

TECHNICAL MANUAL

# PowerPlex® Fusion System for Use on the Applied Biosystems® Genetic Analyzers

Instructions for Use of Products  
DC2402 and DC2408



# PowerPlex<sup>®</sup> Fusion System

## for Use on the Applied Biosystems<sup>®</sup> Genetic Analyzers

All technical literature is available at: [www.promega.com/protocols/](http://www.promega.com/protocols/)  
 Visit the web site to verify that you are using the most current version of this Technical Manual.  
 E-mail Promega Technical Services if you have questions on use of this system: [genetic@promega.com](mailto:genetic@promega.com)

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## 1. Description

STR (short tandem repeat) loci consist of short, repetitive sequence elements 3–7 base pairs in length (1–4). These repeats are well distributed throughout the human genome and are a rich source of highly polymorphic markers, which may be detected using the polymerase chain reaction (5–9). Alleles of STR loci are differentiated by the number of copies of the repeat sequence contained within the amplified region and are distinguished from one another using fluorescence detection following electrophoretic separation.

The PowerPlex® Fusion System<sup>(a,b)</sup> is a 24-locus multiplex for human identification applications including forensic analysis, relationship testing and research use. This five-color system allows co-amplification and fluorescent detection of the 20 autosomal loci in the expanded core CODIS (US) loci (CSF1PO, FGA, TH01, TPOX, vWA, D1S1656, D2S1338, D2S441, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11 and D22S1045), as well as Amelogenin and DYS391 for gender determination. The Penta D and Penta E loci are also included to increase discrimination and allow searching of databases that include profiles with these loci. This extended panel of STR markers is intended to satisfy both CODIS and ESS recommendations.

The PowerPlex® Fusion System and all system components are manufactured in accordance with ISO 18385:2016. All necessary materials are provided to amplify STR regions of human genomic DNA, including a hot-start thermostable DNA polymerase, which is a component of the PowerPlex® Fusion 5X Master Mix.

This manual contains protocols for use of the PowerPlex® Fusion System with the GeneAmp® PCR System 9700, Veriti® 96-Well Thermal Cycler and ProFlex® PCR System in addition to protocols to separate amplified products and detect separated material on the ABI PRISM® 3100 and 3100-*Avant* Genetic Analyzers and Applied Biosystems® 3130, 3130*xl*, 3500 and 3500*xL* Genetic Analyzers. A protocol to operate the fluorescence-detection instrument should be obtained from the instrument manufacturer. Amplification and detection instrumentation may vary. You may need to optimize protocols including amount of template DNA, cycle number, injection conditions and loading volume for your laboratory instrumentation. In-house validation should be performed.

Information about other Promega fluorescent STR systems is available upon request from Promega or online at:  
**[www.promega.com](http://www.promega.com)**



## 2. Product Components and Storage Conditions

PRODUCT	SIZE	CAT.#
PowerPlex® Fusion System	200 reactions	DC2402

Not For Medical Diagnostic Use. This system contains sufficient reagents for 200 reactions of 25µl each.

Includes:

### Pre-amplification Components Box

- 1ml PowerPlex® Fusion 5X Master Mix
- 1ml PowerPlex® Fusion 5X Primer Pair Mix
- 25µl 2800M Control DNA, 10ng/µl
- 5 × 1,250µl Water, Amplification Grade

### Post-amplification Components Box

- 100µl PowerPlex® Fusion Allelic Ladder Mix
- 200µl WEN Internal Lane Standard 500

PRODUCT	SIZE	CAT.#
PowerPlex® Fusion System	800 reactions	DC2408

Not For Medical Diagnostic Use. This system contains sufficient reagents for 800 reactions of 25µl each.

Includes:

### Pre-amplification Components Box

- 4 × 1ml PowerPlex® Fusion 5X Master Mix
- 4 × 1ml PowerPlex® Fusion 5X Primer Pair Mix
- 25µl 2800M Control DNA, 10ng/µl
- 10 × 1,250µl Water, Amplification Grade

### Post-amplification Components Box

- 4 × 100µl PowerPlex® Fusion Allelic Ladder Mix
- 4 × 200µl WEN Internal Lane Standard 500



The PowerPlex® Fusion Allelic Ladder Mix is provided in a separate, sealed bag for shipping. This component should be moved to the post-amplification box after opening. The Water, Amplification Grade, is provided in a separate, sealed bag for shipping. Store this component with the pre-amplification components after opening.

**Storage Conditions:** Upon receipt, store all components at –30°C to –10°C in a nonfrost-free freezer. Make sure the 2800M Control DNA is stored at 2–10°C for **at least 24 hours** before use; do not refreeze. After the first use, store the WEN Internal Lane Standard 500 (WEN ILS 500) at 2–10°C, protected from light; do not refreeze. The PowerPlex® Fusion 5X Primer Pair Mix, PowerPlex® Fusion Allelic Ladder Mix and WEN ILS 500 are light-sensitive and must be stored in the dark. We strongly recommend that pre-amplification and post-amplification reagents be stored and used separately with different pipettes, tube racks, etc.

**Optional:** The PowerPlex® Fusion System components may be stored for up to 1 year at 2–10°C without loss of activity.

## Available Separately

PRODUCT	SIZE	CAT.#
PunchSolution™ Kit	100 preps	DC9271
SwabSolution™ Kit	100 preps	DC8271
5X AmpSolution™ Reagent	500µl	DM1231

The PunchSolution™ Kit is required to process nonlytic card punches prior to direct amplification. The SwabSolution™ Kit is required to process swabs prior to direct amplification. The 5X AmpSolution™ Reagent is required for direct amplification of DNA from storage card punches in a 12.5µl reaction volume. Both the PunchSolution™ Kit and SwabSolution™ Kit include the 5X AmpSolution™ Reagent.

The proper panels, bins and stutter text files and size standard .xml file for use with GeneMapper® ID and ID-X software can be downloaded at:

**[www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/](http://www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/)**

The PowerPlex® 5C Matrix Standard (Cat.# DG4850) is required for initial set up of the color separation matrix (see Section 3.B).

## 3. Before You Begin

### 3.A. Precautions

The application of PCR-based typing for forensic or paternity casework requires validation studies and quality-control measures that are not contained in this manual (10,11). Guidelines for the validation process are published in the *Internal Validation Guide of Autosomal STR Systems for Forensic Laboratories* (12).

The quality of purified DNA or direct-amplification samples, small changes in buffers, ionic strength, primer concentrations, reaction volume, choice of thermal cycler and thermal cycling conditions can affect PCR success. We suggest strict adherence to recommended procedures for amplification and fluorescence detection. Additional research and validation are required if any modifications to the recommended protocols are made.

PCR-based STR analysis is subject to contamination by very small amounts of human DNA. Extreme care should be taken to avoid cross-contamination when preparing template DNA, handling primer pairs, assembling amplification reactions and analyzing amplification products. Reagents and materials used prior to amplification (Master Mix, Primer Pair Mix, 2800M Control DNA and Water, Amplification Grade) are provided in a separate box and should be stored separately from those used following amplification (Allelic Ladder Mix and Internal Lane Standard). Always include a negative control reaction (i.e., no template) to detect reagent contamination. We highly recommend the use of gloves and aerosol-resistant pipette tips.

Some reagents used in the analysis of STR products are potentially hazardous and should be handled accordingly. Formamide is an irritant and a teratogen; avoid inhalation and contact with skin. Read the warning label, and take appropriate precautions when handling this substance. Always wear gloves and safety glasses when working with formamide.



### 3.B. Spectral Calibration

Proper spectral calibration is critical to evaluate multicolor systems with the ABI PRISM® 3100 and 3100-*Avant* Genetic Analyzers and Applied Biosystems® 3130, 3130xl, 3500 and 3500xL Genetic Analyzers. A matrix must be generated for each individual instrument.

For protocols and additional information about spectral calibration on these instruments, see the *PowerPlex® 5C Matrix Standard Technical Manual #TMD049*. This manual is available online at: [www.promega.com/protocols/](http://www.promega.com/protocols/)

## 4. Protocols for DNA Amplification Using the PowerPlex® Fusion System

The PowerPlex® Fusion System was developed for amplification of extracted DNA and direct-amplification samples. Slight protocol variations are recommended for optimal performance with each template source. Protocols for amplification in a 25µl reaction volume using extracted DNA (Section 4.A), lytic and nonlytic storage card punches (Section 4.B) and swabs (Section 4.C) are included in the following amplification sections. Protocols for amplification in a 12.5µl reaction volume using lytic and nonlytic storage card punches and swabs are included in Sections 9.C and 9.D, respectively.

The PowerPlex® Fusion System is compatible with the GeneAmp® PCR System 9700 with a gold-plated silver or silver sample block, the Veriti® 96-Well Thermal Cycler and the ProFlex® PCR System.

**Note:** It may be possible to use thermal cyclers other than those listed in this technical manual. Use of thermal cyclers not listed here may require optimization of cycling conditions and validation in your laboratory. Use of thermal cyclers with an aluminum block is **not** recommended with the PowerPlex® Fusion System.

The use of gloves and aerosol-resistant pipette tips is highly recommended to prevent cross-contamination. Keep all pre-amplification and post-amplification reagents in separate rooms. Prepare amplification reactions in a room dedicated for reaction setup. Use equipment and supplies dedicated for amplification setup.



Meticulous care must be taken to ensure successful amplification. A guide to amplification troubleshooting is provided in Section 7.

### 4.A. Amplification of Extracted DNA in a 25µl Reaction Volume

The following protocol has been routinely used to amplify 0.25–0.5ng of template DNA in a 25µl reaction volume using the PowerPlex® Fusion System.

#### Materials to Be Supplied by the User

- GeneAmp® PCR System 9700 with a gold-plated silver or silver PCR sample block, Veriti® 96-Well Thermal Cycler or ProFlex® PCR System (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plate or 0.2ml MicroAmp® reaction tubes (Applied Biosystems)
- aerosol-resistant pipette tips

## Amplification Setup

1. Thaw the PowerPlex® Fusion 5X Master Mix, PowerPlex® Fusion 5X Primer Pair Mix and Water, Amplification Grade, completely.  
**Note:** Centrifuge tubes briefly to bring contents to the bottom, and then vortex reagents for 15 seconds before each use. Do not centrifuge the 5X Primer Pair Mix or 5X Master Mix after vortexing, as this may cause the reagents to be concentrated at the bottom of the tube.
2. Determine the number of reactions to be set up. This should include positive and negative control reactions. Add 1 or 2 reactions to this number to compensate for pipetting error. While this approach does consume a small amount of each reagent, it ensures that you will have enough PCR amplification mix for all samples. It also ensures that each reaction contains the same PCR amplification mix.
3. Use a clean plate for reaction assembly, and label it appropriately. Alternatively, determine the number of clean, 0.2ml reaction tubes required, and label them appropriately.
4. Add the final volume of each reagent listed in Table 1 to a clean tube.

**Table 1. PCR Amplification Mix for Amplification of Extracted DNA.**

PCR Amplification Mix Component <sup>1</sup>	Volume Per Reaction	×	Number of Reactions	=	Final Volume
Water, Amplification Grade	to a final volume of 25µl	×		=	
PowerPlex® Fusion 5X Master Mix	5µl	×		=	
PowerPlex® Fusion 5X Primer Pair Mix	5µl	×		=	
template DNA (0.25–0.5ng) <sup>2,3,4</sup>	up to 15µl				
<b>total reaction volume</b>	<b>25µl</b>				

<sup>1</sup>Add Water, Amplification Grade, to the tube first, and then add PowerPlex® Fusion 5X Master Mix and PowerPlex® Fusion 5X Primer Pair Mix. The template DNA will be added at Step 6.

<sup>2</sup>Store DNA templates in TE<sup>-4</sup> buffer (10mM Tris-HCl [pH 8.0], 0.1mM EDTA) or TE<sup>-4</sup> buffer with 20µg/ml glycogen. If the DNA template is stored in TE buffer that is not pH 8.0 or contains a higher EDTA concentration, the volume of DNA added should not exceed 20% of the final reaction volume. PCR amplification efficiency and quality can be greatly altered by changes in pH (due to added Tris-HCl), available magnesium concentration (due to chelation by EDTA) or other PCR inhibitors, which may be present at low concentrations depending on the source of the template DNA and the extraction procedure used.

<sup>3</sup>Apparent DNA concentrations can differ, depending on the DNA quantification method used (13). We strongly recommend that you perform experiments to determine the optimal DNA amount based on your DNA quantification method.

<sup>4</sup>The PowerPlex® Fusion System was optimized and balanced for 0.25–0.5ng of DNA template. The amount of DNA template used in your laboratory should be based on the results of your internal validation and may be different.



#### 4.A. Amplification of Extracted DNA in a 25 $\mu$ l Reaction Volume (continued)

5. Vortex the PCR amplification mix for 5–10 seconds, and then pipet PCR amplification mix into each reaction well.



Failure to vortex the PCR amplification mix sufficiently can result in poor amplification or locus-to-locus imbalance.

**Note:** Do not store the PCR amplification mix for a prolonged period. Add the mix to the wells of the reaction plate as soon as the mix is prepared. Add DNA as soon as possible to each well and follow immediately by thermal cycling.

6. Add template DNA for each sample to the respective well containing PCR amplification mix.

**Note:** The PowerPlex<sup>®</sup> Fusion System is optimized and balanced using 0.25–0.5ng of DNA template. The amount of DNA template used in your laboratory should be based on the results of your internal validation and may be different.

7. For the positive amplification control, vortex the tube of 2800M Control DNA, and then dilute an aliquot to 0.5ng in the desired template DNA volume. Add 0.5ng of diluted DNA to a reaction well containing PCR amplification mix.

8. For the negative amplification control, pipet Water, Amplification Grade, or TE<sup>-4</sup> buffer instead of template DNA into a reaction well containing PCR amplification mix.

9. Seal or cap the plate, or close the tubes.

**Optional:** Briefly centrifuge the plate to bring contents to the bottom of the wells and remove any air bubbles.

## Thermal Cycling

Amplification and detection instrumentation may vary. You may need to optimize protocols including the amount of template DNA, cycle number, injection conditions and loading volume for your laboratory instrumentation. Testing at Promega shows that 30 cycles works well for 0.5ng of purified DNA template. In-house validation should be performed.

1. Place the reaction plate or tubes in the thermal cycler.
2. Select and run the recommended protocol, which is provided in Figure 1.

### Notes:

1. When using the ProFlex® PCR System, use the 9700 Simulation Mode.
2. When using the Veriti® 96-Well Thermal Cycler, set the ramping rate to 100%.
3. When using the GeneAmp® PCR System 9700, the program must be run with Max Mode as the ramp speed. This requires a gold-plated silver or silver sample block. The ramp speed is set after the thermal cycling run is started. When the 'Select Method Options' screen appears, select "Max" for the ramp speed and enter the reaction volume.

### Thermal Cycling Protocol

96°C for 1 minute, then:

94°C for 10 seconds

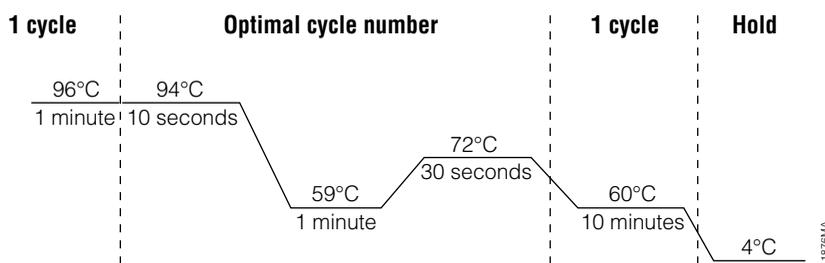
59°C for 1 minute

72°C for 30 seconds

for 30 cycles, then:

60°C for 10 minutes

4°C soak



**Figure 1. Thermal cycling protocol for the GeneAmp® PCR System 9700, Veriti® 96-Well Thermal Cycler and ProFlex® PCR System.**

3. After completion of the thermal cycling protocol, proceed with fragment analysis or store amplified samples at  $-20^{\circ}\text{C}$  in a light-protected box.

**Note:** Long-term storage of amplified samples at  $4^{\circ}\text{C}$  or higher may produce artifacts.



#### 4.B. Direct Amplification of DNA from Storage Card Punches in a 25µl Reaction Volume

##### Materials to Be Supplied by the User

- GeneAmp® PCR System 9700 with a gold-plated silver or silver sample block, Veriti® 96-Well Thermal Cycler or ProFlex® PCR System (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plate or 0.2ml MicroAmp® reaction tubes (Applied Biosystems)
- aerosol-resistant pipette tips
- PunchSolution™ Kit (Cat. # DC9271) for nonlytic card punches
- 1.2mm Harris Micro-Punch or equivalent manual punch and cutting mat or automated punch system

This section contains a protocol for direct amplification of DNA from storage card punches in a 25µl reaction volume using the PowerPlex® Fusion System and GeneAmp® PCR System 9700, Veriti® 96-Well Thermal Cycler or ProFlex® PCR System. A protocol for direct amplification of DNA from storage card punches in a 12.5µl reaction volume is provided in Section 9.C.

We recommend amplifying one or two 1.2mm punches of a storage card containing buccal cells or one 1.2mm punch of a storage card containing whole blood in a 25µl reaction volume using the protocols detailed below.

**Note:** You will need to optimize and validate the number of storage card punches per reaction in your laboratory. See the PCR optimization recommendations at the end of the section.

##### Lytic storage card sample types include:

- Buccal cells collected on FTA® cards with Whatman EasiCollect™ or Fitzco Sampact™ devices
- Buccal cells collected with swabs transferred to FTA® or Indicating FTA® cards
- Liquid blood (from collection or storage Vacutainer® tubes or finger sticks) spotted onto FTA® cards

##### Nonlytic storage card sample types include:

- Buccal samples on Bode Buccal DNA Collector™ devices
- Blood and buccal samples on nonlytic cards (e.g., S&S 903)

Pretreat nonlytic sample types with the PunchSolution™ Kit (Cat. # DC9271) to lyse the samples before adding the PCR amplification mix. For more information, see the *PunchSolution™ Kit Technical Manual #TMD038*. Failure to pretreat these samples may result in incomplete profiles.

Use a manual punch tool with a 1.2mm tip to manually create sample disks from a storage card. Place tip near the center of the sample spot, and with a twisting or pressing action, cut a 1.2mm sample disk. Use the plunger to eject the disk into the appropriate well of a reaction plate.

Automated punchers also can be used to create sample disks. Refer to the user's guide for your instrument for assistance with generating 1.2mm disks, technical advice and troubleshooting information.

**Note:** Static may be problematic when adding a punch to a well. For lytic card punches, adding PCR amplification mix to the well before adding the punch may help alleviate static problems. For nonlytic card punches, adding PunchSolution™ Reagent to the well before adding the punch during pretreatment may help alleviate static problems.

## Amplification Setup

1. Thaw the PowerPlex® Fusion 5X Master Mix, PowerPlex® Fusion 5X Primer Pair Mix and Water, Amplification Grade, completely.

**Note:** Centrifuge tubes briefly to bring contents to the bottom, and then vortex reagents for 15 seconds before each use. Do not centrifuge the 5X Primer Pair Mix or 5X Master Mix after vortexing, as this may cause the reagents to be concentrated at the bottom of the tube.

2. Determine the number of reactions to be set up. This should include positive and negative control reactions. Add 1 or 2 reactions to this number to compensate for pipetting error. While this approach does consume a small amount of each reagent, it ensures that you will have enough PCR amplification mix for all samples. It also ensures that each reaction contains the same PCR amplification mix.
3. Use a clean plate for reaction assembly, and label it appropriately. Alternatively, determine the number of clean, 0.2ml reaction tubes required, and label them appropriately.
4. Add the final volume of each reagent listed in Table 2 to a clean tube.

**Table 2. PCR Amplification Mix for Direct Amplification of DNA from Storage Card Punches in a 25µl Reaction Volume.**

PCR Amplification Mix Component <sup>1</sup>	Volume Per Reaction	×	Number of Reactions	=	Final Volume
Water, Amplification Grade	15µl	×		=	
PowerPlex® Fusion 5X Master Mix	5µl	×		=	
PowerPlex® Fusion 5X Primer Pair Mix	5µl	×		=	
<b>total reaction volume</b>	<b>25µl</b>				

<sup>1</sup>Add Water, Amplification Grade, to the tube first, and then add PowerPlex® Fusion 5X Master Mix and PowerPlex® Fusion 5X Primer Pair Mix. For lytic card punches, the template DNA will be added at Step 6.

5. Vortex the PCR amplification mix for 5–10 seconds, and then pipet 25µl of PCR amplification mix into each reaction well.



Failure to vortex the PCR amplification mix sufficiently can result in poor amplification or locus-to-locus imbalance.

**Note:** Do not store the PCR amplification mix for a prolonged period. Add the mix to the wells of the reaction plate as soon as the mix is prepared. Add the punches as soon as possible to each well and follow immediately by thermal cycling.

6. For lytic storage cards, add one or two 1.2mm punches from a card containing buccal cells or one 1.2mm punch from a card containing whole blood to the appropriate wells of the reaction plate. For nonlytic card punches, add the PCR amplification mix to the plate containing the PunchSolution™ Reagent-treated punches.

**Note:** It also is acceptable to add the lytic card punch first, and then add the PCR amplification mix.



#### 4.B. Direct Amplification of DNA from Storage Card Punches in a 25 $\mu$ l Reaction Volume (continued)

7. For the positive amplification control, vortex the tube of 2800M Control DNA, and then add 1 $\mu$ l (10ng) to a reaction well containing 25 $\mu$ l of PCR amplification mix.

**Notes:**

1. Do not include blank storage card punches in the positive control reactions.
  2. Optimization of the amount of 2800M Control DNA may be required, depending on cycling conditions and laboratory preferences.
8. Reserve a well containing PCR amplification mix as a negative amplification control.  
**Note:** An additional negative control with a blank punch may be performed to detect contamination from the storage card or punch device.
  9. Seal or cap the plate, or close the tubes. Briefly centrifuge reactions to bring storage card punches to the bottom of the wells and remove any air bubbles.

