

SOFTGENETICS®

Software PowerTools for Genetic Analysis

GeneMarker® HID STR Human Identity Software

- NDIS Approved Expert System
- Fast, Accurate, and User-friendly
 - ~ Documented time savings of up to 40%¹
 - ~ Up to 70% less analyst intervention²
- User Management with Audit Trail
- Mixture Analysis
- Relationship Testing
 - ~ Kinship
 - ~ Paternity
- Database Search Tools:
 - ~ Missing Persons Search
 - ~ Mass Disasters
 - ~ State DNA Index System (SDIS) Search
- Quality Control and Validation Tools
- Compatible with all Major CE systems, Rapid instruments, and Human ID Chemistries.

You will see the difference!

GeneMarker® HID

Human Identity Software

GeneMarker®HID Software is an NDIS approved expert system designed for human identification and forensics applications. GeneMarkerHID Software offers several advantages including time savings¹, ease of use², and a suite of integrated post genotyping applications, thereby making it an excellent alternative to Genotyper®, GeneMapper®, GeneMapper®IDX, and other fragment analysis programs.

Features:

- NDIS Approved expert system
- Accurate Size/Allele Calls
- Linked Navigation
- Running Audit Trail
- Automated Control Concordances
- All Major Chemistries

Project Review Tools:

- All Color Browser
- Panel Editor
- Replicate Comparison Tool
- Project Comparison Tool
- CODIS Compatible Export
- Contamination Check/Elimination
- Database Search

Human ID Applications:

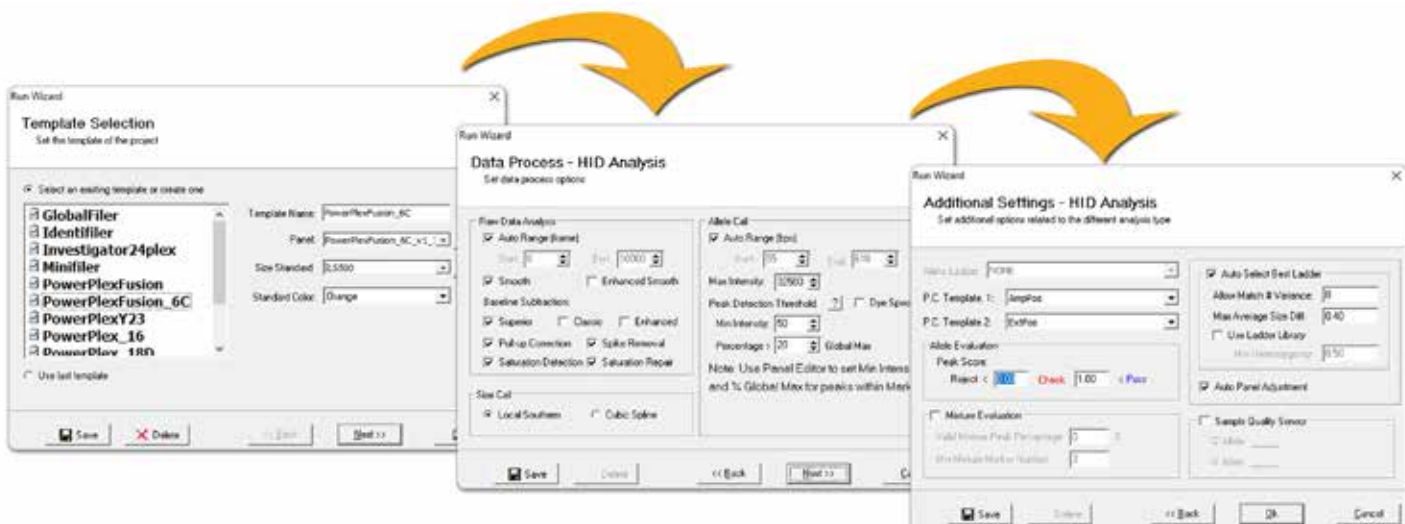
- Allele Specific Stutter Filters
- Database Searching
- Mixture Deconvolution
- Percent Match Search
- Kinship Analysis
- Paternity Testing

GeneMarkerHID Software is compatible with all major commercially available Human Identity chemistries, as well as CE instruments, and Rapid Systems (Including 6 dye chemistries). The program's built-in panel editor tool also provides extensive support for custom chemistries. GeneMarkerHID Software can be run on Windows® Vista, 7, 8, and 10 Operating Systems.



