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**IDENTIFYING THE FACTORS NECESSARY FOR SUCCESSFUL DNA
PROFILING FROM SPENT CARTRIDGE CASINGS**

FINAL REPORT

2013-DN-BX-K039

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ABSTRACT

Crimes involving firearms are widespread in the United States, and in many instances it is vitally important that law enforcement be able to identify the individual involved. In general, the weapon used in a shooting is not recovered from the scene, however spent cartridge casings, ejected during firearm use can be recovered by law enforcement. Fingerprints are rarely obtained from casings, thus many have attempted to obtain DNA from them, typically with little success. Thus, the goals of this research were to test and optimize methods for obtaining DNA from spent cartridge casings, along with testing different DNA analysis methods. In this research, volunteers loaded live cartridges into the magazines of firearms, which were fired and casings collected. These collections were used to test several variables that might influence successful DNA analysis from spent cartridges.

The first experiments involved swabbing or soaking casings. Different vessels for soaking the outside of a casing were investigated, along with other factors. The optimized protocol involved soaking casings in the bulb of a plastic transfer pipette for 30 min, removing the liquid and swabbing the casing and bulb, and incubating the swab and solution at 85°C for 10 min. The swabbing protocol was a standard double swab strategy widely used in crime laboratories, where the first swab is wetted and used to swab the object, followed by a dry swab that picks up residual liquid. Finally, a kit specifically designed for DNA isolation from fingerprints (Fingerprint DNA Finder, or FDF) was tested, following the manufacturer's instructions.

DNAs from swabbings and soakings were extracted via standard organic extraction followed by filtration, or using a commercial, silica-based kit (QIAamp). DNA yields were compared. Swabbing resulted in significantly higher DNA yields than did soaking, followed by

FDF. Likewise, organic extraction resulted in significantly higher DNA yields than did QIAamp and FDF.

Next, three DNA typing methodologies were investigated: STR amplification using Promega Fusion, STR amplification using Life Technologies' MiniFiler, and mitochondrial DNA amplification and sequencing. The MiniFiler kit generally resulted in a higher percentage of possible alleles being amplified, however the Fusion kit targets so many more loci, it resulted in more overall data. MtDNA was successfully amplified from all samples. Non-handler alleles/polymorphisms were seen in a large number of samples, likely because casings, magazines, firearms, etc., were not cleaned in advance, in order to make scenarios and results as 'real world' as possible.

Two strategies for swabbing casings: individually double swabbing each or cumulatively double swabbing sets of three with a single pair of swabs, were examined. Cumulative swabbing was faster and resulted in more DNA per swab pair, although not three times as much as individual swabbing. More STR alleles were also recovered, however this was offset by a substantial increase in non-handler alleles from cumulatively swabbed casings.

Loading/firing order, which could influence DNA yields in a variety of ways, did not have a discernable impact on DNA yields or typing results. In contrast, the caliber of the cartridge did affect DNA results, with 0.45 caliber casings resulting in greater DNA yields than 0.22 caliber casings, when both individually and cumulatively swabbed. Likewise, cyanoacrylate fuming, which is a common procedure for enhancing fingerprints on items such as cartridge casings, also affected DNA yields, in a detrimental way.

In the end, a significantly superior method for isolating and purifying DNA from spent cartridge casings was identified, as were a large number of variables that did or did not affect

DNA yields from casings. Such results should prove to be highly beneficial for the successful analysis of DNA from casings associated with crime scenes.

DRAFT

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INTRODUCTION

Hundreds of thousands of crimes are committed using firearms every year in the United States (National Institute of Justice, 2013), including the most violent crimes such as homicide, rape, robbery, and aggravated assault. As an example, in 2014, 11,961 homicides were reported to the FBI, 70% of which involved firearms, primarily handguns (Uniform Crime Reports, <https://www.fbi.gov/stats-services/crimestats>). Because firearm violence is so prevalent, it is crucial that law enforcement be able to identify the person who loaded and fired a weapon during the commission of a crime. The goal of this research project was to determine if the handler of a handgun could be identified through the DNA left behind on the ammunition after it was fired, and to optimize our chances of doing so.

Cartridge Casings: Class and Individual Characteristics

Though often referred to as a “bullet”, firearm cartridges are actually composed of four elements: the projectile, the primer, the gunpowder, and the casing. The projectile for most handgun and rifle ammunition is a single bullet. In shotgun ammunition, the cartridge, or shell, contains a number of projectiles called shot, or a single slug. The primer is the component of the cartridge that is struck to generate a spark, which ignites the gunpowder and causes the weapon to fire. Black powder was originally used in firearms, but modern weapons use smokeless powder (Saferstein, 2005). The casing is the metal container that surrounds the projectile, primer, and powder. Casings are commonly made of brass, although nickel, aluminum, and steel are also used (Saferstein, 2005). When a pistol or rifle is fired, the casing is ejected, and is often left behind and collected by crime scene investigators as evidence.

There are several class and individualizing features of cartridges that are used to associate them with a firearm. One class level trait is the caliber of the ammunition, or the measurement of its width. For example, a 0.22 caliber bullet has a diameter of 0.22 in, and the width of the casing is the same or slightly wider. The caliber of the ammunition corresponds to the caliber of the weapon designed to fire it, which helps firearms examiners identify the type of gun used to commit a crime. Other class characteristics of casings that can associate them with a particular make and model of firearm include the type of cartridge (rimfire or centerfire), type of rim (rimmed, semi-rimmed, rimless, belted, or rebated), shape and location of the firing pin impression, and presence and location of extractor and ejector marks, which are examined using a low-power microscope (Saferstein, 2005).

Individual characteristics are then examined to connect a casing to a particular firearm. For example, marks on the casing such as firing pin impressions, breech face marks, and ejector marks can all be used to associate the casing with a particular gun (e.g., Saribey et al., 2009). A firearm examiner first test fires the suspected firearm to obtain known cartridge casings for comparison, and the known and unknown samples are then evaluated using a comparison microscope. However, while this method is useful for associating a cartridge casing with a gun, it cannot identify the person who loaded or fired it.

Obtaining Fingerprints from Spent Cartridge Casings

Fingerprints may be left on the casing surface when a cartridge is loaded into a magazine, which can be useful for identification of the handler as no two individuals are thought to share the same fingerprint. Such prints, if recoverable, have the potential to identify the individual who loaded the weapon. Given (1976) first examined the effect that firing a cartridge had on the

recovery of identifiable fingerprints from cartridge casings, under idealized circumstances. Six volunteers placed prints on individual chloroform-cleaned sets of brass and nickel-plated 0.38 caliber cartridges, half of which were subsequently fired using a Smith & Wesson model 19, .357 Combat Magnum. The time between the handling and firing of cartridges was varied, as was the time between firing and recovery of prints, which was attempted using black fingerprint powder. Time did not cause substantial degradation of the fingerprints, though it was proposed that the evaporation of water resulted in a decrease in the adherence of powder to the prints. Degradation of fingerprints as a result of firing was purportedly due to blowback of hot gasses along surfaces of the casing not tightly sealed against the chamber wall, and friction between the casing and gun barrel. When the gunpowder ignites, internal pressure causes the casing to expand; fingerprints were most commonly recovered from near the head of the casing (by the rim), possibly because it is where the metal of the casing is the thickest and therefore experiences less expansion and friction. Additionally, it was noted that prints were recovered more successfully from brass cartridges than from nickel.

Bentsen et al. (1996) furthered Given's work by testing a variety of methods to enhance latent fingerprints on spent casings. The authors investigated the recovery of fingerprints purposefully rolled onto cartridges, which were subsequently fired and analyzed. The ammunition was fired with a 0.38 Webley revolver, which the authors stated "was selected because of its lower thermodynamics of detonation and minimum handling of test rounds during loading compared to magazine or belt-fed weapons...ridge detail loss during the ejection process should be minimal in comparison to self-loading systems". The sensitivity of multiple latent print visualization techniques was investigated based on the amount and quality of ridge detail. The two most sensitive methods were vacuum cyanoacrylate fuming with Panacryl Brilliant Flavine

staining, and selenious acid surface oxidation. Of the 21 combinations of weapons and ammunition studied post-firing using these two methods, 23.8% yielded identifiable ridge detail and 57.1% included some ridge detail. However, when applied to 104 criminal incidents, only two prints (one of which was associated to a CSI, and the other of which was never identified) were recovered using the cyanoacrylate method. The casework results clearly show fingerprints are rarely recovered from spent casings. The authors noted the loss of fingerprint ridge detail may be attributed to several variables: physical damage during cartridge loading or casing ejection, gaseous blowback during firing, or interference of propellant by-products as a result of gaseous blowback.

The lack of success in obtaining useable fingerprints from spent cartridge casings was further demonstrated by Spear et al. (2005). Forty-eight fingerprints, characterized as bloody, oily, or sweaty, were intentionally placed on cartridges, half of which were fired. Bloody prints were processed using amido black, while sweaty and oily prints were visualized using cyanoacrylate fuming followed by rhodamine 6G dye. Five useable prints were obtained from the unfired cartridges, of which two were bloody and three were oily. Only a single bloody print was recovered from the spent casings, which the authors acknowledged is not frequently encountered on casings submitted as evidence. Excluding bloody prints, 3 out of 32 (9%) cartridges displayed useable prints, all of which were unfired. It was also noted that casings, which displayed a print, were all of the larger caliber sizes used in the study (0.45 or 9 mm as opposed to 0.22).

Isolation and Characterization of Touch DNA

A potential alternative to developing fingerprints on casings is analyzing DNA left on them as they are loaded into a weapon or magazine. ‘Touch DNA’ has been successfully obtained from items, however its viability from spent cartridge casings using current techniques is suspect. The first published success in obtaining genetic information from touch samples was by van Oorschot and Jones (1997), who demonstrated that STR alleles could be produced from swabs of handled objects including briefcase handles, pens, and car keys. These types of samples quickly became popular submissions to forensic laboratories, and DNA evidence was obtained from weapons such as knives, screwdrivers, and ligatures, as well as from door handles, door bells, and adhesive tape involved in crimes (reviewed by Wickenheiser, 2002). The success of touch sample analysis, however, has remained highly variable. Researchers have shown that the amount of DNA transferred through physical contact depends on many variables, including the individual handler, the surface being handled, and environmental conditions (Phipps and Petricevic, 2007; Daly et al., 2010). For example, rough, porous surfaces are more likely to yield DNA than smooth, non-porous ones (Daly et al., 2012). Surprisingly, the amount of time spent handling the substrate has not been found to affect the amount of DNA deposited, and full profiles have been reported from a contact time of 1 s from paper (Balogh et al., 2003a) and 5 s from fabrics (Linacre et al., 2010).

Several modifications to the procedures used by forensic scientists have been suggested to increase the success of DNA analysis from low template samples. The quantity of DNA collected via swabbing can be raised through the use of detergent-based wetting solutions (Thomasma and Foran, 2013), and pre-treatment of centrifugal filtration devices has been shown to decrease DNA loss during extraction (Doran and Foran, 2014). Following extraction, the

amplification of STR alleles has been improved by increasing the number of polymerase chain reaction (PCR) cycles (Gill, 2001) and reducing PCR reaction volumes (Gaines et al., 2002). Detection of alleles can be enhanced through post-PCR clean up and increased injection times (Smith and Ballantyne, 2007; Westen et al., 2009), which allows for the production of more complete profiles.

Despite these advances, challenges in processing low copy number samples remain, several of which were discussed by Budowle et al. (2009). Stochastic sampling, in which alleles are randomly amplified, may result in heterozygote peak imbalance and/or drop out of one or both alleles at a locus. Stutter peaks, which are generally less than 20% of the associated allele peak height in high template samples (e.g., Leclair et al., 2004), can be as tall as their parent allele, and in some instances might exceed the true peak's height. Contamination and drop-in can also have an intensity as strong as true alleles in low template samples, making interpretation difficult and unreliable. One method for overcoming these challenges is to perform replicate analysis, in which two or more aliquots of the sample are amplified separately (Budowle et al., 2009) and results are compared.

Previous Studies on DNA from Cartridge Casings

The analysis of touch DNA is becoming increasingly successful, but samples obtained from spent cartridge casings present additional challenges. DNA is likely deposited onto the surface of the casing during the loading process, however, when the cartridge is fired it is subjected to extremely high temperatures (the barrel of the gun may reach 1,200°C [Lawton, 2001]), pressure, and mechanical stress (U.S. Army Materiel Command, 1965), which likely have a strong degradative effect on DNA. Additionally, the metal composition of the casing and

the gunshot residue expelled during firing might inhibit PCR. Consequently, authors have noted that crime laboratories often do not attempt to recover DNA from spent casings (e.g., Horsman-Hall et al., 2009).

The feasibility of recovering DNA profiles from spent cartridge casings has been the focus of multiple studies over the past several years. In the aforementioned study, Spear et al. (2005) attempted to recover DNA from planted fingerprints. After the casings were processed for fingerprints, they were swabbed and DNA was organically extracted and amplified with an AmpF ℓ STR Profiler Plus Kit. Only three of the 48 casings generated a DNA profile, all of which came from bloody fingerprints. One of the three resulted from a fired casing and nine of the ten loci in that profile contained allelic information, although it was not specified whether the alleles were consistent with the blood donor. Additionally, it is not clear if fingerprint processing prior to DNA analysis had an effect on the STR results.

Horsman-Hall et al. (2009) analyzed the effect that firing had on the recovery of DNA from spent casings. A single donor, said to leave behind substantial DNA in touch samples (although how this was determined was not described), who had not washed their hands for at least an hour, handled ten cartridges, each for at least 30 s. Five were loaded into a cleaned rifle by a gloved individual and were fired, while the remaining five were tested unfired. No magazine was used. DNA was recovered using a double swab technique, in which the first swab was wetted with 40 μ L water, and was extracted using either an organic procedure (followed by Microcon purification) or DNA IQ with one of three digestion buffers (proteinase K + 20% sarkosyl, DNA IQ Lysis Buffer, or proteinase K + sodium dodecyl sulfate [SDS]). DNA was quantified using a Plexor HY System, and STRs were amplified using AmpF ℓ STR MiniFiler, AmpF ℓ STR Identifiler, and PowerPlex 16 BIO kits. Organic extraction yielded significantly less

DNA than the three DNA IQ methods. There was no significant difference between the DNA yields of the fired and unfired casings, which produced an average MiniFiler profile of $81 \pm 20\%$ and $85 \pm 12\%$, respectively, indicating that firing did not affect DNA profiling under these idealized conditions, although the small sample size would necessarily influence the statistical findings. MiniFiler produced a significantly greater number of alleles than either PowerPlex 16 BIO or Identifiler.

In a retrospective study at the Forensic Laboratory for DNA Research in the Netherlands, Dieltjes et al. (2011) developed a method to recover and extract DNA, and described some results. The authors used a Qiagen QIAamp DNA Mini Kit on 4,085 items (cartridges, bullets, and casings) collected among 616 cases, and performed a modified version of the manufacturer's protocol for bloodstains. Casings were soaked in sterile 10-mL round bottom tubes with 400 μ L of buffer and rotated at a non-specified angle for 30 minutes. Following soaking, casings were swabbed with a dry sterile cotton swab and the samples underwent a pre-digestion incubation for 10 minutes at 85°C. DNAs were amplified with PowerPlex 16. The authors noted "since the success rates for cartridges and casings were rather similar, we combined their results". The success rate per criminal case was defined as "the number of criminal cases in which at least one DNA profile could be reported". The average success rate of obtaining a reproducible STR profile (defined as amplifications of a locus two or more times from a single DNA extract) from cartridges/casings was 26.5%. Examining all three types of evidence, the authors obtained 283 reproducible STR profiles (98.9% contained STR data at four or more loci), 84.1% of which were consistent with a single individual (i.e., 2 or fewer peaks per locus). Additionally, 51 STR profiles were full—containing alleles from all 15 loci. However, the authors did not clarify which items yielded which results, thus it is unknown how much of the STR data was from spent

casings. Furthermore, it was not made clear if known STR profiles were available to make comparisons with the 4,085 cartridges, bullets, and casings analyzed.

Shortcomings of Previous Studies

Loading Order

One variable that has the potential to influence the amount of DNA recovered from spent cartridge casings is the order in which the cartridges are loaded and subsequently fired. It is possible that most of the loose cells on an individual's fingers are deposited on the first cartridges loaded, with the number of cells decreasing with each subsequent cartridge. Conversely, the last cartridge loaded requires more force to load into a magazine, which might result in the transfer of a greater number of cells. Additionally, the temperature of the weapon when it is fired may alter the amount of DNA that is present on a spent casing. The temperature inside a firearm will increase as more cartridges are fired, thus the first loaded (last fired) cartridge is exposed to the most heat, potentially having a degradative effect on DNA.

DNA Isolation

Current protocols used by the Michigan State Police Forensic Science Division to analyze touch DNA from spent casings involve swabbing the casings and processing the swabs according to the laboratory's standard operating procedure for swabs (forensic scientist Sarah Rambadt, personal communication). However, touch DNA is often degraded and present in low copy number (LCN; generally less than 100 pg of DNA; Gill et al., 2000) meaning analysis from spent casings has limited success. Multiple techniques exist for the isolation and purification of DNA, including organic (Maniatis et al., 1982; Comey et al., 1994), silica-based (Boom et al., 1990;

Greenspoon et al., 1998), and non-binding separation (Kopka et al., 2011) methods. Therefore it is possible that optimization of one or more of these may improve the amount of touch DNA recovered for subsequent analyses.

Standard phenol-chloroform DNA extractions involve digestion of the cell membrane and proteins with a lysis buffer containing a detergent (e.g., SDS), proteinase K, a buffering agent (e.g., Tris), and a chelating agent (e.g., ethylenedinitrilotetraacetic acid [EDTA]). Digestion at ~56°C helps inactivate nucleases and break down cellular membranes, releasing DNA. Following the addition of phenol, the solution is vortexed and centrifuged, resulting in an organic portion (containing degraded proteins and cellular debris) and an aqueous portion (containing nucleic acids). The aqueous layer is added to chloroform to remove residual phenol. This process may be followed by additional purification and concentration methods using a centrifugal filter unit.

Silica-based extraction methods, which come in a variety of commercially available forms, consist of silica covered beads or columns that selectively bind DNA under high salt conditions. Cation bridges are formed via chaotropic agents (e.g., sodium iodide) between the negatively charged silica and the negatively charged DNA backbone (Melzak et al., 1996). Residual proteins and impurities are washed away, after which a low salt solution is used to elute the DNAs from the silica.

Kopka et al. (2011) developed a Fingerprint DNA Finder (FDF) Kit that utilizes a non-binding DNA separation method. They stated “the DNA extraction system is based on a reversal of the silica principle”. The same set of authors (Cardozo et al., 2012) described this method as using “porous matrices associated with polyanilines nano-layers, which are able to retain selectively biopolymers and potential PCR inhibiting substances, while nucleic acids are never

bound and remain in solution”, based on earlier technology developed by Kapustin et al. (2003). The validation study of the FDF Kit (Kopka et al., 2011) included analysis of DNA samples from multiple components (trigger, magazine, slide barrel, and hammer) of four pistols and a revolver, along with cartridge casings fired from them. Only results for three partial electropherograms (samples from a trigger, magazine, and slide barrel of a single firearm) were presented, which were consistent with the handler. The authors stated “the profile was altered in the fired cartridge case (not shown). Similar results were obtained with all guns tested and with all replicate samples from the same gun”. Data presented by Kopka et al. (2011) are scarce, consequently it is unclear what success in DNA recovery FDF Kits may have on spent cartridge casings.

DNA Analysis

Today, there is a wide variety of STR kits commercially available. Typical kits target amplicons between 100 and 450 bp (e.g., Identifiler, PowerPlex 16). However, moving PCR primers closer to the STR region to reduce amplicon size allows for more successful amplification from degraded samples (Wiegand and Kleiber, 2001). As a result, new “miniplex” STR kits were introduced, such as MiniFiler, which targets nine loci all smaller than 300 bp and is advertised as being useful for degraded and challenging samples. Other “megaplex” kits have also been developed, such as the Promega PowerPlex Fusion System that amplifies 24 loci, 14 of which are smaller than 300 bp, and Promega claims it is highly sensitive and inhibitor-tolerant, working well with low template samples.

MtDNA analysis is of great value to forensic science because mtDNA is often still recoverable after nuclear DNA has degraded. While nuclear DNA is present in only two copies, there are hundreds of mtDNA copies per cell (Robin and Wong, 1988), making it more likely

that a profile can be obtained from low template samples. Multiple characteristics of mtDNA also protect it from degradation (Foran, 2006). It is possible that the circular nature of mtDNA prevents exonucleases from digesting it. Additionally, mtDNA is located in the mitochondria of the cell, rather than in the nucleus, and is protected by the mitochondria themselves. Due to these factors, mtDNA profiling has been highly successful when working with ancient and degraded samples (e.g., O'Rourke et al., 2000). There are, however, limitations to the use of mtDNA analysis. MtDNA it is maternally inherited, so it is not unique to an individual and therefore cannot be used for positive identification. This maternal inheritance can be useful, though, when a reference sample for an individual is not available but a sample can be obtained from a maternal relative. Regardless, mtDNA analysis has the potential to be more successful than nuclear DNA analysis when it comes to highly compromised DNA samples, such as would be expected from spent cartridge casings.

Pre-Processing for Fingerprints

von Wurmb et al. (2001) examined the effect of cyanoacrylate fuming on PCR efficiency. Blood was placed on glass slides in 5, 10, and 50 μ L aliquots, while saliva was placed in 2, 5, 10 and 50 μ L aliquots. All stains were allowed to dry overnight. Half of the slides for each body fluid were fumed with cyanoacrylate for 1 h, while the remaining were left untreated. Samples were divided into two groups and extracted using either the Chelex method (Walsh et al., 1991) or an Invisorb Forensic Kit. Pure cyanoacrylate was also extracted and added to known amounts of control DNA to determine if it had an inhibitory effect. Short tandem repeats (STRs) were amplified using an AmpF ℓ STR Profiler Plus kit. The results showed cyanoacrylate had a negative effect on PCR efficiency.

The effect of cyanoacrylate fuming on the recovery of touch DNA from pipe bombs was examined by Gicale (2011). Twenty-four volunteers each assembled two pipe bombs, one of which was fumed with cyanoacrylate for 15 min after deflagration. DNA was isolated using a double swab technique with the first swab was wetted with digestion buffer, followed by organic extraction, quantification using a Quantifiler Human DNA Quantification Kit, and amplification using MiniFiler. Slightly more DNA was recovered from fumed pipe bombs than from non-fumed bombs (averaging 29 and 19 pg, respectively), though the difference was not significant.

Project Design

The study described here had several facets, all of which, in the end, were designed to examine and improve DNA typing results from spent cartridge casings. A key research factor was that, even though the study was based on “touch DNA”, it is quite easy to generate large sample sizes, given that cartridges are readily available from commercial vendors and spent casings can be produced in very short periods of time. Owing to this, it was possible to examine different calibers of ammunition, DNA collection methods, type of DNA testing, etc., making for a very thorough and rigorous, and thus highly informative, body of research.

Based on published materials, research previously conducted in our laboratory, and personal communications with the Michigan State Police crime laboratories, who have participated in all of our previous studies on DNA from spent cartridge casings, the following questions were addressed:

- How does swabbing a casing compare to soaking it (Dieltjes et al. 2011), with regard to DNA yield and profiling success?

- How do swabbing strategies (swabbing casings individually versus swabbing multiple cartridges with a single swab) influence DNA yield and profiling success?
- How does an organic extraction compare to a silica based commercial kit (e.g., Qiagen) or a kit designed for DNA retrieval from fingerprints (FDF), with regard to DNA yield and profiling success?
- How do different STR kits (MiniFiler, Fusion) influence the success of DNA profiling from casings?
- How does the success and probative value of nuclear DNA testing of casings compare to that of mtDNA analysis, given the strengths and weaknesses of each?
- How does the caliber of the ammunition influence DNA analysis?
- And finally, how does processing a casing for fingerprints (cyanoacrylate fuming) compare to not processing it, with regard to DNA yield and profiling success?

The nature of touch samples is that different amounts of cells/DNA are deposited on a handled item, thus necessitating large sample sizes. In some studies this has been partially circumvented by depositing a surrogate for skin cells such as blood or cells from a cell line or buccal swab. However, these scenarios are so artificial that any results could easily misrepresent what happens in the ‘real world’, where touch cells certainly do not begin as a liquid suspension that is allowed to dry. Because of this, volunteers were asked to physically handle materials before testing was conducted, so that results much more closely mimic what crime laboratories encounter.

The overall strategy for testing was to have volunteers load firearm magazines with cartridges, and then provide a buccal swab. Swabs and cartridges were randomly assigned a letter

and number respectively, which were associated with one-another (blind to all investigators). In this way, the known (buccal swab) for each experiment was associated back to cartridge casings, but otherwise all samples were completely de-identified. This anonymous testing strategy had MSU IRB approval, and was conducted in conjunction with the Michigan State Police Forensic Science Division. Magazines were loaded and weapons fired by MSP personnel at their firing ranges. Casings were collected, placed in new paper bags, and assigned to the various experiments listed above (e.g., fumed on-site or returned to our laboratory).

Considerations Included in the Research

1. In some instances, researchers have been concerned about ‘shedder status’ of handlers in these types of studies. Realistically, the shedder status of an individual who has loaded a weapon will not be known, thus trying to account for it, or take advantage of it, is questionable. More importantly, in the studies undertaken, a given volunteer loaded multiple cartridges into a magazine of a gun and the spent casings from that volunteer were divided among the variables under consideration for that portion of the study (e.g., fumed or not fumed). In this way, good or bad shedders (if such a dichotomy actually exists) were controlled for.
2. It is possible that cartridges have background DNA on them when purchased. A subset of cartridges were swabbed and tested to determine if this was a potential problem. Some researchers have cleaned cartridges prior to handling (e.g., Horsman-Hall et al. 2009) however this creates an unrealistic scenario, therefore we did not clean cartridges prior to loading.

3. The order in which cartridges are loaded into or fired from a magazine has the potential to influence the number of cells deposited based on which cartridge was loaded first, the amount of force used, and the temperature inside the weapon. Because of this we purposefully assigned casings to a treatment on an alternating (round robin) basis, changing orders between volunteers.

DRAFT

MATERIALS AND METHODS

Materials

Ammunition utilized throughout this study included .40-caliber Remington, American Eagle Federal, Blazer Brass Federal, Winchester Full Metal Jacket, and TulAmmo MAXX Smith & Wesson brass cartridges, .45-caliber American Eagle Auto brass cartridges, and .22-caliber LR Federal Premium Champion Target rim fire brass cartridges. One to four cartridges from each box of ammunition were randomly selected, swabbed as described below, and DNA was extracted and quantified to determine if background DNA was present. The resulting DNA quantities were low or undetectable, so ammunition was not cleaned prior to handling.

Cotton swabs (860-PPC, Puritan Medical Products, Guilford, ME) and tubes were autoclaved at 135°C for 45 min, followed by a 1 h dry cycle. Solutions were filtered using a 0.22 µm Millex-GS syringe driven filter unit (Millipore Corporation, Billerica, MA). All supplies (tubes, racks, scissors, hemostats, cotton swabs, pipettes, tips, etc.) and appropriate reagents used in pre-amplification procedures were ultraviolet (UV) irradiated for at least 5 min (approximately 2.5 J/cm²), per side if applicable, in a Spectrolinker XL-1500 UV Crosslinker (Spectronics Corporation, Westbury, NY). A laboratory coat, face mask, sleeves, and two pairs of gloves were worn. Reagent blanks were created with each DNA extraction and they, along with positive and negative controls, were quantified with every rtPCR assay.

Optimizing Methods for Cell Recovery from Cartridge Casings

Spent .40-caliber Smith & Wesson brass cartridge casings were used in optimization experiments. Casings were cleaned with 1% Liquinox detergent (Alconox, White Plains, NY) and water, then decontaminated with ELIMINase (Decon Laboratories, King of Prussia, PA) as

per the manufacturer's instructions. Casings were rubbed with water twice, dried with a Kimwipe (Kimberly-Clark Corporation, Irving, TX), and exposed to UV light sitting upright (casing head closest to the bulbs) for a minimum of 5 min. Volunteers handled casings for 5 s in a random order.

Swabbing Cartridge Casings

A double swab technique (Sweet et al., 1997) was used in conjunction with organic or QIAamp DNA Investigator Kit (Qiagen, Hilden, Germany) extractions (detailed below). The first cotton swab was wetted with 150 μ L of digestion buffer (0.1% SDS, 20 mM Tris [pH 7.5], 50 mM EDTA) for organic extraction or 150 μ L of Buffer ATL (tissue lysis buffer) for QIAamp extraction. Casings, held using hemostats, were double-swabbed individually, and swab heads were clipped and added to 1.5 mL microcentrifuge tubes containing 400 μ L of digestion/tissue lysis buffer and either 5 μ L of proteinase K (20 mg/mL) for an organic extraction or 20 μ L of proteinase K (Qiagen). Tubes were vortexed for 10 s and incubated either for 1 h or overnight at 55°C. A Fingerprint DNA Finder Kit (FDF Kit; NEXTTEC Biotechnologie GmbH, Hilgertshausen, Germany) extraction was also tested, using a single swab (per the manufacturer), and the manufacturer's overall protocol was followed. Swabs were wetted with 30 μ L of Kit Lysis Buffer (Buffer FP and proteinase K) and used to swab a casing. The swab heads were clipped and added to spin baskets in 1.5 mL microcentrifuge tubes. Fifty additional microliters of Lysis Buffer were added to the swabs, tubes were vortexed for 10 s, and incubated for 30 min at 55°C.

In later experiments, casings were either individually double swabbed as above, or cumulatively swabbed by holding three casings in individual hemostats. The first wetted swab

was used to swab the outside surface of each of the three casings, followed by a dry swab. Both swab heads were placed in a single tube and processed as described.

Soaking Cartridge Casings

A modified version of the soaking method performed by Dieltjes et al. (2011) was used in combination with organic extraction or QIAamp extraction on spent cartridge casings. Ten milliliter beakers, 15 mL conical tubes, 15 mL culture test tubes, 5 mL stuffed pipette tips, and various sizes of the bulb portion of transfer pipettes were tested as possible vessels for soaking casings. Based on preliminary findings, the bulb portion of a Samco General-Purpose Transfer Pipette (Thermo Fisher Scientific, Waltham, MA) 13 mm in diameter (Figure 1) was selected for subsequent soakings.



Figure 1. Example of pipette bulb as the soaking vessel for a casing in 700uL of digestion/tissue lysis buffer.

Pre-digestion and Digestion Treatments Investigated Within the Soaking Procedure

Three variables within the soaking method were examined to either minimize DNA loss or maximize DNA recovery. 1) The inside surface of transfer pipette bulbs were pre-treated with 1 μ L of 10 μ g/ μ L yeast (*Saccharomyces cerevisiae*) RNA (Alfa Aesar, Ward Hill, MA) and 499 μ L of low TE (10 mM Tris [pH 7.5], 0.1 mM EDTA) prior to soaking handled casings. DNA

yields from pre-treated and non-pre-treated bulbs were compared. 2) Casings were shaken at 900 rpm on an Orbit P2 Digital Shaker (Labnet International, Edison, NJ) during the soaking period. DNA yields from shaken and non-shaken casings were compared. 3) Following the soaking period, tubes were incubated at 85°C for 10 min and vortexed every 3 min for 10 s. DNA yields from samples subjected to a 85°C incubation or not were compared.

The effect of shaking during digestion at 600 rpm (FDF) or 900 rpm (organic and QIAamp extractions) on an Orbit P2 Digital Shaker was examined, as was digestion time (1 h or overnight at 55°C) for organic and QIAamp extractions. Once all of these variables were examined, optimized procedures for cell recovery, detailed in the Results, were used for subsequent testing.

Optimizing Methods for DNA Extraction

Organic Extraction

Swab heads were transferred to spin baskets (Fitzco, Spring Park, MN) and centrifuged at 20,000 g for 4 min. Heads were discarded and flow-throughs were transferred to the original tubes. Equal volumes of phenol were added to the tubes, which were vortexed for 10 s and centrifuged at maximum speed for 5 min. Aqueous layers were transferred to new 1.5 mL microcentrifuge tubes containing equal volumes of chloroform. Tubes were vortexed for 10 s and centrifuged at maximum speed for 5 min. Amicon Ultra-0.5 mL, 30 kDa filtration columns (Millipore Corporation) were pre-treated with 1 µL of 10 µg/µL yeast RNA and 499 µL of low TE (Doran and Foran, 2014), centrifuged at 14,000 g for 10 min, and flow-throughs were discarded. Aqueous layers were transferred to the pre-treated spin columns, centrifuged at 14,000 g for 10 min, and flow-throughs discarded. DNAs were washed with 300 µL of TE (10 mM Tris

[pH 7.5], 1 mM EDTA), centrifuged at 14,000 g for 10 min, and flow-throughs discarded. Two additional washes were performed with 300 µL of low TE. Filtration columns were inverted into new Amicon collection tubes and centrifuged at 1,000 g for 3 min to collect retentates. Organic extractions were performed on DNAs from buccal swabs in the same manner, except two washes with TE and one with low TE were performed. DNAs were stored at -20°C.

