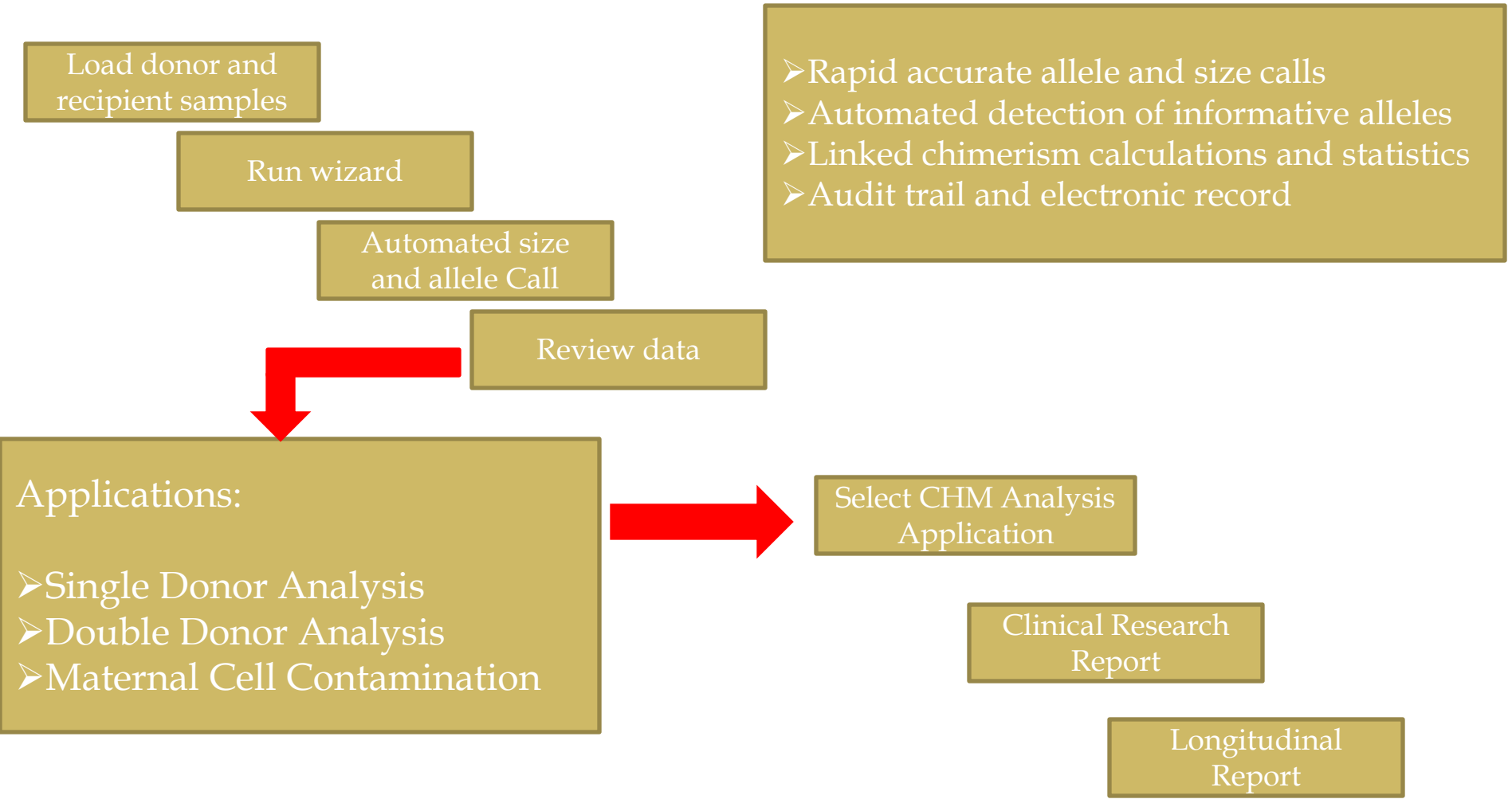
Dotmatics
SoftGenetics

ChimeRMarker

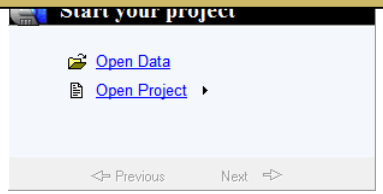
Quick Start Guide

ChimeRMarker Workflow

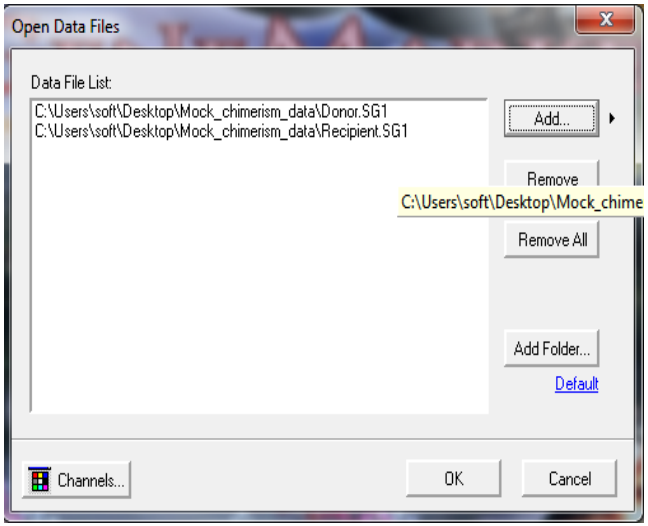


Loading Data and Specifying Identifiers

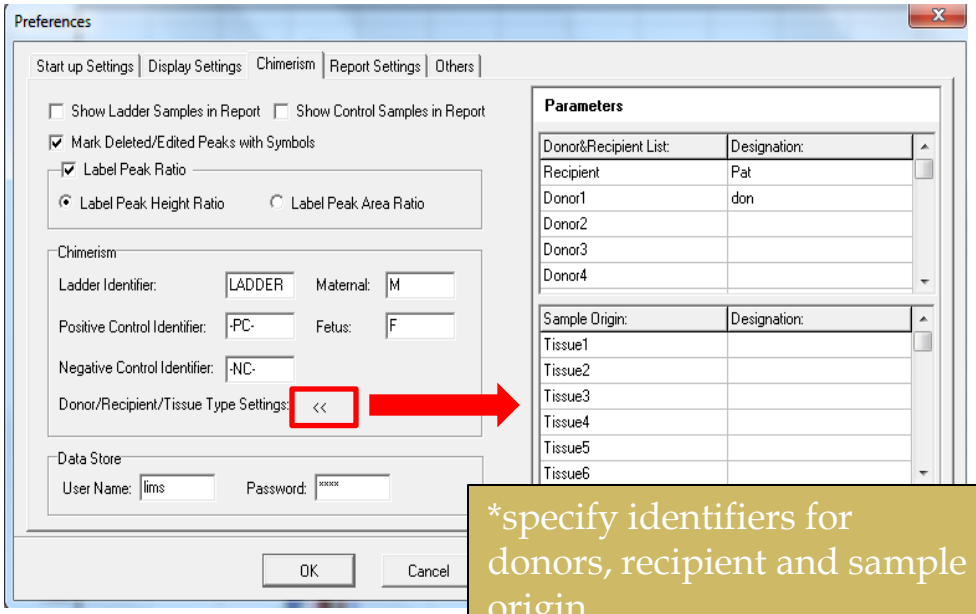
➢Start Your Project:
➢Open Data



➢Open Data Files:
➢Add
➢Select Files (CTRL+A)



