Investigator Template Files for Genotyper® User Guide

For analysis of Investigator Human

Identification PCR Kits with Genotyper Software

QIAGEN®

Sample & Assay Technologies

QIAGEN Sample and Assay Technologies

QIAGEN is the leading provider of innovative sample and assay technologies, enabling the isolation and detection of contents of any biological sample. Our advanced, high-quality products and services ensure success from sample to result.

QIAGEN sets standards in:

- Purification of DNA, RNA, and proteins
- Nucleic acid and protein assays
- microRNA research and RNAi
- Automation of sample and assay technologies

Our mission is to enable you to achieve outstanding success and breakthroughs. For more information, visit www.qiagen.com.

Contents

Product Warranty and Satisfaction Guarantee

QIAGEN guarantees the performance of all products in the manner described in our product literature. The purchaser must determine the suitability of the product for its particular use. Should any product fail to perform satisfactorily due to any reason other than misuse, QIAGEN will replace it free of charge or refund the purchase price. We reserve the right to change, alter, or modify any product to enhance its performance and design. If a QIAGEN product does not meet your expectations, simply call your local Technical Service Department or distributor. We will credit your account or exchange the product — as you wish. Separate conditions apply to QIAGEN scientific instruments, service products, and to products shipped on dry ice. Please inquire for more information.

A copy of QIAGEN terms and conditions can be obtained on request, and is also provided on the back of our invoices. If you have questions about product specifications or performance, please call QIAGEN Technical Services or your local distributor (see back cover or visit www.qiagen.com).

Technical Assistance

At QIAGEN, we pride ourselves on the quality and availability of our technical support. Our Technical Service Departments are staffed by experienced scientists with extensive practical and theoretical expertise in sample and assay technologies and the use of QIAGEN products. If you have any questions or experience any difficulties regarding Genotyper Software or QIAGEN products in general, please do not hesitate to contact us.

QIAGEN customers are a major source of information regarding advanced or specialized uses of our products. This information is helpful to other scientists as well as to the researchers at QIAGEN. We therefore encourage you to contact us if you have any suggestions about product performance or new applications and techniques.

For technical assistance and more information, please see our Technical Support Center at www.qiagen.com/Support or call one of the QIAGEN Technical Service Departments or local distributors (see back cover or visit www.qiagen.com).

Introduction

About this user guide

This user guide provides information about the functions and features of Investigator Template Files used in conjunction with Genotyper Software. Please refer to the *Genotyper Software User Guide* for complete information.

This user guide describes the features of the software and associated tools and enables the user to manage and modify files and analyses.

This user guide provides information about Genotyper Software in the following sections:

■ Introduction

■ Setup on the Analysis Computer

■ Calibration using Allelic Ladders

■ Evaluation of Analysis Data

■ Macros for Investigator Human Identification PCR Kits

■ Adjustment of Categories

■ Troubleshooting Guide

Throughout this document, analysis of PCR products generated using the Investigator ESSplex Kit, ABI PRISM® 3130 Genetic Analyzer, and DNA Size Standard 550 (BTO) are shown as an example. Analyses were performed using Genotyper Software version 3.7 for Windows® and Investigator ESSplex Template Files.

About Investigator Template Files and Genotyper Software

Genotyper Software is a flexible genotyping software package that provides DNA sizing and quality allele calls for all Applied Biosystems® electrophoresis-based genotyping systems. This software specializes in multi-application functionality, including amplified fragment length polymorphism (AFLP®), loss of heterozygosity (LOH), microsatellite, and single-nucleotide polymorphism (SNP) genotyping analysis. Genotyper Software can help users increase data processing efficiency. The software uses process quality values (PQVs) for automated identification that reduces data review time for high-throughput genotyping.

GeneScan® and Genotyper software together form a software package for HID products. It is specifically designed for human identification applications and enables highly accurate allele calls, including analysis of tri-, tetra-, penta-, and hexa-nucleotide repeat motifs.

Investigator Template Files are software sets (macros) for the Genotyper Software in order to simplify data analysis. Investigator Template Files may be used with ABI PRISM® single- and multi-capillary instruments of Applied Biosystems.

Genotyper Software (used in conjunction with Investigator Template Files) assigns the analyzed DNA fragments relative to their length to the allele designation of the short tandem repeat (STR) loci. Optionally, the corresponding fragment length of peaks in base pairs (bp) or peak height in relative fluorescent units (RFU) can be indicated. These data (genotypes) can be tabulated and exported.

Investigator Template Files are available for all Investigator Human Identification PCR Kits for Genotyper Software version 3.7 (Windows®) and version 2.5 (Macintosh®).

Note: Both Genotyper and GeneScan Software applications from Applied Biosystems have been discontinued and are unavailable for purchase (as of June 1, 2004). Applied Biosystems support for these products ended June 1, 2009.

Validity for human identification products

Investigator Human Identification PCR Kits require calibration with an allelic ladder. Therefore, the software used must be compatible with human identification (HID) products for forensic applications. Investigator Template Files are valid with the Genotyper Software.

Setup on the Analysis Computer

Investigator Template Files for Genotyper Software are available to download free from the online catalog pages of all Investigator Human Identification PCR Kits at the QIAGEN Web site (www.qiagen.com) or on a CD-ROM, on request.

Before using the Genotyper Software for the first time, Investigator Template Files must be saved to the local analysis computer (Windows® PC), by either downloading the files from the Internet or copying the files from a CD-ROM. Macintosh users should use only the CD-ROM in order to avoid non-conformities during conversion.

Using Genotyper Software and Investigator Template Files

1. **Install Genotyper Software according to the manufacturer's instructions.**
2. **To use GTA-templates of the Investigator Human Identification PCR Kits with Genotyper Software, an "Investigator folder" should be created on the local hard drive.**
3. **Choose the current template file of the Investigator Human Identification PCR Kit. Double-click the GTA-template and the Genotyper Software will open automatically.**

Calibration Using Allelic Ladders

Analysis with Genotyper Software is performed using related analysis data, i.e., previously analyzed DNA samples, with a known allelic ladder as a GTA-file. In order to analyze DNA samples using Genotyper Software, calibration with the allelic ladder must first be carried out. The allelic ladder of the Investigator Human Identification PC Kit should ideally be analyzed before and after the DNA samples under investigation.