#### Thermal Cycling

Amplification and detection instrumentation may vary. You will need to optimize protocols including the number of storage card punches, cycle number (25–28 cycles), injection conditions and loading volume for your laboratory instrumentation. Testing at Promega shows that 27 cycles works well for a variety of storage card sample types. Cycle number should be optimized in each laboratory for each sample type.

1. Place the reaction plate or tubes in the thermal cycler.
2. Select and run the recommended protocol, which is provided in Figure 2.

**Notes:**

1. When using the ProFlex<sup>®</sup> PCR System, use the 9700 Simulation Mode as the ramp speed.
2. When using the Veriti<sup>®</sup> 96-Well Thermal Cycler, set the ramping rate to 100%.
3. When using the GeneAmp<sup>®</sup> PCR System 9700, the program must be run with Max Mode as the ramp speed. This requires a gold-plated silver or silver sample block. The ramp speed is set after the thermal cycling run is started. When the 'Select Method Options' screen appears, select "Max" for the ramp speed and enter the reaction volume.
4. The final extension for direct amplification was extended to 20 minutes compared to 10 minutes for the extracted DNA protocol to allow sufficient time for adenylation of large amounts of amplicon.

### Thermal Cycling Protocol

96°C for 1 minute, then:

94°C for 10 seconds

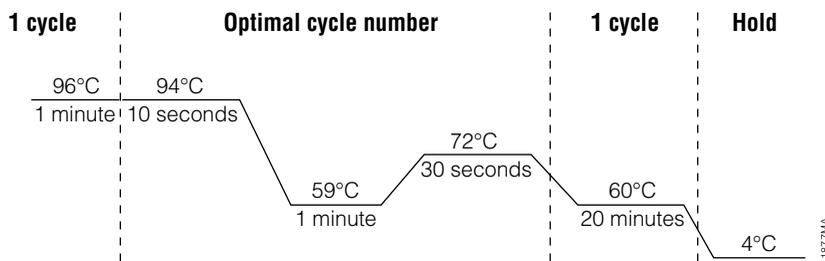
59°C for 1 minute

72°C for 30 seconds

for 27 cycles, then:

60°C for 20 minutes

4°C soak



**Figure 2. Thermal cycling protocol for the GeneAmp® PCR System 9700, Veriti® 96-Well Thermal Cycler and ProFlex® PCR System.**

3. After completion of the thermal cycling protocol, proceed with fragment analysis or store amplified samples at –20°C in a light-protected box.

**Note:** Long-term storage of amplified samples at 4°C or higher may produce artifacts.

### PCR Optimization

Cycle number should be optimized based on the results of an initial experiment to determine the sensitivity with your collection method, number of punches, sample types and instrumentation.

1. Choose several samples that represent typical sample types you encounter in the laboratory. Prepare them as you would using your normal workflow.
2. Depending on your preferred protocol, place one or two 1.2mm storage card punches containing buccal cells or one 1.2mm punch of a storage card containing whole blood in each well of a reaction plate. Be sure to pretreat nonlytic samples with the PunchSolution™ Kit (Cat.# DC9271).
3. Prepare four identical reaction plates with punches from the same samples.
4. Amplify samples using the thermal cycling protocol provided above, but subject each plate to a different cycle number (25–28 cycles).
5. Following amplification, use your laboratory's validated separation and detection protocols to determine the optimal cycle number for the sample type and number of storage card punches.



#### 4.C. Direct Amplification of DNA from Swabs in a 25µl Reaction Volume

##### Materials to Be Supplied by the User

- GeneAmp® PCR System 9700 with a gold-plated silver or silver sample block, Veriti® 96-Well Thermal Cycler or ProFlex® PCR System (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plate or 0.2ml MicroAmp® reaction tubes (Applied Biosystems)
- aerosol-resistant pipette tips
- SwabSolution™ Kit (Cat.# DC8271)

This section contains a protocol for amplifying DNA from swab extracts in a 25µl reaction volume using the PowerPlex® Fusion System and GeneAmp® PCR System 9700, Veriti® 96-Well Thermal Cycler or ProFlex® PCR System. A protocol for direct amplification of DNA from swab extracts in a 12.5µl reaction volume is provided in Section 9.D.

Pretreat OmniSwab™ (QIAGEN) or cotton swabs with the SwabSolution™ Kit (Cat.# DC8271) as described in the *SwabSolution™ Kit Technical Manual #TMD037* to generate a swab extract.

##### Amplification Setup

1. Thaw the PowerPlex® Fusion 5X Master Mix, PowerPlex® Fusion 5X Primer Pair Mix and Water, Amplification Grade, completely.  
**Note:** Centrifuge tubes briefly to bring contents to the bottom, and then vortex reagents for 15 seconds before each use. Do not centrifuge the 5X Primer Pair Mix or 5X Master Mix after vortexing, as this may cause the reagents to be concentrated at the bottom of the tube.
2. Determine the number of reactions to be set up. This should include positive and negative control reactions. Add 1 or 2 reactions to this number to compensate for pipetting error. While this approach does consume a small amount of each reagent, it ensures that you will have enough PCR amplification mix for all samples. It also ensures that each reaction contains the same PCR amplification mix.
3. Use a clean plate for reaction assembly, and label it appropriately. Alternatively, determine the number of clean, 0.2ml reaction tubes required, and label them appropriately.

- Add the final volume of each reagent listed in Table 3 to a clean tube.

**Table 3. PCR Amplification Mix for Direct Amplification of DNA from Swabs in a 25 $\mu$ l Reaction Volume.**

PCR Amplification Mix Component <sup>1</sup>	Volume Per Reaction	×	Number of Reactions	=	Final Volume
Water, Amplification Grade	13 $\mu$ l	×		=	
PowerPlex <sup>®</sup> Fusion 5X Master Mix	5 $\mu$ l	×		=	
PowerPlex <sup>®</sup> Fusion 5X Primer Pair Mix	5 $\mu$ l	×		=	
swab extract	2 $\mu$ l				
<b>total reaction volume</b>	<b>25<math>\mu</math>l</b>				

<sup>1</sup>Add Water, Amplification Grade, to the tube first, and then add PowerPlex<sup>®</sup> Fusion 5X Master Mix and PowerPlex<sup>®</sup> Fusion 5X Primer Pair Mix. The swab extract will be added at Step 6.

- Vortex the PCR amplification mix for 5–10 seconds, and then pipet 23 $\mu$ l of PCR amplification mix into each reaction well.



Failure to vortex the PCR amplification mix sufficiently can result in poor amplification or locus-to-locus imbalance.

**Note:** Do not store the PCR amplification mix for a prolonged period. Add the mix to the wells of the reaction plate as soon as the mix is prepared. Add the swab extract as soon as possible to each well and follow immediately by thermal cycling.

- Pipet 2 $\mu$ l of swab extract for each sample into the appropriate well of the reaction plate.
- For the positive amplification control, vortex the tube of 2800M Control DNA, and then dilute an aliquot to 5ng/ $\mu$ l. Add 2 $\mu$ l (10ng) to a reaction well containing 23 $\mu$ l of PCR amplification mix.

**Note:** Optimization of the amount of 2800M Control DNA may be required, depending on thermal cycling conditions and laboratory preferences.

- For the negative amplification control, pipet 2 $\mu$ l of Water, Amplification Grade, or TE<sup>-4</sup> buffer instead of swab extract into a reaction well containing PCR amplification mix.

**Note:** Additional negative controls can be included. Assemble a reaction containing the swab extract prepared from a blank swab, or assemble a reaction where the SwabSolution<sup>™</sup> Reagent is processed as a blank without a swab.

- Seal or cap the plate, or close the tubes.

**Optional:** Briefly centrifuge the plate to bring contents to the bottom of the wells and remove any air bubbles.

#### 4.C. Direct Amplification of DNA from Swabs in a 25µl Reaction Volume (continued)

##### Thermal Cycling

Amplification and detection instrumentation may vary. You will need to optimize protocols including the amount of template DNA, cycle number (25–28 cycles), injection conditions and loading volume for your laboratory instrumentation. Testing at Promega shows that 27 cycles works well for a variety of swab sample types. Cycle number will need to be optimized in each laboratory for each sample type.

1. Place the reaction plate or tubes in the thermal cycler.
2. Select and run the recommended protocol, which is provided in Figure 3.

##### Notes:

1. When using the ProFlex® PCR System, use the 9700 Simulation Mode as the ramp speed.
2. When using the Veriti® 96-Well Thermal Cycler, set the ramping rate to 100%.
3. When using the GeneAmp® PCR System 9700, the program must be run with Max Mode as the ramp speed. This requires a gold-plated silver or silver sample block. The ramp speed is set after the thermal cycling run is started. When the ‘Select Method Options’ screen appears, select “Max” for the ramp speed and enter the reaction volume.
4. The final extension for direct amplification was extended to 20 minutes compared to 10 minutes for the extracted DNA protocol to allow sufficient time for adenylation of large amounts of amplicon.

##### Thermal Cycling Protocol

96°C for 1 minute, then:

94°C for 10 seconds

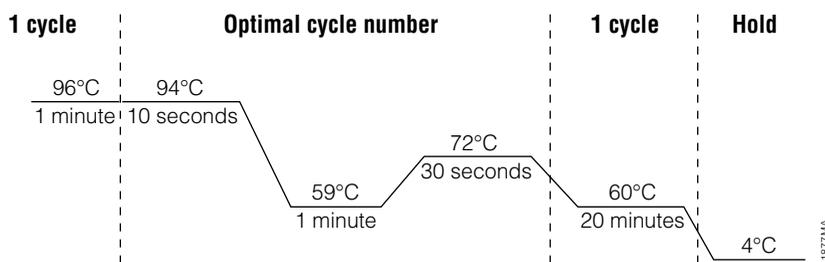
59°C for 1 minute

72°C for 30 seconds

for 27 cycles, then:

60°C for 20 minutes

4°C soak



**Figure 3. Thermal cycling protocol for the GeneAmp® PCR System 9700, Veriti® 96-Well Thermal Cycler and ProFlex® PCR System.**

3. After completion of the thermal cycling protocol, proceed with fragment analysis or store amplified samples at  $-20^{\circ}\text{C}$  in a light-protected box.

**Note:** Long-term storage of amplified samples at  $4^{\circ}\text{C}$  or higher may produce artifacts.

### PCR Optimization

Cycle number should be optimized based on the results of an initial experiment to determine the sensitivity with your collection method, sample types and instrumentation.

1. Choose several samples that represent typical sample types you encounter in the laboratory. Prepare them as you would using your normal workflow.
2. Prepare four identical reaction plates with aliquots of the same swab extracts.
3. Amplify samples using the thermal cycling protocol provided above, but subject each plate to a different cycle number (25–28 cycles).

**Note:** This recommendation is for  $2\mu\text{l}$  of swab extract. Additional cycle number testing may be required.

4. Following amplification, use your laboratory's validated separation and detection protocols to determine the optimal cycle number for the sample type.

### 5. Instrument Setup and Sample Preparation

#### 5.A. Detection of Amplified Fragments Using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer

##### Materials to Be Supplied by the User

- $95^{\circ}\text{C}$  dry heating block, water bath or thermal cycler
- crushed ice, ice-water bath or a freezer plate block
- centrifuge compatible with a 96-well plate
- aerosol-resistant pipette tips
- 3500/3500xL capillary array, 36cm
- plate retainer and base set (standard)
- POP-4® polymer for the Applied Biosystems® 3500 or 3500xL Genetic Analyzer
- anode buffer container
- cathode buffer container
- MicroAmp® optical 96-well plate (or equivalent) and septa (Applied Biosystems)
- Hi-Di™ formamide (Applied Biosystems Cat.# 4311320)



The quality of formamide is critical. Use only the recommended formamide. Freeze formamide in aliquots at  $-20^{\circ}\text{C}$ . Multiple freeze-thaw cycles or long-term storage at  $4^{\circ}\text{C}$  may cause breakdown of formamide. Poor-quality formamide may contain ions that compete with DNA during injection, which results in lower peak heights and reduced sensitivity. A longer injection time may not increase the signal.



Formamide is an irritant and a teratogen; avoid inhalation and contact with skin. Read the warning label, and take appropriate precautions when handling this substance. Always wear gloves and safety glasses when working with formamide.



## 5.A. Detection of Amplified Fragments Using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer (continued)

### Sample Preparation

1. Prepare a loading cocktail by combining and mixing internal lane standard (ILS) and formamide as follows:  
[(0.5µl ILS) × (# samples)] + [(9.5µl formamide) × (# samples)]

**Note:** The volume of internal lane standard used in the loading cocktail can be adjusted to change the intensity of the size standard peaks based on laboratory preferences.

2. Vortex for 10–15 seconds to mix.
3. Pipet 10µl of formamide/internal lane standard mix into each well.
4. Add 1µl of amplified sample (or 1µl of Allelic Ladder Mix) to each well. Cover wells with appropriate septa.

#### **Notes:**

1. Instrument detection limits vary; therefore, injection time, injection voltage or the amount of sample mixed with loading cocktail may need to be increased or decreased. To modify the injection time in the run module, select **Instrument Protocol** from the Library menu in the data collection software. If peak heights are higher than desired, use less DNA template in the amplification reactions or reduce the number of cycles in the amplification program to achieve the desired signal intensity.
  2. Use a volume of allelic ladder that results in peak heights that are all consistently above the peak amplitude threshold determined as part of your internal validation.
5. Centrifuge the plate briefly to remove air bubbles from the wells.
  6. Denature samples at 95°C for 3 minutes, and then immediately chill on crushed ice, a freezer plate block or in an ice-water bath for 3 minutes. Denature samples just prior to loading the instrument.

## Instrument Preparation

Refer to the *Applied Biosystems 3500/3500xL Genetic Analyzer User Guide* for the instrument maintenance schedule and instructions to install the capillary array, buffers and polymer pouch, and perform a spatial calibration. Samples may be analyzed as described in the *Applied Biosystems 3500/3500xL Genetic Analyzer User Guide*.

1. Open the 3500 Data Collection Software. The 'Dashboard' screen will launch (Figure 4). To ensure that you are viewing the most up-to-date information, press the **Refresh** button. Ensure that the Consumables Information and Maintenance Notifications are acceptable.

Set the oven temperature to 60°C, and then select **Start Pre-Heat**. When the Oven Temperature and Detection Cell Temperature turn green, you may proceed with the first injection.



**Consumables Information Table:**

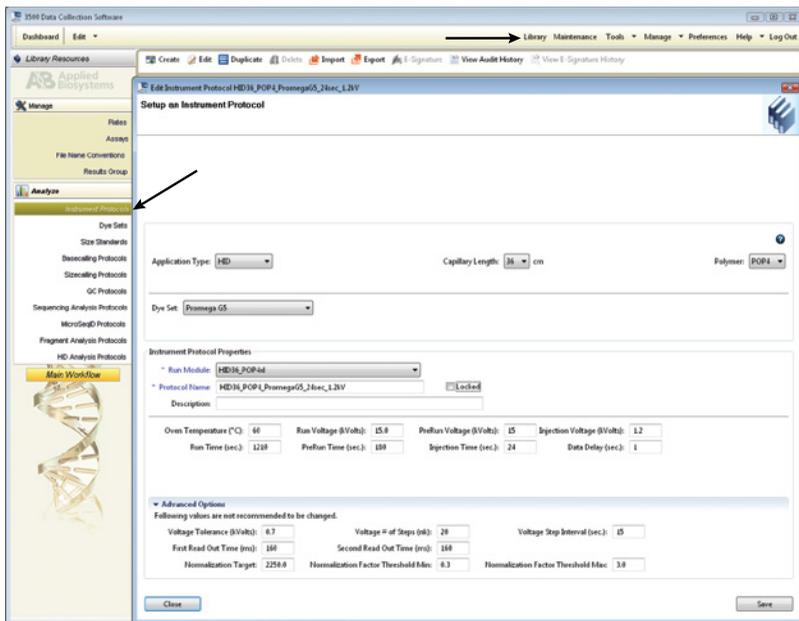
Consumable	Name	Status	Days on Instrument	Expiration Date	Lot Number	Part Number
Polymer	POP4	48 Samples Remaining	5	06-Jan-2011 06..	1006009	4393715
Anode Buffer	ABC	7 Days Remaining	0	13-Mar-2011 07..	1006014	4393927
Cathode Buffer	CBC	7 Days Remaining	0	23-Mar-2011 07..	1007021	4401256
Capillary Array	36cm - 24 cap	94 Injections Remaining	51	03-Feb-2011 02..	01	4404067 - Serial # M4309K0003

Figure 4. The Dashboard.

**5.A. Detection of Amplified Fragments Using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer (continued)**

2. Prior to the first analysis using the PowerPlex® Fusion System, you must create an Instrument Protocol, Size Standard, QC Protocol, Assay, File Name Convention and Results Group.
  - 2.a. To create a new Instrument Protocol, navigate to the Library, select **Instrument Protocols**, and then select **Create**. Alternatively, a previously created Instrument Protocol may be used.

Figure 5 shows the settings used at Promega for the Applied Biosystems® 3500xL Genetic Analyzer for the application type, dye set, capillary length, polymer, run module and appropriate protocol information. The only setting that was changed from the default settings is Dye Set.



**Figure 5. The ‘Create New Instrument Protocol’ window.**

The recommended settings are:

---

Application Type	HID
Capillary Length	36cm
Polymer	POP-4®
Dye Set	G5 (Promega G5 spectral)
Run Module	HID36_POP4(xl)
Injection Time <sup>1</sup>	15 seconds for the Applied Biosystems® 3500 Genetic Analyzer 24 seconds for the Applied Biosystems® 3500xL Genetic Analyzer
Injection Voltage	1.2kV
Run Voltage <sup>2</sup>	15kV
Run Time	1,210–1,500 seconds

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<sup>1</sup>Injection time may be modified to increase or decrease peak heights.

<sup>2</sup>The default run voltage is 15kV. Changing the run voltage may necessitate a change in run time. Changing the run voltage and run time can affect peak morphology and resolution. For more information refer to the Applied Biosystems Technical Note titled *Advanced Topics: Optional Alternate Running Conditions for 3500 Genetic Analyzers in the Human Identification (HID) Laboratory*.

When creating an Instrument Protocol, be sure to select the same dye set that was used to perform the Promega 5-dye spectral calibration.



Run time and other instrument settings should be optimized and validated in your laboratory.

When optimizing injection conditions in your laboratory, you may choose to create specific Instrument Protocols for each condition tested. If a single Instrument Protocol is used, follow the instructions in the *Applied Biosystems 3500/3500xL Genetic Analyzer User Guide* to edit a library entry.

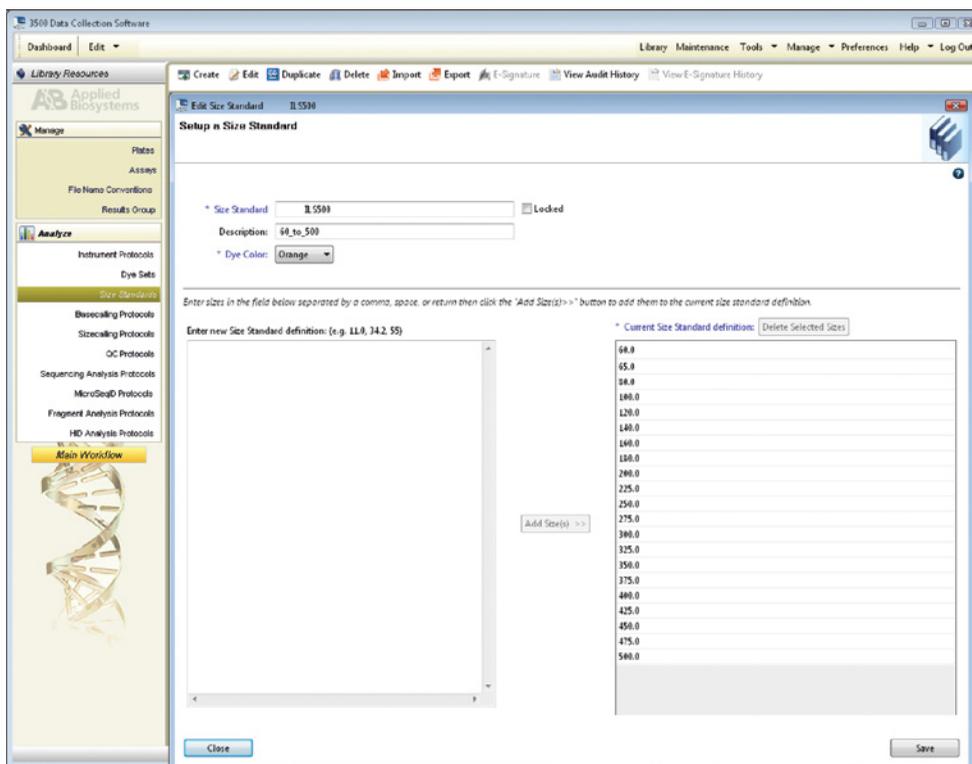
Assign a descriptive protocol name.

**Note:** For more detailed information refer to the *Applied Biosystems 3500/3500xL Genetic Analyzer User Guide*.

## 5.A. Detection of Amplified Fragments Using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer (continued)

- 2.b. To create a new Size Standard for the QC protocol, navigate to the Library. Select **Size Standards**, and then select **Create**. Alternatively, a previously created Size Standard may be used.