View->Preference-> Chimerism



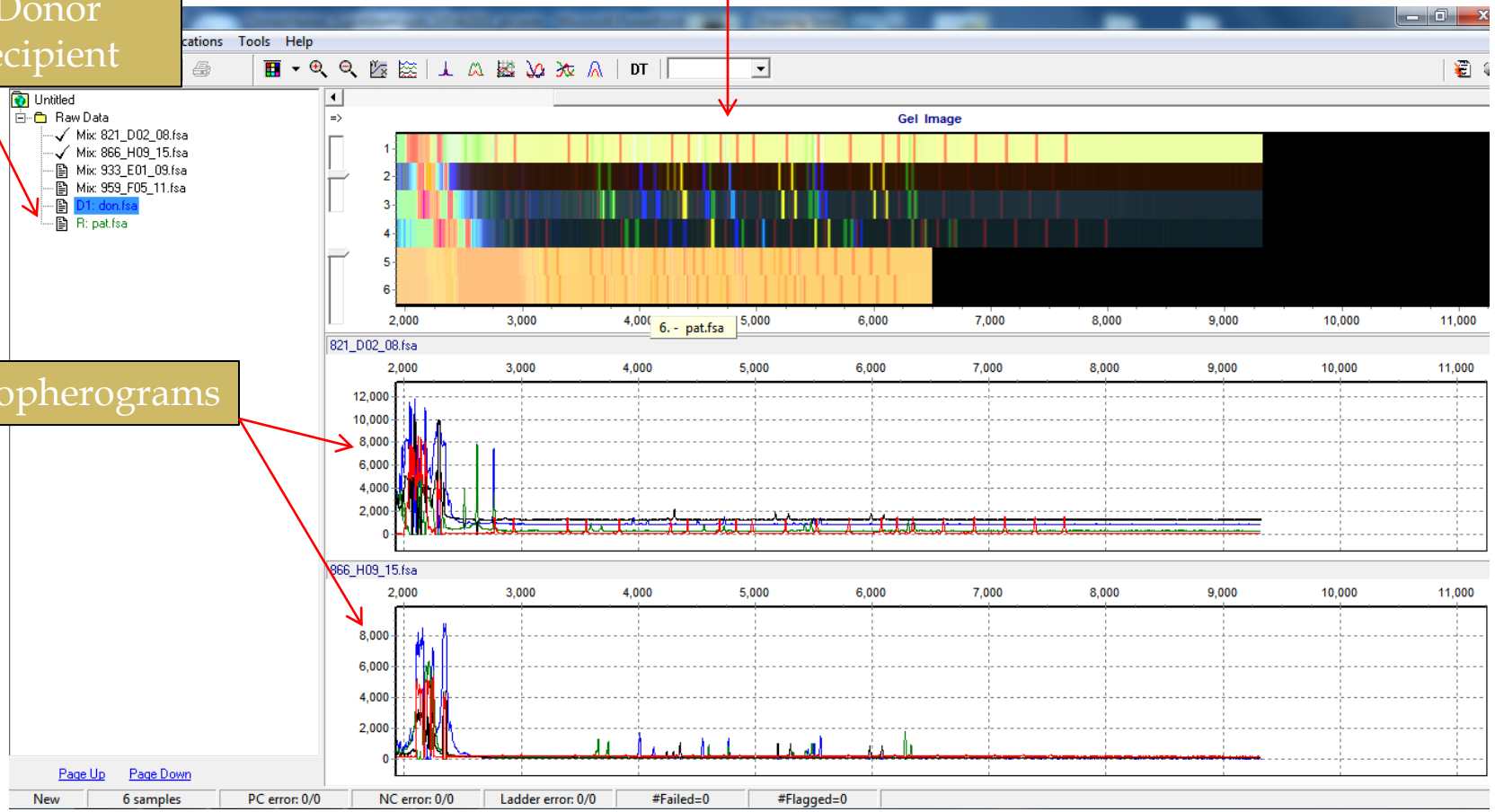
*specify identifiers for donors, recipient and sample origin

See ChimerMarker Manual Chapter 2

Raw Data Screen

Synthetic Gel Image

List of Files
D1= Donor
R=Recipient



Electropherograms

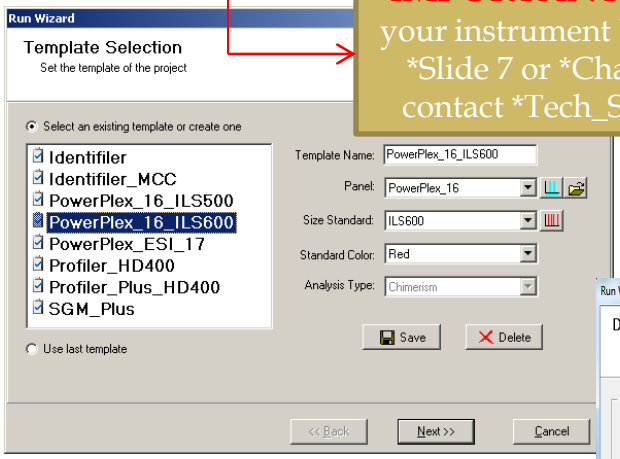
See ChimerMarker Manual
Chapter 3

Size & Allele Calls using Run Wizard

➢Click on Run Icon to begin

Run Wizard Template Selection:
•Select the appropriate Panel and Size Standard from Drop Down Menu.

IMPORTANT: Please calibrate panels to your instrument before proceeding. Refer to *Slide 7 or *Chapter 6 in User Manual or contact *Tech_Support@softgenetics.com



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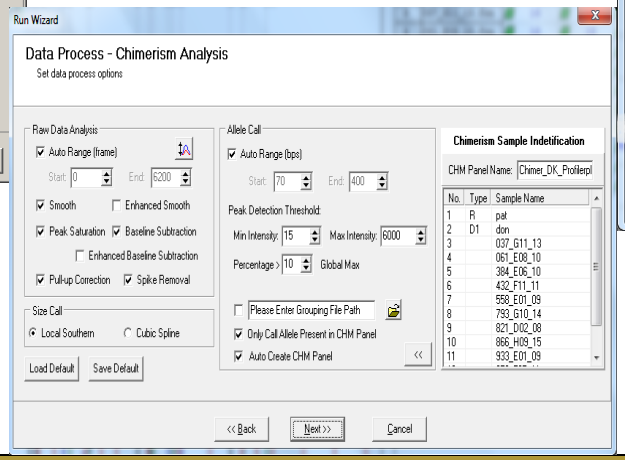
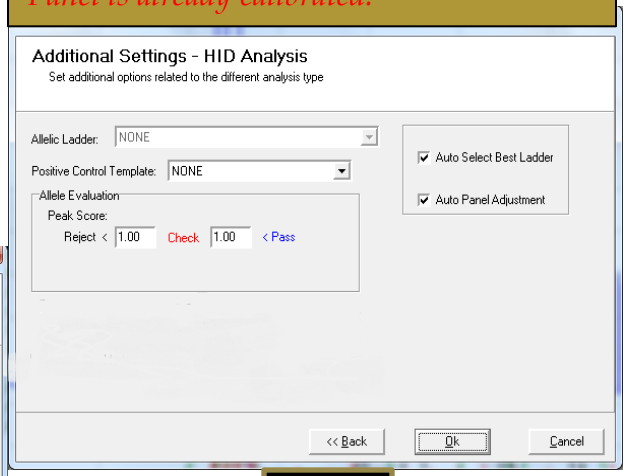
Page 2



Additional Settings:

*Select *Auto Select Best Ladder* and *Auto Panel Adjustment*
These two options can only be used if Panel is already calibrated.



