



Technology Transition Workshop | *Brad Dixon*

GenPlex™ HID Training Class II
Data Analysis Using GeneMapper®
Software v4.0 / 4.1

GenPlex™ HID System Analysis Workflow

- **Set up the SNPlex™ system analysis:**
 1. **Import the panel, bin set and AIF (SNP set).**
 2. **Create an analysis method.**
 3. **Create projects for each run in the study:**
 - a. **Create a new project and add samples to it.**
 - b. **Set the analysis parameters in the Samples tab.**
 - c. **Perform an initial analysis.**
- **Analyze and examine the data**
- **Export the results**
- **Export the desired data for further analysis**




GeneMapper® Software Managers

The screenshot displays the GeneMapper software interface. The main window is titled "GeneMapper - Untitled [Generic] - gm Is Logged In Database fosfangrnL03". The menu bar includes File, Edit, Analysis, View, Tools, and Help. A toolbar contains icons for file operations and a "Table Setting" dropdown menu set to "SNPlex_v3". A red box highlights the "GeneMapper Manager" menu item, which is expanded to show "Panel Manager" (Ctrl+J) and "Study Manager". Below the main window, a "GeneMapper Manager" window is open, showing a table of projects. The table has columns for Project, Type, Last Saved, Owner, and # of Samples. The data is as follows:

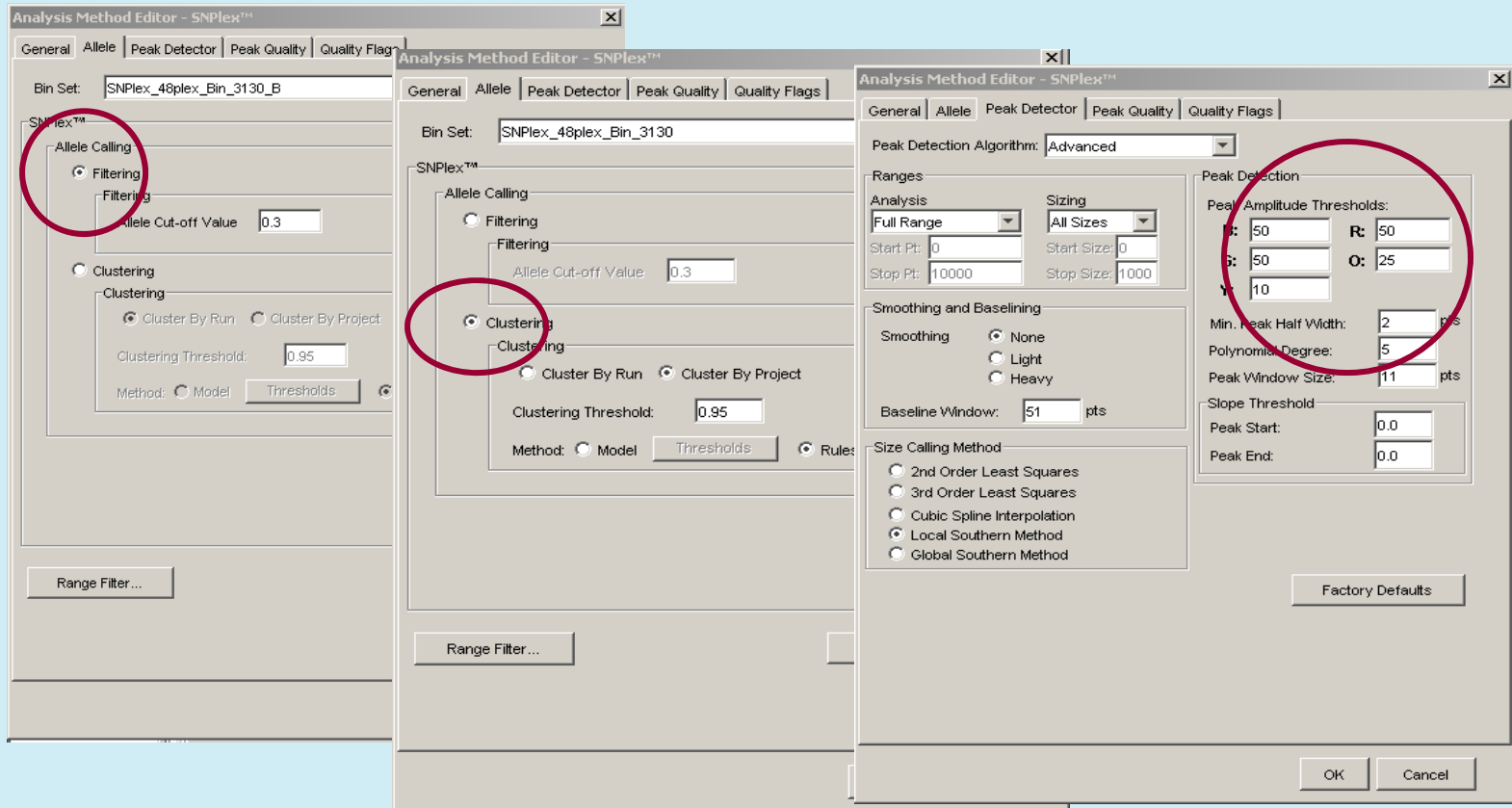
Project	Type	Last Saved	Owner	# of Samples
01-12-2009-Cic-T-GENE	Generic	2009-01-12 15:19:1	gm	64
01282009	Generic	2009-01-28 15:23:1	gm	16
0202-EGFR_KRAS_ATCC	Generic	2009-10-01 13:46:1	gm	77
02022009-NCR-EGFRKRAS	Generic	2009-10-01 13:30:5	gm	96
02022009_ATCC_EGFRKRAS	SNPlex	2009-10-01 13:35:3	gm	77
02172009_Control DNAs	Generic	2009-02-19 04:40:4	gm	16
02182009-Enzymes-HumicAcid	Generic	2009-04-27 17:57:3	gm	96
02182009-control-DNAs	SNPlex	2009-03-10 09:27:5	gm	16
02182009controlDNA_Biochain20	SNPlex	2009-03-10 09:34:2	gm	42
02252009-Balancing1	Generic	2009-02-26 12:29:4	gm	32
022609trial	Generic	2009-02-27 10:07:5	gm	24
03052009-QC-Balancing	Generic	2009-03-05 15:48:3	gm	96
03092009_QC_Maura	SNPlex	2009-03-09 12:48:4	gm	19