For calibration, the measured allele sizes are transferred automatically to the expected sizes within the project. In general, calibration is based upon the most current run of the allelic ladder. If more runs will be used, calibration uses all allelic ladders and the correct assignment of alleles should be verified. If alleles are not assigned correctly, DNA samples should undergo further runs with an appropriate allelic ladder.

Calibration using multi-capillary analyzers

To ensure a reliable allelic assignment on multi-capillary analyzers, a number of allelic ladders should be run on different capillaries.

Room temperature may influence the running performance of PCR products and may result in split peaks — especially at low temperatures — or an altered run velocity of DNA fragments. Ensure that environmental conditions recommended by the instrument manufacturer are maintained at all times.

System parameters

Different analysis instruments, DNA size standards, or polymers may result in different fragment lengths. Thus, DNA samples and allelic ladders from one sample set should be analyzed using the same system parameters.

Evaluation of Analysis Data

1. **Open the template file of the Investigator Human Identification PCR Kit; Genotyper Software will open automatically.**

2. **Go to "Import data".**

3. **Select "File", followed by "Import" and then "From GeneScan File".**

4. **Select "GeneScan Analysis Data Files: Add Sample Files".**

5. **Select "Add", and then click "Finish".**

   The data files will appear at the top of the window.

6. **To import, choose the dye colors of the Investigator Human Identification PCR Kit and color for the DNA Size Standard (e.g., B, Y, G, R, O). Go to "Edit", choose "Set Preferences", followed by "Import Colors".**

7. **To run the macro, highlight or double-click the appropriate macro (found in the bottom left corner of the main window). Click "Run Macro".**

Note: Before analyzing data, always run the Macro Calibrate Ladder first, see page 12.

The general procedure for analysis is:

- Check size standard
- Check allelic ladder
- Check positive control
- Check negative control
- Review sample data

Macros for Investigator Human Identification PCR Kits

This section is divided into the following subsections:

- Size standards
- Calibrate ladder
- Label 20% Filter
- Label 10% Filter
- Blue, green, yellow, and red panels
- Horizontal table for 2 alleles
- Vertical table for 10 alleles
- Calculation of category offsets

Note: The macro "Calibrate Ladder" is essential for the analysis results from Investigator Human Identification PCR Kits. Use of additional Investigator Template Files is optional.

Size standards

SST-BTO

To check the correct assignment of the labels to the sample, click the O icon) in the upper left of the main window. The red panels of all samples are then displayed in the plot window.

Compare the sample fragments sizes with the sizes of the DNA size standard 550 (BTO), which should be: 60, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 250, 260, 280, 300, 320, 340, 360, 380, 400, 425, 450, 475, 500, 525, and 550 bp.

If sizes differ, further analysis should be performed using GeneScan Software. If necessary, create a new size standard definition within the GeneScan Software.
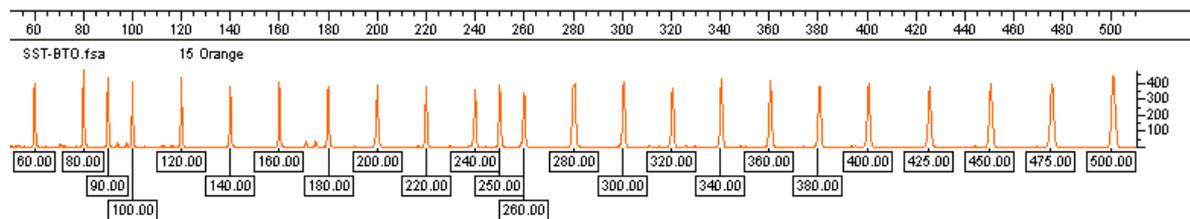

Figure 1. Electropherogram of the DNA size standard 550 (BTO). Fragment lengths are shown in base pairs.

SST-ROX

For Investigator Human Identification PCR Kits in 4 Color Assay with the fluorescent labels 6-FAM®, HEX, NED, and ROX (matrix DS-30), the DNA Size Standard 550 (ROX) in the red panel (R icon) is necessary.

Calibrate ladder

■ The shortcut key to initiate the macro "Calibrate Ladder" is Ctrl + O

■ Use this macro to calibrate the current project (GTA-file) with an allelic ladder

■ After calibration, the macro "Label 20% Filter" will run automatically

Identification of the allelic ladder

All colors of the imported allelic ladder must be defined as "ladder" in the "Dye/Lanes" window. Go to "Views" and select "Show Dye/Lanes Window". Then, add the term "ladder" to every color in the "Sample Info" text field (Figure 2).

Figure 2. Dye/Lanes window.
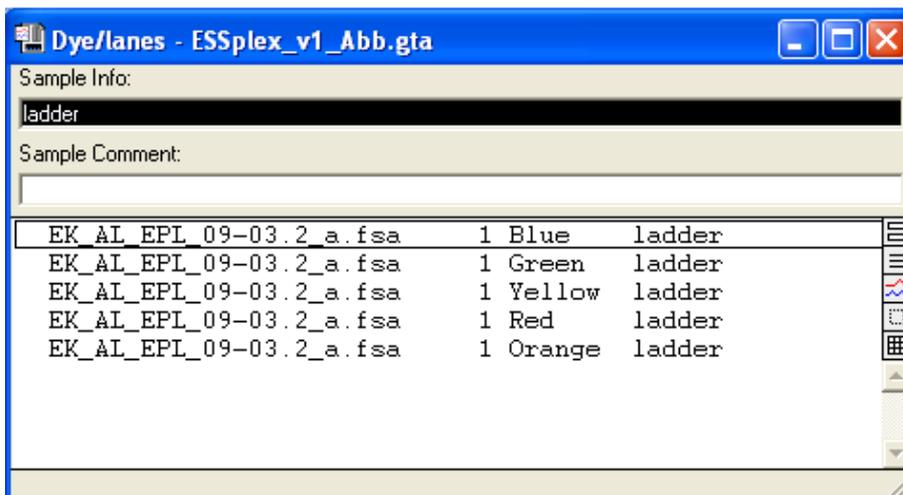
Note: Peaks in the allelic range that are not identified by the GeneScan software cannot be labeled by the GeneScan Software.

Controls

In order to check allele designations, compare the alleles of the allelic ladder and control DNA of the test kit with data from the latest version of the Handbook corresponding to the Investigator Human Identification PCR Kit being used.

