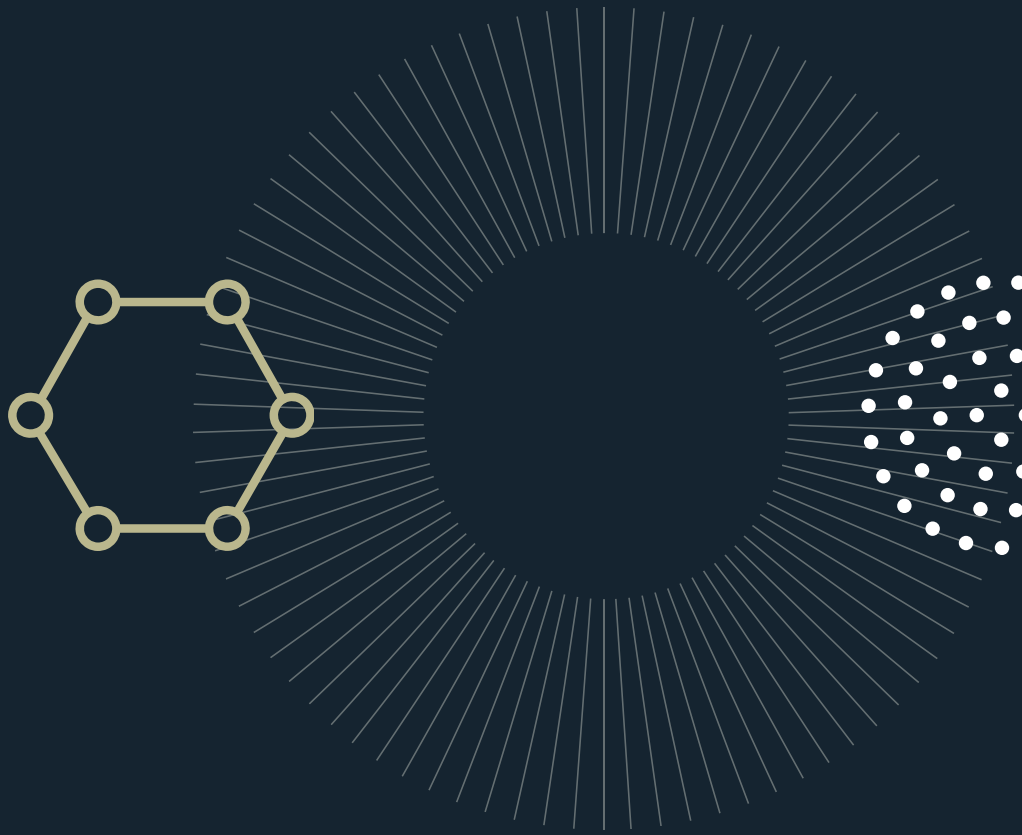
Dotmatics

SoftGenetics

GeneMarker HID

Quick Start Guide



GeneMarker HID Workflow

STR Human Identity Software

GeneMarkerHID supports numerous applications for Human Identity, including: Database Searches, Mixture Analysis, Kinship Analysis, and Paternity Testing.

Load Raw Data

Choose Template

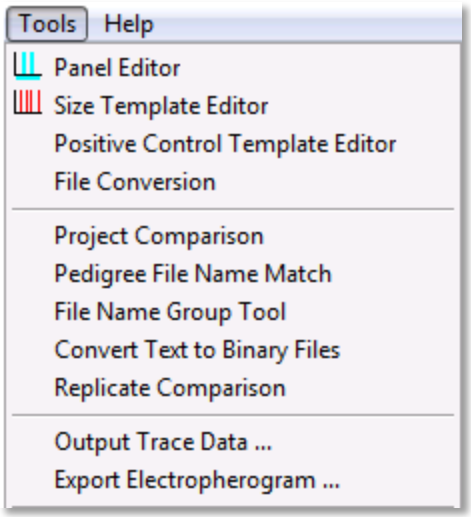
Process Samples

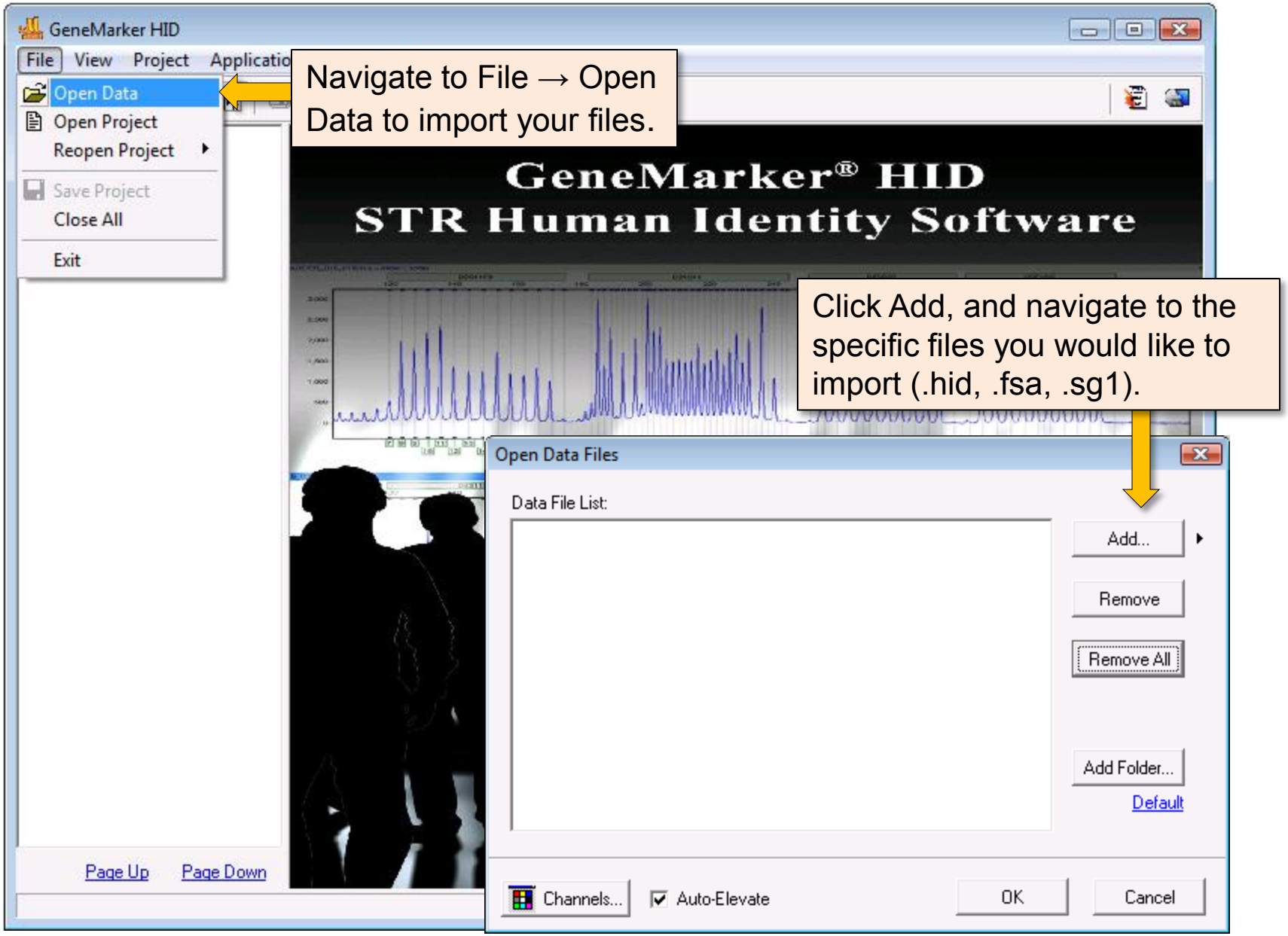
Review Size and Allele Calls

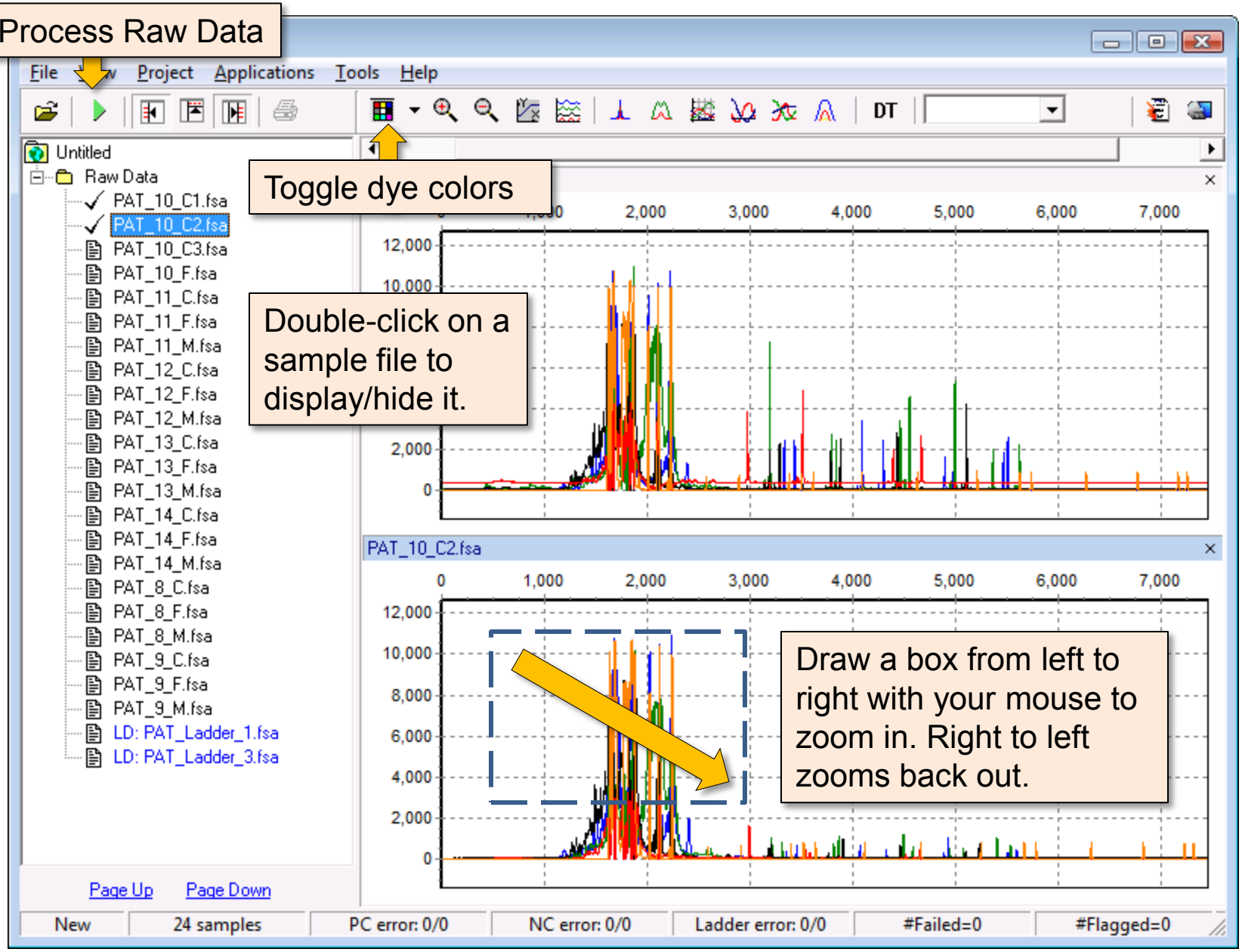
Run Application(s)