User Operation

Thanks to its linked navigation and 'point and click' interface, GeneMarkerHID Software is easy to use for experts and beginners alike. The "Run Wizard" simplifies parameter setting by guiding the user through three simple steps, thereby making repetitive analyses quick, easy, and accurate. The user may select one of several preloaded templates, or create and save their own. GeneMarkerHID Software's patented pattern recognition technology automatically corrects for most chemistry errors, including peak saturation, noise, bleed-through, instrument spikes, and stutter, thereby reducing user intervention by up to 70%².

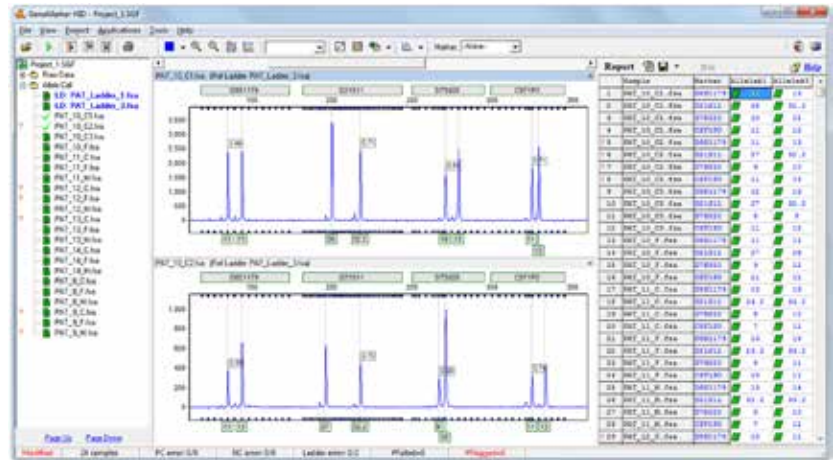


The three pages of the Run Wizard allow the user to customize the analysis parameters for each project. Groups of settings can be saved as templates for future analyses.

Main Analysis Window

After Data Processing, results are displayed in the Main Analysis Window. Colored icons on the left indicate the success of size calling, while colored icons in the report table indicate the strength of a given allele call. Flags alert the user to any fired rules. Flexible reporting options to meet laboratory LIMS requirements and export to probabilistic software programs.

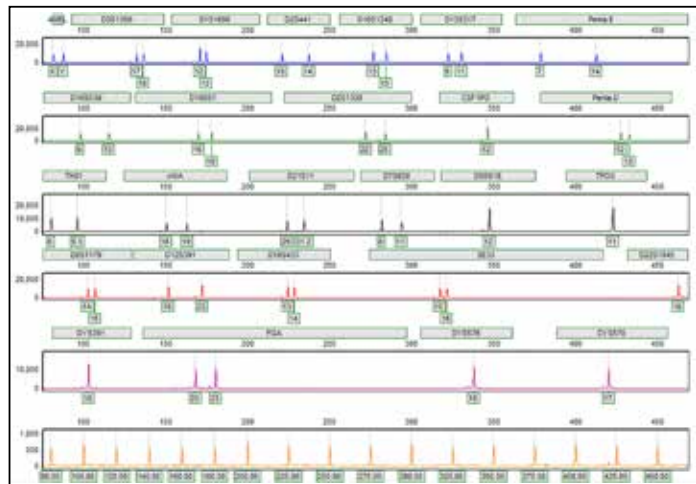
The main analysis window: Colored icons indicate the success of size calling (left) and allele calls (right). The linked electropherogram in the center of the screen allows the user to edit, delete, and confirm calls.



Linked navigation allows the user to quickly and easily survey the results. A simple right-click allows the user to insert, delete, and edit alleles – actions that are all recorded by the software. Display options allow the user to customize what information is shown. The Main analysis window also serves as a portal to other tools and post-genotyping applications discussed below.