Label 20% Filter

■ The shortcut keys to initiate the macro "Label 20% Filter" are Ctrl + 1; Ctrl + 2; Ctrl + 3

■ Use this macro for analysis of samples containing one DNA; unsuitable for DNA mixtures

■ Using the macro "Label "20% Filter", peaks are indicated with their allele designation (Figure 3)

■ Using the macro "Label 20% Filter incl. bp", peaks are indicated with their allele designation and their size in base pairs

■ Using the macro "Label 20% Filter incl. peak height", peaks are indicated with their allele designation and their peak height in relative fluorescence units (RFU)

■ A plot window will open up automatically with the following entries:

   ■ DNA samples

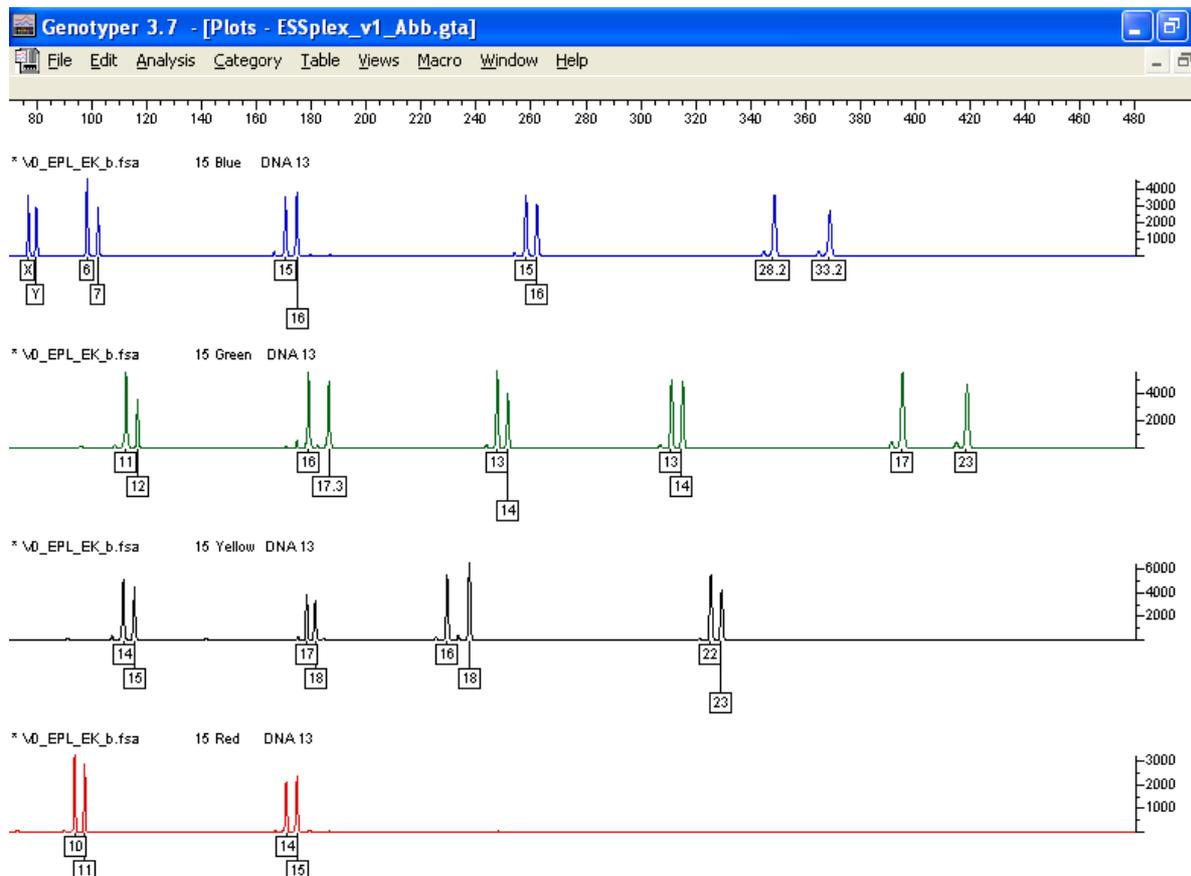   ■ Allelic ladder

   ■ DNA size standard, if imported

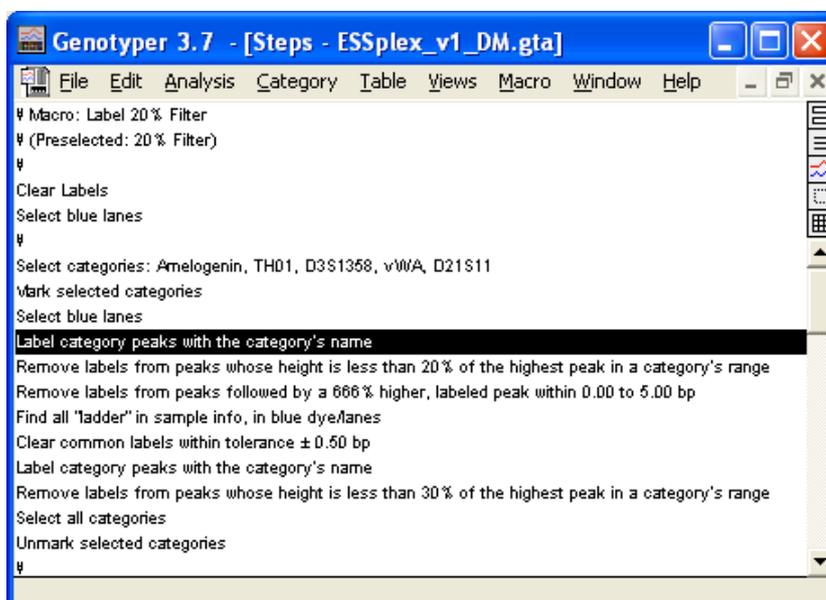**Figure 3. Plot Window after execution of Macro "Label 20% Filter".**

Labeling of all relevant peaks

■ Peak designations below 20% of the height of the highest peak in the category (STR loci) are not shown in the macro "Label 20% Filter". To change the preselected 20% filter of the macro see "Changing Filter Value", page 16.

■ Filter options are integrated into the macro in order to avoid stutter peaks and template-independent nucleotide addition (minusA peaks).