Print or Export Results

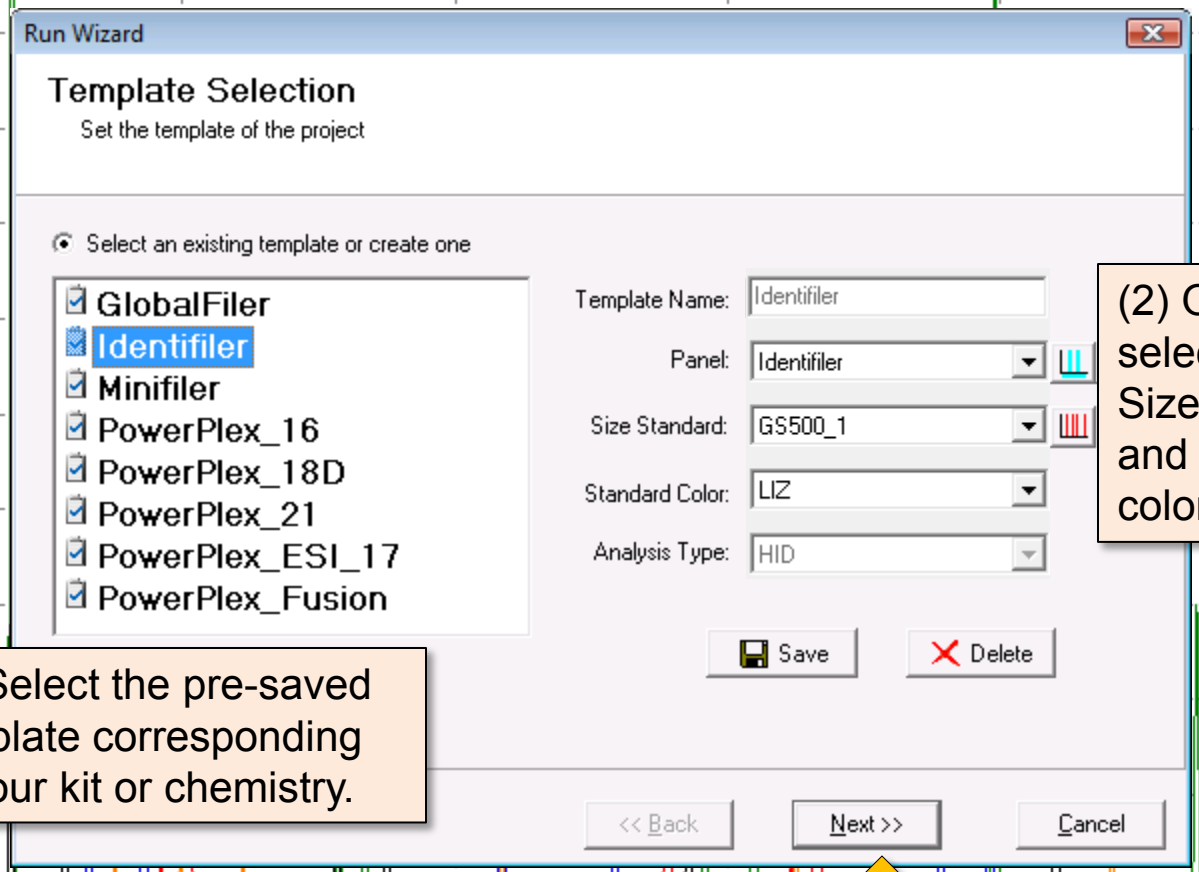
Select your process settings manually, or use one of GeneMarkerHID's pre-made templates (Fusion®, Globalfiler®, Identifiler®, PowerPlex®16, etc.) or create your own.




GeneMarker HID
File View Project Applicatio
Open Data
Open Project
Reopen Project
Save Project
Close All
Exit
Navigate to File → Open Data to import your files.
GeneMarker® HID
STR Human Identity Software
Click Add, and navigate to the specific files you would like to import (.hid, .fsa, .sg1).
Open Data Files
Data File List:
Add...
Remove
Remove All
Add Folder...
Default
Page Up
Page Down
Channels...
Auto-Elevate
OK
Cancel


Process Raw Data
File
Project
Applications
Tools
Help
DT
Untitled
Raw Data
PAT_10_C1.fsa
PAT_10_C2.fsa
PAT_10_C3.fsa
PAT_10_F.fsa
PAT_11_C.fsa
PAT_11_F.fsa
PAT_11_M.fsa
PAT_12_C.fsa
PAT_12_F.fsa
PAT_12_M.fsa
PAT_13_C.fsa
PAT_13_F.fsa
PAT_13_M.fsa
PAT_14_C.fsa
PAT_14_F.fsa
PAT_14_M.fsa
PAT_8_C.fsa
PAT_8_F.fsa
PAT_8_M.fsa
PAT_9_C.fsa
PAT_9_F.fsa
PAT_9_M.fsa
LD: PAT_Ladder_1.fsa
LD: PAT_Ladder_3.fsa
Toggle dye colors
Double-click on a sample file to display/hide it.
PAT_10_C2.fsa
Draw a box from left to right with your mouse to zoom in. Right to left zooms back out.
Page Up
Page Down
New
24 samples
PC error: 0/0
NC error: 0/0
Ladder error: 0/0
#Failed=0
#Flagged=0

Click the icon or navigate to Project ⟶ Run to process your data:



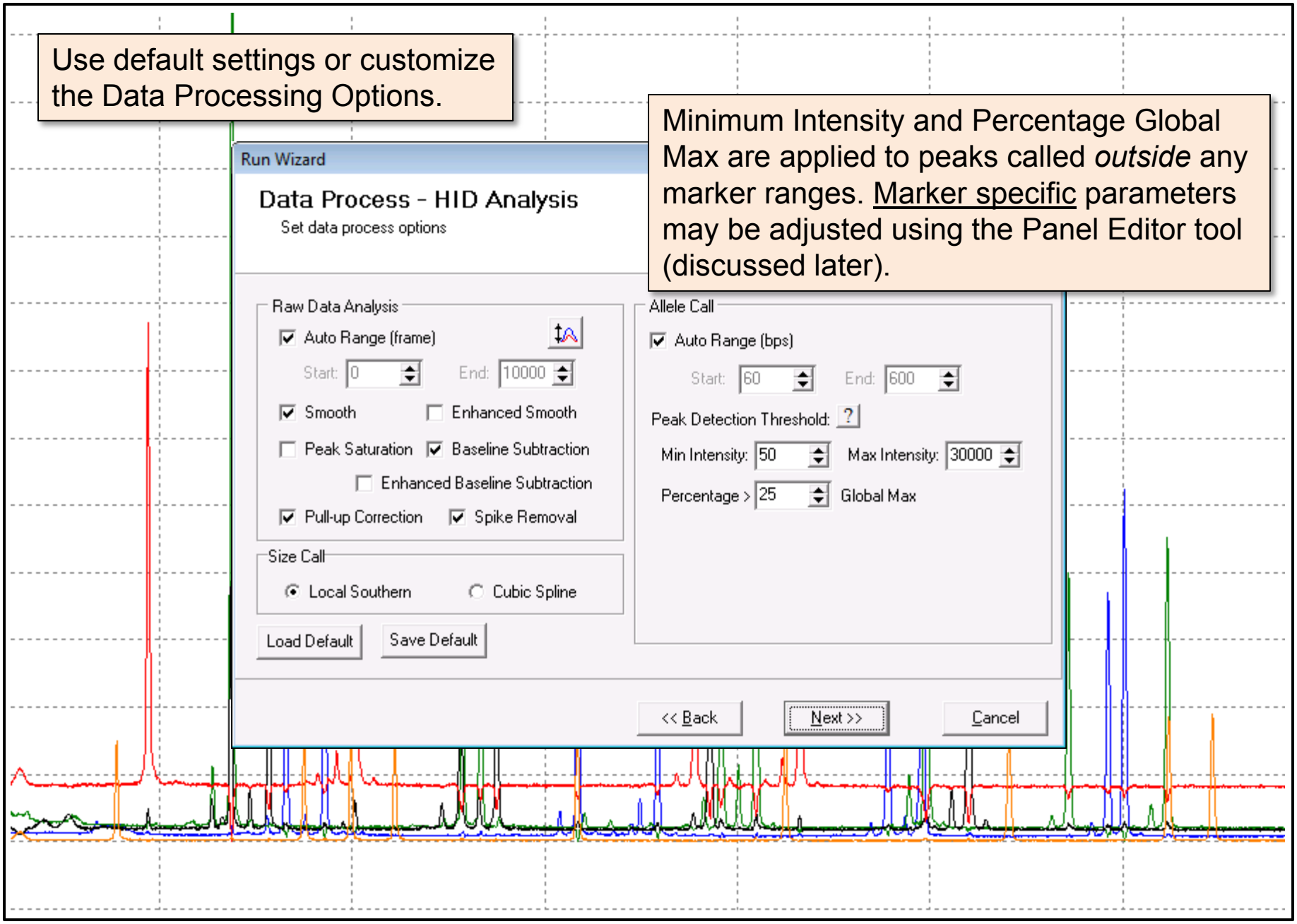
(1) Select the pre-saved template corresponding to your kit or chemistry.

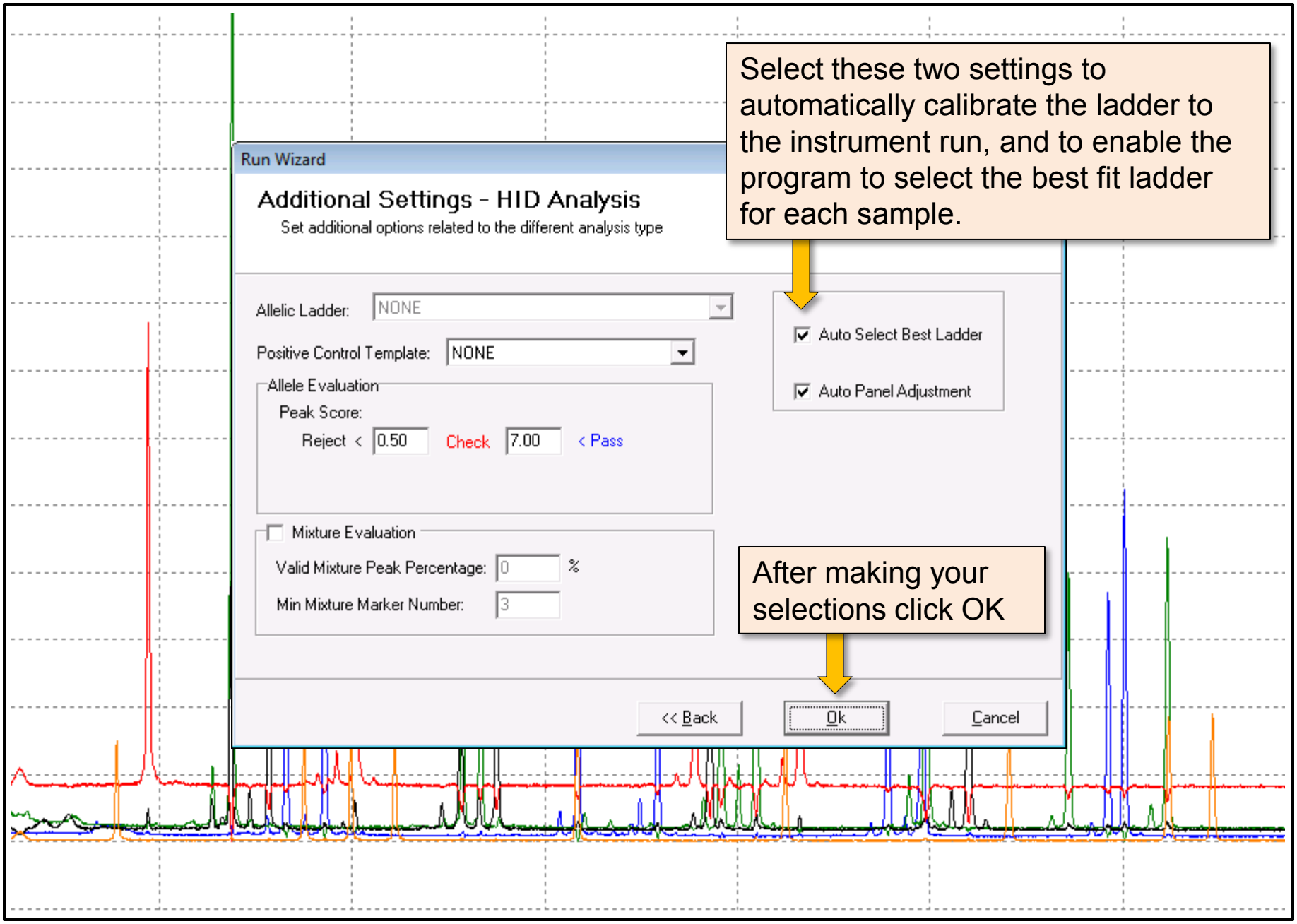
(2) Or, manually select your Panel, Size Standard, and Standard color.