Page 3

Data Processing:
➢Select "Auto Create CHM Panel" to have ChimerMarker automatically create a Chimertyping panel and apply it.
➢ Deselect to manually create Chimertyping panel

See ChimerMarker Manual Chapter 2 and 3

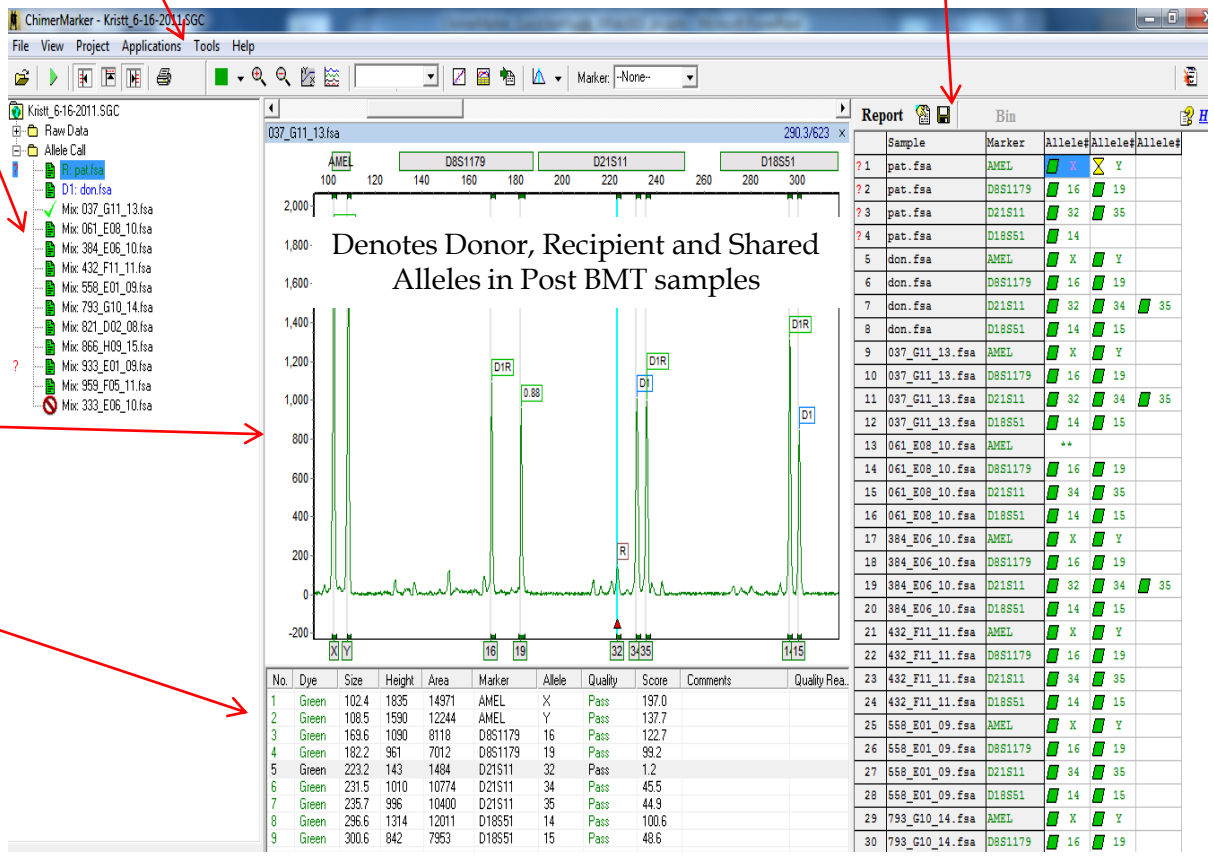
Review Size and Allele Cells

Main Toolbar

Allele Report Table

Size Called Samples

Green=High Lane Quality
Yellow=Requires Verification
Red=Size Did Not Occur

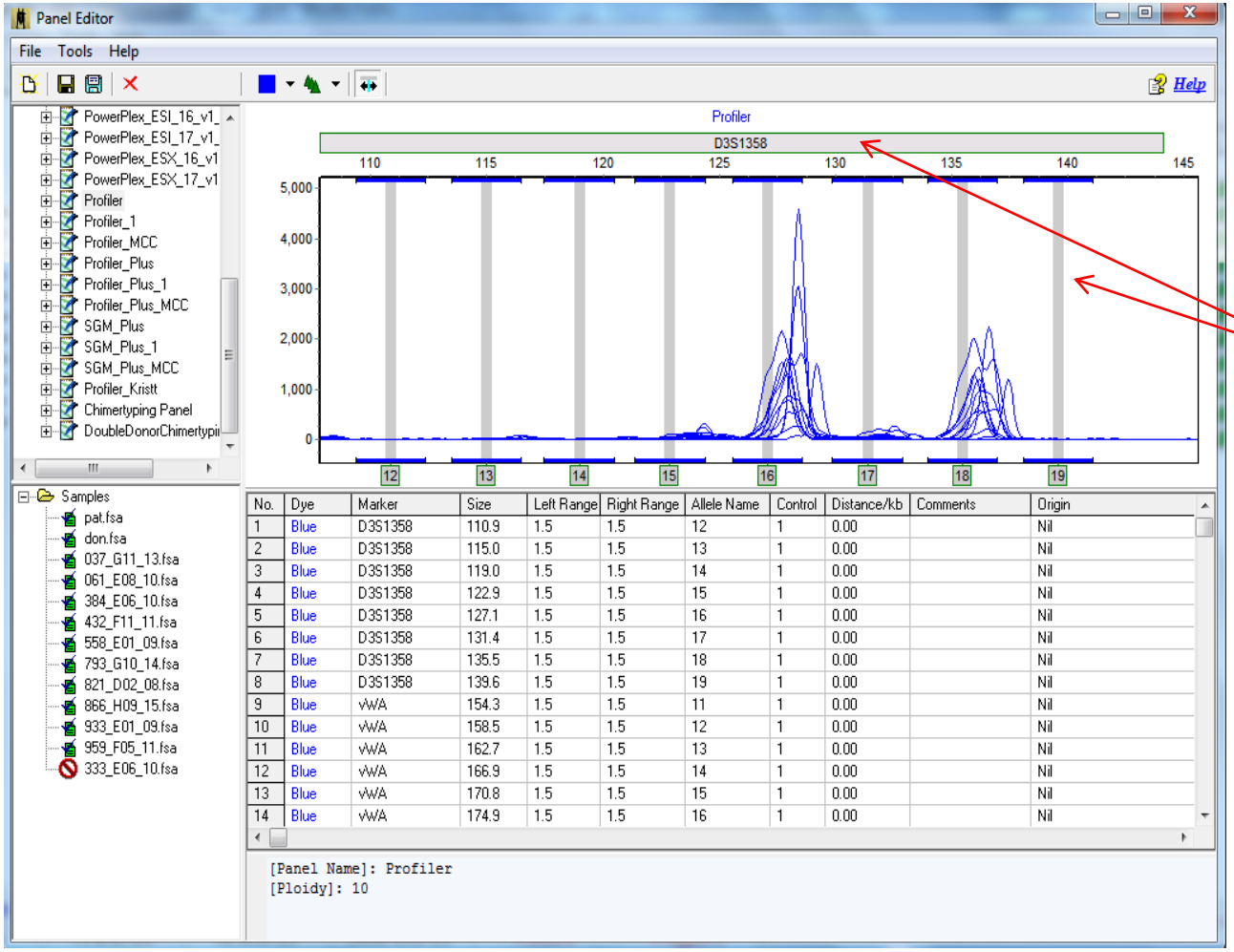


Electropherograms

Peak Chart/Table

Panel Editor

*Tools →Panel Editor→ Select Panel of Interest under "Panel Template"



No.	Dye	Marker	Size	Left Range	Right Range	Allele Name	Control	Distance/kb	Comments	Origin
1	Blue	D3S1358	110.9	1.5	1.5	12	1	0.00		Nil
2	Blue	D3S1358	115.0	1.5	1.5	13	1	0.00		Nil
3	Blue	D3S1358	119.0	1.5	1.5	14	1	0.00		Nil
4	Blue	D3S1358	122.9	1.5	1.5	15	1	0.00		Nil
5	Blue	D3S1358	127.1	1.5	1.5	16	1	0.00		Nil
6	Blue	D3S1358	131.4	1.5	1.5	17	1	0.00		Nil
7	Blue	D3S1358	135.5	1.5	1.5	18	1	0.00		Nil
