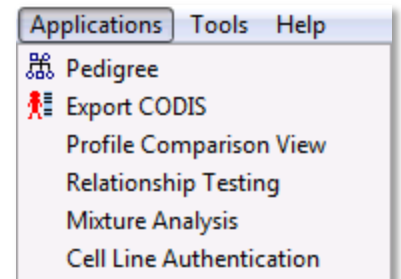
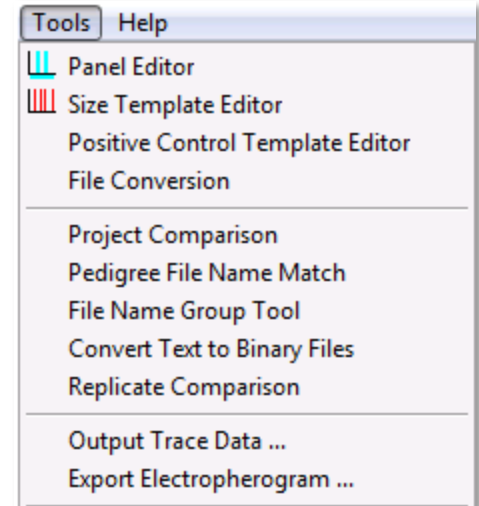
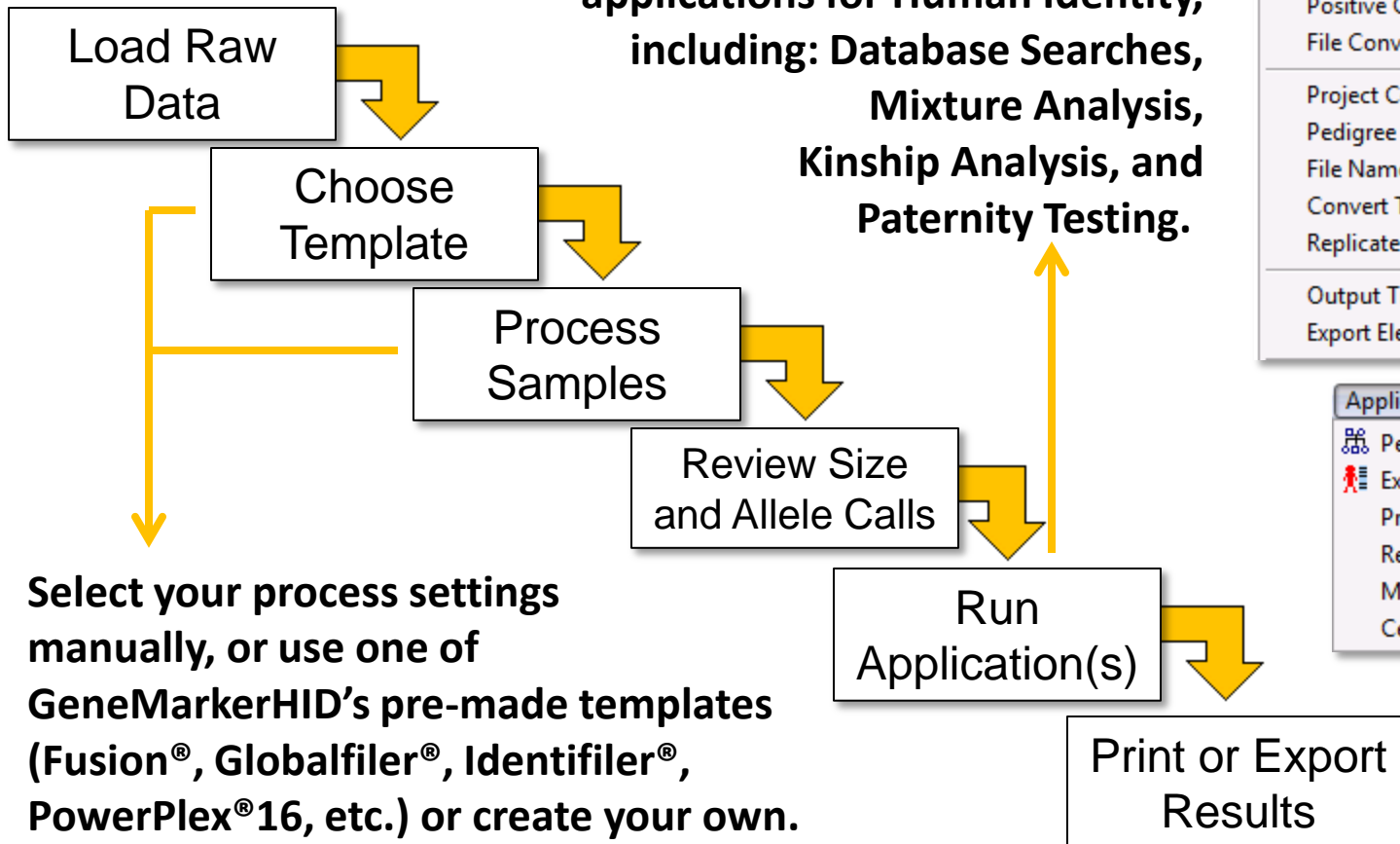




# GeneMarker<sup>®</sup>HID Workflow

STR Human Identity Software

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



The screenshot displays the GeneMarker HID software interface. The main window title is "GeneMarker HID" and the subtitle is "STR Human Identity Software". The "File" menu is open, showing options: "Open Data", "Open Project", "Reopen Project", "Save Project", "Close All", and "Exit". A yellow arrow points to the "Open Data" option. Below the menu, a DNA electropherogram is visible. An "Open Data Files" dialog box is open in the foreground, featuring a "Data File List" area, buttons for "Add...", "Remove", "Remove All", and "Add Folder...", and a "Default" link. A yellow arrow points to the "Add..." button. At the bottom of the dialog box, there are checkboxes for "Channels..." and "Auto-Elevate", and "OK" and "Cancel" buttons.

