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Investigator® ESSplex SE GO! Handbook

For multiplex amplification of the new European standard set of loci, plus SE33, and Amelogenin

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Contents

Kit Contents

Investigator ESSplex SE GO! Kit	**(200)**	**(1000)**
Catalog no.	**381566**	**381568**
Number of 25 µl reactions	**200**	**1000**
Fast Reaction Mix*	1500 µl	5 x 1500 µl
Primer Mix ESSplex SE GO!	2 x 1750 µl	10 x 1750 µl
Control DNA 9948 (5 ng/µl)	50 µl	50 µl
DNA size standard 550 (BTO)	110 µl	5 x 110 µl
Allelic ladder ESSplex SE GO!	50 µl	5 x 50 µl
Quick-Start Protocol	1	1

* Contains HotStarTaq® Plus DNA Polymerase, dNTPs, $MgCl_2$, and bovine serum albumin (BSA).

Storage

The Investigator ESSplex SE GO! Kit is shipped on dry ice. It should be stored immediately upon receipt at –30 to –15°C in a constant-temperature freezer. Avoid repeated thawing and freezing. Primer mix and allelic ladder must be stored protected from the light. DNA samples and post-PCR reagents (allelic ladder and DNA size standard) should be stored separately from the PCR reagents. Under these conditions, the components are stable until the expiration date indicated on the kit.

Once opened, the Investigator ESSplex SE GO! Kit should be stored at 2–8°C for a maximum of 2 weeks.

Intended Use

The Investigator ESSplex SE GO! Kit is intended for molecular biology applications in forensic, human identity, and paternity testing. This product is not intended for the diagnosis, prevention, or treatment of a disease.

All due care and attention should be exercised in the handling of the products. We recommend all users of QIAGEN products to adhere to the NIH guidelines that have been developed for recombinant DNA experiments, or to other applicable guidelines.

Safety Information

When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, please consult the appropriate safety data sheets (SDSs). These are available online in convenient and compact PDF format at www.qiagen.com/safety where you can find, view, and print the SDS for each QIAGEN kit and kit component.

Quality Control

In accordance with QIAGEN's ISO-certified Quality Management System, each lot of Investigator ESSplex SE GO! Kit is tested against predetermined specifications to ensure consistent product quality.

Introduction

The Investigator ESSplex SE GO! Kit is used for multiplex PCR in forensic human identity and paternity testing. The 15 polymorphic STR markers recommended by the European Network of Forensic Science Institutes (ENFSI) and the European DNA Profiling Group (EDNAP) as the new European Standard Set of loci (D1S1656, D2S441, D2S1338, D3S1358, D8S1179, D10S1248, D12S391, D16S539, D18S51, D19S433, D21S11, D22S1045, FGA [FIBRA], TH01 [TC11], and vWA), plus SE33 [ACTBP2], and the gender-specific Amelogenin are amplified simultaneously.

The Investigator ESSplex SE GO! Kit has been developed specifically for rapid direct amplification from blood or buccal cells on FTA™ and other paper, and buccal swabs. The kit utilizes QIAGEN's fast cycling PCR technology, which allows amplification in around 45 minutes and provides highly robust results. Punches from FTA and other filter papers can be used without the need for pretreatment. For buccal swabs, a fast and convenient room temperature lysis protocol is provided to create a crude lysate for amplification. The primers are fluorescence-labeled with one of the following dyes:

- 6-FAM™: Amelogenin, TH01, D3S1358, vWA, D21S11
- BTG: D16S539, D1S1656, D19S433, SE33
- BTY: D10S1248, D22S1045, D12S391, D8S1179, D2S1338
- BTR: D2S441, D18S51, FGA

The recommended amount of sample is one punch of 1.2 mm diameter for FTA and other filter papers, or 2 µl of a buccal swab lysate.

The Investigator ESSplex SE GO! Kit was validated using the GeneAmp® PCR System 9700 (with Gold-plated 96-Well Silver Block) and the Applied Biosystems® 3500™ Genetic Analyzer.

Table 1 shows the STR loci with their chromosomal mapping and repeat motifs, which are concordant with the International Society for Forensic Genetics (ISFG) guidelines for the use of microsatellite markers (Bär et al., 1997).

For information about known microvariants not contained in the Investigator ESSplex SE GO! Allelic Ladder, see the National Institute of Standards and Technology (NIST) web site (www.cstl.nist.gov/biotech/strbase/).

Table 1. Locus-specific information of the Investigator ESSplex SE GO! Kit

Locus	GenBank® accession number	Repeat motif of the reference allele	Chromosomal mapping
Amelogenin X	M55418	–	Xp22.1-22.3
Amelogenin Y	M55419	–	Yp11.2
D1S1656	NC_000001.9	$[TAGA]_{16}$ $[TGA][TAGA][TAGG]_1[TG]_5$	1q42
D2S441	AL079112	$[TCTA]_{12}$	2p14
D2S1338	G08202	$[TGCC]_6[TTCC]_{11}$	2q35
D3S1358	11449919	TCTA $[TCTG]_2$ $[TCTA]_{15}$	3p25.3
D8S1179	G08710	$[TCTA]_{12}$	8q23.1-23.2
D10S1248	AL391869	$[GGAA]_{13}$	10q26.3
D12S391	G08921	$[AGAT]_5$ GAT $[AGAT]_7$ $[AGAC]_6$ AGAT	12p13.2
D16S539	G07925	$[GATA]_{11}$	16q24.1
D18S51	L18333	$[AGAA]_{13}$	18q21.3
D19S433	G08036	AAGG [AAAG] AAGG TAGG $[AAGG]_{11}$	19q12
D21S11	AP000433	$[TCTA]_4$ $[TCTG]_6$ $[TCTA]_3$ TA $[TCTA]_3$ TCA $[TCTA]_2$ TCCATA $[TCTA]_{11}$	21q21.1
D22S1045	AL022314	$[ATT]_{14}$ ACT $[ATT]_2$	22q12.3
FGA (FIBRA)	M64982	$[TTTC]_3$ TTTTTTCT $[CTTT]_{13}$ CTCC $[TTCC]_2$	4q28.2
SE33 (ACTBP2)	NG000840	$[AAAG]_9$ AA $[AAAG]_{16}$	6q14.2
TH01 (TC11)	D00269	$[TCAT]_9$	11p15.5
vWA	M25858	TCTA $[TCTG]_4$ $[TCTA]_{13}$	12p13.31

Equipment and Reagents to Be Supplied by User

When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, consult the appropriate safety data sheets (SDSs), available from the product supplier.

All protocols

- Hi-Di™ Formamide, 25 ml (Applied Biosystems, cat. no. 4311320)
- Matrix Standards BT5 for single-capillary instruments, e.g., ABI PRISM® 310 Genetic Analyzer (QIAGEN, cat. no. 386113)
- Matrix Standards BT5 for multi-capillary instruments, e.g., ABI PRISM 3100 and Applied Biosystems 3130 and 3500 Genetic Analyzers (QIAGEN, cat. nos. 386123 or 386125)
- Pipets and pipet tips
- One of the following DNA analyzers:*
  ABI PRISM 310 Genetic Analyzer
  ABI PRISM 3100-*Avant*™/3100 Genetic Analyzer
  Applied Biosystems 3130/3130*x*/Genetic Analyzer
  Applied Biosystems 3500/3500xL Genetic Analyzer
- One of the following PCR thermal cyclers:*
  QIAGEN Rotor-Gene® Q
  GeneAmp PCR System 9700
  Bio-Rad PTC-200
  Biometra UNO-Thermoblock
  Eppendorf® Mastercycler® ep
- PCR tubes or plates
- Microcentrifuge for PCR tubes or plates

For protocols based on blood or buccal cells on paper

- Uni-Core Punch 1.2 mm (GE Healthcare, cat. no. WB100028) or 1.2 mm Aluminum Micro-Punch with Mat (GE Healthcare, cat. no. WB100005)

For protocols based on buccal cells on paper

- Investigator STR GO! Punch Buffer (1000) or (200) (cat. no. 386528 or 386526)

*This is not a complete list of suppliers and does not include many important vendors of biological supplies.

For protocols based on buccal swab lysates

- Investigator STR GO! Lysis Buffer (QIAGEN, cat. no. 386516)
- 2 ml microcentrifuge tubes
- Shaker for 2 ml microcentrifuge tubes

Validity analysis software 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. We recommend GeneMapper® *ID-X*, GeneMapper *ID*, or Genotyper® Software. The Investigator Template Files facilitate data analysis and are valid with the software mentioned above.

Important Notes

The experimental conditions outlined in the protocols have been found to give the best results. However, depending on the sample material, PCR cycle numbers may be adapted to ensure the highest possible first round success rates. We recommend running a representative batch of samples in order to confirm that the cycle numbers given in this protocol are optimal. Increase the cycle number by one if the signals in the resulting electropherograms are too low. Decrease the cycle number by one if the signals in the resulting electropherograms are too high.

Protocol: PCR Amplification from Blood on FTA and Other Paper

This protocol is for direct PCR amplification of STR loci from punches of blood on FTA and other paper using the Investigator ESSplex SE GO! Kit.

Important points before starting

- Set up all reaction mixtures in an area separate from that used for DNA isolation and PCR product analysis (post-PCR).
- Use disposable tips containing hydrophobic filters to minimize cross-contamination risks.

Things to do before starting

- Before opening the tubes containing PCR components, vortex and then centrifuge briefly to collect the contents at the bottom of the tubes.

Procedure

1. **Take a 1.2 mm punch from the center of the blood spot with a suitable tool (e.g., Uni-Core Punch).**

   Important: Do not use more than one punch at a time.

2. **Prepare a master mix according to Table 2.**

   As some loss of reagents can occur during transfers, prepare the mix with additional reactions included. Also include positive and negative control reactions. The master mix contains all of the components needed for PCR except the template (sample) DNA.

3. **Mix the reaction mix thoroughly, and dispense 25 µl into PCR tubes or the well of a PCR plate.**
4. **Transfer one 1.2 mm disc to each reaction.**

   Note: Do not mix the reaction after disc transfer.

5. **Prepare positive and negative controls.**

   Positive control: Use 2 µl of the Control DNA (i.e., 10 ng).

   Note: Amounts of Control DNA may have to be adapted after setting optimal PCR cycle number in your laboratory if signals are too low or too high.

   Negative control: Do not add any template DNA. Do not add a blank disc or water to the negative control well.