8	Blue	D3S1358	139.6	1.5	1.5	19	1	0.00		Nil
9	Blue	vWA	154.3	1.5	1.5	11	1	0.00		Nil
10	Blue	vWA	158.5	1.5	1.5	12	1	0.00		Nil
11	Blue	vWA	162.7	1.5	1.5	13	1	0.00		Nil
12	Blue	vWA	166.9	1.5	1.5	14	1	0.00		Nil
13	Blue	vWA	170.8	1.5	1.5	15	1	0.00		Nil
14	Blue	vWA	174.9	1.5	1.5	16	1	0.00		Nil

*If one or more allele is not aligned correctly to its bin:

- Adjust and calibrate panel
  - Hold Shift key + Left-mouse click on Marker Label or Bin and drag it left or right to align it to the alleles.
- Adjust marker parameters-> Filter out noise

See ChimerMarker Manual Chapter 6

Navigation

Zoom in:

-In electropherogram, hold left mouse click and drag a box from upper left to lower right

Zoom Out:

-In electropherogram, hold left mouse click and drag a box from lower right to upper left.

Scroll:

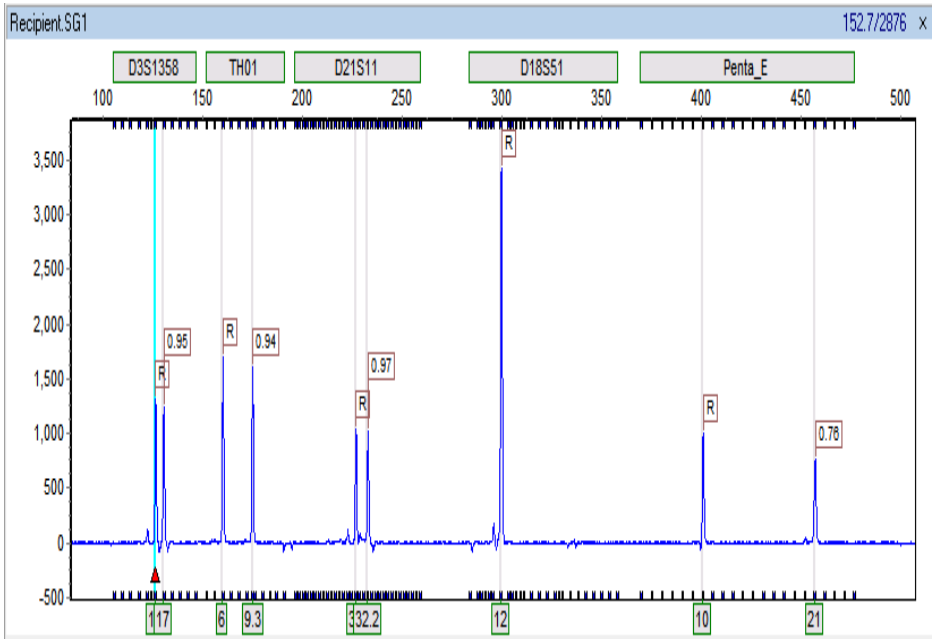
-In electropherogram, hold right mouse click and drag trace left or right.

One Color Viewing

-Click the *Show Color* Icon

Hide Option:

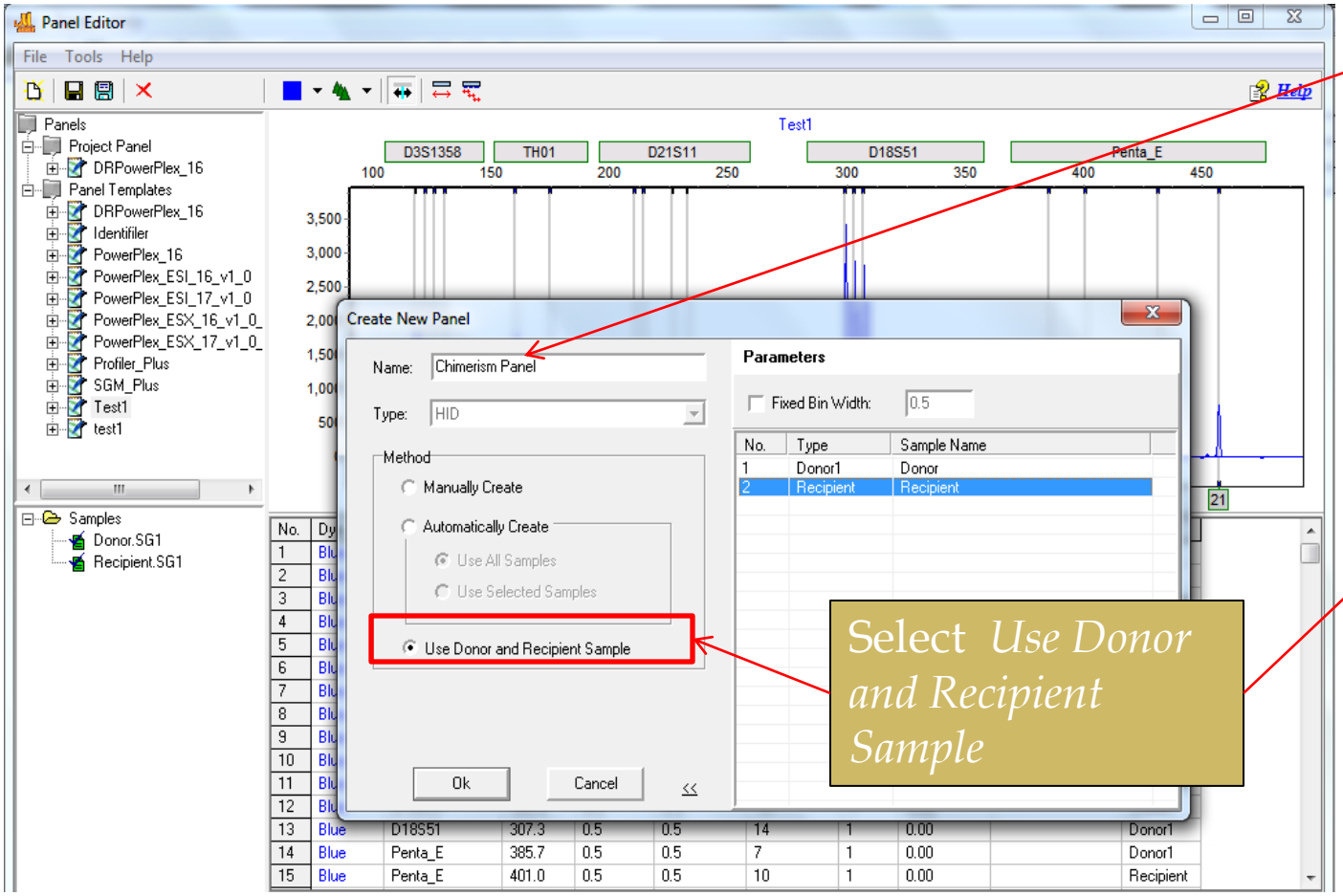
-Click the *Show/Hide* Icons
remove flie list, gel image, report table



See ChimerMarker Manual
Chapter 4

Making a Chimerism Panel

*If you selected "Auto Create CHM Panel" in the Run Wizard dialog, skip this step and move onto page 10