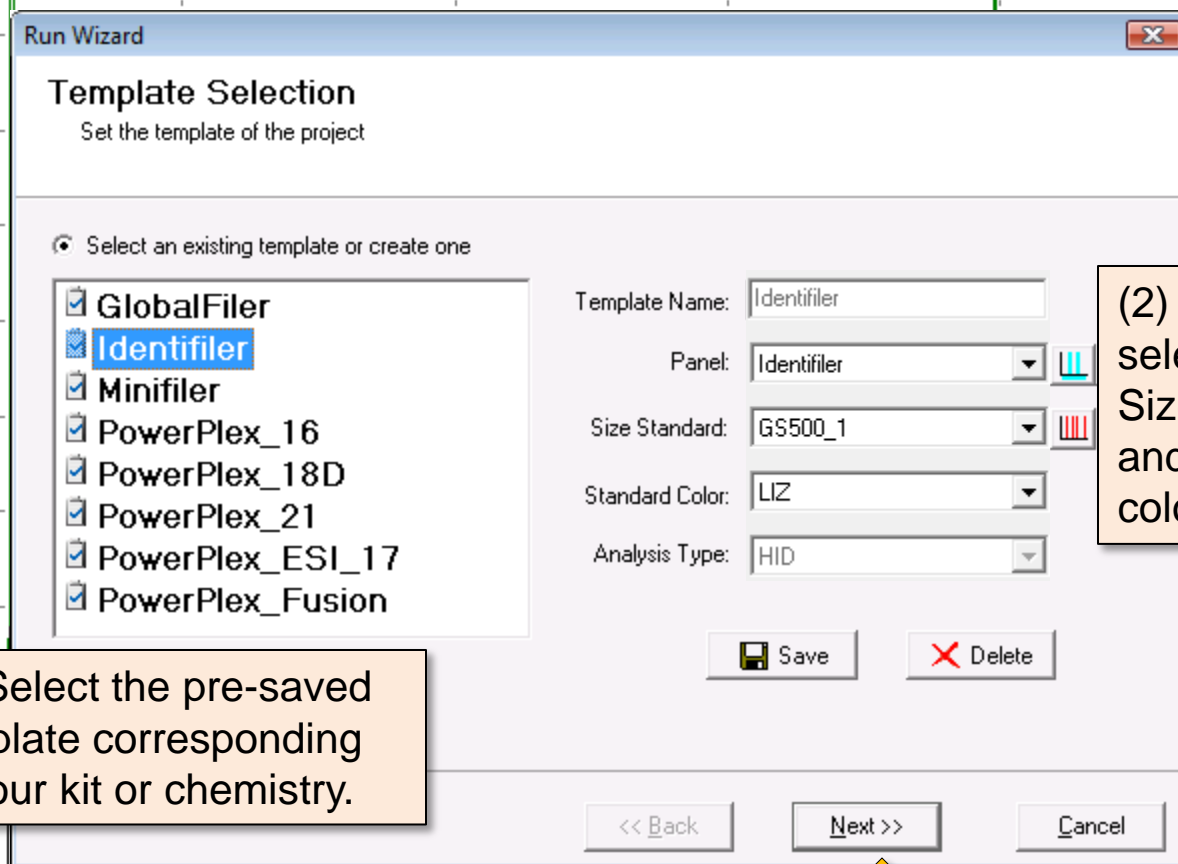
Navigate to File → Open Data to import your files.

Click Add, and navigate to the specific files you would like to import (.hid, .fsa, .sg1).

Process Raw Data

The screenshot displays a software window titled "Process Raw Data" with a menu bar (File, Project, Applications, Tools, Help) and a toolbar. On the left, a file tree under "Raw Data" lists files such as PAT\_10\_C1.fsa, PAT\_10\_C2.fsa (selected), PAT\_10\_C3.fsa, and various PAT\_11, PAT\_12, PAT\_13, PAT\_14, PAT\_8, PAT\_9 files, along with ladder files. Two chromatograms are shown: a top one for the entire dataset and a bottom one for "PAT\_10\_C2.fsa" which is zoomed in. A yellow arrow points to a "Toggle dye colors" icon in the toolbar. Another yellow arrow points to a callout box that says "Double-click on a sample file to display/hide it." A third yellow arrow points to a callout box that says "Draw a box from left to right with your mouse to zoom in. Right to left zooms back out." The bottom status bar shows "New", "24 samples", "PC error: 0/0", "NC error: 0/0", "Ladder error: 0/0", "#Failed=0", and "#Flagged=0".

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



Run Wizard

Template Selection

Set the template of the project

Select an existing template or create one

- GlobalFiler
- Identifiler**
- Minifiler
- PowerPlex\_16
- PowerPlex\_18D
- PowerPlex\_21
- PowerPlex\_ESI\_17
- PowerPlex\_Fusion

Template Name: Identifiler

Panel: Identifiler

Size Standard: GS500\_1

Standard Color: LIZ

Analysis Type: HID

Save Delete

<< Back Next >> Cancel

(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).

**Run Wizard**

**Data Process - HID Analysis**  
Set data process options

**Raw Data Analysis**

Auto Range (frame) 

Start:  End:

Smooth  Enhanced Smooth

Peak Saturation  Baseline Subtraction

Enhanced Baseline Subtraction

Pull-up Correction  Spike Removal

**Allele Call**

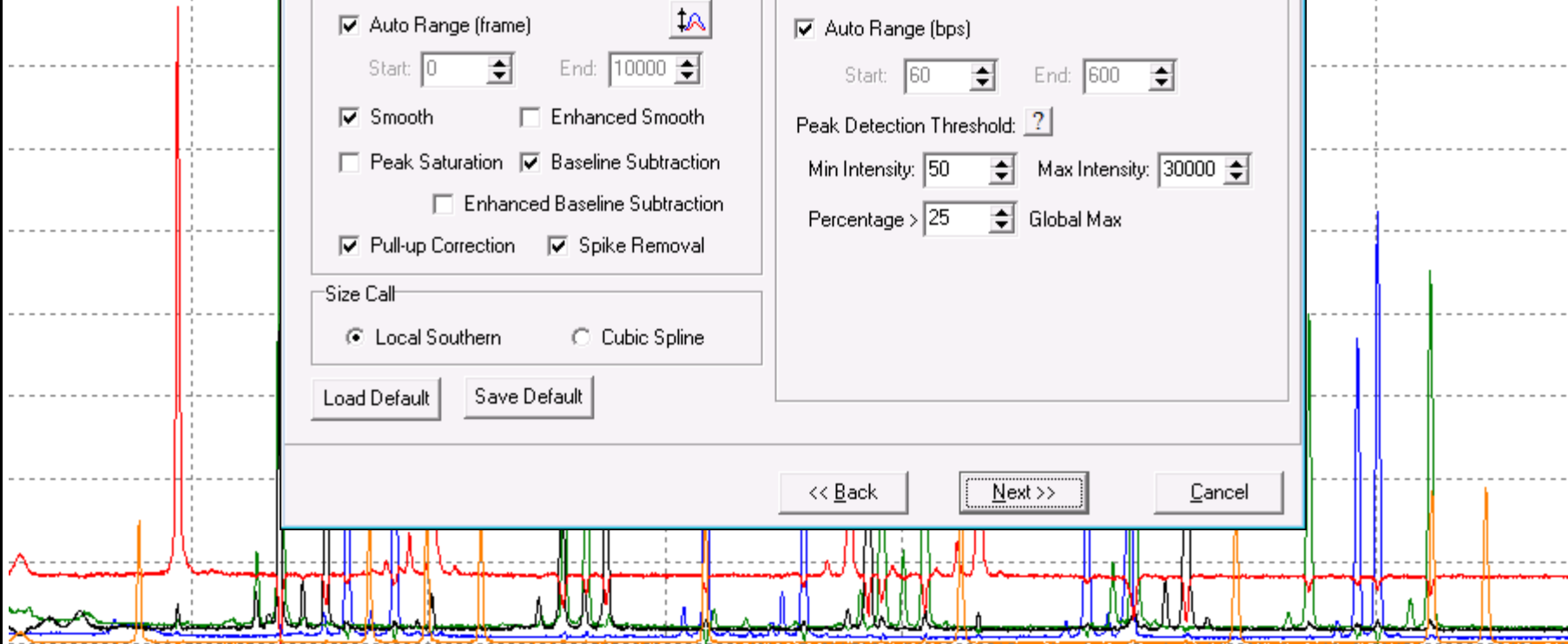
Auto Range (bps)

Start:  End:

Peak Detection Threshold:  ?

Min Intensity:  Max Intensity:

Percentage >  Global Max

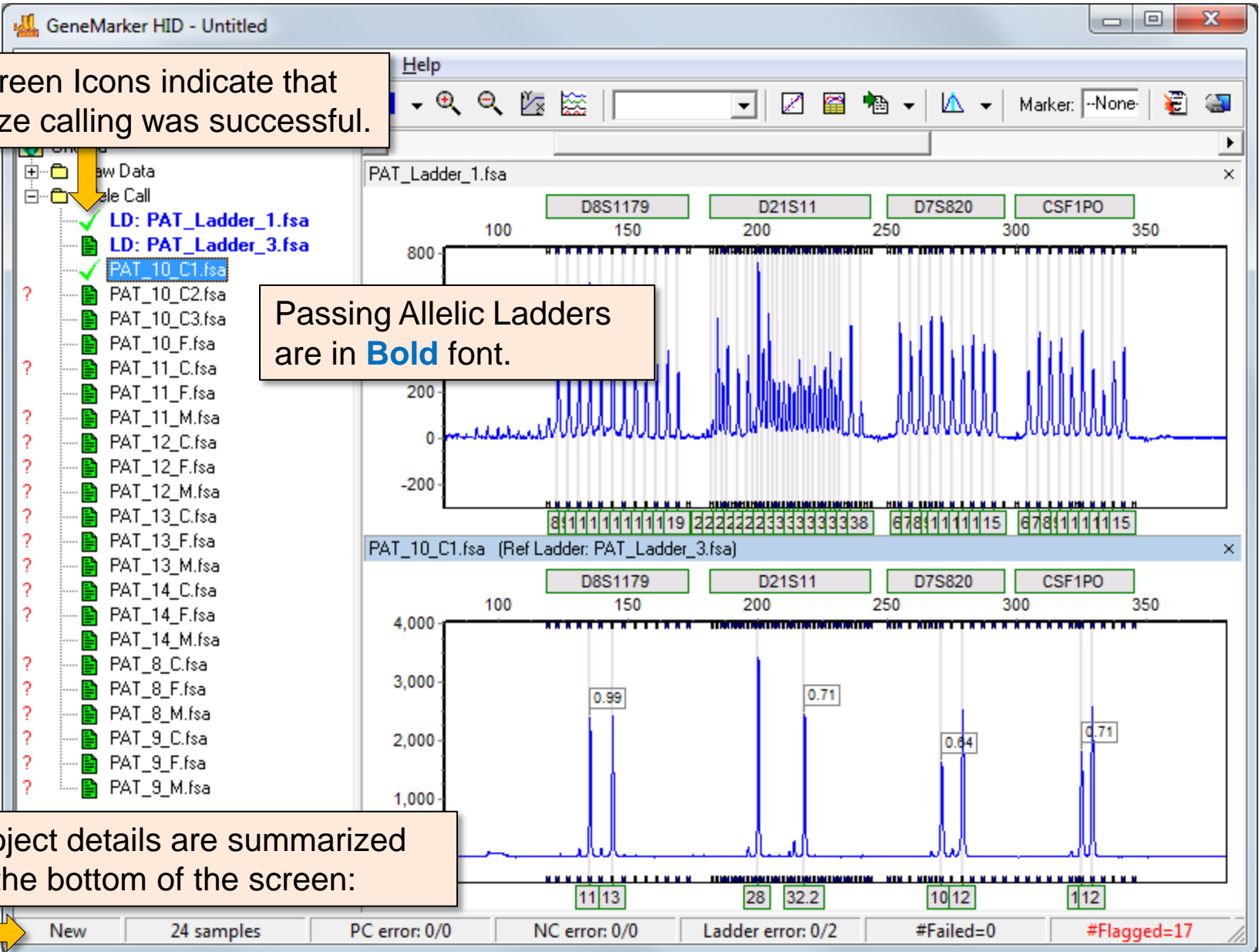




Green Icons indicate that size calling was successful.

Passing Allelic Ladders are in **Bold** font.