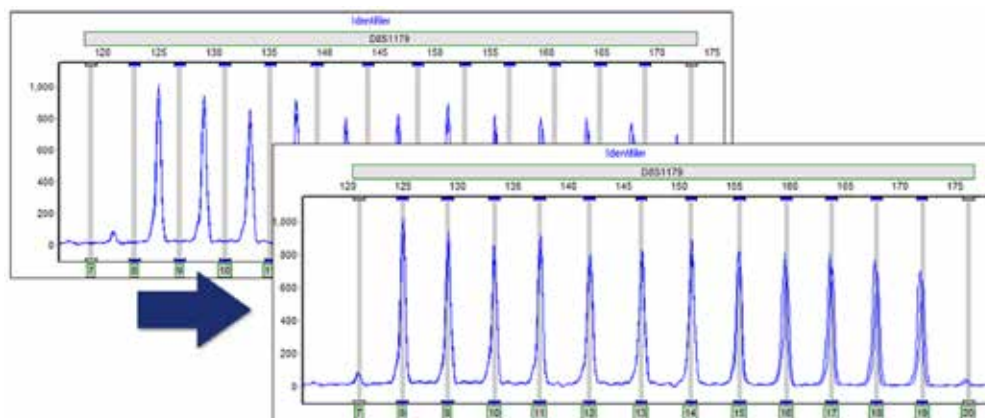
All Color Browser

The All Color Browser is another viewing option that allows the user to see every dye channel simultaneously. This view is particularly useful for detecting pull up and other artifacts, as well as making edits or comments.



Automated Panel Calibration

During data processing, GeneMarkerHID Software automatically calibrates the selected genotyping panel using Allelic Ladder samples that have been uploaded into the project. If multiple ladders have been uploaded, the program selects the best ladder for each sample.



The Panel Editor tool allows easy visualization and organization of genotyping panels. During panel calibration, panel bins are automatically aligned to ladder peaks, increasing accuracy.

Marker-Specific Parameters

In addition to the analysis settings discussed in the Run Wizard, GeneMarkerHID Software fully supports Marker-Specific analysis thresholds including:

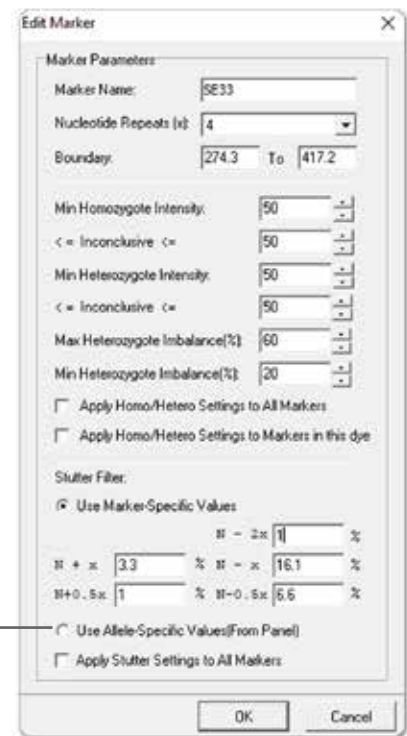
- Homo and Heterozygote RFU thresholds
- Inconclusive (Stochastic) Ranges
- Heterozygous Imbalance thresholds
- Stutter Filters

These settings allow the user to fully customize their analysis parameters for each marker and save them for future analyses.

Allele Specific Stutter Capability

Allows incorporation of Allele specific stutter values from validation studies. Especially beneficial for markers with complex repeat patterns and LUS effects.

*Marker specific settings for SE33
Select to apply specific stutter filters.
Marker stutter is grayed out when allele specific is selected.*



User Management and Audit Trail

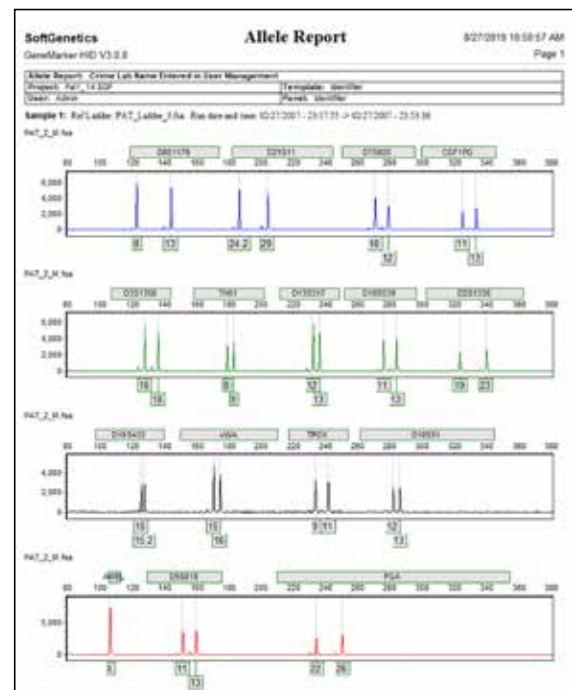
GeneMarkerHID Software is equipped with an extensive user management system and built-in audit trail. User management provides control of user access rights and generates an edit history for each sample profile in the project. Access rights for each user are set by the administrator – thereby providing assurance that unauthorized individuals don't accidentally modify or alter a project or settings. User Management is also linked with reports – report headers contain the analyst, date, institution name, and project information. Password control is also available, requiring users to log in with their password before opening the program.