Software and Other Patches Needed: Online or CD

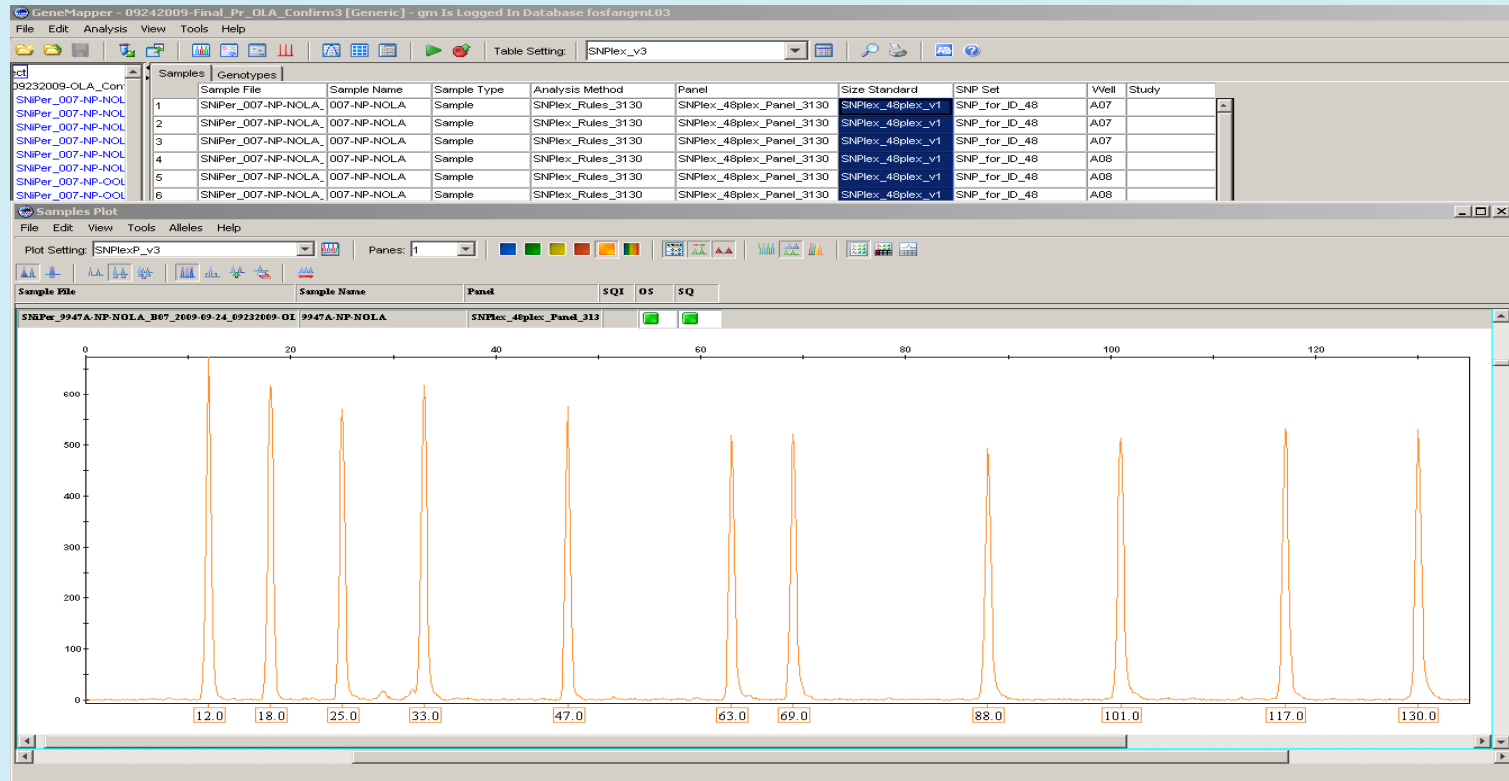
<http://www.appliedbiosystems.com/support/software/snplex/updates.cfm>

 3130_Global_QC_parameters.xml	XML Document
 SNPlex_48plex_3130_Bins.txt	Text Document
 SNPlex_48plex_3130_Panels.txt	Text Document
 SNPlex_48plex_v1.xml	XML Document
