



PowerPlex® ESX 17 System for Use on the Spectrum Compact CE System Technical Manual

Instructions for Use of Product DC6720



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All technical literature is available at: 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

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® ESX 17 System^(a,b) is used for human identification applications including forensic analysis, relationship testing and research use. This system allows co-amplification and four-color fluorescent detection of seventeen loci (sixteen STR loci and Amelogenin), including D18S51, D21S11, TH01, D3S1358, Amelogenin, D16S539, D2S1338, D1S1656, D10S1248, FGA, D8S1179, vWA, D22S1045, SE33, D19S433, D12S391 and D2S441.

The PowerPlex® ESX 17 System amplifies the loci recommended by the European Network of Forensic Science Institutes (ENFSI) and European DNA Profiling Group (EDNAP) as mini-STRs (<125bp; D2S441, D10S1248 and D22S1045) or midi-STRs (125–185bp; D1S1656 and D12S391). To complement this design and allow maximal recovery of allelic information from degraded samples, the PowerPlex® ESI 17 Pro System, which amplifies the same seventeen loci present in the PowerPlex® ESX 17 System, is designed to amplify six of the original seven European Standard Set (ESS) loci (D3S1358, D18S51, TH01, vWA, D8S1179 and the more common FGA alleles) along with D16S539 and D19S433 as smaller amplicons (<250bp), while the new ENFSI/EDNAP loci are present as larger amplicons. Therefore, these two STR systems can be used to complement each other when analyzing degraded or challenging samples to maximize recovery of allelic information from as many loci as possible and also allow confirmation of results obtained with the other system.

The PowerPlex® ESX 17 System provides all materials to amplify STR regions of human genomic DNA, including hot-start *Taq* DNA polymerase, which is a component of the PowerPlex® ESX 5X Master Mix. This manual contains a protocol for use of the PowerPlex® ESX 17 System with the GeneAmp® PCR System 9700 in addition to a protocol to separate amplified products and detect separated material on the Spectrum Compact CE System. A protocol to operate the Spectrum Compact CE System is available separately. See the *Spectrum Compact CE System Operating Manual #TMD058*. 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. 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

Product Components and Storage Conditions

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PRODUCT	SIZE	CAT.#
PowerPlex® ESX 17 System	400 reactions	DC6720

Not For Medical Diagnostic Use. This system contains sufficient reagents for 400 reactions of 25µl each. Includes:

Pre-Amplification Components Box

- 4 × 500µl PowerPlex® ESX 5X Master Mix
- 4 × 250µl PowerPlex® ESX 17 10X Primer Pair Mix
- 25µl 2800M Control DNA, 10ng/µl
- 10 × 1,250µl Water, Amplification Grade

Post-Amplification Components Box

- 4 × 50µl PowerPlex® ESX 17 Allelic Ladder Mix
- 2 × 200µl WEN Internal Lane Standard 500



The PowerPlex® ESX 17 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 also 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, except for the 2800M Control DNA, which should be stored at 2–10°C. Make sure that the 2800M Control DNA is stored at 2–10°C for **at least 24 hours** before use. After the first use, store the WEN Internal Lane Standard (WEN ILS) 500 at 2–10°C, protected from light. Do not refreeze. The PowerPlex® ESX 17 10X Primer Pair Mix, PowerPlex® ESX 17 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® ESX 17 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
GeneMarker®HID Software for Spectrum CE Systems, Local	1 seat	CE3001
GeneMarker®HID Software for Spectrum CE Systems, Network	1 seat	CE3010
GeneMarker®HID Software for Spectrum CE Systems, Client	1 seat	CE3011

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 and swab extracts. Both the PunchSolution™ Kit and SwabSolution™ Kit contain the 5X AmpSolution™ Reagent.

The proper panels, bins and stutter text files for use with GeneMapper® *ID-X* software are available for download at: www.promega.com/PowerPlexPanels

The proper panel .xml file for use with GeneMarker®HID Software for Spectrum CE Systems (GMHID-Spectrum) is preloaded in GMHID-Spectrum or downloadable at www.promega.com/PowerPlexPanels

The PowerPlex® 5C Matrix Standard (Cat.# DG4850) is required for initial setup of the color separation matrix (see Section 3.2).

Before You Begin

3.1. 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, 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.

3.2. Spectral Calibration

Proper spectral calibration is critical to evaluate multicolor systems with the Spectrum Compact CE System. A matrix must be generated for each individual instrument.

For protocol and additional information about matrix generation and spectral calibration, see the *PowerPlex® Matrix Standards for the Spectrum Compact CE System Technical Manual* #TMD062. This manual is available online at: www.promega.com/protocols/

Protocols for DNA Amplification Using the PowerPlex® ESX 17 System

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The PowerPlex® ESX 17 System is optimized for the GeneAmp® PCR System 9700.

Protocols for amplification in a 25µl reaction volume using extracted DNA (Section 4.1), lytic and nonlytic storage card punches (Section 4.2) and swabs (Section 4.3) are included in the following amplification sections.

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 9.

4.1. Amplification of Extracted DNA

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. The PowerPlex® ESX 17 System is optimized and balanced for 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. Testing at Promega shows that 30 cycles work well for 0.5ng of purified DNA templates. Developmental validation of the kit showed routine generation of full profiles using 30 cycles of amplification with lower amounts of DNA template down to 62.5pg. Partial profiles were typically observed for DNA template of 32pg and below (13). In-house optimization and validation should be performed to establish the performance of the kit in your laboratory (12).

Materials to be Supplied by the User

- GeneAmp® PCR System 9700 (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plates or 0.2ml MicroAmp® reaction tubes (Applied Biosystems)
- aerosol-resistant pipette tips

Amplification Setup

1. Thaw the PowerPlex® ESX 5X Master Mix, PowerPlex® ESX 17 10X Primer Pair Mix and Water, Amplification Grade, completely.
Note: Centrifuge tubes briefly to bring contents to the bottom, then vortex reagents for 15 seconds before each use. Do not centrifuge the 10X 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 MicroAmp® 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 Purified DNA.

PCR Amplification Mix Component ¹	Volume per Reaction	×	Number of Reactions	=	Final Volume
	to a final volume of				
Water, Amplification Grade	25µl	×		=	
PowerPlex® ESX 5X Master Mix	5.0µl	×		=	
PowerPlex® ESX 17 10X Primer Pair Mix	2.5µl	×		=	
template DNA (0.5ng) ^{2,3,4}	up to 17.5µl				
total reaction volume	25µl				

¹Add Water, Amplification Grade, to the tube first, then add PowerPlex® ESX 5X Master Mix and PowerPlex® ESX 17 10X Primer Pair Mix. The template DNA will be added at Step 6.

²Store DNA templates in TE⁻⁴ buffer (10mM Tris-HCl [pH 8.0], 0.1mM EDTA). 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.

³Apparent DNA concentrations can differ, depending on the DNA quantification method used (14). We strongly recommend that you perform experiments to determine the optimal DNA amount based on your DNA quantification method.

⁴The PowerPlex® ESX 17 System is optimized and balanced for 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.

5. Vortex the PCR amplification mix for 5–10 seconds, 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 the template DNA for each sample to the respective well containing PCR amplification mix.

Note: The PowerPlex® ESX 17 System is optimized and balanced using 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, then dilute an aliquot to 0.5ng in the desired template 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⁻⁴ buffer instead of template DNA into a reaction well containing PCR amplification mix.
9. Seal 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

This section contains a protocol for use of the PowerPlex® ESX 17 System with the GeneAmp® PCR System 9700.

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 each laboratory instrument. Testing at Promega shows that 30 cycles work well for 0.5ng of purified DNA templates. In-house validation should be performed.

1. Place the reaction plate or tubes in the thermal cycler.
2. Select and run the recommended protocol.

Note: When using the GeneAmp® PCR System 9700, the program must be run with 9600 as the ramp speed. The ramp speed is set after the thermal cycling run is started. The 'Select Method Options' screen appears. Select **9600** for the ramp speed, and enter the reaction volume.

Thermal Cycling Protocol¹

96°C for 2 minutes, then:

94°C for 30 seconds

59°C for 2 minutes

72°C for 90 seconds

for 30 cycles, then:

60°C for 45 minutes

4°C soak

3. After completion of the thermal cycling protocol, proceed to 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.

4.2. Direct Amplification of DNA from Storage Card Punches

Materials to be Supplied by the User

- GeneAmp® PCR System 9700 (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plates 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

This section contains a protocol for direct amplification of DNA from storage card punches using the PowerPlex® ESX 17 System and GeneAmp® PCR System 9700.

When using the protocol detailed below, add the number of 1.2mm storage card punches indicated below to each 25µl amplification reaction.

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 this section.

Lytic card sample types include:

- Buccal cells collected on FTA® cards with Whatman EasiCollect™ or Fitzco Sampact™ devices (one or two punches per 25µl amplification reaction)
- Buccal cells collected with swabs transferred to FTA® or Indicating FTA® cards (one or two punches per 25µl amplification reaction)
- Liquid blood (from collection or storage Vacutainer® tubes or finger sticks) spotted onto FTA® cards (one punch per 25µl amplification reaction)

Nonlytic card sample types include:

- Buccal samples on Bode Buccal DNA Collector™ devices (one punch per 25µl amplification reaction)
- Blood and buccal samples on nonlytic cards (e.g., S&S 903) (one punch per 25µl amplification reaction)

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® ESX 5X Master Mix, PowerPlex® ESX 17 10X Primer Pair Mix and Water, Amplification Grade, completely.

Note: Centrifuge tubes briefly to bring contents to the bottom, then vortex reagents for 15 seconds before each use. Do not centrifuge the 10X 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 reagent briefly at 37°C, 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 MicroAmp® 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 2 to a clean tube.

Table 2. PCR Amplification Mix for Direct Amplification of DNA from Storage Card Punches.

PCR Amplification Mix Component ¹	Volume per Reaction	×	Number of Reactions	=	Final Volume
Water, Amplification Grade	12.5µl	×		=	
PowerPlex® ESX 5X Master Mix	5.0µl	×		=	
PowerPlex® ESX 17 10X Primer Pair Mix	2.5µl	×		=	
5X AmpSolution™ Reagent	5.0µl	×		=	
total reaction volume	25µl				

¹Add Water, Amplification Grade, to the tube first, and then add PowerPlex® ESX 5X Master Mix, PowerPlex® ESX 17 10X 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, 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.

7. For lytic storage cards, add one or two 1.2mm punches from a storage card containing a buccal sample or one 1.2mm punch from a storage 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, then add the PCR amplification mix.

8. For the positive amplification control, add 1µl (10ng) of the 2800M Control DNA to a reaction well containing 25µl 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, 10ng 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. Reserve a well containing PCR amplification mix as a negative amplification control.
10. Seal or cap the plate, or close the tubes. Briefly centrifuge the reactions to bring storage card punches to the bottom of the wells and remove any air bubbles.

Note: Place the amplification plate or tubes in the thermal cycler, and start the thermal cycling program as soon as the PCR amplification mix is added to all wells. Prolonged storage of assembled reactions prior to cycling may result in poor performance (i.e., lower peak heights for large amplicons).

Thermal Cycling

Amplification and detection instrumentation may vary. You will need to optimize protocols including the number of storage card punches, cycle number, injection conditions and loading volume for your laboratory instrumentation. Testing at Promega shows that 24 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.

Note: When using the GeneAmp® PCR System 9700, the program must be run with 9600 as the ramp speed. The ramp speed is set after the thermal cycling run is started. The 'Select Method Options' screen appears. Select **9600** for the ramp speed, and enter the reaction volume.

Thermal Cycling Protocol¹

96°C for 2 minutes, then:

94°C for 30 seconds

59°C for 2 minutes

72°C for 90 seconds

for 24 cycles, then:

60°C for 45 minutes

4°C soak

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, 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. 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 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.
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.

4.3. Direct Amplification of DNA from Swabs

Materials to be Supplied by the User

- GeneAmp® PCR System 9700 (Applied Biosystems)
- centrifuge compatible with 96-well plates or reaction tubes
- MicroAmp® optical 96-well reaction plates or 0.2ml MicroAmp® reaction tubes (Applied Biosystems)
- aerosol-resistant pipette tips
- SwabSolution™ Kit (Cat.# DC8271)
- 5X AmpSolution™ Reagent (Cat.# DM1231), also supplied with the SwabSolution™ Kit

This section contains a protocol for amplifying DNA from swab extracts using the PowerPlex® ESX 17 System and GeneAmp® PCR System 9700.

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.

Amplification Setup

1. Thaw the PowerPlex® ESX 5X Master Mix, PowerPlex® ESX 17 10X Primer Pair Mix and Water, Amplification Grade, completely.

Note: Centrifuge tubes briefly to bring contents to the bottom, then vortex reagents for 15 seconds before each use. Do not centrifuge the 10X 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 reagent briefly at 37°C, 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 MicroAmp® 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 3 to a clean tube.

Table 3. PCR Amplification Mix for Direct Amplification of DNA from Swabs.

PCR Amplification Mix Component ¹	Volume per Reaction	×	Number of Reactions	=	Final Volume
Water, Amplification Grade	10.5µl	×		=	
PowerPlex® ESX 5X Master Mix	5.0µl	×		=	
PowerPlex® ESX 17 10X Primer Pair Mix	2.5µl	×		=	
5X AmpSolution™ Reagent	5.0µl	×		=	
swab extract	2.0µl				
total reaction volume	25µl				

¹Add Water, Amplification Grade, to the tube first, and then add PowerPlex® ESX 5X Master Mix and PowerPlex® ESX 17 10X Primer Pair Mix. The swab extract will be added at Step 7.