Reporting Options

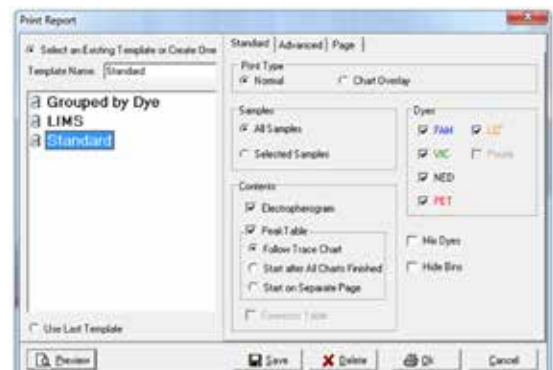
GeneMarkerHID Software supports numerous electronic and print reporting options, including:

- Complete PDF Reports
- Excel/Text table Reports
- CODIS Compatible Exports
- Importation to LIMS system

GeneMarkerHID Software's extensive reporting customization options allow a vast array of different reporting formats and layouts. Print templates enable the user to save groups of settings under a single template name, enabling effortless printing of common reports.



Above is one of many possible print reports that may be generated in GeneMarkerHID Software. Detailed print settings (right) allow extensive customization of reports. Templates can be created and recalled for frequently used formats.



Linked Applications

Mixture Analysis Tool

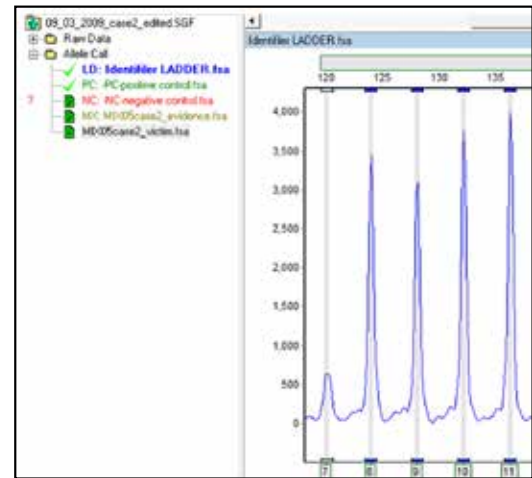
GeneMarkerHID Software comes preloaded with a Mixture Analysis Tool. The tool can completely deconvolute mixtures with two contributors, and can calculate the probability of inclusion for mixtures with three contributors. In addition, GeneMarkerHID Software's mixture analysis tool automatically:

- Identifies the number of potential contributors in each mixture
- Displays all possible allele combinations at each locus
- Performs all PI, PE, LR, and RMNE calculations
- Ranks the most likely genotype combinations (with or without single source reference profiles)
- Deconvolutes major and minor contributors from mixture
- Searches database for consensus contributor genotypes

Using the recommendations of the DNA Commission of the international Society of Forensic Genetics (Gill et al. 2006) and methods of Clayton et al. 1998 and Gill et al. 1998, the mixture analysis application automatically determines the most likely genotype combination at each locus, and then determines the most probable contributor genotypes (major and minor).

If no files in the current project match a contributor genotype, the user may query GeneMarkerHID Software's built-in relationship testing database for possible matches. In addition, consensus contributor genotypes may be uploaded to the database for future searches.

In the main analysis window, sample names are colored according to the sample type. Mixture profiles are displayed in olive-green, negative controls in red, positive controls in green, and ladder profiles in blue.



In the Mixture Analysis Application, peaks are visually displayed in the trace comparison, while the peak table contains all data including PI, PE, LR, and RMNE. The peak table may be exported as .txt tab delimited or excel file. All results are presented in report tables that may be saved or copy/pasted into existing documents.