 SNPlex_Rules_3130.xml	XML Document

Analysis Algorithms: Filtering versus Clustering



Analysis Setup



Size standard: 12 – 130 bp

Size Standard

Size Standard Editor [X]

Edit

Size Standard Description

Name: SNIPlex_48plex_v1

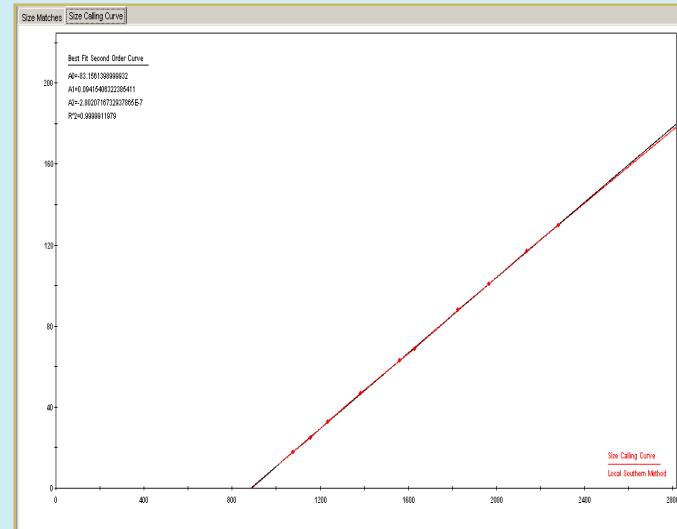
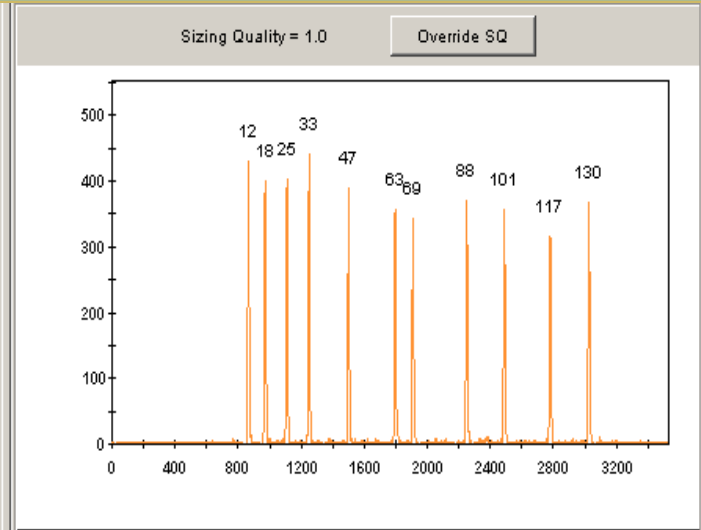
Description: Factory Provided