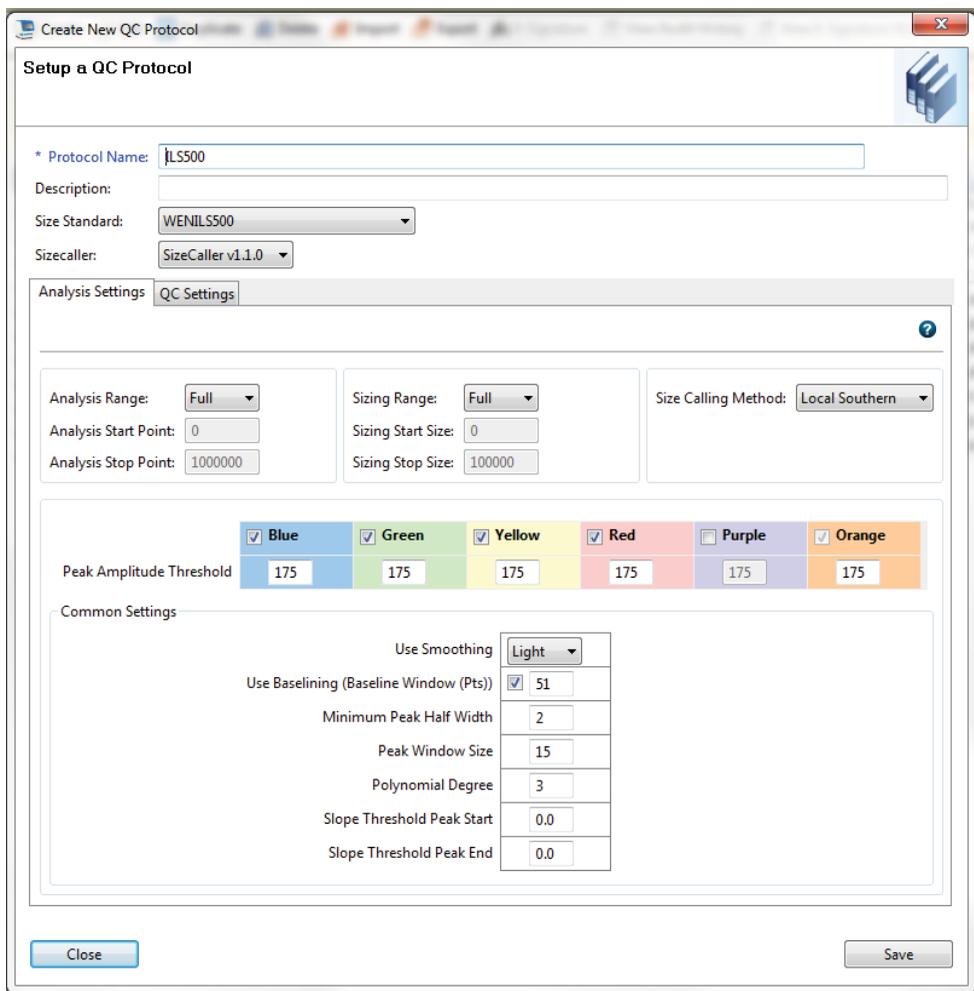
Assign the Size Standard a descriptive name such as “ILS500”. Choose **Orange** as the Dye Color. The fragments in the size standard are 60, 65, 80, 100, 120, 140, 160, 180, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475 and 500 bases. See Figure 6.



**Figure 6. The ‘Create New Size Standard’ window.**

2.c. To create a new QC Protocol, navigate to the Library. Select **QC Protocols**, and then select **Create**. Alternatively, a previously created QC Protocol may be used.

Assign a descriptive protocol name such as “ILS 500”. Select the size standard created in Step 2.b. The settings for the QC protocol should be based on the internally validated conditions for the PowerPlex® Fusion System on the Applied Biosystems® 3500 or 3500xL Genetic Analyzer. Figure 7 shows one option for these settings.



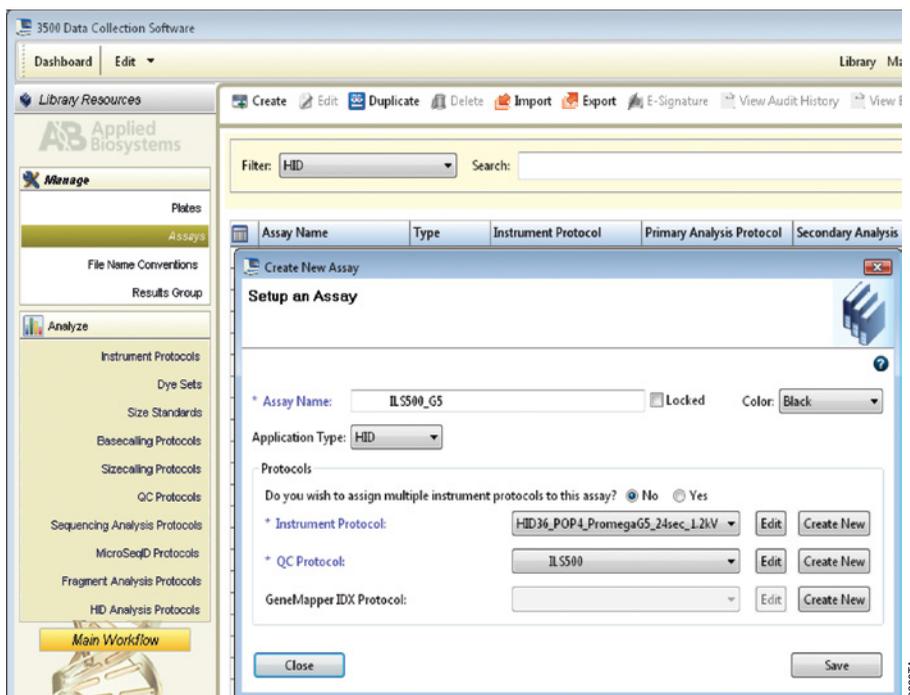
**Figure 7. The ‘Create New QC Protocol’ window.**

## 5.A. Detection of Amplified Fragments Using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer (continued)

- 2.d. To create a new Assay, navigate to the Library. Select **Assays**, and then select **Create**. Alternatively, a previously created Assay may be used.

In the ‘Create New Assay’ window (Figure 8), select the application type **HID**. Choose the Instrument Protocol created in Step 2.a and the QC Protocol created in Step 2.c. Assign a descriptive assay name. An Assay is required for all named samples on a plate.

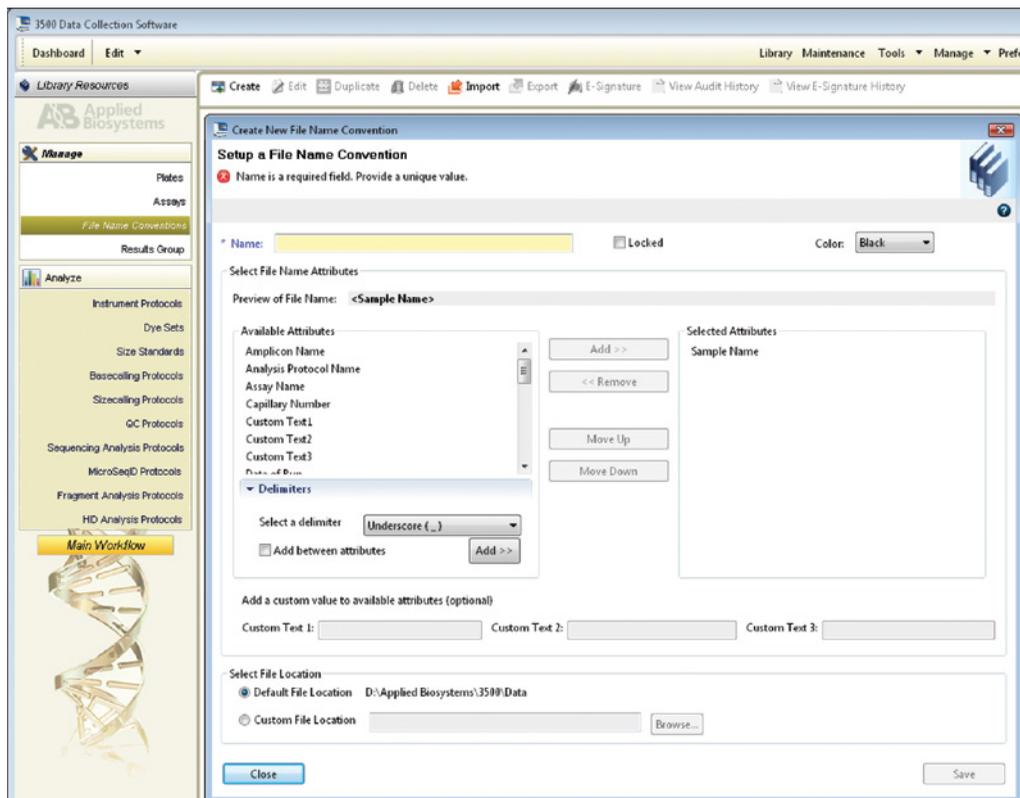
**Note:** If autoanalysis of sample data is desired, refer to the instrument user’s manual for instructions.



**Figure 8.** The ‘Create New Assay’ window.

2.e. To create a new File Name Convention (Figure 9), navigate to the Library. Select **File Name Conventions**, and then select **Create**. Alternatively, a previously created File Name Convention may be used.

Select the File Name Attributes according to your laboratory practices, and save with a descriptive name.

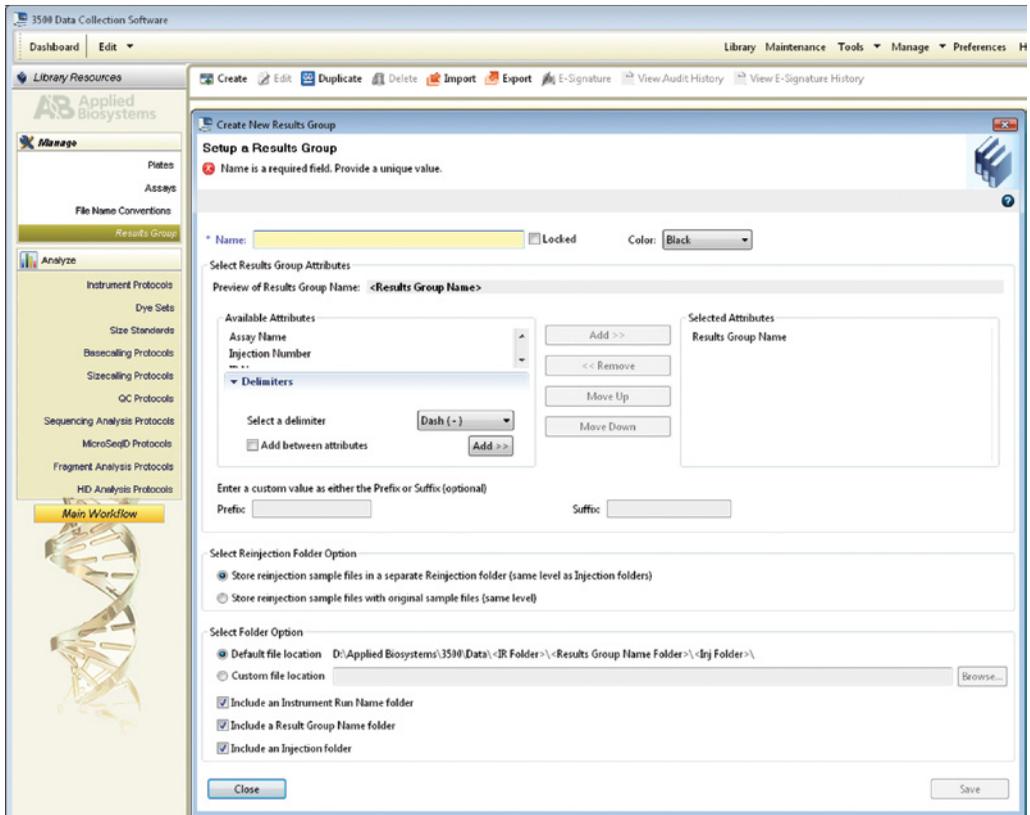


**Figure 9. The ‘Create New File Name Convention’ window.**

## 5.A. Detection of Amplified Fragments Using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer (continued)

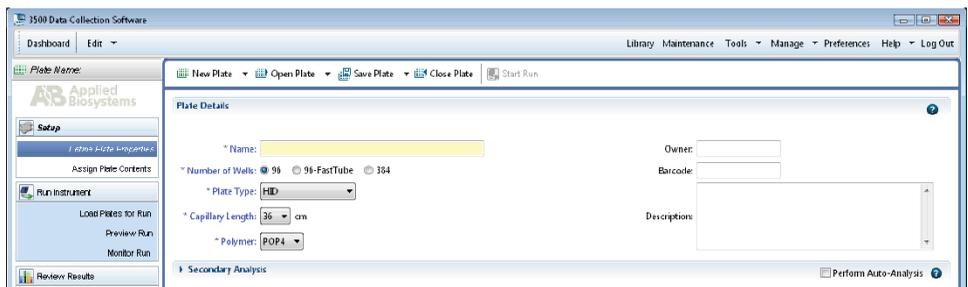
- 2.f. To create a new Results Group (Figure 10), navigate to the Library. Select **Results Group**, and then select **Create**. Alternatively, a previously created Results Group may be used.

Select the Results Group Attributes according to your laboratory practices. Save with a descriptive name.



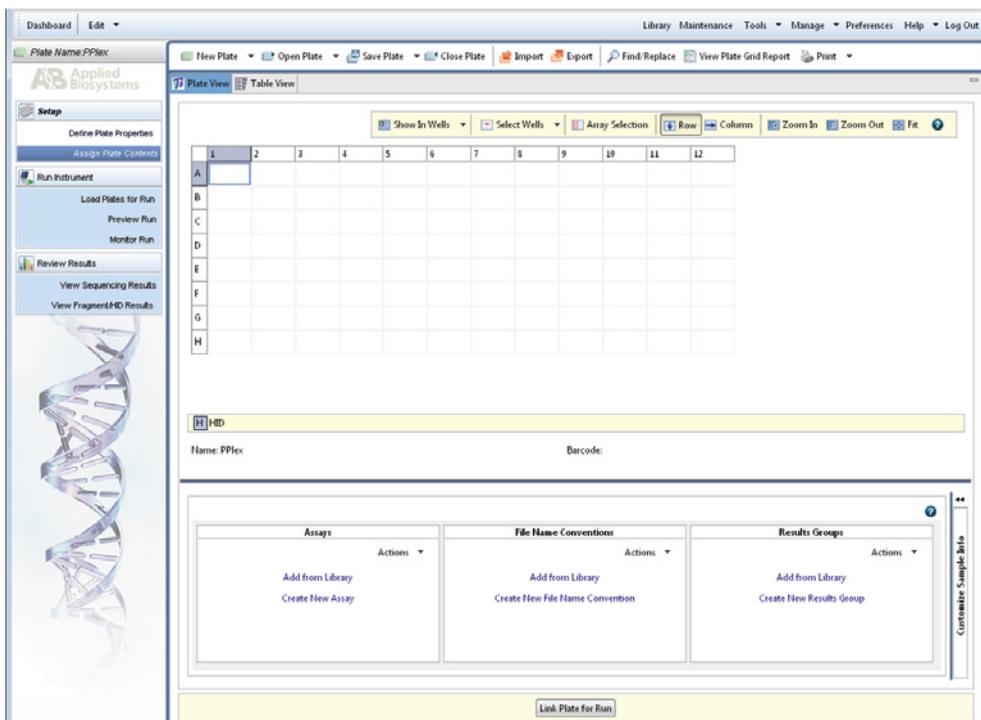
**Figure 10. The ‘Create New Results Group’ window.**

3. To create a New Plate, navigate to the Library, and from the Manage menu, select **Plates**, and then **Create**.
4. Assign a descriptive plate name. Select the plate type **HID** from the drop-down menu (Figure 11).



**Figure 11. Defining plate properties.**

5. Select **Assign Plate Contents** (Figure 12).

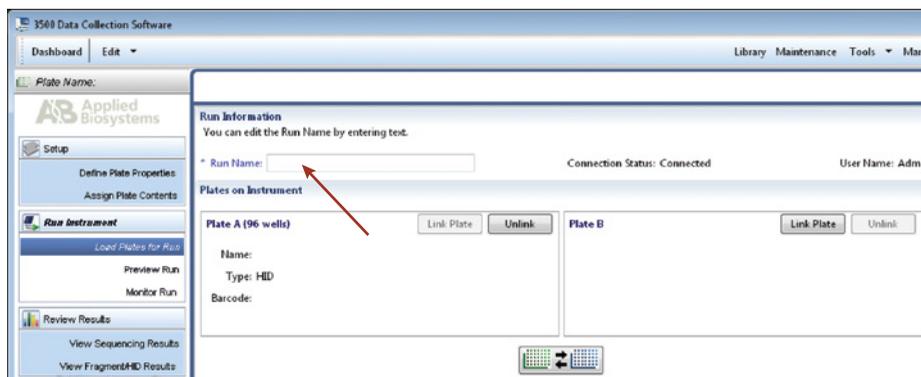


**Figure 12. Assigning plate contents.**

## 5.A. Detection of Amplified Fragments Using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer (continued)

6. Assign sample names to wells.
7. In the lower left portion of the screen, under Assays, use the 'Add from Library' option to select the Assay created in Step 2.d or one previously created. Click on the **Add to Plate** button, and close the window.
8. Under File Name Conventions, use the 'Add from Library' option to select the File Name Convention created in Step 2.e or one previously created. Click on the **Add to Plate** button, and close the window.
9. Under Results Groups, use the 'Add from Library' option to select the Results Group created in Step 2.f or one previously created. Click on the **Add to Plate** button, and close the window.
10. Highlight the sample wells, and then select the boxes in the Assays, File Name Conventions and Results Groups that pertain to those samples.
11. Select **Link Plate for Run**.
12. The 'Load Plate' window will appear. Select **Yes**.
13. In the 'Run Information' window (Figure 13), assign a Run Name. Select **Start Run** (not shown).

Each injection will take approximately 40 minutes.



**Figure 13. Assigning a run name.**

## 5.B. Detection of Amplified Fragments Using the ABI PRISM® 3100 or 3100-*Avant* Genetic Analyzer with Data Collection Software, Version 2.0, or the Applied Biosystems® 3130 or 3130*xl* Genetic Analyzer with Data Collection Software, Version 3.0 or 4.0

### Materials to Be Supplied by the User

- 95°C dry heating block, water bath or thermal cycler
- crushed ice, ice-water bath or freezer plate block
- centrifuge compatible with 96-well plates
- aerosol-resistant pipette tips
- 3100 or 3130 capillary array, 36cm
- plate retainer and base set (standard)
- POP-4® polymer for the Applied Biosystems® 3130 or 3130*xl* Genetic Analyzers
- 10X genetic analyzer buffer with EDTA
- MicroAmp® optical 96-well plate (or equivalent) and septa (Applied Biosystems)
- Hi-Di™ formamide (Applied Biosystems Cat.# 4311320)

 The quality of formamide is critical. Use only the recommended formamide. Freeze formamide in aliquots at –20°C. Multiple freeze-thaw cycles or long-term storage at 4°C may cause breakdown of formamide. Poor-quality formamide may contain ions that compete with DNA during injection, which results in lower peak heights and reduced sensitivity. A longer injection time may not increase the signal.

 Formamide is an irritant and a teratogen; avoid inhalation and contact with skin. Read the warning label, and take appropriate precautions when handling this substance. Always wear gloves and safety glasses when working with formamide.

### Sample Preparation

1. Prepare a loading cocktail by combining and mixing internal lane standard (ILS) and formamide as follows:  
[(0.5µl ILS) × (# samples)] + [(9.5µl formamide) × (# samples)]

**Note:** The volume of internal lane standard used in the loading cocktail can be adjusted to change the intensity of the size standard peaks based on laboratory preferences.

2. Vortex for 10–15 seconds to mix.
3. Pipet 10µl of formamide/internal lane standard mix into each well.
4. Add 1µl of amplified sample (or 1µl of Allelic Ladder Mix) to each well. Cover the wells with appropriate septa.

#### Notes:

1. Instrument detection limits vary; therefore, injection time, injection voltage or the amount of sample mixed with loading cocktail may need to be adjusted. Use the Module Manager in the data collection software to modify the injection time or voltage in the run module (see Instrument Preparation below).
2. Use a volume of allelic ladder that results in peak heights that are all consistently above the peak amplitude threshold determined as part of your internal validation.

## 5.B. Detection of Amplified Fragments Using the ABI PRISM® 3100 or 3100-*Avant* Genetic Analyzer with Data Collection Software, Version 2.0, or the Applied Biosystems® 3130 or 3130*xl* Genetic Analyzer with Data Collection Software, Version 3.0 or 4.0 (continued)

5. Centrifuge the plate briefly to remove air bubbles from the wells.
6. Denature samples at 95°C for 3 minutes, and then immediately chill on crushed ice, a freezer plate block or in an ice-water bath for 3 minutes. Denature samples just prior to loading the instrument.

### Instrument Preparation

Refer to the instrument user's manual for instructions on cleaning, installing the capillary array, performing a spatial calibration and adding polymer.

Analyze samples as described in the user's manual for the ABI PRISM® 3100 or 3100-*Avant* Genetic Analyzer and the Applied Biosystems® 3130 or 3130*xl* Genetic Analyzer with the following exceptions.

1. In the Module Manager, select **New**. Select **Regular** in the Type drop-down list, and select **HIDFragmentAnalysis36\_POP4** in the 'Template' drop-down list. Confirm that the injection time is 5 seconds, the injection voltage is 3kV and the run time is 1,500 seconds. Give a descriptive name to your run module, and select **OK**.  
**Note:** Instrument sensitivities can vary. The injection time and voltage may be adjusted in the Module Manager. A suggested range for the injection time is 3–22 seconds and for the injection voltage is 1–3kV.
2. In the Protocol Manager, select **New**. Type a name for your protocol. Select **Regular** in the 'Type' drop-down list, and select the run module you created in the previous step in the 'Run Module' drop-down list. Lastly, select **G5** in the dye-set drop-down list. Select **OK**.
3. In the Plate Manager, create a new plate record as described in the instrument user's manual. In the dialog box that appears, select **GeneMapper—Generic** in the 'Application' drop-down list, and select the appropriate plate type (96-well). Add entries in the owner and operator windows, and select **OK**.  
**Note:** If autoanalysis of sample data is desired, refer to the instrument user's manual for instructions.
4. In the GeneMapper® plate record, enter sample names in the appropriate cells. Scroll to the right. In the 'Results Group 1' column, select the desired results group. In the 'Instrument Protocol 1' column, select the protocol you created in Step 2. Be sure this information is present for each row that contains a sample name. Select **OK**.  
**Note:** To create a new results group, select **New** in the drop-down menu in the 'Results Group' column. Select the 'General' tab, and enter a name. Select the 'Analysis' tab, and select **GeneMapper—Generic** in the 'Analysis Type' drop-down list.
5. Place samples in the instrument, and close the instrument doors.
6. In the spectral viewer, select **Dye Set G5**, and confirm that the active dye set is the file generated for the PowerPlex® 5-dye chemistry.