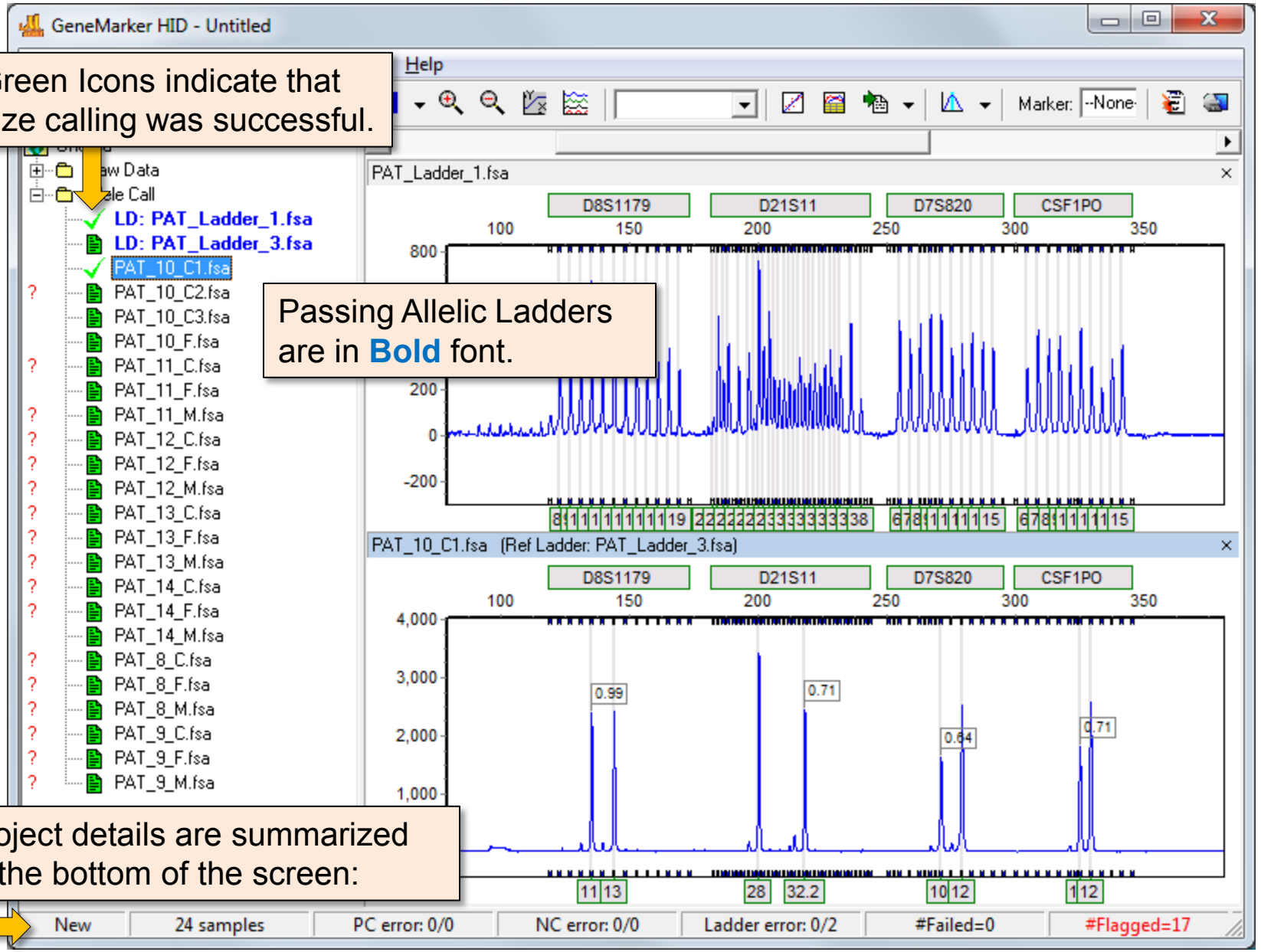
(3) After making your selections, click Next >>

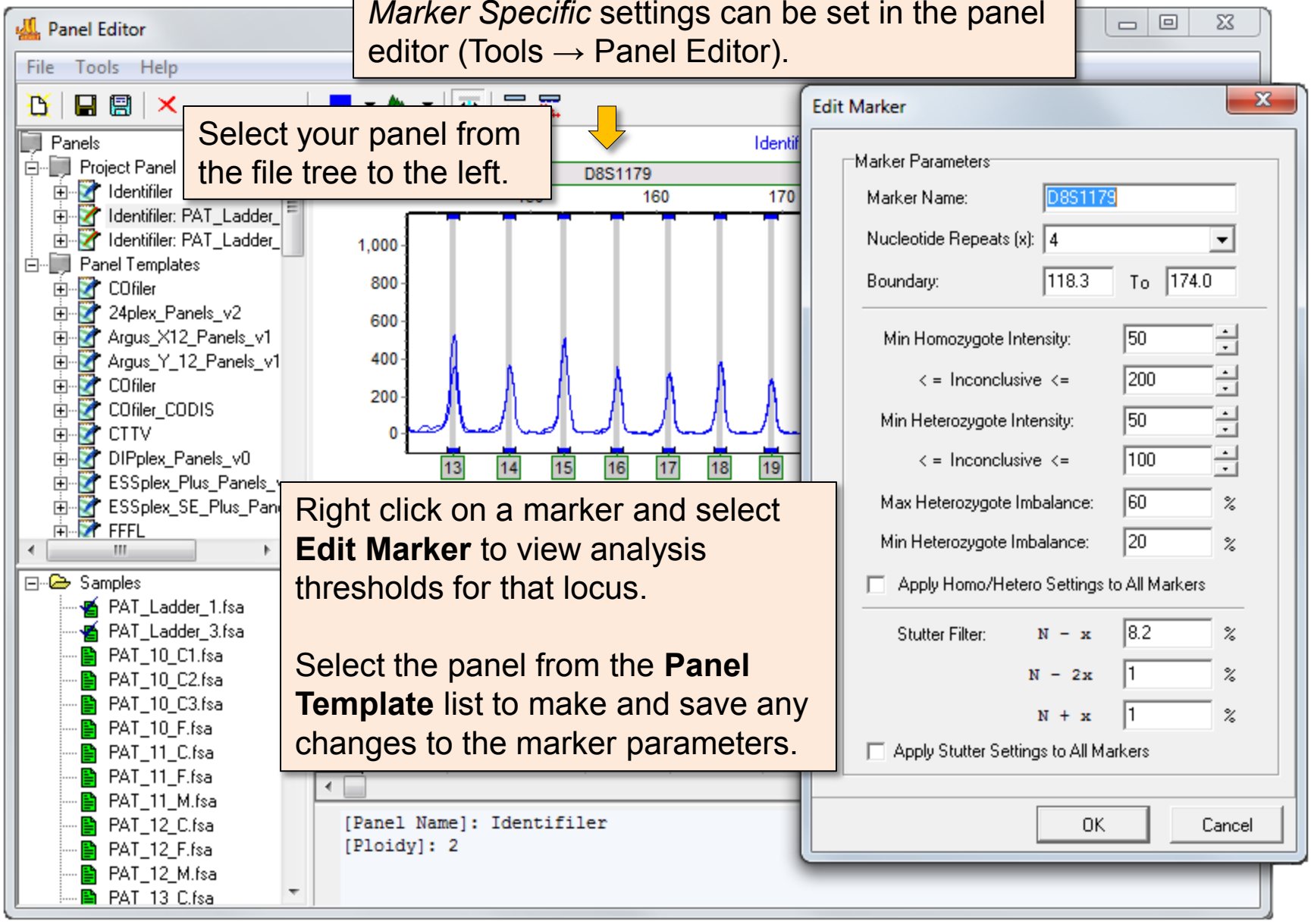
Use default settings or customize the Data Processing Options.

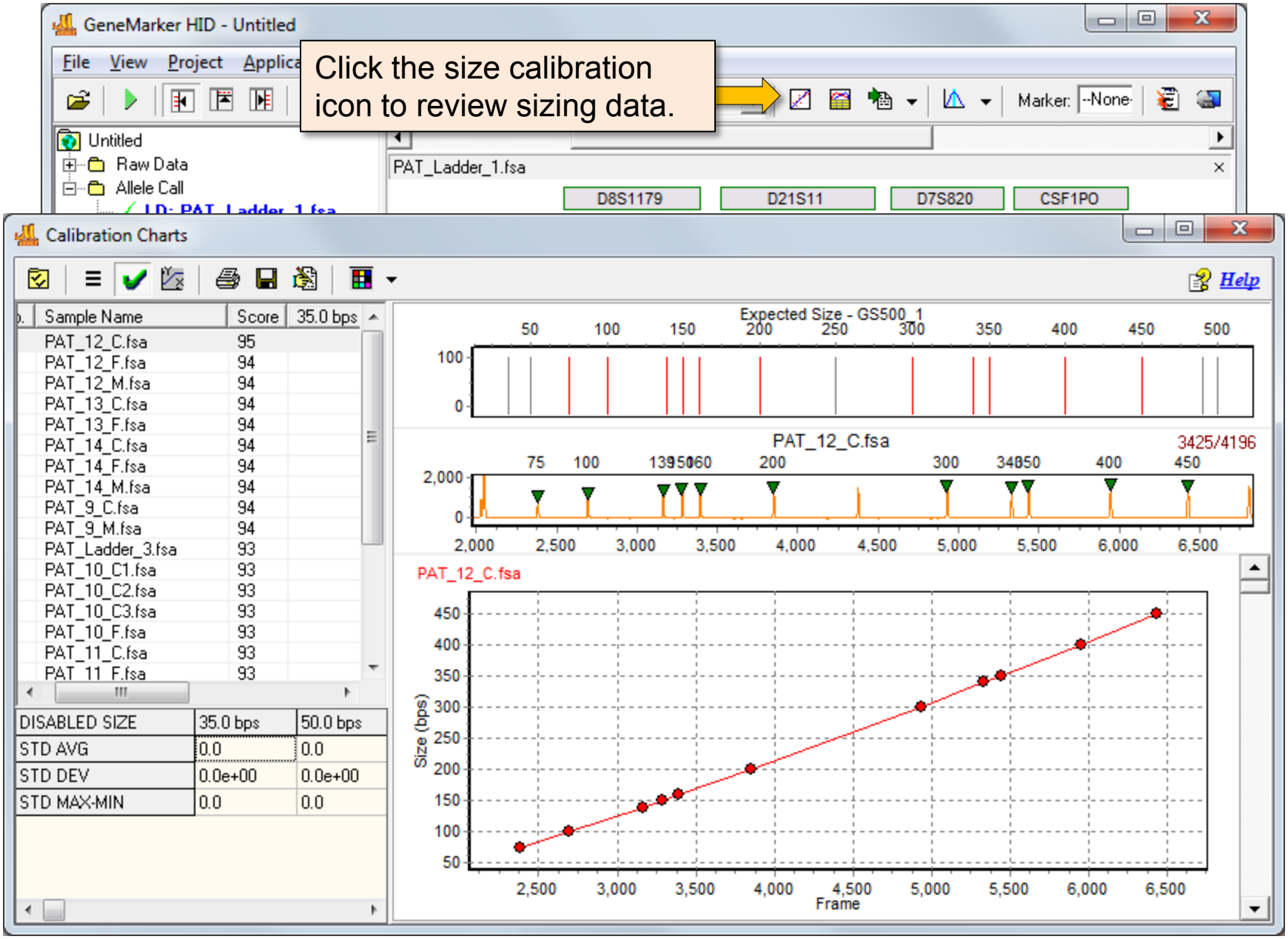
Minimum Intensity and Percentage Global Max are applied to peaks called *outside* any marker ranges. Marker specific parameters may be adjusted using the Panel Editor tool (discussed later).

