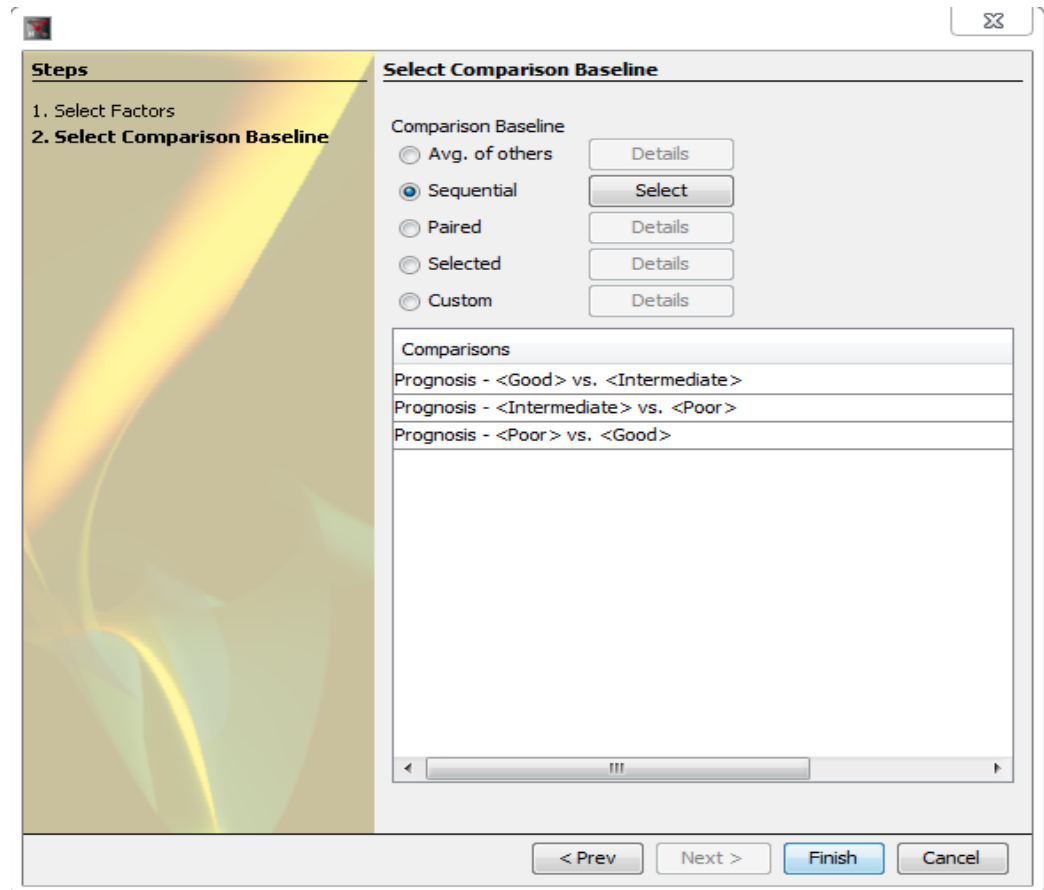
- c. Click the comparisons tab (arrow) and click the **Add** button to open the dialog to set up a comparison analysis.



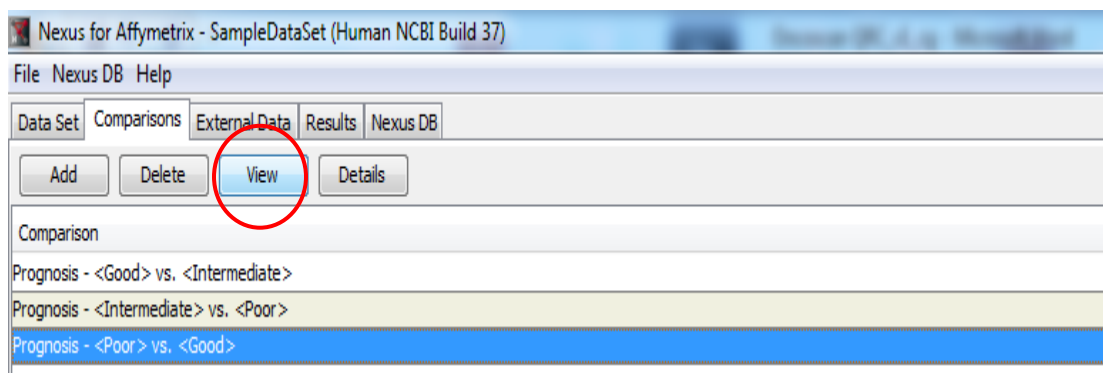
- d. Select the factor that identifies the different groups of interest. In this example check Prognosis.