QIAamp DNA Investigator Extraction

Swab heads were transferred to spin baskets and centrifuged at 20,000 g for 4 min. Heads were discarded and flow-throughs were collected in the original tubes. DNA isolations and purifications were performed per the manufacturer's protocol for surface and buccal swabs, including the addition of carrier RNA to Buffer AL (per the manufacturer), with the following modification: three elutions were collected for each DNA extraction by adding 20 µL of Buffer ATE to column membranes, incubating at room temperature for 5 min, and centrifuging at maximum speed for 3 min (Hebda et al., 2014).

Fingerprint DNA Finder Extraction

Prior to performing FDF extractions on DNA recovered from spent casings, known male DNA (Promega, Madison, WI) was extracted with solutions from an FDF Kit (Buffer FP and Prep Solution) that were either UV irradiated for 10 min or not treated. Based on lower DNA yields, none of the reagents in the FDF extractions were UV irradiated for subsequent experiments. DNAs were extracted and purified according to the manufacturer's protocol for isolation of genomic DNA from fingerprints and low template DNA samples.

DNA Quantification via Real-Time PCR Analysis

Volumes of the DNA extracts were measured prior to DNA quantification. PCR amplification was performed on an iCycler Thermal Cycler (Bio-Rad Laboratories, Hercules, CA) and fluorescence was detected using an iQ5 Multicolor Real-Time PCR Detection System (Bio-Rad Laboratories). DNAs yields were determined using either a Quantifiler Human DNA Quantification Kit (Life Technologies, Carlsbad, CA) according to the manufacturer's instructions, with volumes reduced to 15 μ L, or an Alu assay (Nicklas and Buel, 2005). Table 1 contains the sequences of Alu primers, probes, and internal positive control (IPC) template DNA (Lindquist et al., 2011) used for quantification. Primers, probes, and IPC template were produced by Sigma-Aldrich (St. Louis, MO) or Integrated DNA Technologies (Coralville, IA). Alu primers were filtered through Microcon YM-100 membranes (Millipore Corporation) before use. Alu standards were created via serial dilutions of Standard Reference Material 2372 Human DNA Quantitation Standard Component A (genomic DNA from a single male donor; 57 ng/ μ L; National Institute of Standards and Technology, Gaithersburg, MD) in low TE containing 20 μ g/mL glycogen, yielding six DNA standards at concentrations of 2000, 200, 20, 2, 0.2, and 0.02 pg/ μ L.

Real-time PCR reactions were set up in 0.2 mL optically clear flat-capped PCR strips (USA Scientific, Ocala, FL) with final volumes of 15 μ L. Alu rtPCR reactions consisted of 7.5 μ L of iQ Supermix (Bio-Rad Laboratories), 500 nM Alu forward primer, 900 nM Alu reverse primer, 250 nM Alu probe, 1 μ M IPC forward and reverse primer, 250 nM IPC probe, 1 μ L of the working concentration of IPC template DNA (1:1 billion dilution of 100 μ M stock), 0.625 units of Taq DNA polymerase (5 U/ μ L; Empirical Bioscience, Grand Rapids, MI), 0.625 μ L of

water, and 1 μ L of DNA. DNA standards were run in duplicate. rtPCR cycling parameters included: 3 min at 95°C, followed by 50 cycles of 15 s at 95°C and 1 min at 60°C.

Table 1. Primer, probe, and IPC template sequences for real-time PCR. HEX and 6FAM are fluorescent dyes attached to the 5' end of the probes. BHQ1 and IABkFQ are black hole quenchers attached to the 3' end of the probes. ZEN is an internal quencher. The Alu primers and probe were designed by Nicklas and Buel (2005). The IPC primers, probe, and template were designed by Lindquist et al. (2011).

Primer Name	Sequence	Amplicon Length
F Alu	5'-GAG ATC GAG ACC ATC CCG GCT AAA-3'	113 bp
R Alu	5'-CTC AGC CTC CCA AGT AGC TG-3'	
Alu probe	5'-HEX-GGG CGT AGT GGC GGG-BHQ1-3'	
F IPC	5'-AAG CGT GAT ATT GCT CTT TCG TAT AG-3'	77 bp
R IPC	5'-ACA TAG CGA CAG ATT ACA ACA TTA GTA TTG-3'	
IPC probe	5'-6FAM-TAC CAT GGC-ZEN-AAT GCT-IABkFQ-3'	
IPC template	5'-AAG CGT GAT ATT GCT CTT TCG TAT AGT TAC CAT GGC AAT GCT TAG AAC AAT ACT AAT GTT GTA ATC TGT CGC TAT GT-3'	

Data were analyzed with iQ5 Optical System Software. A standard curve was generated based on the C_t values of the DNA standards, and DNA concentrations of the samples were extrapolated. DNA yields (pg) were calculated by multiplying rtPCR concentrations (pg/ μ L) by DNA extract volumes (μ L).

STR Analysis of DNA from Spent Cartridge Casings

Loading and Firing Cartridges

Forty caliber cartridges were loaded into the magazine of the appropriate caliber weapon by volunteers¹ in sets of nine or twelve, and magazines were placed into the firearm. Cartridges were fired in sets of three by glove-wearing Michigan State Police Forensic Science Division firearm examiners through a pop-up mesh laundry hamper. Casings were transferred from the hamper to paper bags using hemostats (wiped with 10% bleach in between volunteer handlers), and were assigned to the different procedures and experiments in a round robin manner so as to take into account loading/firing order. DNAs were isolated from the spent casings using the optimized protocols, and quantified.

STR Amplification using PowerPlex Fusion

STRs were amplified² using a PowerPlex Fusion System (Promega) and an Applied Biosystems 2720 Thermal Cycler (Life Technologies). Six microliters of DNA extract from each casing (or 1 ng if available) was added to 2 μ L 5X Master Mix and 2 μ L 5X Primer Pair Mix in a 0.2 mL PCR tube. DNA extracts from buccal swabs were diluted 1:300 with water, and 1 μ L was added to 5 μ L water, 2 μ L 5X Master Mix, and 2 μ L 5X Primer Pair Mix. Amplification was conducted using an initial denaturation step of 96°C for 1 min, 30 cycles of 94°C for 10 s, 59°C for 1 min, and 72°C for 30s, and a final 10 min 60°C extension.

Amplified DNA was denatured at 95°C for 3 min and placed on ice for 3 min. One microliter was added to 10 μ L Hi-Di Formamide (Life Technologies) and 1 μ L CC5 Internal

¹ Volunteers also provided a buccal swab, the DNA profile from which could be compared to those derived from experimental procedures. All samples were completely deidentified, and all procedures were approved by the Michigan State University Institutional Review Board (IRB number 12-770).

² Samples were tested from highest DNA yields to lowest until 0 handler alleles were recovered from multiple samples, after which STR testing was terminated.

Lane Standard 500 (Promega). DNA was electrophoresed on an AB3500 Genetic Analyzer (Life Technologies). Capillary electrophoresis was performed using the parameters: oven temperature 60°C; pre-run voltage 15 kV; pre-run time 180 s; injection voltage 1.2 kV; injection time 24 s; run voltage 15 kV; run time 1500 s; capillary length 50 cm.

Allele calls were made using GeneMapper v4.1 software (Life Technologies) at a threshold value of 100 relative fluorescence units (RFUs) and were verified using OSIRIS v2.2 (Goor et al., 2011). Alleles were compared to reference profiles and were classified as consistent or not consistent with the handler. Percent profiles were calculated by dividing the number of consistent alleles by the total number of possible alleles for that individual.

STR Amplification using MiniFiler

MiniSTRs from approximately 15 samples with the highest DNA concentrations for each of the five methods³ were amplified using MiniFiler (Life Technologies) and an Applied Biosystems 2720 Thermal Cycler. PCR reactions were prepared in a final volume of 10 µL, consisting of 4 µL MiniFiler Master Mix, 1 µL MiniFiler Primer Set, and 5 µL DNA (or 1 ng if available). PCR cycling conditions were 11 min at 95°C followed by 30 cycles of 20 s at 94°C, 2 min at 59°C, and 1 min at 72°C, and a final extension step of 45 min at 60°C.

One microliter of amplified DNA was added to 9 µL Hi-Di Formamide and 0.3 µL GeneScan 500 LIZ Size Standard (Life Technologies). Capillary electrophoresis was performed using the parameters: oven temperature 60°C; pre-run voltage 15 kV; pre-run time 180 s; injection voltage 1.6 kV; injection time 8 s; run voltage 19.5 kV; run time 1330 s; capillary length 50 cm. Allele calls were made as above.

³ If all DNA from a sample had previously been utilized, it was replaced with a sample that still had DNA.

MtDNA Sequencing of DNA from Spent Cartridge Casings

Mitochondrial DNA was analyzed from DNA extracts of different swabbing strategies and cartridge calibers. Samples were divided into three groups based on DNA quantitation (high, medium, and low). DNAs from eight individually swabbed 0.45 caliber casings, cumulatively swabbed 0.45 caliber casings, individually swabbed 0.22 caliber casings, and cumulatively swabbed 0.22 caliber casings were amplified from each group, and sequenced through HV1 and HV2 using the primers in Table 2.

PCR for mtDNA amplification was conducted in 30 μ L volumes, consisting of 3 μ L GeneAmp 10X PCR Buffer II (Life Technologies), 3 μ L 25 mM $MgCl_2$ (Life Technologies), 3 μ L of 2 mM deoxynucleoside 5'-triphosphates, 3 μ L 4 mg/mL bovine serum albumin (BSA; Thermo Fisher Scientific), 3 μ L of 20 μ M forward primer and reverse primer, 11 μ L water, 1 unit AmpliTaq Gold polymerase (Life Technologies), and 1 μ L template DNA. Cycling parameters were 10 min at 94°C, 38 cycles of 30 s at 94°C, 30 s at 60°C, and 30 s at 72°C, and a final extension of 5 min at 72°C.

Table 2. Primers used to amplify and sequence mtDNA from casings and reference samples. All samples were amplified with F15989, R16410, F15, and R499. F16190 and R285 replaced F15989 and R499 respectively if amplification or sequencing failed.

Primer Name	Region	Sequence
F15989	HV1	5'-CCC AAA GCT AAG ATT CTA AT-3'
R16410	HV1	5'-GAG GAT GGT GGT CAA GGG AC-3'
F16190	HV1	5'-CCC CAT GCT TAC AAG CAA GT-3'
F15	HV2	5'-CAC CCT ATT AAC CAC TCA CG-3'
R499	HV2	5'-CGG GGG TTG TAT TGA TGA GAT T-3'
R285	HV2	5'-GTT ATG ATG TCT GTG TGG AA-3'

Five microliters of PCR product was electrophoresed on a 1% agarose gel. Post PCR clean-up was performed using Diffinity RapidTips (Diffinity Genomics, Inc., West Henrietta, NY). PCR products were aspirated through a RapidTip approximately 15 times, and were transferred to a new tube.

Sequencing reactions included 2.5 μ L BigDye Terminator v3.1 Cycle Sequencing master mix, consisting of 1.82 μ L of BDX64 BigDye enhancing buffer (MCLAB, San Francisco, CA), 0.68 μ L of BigDye Terminator v3.1 Ready Reaction Mix (Life Technologies), 1 μ L 20 μ M forward or reverse primer, 1 – 3 μ L amplified DNA (depending on agarose gel band intensity), and water to a final volume of 10 μ L. Cycling parameters were 3 min at 96°C followed by 30 cycles of 10 s at 96°C, 5 s at 50°C, and 2 min at 60°C.

Sequencing reactions were combined with 2.5 μ L stop solution (1 μ L of 3 M sodium acetate, 1 μ L of 100 mM EDTA, and 0.5 μ L of 20 mg/mL glycogen) in a 1.5 mL tube. Thirty-five microliters cold 95% ethanol was added to each sequencing reaction, which was vortexed for 10 s and centrifuged at maximum speed for 10 min. The supernatant was removed, and the pellet washed with 180 μ L cold 70% ethanol. The samples were centrifuged at maximum speed for 5 min, and the supernatant removed. The 70% wash step was repeated two more times, and DNAs were vacuum dried for 10 min. Ten microliters of Hi-Di Formamide was added and was vortexed for 10 s.

DNAs were electrophoresed on an AB3500 Genetic Analyzer using the parameters: oven temperature 60°C; injection time 8 s; injection voltage 1.6 kV; run time 1400 s; run voltage 19.5 kV; capillary length 50 cm. Sequences were aligned and analyzed using BioEdit v7.2 software (Hall, 1999), and compared to the Cambridge Reference Sequence (Anderson et al., 1981). Polymorphisms were identified and compared to volunteer reference sequences, and profiles

were classified as described below. Mixtures were called when two peaks were detected at the same position in both the forward and reverse sequences.

Cyanoacrylate Fuming of Casings

Sets of nine .40-caliber cartridges were loaded into a magazine by volunteers, which were fired and collected as above. Three casings from each volunteer were taken to the MSP fingerprint unit (on site) and fumed using the MSP's standard protocol. This consisted of raising the humidity inside the chamber, followed by a fuming step and a ventilation step, taking 1 – 1.5 h. Another three casings from each volunteer were returned to the MSU Forensic Biology Laboratory to be fumed. The MSU fuming chamber consisted of an electric candle warmer (Rimports USA LLC, Provo, UT) in the center of a 24 x 16 x 13 in, 15 gallon plastic storage container (Incredible Plastics, Warren, Ohio). A beaker containing 200 mL of water was placed on the candle warmer. Casings were positioned in the chamber on weigh paper surrounding the candle warmer and the container was closed. After 15 min, a tea-light foil container holding approximately 4 mL of cyanoacrylate was added to the candle warmer, and the casings were fumed for 20 min. The cyanoacrylate was removed from the container, which was left slightly open to ventilate for 10 min before the casings were removed and placed back in their corresponding paper bags. Sets of 15 – 18 casings were placed in the fuming chamber at a time, and this process was repeated three times. The casings were stored at -20°C.

The remaining three casings from each volunteer were not fumed. Sets of three fired casing were collected and subjected to the fuming/non-fuming treatments in a round robin fashion.

Data Analysis

Comparison of DNA Yields

Statistical tests were performed using XLSTAT 2014.2.01, with a significance level of 0.05. A Shapiro-Wilk test was conducted to determine normality for nuclear DNA quantification data; if $p < 0.05$ existed for any of the cell recovery and DNA extraction methods then non-parametric analyses were performed. A Kruskal-Wallis test was used to make multiple comparisons, and pairwise comparisons were made using Mann-Whitney.

Comparison of DNA Profiles

Casing STR profiles were compared to volunteers' reference profiles, and alleles were designated as handler or non-handler. Descriptive statistics (average # handler alleles, # possible handler alleles, % handler profile, and # non-handler alleles) were calculated for each optimized method. As described above, the percentage of a cartridge handler's profile was determined based on the number of alleles consistent with the handler divided by the number of possible alleles from each volunteer. Homozygous alleles in the reference profiles were counted as one possible allele.

The percentages of handlers' profiles present in MiniFiler and Fusion profiles were tested for normality using a Shapiro-Wilk test; if $p < 0.05$ existed for any of the cell recovery and DNA extraction methods then non-parametric analyses were performed. A Kruskal-Wallis test was performed on the non-parametric data to determine if a significant difference existed among the optimized methods. Pairwise comparisons were performed using the Mann-Whitney test to determine if certain cell recovery and DNA extraction methods generated significantly greater percentages of handlers' profiles, as well as if the number of handler and non-handler alleles

differed using MiniFiler and Fusion. In some instances box plots were constructed to illustrate the distribution of the data.

MtDNA profiles were classified as consistent with a handler, not consistent with a handler, mixture containing the handler's haplotype, or mixture not containing the handler's haplotype. Fisher's exact test was conducted to determine whether quantitation level, as well as swabbing strategy and cartridge caliber, had a statistically significant effect on mtDNA profile classification.

DNA quantities recovered with each optimized method were linearly correlated to the number of handler alleles amplified in Fusion profiles. Fusion profiles were also evaluated for the frequency of handler alleles at each locus to assess if the DNA recovered from spent casings was degraded.

RESULTS

Optimized Methods for Soaking Cartridge Casings

A variety of factors were tested during optimization of the soaking procedure, including: pre-treatment of the bulbs, shaking during the soaking phase, incubation at 85°C prior to the digestion phase, shaking during the digestion phase, and varying digestion times. Complete data of all factors tested, including non-optimal factors not presented here, can be found in Mottar (2014). The optimized protocol was as follows: Samco General-Purpose Transfer Pipettes were UV irradiated for 10 min, bulbs were cut off, set upright in a rack, and irradiated for an additional 10 min. Casings were placed in bulbs containing 700 µL of digestion buffer (organic extraction) or Buffer ATL (QIAamp extraction) and soaked for 30 min. Casings were removed and buffer solutions were transferred to 1.5 mL microcentrifuge tubes. Bulbs and the outside surface of casings were swabbed with a dry swab. Swab heads were clipped and added to soaking solutions. Tubes were incubated at 85°C for 10 min, vortexing every 3 min for 10 s. Either 5 µL of proteinase K (20 mg/mL) or 20 µL of proteinase K (Qiagen) were added to tubes, which were vortexed for 10 s and incubated with shaking at 900 rpm for 1 h at 55°C. Based on minimal DNA loss and lower DNA yields, bulbs were not pre-treated and casings were not shaken during the soak period, respectively. This protocol was used to compare cartridge casings soaking and swabbing procedures.

The Influence of Cell Recovery and DNA Extraction Methods on DNA Yields and Profiling

Comparisons of DNA Yields

Volunteers loaded a total of 420 casings that were assayed using the five cell recovery and DNA extraction methods: 90 casings each for swabbing or soaking with either organic or

Qiagen extraction, and 60 casings for FDF extraction. None of the DNA extracts contained detectable PCR inhibition. Median DNA yield results are displayed in Figure 2. Specific DNA concentrations, extract volumes, and yields from each casing can be found in Appendix A and in Mottar (2014) (organized according to the cell recovery and DNA extraction method). DNA yields among all five methods were not normally distributed (Shapiro Wilk, $p < 0.0001$) and there was a significant difference in DNA yields among methods (Kruskal-Wallis, $p < 0.0001$). Further, DNA yields differed significantly when pairwise relationships were analyzed between methods (Table 3). Double swabbing recovered a significantly greater amount of DNA than soaking (Mann-Whitney; organic extractions, $p = 0.0180$; QIAamp extractions, $p < 0.0001$). Additionally, organic extraction recovered significantly more DNA than did QIAamp and FDF extractions (Table 3).

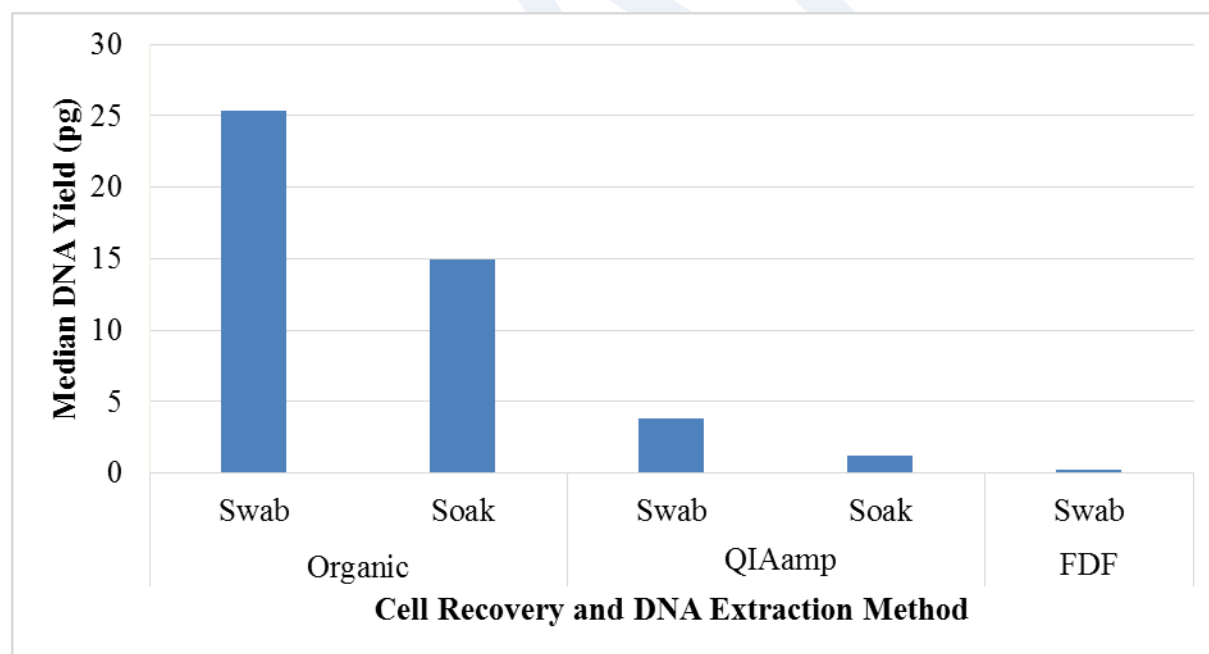


Figure 2. Median DNA quantities recovered using optimized cell recovery and DNA extraction methods. Median DNA yields from organic extractions (double swab = 25.32 pg and soak = 14.95 pg) were significantly higher than the median DNA yields from QIAamp extractions (double swab = 3.81 pg and soak = 1.18 pg) and the median DNA yield from FDF extractions (0.20 pg).

Table 3. Mann-Whitney pairwise comparisons of DNA quantities retrieved with the optimized cell recovery and DNA extraction methods (bold = significantly greater DNA yields).

Pair		P-Value
Double Swab + Organic	Soak + Organic	0.018
Double Swab + Organic	Double Swab + QIAamp	< 0.0001
Double Swab + Organic	Soak + QIAamp	< 0.0001
Double Swab + Organic	FDF	< 0.0001
Soak + Organic	Double Swab + QIAamp	< 0.0001
Soak + Organic	Soak + QIAamp	< 0.0001
Soak + Organic	FDF	< 0.0001
Double Swab + QIAamp	Soak + QIAamp	< 0.0001
Double Swab + QIAamp	FDF	< 0.0001
Soak + QIAamp	FDF	< 0.0001

Comparison of MiniFiler and Fusion STR Profiles

Descriptive statistics for the STR profiles from DNAs amplified with MiniFiler and Fusion using the five techniques are displayed in Table 4. The details of each profile, including the number of consistent handler alleles, the number of possible handler alleles, the percentages of handlers' profile, and the number of non-handler alleles present in each profile can be found in Appendix B and C, and in Mottar (2014). The highest average number of alleles consistent with the handler was 10.8 (MiniFiler) and 27.33 (Fusion) with double swabbing and organic extractions. Average number of alleles for the other combinations were: 10.31 (MiniFiler) and 22.37 (Fusion) with soaking and organic extractions, 1.57 (MiniFiler) and 5.71 (Fusion) with double swabbing and QIAamp extractions, 2.57 (MiniFiler) and 6.57 (Fusion) with soaking and QIAamp extractions, and 0.57 (MiniFiler) and 1.57 (Fusion) with FDF extractions. Overall, double swabbing with organic extraction generated the highest average percentage of handlers' profiles and number of non-handler alleles with both amplification kits.

Table 4. Descriptive statistics of profiles amplified with MiniFiler and Fusion (bold). The cell recovery and DNA extraction method utilized is denoted by A = double swab + organic extraction; B = soak + organic extraction; C = double swab + QIAamp extraction; D = soak + QIAamp extraction; E = FDF extraction

Method	A	A	B	B	C	C	D	D	E	E
Avg. # Handler Alleles	10.80	27.33	10.31	22.37	1.57	5.71	2.57	6.57	0.57	1.57
Avg. # Possible Handler Alleles	16.33	41.67	15.75	41.12	15.57	40.36	15.71	40.57	15.71	41.14
Avg. % Handler Profile	67.0	66.2	65.8	54.9	9.7	14.1	15.9	16.0	3.5	3.8
Median % Handler Profile	75.0	69.8	67.8	41.6	5.9	5.3	9.4	13.1	0.0	0.0
Avg. # Non-handler Alleles	2.47	3.47	1.94	2.94	1.29	1.36	2.07	2.93	1.43	0.71

Table 5 presents Mann-Whitney pairwise comparisons of the number of handler and non-handler alleles present in MiniFiler and Fusion profiles. A significantly greater number of handler alleles was amplified from a DNA extract with Fusion than with MiniFiler, except for those isolated with FDF. The number of non-handler alleles present in the profiles that were generated using the five optimized methods did not differ significantly between MiniFiler and Fusion.

Table 5. Mann-Whitney pairwise comparisons examining the number of handler and non-handler alleles present in MiniFiler and Fusion profiles generated with the five methods: A = double swab + organic extraction; B = soak + organic extraction; C = double swab + QIAamp extraction; D = soak + QIAamp extraction; E = FDF extraction
(Bold = significantly greater number of handler alleles)

Pair		# Handler Alleles P-Value	# Non-handler Alleles P-Value
MiniFiler A	Fusion A	< 0.0001	0.4490
MiniFiler B	Fusion B	0.0004	0.3460
MiniFiler C	Fusion C	0.0120	0.9620
MiniFiler D	Fusion D	0.0110	0.6510
MiniFiler E	Fusion E	0.8100	0.3560

Analysis of Fusion STR Profiles

To increase sample size and statistical power, a new set of cartridge firings was undertaken. Because the Fusion STR kit gave superior results to MiniFiler, the former was used to compare cell recovery and DNA extraction methods (Figure 3). All Fusion profiles can be found in Appendix D and in Mottar (2014). The same trends were seen as in earlier experiments, with swabbing and organic extraction resulting in the highest percent recovery of handler alleles. The percentages of handlers' profiles from all methods, except organic extractions, were not normally distributed (Shapiro Wilk, $p < 0.0001$) (Table 6). Further, there was a significant difference in the percentages of handlers' profiles among methods (Kruskal-Wallis, $p < 0.0001$).

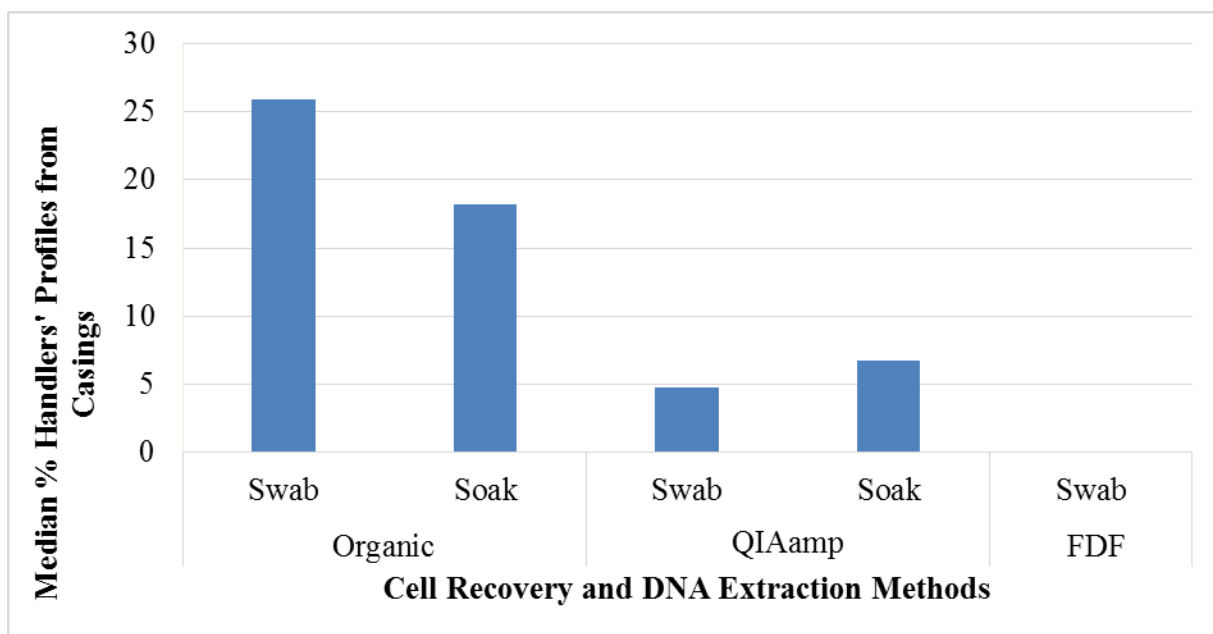


Figure 3. Median percentages of handlers' profiles recovered using optimized cell recovery and DNA extraction methods followed by amplification with Fusion. Median percentages of handlers' profiles from organic extractions (double swab = 25.8% [n = 90] and soak = 18.2% [n = 89]) were higher than handlers' profiles from QIAamp extractions (double swab = 4.8% [n = 56] and soak = 6.7% [n = 36]). The median percentage of handlers' profiles from FDF extractions was 0.0% (n = 14).

Table 6. Shapiro Wilk test for normality on the percentages of handlers' profiles processed with the optimized cell recovery and DNA extraction methods and amplified using Fusion.

Cell Recovery and DNA Extraction Method	P-Value
Double Swab + Organic	0.677
Soak + Organic	0.071
Double Swab + QIAamp	0.012
Soak + QIAamp	0.002
FDF	< 0.0001

Cell recovery and DNA extraction methods differed significantly in all but one pairwise comparison (double swabbing vs. soaking with QIAamp extractions) when the percentages of handlers' profiles were analyzed (Table 7). In general, DNA concentrations of approximately 0.05 pg/μL or higher (~0.3 pg of input DNA) produced some allelic data (see Appendix C and Mottar, 2014).

Table 7. Mann-Whitney pairwise comparisons of the percentages of handlers' profiles processed with the optimized cell recovery and DNA extraction methods and amplified using Fusion (bold = significantly greater percentages of handlers' profiles).

Pair		P-Value
Double Swab + Organic	Soak + Organic	0.0400
Double Swab + Organic	Double Swab + QIAamp	< 0.0001
Double Swab + Organic	Soak + QIAamp	< 0.0001
Double Swab + Organic	FDF	< 0.0001
Soak + Organic	Double Swab + QIAamp	< 0.0001
Soak + Organic	Soak + QIAamp	< 0.0001
Soak + Organic	FDF	< 0.0001
Double Swab + QIAamp	Soak + QIAamp	0.3230
Double Swab + QIAamp	FDF	0.0130
Soak + QIAamp	FDF	0.0040

Table 8 shows descriptive statistics of the individual profiles of DNAs amplified with Fusion. Full datasets can be found Appendix D and in Mottar 2014. The average number of alleles consistent with the handler was 12.4 with double swabbing and organic extractions, 9.7 with soaking and organic extractions, 3.0 with double swabbing and QIAamp extractions, 3.6 with soaking and QIAamp extractions, and 1.1 with FDF extractions. The average number of non-handler alleles was highest in samples that were double swabbed and organically extracted (4.71 alleles).

Table 8. Descriptive statistics of individual profiles of DNAs amplified with Fusion. The cell recovery and DNA extraction method utilized is denoted by A = double swab + organic extraction; B = soak + organic extraction; C = double swab + QIAamp extraction; D = soak + QIAamp extraction; E = FDF extraction. Samples were tested from highest concentration to lowest until 0 handler alleles were recovered from multiple samples, after which STR testing was terminated. Includes data from Table 4.

PowerPlex Fusion					
Cell Recovery and DNA Extraction Method	A	B	C	D	E
Sample Size	90	89	56	36	14

Avg. # Handler Alleles	12.43	9.69	3.05	3.64	1.07
Avg. # Possible Handler Alleles	41.76	41.75	41.59	42.11	41.36
Avg. % Handler Profile	30.0	23.3	7.4	8.7	2.7
Avg. # Non-handler Alleles	4.71	2.79	0.95	2.00	0.71

Table 9 shows the linear correlations between DNA yields from casings using the five methods and the number of handler alleles amplified with Fusion. There was a positive linear correlation between DNA yields and the handler alleles amplified for each method, which demonstrated more handler alleles were amplified as the amount of DNA input increased. The correlation coefficient (r) values ranged from 0.64 to 0.94.

Table 9. The degree of linear correlation between the DNA yields and the amount of handler alleles amplified in Fusion profiles. The cell recovery and DNA extraction method utilized is denoted by A = double swab + organic extraction; B = soak + organic extraction; C = double swab + QIAamp extraction; D = soak + QIAamp extraction; E = FDF extraction.