6. **Briefly centrifuge reactions to ensure discs are fully submerged.**

7. **Program the thermal cycler according to the manufacturer's instructions, using the conditions given in Table 3.**

   Note: If using the GeneAmp 9700 thermal cycler with an Aluminum block, use "Std Mode", or with a Silver block or Gold-plated Silver block, use "Max Mode". Do not use "9600 Emulation Mode".

8. **After the cycling protocol is completed, store samples at –30 to –15°C protected from the light, or proceed directly with running the electrophoresis.**

Table 2. Master Mix setup

Component	Volume per reaction
Fast Reaction Mix	7.5 µl
Primer Mix	17.5 µl
Total volume	**25 µl**

Table 3. Cycling protocol for blood on FTA and other paper

Temperature	Time	Number of cycles
95°C*	8 min	–
96°C 61°C	10 s 38 s	25
68°C	1 min	–
10°C	∞	–

* Hot-start to activate DNA polymerase.

Protocol: PCR Amplification from Buccal Cells on FTA and Other Paper

This protocol is for direct PCR amplification of STR loci from punches of buccal cells on FTA and other paper using the Investigator ESSplex SE GO! Kit.

Important points before starting

- Set up all reaction mixtures in an area separate from that used for DNA isolation and PCR product analysis (post-PCR).
- Use disposable tips containing hydrophobic filters to minimize cross-contamination risks.

Things to do before starting

- Before opening the tubes containing PCR components, vortex and then centrifuge briefly to collect the contents at the bottom of the tubes.

Procedure

1. **Take a 1.2 mm punch with a suitable tool (e.g., Uni-Core Punch).**
   Note: If using a Whatman EasiCollect™ and a buccal cell sample, take the punch from a whitish area. This color indicates successful sample transfer.

   Important: Do not use more than one punch at a time.
2. **Prepare a master mix according to Table 4.**
   As some loss of reagents can occur during transfers, prepare the mix with additional reactions included. Also include positive and negative control reactions. The master mix contains all of the components needed for PCR except the template (sample) DNA.
3. **Mix the reaction mix thoroughly, and dispense 27 µl into PCR tubes or the well of a PCR plate.**
4. **Transfer one 1.2 mm disc to each reaction.**
   Note: Do not mix the reaction after disc transfer.

5. **Prepare positive and negative controls.**

   Positive control: Use 1 µl Control DNA (i.e., 5 ng).

   Note: Amounts of Control DNA may have to be adapted after setting optimal PCR cycle number in your laboratory if signals are too low or too high.

   Negative control: Do not add any template DNA. Do not add a blank disc or water to the negative control PCR tube or well.

6. **Briefly centrifuge reactions to ensure discs are fully submerged.**
7. **Program the thermal cycler according to the manufacturer's instructions, using the conditions given in Table 5 .**

   Note: If using the GeneAmp 9700 thermal cycler with an Aluminum block, use "Std Mode", or with a Silver block or Gold-plated Silver block, use "Max Mode". Do not use "9600 Emulation Mode".

8. **After the cycling protocol is completed, store samples at –30 to –15°C protected from the light, or proceed directly with running the electrophoresis.**

Table 4. Master Mix setup for buccal cells on FTA and other paper

Component	Volume per reaction
Fast Reaction Mix	7.5 µl
Primer Mix	17.5 µl
Investigator STR GO! Punch Buffer	2.0 µl
Total volume	**27.0 µl**

Table 5. Cycling protocol for buccal cells on FTA and other paper

Temperature	Time	Number of cycles
95°C*	8 min	–
96°C 61°C	10 s 38 s	28
68°C	1 min	–
10°C	∞	–

* Hot-start to activate DNA polymerase.

Protocol: PCR Amplification from Buccal Swab Lysates

This protocol is for direct PCR amplification of STR loci from crude lysates of buccal swabs using the Investigator ESSplex SE GO! Kit.

Important points before starting

- Set up all reaction mixtures in an area separate from that used for DNA isolation and PCR product analysis (post-PCR).
- Use disposable tips containing hydrophobic filters to minimize cross-contamination risks.

Things to do before starting

- Before opening the tubes containing PCR components, vortex and then centrifuge briefly to collect the contents at the bottom of the tubes.

Procedure

1. **Place the swab in a 2 ml microcentrifuge tube.**
   Carefully cut, break off, or eject the end part of the swab.

   Note: Prepare a blank swab as negative control.
2. **Add 500 µl of STR GO! Lysis Buffer to the sample.**
3. **Incubate at room temperature for 5 min with shaking at 1200 rpm in a thermomixer.**
   Optional: For challenging samples results may be improved by incubating at 95°C with shaking at 1200 rpm.
4. **Prepare a master mix according to Table 6.**
   As some loss of reagents can occur during transfers, prepare the mix with additional reactions included. Also include positive and negative control reactions. The master mix contains all of the components needed for PCR except the template (sample) DNA.
5. **Mix the reaction mix thoroughly, and dispense 25 µl into PCR tubes or the well of a PCR plate.**
6. **Transfer 2 µl of swab lysate to each reaction.**
7. **Prepare positive and negative controls.**
   Positive control: Use 1 µl Control DNA (i.e., 5 ng).

   Note: Amounts of Control DNA may have to be adapted after setting optimal PCR cycle number in your laboratory if signals are too low or too high.

Negative control: Use a blank swab lysate.

8. **Program the thermal cycler according to the manufacturer's instructions, using the conditions given in Table 7.**

   Note: If using the GeneAmp 9700 thermal cycler with an Aluminum block, use "Std Mode", or with a Silver block or Gold-plated Silver block, use "Max Mode". Do not use "9600 Emulation Mode".

9. **After the cycling protocol is completed, store samples at –30 to –15°C protected from the light, or proceed directly with running the electrophoresis.**

Table 6. Master Mix setup

Component	Volume per reaction
Fast Reaction Mix	7.5 µl
Primer Mix	17.5 µl
Total volume	**25 µl**

Table 7. Cycling protocol for buccal swab lysates

Temperature	Time	Number of cycles
95°C*	8 min	–
96°C 61°C	10 s 38 s	28
68°C	1 min	–
10°C	∞	–

* Hot-start to activate DNA polymerase.

Protocol: Electrophoresis Using the ABI PRISM 310 Genetic Analyzer

For general instructions on instrument setup, matrix generation, and application of the GeneScan® or GeneMapper® *ID* Software, refer to the *ABI PRISM 310 Genetic Analyzer User's Manual*. Electrophoresis using the GeneScan Software is described below.

The virtual filter set G5 is used for combined application of the 5 fluorescent labels 6-FAM, BTG, BTY, BTR, and BTO. This matrix standard is known as BT5.

The materials required for electrophoresis are given in Table 8.

Table 8. Materials required for electrophoresis

Material	Specifications
Capillary	47 cm/50 µm (green)
Polymer	POP-4™ for ABI PRISM 310 Genetic Analyzer
Buffer	10x Genetic Analyzer Buffer with EDTA

Matrix generation

Before conducting DNA fragment size analysis with the filter set G5, a matrix with the 5 fluorescent labels 6-FAM, BTG, BTY, BTR, and BTO must be generated (Table 9).

Table 9. The 5 fluorescent labels of BT5

Color	Matrix standard
Blue (B)	6-FAM
Green (G)	BTG
Yellow (Y)	BTY
Red (R)	BTR
Orange (O)	BTO

1. **Five electrophoresis runs should be conducted, one for each fluorescent label, under the same conditions as for the samples and allelic ladders of the Investigator ESSplex SE GO! Kit, in order to generate suitable matrix files (Table 10).**

Table 10. Matrix setup for a single capillary instrument (ABI PRISM 310 Genetic Analyzer)

Matrix sample	Component	Volume
Matrix sample 1	Hi-Di Formamide	12.0 µl
	Matrix standard 6-FAM	1.0 µl
Matrix sample 2	Hi-Di Formamide	12.0 µl
	Matrix standard BTG	1.0 µl
Matrix sample 3	Hi-Di Formamide	12.0 µl
	Matrix standard BTY	1.0 µl
Matrix sample 4	Hi-Di Formamide	12.0 µl
	Matrix standard BTR	1.0 µl
Matrix sample 5	Hi-Di Formamide	12.0 µl
	Matrix standard BTO	1.0 µl

2. **Denature for 3 min at 95°C.**
3. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.
4. **Load the samples on the tray.**
5. **Create a Sample Sheet and enter the sample designation. Table 11 shows the injection list for the matrix generation.**

Table 11. Injection list for matrix generation

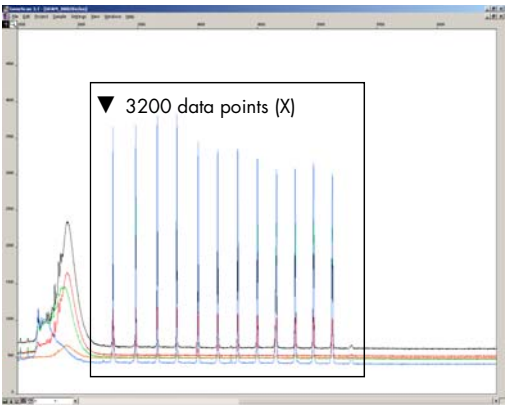
Parameter	Settings
Module File	GS STR POP-4 (1 ml) G5
Matrix File	None
Size Standard	None*
Injection Time (s)	5
Injection Voltage (kV)	15
Run Voltage (kV)	15
Run Temperature (°C)	60
Run Time (min)	24

* Always prepare matrix standards without DNA Size Standard (BTO).

Procedure

1. **Run the GeneScan Software.**
2. **Select "New" from the File menu, and then select "Project".**
3. **Open the folder of the current run and select "Add Sample Files".**
4. **Select a matrix sample in the "Sample File" column.**
5. **Click "Sample" and then "Raw Data".**
6. **Check the matrix samples for a flat baseline. As shown in the figure (next page), there should be at least 5 peaks with peak heights of 1000–4000 RFU for each matrix sample.**

   Note: The optimal range is 2000–4000 RFU.

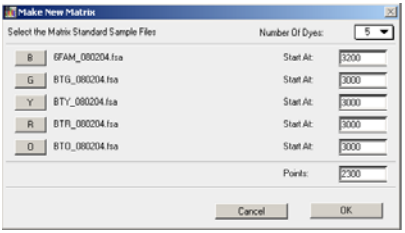


Electropherogram with raw data of the matrix standard 6-FAM.