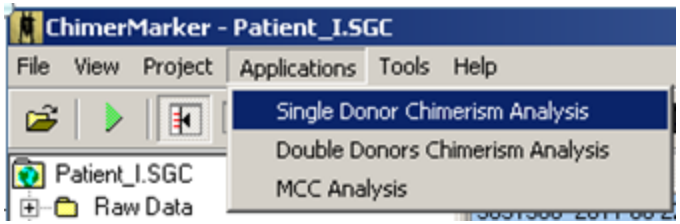
Specified Unique Panel Name

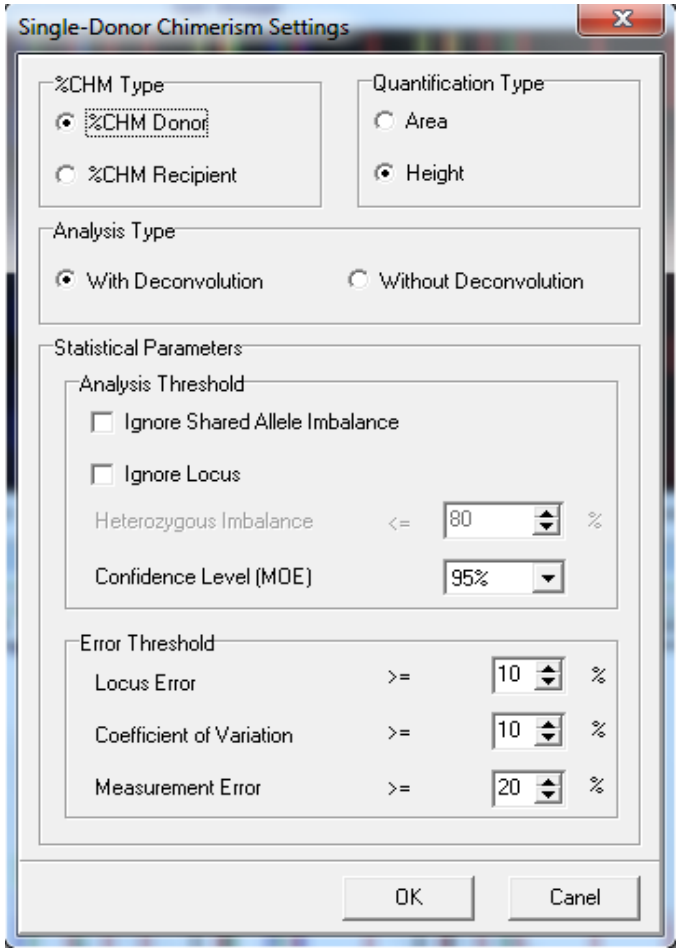
Select *Use Donor and Recipient Sample*

*Same procedure would apply to Double Donor Chimertyping Panel

See ChimerMarker Manual Chapter 6

Chimerism Analysis



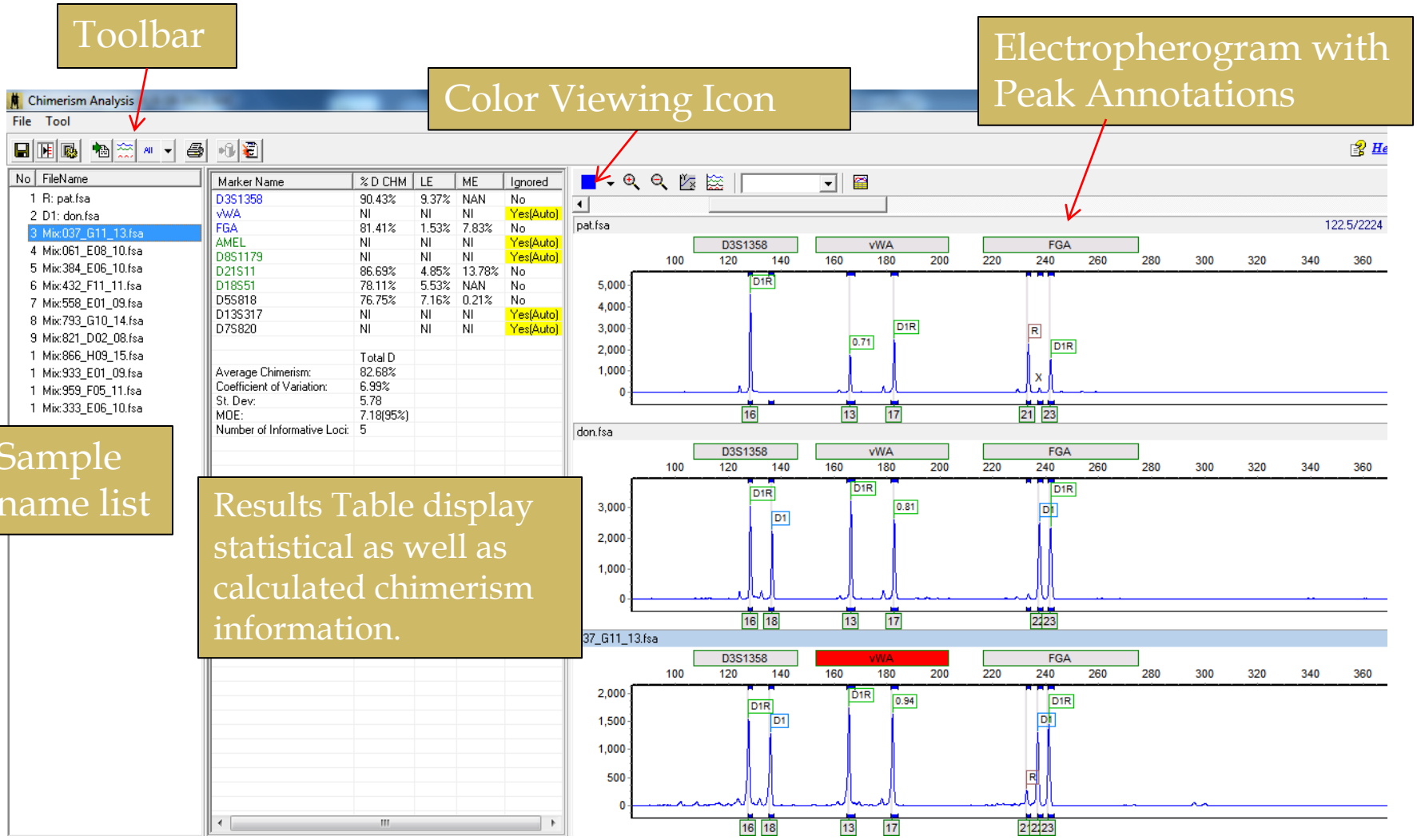


Select from the Applications drop-down menu

Single Donor Chimerism Settings:

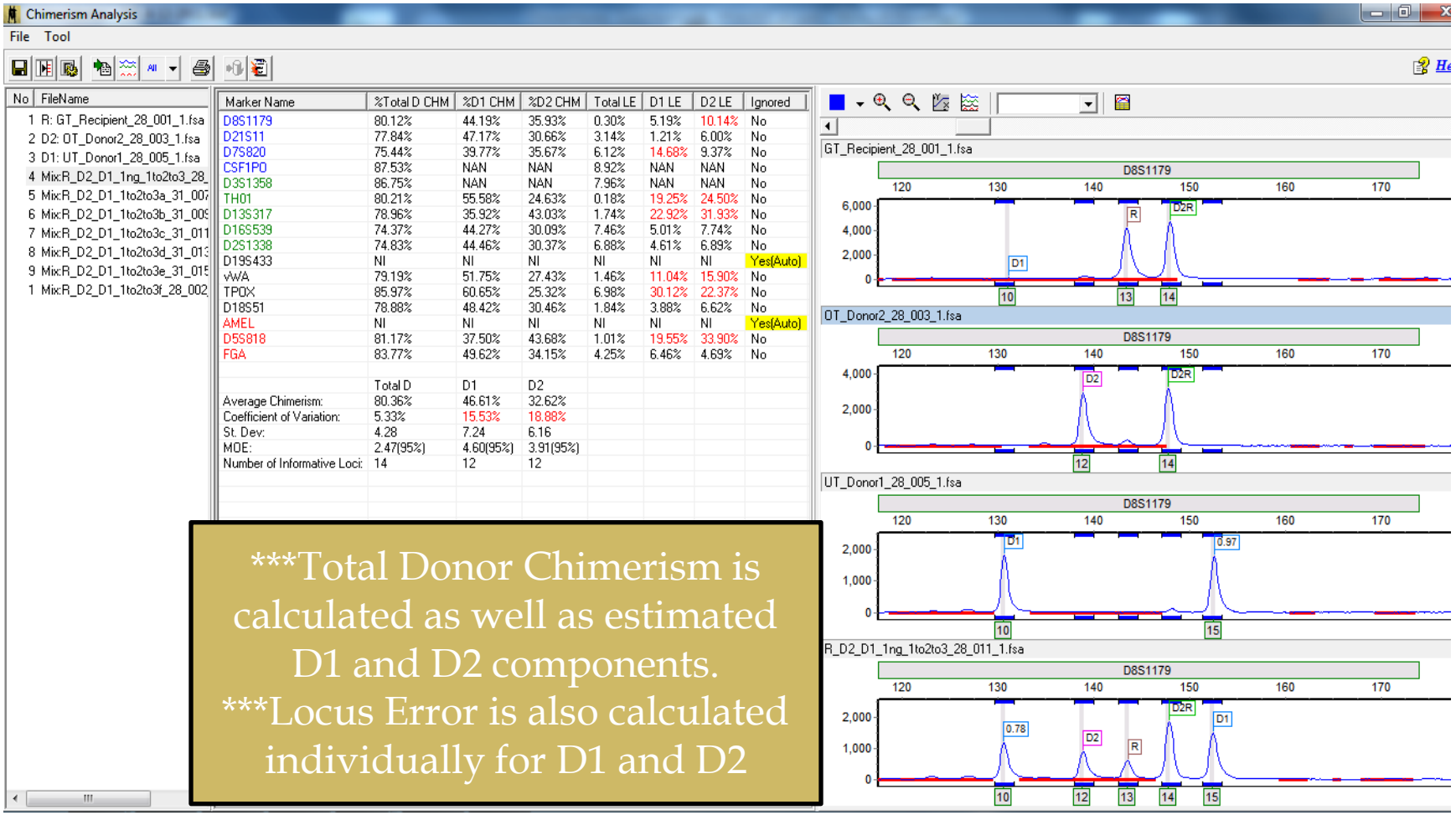
- %CHM Type: Calculate by % Recipient or % Donor (applicable to Double Donor)
- Ignore Share Allele Imbalance: Ignore markers that contain unique allele that is greater in intensity or area than shared allele.
- Quantification Type: Calculate Chimerism using Peak Area or Height (applicable to Double Donor)
- Analysis Type:
  - *With Deconvolution*: Will use unshared allele information to deconvolute shared peak and calculate Chimerism
  - *Without Deconvolution*: Will ignore locus with shared peak and only use unshared alleles
- Statistical Parameters: Parameters to flag locus or sample using set threshold. (applicable to Double Donor)

Single Donor Chimerism Analysis Results



See ChimerMarker Manual Chapter 2

Double Donor Chimerism Analysis Results



***Total Donor Chimerism is calculated as well as estimated D1 and D2 components.
***Locus Error is also calculated individually for D1 and D2