Cell Recovery and DNA Extraction Method	A	B	C	D	E
Sample Size	90	89	56	36	14
Avg. DNA Yield (pg)	12.50	11.50	1.26	3.29	0.19
Avg. # Handler Alleles	12.43	9.69	3.05	3.64	1.07
r	0.70	0.64	0.87	0.94	0.71

Once an optimal method for DNA recovery and STR analysis from spent cartridge casings was established, a number of other factors were examined, including cartridge caliber, swabbing strategy (individually swabbing casings versus cumulatively swabbing multiple casings with a single pair of swabs), loading/firing order of the cartridges, and cyanoacrylate fuming of casings. The first two of these were investigated together, wherein volunteers loaded 0.22 caliber cartridges into a magazine first, then 0.45 caliber cartridges into a second magazine, or vice versa. Both DNA yields and STR profiles were considered.

The Influence of Swabbing Strategy and Cartridge Caliber

Comparison of DNA Yields Based on Swabbing Strategy and Cartridge Caliber

Figure 4 displays median DNA yields based on swabbing strategy and cartridge caliber, while the distribution of the data is shown in Figure 5. More DNA was recovered from 0.45 caliber casings than from 0.22 caliber casings, and cumulative swabbing resulted in higher yields than individual swabbing. Cumulatively swabbed 0.45 casings resulted in the largest median DNA yield (46.41 pg), followed by individually swabbed 0.45 casings (18.13 pg), cumulatively swabbed 0.22 casings (17.40 pg), and individually swabbed 0.22 casings (13.31 pg). The DNA concentration of approximately 37% of individually swabbed 0.22, 15% of individually swabbed 0.45, 13% of cumulatively swabbed 0.22, and 2% of cumulatively swabbed 0.45 caliber casings fell at or below the lowest quantitation standard. Pairwise comparisons are shown in Table 10. All differences were significant with the exception of individually swabbed 0.45 and cumulatively swabbed 0.22 casings. Detailed quantitation results for each casing can be found in Appendix E and in Ray (2015).

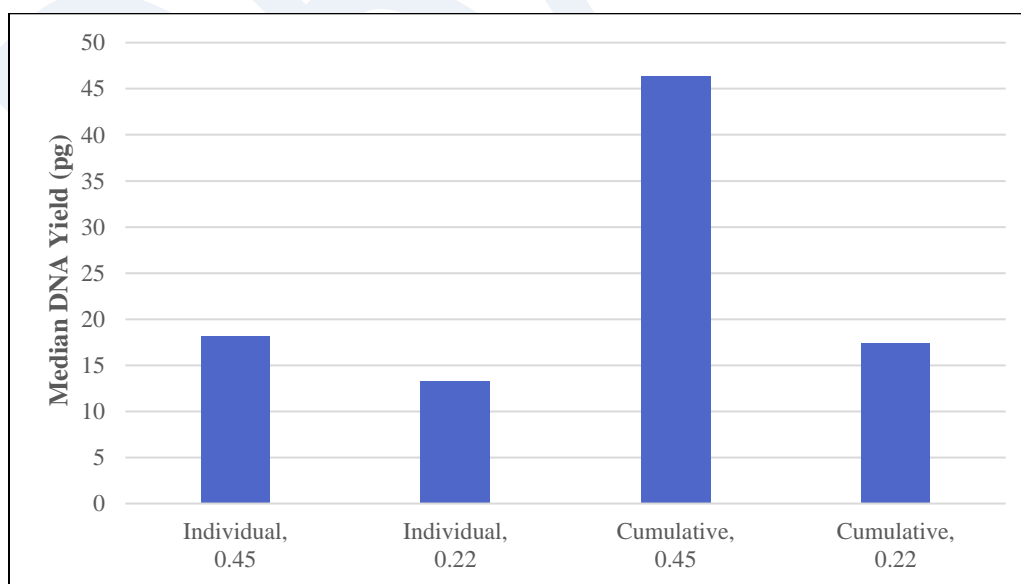


Figure 4. Median DNA yield (pg) based on swabbing strategy and cartridge caliber. Individual/cumulative refers to the swabbing strategy and 0.45/0.22 refers to the caliber.

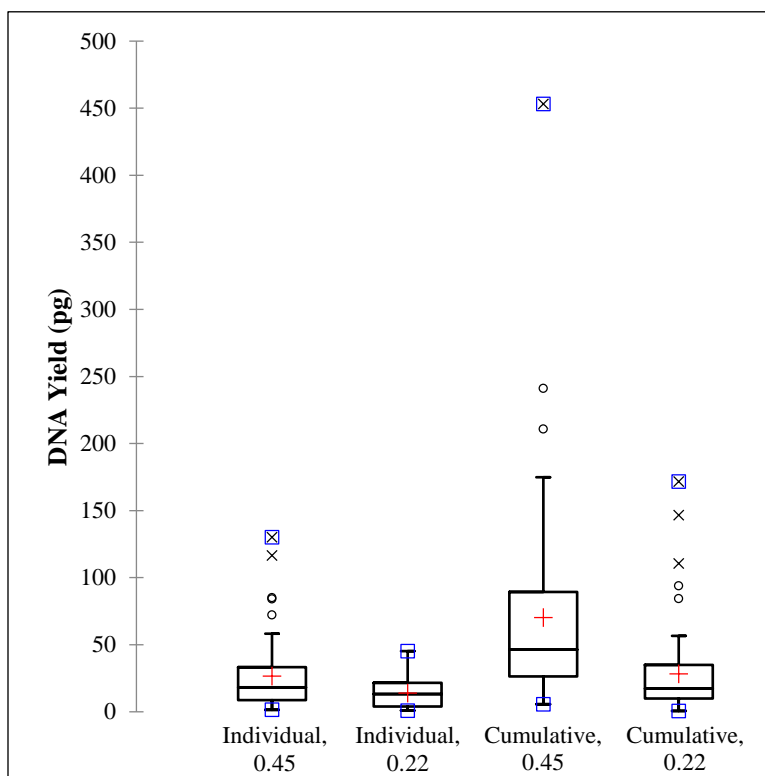


Figure 5. Box plots displaying the distribution of the DNA yield (pg) based on swabbing strategy and cartridge caliber. The box encompasses the interquartile range (the distance between the lower and upper quartiles), with the line through the box symbolizing the median. The mean is represented by a red +, extreme outliers are represented by x, mild outliers are represented by °, and maximum/minimum values are represented by blue squares. The whiskers represent the maximum/minimum values that are not outliers. Individual/cumulative refers to the swabbing strategy and 0.45/0.22 refers to the caliber.

Table 10. Mann-Whitney pairwise comparisons for DNA yield (pg). Individual/cumulative refers to the swabbing strategy, and 0.45/0.22 refers to the caliber.

Pair		P-Value
Individual, 0.45	Individual, 0.22	0.0023
Individual, 0.45	Cumulative, 0.45	< 0.0001
Individual, 0.45	Cumulative, 0.22	0.9728
Individual, 0.22	Cumulative, 0.22	0.0039
Individual, 0.22	Cumulative, 0.45	< 0.0001
Cumulative, 0.45	Cumulative, 0.22	< 0.0001

Influence of Handling Order of 0.45 or 0.22 Caliber Cartridges on DNA Yields from Spent Casings

The median DNA yields from casings handled first or second are compared in Figure 6. More DNA was recovered from the 0.22 caliber casings (both individually and cumulatively swabbed) when they were handled first than when they were handled second. Similarly, greater amounts of DNA were recovered from cumulatively swabbed 0.45 casings when they were handled first than when they were handled second. In contrast, more DNA was recovered from the individually swabbed 0.45 casings that were handled second rather than first. However, the only significant difference in DNA yields based on handling order was in the cumulatively swabbed 0.22 casings (Table 11), indicating handling order did not play a substantial role in DNA yields.

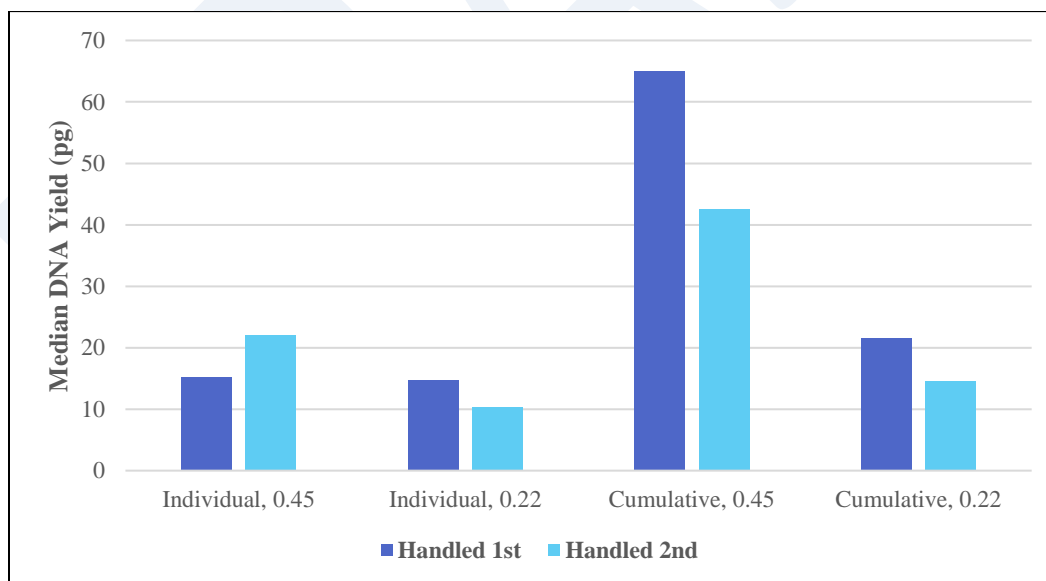


Figure 6. Median DNA yields (pg) of 0.45/0.22 caliber casings based on swabbing strategy. Individual/cumulative refers to the swabbing strategy.

Table 11. Mann-Whitney pairwise comparisons between the DNA yields (pg) from casings handled first and second based on swabbing strategy and cartridge caliber. Individual/cumulative refers to the swabbing strategy, and 0.45/0.22 refers to the caliber.

	P-Value
Individual, 0.45	0.947
Individual, 0.22	0.462
Cumulative, 0.45	0.109
Cumulative, 0.22	0.006

Comparison of Fusion STR Profiles Based on Cartridge Caliber and Swabbing Strategy

The median number of handler and non-handler alleles based on swabbing strategy and cartridge caliber are displayed in Figure 7. The cumulatively swabbed 0.45 casings resulted in the largest median number of handler alleles (17.5), followed by cumulatively swabbed 0.22 casings (8.5), individually swabbed 0.45 casings (6.0), and individually swabbed 0.22 casings (4.0). The distribution of the handler alleles is shown in Figure 8. Pairwise comparisons are shown in Table 12.

The median number of non-handler alleles was 4.5 for cumulatively swabbed 0.45 caliber casings, 2.5 for individually swabbed 0.45 caliber casings, 2.0 for cumulatively swabbed 0.22 caliber casings, and 1.0 for individually swabbed 0.22 caliber casings. Table 12 shows the pairwise comparisons for caliber size and swabbing strategy. The distribution of the non-handler alleles is shown in Figure 9. All STR data can be found in Appendix F and in Ray (2015).

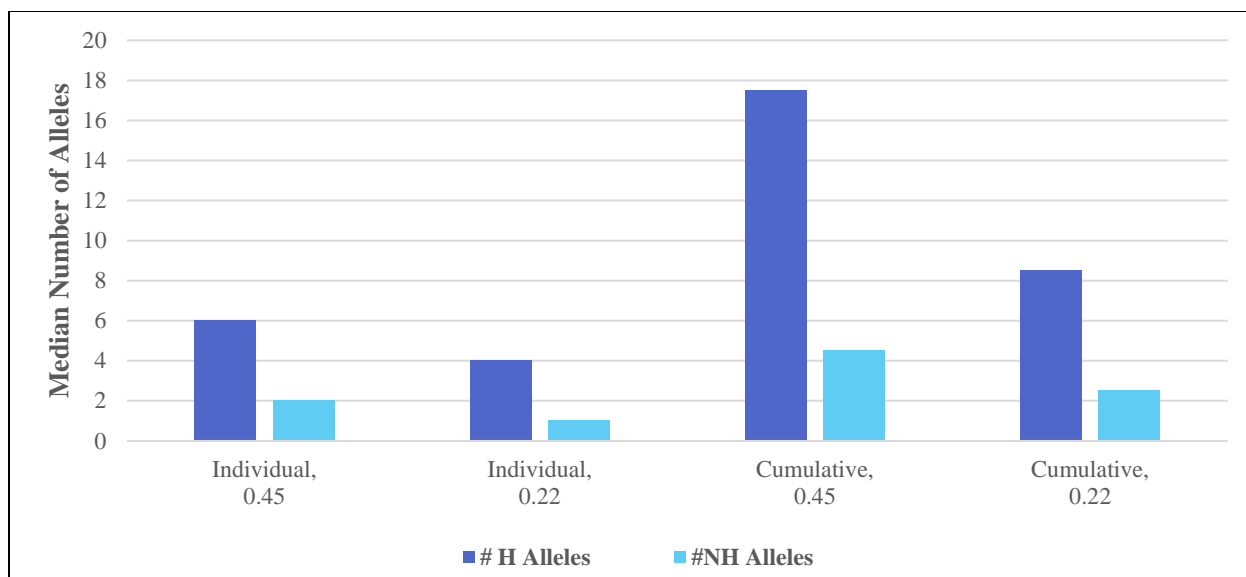


Figure 7. Median number of handler (H) and non-handler (NH) alleles based on swabbing strategy and cartridge caliber. Individual/cumulative refers to the swabbing strategy.

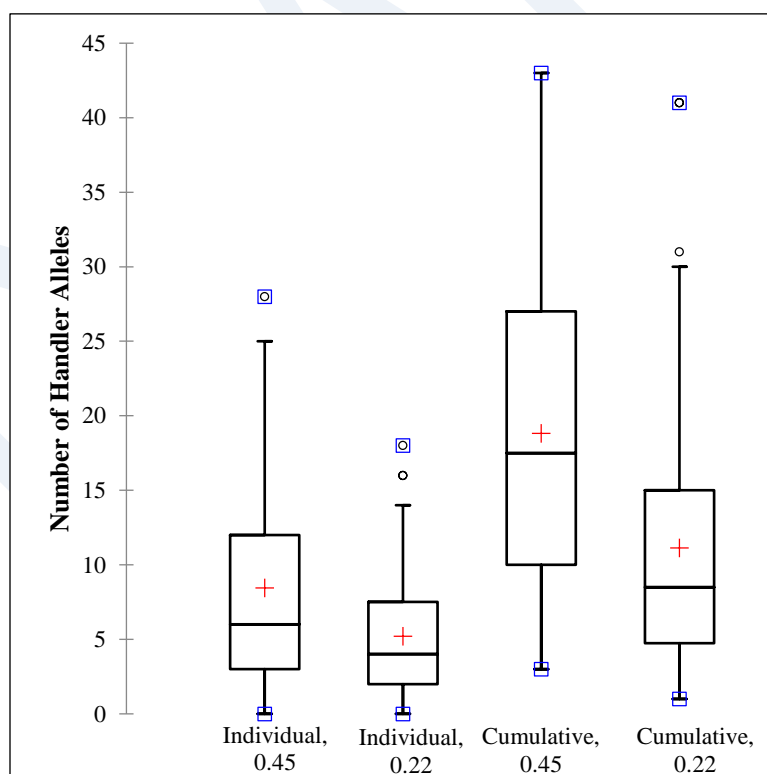


Figure 8. Box plots displaying the distribution of the number of handler alleles based on swabbing strategy and cartridge caliber. The box encompasses the interquartile range (the distance between the lower and upper quartiles), with the line through the box symbolizing the

median. The mean is represented by a red +, mild outliers are represented by °, and maximum/minimum values are represented by blue squares. The whiskers represent the maximum/minimum values that are not outliers. Individual/cumulative refers to the swabbing strategy and 0.45/0.22 refers to the caliber.

Table 12. Mann-Whitney pairwise comparisons of the number of handler alleles (H), non-handler alleles (NH), and percent profile obtained. Individual/cumulative refers to the swabbing strategy and 0.45/0.22 refers to the caliber.

Pair		# H Alleles (P-Value)	# NH Alleles (P-Value)	% Profile (P-Value)
Individual, 0.45	Individual, 0.22	0.0062	0.0964	0.0070
Individual, 0.45	Cumulative, 0.45	< 0.0001	< 0.0001	< 0.0001
Individual, 0.45	Cumulative, 0.22	0.0860	0.0125	0.0930
Individual, 0.22	Cumulative, 0.45	< 0.0001	< 0.0001	< 0.0001
Individual, 0.22	Cumulative, 0.22	< 0.0001	< 0.0001	< 0.0001
Cumulative, 0.45	Cumulative, 0.22	< 0.0001	0.0145	< 0.0001

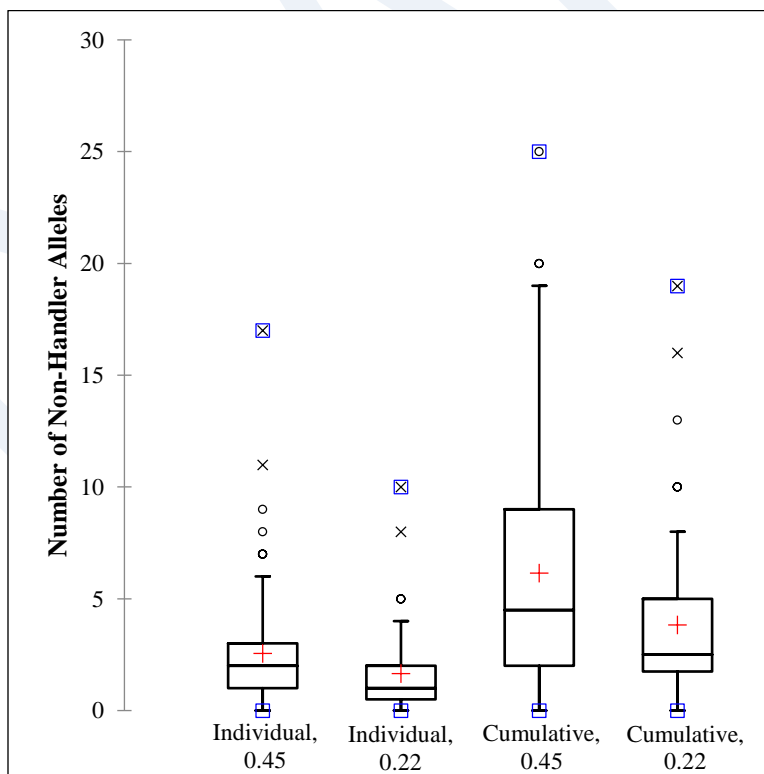


Figure 9. Box plots displaying the distribution of the number of non-handler alleles based on swabbing strategy and cartridge caliber. The box encompasses the interquartile range (the

distance between the lower and upper quartiles), with the line through the box symbolizing the median. The mean is represented by a red +, extreme outliers are represented by x, mild outliers are represented by °, and maximum/minimum values are represented by blue squares. The whiskers represent the maximum/minimum values that are not outliers. Individual/cumulative refers to the swabbing strategy and 0.45/0.22 refers to the caliber.

Cartridge Loading and Firing Order

Influence of Loading/Firing Order on DNA Yields and STR Results

Half of the volunteers loaded 0.45 caliber cartridges into ‘Magazine 1’, and then loaded 0.22 caliber cartridges into ‘Magazine 2’. The other half of volunteers loaded magazines in the opposite order. Table 13 displays the median DNA yield and number of handler alleles obtained based on swabbing strategy, caliber, and firing order (first loaded = last fired), in sets of three. Pairwise comparisons of DNA yields and number of handler alleles between the first and last casings (Table 14) showed that no differences were significant.

Table 13. Median DNA yields (pg) and number of handler (H) alleles from spent casings. Casing number 1 – 3 refers to the casings from the 1st, 2nd, and 3rd cartridges fired, 4 – 6 refers to the 4th, 5th, and 6th, etc. Individual/cumulative refers to the swabbing strategy and 0.45/0.22 refers to the caliber.

		Magazine 1		Magazine 2	
Casing #		1 – 3	4 – 6	7 – 9	10 – 12
Individual, 0.45	Yield (pg)	12.26	17.83	29.04	25.28
	# H Alleles	3.0	6.0	9.0	10.0
Individual, 0.22	Yield (pg)	4.75	9.32	14.24	24.77
	# H Alleles	3.0	5.0	6.0	3.5
Cumulative, 0.45	Yield (pg)	43.55	64.78	31.82	44.71
	# H Alleles	20.0	22.0	14.0	15.0
Cumulative, 0.22	Yield (pg)	18.14	16.63	18.71	14.88
	# H Alleles	8.0	9.0	8.0	10.0

Table 14. Mann-Whitney pairwise comparisons of DNA yields (pg) and number of handler (H) alleles between casings from the first and last fired cartridges from each magazine based on swabbing strategy and cartridge caliber. Individual/cumulative refers to the swabbing strategy and 0.45/0.22 refers to the caliber.

		Casings 1 – 3 vs. 4 – 6	Casings 7 – 9 vs. 10 – 12
Individual, 0.45	DNA Yield (P-Value)	0.46	0.68
	# H Alleles (P-Value)	0.16	0.98
Individual, 0.22	DNA Yield (P-Value)	0.28	0.01
	# H Alleles (P-Value)	0.03	0.72
Cumulative, 0.45	DNA Yield (P-Value)	0.56	0.74
	# H Alleles (P-Value)	0.75	0.90
Cumulative, 0.22	DNA Yield (P-Value)	0.74	0.07
	# H Alleles (P-Value)	0.87	0.48

The Influence of DNA Concentration and Degradation on STR Profiles

Correlation Between DNA Concentration and STR Profiling

The correlation coefficient between DNA concentration and the number of handler alleles generated using Fusion for each swabbing strategy and caliber is shown in Table 15. C

Positive correlations existed in all instances, although they were variable, ranging from 0.3030 (individual, 0.22) to 0.8061 (cumulative, 0.22).

Table 15. The correlation between DNA concentration (pg/μL) and the number of handler alleles generated using Fusion for each caliber and swabbing strategy. Individual/cumulative refers to the swabbing strategy, and 0.45/0.22 refers to the caliber.

	Correlation Coefficient (r)
Individual, 0.45	0.5647
Individual, 0.22	0.3030
Cumulative, 0.45	0.5825
Cumulative, 0.22	0.8061

Degradation of DNA Recovered from Spent Cartridge Casings

The frequencies of alleles consistent with the handler at each locus are presented in Figure 10. DNA from spent casings showed indication of degradation, with the smaller amplicons much more likely to successfully amplify than larger ones.

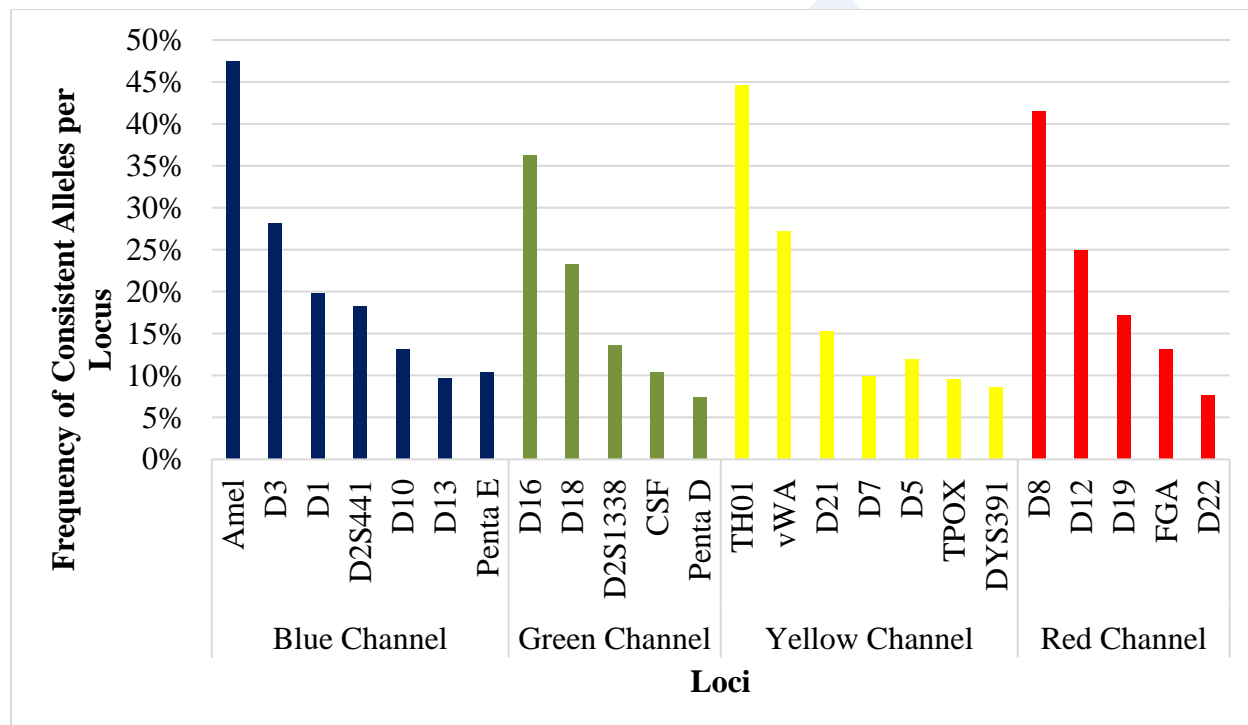


Figure 10. Frequency of consistent handler alleles amplified at each locus, illustrating greater success in the amplification of shorter amplicons. The loci are arranged according to their amplicon sizes (short to long) for each dye channel, and overall, smaller amplicons had higher frequencies of amplification. Frequencies of the smallest locus in each channel: Amel = 47.5%, D16 = 36.3%, TH01 = 44.6%, D8 = 41.5%. Frequencies of the largest locus in each channel: Penta E = 10.4%, Penta D = 7.5%, DYS391 = 8.6%, D22 = 7.6%.

MtDNA Analysis from Spent Cartridge Casings

Comparison of MtDNA Profiles Among Calibers and Swabbing Strategies

MtDNA profiles were successfully generated from all 96 DNA extracts tested (based on relative nuclear DNA yields designated as high, medium, or low, for each caliber and swabbing

strategy). Figure 11 displays the classification results from all profiles, of which 50 were consistent (52%), 25 were mixed-consistent (26%), 18 were inconsistent (19%), and 3 were mixed-inconsistent (3%) with the handler. In total, 78% of the generated profiles included the handlers' haplotype and 29% contained a mixture. All mtDNA profiles can be found in Appendix G and in Ray (2015).

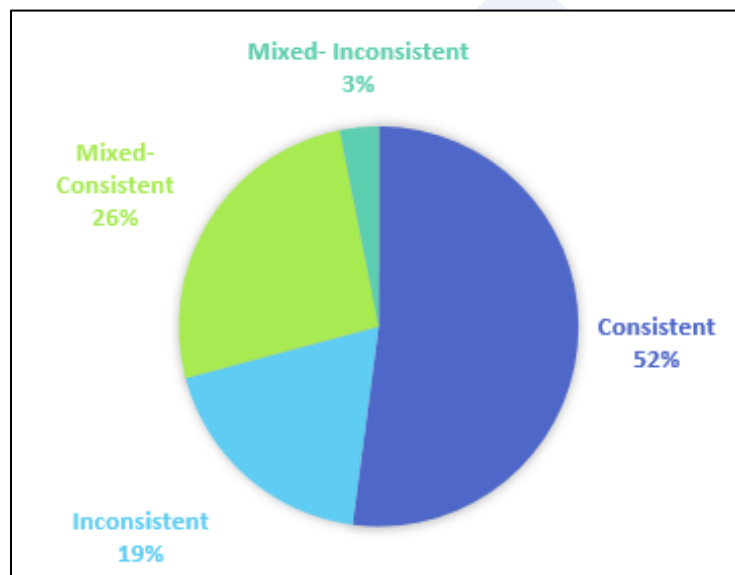


Figure 11. Classification of mtDNA profiles for all samples (n = 96).

Figure 12 displays the mtDNA profile classifications for each DNA quantitation level (high, medium, and low). Overall, higher DNA quantities resulted in more mtDNA profiles consistent with the handler, although a Fisher's exact test indicated that mtDNA profile classification was independent of quantitation level ($p = 0.433$).

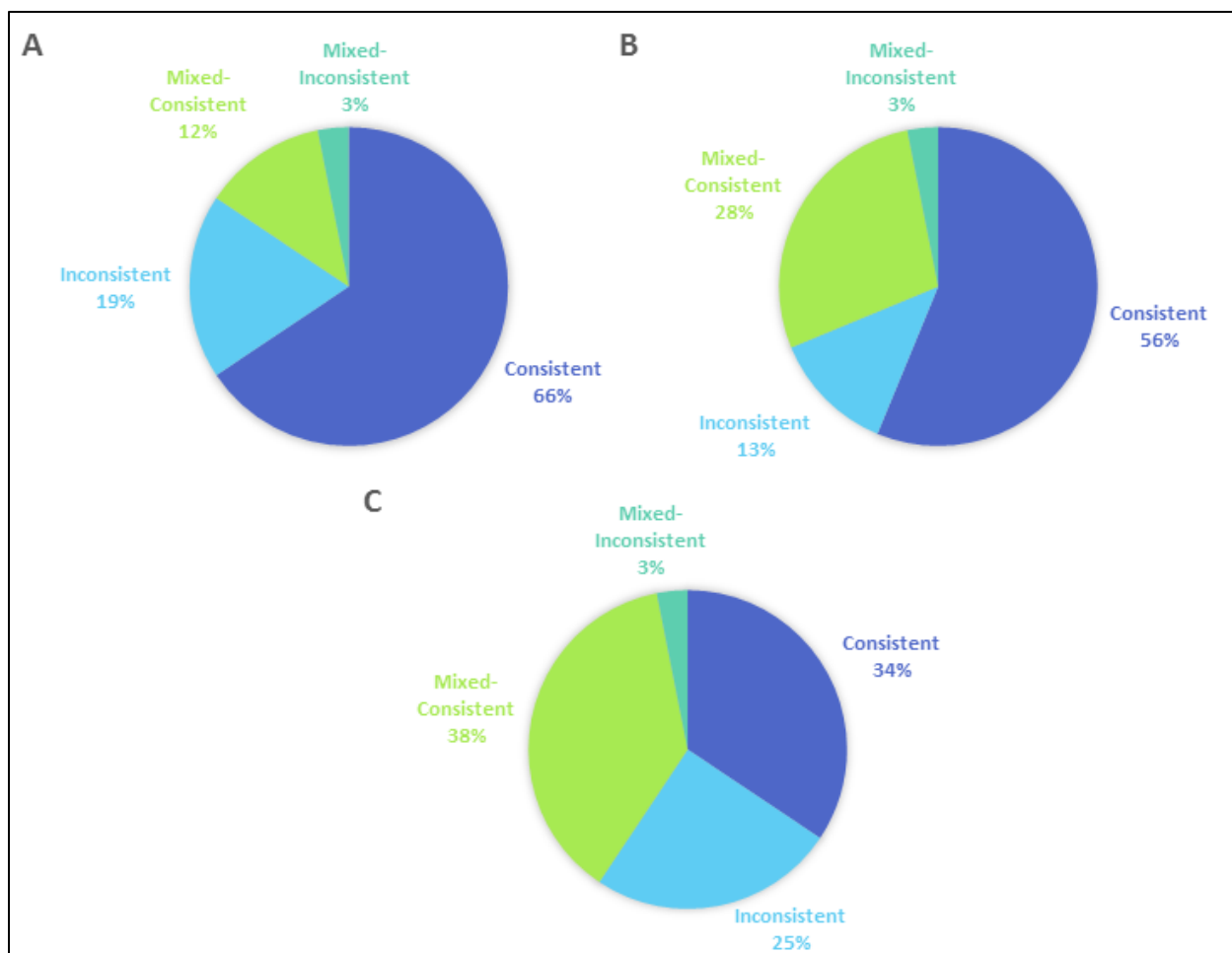


Figure 12. Classification of mtDNA profiles for the high (A), medium (B), and low (C) DNA quantity samples (n = 32 for each chart).

Cumulatively and individually swabbed casings produced similar numbers of inconsistent profiles, however individually swabbed casings had far fewer mixtures (Figure 13). The cumulatively swabbed casings resulted in 29 consistent, 19 mixed-consistent, 10 inconsistent, and no mixed-inconsistent profiles, while the individually swabbed casings resulted in 31 consistent, 6 mixed-consistent, 8 inconsistent, and 3 mixed-inconsistent profiles. Fisher's exact test produced a p-value of 0.035, indicating the two variables are dependent/linked. Individually swabbed samples produced significantly more consistent profiles and significantly fewer mixed-

consistent profiles, while the number of inconsistent and mixed-inconsistent profiles did not differ significantly.