6. Vortex the PCR amplification mix for 5–10 seconds, then pipet 23µl 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. Pipet 2µl of swab extract for each sample into the appropriate well of the reaction plate or tube.
8. For the positive amplification control, vortex the tube of 2800M Control DNA, then dilute to 2.5ng/µl. Add 2µl (5ng) to a reaction well containing 23µl of PCR amplification mix.

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

9. For the negative amplification control, pipet 2µl of Water, Amplification Grade, or TE⁻⁴ 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.

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

Optional: Briefly centrifuge the reactions to bring contents 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 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 swab sample types. Cycle number will need to be optimized in each laboratory for each sample type that is amplified.

1. Place the reaction plates in the thermal cycler.
2. Select and run the recommended protocol.

Note: When using the GeneAmp® PCR System 9700, the program must be run with 9600 as the ramp speed. The ramp speed is set after the thermal cycling run is started. The ‘Select Method Options’ screen appears. Select **9600** for the ramp speed, and enter the reaction volume.

Thermal Cycling Protocol¹

96°C for 2 minutes, then:

94°C for 30 seconds

59°C for 2 minutes

72°C for 90 seconds

for 26 cycles, then:

60°C for 45 minutes

4°C soak

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, 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 or 27 cycles).

Note: This recommendation is for 2µl 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.

Detection of Amplified Fragments Using the Spectrum Compact CE System

5

Note: Instructions for detecting amplified fragments using the Spectrum Compact CE System can be used with the HITACHI DS3000 Compact CE Sequencer.

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 8-tube strips
- aerosol-resistant pipette tips
- Spectrum Compact Capillary Cartridge, 4-Capillary 36cm (Cat.# CE2340)
- Spectrum Compact Polymer4 (Cat.# CE2304)
- Spectrum Compact Buffer (Cat.# CE2300)
- Spectrum Compact Cathode Septa Mat (Cat.# CE2301)
- Spectrum Compact Cathode Retainer (Cat.# CE2302)
- Spectrum Compact Strip Base & Retainer, 32-Well (Cat.# CE2332)
- Strip Septa Mat, 8-Well (Cat.# CE2308)
- MicroAmp® Optical 8-Tube Strip, 0.2ml (Applied Biosystems Cat.# 4316567)
- 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.

Notes:

1. Only use MicroAmp® Optical 8-Tube Strips, 0.2ml (Applied Biosystems Cat.# 4316567) as a source of 8-well strip tubes. Use of other 8-well strip tubes may affect performance or damage the Spectrum Compact CE System.
2. Wear gloves when handling consumables and sample cartridges.

Sample Layout

Samples prepared in 8-well strip tubes are assembled into the strip base and retainer (Figure 1) to form the sample cartridge (Figure 2), which can be loaded onto the Spectrum Compact CE System. Samples are injected in groups of four, such that one 8-well strip tube can be used for two injections. Each 8-well strip tube corresponds to one lane (A, B, C or D) of the sample cartridge. Samples are injected in groups of four across a lane (not by column). For example, samples in well positions A1 through A4 are injected together, followed by samples in well positions A5 through A8 for the second injection. This pattern is then repeated for samples in lanes B, C and D. Refer to the *Spectrum Compact CE System Operating Manual #TMD058* for information on changing the order of injections during run setup.

		Wells							
		1	2	3	4	5	6	7	8
Lanes	A	Injection 1				Injection 2			
	B	Injection 3				Injection 4			
	C	Injection 5				Injection 6			
	D	Injection 7				Injection 8			

5.1. Sample Preparation

1. Prepare a loading cocktail by combining and mixing internal lane standard (ILS) and Hi-Di™ formamide as follows: $[(0.5\mu\text{l ILS}) \times (\# \text{ samples})] + [(9.5\mu\text{l formamide}) \times (\# \text{ samples})]$
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 of the 8-well strip tube(s).

4. Add 1 µl of amplified sample (or 1 µl of Allelic Ladder Mix) to each well. Cover wells with the Strip Septa Mat, 8-Well.

Notes:

1. To prevent cross-contamination, do not reuse Strip Septa Mat, 8-Well. Always use a new Strip Septa Mat, 8-Well, for each 8-well strip tube.
2. Instrument detection limits vary; therefore, injection time or the amount of sample mixed with loading cocktail may need to be increased or decreased. To modify the injection time, refer to the *Spectrum Compact CE System Operating Manual #TMD058*. 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.
3. 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.
4. Include an injection of allelic ladder every 4 injections (16 samples).
5. Centrifuge the 8-well strip tube(s) briefly to remove air bubbles from the wells.
6. Denature samples at 95°C for 3 minutes, and then immediately chill on crushed ice or a freezer plate block or in an ice-water bath for 3 minutes. Denature samples just prior to loading the instrument.

5.2. Assembling Sample Cartridge

1. Place the 8-well strip tube(s) with the Strip Septa Mat, 8-well, into the strip base (Figure 1). When using fewer than 4 strips in the run, you can place the strips in any lane.

Note: Lane names A to D and well numbers 1 to 8 are embossed on the strip base. Be sure to check the lane name when placing a sample 8-well strip tube into the strip base to make certain that the correct 8-well strip tube is in the correct lane.

Additionally, well numbers 1 to 8 are embossed on each 8-well strip tube. When placing a sample 8-well strip tube into the strip base, be sure that the well numbers on each sample 8-well strip tube match those on the strip base.

2. To complete the assembly, place the retainer over the strip(s) in the strip base, aligning the lane names A to D and well numbers 1 to 8 on the retainer to those on the strip base and pressing until the retainer clicks into the strip base (Figure 2).

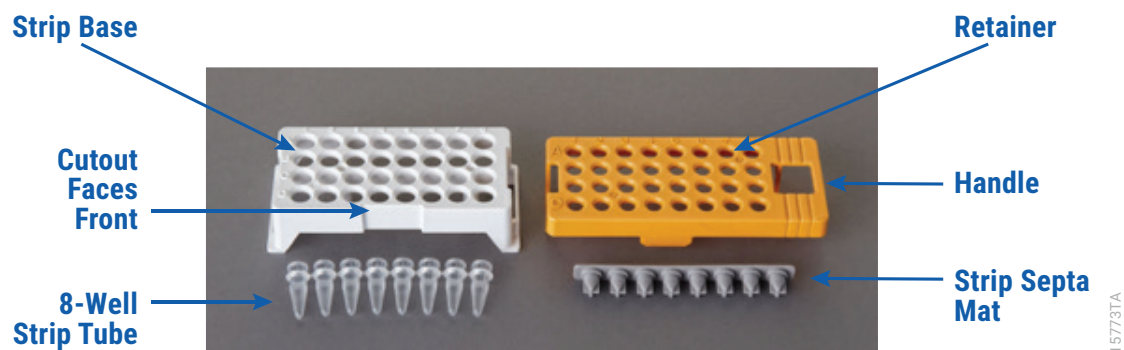


Figure 1. Assembling the Spectrum Compact Strip Base and Retainer.

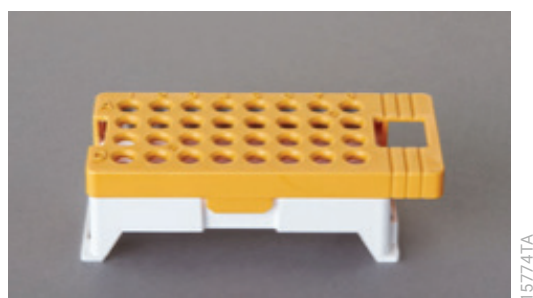


Figure 2. Assembled Spectrum Compact Sample Cartridge.

5.3. Instrument Preparation

These instructions are intended as a guide for running samples on the Spectrum Compact CE System (after successful spatial calibration and spectral calibration with the PowerPlex® 5C Matrix Standard). They are not intended as comprehensive instructions for using the Spectrum Compact CE System. Refer to the *Spectrum Compact CE System Operating Manual* #TMD058 for instrument maintenance, instructions for installing consumables, performing a spatial calibration and managing protocols (Assay, Instrument, and Sizecalling protocols). Refer to the *PowerPlex® Matrix Standards for the Spectrum Compact CE System Technical Manual* #TMD062 for instructions on performing a spectral calibration.

1. Before starting a run, ensure all consumables are installed and in sufficient supply. For best quality results, use unexpired reagents that are within the recommended use range (Figure 4 and Table 4). Refer to the 'Consumables' screen to determine if any consumables need to be replaced. To access the 'Consumables' screen, select the **Consumables** icon in the Header on the 'Main Menu' screen (Figure 3). The 'Consumables' screen displays information for the four consumables on the instrument: Polymer, Capillary Cartridge and Anode and Cathode Buffers.



Figure 3. Spectrum Compact CE System Software 'Main Menu' screen.

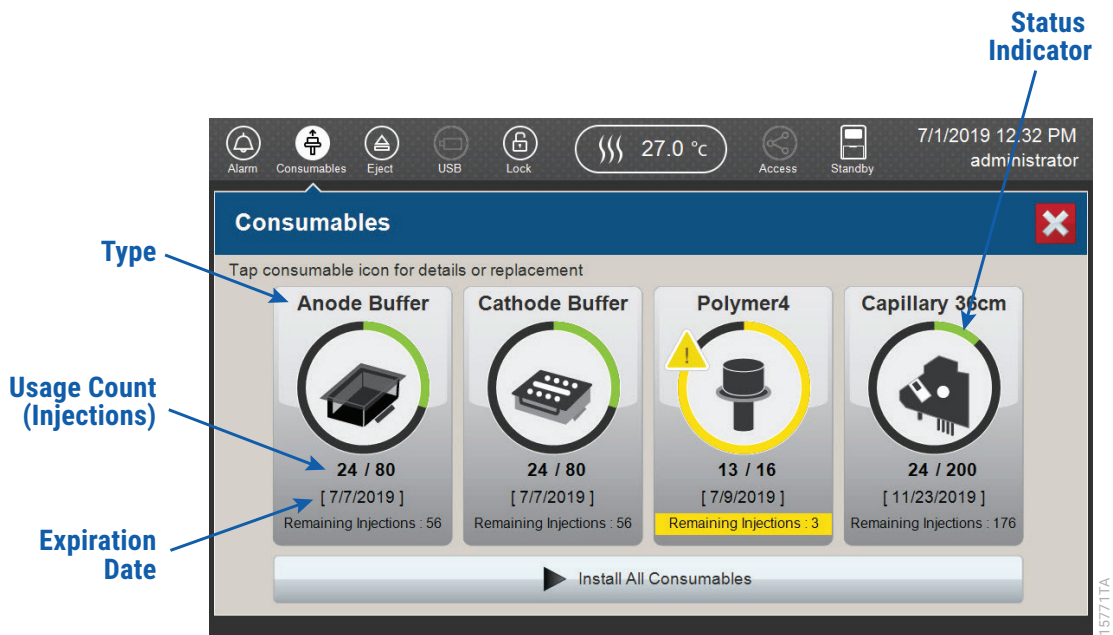





Figure 4. Spectrum Compact CE System 'Consumables' screen. Usage count (number of injections), on-instrument expiration date and remaining injections are displayed on the 'Consumables' screen for each consumable, as well as polymer type.

A consumable status indicator will appear on the icons of consumables that need attention. There are three indicators (Table 4).

Table 4. Consumable Warning Symbols.

Symbol	Description
	Reaching consumable expiration date, on-instrument expiration date or injection limit for consumable.
	Consumable expiration date, on-instrument expiration date or injection limit for consumable has passed.
	Cannot perform a run because maximum injection count reached for this consumable.

2. Select the **Oven Temperature** icon in the Header on the 'Main Menu' screen as shown in Figure 5 to start preheating the oven temperature to 60°C. The temperature displayed will change as the temperature of the oven increases. When 60°C is reached a check mark will appear adjacent to the temperature.

Note: We recommend that you preheat the oven for at least 30 minutes prior to starting a run. The oven will automatically turn off after 2 hours if a run is not started.

Oven Temperature Icon

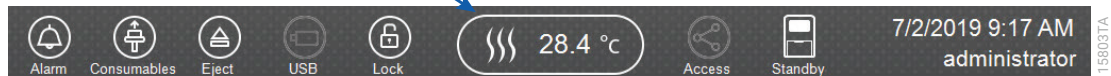


Figure 5. Preheating Oven.

3. Select **Fragment Analysis** on the 'Main Menu' screen (Figure 6).



Figure 6. Spectrum Compact CE System Software 'Main Menu' screen.

- Use the default name that includes date, time and “Fragment” or enter a Run ID on the ‘Set Run ID’ screen (Figure 7). Select the Run ID box to open the ‘Run ID’ window and a keypad will become active on the touch screen. Alternatively, the Run ID can be entered using a traditional keyboard if one is connected to the Spectrum Compact CE System.

Notes:

- The Run ID will be included in the file names for the samples.
- The following table lists rules for characters that can be used for a Run ID, Strip ID and sample name.