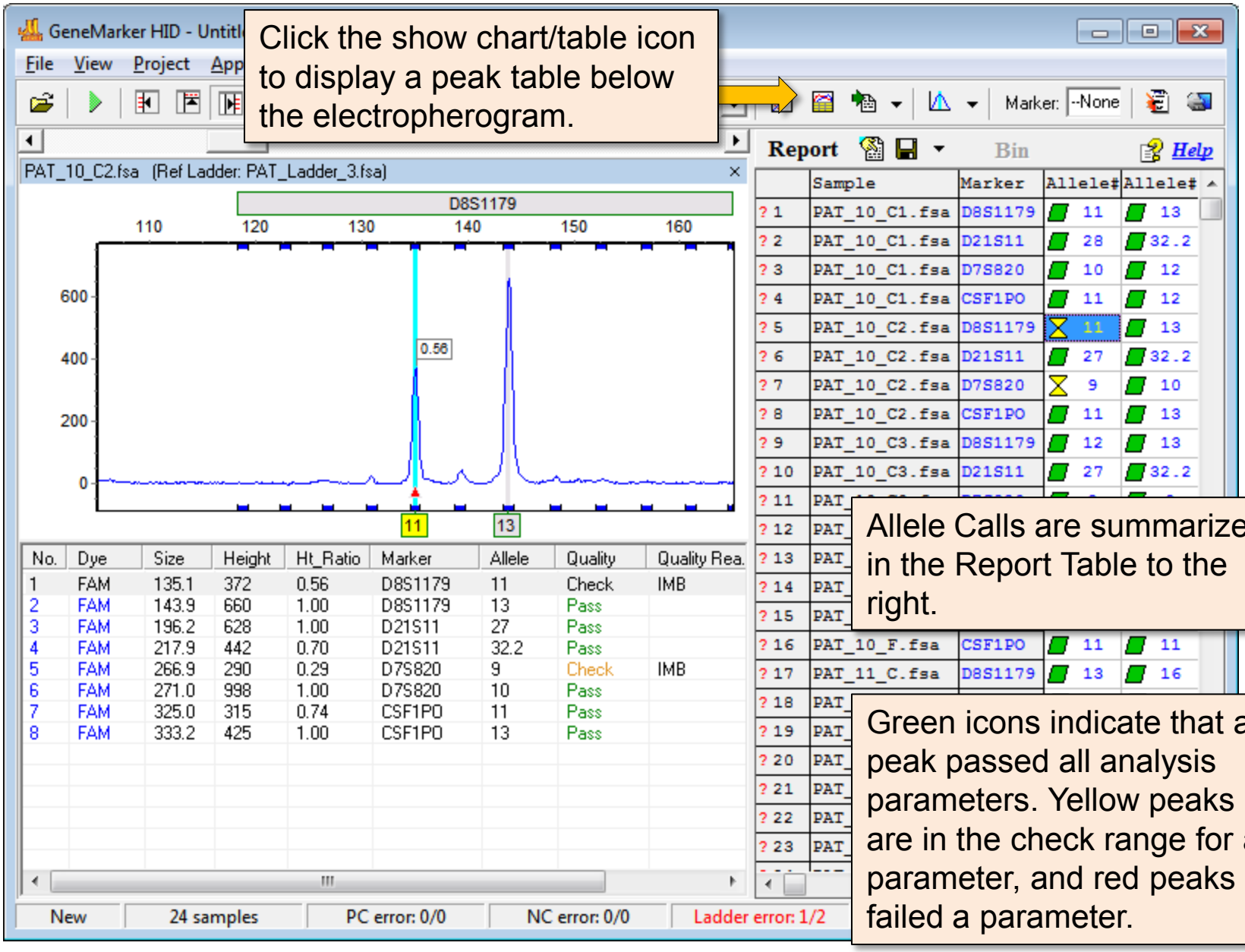


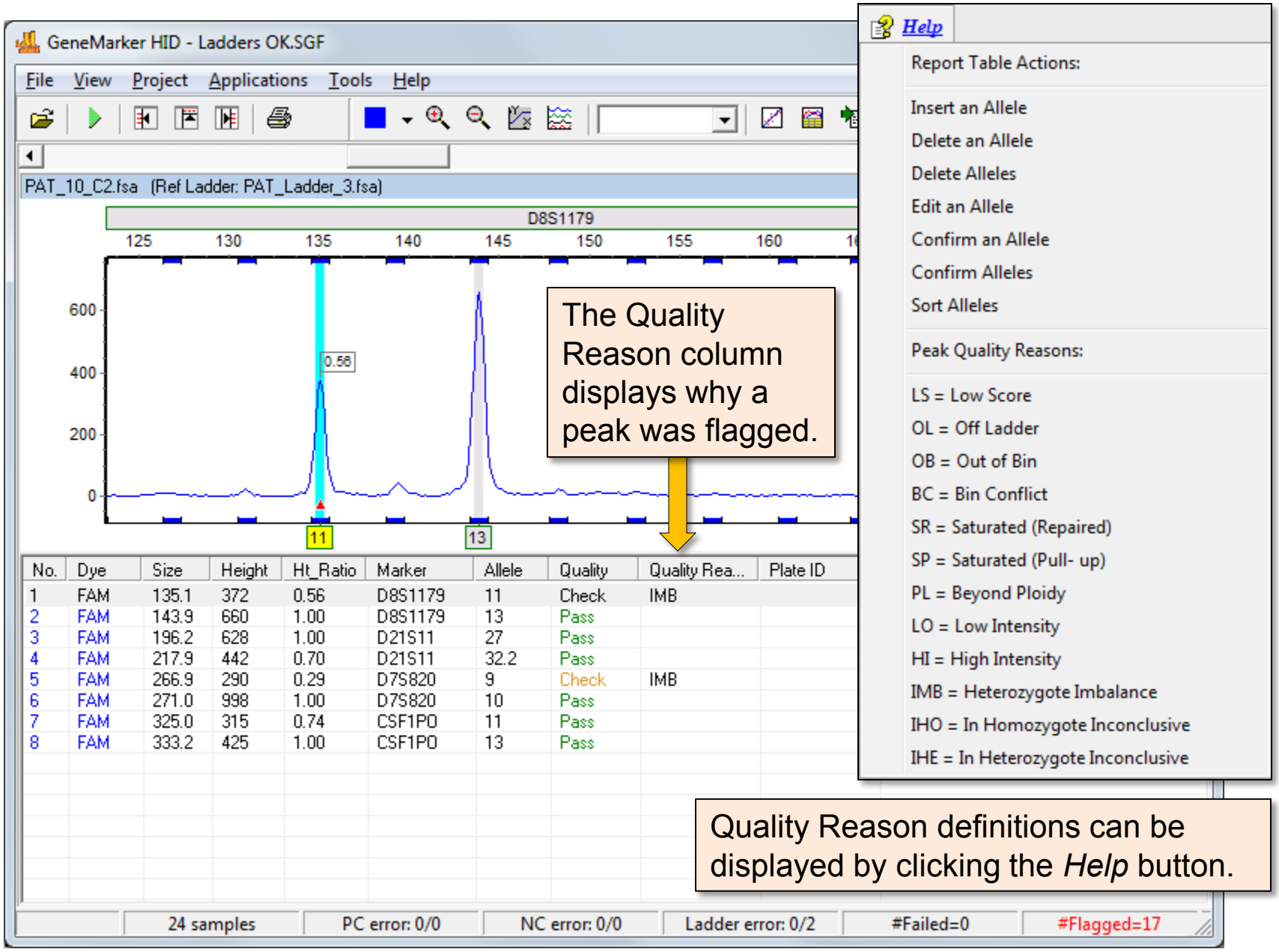

Select these two settings to automatically calibrate the ladder to the instrument run, and to enable the program to select the best fit ladder for each sample.
Run Wizard
Additional Settings - HID Analysis
Set additional options related to the different analysis type
Allelic Ladder:
NONE
Positive Control Template:
NONE
Auto Select Best Ladder
Auto Panel Adjustment
Allele Evaluation
Peak Score:
Reject <
0.50
Check
7.00
< Pass
Mixture Evaluation
Valid Mixture Peak Percentage:
0
%
Min Mixture Marker Number:
3
After making your selections click OK
<< Back
Ok
Cancel

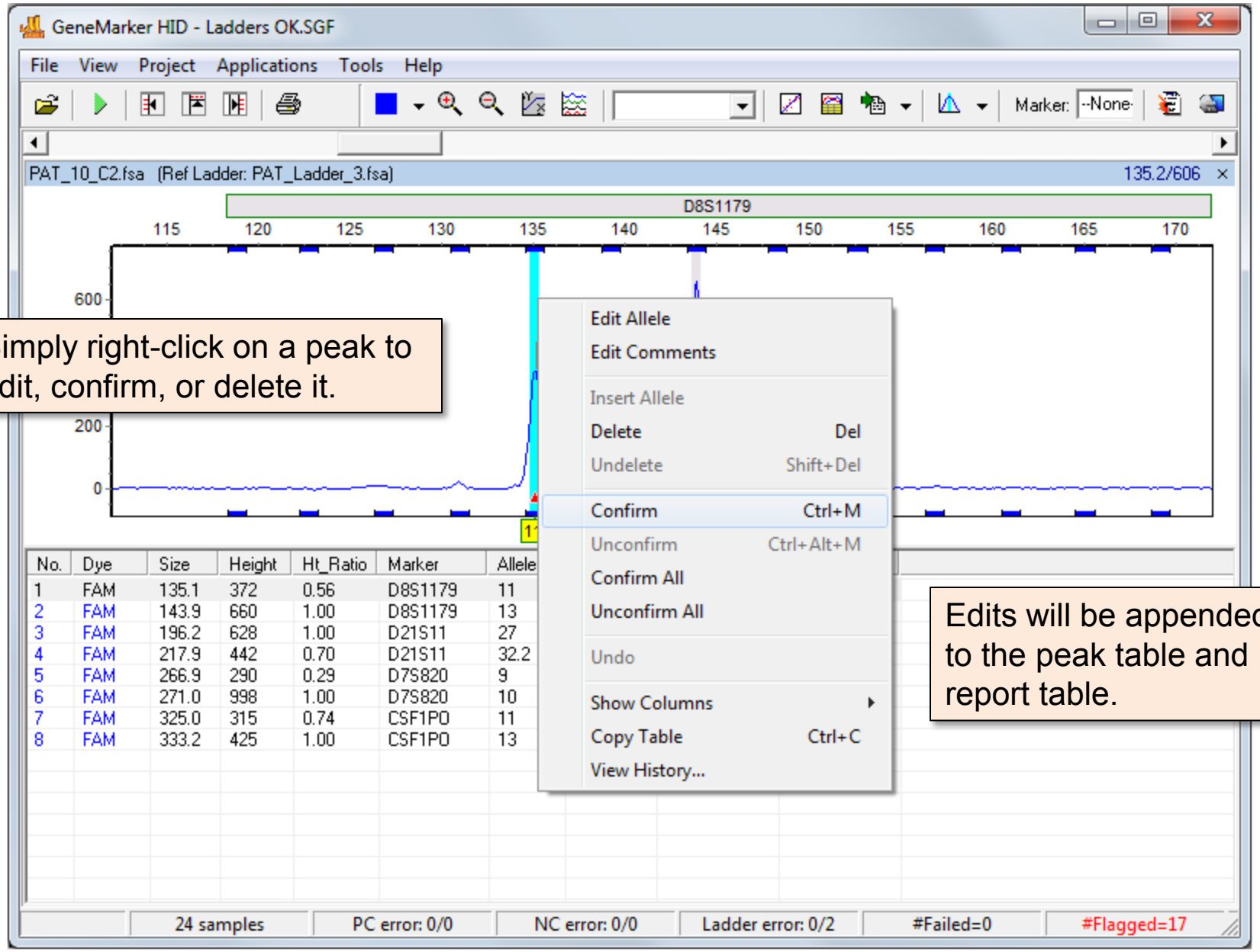

GeneMarker HID - Untitled
Help
Marker: --None-
Green Icons indicate that size calling was successful.
Passing Allelic Ladders are in **Bold** font.
Project details are summarized at the bottom of the screen:
LD: PAT_Ladder_1.fsa
LD: PAT_Ladder_3.fsa
PAT_10_C1.fsa
PAT_10_C2.fsa
PAT_10_C3.fsa
PAT_10_F.fsa
PAT_11_C.fsa
PAT_11_F.fsa
PAT_11_M.fsa
PAT_12_C.fsa
PAT_12_F.fsa
PAT_12_M.fsa
PAT_13_C.fsa
PAT_13_F.fsa
PAT_13_M.fsa
PAT_14_C.fsa
PAT_14_F.fsa
PAT_14_M.fsa
PAT_8_C.fsa
PAT_8_F.fsa
PAT_8_M.fsa
PAT_9_C.fsa
PAT_9_F.fsa
PAT_9_M.fsa
PAT_Ladder_1.fsa
D8S1179
D21S11
D7S820
CSF1PO
PAT_10_C1.fsa (Ref Ladder: PAT_Ladder_3.fsa)
0.99
0.71
0.64
0.71
New
24 samples
PC error: 0/0
NC error: 0/0
Ladder error: 0/2
#Failed=0
#Flagged=17