See ChimerMarker Manual Chapter 2

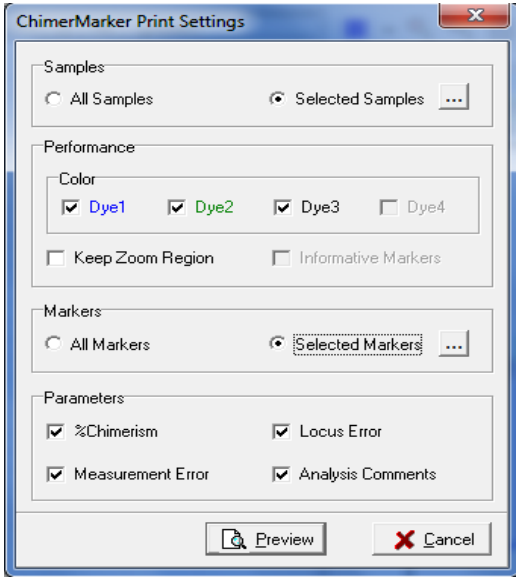
Print or Save Report

Save Report:
File→Save Report

Click on Print Icon 

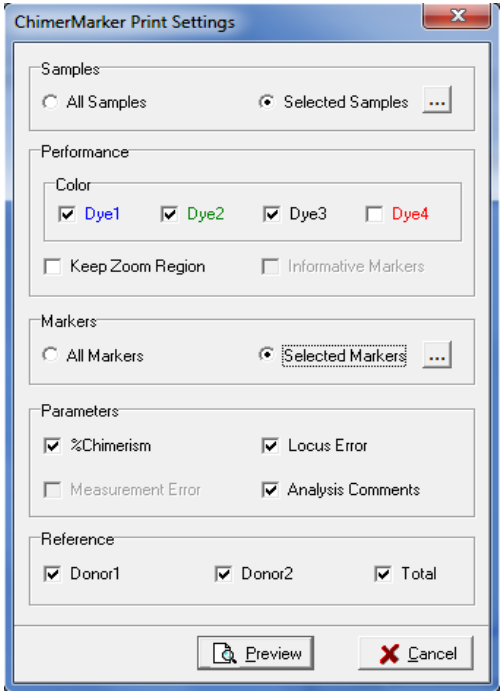
Print Options for Single Donor:

- Print all Samples or Select Specific Samples
- Print all Markers or Select Specific Markers
- Print all or only specific parameters.



Print Options for Double Donor:

- Print all Samples or Select Specific Samples
- Print all Markers or Select Specific Markers
- Print all or only specific parameters.
- Print all Reference components or specific components only.
- Keep Zoom Region prints current region of electropherogram



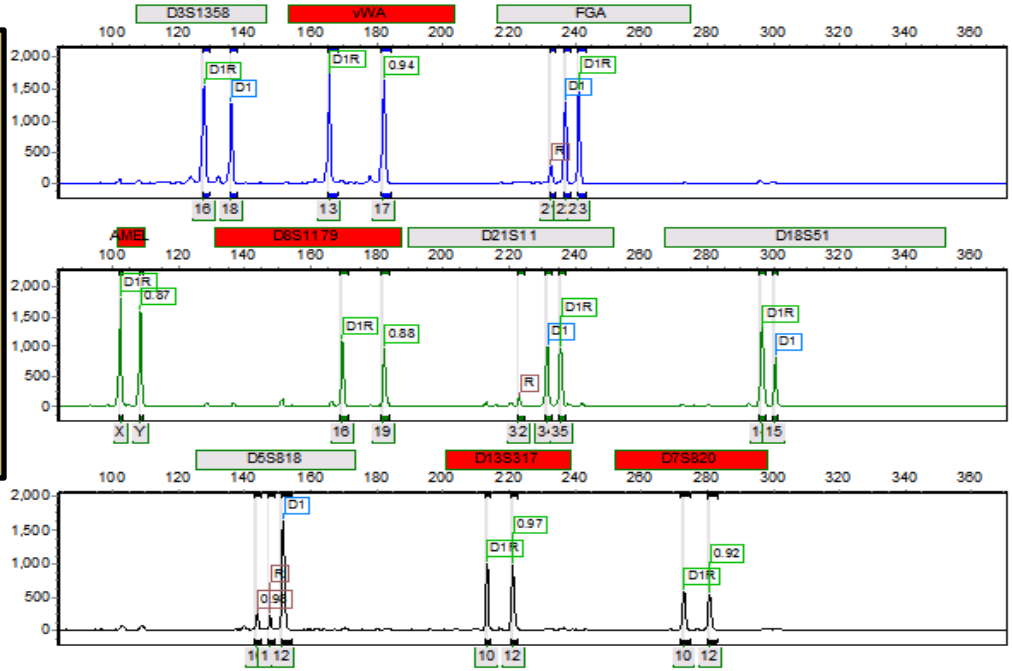
Comprehensive Report

Header Information

Results Table

Chimerism Analysis Report - SoftGenetics	
Software: ChimerMarker V2.8.1	Analysis Type: Single-Donor Chimerism With Deconvolution
Project: Kristt_6-16-2011.SGC	Panel: DK_Test_CHM
User:	Quantification Type: Height
Report Time: 11/01/2011 - 10:10:00	Coefficient of Variation: 10.00%
Chimerism Type: % Donor Chimerism	Locus Error: 10.00%
Confidence Level (MOE): 95%	Measurement Error: 20.00%
Sample Name: 206037	Machine: demo_3100
Comments:	Run Time: 05/03/2011 - 11:52:15 -> 05/03/2011 - 12:33:49

037_G11_13.fsa



Conclusion		
Comments		
	Date	Initial
Authorization 1		
Authorization 2		

Marker	ME	LE	CHM	Ignored
D3S1358	NAN	9.37%	90.43%	No
vWA	NI	NI	NI	Yes(Auto)
FGA	7.83%	1.54%	81.41%	No
AMEL	NI	NI	NI	Yes(Auto)
D8S1179	NI	NI	NI	Yes(Auto)
D21S11	13.78%	4.85%	86.69%	No
D18S51	NAN	5.53%	78.11%	No
D5S818	0.21%	7.17%	76.75%	No
D13S317	NI	NI	NI	Yes(Auto)
D7S820	NI	NI	NI	Yes(Auto)