7. **Select an analysis range with a flat baseline and re-inject the matrix sample, if necessary.**
8. **Record start and end value (data points) of the analysis range; e.g., start value 3200, end value 5500.**
9. **Calculate the difference between the end and start values; e.g., 5500–3200=2300 data points.**

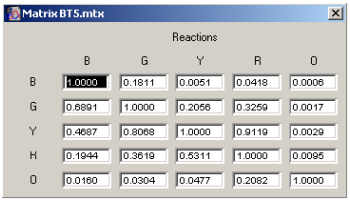
Generation of a matrix

1. **Select "New" in the File menu, and then select "Matrix".**
2. **Import the matrix samples for all dyes (B, G, Y, R, and O).**
3. **Enter a "Start At" value, e.g., 3200.**
4. **Under "Points", enter the calculated difference between end and start values, e.g., 2300.**
5. **Click "OK" to calculate the new matrix.**



Matrix sample selection.

6. **Select "Save as" in the File menu to save the new matrix in the matrix folder.**



New matrix BT5.

Checking the matrix

1. **To check the new matrix with current samples, select "New" in the File menu, and then select "Project".**
2. **Open the folder of the respective run and select "Add Sample Files".**
3. **Select the sample(s) in the Sample File column.**
4. **Click "Sample" and then "Install New Matrix" to open the matrix folder and select the new matrix.**
5. **Re-analyze the samples.**

   Note: There should be no pull-up peaks between the dye panels (B, G, Y, R, O) with the new matrix.

Sample preparation

1. **Set up a mixture of formamide and DNA size standard according to Table 12.**

Table 12. Setup of formamide and DNA size standard mixture

Component	Volume per sample
Hi-Di Formamide	12.0 µl
DNA Size Standard 550 (BTO)	0.5 µl

2. **Aliquot 12 µl of the mixture to a tube for each sample to be analyzed.**
3. **Add 1 µl PCR product or allelic ladder (diluted, if necessary).**
4. **Denature for 3 min at 95°C.**
5. **Snap freeze by placing the plate on ice for 3 min.**

   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.

6. **Load the samples on the tray.**

Setting up the GeneScan Software

Create a Sample Sheet and enter sample designation.

Table 13. Injection list for ABI PRISM 310 Genetic Analyzer

Component	Settings
Module File	GS STR POP-4 (1 ml) G5
Matrix File	e.g., Matrix BT5
Size Standard	e.g., SST-BTO_60-500bp
Injection Time (s)	5*
Injection Voltage (kV)	15
Run Voltage (kV)	15
Run Temperature (°C)	60
Run Time (min)	28†

* Deviating from standard settings, the injection time may range between 1 and 10 s depending on the type of sample. If samples with very high signal intensities are recorded, a shorter injection time may be selected. For samples with low DNA content, an injection time up to 10 s may be necessary.

† D he run time for Investigator ESSplex SE GO! was modified in order to be able to analyze fragments with lengths of up to 500 bp.

Analysis parameters

Table 14 lists the recommended analysis parameters.

Table 14. Recommended analysis parameters for the ABI PRISM 310 Genetic Analyzer

Parameter	Settings
Analysis Range	Start: 2000 Stop: 10,000
Data Processing	Baseline: Checked Multi-component: Checked Smooth options: Light
Peak Detection	Peak Amplitude Thresholds B:* Y:* G:* R:* O:* Min. Peak Half Width: 2 pts Polynomial Degree: 3 Peak Window Size: 11 pts†
Size Call Range	Min: 60 Max: 550
Size Calling Method	Local Southern Method
Split Peak Correction	None

* The peak amplitude threshold (cutoff value) corresponds to the minimum peak height that will be detected by the GeneScan or GeneMapper *ID* Software. Thresholds are usually 50–200 RFU and should be determined individually by the laboratory. Recommendation: The minimal peak height should be 3-times as high as the background noise of the baseline.

† Only the setting for Peak Window Size is different to defaults from Applied Biosystems for HID analysis.

Note: For information on the use of the recommended Template Files (as analysis parameters), refer to the appropriate Investigator Template Files User Guide (Genotyper®, GeneMapper *ID*, or GeneMapper *ID-X*).

Protocol: Electrophoresis using the ABI PRISM 3100-*Avant*/3100 Genetic Analyzer

For detailed instructions on instrument setup, spectral calibration, application of the ABI PRISM 3100 Data Collection software version 1.01 or 1.1 and the GeneScan software, refer to the *ABI PRISM 3100*-Avant*/3100 Genetic Analyzer User's Manual*.

The system with 4 capillaries is the ABI PRISM 3100-*Avant* Genetic Analyzer and the system with 16 capillaries is the ABI PRISM 3100 Genetic Analyzer.

The virtual filter set G5 is used for combined application of the 5 fluorescent labels 6-FAM, BTG, BTY, BTR, and BTO. This matrix standard is known as BT5.

The materials required for electrophoresis are given in Table 15.

Table 15. Materials required for electrophoresis

Material	Specifications
Capillary	36 cm Capillary Array for ABI PRISM 3100-*Avant*/3100 Genetic Analyzer
Polymer	POP-4 Polymer for ABI PRISM 3100-*Avant*/3100 Genetic Analyzer
Buffer	10x Genetic Analyzer Buffer with EDTA

Spectral calibration/matrix generation

Proper spectral calibration is critical for evaluation of multicolor systems with the ABI PRISM 3100/3100-*Avant* Genetic Analyzer and should be done before conducting fragment length analysis. The calibration procedure creates a matrix which is used to correct the overlapping of fluorescence emission spectra of the dyes.

Spectral calibration comprises the following steps:

- Preparation of the spectral calibration standards
- Loading the standards to the 96-well reaction plate (one sample per capillary)
- Entering the plate composition
- Performing a spectral calibration run and checking the matrix

Preparing the spectral calibration standards

Example for 4 capillaries (ABI PRISM 3100-*Avant* Genetic Analyzer)

1. **Set up a mixture of formamide and Matrix Standard BT5 according to Table 16.**

Table 16. Setup of formamide and Matrix Standard BT5 mixture for 4 capillaries

Component	Volume
Hi-Di Formamide	60 µl
Matrix Standard BT5 multi cap.	5 µl

2. **Load 12 µl of the mixture to 96-well plate; e.g., positions A1–D1.**
3. **Denature for 3 min at 95°C.**
4. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.

Example for 16 capillaries (ABI PRISM 3100 Genetic Analyzer)

1. **Set up a mixture of formamide and Matrix Standard BT5 according to Table 17.**

Table 17. Setup of formamide and Matrix Standard BT5 mixture for 16 capillaries

Component	Volume
Hi-Di Formamide	204 µl
Matrix Standard BT5 multi cap.	17 µl

2. **Load 12 µl of the mixture to 96-well plate; e.g., positions A1–H1 and A2–H2.**
3. **Denature for 3 min at 95°C.**
4. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.

Performing a spectral calibration run

The parameter file for DyeSet*G5* must be modified once to achieve successful calibration with the Data Collection Software version 1.0.1 or 1.1.

Spectral parameter

1. **To change settings in the parameter file, go to the following path:**
   D:\AppliedBio\Support Files\Data Collection SupportFiles\CalibrationData\Spectral Calibration\ParamFiles
2. **Select "MtxSTD{Genescan_SetG5} to open the PAR file.**
3. **Change "Condition Bounds Range" to [1.0, 20.0].**
4. **If the calibration was unsuccessful, also change Sensitivity to 0.1 and Quality to 0.8.**
5. **Select "Save As" in the File menu and save the parameter file under a new name; e.g., MtxStd{Genescan_SetG5_BT5}.par.**

   Note: Always use this parameter file for spectral calibration runs using QIAGEN Matrix Standard BT5.

Plate Editor for spectral calibration

1. **Place the 96-well plate on the autosampler tray.**
2. **Run the ABI PRISM 3100 Data Collection Software.**
3. **In Plate View, click "New" to open the Plate Editor dialog box.**
4. **Enter a name for the plate.**
5. **Select a Spectral Calibration.**
6. **Select "96-Well" as plate type, and click "Finish".**

Table 18. Plate Editor for spectral calibration

Parameter	Settings
Sample Name	Enter name for the matrix samples
Dye Set	*G5*
Spectral Run Module	Default (e.g., Spect36_POP4)
Spectral Parameters	MtxStd{GeneScan_SetG5_BT5}.par (parameters created before)

7. **Click the column header to select the entire column, and select "Fill Down" from the Edit menu to apply the information to the selected samples. Confirm by clicking "OK".**
8. **Link the reaction plate on the autosampler tray with the created plate ID and start the run.**
9. **Upon completion of the run, check in the Spectral Calibration Result dialog box that all capillaries have successfully passed calibration (label A).**
   If individual capillaries are labeled X, refer to the *ABI PRISM 3100-*Avant*/3100 Genetic Analyzer User's Manual.*
10. **Click "OK" to confirm completion of the run.**

Checking the matrix

1. **Select "Display Spectral Calibration" from the Tools menu, then "Dye Set" and "G5" to review the spectral calibration profile for each capillary.**
2. **The quality value (Q value) must be greater than 0.95 and the condition number (C value) must be between 1 and 20. Both values must be within the predetermined range.**
3. **Check for a flat baseline in the matrix samples. There should be 5 peaks with heights of 1000–5000 RFU in each matrix sample.**
   Note: The optimal range is 2000–4000 RFU.
4. **Check the new matrix with the current samples. There should be no pull-up peaks between the dye panels (B, G, Y, R, and O) with the new matrix.**
5. **If the calibration failed, follow instructions in the section "Spectral parameter" on page 27.**
6. **If all capillaries have passed the calibration, the last calibration file for Dye Set G5 must be activated manually. Click "Set Active Spectral Calibration" under the Tools menu.**
7. **Rename the calibration file under Set Matrix Name (e.g., BT5_Date of calibration).**

Sample preparation

1. **Set up a mixture of formamide and DNA size standard according to Table 19.**

Table 19. Setup of formamide and DNA size standard mixture

Component	Volume per sample
Hi-Di Formamide	12 µl
DNA Size Standard 550 (BTO)	0.5 µl

2. **Aliquot 12 µl of the mixture to a tube for each sample to be analyzed.**
3. **Add 1 µl PCR product or allelic ladder (diluted, if necessary).**
4. **Denature for 3 min at 95°C.**
5. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.
6. **Load the samples on the tray.**

Since injections take place simultaneously on all capillaries, 4 or 16 samples must be pipetted onto the plate of multi-capillary analyzers. If fewer samples are analyzed, the empty positions must be filled with 12 µl Hi-Di Formamide.

To ensure a reliable allelic assignment on multi-capillary analyzers, several ladders should be run.