Size Standard Dye: Orange

Size Standard Table

	Size in Basepairs	
1	12.0	[Insert] [Delete]
2	18.0	
3	25.0	
4	33.0	
5	47.0	
6	63.0	
7	69.0	
8	88.0	

[OK] [Cancel]

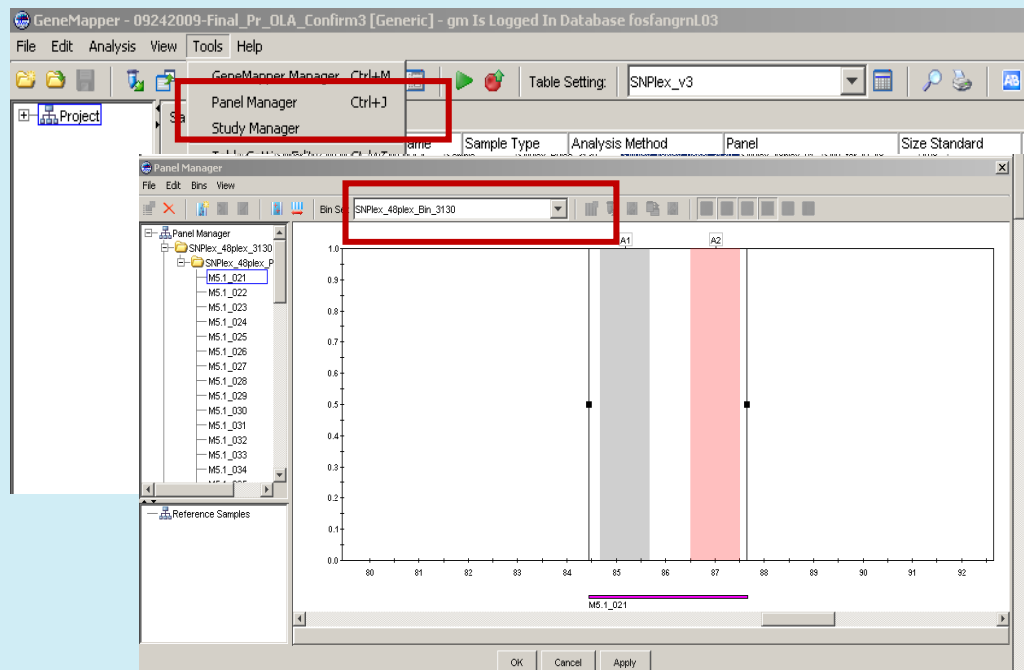


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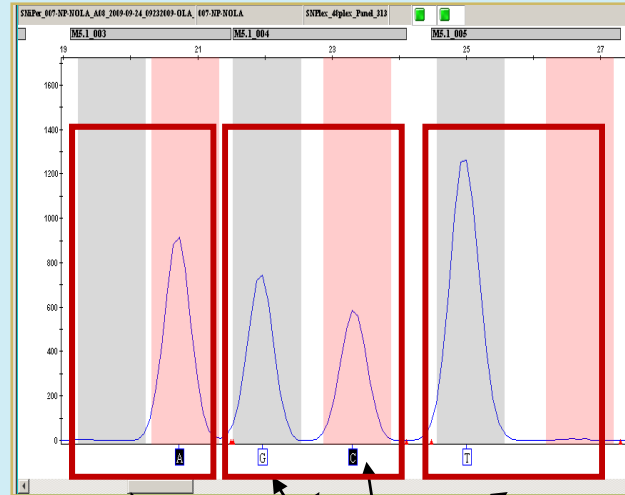