■ Peaks in the allelic range labeled with "allele?" can not be assigned to an allele size. These labels have to be checked manually and may be deleted by clicking on it (see 'Many peaks of the sample are termed "allele?"' in the troubleshooting guide", page 23). If necessary, scale down the window.

New peak designations (labels)

Perform the following steps to change peak designation:

1. Unlock the Template File by going to "File" and selecting "Unlock".
2. Select the macro to be adjusted.
3. Go to "View" and select "Show Step Window" to open the step window.
4. Select the step to be adjusted by clicking on the appropriate line in the step window (e.g., Label category peaks, see screenshot below).

"The "Labels" tab is used for designation of the peaks.

5. Go to "Macro" and select "Edit Step" to edit this step
6. Click the desired peak designation (e.g., size in bp, peak height, peak area) on the window that appears and confirm the changes by

clicking "Replace".

Edit peak designations.

7. **Repeat the process with all categories to be adjusted.**
8. **When all changes are complete, lock the Template File by going to "File" and selecting "Lock".**
9. **Click "Save As" and save the file with a new filename.**

Note: The Macro "Label 20% filter" is unsuitable for the analysis of DNA mixtures.

New filter options must be defined by the user. Alternatively, the macro "Label 10% Filter" can be used.

Label 10% Filter

■   The shortcut key to initiate the macro "Label 10% Filter" is Ctrl + 4

■   Use this macro for the analysis of stains or samples containing more than one DNA (e.g., for forensic casework)

■   Peaks will be labeled with the appropriate allele

■   A plot window will open up automatically with the following entries:

■   DNA samples

- Allelic ladder

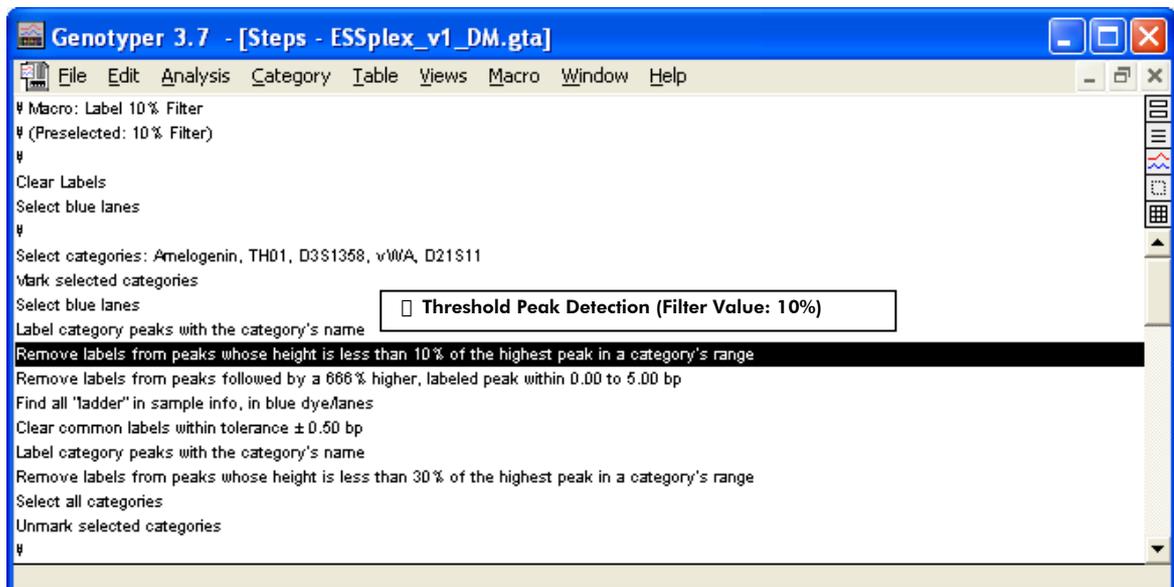- DNA size standard, if imported

Basic setting for improved peak detection

- In the macro "Label 10% Filter", all peak designations higher than 10% of the highest peak height in the category are labeled thereby improving peak detection (preselected: 10% filter).

- Filter options are already integrated into the macro in order to avoid stutter peaks and template-independent nucleotide addition (minusA peaks).
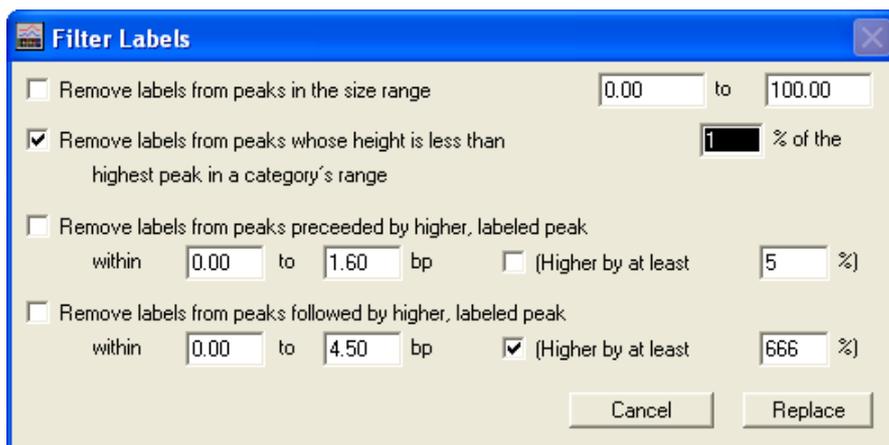
Changing Filter Value

Perform the following steps to change the lower threshold for the peak detection (preselection filter 20%) in the Genotyper macro.

1. **Go to "File" and select "Unlock" to unlock the Template File.**
2. **Select the macro to be adjusted.**
3. **Go to "Views" and select "Show Step Window".**
4. **For improved detection of categories (STR-loci) select the step "Remove Labels…" by clicking on the appropriate line in the step window.**

Genotyper 3.7 - [Steps - ESSplex_v1_DM.gta]

File Edit Analysis Category Table Views Macro Window Help

¥ Macro: Label 10% Filter
¥ (Preselected: 10% Filter)
¥
Clear Labels
Select blue lanes
¥
Select categories: Amelogenin, TH01, D3S1358, vWA, D21S11
Mark selected categories
Select blue lanes   Threshold Peak Detection (Filter Value: 10%)
Label category peaks with the category's name
Remove labels from peaks whose height is less than 10% of the highest peak in a category's range
Remove labels from peaks followed by a 666% higher, labeled peak within 0.00 to 5.00 bp
Find all 'ladder' in sample info, in blue dye/lanes
Clear common labels within tolerance ± 0.50 bp
Label category peaks with the category's name
Remove labels from peaks whose height is less than 30% of the highest peak in a category's range
Select all categories
Unmark selected categories
¥

Step Window of Macro "Label 10% Filter".