Room temperature may influence the performance of PCR products on multi-capillary instruments, so that shoulder peaks or split peaks occur especially at low temperatures. Ensure ambient conditions are kept as recommended by the instrument manufacturer.

Setting up the GeneScan Software

1. **Edit the default run module in Dye Set G5 once for the first run. Select "Module Editor" to open the dialog box.**
2. **Select the appropriate Run Module as template from the GeneScan table (see Table 20).**
3. **Modify the Injection Voltage to 3 kV and the Injection Time to 10 s.**
4. **Click "Save As" and enter the name of the new module (e.g., 3kV_10s_500bp). Confirm by clicking "OK".**
5. **Click "Close" to exit the Run Module Editor.**

Table 20. Run Module 3kV_10s_500bp for ABI PRISM 3100-*Avant*/3100 Genetic Analyzer

Parameter	Setting
Run Temperature (°C)	Default
Cap Fill Volume	Default
Maximum Current (A)	Default
Current Tolerance (A)	Default
Run Current (A)	Default
Voltage Tolerance (kV)	Default
Pre-Run Voltage (kV)	Default
Pre-Run Time (s)	Default
Injection Voltage (kV)	3.0
Injection Time (s)	10*
Run Voltage (kV)	Default
Number of Steps	Default
Voltage Step Interval	Default
Data Delay Time (s)	Default
Run Time (min)	26†

* Deviating from the standard settings, the injection time may range between 1 and 20 s depending on the type of sample. If samples with very high signal intensities are recorded, a shorter injection time may be selected. For samples with low DNA content, an injection time of up to 20 s may be necessary.

† The run time for Investigator ESSplex SE GO! was modified in order to be able to analyze fragments with lengths of up to 500 bp.

Starting the run

1. **Place the prepared 96-well plate on the autosampler tray.**
2. **Run the ABI PRISM 3100 Data Collection Software.**
3. **In Plate View, click "New" to open the Plate Editor dialog box.**
4. **Enter a name for the plate.**
5. **Select "GeneScan" as the application type.**

6. **Select "96-Well" as plate type, and click "Finish".**

Table 21. Settings in Plate Editor

Parameter	Settings
Sample Name	Enter name for the matrix samples
Dyes	O
Color Info	Ladder or sample
Project Name	e.g., 3100_Project1
Dye Set	G5
Run Module	3kV_10s_500bp*
Analysis Module 1	DefaultAnalysis.gsp

* See Table 20, "Run Module 3kV_10s_500bp for ABI PRISM 3100-*Avant*/3100 Genetic Analyzer".

7. **Complete the table in the Plate Editor and click "OK".**
8. **Click the column header to highlight the entire column and select "Fill Down" from the Edit menu to apply the information to the selected samples.**
9. **Link the reaction plate on the autosampler tray to the created plate ID and start the run.**
10. **Upon completion of the run, view the data as Color Data in the Array View of the 3100 Data Collection Software or as Analyzed Sample Files under D:/AppliedBio/3100/DataExtractor/ExtractRuns.**

Analysis parameters

Table 22 lists the recommended analysis parameters.

Table 22. Recommended analysis parameters for the ABI PRISM 3100-*Avant*/3100 Genetic Analyzer

Parameter	Settings
Analysis Range	Start: 2000 Stop: 10,000
Data Processing	Baseline: Checked Multi-component: Checked Smooth options: Light
Peak Detection	Peak Amplitude Thresholds B:* Y:* G:* R:* O:* Min. Peak Half Width: 2 pts Polynomial Degree: 3 Peak Window Size: 11 pts†
Size Call Range	Min: 60 Max: 550
Size Calling Method	Local Southern Method
Split Peak Correction	None

* The peak amplitude threshold (cutoff value) corresponds to the minimum peak height that will be detected by the GeneScan or GeneMapper *ID* Software. Thresholds are usually 50–200 RFU and should be determined individually by the laboratory. Recommendation: The minimal peak height should be 3-times higher than the background noise of the baseline.

† Only the setting for Peak Window Size is different to defaults from Applied Biosystems for HID analysis.

Note: For information on the use of the recommended Template Files (as analysis parameters), refer to the appropriate Investigator Template Files User Guide (Genotyper, GeneMapper *ID*, or GeneMapper *ID-X*).

Protocol: Electrophoresis Using the Applied Biosystems 3130/3130*x*/Genetic Analyzer

For detailed instructions on instrument setup, spectral calibration, or application of the ABI PRISM Data Collection Software version 3.0 and the GeneMapper *ID* Software, refer to the *Applied Biosystems 3130/3130*xl *Genetic Analyzers Getting Started Guide*.

The system with 4 capillaries is the Applied Biosystems 3130 Genetic Analyzer and the system with 16 capillaries is the Applied Biosystems 3130*x*/Genetic Analyzer.

The virtual filter set Any5Dye is used for combined application of the 5 fluorescent labels 6-FAM, BTG, BTY, BTR, and BTO. This matrix standard is known as BT5.

The materials required for electrophoresis are given in Table 23.

Table 23. Materials required for electrophoresis

Material	Specifications
Capillary	36 cm Capillary Array for Applied Biosystems 3130/3130*x*/Genetic Analyzer
Polymer	POP-4 Polymer for Applied Biosystems 3130/3130*x*/ Genetic Analyzer
Buffer	10x Genetic Analyzer Buffer with EDTA

Spectral calibration/matrix generation

Before conducting DNA fragment size analysis, it is necessary to perform a spectral calibration with the 5 fluorescent labels 6-FAM, BTG, BTY, BTR, and BTO for each analyzer. The calibration procedure creates a matrix which is used to correct the overlapping of fluorescence emission spectra of the dyes.

Spectral calibration is comprised of the following steps:

- Preparation of the spectral calibration standards
- Loading the standards to the 96-well reaction plate (one sample per capillary)
- Creating the instrument protocol for spectral calibration (Protocol Manager)
- Defining the plate composition in the plate editor (Plate Manager)

■ Performing a spectral calibration run and checking the matrix

Preparing the spectral calibration standards

Example for 4 capillaries (Applied Biosystems 3130 Genetic Analyzer)

1. **Set up a mixture of formamide and Matrix Standard BT5 according to Table 24.**

Table 24. Setup of formamide and Matrix Standard BT5 mixture for 4 capillaries

Component	Volume
Hi-Di Formamide	60 µl
Matrix Standard BT5 multi cap.	5 µl

2. **Load 12 µl of the mixture into each of the 4 wells in a 96-well plate, e.g., positions A1–D1.**
3. **Denature for 3 min at 95°C.**
4. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.

Example for 16 capillaries (Applied Biosystems 3130*x*/Genetic Analyzer)

1. **Set up a mixture of formamide and Matrix Standard BT5 according to Table 25.**

Table 25. Setup of formamide and Matrix Standard BT5 mixture for 16 capillaries

Component	Volume
Hi-Di Formamide	204 µl
Matrix Standard BT5 multi cap.	17 µl

2. **Load 12 µl of the mixture into each of the 16 wells in a 96-well plate, e.g., positions A1–H1 and A2–H2.**
3. **Denature for 3 min at 95°C.**
4. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.

Performing spectral calibration run

1. **Place the 96-well plate on the autosampler tray.**
2. **In the Protocol Manager of the Data Collection Software, open the Instrument Protocol window.**
3. **Click "New" to open the Protocol Editor dialog box.**
4. **Complete the dialog box with information from Table 26 and click "OK".**

Table 26. Instrument protocol for spectral calibration

Protocol Editor	Settings
Name	User (e.g., Spectral36_POP4_BT5)
Type	SPECTRAL
Dye Set	Any5Dye
Polymer	User (e.g., POP4)*
Array Length	User (e.g., 36cm)*
Chemistry	Matrix Standard
Run Module	Default (e.g., Spect36_POP4_1)*

* Depends on the type of polymer and length of capillary used.

5. **Click "New" in the Plate Manager of the Data Collection Software to open the New Plate Dialog box.**
6. **Enter information from Table 27 and click "OK". A new table in the Plate Editor opens automatically (Table 28).**

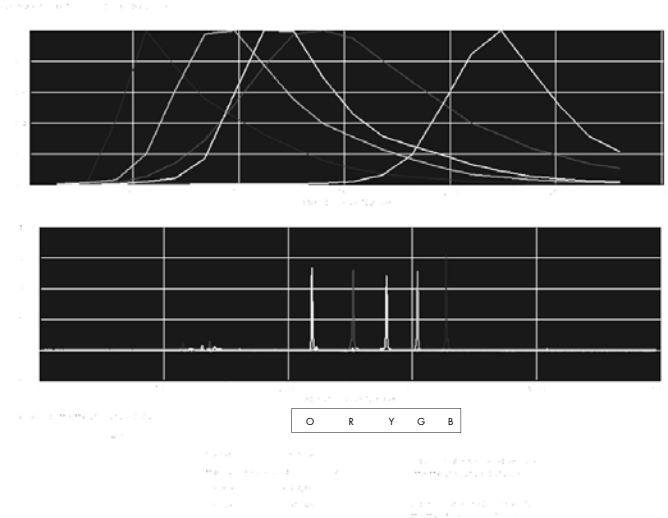
Table 27. Plate Editor for spectral calibration (I)

New plate dialog	Settings
Name	e.g., Spectral_BT5_date
Application	Spectral Calibration
Plate Type	96-well
Owner Name/ Operator Name	…

Table 28. Plate Editor for spectral calibration (II)

Parameter	Settings
Sample Name	Enter name for the matrix samples
Priority	e.g., 100
Instrument Protocol 1	Spectral36_POP4_BT5 (setting described before)

7. **Click the column header to select the entire column, and select "Fill Down" from the Edit menu to apply the information to the selected samples. Confirm by clicking "OK".**
8. **Link the reaction plate on the autosampler tray with the created plate ID (position A or B) and start the run.**



Electropherogram of spectral calibration with matrix standard BT5 on an Applied Biosystems 3130 Genetic Analyzer.