Analysis Requirements

- Panel and binset: together identify marker / ZipChute® Probe
 - 3130xI systems panel and binset
- Components:
 - (1) Panel
 - (2) Binset
 - (3) Specific for 3130xI systems



Panel and Binset: Identify Marker and ZipChute® Probe



Marker + **Bin** = ZipChute® Probe identification

SNP + **Allele** = Genotype determined

Import and Select SNP Set

The screenshot shows the GeneMapper Manager interface. The 'SNP Set Editor' dialog box is open, displaying the following information:

- SNP Set Description:**
 - Name: SNP_for_ID_48
 - Description: (empty)
- SNP Set Table:**

Marker Name	SNP Name	Zip Name	Allele1	Allele2
M5.1_001	rs740910	M5.1_001_2_A	T	C
M5.1_002	rs1490413	M5.1_002_2_A	A	G
M5.1_003	rs1335873	M5.1_003_2_A	T	A
M5.1_004	rs1979255	M5.1_004_2_A	G	C
M5.1_005	rs1493232	M5.1_005_2_A	T	G
M5.1_006	rs2040411	M5.1_006_2_A	T	C
M5.1_007	Amel	M5.1_007_2_A	Amel1	Amel2
M5.1_008	rs1528460	M5.1_008_2_A	G	A
M5.1_009	rs717302	M5.1_009_2_A	A	G
M5.1_010	rs251934	M5.1_010_2_A	T	C
M5.1_011	rs8037429	M5.1_011_2_A	C	T
M5.1_012	rs891700	M5.1_012_2_A	A	G
M5.1_013	rs901398	M5.1_013_2_A	G	A
M5.1_014	rs873196	M5.1_014_2_A	C	T
M5.1_015	rs964681	M5.1_015_2_A	G	A
M5.1_016	rs737681	M5.1_016_2_A	G	A