5. **Go to "Macro" and select "Edit Step", to edit the step.**
6. **Go to "Filter Labels" and amend the value for the lower threshold of the filter (see black shaded field in screenshot, next page)**

Edit Filter Values.

7. **When all changes are complete, lock the Template File by going to "File" and selecting "Lock".**

8. **Click "Save As" and save the file with a new filename.**

Blue, green, yellow, and red panels

■ The shortcut keys required are Ctrl + 5, Ctrl + 6, Ctrl + 7, Ctrl + 8

■ Used to compare samples with the appropriate allelic ladder

■ Shows the labels generated with the label macro used (see "Label 20% Filter", page 13 and "Label 10% Filter", page 15)

■ To simplify allocation, zoom in on the appropriate area: Go to "Views" and click "Zoom", followed by "Zoom to" (e.g., 70–220 bp)
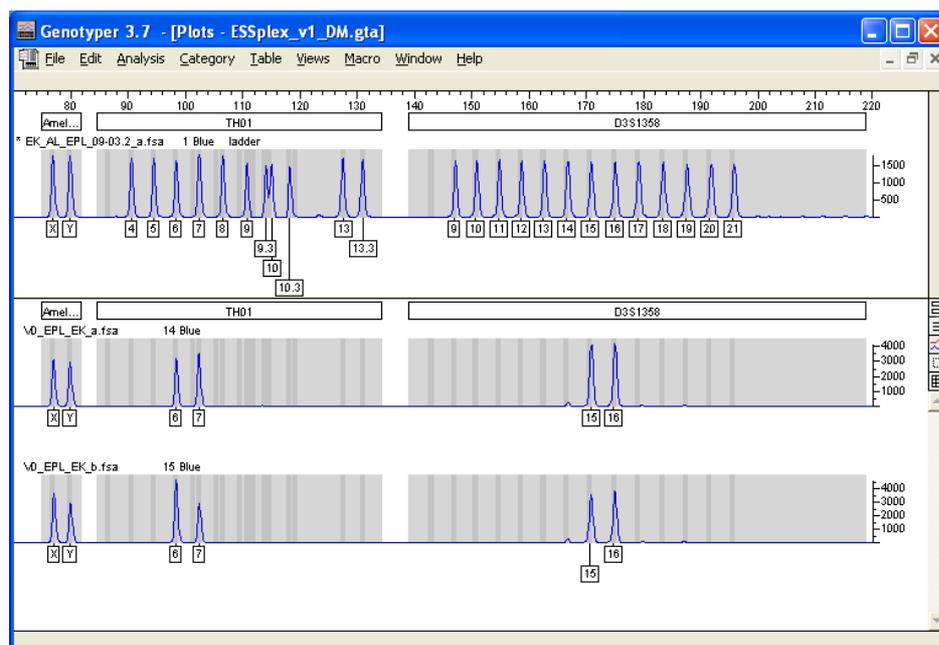

Figure 4. Plot Window after execution of the Macro "Blue Panels" with allelic ladder and DNA samples.

Show categories

To display all categories (STR loci) in the panel of one color, check the "Category boundaries" check box.

Go to "Views" select "Plot Options", followed by "Plot Window, Upper Panel" and "Plot Window, Lower Panel".

In "Plot Window, Upper Panel", the allelic ladder is fixed at the top of the window. In "Plot Window, Lower Panel", the DNA samples are shown at the bottom of the window. Genotyper Software is unable to show categories when different panel colors are displayed one below the other.

Horizontal Table for 2 Alleles

- The shortcut key to initiate the macro "Horizontal table for 2 alleles" is Ctrl + 9

- Use this macro to analyze samples of one DNA, e.g., for a DNA database

- This macro displays the allele designation of two peaks of each marker

- This macro generates a table after the label macro has been performed

- This macro displays the allele designation of up to 2 peaks per category (STR locus) for each sample in one line

- For genetically homozygote peaks, the allele designation will be displayed twice

- In order to discriminate between individual samples, the "Sample Info" field for each sample color must be completed with an appropriate description. Go to "Views" and select "Show Dye/Lanes Window"

- Use "Table" and "Update Table" to copy the current allele designation for peaks to the table. Misnomers resulting from pull-up peaks between different panels can be deleted manually by clicking on the peak.

Genotyper 3.7 - [Table - ESSplex_v1_DM.gta]

File Edit Analysis Category Table Views Macro Window Help

Sample Info	Amelogenin 1	Amelogenin 2	TH01 1	TH01 2	D3S1358 1	D3S1358 2	vWA 1	vWA 2
ladder	X	Y	4	5	9	10	11	12
	X	Y	6	7	15	16	15	16
DNA 13	X	Y	6	7	15	16	15	16

Figure 5. Output File after execution of the macro "Horizontal Table for 2 Alleles".
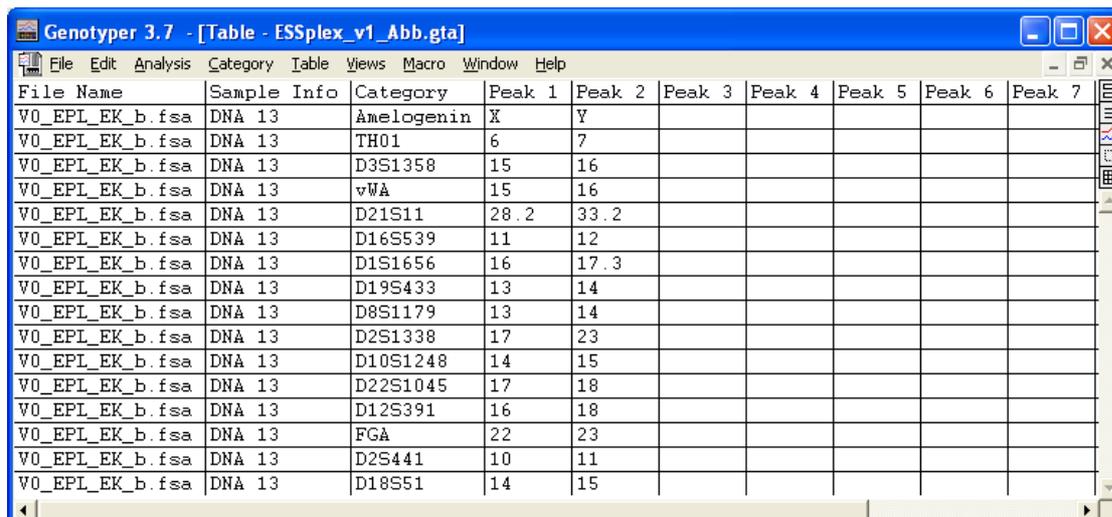
Table export

Perform the following steps to export the table to Microsoft® Excel®.