It is critical to select the correct G5 spectral calibration for the PowerPlex® 5-dye chemistry.

If the PowerPlex® 5-dye chemistry is not the active dye set, locate the PowerPlex® 5-dye spectral calibration in the List of Calibrations for Dye Set G5, and select **Set**.

7. In the run scheduler, locate the plate record that you just created in Steps 3 and 4, and click once on the name to highlight it.
8. Once the plate record is highlighted, click the plate graphic that corresponds to the plate on the autosampler that contains your amplified samples.
9. When the plate record is linked to the plate, the plate graphic changes from yellow to green, and the green **Run Instrument** arrow becomes enabled.
10. Click on the green **Run Instrument** arrow on the toolbar to start the sample run.
11. Monitor electrophoresis by observing the run, view, array or capillaries viewer window in the data collection software. Each injection will take approximately 40 minutes.

## 6. Data Analysis

The instructions in this section are for use with GeneMapper® *ID-X* software or GeneMapper® *ID* software, version 3.2. Due to potential differences between software versions, some of the instructions may not apply to all software versions.

### 6.A. Importing PowerPlex® Fusion Panels, Bins and Stutter Text Files into GeneMapper® *ID-X* Software

To facilitate analysis of data generated with the PowerPlex® Fusion System, we have created panels, bins and stutter text files to allow automatic assignment of genotypes using GeneMapper® *ID-X* software. We recommend that users receive training from Applied Biosystems on the GeneMapper® *ID-X* software to familiarize themselves with proper operation of the software.

#### Getting Started

1. To obtain the proper panels, bins and stutter text files and WEN\_ILS\_500\_IDX.xml file for the PowerPlex® Fusion System, go to: **[www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/](http://www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/)**
2. Select the PowerPlex® System that you are using, and select **GeneMapper ID-X**. Enter your contact information, and select **Submit**.
3. Save the PowerPlex\_Fusion\_Panels\_IDX\_vX.x.txt, PowerPlex\_Fusion\_Bins\_IDX\_vX.x.txt and PowerPlex\_Fusion\_Stutter\_IDX\_vX.x.txt files, where “X.x” refers to the most recent version of the panels, bins and stutter text files, to a known location on your computer.
4. Save the WEN\_ILS\_500\_IDX.xml file to a known location on your computer.

## 6.A. Importing PowerPlex® Fusion Panels, Bins and Stutter Text Files into GeneMapper® ID-X Software (continued)

### Importing Panels, Bins and Stutter Text Files

1. Open the GeneMapper® ID-X software.
2. Select **Tools**, and then **Panel Manager**.
3. Highlight the 'Panel Manager' icon in the upper left navigation pane.
4. Select **File**, and then **Import Panels**.
5. Navigate to the panels text file downloaded in the Getting Started section. Select the file, and then **Import**.
6. Select **GeneMapper ID-X Security Group** as the Security Group. This allows access for all users of the software. Other security groups may be used.
7. In the navigation pane, highlight the PowerPlex Fusion panels folder that you just imported in Step 5.
8. Select **File**, and then **Import Bin Set**.
9. Navigate to the bins text file downloaded in the Getting Started section. Select the file, and then **Import**.
10. In the navigation pane, highlight the PowerPlex Fusion panels folder that you just imported in Step 5.
11. Select **File**, and then **Import Marker Stutter**. A warning will appear asking if you want to overwrite current values. Select **Yes**.
12. Navigate to the stutter text file downloaded in the Getting Started section. Select the file, and then **Import**.
13. At the bottom of the 'Panel Manager' window, select **OK**. This will save the panels, bins and stutter text files and close the window.

**Note:** If you are using GeneMapper® ID-X software, version 1.4 or higher, before closing the Panel Manager check the boxes to indicate DYS391 is a Y-marker. See Figure 14. This option is available only in GeneMapper® ID-X software, version 1.4 and higher, and is not available for older versions of GeneMapper® ID-X software.

Marker Name	Dye Color	Min Size	Max Size	Control Alleles	Marker	Comments	Y Marker	Label Alleles
1 AMEL	Blue	80.0	92.0	X,Y	9	none	<input type="checkbox"/>	X,Y
2 D3S1359	Blue	93.0	150.0	17,19	4	none	<input type="checkbox"/>	9,10,11,12,13,14,15,16,17,18,19,20
3 D1S1656	Blue	151.0	207.0	12,13	4	none	<input type="checkbox"/>	9,10,11,12,13,14,14.3,15,15.3,16,16.3,17,17.3,18,18.3,19,19.3,20.3
4 D2S441	Blue	207.5	247.5	10,14	4	none	<input type="checkbox"/>	8,9,10,11,11.3,12,13,14,15,16,17
5 D10S1248	Blue	248.0	295.0	13,15	4	none	<input type="checkbox"/>	8,9,10,11,12,13,14,15,16,17,18,19
6 D13S317	Blue	295.2	350.0	9,11	4	none	<input type="checkbox"/>	5,6,7,8,9,10,11,12,13,14,15,16,17
7 Penta E	Blue	354.5	474.9	7,14	5	none	<input type="checkbox"/>	5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24
8 D16S539	Green	73.0	129.0	9,13	4	none	<input type="checkbox"/>	4,5,6,7,8,9,10,11,12,13,14,15,16
9 D18S51	Green	129.1	215.5	16,18	4	none	<input type="checkbox"/>	7,8,9,10,10.2,11,12,13,13.2,14,15,16,17,18,19,20,21,22,23,24,25,26,27
10 D2S1338	Green	218.0	299.0	22,25	4	none	<input type="checkbox"/>	10,12,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28
11 CSF1PO	Green	309.0	363.0	12	4	none	<input type="checkbox"/>	5,6,7,8,9,10,11,12,13,14,15,16
12 Penta D	Green	370.0	461.0	12,13	5	none	<input type="checkbox"/>	2,2.2,3,2.5,6,7,8,9,10,11,12,13,14,15,16,17
13 TH01	Yellow	69.0	118.0	6,9,3	4	none	<input type="checkbox"/>	3,4,5,6,7,8,9,9.3,10,11,13,3
14 vWA	Yellow	122.0	192.0	16,19	4	none	<input type="checkbox"/>	10,11,12,13,14,15,16,17,18,19,20,21,22,23,24
15 D21S11	Yellow	198.0	266.5	29,31.2	4	none	<input type="checkbox"/>	24,24.2,25,25.2,26,27,28,28.2,29,29.2,30,30.2,31,31.2,32,32.2,33,33.2,34,34.2,35,35.2,36,37,38
16 D7S820	Yellow	267.0	316.0	8,11	4	none	<input type="checkbox"/>	5,6,7,8,9,10,11,12,13,14,15,16
17 D5S818	Yellow	316.5	379.0	12	4	none	<input type="checkbox"/>	6,7,8,9,10,11,12,13,14,15,16,17,18
18 TPOX	Yellow	387.0	443.5	11	4	none	<input type="checkbox"/>	4,5,6,7,8,9,10,11,12,13,14,15,16
19 DYS391	Yellow	443.6	495.0	10	4	none	<input checked="" type="checkbox"/>	5,6,7,8,9,10,11,12,13,14,15,16
20 D8S1179	Red	72.0	131.2	14,15	4	none	<input type="checkbox"/>	7,8,9,10,11,12,13,14,15,16,17,18,19
21 D12S391	Red	131.4	191.0	18,23	4	none	<input type="checkbox"/>	14,15,16,17,17.3,18,18.3,19,20,21,22,23,24,25,26,27
22 D19S433	Red	191.5	256.5	13,14	4	none	<input type="checkbox"/>	5,2.6,2.8,9,10,11,12,12.2,13,13.2,14,14.2,15,15.2,16,16.2,17,17.2,18,18.2
23 FGA	Red	257.0	415.0	20,23	4	none	<input type="checkbox"/>	14,15,16,17,18,18.2,19,19.2,20,20.2,21,21.2,22,22.2,23,23.2,24,24.2,25,25.2,26,27,28,29,30,31,2,32,2.33,2,42,2.43,2.44,2.45,2.46,2.48,2.50,2
24 D22S1045	Red	420.0	472.0	16	3	none	<input type="checkbox"/>	7,8,9,10,11,12,13,14,15,16,17,18,19,20

Figure 14. The GeneMapper® ID-X Software Y-Marker Check Box.

## **6.B. Importing the WEN ILS 500 IDX Size Standard into GeneMapper® ID-X Software**

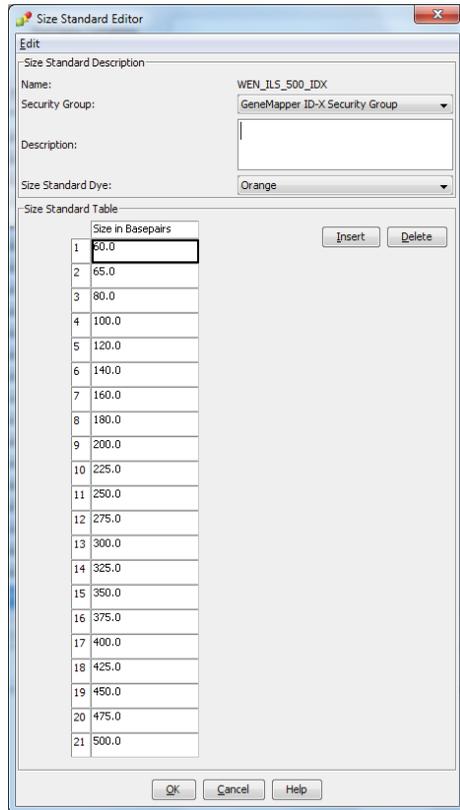
There are two options when creating a size standard. Use this protocol or the alternative protocol in Section 6.C.

1. Select **Tools**, and then **GeneMapper ID-X Manager**.
2. Select the 'Size Standard' tab.
3. Select **Import**.
4. Navigate to the location of the WEN\_ILS\_500\_IDX.xml file downloaded in Section 6.A.
5. Highlight the file, and then select **Import**.
6. Select **GeneMapper ID-X Security Group**. This allows access for all users of the software. Other security groups may be used.
7. Select **Done** to save changes and close the GeneMapper® ID-X Manager.

## **6.C. Creating a Size Standard with GeneMapper® ID-X Software**

1. Select **Tools**, and then **GeneMapper ID-X Manager**.
2. Select the 'Size Standard' tab.
3. Select **New**.
4. In the 'Size Standard Editor' window (Figure 15), select **GeneMapper ID-X Security Group** as the Security Group. This allows access for all users of the software. Other security groups may be used.
5. Enter a detailed name, such as "WEN\_ILS\_500\_IDX".
6. Choose **Orange** for the Size Standard Dye.
7. Enter the sizes of the internal lane standard fragments (60, 65, 80, 100, 120, 140, 160, 180, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475 and 500 bases). See Section 9.B, Figure 27.
8. Select **OK**.

### 6.C. Creating a Size Standard with GeneMapper® ID-X Software (continued)



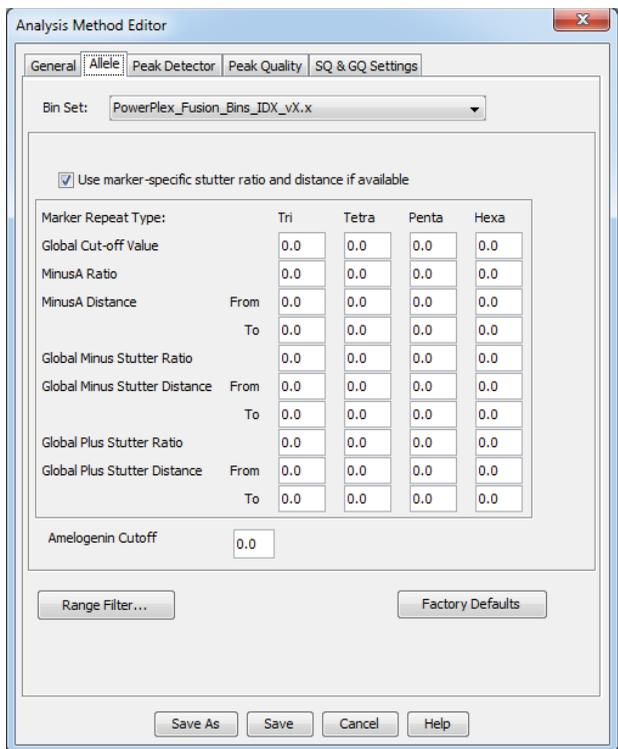
**Figure 15. The GeneMapper® ID-X Software Size Standard Editor.**

### 6.D. Creating a Casework Analysis Method with GeneMapper® ID-X Software

These instructions are intended as a guide to start analyzing data in GeneMapper® ID-X software. They are not intended as comprehensive instructions for using GeneMapper® ID-X software. We recommend that users contact Applied Biosystems for training on the software.

1. Select **Tools**, and then **GeneMapper ID-X Manager**.
2. Select the 'Analysis Methods' tab.
3. Select **New**, and a new analysis method dialog box will open.
4. In the 'Analysis Method Editor' window, select **GeneMapper ID-X Security Group** as the Security Group. This allows access for all users of the software. Other security groups may be used.

5. Enter a descriptive name for the analysis method, such as “PowerPlex Fusion”.
6. Select the ‘Allele’ tab (Figure 16).
7. Select the bins text file that was imported in Section 6.A.
8. Ensure that the “Use marker-specific stutter ratio and distance if available” box is checked. We recommend the settings shown in Figure 16 for proper filtering of stutter peaks when using the PowerPlex® Fusion System. You may need to optimize these settings. In-house validation should be performed.



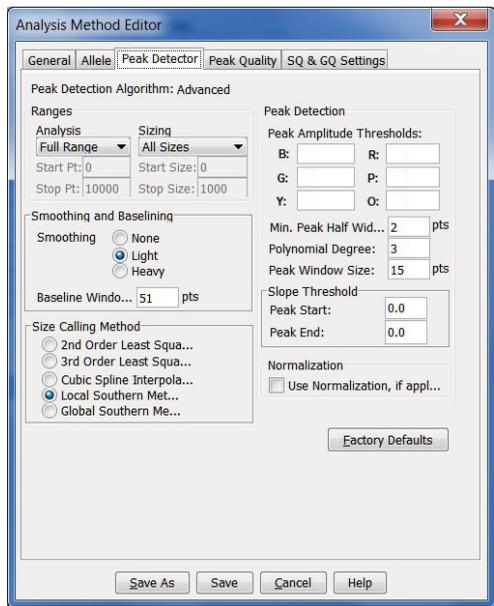
**Figure 16. The GeneMapper® ID-X Software ‘Allele’ tab.**

### 6.D. Creating a Casework Analysis Method with GeneMapper® ID-X Software (continued)

9. Select the 'Peak Detector' tab (Figure 17). You will need to optimize these settings. In-house validation should be performed.

**Notes:**

1. Select full range or partial range for the analysis range. When using a partial range, choose an appropriate analysis range based on your data. Choose a start point after the primer peak and just before the first defined internal lane standard peak to help ensure proper sizing of the internal lane standard.
2. The peak amplitude thresholds are the minimum peak heights at which the software will call a peak. Individual laboratories should determine their peak amplitude thresholds from internal validation studies.
3. The Normalization box can be checked or unchecked.



**Figure 17. The GeneMapper® ID-X Software 'Peak Detector' tab.**

10. Select the 'Peak Quality' tab. You may change the settings for peak quality.

**Note:** For Steps 10 and 11, see the GeneMapper® ID-X user's manual for more information. The settings in Steps 10 and 11 should be based on the results of your internal validation.

11. Select the 'SQ & GQ Settings' tab. You may change these settings.
12. Select **Save** to save the new analysis method.
13. Select **Done** to exit the GeneMapper® ID-X Manager.

## Processing Data for Casework Samples

1. Select **File**, and then **New Project**.
2. Select **Edit**, and then **Add Samples to Project**.
3. Browse to the location of the run files. Highlight desired files, and then select **Add to list** followed by **Add**.
4. In the ‘Sample Type’ column, use the drop-down menu to select **Allelic Ladder**, **Sample**, **Positive Control** or **Negative Control** as appropriate for the sample. Every folder in the project must contain at least one allelic ladder injection that is designated as **Allelic Ladder** in the ‘Sample Type’ column for proper genotyping.  
**Note:** The positive control DNA defined in the GeneMapper® *ID-X* panel file is the 2800M Control DNA. Redefine the genotype in the panel file if using a different positive control DNA.
5. In the ‘Analysis Method’ column, select the analysis method created previously in this section.
6. In the ‘Panel’ column, select the panels text file that was imported in Section 6.A.
7. In the ‘Size Standard’ column, select the size standard that was imported in Section 6.B or created in Section 6.C.
8. Select **Analyze** (green arrow button) to start data analysis.  
**Note:** By default, the software is set to display the ‘Analysis Requirements Summary’ window and the ‘Allelic Ladder Analysis Summary’ window if an analysis requirement is not met. After analysis is complete, the default setting is to show the ‘Analysis Summary’ tab. If these default settings are changed, manual troubleshooting may be necessary.
9. If all analysis requirements are met, the ‘Save Project’ window will open (Figure 18).



**Figure 18. The ‘Save Project’ window.**

10. Enter the project name.
11. Choose the applicable security group from the drop-down menu, and then select **OK**.

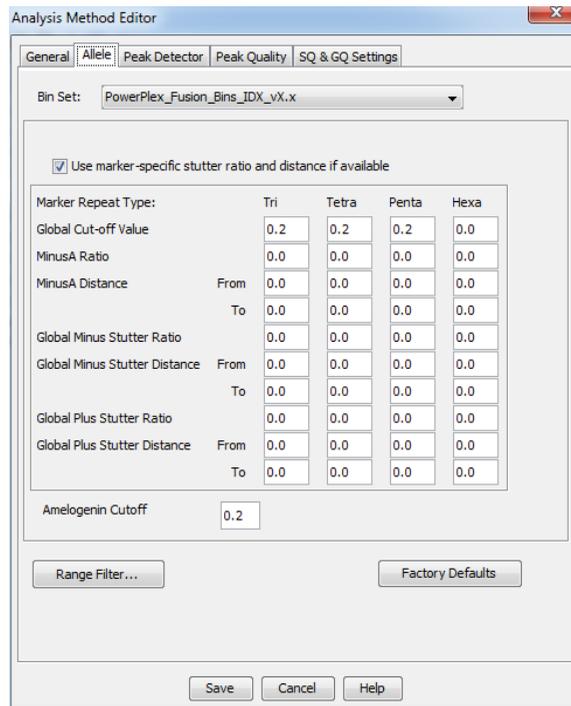
When the analysis is finished, the ‘Analysis Summary’ screen will appear. We recommend that you review any yellow or red marker header bars in the plots view and handle them according to laboratory standard operating procedures.

The values displayed in the ‘Analysis Method Peak Quality’ and ‘SQ & GQ Settings’ tabs are defaults and will affect the quality values displayed in the plot settings. We recommend that you modify the values in these tabs to fit your laboratory’s data analysis protocols.

### 6.E. Creating a Databasing or Paternity Analysis Method with GeneMapper® ID-X Software

These instructions are intended as a guide to start analyzing data in GeneMapper® ID-X software. They are not intended as comprehensive instructions for using the GeneMapper® ID-X software. We recommend that users contact Applied Biosystems for training on the software.

1. Select **Tools**, and then **GeneMapper ID-X Manager**.
2. Select the 'Analysis Methods' tab.
3. Select **New**, and a new analysis method dialog box will open.
4. In the 'Analysis Method Editor' window, select **GeneMapper ID-X Security Group** as the Security Group. This allows access for all users of the software. Other security groups may be used.
5. Enter a descriptive name for the analysis method, such as "PowerPlex Fusion 20% Filter".
6. Select the 'Allele' tab (Figure 19).
7. Select the bins text file that was imported in Section 6.A.



**Figure 19. The GeneMapper® ID-X Software 'Allele' tab with settings for using a 20% peak filter.**

8. Ensure that the “Use marker-specific stutter ratio and distance if available” box is checked. Doing this will assign locus-specific stutter filters and distances from the imported stutter file. Ensure that the appropriate global filter is applied to this analysis method. For example, for a 20% filter enter “0.20” for the Amelogenin Cutoff and Global Cutoff Value for Tri, Tetra and Penta repeats (Figure 19). You may need to optimize these settings. In-house validation should be performed.
9. Select the ‘Peak Detector’ tab (Figure 17). You will need to optimize these settings. In-house validation should be performed.

**Notes:**

1. Select full range or partial range for the analysis range. When using a partial range, choose an appropriate analysis range based on your data. Choose a start point after the primer peak and just before the first defined internal lane standard peak to help ensure proper sizing of the internal lane standard.
  2. The peak amplitude thresholds are the minimum peak heights at which the software will call a peak. Individual laboratories should determine their peak amplitude thresholds from internal validation studies.
  3. The normalization box can be checked or unchecked.
10. Select the ‘Peak Quality’ tab. You may change the settings for peak quality.  
**Note:** For Steps 10 and 11, see the GeneMapper® *ID-X* user’s manual for more information. The settings in Steps 10 and 11 should be based on the results of your internal validation.
  11. Select the ‘SQ & GQ Settings’ tab. You may change these settings.
  12. Select **Save** to save the new analysis method.
  13. Select **Done** to exit the GeneMapper® *ID-X* Manager.

**Processing Data for Databasing or Paternity Samples**

1. Select **File**, and then **New Project**.
2. Select **Edit**, and then **Add Samples to Project**.
3. Browse to the location of run files. Highlight desired files, and then select **Add to list** followed by **Add**.
4. In the ‘Sample Type’ column, use the drop-down menu to select **Allelic Ladder**, **Sample**, **Positive Control** or **Negative Control** as appropriate for the sample. Every folder in the project must contain at least one allelic ladder injection that is designated as **Allelic Ladder** in the ‘Sample Type’ column for proper genotyping.  
**Note:** The positive control DNA defined in the GeneMapper® *ID-X* panel file is the 2800M Control DNA. Redefine the genotype in the panel file if using a different positive control DNA.
5. In the ‘Analysis Method’ column, select the analysis method created previously in this section.
6. In the ‘Panel’ column, select the panels text file that was imported in Section 6.A.
7. In the ‘Size Standard’ column, select the size standard that was imported in Section 6.B or created in Section 6.C.