Checking the matrix

1. **The quality value (Q value) of each capillary must be greater than 0.95 and the condition number range (C value) must be between 1 and 20.**
2. **Check for a flat baseline in the matrix samples. As shown in the figure on the previous page, there should be 5 peaks with peak heights of about 1000–5000 RFU in each matrix sample.**

   Note: The optimal range is 2000–4000 RFU.
3. **Check the new matrix with the current samples. There should be no pull-up peaks between the dye panels (B, G, Y, R, O) with the new matrix.**
4. **If calibration failed, use the optimized values of the Matrix Standard BT5 and repeat the calibration run.**
5. **If all capillaries have passed the test, the last calibration file for the Dye Set Any5Dye is activated automatically in the Spectral Viewer. Rename the calibration file (e.g., BT5_Date of calibration).**

Sample preparation

1. **Set up a mixture of formamide and DNA size standard according to Table 29.**

Table 29. Setup of formamide and DNA size standard mixture

Component	Volume per sample
Hi-Di Formamide	12.0 µl
DNA Size Standard 550 (BTO)	0.5 µl

2. **Aliquot 12 µl of the mixture to a tube for each sample to be analyzed.**
3. **Add 1 µl PCR product or allelic ladder (diluted, if necessary).**
4. **Denature for 3 min at 95°C.**
5. **Snap freeze by placing the plate on ice for 3 min.**

   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.
6. **Load the samples on the tray.**

Since injections take place simultaneously on all capillaries, 4 or 16 samples must be pipetted onto the plate of multi-capillary analyzers. If fewer samples are analyzed, the empty positions must be filled with 12 µl Hi-Di Formamide.

To ensure a reliable allelic assignment on multi-capillary analyzers, several ladders should be run.

Room temperature may influence the performance of PCR products on multi-capillary instruments, so that shoulder peaks or split peaks occur especially at low temperatures. Ensure ambient conditions are kept, as recommended by the instrument manufacturer.

Setting up the Data Collection Software

1. **Edit the Run Module once for the first run. In the Module Manager of the Data Collection Software, click "New" to open the Run Module Editor dialog box.**

   Note: Modify the Run Module Default settings from "HIDFragmentAnalysis36_POP4_1" to those shown in Table 30.

2. **Modify the Injection Voltage to 3 kV and the Injection Time to 10 s (Table 30).**
3. **Click "Save As", enter a name for the new Run Module (e.g., 3kV_10s_500bp), and confirm by clicking "OK".**
4. **Click "Close" to exit the Run Module Editor.**

Table 30. Run Module 3kV_10s_500bp for Applied Biosystems 3130/3130*x*/ Genetic Analyzer

Parameter	Settings
Oven Temperature (°C)	Default
Poly Fill Volume	Default
Current Stability (µA)	Default
Pre-Run Voltage (kV)	Default
Pre-Run Time (s)	Default
Injection Voltage (kV)	3.0
Injection Time (s)	10*
Voltage Number of Steps	Default
Voltage Step Interval	Default
Data Delay Time (s)	Default
Run Voltage (kV)	Default
Run Time (s)	1560†

* Deviating from the standard settings, the injection time may range between 1 and 20 s depending on the type of sample. If samples with very high signal intensities are recorded, a shorter injection time may be selected. For samples with low DNA content, an injection time of up to 20 s may be necessary.

† The run time for Investigator ESSplex SE GO! was modified in order to be able to analyze fragments with lengths of up to 500 bp.

Starting the run

1. **Place the prepared 96-well plate on the autosampler tray.**
2. **Open the Protocol Manager of the Data Collection Software.**
3. **Click "New" in the Instrument Protocol window to open the Protocol Editor dialog box and enter the information in Table 31.**
4. **Click "OK" to exit the Protocol Editor.**

Table 31. Settings in Instrument Protocol

Protocol Editor	Settings
Name	Run36_POP4_BT5_26min
Type	REGULAR
Run Module	3kV_10s_500bp*
Dye Set	Any5Dye

* See Table 30, "Run Module 3kV_10s_500bp for for Applied Biosystems 3130/3130*x*/ Genetic Analyzer".

5. **Before each run, it is necessary to create a plate definition. In the Plate Manager of the Data Collection Software, click "New" to open the New Plate Dialog box.**
6. **Enter the information in Table 32.**

Table 32. GeneMapper Plate Editor (I)

Protocol Editor	Settings
Name	e.g., Plate_BT5_Date
Application	Select GeneMapper Application
Plate type	96-Well
Owner Name/ Operator Name	…

7. **Click "OK" and a new table in the Plate Editor opens automatically (Table 33).**
8. **Click the column header to select the entire column. Select "Fill Down" from the Edit menu to apply the information to all selected samples. Click "OK".**
9. **In the Run Scheduler, click "Find All", and select "Link" to link the reaction plate on the autosampler tray to the newly created plate record (position A or B).**

Table 33. GeneMapper Plate Editor (II)

Parameter	Settings
Sample Name	Enter the name for the samples
Priority	e.g., 100 (Default)
Sample Type	Sample or Allelic Ladder
Size Standard	e.g., SST-BTO_60-500bp
Panel	e.g., ESSplex SE Plus Panels
Analysis Method	e.g., Analysis_HID_3130
Snp Set	–
User-defined 1-3	–
Results Group 1	(Select results group)
Instrument Protocol 1	Run36_POP4_BT5_26min (setting described before)

10. Start the run.

11. During the run, view Error Status in the Event Log or examine the quality of the raw data for each capillary in the Capillaries Viewer or the Cap/Array Viewer.

12. View data as an overview in Run History or Cap/Array Viewer of the Data Collection Software.

Run data are saved in the Run Folder of the previously chosen Result Group.

Analysis parameters/analysis method

Table 34 lists the recommended analysis parameters.

Table 34. Recommended settings for the Applied Biosystems 3130/3130*x*/ Genetic Analyzer

Parameter	Settings
Peak Detection Algorithm	Advanced
Ranges	Analysis: Partial Range Start Point: 2000; Stop Point: 10,000 Sizing: All Sizes
Smoothing and Baselining	Smoothing: Light Baseline Window: 51 pts
Size Calling Method	Local Southern Method
Peak Detection	Peak Amplitude Thresholds B:* Y:* G:* R:* O:* Min. Peak Half Width: 2 pts Polynomial Degree: 3 Peak Window Size: 11 pts† Slope Thresholds: 0.0

* The peak amplitude threshold (cutoff value) corresponds to the minimum peak height that will be detected by the GeneMapper *ID* Software. The thresholds are usually 50–200 RFU and should be determined individually by the laboratory. Recommendation: The minimal peak height should be 3-times higher than the background noise of the baseline.

† Only the setting for Peak Window Size is different to defaults from Applied Biosystems for HID analysis.

Note: For information on the use of the recommended Template Files (as analysis parameters), refer to the appropriate Investigator Template Files User Guide (Genotyper, GeneMapper *ID*, or GeneMapper *ID-X*).

Protocol: Electrophoresis Using the Applied Biosystems 3500/3500xL Genetic Analyzer

This Investigator Kit is validated for use on the 3500/3500xL Genetic Analyzer, which requires the 3500 Data Collection Software v1 or v2 or HID Updater 3500 Data Collection v2.0 software.

Note: The user must be logged on to the PC as local administrator or with equivalent access rights to allow data to be written to the appropriate files.

For detailed instructions on instrument setup, spectral calibration, or application of the Applied Biosystems 3500 Series Data Collection Software version 1.0 and the GeneMapper *ID-X* Software version 1.2, refer to the *Applied Biosystems 3500/3500xL Genetic Analyzers User Guide*.

The system with 8 capillaries is the Applied Biosystems 3500 Genetic Analyzer and the system with 24 capillaries is the Applied Biosystems 3500xL Genetic Analyzer.

The virtual filter set AnyDye is used for combined application of the 5 fluorescent labels 6-FAM, BTG, BTY, BTR, and BTO. This matrix standard is known as BT5.

The materials required for electrophoresis are given in Table 35.

Table 35. Materials required for electrophoresis

Material	Specifications
Capillary	36 cm Array for Applied Biosystems 3500/3500xL Genetic Analyzer
Polymer	POP-4 for Applied Biosystems 3500/3500xL Genetic Analyzer
Buffer	Anode Buffer Container (ABC) 3500 Series Cathode Buffer Container (CBC) 3500 Series

Spectral calibration/matrix generation

Before conducting DNA fragment size analysis, it is necessary to perform a spectral calibration with the 5 fluorescent labels 6-FAM, BTG, BTY, BTR, and BTO for each analyzer (Table 36). The calibration procedure creates a matrix which is used to correct the overlapping of fluorescence emission spectra of the dyes.

IMPORTANT: Spectral calibration must be performed for each new capillary array.

Spectral calibration comprises the following steps:

- Preparation of the instrument
- Preparation of the standard calibration plate
- Plate assembly and loading the plate in the instrument
- Software set up of dye set BT5
- Performing a spectral calibration run
- Checking the matrix

Preparation of the instrument

Before the spectral calibration process, ensure that the spatial calibration has been performed. This process is described in detail in the *Applied Biosystems 3500/3500xL Genetic Analyzers User Guide*.

Table 36. The 5 fluorescent labels of BT5

Color	Matrix standard
Blue (B)	6-FAM
Green (G)	BTG
Yellow (Y)	BTY
Red (R)	BTR
Orange (O)	BTO

Preparation of the standard calibration plate

Example for 8 capillaries (Applied Biosystems 3500 Genetic Analyzer)

1. **Set up a mixture of formamide and Matrix Standard BT5 according to Table 37.**

Table 37. Setup of formamide and Matrix Standard BT5 mixture for 8 capillaries

Component	Volume
Hi-Di Formamide	90 µl
Matrix Standard BT5 multi cap.	10 µl

2. **Load 10 µl of the mixture into each of the 8 wells in a 96-well plate, e.g., positions A1–H1.**
3. **Denature for 3 min at 95°C.**
4. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.

Example for 24 capillaries (Applied Biosystems 3500xL Genetic Analyzer)

1. **Set up a mixture of formamide and Matrix Standard BT5 according to Table 38.**

Table 38. Setup of formamide and Matrix Standard BT5 mixture for 24 capillaries

Component	Volume
Hi-Di Formamide	225 µl
Matrix Standard BT5 multi cap.	25 µl

2. **Load 10 µl of the mixture into each of the 24 wells in a 96-well plate, e.g., positions A1–H1, A2–H2, and A3–H3.**
3. **Denature for 3 min at 95°C.**
4. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.