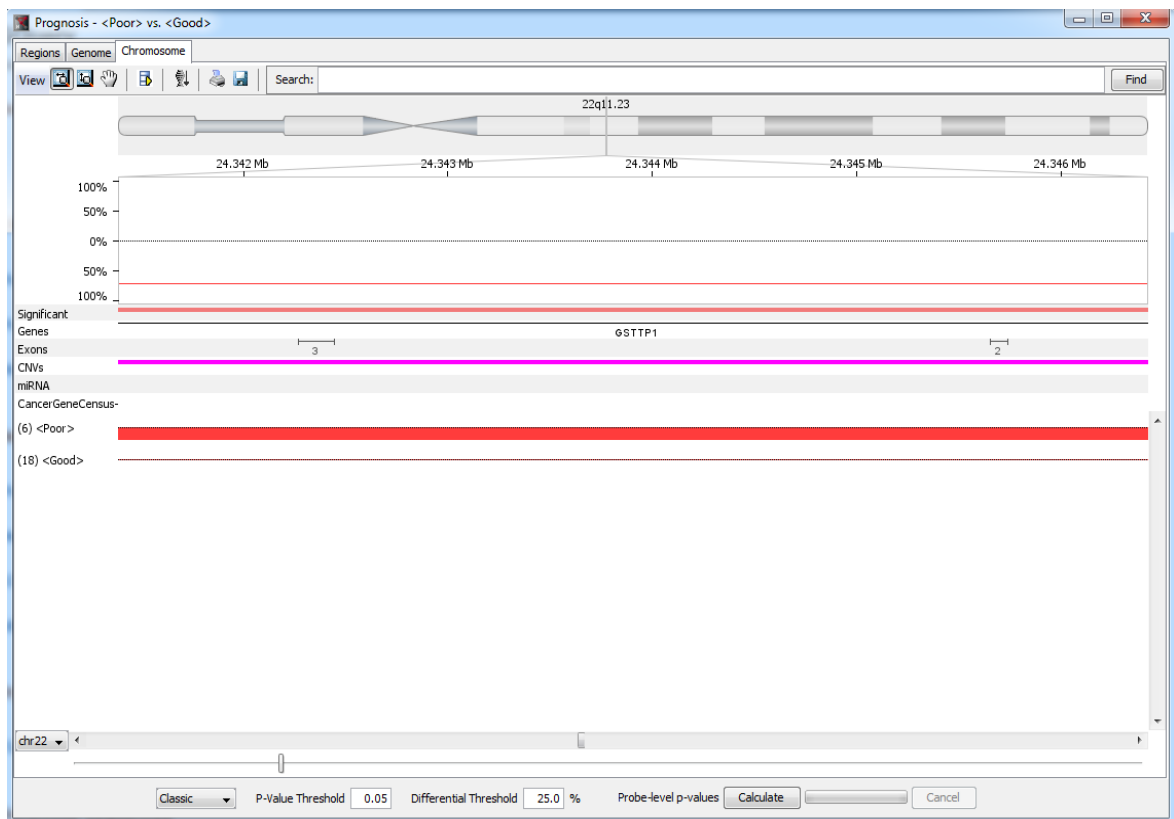
- e. Select the baseline to be used in the analysis. In this example, select “Sequential” which will analyze each group against the other 2 groups individually. Click **Finish**.



- f. Highlight the comparison you would like to view (e.g., Poor vs. Good). The View button should now be enabled, click **View** to see the results.