## 6.E. Creating a Databasing or Paternity Analysis Method with GeneMapper® ID-X Software (continued)

8. Select **Analyze** (green arrow button) to start data analysis.

**Note:** By default, the software is set to display the ‘Analysis Requirements Summary’ and the ‘Allelic Ladder Analysis Summary’ windows if an analysis requirement is not met. After analysis is complete, the default setting is to show the ‘Analysis Summary’ tab. If these default settings are changed, manual troubleshooting may be necessary.

9. If all analysis requirements are met, the ‘Save Project’ window will open (Figure 18).
10. Enter the project name.
11. Choose the applicable security group from the drop-down menu, and then select **OK**.

When the analysis is finished, the ‘Analysis Summary’ screen will appear. We recommend that you review any yellow or red marker header bars in the plots view and handle them according to laboratory standard operating procedures.

The values displayed in the ‘Analysis Method Peak Quality’ and ‘SQ & GQ Settings’ tabs are defaults and will affect the quality values displayed in the plot settings. We recommend that you modify the values in these tabs to fit your laboratory’s data analysis protocols.

## 6.F. Importing PowerPlex® Fusion Panels and Bins Text Files with GeneMapper® ID Software, Version 3.2

To facilitate analysis of data generated with the PowerPlex® Fusion System, we have created panels and bins text files to allow automatic assignment of genotypes using GeneMapper® ID software, version 3.2. We recommend that users of GeneMapper® ID software, version 3.2, complete the *Applied Biosystems GeneMapper® ID Software Human Identification Analysis Tutorial* to familiarize themselves with proper operation of the software. For GeneMapper® ID software, version 3.1, we recommend upgrading to version 3.2.

**Note:** Run files generated using the Applied Biosystems® 3500 or 3500xL Genetic Analyzer cannot be analyzed using GeneMapper® ID Software, version 3.2. You must analyze these files with GeneMapper® ID-X software.

### Getting Started

1. To obtain the proper panels and bins text files and WEN\_ILS\_500.xml file for the PowerPlex® Fusion System go to: [www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/](http://www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/)
2. Select the PowerPlex® System that you are using, and select **GeneMapper ID**. Enter your contact information, and select **Submit**.
3. Save the PowerPlex\_Fusion\_Panels\_vX.x.txt and PowerPlex\_Fusion\_Bins\_vX.x.txt files, where “X.x” refers to the most recent version of the panels and bins text files, to a known location on your computer.
4. Save the WEN\_ILS\_500.xml file to a known location on your computer.

## Importing Panels and Bins Text Files

These instructions loosely follow the Applied Biosystems GeneMapper® *ID* software tutorial, pages 1–4.

1. Open the GeneMapper® *ID* software, version 3.2.
2. Select **Tools**, and then **Panel Manager**.
3. Highlight the ‘Panel Manager’ icon in the upper left navigation pane.
4. Select **File**, and then **Import Panels**.
5. Navigate to the panels text file downloaded in the Getting Started section. Select the file, and then **Import**.
6. In the navigation pane, highlight the PowerPlex Fusion panels folder that you just imported in Step 5.
7. Select **File**, and then **Import Bin Set**.
8. Navigate to the bins text file downloaded in the Getting Started section. Select the file, and then **Import**.
9. At the bottom of the ‘Panel Manager’ window, select **OK**. This will save the panels and bins text files and close the window.

## 6.G. Importing the WEN ILS 500 Size Standard into GeneMapper® *ID* Software, Version 3.2

There are two options when creating a size standard. Use this protocol or the alternative protocol in Section 6.H.

The WEN\_ILS\_500.xml file is available for download at:

**[www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/](http://www.promega.com/resources/software-firmware/str-analysis/genemapper-id-software-panels-and-bin-sets/)**

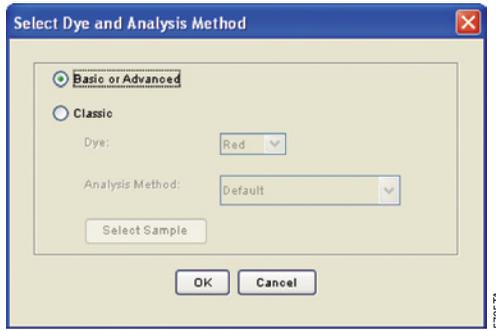
Save the WEN\_ILS\_500.xml file to a known location on your computer.

1. Select **Tools**, and then **GeneMapper Manager**.
2. Select the ‘Size Standard’ tab.
3. Select **Import**.
4. Browse to the location of the WEN\_ILS\_500.xml file downloaded in Section 6.F.
5. Highlight the file, and then select **Import**.
6. Select **Done** to save changes and exit the GeneMapper® Manager.

## 6.H. Creating a Size Standard with GeneMapper® *ID* Software, Version 3.2

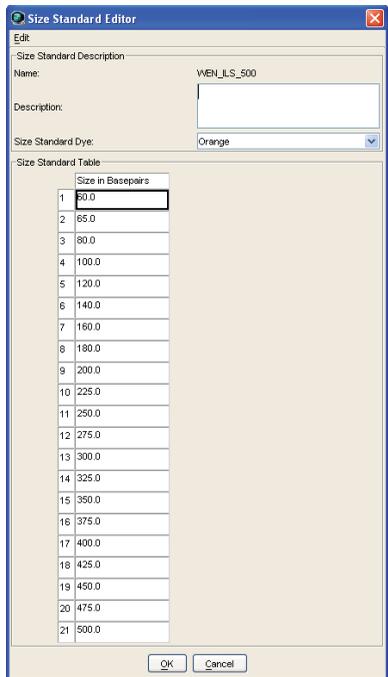
1. Select **Tools**, and then **GeneMapper Manager**.
2. Select the ‘Size Standard’ tab.
3. Select **New**.
4. Select **Basic or Advanced** (Figure 20). The type of analysis method selected must match the type of analysis method created earlier. Select **OK**.

**6.H. Creating a Size Standard with GeneMapper® ID Software, Version 3.2 (continued)**



**Figure 20. The ‘Select Dye and Analysis Method’ window.**

5. Enter a detailed name, such as “WEN\_ILS\_500”, in the Size Standard Editor (Figure 21).
6. Choose **Orange** for the Size Standard Dye.
7. Enter the sizes of the internal lane standard fragments (60, 65, 80, 100, 120, 140, 160, 180, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475 and 500 bases). See Section 9.B, Figure 27.
8. Select **OK**.



**Figure 21. The GeneMapper® ID Software Size Standard Editor.**

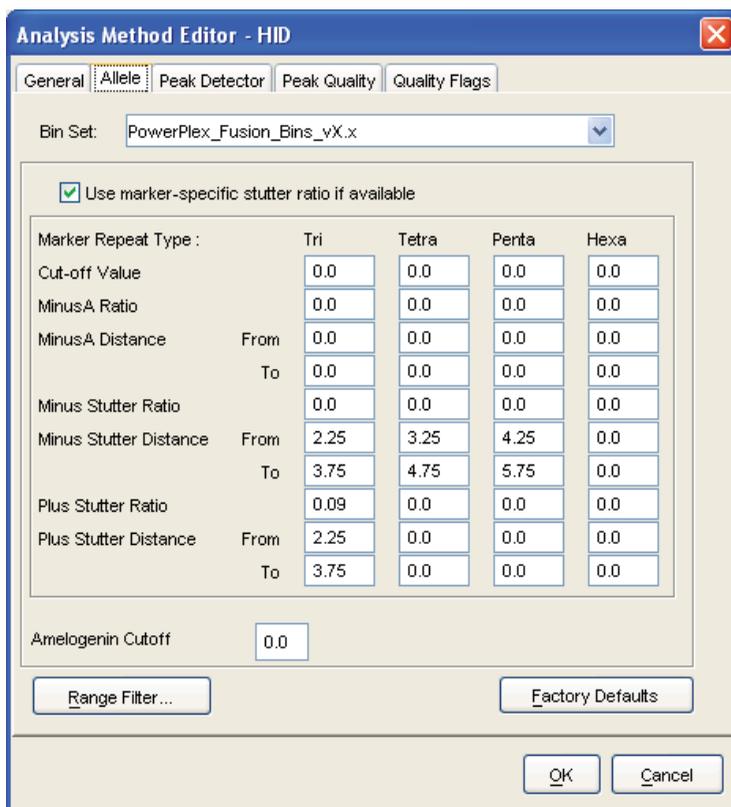
## 6.I. Creating a Casework Analysis Method with GeneMapper® ID Software, Version 3.2

These instructions are intended as a guide to start analyzing data in GeneMapper® ID software. They are not intended as comprehensive instructions for using GeneMapper® ID software. We recommend that users contact Applied Biosystems for training on the software. These instructions loosely follow the Applied Biosystems GeneMapper® ID software tutorial, pages 5–11.

1. Select **Tools**, and then **GeneMapper Manager**.
2. Select the 'Analysis Methods' tab.
3. Select **New**, and a new analysis method dialog box will open.
4. Select **HID**, and select **OK**.

**Note:** If you do not see the HID option, you do not have the GeneMapper® ID software. Contact Applied Biosystems.

5. Enter a descriptive name for the analysis method, such as “PowerPlex Fusion”.
6. Select the 'Allele' tab (Figure 22).



Marker Repeat Type :		Tri	Tetra	Penta	Hexa
Cut-off Value		0.0	0.0	0.0	0.0
MinusA Ratio		0.0	0.0	0.0	0.0
MinusA Distance	From	0.0	0.0	0.0	0.0
	To	0.0	0.0	0.0	0.0
Minus Stutter Ratio		0.0	0.0	0.0	0.0
Minus Stutter Distance	From	2.25	3.25	4.25	0.0
	To	3.75	4.75	5.75	0.0
Plus Stutter Ratio		0.09	0.0	0.0	0.0
Plus Stutter Distance	From	2.25	0.0	0.0	0.0
	To	3.75	0.0	0.0	0.0

Amelogenin Cutoff: 0.0

**Figure 22. The GeneMapper® ID Software 'Allele' tab.**



## 6.I. Creating a Casework Analysis Method with GeneMapper® ID Software, Version 3.2 (continued)

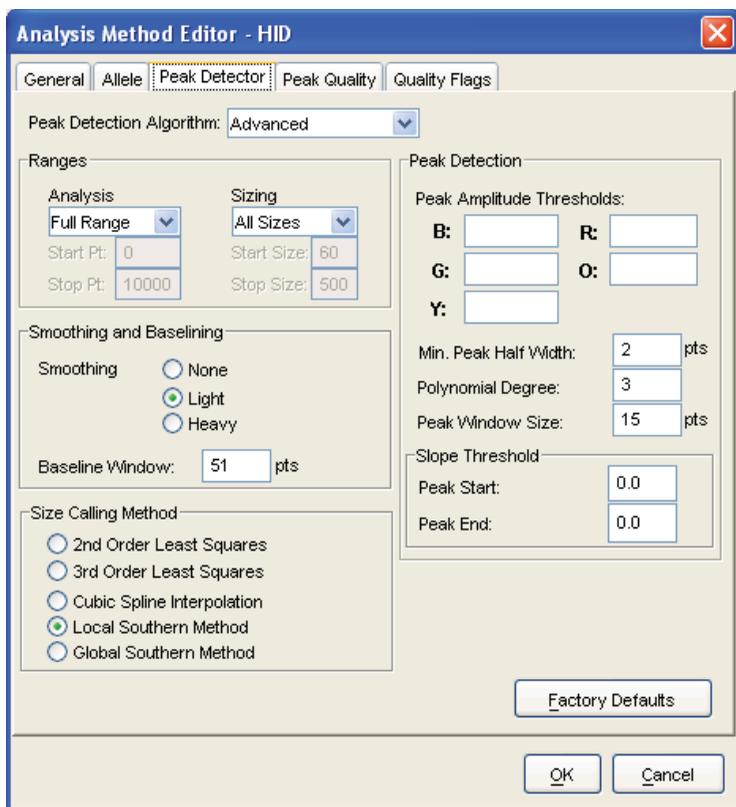
7. Select the bins text file that was imported in Section 6.F.
8. Ensure that the “Use marker-specific stutter ratio if available” box is checked.
9. Enter the values shown in Figure 22 for proper filtering of stutter peaks when using the PowerPlex® Fusion System. For an explanation of the proper usage and effects of these settings, refer to the Applied Biosystems user bulletin titled *Installation Procedures and New Features for GeneMapper ID Software 3.2*.

**Note:** Some of these settings have been optimized and are different from the recommended settings in the user bulletin. You will need to optimize these settings. In-house validation should be performed.

10. Select the ‘Peak Detector’ tab (Figure 23). You will need to optimize these settings. In-house validation should be performed.

### Notes:

1. Select full range or partial range for the analysis range. When using a partial range, choose an appropriate analysis range based on your data. Choose a start point after the primer peak and just before the first defined internal lane standard peak to help ensure proper sizing of the internal lane standard.
2. The peak amplitude thresholds are the minimum peak heights at which the software will call a peak. Individual laboratories should determine their peak amplitude thresholds from internal validation studies.



**Figure 23. The GeneMapper® ID Software ‘Peak Detector’ tab.**

11. Select the ‘Peak Quality’ tab. You may change the settings for peak quality.

**Note:** For Steps 11 and 12, see the GeneMapper® ID user’s manual for more information.

12. Select the ‘Quality Flags’ tab. You may change these settings.

13. Select **OK** to save your settings.



## 6.I. Creating a Casework Analysis Method with GeneMapper® ID Software, Version 3.2 (continued)

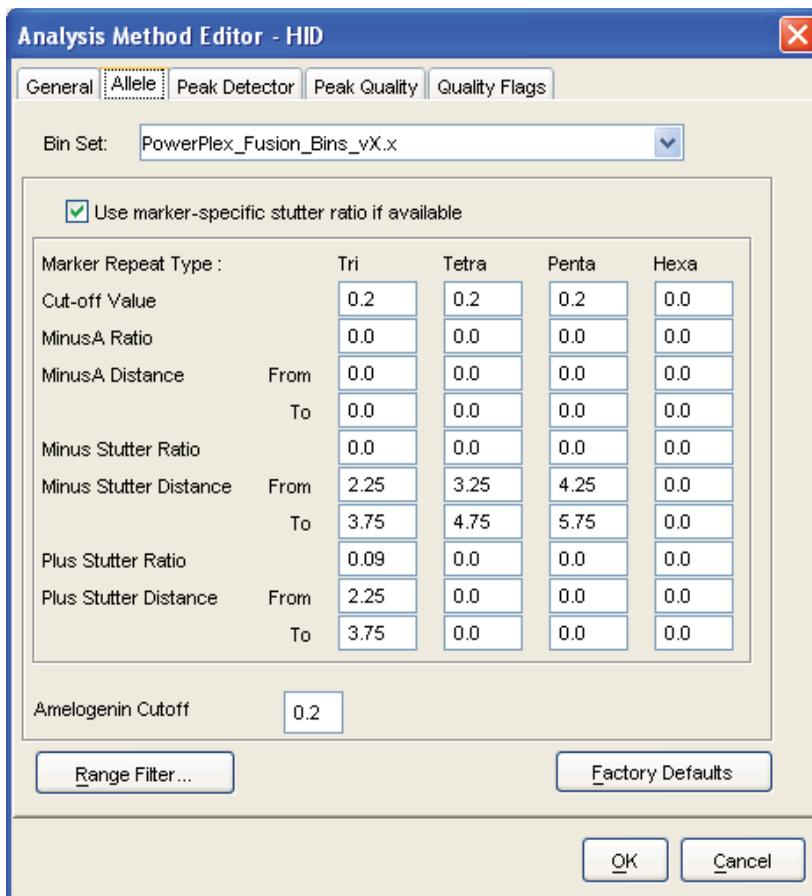
### Processing Data for Casework Samples

1. Select **File**, and then **New Project**.
2. Select **Edit**, and then **Add Samples to Project**.
3. Browse to the location of the run files. Highlight desired files, and then select **Add to list** followed by **Add**.
4. In the 'Sample Type' column, use the drop-down menu to select **Ladder**, **Sample**, **Positive Control** or **Negative Control** as appropriate for the sample. Every folder in the project must contain at least one allelic ladder injection that is designated as **Ladder** in the 'Sample Type' column for proper genotyping.  
**Note:** The positive control DNA defined in the GeneMapper® ID panel file is the 2800M Control DNA. Redefine the genotype in the panel file if using a different positive control DNA.
5. In the 'Analysis Method' column, select the analysis method created previously in this section.
6. In the 'Panel' column, select the panels text file that was imported in Section 6.F.
7. In the 'Size Standard' column, select the size standard that was imported in Section 6.G or created in Section 6.H.
8. Select **Analyze** (green arrow button) to start data analysis.

## 6.J. Creating a Databasing or Paternity Analysis Method with GeneMapper® ID Software, Version 3.2

1. Select **Tools**, and then **GeneMapper Manager**.
2. Select the 'Analysis Methods' tab.
3. Select **New**, and a new analysis method dialog box will open.
4. Select **HID**, and select **OK**.  
**Note:** If you do not see the HID option, you do not have the GeneMapper® ID software. Contact Applied Biosystems.
5. Enter a descriptive name for the analysis method, such as "PowerPlex\_Fusion\_20%filter".

6. Select the 'Allele' tab (Figure 24).



**Figure 24. The GeneMapper® ID Software 'Allele' tab with settings for using a 20% peak filter.**

7. Select the bins text file that was imported in Section 6.F.
8. Ensure that the "Use marker-specific stutter ratio if available" box is checked. Ensure that the appropriate global filter is applied to this analysis method. For example, for a 20% filter enter "0.20" for the Amelogenin and Global Cut-off Value for Tri, Tetra and Penta repeats (Figure 24).

**Note:** If you do not check the "Use marker-specific stutter ratio if available" box, you will need to optimize these settings. In-house validation should be performed.



## 6.J. Creating a Databasing or Paternity Analysis Method with GeneMapper® ID Software, Version 3.2 (continued)

9. Enter the values shown in Figure 24 for proper filtering of peaks when using the PowerPlex® Fusion System. For an explanation of the proper usage and effect of these settings, refer to the Applied Biosystems user bulletin titled *Installation Procedures and New Features for GeneMapper ID Software 3.2*.
10. Select the 'Peak' Detector tab (Figure 23). You will need to optimize these settings. In-house validation should be performed.

### Notes:

1. Select full range or partial range for the analysis range. When using a partial range, choose an appropriate analysis range based on your data. Choose a start point after the primer peak and just before the first defined internal lane standard peak to help ensure proper sizing of the internal lane standard.
  2. The peak amplitude thresholds are the minimum peak heights that the software will call as a peak. Individual laboratories should determine their peak amplitude thresholds from internal validation studies.
11. Select the 'Peak Quality' tab. You may change the settings for peak quality.  
**Note:** For Steps 11 and 12, see the GeneMapper® ID user's manual for more information.
  12. Select the 'Quality Flags' tab. You may change these settings.
  13. Select **OK** to save your settings.

## Processing Data for Databasing or Paternity Samples

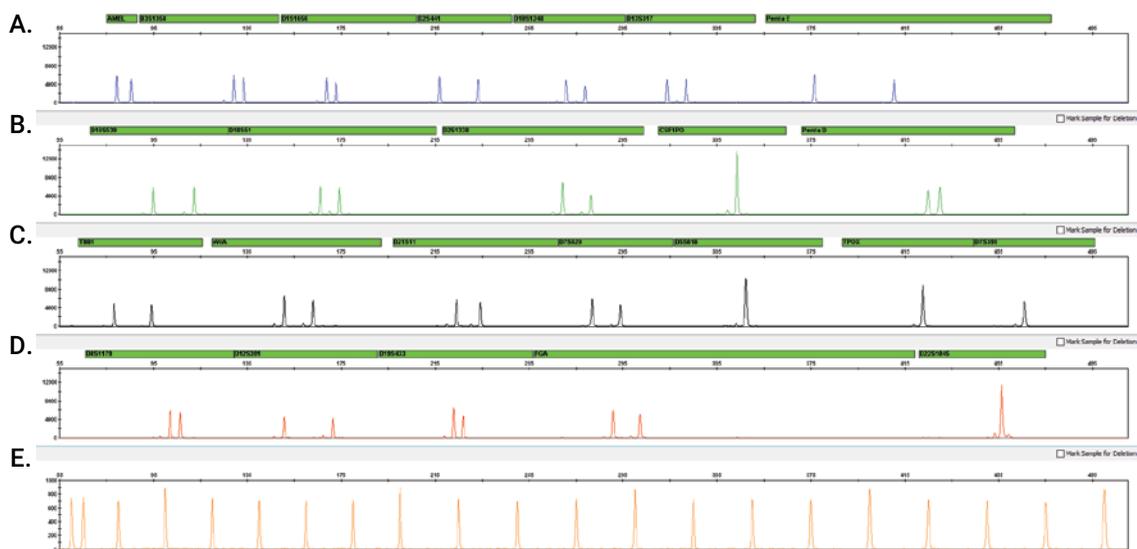
1. Select **File**, and then **New Project**.
2. Select **Edit**, and then **Add Samples to Project**.
3. Browse to the location of the run files. Highlight the desired files, and then select **Add to list** followed by **Add**.
4. In the 'Sample Type' column, use the drop-down menu to select **Ladder**, **Sample**, **Positive Control** or **Negative Control** as appropriate for the sample. Every folder in the project must contain at least one allelic ladder injection that is designated as **Ladder** in the 'Sample Type' column for proper genotyping.  
**Note:** The positive control DNA defined in the GeneMapper® ID panel file is the 2800M Control DNA. Redefine the genotype in the panel file if using a different positive control DNA.
5. In the 'Analysis Method' column, select the analysis method created previously in this section.
6. In the 'Panel' column, select the panels text file that was imported in Section 6.F.
7. In the 'Size Standard' column, select the size standard that was imported in Section 6.G or created in Section 6.H.
8. Select **Analyze** (green arrow button) to start the data analysis.