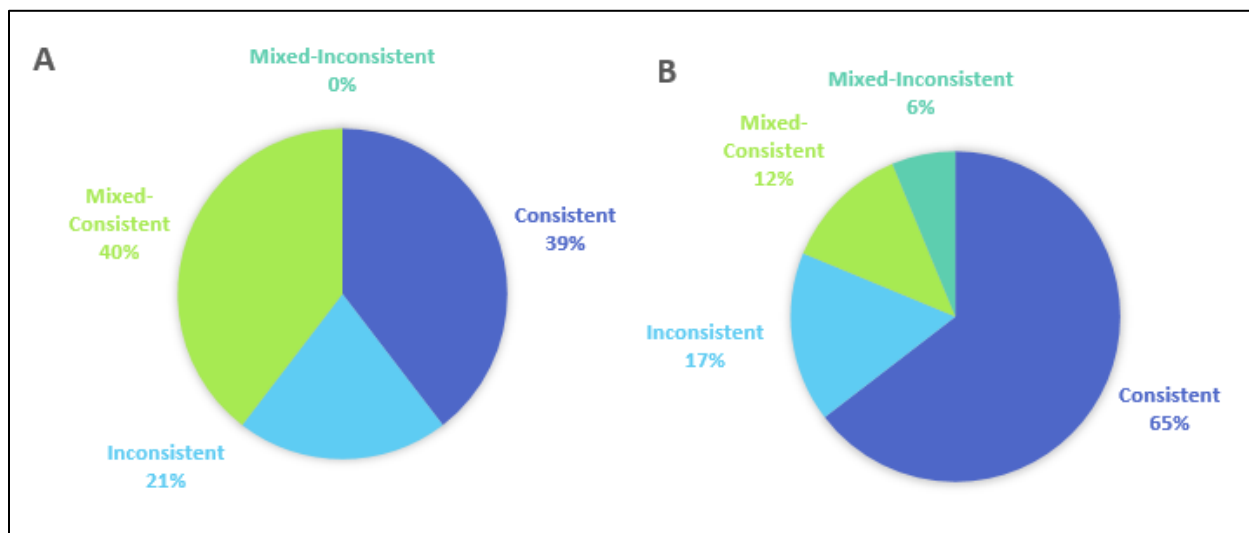


Figure 13. Percentage of each mtDNA profile category for cumulatively swabbed casings (A) and individually swabbed casings (B) (n = 48 for each chart).

Figure 14 displays the mtDNA profile classifications for 0.45 and 0.22 caliber casings. Forty-five caliber casings resulted in 26 consistent, 14 mixed-consistent, 6 inconsistent, and 2 mixed-inconsistent profiles, while 0.22 caliber casings resulted in 24 consistent, 11 mixed-consistent, 12 inconsistent, and 1 mixed-inconsistent profile. Fisher's exact test produced a p-value of 0.321, indicating that mtDNA profile classification was independent of cartridge caliber.

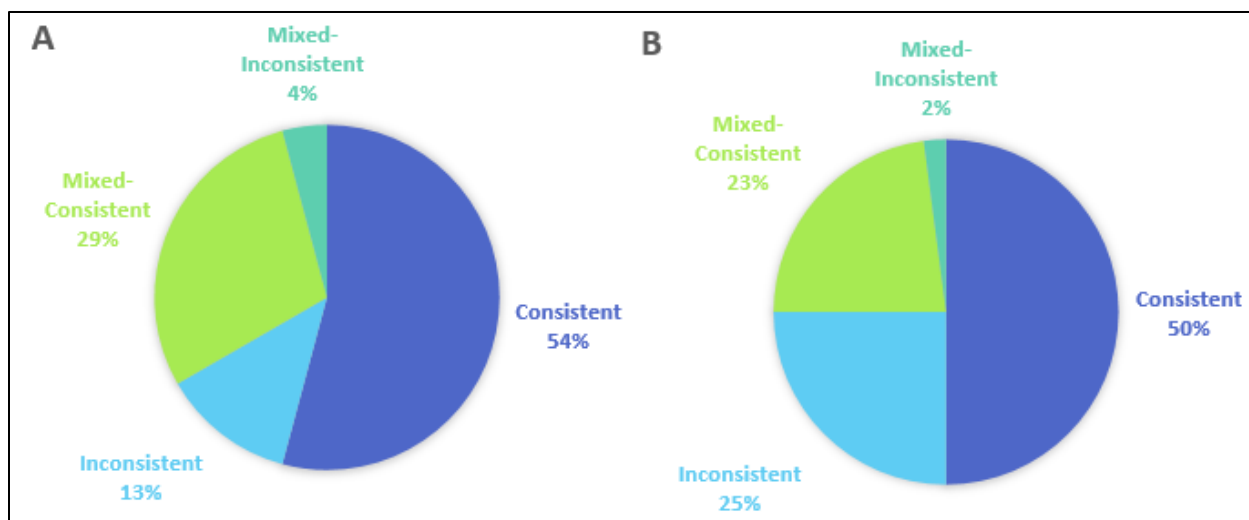


Figure 14. Percentage of each mtDNA profile category for 0.45 caliber casings (A) and 0.22 caliber casings (B) (n = 48 for each chart).

Comparison of MtDNA and STR Results

Overall, the mtDNA and STR results corresponded well with one another. Figure 15 shows the median number of handler and non-handler STR alleles for samples of each mtDNA profile classification. DNA extracts that produced an inconsistent mtDNA profile also had a relatively high number of non-handler alleles when compared to extracts that resulted in a mtDNA profile consistent with the handler. Consistent mtDNA profiles had a median of 11 handler and 2 non-handler alleles, mixed-consistent profiles had a median of 9 handler and 3 non-handler alleles, and inconsistent profiles had a median of 7.5 handler and 3 non-handler alleles. The classification of each mtDNA profile and the corresponding number of handler and non-handler alleles for each sample are in Appendix H and in Ray (2015).

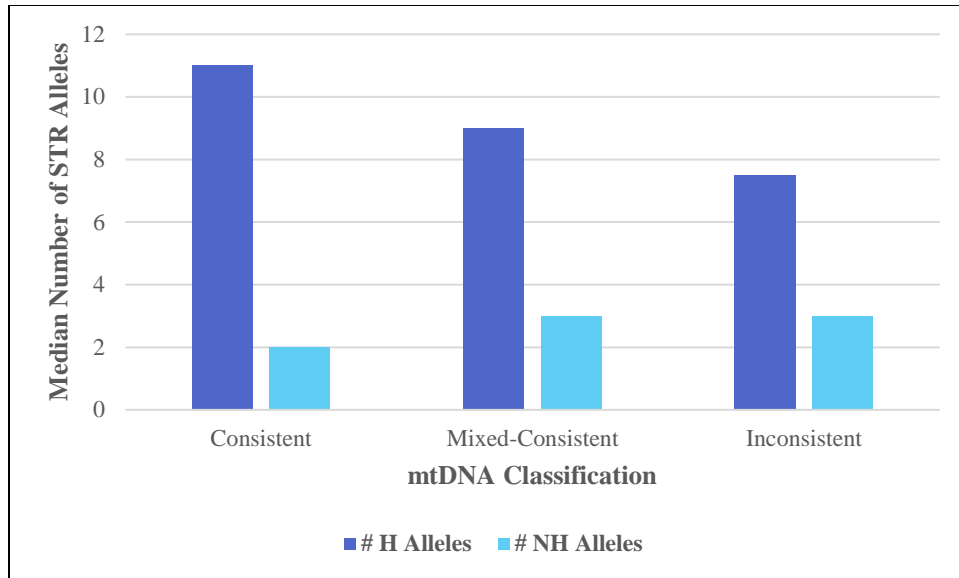


Figure 15. Medium number of handler (H) and non-handler (NH) STR alleles for each classification of mtDNA profile. Only three samples were classified as mixed-inconsistent, which are not included in this graph.

The Influence of Cyanoacrylate Fuming of Casings on DNA Results

Comparison of DNA Yields from Fumed and Non-Fumed Casings

The median DNA yields of fumed and non-fumed casings and the distributions of the data are shown in Figures 16 and 17, respectively. The non-fumed casings resulted in a median DNA yield of 25.86 pg, while 11.53 was recovered from the MSU-fumed, and 4.95 pg from the MSP-fumed casings. Descriptive statistics are in Table 16. DNA yields were not normally distributed (Shapiro-Wilk, $p < 0.0001$), and there was a significant difference among the non-fumed, MSU-fumed, and MSP-fumed casings (Kruskal-Wallis, $p < 0.0001$). Pairwise comparisons (Table 17) showed that all differences in DNA yield were significant. DNA yield from each casing can be found in Appendix I and in Ray (2015).

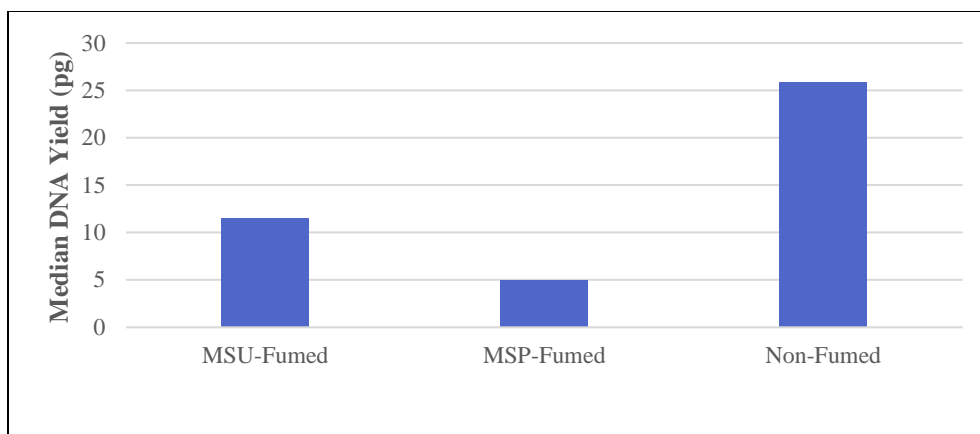


Figure 16. Median DNA (pg) yields among the fumed and non-fumed casings.

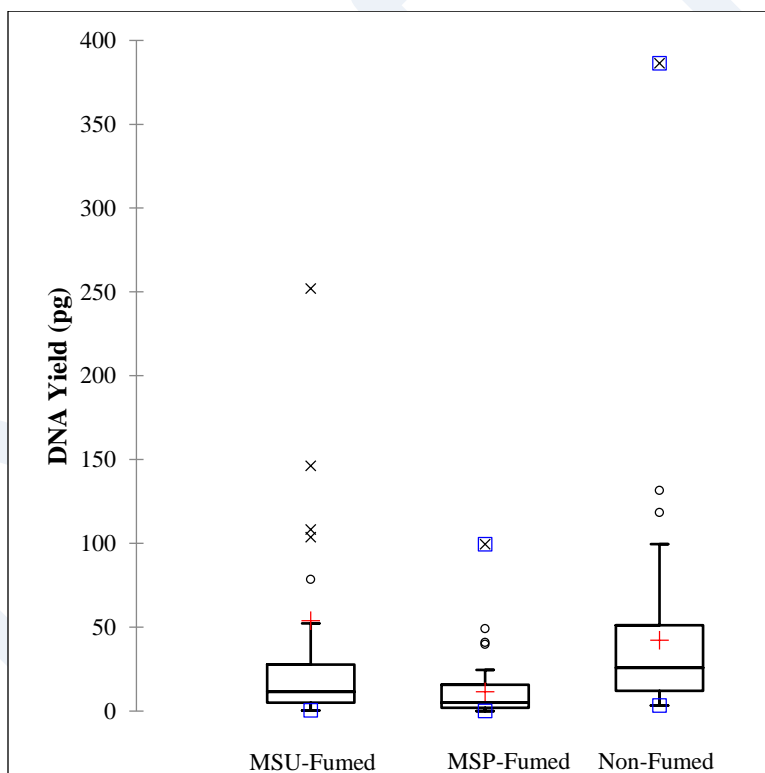


Figure 17. Box plots displaying the distribution of the DNA yields (pg) of fumed and non-fumed casings. The box encompasses the interquartile range (the distance between the lower and upper quartiles), with the line through the box symbolizing the median. The mean is represented by a red +, extreme outliers are represented by x, mild outliers are represented by o, and maximum/minimum values are represented by blue squares. The whiskers represent the maximum/minimum values that are not outliers. The MSU-fumed casings contained an extreme outlier at 1420.2 pg that is not shown.

Table 16. Descriptive statistics of quantitation results of fumed and non-fumed casings.

		MSU-Fumed	MSP-Fumed	Non-Fumed
DNA Concentration (pg/μL)	Median	0.57	0.18	0.99
	Average	2.15	0.41	1.65
	Standard Deviation	7.46	0.58	2.37
DNA Yield (pg)	Median	11.53	4.95	25.86
	Average	53.94	11.47	42.33
	Standard Deviation	199.97	16.88	57.95
n		51	51	51

Table 17. Mann-Whitney pairwise comparisons of DNA yields (pg) for fumed and non-fumed casings.

Pair		P-Value
MSU-Fumed	MSP-Fumed	0.0065
MSU-Fumed	Non-Fumed	0.0024
MSP-Fumed	Non-Fumed	< 0.0001

Comparison of Commercial STR Kits on Fumed and Unfumed Casings

Table 18 displays the median number of handler alleles, non-handler alleles, and percent profile produced using MiniFiler and Fusion from the subset of fumed/unfumed casings that were amplified using both kits. MiniFiler produced a median of 2 alleles consistent with the handler from casings fumed both at MSU and at MSP and 11 for non-fumed casings, while Fusion resulted in medians of 10 (MSU-fumed), 15 (MSP-fumed), and 23 (non-fumed). MiniFiler produced a median of 13% of a full profile for both MSU and MSP fumed casings, while Fusion produced 25% (MSU-fumed) and 36% (MSP-fumed) profiles. The non-fumed casings resulted in median profiles of 67% (MiniFiler) and 60.5% (Fusion). The MSU-fumed casings, MSP-fumed casings, and non-fumed casings produced median percent Fusion profiles of 31%, 42%, and 70%, respectively, when only loci with amplicons smaller than 300 bp were examined. Fusion also generated a higher number of non-handler alleles, resulting in medians of 10 (MSU-fumed), 4 (MSP-fumed) and 3 (non-fumed), compared to medians of 2 (MSU-fumed),

0 (MSP-fumed), and 1 (non-fumed) amplified using MiniFiler. Pairwise comparisons (Table 19) showed that all but three differences between MiniFiler and Fusion were significant (percent profiles from the MSU-fumed casings, percent profiles from the non-fumed casings, and number of non-handler alleles from the non-fumed casings). STR profiles for each DNA extract (from casings and buccal swabs) amplified with MiniFiler and Fusion can be found in Appendix J and in Ray (2015).

Table 18. Median number of handler (H) alleles, non-handler (NH) alleles, and percent profiles produced from fumed and non-fumed casings using MiniFiler and Fusion.

	MSU-Fumed		MSP-Fumed		Non-Fumed	
	MiniFiler	Fusion	MiniFiler	Fusion	MiniFiler	Fusion
Median # H Alleles	2	10	2	15	11	23
Median # NH Alleles	2	10	0	4	1	3
Median % Profile	13	25	13	36	67	61
n	22	22	19	19	11	11

Table 19. Mann-Whitney pairwise comparisons between the number of handler (H) alleles, non-handler (NH) alleles, and percent profiles generated using MiniFiler and Fusion.

Pair	# H Alleles (P-Value)	# NH Alleles (P-Value)	% Profile (P-Value)
MiniFiler vs. Fusion (MSU-Fumed)	< 0.0001	< 0.0001	0.0606
MiniFiler vs. Fusion (MSP-Fumed)	< 0.0001	< 0.0001	0.0003
MiniFiler vs. Fusion (Non-Fumed)	0.0005	0.1912	0.6862

Comparison of Fusion STR Profiles from Fumed and Non-Fumed Casings

All remaining casings were then profiled using Fusion. Figure 18 displays the median number of alleles consistent and not consistent with the handler for the full set of casings (DNA from three casings was not amplified due to low extract volumes). The non-fumed casings

generated the greatest number of alleles consistent with the handler, with a median of 12, while the fumed casings generated medians of 5 (MSU) and 5.5 (MSP). Pairwise comparisons (Table 20) showed that the number of handler alleles did not differ significantly between the MSU-fumed and the MSP-fumed casings, while significantly more were produced from the non-fumed casings. MSU and MSP-fumed casings both resulted in a median percent profile of 13.2%, while non-fumed casings produced 30.8% of a full profile. The percent profile from non-fumed casings was significantly higher than the MSU and MSP-fumed casings. Unlike the number of handler alleles, the MSU-fumed casings resulted in the largest number of non-handler alleles with a median of 7, which was significantly greater than those produced from the MSP-fumed and non-fumed casings. The STR profile for each casing can be found in Appendix K and L, and in Ray (2015).

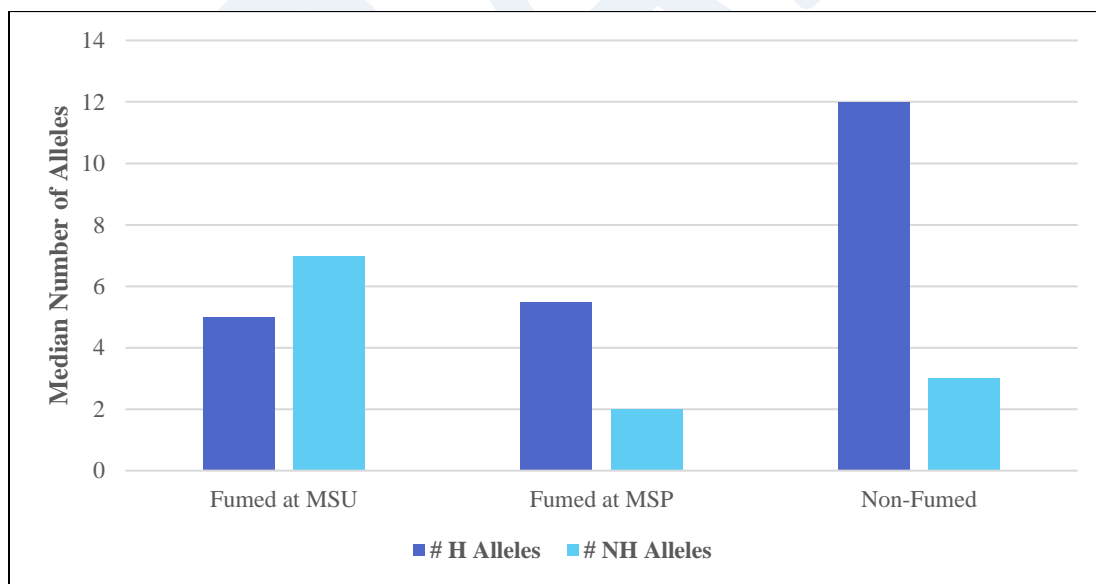


Figure 18. Median number of handler (H) and non-handler (NH) alleles amplified from fumed and non-fumed casings using Fusion.

Table 20. Pairwise comparisons of the number of handler alleles (H) and non-handler alleles (NH) and the percent profiles using the Mann-Whitney test.

Pair		# H Alleles (P-Value)	# NH Alleles (P-Value)	% Profile (P-Value)
MSU-Fumed	MSP-Fumed	0.8690	< 0.0001	0.8418
MSU-Fumed	Non-Fumed	0.0025	0.0027	0.0038
MSP-Fumed	Non-Fumed	0.0034	0.2383	0.0056

DISCUSSION

Spent cartridge casings, often recovered from shooting incidents, have the potential to be a valuable source of evidence used to link a perpetrator to a crime. Current forensic strategies for analyzing spent casings—class characteristics, individual (toolmark) characteristics, and fingerprints—either lack specific information necessary to associate an individual to a crime, are rarely recovered, or both (Given, 1976; Bentsen et al., 1996; Spear et al., 2005). In contrast, DNA analysis has the potential to both differentiate individuals and identify the person(s) responsible for shooting. However, although DNA is a powerful tool, when recovered from spent casings it is often degraded and present in low copy numbers, causing its analysis to be challenging. Currently, crime laboratories process spent cartridge casings for DNA as a last resort due to extremely low DNA yields and minimal allele recovery (Michigan State Police Forensic Science Division, personal communication). Therefore, it is imperative that we improve existing techniques for STR analysis of touch DNA from spent cartridge casings if this strategy is to be used to identify the perpetrators of violent crimes.

The overarching goal of this research was to improve the probative value of spent cartridge casings recovered from crime scenes. The first step towards its achievement was to compare and optimize cell/DNA recovery methods from casings, based on a large number of variables. This was followed by doing the same for DNA extraction methods, again by testing a variety of strategies, including those specifically designed to obtain DNA from touch samples such as spent cartridge casings. Once these methods had been optimized, different DNA analysis techniques were assessed. Finally, several other factors that could influence DNA testing of cartridge casings were examined, including the loading/firing order of cartridges, cartridge caliber, and cyanoacrylate fuming. In the end, all of the factors delineated in the original NIJ

proposal were investigated, and their influence on the successful testing of DNA from cartridge casings determined.

The first portion of the research presented here was designed to objectively examine and optimize methods for isolating cells/DNA from touched cartridge casings. Multiple studies have been conducted that involved different techniques to recover and isolate DNA from spent cartridge casings, including soaking evidence with rotation (Dieltjes et al., 2011), pre-digestion incubation of soaked samples (Dieltjes et al., 2011), organic extraction (Horsman-Hall et al., 2009; Orlando, 2012), silica-based extraction (Horsman-Hall et al., 2009; Dieltjes et al., 2011), and a non-binding DNA extraction strategy (Kopka et al., 2011). Additionally, studies have been performed to increase DNA yields by enhancing cell recovery and DNA extraction, including double swabbing of evidence (Sweet et al., 1997), pre-treatment of purification columns (Doran and Foran, 2014) and altering the duration of digestion with concurrent shaking (QIAamp and FDF manufactures' protocols). In the current study, these variables were tested independently to examine their influences on DNA recovery.

An obvious question is if swabbing a casing, as would generally be done in a crime laboratory, recovers most or all of the cells/DNA from it, or if some other method would result in higher yields. Soaking the outside of a casing is one such option, as presumably all material deposited by a handler would be contacted. Multiple vessels were investigated for performing soaking as a cell/DNA recovery method. The diameters of beakers and test tubes were large, requiring a sizeable buffer volume to fully soak the outside surface of casings. Five milliliter stuffed pipette tips were smaller, which helped reduce soak solution volumes, but after a short time they started to leak. The bulb portion of transfer pipettes proved to be a useful vessel for soaking. They were close-fitting around the casings, which minimized buffer volumes and

maximized the submerged surface area. Transfer pipettes are often supplied sterile, and are inexpensive, disposable, and offered in a variety of sizes to accommodate different ammunition calibers. The possibility of DNA loss because of binding to the plastic of the bulb led to the investigation of pre-treatment to avoid this. Recent research at the MSU Forensic Biology Laboratory found pre-treatment application of DNA purification columns with yeast rRNA substantially reduced DNA loss (Doran and Foran, 2014). Yeast rRNA was applied to the bulbs to determine if it would help improve DNA recovery. Yields from pre-treated bulbs increased minimally, indicating negligible improvements in DNA recovery and little, if any, DNA adhesion onto the soaking vessel.

The inclusion of agitation during the soaking period has the potential to help loosen cells and DNA from casings, aiding in the amount of DNA recovered. Dieltjes et al. (2011) soaked items (cartridges, bullets, and casings) for 30 minutes with simultaneous rotation and reported the production of a blue colored lysis solution, and further reported that the soaked item itself turned blue at longer soaking times. They attributed this to oxidation of the soaked items, and claimed to “solve the oxidation problem” by limiting the soak period to 30 minutes with subsequent swabbing. Blue soak solutions were generated with their adjusted protocol when performed in this study, and adding agitation during this step resulted in even more discoloration, indicating casings oxidized quicker. Shaken samples routinely had decreased DNA yields with both extraction methods. It is possible that copper ions (most likely Cu^{+2}) swamped out the EDTA in the soaking solution, leading to DNA degradation when other divalent cations acted as cofactors for nucleases. Furthermore, other casing metals (e.g., zinc) along with primer components of the gunshot residue (GSR) could have inhibited PCR. Horsman-Hall et al. (2009) and Orlando (2012) noted PCR inhibition from the metals of the cartridge casings or primer

components of the GSR; the former in 11% of the DNAs recovered from shotgun shells and the latter in DNA extracts from cumulative and single swabbed casings. However, PCR inhibition was not observed in the current study, thus it seems likely that the DNA loss from shaking was real.

Incubation at 85°C prior to DNA isolation is included in Qiagen's protocol for eluting dried bloodstains off FTA paper (Smith and Burgoyne, 2004). Dieltjes et al. (2011) followed this protocol and successfully obtained DNA, despite recovering it from ammunition and not bloodstains. In the current study, pre-digestion incubation of soaking solution and accompanying swabs increased DNA recovery using both organic and QIAamp extractions. This may be attributable to cells being loosened from the swabs, making them more accessible for lysis. Additionally, common nucleases such as DNase I and II are inactivated at temperatures well below this (68°C and 30°C, respectively; Sigma-Aldrich Nucleases, 2014). Thus, subjecting samples to this high temperature could have limited nuclease activity and prevented DNA degradation (further discussed below).

QIAamp and FDF manufacturers recommend incubating swabs in lysis buffer for at least one hour or 30 min, respectively. In this study there was no obvious correlation between digestion time and DNA yields, although only two time points (one hour and overnight) were examined. It was clear however, that yields were reduced overnight. It is conceivable that nucleases were not inactivated by EDTA during this step due to the presence of metal ions and/or primer components. Both organic and QIAamp extracted samples that were soaked and digested overnight recovered slightly more DNA than those double swabbed and digested overnight, which could have resulted from the former undergoing the 85°C incubation. On the other hand,

the one hour incubation may not have been long enough for complete digestion of cells, and an incubation time between one hour and overnight may be advantageous.

The standard protocols for organic and QIAamp extractions at the MSU Forensic Biology Laboratory do not include shaking during digestion, although the QIAamp instructions incorporate it. Since the FDF protocol has agitation at 600 rpm during digestion, this step was incorporated into the extraction methods to examine its effect on DNA recovery. Shaking at 900 rpm was selected for organic and QIAamp extractions, as this was the speed recommended by Qiagen. Shaking did increase DNA yields when compared to non-shaken samples, which may have resulted from increased detachment of cells from swabs, which rendered them more accessible for lysis and DNA isolation. Further, it is possible agitation could have physically lysed the cells or aided in the process by increasing the number of cells exposed to the SDS and proteinase K.

The final optimized soaking method, which aimed to maximize yields associated with touch DNA on casings, included: (1) soak in transfer pipette bulbs, (2) pre-digest soaking solution and accompanying swab at 85°C for 10 min, (3) digest samples for one hour with concurrent shaking, (4) extract DNAs either organically or with QIAamp. The double swab method included shaking the sample during the one hour digestion. Once these strategies had been established, the influence of multiple other factors could be examined. The first of these was comparison of DNA yields among the soaking, swabbing, and FDF methods when testing live cartridges that volunteers loaded into the magazine of a weapon and were then fired.

An important factor in this study was the variability that is inherent in the amount of DNA left through simple handling of an object. Several authors have noted the variability between and within individuals transferring DNA on handled items (Lowe et al., 2002;

Alessandrini et al., 2003; Bright and Petricevic, 2004; Phipps and Petricevic, 2007; Thomasma and Foran, 2013). Lowe et al. (2002) were the first to investigate the amount of DNA individuals deposit on handled objects. They attempted to categorize people according to ‘shedder type’ based on how much DNA they deposited or ‘shed’ 15 minutes after hand washing. The authors deemed 18 of 30 volunteers ‘good shedders’, defined as 80 – 100% of an individuals’ SGM Plus profile when assessing STR results generated from handled tubes. Phipps and Petricevic (2007) attempted to replicate the study by Lowe et al. (2002), however, among 60 volunteers none were classified as ‘good shedders’. The authors noted differences in the protocols, where Lowe et al. (2002) undertook QIAamp extractions and wiped tubes with a wet swab prior to handling, while they performed organic extractions and did not swab prior to handling. Phipps and Petricevic (2007) suggested discrepancies between the studies may have resulted from the extraction performed or the damp surface created during swabbing that possibly assisted with DNA transfer. Additionally, they found the amount of DNA ‘shed’ by a single person varied day-to-day and even depended on the hand used. Beyond ‘shedder type’, it has been hypothesized that skin condition (dry or oily), substrate surfaces (porous or non-porous), and the amount of physical contact with one’s self and others impact transferred DNA quantities (Wickenheiser, 2002; Alessandrini et al., 2003). Owing to this, a large number of volunteers was used in the current study, as was a large number of trials, which is in contrast to earlier studies of DNA from spent casings.

Once optimized, soaking versus double swabbing versus FDF were compared. The double swab method, developed by Sweet et al. (1997), was designed to increase DNA yields, and has been widely used. The method is thought to rehydrate, loosen, and collect shed cells from surfaces using a wetted swab, while a second dry swab retrieves additional cells that may

not have adhered to the first one. Pang and Cheung (2007) double swabbed 20 touched items, individually extracted the swabs, and amplified the DNAs with Identifiler. The authors found 80% of the first swabs and 60% of the second swabs recovered enough DNA to generate allelic data, demonstrating the importance of both swabs. Additionally, van Oorschot et al. (2010) recommend swabbing objects with multiple swabs and considered it common practice to enhance DNA yields. However, double swabbing has never been compared to soaking when recovering DNA from spent cartridge casings, and the latter method had the potential to improve upon simple swabbing. In this study, double swabbing recovered a significantly greater amount of DNA than did soaking (69.4 % and 222.9% increase with organic and QIAamp[®] extractions, respectively; FDF findings appear below). The finding was consistent with Bright and Petricevic (2004) who reported double swabbing yielded more DNA than soaking (avg. = 0.16 and 0.08 ng, respectively) when analyzing trace DNA from shoe insoles.

DNA recoveries in the current study were also significantly influenced by the extraction methods, with organic extractions producing significantly higher yields than QIAamp or FDF. In contrast, Horsman-Hall et al. (2009) reported significantly higher DNA yields from spent cartridge casings using a silica-based extraction compared to organic extraction and Microcon purification. The primary difference between the two studies was that Horsman-Hall et al. (2009) did not pre-treat the purification columns, as was done in the current study, which has been shown to improve DNA yields substantially (Doran and Foran, 2014). It would be interesting to determine if the results of Horsman-Hall et al. (2009) would differ had they undertaken this step.

Lower DNA yields generated with QIAamp extractions in the current study could have resulted from DNA loss on the column or problems associated with silica binding. Hebda et al. (2014), examined multiple elution steps with QIAamp extractions and found a measurable

amount of DNA was still eluting off the columns beyond three elutions. Therefore, it is feasible that yields could have increased with more elutions, but that also would have further diluted the DNA. Additionally, silica has previously been used to remove heavy metals (e.g., copper, cadmium, and zinc) from aqueous solutions (Bowe, 2003). Thus, it is possible copper ions or metals from GSR (e.g., lead and barium) bound to the negatively-charged DNA or silica, interfering with DNA binding, causing its loss.

The FDF method demonstrated the lowest DNA yields of all, even though the kit was specifically designed for obtaining DNA from fingerprints. The manufacturer claims “proteins, detergents and low molecular weight compounds are retained by the nexttec sorbent”. However, if the DNA was highly degraded it is possible those fragments were retained on the column, especially since the manufacturer does not provide a molecular weight cutoff for retention. It also seems likely that lower DNA yields resulted from the single swab recovery method. The technique required 30 µL of Lysis Buffer to be applied to swabs (compared to 150 µL used with organic and QIAamp extractions), and so cells may not have been rehydrated, hindering their removal. Kopka et al. (2011) provided limited data in their validation of the FDF Kit, consequently it is difficult to make a direct comparison to the result presented here. In reference to spent casing data, they stated “these [STR profiles] are not reliable. The allele peaks are near or below the amplitude threshold of 50 rfu and should therefore be interpreted very carefully”. If the allele peaks were that weak, it is quite possible they also obtained extremely low DNA yields, similar to those obtained using FDF throughout this work.

The strategy used to recover cells/DNA from spent casings (or other objects) also has the potential to affect DNA yields and typing results. One would expect that cumulatively swabbing casings that were presumed to have been fired from the same weapon by a single individual

would increase yields of that individual's DNA, resulting in better STR profiles. On the other hand, it is possible that some DNA is lost from the swab through deposition onto subsequent casings swabbed. It is also possible that DNA from more than one individual is more likely to be encountered as casings are cumulatively swabbed. In the research described here, cumulative swabbing resulted in higher DNA yields than did individual swabbing, however they were not three times larger, so cumulative swabbing recovered more DNA per swab but not per casing. The most probable reason for this is that DNA retrieved from one casing was indeed deposited onto subsequently swabbed casings. Hebda et al. (2014) examined the effects of cumulative swabbing when studying the collection and analysis of DNA from fingernail evidence. Blood from a male volunteer was placed on two of four female fingernails, which were cumulatively swabbed with a single swab wetted with digestion buffer, alternating between bloody and clean. The clean nails were re-swabbed using the double swab technique and DNA was extracted, quantified, and Y-STRs were amplified to assay blood transfer; enough blood was transmitted to the clean nails to produce full Y-STR profiles. It is likely that DNA was also transferred in the current research, as cells picked up from an earlier swabbed casing were deposited onto those that were subsequently swabbed, resulting in the reduction of important genetic evidence.