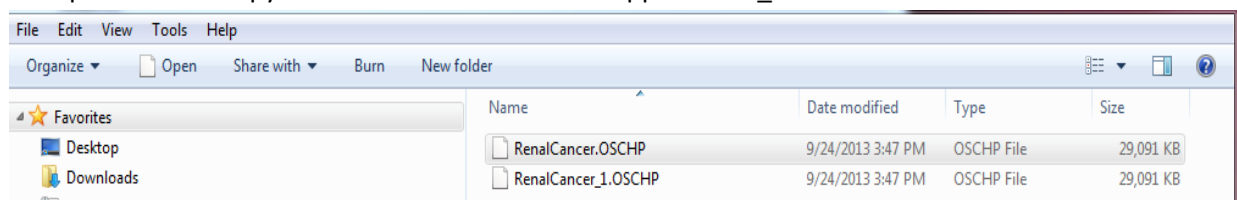
8. Use the “Regions”, “Genome”, and “Chromosome” tabs to explore the copy number changes between selected groups. Below illustrates a region on Chromosome 22 covering the GSTTP1 gene in which the patients with Poor Prognosis show a loss and the patients with Good Prognosis have no aberration.



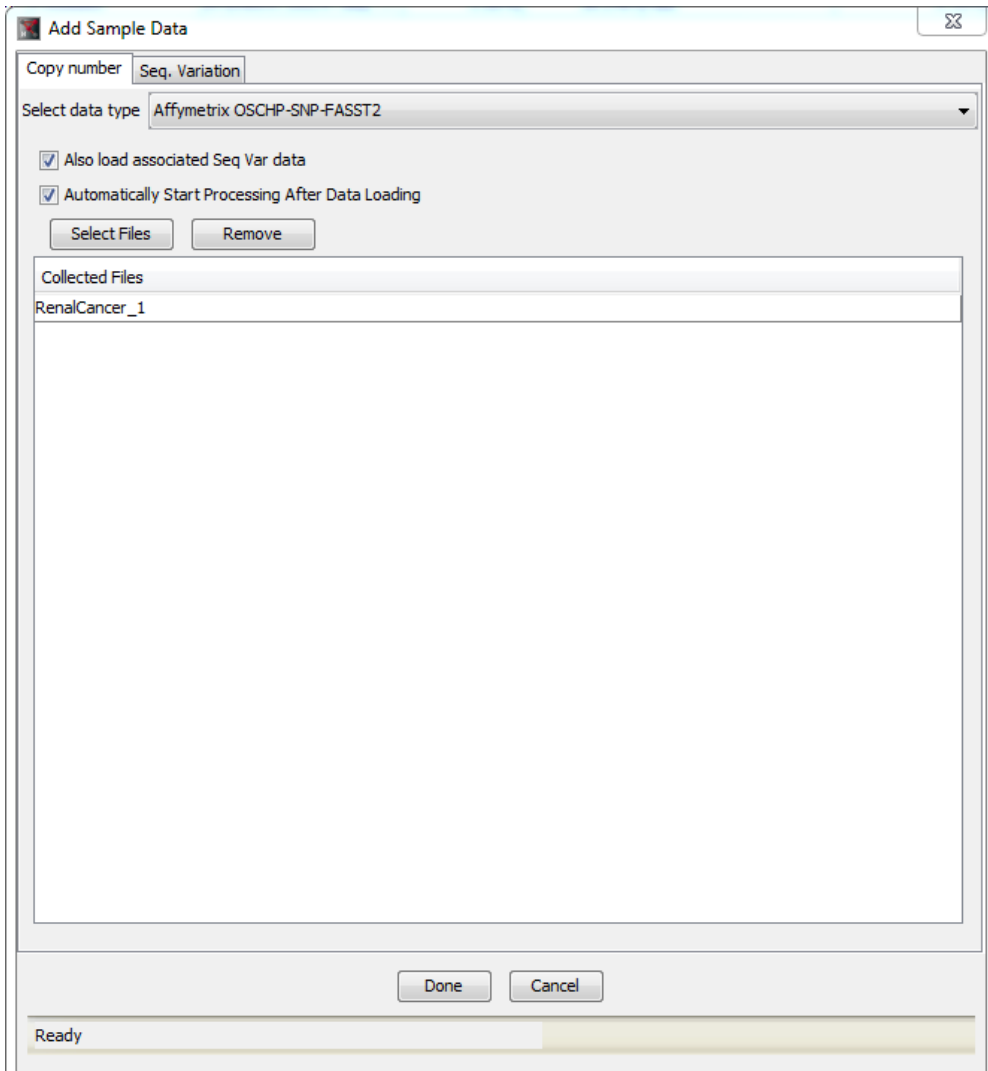
Analysis of OncoScan™ Assay Data using SNPFAST2