Project details are summarized at the bottom of the screen:





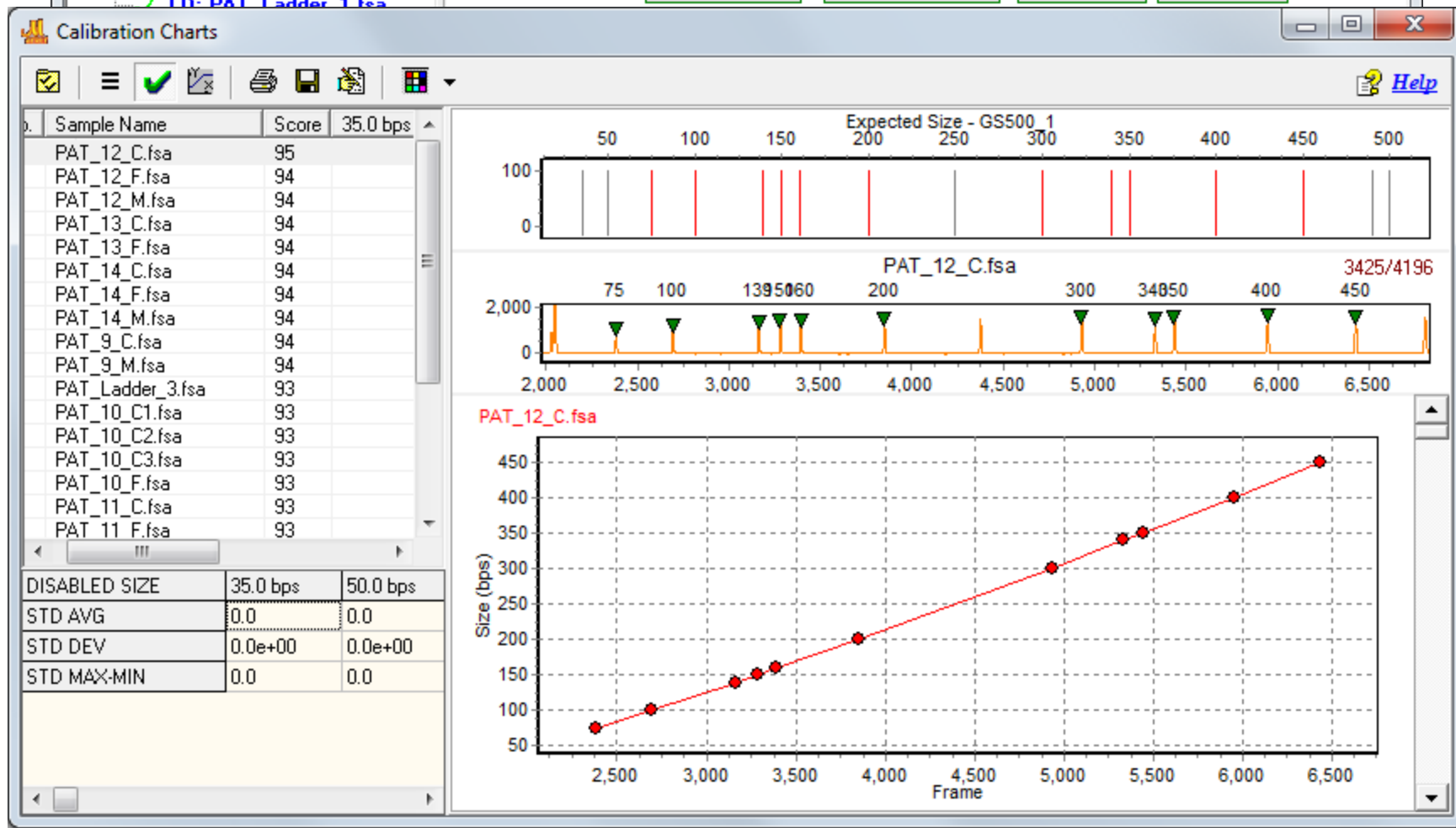
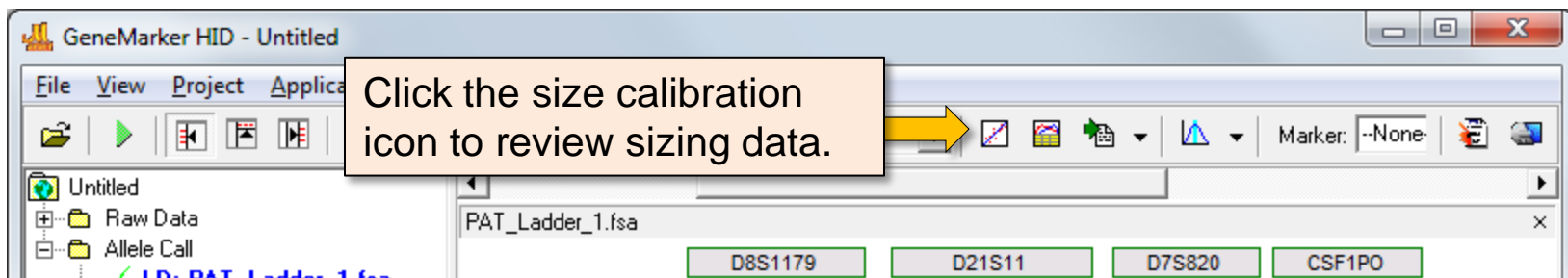
Marker Specific settings can be set in the panel editor (Tools → Panel Editor).

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.

The screenshot displays the 'Panel Editor' window with a file tree on the left containing 'Project Panel' and 'Panel Templates'. A central plot shows a DNA profile for marker 'D8S1179' with peaks at loci 13-19. An 'Edit Marker' dialog box is open on the right, showing parameters for 'D8S1179' such as 'Nucleotide Repeats (x): 4', 'Boundary: 118.3 To 174.0', and various intensity and imbalance thresholds. A status bar at the bottom shows '[Panel Name]: Identifiler' and '[Ploidy]: 2'.