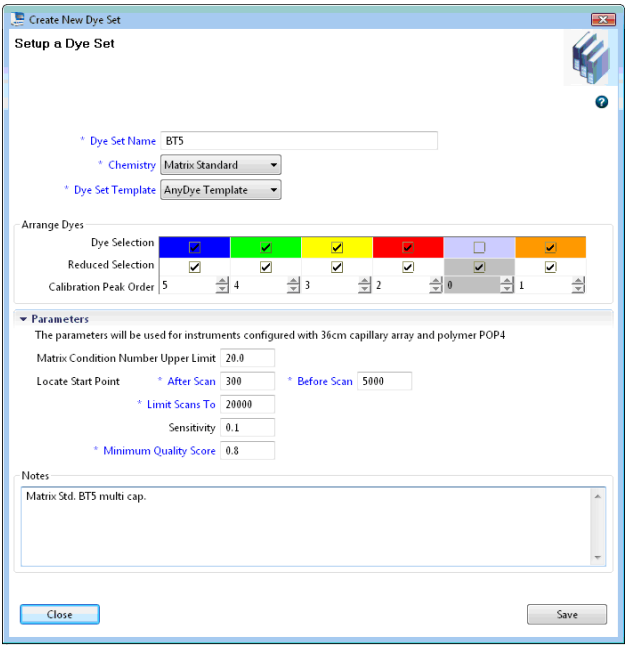
Plate assembly and loading the plate in the instrument

The necessary steps are described in detail in the *Applied Biosystems 3500/3500xL Genetic Analyzers User Guide*.

Software setup of dye set BT5

Prior to the spectral calibration, a dye set for the Matrix Standard BT5 must be set up.

1. **To create a new dye set, go to "Library" and select "Analyze", followed by "Dye Sets" and click "Create".**
2. **Enter a "Dye Set Name", e.g., BT5.**
3. **Select "Matrix Standard" as a chemistry and "AnyDye Template" as a dye set template.**
4. **Disable "Purple" in the field "Arrange Dyes". Ensure that all other colors are enabled.**
5. **Under "Calibration Peak Order" the colors need to be arranged as follows: 5 – blue, 4 – green, 3 – yellow, 2 – red, and 1 – orange.**
6. **Do not alter the "Parameter" settings.**
7. **Click "Save" to confirm the changes.**



Setup of dye set BT5.

Performing a spectral calibration run

Once the multiwell plates containing the spectral calibration mixture are placed in the autosampler tray, the spectral calibration process can be started.

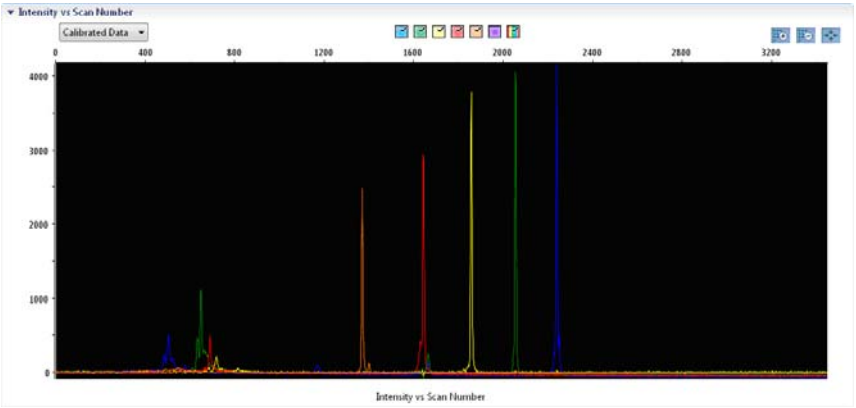
1. **To access the Spectral Calibration screen, select "Maintenance" on the Dashboard of the 3500 Series Data Collection software.**

2. **The number of wells in the spectral calibration plate and their location in the instrument must be specified.**
3. **Select "Matrix Standard" as a chemistry standard and "BT5" for Dye Set Name.**
4. **(Optional) Enable "Allow Borrowing".**
5. **Click "Start Run".**

Checking the matrix

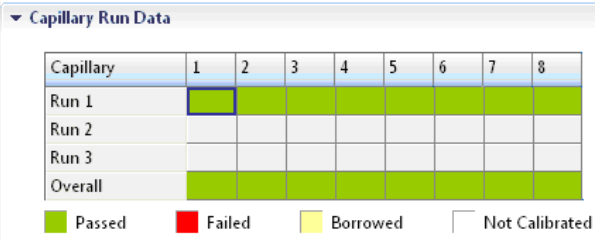
Click a capillary in the table in order to display the results for each capillary (spectral data, Quality value, and Condition Number) below the run results table.

- The quality value (Q value) of each capillary must be greater than 0.8 and the number range (C value) must be between 1 and 20.
- Check the matrix samples for a flat baseline. As shown in the figure, there should be 5 peaks with peak heights of about 1000–5000 RFU for each matrix sample (Note: The optimal range is 2000–4000 RFU).



Electropherogram of spectral calibration of the matrix standard BT5 on an Applied Biosystems 3500 Genetic Analyzer.

When a spectral calibration is successfully completed, the "Overall" row displays green results. If the "Overall" row displays red results, refer to the "spectral calibration troubleshooting" section of the *Applied Biosystems 3500/3500xL Genetic Analyzers User Guide*.



Example of successful spectral calibration of the matrix standard BT5 for all capillaries on an Applied Biosystems 3500 Genetic Analyzer.

For each capillary, select and display the spectral and raw data. Check that the data meet the following criteria:

- The order of the peaks in the spectral profile from left to right read orange-red-yellow-green-blue
- No extraneous peaks appear in the raw data profile
- Peak morphology in the spectral profile shows no gross overlaps, dips, or other irregularities. Separate and distinct peaks should be visible

If the data for all capillaries meet the criteria above, click "Accept Results". If any capillary data does not meet the criteria above, click "Reject Results", and refer to the "spectral calibration troubleshooting" section of the *Applied Biosystems 3500/3500xL Genetic Analyzers User Guide*.

Sample preparation

1. **Set up a mixture of formamide and DNA size standard according to Table 39.**

Table 39. Setup of formamide and DNA size standard mixture

Component	Volume per sample
Hi-Di Formamide	12.0 µl
DNA Size Standard 550 (BTO)	0.5 µl

2. **Aliquot 12 µl of the mixture to a tube for each sample to be analyzed.**
3. **Add 1 µl PCR product or allelic ladder (diluted, if necessary).**
4. **Denature for 3 min at 95°C.**

5. **Snap freeze by placing the plate on ice for 3 min.**
   Alternatively, the thermal cycler set to 4°C may be used to cool the plate.
6. **Load the samples on the tray.**

Since injections take place simultaneously on all capillaries, 8 or 24 samples must be pipetted onto the plate of multi-capillary analyzers. If fewer samples are analyzed, the empty positions must be filled with 12 µl Hi-Di Formamide.

To ensure a reliable allelic assignment on multi-capillary analyzers, inject one allelic ladder for each set of 24 samples:

- 8-capillary instruments: One allelic ladder per 3 injections
- 24-capillary instruments: One allelic ladder per 1 injection

Important: The actual room temperature may influence the performance of PCR products on multi-capillary instruments, so shoulder peaks or split peaks may occur, especially at lower temperatures. **Ensure that ambient conditions are maintained as recommended by the instrument manufacturer.** Also ensure buffers are equilibrated to ambient conditions.

Setting up a run

If you are using the Investigator ESSplex SE GO! Kit for the first time on an Applied Biosystems 3500 Genetic Analyzer, you will first need to set up a number of protocols:

- Instrument Protocol
- Size Standard
- QC Protocol
- Assay

All protocols can be set up via the Dashboard of the 3500 Series Data Collection software.

1. **To set up the Instrument Protocol, go to "Library" and select "Analyze", followed by "Instrument Protocols" and click "Create".**
   Note: Modify the Run Module Default settings from "HID36_POP4" as shown in Table 40.
2. **The parameters in Table 40 must be entered or selected.**

Table 40. Instrument Protocol parameters for Applied Biosystems 3500/3500xL Genetic Analyzer

Parameter	Setting
Application Type	HID
Capillary Length	36 cm
Polymer	POP4
Dye Set	e.g., BT5
Run Module	HID36_POP4
Protocol Name	e.g., Investigator ESSplex SE GO!
Oven Temperature (°C)	Default
Run Voltage (kV)	Default
PreRun Voltage (kV)	Default
Injection Voltage (kV)	3.0
Run Time (s)	1300
PreRun Time (s)	Default
Injection Time (s)	8.0*
Data Delay (s)	Default
Advanced Options	Default

* Deviating from the standard settings, the injection time may range between 1 and 20 s depending on the type of sample. If samples with very high signal intensities are recorded, a shorter injection time may be selected. For samples with low DNA content, an injection time of up to 20 s may be necessary.

3. **Click "Save" to confirm the changes.**
4. **To set up the Size Standard, go to "Library", select "Analyze", followed by "Size Standards", and click "Create".**
5. **The parameters in Table 41 must be entered or selected.**

   The DNA Size Standard 550 (BTO) should be used with the following lengths of fragments: 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.

Table 41. Size standard parameters

Parameter	Setting
Size Standard	e.g., SST-BTO_60-500bp
Dye Color	Orange

6. **Click "Save" to confirm the changes.**
7. **To set up the QC Protocol, go to "Library" and select "Analyze", followed by "QC Protocols", and click "Create".**
8. **The parameters in Table 42 must be entered or selected.**

Table 42. QC Protocol parameters

Parameter	Setting
Protocol Name	e.g., BTO_550
Size Standard	SST-BTO_60-500bp (from Table 41)
Sizecaller	SizeCaller v1.1.0

9. **Go to "Analysis Settings", followed by "Peak Amplitude Threshold" and disable "Purple". Ensure that all other colors are enabled.**

   Check the recommended analysis settings in Table 45. All other settings should remain as "Default".
10. **Click "Save" to confirm the changes.**
11. **To set up an Assay, go to "Library" and select "Manage", followed by "Assays", and click "Create".**
12. **To analyze Investigator ESSplex SE GO! fragments, the parameters in Table 43 must be selected.**

Table 43. Assay parameters

Parameter	Setting
Assay Name	e.g., Investigator ESSplex SE GO!
Color	Default
Application Type	HID
Instrument Protocol	e.g., Investigator ESSplex SE GO! (from Table 40)
QC Protocols	e.g., BTO_550 (from Table 42)

13. Click "Save" to confirm the changes.

Starting the run

1. **In the Dashboard, click "Create New Plate".**
2. **Go to "Define Plate Properties" and select "Plate Details". Select or enter the parameters in Table 44.**

Table 44. Plate properties

Property	Setting
Name	e.g., Investigator ESSplex SE GO!
Number of Wells	96
Plate Type	HID
Capillary Length	36 cm
Polymer	POP4

3. **Click "Assign Plate Contents" to confirm the changes.**
4. **Enter the designated sample name in each well containing a sample or allelic ladder. This will identify the well positions of each sample for the data collection and processing.**

5. **Choose the correct Assay for the analysis. If you followed the steps under "Setting up the Run", this would be Investigator ESSplex SE GO! from step 11. All named wells on the plate must have an assigned assay.**
6. **Select the wells for which to specify an assay. Check the box next to the assay name to assign it to the selected wells.**
7. **(Optional) Repeat for file name conventions and results group.**
8. **If not already done, load the assembled plate to the instrument and close the instrument door to re-initialize the instrument. Then click "Link Plate for Run". In the next screen, enter the desired Run Name and click "Start Run".**

Analysis parameters/analysis method

Table 45 lists the recommended analysis parameters in the worksheet Peak Detector.