Comparison of MiniFiler and Fusion profiling, both of which target small amplicons (with some larger ones as well in Fusion), was conducted in two ways: the total number of possible alleles obtained, or the percentage of a handler's profile obtained based on that kit (along with the level of non-handler alleles). When comparing the percentage of a profile produced, MiniFiler outperformed Fusion for organic extractions, however this resulted from the higher number of Fusion alleles that each loader could have provided due to the increased number of loci assayed. For example, one DNA sample amplified with MiniFiler generated 12

alleles consistent with the loader (85.7% of the loader's profile), while the same sample amplified with Fusion yielded 22 loader alleles (57.9% of the loader's profile). When the large difference in alleles amplified is taken into account, Fusion outperformed MiniFiler in all respects. Fusion amplified significantly more loader alleles from both organic and QIAamp extracts, while the number of non-loader alleles did not differ significantly between the kits. These results demonstrate the improved quality and quantity of genetic information obtained with Fusion (and most likely other newer kits that target more loci). Oostdik et al. (2014) validated Fusion and found strong amplification with minimal artifacts when analyzing less than pristine samples, confirming the findings of this study. In the current study, there was no statistical difference between MiniFiler and Fusion when comparing the number of amplified loader alleles from FDF extracts, however, only 2 of the 7 samples produced any allelic data, and in both cases Fusion amplified more loader alleles. All in all, Fusion generated more than twice the number of alleles than did MiniFiler, a fact that was also true for cyanoacrylate fumed samples (below).

Comparing the STR results in the current study to previous ones, it is clear that optimization improved genotyping success from spent casings. Orlando (2012) recovered mostly (~70%) partial Identifiler Plus profiles (7 or less loci with alleles) and of those, most were not consistent with the loader. Horsman-Hall et al. (2009) utilized MiniFiler with a 20 s injection time (compared to 8 s in this study), and noted 11% of the profiles contained loaders' alleles at all 9 possible loci and 20% had loader alleles at over half of the loci. MiniFiler profiles (double swab + organic) in this study were more complete than those generated by Horsman-Hall et al. (2009), wherein 20% were full profiles and 53% contained over half of the possible loader alleles. Amplifying the same DNA extracts as were analyzed with MiniFiler, Fusion generated

13% full profiles and 67% containing over half of the possible loader alleles. Clearly this more sensitive kit targeting more loci is advantageous when it comes to low quantity and highly compromised samples like those obtained from fired cartridge casings.

In contrast to nuclear DNA, mtDNA amplified from all samples tested, including those that produced few or no STR results. MtDNA analysis is more sensitive than nuclear DNA analysis, as there are hundreds of copies of mtDNA per cell (Robin and Wong, 1988) potentially making its amplification more successful when analyzing touch samples (e.g., Balogh et al., 2003b). Additionally, mtDNA is better protected from degradation than nuclear DNA (Foran, 2006), which is beneficial when working with degraded samples such as DNA from spent cartridge casings. Consequently, all casings had enough high quality mtDNA for HV1 and HV2 to successfully amplify. However, samples with a high nuclear DNA yield generated more accurate sequences (i.e. consistent with the handler) than low yielding samples, but the difference was not significant.

Given the mtDNA results, it is very plausible that its analysis might be the better option for examining DNA from evidentiary casings. However, there are drawbacks to analyzing mtDNA in a crime laboratory that do not exist for STR analysis. MtDNA profiles are not unique, and consequently, mtDNA cannot be utilized to positively identify the loader of a firearm, although it can be used to include, and more importantly to completely exclude, a suspect. Sequencing is also much more time consuming than STR analysis, and of course many crime laboratories do not perform mtDNA analysis, and may instead have to send samples to agencies such as the regional FBI laboratories for testing, which already have a backlog of cases (U.S. Department of Justice, 2012). Regardless, the success of mtDNA analysis compared to STRs when testing cartridge casings is noteworthy.

Several other factors have the potential to influence DNA profiling results from spent cartridge casings. One considered in this research was the order in which the cartridges were placed into the magazine and subsequently fired. It is possible that the bulk of free cells are deposited on the first cartridge loaded into a magazine, with a substantial drop off after that. On the other hand, it takes increasingly more pressure to load each cartridge into a magazine, which itself could deposit more cells. On the flip side, the last cartridge loaded is the first fired, which could have its own influences on DNA recovery.

In spite of these considerations, loading/firing order did not have a significant effect on DNA yield in the current research, for which there are several potential explanations. One is that the order the cartridges were loaded/fired simply does not influence DNA yield. However, van Oorschot et al. (2003) stated that the amount of DNA transferred to items “can drop significantly after the initial touch”, although their experiment involved only four volunteers repeatedly placing their hand on sheets of plastic. DNA was then extracted and amplified using Profiler Plus, and STR peak heights were used as a metric of the amount of DNA deposited, which is not a generally accepted method for determining DNA yield. It is possible that firing order did not significantly affect DNA yields in the current study because the temperature of the casings did not get high enough to have a degradative effect. The temperature of the barrel of a fired gun can reportedly reach 1,200°C (Lawton, 2001), but the casing likely does not get that hot as it is quickly ejected from the firearm. Or, it may be that both loading and firing order do have an effect on DNA yield, but one counteracts the other. For example, the first loaded cartridge might contain the most DNA prior to firing, but the temperature increase inside the gun as preceding cartridges are fired degrades it to the point that the amount of DNA recovered is similar to the last loaded/first fired cartridge. In reality, the order that cartridges were fired will likely never be

readily apparent at a crime scene, or at least considered during casing collection, thus it is perhaps reassuring to know that it does not seem to be an important consideration for DNA yields.

Another characteristic of cartridges that had an effect on the recovery of DNA in this research was caliber. There are two potential reasons for why the 0.45 caliber casings yielded significantly more DNA than did the 0.22 caliber casings. First, the former have a greater surface area on which DNA can be deposited (see below), and second, the increased force and time required to load the bigger cartridges may have resulted in additional cells being transferred to the casing surface. Or, both may have had an effect. Spear et al. (2005) reported similar findings when investigating the recovery of fingerprints from spent casings. The authors placed prints on cartridges ranging in size from 0.22 to 0.45 caliber, and half were fired. Only one identifiable print was obtained from the spent casings and five from the unfired cartridges, all six of which were 9 mm (approximately 0.35 in) or 0.45 caliber. Based on the results of the current research, as well as previous studies, forensic examiners should consider cartridge caliber when deciding whether to attempt DNA recovery from a casing, and when determining what methods to use during processing.

An interesting finding in this research was the interplay between cartridge caliber and swabbing strategy. While cumulative swabbing three casings did not triple DNA yields for either caliber, the increase over swabbing a single casing was much larger for the 0.45 caliber casings than for 0.22 caliber. This probably stemmed from the difference in surface area between the two. The surface area of a 0.45 caliber casing is approximately three times that of a 0.22 caliber casing, so when multiple 0.45 caliber casings are swabbed there is a greater increase in the total surface area (the surface area increases by 18 cm² and 6 cm² for 0.45 and 0.22 caliber casings,

respectively), potentially affecting overall DNA yields. Another factor that may have caused this discrepancy is the accuracy of the DNA quantitation. If a sample falls outside the range of a standard curve, the calculation of its DNA concentration is likely not as accurate as samples that fall within the curve. The lowest quantitation standard in this research was near the limit of detection of the assay, so adding another standard dilution was not an option. More individually swabbed 0.22 caliber samples fell at or below the smallest quantitation standard than any other caliber/swabbing strategy, so the calculated DNA concentrations for these samples could be expected to be less accurate. The median DNA yield for the individually swabbed 0.22 casings could thus be artificially high, making it appear as though there was not a large difference between individually and cumulatively swabbed 0.22 caliber casings.

Once a casing has been collected from a shooting scene, it is likely to be transported to a crime laboratory for analysis such as visualization of fingerprints, microscopic examination, and DNA profiling. How the casing is handled upon discovery and collection has the potential to affect the amount of DNA recovered from it. Fingerprints are typically enhanced using chemical or physical means that might remove touch DNA, trap it in place, introduce contaminant DNA, or introduce substances that interfere with DNA extraction or analysis. If the casing is manipulated by a firearms examiner, any cells that were deposited onto the casing when the cartridge was loaded could be inadvertently lost, and may even be replaced by DNA from the examiner if precautions are not taken. Additionally, the manner in which the casing is processed for DNA can also affect yields, as there are many extraction and analysis techniques employed by forensic scientists to analyze DNA. Several of these factors were examined in the current research.

Cyanoacrylate fuming is a common fingerprint enhancement technique that can be performed using a portable or stationary fuming chamber. The purpose of testing two methods in this study was to determine not only if cyanoacrylate fuming had an effect on the recovery and analysis of DNA from spent casings, but also whether fuming casings on site was more beneficial than transporting them prior to fuming. For example, fuming casings immediately after collection may glue cells to the surface and prevent loss during transportation. On the other hand, cyanoacrylate itself might interfere with DNA retrieval and/or analysis. Transportation did not affect DNA recovery from fumed casings in the current research, as the MSU-fumed casings (which were transported before fuming) resulted in significantly higher DNA yields than those fumed by the MSP. However, the MSP-fumed casings were coated in a heavier layer of cyanoacrylate than those fumed at MSU, so it is possible that the amount of cyanoacrylate affected the DNA yields. Even more DNA was recovered from the non-fumed casings, thus it is likely that the cyanoacrylate residue hindered DNA extraction, potentially because the cells were trapped in the cyanoacrylate, which remained in the interface between the organic and aqueous layers.

Several researchers have examined the influence of cyanoacrylate fuming on DNA recovery and also found it to be deleterious. von Wurmb et al. (2001) placed blood and saliva on glass slides, half of which were fumed with cyanoacrylate, cells/DNA was removed (details not given) and a Chelex extraction performed. STRs were amplified using Profiler Plus, and while profiles were generated from all samples, cyanoacrylate “had a negative effect on the signal intensity”. The authors also reported that when cyanoacrylate was directly added to controlled amounts of purified DNA, PCR was inhibited, although this probably occurred because Chelex does not separate DNA from substances like cyanoacrylate in the solution. Pitilertpanya and

Palmback (2007) placed fingerprints on soda cans, fumed them with cyanoacrylate, extracted DNA using a QIAamp extraction kit, and amplified STRs using a COfiler kit. No quantitative data or statistics were presented, but the authors stated that more cyanoacrylate resulted in “worse” profiles and non-fumed prints produced “better DNA profiles”, which is consistent with the findings of the current study. In contrast, other researchers have found that cyanoacrylate fuming did not have an effect on DNA analysis. Gicale (2011) examined the recovery of DNA from deflagrated pipe bombs fumed with cyanoacrylate by having volunteers assemble bombs, fuming half on site for 15 min following deflagration, and extracting DNA; there was no statistical difference in DNA yields between the two. Bille et al. (2009) also examined cyanoacrylate fuming of pipe bombs, but used a cell suspension to deliver a constant amount of DNA, and deflagrated bombs were exposed to cyanoacrylate for 10 min. Only six bombs were tested and no statistics were reported, although DNA yields from fumed and un-fumed bombs were similar. These conflicting results are likely due to variations in experimental design, sample type (blood, saliva, touch samples, etc.), fuming method, and DNA extraction technique. Cyanoacrylate fuming may therefore not have the same effect on all types of samples, so both the sample and processing methods must be taken into account by the DNA analyst, and extraction procedures that do not separate molecules such as cyanoacrylate from the DNA (e.g., Chelex) should be avoided.

Based on the results of the current study, cyanoacrylate fuming spent casings is not recommended for several reasons. The purpose of this technique is to enhance latent fingerprints, which is rarely successful when working with casings (e.g., Bentsen et al., 1996). Furthermore, even when fingerprints are visible on spent casings they are often partial or have poor ridge detail, and are not easily identifiable (Bentsen et al., 1996). Fingerprints were not observed on

any casings in this study while STR results were produced from most, indicating that DNA is far more likely to provide investigative information from spent casings. In this study, cyanoacrylate fuming casings prior to DNA processing was detrimental to the identification of the loader, as it resulted in lower DNA yields and more non-handler alleles.

The greatest impediment to accurately identifying the individual who loaded a magazine in this research was the presence of DNA not consistent with the handler, as 75 – 85% of STR profiles and around half of mtDNA sequences contained at least one non-handler allele/polymorphism overall, although varied widely based on the research question (e.g., single swabbing casings versus cumulatively swabbing them). There were multiple potential sources of these non-handler DNAs. Cartridges were not cleaned prior to loading, and DNA might have already been present on them (although spot tests indicated this was non problematic). Some volunteers placed the cartridges on the table top prior to loading them into a magazine, which was not a clean surface and could have held DNA from other individuals. The same magazines were loaded by each volunteer and all cartridges of the same caliber were fired by a single weapon, so DNA may have been transferred between the casings and the magazine/firearm. The shooter wore gloves when firing the cartridges, but the casings sometimes made contact with the individual's lab coat. DNA from the shooter, or laboratory personnel, could not be identified due to the small number of alleles produced and the anonymous method used to collect buccal swabs, and the non-handler alleles did not appear to be from one consistent individual. The casings within each collection were captured using a single apparatus and as a result DNA might have been transferred between the collection apparatus and the casings. Although some of these sources of inconsistent alleles/polymorphisms may be a product of the research setting (e.g., it is unlikely that 20 different individuals would load the same gun over the course of a few hours),

others are likely to be present in a forensic scenario. For instance, a criminal will not clean ammunition prior to loading it, and ejected casings will come into contact with a surface.

Non-handler alleles/polymorphisms were prevalent in cumulatively swabbed casings, although cumulatively swabbing did result in higher DNA yields and time savings. In this regard, individual swabbing each casing may be superior as a method of accurately identifying the person who loaded a firearm. This was especially true when analyzing mtDNA, since both strategies generated complete sequences (i.e., higher yields were not advantageous). However, when STRs were amplified, the decrease in the number of non-handler alleles produced from the individual swabbed casings was accompanied by a decrease in the number of handler alleles. Due to this trade-off between many handler and few non-handler alleles, cumulative swabbing could be more advantageous if STRs are to be analyzed from spent casings, particularly when working with smaller caliber (e.g., 0.22) casings, which did not frequently yield more than a few alleles when swabbed individually. Another trade-off of individual swabbing is the amount of time it takes. If a crime scene involves a large number of casings it may not be feasible to swab them all individually, even if that would generate less mixtures, as swabbing casings individually is time consuming.

Non-handler alleles were much more abundant in the STR profiles than in the mtDNA sequences, and many casings produced several non-handler alleles but no non-handler polymorphisms (keep in mind that buccal (known) mitochondrial haplotypes were generated, thus it could be determined if haplotypes were shared). It is thus likely that some of the non-handler STR alleles were actually artifacts such as drop-in and high stutter, rather than contaminant DNA, which are well known stochastic effects stemming from very low copy DNA analysis (e.g., Budowle et al., 2009). Another general observation in the current research was that

many non-handler STR alleles were in a stutter position, however classification of them as stutter was not possible owing to frequent peak height imbalance, which is also prevalent in low copy number samples (e.g., Gill et al., 2000).

Other factors that could have influenced the results of this study, besides the inherent variability in touch samples, include: 1) Variability in loading cartridges into magazines. Some volunteers had a great deal of experience working with firearms and quickly and effortlessly loaded cartridges, while others had never handled ammunition and expended more time and energy. For example, one volunteer took up to two minutes to load each cartridge. Also, volunteers typically found it easier to load 0.22 caliber cartridges than 0.40 and 0.45 caliber cartridges, and required less time and force to load them. 2) Shared magazines and firearms. Because the order that volunteers loaded magazines was recorded, it was possible to make at least a rough assessment of any transfer of DNA among handlers and spent casings via magazines or firearms. In general, no systematic contamination was discernable, although approximately a third of the non-handler alleles obtained could have originated from the preceding loader. The most extreme example was from one volunteer whose STR profile from a casing contained 20 non-handler alleles, 16 of which were consistent with the individual who had loaded the magazine immediately prior. On the other hand, there were also instances where prior loaders could be excluded.

CONCLUSIONS

Given the myriad factors that can come into play when analyzing DNA from spent cartridge casings, it is impossible to generate a single answer as to when, how, and how often desirable results will be obtained. However, the goal in this body of research was to thoroughly compare as large a number of these variables as practical, in order to determine which are most important, and in what way. Further, such variables were examined under ‘real world’ conditions, in that no special precautions were taken to place or remove DNA from cartridges, or otherwise create artificial conditions that would not be relevant to actual casework.

Overall, the results of this study demonstrate that significantly higher quantities of DNA are recovered from spent cartridge casings using the optimized double swab method and organic extraction than using an optimized soaking method or extracting DNAs with QIAamp or FDF Kits. Additionally, significantly more loader alleles are amplified using Fusion than MiniFiler, without substantially increasing the number of non-loader alleles. MtDNA analysis performed even better, producing genetic data for all samples, although it has well known drawbacks. All methods also generated some level of non-handler alleles/polymorphisms, so none is perfect. Cumulatively swabbing casings resulted in higher DNA yields and more handler alleles, although it also resulted in increased mixture levels compared to individually processing casings, thus this tradeoff needs to be considered.

Loading order was found to have no detectable influence on DNA profiling results, meaning that CSIs and lab personnel need not try to determine which casings were ejected in which order. On the other hand, cyanoacrylate treatment of spent casings did reduce DNA yields, and should be avoided if DNA testing is to be undertaken using current techniques. Taken together, the results of this research have the potential to provide strong investigative leads to

violent crimes by associating an individual to a shooting incident. This highly comprehensive study provides a foundation for crime laboratories that wish to utilize DNA analysis as a viable tool for investigating spent cartridge casings, increasing their probative value by aiding in identification of the loader of a firearm.

DRAFT

DISSEMINATION OF RESEARCH FINDINGS

Germain, Ray and Foran Comparison of DNA Analysis Methods for Typing Firearm Loaders Based on DNA from Spent Cartridge Casings. The Midwestern Association of Forensic Scientists Annual Meeting, Sept. 2015, Mackinac Island, MI

Ray, Mottar and Foran Examination of Factors That Affect the Recovery and Analysis of DNA From Spent Cartridge Casings. Poster The American Academy of Forensic Sciences Annual Meeting, Feb. 2015, Orlando, FL

Mottar, Ray and Foran Maximizing DNA Recovery and Short Tandem Repeat (STR) Data From Spent Cartridge Casings. The American Academy of Forensic Sciences Annual Meeting, Feb. 2015, Orlando, FL

Mottar and Foran Optimizing Techniques for DNA Recovery and Extraction from Spent Cartridge Casings. The American Academy of Forensic Sciences Annual Meeting, Feb. 2014, Seattle, WA

Metchikian, Orlando and Foran Mitochondrial DNA Recovery and Analysis From Spent Cartridge Casings. The American Academy of Forensic Sciences Annual Meeting, Feb. 2013, Washington, DC

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APPENDIX A. DNA QUANTITIES FROM SPENT CASINGS ASSAYED WITH OPTIMIZED CELL RECOVERY AND DNA EXTRACTION METHODS^{1, 2, 3, 4}

Table A1. DNA quantities recovered from spent cartridge casings using a double swab technique (Sweet *et al.*, 1997) and organic extraction.

Casing Identifier	DNA Concentration (pg/ μ L)	DNA Extract Volume (μ L)	DNA Yield (pg)
30.6	2.88E+01	25.40	731.52
34.4	1.77E+01	24.00	424.80
13-7B	1.61E+01	24.00	386.40
28.2	1.39E+01	27.80	386.42
19-2A	5.39E+00	24.20	130.44
23-2A	5.14E+00	25.60	131.58
1-1C	4.75E+00	26.00	123.50
21-1B	4.69E+00	27.00	126.63
23-2B	4.15E+00	24.00	99.60
41-4B	4.04E+00	29.30	118.37
13-7A	3.69E+00	25.20	92.99
50-5B	3.68E+00	25.50	93.84
43.3	3.46E+00	26.20	90.65
13-7C	2.93E+00	27.50	80.58
33-7B	2.65E+00	24.40	64.66
18-3A	2.51E+00	26.40	66.26
3-4A	2.42E+00	29.00	70.18
2-3A	2.21E+00	28.80	63.65
33-7A	2.16E+00	24.50	52.92
8-5C	1.97E+00	29.00	57.13
50-5A	1.94E+00	25.70	49.86

¹ The casings are organized based on DNA concentration arranged in descending order.

² Casings identifiers: decimal = collected individually. number hyphenated with another number & a letter = collected in triplicate (first number = loader; second number = casing set; letter = individual casing from set)

³ In Collection 1, casings loaded by RR & CC were collected in triplicate and individually due to a confusion in available supplies. As a result, Table B1 contains casings identified in both forms. The only difference between Collections 2 & 3 and triplicate casings from RR & CC is that in Collection 1 each volunteer loaded enough casings for each method to recover DNA from only one casing, rather than three.

⁴ In Collection 3, casing sets were incorrectly labeled resulting in 8 sets of “7-#”. There should have been 4 sets of “7-#” (loader P) and 4 sets of “18-#” (loader Z). Consequently, the sets were temporarily assigned to either P or Z. The volunteer’s profile that was most consistent with each casing was determined following STR analysis. In situations where minimal allelic information was available and a ‘correct’ association could not be made, then individual casings were given an identifier that could associate to either volunteer (*e.g.*, 7/18-1A.1).

Table A1 (cont'd).

Casing Identifier	DNA Concentration (pg/ μL)	DNA Extract Volume (μL)	DNA Yield (pg)
40-3B	1.83E+00	28.80	52.70
26-4B	1.78E+00	26.80	47.70
20-4B	1.75E+00	28.40	49.70
26-4A	1.70E+00	24.50	41.65
20-4A	1.70E+00	28.00	47.60
17-2A	1.68E+00	22.60	37.97
8-5B	1.66E+00	25.00	41.50
38-2B	1.55E+00	27.20	42.16
48.5	1.49E+00	22.40	33.38
20-4C	1.48E+00	27.40	40.55
27-5B	1.39E+00	18.80	26.13
23-2C	1.38E+00	25.20	34.78
26-4C	1.38E+00	27.00	37.26
27-5A	1.38E+00	21.20	29.26
27-5C	1.31E+00	24.50	32.10
17-2B	1.28E+00	26.00	33.28
1-1A	1.26E+00	25.80	32.51
33-7C	1.19E+00	25.60	30.46
18-3B	1.11E+00	26.00	28.86
21-1A	1.01E+00	27.20	27.47
36-1A	9.91E-01	22.20	22.00
19.2	9.89E-01	25.90	25.62
38-2A	9.87E-01	26.20	25.86
50-5C	9.58E-01	27.40	26.25
8-5A	9.57E-01	27.00	25.84
36-1C	8.94E-01	28.00	25.03
6-2A	8.87E-01	27.20	24.13
17-2C	8.61E-01	24.20	20.84
2-3C	8.25E-01	26.00	21.45
1-1B	8.04E-01	30.00	24.12
38-2C	7.87E-01	26.00	20.46
41-4C	7.36E-01	25.50	18.77
21-1C	7.36E-01	27.00	19.87
11-4C	6.89E-01	27.40	18.88
40-3A	6.83E-01	27.00	18.44
36-1B	5.80E-01	25.00	14.50
12-1A	5.47E-01	23.70	12.96
41-4A	5.42E-01	24.00	13.01

Table A1 (cont'd).

Casing Identifier	DNA Concentration (pg/ μL)	DNA Extract Volume (μL)	DNA Yield (pg)
3-4B	5.35E-01	26.00	13.91
11-4A	5.20E-01	27.30	14.20
2-3B	5.19E-01	33.00	17.13
12-1C	5.18E-01	25.00	12.95
25-3C	4.79E-01	24.00	11.50
37-1A	4.75E-01	25.20	11.97
24-6B	4.73E-01	27.00	12.77
18-3C	4.63E-01	23.30	10.79
11-4B	4.48E-01	26.00	11.65
15-1C	3.81E-01	27.60	10.52
6-2C	3.70E-01	26.50	9.81
15-1B	3.67E-01	30.80	11.30
25-3B	3.54E-01	24.80	8.78
40-3C	3.53E-01	27.20	9.60
3-4C	3.40E-01	24.00	8.16
35-2B	3.18E-01	26.60	8.46
10-6B	3.14E-01	27.80	8.73
24-6C	3.06E-01	27.40	8.38
12-1B	3.04E-01	23.60	7.17
25-3A	2.95E-01	26.80	7.91
6-2B	2.79E-01	27.00	7.53
10-6A	2.59E-01	26.20	6.79
35-2A	2.57E-01	27.30	7.02
7-3A	2.46E-01	28.00	6.89
10-6C	2.28E-01	28.40	6.48
7-3B	1.89E-01	28.40	5.37
15-1A	1.74E-01	25.20	4.38
24-6A	1.24E-01	26.80	3.32
37.1	1.06E-01	24.40	2.59
7-3C	5.61E-02	28.00	1.57
35-2C	4.07E-02	25.00	1.02

Table A2. DNA quantities recovered from spent cartridge casings using a soaking technique and organic extraction.

Casing Identifier	DNA Concentration (pg/ μL)	DNA Extract Volume (μL)	DNA Yield (pg)
34.3	5.05E+01	28.20	1424.10
30.5	1.71E+01	27.60	471.96
13-1A	1.36E+01	26.00	353.60
23-3C	5.92E+00	26.60	157.47
28.1	4.75E+00	27.80	132.05
8-6A	4.63E+00	24.00	111.12
13-1B	4.60E+00	25.00	115.00
8-6B	3.82E+00	25.00	95.50
13-1C	3.60E+00	25.80	92.88
23-3A	3.56E+00	25.60	91.14
19-1A	2.82E+00	27.50	77.55
50-6A	2.72E+00	24.60	66.91
23-3B	2.71E+00	24.00	65.04
41-5A	2.16E+00	23.00	49.68
38-3C	2.16E+00	25.60	55.30
8-6C	2.06E+00	25.60	52.74
50-6C	1.90E+00	26.00	49.40
21-2B	1.74E+00	28.40	49.42
38-3B	1.55E+00	23.20	35.96
38-3A	1.49E+00	24.80	36.95
26-5C	1.41E+00	28.00	39.48
50-6B	1.39E+00	27.00	37.53
26-5A	1.35E+00	20.20	27.27
20-1A	1.33E+00	28.00	37.24
27-6A	1.32E+00	27.60	36.43
33-1C	1.30E+00	24.40	31.72
41-5C	1.30E+00	24.80	32.24
17-3C	1.26E+00	28.30	35.66
21-2A	1.22E+00	28.50	34.77
37-2A	1.20E+00	26.40	31.68
27-6B	1.20E+00	28.00	33.60
17-3B	1.20E+00	30.00	36.00
27-6C	1.16E+00	23.00	26.68
43.1	1.14E+00	20.60	23.48
26-5B	1.11E+00	24.30	26.97
25-4C	1.02E+00	25.20	25.70
2-4C	9.15E-01	25.20	23.06
33-1B	8.86E-01	25.20	22.33

Table A2 (cont'd).

Casing Identifier	DNA Concentration (pg/ µL)	DNA Extract Volume (µL)	DNA Yield (pg)
33-1A	8.79E-01	24.20	21.27
41-5B	8.61E-01	22.80	19.63
3-5B	7.88E-01	25.00	19.70
20-1B	7.79E-01	28.20	21.97
11-1C	6.91E-01	30.20	20.87
48.4	6.71E-01	31.00	20.80
2-4B	6.13E-01	24.50	15.02
19.1	5.95E-01	25.00	14.88
2-4A	5.52E-01	24.60	13.58
10-7A	4.96E-01	24.00	11.90
21-2C	4.76E-01	27.80	13.23
37.6	4.67E-01	29.20	13.64
36-2A	4.65E-01	24.00	11.16
36-2B	4.22E-01	26.00	10.97
20-1C	4.06E-01	28.00	11.37
25-4A	3.95E-01	26.20	10.35
18-4C	3.88E-01	28.00	10.86
12-2C	3.69E-01	27.50	10.15
3-5A	3.67E-01	26.80	9.84
40-4C	3.27E-01	23.20	7.59
1-2C	2.94E-01	31.70	9.32
12-2B	2.88E-01	28.20	8.12
40-4A	2.76E-01	25.20	6.96
10-7B	2.75E-01	25.70	7.07
25-4B	2.72E-01	25.00	6.80
36-2C	2.70E-01	24.70	6.67
15-2C	2.59E-01	22.00	5.70
24-7C	2.54E-01	24.00	6.10
6-3C	2.46E-01	26.60	6.54
18-4A	2.40E-01	31.30	7.51
3-5C	2.38E-01	25.00	5.95
1-2B	2.35E-01	27.40	6.44
24-7A	2.22E-01	26.40	5.86
1-2A	2.09E-01	29.80	6.23
7-4A	2.00E-01	31.20	6.24
10-7C	1.93E-01	30.00	5.79
12-2A	1.91E-01	27.90	5.33
17-3A	1.75E-01	29.00	5.08

Table A2 (cont'd).

Casing Identifier	DNA Concentration (pg/ μL)	DNA Extract Volume (μL)	DNA Yield (pg)
35-3A	1.62E-01	28.20	4.57
15-2B	1.36E-01	25.50	3.47
40-4B	1.23E-01	26.00	3.20
18-4B	1.15E-01	29.20	3.36
11-1A	1.07E-01	28.00	3.00
6-3B	9.43E-02	29.80	2.81
11-1B	9.01E-02	31.20	2.81
15-2A	8.22E-02	22.60	1.86
24-7B	6.91E-02	28.60	1.98
7-4C	5.42E-02	28.50	1.54
35-3B	3.95E-02	29.00	1.15
6-3A	2.94E-02	28.20	0.83
7-4B	2.03E-02	27.50	0.56
35-3C	1.99E-02	28.30	0.56

Table A3. DNA quantities recovered from spent cartridge casings using a double swab technique (Sweet *et al.*, 1997) and QIAamp® DNA Investigator extraction.

Casing Identifier	DNA Concentration (pg/ µL)	DNA Extract Volume (µL)	DNA Yield (pg)
13-2B	1.25E+00	57.00	71.25
34.6	1.17E+00	58.90	68.91
21-3B	9.04E-01	58.40	52.79
21-3A	4.79E-01	59.00	28.26
28.4	4.71E-01	58.80	27.69
12-3A	3.92E-01	58.50	22.93
20-2B	3.89E-01	56.80	22.10
13-2A	3.58E-01	57.70	20.66
23-4C	3.16E-01	59.80	18.90
17-4A	3.00E-01	58.40	17.52
38-4B	2.84E-01	57.50	16.33
2-5B	2.80E-01	57.60	16.13
17-4C	2.57E-01	57.20	14.70
21-3C	2.50E-01	56.70	14.18
8-7A	2.29E-01	57.40	13.14
38-4A	2.15E-01	56.80	12.21
23-4A	2.14E-01	58.80	12.58
26-6A	2.00E-01	59.00	11.80
23-4B	1.90E-01	57.20	10.87
8-7B	1.83E-01	58.20	10.65
41-6B	1.82E-01	58.40	10.63
13-2C	1.77E-01	57.70	10.21
48.1	1.65E-01	57.40	9.47
33-2C	1.49E-01	56.60	8.43
11-2A	1.41E-01	56.30	7.94
37-1B	1.38E-01	59.00	8.14
20-2A	1.36E-01	57.20	7.78
30.2	1.27E-01	58.20	7.39
6-4C	1.27E-01	59.20	7.52
20-2C	1.23E-01	58.40	7.18
2-5C	1.08E-01	57.20	6.18
2-5A	1.05E-01	57.60	6.05
26-6C	1.04E-01	57.80	6.01
7/18-1B.1	1.01E-01	57.40	5.80
41-6A	9.60E-02	57.70	5.54
1-3A	9.47E-02	60.00	5.68
7/18-1C.1	9.43E-02	58.00	5.47

Table A3 (cont'd).