GeneMarker HID - Untitled

File View Project App

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

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	

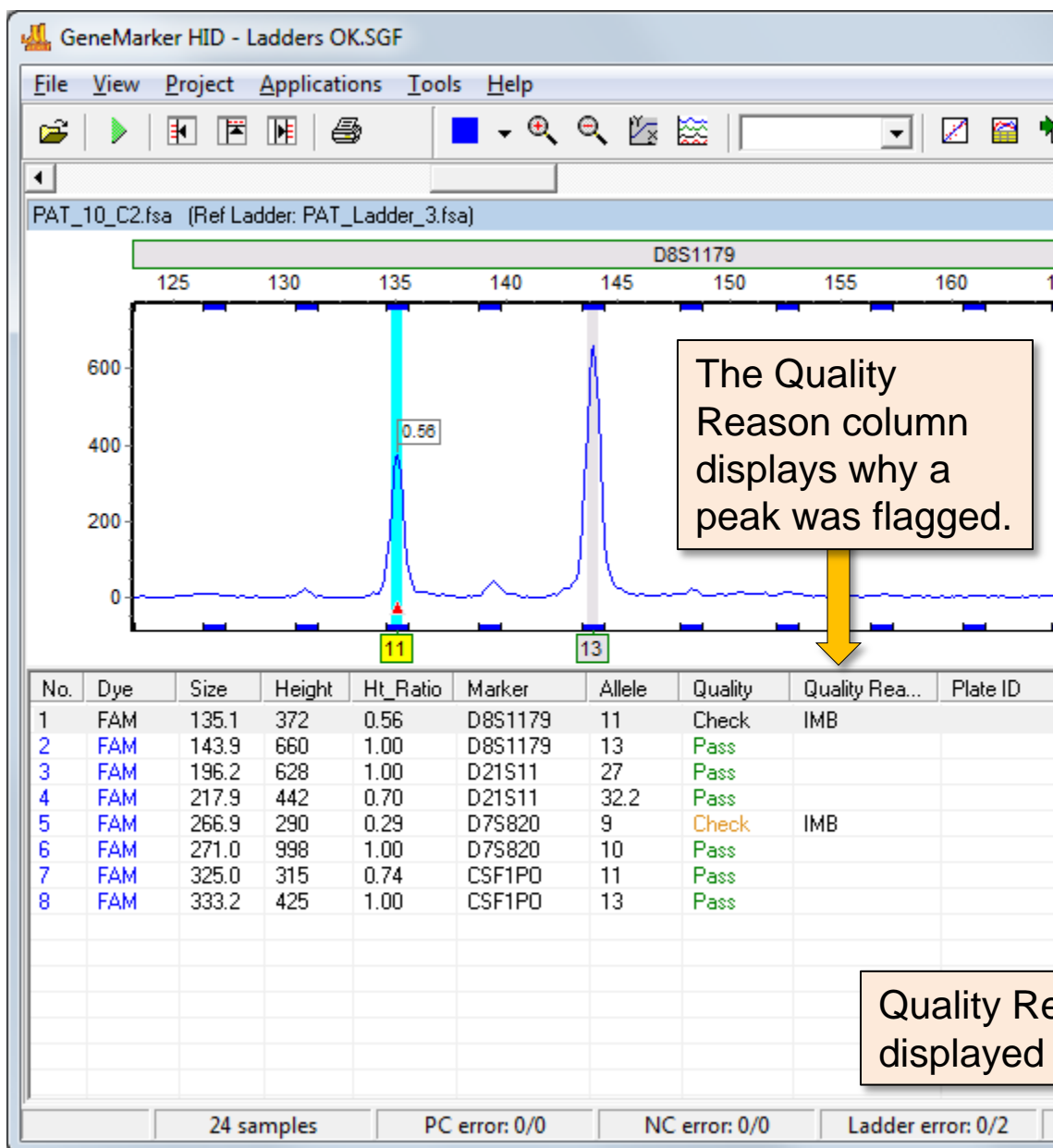
Report Bin Help

	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
? 11	PAT_10_C3.fsa	D7S820	9	10
? 12	PAT_10_C3.fsa	CSF1PO	11	13
? 13	PAT_10_C3.fsa	D8S1179	12	13
? 14	PAT_10_C3.fsa	D21S11	27	32.2
? 15	PAT_10_C3.fsa	D7S820	9	10
? 16	PAT_10_F.fsa	CSF1PO	11	11
? 17	PAT_11_C.fsa	D8S1179	13	16
? 18	PAT_11_C.fsa	D21S11	27	32.2
? 19	PAT_11_C.fsa	D7S820	9	10
? 20	PAT_11_C.fsa	CSF1PO	11	13
? 21	PAT_11_C.fsa	D8S1179	12	13
? 22	PAT_11_C.fsa	D21S11	27	32.2
? 23	PAT_11_C.fsa	D7S820	9	10

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



The Quality Reason column displays why a peak was flagged.

[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.

GeneMarker HID - Ladders OK.SGF

File View Project Applications Tools Help

PAT\_10\_C2.fsa (Ref Ladder: PAT\_Ladder\_3.fsa) 135.2/606 x

D8S1179

115 120 125 130 135 140 145 150 155 160 165 170

600

200

0


1

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

No.	Dye	Size	Height	Ht_Ratio	Marker	Allele
1	FAM	135.1	372	0.56	D8S1179	11
2	FAM	143.9	660	1.00	D8S1179	13
3	FAM	196.2	628	1.00	D21S11	27
4	FAM	217.9	442	0.70	D21S11	32.2
5	FAM	266.9	290	0.29	D7S820	9
6	FAM	271.0	998	1.00	D7S820	10
7	FAM	325.0	315	0.74	CSF1PO	11
8	FAM	333.2	425	1.00	CSF1PO	13

24 samples    PC error: 0/0    NC error: 0/0    Ladder error: 0/2    #Failed=0    #Flagged=17

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.

The screenshot shows the 'Print Report' dialog box. At the top, there are three tabs: 'Standard', 'Advanced', and 'Page'. The 'Standard' tab is active. Below the tabs, there are several sections:

- Print Type:** Radio buttons for 'Normal' (selected) and 'Chart Overlay'.
- Samples:** Radio buttons for 'All Samples' (selected) and 'Selected Samples'.
- Contents:** Checkboxes for 'Electropherogram', 'Peak Table', 'Follow Trace Chart' (selected), 'Start after All Charts Finished', 'Start on Separate Page', and 'Forensics Table'.
- Dyes:** Checkboxes for 'FAM', 'VIC', 'NED', 'PET', 'LIZ', and 'Purple'.

At the bottom of the dialog, there are five buttons: 'Preview', 'Save', 'Delete', 'Ok', and 'Cancel'. A yellow arrow points to the 'Preview' button.