Acceptable Characters	1 to 30 characters for Strip IDs
	1 to 50 characters for Run IDs and sample names
	Upper and lowercase alphabetic characters
	Numbers
	Symbols unless listed below
Unacceptable Characters	¥ / : , ; * ? ' < >
	Spaces

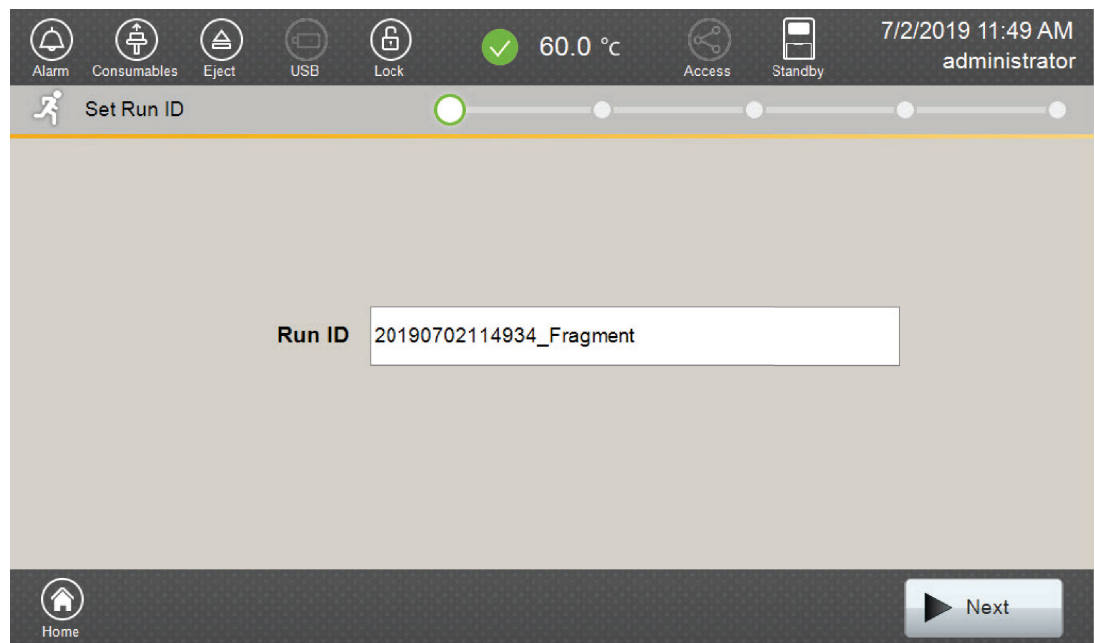


Figure 7. ‘Set Run ID’ screen.

- Select **Next** to proceed to the message screen for placement of strips into the sample cartridge.
- Follow the message screen for placement of strips into the sample cartridge (Figure 8).

Note: Ensure that the correct strip tube is placed into the correct lane (A through D) on the strip base and that wells 1 to 8 of the strip tube are correctly aligned with well positions 1 to 8 on the strip base.



Figure 8. 'Setup the Strip' screen.

5.4. Assigning Run Information to Samples

There are four methods to assign run information to samples:

1. Creating new strip information
2. Reusing run information from a list of completed runs
3. Loading saved strip information
4. Importing strip information

The following instructions are for creating new strip information only. For details on the remaining three methods, please see the *Spectrum Compact CE System Operating Manual* #TMD058.

Note: The Spectrum Compact CE System includes software for remote access to the instrument. This software allows a user to create and setup sample strips by remotely accessing the Spectrum Compact CE System software using a PC connected directly or via a lab network to the instrument. This software also allows a user to edit protocols and assays, monitor runs and export data. Refer to the *Spectrum Compact CE System Remote Access Software Manual* #TMD064.

1. Select **Next** on the 'Setup the Strip' screen shown in Figure 8. This will take you to the 'Setup Strip Information' screen shown in Figure 9.

Note: The 'Setup Strip Information' screen is divided into two sections: Sample Information and Strip ID.

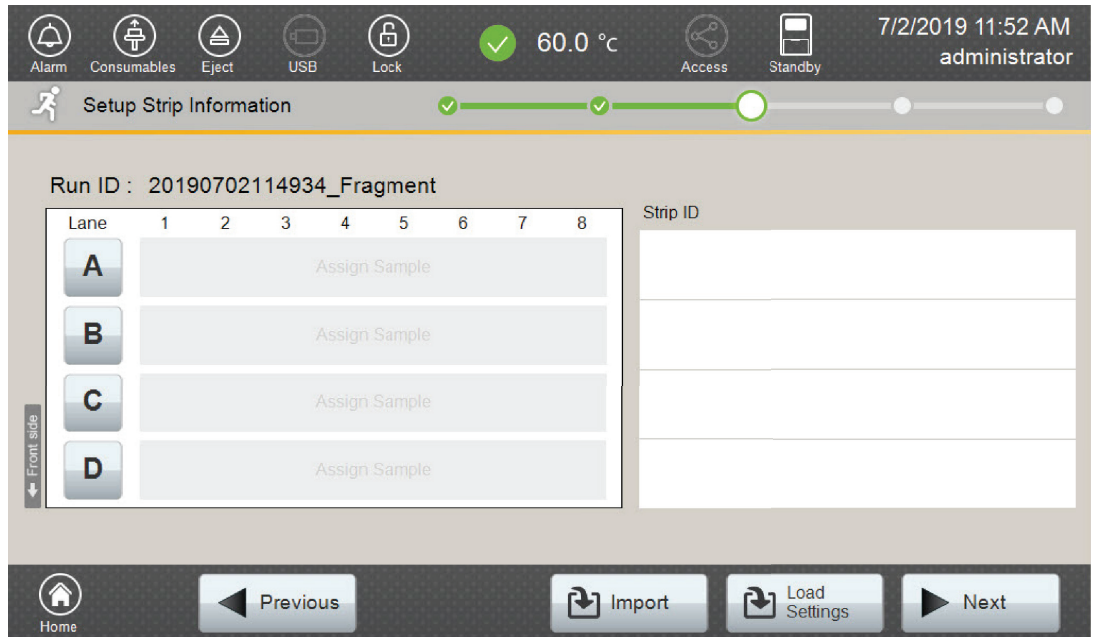


Figure 9. 'Setup Strip Information' screen.

2. Select a lane icon (A, B, C or D) to enter information for that 8-well strip tube. This opens the 'Edit Strip Information' screen for that lane (Figure 10). This screen displays fields for defining the Strip ID, run assay, sample name and sample type for that lane. Each well in the strip is represented along the left side of the screen. The first injection set of the strip (Wells 1–4) is displayed on the screen. You can use the arrows on the right side of the screen to scroll to the second injection set (Wells 5–8).

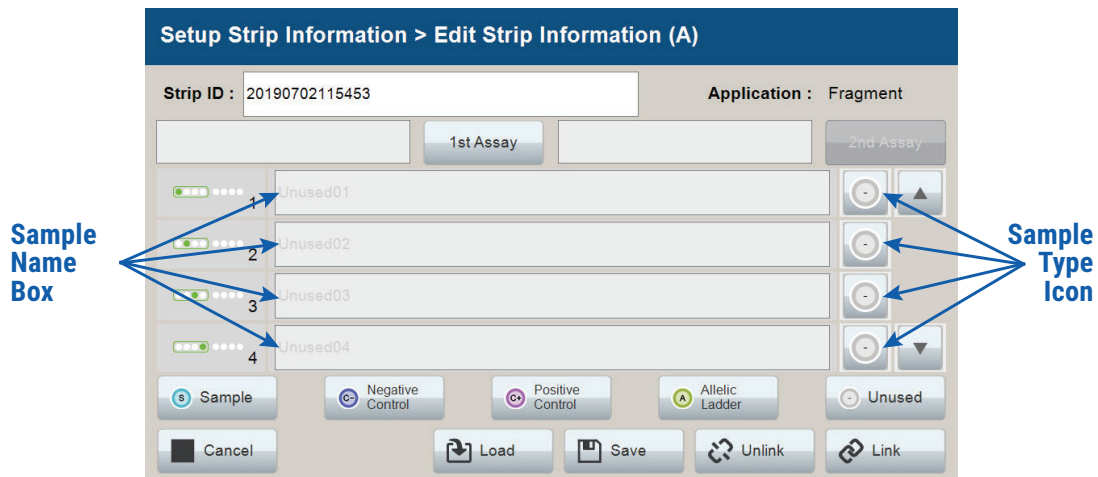


Figure 10. 'Edit Strip Information' screen.

3. The default Strip ID is date and time. It can be modified by selecting the Strip ID box. This opens the 'Set Strip ID' window and a keypad will become active on the touch screen (Figure 11). Alternatively, the Strip ID can be entered using a traditional keyboard if one is connected to the Spectrum Compact CE System. Enter the appropriate Strip ID, and then select **OK** to exit and return to the 'Edit Strip Information' screen.

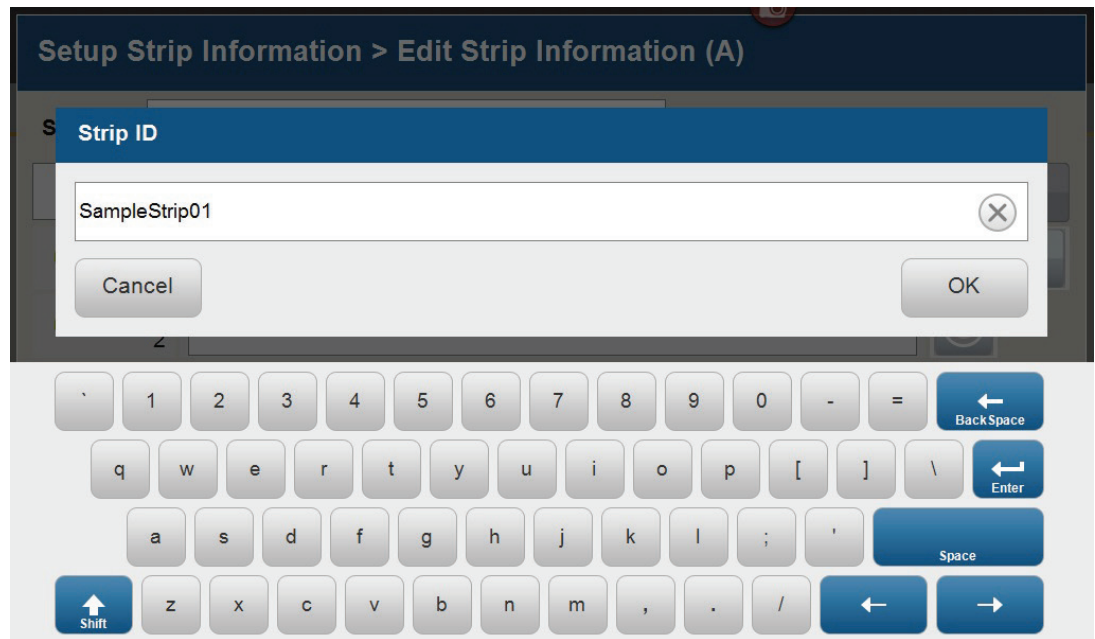







Figure 11. 'Set Strip ID' window.

4. Select a sample type on the 'Edit Strip Information' screen (Figure 12). Sample types must be selected for each well position before the Sample Name box becomes active for entry of sample name. Sample types are as follows.

Symbol	Sample Type
	Sample
	Negative Control
	Positive Control
	Allelic Ladder
	Unused

5. To assign a sample type to a well, select the appropriate sample type along the bottom of the 'Edit Strip Information' screen (Figure 12), and then select the **Sample Type** icon to the right of the sample name field for the desired well. This icon will then display the sample type selected for that well (Figure 13).

Note: A sample type other than 'Unused' must be assigned to at least one well in each injection set. If all of the four wells in an injection set are assigned as 'Unused', the injection set will not be run. If all eight wells in a strip are assigned as 'Unused', a warning message will be displayed, and no strip information will be assigned. Unused wells for any set of four wells being injected should contain formamide alone. Do not leave uninjected wells empty.

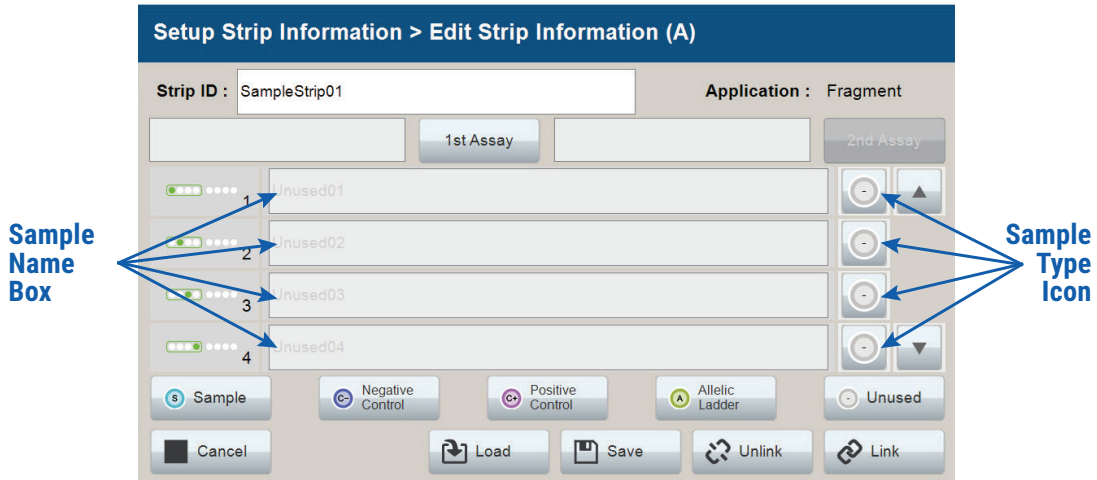


Figure 12. Sample Type and Sample Name on 'Edit Strip Information' screen.

- Enter a sample name for each well position by selecting the Sample Name box adjacent to the well number on the 'Edit Strip Information' screen (Figure 13). This opens the 'Set Sample Name' window and a keypad will become active on the touch screen (Figure 14). Alternatively, the Sample Name can be entered using a traditional keyboard if one is connected to the Spectrum Compact CE System. Enter the appropriate sample name, and then select **OK** to exit and return to the 'Edit Strip Information' screen.