Marker Specific settings can be set in the panel editor (Tools → Panel Editor).
Select your panel from the file tree to the left.
Right click on a marker and select **Edit Marker** to view analysis thresholds for that locus.
Select the panel from the **Panel Template** list to make and save any changes to the marker parameters.
Panel Editor
File Tools Help
Panels
Project Panel
Identifiler
Identifiler: PAT_Ladder_
Identifiler: PAT_Ladder_
Panel Templates
COfiler
24plex_Panels_v2
Argus_X12_Panels_v1
Argus_Y_12_Panels_v1
COfiler
COfiler_CODIS
CTTV
DIPplex_Panels_v0
ESSplex_Plus_Panels_
ESSplex_SE_Plus_Pan
FFFL
Samples
PAT_Ladder_1.fsa
PAT_Ladder_3.fsa
PAT_10_C1.fsa
PAT_10_C2.fsa
PAT_10_C3.fsa
PAT_10_F.fsa
PAT_11_C.fsa
PAT_11_F.fsa
PAT_11_M.fsa
PAT_12_C.fsa
PAT_12_F.fsa
PAT_12_M.fsa
PAT_13_C.fsa
D8S1179
160
170
1,000
800
600
400
200
0
13
14
15
16
17
18
19
[Panel Name]: Identifiler
[Ploidy]: 2
Edit Marker
Marker Parameters
Marker Name: D8S1179
Nucleotide Repeats (x): 4
Boundary: 118.3 To 174.0
Min Homozygote Intensity: 50
< = Inconclusive <= 200
Min Heterozygote Intensity: 50
< = Inconclusive <= 100
Max Heterozygote Imbalance: 60 %
Min Heterozygote Imbalance: 20 %
Apply Homo/Hetero Settings to All Markers
Stutter Filter: N - x 8.2 %
N - 2x 1 %
N + x 1 %
Apply Stutter Settings to All Markers
OK
Cancel


GeneMarker HID - Untitled
File View Project Applica
Click the size calibration icon to review sizing data.
Marker: --None-
Untitled
Raw Data
Allele Call
PAT_Ladder_1.fsa
D8S1179
D21S11
D7S820
CSF1PO
Calibration Charts
Help
Sample Name Score 35.0 bps
PAT_12_C.fsa 95
PAT_12_F.fsa 94
PAT_12_M.fsa 94
PAT_13_C.fsa 94
PAT_13_F.fsa 94
PAT_14_C.fsa 94
PAT_14_F.fsa 94
PAT_14_M.fsa 94
PAT_9_C.fsa 94
PAT_9_M.fsa 94
PAT_Ladder_3.fsa 93
PAT_10_C1.fsa 93
PAT_10_C2.fsa 93
PAT_10_C3.fsa 93
PAT_10_F.fsa 93
PAT_11_C.fsa 93
PAT_11_F.fsa 93
DISABLED SIZE 35.0 bps 50.0 bps
STD AVG 0.0 0.0
STD DEV 0.0e+00 0.0e+00
STD MAX-MIN 0.0 0.0
Expected Size - GS500_1
PAT_12_C.fsa
3425/4196
PAT_12_C.fsa
Size (bps)
Frame

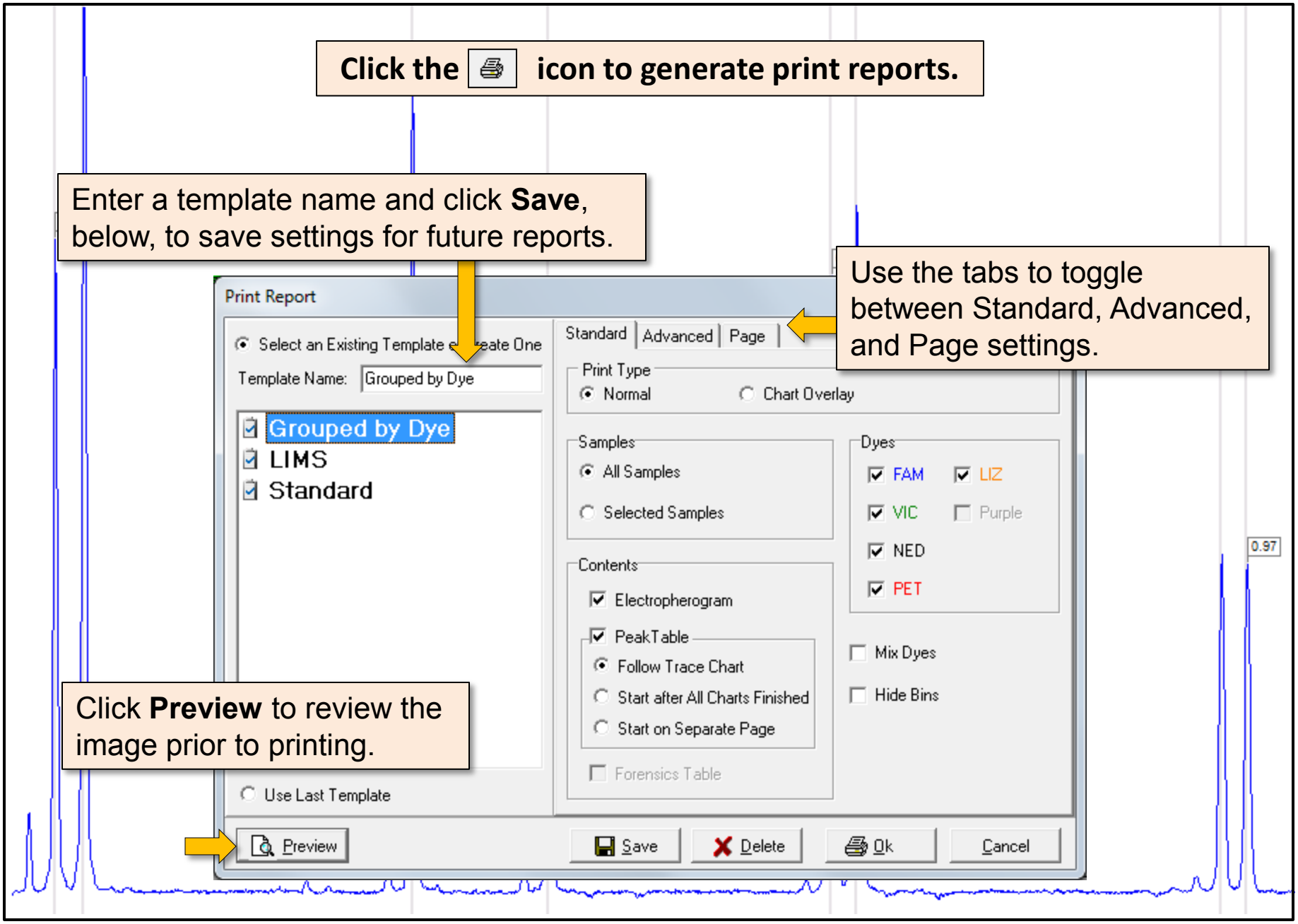

Click the show chart/table icon to display a peak table below the electropherogram.
GeneMarker HID - Untitl
File View Project App
Marker: --None
PAT_10_C2.fsa (Ref Ladder: PAT_Ladder_3.fsa)
D8S1179
110 120 130 140 150 160
600 400 200 0
0.56
11 13
Report
Bin
Help
Sample Marker Allele# Allele#
? 1 PAT_10_C1.fsa D8S1179 11 13
? 2 PAT_10_C1.fsa D21S11 28 32.2
? 3 PAT_10_C1.fsa D7S820 10 12
? 4 PAT_10_C1.fsa CSF1PO 11 12
? 5 PAT_10_C2.fsa D8S1179 11 13
? 6 PAT_10_C2.fsa D21S11 27 32.2
? 7 PAT_10_C2.fsa D7S820 9 10
? 8 PAT_10_C2.fsa CSF1PO 11 13
? 9 PAT_10_C3.fsa D8S1179 12 13
? 10 PAT_10_C3.fsa D21S11 27 32.2
? 16 PAT_10_F.fsa CSF1PO 11 11
? 17 PAT_11_C.fsa D8S1179 13 16
No. Dye Size Height Ht_Ratio Marker Allele Quality Quality Rea.
1 FAM 135.1 372 0.56 D8S1179 11 Check IMB
2 FAM 143.9 660 1.00 D8S1179 13 Pass
3 FAM 196.2 628 1.00 D21S11 27 Pass
4 FAM 217.9 442 0.70 D21S11 32.2 Pass
5 FAM 266.9 290 0.29 D7S820 9 Check IMB
6 FAM 271.0 998 1.00 D7S820 10 Pass
7 FAM 325.0 315 0.74 CSF1PO 11 Pass
8 FAM 333.2 425 1.00 CSF1PO 13 Pass
Allele Calls are summarized in the Report Table to the right.
Green icons indicate that a peak passed all analysis parameters. Yellow peaks are in the check range for a parameter, and red peaks failed a parameter.
New 24 samples PC error: 0/0 NC error: 0/0 Ladder error: 1/2


GeneMarker HID - Ladders OK.SGF
File View Project Applications Tools Help
PAT_10_C2.fsa (Ref Ladder: PAT_Ladder_3.fsa)
D8S1179
125 130 135 140 145 150 155 160
600
400
200
0
0.56
11
13
The Quality Reason column displays why a peak was flagged.
No. Dye Size Height Ht_Ratio Marker Allele Quality Quality Rea... Plate ID
1 FAM 135.1 372 0.56 D8S1179 11 Check IMB
2 FAM 143.9 660 1.00 D8S1179 13 Pass
3 FAM 196.2 628 1.00 D21S11 27 Pass
4 FAM 217.9 442 0.70 D21S11 32.2 Pass
5 FAM 266.9 290 0.29 D7S820 9 Check IMB
6 FAM 271.0 998 1.00 D7S820 10 Pass
7 FAM 325.0 315 0.74 CSF1PO 11 Pass
8 FAM 333.2 425 1.00 CSF1PO 13 Pass
24 samples
PC error: 0/0
NC error: 0/0
Ladder error: 0/2
#Failed=0
#Flagged=17
Help
Report Table Actions:
Insert an Allele
Delete an Allele
Delete Alleles
Edit an Allele
Confirm an Allele
Confirm Alleles
Sort Alleles
Peak Quality Reasons:
LS = Low Score
OL = Off Ladder
OB = Out of Bin
BC = Bin Conflict
SR = Saturated (Repaired)
SP = Saturated (Pull- up)
PL = Beyond Ploidy
LO = Low Intensity
HI = High Intensity
IMB = Heterozygote Imbalance
IHO = In Homozygote Inconclusive
IHE = In Heterozygote Inconclusive
Quality Reason definitions can be displayed by clicking the *Help* button.