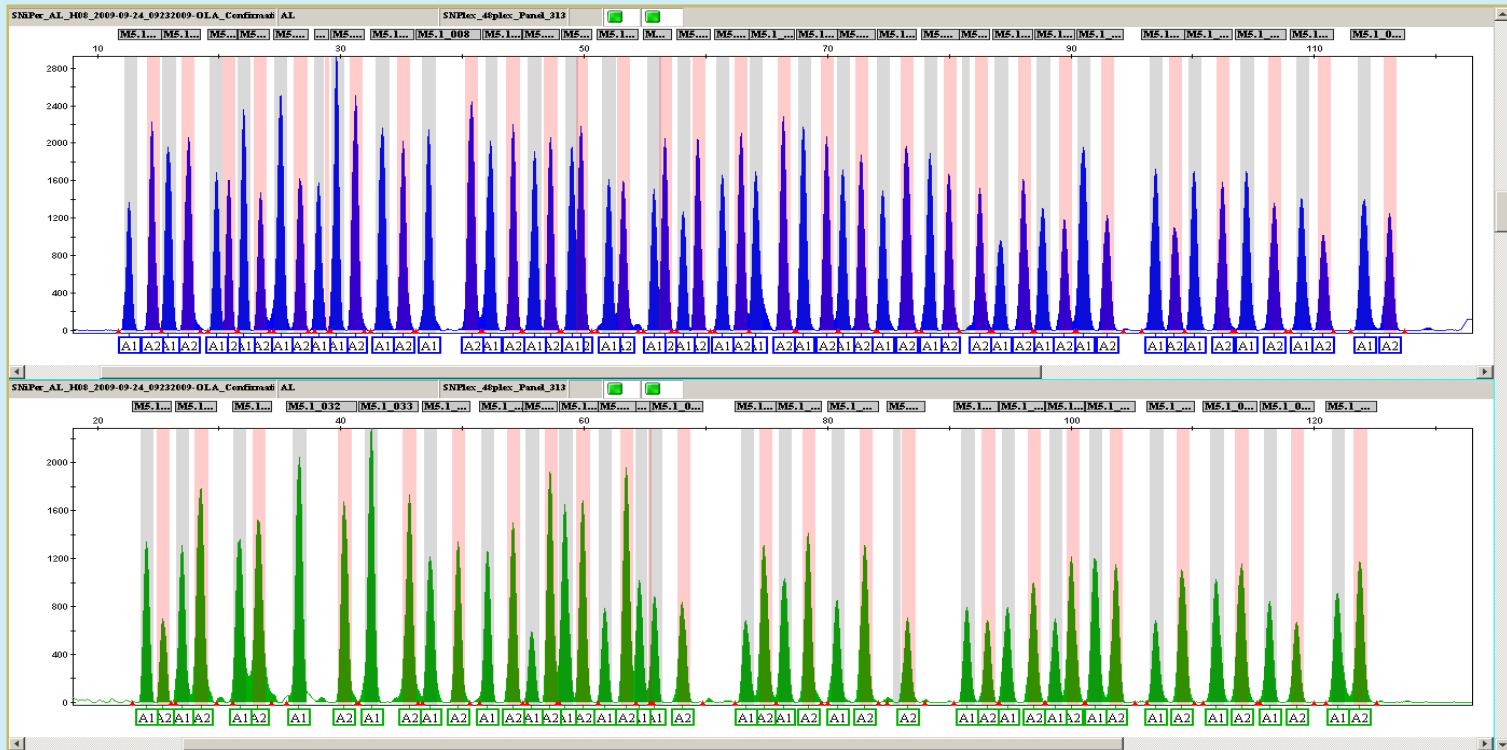
- Associates SNPs of a given multiplex with their respective ZipChute® Probe pairs
- Markers = ZipChute® Probe pairs
- Import into software once

Analysis Requirements: Sample Type

The screenshot shows a software interface with a table titled 'SNIPlex_v3'. The table has columns for Sample File, Sample Name, Sample Type, Analysis Method, Panel, Size Standard, SNP Set, and Well. The 'Sample Type' column is highlighted with a red box. The table contains 13 rows of data, including Allelic Ladder, Negative Control, Positive Control, and Sample types.

	Sample File	Sample Name	Sample Type	Analysis Method	Panel	Size Standard	SNP Set	Well
83	SNIPer_AL_H12_2009-	AL	Allelic Ladder	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	H12
84	SNIPer_AL_H12_2009-	AL	Allelic Ladder	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	H12
85	SNIPer_BC_4-NP-NOLA	BC_4-NP-NOLA	Negative Control	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G07
86	SNIPer_BC_4-NP-NOLA	BC_4-NP-NOLA	Positive Control	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G07
87	SNIPer_BC_4-NP-NOLA	BC_4-NP-NOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G07
88	SNIPer_BC_4-NP-NOLA	BC_4-NP-NOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G08
89	SNIPer_BC_4-NP-NOLA	BC_4-NP-NOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G08
90	SNIPer_BC_4-NP-NOLA	BC_4-NP-NOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G08
91	SNIPer_BC_4-NP-OOLA	BC_4-NP-OOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G09
92	SNIPer_BC_4-NP-OOLA	BC_4-NP-OOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G09
93	SNIPer_BC_4-NP-OOLA	BC_4-NP-OOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G09
94	SNIPer_BC_4-NP-OOLA	BC_4-NP-OOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G10
95	SNIPer_BC_4-NP-OOLA	BC_4-NP-OOLA	Sample	SNIPlex_Rules_3130	SNIPlex_48plex_Panel_3130	SNIPlex_48plex_v1	SNP_for_ID_48	G10