Casing Identifier	DNA Concentration (pg/ μ L)	DNA Extract Volume (μ L)	DNA Yield (pg)
38-4C	9.31E-02	57.30	5.33
7/18-1A.2	9.18E-02	57.80	5.31
8-7C	8.74E-02	58.60	5.12
1-3C	8.69E-02	57.80	5.02
27-7C	7.50E-02	56.20	4.22
1-3B	7.28E-02	60.00	4.37
17-4B	6.70E-02	58.20	3.90
33-2B	6.69E-02	55.70	3.73
26-6B	6.55E-02	59.70	3.91
25-5C	6.23E-02	59.00	3.68
11-2C	5.97E-02	57.00	3.40
12-3B	5.79E-02	56.80	3.29
27-7B	5.66E-02	58.80	3.33
12-3C	5.54E-02	59.20	3.28
7/18-1A.1	5.51E-02	59.00	3.25
50-7B	5.45E-02	58.00	3.16
3-6C	5.33E-02	58.20	3.10
50-7C	5.04E-02	58.50	2.95
11-2B	4.91E-02	57.30	2.81
41-6C	4.74E-02	59.20	2.81
50-7A	4.42E-02	56.90	2.51
36-3B	4.26E-02	58.60	2.50
25-5B	3.99E-02	57.30	2.29
6-4A	3.86E-02	59.50	2.30
19-2B	3.79E-02	57.80	2.19
15-3B	3.32E-02	56.20	1.87
6-4B	3.22E-02	57.00	1.84
27-7A	3.20E-02	57.20	1.83
25-5A	3.14E-02	58.20	1.83
37.3	2.67E-02	58.40	1.56
7/18-1B.2	2.64E-02	57.00	1.50
33-2A	2.59E-02	57.00	1.48
10-1B	2.56E-02	58.20	1.49
3-6B	1.90E-02	58.00	1.10
19.4	1.84E-02	55.00	1.01
40-5B	1.77E-02	57.60	1.02
7/18-1C.2	1.70E-02	57.20	0.97
36-3A	1.68E-02	57.70	0.97

Table A3 (cont'd).

Casing Identifier	DNA Concentration (pg/ μL)	DNA Extract Volume (μL)	DNA Yield (pg)
3-6A	1.63E-02	58.00	0.95
40-5A	1.50E-02	57.60	0.86
15-3A	1.36E-02	56.20	0.76
40-5C	1.36E-02	59.00	0.80
36-3C	1.03E-02	56.80	0.59
24-1B	9.96E-03	56.00	0.56
10-1C	9.24E-03	57.30	0.53
15-3C	9.23E-03	56.20	0.52
35-4A	8.60E-03	57.50	0.49
24-1C	5.73E-03	57.40	0.33
10-1A	4.36E-03	58.00	0.25
35-4C	3.70E-03	58.40	0.22
35-4B	2.86E-03	56.40	0.16
43.5	1.52E-03	57.80	0.09
24-1A	0.00E+00	57.20	0.00

Table A4. DNA quantities recovered from spent cartridge casings using a soaking technique and QIAamp® DNA Investigator extraction.

Casing Identifier	DNA Concentration (pg/ µL)	DNA Extract Volume (µL)	DNA Yield (pg)
3-7C	8.85E+00	57.00	504.45
13-3A	3.46E+00	58.00	200.68
23-5C	1.11E+00	59.30	65.82
27-1B	7.00E-01	58.00	40.60
23-5B	6.87E-01	60.60	41.63
23-5A	6.49E-01	57.20	37.12
26-7B	5.45E-01	57.40	31.28
26-7A	4.71E-01	58.20	27.41
25-6A	4.00E-01	58.30	23.32
21-4A	3.74E-01	56.60	21.17
27-1C	2.92E-01	57.00	16.64
30.1	2.28E-01	59.60	13.59
36-4B	1.70E-01	59.00	10.03
13-3C	1.63E-01	58.00	9.45
34.5	1.59E-01	59.20	9.41
12-4B	1.49E-01	58.00	8.64
36-4C	1.28E-01	57.20	7.32
8-1B	1.22E-01	60.00	7.32
7/18-2C.1	1.06E-01	56.90	6.03
33-3C	1.04E-01	59.00	6.14
11-3C	9.93E-02	58.40	5.80
38-5A	6.43E-02	59.00	3.79
11-3A	6.07E-02	56.00	3.40
26-7C	5.38E-02	57.40	3.09
10-2A	5.31E-02	59.40	3.15
17-1C	5.23E-02	57.40	3.00
8-1C	5.18E-02	57.80	2.99
33-3B	5.11E-02	57.60	2.94
25-6C	5.09E-02	57.50	2.93
25-6B	5.08E-02	59.20	3.01
37-2B	4.81E-02	59.00	2.84
41-7C	4.76E-02	58.40	2.78
50-1C	4.40E-02	59.80	2.63
17-1A	4.05E-02	56.40	2.28
6-1A	4.01E-02	57.20	2.29
7/18-2B.1	3.95E-02	59.60	2.35
40-6B	3.38E-02	60.20	2.03
50-1A	3.00E-02	58.70	1.76

Table A4 (cont'd).

Casing Identifier	DNA Concentration (pg/ µL)	DNA Extract Volume (µL)	DNA Yield (pg)
33-3A	2.97E-02	58.80	1.75
2-6B	2.64E-02	57.70	1.52
17-1B	2.56E-02	57.00	1.46
27-1A	2.54E-02	57.80	1.47
10-2C	2.28E-02	57.00	1.30
15-4C	2.22E-02	57.50	1.28
13-3B	2.03E-02	59.00	1.20
10-2B	1.95E-02	59.90	1.17
38-5B	1.85E-02	58.50	1.08
28.3	1.58E-02	59.20	0.94
19.3	1.47E-02	59.50	0.87
3-7A	1.46E-02	59.00	0.86
2-6C	1.37E-02	60.20	0.82
11-3B	1.35E-02	55.20	0.75
2-6A	1.32E-02	57.40	0.76
40-6A	1.22E-02	59.60	0.73
3-7B	1.13E-02	57.80	0.65
8-1A	1.11E-02	58.60	0.65
41-7B	1.11E-02	59.40	0.66
36-4A	1.07E-02	60.00	0.64
43.4	1.05E-02	58.00	0.61
1-4B	9.85E-03	57.00	0.56
6-1B	8.69E-03	58.00	0.50
20-3C	8.36E-03	56.50	0.47
12-4A	8.16E-03	56.50	0.46
50-1B	7.89E-03	59.60	0.47
19-1B	7.17E-03	60.40	0.43
41-7A	6.64E-03	58.40	0.39
6-1C	6.46E-03	57.80	0.37
24-2C	6.41E-03	57.00	0.37
15-4B	6.30E-03	59.90	0.38
38-5C	6.15E-03	58.20	0.36
40-6C	6.03E-03	59.20	0.36
24-2A	5.81E-03	59.50	0.35
48.6	5.76E-03	58.50	0.34
7/18-2A.1	5.43E-03	58.00	0.31
37.2	5.04E-03	59.00	0.30
20-3B	4.92E-03	56.60	0.28

Table A4 (cont'd).

Casing Identifier	DNA Concentration (pg/ μL)	DNA Extract Volume (μL)	DNA Yield (pg)
20-3B	4.92E-03	56.60	0.28
35-1A	4.19E-03	57.60	0.24
15-4A	3.78E-03	56.80	0.21
1-4C	3.59E-03	57.20	0.21
24-2B	3.28E-03	58.50	0.19
21-4C	2.77E-03	56.20	0.16
1-4A	2.31E-03	56.20	0.13
35-1C	1.71E-03	56.40	0.10
7/18-2C.2	1.66E-03	56.40	0.09
12-4C	1.36E-03	58.80	0.08
7/18-2A.2	1.12E-03	59.40	0.07
35-1B	7.62E-04	57.20	0.04
20-3A	6.58E-04	56.80	0.04
21-4B	1.90E-04	56.00	0.01
7/18-2B.2	1.89E-04	56.20	0.01

Table A5. DNA quantities recovered from spent cartridge casings using a single swab technique and FDF[®] extraction.

Casing Identifier	DNA Concentration (pg/ µL)	DNA Extract Volume (µL)	DNA Yield (pg)
34.1	2.82E-01	75.00	21.15
30.3	5.14E-02	74.80	3.84
8-2A	1.65E-02	69.50	1.15
48.2	1.18E-02	67.80	0.80
37.4	1.10E-02	73.60	0.81
33-4B	1.07E-02	71.00	0.76
19-1C	9.48E-03	71.40	0.68
37-2C	9.29E-03	75.00	0.70
28.5	8.93E-03	68.60	0.61
27-2B	7.81E-03	68.40	0.53
19.5	7.30E-03	72.20	0.53
25-7C	7.19E-03	66.80	0.48
24-3B	7.19E-03	66.80	0.48
43.6	7.18E-03	68.60	0.49
50-2C	5.82E-03	70.90	0.41
26-1B	5.77E-03	70.50	0.41
27-2C	4.92E-03	69.00	0.34
50-2A	4.89E-03	69.80	0.34
3-1B	3.97E-03	71.00	0.28
50-2B	3.93E-03	72.20	0.28
27-2A	3.71E-03	65.40	0.24
8-2B	3.67E-03	70.30	0.26
2-7A	3.61E-03	63.60	0.23
13-4A	3.50E-03	74.20	0.26
41-1B	3.24E-03	68.40	0.22
25-7A	3.14E-03	70.80	0.22
26-1C	3.13E-03	69.90	0.22
41-1C	3.10E-03	69.50	0.22
26-1A	3.04E-03	70.40	0.21
23-6B	3.00E-03	67.50	0.20
3-1C	2.88E-03	69.40	0.20
8-2C	2.78E-03	68.20	0.19
38-6B	2.17E-03	66.60	0.14
23-6A	2.08E-03	68.20	0.14
33-4C	2.03E-03	68.00	0.14
15-5B	1.99E-03	67.20	0.13
10-3C	1.98E-03	72.00	0.14
15-5C	1.95E-03	75.50	0.15

Table A5 (cont'd).

Casing Identifier	DNA Concentration (pg/ μL)	DNA Extract Volume (μL)	DNA Yield (pg)
38-6C	1.84E-03	70.20	0.13
2-7C	1.71E-03	67.70	0.12
23-6C	1.69E-03	73.20	0.12
24-3A	1.68E-03	70.20	0.12
3-1A	1.54E-03	65.80	0.10
25-7B	1.53E-03	74.20	0.11
2-7B	1.51E-03	68.00	0.10
40-7A	1.29E-03	63.70	0.08
10-3A	1.28E-03	69.80	0.09
40-7C	1.10E-03	71.00	0.08
36-5C	9.65E-04	62.80	0.06
24-3C	8.56E-04	71.40	0.06
36-5B	7.38E-04	71.50	0.05
40-7B	7.08E-04	70.50	0.05
13-4B	6.15E-04	71.80	0.04
15-5A	5.98E-04	69.80	0.04
33-4A	5.84E-04	72.00	0.04
13-4C	5.16E-04	73.00	0.04
38-6A	4.95E-04	71.00	0.04
41-1A	4.09E-04	65.80	0.03
36-5A	1.29E-04	64.00	0.01
10-3B	2.47E-06	71.40	0.00

APPENDIX B. COMPARISON OF AMF_{STR}[®] MINIFILER[™] STR PROFILES AND POWERPLEX[®] FUSION STR PROFILES

Red font = non-loader allele

Italicized font = allele is consistent with the loader but could have originated from the previous loader

** = non-loader allele could have originated from the previous loader*

† = off-ladder allele (the number of † symbols represents the number of off-ladder alleles)

N/A = not applicable

NT = locus was not tested (several loci examined with PowerPlex[®] Fusion are not included in MiniFiler[™])

Blank = no alleles recovered at that locus

Table B1. Alleles amplified with AmpF_{STR}[®] MiniFiler[™] and PowerPlex[®] Fusion from spent cartridge casings loaded by volunteer CC during Collection 1.

Locus	Mini 19-1A	Fusion 19-1A	Mini 19-1C	Fusion 19-1C	Mini 19-2A	Fusion 19-2A	CC
Amel	X	X,Y*			X,Y*	X	X
D3	NT		NT		NT	15	14,15
D1	NT	12	NT		NT	11,17.3	11,17.3
D2S441	NT	14	NT		NT	10,14	10,14
D10	NT	13,14,15	NT		NT	16	14,16
D13	13	13			11,12,13	13	13
Penta E	NT		NT		NT	12,13	12,13
D16	9,10,11	11,12			11,12	11,12	11,12
D18	12,14	12,13			12,13,17*	12,16	12
D2S1338	17,21	17			17	17	17
CSF	12	11			†,12	11,12	11,12
Penta D	NT	13	NT		NT		9,12
THO1	NT	6*,7,8,9.3	NT		NT	7,9.3	7,9.3
vWA	NT	18	NT		NT	16,17	17
D21	28,32.2	32.2			32.2	27,28,32.2	28,32.2
D7	8,12	12			9,12	9,12	9,12
D5	NT	13*	NT		NT	9,12	9,12
TPOX	NT		NT		NT	8	8,11
DYS391	NT		NT		NT		N/A
D8	NT	12,13	NT		NT	12,13,15	12,13
D12	NT		NT		NT	17,24	17,24
D19	NT	14.2,15	NT		NT	14.2,15.2	14.2,15.2
FGA	24*	22.2			23,25		23,25
D22	NT		NT		NT	16	16

Table B2. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer Q during Collection 1.

Locus	Mini 28.1	Fusion 28.1	Mini 28.2	Fusion 28.2	Mini 28.4	Fusion 28.4	Mini 28.5	Fusion 28.5	Q
Amel	X,Y	Y	X,Y	X,Y					X,Y
D3	NT	17	NT	15,16,17	NT	17	NT		15,17
D1	NT		NT	12,16.3	NT		NT		12,16.3
D2S441	NT		NT	11	NT		NT		11
D10	NT		NT	13,15	NT		NT		13,15
D13	11,13		11,13	11					11,13
Penta E	NT	13	NT	7,11	NT		NT		7,11
D16	9,11,13*	11	11	11		11			11
D18	13,15*	13,14	13,14	13,14					13,14
D2S1338	19,23,24		23,24	18,23,24	24				23,24
CSF	10,11		10,11,†	10,11	10				10,11
Penta D	NT		NT	10	NT		NT		2.2,10
THO1	NT	7*,8,9	NT	8,9	NT		NT		8,9
vWA	NT	16	NT	16,18	NT	16	NT		16,18
D21	29*,30		30,32.2	30		32.2			30,32.2
D7	8,11		8,11	8,11					8,11
D5	NT		NT	13	NT		NT		13
TPOX	NT		NT	8	NT		NT		8
DYS391	NT		NT	10	NT		NT		10
D8	NT	13,17	NT	13,17	NT	17	NT		13,17
D12	NT	18	NT	18	NT		NT		18
D19	NT		NT	13,15	NT	15	NT		13,15
FGA	22,24		22,24	24		16,16.1,18			22,24
D22	NT		NT		NT		NT		11,12

Table B3. Alleles amplified with AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$ and PowerPlex $^{\text{®}}$ Fusion from spent cartridge casings loaded by volunteer LL during Collection 1.

Locus	Mini 30.1	Fusion 30.1	Mini 30.2	Fusion 30.2	Mini 30.5	Fusion 30.5	Mini 30.6	Fusion 30.6	LL
Amel					X	X	X	X	X
D3	NT	15	NT	15	NT	15	NT	15	15
D1	NT		NT		NT	17,18.3	NT	17,18.3	17,18.3
D2S441	NT	14	NT		NT	11.3,14	NT	11.3,14	11.3,14
D10	NT		NT		NT	13,15	NT	13,15	13,15
D13	12				12	12	12	12	12
Penta E	NT		NT		NT	14,17	NT	14,17	14,17
D16	11	†			11,13	11,13	11,13	11,13	11,13
D18					14,15	14,15	14,15,16,17*	14,15	14,15
D2S1338	20				17,18,19*,20,26	17,20	17,18,20,23*,26	17,20	17,20
CSF	12				11,12	11,12	11,12	11,12	11,12
Penta D	NT		NT		NT	9	NT	9	9
THO1	NT		NT	7	NT	7	NT	7	7
vWA	NT	16	NT		NT	16,17	NT	16,17	16,17
D21					29,31.2	29,31.2	29,30*,31.2	29,31.2	29,31.2
D7					8	8	8	8	8
D5	NT		NT		NT	10,12	NT	10,12	10,12
TPOX	NT		NT		NT	8	NT	8	8
DYS391	NT		NT		NT		NT	10	N/A
D8	NT	13	NT		NT	13,14,20	NT	13,14	13,14
D12	NT		NT		NT	18,25	NT	18,25	18,25
D19	NT		NT		NT	13,14	NT	13,14	13,14
FGA	20,30.2,†	23			19,23,25	19,23	19,23	19,23,†	19,23
D22	NT		NT	†	NT	†,15	NT	15	15

Table B4. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer YY during Collection 1.

Locus	Mini 34.1	Fusion 34.1	Mini 34.3	Fusion 34.3	Mini 34.4	Fusion 34.4	Mini 34.5	Fusion 34.5	Mini 34.6	Fusion 34.6	YY
Amel			X,Y	X,Y	X,Y	X,Y				X,Y	X,Y
D3	NT	15	NT	15	NT	15	NT		NT	15	15
D1	NT	15	NT	15,16	NT	15,16	NT		NT	15,16	15,16
D2S441	NT		NT	10,14	NT	10,14	NT	13,14	NT		10,14
D10	NT		NT	14,16	NT	14,16	NT		NT	14	14,16
D13	14		9,14	9,14	9,11,14	9,14			9,14		9,14
Penta E	NT		NT	12,13	NT	12,13	NT		NT	12,13	12,13
D16	12	12	12	12	12	12			12	11,12	12
D18			12,17	12,17	12,17	12,17			12,17	12,17	12,17
D2S1338			18,23	18,23	18,23	18,23	23		23	18	18,23
CSF	11		11,12	11,12	11,12	11,12	11		11,12		11,12
Penta D	NT		NT	9,14	NT	9,14	NT		NT		9
THO1	NT	9.3	NT	6,9.3	NT	6,9.3	NT	6	NT	6,9.3	6,9.3
vWA	NT		NT	19	NT	19	NT		NT	19	19
D21			29,30	29,30	29,30	29,30	29		28,29,30	29	29,30
D7			9	9	9	9	9		9	9	9
D5	NT		NT	12,13	NT	12,13	NT		NT		12,13
TPOX	NT		NT	8,11	NT	8,11	NT		NT	11	8,11
DYS391	NT		NT	11	NT	11	NT		NT	11	11
D8	NT	13	NT	13	NT	13	NT	13	NT	13	13
D12	NT		NT	19	NT	19	NT	19	NT	19	19
D19	NT		NT	13	NT	13	NT		NT	13	13
FGA		†,21	21,24	21,24	21,24,25	21,24	†		24	21,23,2,24	21,24
D22	NT	†	NT	15	NT	15	NT		NT	15	15

Table B5. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer RR during Collection 1.

Locus	Mini 37-2A	Fusion 37-2A	Mini 37-2B	Fusion 37-2B	RR
Amel		<i>X</i>			X,Y
D3	NT	16	NT		16,17
D1	NT	16.3	NT		14,16.3
D2S441	NT	11	NT		11,16
D10	NT		NT		13,15
D13	14				8,14
Penta E	NT		NT		7,18
D16	9,11,12	9,12			11,12
D18	12*,16,17	15,16,17			16,17
D2S1338	20	18			20,25
CSF		10			10,13
Penta D	NT		NT		9,12
THO1	NT	7,9.3*	NT		6,7
vWA	NT	15,19	NT		15,18
D21	30				30
D7	12		10		10,12
D5	NT	12	NT		12,13
TPOX	NT		NT		8
DYS391	NT		NT		11
D8	NT	13*	NT	13*	11,15
D12	NT	22	NT		18,22
D19	NT	14.2*	NT		13,15
FGA	20				20,24
D22	NT		NT		15

Table B6. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer U during Collection 2.

Locus	Mini 2-3A	Fusion 2-3A	Mini 2-5B	Fusion 2-5B	U
Amel	X	X			X
D3	NT	15	NT		15
D1	NT	11,17.3	NT		11,17.3
D2S441	NT	10,15	NT		10,15
D10	NT	12	NT		12,14
D13	9				9,13
Penta E	NT		NT		12,15
D16	11	11,13			11,13
D18	14,15	13*,14,15	15		14,15
D2S1338	17,25	25			17,25
CSF	12	12	13		10,12
Penta D	NT	10	NT		10,11
THO1	NT	6,7	NT		6,7
vWA	NT	14	NT		14,20
D21	28,30	28,30,31			28,30
D7	11				11
D5	NT	11	NT		11
TPOX	NT	8,11	NT		8,11
DYS391	NT		NT		N/A
D8	NT	12	NT		12
D12	NT	23	NT	20	17,23
D19	NT	13	NT		13
FGA	24,†,†,†	17.2,24,25	†	46.2	24,25
D22	NT	16	NT		16

Table B7. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer MM during Collection 2.

Locus	Mini 3-4A	Fusion 3-4A	Mini 3-7C	Fusion 3-7C	MM
Amel		Y*	X	X	X
D3	NT	18*	NT	15	14,16
D1	NT		NT	12,15.3	12,16
D2S441	NT		NT	14*	10,11
D10	NT		NT	13*	14,15
D13			11	11	8,12
Penta E	NT		NT	11,12	7,21
D16		12	11,13*	11,13*	12
D18			16,18	16,18	14,14.2
D2S1338			17,19	17,19	17,23
CSF	†		11,12	11,12	12,13
Penta D	NT		NT	10,12*	13
THO1	NT		NT	9.3	9,9.3
vWA	NT		NT	16,17	17
D21			29,32.2	29,32.2	29,31.2
D7			8,12*	8,12*	9,11
D5	NT		NT	10,12	9,10
TPOX	NT		NT	8	8
DYS391	NT		NT		N/A
D8	NT		NT	11,13	13,15
D12	NT	22	NT	13,18,22	18,22
D19	NT		NT	14,15*	14,15.2
FGA	47.2,†,†,†	17.2	22,22.2,24	22.2,24	22,26
D22	NT		NT	16*,17	11,12

Table B8. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer S during Collection 2.

Locus	Mini 8-2A	Fusion 8-2A	Mini 8-6A	Fusion 8-6A	Mini 8-6B	Fusion 8-6B	S
Amel			X	X	X	X	X
D3	NT		NT	18	NT		18
D1	NT		NT	12,15	NT	12,15	12,15
D2S441	NT		NT	11,11.3	NT	11.3	11,11.3
D10	NT		NT	15	NT	15	13,15
D13			12,13		13	12	12,13
Penta E	NT		NT	13	NT	12	12,13
D16			11	11	11	11	11
D18			12,16	12,16	12,16	12	12,16
D2S1338	20		17,19,25	17	17,23*,25	17,25	17,25
CSF	14,†,†		10,†,10.2,11	10	10,11,12*	10,11	10,11
Penta D	NT		NT	10,13	NT		10,13
THO1	NT		NT	6,9	NT	6,9	6,9
vWA	NT		NT	17,18	NT	16,17,18	17,18
D21			28	28	28	28,31	28
D7	9*		10	10		10	10
D5	NT		NT	10,12	NT	12	10,12
TPOX	NT		NT		NT		8,11
DYS391	NT		NT		NT		N/A
D8	NT		NT	13,16	NT	13,16	13,16
D12	NT		NT	18,18.3	NT	18,18.3	18,18.3
D19	NT		NT	15	NT	15	13.2,15
FGA	29.2,†	†	22,23,†	†	22,†,†,†	22,23	22,23
D22	NT		NT	15	NT	15	15

Table B8 (cont'd).

Locus	Mini 8-7A	Fusion 8-7A	Mini 8-7B	Fusion 8-7B	S
Amel					X
D3	NT	18	NT		18
D1	NT		NT		12,15
D2S441	NT		NT		11,11.3
D10	NT		NT		13,15
D13				<i>12</i>	12,13
Penta E	NT		NT		12,13
D16					11
D18		12			12,16
D2S1338		<i>17</i>			17,25
CSF	†		†,†,†		10,11
Penta D	NT		NT		10,13
THO1	NT	6,9	NT		6,9
vWA	NT	<i>17</i>	NT		17,18
D21					28
D7					10
D5	NT		NT		10,12
TPOX	NT		NT		8,11
DYS391	NT		NT		N/A
D8	NT	†	NT		13,16
D12	NT		NT		18,18.3
D19	NT	†	NT	†	13.2,15
FGA	23, 32.2 ,†,†	†	20,28,48.2 ,†,†,†,†,†,†	†	22,23
D22	NT		NT	20	15

Table B9. Alleles amplified with AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$ and PowerPlex $^{\text{®}}$ Fusion from spent cartridge casings loaded by volunteer V during Collection 2.

Locus	Mini 13-1A	Fusion 13-1A	Mini 13-1B	Fusion 13-1B	Mini 13-1C	Fusion 13-1C	V
Amel	X,Y	X,Y	X,Y	X,Y		X,Y	X,Y
D3	NT	14	NT	14	NT	14	14
D1	NT	17.3	NT	16.3,17.3	NT	16.3	16.3,17.3
D2S441	NT	11,11.3	NT		NT	11	11,11.3
D10	NT	15,16	NT	15	NT	15,16	15,16
D13	10,12	10,12	10,12		10,12	10	10,12
Penta E	NT	5,14	NT		NT	5,14	5,14
D16	11,12	11,12	11,12	11,12		12	11,12
D18	16,17	16,17	16	17	13,16,17	13,16	16,17
D2S1338	20,22	20,22	20,22		20,22	20,22	20,22
CSF	10,11	11	10,11		10,†	10	10,11
Penta D	NT	11,12	NT		NT	11	11,12
THO1	NT	9,9.3	NT	9,9.3	NT	6*,9,9.3	9,9.3
vWA	NT	16,18	NT	16	NT	16,18	16,18
D21	28,32.2	28,32.2	28		28,29	28,29	28,32.2
D7	11,12	12			11,12	11	11,12
D5	NT	12	NT	12	NT	12	12
TPOX	NT	8	NT	8	NT	8	8
DYS391	NT	11	NT		NT		11
D8	NT	9,12	NT	9	NT	9,12,13*,†	9,12
D12	NT	21,23	NT	21,23	NT	21,23	21,23
D19	NT	12,14	NT	11,12,14	NT	14	12,14
FGA	21.2,22,†,†	21.2,22	21.2	†	22,†,†,†,†	22	21.2,22
D22	NT	11,16	NT		NT		11,16

Table B9 (cont'd).

Locus	Mini 13-2A	Fusion 13-2A	Mini 13-2B	Fusion 13-2B	Mini 13-3A	Fusion 13-3A	V
Amel	X			X,Y	X,Y	X,Y	X,Y
D3	NT		NT		NT	14	14
D1	NT		NT		NT	16.3,17.3	16.3,17.3
D2S441	NT	11	NT	11,11.3	NT		11,11.3
D10	NT		NT	15,16	NT	16	15,16
D13					10,12		10,12
Penta E	NT		NT		NT		5,14
D16			11	11,12	11,12	11,12	11,12
D18			17	17	16,17	16,17	16,17
D2S1338		22	20		20,22	20,22	20,22
CSF	9,†		16,†,†		10,11	11	10,11
Penta D	NT	12	NT	12	NT	12	11,12
THO1	NT	3,9	NT	9.3	NT	9,9.3	9,9.3
vWA	NT		NT	16,17*	NT	16,18	16,18
D21				28			28,32.2
D7						11	11,12
D5	NT		NT		NT		12
TPOX	NT		NT		NT		8
DYS391	NT		NT		NT		11
D8	NT	9,12	NT	9,15	NT	9,12	9,12
D12	NT		NT		NT	21,23	21,23
D19	NT		NT		NT	11,12,14	12,14
FGA	21,†,†,†,†,†,†,†	21.2,41.2	†,†	21.2,22	21.2,22	†	21.2,22
D22	NT	11	NT		NT	11	11,16

Table B9 (cont'd).

Locus	Mini 13-3C	Fusion 13-3C	Mini 13-7A	Fusion 13-7A	Mini 13-7B	Fusion 13-7B	Mini 13-7C	Fusion 13-7C	V
Amel				X,Y	X,Y	X,Y		X,Y	X,Y
D3	NT		NT	14,18*	NT	14	NT	14	14
D1	NT		NT	16.3,17.3	NT	16.3,17.3	NT		16.3,17.3
D2S441	NT		NT	11,11.3	NT	11,11.3	NT	11,11.3	11,11.3
D10	NT		NT		NT	15,16	NT	15,16	15,16
D13			12	10	10,12	10,12	12		10,12
Penta E	NT		NT	5,14	NT	5,14	NT	5,14	5,14
D16		12	11,12	11,12	11,12	11,12	11,12	12	11,12
D18			16	17	16,17	16,17	16	16,17	16,17
D2S1338			17*,20,22,25*	20,22	20,22	20,22	20,22	20	20,22
CSF	15		†	11	10,11	10,11	10,11	10	10,11
Penta D	NT		NT	12	NT	11,12	NT	12	11,12
THO1	NT		NT	9,9.3	NT	9,9.3	NT	9,9.3	9,9.3
vWA	NT	16,18	NT	16,18	NT	16,18	NT	14,17*,18	16,18
D21		36.2	32.2	28,32.2	28,32.2	28,32.2	28	28	28,32.2
D7				12	11	11,12	11	11,12	11,12
D5	NT		NT	12	NT	12	NT		12
TPOX	NT		NT		NT	8	NT		8
DYS391	NT		NT	11	NT	11	NT	11	11
D8	NT		NT	9,12	NT	9,12	NT	9,12	9,12
D12	NT		NT	20,21,23	NT	21,23	NT	23	21,23
D19	NT		NT		NT	12	NT	12	12,14
FGA	†,†,†,†,†,†	†,†	21.2,31.2,†,†	22	21.2,22,†	21.2,22	21.2,†,†	22,23*,32.2	21.2,22
D22	NT	†	NT		NT	11,16	NT	11,16	11,16

Table B10. Alleles amplified with AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$ and PowerPlex $^{\text{®}}$ Fusion from spent cartridge casings loaded by volunteer L during Collection 2.

Locus	Mini 23-2A	Fusion 23-2A	Mini 23-2B	Fusion 23-2B	Mini 23-3A	Fusion 23-3A	L
Amel	X	X	X	X		X	X
D3	NT	16	NT	16,17	NT	15,16	16
D1	NT	16,17.3	NT	16,17.3	NT	16,17.3	16,17.3
D2S441	NT	11	NT	11	NT	11	11
D10	NT		NT	15	NT		13,15
D13	13	13	13		13		13
Penta E	NT	7	NT	7	NT	7	7
D16	11	11	11	11	11	11	11
D18	15,16	15,16	15,16	15	15,16		15,16
D2S1338	17	17	17,19	17	17		17
CSF	12,13,†,†	13	12,13,†,†		†		12,13
Penta D	NT		NT	8.2	NT		9,11
THO1	NT	8,9.3	NT	8,9.3	NT	7,8,9.3	8,9.3
vWA	NT	14	NT	14,18	NT	16,18	14,18
D21	27,30	30		30	27	30	27,30
D7	8,10	8			8		8,10
D5	NT		NT		NT		11,12
TPOX	NT		NT		NT		8
DYS391	NT		NT		NT		N/A
D8	NT	13,14	NT	13,14	NT	13	13,14
D12	NT	20	NT	18,20	NT	18	18,20
D19	NT		NT	14,15	NT	14,15	14,15
FGA	23.2,30,†,†,†	21,23	21,23	21,†,†	23,28	†	21,23
D22	NT		NT	†,16	NT		15,16

Table B10 (cont'd).

Locus	Mini 23-3B	Fusion 23-3B	Mini 23-3C	Fusion 23-3C	Mini 23-4A	Fusion 23-4A	L
Amel	<i>X</i>	<i>X,Y*</i>	<i>X</i>	<i>X</i>			<i>X</i>
D3	NT	16	NT	16	NT		16
D1	NT	16	NT	<i>17.3</i>	NT		16,17.3
D2S441	NT	<i>11</i>	NT	<i>11</i>	NT		11
D10	NT		NT		NT		13,15
D13	13		13	<i>12*</i>			13
Penta E	NT		NT		NT		7
D16	<i>11</i>	<i>11</i>	<i>11</i>	<i>11</i>			11
D18	15,16	16	<i>12*,15,16</i>	16			15,16
D2S1338	<i>17</i>	<i>17</i>	<i>17,18,22</i>	<i>17</i>			17
CSF	<i>5</i>		<i>12,†</i>	<i>12</i>	†		12,13
Penta D	NT		NT	<i>6</i>	NT		9,11
THO1	NT	8,9.3	NT	8,9.3	NT	9.3	8,9.3
vWA	NT	<i>14,16</i>	NT	<i>14,17*,18</i>	NT		14,18
D21	27		27	27,30			27,30
D7	10	10		<i>9,10</i>			8,10
D5	NT	11	NT	12	NT		11,12
TPOX	NT		NT	8	NT		8
DYS391	NT		NT		NT		N/A
D8	NT		NT	<i>13,14,15,15.1</i>	NT		13,14
D12	NT	18	NT	18,20,†	NT		18,20
D19	NT	<i>15</i>	NT	<i>14,15</i>	NT	<i>15</i>	14,15
FGA	<i>23,25,32,†,†</i>	21	<i>21,23,†,†</i>	<i>21,†</i>		†	21,23
D22	NT		NT		NT		15,16

Table B10 (cont'd).