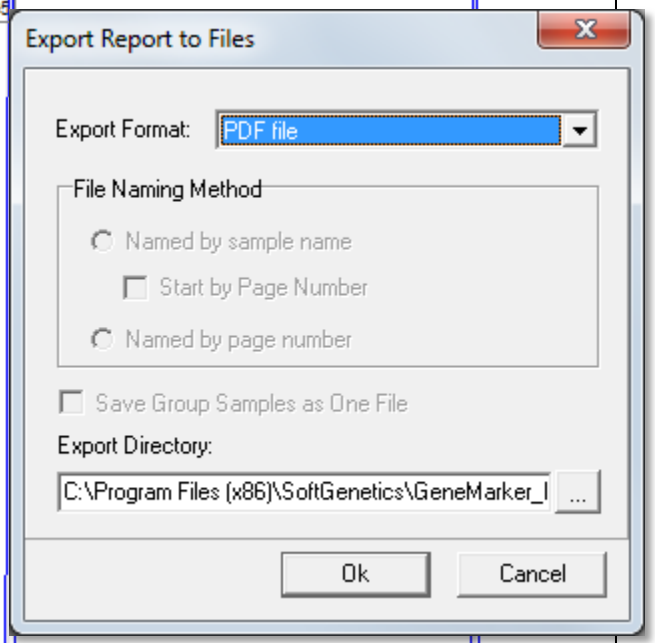


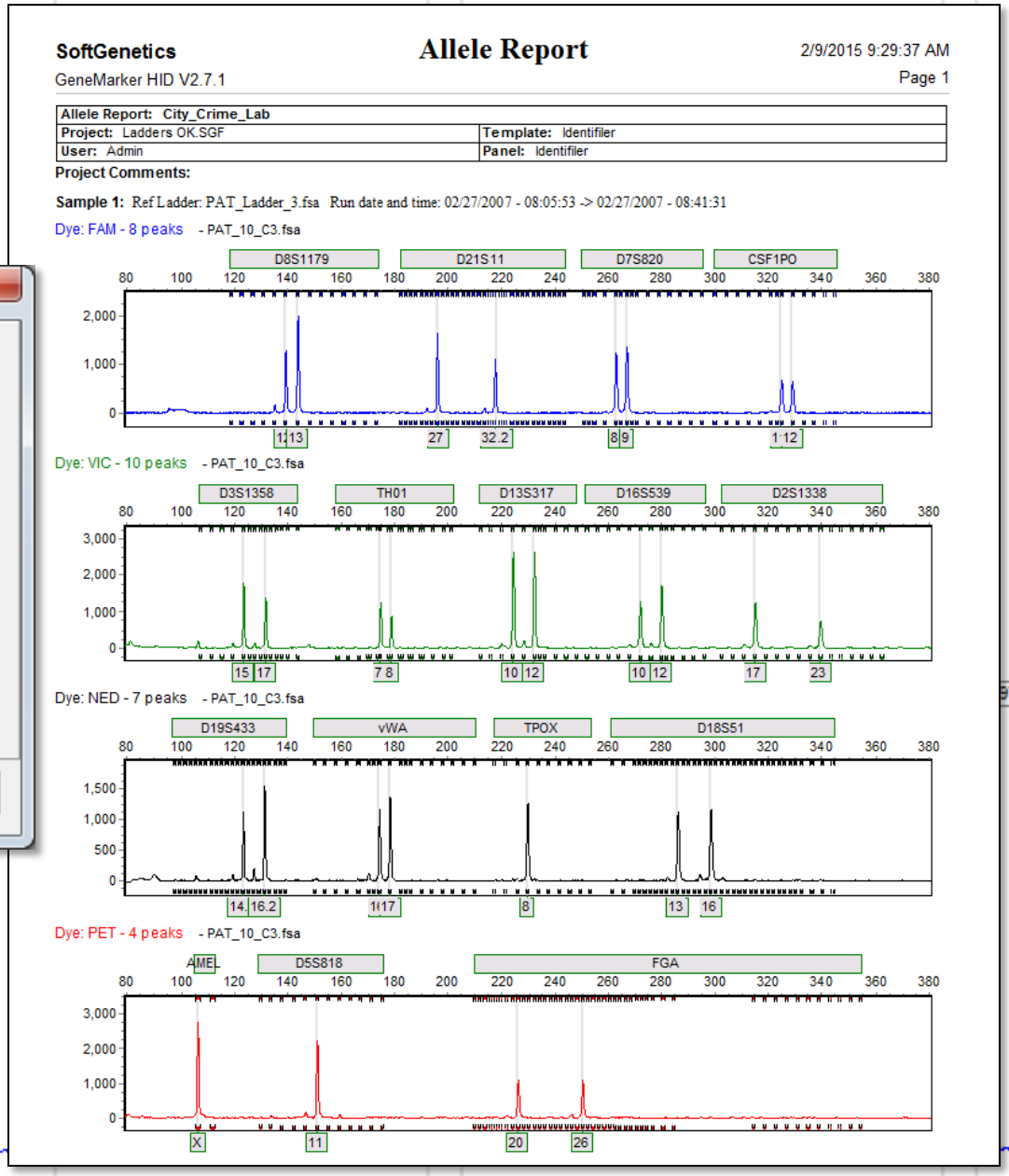
Simply right-click on a peak to edit, confirm, or delete it.

Edits will be appended to the peak table and report table.


Click the icon to generate print reports.
Enter a template name and click **Save**, below, to save settings for future reports.
Use the tabs to toggle between Standard, Advanced, and Page settings.
Click **Preview** to review the image prior to printing.
Print Report
Select an Existing Template
Create One
Template Name:
Grouped by Dye
Grouped by Dye
LIMS
Standard
Use Last Template
Standard
Advanced
Page
Print Type
Normal
Chart Overlay
Samples
All Samples
Selected Samples
Dyes
FAM
LIZ
VIC
Purple
NED
PET
Contents
Electropherogram
PeakTable
Follow Trace Chart
Start after All Charts Finished
Start on Separate Page
Forensics Table
Mix Dyes
Hide Bins
Preview
Save
Delete
Ok
Cancel
0.97

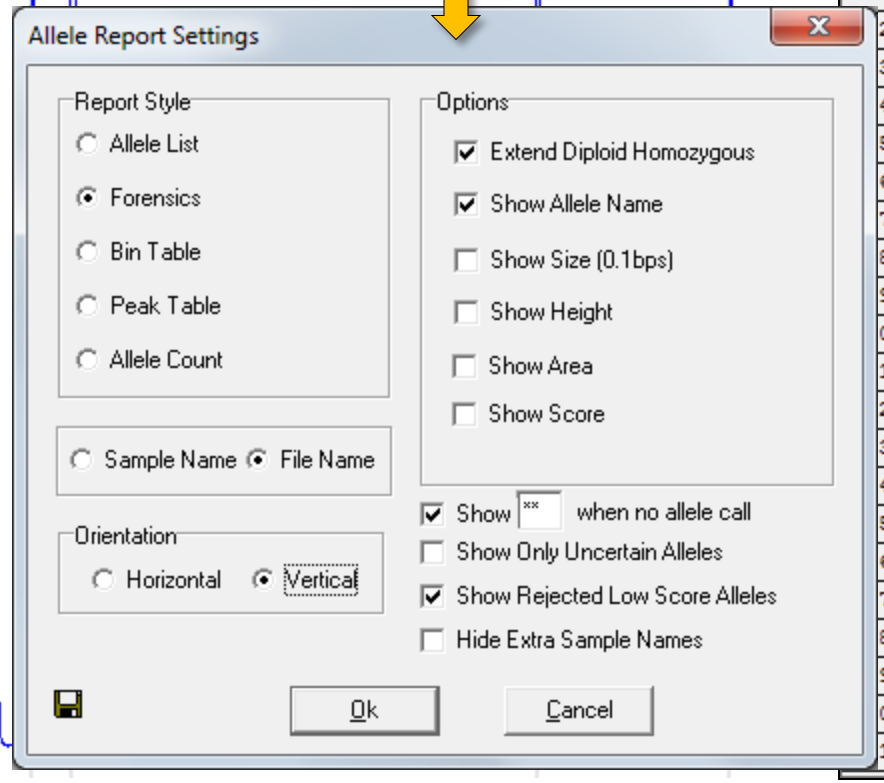
Reports can be printed directly, or saved as a PDF, JPEG, or PNG image.

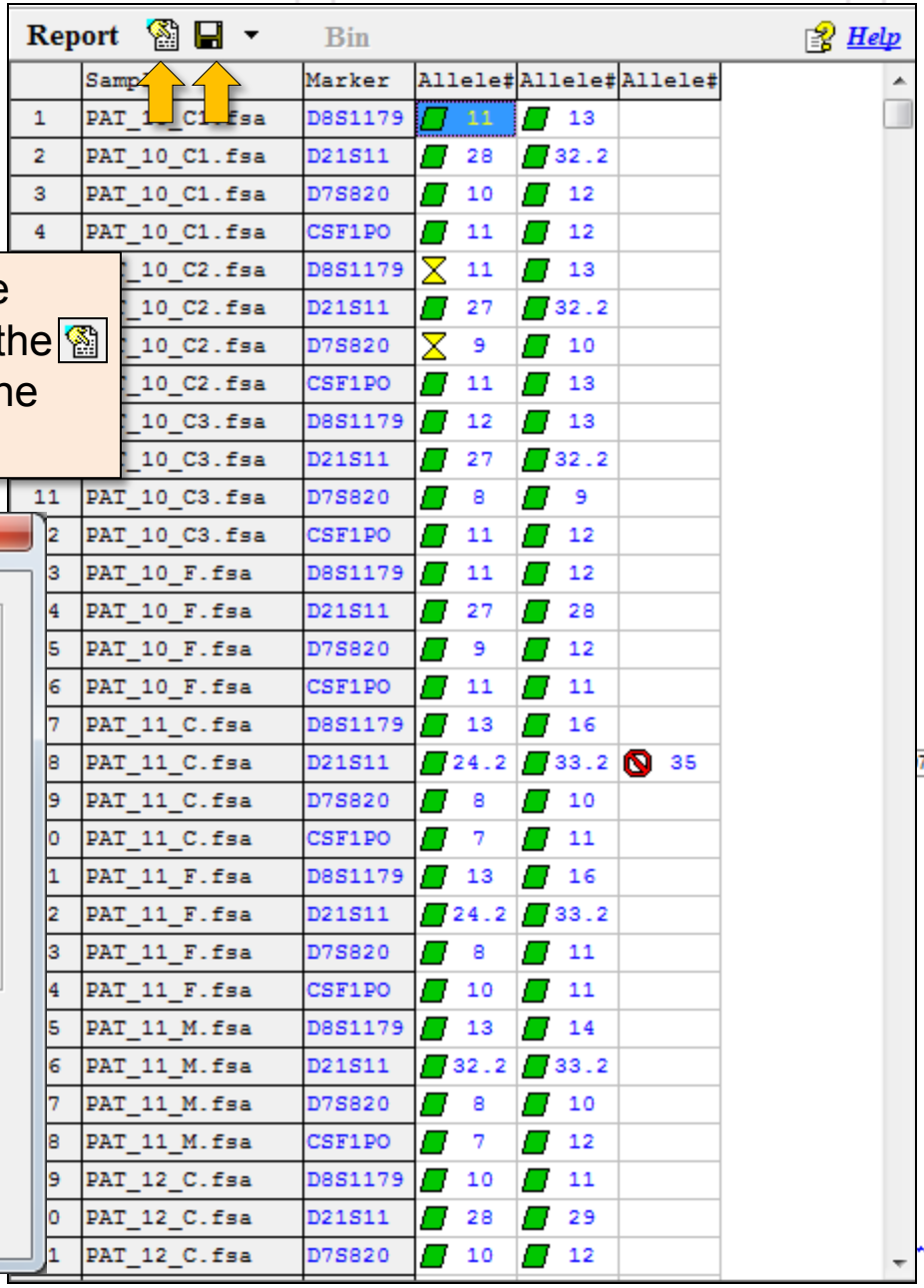




The Report Table can be saved as an excel or text file by simply clicking the icon.

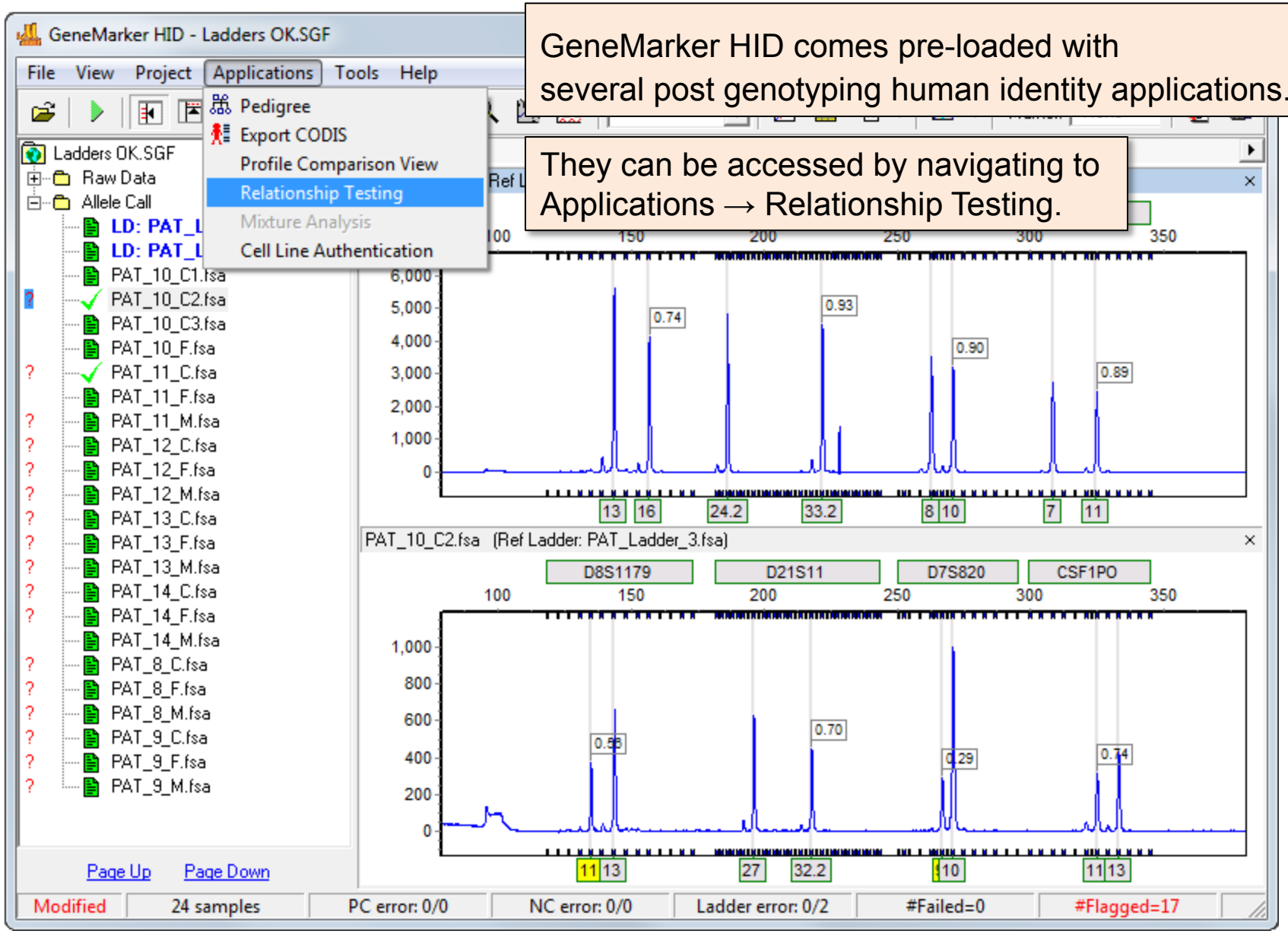
The Report Table will be saved in the same format in which it is being displayed. Click the icon to modify the contents and format of the report table.