Affymetrix recommends analyzing OncoScan™ Assay data using our TuScan algorithm. The Nexus Express software does enable you to analyze the data using the BioDiscovery SNPFAST2 algorithm as well. If you would like to view your data using SNPFAST2, please follow the following steps. To enabling comparison of the different segmentation algorithms in the same project, please make a copy of the OSCHP file on your computer.

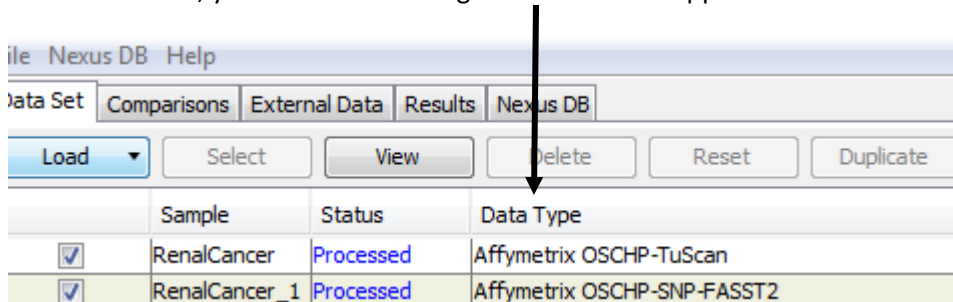
1. Duplicate your data on your computer.
 - a. Example: Make a copy of RenalCancer.OSCHP and append an “_1”



- b. Load the copy “RenalCancer_1” into your project making sure to select “Affymetrix OSCHP SNP-FASST2” from the select data type list. Click on “Select Files” to choose the OSCHP file you would like to bring in using SNPFASST2 and then select “Done”.



- c. In the Dataset Tab, you can see which algorithm has been applied to each OSCHP file.



- d. Click on “Processed” under Status for the sample(s) run with SNP-FASST2 (e.g. RenalCancer_1.OSCHP). Check that the “Min number of probes per segment” is set to 10 (black oval).

Settings

Select data type: Affymetrix OSCHP-SNP-FASST2

Parameters

Ratio Column: Log2Ratio

Recenter Probes

Type: Median

Analysis

Type: SNP-FASST2 Segmentation

Significance Threshold	5.0E-7
Max Continuous Probe Spacing (Kbp)	1000.0
Min number of probes per segment	10
High Gain	0.7
Gain	0.1
Loss	-0.15
Big Loss	-1.1
Male Sex Chromosomes Big Loss	-1.1
3:1 Sex chromosome gain	1.2
4:1 Sex chromosome gain	1.7
Homozygous Frequency Threshold	0.85
Homozygous Value Threshold	0.8
Heterozygous Imbalance Threshold	0.4
Minimum LOH Length (KB)	500
Minimum SNP Probe Density (Probes/MB)	0.0

Set as Current Close

- e. If you would like to change the “Min number of probes per segment” from the recommended 10, please go back to the Dataset Tab. Highlight the sample file that was run with SNPFASST2 and click on “Duplicate”.