1. **Go to "Table" and choose "Export to File".**
   Save the file with the extension ".xls".

2. **Open Microsoft Excel software and load the table.**

3. **The conversion procedure opens automatically. Follow the conversion procedure.**

Vertical Table for 10 Alleles

- Use this macro to analyze stains or mixed samples of different DNAs

- This macro displays the allele designation of up to 10 peaks for each marker

- This macro generates a table after the label macro has been performed

- This macro displays the allele designation of up to 10 alleles per category (STR locus) and generates a vertical table. The categories are all listed in one line (e.g., ESSplex: all categories x 10 alleles)

- In "Sample Info", the filename of the sample is displayed automatically

- For genetically homozygote peaks, the allele designation will be displayed twice

- Use "Table" and "Update Table" to copy the current allele designation for peaks to the table. Misnomers resulting from pull-up peaks between different panels can be deleted manually by clicking on the peak.

File Name	Sample Info	Category	Peak 1	Peak 2	Peak 3	Peak 4	Peak 5	Peak 6	Peak 7
V0_EPL_EK_b.fsa	DNA 13	Amelogenin	X	Y					
V0_EPL_EK_b.fsa	DNA 13	TH01	6	7					
V0_EPL_EK_b.fsa	DNA 13	D3S1358	15	16					
V0_EPL_EK_b.fsa	DNA 13	vWA	15	16					
V0_EPL_EK_b.fsa	DNA 13	D21S11	28.2	33.2					
V0_EPL_EK_b.fsa	DNA 13	D16S539	11	12					
V0_EPL_EK_b.fsa	DNA 13	D1S1656	16	17.3					
V0_EPL_EK_b.fsa	DNA 13	D19S433	13	14					
V0_EPL_EK_b.fsa	DNA 13	D8S1179	13	14					
V0_EPL_EK_b.fsa	DNA 13	D2S1338	17	23					
V0_EPL_EK_b.fsa	DNA 13	D10S1248	14	15					
V0_EPL_EK_b.fsa	DNA 13	D22S1045	17	18					
V0_EPL_EK_b.fsa	DNA 13	D12S391	16	18					
V0_EPL_EK_b.fsa	DNA 13	FGA	22	23					
V0_EPL_EK_b.fsa	DNA 13	D2S441	10	11					
V0_EPL_EK_b.fsa	DNA 13	D18S51	14	15					

Figure 6. Output file after execution of the macro "Vertical Table for 10 Alleles".

Calculation of category offsets

- Macros for calibration of individual categories

- This macro must be used with the macro "Calibrate Ladder".

Adjustment of Categories

Perform the following steps to adjust categories:

1. **Open the Template File corresponding to the Investigator Human Identification PCR Kit being used. Genotyper Software will open automatically.**
2. **Go to "File" and select "Unlock" to unlock the Template File (see lock symbol at the lower left sidebar).**
3. **Go to "Views" and select "Show Categories", followed by "Open categories".**
4. **Go to "Category" and then "Edit Category". Select the allele to be adjusted from the table.**
5. **Change the desired allele features (tolerance range, fragment length).**
6. **Click "Replace" to confirm the changes.**
7. **Got to "File" and click "Save As" to save the file with a new filename.**

Note: Additional categories for newly found (intermediate) alleles can be created in the same way. Here, a tolerance range of ±0.45 bp should be chosen. However, these added categories are not evaluated by the automatic calibration of the macro "Calibrate Ladder".

QIAGEN assumes no liability for changes made to Investigator Template Files. The actual versions of Investigator Template Files for all test kits are available at the Web catalog page of each Investigator Human Identification PCR Kit on the QIAGEN Web site (www.qiagen.com).

Troubleshooting Guide

This troubleshooting guide may be helpful in solving any problems that may arise. For more information, see also the Frequently Asked Questions page at our Technical Support Center: www.qiagen.com/FAQ/FAQList.aspx. The scientists in QIAGEN Technical Services are always happy to answer any questions you may have about either the information and protocols in this handbook or sample and assay technologies (for contact information, see back cover or visit www.qiagen.com).

	Comments and suggestions
Error message during program start: "Could not start the application because there is not enough memory."	
Both Genotyper and GeneScan Software applications from Applied Biosystems have been discontinued and are unavailable for purchase (as of June 1, 2004).	Applied Biosystems support for these products ended June 1, 2009.
	Use an appropriate Windows-based computer.
	A computer with less than 1 GB memory may not work with Genotyper software.
The template file cannot be opened	
a) Genotyper Software is not the most recent version (Macintosh version 2.5; Windows version 3.7)	Upgrade the Genotyper Software.
	The old Macintosh Genotyper version 2.1 can be updated via a free download, available from Applied Biosystems.
b) Genotyper Software was not installed on the local computer	Install Genotyper Software on the local Computer.
c) Template Files or the CD-ROM were damaged	Download the files again from www.qiagen.com or reorder the CD-ROM.

Comments and suggestions

Error message during analysis: "Could not complete your request because the labeled peak could not be found."

a) An additional signal can be identified as a peak of the allelic ladder because of malfunction during the electrophoresis. If peaks of the allelic ladder are miscalled, the ladder can not be used for the analysis.

Use a different injection of the allelic ladder and check the data of the analyzed sizes from the Size Standard (in bp) of the allelic ladder.