	Samp	Marker	Allele#	Allele#	Allele#
1	PAT_1_C1.fsa	D8S1179	11	13	
2	PAT_10_C1.fsa	D21S11	28	32.2	
3	PAT_10_C1.fsa	D7S820	10	12	
4	PAT_10_C1.fsa	CSF1PO	11	12	
	_10_C2.fsa	D8S1179	11	13	
	_10_C2.fsa	D21S11	27	32.2	
	_10_C2.fsa	D7S820	9	10	
	_10_C2.fsa	CSF1PO	11	13	
	_10_C3.fsa	D8S1179	12	13	
	_10_C3.fsa	D21S11	27	32.2	
11	PAT_10_C3.fsa	D7S820	8	9	
2	PAT_10_C3.fsa	CSF1PO	11	12	
3	PAT_10_F.fsa	D8S1179	11	12	
4	PAT_10_F.fsa	D21S11	27	28	
5	PAT_10_F.fsa	D7S820	9	12	
6	PAT_10_F.fsa	CSF1PO	11	11	
7	PAT_11_C.fsa	D8S1179	13	16	
8	PAT_11_C.fsa	D21S11	24.2	33.2	35
9	PAT_11_C.fsa	D7S820	8	10	
0	PAT_11_C.fsa	CSF1PO	7	11	
1	PAT_11_F.fsa	D8S1179	13	16	
2	PAT_11_F.fsa	D21S11	24.2	33.2	
3	PAT_11_F.fsa	D7S820	8	11	
4	PAT_11_F.fsa	CSF1PO	10	11	
5	PAT_11_M.fsa	D8S1179	13	14	
6	PAT_11_M.fsa	D21S11	32.2	33.2	
7	PAT_11_M.fsa	D7S820	8	10	
8	PAT_11_M.fsa	CSF1PO	7	12	
9	PAT_12_C.fsa	D8S1179	10	11	
0	PAT_12_C.fsa	D21S11	28	29	
1	PAT_12_C.fsa	D7S820	10	12	

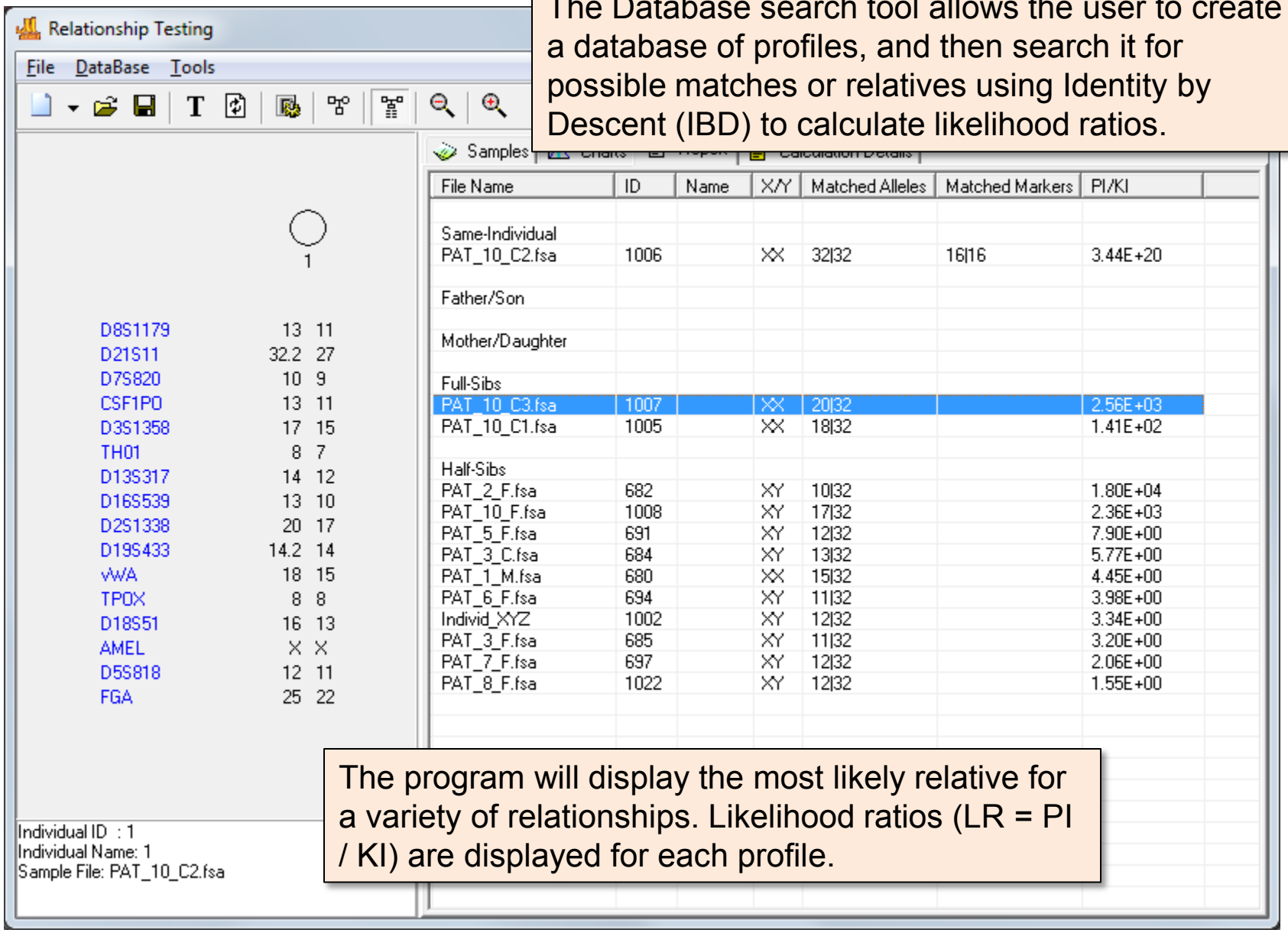
Post Genotyping Applications



GeneMarker HID comes pre-loaded with several post genotyping human identity applications.

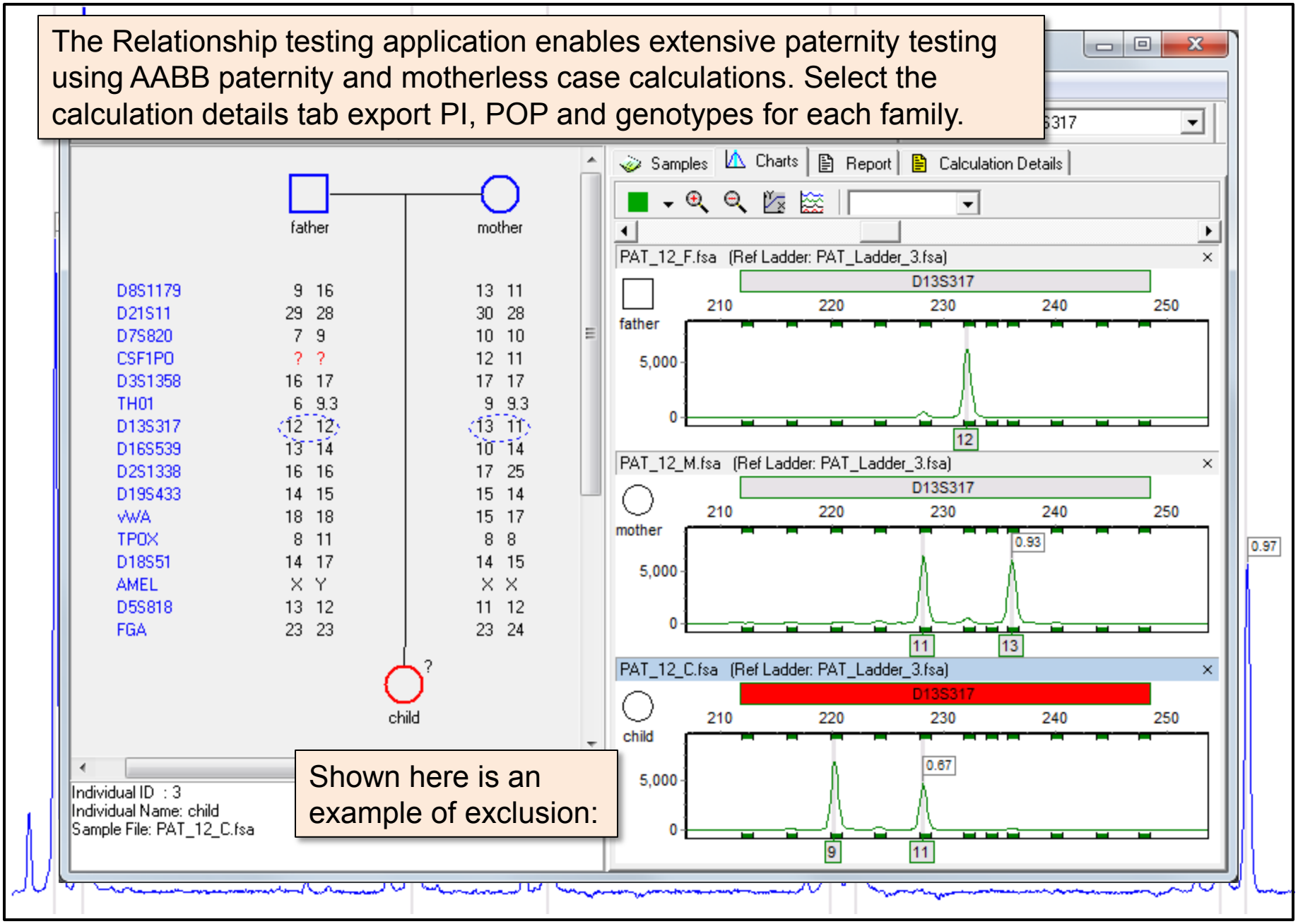
They can be accessed by navigating to Applications → Relationship Testing.

The Database search tool allows the user to create a database of profiles, and then search it for possible matches or relatives using Identity by Descent (IBD) to calculate likelihood ratios.