No.	Marker	Major	Minor	Major Mx	Residual
1-1	D0S1179	11,13	11,14	0.87	0.0000
1-2	D0S1179	11,13	14,14	0.93	0.0005
1-3	D0S1179	11,13	13,14	0.89	0.0091
2-1	D21S11	28,32,2	30,31	0.83	0.0098
3-1	D7S820	8,10	8,11	0.87	0.0011
4-1	CSF1PO	7,10	12,13	0.90	0.0033
5-1	D3S1358	15,15	15,16	0.89	0.0000
5-2	D3S1358	15,15	16,16	0.94	0.0090
6-1	TH01	7,9,3	8,10	0.89	0.0092
7-1	D13S317	12,14	8,9	0.85	0.0032
8-1	D16S539	10,11	9,12	0.85	0.0010
9-1	D2S1330	17,21	16,24	0.90	0.0020
10-1	D19S433	13,13	13,14	0.84	0.0001
10-2	D19S433	13,13	12,14	0.82	0.0050
10-3	D19S433	13,13	14,14	0.92	0.0054
11-1	vWA	15,15	16,19	0.89	0.0006
12-1	TPDX	9,10	8,11	0.85	0.0062
13-1	D18S51	17,18	12,15	0.84	0.0012

No.	Marker	Mixture	PI	PE	Contributor 1	Contributor 2	LR
1	D0S1179	11,13,14	0.31586	0.68414	11,14	11,13	208.905
2	D21S11	28,30,31,32,2	0.32685	0.67315	30,31	28,32,2	1175.021
3	D7S820	8,9,10,11	0.77414	0.22586	9,11	8,10	144.475
4	CSF1PO	7,10,12,13	0.41470	0.58530	12,13	7,10	1684.433
5	D3S1358	15,16	0.40853	0.59147	15,16	15	34.717
6	TH01	7,8,9,3,10	0.53997	0.46003	8,10	7,9,3	3024.934
7	D13S317	8,9,12,14	0.27984	0.72016	8,9	12,14	19594.529
8	D16S539	9,10,11,12	0.68160	0.31840	9,12	10,11	176.595
9	D2S1330	15,17,21,24	0.14541	0.85459	16,24	17,21	2798.716
10	D19S433	12,13,14	0.34027	0.65973	12,14	13	126.352
11	vWA	15,16,19	0.24614	0.75386	16,19	15	338.906
12	TPDX	8,9,10,11	0.73706	0.26294	8,11	9,10	193.028
13	D18S51	12,15,17,18	0.26381	0.73619	12,15	17,18	1069.590
14	AMEL	X,Y	-	X	X,Y	-	-
15	D5S818	8,11,12,13	0.76054	0.23946	11,12	8,13	263.901
16	FGA	20,23,24	0.12168	0.87832	23,24	20,24	362.640
Cumulative:			2.95E-07	1.2.95E-07			1.52E+41

The mixture analysis application: Possible genotype combinations are shown on the left, and PI, PE, and LR values are calculated on the right. The dialogs in the bottom left allow the user to change which individuals are being contested.

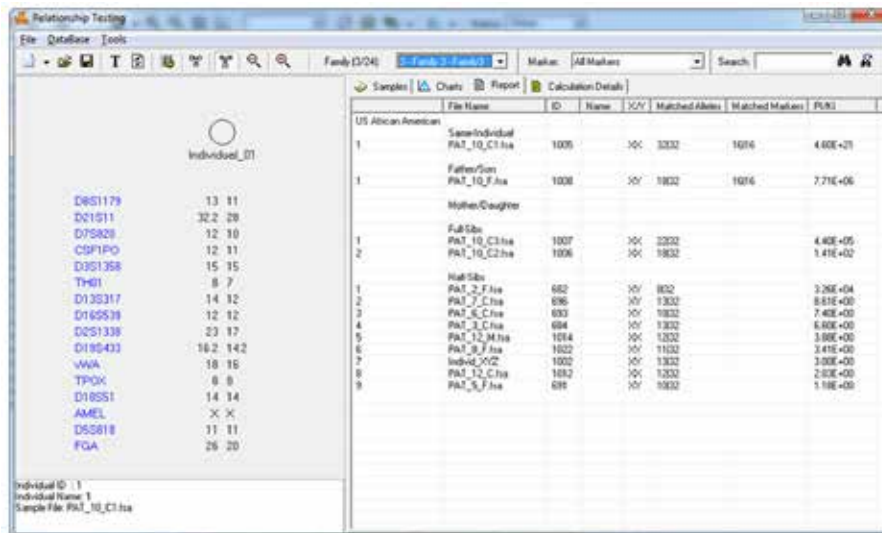
Database Searching

GeneMarkerHID Software's linked, searchable database enables hundreds of thousands of profiles to be imported into the program and saved for future searches. Genotypes can be imported from the current project, from a text file, or from CODIS .cmf files. This lends itself to numerous applications, including:

- Missing Persons Search
- SDIS Search
- Mass Disaster Identification
- Crime Scene Suspect or Familial Search
- Kinship Analysis Statistics for Three Generations

Using the Relationship Testing application, the user may query a sample against the database for potential matches across different populations at varying relationship levels. For each potential match, an Identity by Descent (IBD) calculation is used to determine the likelihood ratio of each possible relation to the test sample. Calculation details and the electropherogram are easily accessible for analyst review.