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

### Export Report to Files

Export Format: PDF file

#### File Naming Method

- Named by sample name
- Start by Page Number
- Named by page number

Save Group Samples as One File

#### Export Directory:

C:\Program Files (x86)\SoftGenetics\GeneMarker\_I ...

Ok

Cancel

## SoftGenetics

## Allele Report

2/9/2015 9:29:37 AM

GeneMarker HID V2.7.1

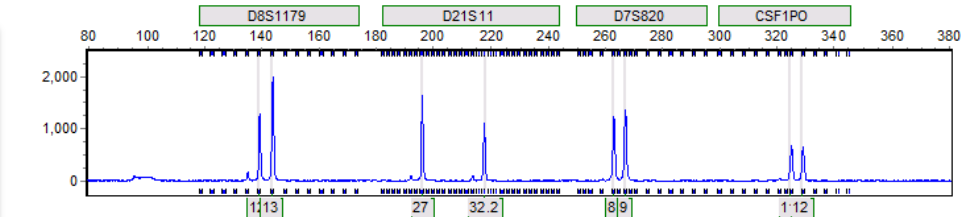
Page 1

Allele Report: City_Crime_Lab	
Project: Ladders OK.SGF	Template: Identifier
User: Admin	Panel: Identifier

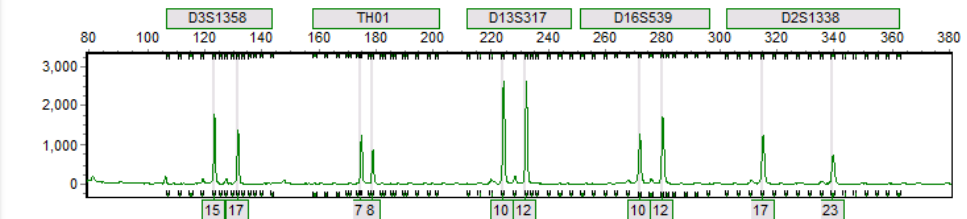
#### Project Comments:

Sample 1: Ref Ladder: PAT\_Ladder\_3.fsa Run date and time: 02/27/2007 - 08:05:53 -> 02/27/2007 - 08:41:31

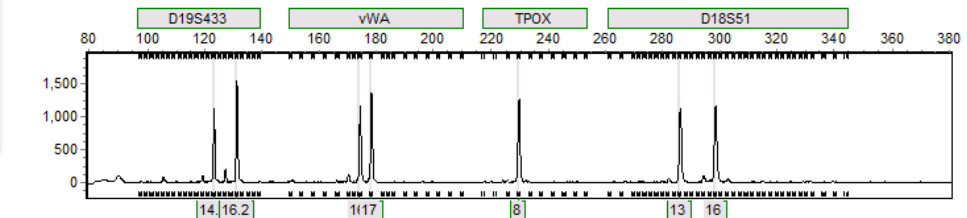
Dye: FAM - 8 peaks - PAT\_10\_C3.fsa



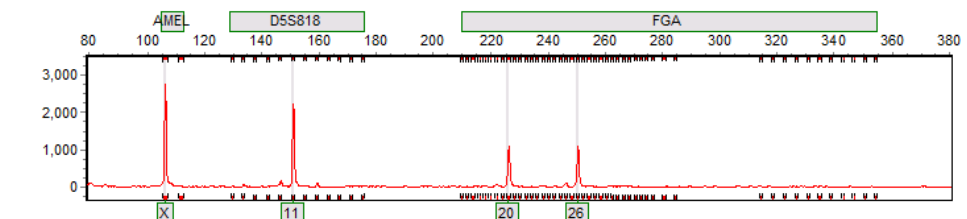
Dye: VIC - 10 peaks - PAT\_10\_C3.fsa





Dye: NED - 7 peaks - PAT\_10\_C3.fsa



Dye: PET - 4 peaks - PAT\_10\_C3.fsa



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.

Report		Bin	Help		
	Sample	Marker	Allele#	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	
	PAT_10_C2.fsa	D8S1179	11	13	
	PAT_10_C2.fsa	D21S11	27	32.2	
	PAT_10_C2.fsa	D7S820	9	10	
	PAT_10_C2.fsa	CSF1PO	11	13	
	PAT_10_C3.fsa	D8S1179	12	13	
	PAT_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	

### Allele Report Settings

**Report Style**

Allele List

Forensics

Bin Table

Peak Table

Allele Count

Sample Name  File Name

**Orientation**

Horizontal  Vertical

**Options**

Extend Diploid Homozygous

Show Allele Name

Show Size (0.1bps)