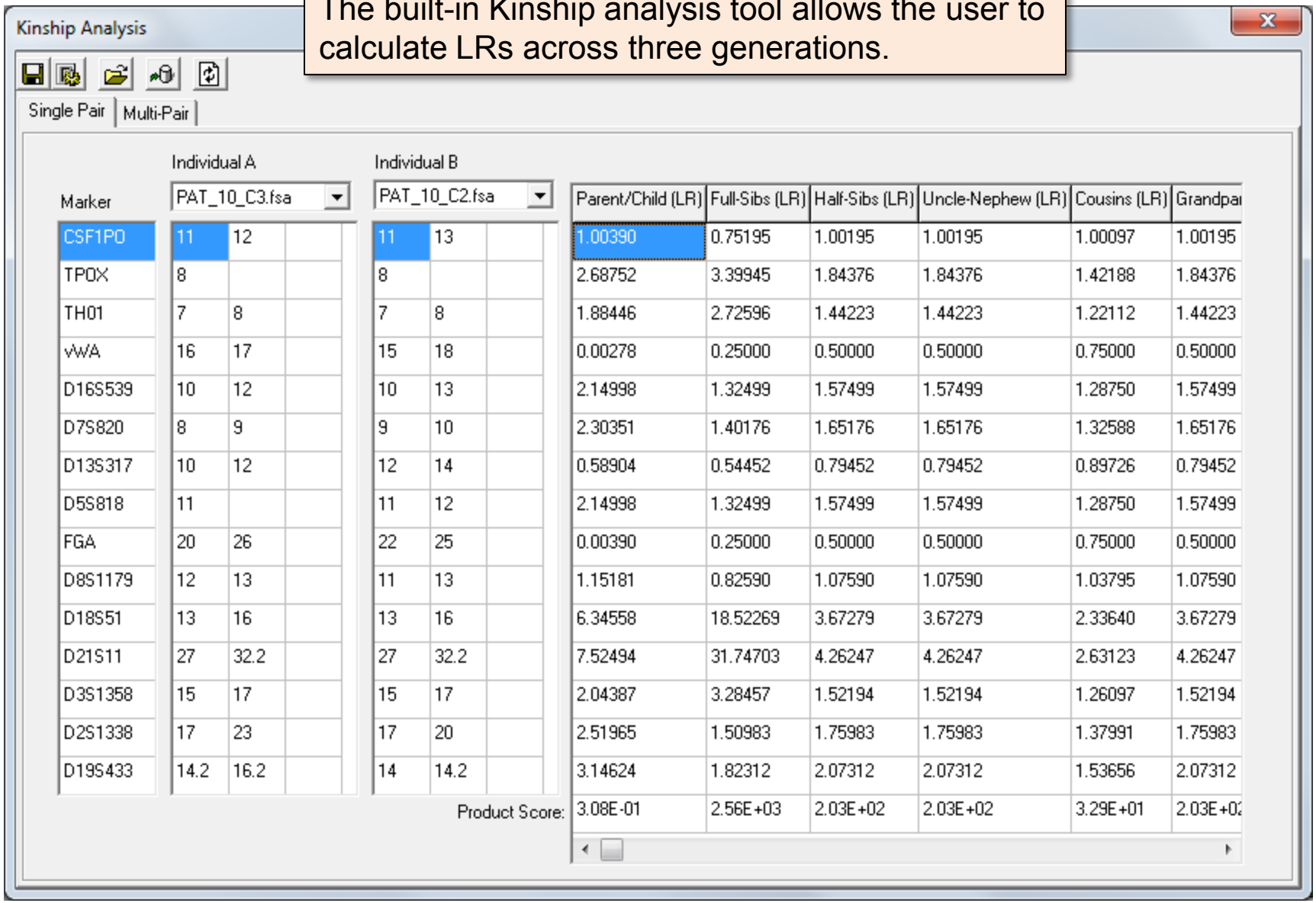
The program will display the most likely relative for a variety of relationships. Likelihood ratios (LR = PI / KI) are displayed for each profile.

The Relationship testing application enables extensive paternity testing using AABB paternity and motherless case calculations. Select the calculation details tab export PI, POP and genotypes for each family.

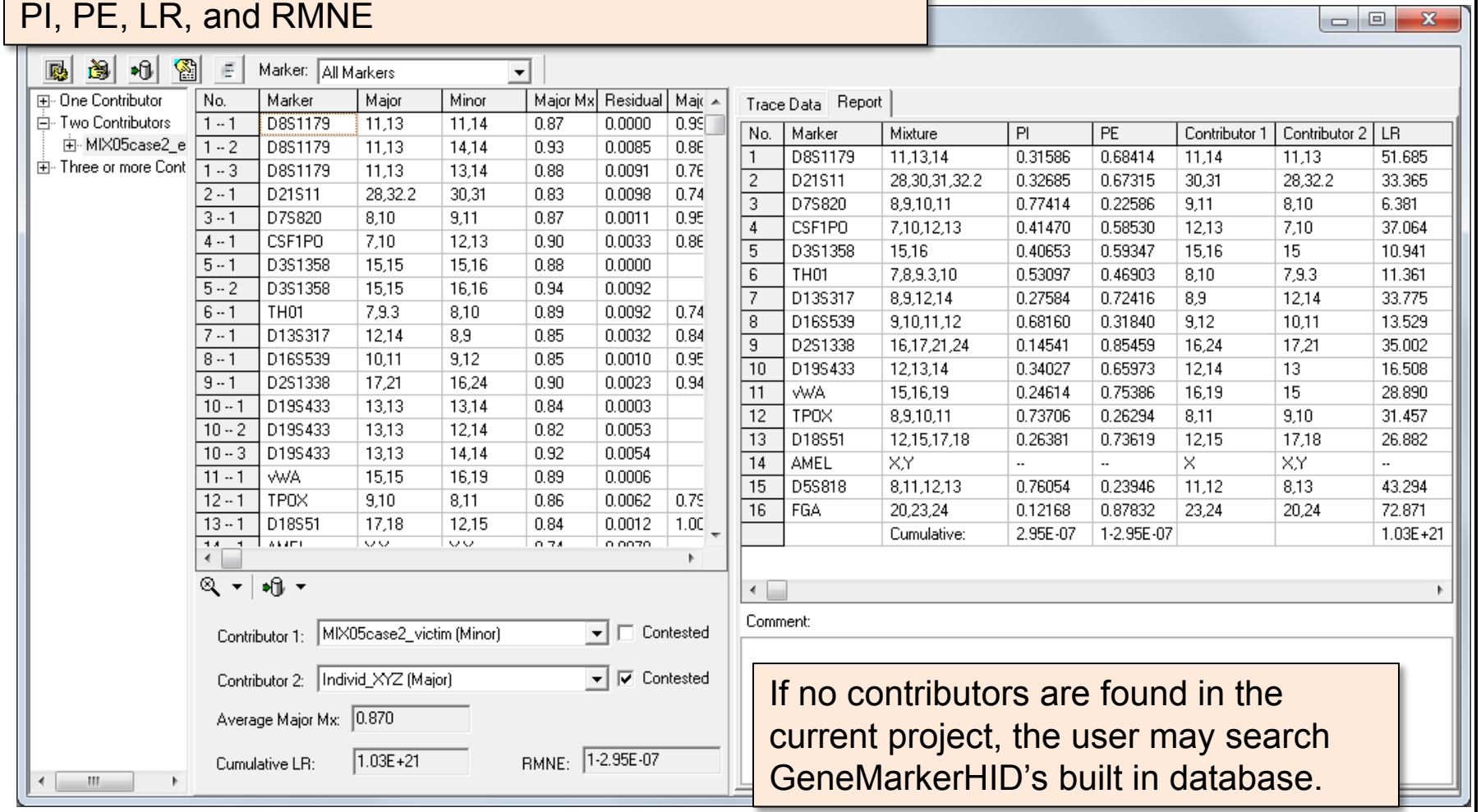


Shown here is an example of exclusion:

The built-in Kinship analysis tool allows the user to calculate LRs across three generations.



The preloaded mixture analysis tool can completely deconvolute mixtures with two contributors, and calculate PI, PE, LR, and RMNE



No.	Marker	Major	Minor	Major Mx	Residual	Maj
1 -- 1	D8S1179	11,13	11,14	0.87	0.0000	0.9
1 -- 2	D8S1179	11,13	14,14	0.93	0.0085	0.8
1 -- 3	D8S1179	11,13	13,14	0.88	0.0091	0.7
2 -- 1	D21S11	28,32.2	30,31	0.83	0.0098	0.74
3 -- 1	D7S820	8,10	9,11	0.87	0.0011	0.9
4 -- 1	CSF1PO	7,10	12,13	0.90	0.0033	0.8
5 -- 1	D3S1358	15,15	15,16	0.88	0.0000	
5 -- 2	D3S1358	15,15	16,16	0.94	0.0092	
6 -- 1	TH01	7,9.3	8,10	0.89	0.0092	0.74
7 -- 1	D13S317	12,14	8,9	0.85	0.0032	0.84
8 -- 1	D16S539	10,11	9,12	0.85	0.0010	0.9
9 -- 1	D2S1338	17,21	16,24	0.90	0.0023	0.94
10 -- 1	D19S433	13,13	13,14	0.84	0.0003	
10 -- 2	D19S433	13,13	12,14	0.82	0.0053	
10 -- 3	D19S433	13,13	14,14	0.92	0.0054	
11 -- 1	vWA	15,15	16,19	0.89	0.0006	
12 -- 1	TPOX	9,10	8,11	0.86	0.0062	0.7
13 -- 1	D18S51	17,18	12,15	0.84	0.0012	1.0

No.	Marker	Mixture	PI	PE	Contributor 1	Contributor 2	LR
1	D8S1179	11,13,14	0.31586	0.68414	11,14	11,13	51.685
2	D21S11	28,30,31,32.2	0.32685	0.67315	30,31	28,32.2	33.365
3	D7S820	8,9,10,11	0.77414	0.22586	9,11	8,10	6.381
4	CSF1PO	7,10,12,13	0.41470	0.58530	12,13	7,10	37.064
5	D3S1358	15,16	0.40653	0.59347	15,16	15	10.941
6	TH01	7,8,9.3,10	0.53097	0.46903	8,10	7,9.3	11.361
7	D13S317	8,9,12,14	0.27584	0.72416	8,9	12,14	33.775
8	D16S539	9,10,11,12	0.68160	0.31840	9,12	10,11	13.529
9	D2S1338	16,17,21,24	0.14541	0.85459	16,24	17,21	35.002
10	D19S433	12,13,14	0.34027	0.65973	12,14	13	16.508
11	vWA	15,16,19	0.24614	0.75386	16,19	15	28.890
12	TPOX	8,9,10,11	0.73706	0.26294	8,11	9,10	31.457
13	D18S51	12,15,17,18	0.26381	0.73619	12,15	17,18	26.882
14	AMEL	X,Y	--	--	X	X,Y	--
15	D5S818	8,11,12,13	0.76054	0.23946	11,12	8,13	43.294
16	FGA	20,23,24	0.12168	0.87832	23,24	20,24	72.871
		Cumulative:	2.95E-07	1-2.95E-07			1.03E+21

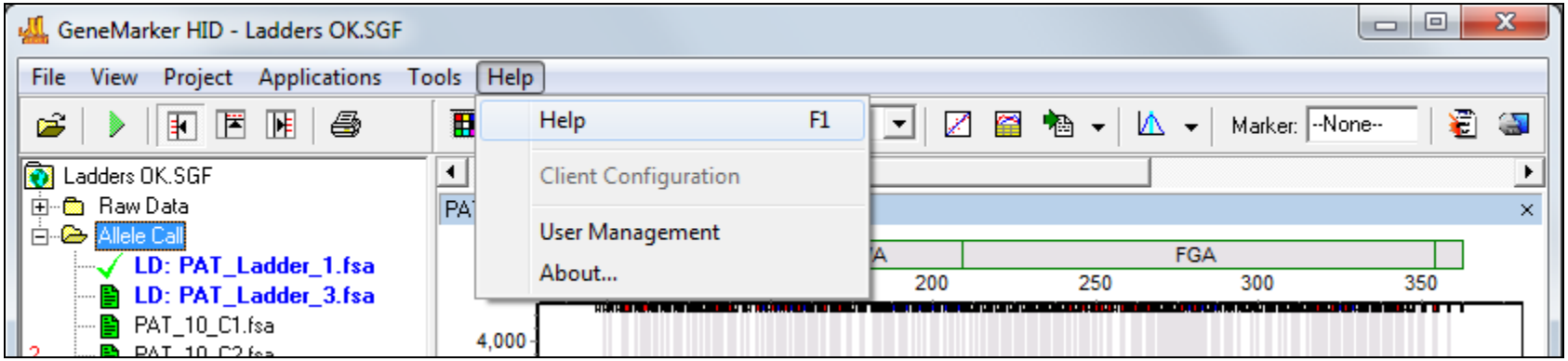
If no contributors are found in the current project, the user may search GeneMarkerHID's built in database.

More Information

Thank you for your interest in GeneMarker HID

STR Human Identity Software

Have more questions? Please email tech_support@softgenetics.com or call 814-237-9340 to…

- Obtain more information about GeneMarkerHID
- Request a Quotation
- Schedule a **Free**, online training session with a SoftGenetics expert

Finally, please note that the **User Manual** is always available by navigating to **Help → Help.**