Genotypes can be imported into the database directly from the current project, limiting data transfer; they may also be imported from CODIS or text files.



The Database Search Tool: Profiles may be tested against a database of known genotypes. Likelihood Ratios ($LR = PI/KI$) are displayed for the most likely candidate at each relationship level.

The linked kinship analysis tool allows direct comparison of two individual profiles on a variety of different relationship levels: siblings, parent-child, uncle-nephew, and so on. Likelihood ratios and probabilities are available for analyst review and can be saved as a text file, an excel file, or may be copy/pasted.

The built-in Kinship Analysis tool allows the user to calculate probabilities and likelihood ratios across three generations. Report tables may be saved as .txt tab-delimited files, or may be copy/pasted into an existing document.

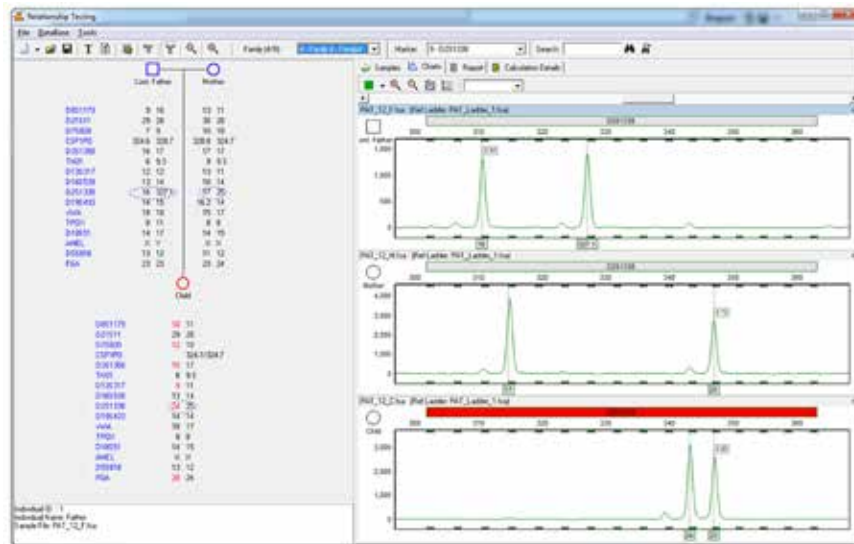
Marker	Individual A	Individual B	Parent/Child (L/R)	Full Sibs (L/R)	Half Sibs (L/R)	Uncle/Nephew (L/R)	Cousins (L/R)	Grandchild
D7S828	11 12	11 13	1.5029	0.79195	1.00195	1.00195	1.00007	1.00195
TP01	8	8	2.68792	2.38945	1.94376	1.64376	1.42188	1.84376
TH01	7 8	7 8	1.88445	2.72596	1.44223	1.44223	1.22112	1.44223
vWA	16 18	15 18	1.81249	1.05624	1.30624	1.30624	1.15312	1.30624
D16S539	12	10 13	0.00201	0.25000	0.50000	0.50000	0.75000	0.50000
D7S820	10 12	9 10	0.75420	0.62719	0.87719	0.87719	0.33859	0.87719
D13S317	12 14	12 14	7.79647	12.57203	4.37624	4.37624	2.68812	4.37624
D8S1179	11	11 12	2.14988	1.32899	1.57499	1.57499	1.26750	1.57499
FGA	20 26	22 25	0.00390	0.25000	0.50000	0.50000	0.75000	0.50000
D21S11	11 13	11 13	6.78096	16.95162	3.00648	3.00648	2.44024	3.00648
D5S818	14	13 15	0.00302	0.25000	0.50000	0.50000	0.75000	0.50000
D21S11	26 32.2	27 32.2	4.29907	2.39968	2.64998	2.64998	1.82499	2.64998
D51198	15	15 17	1.85362	1.07891	1.32691	1.32691	1.16346	1.32691
D2S1338	17 23	17 20	2.51365	1.50863	1.75983	1.75983	1.37991	1.75983
D16S433	14.2 16.2	14 14.2	3.14624	1.82312	2.07312	2.07312	1.53658	2.07312
Product Score			0.006400	1.41E+02	1.31E+02	1.31E+02	3.02E+01	1.31E+02