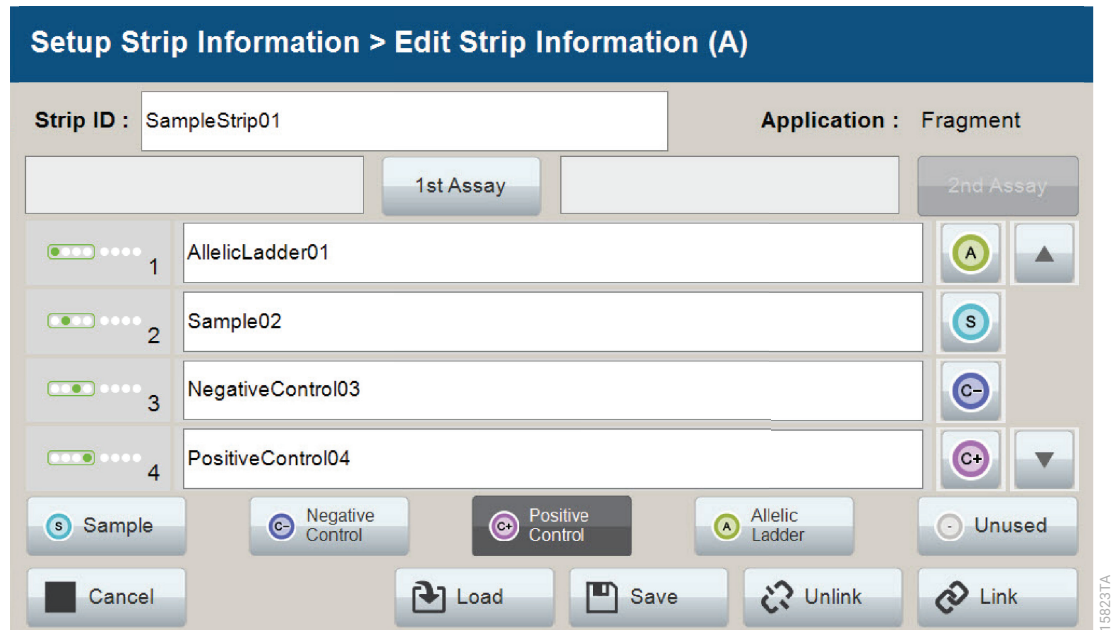


Figure 13. Sample Name Entry on 'Edit Strip Information' screen.

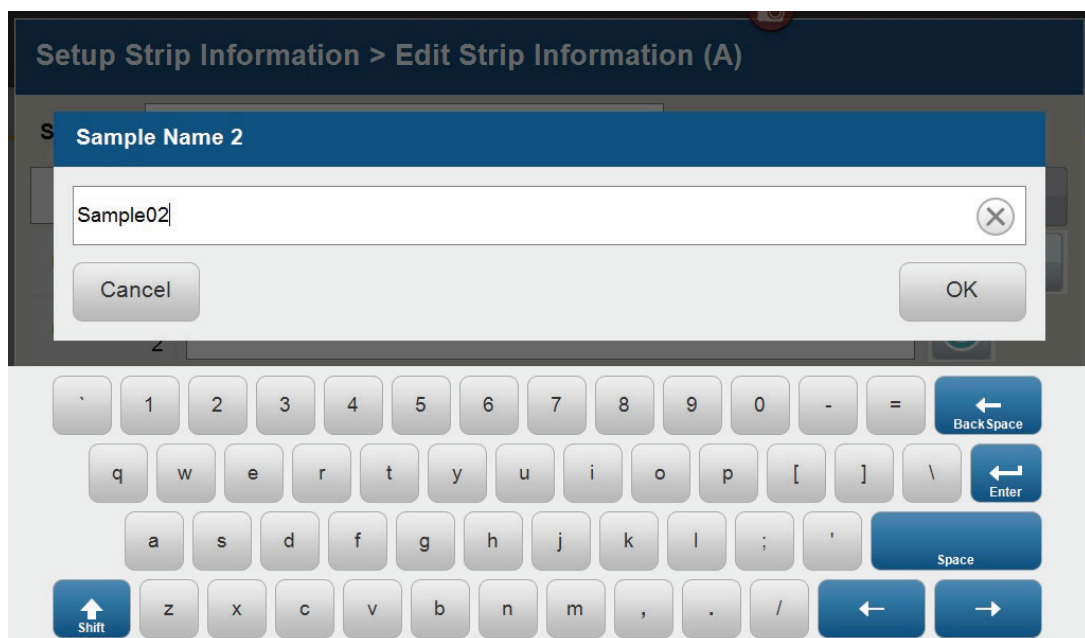


Figure 14. 'Set Sample Name' window.

- The Spectrum Compact Control Software includes preloaded run assays for use with chemistries available from Promega. Refer to the *Spectrum Compact CE System Operating Manual #TMD058* for information on creating or modifying assays. To assign a run assay to an injection set, select **1st Assay** on the right side of the 1st Assay field (Figure 13). This opens the 'Select Assay' window (Figure 15). Select "Promega_5Dye_WENILS_36_P4" from the drop-down list (Figure 15) and then select **Apply**.

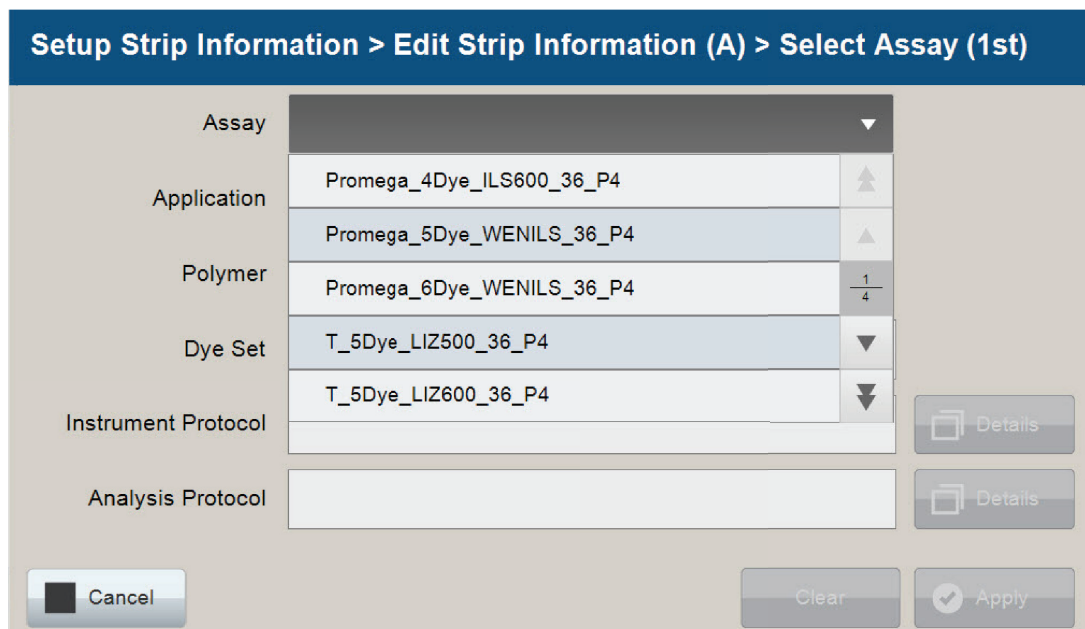


Figure 15. 'Select Assay' window.

8. You can verify the settings of the Instrument Protocol and Analysis Protocol associated with the assay chosen by selecting **Details** next to these fields (Figure 16). This will display a window showing the settings in these protocols but will not allow you to edit these settings. Refer to the *Spectrum Compact CE System Operating Manual #TMD058* to edit the Instrument Protocol or Analysis Protocol. When the assay information is confirmed, select **Apply** to return to the 'Edit Strip Information' screen.

The screenshot shows a software window titled "Setup Strip Information > Edit Strip Information (A) > Select Assay (1st)". The window contains several input fields and buttons:

- Assay:** A dropdown menu showing "Promega_5Dye_WENILS_36_P4".
- Application:** A text box containing "Fragment".
- Polymer:** A text box containing "Polymer4".
- Dye Set:** A text box containing "Promega 5-dye".
- Instrument Protocol:** A text box containing "Fragment_Analysis36_Polymer4" with a "Details" button to its right.
- Analysis Protocol:** A text box containing "Sizecalling_protocol_WENILS500" with a "Details" button to its right.
- Buttons:** At the bottom, there are "Cancel", "Clear", and "Apply" buttons.

Figure 16. Accessing Instrument and Analysis Protocols on 'Select Assay' window.

9. Repeat these steps for the 2nd Assay field if a second assay will be run for the strip. A second assay might include a longer or shorter injection time.
10. Use the down arrow on the right side of the 'Edit Strip Information' screen to enter sample information and assign an assay for samples in wells 5–8 of the strip.
11. When all information is entered and verified for the strip, select **Link** on the lower right corner of the 'Edit Strip Information' screen (Figure 17). This will link the strip to the run. If you want to save the strip information to use in future runs, save the information by selecting **Save** at the bottom of the 'Edit Strip Information' screen (Figure 17). This will save the strip information so that it can be loaded later into another run, as well as link the strip to the run. Refer to the *Spectrum Compact CE System Operating Manual #TMD058* for use of saved strip information.

Notes:

1. If you select **Unlink** without having previously selected **Save** at the bottom of the 'Edit Strip Information' screen, you will lose the strip information.
2. If you forget to assign an assay in the 'Edit Strip Information' screen, a warning window stating "Invalid Data Entered" will appear. Close this window and assign an assay on the 'Edit Strip Information' screen before continuing.

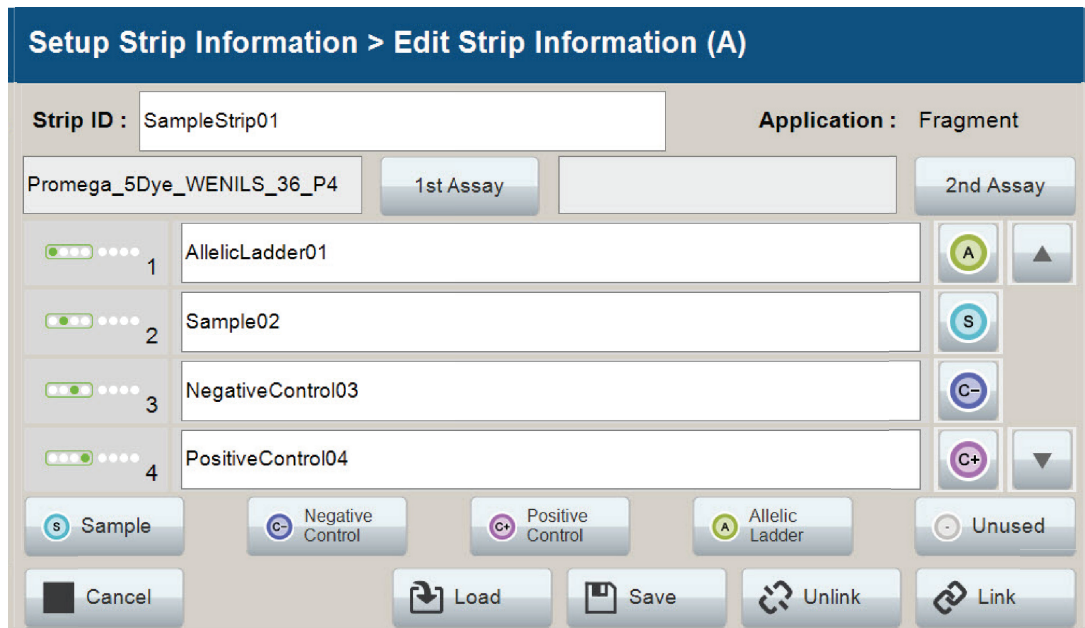


Figure 17. Completed 'Edit Strip Information' screen.

12. Repeat Steps 2–11 for additional lanes as necessary.
13. After all the required lanes have been set up, select **Next** on the 'Setup Strip Information' screen to load the sample cartridge (Figure 18).



Figure 18. Completed 'Setup Strip Information' screen.

5.5. Loading the Sample Cartridge

1. After selecting **Next** on the 'Setup Strip Information' screen, a message window will open, indicating that the autosampler is moving and telling the user to not open the door. In addition, the status indicator flashes green while the autosampler is moving. After autosampler movement is complete, the message window closes, and the status indicator returns to a steady green.

! **Note:** Do not open the door while the autosampler is in motion.

2. Open the instrument door, and then place the sample cartridge on the autosampler following the instructions displayed on the 'Install the Cartridge' screen (Figure 19). Press down on the yellow tab on the autosampler deck that locks the sample cartridge in place before placing sample cartridge into position. Release the tab to lock the sample cartridge in place on the autosampler deck.