## 6.K. Controls

1. Observe the results for the negative control. Using the protocols defined in this manual, the negative control should be devoid of amplification products.
2. Observe the results for the 2800M Control DNA. The expected 2800M DNA allele designations for each locus are listed in Table 8 (Section 9.A).

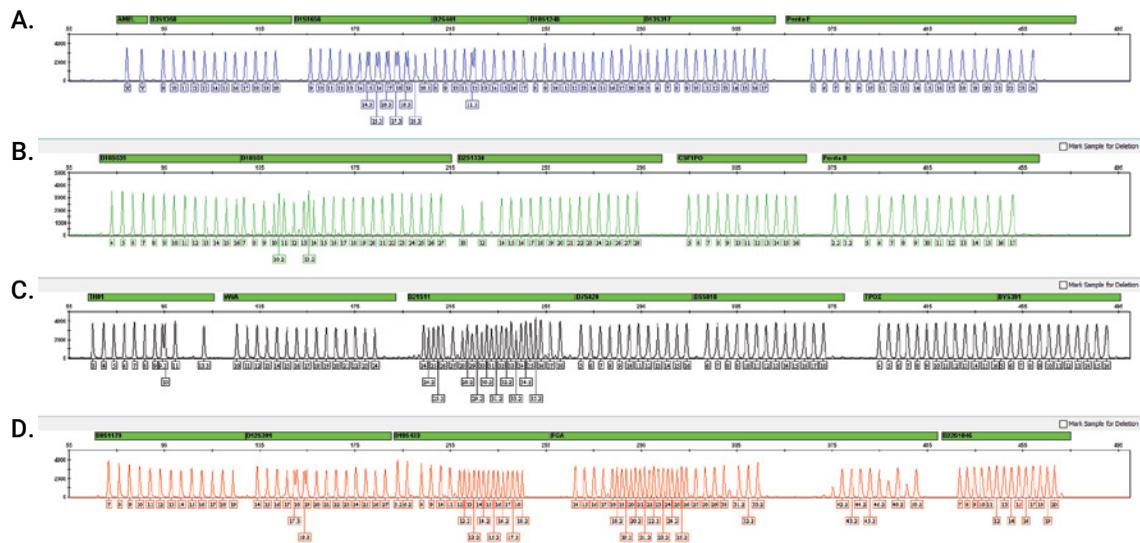
## 6.L. Results

Representative results of the PowerPlex® Fusion System are shown in Figure 25. The PowerPlex® Fusion Allelic Ladder Mix is shown in Figure 26.



**Figure 25. The PowerPlex® Fusion System.** The 2800M Control DNA (0.5ng) was amplified using the PowerPlex® Fusion System and 30 cycles. Amplification products were mixed with WEN Internal Lane Standard 500 and analyzed with an Applied Biosystems® 3500 Genetic Analyzer using a 1.2kV, 8-second injection. Results were analyzed using GeneMapper® *ID-X* software, version 1.4. **Panel A.** An electropherogram showing the peaks of the fluorescein-labeled loci: Amelogenin, D3S1358, D1S1656, D2S441, D10S1248, D13S317 and Penta E. **Panel B.** An electropherogram showing the peaks of the JOE-labeled loci: D16S539, D18S51, D2S1338, CSF1PO and Penta D. **Panel C.** An electropherogram showing the peaks of the TMR-ET-labeled loci: TH01, vWA, D21S11, D7S820, D5S818, TPOX and DYS391. **Panel D.** An electropherogram showing the peaks of the CXR-ET-labeled loci: D8S1179, D12S391, D19S433, FGA and D22S1045. **Panel E.** An electropherogram showing the 60bp to 500bp fragments of the WEN Internal Lane Standard 500.

## 6.L. Results (continued)



**Figure 26. The PowerPlex® Fusion Allelic Ladder Mix.** The PowerPlex® Fusion Allelic Ladder Mix was analyzed with an Applied Biosystems® 3500 Genetic Analyzer using a 1.2kV, 8-second injection. The sample file was analyzed with the GeneMapper® ID-X software, version 1.4, and PowerPlex® Fusion panels and bins text files. **Panel A.** The fluorescein-labeled allelic ladder components and their allele designations. **Panel B.** The JOE-labeled allelic ladder components and their allele designations. **Panel C.** The TMR-ET-labeled allelic ladder components and their allele designations. **Panel D.** The CXR-ET-labeled allelic ladder components and their allele designations.

## Artifacts and Stutter

Stutter products are a common amplification artifact associated with STR analysis. Stutter products often are observed one repeat unit below the true allele peak and, occasionally, two repeat units smaller or one repeat unit larger than the true allele peak. Frequently, alleles with a greater number of repeat units will exhibit a higher percent stutter. A trinucleotide repeat locus, like D22S1045, will have more pronounced stutter in both  $n-3$  and  $n+3$  positions than a typical tetranucleotide repeat locus. The pattern and intensity of stutter may differ slightly between primer sets for the same loci.

The mean plus three standard deviations at each locus is used in the PowerPlex® Fusion panels text file for locus-specific filtering in the GeneMapper® ID software, version 3.2, and in the PowerPlex® Fusion stutter text file for locus-specific filtering in GeneMapper® ID-X software.

In addition to stutter peaks, you may observe the following DNA-dependent (Table 4) and DNA-independent (with or without human genomic DNA) artifact peaks (Table 5).

**Table 4. DNA-Dependent Artifacts Observed in Amplification Reactions with Human Genomic DNA.**

Locus or Dye Label	Artifact Size
Fluorescein	~63–68 bases <sup>1</sup> ~88–112 bases <sup>2</sup>
JOE	~73–85 bases <sup>1</sup> ~214 bases <sup>1</sup> ~247 bases <sup>1</sup>
TMR-ET	~66–72 bases <sup>1</sup> ~172–176 bases <sup>1</sup>
CXR-ET	~175–183 bases <sup>1</sup>
Amelogenin	$n-1^3$
D1S1656	$n-2, n+2^3$
D2S441	$n-1^3$
D13S317	$n-2, n+2^3$
D18S51	$n-2, n+2^3$
D21S11	$n-2, n+2^3$
D7S820	$n-2, n+2^3$
D5S818	$n-2, n+2^3; n-8$ to $n-9^4$
D12S391	$n-2, n+2, n-3^3$
D19S433	$n-2, n+2^3$

<sup>1</sup>Artifact sizes may vary depending on CE instrumentation and environmental conditions in the laboratory.

<sup>2</sup>For artifacts in this size range, rfu approximately 1.5% or less of the main peaks may be observed at the D3S1358 locus.

<sup>3</sup>Number of bases below ( $n-$ ) or above ( $n+$ ) the true allele peak, respectively.

<sup>4</sup>Low intensity peaks (50–200rfu) that migrate approximately 8–9 bases in front of the main allele may represent DNA secondary structure.



## 6.L. Results (continued)

**Table 5. DNA-Independent Artifacts Observed in Amplification Reactions with and without Human Genomic DNA.**

Dye Label	Artifact Size <sup>1</sup>
Fluorescein	~58–59 bases
	~61–63 bases
	~83–86 bases
JOE	~62–67 bases
TMR-ET	~58–62 bases

<sup>1</sup>Artifact sizes may vary depending on CE instrumentation and environmental conditions in the laboratory.

The PowerPlex® Fusion System is optimized for use with POP-4® polymer. This system was not developed for use with POP-7® polymer; if using POP-7® polymer, optimization and in-house validation are required. Some artifacts specific to the PowerPlex® Fusion System with POP-7® polymer have been noted. The global filters used for database analyses will generally filter these artifact peaks. Artifact peaks may be seen in the fluorescein channel at 71–73 bases, 82–84 bases and 98–100 bases. In the JOE channel, artifacts may be seen at 87–89 bases. The signal strength of the JOE-channel artifact increases with storage of the amplification plate at 4°C, most commonly when plates are left at 4°C for a few days. We recommend storing amplification products at –20°C.

## 7. Troubleshooting

For questions not addressed here, please contact your local Promega Branch Office or Distributor. Contact information available at: [www.promega.com](http://www.promega.com). E-mail: [genetic@promega.com](mailto:genetic@promega.com)

### 7.A. Amplification and Fragment Detection

This section provides information about general amplification and detection. For questions about amplification of extracted DNA, see Section 7.B. For questions about direct amplification, see Sections 7.C and 7.D.

#### Symptoms

Faint or absent allele peaks

#### Causes and Comments

The Master Mix was not vortexed well before use. Vortex the Master Mix for 15 seconds before dispensing into the PCR amplification mix.

Primer concentration was too low. Use the recommended primer concentration. Vortex the Primer Pair Mix for 15 seconds before use.

An air bubble formed at the bottom of the reaction tube. Use a pipette to remove the air bubble, or centrifuge the reactions briefly before thermal cycling.

**Symptoms**
**Causes and Comments**

Faint or absent allele peaks (continued)

Thermal cycler, plate or tube problems. Review the thermal cycling protocol. We have not tested reaction tubes, plates or thermal cyclers that are not listed. Calibrate the thermal cycler heating block if necessary.

Repeat sample preparation using fresh formamide. Long-term storage of amplified sample in formamide can result in loss of signal.

Poor capillary electrophoresis injection (ILS peaks also affected). Re-inject the sample.

Laser is starting to fail. Check the laser power.

Poor-quality formamide was used. Use only Hi-Di™ formamide when analyzing samples.

Faint or absent allele peaks for the positive control reaction

Improper storage of the 2800M Control DNA. Store the 2800M Control DNA at 2–10°C. Make sure that the 2800M Control DNA is stored at 2–10°C for at least 24 hours before use; do not refreeze. Vortex before use.

Extra peaks visible in one or all color channels

Contamination with another template DNA or previously amplified DNA. Cross-contamination can be a problem. Use aerosol-resistant pipette tips, and change gloves regularly.

Do not store the PCR amplification mix for a prolonged period. Add the mix to the wells of the reaction plate as soon as the mix is prepared. Add the DNA source as soon as possible to each well and follow immediately by thermal cycling.

Samples were not denatured completely. Heat denature samples for the recommended time, and then cool on crushed ice, a freezer plate block or in an ice-water bath immediately prior to capillary electrophoresis. Do not cool samples in a thermal cycler set at 4°C, as this may lead to artifacts due to DNA reannealing.

Double-stranded DNA migrates faster than single-stranded DNA during capillary electrophoresis. Appearance of “shadow” peaks migrating in front of the main peaks, especially if the shadow peaks are separated by the same distance as the main peaks in a heterozygote, can indicate the presence of double-stranded DNA due to incomplete denaturation or post-injection re-annealing.



## 7.A. Amplification and Fragment Detection (continued)

### Symptoms

Extra peaks visible in one or all color channels (continued)

### Causes and Comments

CE-related artifacts (“spikes”). Minor voltage changes or urea crystals passing by the laser can cause “spikes” or unexpected peaks. Spikes sometimes appear in one color but often are easily identified by their presence in more than one color. Re-inject samples to confirm.

CE-related artifacts (contaminants). Contaminants in the water used with the instrument or to dilute the 10X genetic analyzer buffer may generate peaks in the fluorescein and JOE channels. Use autoclaved deionized water; change vials and wash buffer reservoir.

Incorrect G5 spectral was active when analyzing samples with the Applied Biosystems® 3130 or 3130xl Genetic Analyzer. Re-run samples, and confirm that the PowerPlex® G5 spectral calibration is set for G5. See instructions for instrument preparation in Section 5.B.

Pull-up or bleedthrough. Pull-up can occur when peak heights are too high or if a poor or incorrect matrix is applied to the samples.

- Perform a new spectral calibration, and re-run the samples.
- Confirm the correct spectral calibration was used for the sample run.
- Instrument sensitivities can vary. Optimize the injection conditions. See Section 5.
- Reboot the Applied Biosystems® 3500 or 3500xL Genetic Analyzer and the instrument’s computer. Repeat the spectral calibration. Do not allow borrowing when running the spectral calibration on the Applied Biosystems® 3500 or 3500xL Genetic Analyzer.

Dye blob artifacts. The signal strength of certain dye blob artifacts increases with the storage of the amplification plate at 4°C, sometimes in as short a time period as overnight but more commonly when left at 4°C for a few days. We recommend storing amplification products at –20°C.

An incorrect internal late standard was used. Use the size standard provided in the kit.

The CE polymer was beyond its expiration date, or polymer was stored at room temperature for more than one week.

Maintain instrumentation on a daily or weekly basis, as recommended by the manufacturer.

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**Symptoms**

Extra peaks visible in one or all color channels (continued)

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**Causes and Comments**

Polymer-related artifacts. This system was not developed for use with POP-7<sup>®</sup> polymer; if using POP-7<sup>®</sup> polymer, optimization and in-house validation are required. The use of POP-7<sup>®</sup> polymer can change the migration and sizing location of artifacts compared to the POP-4<sup>®</sup> locations. An artifact can be seen with the POP-7<sup>®</sup> polymer at 87–89bp in the JOE channel and at 71–73, 82–84 or 98–100bp in the fluorescein channel.

Allelic ladder not running the same as samples

Allelic ladder and primer pair mix were not compatible. Ensure that the allelic ladder is from the same kit as the primer pair mix.

Be sure that the allelic ladder and samples are from the same instrument run.

Migration of samples changed slightly over the course of a CE run with many samples. This may be due to changes in temperature or the CE column over time. Use a different injection of allelic ladder to determine sizes.

Poor injection of allelic ladder. Include more than one ladder per instrument run.

Internal size standard was not assigned correctly. Evaluate the sizing labels on the ILS, and correct if necessary.

Peak height imbalance

Miscellaneous balance problems. At the first use, thaw the Primer Pair Mix and Master Mix completely. Vortex the Primer Pair Mix and Master Mix for 15 seconds before use; do not centrifuge the Primer Pair Mix or Master Mix after mixing. Calibrate thermal cyclers and pipettes routinely.

PCR amplification mix was not mixed well. Vortex the PCR amplification mix for 5–10 seconds before dispensing into the reaction tubes or plate.

## 7.B. Amplification of Extracted DNA

The following information is specific to amplification of purified DNA. For information about general amplification and detection, see Section 7.A.

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**Symptoms**

Faint or absent allele peaks

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**Causes and Comments**

Impure template DNA. Depending on the DNA purification procedure used and sample source, inhibitors might be present in the DNA sample. As DNA sample volume increases relative to the total amplification reaction volume, this may be more likely.

Insufficient template. Use the recommended amount of template DNA if available. Quantify template DNA before use if possible.



## 7.B. Amplification of Extracted DNA (continued)

### Symptoms

Faint or absent allele peaks (continued)

### Causes and Comments

High salt concentration or altered pH. If the DNA template is stored in TE buffer that is not pH 8.0 or contains a higher EDTA concentration, the DNA volume should not exceed 20% of the total reaction volume. Carryover of  $K^+$ ,  $Na^+$ ,  $Mg^{2+}$  or EDTA from the DNA sample can negatively affect PCR. A change in pH also may affect PCR. Store DNA in  $TE^{-4}$  buffer (10mM Tris-HCl [pH 8.0], 0.1mM EDTA),  $TE^{-4}$  buffer with 20 $\mu$ g/ml glycogen or nuclease-free water.

The reaction volume was too low. This system is optimized for a final reaction volume of 25 $\mu$ l for extracted DNA. Decreasing the reaction volume may result in suboptimal performance.

Extra peaks visible in one or all color channels

Amplification of more than the recommended amount of purified DNA can result in a higher number of artifact peaks due to overamplification, resulting in saturating signal. Use the recommended amount of template DNA. See Section 6.L for additional information about stutter and artifacts. The amount of template will need to be optimized if you are using reduced reaction volumes.

Artifacts of STR amplification. Amplification of STRs can result in artifacts that appear as peaks one base smaller than the allele due to incomplete addition of the 3' A residue.

- Be sure to perform the recommended extension step at 60°C after thermal cycling.
- Decrease the amount of template DNA. Using more than the recommended amount of template DNA can result in incomplete adenylation.
- Decrease cycle number.
- Increase the final extension time.

Peak height imbalance

Amplification of greater than the recommended amount of template can result in imbalance, with the smaller loci showing more product than larger loci. Use less template or fewer cycles. The amount of template will need to be optimized if you are using reduced reaction volumes.

Degraded DNA sample. DNA template was degraded, and larger loci showed diminished yield.

Insufficient template DNA. Use the recommended amount of template DNA if available. Stochastic effects can occur when amplifying low amounts of template.

**Symptoms**

Peak height imbalance (continued)

**Causes and Comments**

Impure template DNA. Inhibitors that may be present in forensic samples can lead to allele dropout or imbalance.

Imbalance may be seen more often when using the maximum template volume or a reduced amplification reaction volume.

The reaction volume was too low. This system is optimized for a final reaction volume of 25µl. Decreasing the reaction volume may result in suboptimal performance.

**7.C. Direct Amplification of DNA from Storage Card Punches**

The following information is specific to direct amplification of DNA from storage card punches. For additional information about general amplification and detection, see Section 7.A.

**Symptoms**

Faint or absent allele peaks

**Causes and Comments**

For direct amplification reactions that require the addition of AmpSolution™ Reagent, its omission can result in inhibition of the amplification reaction. Review the amplification setup and confirm whether or not AmpSolution™ Reagent is required for your direct amplification reactions.

DNA was not accessible on nonlytic material. Pretreat nonlytic materials with PunchSolution™ Reagent to ensure that DNA is liberated from cellular proteins.

Poor sample deposition. Shedding and collection of donor cells was variable. Increase cycle number.

Poor sample transfer to storage card or variable sampling from storage card. Take punches from a different portion of the card. Increasing cycle number can increase peak heights.

Too much sample in the reaction can result in inhibition, decreasing intensity of peaks (especially larger amplicons). Be sure to use the recommended number of punches. Follow the manufacturer's recommendations when depositing sample onto the storage card.

Amplification was inhibited when using more than one storage card punch with blood. Use only one 1.2mm storage card punch with blood.

The reaction volume was too low. Decreasing the reaction volume from that recommended in the protocol may result in suboptimal performance. Use the recommended number of punches for the reaction volume used.

## 7.C. Direct Amplification of DNA from Storage Card Punches (continued)

### Symptoms

Faint or absent allele peaks (continued)

### Causes and Comments

Active PunchSolution™ Reagent carried over into amplification reactions with nonlytic card punches. Ensure that the heat block reached 70°C and samples were incubated for 30 minutes or until wells are dry. Incubation for shorter time periods may result in incomplete inactivation of the PunchSolution™ Reagent. We have not tested longer incubation times.

Inactive PunchSolution™ Reagent was used to pretreat nonlytic punches. Thaw the PunchSolution™ Reagent at 2–10°C. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Do not refreeze, as this may reduce activity.

Consider using PunchSolution™ Reagent with lytic card punches.

Faint or absent allele peaks  
for the positive control reaction

If the positive control reaction failed to amplify, check to make sure that the correct amount of 2800M Control DNA was added to the reaction. Due to the reduced cycle number, it is necessary to increase the mass of DNA to obtain a profile. Use the recommended amount of 2800M Control DNA per amplification reaction. This mass of DNA should be reduced if cycle number is increased, and increased if the cycle number is decreased. Increase or decrease the mass of 2800M Control DNA by twofold for every one-cycle decrease or increase respectively. We do not recommend including blank punches in the 2800M Control DNA reaction.

Extra peaks visible in one  
or all color channels

Punch was contaminated with DNA from another sample. Perform punches on a blank card between samples to minimize potential carryover between samples.

Amplification of processed punches with high amounts of DNA can result in artifact peaks due to overamplification, resulting in saturating signal on the CE instrument. Be sure to use the recommended number of punches. Use of a larger punch size or a smaller reaction volume may result in overamplification and signal saturation. If the signal is saturated, repeat the amplification with a smaller punch, a larger reaction volume or reduced cycle number.

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**Symptoms**

Extra peaks visible in one or all color channels (continued)

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**Causes and Comments**

Amplification of excess template for a given cycle number can result in overloading of the capillary upon electrokinetic injection. The presence of excess DNA in the capillary makes it difficult to maintain the DNA in a denatured single-stranded state. Some single-stranded DNA renatures and becomes double-stranded. Double-stranded DNA migrates faster than single-stranded DNA during capillary electrophoresis and appears as “shadow” peaks migrating in front of the main peaks (i.e., smaller in size). If this occurs at a heterozygous locus, it is sometimes possible to see two “shadow” peaks that differ in size from one another by approximately the same distance as the single-stranded alleles.

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Artifacts of STR amplification. Direct amplification of high amounts of template can result in a higher number of artifact peaks. Use the recommended punch size and number of punches. Optimize the cycle number. See Section 6.L for additional information on stutter and artifacts.

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Artifacts of STR amplification. Amplification of STRs can result in artifacts that appear as peaks one base smaller than the allele due to incomplete addition of the 3' A residue.

- Be sure to perform the recommended extension step at 60°C after thermal cycling (Section 4.B).
- Decrease cycle number.
- Increase the final extension time.

---

Peak height imbalance

---

Excessive amount of DNA. Amplification of high amounts of template can result in an imbalance, with smaller loci showing more product than larger loci.

- Be sure to use the recommended number of punches. Follow the manufacturer's recommendations when depositing sample onto the card.
- Decrease cycle number.

---

The cycle number was too high. Decrease the cycle number by one cycle, and repeat the amplification.

---

## Symptoms

Peak height imbalance (continued)

## Causes and Comments

For direct amplification reactions that require the addition of AmpSolution™ Reagent, its omission can result in inhibition of the amplification reaction. Review the amplification setup and confirm whether or not AmpSolution™ Reagent is required for your direct amplification reactions.

Amplification was inhibited when using more than one storage card punch with blood. Use only one 1.2mm storage card punch with blood.

If you used two 1.2mm nonlytic card punches, try using one punch treated with 10µl of PunchSolution™ Reagent per 12.5µl or 25µl amplification reaction.

The reaction volume was too low. Decreasing the reaction volume can result in suboptimal performance due to inhibitors present in lytic cards and PunchSolution™ Reagent.

DNA was not accessible on nonlytic material. Small loci may amplify preferentially, with large loci dropping out. Pretreat nonlytic materials with PunchSolution™ Reagent to ensure that DNA is liberated from cellular proteins.