Allelic Ladder

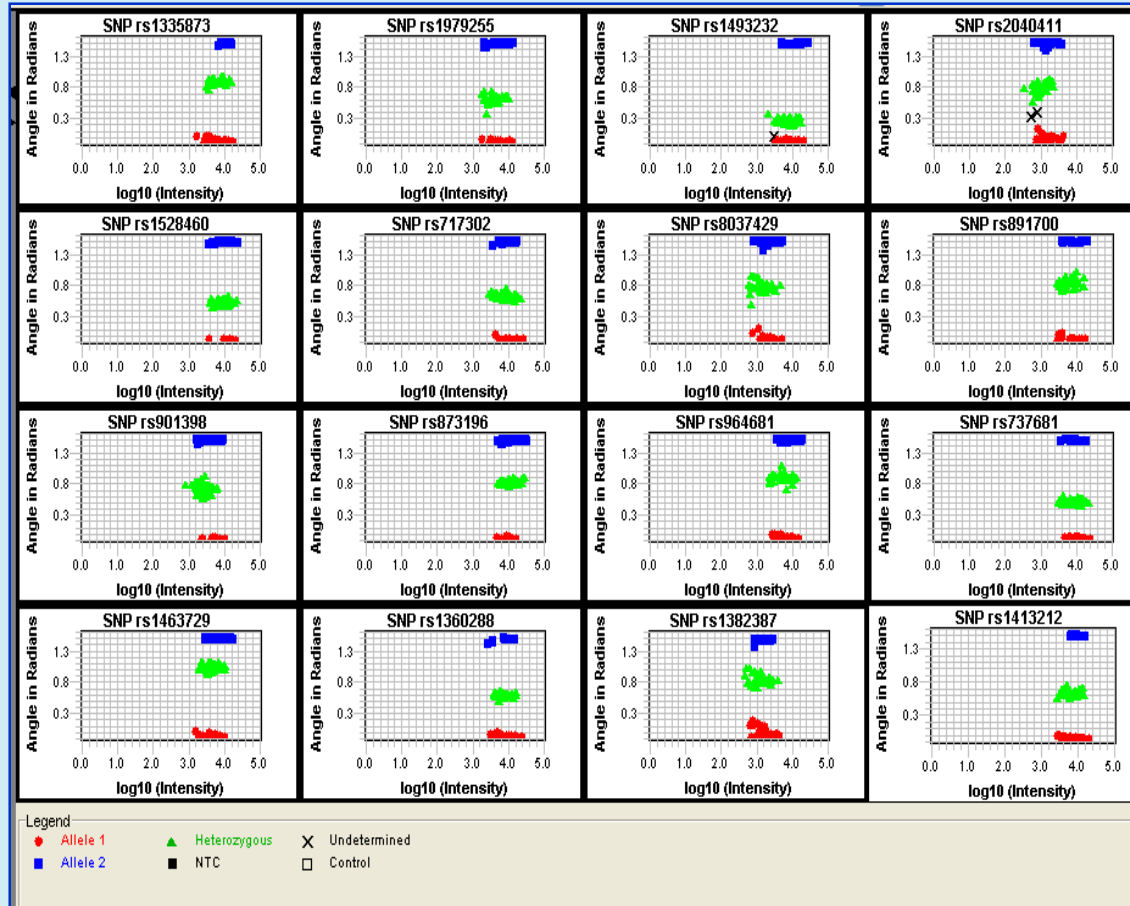


All ZipChute[®] Probes = all possible alleles

GeneMapper[®] Software Workflow / Checklist

- 1. Add samples to project.**
- 2. Review raw data for obvious issues.**
- 3. Apply analysis parameters and analyze.**
- 4. Review samples with 'Failed' Sizing Quality (SQ).**
- 5. Review samples with 'Check' Off-Scale (OS).**
- 6. Review allelic ladder Well Quality (WELLQ).**
- 7. Review positive and negative controls.**
- 8. Review samples with 'Failed' and 'Check' Well Quality (WELLQ).**
- 9. Filter poor quality samples from analysis.**
- 10. Review SNP clusters.**
- 11. Export genotypes.**
- 12. Back up GeneMapper[®] software files.**

Genotyping Using Cluster Analysis Algorithm



Questions?

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