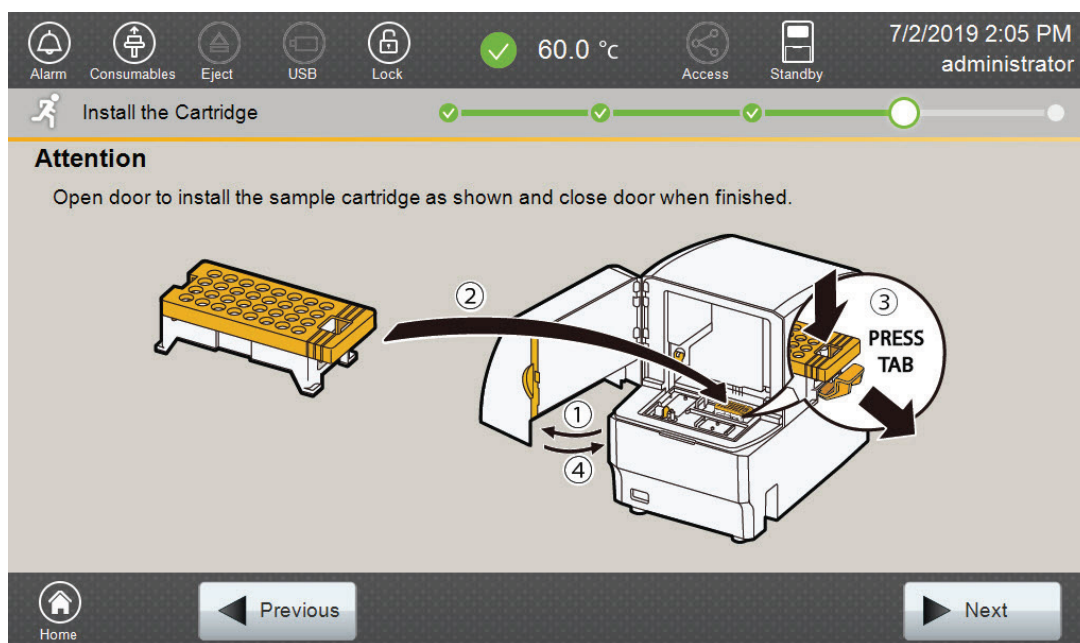


Figure 19. 'Install the Cartridge' screen.

3. When the sample cartridge is locked into place on the autosampler, close the instrument door and wait for the status indicator to stop flashing amber and turn steady green.

! **Note:** Do not open the door while the autosampler is in motion. Follow the instructions displayed on the screen.

4. After the autosampler has returned to its home position, the 'Edit Injection List' screen will be displayed (Figure 20).
5. Select **Run** to start the run.

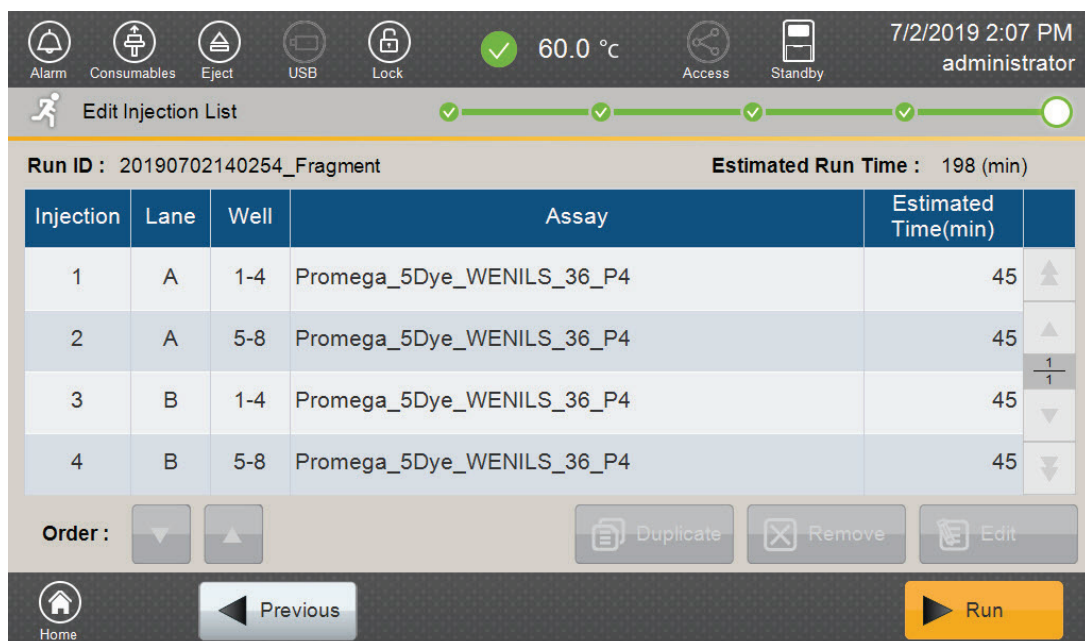


Figure 20. 'Edit Injection List' screen.

- Refer to the *Spectrum Compact CE System Operating Manual* #TMD058, for instructions on editing injection information, monitoring a run, viewing run results and exporting run data.

Data Analysis Using GeneMapper® *ID-X* Software

6

Due to potential differences between software versions, some of the instructions may not apply to all versions of GeneMapper® *ID-X* software.

6.1. Importing PowerPlex® ESX Panels, Bins and Stutter Text Files into GeneMapper® *ID-X* Software

To facilitate analysis of data generated with the PowerPlex® ESX 17 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 for the PowerPlex® ESX 17 System, go to: **www.promega.com/PowerPlexPanels**
2. Select the PowerPlex® ESX 17 System in the drop-down menu, and then select “GeneMapper *ID-X*”. Enter your contact information, and then select **Submit**.
3. Save the PowerPlex_ESX_Panels_IDX_vX.x.txt, PowerPlex_ESX_Bins_IDX_vX.x.txt and PowerPlex_ESX_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.

Importing Panels, Bins and Stutter 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 above. 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 ESX 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 above. Select the file, and then **Import**.
10. In the navigation pane, highlight the PowerPlex ESX panels folder that you just imported in Step 5.
11. Select **File**, and then **Import Marker Stutter**. A warning box 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 above. 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 then close the window.

6.2. Importing the WEN ILS 500 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 6.3.

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 6.1, Getting Started.
5. Highlight the file, and then select **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. Select **Done** to save the changes and close the GeneMapper® ID-X Manager.

6.3. 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 21), 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.

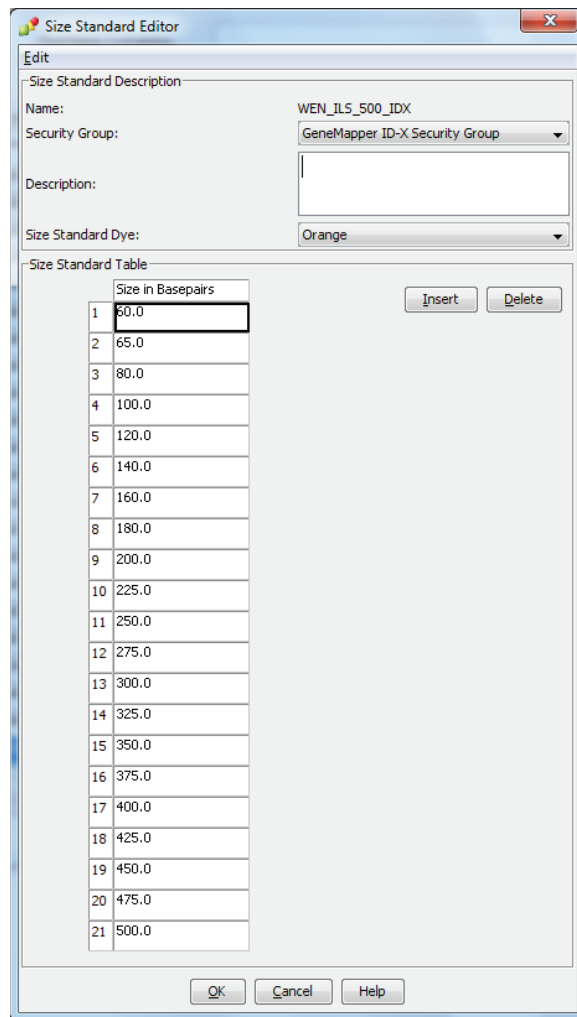


Figure 21. The GeneMapper® ID-X Size Standard Editor.

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 11.2, Figure 33.
8. Select **OK**.

6.4. 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 ESX 17".
6. Select the 'Allele' tab (Figure 22).

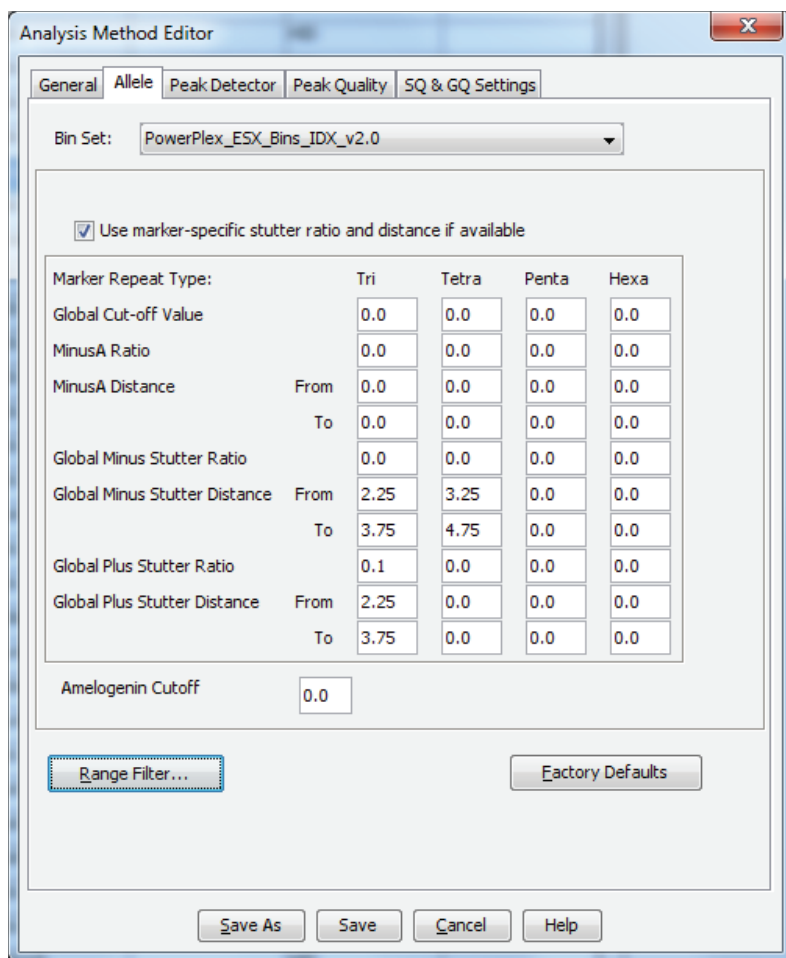


Figure 22. The GeneMapper® ID-X Allele tab.

7. Select the bins text file that was imported in Section 6.1.
8. Ensure that the 'Use marker-specific stutter ratio and distance if available' box is checked.
9. We recommend the values shown in Figure 22 for proper filtering of stutter peaks when using the PowerPlex® ESX 17 System. You may 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.
3. The normalization box can be checked or unchecked.

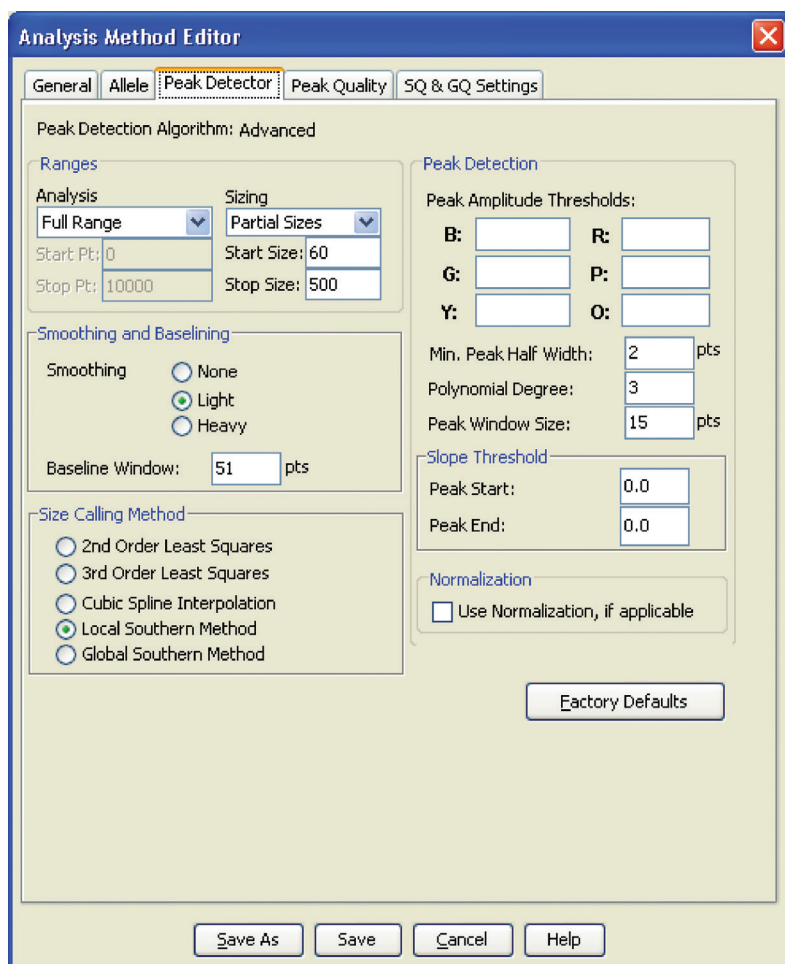


Figure 23. The GeneMapper® ID-X Peak Detector tab.

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

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

12. Select the 'SQ & GQ Settings' tab. You may change these settings.

13. Select **Save** to save the new analysis method.

14. 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. The sample types assigned in Section 5.4 will be included in the 'Sample Type' column. If needed, the drop-down menu in the 'Sample Type' column can be used to select **Allelic Ladder**, **Sample**, **Positive Control** or **Negative Control** as appropriate for the sample. Every run 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.
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 6.1.
7. In the 'Size Standard' column, select the size standard that was imported in Section 6.2 or created in Section 6.3.
8. Select **Analyze** (green arrow button) to start data analysis.