Table 45. Recommended settings for the Applied Biosystems 3500/3500xL Genetic Analyzer

Parameter	Settings
Peak Detection Algorithm	Advanced
Ranges	Analysis: Partial Range Start Point: 1000; Stop Point: 20,000 Sizing: All Sizes
Smoothing and Baselining	Smoothing: Light Baseline Window: 51 pts
Size Calling Method	Local Southern Method
Peak Detection	Peak Amplitude Thresholds B:* Y:* G:* R:* O:* Min. Peak Half Width: 2 pts Polynomial Degree: 3 Peak Window Size: 11 pts† Slope Thresholds: 0.0

* The peak amplitude threshold (cutoff value) corresponds to the minimum peak height that will be detected by the GeneMapper *ID-X* Software. The thresholds are usually 50–200 RFU and should be determined individually by the laboratory. Recommendation: The minimal peak height should be three-times higher than the background noise of the baseline.

† Only the setting for Peak Window Size is different to defaults from Applied Biosystems for HID analysis.

Protocol: Analysis

For general instructions on automatic sample analysis, refer to the appropriate User Guides for GeneMapper ID-X, GeneMapper ID, or GeneScan Software.

Finding the exact lengths of the amplified products depends on the device type, the conditions of electrophoresis, as well as the DNA size standard used. Due to the complexity of some loci, determining the size should be based on evenly distributed references. The DNA Size Standard 550 (BTO) should be used with the following lengths of fragments: 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.

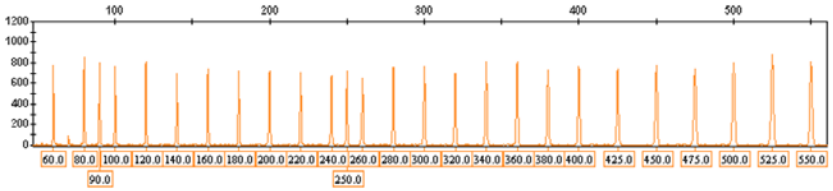


Figure 1. Electropherogram of the DNA Size Standard 550 (BTO), fragments with lengths in bp.

Analysis Software

Allele allocation should be carried out using suitable analysis software (e.g., GeneMapper ID-X, GeneMapper ID, or Genotyper Software) in combination with the Investigator Template Files available for download from www.qiagen.com; see Table 46 and Table 47.

The recommended Investigator Template File for Genotyper Software is the ESSplex SE.

Table 46. Recommended Investigator Template Files for GeneMapper *ID*

File type	File name
Panels	ESSplex SE Plus_Panels
BinSets	ESSplex SE Plus_Bins
Size standard	SST-BTO_60–500bp
Analysis Method	Analysis_HID_310 Analysis_HID_3130
Plot Settings	Plots_5dyes
Table Settings	Table for 2 alleles Table for 10 alleles

Panels and BinSets must always be used; other template files are optional.

Table 47. Recommended Investigator Template Files for GeneMapper *ID-X*

File type	File name
Panels	ESSplex SE Plus_Panels_x
BinSets	ESSplex SE Plus_Bins_x
Stutter	ESSplex SE Plus_Stutter_x
Size standard	SST-BTO_60–500bp
Analysis Method	Analysis_HID_310_200rfu Analysis_HID_3130_200rfu Analysis_HID_3500_200rfu
Plot Settings	Plots_5dyes
Table Settings	310 Data Analysis/31xx Data Analysis

Panels and BinSets must always be used; other template files are optional.

Controls

The alleles listed in Table 48 represent the Control DNA 9948 (included in the Investigator ESSplex SE GO! Kit) and DNA from other commercially available standard cell lines.

Table 48. Allele assignment of the Investigator ESSplex SE GO! Kit

Locus	CCR 9948	CCR 9947A	CCR 3657
Amelogenin	X/Y	X/X	X/Y
D1S1656	14/17	18.3/18.3	13/18.3
D2S441	11/12	10/14	14/14
D2S1338	23/23	19/23	18/22
D3S1358	15/17	14/15	16/18
D8S1179	12/13	13/13	15/16
D10S1248	12/15	13/15	14/16
D12S391	18/24	18/20	18/19
D16S539	11/11	11/12	13/13
D18S51	15/18	15/19	12/20
D19S433	13/14	14/15	13/14
D21S11	29/30	30/30	28/29
D22S1045	16/18	11/14	11/17
FGA	24/26	23/24	18/23
SE33	23.2/26.2	19/29.2	22.2/27.2
TH01	6/9.3	8/9.3	7/9.3
vWA	17/17	17/18	14/19

For further confirmation, the table above displays the alleles of the reference DNA purchased from Coriell Cell Repositories (CCR), as well as 3 reference DNAs purchased from CCR and ATCC up to the standard of Szibor et al. (2003).

Alleles

Table 49 shows the alleles of the allelic ladder. All analyses were performed using POP-4 polymer (Table 49 and Figure 2). Different analysis instruments, DNA size standards, or polymers may result in different fragment lengths. In addition, a visual alignment with the allelic ladder is recommended.

Scaling

- Horizontal: 70–480 bp
- Vertical: Depending on signal intensity

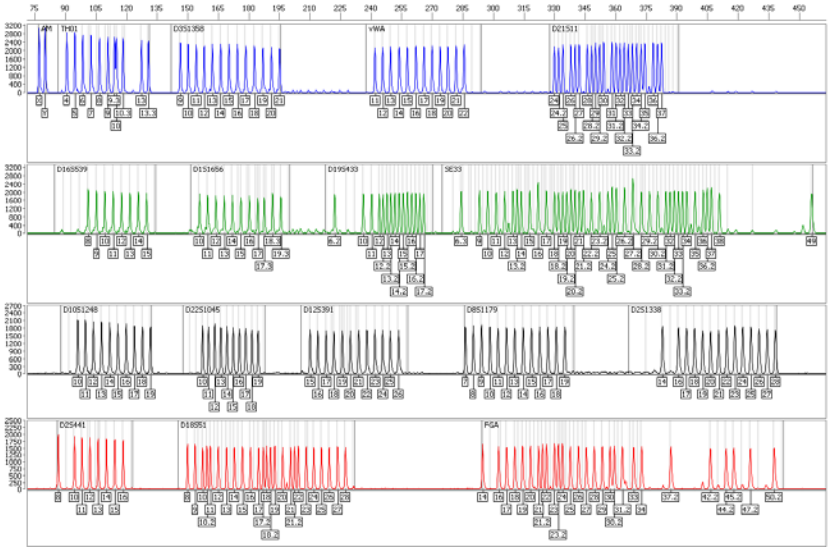


Figure 2. Electropherogram of the allelic ladder ESSplex SE GO! analyzed on an Applied Biosystems 3500 Genetic Analyzer. Allele assignment was performed using Investigator IDproof Software.

Table 49. Allelic ladder fragments included in the Investigator ESSplex SE GO! Kit

Locus	Dye label	Repeat numbers of allelic ladder
Amelogenin	6-FAM	X, Y
TH01	6-FAM	4, 5, 6, 7, 8, 9, 9.3, 10, 10.3, 13, 13.3
D3S1358	6-FAM	9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21
vWA	6-FAM	11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22
D21S11	6-FAM	24, 24.2, 25, 26, 26.2, 27, 28, 28.2, 29, 29.2, 30, 31, 31.2, 32, 32.2, 33, 33.2, 34, 34.2, 35, 36, 36.2, 37
D16S539	BTG	8, 9, 10, 11, 12, 13, 14, 15
D1S1656	BTG	10, 11, 12, 13, 14, 15, 16, 17, 17.3, 18.3, 19.3
D19S433	BTG	6.2, 10, 11, 12, 12.2, 13, 13.2, 14, 14.2, 15, 15.2, 16, 16.2, 17, 17.2
SE33	BTG	6.3, 9, 10, 11, 12, 13, 13.2, 14, 15, 16*, 17, 18, 18.2, 19, 19.2, 20, 20.2, 21, 21.2, 22.2, 23.2, 24.2, 25, 25.2, 26.2, 27.2*, 28.2, 29.2, 30.2, 31.2, 32, 32.2, 33, 33.2, 34, 35, 36, 36.2, 37, 38, 49
D10S1248	BTY	10, 11, 12, 13, 14, 15, 16, 17, 18, 19
D22S1045	BTY	10, 11, 12, 13, 14, 15, 16, 17, 18, 19
D12S391	BTY	15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26

Table continued on next page.

Table 49. continued from previous page.

Locus	Dye label	Repeat numbers of allelic ladder
D8S1179	BTY	7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19
D2S1338	BTY	14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28
D2S441	BTR	8, 10, 11, 12, 13, 14, 15, 16
D18S51	BTR	8, 9, 10, 10.2, 11, 12, 13, 14, 15, 16, 17, 17.2, 18, 18.2, 19, 20, 21, 21.2, 22, 23, 24, 25, 26, 27, 28
FGA	BTR	14, 16, 17, 18, 19, 20, 21, 21.2, 22, 23, 23.2, 24, 25, 26, 27, 28, 29, 30, 30.2, 31.2, 33, 34, 37.2, 42.2, 44.2, 45.2, 47.2, 50.2

* Alleles are heightened within the allelic ladder for better orientation.

For information about known microvariants not contained in the Investigator ESSplex SE GO! allelic ladder, see the National Institute of Standards and Technology (NIST) web site (www.cstl.nist.gov/biotech/strbase/).