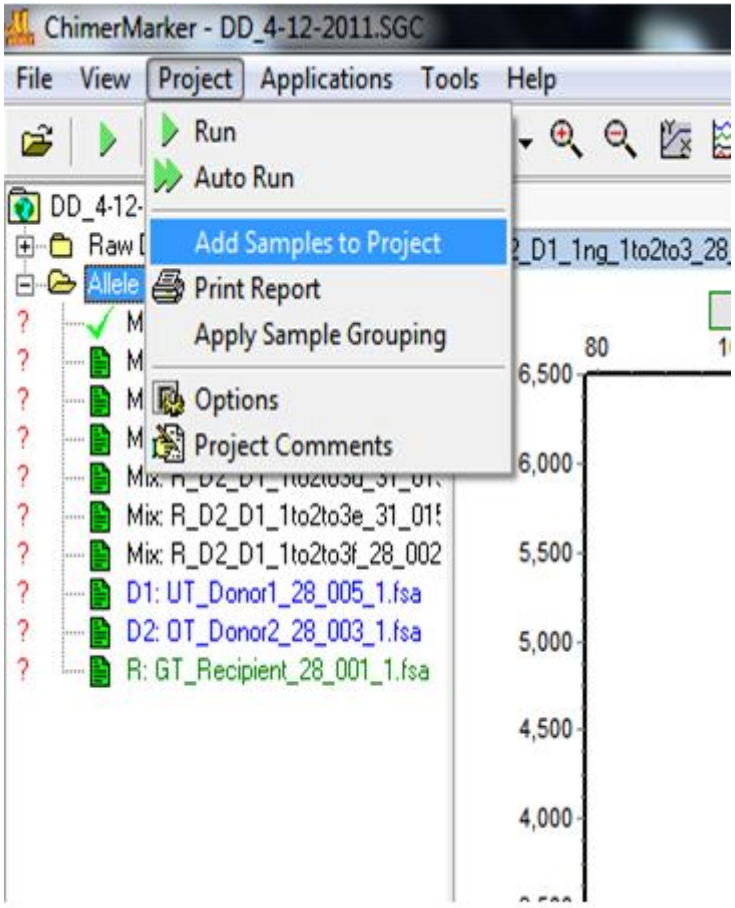
Average Chimerism: 82.68%
St. Dev: 5.78
Coefficient of Variance: 6.99%
MOE: 7.18 (95%)
Number of Informative Loci: 5

Each dye color is printed separately with Peak annotation (D or R)

Average CHM, St. Dev., and CV

See ChimerMarker Manual Chapter 2

Long Term Monitoring:
Adding Subsequent Samples



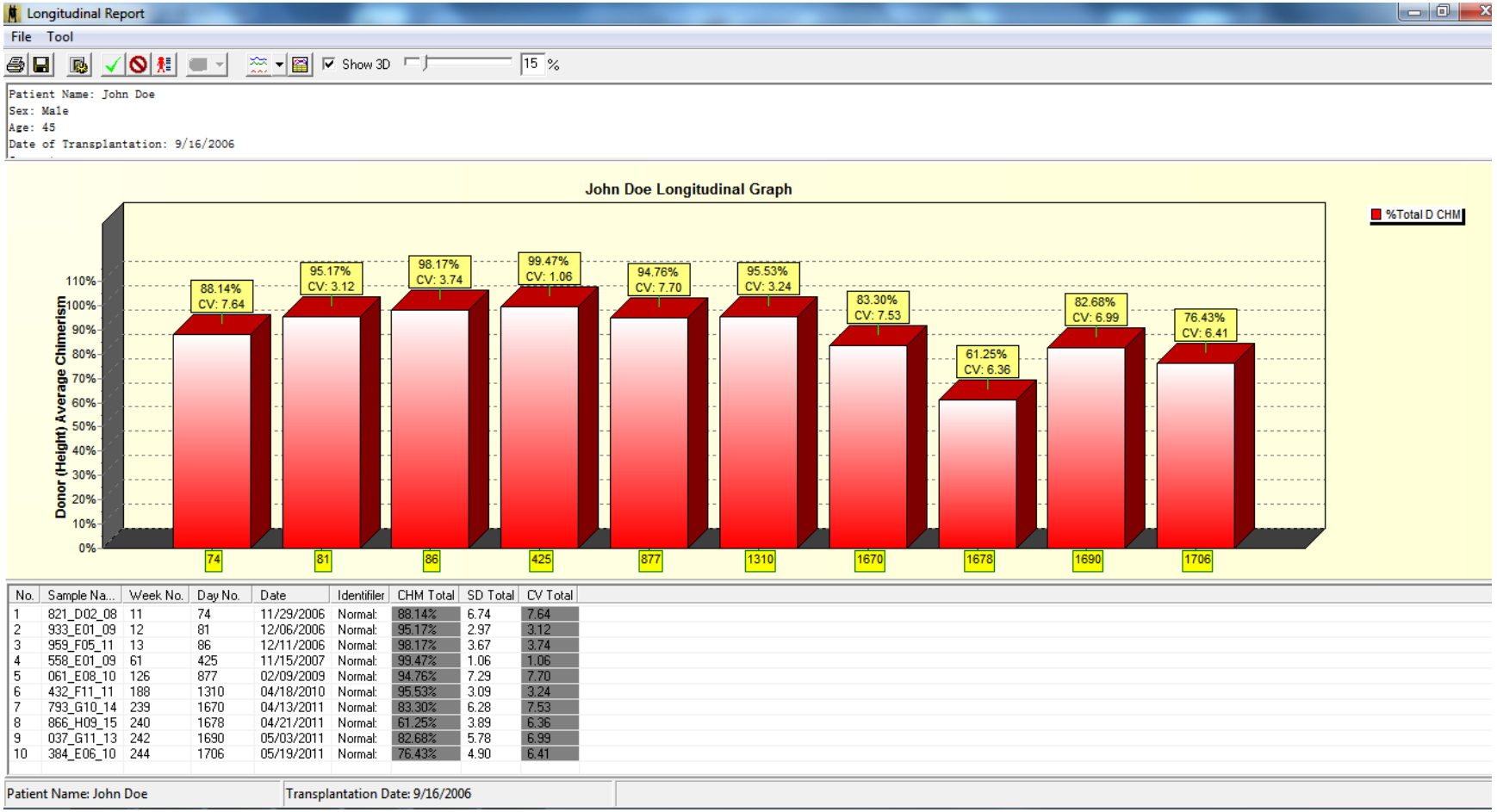
* No need to repeat analysis – Add Samples to Project appends the patient project with follow-up samples over time.

To add additional samples to a saved project:
Project→ Add Samples to Project

See ChimerMarker Manual Chapter 2

Longitudinal Report

All samples within a project can be used to create a long term graph. For more information, please refer to The Longitudinal Webinar. For additional help/questions, please email tech_support@softgenetics.com



No.	Sample Na...	Week No.	Day No.	Date	Identifiler	CHM Total	SD Total	CV Total
1	821_D02_08	11	74	11/29/2006	Normal:	88.14%	6.74	7.64
2	933_E01_09	12	81	12/06/2006	Normal:	95.17%	2.97	3.12
3	959_F05_11	13	86	12/11/2006	Normal:	98.17%	3.67	3.74
4	558_E01_09	61	425	11/15/2007	Normal:	99.47%	1.06	1.06
5	061_E08_10	126	877	02/09/2009	Normal:	94.76%	7.29	7.70
6	432_F11_11	188	1310	04/18/2010	Normal:	95.53%	3.09	3.24
7	793_G10_14	239	1670	04/13/2011	Normal:	83.30%	6.28	7.53
8	866_H09_15	240	1678	04/21/2011	Normal:	61.25%	3.89	6.36
9	037_G11_13	242	1690	05/03/2011	Normal:	82.68%	5.78	6.99
10	384_E06_10	244	1706	05/19/2011	Normal:	76.43%	4.90	6.41

See ChimerMarker Manual Chapter 2