Note: By default, the software is set to display the 'Analysis Requirement Summary' window if an analysis requirement is not met.
9. If all analysis requirements are met, the 'Save Project' window will open (Figure 24).

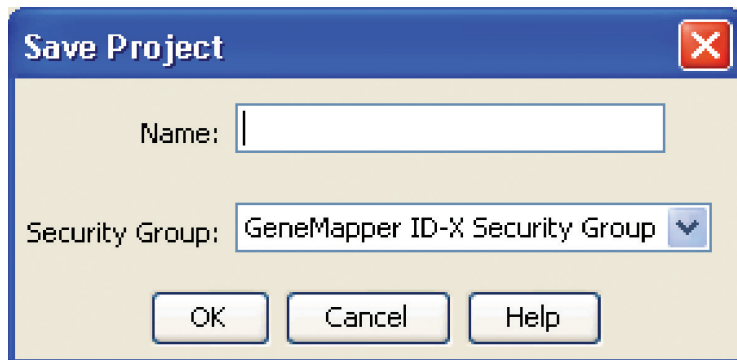


Figure 24. 'Save Project' Window.

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.

6.5. 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 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 ESX 17 20% Filter".
6. Select the 'Allele' tab (Figure 25).
7. Select the bins text file that was imported in Section 6.1.
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 and Tetra repeats (Figure 25). You may need to optimize these settings. In-house validation should be performed.

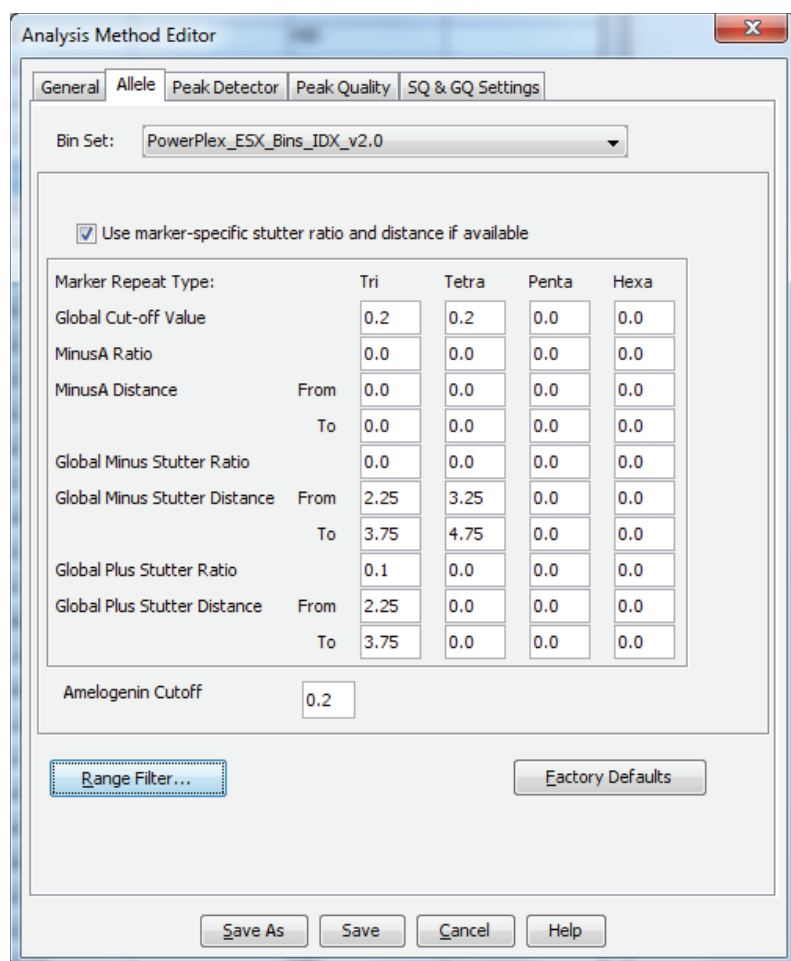


Figure 25. The GeneMapper® ID-X Allele tab with settings for using a 20% peak filter.

9. 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.
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.
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 the run files. Highlight the desired files, and then select **Add to List**, followed by **Add**.
4. The sample types assigned in Section 5.4 will be included in the 'Sample Type' column. If needed, the drop-down menu in the 'Sample Type' column can be used to select **Allelic Ladder**, **Sample**, **Positive Control** or **Negative Control** as appropriate for the sample. Every run 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.
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 6.1.
7. In the 'Size Standard' column, select the size standard that was imported in Section 6.2 or created in Section 6.3.
8. Select **Analyze** (green arrow button) to start data analysis.

Note: By default, the software is set to display the 'Analysis Requirement Summary', 'Allelic Ladder Analysis Summary' and 'Analysis Summary' windows after quality review by the software. Ensure that all requirements are met as each window appears. If you do not have the 'Analysis Requirement Summary' window activated, you may need to additional manual troubleshooting.

9. If all analysis requirements are met, the 'Save Project' window will open (Figure 24)
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.

6.6. Controls in GeneMapper® *ID-X* Software

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 99 (Section 11.1).

Data Analysis Using GeneMarker®HID Software for Spectrum CE Systems

7

7.1. Creating an Analysis Method with GeneMarker®HID Software for Spectrum CE Systems

These instructions are intended as a guide to start analyzing data in GeneMarker®HID Software for Spectrum CE Systems (GMHID-Spectrum). They are not intended as comprehensive instructions for using GMHID-Spectrum. More detailed instructions can be found in the *GeneMarker®HID for Spectrum CE Systems User Manual #TM555*.

The current PowerPlex.xml panel files are preloaded in the software or available at www.promega.com/PowerPlexPanels

1. Open GMHID-Spectrum.
2. To access your data files, select **Open Data** in the Magic Wizard or under the File menu.
3. Select **Add**, then navigate to the directory containing your raw data files and select the desired files.
4. Select **Open**, and the selected files will appear in the Data File List (Figure 26).

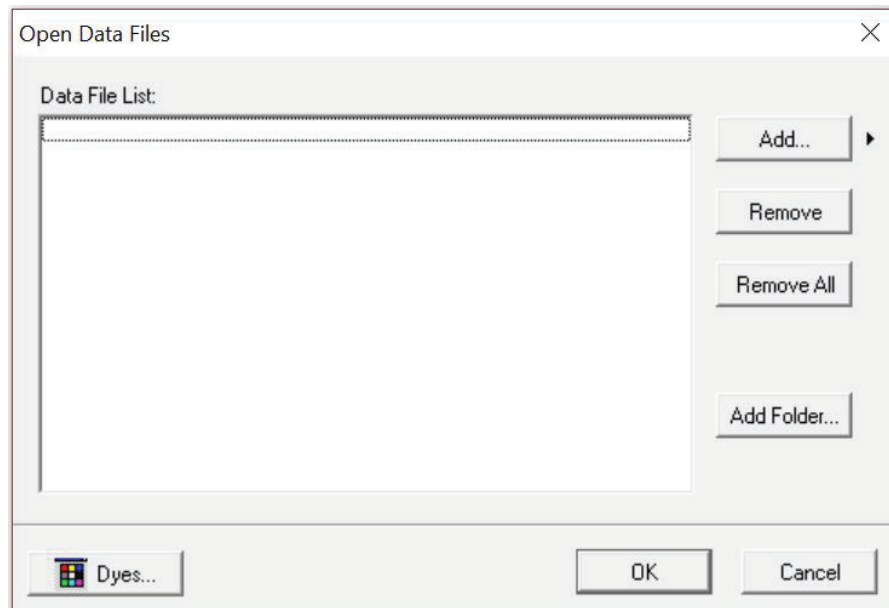


Figure 26. The GMHID-Spectrum Data File List.

5. Select **OK** in the 'Open Data Files' window, and the data will be uploaded into GMHID-Spectrum. In the Raw Data Tree, verify that the sample types (allelic ladder, positive control and negative control) are designated correctly. If sample types are not correct, designate sample types by right-clicking on the file name and selecting **Set Sample Type**.

Note: Sample types are designated in the file name using preferences. In the View menu, select the Forensic tab under Preferences, then enter sample name identifiers for ladder, positive and negative controls.

6. Use the Panel Editor in the Tools menu to select the PowerPlex®_ESX_17 panel from the Panel Template list. Click on the plus symbol to expand the list, right-click on a marker, and then select **Edit**. Enter laboratory-specified values for Min Homozygote Intensity, Homozygote Inconclusive Range, Min Heterozygote Intensity, Heterozygote Inconclusive Range, Min Heterozygote Imbalance and Max Heterozygote Imbalance (Figure 27). This will set values for peaks within the marker range. Refer to *GeneMarker®HID Software for Spectrum CE Systems User Manual #TM555* for more information.

Notes:

1. Individual laboratories should determine their peak amplitude thresholds from internal validation studies.
 2. These settings can be applied to all markers by checking the "Apply Homo/Hetero Settings to All Markers" check box or by dye channel by checking the "Apply Homo/Hetero Settings to Markers in this dye" check box.
7. Select **OK** and close the 'Panel Editor' window. Select **Save Changes** or **Save as New Panel** under the File menu then close the window.

Edit Marker [X]

Marker Parameters:

Marker Name:

Nucleotide Repeats (x):

Boundary: To

Min Homozygote Intensity: [▲▼]

< = Inconclusive <= [▲▼]

Min Heterozygote Intensity: [▲▼]

< = Inconclusive <= [▲▼]

Max Heterozygote Imbalance(%): [▲▼]

Min Heterozygote Imbalance(%): [▲▼]

Apply Homo/Hetero Settings to All Markers

Apply Homo/Hetero Settings to Markers in this dye

Stutter Filter:

Use Marker-Specific Values

N - 2x %

N + x % N - x %

N+0.5x % N-0.5x %

Use Allele-Specific Values(From Panel)

Apply Stutter Settings to All Markers

Figure 27. The 'Edit Marker' window for the D3S1358 marker.

- Click on **Run** in the Magic Wizard or click the **Run Project** icon (green arrow) in the toolbar. The 'Template Selection' screen will appear (Figure 28). Select the PowerPlex_ESX_17 template and the settings shown in Figure 28. Verify the panel that you created in Step 6 is selected in the panel drop-down field. The Size Standard must be ILS500 and the Standard Color must be Orange. Select **Next**.

Note: Changes to the template can be saved at each step during the Run Project process: 'Template Selection', 'Data Process' and 'Additional Settings' screens.

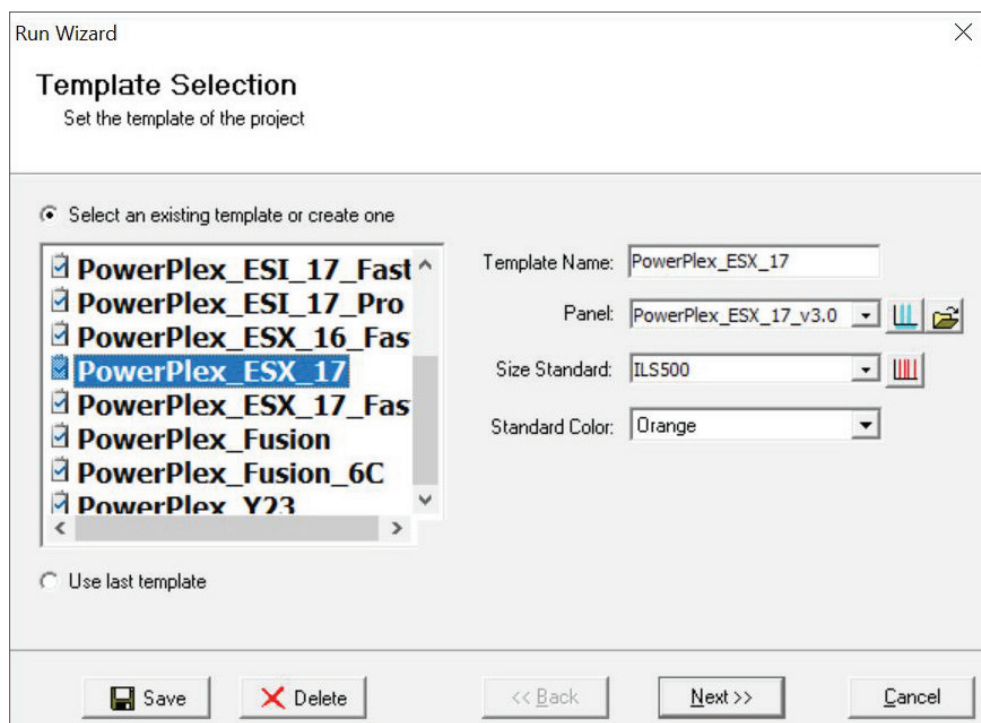


Figure 28. The 'Template Selection' window.

9. The 'Data Process' window will appear (Figure 29). For the Raw Data Analysis, we recommend using Auto Range, Smooth, Superior Baseline Subtraction and Local Southern for the Size Call.

For the Allele Call, we recommend using Auto Range. Setting of the Max Intensity (peaks above which will be flagged) and the Min Intensity for Standard Color should be determined by your laboratory. For peaks outside of the panel range, the settings from the panel can be applied by checking the "Apply Nearest Marker Setting" box. Refer to *GeneMarker®HID Software for Spectrum CE Systems User Manual #TM555* for more information on use of the Peak Detection Threshold. Select **Next**.