Locus	Mini 23-4B	Fusion 23-4B	Mini 23-4C	Fusion 23-4C	L
Amel					X
D3	NT		NT		16
D1	NT	16	NT	15.3,17.3	16,17.3
D2S441	NT		NT		11
D10	NT		NT		13,15
D13					13
Penta E	NT		NT	21	7
D16		11			11
D18					15,16
D2S1338					17
CSF	10		12		12,13
Penta D	NT		NT		9,11
THO1	NT		NT	8	8,9.3
vWA	NT		NT		14,18
D21					27,30
D7					8,10
D5	NT		NT		11,12
TPOX	NT		NT		8
DYS391	NT		NT		N/A
D8	NT		NT		13,14
D12	NT		NT		18,20
D19	NT		NT	†,13	14,15
FGA	22.2,24.2,†,†,†		17,19.2,†		21,23
D22	NT		NT		15,16

Table B10 (cont'd).

Locus	Mini 23-5A	Fusion 23-5A	Mini 23-5B	Fusion 23-5B	Mini 23-5C	Fusion 23-5C	L
Amel		<i>X</i>		<i>X</i>	<i>X</i>	<i>X,Y*</i>	<i>X</i>
D3	NT		NT	16	NT		16
D1	NT		NT		NT		16,17.3
D2S441	NT		NT		NT		11
D10	NT		NT		NT		13,15
D13							13
Penta E	NT		NT		NT		7
D16		<i>†,11</i>				<i>11</i>	11
D18			<i>12*</i>	15	16		15,16
D2S1338							17
CSF	<i>†</i>		<i>†,†,†</i>				12,13
Penta D	NT		NT		NT		9,11
THO1	NT	9.3	NT		NT	9.3	8,9.3
vWA	NT		NT		NT		14,18
D21							27,30
D7	8						8,10
D5	NT		NT		NT		11,12
TPOX	NT		NT		NT	8	8
DYS391	NT		NT		NT		N/A
D8	NT	<i>14,19</i>	NT	<i>13,14</i>	NT		13,14
D12	NT		NT	<i>†</i>	NT	18	18,20
D19	NT		NT	<i>14.2</i>	NT	<i>†</i>	14,15
FGA	<i>†,†,†</i>	<i>30</i>	<i>18.2,†,†,†</i>	<i>†</i>	<i>18.2,†,†</i>	21	21,23
D22	NT		NT		NT		15,16

Table B11. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer T during Collection 2.

Locus	Mini 25-6A	Fusion 25-6A	Mini 25-7C	Fusion 25-7C	T
Amel					X
D3	NT	16	NT		16,17
D1	NT		NT		16,17.3
D2S441	NT		NT		11,14
D10	NT	17	NT		14,17
D13					11
Penta E	NT		NT		11,12
D16					11,12
D18		13			13,17
D2S1338					20,24
CSF	15				10,11
Penta D	NT		NT		8,10
THO1	NT		NT		6,7
vWA	NT		NT		19,20
D21	31.2*				29
D7					8,10
D5	NT		NT		12
TPOX	NT		NT		8,11
DYS391	NT		NT		N/A
D8	NT	13	NT		13,14
D12	NT		NT		19,23
D19	NT		NT		13,16.2
FGA	27.2,†	†,†	19.2,†,†		24
D22	NT	11	NT		11,18

Table B12. Alleles amplified with AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$ and PowerPlex $^{\text{®}}$ Fusion from spent cartridge casings loaded by volunteer XX during Collection 2.

Locus	Mini 26-6A	Fusion 26-6A	Mini 26-7A	Fusion 26-7A	Mini 26-7B	Fusion 26-7B	XX
Amel							X
D3	NT		NT		NT	15	14,15
D1	NT		NT	14	NT		14,17.3
D2S441	NT	11.3	NT	14	NT		12,14
D10	NT		NT		NT		14,16
D13			12				12,13
Penta E	NT		NT		NT		12
D16		6				13	11,13
D18							17,18
D2S1338			17	17		16	17
CSF	†,†		8,12		6,11*,†,†		10,12
Penta D	NT		NT		NT		12
THO1	NT		NT		NT	9	9,9.3
vWA	NT		NT		NT		17,19
D21							29,32
D7				12			9,12
D5	NT		NT		NT		10,13
TPOX	NT		NT		NT		8,12
DYS391	NT		NT		NT		N/A
D8	NT		NT		NT	10	10,13
D12	NT	18.3	NT		NT	22	18,22
D19	NT		NT	13,14	NT		13,14
FGA	27.2,†,†,†,†,†	22.2	28.2,†,†,†		32.2,49.2,†,†,†	21	21,23
D22	NT		NT		NT	14	16,17

Table B13. Alleles amplified with AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$ and PowerPlex $^{\text{®}}$ Fusion from spent cartridge casings loaded by volunteer N during Collection 2.

Locus	Mini 27-1B	Fusion 27-1B	Mini 27-1C	Fusion 27-1C	Mini 27-2B	Fusion 27-2B	N
Amel		X					X
D3	NT	16	NT		NT		16,17
D1	NT		NT		NT		15.3,17.3
D2S441	NT		NT		NT		11
D10	NT		NT		NT		13
D13		14					12,14
Penta E	NT		NT		NT		13,15
D16							12,13
D18	14						13,14
D2S1338							20,23
CSF	5,†,15				14,†		11,12
Penta D	NT	12	NT		NT		10,12
THO1	NT	9.3	NT		NT		6,9.3
vWA	NT	18	NT		NT		17,18
D21							30,32.2
D7							11,12
D5	NT		NT		NT		12
TPOX	NT		NT		NT		8
DYS391	NT		NT		NT		N/A
D8	NT	13	NT		NT		13
D12	NT	19,21.3	NT		NT		19,20
D19	NT	14	NT	†	NT		13,14
FGA	†,19,21,48.2	25.2,29.2	17.2,29.2,†,†	20.3,†	20,†,†	50.2	21,25
D22	NT		NT		NT	†	11,15

Table B14. Alleles amplified with AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$ and PowerPlex $^{\text{®}}$ Fusion from spent cartridge casings loaded by volunteer B during Collection 2.

Locus	Mini 33-4B	Fusion 33-4B	Mini 33-7A	Fusion 33-7A	Mini 33-7B	Fusion 33-7B	B
Amel				X,Y		X,Y	X,Y
D3	NT	18	NT	16,17*,18	NT	16	16,18
D1	NT	17.3	NT	16.3,17.3	NT		16.3,17.3
D2S441	NT		NT	14,15	NT		14,15
D10	NT	13	NT		NT		13,15
D13			12	10	10,12		10,12
Penta E	NT	17.4,18	NT		NT		7,18
D16				9,13	9,13	9,12*,13	9,13
D18			15	15	13,15	13,15	13,15
D2S1338				25	20		20,25
CSF	12		10,†	12	10,12,†,†	12	10,12
Penta D	NT		NT		NT		12,13
THO1	NT	†	NT	8,9,9.3	NT	8,9.3	8,9.3
vWA	NT		NT	18	NT	17,18	17,18
D21			29	29	29		29,31
D7				9			9,12
D5	NT		NT	13	NT		11,13
TPOX	NT		NT		NT		8
DYS391	NT		NT		NT		11
D8	NT		NT	8,13	NT	8,13	8,13
D12	NT	13	NT		NT	22,23	22,23
D19	NT		NT	13,14*	NT		13,15
FGA	24,24.2,33.2	16.1,19.3,23,†,†	20.2,23,†,†	31,†	21,23,48.2		21,23
D22	NT		NT		NT		15,16

Table B15. Alleles amplified with AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$ and PowerPlex $^{\text{®}}$ Fusion from spent cartridge casings loaded by volunteer WW during Collection 2.

Locus	Mini 38-3C	Fusion 38-3C	Mini 38-4A	Fusion 38-4A	Mini 38-4B	Fusion 38-4B	WW
Amel		<i>X</i>		<i>X</i>			<i>X</i>
D3	NT	<i>16</i>	NT		NT		16,18
D1	NT		NT		NT		11,12
D2S441	NT	<i>11</i>	NT		NT	<i>11,14</i>	11,14
D10	NT		NT		NT	16	15,16
D13							8,9
Penta E	NT		NT		NT		11,12
D16	<i>12</i>	<i>12</i>		<i>12</i>	<i>12</i>	<i>11</i>	12
D18	12,15	12,15				12	12,15
D2S1338		17				<i>25</i>	17,21
CSF					†,†,†		11,12
Penta D	NT		NT		NT		10,12
THO1	NT	<i>8,9.3</i>	NT		NT		9.3
vWA	NT	<i>15,17</i>	NT		NT	15	15,17
D21							28,30
D7							10,11
D5	NT		NT		NT		13
TPOX	NT		NT		NT		8,12
DYS391	NT		NT		NT		N/A
D8	NT	10,12	NT		NT	10	10,12
D12	NT	<i>17.3,19.3</i>	NT		NT	<i>18,21.3</i>	18,19.3
D19	NT		NT		NT		13,14
FGA	16,†,†		<i>21*,†,†</i>	†,†	<i>21*</i>		20,24
D22	NT		NT		NT		16

Table B16. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer Y during Collection 2.

Locus	Mini 41-4B	Fusion 41-4B	Mini 41-5A	Fusion 41-5A	Y
Amel		X,Y		X,Y	X,Y
D3	NT	14	NT	17,18	16,17
D1	NT	16.3,17.3*	NT		12,14
D2S441	NT	11.3	NT		14,15
D10	NT	15,16	NT		14,15
D13		12		13	13,14
Penta E	NT	5,14	NT		5,14
D16	11,12	11,12		11,12	11,12
D18	16*,17	16*,17		17	17
D2S1338	20,22	20	24		17,24
CSF	7,10,11	10	†		12,14
Penta D	NT	12	NT		8,13
THO1	NT	9,9.3	NT	9.3	9,9.3
vWA	NT	16,18*	NT	14	14,16
D21	28,32.2	28,32.2			29,30.2
D7	11,12	11,12			8,10
D5	NT	12	NT		12
TPOX	NT	8	NT		8
DYS391	NT	11	NT		11
D8	NT	9,12	NT	10,14	10,14
D12	NT	21,23	NT	20*,†	17,21
D19	NT	12,14*	NT	9,16.2	13,16.2
FGA	25.2,†,†	21.2,22	20.2,†		22,27
D22	NT	11,16	NT		11,16

Table B17. Alleles amplified with AmpFℓSTR® MiniFiler™ and PowerPlex® Fusion from spent cartridge casings loaded by volunteer II during Collection 2.

Locus	Mini 50-5B	Fusion 50-5B	Mini 50-6A	Fusion 50-6A	II
Amel	Y	Y		X,Y	X,Y
D3	NT	17	NT	17	17
D1	NT	15,18.3	NT	15	15,18.3
D2S441	NT	10,11	NT		10,11
D10	NT	13	NT		13,15
D13	12	11,12			11,12
Penta E	NT	13,14	NT		13,14
D16	12	11,12		10,12	12
D18	16,17	16		17	16,17
D2S1338	19,21		21	21	19,21
CSF	12	12	12,†		12
Penta D	NT		NT		9,13
THO1	NT	6,8,9,9.3	NT	8,9.3	8,9.3
vWA	NT	15,17	NT	15,17	15,17
D21	29	31	29	31	29,31
D7	10	12			10,12
D5	NT	12	NT		11,12
TPOX	NT	8	NT		8
DYS391	NT		NT		11
D8	NT	11,13	NT	11,13	11,13
D12	NT	18,20,†	NT	18	18,20
D19	NT	14	NT	13.2,15.2	14,15.2
FGA	20,21,23,25.2,†,†,†,†,†	23,†	†,†	21,†	21,23
D22	NT	15,16	NT		15,16

APPENDIX C. ANALYSIS OF LOADER AND NON-LOADER ALLELES IN STR PROFILES AMPLIFIED WITH AMPF_{STR}[®] MINIFILER[™] AND POWERPLEX[®] FUSION¹

Table C1. Summary of alleles recovered in STR profiles generated from spent cartridge casings using a double swab technique (Sweet *et al.*, 1997) and organic extraction.

Casing Identifier	DNA Conc. (pg/μL)	AmpF _{STR} [®] MiniFiler [™]				PowerPlex [®] Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
30.6	2.88E+01	15	15	100.0	6	38	38	100.0	1
34.4	1.77E+01	16	16	100.0	2	38	38	100.0	1
13-7B	1.61E+01	17	18	94.4	0	43	44	97.7	0
28.2	1.39E+01	17	17	100	0	36	42	85.7	2
19-2A	5.39E+00	12	14	85.7	5	33	40	82.5	4
23-2A	5.14E+00	12	14	85.7	2	22	38	57.9	0
1-1C	4.75E+00	N/A	N/A	N/A	N/A	22	42	52.4	4
21-1B	4.69E+00	N/A	N/A	N/A	N/A	21	42	50.0	4
23-2B	4.15E+00	10	14	71.4	3	23	38	60.5	2
41-4B	4.04E+00	3	17	17.6	11	18	44	40.9	21
13-7A	3.69E+00	8	18	44.4	3	31	44	70.4	2
50-5B	3.68E+00	12	16	75.0	2	30	43	69.8	4
43.3	3.46E+00	N/A	N/A	N/A	N/A	8	41	19.5	20

¹ The casings are organized based on DNA concentration arranged in descending order.

Table C1 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpF ℓ STR® MiniFiler™				PowerPlex® Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
13-7C	2.93E+00	11	18	61.1	0	29	44	65.9	4
33-7B	2.65E+00	12	18	66.7	1	16	46	34.8	1
18-3A	2.51E+00	N/A	N/A	N/A	N/A	19	40	47.5	7
3-4A	2.42E+00	0	16	0.0	1	2	41	4.9	3
2-3A	2.21E+00	12	16	75.0	0	28	39	71.8	3
33-7A	2.16E+00	5	18	27.8	1	23	46	50.0	4
8-5C	1.97E+00	N/A	N/A	N/A	N/A	14	41	34.1	5
50-5A	1.94E+00	N/A	N/A	N/A	N/A	17	43	39.5	11
40-3B	1.83E+00	N/A	N/A	N/A	N/A	12	39	30.8	18
26-4B	1.78E+00	N/A	N/A	N/A	N/A	22	42	52.4	7
20-4B	1.75E+00	N/A	N/A	N/A	N/A	9	39	23.1	10
26-4A	1.70E+00	N/A	N/A	N/A	N/A	22	42	52.4	1
20-4A	1.70E+00	N/A	N/A	N/A	N/A	11	39	28.2	3
17-2A	1.68E+00	N/A	N/A	N/A	N/A	13	46	28.3	1
8-5B	1.66E+00	N/A	N/A	N/A	N/A	20	41	48.8	1
38-2B	1.55E+00	N/A	N/A	N/A	N/A	17	41	41.5	18
48.5	1.49E+00	N/A	N/A	N/A	N/A	9	43	20.9	2
20-4C	1.48E+00	N/A	N/A	N/A	N/A	10	39	25.6	18
27-5B	1.39E+00	N/A	N/A	N/A	N/A	12	40	30.0	6
23-2C	1.38E+00	N/A	N/A	N/A	N/A	12	38	31.6	4
26-4C	1.38E+00	N/A	N/A	N/A	N/A	24	42	57.1	3
27-5A	1.38E+00	N/A	N/A	N/A	N/A	9	40	22.5	7
27-5C	1.31E+00	N/A	N/A	N/A	N/A	15	40	37.5	9
17-2B	1.28E+00	N/A	N/A	N/A	N/A	9	46	19.6	2

Table C1 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpFtSTR® MiniFiler™				PowerPlex® Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
1-1A	1.26E+00	N/A	N/A	N/A	N/A	9	41	21.9	9
33-7C	1.19E+00	N/A	N/A	N/A	N/A	12	46	26.1	0
18-3B	1.11E+00	N/A	N/A	N/A	N/A	14	40	35.0	6
21-1A	1.01E+00	N/A	N/A	N/A	N/A	12	42	28.6	2
36-1A	9.91E-01	N/A	N/A	N/A	N/A	12	44	27.3	1
19.2	9.89E-01	N/A	N/A	N/A	N/A	23	40	57.5	5
38-2A	9.87E-01	N/A	N/A	N/A	N/A	17	41	41.5	0
50-5C	9.58E-01	N/A	N/A	N/A	N/A	20	43	46.5	4
8-5A	9.57E-01	N/A	N/A	N/A	N/A	13	41	31.7	7
36-1C	8.94E-01	N/A	N/A	N/A	N/A	5	44	11.4	5
6-2A	8.87E-01	N/A	N/A	N/A	N/A	10	46	21.7	13
17-2C	8.61E-01	N/A	N/A	N/A	N/A	9	46	19.6	6
2-3C	8.25E-01	N/A	N/A	N/A	N/A	11	39	28.2	3
1-1B	8.04E-01	N/A	N/A	N/A	N/A	11	41	26.8	9
38-2C	7.87E-01	N/A	N/A	N/A	N/A	9	41	21.9	4
41-4C	7.36E-01	N/A	N/A	N/A	N/A	18	44	40.9	8
21-1C	7.36E-01	N/A	N/A	N/A	N/A	7	42	16.7	2
11-4C	6.89E-01	N/A	N/A	N/A	N/A	6	41	14.6	0
40-3A	6.83E-01	N/A	N/A	N/A	N/A	13	39	33.3	10
36-1B	5.80E-01	N/A	N/A	N/A	N/A	3	44	6.8	1
12-1A	5.47E-01	N/A	N/A	N/A	N/A	6	41	14.6	1
41-4A	5.42E-01	N/A	N/A	N/A	N/A	4	44	9.1	3
3-4B	5.35E-01	N/A	N/A	N/A	N/A	1	41	2.4	3

Table C1 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpF ℓ STR® MiniFiler™				PowerPlex® Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
11-4A	5.20E-01	N/A	N/A	N/A	N/A	0	41	0.0	0
2-3B	5.19E-01	N/A	N/A	N/A	N/A	16	39	41.0	1
12-1C	5.18E-01	N/A	N/A	N/A	N/A	6	41	14.6	6
25-3C	4.79E-01	N/A	N/A	N/A	N/A	3	41	7.3	12
37-1A	4.75E-01	N/A	N/A	N/A	N/A	12	44	27.3	0
24-6B	4.73E-01	N/A	N/A	N/A	N/A	5	41	12.2	14
18-3C	4.63E-01	N/A	N/A	N/A	N/A	9	40	22.5	1
11-4B	4.48E-01	N/A	N/A	N/A	N/A	3	41	7.3	2
15-1C	3.81E-01	N/A	N/A	N/A	N/A	1	41	2.4	1
6-2C	3.70E-01	N/A	N/A	N/A	N/A	3	46	6.5	2
15-1B	3.67E-01	N/A	N/A	N/A	N/A	2	41	4.9	2
25-3B	3.54E-01	N/A	N/A	N/A	N/A	7	41	17.1	1
40-3C	3.53E-01	N/A	N/A	N/A	N/A	0	39	0.0	1
3-4C	3.40E-01	N/A	N/A	N/A	N/A	9	41	21.9	4
35-2B	3.18E-01	N/A	N/A	N/A	N/A	18	42	42.8	25
10-6B	3.14E-01	N/A	N/A	N/A	N/A	4	41	9.7	2
24-6C	3.06E-01	N/A	N/A	N/A	N/A	5	41	12.2	2
12-1B	3.04E-01	N/A	N/A	N/A	N/A	2	41	4.9	3
25-3A	2.95E-01	N/A	N/A	N/A	N/A	5	41	12.2	3
6-2B	2.79E-01	N/A	N/A	N/A	N/A	6	46	13.0	6
10-6A	2.59E-01	N/A	N/A	N/A	N/A	0	41	0.0	1
35-2A	2.57E-01	N/A	N/A	N/A	N/A	3	42	7.1	6
7-3A	2.46E-01	N/A	N/A	N/A	N/A	2	45	4.4	1
10-6C	2.28E-01	N/A	N/A	N/A	N/A	0	41	0.0	0

Table C1 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpFtSTR® MiniFiler™				PowerPlex® Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
7-3B	1.89E-01	N/A	N/A	N/A	N/A	4	45	8.9	1
15-1A	1.74E-01	N/A	N/A	N/A	N/A	4	41	9.7	3
24-6A	1.24E-01	N/A	N/A	N/A	N/A	1	41	2.4	2
37.1	1.06E-01	N/A	N/A	N/A	N/A	1	44	2.3	2
7-3C	5.61E-02	N/A	N/A	N/A	N/A	5	45	11.1	3
35-2C	4.07E-02	N/A	N/A	N/A	N/A	1	42	2.4	2

Table C2. Summary of alleles recovered in STR profiles generated from spent cartridge casings using a soaking technique and organic extraction. DNA extract 3-5A is the only sample extracted with an organic extraction and amplified with PowerPlex® Fusion that does not have allelic data due to high levels of contamination.

Casing Identifier	DNA Conc. (pg/μL)	AmpFtSTR® MiniFiler™				PowerPlex® Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
34.3	5.05E+01	16	16	100.0	0	38	38	100.0	1
30.5	1.71E+01	15	15	100.0	4	38	38	100.0	1
13-1A	1.36E+01	18	18	100.0	0	41	44	93.2	0
23-3C	5.92E+00	10	14	71.4	3	24	38	63.1	6
28.1	4.75E+00	15	17	88.2	5	11	42	26.6	2
8-6A	4.63E+00	14	14	100.0	2	29	41	70.7	0
13-1B	4.60E+00	13	18	72.2	0	19	44	43.2	1
8-6B	3.82E+00	11	14	78.6	2	28	41	68.3	2
13-1C	3.60E+00	11	18	61.1	2	30	44	68.2	4
23-3A	3.56E+00	8	14	57.1	1	15	38	39.5	3
19-1A	2.82E+00	9	14	64.3	6	16	40	40.0	11
50-6A	2.72E+00	3	16	18.7	0	17	43	39.5	2
23-3B	2.71E+00	9	14	64.3	3	15	38	39.5	2
41-5A	2.16E+00	1	17	5.9	1	12	44	27.3	3
38-3C	2.16E+00	3	16	18.7	0	13	41	31.7	2
8-6C	2.06E+00	N/A	N/A	N/A	N/A	23	41	56.1	5
50-6C	1.90E+00	N/A	N/A	N/A	N/A	8	43	18.6	1
21-2B	1.74E+00	N/A	N/A	N/A	N/A	20	42	47.6	5
38-3B	1.55E+00	N/A	N/A	N/A	N/A	10	41	24.4	2
38-3A	1.49E+00	N/A	N/A	N/A	N/A	17	41	41.5	13
26-5C	1.41E+00	N/A	N/A	N/A	N/A	17	42	40.5	0
50-6B	1.39E+00	N/A	N/A	N/A	N/A	9	43	20.9	2

Table C2 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$				PowerPlex $^{\text{®}}$ Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
26-5A	1.35E+00	N/A	N/A	N/A	N/A	17	42	40.5	1
20-1A	1.33E+00	N/A	N/A	N/A	N/A	9	39	23.1	1
27-6A	1.32E+00	N/A	N/A	N/A	N/A	10	40	25.0	10
33-1C	1.30E+00	N/A	N/A	N/A	N/A	11	46	23.9	4
41-5C	1.30E+00	N/A	N/A	N/A	N/A	9	44	20.4	3
17-3C	1.26E+00	N/A	N/A	N/A	N/A	10	46	21.7	0
21-2A	1.22E+00	N/A	N/A	N/A	N/A	12	42	28.6	2
37-2A	1.20E+00	9	17	52.9	2	12	44	27.3	7
27-6B	1.20E+00	N/A	N/A	N/A	N/A	10	40	25.0	9
17-3B	1.20E+00	N/A	N/A	N/A	N/A	12	46	26.1	0
27-6C	1.16E+00	N/A	N/A	N/A	N/A	10	40	25.0	5
43.1	1.14E+00	N/A	N/A	N/A	N/A	6	41	14.6	2
26-5B	1.11E+00	N/A	N/A	N/A	N/A	17	42	40.5	2
25-4C	1.02E+00	N/A	N/A	N/A	N/A	6	41	14.6	3
2-4C	9.15E-01	N/A	N/A	N/A	N/A	18	39	46.1	8
33-1B	8.86E-01	N/A	N/A	N/A	N/A	12	46	26.1	1
33-1A	8.79E-01	N/A	N/A	N/A	N/A	12	46	26.1	1
41-5B	8.61E-01	N/A	N/A	N/A	N/A	14	44	31.8	1
3-5B	7.88E-01	N/A	N/A	N/A	N/A	4	41	9.7	10
20-1B	7.79E-01	N/A	N/A	N/A	N/A	4	39	10.2	4
11-1C	6.91E-01	N/A	N/A	N/A	N/A	13	41	31.7	6
48.4	6.71E-01	N/A	N/A	N/A	N/A	5	43	11.6	5
2-4B	6.13E-01	N/A	N/A	N/A	N/A	7	39	17.9	4
19.1	5.95E-01	N/A	N/A	N/A	N/A	5	40	12.5	2

Table C2 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpF ℓ STR $^{\text{®}}$ MiniFiler $^{\text{™}}$				PowerPlex $^{\text{®}}$ Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
2-4A	5.52E-01	N/A	N/A	N/A	N/A	8	39	20.5	3
10-7A	4.96E-01	N/A	N/A	N/A	N/A	5	41	12.2	5
21-2C	4.76E-01	N/A	N/A	N/A	N/A	5	42	11.9	2
37.6	4.67E-01	N/A	N/A	N/A	N/A	8	44	18.2	3
36-2A	4.65E-01	N/A	N/A	N/A	N/A	8	44	18.2	4
36-2B	4.22E-01	N/A	N/A	N/A	N/A	3	44	6.8	2
20-1C	4.06E-01	N/A	N/A	N/A	N/A	9	39	23.1	1
25-4A	3.95E-01	N/A	N/A	N/A	N/A	4	41	9.7	3
18-4C	3.88E-01	N/A	N/A	N/A	N/A	5	40	12.5	0
12-2C	3.69E-01	N/A	N/A	N/A	N/A	3	41	7.3	4
3-5A	3.67E-01	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-4C	3.27E-01	N/A	N/A	N/A	N/A	8	39	20.5	3
1-2C	2.94E-01	N/A	N/A	N/A	N/A	3	41	7.3	2
12-2B	2.88E-01	N/A	N/A	N/A	N/A	4	41	9.7	1
40-4A	2.76E-01	N/A	N/A	N/A	N/A	3	39	5.1	4
10-7B	2.75E-01	N/A	N/A	N/A	N/A	3	41	7.3	2
25-4B	2.72E-01	N/A	N/A	N/A	N/A	4	41	9.7	5
36-2C	2.70E-01	N/A	N/A	N/A	N/A	3	44	6.8	0
15-2C	2.59E-01	N/A	N/A	N/A	N/A	3	41	7.3	7
24-7C	2.54E-01	N/A	N/A	N/A	N/A	5	41	12.2	3
6-3C	2.46E-01	N/A	N/A	N/A	N/A	12	46	26.1	5
18-4A	2.40E-01	N/A	N/A	N/A	N/A	4	40	10.0	1
3-5C	2.38E-01	N/A	N/A	N/A	N/A	4	41	9.7	1

Table C2 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpFlSTR® MiniFiler™				PowerPlex® Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
1-2B	2.35E-01	N/A	N/A	N/A	N/A	5	41	12.2	0
24-7A	2.22E-01	N/A	N/A	N/A	N/A	3	41	7.3	3
1-2A	2.09E-01	N/A	N/A	N/A	N/A	1	41	2.4	1
7-4A	2.00E-01	N/A	N/A	N/A	N/A	2	45	4.4	8
10-7C	1.93E-01	N/A	N/A	N/A	N/A	2	41	4.9	2
12-2A	1.91E-01	N/A	N/A	N/A	N/A	7	41	17.7	0
17-3A	1.75E-01	N/A	N/A	N/A	N/A	10	46	21.7	1
35-3A	1.62E-01	N/A	N/A	N/A	N/A	0	42	0.0	0
15-2B	1.36E-01	N/A	N/A	N/A	N/A	1	41	2.4	3
40-4B	1.23E-01	N/A	N/A	N/A	N/A	2	39	5.1	1
18-4B	1.15E-01	N/A	N/A	N/A	N/A	5	40	12.5	1
11-1A	1.07E-01	N/A	N/A	N/A	N/A	2	41	4.9	3
6-3B	9.43E-02	N/A	N/A	N/A	N/A	1	46	2.2	1
11-1B	9.01E-02	N/A	N/A	N/A	N/A	0	41	0.0	0
15-2A	8.22E-02	N/A	N/A	N/A	N/A	0	41	0.0	0
24-7B	6.91E-02	N/A	N/A	N/A	N/A	1	41	2.4	1
7-4C	5.42E-02	N/A	N/A	N/A	N/A	4	45	8.9	1
35-3B	3.95E-02	N/A	N/A	N/A	N/A	3	42	7.1	0
6-3A	2.94E-02	N/A	N/A	N/A	N/A	1	46	2.2	2
7-4B	2.03E-02	N/A	N/A	N/A	N/A	1	45	2.2	0
35-3C	1.99E-02	N/A	N/A	N/A	N/A	2	42	4.8	0

Table C3. Summary of alleles recovered in STR profiles generated from spent cartridge casings using a double swab technique (Sweet *et al.*, 1997) and QIAamp® DNA Investigator extraction.

Casing Identifier	DNA Conc. (pg/μL)	AmpFSTR® MiniFiler™				PowerPlex® Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
13-2B	1.25E+00	3	18	16.7	1	17	44	38.6	2
34.6	1.17E+00	12	16	75.0	1	25	38	65.8	2
21-3B	9.04E-01	N/A	N/A	N/A	N/A	11	42	26.2	1
21-3A	4.79E-01	N/A	N/A	N/A	N/A	6	42	14.3	3
28.4	4.71E-01	2	17	11.8	0	6	42	14.3	3
12-3A	3.92E-01	N/A	N/A	N/A	N/A	5	41	12.2	0
20-2B	3.89E-01	N/A	N/A	N/A	N/A	5	39	12.8	1
13-2A	3.58E-01	1	18	5.6	2	8	44	18.2	2
23-4C	3.16E-01	1	14	7.1	3	2	38	5.3	0
17-4A	3.00E-01	N/A	N/A	N/A	N/A	2	46	4.3	0
38-4B	2.84E-01	1	16	6.2	1	7	41	17.1	3
2-5B	2.80E-01	1	16	6.2	1	0	39	0.0	2
17-4C	2.57E-01	N/A	N/A	N/A	N/A	0	46	0.0	3
21-3C	2.50E-01	N/A	N/A	N/A	N/A	9	42	21.4	1
8-7A	2.29E-01	1	14	7.1	1	6	41	14.6	0
38-4A	2.15E-01	0	16	0.0	1	2	41	4.9	0
23-4A	2.14E-01	0	14	0.0	0	2	38	5.3	0
26-6A	2.00E-01	0	16	0.0	1	0	42	0.0	4
23-4B	1.90E-01	0	14	0.0	3	2	38	5.3	0
8-7B	1.83E-01	0	14	0.0	3	1	41	2.4	1
41-6B	1.82E-01	N/A	N/A	N/A	N/A	7	44	15.9	2
13-2C	1.77E-01	N/A	N/A	N/A	N/A	0	44	0.0	3
48.1	1.65E-01	N/A	N/A	N/A	N/A	2	43	4.6	1

Table C3 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpF [®] STR [®] MiniFiler [™]				PowerPlex [®] Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
33-2C	1.49E-01	N/A	N/A	N/A	N/A	5	46	10.9	0
11-2A	1.41E-01	N/A	N/A	N/A	N/A	2	41	4.9	0
37-1B	1.38E-01	N/A	N/A	N/A	N/A	3	44	6.8	1
20-2A	1.36E-01	N/A	N/A	N/A	N/A	2	39	5.1	0
30.2	1.27E-01	0	15	0.0	0	2	38	5.3	0
6-4C	1.27E-01	N/A	N/A	N/A	N/A	3	46	6.5	2
20-2C	1.23E-01	N/A	N/A	N/A	N/A	3	39	7.7	1
2-5C	1.08E-01	N/A	N/A	N/A	N/A	3	39	7.7	0
2-5A	1.05E-01	N/A	N/A	N/A	N/A	1	39	2.6	2
26-6C	1.04E-01	N/A	N/A	N/A	N/A	0	42	0.0	0
7/18-1B.1	1.01E-01	N/A	N/A	N/A	N/A	4	40	10.0	3
41-6A	9.60E-02	N/A	N/A	N/A	N/A	1	44	2.3	0
1-3A	9.47E-02	N/A	N/A	N/A	N/A	0	41	0.0	2
7/18-1C.1	9.43E-02	N/A	N/A	N/A	N/A	0	40	0.0	0
38-4C	9.31E-02	N/A	N/A	N/A	N/A	1	41	2.4	1
7/18-1A.2	9.18E-02	N/A	N/A	N/A	N/A	1	45	2.2	0
8-7C	8.74E-02	N/A	N/A	N/A	N/A	6	41	14.6	1
1-3C	8.69E-02	N/A	N/A	N/A	N/A	0	41	0.0	1
27-7C	7.50E-02	N/A	N/A	N/A	N/A	0	40	0.0	0
1-3B	7.28E-02	N/A	N/A	N/A	N/A	0	41	0.0	1
17-4B	6.70E-02	N/A	N/A	N/A	N/A	0	46	0.0	0
33-2B	6.69E-02	N/A	N/A	N/A	N/A	0	46	0.0	1
26-6B	6.55E-02	N/A	N/A	N/A	N/A	2	42	4.7	0
25-5C	6.23E-02	N/A	N/A	N/A	N/A	0	41	0.0	0

Table C3 (cont'd).