Active PunchSolution™ Reagent carried over into amplification reactions with nonlytic card punches. Larger loci are most susceptible to carryover and will drop out before the smaller loci.

- Ensure that the heat block reached 70°C and samples were incubated for 30 minutes or until wells are dry. Incubation for shorter time periods may result in incomplete inactivation of the PunchSolution™ Reagent.
- We recommend treating one 1.2mm nonlytic card punch with 10µl of PunchSolution™ Reagent per 12.5µl or 25µl amplification reaction.
- Reducing the PunchSolution™ Reagent volume may improve results for reactions with reduced amplification volumes. Optimization and validation are required.

Inactive PunchSolution™ Reagent was used to pretreat nonlytic punches. Thaw the PunchSolution™ Reagent at 2–10°C. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Do not refreeze, as this may reduce activity.

Extreme variability in sample-to-sample peak heights

There can be significant individual-to-individual variability in the number of cells on a card, resulting in peak height variability between samples. The PunchSolution™ Kit maximizes the recovery of amplifiable DNA from nonlytic punches but does not normalize the amount of DNA present.

## 7.D. Direct Amplification of DNA from Swabs

The following information is specific to direct amplification of DNA from swabs after pretreatment using the SwabSolution™ Kit. For additional information about general amplification and detection, see Section 7.A.

### Symptoms

Faint or absent allele peaks

### Causes and Comments

Poor sample deposition. Shedding and collection of donor cells was variable. Increase cycle number.

Inactive SwabSolution™ Reagent. Thaw the SwabSolution™ Reagent completely in a 37°C water bath, and mix by gentle inversion. Store the SwabSolution™ Reagent at 2–10°C. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Do not refreeze, as this may reduce activity.

Active SwabSolution™ Reagent carried over into the amplification reaction. Ensure that the heat block reached 70°C (90°C if using a 2.2ml, Square-Well Deep Well Plate) and samples were incubated for the full 30 minutes. Incubation for shorter time periods may result in incomplete reagent inactivation. Do not use an incubator to incubate tubes or plates; heat transfer is inefficient and will result in poor performance. Use only a heat block to maintain efficient heat transfer. We have tested 60-minute incubation times and observed no difference in performance compared to a 30-minute incubation.

For direct amplification reactions that require the addition of AmpSolution™ Reagent, its omission can result in inhibition of the amplification reaction. Review the amplification setup and confirm whether or not AmpSolution™ Reagent is required for your direct amplification reactions.

DNA was not accessible on nonlytic material. Pretreat swabs with SwabSolution™ Reagent to ensure that DNA is liberated from cellular proteins.

Faint or absent peaks for the positive control reaction

If the positive control reaction failed to amplify, check to make sure that the correct amount of 2800M Control DNA was added to the reaction. Due to the reduced cycle numbers used with swab extracts, it is necessary to increase the mass of 2800M Control DNA to obtain a profile. Use the recommended amount of 2800M Control DNA per amplification reaction. This mass of DNA should be reduced if cycle number is increased, and increased if the cycle number is decreased. Increase or decrease by twofold the mass of 2800M Control DNA for every one-cycle decrease or increase, respectively.



## 7.D. Direct Amplification of DNA from Swabs (continued)

### Symptoms

Extra peaks visible in one or all color channels

### Causes and Comments

Swab extract was contaminated. Assemble a reaction containing the swab extract prepared from a blank swab, or assemble a reaction where the SwabSolution™ Reagent is processed and incubated as a blank without a swab.

Artifacts of STR amplification. Amplification of swab extracts with high DNA concentrations can result in artifact peaks due to overamplification, resulting in saturated signal on the CE instrument.

We recommend 2µl of swab extract per reaction. Using more than 2µl may result in overamplification and signal saturation. If signal is saturated, repeat amplification with less swab extract or reduced cycle number.

Amplification of excess template for a given cycle number resulted in overloading of the capillary upon electrokinetic injection. Excess DNA in the capillary is difficult to maintain in a denatured single-stranded state. Some single-stranded DNA renatures and becomes double-stranded. Double-stranded DNA migrates faster than single-stranded DNA during capillary electrophoresis and appears as “shadow” peaks migrating in front of the main peaks (i.e., smaller in size). If this occurs at a heterozygous locus it is possible to observe the presence of two “shadow” peaks that differ in size by approximately the same distance as the single-stranded alleles.

Artifacts of STR amplification. Amplification of STRs can result in artifacts that appear as peaks one base smaller than the allele due to incomplete addition of the 3' A residue.

- Be sure to perform the recommended extension step at 60°C after thermal cycling (Section 4.C)
- Use 2µl of swab extract in a 25µl PowerPlex® Fusion reaction. A larger volume of swab extract may contain more than the recommended amount of DNA template, resulting in incomplete adenylation.
- Decrease cycle number.
- Increase the final extension time.

Peak height imbalance

Excess DNA in the amplification reaction can result in locus-to-locus imbalance within a dye channel such that the peak heights at the smaller loci are greater than those at the larger loci (ski-slope effect). Use less swab extract, or reduce cycle number.

## Symptoms

Peak height imbalance (continued)

## Causes and Comments

Active SwabSolution™ Reagent carried over from swab extracts into the amplification reaction. Larger loci are most susceptible to reagent carryover and will drop out before the smaller loci. Ensure that the heat block reached 70°C (90°C if using 2.2ml, Square-Well Deep Well Plates) and samples were incubated for the full 30 minutes. Incubation for shorter time periods may result in incomplete reagent inactivation. Do not use an incubator to incubate tubes or plates; heat transfer is inefficient and will result in poor performance. Use only a heat block to maintain efficient heat transfer.

The cycle number was too high. Decrease cycle number by one cycle, and repeat the amplification.

Inactive SwabSolution™ Reagent. Thaw the SwabSolution™ Reagent completely in a 37°C water bath, and mix by gentle inversion. Store the SwabSolution™ Reagent at 2–10°C. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Do not re-freeze, as this may reduce activity.

DNA was not accessible on nonlytic material. Small loci may amplify preferentially, with large loci dropping out. Pretreat swabs with SwabSolution™ Reagent to ensure that DNA is liberated from cellular proteins.

Extreme variability in sample-to-sample peak heights

There can be significant individual-to-individual variability in cell deposition onto buccal swabs. This will appear as variability in peak heights between swab extracts. The extraction process maximizes recovery of amplifiable DNA from buccal swabs but does not normalize the amount of DNA present. If variability is extreme, quantify the DNA using a fluorescence-based double-stranded DNA quantification method or qPCR-based quantification method. The quantification values can be used to normalize input template amounts to minimize variation in signal intensity.



## 7.E. GeneMapper® ID-X Software

### Symptoms

Stutter peaks not filtered

### Causes and Comments

Stutter text file was not imported into the Panel Manager when the panels and bins text files were imported.

Be sure that the “Use marker-specific stutter ratio and distance if available” box is checked. If the “Use marker-specific stutter ratio and distance if available” box is not checked, stutter distance must be defined in the ‘Analysis Method Allele’ tab.

Samples in the project not analyzed

The ‘Analysis Requirements Summary’ window was not active, and there was an analysis requirement that was not met. Turn on Analysis Requirements Summary in the ‘Project Options’ menu under File, and correct the necessary analysis requirements to continue analysis.

Edits in label edit viewer cannot be viewed

To view edits made to a project, the project first must be saved. Close the plot view window, return to the main GeneMapper® ID-X page and save the project. Display the plot window again, and then view the label edit table.

Marker header bar for some loci are gray

When an edit is made to a locus, the quality flags and marker header bar automatically change to gray. To change the GQ and marker header bar for a locus to green, override the GQ in the plot window.

Alleles not called

To analyze samples with GeneMapper® ID-X software, at least one allelic ladder must be defined per folder of sample files being analyzed in the project.

Run was too short and larger peaks in ILS were not captured. Not all ILS peaks defined in the size standard were detected during the run.

- Create a new size standard using the internal lane standard fragments present in the sample.
- Re-run samples using a longer run time.

A low-quality allelic ladder was used during analysis. Ensure that only high-quality allelic ladders are used for analysis.

Off-ladder alleles

An allelic ladder from a different run than the samples was used. Re-analyze samples with an allelic ladder from the same run.

The GeneMapper® ID-X software requires that the allelic ladder be imported from the same folder as the sample. Be sure that the allelic ladder is in the same folder as the sample. Create a new project and re-analyze, as described in Section 6.D or 6.E.

**Symptoms**

Off-ladder alleles (continued)

**Causes and Comments**

Panels text file selected for analysis was incorrect for the STR system used. Assign correct panels text file that corresponds to the STR system used for amplification.

The allelic ladder was not identified as an allelic ladder in the 'Sample Type' column.

The internal lane standard was not properly identified in the sample. Manually redefine the sizes of the size standard fragments in the sample.

A low-quality allelic ladder was used during analysis. Ensure that only high-quality allelic ladders are used for analysis.

Incorrect polymer was used. Use of a polymer other than POP-4® polymer may change migration of the fragments. Alleles may migrate outside of the panel range established using POP-4® polymer.

Size standard not called correctly

Starting data point was incorrect for the partial range chosen in Section 6.D or 6.E. Adjust the starting data point in the analysis method. Alternatively, use a full range for the analysis.

Extra peaks in size standard. Open the Size Match Editor. Highlight the extra peak, select **Edit** and select **Delete Size Label**. Select **Auto Adjust Sizes**.

An incorrect size standard was used.

Run was too short and larger peaks in ILS were not captured. Not all ILS peaks defined in the size standard were detected during the run.

- Create a new size standard using the internal lane standard fragments present in the sample.
- Re-run samples using a longer run time.

Peaks in size standard missing

If peaks are low-quality, redefine the size standard for the sample to skip these peaks.

An incorrect size standard was used.

Significantly raised baseline

Poor spectral calibration. Perform a new spectral calibration, and re-run the samples.

Incorrect G5 spectral calibration was active. Re-run samples, and confirm that the PowerPlex® 5-dye G5 spectral is set for G5. See instructions for instrument preparation in Section 5.



## 7.F. GeneMapper® ID Software

### Symptoms

Alleles not called

### Causes and Comments

To analyze samples with GeneMapper® ID software, the analysis parameters and size standard must both have “Basic or Advanced” as the analysis type. If they are different, an error is obtained.

To analyze samples with GeneMapper® ID software, at least one allelic ladder must be defined per folder of sample files being analyzed in the project.

Run was too short and larger peaks in ILS were not captured. Not all ILS peaks defined in the size standard were detected during the run.

- Create a new size standard using the internal lane standard fragments present in the sample.
- Re-run samples using a longer run time.

A low-quality allelic ladder was used during analysis. Ensure that only high-quality allelic ladders are used for analysis.

Off-ladder alleles

An allelic ladder from a different run than the samples was used. Re-analyze samples with an allelic ladder from the same run.

The GeneMapper® ID software requires that the allelic ladder be imported from the same folder as the sample. Be sure that the allelic ladder is in the same folder as the sample. Create a new project and re-analyze as described in Section 6.I or 6.J.

Panels text file selected for analysis was incorrect for the STR system used. Assign correct panels text file that corresponds to the STR system used for amplification.

The allelic ladder was not identified as an allelic ladder in the Sample Type column.

The wrong analysis type was chosen for the analysis method. Be sure to use the HID analysis type.

The internal lane standard was not properly identified in the sample. Manually redefine the sizes of the size standard fragments in the sample.

A low-quality allelic ladder was used during analysis. Ensure that only high-quality allelic ladders are used for analysis.

Incorrect polymer was used. Use of a polymer other than POP-4 polymer may change the migration of the fragments. Alleles may migrate outside of the panel range established using POP-4 polymer.

## Symptoms

## Causes and Comments

Size standard not called correctly

Starting data point was incorrect for the partial range chosen in Section 6.I or 6.J. Adjust the starting data point in the analysis method. Alternatively, use a full range for the analysis.

Extra peaks in advanced mode size standard. Open the Size Match Editor. Highlight the extra peak, select **Edit** and select **delete size label**. Select **auto adjust sizes**.

An incorrect size standard was used.

Run was too short and larger peaks in ILS were not captured. Not all ILS peaks defined in the size standard were detected during the run.

- Create a new size standard using the internal lane standard fragments present in the sample.
- Re-run samples using a longer run time.

Peaks in size standard missing

If peaks are low-quality, redefine the size standard for the sample to skip these peaks.

An incorrect size standard was used.

Error message:

“Either panel, size standard, or analysis method is invalid”

The size standard and analysis method were not in the same mode (“Classic” vs. “Basic or Advanced”). Be sure both files are set to the same mode, either Classic or Basic or Advanced mode.

No alleles called, but no error message appears

Panel text file was not selected for sample. In the ‘Panel’ column, select the appropriate panels text file for the STR system that was used.

No size standard was selected. In the ‘Size Standard’ column, be sure to select the appropriate size standard.

Size standard was not correctly defined, or size peaks were missing. Redefine size standard to include only peaks present in your sample. Terminating analysis early or using short run times will cause larger ladder peaks to be missing. This will cause your sizing quality to be flagged as “red”, and no allele sizes will be called.

Error message:

“Both the Bin Set used in the Analysis Method and the Panel must belong to the same Chemistry Kit”

The bins text file assigned to the analysis method was deleted. In the GeneMapper Manager, select the ‘Analysis Methods’ tab, and open the analysis method of interest. Select the ‘Allele’ tab, and select an appropriate bins text file.

The wrong bins text file was chosen in the analysis method ‘Allele’ tab. Be sure to choose the appropriate bins text file, as shown in Figure 22.



## 7.F. GeneMapper® ID Software (continued)

### Symptoms

Significantly raised baseline

### Causes and Comments

Poor spectral calibration. Perform a new spectral calibration, and re-run the samples.

Use of Classic mode analysis method. Use of Classic mode analysis on samples can result in baselines with more noise than those analyzed using the Basic or Advanced mode analysis method. Advanced mode analysis methods and size standards are recommended.

Incorrect G5 spectral calibration was active. Re-run samples, and confirm that the PowerPlex® 5-dye G5 spectral is set for G5. See instructions for instrument preparation in Section 5.

Error message after attempting to import panels and bins text files: “Unable to save panel data: java.SQLException: ORA-00001: unique constraint (IFA.CKP\_NNN) violated”.

There was a conflict between different sets of panels and bins text files. Check to be sure that the bins are installed properly. If not, delete all panels and bins text files, and re-import files in a different order.

Allelic ladder peaks labeled off-ladder

GeneMapper® ID software was not used, or microsatellite analysis settings were used instead of HID analysis settings. GeneMapper® software does not use the same algorithms as GeneMapper® ID software and cannot correct for sizing differences using the allelic ladder. We recommend using GeneMapper® ID software to analyze PowerPlex® reactions. If using GeneMapper® ID software, version 3.2, be sure that the analysis method selected is an HID method. This can be verified by opening the analysis method using the GeneMapper® Manager, and then selecting the General tab. The analysis type cannot be changed. If the method is not HID, it should be deleted and a new analysis method created.

## 8. References

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## 9. Appendix

### 9.A. Advantages of Using the Loci in the PowerPlex® Fusion System

A single PowerPlex® Fusion System reaction amplifies all core loci required for US expanded CODIS and European databases (Tables 6 and 7). Additionally, the male-specific DYS391 locus is included to identify null Y results for Amelogenin. Table 8 lists the PowerPlex® Fusion System alleles amplified from 2800M Control DNA.

We have carefully selected primers to avoid or minimize artifacts, including those associated with DNA polymerases, such as repeat slippage and terminal nucleotide addition (14,15). Repeat slippage, sometimes called “n–4 peaks”, “stutter” or “shadow peaks”, is due to the loss of a repeat unit during DNA amplification, somatic variation within the DNA or both. The amount of this artifact observed depends primarily on the locus and the DNA sequence being amplified.

Terminal nucleotide addition (16,17) occurs when a thermostable nonproofreading DNA polymerase adds a nucleotide, generally adenine, to the 3′ ends of amplified DNA fragments in a template-independent manner. The efficiency with which this occurs varies with different primer sequences. Thus, an artifact peak one base shorter than expected (i.e., missing the terminal addition) is sometimes seen. We have modified primer sequences and added a final extension step at 60°C (18) to the amplification protocols to provide conditions for essentially complete terminal nucleotide addition when recommended amounts of template DNA are used.

**Table 6. The PowerPlex® Fusion System Locus-Specific Information.**

<b>STR Locus</b>	<b>Label</b>	<b>Chromosomal Location<sup>1</sup></b>	<b>Repeat Sequence<sup>2</sup> 5'→3'</b>
Amelogenin <sup>3</sup>	Fluorescein	Xp22.1–22.3 and Y	NA
D3S1358	Fluorescein	3p21.31 (45.557Mb)	TCTA Complex
D1S1656	Fluorescein	1q42 (228.972Mb)	TAGA Complex
D2S441	Fluorescein	2p14 (68.214Mb)	TCTA
D10S1248	Fluorescein	10q26.3 (130.567Mb)	GGAA
D13S317	Fluorescein	13q31.1 (81.62Mb)	TATC
Penta E	Fluorescein	15q26.2 (95.175Mb)	AAAGA
D16S539	JOE	16q24.1 (84.944Mb)	GATA
D18S51	JOE	18q21.33 (59.1Mb)	AGAA (19)
D2S1338	JOE	2q35 (218.705Mb)	TGCC/TTCC
CSF1PO	JOE	5q33.1 (149.436Mb)	AGAT
Penta D	JOE	21q22.3 (43.88Mb)	AAAGA
TH01	TMR-ET	11p15.5 (2.149Mb)	AATG (19)
vWA	TMR-ET	12p13.31 (5.963Mb)	TCTA Complex (19)
D21S11	TMR-ET	21q21.1 (19.476Mb)	TCTA Complex (19)
D7S820	TMR-ET	7q21.11 (83.433Mb)	GATA
D5S818	TMR-ET	5q23.2 (123.139Mb)	AGAT
TPOX	TMR-ET	2p25.3 (1.472Mb)	AATG
DYS391	TMR-ET	Y	TCTA
D8S1179	CXR-ET	8q24.13 (125.976Mb)	TCTA Complex (19)
D12S391	CXR-ET	12p12 (12.341Mb)	AGAT/AGAC Complex
D19S433	CXR-ET	19q12 (35.109Mb)	AAGG Complex
FGA	CXR-ET	4q28 (155.866Mb)	TTTC Complex (19)
D22S1045	CXR-ET	22q12.3 (35.779Mb)	ATT

<sup>1</sup>Information about the chromosomal location of these loci can be found in references 20 and 21 at:

**<https://strbase.nist.gov//chrom.htm>**

<sup>2</sup>The August 1997 report (22,23) of the DNA Commission of the International Society for Forensic Haemogenetics (ISFH) states, “1) for STR loci within coding genes, the coding strand shall be used and the repeat sequence motif defined using the first possible 5' nucleotide of a repeat motif; and 2) for STR loci not associated with a coding gene, the first database entry or original literature description shall be used”.

<sup>3</sup>Amelogenin is not an STR.

NA = Not applicable



**Table 7. The PowerPlex® Fusion System Allelic Ladder Information.**

<b>STR Locus</b>	<b>Label</b>	<b>Size Range of Allelic Ladder Components<sup>1,2</sup> (bases)</b>	<b>Repeat Numbers of Allelic Ladder Components<sup>3</sup></b>
Amelogenin <sup>4</sup>	Fluorescein	89, 95	X, Y
D3S1358	Fluorescein	103–147	9–20
D1S1656	Fluorescein	161–208	9–14, 14.3, 15, 15.3, 16, 16.3, 17, 17.3, 18, 18.3, 19, 19.3, 20.3
D2S441	Fluorescein	214–250	8–11, 11.3, 12–17
D10S1248	Fluorescein	255–299	8–19
D13S317	Fluorescein	302–350	5–17
Penta E	Fluorescein	371–466	5–24
D16S539	JOE	84–132	4–16
D18S51	JOE	134–214	7–10, 10.2, 11–13, 13.2, 14–27
D2S1338	JOE	224–296	10, 12, 14–28
CSF1PO	JOE	318–362	5–16
Penta D	JOE	377–450	2.2, 3.2, 5–17
TH01	TMR-ET	72–115	3–9, 9.3, 10–11, 13.3
vWA	TMR-ET	127–183	10–24
D21S11	TMR-ET	203–259	24, 24.2, 25, 25.2, 26–28, 28.2, 29, 29.2, 30, 30.2, 31, 31.2, 32, 32.2, 33, 33.2, 34, 34.2, 35, 35.2, 36–38
D7S820	TMR-ET	269–313	5–16
D5S818	TMR-ET	321–369	6–18
TPOX	TMR-ET	393–441	4–16
DYS391	TMR-ET	442–486	5–16
D8S1179	CXR-ET	76–124	7–19
D12S391	CXR-ET	133–185	14–17, 17.3, 18, 18.3, 19–27
D19S433	CXR-ET	193–245	5.2, 6.2, 8–12, 12.2, 13, 13.2, 14, 14.2, 15, 15.2, 16, 16.2, 17, 17.2, 18, 18.2
FGA	CXR-ET	265–411	14–18, 18.2, 19, 19.2, 20, 20.2, 21, 21.2, 22, 22.2, 23, 23.2, 24, 24.2, 25, 25.2, 26–30, 31.2, 32.2, 33.2, 42.2, 43.2, 44.2, 45.2, 46.2, 48.2, 50.2
D22S1045	CXR-ET	425–464	7–20

<sup>1</sup>The length of each allele in the allelic ladder has been confirmed by sequence analysis.

<sup>2</sup>When using an internal lane standard, such as the WEN Internal Lane Standard 500, the calculated sizes of allelic ladder components may differ from those listed. This occurs because different sequences in allelic ladder and ILS components may cause differences in migration. The dye label and linker also affect migration of alleles.

<sup>3</sup>For a current list of microvariants, see the Variant Allele Report published at the U.S. National Institute of Standards and Technology (NIST) web site at: [https://strbase.nist.gov/var\\_tab.htm](https://strbase.nist.gov/var_tab.htm)

<sup>4</sup>Amelogenin is not an STR.