Always use the DNA Size Standard 550 for Investigator Human Identification PCR Kits.

b) One peak of the allelic ladder is below the peak detection value (50–200 RFU) of the analysis method used, and thus, is not identified as a peak

The allelic ladder must be loaded onto the analysis instrument at a higher concentration than samples to be analyzed.

Alternatively, allelic ladder data can be analyzed with a lower peak detection value in Genotyper or GeneScan Software.

d) One peak of the allelic ladder is not identified because it is outside the expected size range of the software (in bp)

Compare the length of the fragments (in bp) of the first allele in one color of the allelic ladder with the corresponding value in the categories. Then compare it with the other alleles.

e) Deviant fragment lengths due to unsuitable size standard

Always use the DNA Size Standard 550 for Investigator Human Identification PCR Kits.

Error message during analysis "Could not complete your request because no dye/lanes are selected."

a) The allelic ladder file was not loaded

Import the file with the allelic ladder.

b) The allelic ladder file was not identified

For every color of the allelic ladder, the term "ladder" must be listed. Go to "Views" and select "Show Dye/Lanes Window". Add "ladder" in the text field "Sample Info".

c)	Not all five dye colors (blue, green, yellow, red, orange) have been imported	Go to "Edit" and choose "Select preferences". Choose all dye colors and import them again.

Many peaks of the sample are termed "allele?"

a)	Bubbles in the capillary lead to pull-up peaks in all color panels ("spikes") that result in allele misnomer	Repeat electrophoresis to confirm results.
b)	Signal intensities are too high. If the peak heights of the samples are outside the linear detection range (>4000 RFU/ABI310;>5000 RFU/ABI3130), the frequency of stutters, split peaks, and artifacts may increase	Reduce the injection time by up to 1 s, reduce the amount of the PCR amplification product for analysis, or reduce the quantity of DNA for PCR.
c)	The DNA size standard 550 (BTO or ROX) was not defined or was identified incorrectly	Click on icon $\boxed{O}$ for BTO or $\boxed{R}$ for ROX panels in the left upper corner of the Genotyper Software and display the orange or red fragments of all samples in the Plot Window.
d)	Data from different analyzers (e.g., ABI 310 and ABI 3130) have been saved within one GTA-file	Data from different analyzers must always be saved in different GTA-files.

Point alleles are not found

Point alleles were not separated in the GeneScan analysis	Point alleles are alleles with at least 1 bp difference to the next integer allele.
	Check the settings of the analysis method. Lower the Peak Window Size value to 11 points. Then, analyze the DNA samples again using the new parameters.

References

QIAGEN maintains a large, up-to-date online database of scientific publications utilizing QIAGEN products. Comprehensive search options allow you to find the articles you need, either by a simple keyword search or by specifying the application, research area, title, etc.

For a complete list of references, visit the QIAGEN Reference Database online at www.qiagen.com/RefDB/search.asp or contact QIAGEN Technical Services or your local distributor.

Ordering Information

Product	Contents	Cat. no.
Investigator Template Files (for Windows)	All template files for Investigator Human Identification PCR Kits for use with GeneMapper ID, Genotyper, and Genotyper software, as well as DIPSorter freeware (CD-ROM)	389900
Related products		
Investigator ESSplex Kit (100)*	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	381515
Investigator Triplex AFS QS Kit (100)*	Primer mix including internal control (QS), reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	380315
Investigator Triplex DSF Kit (100)*	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	380325
Investigator Decaplex SE Kit (100)*	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	381025
Investigator Argus X-12 Kit (25)*	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	383213
Investigator Argus Y-12 QS Kit (100)*	Primer mix including internal control (QS), reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	383615
Investigator DIPplex Kit (25)*	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	384013

* Larger kit size available; please inquire.

Product	Contents	Cat. no.
Matrix Standard BT5 single cap. (5 x 25)	Matrix standards 6-FAM, BTG, BTY, BTR, and BTO for single-capillary analyzers	386113
Matrix Standard BT5 multi cap. (25)	Matrix standards 6-FAM, BTG, BTY, BTR, and BTO for multi-capillary analyzers	386123
Matrix Standard BT5 multi cap. (50)	Matrix standards 6-FAM, BTG, BTY, BTR, and BTO for multi-capillary analyzers	386125

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

Trademarks: QIAGEN® (QIAGEN Group); 6-FAM®, ABI PRISM®, Applied Biosystems®, GeneMapper®, GeneScan®, Genotyper®, ROX™ (Life Technologies); AFLP® (Keygene N.V.); Excel®, Microsoft®, Windows® (Microsoft Corporation); Macintosh® (Apple Inc.).

Software License Agreement and Warranty Statement

IMPORTANT: PLEASE READ THIS LICENSE AGREEMENT CAREFULLY. QIAGEN LICENSES THIS SOFTWARE TO YOU ("LICENSEE") ONLY UPON THE ACCEPTANCE OF ALL OF THE TERMS IN THIS LICENSE AGREEMENT. BY USING THIS SOFTWARE PACKAGE, LICENSEE CONSENTS TO BE BOUND BY THE TERMS OF THIS LICENSE.

Software License

The software which accompanies this license (the "Software") is the property of QIAGEN and is protected by copyright law. The software under this license is licensed, not sold, to Licensee by QIAGEN upon the conditions contained in this License. QIAGEN retains full title to the Software. This license is valid for the Investigator Template Files for Genotyper.

The Software may be used solely in accordance with the *Investigator Template Files for Genotyper User Guide* and for use with components contained in the Software only. QIAGEN grants no license under any of its intellectual property to use or incorporate the enclosed components of this Software with any components not included within this Software except as described in the *Investigator Template Files for Genotyper User Guide* and additional protocols available at www.qiagen.com.

Permitted Uses

Licensee may:

1. Make one copy of the Software for archival purposes, or copy the Software onto the hard disk of Licensee's computer and retain the original for archival purposes.

2. Use the Software on a network, only if Licensee has a licensed copy of the Software for each computer that can access the Software over that network.

Restricted Uses

Licensee may not (except as provided by statutory law):

1. Sublicense, rent, loan, lease or otherwise transfer any portion of the Software.

2. Reverse engineer, de-compile, disassemble, modify, translate, make any attempt to discover the source code of the Software, or create derivative works from the Software.

3. Copy the software or accompanying documentation, except as specifically permitted herein.

4. Use a previous version or copy of the Software after receipt of a disk replacement set or an upgraded version as a replacement of the prior version.