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
Many samples show off-scale alleles	
PCR cycle number too high	Determine optimal cycle number by running a representative batch of samples. Re-inject off-scale samples occurring under optimal cycle conditions using a reduced injection time
Many samples show faint or no signal	
PCR cycle number too low	Determine optimal cycle number by running a representative batch of samples.
Unbalanced profiles, low signals	
a) Incorrect volume of Fast Reaction Mix or Primer mix	Check reaction setup and repeat amplification
b) Master mix not vortexed before distribution	Vortex master mix thoroughly
c) Sample size too large	Do not use more than one 1.2 mm punch, or punches with larger diameter
Swab samples show low signal for high-molecular-weight markers	
Lysis incomplete	Perform optional lysis at 95°C

Comments and suggestions	
Sample preparation	
Sample signal intensity must be increased	Reduce the volume of the DNA Size Standard 550 (BTO) to peak heights of about 500 RFU. Purify the PCR products before starting the analysis. We recommend the MinElute® PCR Purification Kit (QIAGEN, cat. nos. 28004 and 28006) for rapid and effective purification (see "Ordering Information", page 67)
Matrix/spectral calibration is not appropriate	
There are pull-up peaks between the dye panels (B, G, Y, R, O) with the current matrix/ spectral calibration	This matrix cannot be used for the analysis. Repeat the matrix generation/spectral calibration. Be sure to carefully follow the correct protocol for the specific analysis instrument.
Many peaks are labeled as off-ladder (OL) alleles in the samples	
a) DNA Size Standard 550 (BTO) was not defined or identified correctly	Click the orange "Size Match Editor" icon in the upper toolbar or the GeneMapper *ID* or GeneMapper *ID-X* Software. Mark the orange fragments of all samples. Always use the DNA Size Standard 550 included in Investigator Human Identification PCR Kits.
b) Signal intensities are too high. If the peak heights of the samples are outside the linear detection range (>4000 RFU/>5000 RFU)*, stutters, split peaks, and artifacts may be increased	Reduce the injection time in increments to a minimum of 1 s, reduce the amount of the PCR amplification product for analysis, or reduce the quantity of DNA for PCR.

*>4000 RFU for the ABI PRISM 310 Genetic Analyzer; >5000 RFU for the Applied Biosystems 3100/3130/3500 Genetic Analyzer.

	Comments and suggestions
c) Bubbles in the capillary lead to pull-up peaks in all color panels ("spikes") that result in allele misnomer	Repeat electrophoresis to confirm results.
d) Differences in the run performance among the capillaries of a multi-capillary analyzer may result in allelic assignment shift	For reliable allelic assignment on multi-capillary analyzers, a number of allelic ladders should be run.
Injection/file of the allelic ladder is not appropriate	
a) An additional signal can be identified as peak of the allelic ladder because of dysfunctions during the electrophoresis. If peaks of the allelic ladder are miscalled, the ladder cannot be used for the analysis	Use a different injection/file 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	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 Analysis Software.
c) 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.

	Comments and suggestions
d) Point alleles are not found	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.

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.

Cited references

Bär, W., et al. (1997) DNA recommendations. Further report of the DNA Commission of the ISFG regarding the use of short tandem repeat systems. Int. J. Legal Med. **110,** 175.

Hill, C.R., Kline, M.C., Coble, M.D., and Butler, J.M. (2008) Characterization of 26 miniSTR loci for improved analysis of degraded DNA samples. J. Forensic Sci., **53,** 73.

Szibor, R., et al. (2003) Cell line DNA typing in forensic genetics – the necessity of reliable standards. Forensic Sci. Int. **138,** 37.

Appendix: Interpretation of Results

Post-PCR analysis and automatic allele assignment with suitable analysis software ensure a precise and reliable discrimination of alleles.

General procedure for the analysis

1. **Check the DNA size standard.**
2. **Check the allelic ladder.**
3. **Check the positive control.**
4. **Check the negative control.**
5. **Analyze and interpret the sample data.**

Pull-up peaks

Pull-up peaks may occur if peak heights are outside the linear detection range (see "Troubleshooting Guide", page 61), or if an incorrect matrix was applied. They appear at positions of specific peaks in other color channels, typically with lower signal intensities. Peak heights should not exceed thresholds in order to prevent pull-up peaks.

Stutter peaks

The occurrence of stutter peaks depends on the sequence of the repeat structure and the number of alleles. n –4 peaks are caused by a loss of a repeat unit during amplification of tetranucleotide STR motifs, caused by slippage effects of the *Taq* DNA Polymerase, whereas n –3 peaks appear particularly during amplification of the trinucleotide STR motif D22S1045. These peaks should be interpreted using the Investigator Template Files for GeneMapper *ID-X*, GeneMapper *ID*, and Genotyper Software.

Template-independent addition of nucleotides

Because of its terminal transferase activity, the *Taq* DNA Polymerase may cause incomplete adenylation at the 3'-end of the amplified DNA fragments. The artifact peak is one base shorter than expected (–1 peaks). All primers included in the Investigator ESSplex SE GO! Kit are designed to minimize these artifacts. Peak height of the artifact correlates with the amount of DNA. Laboratories should define their own limits for analysis of the peaks.

Artifacts

Room temperature may influence the performance of PCR products on multi-capillary instruments, so that shoulder peaks or split peaks occur. If shoulder or split peaks appear, we recommend injecting the sample again. Ensure ambient conditions are kept, as recommended by the instrument manufacturer. Ensure buffers are equilibrated to ambient conditions as well.

Ordering Information

Product	Contents	Cat. no.
Investigator ESSplex SE GO! Kit (200)	Primer Mix, Fast Reaction Mix including HotStarTaq Plus DNA Polymerase, Control DNA, allelic ladder ESSplex SE GO! and DNA size standard 550 (BTO)	381566
Investigator ESSplex SE GO! Kit (1000)	Primer Mix, Fast Reaction Mix including HotStarTaq Plus DNA Polymerase, Control DNA, allelic ladder ESSplex SE GO! and DNA size standard 550 (BTO)	381568
Accessories		
Investigator STR GO! Lysis Buffer (200)	Lysis buffer for 200 swab samples	386516
Investigator STR GO! Punch Buffer (200)*	Lysis buffer for 200 samples of epithelial cells on paper	386526
Matrix Standard BT5 multi cap. (25)	Matrix standard 6-FAM, BTG, BTY, BTR, and BTO	386123
Matrix Standard BT5 multi cap. (50)	Matrix standard 6-FAM, BTG, BTY, BTR, and BTO	386125
DNA Size Standard 550 (BTO) (100)	DNA Size Standard 550 (BTO) for 100 reactions	386015
Related products		
Investigator Human Identification PCR Kits		
Investigator 24plex QS Kit (100)*	Primer mix, Fast Reaction Mix 2.0, Control DNA, allelic ladder 24plex, DNA size standard 550 (BTO), and nuclease-free water	382415
Investigator 24plex GO! Kit (200)*	Primer mix, Fast Reaction Mix 2.0, Control DNA, allelic ladder 24plex, DNA size standard 550 (BTO)	382426

* Larger kit sizes are available; please inquire.

Product	Contents	Cat. no.
Investigator ESSplex SE Plus Kit (100)*	Primer mix, Fast Reaction Mix including HotStarTaq Plus DNA Polymerase, Control DNA, allelic ladder ESSplex SE Plus, DNA size standard 550 (BTO), and nuclease-free water	381545
Investigator IDplex Plus Kit (100)*	Primer mix, Fast Reaction Mix including HotStarTaq Plus DNA Polymerase, Control DNA, allelic ladder IDplex Plus, DNA size standard 550 (BTO), and nuclease-free water	381625
Investigator ESSplex Plus Kit (100)*	Primer mix, Fast Reaction Mix including HotStarTaq Plus DNA Polymerase, Control DNA, allelic ladder ESSplex Plus, DNA size standard 550 (BTO), and nuclease-free water	381535
Investigator IDplex GO! Kit (200)*	Primer Mix, Fast Reaction Mix including HotStarTaq Plus DNA Polymerase, Control DNA, allelic ladder IDplex GO! and DNA size standard 550 (BTO)	381636
Investigator HDplex Kit (100)	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	381215
Investigator Triplex AFS QS Kit (400)	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	380317
Investigator Triplex DSF Kit (400)	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	380327

* Larger kit sizes are available; please inquire.

Product	Contents	Cat. no.
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, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	383615
Investigator DIPplex Kit (100)	Primer mix, reaction mix, DNA Polymerase, Control DNA, allelic ladder, DNA size standard, and nuclease-free water	384015
Investigator Quantiplex Kit (200)	Primer mix IC FQ, reaction mix FQ, control DNA Z1, dilution buffer	387016
Investigator Quantiplex HYres Kit (200)	Primer mix IC YQ, reaction mix YQ, control DNA Z1, dilution buffer	387116
DNA extraction and purification		
QIAamp® DNA Investigator Kit (50)*	50 QIAamp MinElute Columns, Proteinase K, Carrier RNA, Buffers, Collection Tubes (2 ml)	56504
EZ1® DNA Investigator Kit (48)	Reagent Cartridges (DNA Investigator), Disposable Filter-Tips, Disposable Tip-Holders, Sample Tubes (2 ml), Elution Tubes (1.5 ml), Buffer G2, Proteinase K, Carrier RNA	952034
MinElute PCR Purification Kit (50)*	50 MinElute Spin Columns, Buffers, Collection Tubes (2 ml)	28004

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.

* Larger kit sizes are available; please inquire.

Notes

Limited License Agreement for the Investigator ESSplex SE GO! Kit

Use of this product signifies the agreement of any purchaser or user of the product to the following terms:

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Australia ■ techservice-au@qiagen.com

Austria ■ techservice-at@qiagen.com

Belgium ■ techservice-bnl@qiagen.com

Brazil ■ suportetecnico.brasil@qiagen.com

Canada ■ techservice-ca@qiagen.com

China ■ techservice-cn@qiagen.com

Denmark ■ techservice-nordic@qiagen.com

Finland ■ techservice-nordic@qiagen.com

France ■ techservice-fr@qiagen.com

Germany ■ techservice-de@qiagen.com

Hong Kong ■ techservice-hk@qiagen.com

India ■ techservice-india@qiagen.com

Ireland ■ techservice-uk@qiagen.com

Italy ■ techservice-it@qiagen.com

Japan ■ techservice-jp@qiagen.com

Korea (South) ■ techservice-kr@qiagen.com

Luxembourg ■ techservice-bnl@qiagen.com

Mexico ■ techservice-mx@qiagen.com

The Netherlands ■ techservice-bnl@qiagen.com

Norway ■ techservice-nordic@qiagen.com

Singapore ■ techservice-sg@qiagen.com

Sweden ■ techservice-nordic@qiagen.com

Switzerland ■ techservice-ch@qiagen.com

UK ■ techservice-uk@qiagen.com

USA ■ techservice-us@qiagen.com

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