Show Height

Show Area


Show Score

Show "x" when no allele call

Show Only Uncertain Alleles

Show Rejected Low Score Alleles

Hide Extra Sample Names

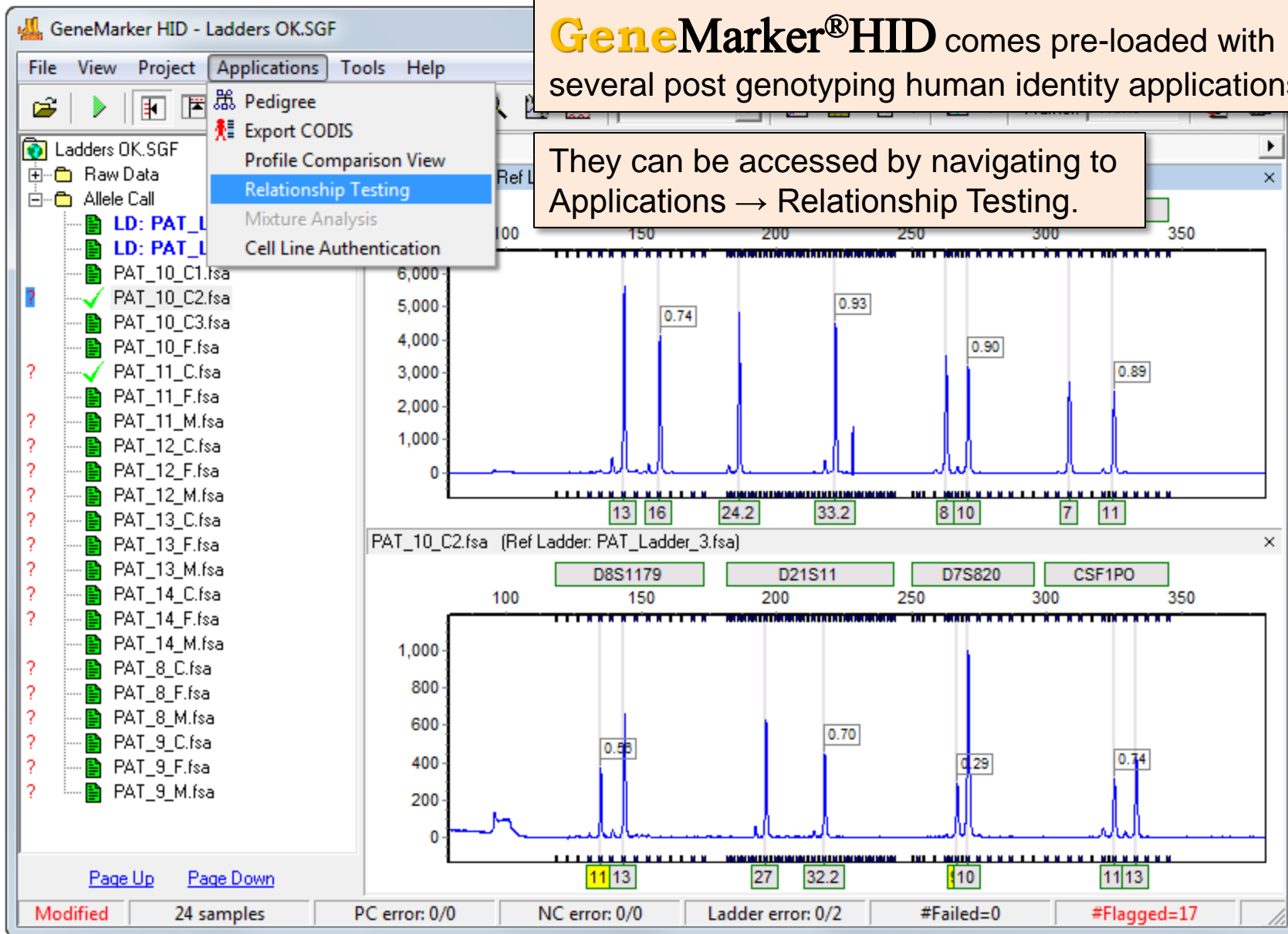

Ok
Cancel



# Post Genotyping Applications

**GeneMarker<sup>®</sup>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 screenshot shows the 'Relationship Testing' software interface. On the left, a list of profiles is displayed with their IDs and marker counts. The profile 'PAT\_10\_C2.fsa' is selected, with ID 1. Below the list, the individual's ID and name are confirmed as 1 and 'PAT\_10\_C2.fsa' respectively.

The main window displays a table of search results for various relationships. The table columns are File Name, ID, Name, X/Y, Matched Alleles, Matched Markers, and PI/KI. The most likely relative is highlighted in blue: PAT\_10\_C3.fsa (ID 1007, X/Y XX, Matched Alleles 20|32, Matched Markers 16|16, PI/KI 2.56E+03).

File Name	ID	Name	X/Y	Matched Alleles	Matched Markers	PI/KI
Same-Individual						
PAT_10_C2.fsa	1006		XX	32 32	16 16	3.44E+20
Father/Son						
Mother/Daughter						
Full-Sibs						
PAT_10_C3.fsa	1007		XX	20 32		2.56E+03
PAT_10_C1.fsa	1005		XX	18 32		1.41E+02
Half-Sibs						
PAT_2_F.fsa	682		XY	10 32		1.80E+04
PAT_10_F.fsa	1008		XY	17 32		2.36E+03
PAT_5_F.fsa	691		XY	12 32		7.90E+00
PAT_3_C.fsa	684		XY	13 32		5.77E+00
PAT_1_M.fsa	680		XX	15 32		4.45E+00
PAT_6_F.fsa	694		XY	11 32		3.98E+00
Individ_XYZ	1002		XY	12 32		3.34E+00
PAT_3_F.fsa	685		XY	11 32		3.20E+00
PAT_7_F.fsa	697		XY	12 32		2.06E+00
PAT_8_F.fsa	1022		XY	12 32		1.55E+00

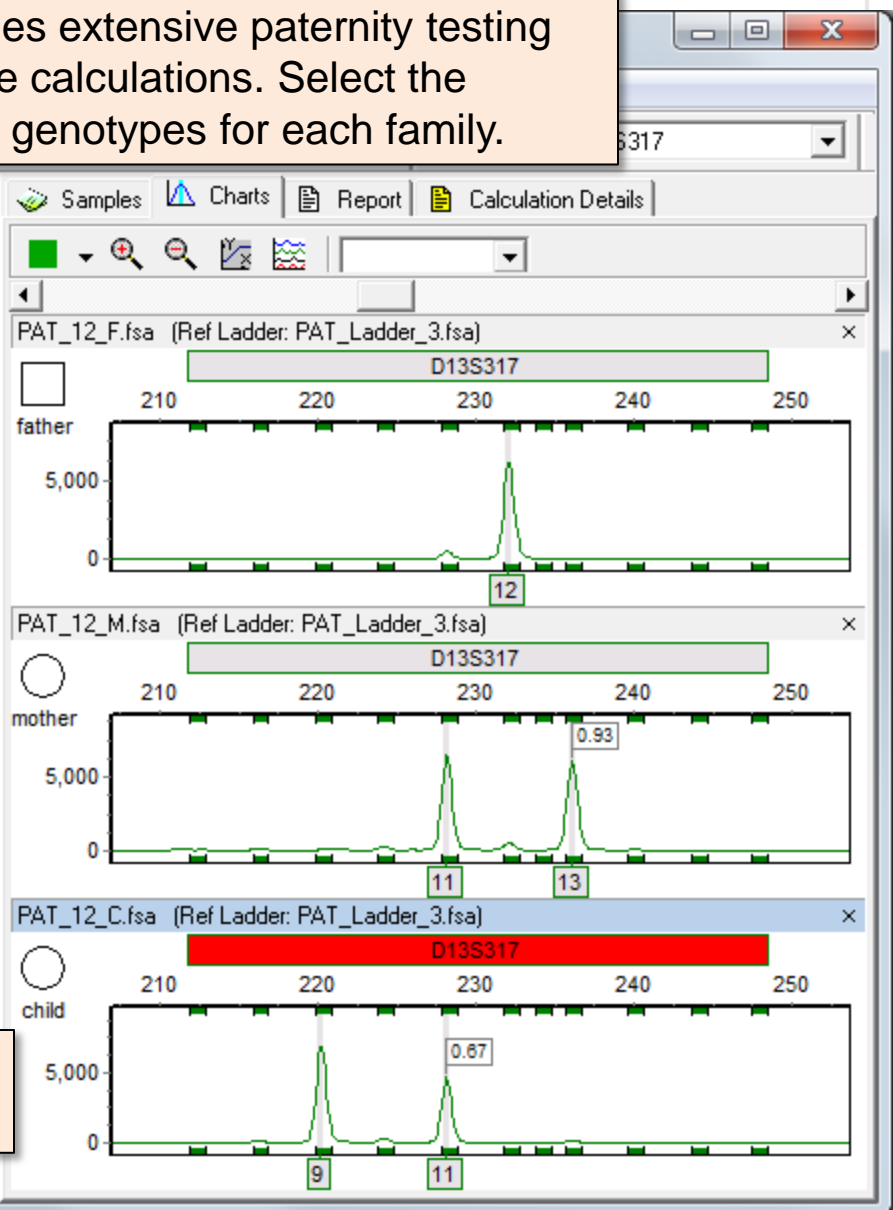
The program will display the most likely relative for a variety of relationships. Likelihood ratios (LR = PI / KI) are displayed for each profile.