Paternal Testing

GeneMarkerHID Software's paternity testing application is a versatile tool with many capabilities, including:

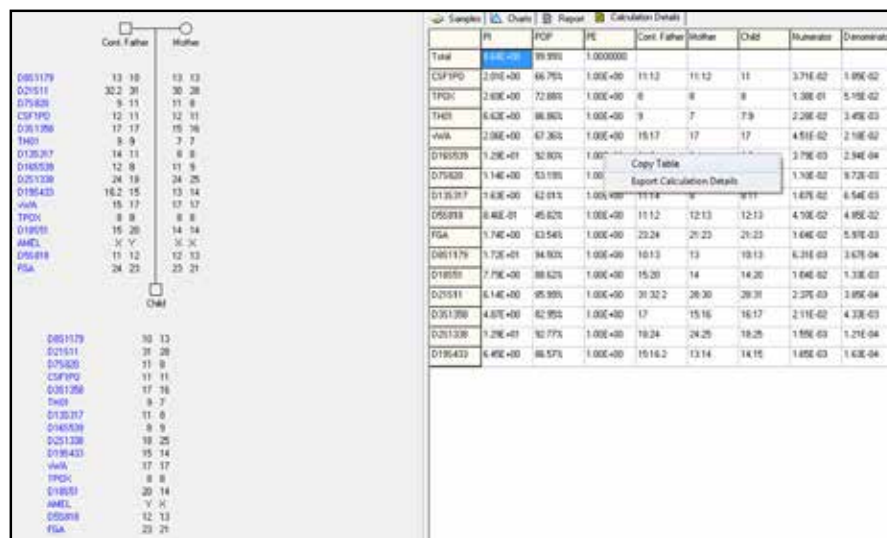
- Automated (and manual) Pedigree Drawing
- Identity By Descent (IBD) Calculations
- AABB paternity trio and motherless case calculations
- Reverse Parentage Testing
- Easy visualization of results
- Separate Kinship Analysis tool

The relationship testing module is embedded within GeneMarkerHID Software, allowing the user to proceed directly from data processing to paternity and/or kinship analysis. Profiles from the current project are used to automatically construct pedigrees and family trees. Conflicting genotypes are automatically flagged and linked to an electropherogram comparison for user review.



An example pedigree demonstrating exclusion: Conflicting alleles are highlighted in red. The pedigree is linked to an electropherogram, allowing the user to review potential conflicts in more detail.

The user may select one of several preloaded allele frequency tables or create their own to contest individuals within their pedigrees. Paternity Index (PI), Probability of Exclusion (PE), and Probability of Paternity (POP) calculations are available for this purpose. A wide variety of settings allow the user to customize the procedure, and take into account variables such as mutation rates and step-wise mutations.



An example pedigree demonstrating inclusion: PI, POP, and PE scores are calculated for each marker. The table can be copied directly or exported as a text file.

Percent Match and Cell Line Authentication Tool

The percent match tool uses a percent-similarity calculation to compare profiles in the current project to a database of known genotypes. This lends itself to several applications including the following:

- Cell Line Authentication

Results are ranked in order of their percent match score, with differences highlighted in yellow. Results can be exported in the form of an excel or text file.

The Percent Match Tool: After querying a sample against the database, results will be ranked on the right according to their percent match score. Here the tool is being used to demonstrate that all peaks from a Y-STR profile are included in a mixture sample.

Contamination Check/Elimination Database Search

- Y-STR Comparison
- Database Search when allele frequencies are not available

Improvements to the sensitivity of the polymerase chain reaction (PCR) have necessitated increased diligence in detecting possible contaminants. Contamination may jeopardize data analysis and can originate from many common sources, particularly from the skin or hair of a staff member. GeneMarkerHID software solves this problem by enabling the user to create a database of staff profiles as an elimination database. This database can then be compared against profiles in the current project to search for any contamination. Profiles of the current project may also be compared to one another to detect possible profile-to-profile contamination.