5. Remove or alter any proprietary notices, labels, or marks on the software or accompanying documentation.

Communication

Licensee shall communicate the terms and restrictions contained in this license agreement to all persons under Licensee's direction or control who may have access to the Software. Licensee is responsible for any breach of this License resulting from an act by its employees or any other person acting on behalf of the Licensee.

Compliance with Laws

Licensee shall be responsible for its compliance with any laws or regulations governing the import or export of the Software.

Termination

Any failure to comply with the terms and conditions of this License may result in immediate termination.

Limitation of Warranty

THIS SOFTWARE IS PROVIDED "AS IS" AND QIAGEN DOES NOT WARRANT THAT THE OPERATION OF THE SOFTWARE WILL MEET LICENSEE'S PARTICULAR REQUIREMENTS OR BE UNINTERRUPTED OR ERROR FREE. TO THE EXTENT PERMITTED BY APPLICABLE STATUTORY LAW, QIAGEN MAKES NO OTHER WARRANTY, EITHER EXPRESSED OR IMPLIED, WITH RESPECT TO THIS SOFTWARE. QIAGEN SPECIFICALLY DISCLAIMS IMPLIED TERMS INCLUDING BUT NOT LIMITED TO WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE. THE ENTIRE RISK AS TO THE QUALITY AND PERFORMANCE OF THE SOFTWARE IS WITH YOU. SHOULD THE SOFTWARE PROVE DEFECTIVE, YOU ASSUME THE COST OF ALL NECESSARY SERVICING, REPAIR OR CORRECTION. IN NO EVENT WILL ANY COPYRIGHT HOLDER BE LIABLE TO YOU FOR DAMAGES, INCLUDING ANY GENERAL, SPECIAL, INCIDENTAL OR CONSEQUENTIAL DAMAGES ARISING OUT OF THE USE OR INABILITY TO USE THE SOFTWARE (INCLUDING BUT NOT LIMITED TO LOSS OF DATA OR DATA BEING RENDERED INACCURATE OR LOSSES SUSTAINED BY YOU OR THIRD PARTIES OR A FAILURE OF THE SOFTWARE TO OPERATE WITH ANY OTHER SOFTWARE).

Technical Support

Technical support may be provided via e-mail and/or website postings. While every effort is made to provide timely technical support no guarantees whatsoever are implied that technical support will be provided or that technical support, when provided, will be accurate. Software offered on this site is basically unsupported and supplied on an as-is basis unless you have obtained a specific maintenance contract agreement with the copyright holders.

Exclusive Remedies

The remedies provided herein are Licensee's sole and exclusive remedies. In no event shall QIAGEN be liable for any direct, special, incidental or consequential damages, whether based on contract, tort, or any other legal theory. Some jurisdictions do not allow the exclusion of limitation of incidental or consequential damages, so the above limitation may not apply. In the case the above limitations do not apply, the licensee agrees that the cumulative limitation of liability will be a maximum of USD $1,000.00.

Third Party Software

To the extent the Software includes any operating programs, such as Microsoft Windows, such software is provided to the end user "as is," without warranty of any kind.

Australia ▪ Orders 03-9840-9800 ▪ Fax 03-9840-9888 ▪ Technical 1-800-243-066

Austria ▪ Orders 0800/28-10-10 ▪ Fax 0800/28-10-19 ▪ Technical 0800/28-10-11

Belgium ▪ Orders 0800-79612 ▪ Fax 0800-79611 ▪ Technical 0800-79556

Brazil ▪ Orders 0800-557779 ▪ Fax 55-11-5079-4001 ▪ Technical 0800-557779

Canada ▪ Orders 800-572-9613 ▪ Fax 800-713-5951 ▪ Technical 800-DNA-PREP (800-362-7737)

China ▪ Orders 021-3865-3865 ▪ Fax 021-3865-3965 ▪ Technical 800-988-0325

Denmark ▪ Orders 80-885945 ▪ Fax 80-885944 ▪ Technical 80-885942

Finland ▪ Orders 0800-914416 ▪ Fax 0800-914415 ▪ Technical 0800-914413

France ▪ Orders 01-60-920-926 ▪ Fax 01-60-920-925 ▪ Technical 01-60-920-930 ▪ Offers 01-60-920-928

Germany ▪ Orders 02103-29-12000 ▪ Fax 02103-29-22000 ▪ Technical 02103-29-12400

Hong Kong ▪ Orders 800 933 965 ▪ Fax 800 930 439 ▪ Technical 800 930 425

Ireland ▪ Orders 1800 555 049 ▪ Fax 1800 555 048 ▪ Technical 1800 555 061

Italy ▪ Orders 02-33430-420 ▪ Fax 02-33430-426 ▪ Technical 800-787980

Japan ▪ Telephone 03-6890-7300 ▪ Fax 03-5547-0818 ▪ Technical 03-6890-7300

Korea (South) ▪ Orders 1544 7145 ▪ Fax 1544 7146 ▪ Technical 1544 7145

Luxembourg ▪ Orders 8002-2076 ▪ Fax 8002-2073 ▪ Technical 8002-2067

Mexico ▪ Orders 01-800-7742-639 ▪ Fax 01-800-1122-330 ▪ Technical 01-800-7742-639

The Netherlands ▪ Orders 0800-0229592 ▪ Fax 0800-0229593 ▪ Technical 0800-0229602

Norway ▪ Orders 800-18859 ▪ Fax 800-18817 ▪ Technical 800-18712

Singapore ▪ Orders 65-67775366 ▪ Fax 65-67785177 ▪ Technical 65-67775366

Spain ▪ Orders 91-630-7050 ▪ Fax 91-630-5145 ▪ Technical 91-630-7050

Sweden ▪ Orders 020-790282 ▪ Fax 020-790582 ▪ Technical 020-798328

Switzerland ▪ Orders 055-254-22-11 ▪ Fax 055-254-22-13 ▪ Technical 055-254-22-12

UK ▪ Orders 01293-422-911 ▪ Fax 01293-422-922 ▪ Technical 01293-422-999

USA ▪ Orders 800-426-8157 ▪ Fax 800-718-2056 ▪ Technical 800-DNA-PREP (800-362-7737)

QIAGEN

Sample & Assay Technologies