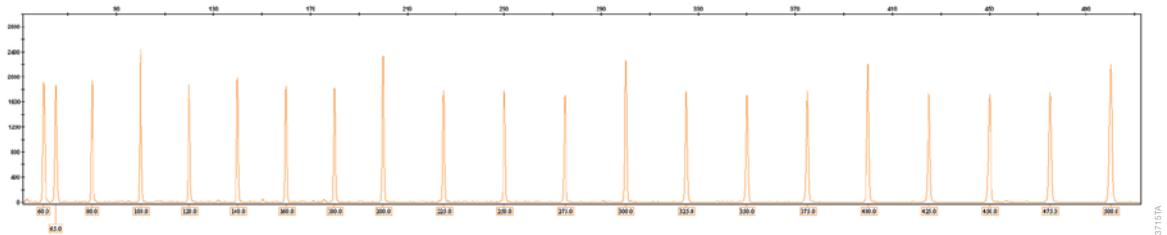
**Table 8. The PowerPlex® Fusion System Allele Determinations for 2800M Control DNA.**

<b>STR Locus</b>	<b>2800M</b>
Amelogenin	X, Y
D3S1358	17, 18
D1S1656	12, 13
D2S441	10, 14
D10S1248	13, 15
D13S317	9, 11
Penta E	7, 14
D16S539	9, 13
D18S51	16, 18
D2S1338	22, 25
CSF1PO	12, 12
Penta D	12, 13
TH01	6, 9.3
vWA	16, 19
D21S11	29, 31.2
D7S820	8, 11
D5S818	12, 12
TPOX	11, 11
DYS391	10
D8S1179	14, 15
D12S391	18, 23
D19S433	13, 14
FGA	20, 23
D22S1045	16, 16



### 9.B. The WEN Internal Lane Standard 500

The WEN Internal Lane Standard 500 contains 21 DNA fragments of 60, 65, 80, 100, 120, 140, 160, 180, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475 and 500 bases in length (Figure 27). Each fragment is labeled with WEN dye and can be detected separately (as a fifth color) in the presence of PowerPlex® Fusion-amplified material. The WEN ILS 500 is designed for use in each CE injection to increase precision in analyses when using the PowerPlex® Fusion System. Protocols to prepare and use this internal lane standard are provided in Section 5.



**Figure 27. WEN Internal Lane Standard 500.** An electropherogram showing the WEN Internal Lane Standard 500 fragments.

### 9.C. Direct Amplification of DNA from Storage Card Punches in a 12.5µl Reaction Volume

Testing at Promega has shown successful direct amplification of DNA from storage card punches in a 12.5µl reaction volume (24). This section contains a protocol for direct amplification of DNA from storage card punches in a 12.5µl reaction volume using the PowerPlex® Fusion System and GeneAmp® PCR System 9700 or ProFlex® PCR System. When using the protocol detailed below, add only one 1.2mm storage card punch to each 12.5µl amplification reaction.

#### Materials to Be Supplied by the User

- GeneAmp® PCR System 9700 with a gold-plated silver or silver sample block or ProFlex® PCR System (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plate or 0.2ml MicroAmp® reaction tubes (Applied Biosystems)
- aerosol-resistant pipette tips
- PunchSolution™ Kit (Cat.# DC9271) for nonlytic card punches
- 5X AmpSolution™ Reagent (Cat.# DM1231, also supplied with the PunchSolution™ Kit)
- 1.2mm Harris Micro-Punch or equivalent manual punch and cutting mat or automated punch system

#### Notes:

1. It may be possible to use thermal cyclers other than those listed in this technical manual. Use of thermal cyclers not listed here may require optimization of cycling conditions and validation in your laboratory. Use of thermal cyclers with an aluminum block is **not** recommended with the PowerPlex® Fusion System.
2. You will need to optimize and validate the number of storage card punches per reaction in your laboratory. See the PCR Optimization recommendations at the end of this section.

#### Lytic storage card sample types include:

- Buccal cells collected on FTA® cards with Whatman EasiCollect™ or Fitzco Sampact™ devices
- Buccal cells collected with swabs transferred to FTA® or Indicating FTA® cards
- Liquid blood (from collection or storage Vacutainer® tubes or finger sticks) spotted onto FTA® cards

#### Nonlytic storage card sample types include:

- Buccal samples on Bode Buccal DNA Collector™ devices
- Blood and buccal samples on nonFTA card punches (e.g., S&S 903)

### 9.C. Direct Amplification of DNA from Storage Card Punches in a 12.5µl Reaction Volume (continued)

Pretreat nonlytic sample types with the PunchSolution™ Kit (Cat. # DC9271) to lyse the samples before adding the PCR amplification mix. For more information, see the *PunchSolution™ Kit Technical Manual #TMD038*. Failure to pretreat these samples may result in incomplete profiles.

Use a manual punch tool with a 1.2mm tip to manually create sample disks from a storage card. Place tip near the center of the sample spot, and with a twisting or pressing action, cut a 1.2mm sample disk. Use the plunger to eject the disk into the appropriate well of a reaction plate.

Automated punchers also can be used to create sample disks. Refer to the user's guide for your instrument for assistance with generating 1.2mm disks, technical advice and troubleshooting information.

**Note:** Static may be problematic when adding a punch to a well. For lytic card punches, adding PCR amplification mix to the well before adding the punch may help alleviate static problems. For nonlytic card punches, adding PunchSolution™ Reagent to the well before adding the punch during pretreatment may help alleviate static problems.

#### Amplification Setup

1. Thaw the PowerPlex® Fusion 5X Master Mix, PowerPlex® Fusion 5X Primer Pair Mix and Water, Amplification Grade, completely.

**Note:** Centrifuge tubes briefly to bring contents to the bottom, and then vortex reagents for 15 seconds before each use. Do not centrifuge the 5X Primer Pair Mix or 5X Master Mix after vortexing, as this may cause the reagents to be concentrated at the bottom of the tube.

2. Vortex the 5X AmpSolution™ Reagent for 10–15 seconds.

**Note:** The 5X AmpSolution™ Reagent should be thawed completely, mixed by vortexing and stored at 2–10°C. The reagent may be turbid after thawing or storage at 4°C. If this occurs, warm the buffer briefly at 37°C, and then vortex until clear. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Storing reagents in the refrigerator door can compromise stability.

3. Determine the number of reactions to be set up. This should include positive and negative control reactions. Add 1 or 2 reactions to this number to compensate for pipetting error. While this approach does consume a small amount of each reagent, it ensures that you will have enough PCR amplification mix for all samples. It also ensures that each reaction contains the same PCR amplification mix.
4. Use a clean plate for reaction assembly, and label it appropriately. Alternatively, determine the number of clean, 0.2ml reaction tubes required, and label them appropriately.

5. Add the final volume of each reagent listed in Table 9 to a clean tube.

**Table 9. PCR Amplification Mix for Direct Amplification of DNA from Storage Card Punches in a 12.5µl Reaction Volume.**

PCR Amplification Mix Component <sup>1</sup>	Volume Per Reaction	×	Number of Reactions	=	Final Volume
Water, Amplification Grade	5.0µl	×		=	
PowerPlex® Fusion 5X Master Mix	2.5µl	×		=	
PowerPlex® Fusion 5X Primer Pair Mix	2.5µl	×		=	
5X AmpSolution™ Reagent	2.5µl	×		=	
<b>total reaction volume</b>	<b>12.5µl</b>				

<sup>1</sup>Add Water, Amplification Grade, to the tube first, and then add PowerPlex® Fusion 5X Master Mix, PowerPlex® Fusion 5X Primer Pair Mix and 5X AmpSolution™ Reagent. For lytic card punches, the template DNA will be added at Step 7.

6. Vortex the PCR amplification mix for 5–10 seconds, and then pipet 12.5µl of PCR amplification mix into each reaction well.



Failure to vortex the PCR amplification mix sufficiently can result in poor amplification or locus-to-locus imbalance.

**Note:** Do not store the PCR amplification mix for a prolonged period. Add the mix to the wells of the reaction plate as soon as the mix is prepared. Add the punches as soon as possible to each well and follow immediately by thermal cycling.

7. For lytic storage cards, add one 1.2mm punch from a card containing buccal cells or one 1.2mm punch from a card containing whole blood to the appropriate wells of the reaction plate. For nonlytic card punches, add the PCR amplification mix to the PunchSolution™ Reagent-treated punches.

**Note:** It also is acceptable to add the lytic card punch first, and then add the PCR amplification mix.

8. For the positive amplification control, vortex the tube of 2800M Control DNA, and then dilute an aliquot to 5ng/µl. Add 1µl (5ng) of the 2800M Control DNA to a reaction well containing 12.5µl of PCR amplification mix.

**Notes:**

1. Do not include blank storage card punches in the positive control reactions.
2. Optimization of the amount of 2800M Control DNA may be required depending on thermal cycling conditions and laboratory preferences. Typically, 5ng of 2800M Control DNA is sufficient to provide a robust profile using the cycle numbers recommended here. A one-cycle reduction in cycle number will require a twofold increase in mass of DNA template to generate similar signal intensity. Similarly, a one-cycle increase in cycle number will require a twofold reduction in the amount of 2800M Control DNA to avoid signal saturation.



### 9.C. Direct Amplification of DNA from Storage Card Punches in a 12.5µl Reaction Volume (continued)

9. Reserve a well containing PCR amplification mix as a negative amplification control.

**Note:** An additional negative control with a blank punch may be performed to detect contamination from the storage card or punch device.

10. Seal or cap the plate, or close the tubes. Briefly centrifuge the plate to bring storage card punches to the bottom of the wells and remove any air bubbles.

#### Thermal Cycling

Amplification and detection instrumentation may vary. You will need to optimize protocols, including cycle number, injection conditions and loading volume for your laboratory instrumentation. Testing at Promega shows that 26 cycles works well for a variety of sample types. Cycle number will need to be optimized in each laboratory for each sample type.

**Note:** It may be possible to use thermal cyclers other than those listed in this technical manual. Use of thermal cyclers not listed here may require optimization of cycling conditions and validation in your laboratory. Use of thermal cyclers with an aluminum block is **not** recommended with the PowerPlex® Fusion System.

1. Place the reaction plate or tubes in the thermal cycler.
2. Select and run the recommended protocol, which is provided in Figure 28.

#### Notes:

1. When using the ProFlex® PCR System, use the 9700 Simulation Mode as the ramp speed.
2. When using the GeneAmp® PCR System 9700, the program must be run with Max Mode as the ramp speed. This requires a gold-plated silver or silver sample block. The ramp speed is set after the thermal cycling run is started. When the 'Select Method Options' screen appears, select "Max" for the ramp speed and enter the reaction volume.
3. The final extension for direct amplification was extended to 20 minutes compared to 10 minutes for the extracted DNA protocol to allow sufficient time for adenylation of large amounts of amplicon.

#### Thermal Cycling Protocol

96°C for 1 minute, then:

94°C for 10 seconds

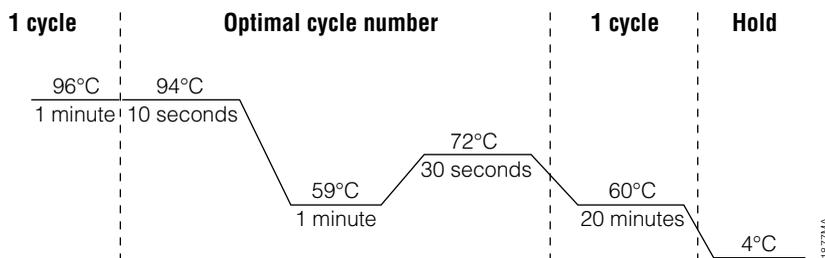
59°C for 1 minute

72°C for 30 seconds

for 26 cycles, then:

60°C for 20 minutes

4°C soak



**Figure 28. Thermal cycling protocol for the GeneAmp® PCR System 9700 and ProFlex® PCR System.**

3. After completion of the thermal cycling protocol, proceed with fragment analysis or store amplified samples at  $-20^{\circ}\text{C}$  in a light-protected box.

**Note:** Long-term storage of amplified samples at  $4^{\circ}\text{C}$  or higher may produce artifacts.

### PCR Optimization

Cycle number should be optimized based on the results of an initial experiment to determine the sensitivity with your collection method, sample types, number of punches and instrumentation.

1. Choose several samples that represent typical sample types you encounter in the laboratory. Prepare them as you would using your normal workflow.
2. Place one 1.2mm storage card punch containing a buccal sample or one 1.2mm punch of a storage card containing whole blood into each well of a reaction plate. Be sure to pretreat nonlytic samples with the PunchSolution™ Kit (Cat.# DC9271).
3. Prepare three identical reaction plates with punches from the same samples.
4. Amplify samples using the thermal cycling protocol provided above, but subject each plate to a different cycle number (25, 26 and 27 cycles).
5. Following amplification, use your laboratory's validated separation and detection protocols to determine the optimal cycle number for the sample type.



## 9.D. Direct Amplification of DNA from Swabs in a 12.5µl Reaction Volume

Testing at Promega has shown successful direct amplification of DNA from swabs in a 12.5µl reaction volume (24). This section contains a protocol for amplifying DNA from swab extracts in a 12.5µl reaction volume using the PowerPlex® Fusion System and GeneAmp® PCR System 9700 or ProFlex® PCR System.

### Materials to Be Supplied by the User

- GeneAmp® PCR System 9700 with a gold-plated silver or silver sample block or ProFlex® PCR System (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plate or 0.2ml MicroAmp® reaction tubes (Applied Biosystems)
- aerosol-resistant pipette tips
- SwabSolution™ Kit (Cat.# DC8271)

Pretreat OmniSwab™ (QIAGEN) or cotton swabs using the SwabSolution™ Kit (Cat.# DC8271) as described in the *SwabSolution™ Kit Technical Manual #TMD037* to generate a swab extract.

**Note:** It may be possible to use thermal cyclers other than those listed in this technical manual. Use of thermal cyclers not listed here may require optimization of cycling conditions and validation in your laboratory. Use of thermal cyclers with an aluminum block is **not** recommended with the PowerPlex® Fusion System.

### Amplification Setup

1. Thaw the PowerPlex® Fusion 5X Master Mix, PowerPlex® Fusion 5X Primer Pair Mix and Water, Amplification Grade, completely.  
**Note:** Centrifuge tubes briefly to bring contents to the bottom, and then vortex reagents for 15 seconds before each use. Do not centrifuge the 5X Primer Pair Mix or 5X Master Mix after vortexing, as this may cause the reagents to be concentrated at the bottom of the tube.
2. Determine the number of reactions to be set up. This should include positive and negative control reactions. Add 1 or 2 reactions to this number to compensate for pipetting error. While this approach does consume a small amount of each reagent, it ensures that you will have enough PCR amplification mix for all samples. It also ensures that each reaction contains the same PCR amplification mix.
3. Use a clean plate for reaction assembly, and label it appropriately. Alternatively, determine the number of clean, 0.2ml reaction tubes required, and label them appropriately.

- Add the final volume of each reagent listed in Table 10 to a clean tube.

**Table 10. PCR Amplification Mix for Direct Amplification of DNA from Swabs in a 12.5µl Reaction Volume.**

PCR Amplification Mix Component <sup>1</sup>	Volume Per Reaction	×	Number of Reactions	=	Final Volume
Water, Amplification Grade	5.5µl	×		=	
PowerPlex® Fusion 5X Master Mix	2.5µl	×		=	
PowerPlex® Fusion 5X Primer Pair Mix	2.5µl	×		=	
swab extract	2.0µl				
<b>total reaction volume</b>	<b>12.5µl</b>				

<sup>1</sup>Add Water, Amplification Grade, to the tube first, and then add PowerPlex® Fusion 5X Master Mix and PowerPlex® Fusion 5X Primer Pair Mix. The swab extract will be added at Step 6.

- Vortex the PCR amplification mix for 5–10 seconds, and then pipet 10.5µl of PCR amplification mix into each reaction well.



Failure to vortex the PCR amplification mix sufficiently can result in poor amplification or locus-to-locus imbalance.

**Note:** Do not store the PCR amplification mix for a prolonged period. Add the mix to the wells of the reaction plate as soon as the mix is prepared. Add the swab extract as soon as possible to each well and follow immediately by thermal cycling.

- Pipet 2µl of swab extract for each sample into the appropriate well of the reaction plate.
- For the positive amplification control, vortex the tube of 2800M Control DNA, and then dilute an aliquot to 2.5ng/µl. Add 2µl (5ng) to a reaction well containing 10.5µl of PCR amplification mix.

**Note:** Optimization of the amount of 2800M Control DNA may be required depending on thermal cycling conditions and laboratory preferences.

- For the negative amplification control, pipet 2µl of Water, Amplification Grade, or TE<sup>-4</sup> buffer instead of swab extract into a reaction well containing PCR amplification mix.

**Note:** Additional negative controls can be included. Assemble a reaction containing the swab extract prepared from a blank swab, or assemble a reaction where the SwabSolution™ Reagent is processed as a blank without a swab.

- Seal or cap the plate, or close the tubes.

**Optional:** Briefly centrifuge the plate to bring contents to the bottom of the wells and remove any air bubbles.



## 9.D. Direct Amplification of DNA from Swabs in a 12.5µl Reaction Volume (continued)

### Thermal Cycling

Amplification and detection instrumentation may vary. You will need to optimize protocols including the amount of template DNA, cycle number, injection conditions and loading volume for your laboratory instrumentation. Testing at Promega shows that 26 cycles works well for a variety of sample types. Cycle number will need to be optimized in each laboratory for each sample type.

**Note:** It may be possible to use thermal cyclers other than those listed in this technical manual. Use of thermal cyclers not listed here may require optimization of cycling conditions and validation in your laboratory. Use of thermal cyclers with an aluminum block is **not** recommended with the PowerPlex® Fusion System.

1. Place the reaction plate or tubes in the thermal cycler.
2. Select and run the recommended protocol, which is provided in Figure 29.

#### Notes:

1. When using the ProFlex® PCR System, use the 9700 Simulation Mode as the ramp speed.
2. When using the GeneAmp® PCR System 9700, the program must be run with Max Mode as the ramp speed. This requires a gold-plated silver or silver sample block. The ramp speed is set after the thermal cycling run is started. When the 'Select Method Options' screen appears, select "Max" for the ramp speed and enter the reaction volume.
3. The final extension for direct amplification was extended to 20 minutes, compared to 10 minutes, for the extracted DNA protocol to allow sufficient time for adenylation of large amounts of amplicon.

#### Thermal Cycling Protocol

96°C for 1 minute, then:

94°C for 10 seconds

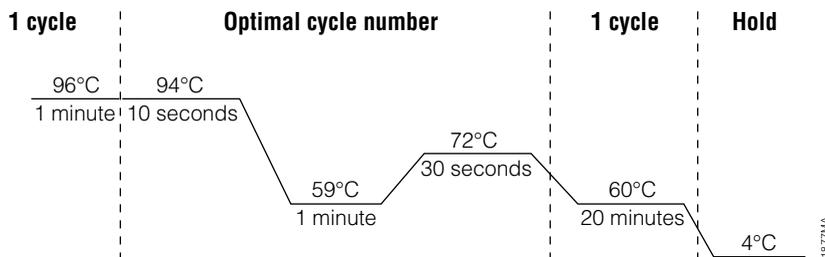
59°C for 1 minute

72°C for 30 seconds

for 26 cycles, then:

60°C for 20 minutes

4°C soak



**Figure 29. Thermal cycling protocol for the GeneAmp® PCR System 9700 and ProFlex® PCR System.**

2. After completion of the thermal cycling protocol, proceed with fragment analysis or store amplified samples at  $-20^{\circ}\text{C}$  in a light-protected box.

**Note:** Long-term storage of amplified samples at  $4^{\circ}\text{C}$  or higher may produce artifacts.

### PCR Optimization

Cycle number should be optimized based on the results of an initial experiment to determine the sensitivity with your collection method, sample types and instrumentation.

1. Choose several samples that represent typical sample types you encounter in the laboratory. Prepare them as you would using your normal workflow.
2. Prepare three identical reaction plates with aliquots of the same swab extracts.
3. Amplify samples using the thermal cycling protocol provided above, but subject each plate to a different cycle number (25, 26 and 27 cycles).

**Note:** This recommendation is for  $2\mu\text{l}$  of swab extract. Additional cycle number testing may be required.

4. Following amplification, use your laboratory's validated separation and detection protocols to determine the optimal cycle number for the sample type.

### 9.E. Composition of Buffers and Solutions

#### TE<sup>-4</sup> buffer (10mM Tris-HCl, 0.1mM EDTA [pH 8.0])

1.21g Tris base  
0.037g EDTA ( $\text{Na}_2\text{EDTA} \cdot 2\text{H}_2\text{O}$ )

Dissolve Tris base and EDTA in 900ml of deionized water. Adjust to pH 8.0 with HCl. Bring the final volume to 1 liter with deionized water.

#### TE<sup>-4</sup> buffer with 20 $\mu\text{g}/\text{ml}$ glycogen

1.21g Tris base  
0.037g EDTA ( $\text{Na}_2\text{EDTA} \cdot 2\text{H}_2\text{O}$ )  
20 $\mu\text{g}/\text{ml}$  glycogen

Dissolve Tris base and EDTA in 900ml of deionized water. Adjust to pH 8.0 with HCl. Add glycogen. Bring the final volume to 1 liter with deionized water.



## 9.F. Related Products

Product	Size	Cat.#
PowerPlex® 5C Matrix Standard	5 preps	DG4850
PunchSolution™ Kit	100 preps	DC9271
SwabSolution™ Kit	100 preps	DC8271
5X AmpSolution™ Reagent	500µl	DM1231
WEN Internal Lane Standard 500	200µl	DG5001
2800M Control DNA (10ng/µl)	25µl	DD7101
2800M Control DNA (0.25ng/µl)	500µl	DD7251
Water, Amplification Grade	6,250µl (5 × 1,250µl)	DW0991

Not for Medical Diagnostic Use.

## 9.G. Summary of Changes

The following changes were made to the 7/20 revision of this document:

1. Added use of the ProFlex® PCR System.
2. Updated Section 6.L.
3. Incorporated other general text updates.

<sup>(a)</sup>U.S. Pat. No. 9,139,868, European Pat. No. 2972229 and other patents pending.

<sup>(b)</sup>TMR-ET, CXR-ET and WEN dyes are proprietary.

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