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.

	father		mother
D8S1179	9 16		13 11
D21S11	29 28		30 28
D7S820	7 9		10 10
CSF1PO	? ?		12 11
D3S1358	16 17		17 17
TH01	6 9.3		9 9.3
D13S317	12 12		13 11
D16S539	13 14		10 14
D2S1338	16 16		17 25
D19S433	14 15		15 14
vWA	18 18		15 17
TPOX	8 11		8 8
D18S51	14 17		14 15
AMEL	X Y		X X
D5S818	13 12		11 12
FGA	23 23		23 24
			child ?

Shown here is an example of exclusion:

Individual ID : 3  
 Individual Name: child  
 Sample File: PAT\_12\_C.fsa



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

Kinship Analysis

Single Pair | Multi-Pair

Marker	Individual A		Individual B		Parent/Child (LR)	Full-Sibs (LR)	Half-Sibs (LR)	Uncle-Nephew (LR)	Cousins (LR)	Grandpa
	PAT_10_C3.fsa		PAT_10_C2.fsa							
CSF1PO	11	12	11	13	1.00390	0.75195	1.00195	1.00195	1.00097	1.00195
TPDX	8		8		2.68752	3.39945	1.84376	1.84376	1.42188	1.84376
TH01	7	8	7	8	1.88446	2.72596	1.44223	1.44223	1.22112	1.44223
vWA	16	17	15	18	0.00278	0.25000	0.50000	0.50000	0.75000	0.50000
D16S539	10	12	10	13	2.14998	1.32499	1.57499	1.57499	1.28750	1.57499
D7S820	8	9	9	10	2.30351	1.40176	1.65176	1.65176	1.32588	1.65176
D13S317	10	12	12	14	0.58904	0.54452	0.79452	0.79452	0.89726	0.79452
D5S818	11		11	12	2.14998	1.32499	1.57499	1.57499	1.28750	1.57499
FGA	20	26	22	25	0.00390	0.25000	0.50000	0.50000	0.75000	0.50000
D8S1179	12	13	11	13	1.15181	0.82590	1.07590	1.07590	1.03795	1.07590
D18S51	13	16	13	16	6.34558	18.52269	3.67279	3.67279	2.33640	3.67279
D21S11	27	32.2	27	32.2	7.52494	31.74703	4.26247	4.26247	2.63123	4.26247
D3S1358	15	17	15	17	2.04387	3.28457	1.52194	1.52194	1.26097	1.52194
D2S1338	17	23	17	20	2.51965	1.50983	1.75983	1.75983	1.37991	1.75983
D19S433	14.2	16.2	14	14.2	3.14624	1.82312	2.07312	2.07312	1.53656	2.07312
Product Score:					3.08E-01	2.56E+03	2.03E+02	2.03E+02	3.29E+01	2.03E+02

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

The screenshot displays a software interface for mixture analysis. On the left, a tree view shows a project named 'MIX05case2\_e' with a table of marker data. The table has columns for 'No.', 'Marker', 'Major', 'Minor', 'Major Mx', 'Residual', and 'Major LR'. The 'Major LR' column is highlighted in orange. Below the table, there are input fields for 'Contributor 1' (set to 'MIX05case2\_victim (Minor)'), 'Contributor 2' (set to 'Individ\_XYZ (Major)'), 'Average Major Mx' (0.870), 'Cumulative LR' (1.03E+21), and 'RMNE' (1-2.95E-07). On the right, a 'Trace Data Report' table shows the same data in a different format, with columns for 'No.', 'Marker', 'Mixture', 'PI', 'PE', 'Contributor 1', 'Contributor 2', and 'LR'. The 'Cumulative' row at the bottom of the report shows a PI of 2.95E-07 and a PE of 1-2.95E-07.

No.	Marker	Major	Minor	Major Mx	Residual	Major LR
1 -- 1	D8S1179	11,13	11,14	0.87	0.0000	0.95E+01
1 -- 2	D8S1179	11,13	14,14	0.93	0.0085	0.8E+01
1 -- 3	D8S1179	11,13	13,14	0.88	0.0091	0.7E+01
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	0.9E+01
4 -- 1	CSF1PO	7,10	12,13	0.90	0.0033	0.8E+01
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	0.9E+01
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	0.7E+01
13 -- 1	D18S51	17,18	12,15	0.84	0.0012	1.0C

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.

# Thank you for your interest in **GeneMarker®HID**

STR Human Identity Software

Have more questions? Please email [tech\\_support@softgenetics.com](mailto: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**.