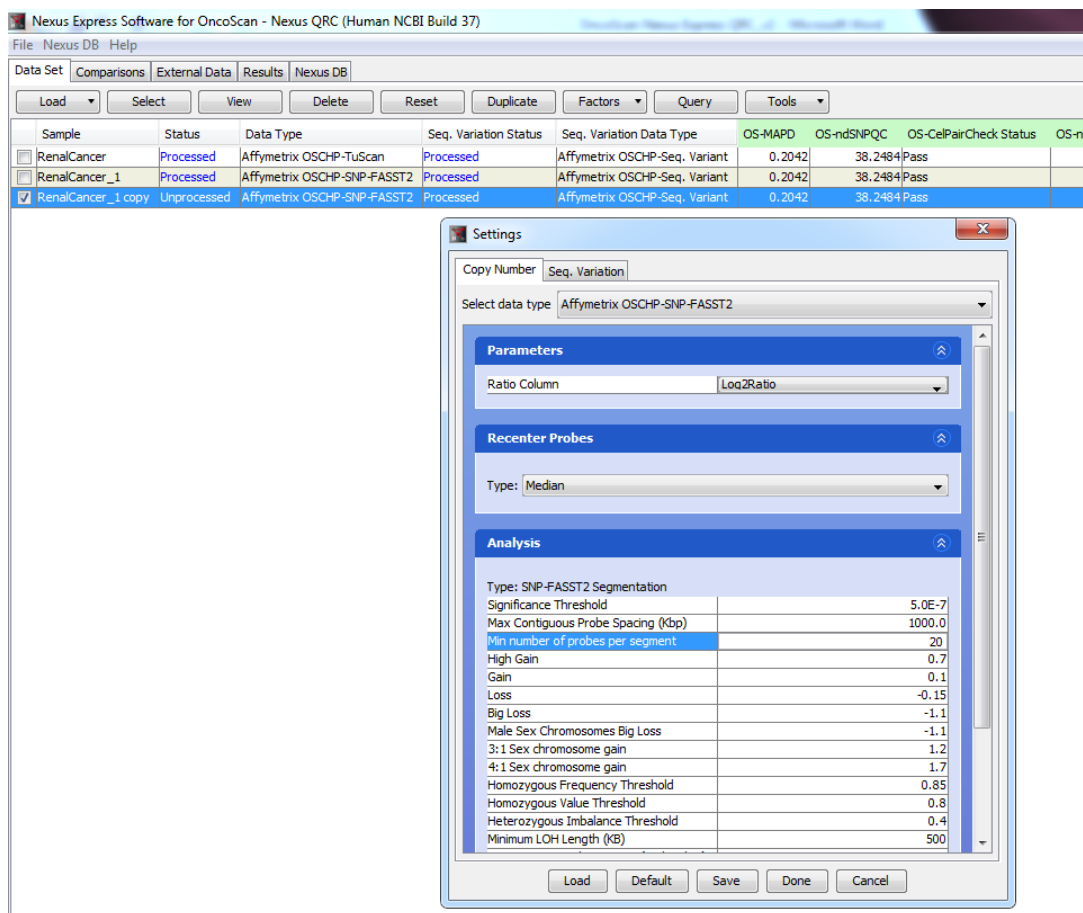
File Nexus DB Help

Data Set Comparisons External Data Results Nexus DB

Load Select View Delete Reset Duplicate Factors Query

	Sample	Status	Data Type	Seq. Variation Status	Seq. Variation Data Type
☒	RenalCancer	Processed	Affymetrix OSCHP-TuScan	Processed	Affymetrix OSCHP-Seq. Variant
☐	RenalCancer_1	Processed	Affymetrix OSCHP-SNP-FASST2	Processed	Affymetrix OSCHP-Seq. Variant
☐	RenalCancer_1 copy	Unprocessed	Affymetrix OSCHP-SNP-FASST2	Processed	Affymetrix OSCHP-Seq. Variant

- f. Uncheck all boxes except for those OSCHP files you would like to process using a different “Min number of probes per segment”. Go to File → Settings , make sure the data type is on “Affymetrix OSCHP SNP-FASST2” and then you can alter the “Min number of probes per segment” value (e.g. 20). Click the “Done” button.



- g. Click on “View” to process the data.

Data Set	Comparisons	External Data	Results	Nexus DB			
Load	Select	View	Delete	Reset	Duplicate	Factors	Query
	Sample /	Status	Data Type	Seq. Variation Status	Seq. Variation Data Type		
☐	RenalCancer	Processed	Affymetrix OSCHP-TuScan	Processed	Affymetrix OSCHP-Seq. Variant		
☐	RenalCancer_1	Processed	Affymetrix OSCHP-SNP-FASST2	Processed	Affymetrix OSCHP-Seq. Variant		
☐	RenalCancer_1 copy	Processed	Affymetrix OSCHP-SNP-FASST2	Processed	Affymetrix OSCHP-Seq. Variant		

- h. Please return to Step C on page for to follow the workflow. Please keep in mind that linear copy number is not available for the SNPFASST2 algorithm.