Group No.	Comparison Sample	Reference Sample	Matched/Total Reference	Similarity Ratio	Matched Markers(All)
1	PAT_8_C.fsa	DB:bob_smith.fsa	29/29	100.00%	D8S1179(10,13), C
2	PAT_8_F.fsa	DB:sara_jones.fsa	29/29	100.00%	D8S1179(10,13), C

The contamination check tool provides several options for customization. The user can choose to exclude different sample types, including negative controls, positive controls, ladders, and samples with a user-specified number of null alleles. The user may also choose to perform the comparison between all samples, or a specific sample. Finally, the user can choose to compare profiles to profiles within the project, to samples within a database, or both.

Automated Control Concordances

Any control samples are flagged in the file name tree and in the summary bar at the bottom of the main analysis screen if they differ from the expected genotype.

Positive controls

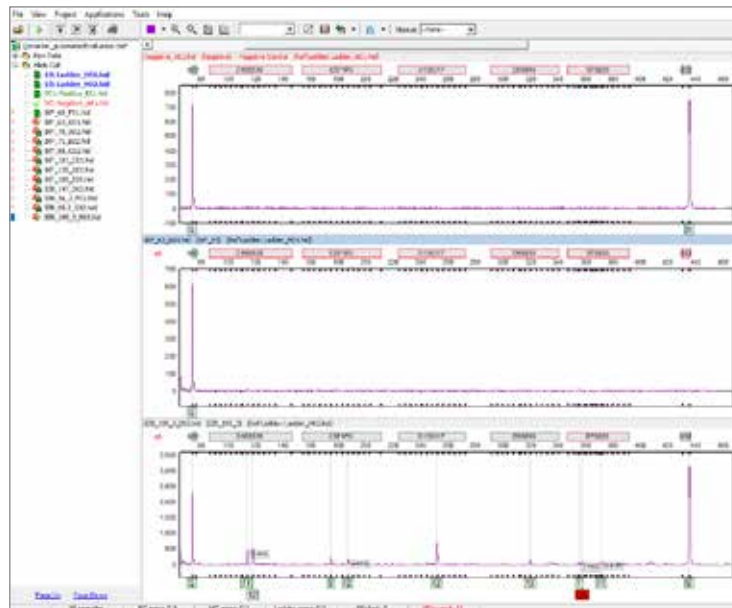
Customize the analysis parameters with up to 2 different positive control genotypes. The setting accommodates SOPs that use one DNA source for an amplification positive control and a different DNA source for the extraction positive control.

Negative controls will be flagged if any peaks are detected above the analytical threshold.



Quality Sensor Evaluation

Settings are available to automatically evaluate the Quality Sensor fragments to assist labs in trouble-shooting problematic samples. Samples are flagged qS in the file name tree and electropherogram if the Quality Sensor fragments fire any of the rules indicating potential 1) amplification failure, 2) inhibition or 3) degradation.



The figure illustrates typical results of the automated quality sensor evaluation. To display a pop-up message of the rule fired, mouse over the qS at the electropherogram. The first electropherogram is a passing negative control, the only peaks detected are the Q and S alleles. The middle electropherogram has Q/S peak imbalance, indicating potential inhibition. The third electropherogram has balanced Q/S fragments but an exponential decrease in total peak height with increasing fragment size, indicating potential degradation.

Please open disc to review your applications of interest and to install a 30-day trial of GeneMarkerHID Software.

Disk Contains

Applications Notes
30-day free GeneMarkerHID Trial
User Manual
Demonstration Data

Minimum Hardware Requirements

PC

32 or 64 bit Windows® Operating System: 7, 8, or 10
Processor: Pentium III, 1GHZ
RAM: 128MB
20GB Minimum available hard disk space.

Intel Powered Macintosh Computer

Virtual Windows Machine running on OS: 10.4.6 or higher.
RAM: 2GB
20GB Minimum available on hard disk

References

- 1) Holland, Mitchell and Walther Parson. GeneMarkerHID: A Reliable Software Tool for the Analysis of Forensic STR Data. J Forensic Sci. 2011. 56:29-35.
- 2) Schmidt, Ronald. Evaluation of GeneMapper ID-X and GeneMarker HID for use in Forensic DNA Analysis. 2012; <http://www.marshall.edu/forensics/files/2012/09/Schmidt-Ron-Poster-New.pdf>.

If trial disc is not present please email info@softgenetics.com
for a free 30-day trial

SOFTGENETICS®

Software PowerTools for Genetic Analysis

SoftGenetics
Oakwood Centre
100 Oakwood Avenue
Suite 350
State College PA 16803 USA
1-888-791-1270
info@softgenetics.com
www.softgenetics.com

Registered Trademarks are property of their respective owners.

Copyright © 2019