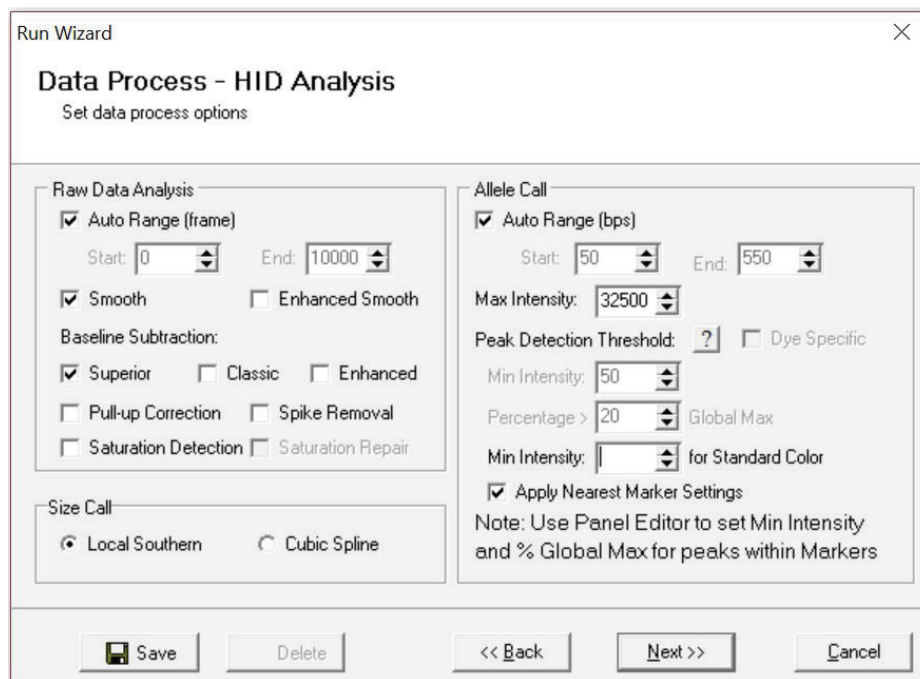


Figure 29. The 'Data Process' window for an analysis method.

- The 'Additional Settings' window will appear (Figure 30). Select **ESX_17** as the P.C. Template 1 and verify that the boxes are checked for "Auto Select Best Ladder" and "Auto Panel Adjust". The values displayed in the 'Allele Evaluation' dialogue box are defaults and will affect the quality values displayed in the plot settings. For more information on quality values, use of a second positive control and mixture evaluation, refer to the *GeneMarker®HID Software for Spectrum CE Systems User Manual #TM555*. Select **OK** to analyze the raw data.

Figure 30. The 'Additional Settings' window.

- When the analysis is complete, the 'Main Analysis' window will appear. We recommend that you review any yellow or red flagged markers and handle them according to your laboratory's standard operating procedures.

Note: Quality and display settings are set using Preferences under the View menu. Refer to *GeneMarker®HID Software for Spectrum CE Systems User Manual #TM555* for more information.

7.2. Controls in the GMHID-Spectrum Software

- Observe the results for the negative control. Using the protocols defined in this manual, the negative controls should be devoid of amplification products.
- Observe the results for the 2800M Control DNA. The expected 2800M allele designations for each locus are listed in Table 9 (Section 11.1).

Representative results of the PowerPlex® ESX 17 System are shown in Figure 31. The PowerPlex® ESX 17 Allelic Ladder Mix is shown in Figure 32.

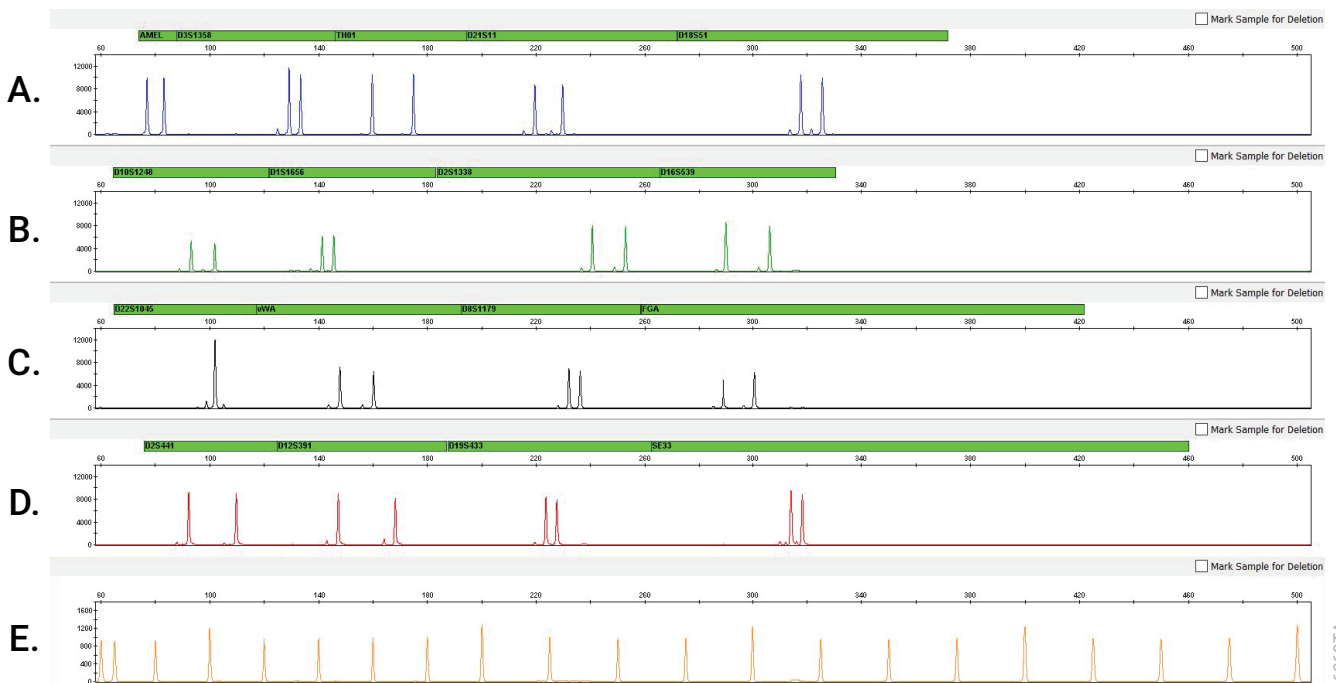
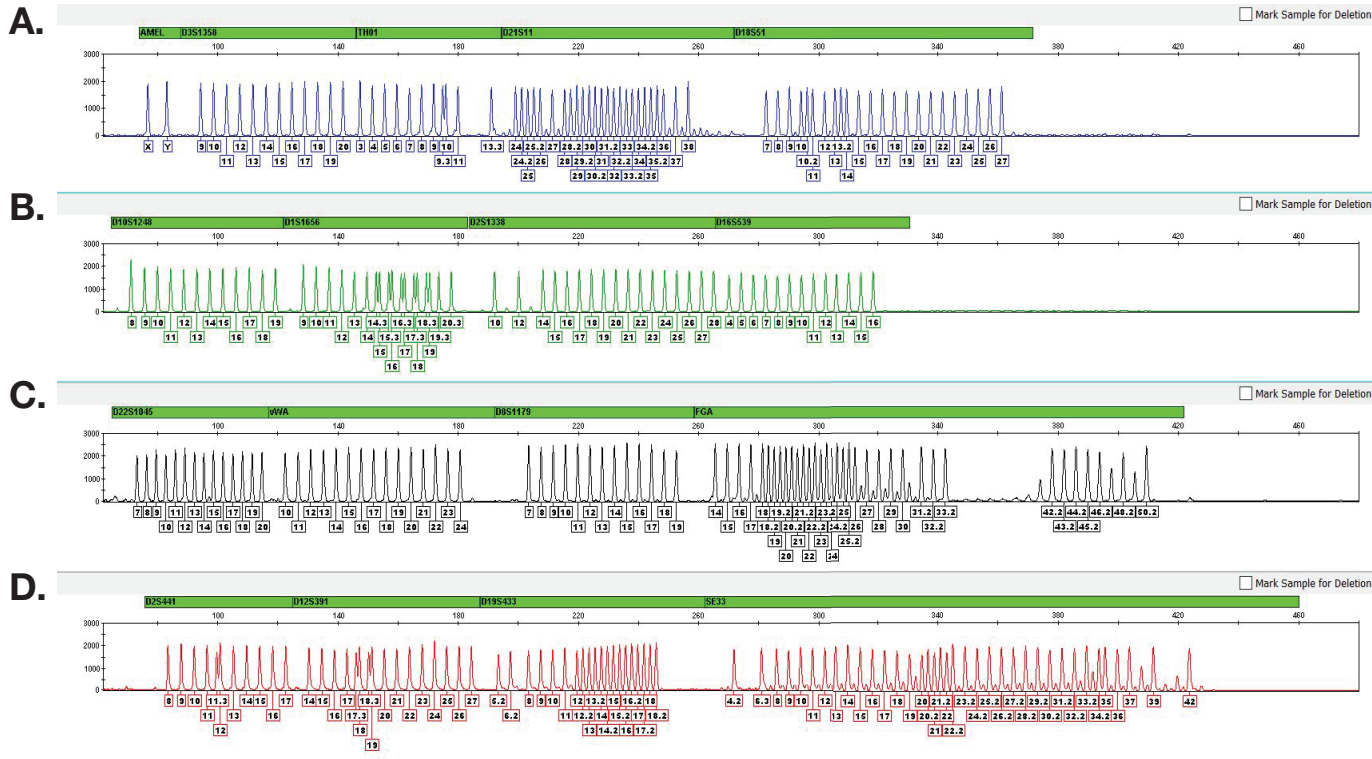


Figure 31. The PowerPlex® ESX 17 System. The 2800M Control DNA (0.5ng) was amplified using the PowerPlex® ESX 17 System. Amplification products were mixed with WEN Internal Lane Standard 500 and analyzed with a Spectrum Compact CE System and a 1.6kV, 9-second injection. Results were analyzed using GeneMapper® ID-X software, version 1.4, and PowerPlex® ESX panels and bins text files. **Panel A.** An electropherogram showing the peaks of the fluorescein-labeled loci: Amelogenin, D3S1358, TH01, D21S11 and D18S51. **Panel B.** An electropherogram showing the peaks of the JOE-labeled loci: D10S1248, D1S1656, D2S1338 and D16S539. **Panel C.** An electropherogram showing the peaks of the TMR-ET-labeled loci: D22S1045, vWA, D8S1179 and FGA. **Panel D.** An electropherogram showing the peaks of the CXR-ET-labeled loci: D2S441, D12S291, D19S433 and SE33. **Panel E.** An electropherogram showing the 60bp to 500bp fragments of the WEN Internal Lane Standard 500.



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Figure 32. The PowerPlex® ESX 17 Allelic Ladder Mix. The PowerPlex® ESX 17 Allelic Ladder Mix was analyzed with a Spectrum Compact CE System and a 1.6kV, 9-second injection. The sample file was analyzed with the GeneMapper® ID-X software, version 1.4, and PowerPlex® ESX 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 (15,16).

Stutter products are often 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 stutter plus three standard deviations observed at each locus is used in the PowerPlex® ESX 17 stutter text file for locus-specific filtering in GeneMapper® *ID-X* software and in the panel file included in GMHID-Spectrum.

In addition to stutter peaks, you may observe the following low-level DNA-dependent artifact peaks (Table 5) and DNA-independent (with or without human genomic DNA) artifact peaks (Table 6) with the PowerPlex® ESX 17 System loci.

Table 5. DNA-Dependent Artifacts Observed in Amplification Reactions with Human Genomic DNA.

Locus or Dye Label	Artifact Size
Fluorescein	~61–63 bases ~71–73 bases
Amelogenin	$n-1$
D21S11	$n-2$, $n+2$
D1S1656	$n-2$, $n+2$
D2S441	$n-2$, $n+2$
SE33	$n-2$, $n+2$

Table 6. DNA-Independent Artifacts Observed in Amplification Reactions with and without Human Genomic DNA.

Dye Label	Artifact Size¹
Fluorescein	~64–67 bases
JOE	~67–69 bases
TMR-ET	~59–61 bases

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

Troubleshooting

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

Refer to the *Spectrum Compact CE System Operating Manual* #TMD058 for instrument troubleshooting. For troubleshooting GMHID-Spectrum, refer to the *GeneMarker[®]HID Software for Spectrum CE Systems User Manual* #TM555.

9.1. Amplification and Fragment Detection

Symptoms	Causes and Comments
Faint or absent allele peaks	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.
	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 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°C to +10°C. Make sure that the 2800M Control DNA is stored at +2°C to +10°C for at least 24 hours before use. Vortex before use.

Symptoms	Causes and Comments
<p>Extra peaks visible in one or all color channels</p>	<p>Contamination with another template DNA or previously amplified DNA. Cross-contamination can be a problem. Use aerosol-resistant pipette tips and change gloves regularly.</p>
	<p>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.</p>
	<p>Samples were not denatured completely. Heat-denature samples for the recommended time, and cool on crushed ice or 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 re-annealing.</p>
	<p>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.</p>
	<p>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.</p>
	<p>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.</p> <ul style="list-style-type: none"> • Perform a new spectral calibration and rerun the samples. • Confirm that the correct spectral was used for the sample run. • Instrument sensitivities can vary. Optimize the injection conditions. Refer to the instrument user manual.
	<p>Dye blob artifacts. The signal strength of certain dye blob artifacts increases with 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.</p>
	<p>An incorrect internal lane standard was used. Use the size standard provided in the kit.</p>

Symptoms	Causes and Comments
Allelic ladder not running the same as samples	Be sure the allelic ladder and samples are from the same instrument run.
	Allelic ladder and primer pair mix were not compatible. Ensure that the allelic ladder is from the same kit as the primer pair mix.
	Migration of samples changed slightly over the course of a CE run with many samples. This may be due to changes in temperature 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. Include one allelic ladder for every 16 samples.
	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.

9.2. Amplification of Extracted DNA

The following information is specific to amplification of purified DNA. For information about general amplification and detection, see Section 9.1.

Symptoms	Causes and Comments
Faint or absent allele peaks	Impure template DNA. Depending on the DNA purification procedure used and sample source, inhibitors might be present in the DNA sample. This may be more of an issue as DNA sample volume increases as a percentage of the total amplification reaction volume.
	Insufficient template. Use the recommended amount of template DNA if available. Quantify template DNA before use if possible.
	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) or TE ⁻⁴ buffer with 20µg/ml glycogen.
	The reaction volume was too low. This system is optimized for a final reaction volume of 25µl for extracted DNA. Decreasing the reaction volume may result in suboptimal performance.

Symptoms	Causes and Comments
<p>Extra peaks visible in one or all color channels</p>	<p>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 Results section for additional information about stutter and artifacts. The amount of template will need to be optimized if you are using reduced reaction volumes.</p>
	<p>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.</p> <ul style="list-style-type: none"> • 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.
<p>Peak height imbalance</p>	<p>Amplification of greater than the recommended amount of template can result in an imbalance, with 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.</p>
	<p>Degraded DNA sample. DNA template was degraded, and larger loci showed diminished yield.</p>
	<p>Insufficient template DNA. Use the recommended amount of template DNA if available. Stochastic effects can occur when amplifying low amounts of template.</p>
	<p>Impure template DNA. Inhibitors that may be present in forensic samples can lead to allele dropout or imbalance.</p>
	<p>Imbalance may be seen more often when using the maximum template volume or a reduced amplification reaction volume.</p>
	<p>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.</p>

9.3. 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 9.1.

Symptoms	Causes and Comments
Faint or absent allele peaks	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.
	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°C to +10°C. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Do not refreeze, as this may reduce activity.

Symptoms	Causes and Comments
Faint or absent allele peaks in the positive control reaction	<p>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 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. We do not recommend including blank punches in the 2800M Control DNA reaction.</p>
Extra peaks visible in one or all color channels	<p>Punch contaminated with DNA from another sample. Perform punches on a blank card between samples to minimize potential for carryover between samples.</p>
	<p>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.</p>
	<p>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. 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.</p>
	<p>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 Results section for additional information on stutter and artifacts.</p>
	<p>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.</p> <ul style="list-style-type: none"> • Be sure to perform the recommended extension step at 60°C after thermal cycling. • Decrease cycle number. • Increase the final extension time.

Symptoms	Causes and Comments
Peak height imbalance	<p>Excessive amount of DNA. Amplification of high amounts of template can result in an imbalance, with smaller loci showing more product than larger loci.</p> <ul style="list-style-type: none"> • Be sure to use the recommended number of punches. Follow the manufacturer’s recommendations when depositing sample onto the card. • Decrease cycle number.
	<p>The cycle number was too high. Decrease the cycle number by one cycle and repeat the amplification.</p>
	<p>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.</p>
	<p>Amplification was inhibited when using more than one storage card punch with blood. Use only one 1.2mm storage card punch with blood.</p>
	<p>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.</p>
	<p>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.</p>
	<p>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.</p> <ul style="list-style-type: none"> • 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 and using one punch 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.
	<p>Inactive PunchSolution™ Reagent was used to pretreat nonlytic punches. Thaw the PunchSolution™ Reagent at +2°C to +10°C. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Do not refreeze, as this may reduce activity.</p>

Symptoms	Causes and Comments
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.

9.4. 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 9.1.

Symptoms	Causes and Comments
Faint or absent allele peaks	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°C to +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.

Symptoms	Causes and Comments
Faint or absent peaks for the positive control reaction	<p>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.</p>
Extra peaks visible in one or all color channels	<p>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.</p>
	<p>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.</p> <p>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.</p>
	<p>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. 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.</p>
	<p>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.</p> <ul style="list-style-type: none"> • Be sure to perform the recommended extension step at 60°C after thermal cycling. • Use 2µl of swab extract in an amplification 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.

Symptoms	Causes and Comments
<p>Peak height imbalance</p>	<p>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.</p>
	<p>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.</p>
	<p>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°C to +10°C. Do not store reagents in the refrigerator door, where the temperature can fluctuate. Do not re-freeze, as this may reduce activity.</p>
	<p>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.</p>
<p>Extreme variability in sample-to-sample peak heights</p>	<p>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, quantitate the DNA using a fluorescence-based double-stranded DNA quantitation method or qPCR-based quantitation method. The quantitation values can be used to normalize input template amounts to minimize variation in signal intensity.</p>

9.5. GeneMapper® ID-X Software

Symptoms	Causes and Comments
Stutter peaks not filtered	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 Requirement Summary’ window was not active, and there was an analysis requirement that was not met. Turn on ‘Analysis Requirement 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 changes 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.
	<p>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.</p> <ul style="list-style-type: none"> • 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.

Symptoms	Causes and Comments
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® <i>ID-X</i> 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 the section 'Processing Data for Casework Samples' or 'Processing Data for Databasing or Paternity Samples.'
	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 Polymer4 may change migration of the fragments, causing alleles to migrate outside of the panel range.
Size standard not called correctly	Starting data point was incorrect for the partial range chosen for the analysis in the GeneMapper® <i>ID-X</i> Peak Detector tab as described in sections 'Creating a Casework Analysis Method' or 'Creating a Databasing or Paternity Analysis Method.' Adjust the starting data point or 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. <ul style="list-style-type: none"> • 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.
	Confirm that the correct spectral was used to run the samples.

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11.1. Advantages of Using the Loci in the PowerPlex® ESX 17 System

The loci included in the PowerPlex® ESX 17 System (Table 7 and Table 8) were selected because they meet the recommendations of the European Network of Forensic Science Institutes (ENFSI). The PowerPlex® ESX 17 System amplifies all ENFSI core loci plus SE33 in a single reaction. Table 9 lists the PowerPlex® ESX 17 System alleles revealed in 2800M Control DNA.

Terminal nucleotide addition (17,18) occurs when *Taq* 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 band 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 (19) to the amplification protocols to provide conditions for essentially complete terminal nucleotide addition when recommended amounts of template DNA are used.

Table 7. The PowerPlex® ESX 17 System Locus-Specific Information.

STR Locus	Label	Chromosomal Location¹	Repeat Sequence² 5'→3'
D18S51	Fluorescein	18q21.33 (59.1Mb)	AGAA (20)
D21S11	Fluorescein	21q21.1 (19.476Mb)	TCTA Complex (20)
TH01	Fluorescein	11p15.5 (2.149Mb)	AATG (20)
D3S1358	Fluorescein	3p21.31 (45.557Mb)	TCTA Complex
Amelogenin ³	Fluorescein	Xp22.1–22.3 and Y	NA
D16S539	JOE	16q24.1 (84.944Mb)	GATA
D2S1338	JOE	2q35 (218.705Mb)	TGCC/TTCC
D1S1656	JOE	1q42 (228.972Mb)	TAGA Complex
D10S1248	JOE	10q26.3 (130.567Mb)	GGAA
FGA	TMR-ET	4q28 (155.866Mb)	TTTC Complex (20)
D8S1179	TMR-ET	8q24.13 (125.976Mb)	TCTA Complex (20)
vWA	TMR-ET	12p13.31 (5.963Mb)	TCTA Complex (20)
D22S1045	TMR-ET	22q12.3 (35.779Mb)	ATT
SE33	CXR-ET	6q14 (89.043Mb)	AAAG Complex
D19S433	CXR-ET	19q12 (35.109Mb)	AAGG Complex
D12S391	CXR-ET	12p12 (12.341Mb)	AGAT/AGAC Complex
D2S441	CXR-ET	2p14 (68.214Mb)	TCTA

¹Information about chromosomal location of these loci can be found in references 21 and 22 and at: <https://strbase.nist.gov/chrom.htm>

²The August 1997 report (23,24) 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.”

³Amelogenin is not an STR.

NA = Not Applicable

Table 8. The PowerPlex® ESX 17 System Allelic Ladder Information.

STR Locus	Label	Size Range of Allelic Ladder Components^{1,2} (bases)	Repeat Numbers of Allelic Ladder Components³
D18S51	Fluorescein	286–366	7–10, 10.2, 11–13, 13.2, 14–27
D21S11	Fluorescein	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
TH01	Fluorescein	152–195	3–9, 9.3, 10–11, 13.3
D3S1358	Fluorescein	103–147	9–20
Amelogenin ⁴	Fluorescein	87, 93	X, Y
D16S539	JOE	273–321	4–16
D2S1338	JOE	197–269	10, 12, 14–28
D1S1656	JOE	137–184	9–14, 14.3, 15, 15.3, 16, 16.3, 17, 17.3, 18, 18.3, 19, 19.3, 20.3
D10S1248	JOE	83–127	8–19
FGA	TMR-ET	264–410	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
D8S1179	TMR-ET	203–251	7–19
vWA	TMR-ET	124–180	10–24
D22S1045	TMR-ET	79–118	7–20
SE33	CXR-ET	267–417	4.2, 6.3, 8–20, 20.2, 21, 21.2, 22, 22.2, 23.2, 24.2, 25.2, 26.2, 27.2, 28.2, 29.2, 30.2, 31.2, 32.2, 33.2, 34.2, 35–37, 39, 42
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
D12S391	CXR-ET	130–182	14–17, 17.3, 18, 18.3, 19–27
D2S441	CXR-ET	88–124	8–11, 11.3, 12–17

¹The length of each allele in the allelic ladder has been confirmed by sequence analyses.

²When 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.

³For 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

⁴Amelogenin is not an STR.

Table 9. The PowerPlex® ESX 17 System Allele Determinations for the 2800M Control DNA.

STR Locus	2800M
D18S51	16, 18
D21S11	29, 31.2
TH01	6, 9.3
D3S1358	17, 18
Amelogenin	X, Y
D16S539	9, 13
D2S1338	22, 25
D1S1656	12, 13
D10S1248	13, 15
FGA	20, 23
D8S1179	14, 15
vWA	16, 19
D22S1045	16, 16
SE33	15, 16
D19S433	13, 14
D12S391	18, 23
D2S441	10, 14

11.2. 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 33). Each fragment is labeled with WEN dye and can be detected separately (as a fifth color) in the presence of PowerPlex® ESX 17-amplified material. The WEN ILS 500 is designed for use in each CE injection to increase precision in analyses when using the PowerPlex® ESX 17 System. Protocols to prepare and use this internal lane standard are provided in Section 5.

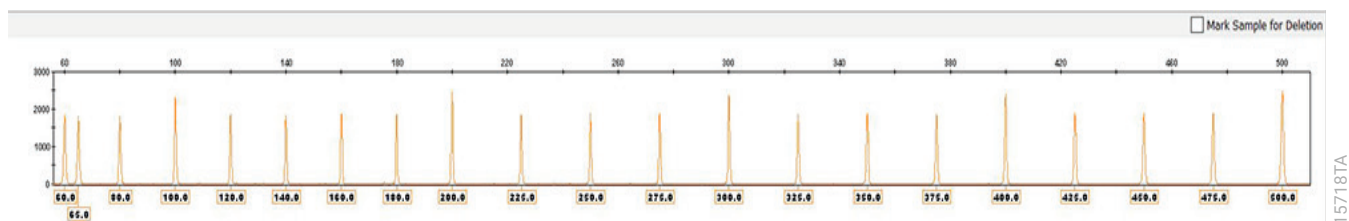


Figure 33. WEN Internal Lane Standard 500. An electropherogram showing the WEN Internal Lane Standard 500 fragments.

11.3. Composition of Buffers and Solutions

TE⁻⁴ buffer (10mM Tris-HCl, 0.1mM EDTA [pH 8.0])

1.21g Tris base

0.037g EDTA (Na₂EDTA • 2H₂O)

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⁻⁴ buffer with 20µg/ml glycogen

1.21g Tris base

0.037g EDTA (Na₂EDTA • 2H₂O)

20µg/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.

11.4. Related Products

Accessory Components

PRODUCT	SIZE	CAT.#
PowerPlex® 5C Matrix Standard	5 preps	DG4850
WEN Internal Lane Standard 500	200µl	DG5001
PunchSolution™ Kit	100 preps	DC9271
SwabSolution™ Kit	500µl	DC8271
5X AmpSolution™ Reagent	500µl	DM1231
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.

Spectrum Compact CE System Accessories and Consumables

PRODUCT	SIZE	CAT.#
Spectrum Compact Capillary Cartridge, 4-Capillary, 36cm	1 each	CE2340
Spectrum Compact Polymer4	4 × 64 wells	CE2304
Spectrum Compact Buffer	2 pairs	CE2300
Spectrum Compact Cathode Septa Mat	10 each	CE2301
Spectrum Compact Cathode Retainer	4 each	CE2302
Spectrum Compact Strip Base & Retainer, 32-Well	4 each	CE2332
Strip Septa Mat, 8-well	24 each	CE2308

Not for Medical Diagnostic Use.

The following changes were made to the 9/21 revision of this document:

1. Expanded character rules table in Section 5.3.
2. Updated disclaimers.

^(a)U.S. Pat. No. 9,139,868, European Pat. No. 2972229, Japanese Pat. No. 6367307 and other patents pending.

^(b)TMR-ET, CXR-ET and WEN dyes are proprietary.

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