Casing Identifier	DNA Conc. (pg/μL)	AmpF [®] STR [®] MiniFiler [™]				PowerPlex [®] Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
11-2C	5.97E-02	N/A	N/A	N/A	N/A	1	41	2.4	0
12-3B	5.79E-02	N/A	N/A	N/A	N/A	0	41	0.0	1
27-7B	5.66E-02	N/A	N/A	N/A	N/A	1	40	2.5	0
12-3C	5.54E-02	N/A	N/A	N/A	N/A	1	41	2.4	0
7/18-1A.1	5.51E-02	N/A	N/A	N/A	N/A	2	40	5.0	0
50-7B	5.45E-02	N/A	N/A	N/A	N/A	0	43	0.0	1
3-6C	5.33E-02	N/A	N/A	N/A	N/A	2	41	4.9	1
50-7C	5.04E-02	N/A	N/A	N/A	N/A	0	43	0.0	0
11-2B	4.91E-02	N/A	N/A	N/A	N/A	0	41	0.0	0
41-6C	4.74E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
50-7A	4.42E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36-3B	4.26E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
25-5B	3.99E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6-4A	3.86E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19-2B	3.79E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-3B	3.32E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6-4B	3.22E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
27-7A	3.20E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
25-5A	3.14E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
37.3	2.67E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7/18-1B.2	2.64E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
33-2A	2.59E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10-1B	2.56E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-6B	1.90E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C3 (cont'd).

		AmpF [®] STR [®] MiniFiler [™]				PowerPlex [®] Fusion			
Casing Identifier	DNA Conc. (pg/μL)	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
19.4	1.84E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-5B	1.77E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7/18-1C.2	1.70E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36-3A	1.68E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-6A	1.63E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-5A	1.50E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-3A	1.36E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-5C	1.36E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36-3C	1.03E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24-1B	9.96E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10-1C	9.24E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-3C	9.23E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
35-4A	8.60E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24-1C	5.73E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10-1A	4.36E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
35-4C	3.70E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
35-4B	2.86E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
43.5	1.52E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24-1A	0.00E+00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C4. Summary of alleles recovered in STR profiles generated from spent cartridge casings using a soaking technique and QIAamp® DNA Investigator extraction.

		AmpFtSTR® MiniFiler™				PowerPlex® Fusion			
Casing Identifier	DNA Conc. (pg/μL)	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
3-7C	8.85E+00	5	14	35.7	11	13	41	31.7	27
13-3A	3.46E+00	14	18	77.8	0	26	44	59.0	1
23-5C	1.11E+00	2	14	14.3	1	6	38	15.8	1
27-1B	7.00E-01	2	17	11.8	4	9	40	22.5	3
23-5B	6.87E-01	0	14	0.0	2	5	38	13.2	1
23-5A	6.49E-01	1	14	7.1	0	4	38	10.5	2
26-7B	5.45E-01	0	16	0.0	2	6	42	14.3	2
26-7A	4.71E-01	3	16	18.7	1	6	42	14.3	0
25-6A	4.00E-01	0	14	0.0	3	5	41	12.2	0
21-4A	3.74E-01	N/A	N/A	N/A	N/A	3	42	7.1	6
27-1C	2.92E-01	0	17	0.0	2	0	40	0.0	1
30.1	2.28E-01	4	15	26.7	2	5	38	13.1	0
36-4B	1.70E-01	N/A	N/A	N/A	N/A	3	44	6.8	5
13-3C	1.63E-01	0	18	0.0	1	3	44	6.8	1
34.5	1.59E-01	4	16	25.0	0	4	38	10.5	1
12-4B	1.49E-01	N/A	N/A	N/A	N/A	6	41	14.6	3
36-4C	1.28E-01	N/A	N/A	N/A	N/A	3	44	6.8	0
8-1B	1.22E-01	N/A	N/A	N/A	N/A	3	41	7.3	3
7/18-2C.1	1.06E-01	N/A	N/A	N/A	N/A	4	45	8.9	3
33-3C	1.04E-01	N/A	N/A	N/A	N/A	3	46	6.5	2
11-3C	9.93E-02	N/A	N/A	N/A	N/A	2	41	4.9	3
38-5A	6.43E-02	N/A	N/A	N/A	N/A	0	41	0.0	1
11-3A	6.07E-02	N/A	N/A	N/A	N/A	1	41	2.4	2

Table C4 (cont'd).

		AmpFtSTR® MiniFiler™				PowerPlex® Fusion			
Casing Identifier	DNA Conc. (pg/μL)	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
26-7C	5.38E-02	N/A	N/A	N/A	N/A	1	42	2.4	0
10-2A	5.31E-02	N/A	N/A	N/A	N/A	0	41	0.0	1
17-1C	5.23E-02	N/A	N/A	N/A	N/A	1	46	2.2	0
8-1C	5.18E-02	N/A	N/A	N/A	N/A	0	41	0.0	0
33-3B	5.11E-02	N/A	N/A	N/A	N/A	1	46	2.2	0
25-6C	5.09E-02	N/A	N/A	N/A	N/A	2	41	4.9	0
25-6B	5.08E-02	N/A	N/A	N/A	N/A	1	41	2.4	0
37-2B	4.81E-02	1	17	5.8	0	0	44	0.0	1
41-7C	4.76E-02	N/A	N/A	N/A	N/A	1	44	2.3	0
50-1C	4.40E-02	N/A	N/A	N/A	N/A	0	43	0.0	1
17-1A	4.05E-02	N/A	N/A	N/A	N/A	1	46	2.2	0
6-1A	4.01E-02	N/A	N/A	N/A	N/A	0	46	0.0	1
7/18-2B.1	3.95E-02	N/A	N/A	N/A	N/A	3	45	6.7	0
40-6B	3.38E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
50-1A	3.00E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
33-3A	2.97E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2-6B	2.64E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17-1B	2.56E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
27-1A	2.54E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10-2C	2.28E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-4C	2.22E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
13-3B	2.03E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10-2B	1.95E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
38-5B	1.85E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C4 (cont'd).

		AmpFtSTR® MiniFiler™				PowerPlex® Fusion			
Casing Identifier	DNA Conc. (pg/μL)	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
28.3	1.58E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19.3	1.47E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-7A	1.46E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2-6C	1.37E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
11-3B	1.35E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2-6A	1.32E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-6A	1.22E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-7B	1.13E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8-1A	1.11E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
41-7B	1.11E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36-4A	1.07E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
43.4	1.05E-02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1-4B	9.85E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6-1B	8.69E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20-3C	8.36E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12-4A	8.16E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
50-1B	7.89E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
19-1B	7.17E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
41-7A	6.64E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6-1C	6.46E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24-2C	6.41E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-4B	6.30E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
38-5C	6.15E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-6C	6.03E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C4 (cont'd).

		AmpFtSTR® MiniFiler™				PowerPlex® Fusion			
Casing Identifier	DNA Conc. (pg/μL)	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
24-2A	5.81E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
48.6	5.76E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7/18-2A.1	5.43E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
37.2	5.04E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20-3B	4.92E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
35-1A	4.19E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-4A	3.78E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1-4C	3.59E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24-2B	3.28E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
21-4C	2.77E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1-4A	2.31E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
35-1C	1.71E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7/18-2C.2	1.66E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12-4C	1.36E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7/18-2A.2	1.12E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
35-1B	7.62E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
20-3A	6.58E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
21-4B	1.90E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
7/18-2B.2	1.89E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C5. Summary of alleles recovered in STR profiles generated from spent cartridge casings using a single swab and FDF[®] extraction.

Casing Identifier	DNA Conc. (pg/μL)	AmpF [®] STR [®] MiniFiler [™]				PowerPlex [®] Fusion			
		# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
34.1	2.82E-01	3	16	18.7	0	6	38	15.8	0
30.3	5.14E-02	N/A	N/A	N/A	N/A	4	38	10.5	1
8-2A	1.65E-02	0	14	0.0	4	0	41	0.0	0
48.2	1.18E-02	N/A	N/A	N/A	N/A	0	43	0.0	1
37.4	1.10E-02	N/A	N/A	N/A	N/A	0	44	0.0	1
33-4B	1.07E-02	1	18	5.6	3	5	46	10.9	4
19-1C	9.48E-03	0	14	0.0	0	0	40	0.0	0
37-2C	9.29E-03	N/A	N/A	N/A	N/A	0	44	0.0	0
28.5	8.93E-03	0	17	0.0	0	0	42	0.0	0
27-2B	7.81E-03	0	17	0.0	2	0	40	0.0	1
19.5	7.30E-03	N/A	N/A	N/A	N/A	0	40	0.0	1
25-7C	7.19E-03	0	14	0.0	1	0	41	0.0	0
24-3B	7.19E-03	N/A	N/A	N/A	N/A	0	41	0.0	1
43.6	7.18E-03	N/A	N/A	N/A	N/A	0	41	0.0	0
50-2C	5.82E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
26-1B	5.77E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
27-2C	4.92E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
50-2A	4.89E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-1B	3.97E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
50-2B	3.93E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
27-2A	3.71E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8-2B	3.67E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2-7A	3.61E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C5 (cont'd).

		AmpF [®] STR [®] MiniFiler [™]				PowerPlex [®] Fusion			
Casing Identifier	DNA Conc. (pg/μL)	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
13-4A	3.50E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
41-1B	3.24E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
25-7A	3.14E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
26-1C	3.13E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
41-1C	3.10E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
26-1A	3.04E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
23-6B	3.00E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-1C	2.88E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
8-2C	2.78E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
38-6B	2.17E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
23-6A	2.08E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
33-4C	2.03E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-5B	1.99E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10-3C	1.98E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-5C	1.95E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
38-6C	1.84E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2-7C	1.71E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
23-6C	1.69E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24-3A	1.68E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3-1A	1.54E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
25-7B	1.53E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2-7B	1.51E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-7A	1.29E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C5 (cont'd).

		AmpF ℓ STR $^{\circ}$ MiniFiler $^{\text{TM}}$				PowerPlex $^{\circ}$ Fusion			
Casing Identifier	DNA Conc. (pg/ μ L)	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
10-3A	1.28E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-7C	1.10E-03	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36-5C	9.65E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
24-3C	8.56E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36-5B	7.38E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
40-7B	7.08E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
13-4B	6.15E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
15-5A	5.98E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
33-4A	5.84E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
13-4C	5.16E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
38-6A	4.95E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
41-1A	4.09E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
36-5A	1.29E-04	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
10-3B	2.47E-06	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Table C6. Summary of alleles recovered in consensus and individual STR profiles generated from DNA extracts retrieved via a double swab technique (Sweet *et al.*, 1997) and organic extraction. Consensus profiles are presented first (Con. = Consensus) and the next three casing identifiers are the individual profiles.

Casing Identifier	PowerPlex® Fusion			
	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 2-3	18	39	46.15	0
2-3A	28	39	71.8	3
2-3B	16	39	41	1
2-3C	11	39	28.2	3
Con. 3-4	1	41	2.44	0
3-4A	2	41	4.9	3
3-4B	1	41	2.4	3
3-4C	9	41	21.9	4
Con. 8-5	14	41	34.15	0
8-5A	13	41	31.7	7
8-5B	20	41	48.8	1
8-5C	14	41	34.1	5
Con. 10-6	0	41	0	0
10-6A	0	41	0	1
10-6B	4	41	9.7	2
10-6C	0	41	0	0
Con. 13-7	40	44	90.91	0
13-7A	31	44	70.4	2
13-7B	43	44	97.7	0
13-7C	29	44	65.9	4
Con. 15-1	1	41	2.44	0
15-1A	4	41	9.7	3
15-1B	2	41	4.9	2
15-1C	1	41	2.4	1
Con. 23-2	19	38	50	0
23-2A	22	38	57.9	0
23-2B	23	38	60.5	2
23-2C	12	38	31.6	4

Table C6 (cont'd).

Casing Identifier	PowerPlex® Fusion			
	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 24-6	2	41	4.88	2
24-6A	1	41	2.4	2
24-6B	5	41	12.2	14
24-6C	5	41	12.2	2
Con. 25-3	2	41	4.88	1
25-3A	5	41	12.2	3
25-3B	7	41	17.1	1
25-3C	3	41	7.3	12
Con. 26-4	22	42	52.38	0
26-4A	22	42	52.4	1
26-4B	22	42	52.4	7
26-4C	24	42	57.1	3
Con. 27-5	9	40	22.5	3
27-5A	9	40	22.5	7
27-5B	12	40	30	6
27-5C	15	40	37.5	9
Con. 33-7	16	46	34.78	0
33-7A	23	46	50	4
33-7B	16	46	34.8	1
33-7C	12	46	26.1	0
Con. 36-1	3	44	6.82	0
36-1A	12	44	27.3	1
36-1B	3	44	6.8	1
36-1C	5	44	11.4	5
Con. 38-2	13	41	31.71	1
38-2A	17	41	41.5	0
38-2B	17	41	41.5	18
38-2C	9	41	21.9	4
Con. 40-3	7	39	17.95	4
40-3A	13	39	33.3	10
40-3B	12	39	30.8	18
40-3C	0	39	0	1

Table C6 (cont'd).

Casing Identifier	PowerPlex® Fusion			
	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 41-4	7	44	15.91	2
41-4A	4	44	9.1	3
41-4B	18	44	40.9	21
41-4C	18	44	40.9	8
Con. 50-5	20	43	46.51	2
50-5A	17	43	39.5	11
50-5B	30	43	69.8	4
50-5C	20	43	46.5	4
Con. 1-1	13	41	31.71	4
1-1A	9	41	21.9	9
1-1B	11	41	26.8	9
1-1C	22	42	52.4	4
Con. 6-2	5	46	10.87	3
6-2A	10	46	21.7	13
6-2B	6	46	13	6
6-2C	3	46	6.5	2
Con. 7-3	2	45	4.44	0
7-3A	2	45	4.4	1
7-3B	4	45	8.9	1
7-3C	5	45	11.1	3
Con. 11-4	0	41	0	0
11-4A	0	41	0	0
11-4B	3	41	7.3	2
11-4C	6	41	14.6	0
Con. 12-1	3	41	7.32	0
12-1A	6	41	14.6	1
12-1B	2	41	4.9	3
12-1C	6	41	14.6	6
Con. 17-2	9	46	19.57	0
17-2A	13	46	28.3	1
17-2B	9	46	19.6	2
17-2C	9	46	19.6	6

Table C6 (cont'd).

Casing Identifier	PowerPlex® Fusion			
	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 18-3	10	40	25	0
18-3A	19	40	47.5	7
18-3B	14	40	35	6
18-3C	9	40	22.5	1
Con. 20-4	7	39	17.95	5
20-4A	11	39	28.2	3
20-4B	9	39	23.1	10
20-4C	10	39	25.6	18
Con. 21-1	13	42	30.95	0
21-1A	12	42	28.6	2
21-1B	21	42	50	4
21-1C	7	42	16.7	2
Con. 35-2	3	42	7.14	3
35-2A	3	42	7.1	6
35-2B	18	42	42.8	25
35-2C	1	42	2.4	2

Table C7. Summary of alleles recovered in consensus and individual STR profiles generated from DNA extracts retrieved via a soaking technique and organic extraction. Consensus profiles are presented first (Con. = Consensus) and the next three casing identifiers are the individual profiles.

	PowerPlex® Fusion			
Casing Identifier	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 2-4	7	39	17.95	0
2-4A	8	39	20.5	3
2-4B	7	39	17.9	4
2-4C	18	39	46.1	8
Con. 3-5	2	41	4.88	0
3-5A	N/A	N/A	N/A	N/A
3-5B	4	41	9.7	10
3-5C	4	41	9.7	1
Con. 8-6	28	41	68.29	0
8-6A	29	41	70.7	0
8-6B	28	41	68.3	2
8-6C	23	41	56.1	5
Con. 10-7	1	41	2.44	1
10-7A	5	41	12.2	5
10-7B	3	41	7.3	2
10-7C	2	41	4.9	2
Con. 13-1	32	44	72.73	0
13-1A	41	44	93.2	0
13-1B	19	44	43.2	1
13-1C	30	44	68.2	4
Con. 15-2	0	41	0	1
15-2A	0	41	0	0
15-2B	1	41	2.4	3
15-2C	3	41	7.3	7
Con. 23-3	19	38	50	1
23-3A	15	38	39.5	3
23-3B	15	38	39.5	2
23-3C	24	38	63.1	6

Table C7 (cont'd).

Casing Identifier	PowerPlex® Fusion			
	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 24-7	2	41	4.88	0
24-7A	3	41	7.3	3
24-7B	1	41	2.4	1
24-7C	5	41	12.2	3
Con. 25-4	4	41	9.76	0
25-4A	4	41	9.7	3
25-4B	4	41	9.7	5
25-4C	6	41	14.6	3
Con. 26-5	18	42	42.86	0
26-5A	17	42	40.5	1
26-5B	17	42	40.5	2
26-5C	17	42	40.5	0
Con. 27-6	9	40	22.5	5
27-6A	10	40	25	10
27-6B	10	40	25	9
27-6C	10	40	25	5
Con. 33-1	10	46	21.74	0
33-1A	12	46	26.1	1
33-1B	12	46	26.1	1
33-1C	11	46	23.9	4
Con. 36-2	2	44	4.55	1
36-2A	8	44	18.2	4
36-2B	3	44	6.8	2
36-2C	3	44	6.8	0
Con. 38-3	12	41	29.27	0
38-3A	17	41	41.5	13
38-3B	10	41	24.4	2
38-3C	13	41	31.7	2
Con. 40-4	1	39	2.56	0
40-4A	3	39	5.1	4
40-4B	2	39	5.1	1
40-4C	8	39	20.5	3

Table C7 (cont'd).

Casing Identifier	PowerPlex® Fusion			
	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 41-5	8	44	18.18	0
41-5A	12	44	27.3	3
41-5B	14	44	31.8	1
41-5C	9	44	20.4	3
Con. 50-6	10	43	23.26	0
50-6A	17	43	39.5	2
50-6B	9	43	20.9	2
50-6C	8	43	18.6	1
Con. 1-2	1	41	2.44	0
1-2A	1	41	2.4	1
1-2B	5	41	12.2	0
1-2C	3	41	7.3	2
Con. 6-3	1	46	2.17	0
6-3A	1	46	2.2	2
6-3B	1	46	2.2	1
6-3C	12	46	26.1	5
Con. 7-4	0	45	0	0
7-4A	2	45	4.4	8
7-4B	1	45	2.2	0
7-4C	4	45	8.9	1
Con. 11-1	0	41	0	0
11-1A	2	41	4.9	3
11-1B	0	41	0	0
11-1C	13	41	31.7	6
Con. 12-2	3	41	7.32	0
12-2A	7	41	17.7	0
12-2B	4	41	9.7	1
12-2C	3	41	7.3	4
Con. 17-3	8	46	17.39	0
17-3A	10	46	21.7	1
17-3B	12	46	26.1	0
17-3C	10	46	21.7	0

Table C7 (cont'd).

Casing Identifier	PowerPlex® Fusion			
	# Loader Alleles	# Possible Loader Alleles	% Loader Profile	# Non-loader Alleles
Con. 18-4	3	40	7.5	0
18-4A	4	40	10	1
18-4B	5	40	12.5	1
18-4C	5	40	12.5	0
Con. 20-1	7	39	17.95	0
20-1A	9	39	23.1	1
20-1B	4	39	10.2	4
20-1C	9	39	23.1	1
Con. 21-2	7	42	16.67	0
21-2A	12	42	28.6	2
21-2B	20	42	47.6	5
21-2C	5	42	11.9	2
Con. 35-3	0	42	0	0
35-3A	0	42	0	0
35-3B	3	42	7.1	0
35-3C	2	42	4.8	0

APPENDIX D. POWERPLEX® FUSION STR PROFILES^{1,2}

Red = non-loader allele

Italicized = allele is consistent with the loader but could have originated from the previous loader

** = non-loader allele could have originated from the previous loader*

† = off-ladder allele (each † symbol represents a different off-ladder allele)

N/A = not applicable

Blank = no alleles recovered at that locus

The cell recovery and DNA extraction method utilized to recover and extract DNAs from spent cartridge casings is denoted with one of the following letters:

A = double swab + organic extraction

B = soak + organic extraction

C = double swab + QIAamp® extraction

D = soak + QIAamp® extraction

E = single swab + FDF® extractions

¹ Two magazines were alternated among loaders in Collection 3, therefore two sets of STR profiles are presented for each volunteer from that collection. first set (blue) = alleles italicized/asterisk based on the loader immediately prior (contamination from firearm); second set (green) = alleles italicized/asterisk based on the preceding magazine loader (contamination from magazine)

² Volunteer P = 1st to load & fire the pistol; Thus, profiles from P were compared to vol. DD (owner of the firearm). Volunteer KK = 1st to load the 2nd magazine; Thus, profiles from KK were only compared to the immediately prior loader.

Table D1. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer CC and collected individually during Collection 1.

Locus	19.1	19.2	19.5	CC
Amel	X	X,Y*		X
D3		15		14,15
D1				11,17.3
D2S441		14		10,14
D10		14,16		14,16
D13				13
Penta E				12,13
D16	11	11,12		11,12
D18				12
D2S1338		16,17		17
CSF		11,12		11,12
Penta D				9,12
THO1	7,9.3	6*,7,8,9.3		7,9.3
vWA		17		17
D21	29	28		28,32.2
D7				9,12
D5		9		9,12
TPOX				8,11
DYS391				N/A
D8	12,14	12,13		12,13
D12		17,24		17,24
D19		14.2,15*,15.2	16.2	14.2,15.2
FGA		25		23,25
D22				16
Method	B	A	E	

Table D2. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer CC and collected in triplicate during Collection 1.

Locus	19-1A	19-1C	19-2A	CC
Amel	X,Y*		X	X
D3			15	14,15
D1	12		11,17.3	11,17.3
D2S441	14		10,14	10,14
D10	13,14,15		16	14,16
D13	13		13	13
Penta E			12,13	12,13
D16	11,12		11,12	11,12
D18	12,13		12,16	12
D2S1338	17		17	17
CSF	11		11,12	11,12
Penta D	13			9,12
THO1	6*,7,8,9.3		7,9.3	7,9.3
vWA	18		16,17	17
D21	32.2		27,28,32.2	28,32.2
D7	12		9,12	9,12
D5	13*		9,12	9,12
TPOX			8	8,11
DYS391				N/A
D8	12,13		12,13,15	12,13
D12			17,24	17,24
D19	14.2,15		14.2,15.2	14.2,15.2
FGA	22.2			23,25
D22			16	16
Method	B	E	A	

Table D3. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer Q and collected individually during Collection 1.

Locus	28.1	28.2	28.4	28.5	Q
Amel	Y	X,Y			X,Y
D3	17	15,16,17	17		15,17
D1		12,16.3			12,16.3
D2S441		11			11
D10		13,15			13,15
D13		11			11,13
Penta E	13	7,11			7,11
D16	11	11	11		11
D18	13,14	13,14			13,14
D2S1338		18,23,24			23,24
CSF		10,11			10,11
Penta D		10			2.2,10
THO1	7*,8,9	8,9			8,9
vWA	16	16,18	16		16,18
D21		30	32.2		30,32.2
D7		8,11			8,11
D5		13			13
TPOX		8			8
DYS391		10			10
D8	13,17	13,17	17		13,17
D12	18	18			18
D19		13,15	15		13,15
FGA		24	16,16.1,18		22,24
D22					11,12
Method	B	A	C	E	

Table D4. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer LL and collected individually during Collection 1.

Locus	30.1	30.2	30.3	30.5	30.6	LL
Amel				X	X	X
D3	15	15	15	15	15	15
D1				17,18.3	17,18.3	17,18.3
D2S441	14		11.3	11.3,14	11.3,14	11.3,14
D10				13,15	13,15	13,15
D13				12	12	12
Penta E				14,17	14,17	14,17
D16	†			11,13	11,13	11,13
D18				14,15	14,15	14,15
D2S1338				17,20	17,20	17,20
CSF				11,12	11,12	11,12
Penta D				9	9	9
THO1		7	7	7	7	7
vWA	16			16,17	16,17	16,17
D21				29,31.2	29,31.2	29,31.2
D7				8	8	8
D5				10,12	10,12	10,12
TPOX				8	8	8
DYS391					10	N/A
D8	13		†,13.3	13,14,20	13,14	13,14
D12			25	18,25	18,25	18,25
D19				13,14	13,14	13,14
FGA	23		†	19,23	19,23,†	19,23
D22		†		†,15	15	15
Method	D	C	E	B	A	

Table D5. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer YY and collected individually during Collection 1.

Locus	34.1	34.3	34.4	34.5	34.6	YY
Amel		X,Y	X,Y		X,Y	X,Y
D3	15	15	15		15	15
D1	15	15,16	15,16		15,16	15,16
D2S441		10,14	10,14	13,14		10,14
D10		14,16	14,16		14	14,16
D13		9,14	9,14			9,14
Penta E		12,13	12,13		12,13	12,13
D16	12	12	12		11,12	12
D18		12,17	12,17		12,17	12,17
D2S1338		18,23	18,23		18	18,23
CSF		11,12	11,12			11,12
Penta D		9,14	9,14			9
THO1	9.3	6,9.3	6,9.3	6	6,9.3	6,9.3
vWA		19	19		19	19
D21		29,30	29,30		29	29,30
D7		9	9		9	9
D5		12,13	12,13			12,13
TPOX		8,11	8,11		11	8,11
DYS391		11	11		11	11
D8	13	13	13	13	13	13
D12		19	19	19	19	19
D19		13	13		13	13
FGA	†,21	21,24	21,24		21,23.2,24	21,24
D22	†	15	15		15	15
Method	E	B	A	D	C	

Table D6. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer RR and collected individually during Collection 1.

Locus	37.1	37.4	37.6	RR
Amel			Y	X,Y
D3			14*,17	16,17
D1	14.3		14,16.3	14,16.3
D2S441				11,16
D10				13,15
D13				8,14
Penta E				7,18
D16			11	11,12
D18				16,17
D2S1338			25	20,25
CSF	11*	12*		10,13
Penta D				9,12
THO1			3,7	6,7
vWA			15	15,18
D21				30
D7				10,12
D5				12,13
TPOX				8
DYS391				11
D8			13*	11,15
D12	18			18,22
D19			†	13,15
FGA	†			20,24
D22				15
Method	A	E	B	

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Table D7. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer RR and collected in triplicate during Collection 1.

Locus	37-1A	37-1B	37-2A	37-2B	37-2C	RR
Amel	X	Y	X			X,Y
D3			16			16,17
D1		16	16.3			14,16.3
D2S441			11			11,16
D10	13					13,15
D13	14					8,14
Penta E						7,18
D16	11,12		9,12			11,12
D18			15,16,17			16,17
D2S1338	20		18			20,25
CSF			10			10,13
Penta D						9,12
THO1	6,7		7,9.3*			6,7
vWA	15,18		15,19			15,18
D21						30
D7						10,12
D5	13		12			12,13
TPOX						8
DYS391						11
D8	11	11	13*	13*		11,15
D12			22			18,22
D19			14.2*			13,15
FGA		20				20,24
D22						15
Method	A	C	B	D	E	

Table D8. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer M and collected individually during Collection 1.

Locus	43.1	43.3	43.6	M
Amel	<i>Y</i>	<i>X,Y</i>		X,Y
D3	<i>15</i>	<i>15,17*</i>		15,16
D1	16	12*		16
D2S441		11*		10,14
D10				13,14
D13		11*,13*		12,14
Penta E		7		7,12
D16	11	11*		9,12
D18		13*,14*		12,17
D2S1338				19,23
CSF				12
Penta D		2.2*,10*		9
THO1	6,9.3	8*,9*		9.3
vWA		18*		16,19
D21		24.2,30		26.2,30
D7				8,9
D5	13*			12
TPOX		8		8,11
DYS391		10*		11
D8		13		13,14
D12		18*,27		19,21
D19	13	13,15*		13,14
FGA	22	18.2,27.3		21,22
D22				15
Method	B	A	E	

Table D9. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer GG and collected individually during Collection 1.

Locus	48.1	48.2	48.4	48.5	GG
Amel	Y		X,Y	X,Y	X,Y
D3	15				14,15
D1			16.3		15.3,17.3
D2S441					11,12
D10					13,15
D13				12	12
Penta E					13,19
D16			†	11,12	12,13
D18					13,16
D2S1338					19,25
CSF				11	11,13
Penta D				10	10,13
TH01			7,9.3	8	8,9.3
vWA					15,17
D21			30*,31.2		29,31.2
D7					9,10
D5					11
TPOX					8
DYS391				10	10
D8			14*	12	12,13
D12			25		20,21
D19			16	19.2	13,16
FGA	25	18			21
D22		†			11,17
Method	C	E	B	A	

Table D10. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer U during Collection 2.

Locus	2-3A	2-3B	2-3C	2-4A	2-4B	2-4C	2-5A	2-5B	2-5C	U
Amel	X	X,Y*	X	X	X	X				X
D3	15	15	15	17*		15,18			15	15
D1	11,17.3	11	17.3			11				11,17.3
D2S441	10,15	15				10,15				10,15
D10	12	12	14			12,14				12,14
D13										9,13
Penta E		15		12		13,15				12,15
D16	11,13		11,13	11,13	11,13	11,13				11,13
D18	13*,14,15		14,15		16	14				14,15
D2S1338	25	17,25			25					17,25
CSF	12	10				10				10,12
Penta D	10									10,11
THO1	6,7	6,7	7	9.3	7	†,6,9.3				6,7
vWA	14	14	15			18	18			14,20
D21	28,30,31			28	28	32.2				28,30
D7						9				11
D5	11	11		11		11				11
TPOX	8,11	11		11	11	8,11				8,11
DYS391										N/A
D8	12	12	12,13*,15		13*,13.2,16	13*			12	12
D12	23		17	17	†	17	14	20		17,23
D19	13	13		14			13			13
FGA	17.2,24,25					19.2		46.2	25,†	24,25
D22	16					16				16
Method	A	A	A	B	B	B	C	C	C	

Table D11. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer MM during Collection 2.

Locus	3-4A	3-4B	3-4C	3-5B	3-5C	3-6C	3-7C	MM
Amel	Y*		X				X	X
D3	18*			15			15	14,16
D1				18.3		12	12,15.3	12,16
D2S441			11				14*	10,11
D10							13*	14,15
D13			8				11	8,12
Penta E							11,12	7,21
D16	12	11		†,12,13*	11		11,13*	12
D18			15*,17	13*	14		16,18	14,14.2
D2S1338				25*			17,19	17,23
CSF				11			11,12	12,13
Penta D			13			13	10,12*	13
THO1		9.3	6,9,9.3	7			9.3	9,9.3
vWA							16,17	17
D21				32.2			29,32.2	29,31.2
D7		8					8,12*	9,11
D5			11*				10,12	9,10
TPOX							8	8
DYS391								N/A
D8		12	†,13,15	13,15	15,†	9	11,13	13,15
D12	22		18	18,23*	18,22		13,18,22	18,22
D19							14,15*	14,15.2
FGA	17.2			24			22.2,24	22,26
D22							16*,17	11,12
Method	A	A	A	B	B	C	D	

Table D12. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer S during Collection 2.

Locus	8-1B	8-1C	8-2A	8-5A	8-5B	8-5C	S
Amel				X	X	X	X
D3				18	18	18	18
D1				11,15	12,15		12,15
D2S441						11	11,11.3
D10				15		15	13,15
D13				13	13		12,13
Penta E					13		12,13
D16				11	11	11	11
D18				12	12	12	12,16
D2S1338						17	17,25
CSF				11	13*		10,11
Penta D							10,13
TH01	6			7,9	6,9		6,9
vWA					18		17,18
D21				29*,34			28
D7				12	10	10	10
D5					12	10	10,12
TPOX				8	11		8,11
DYS391							N/A
D8	13,16			10,13,16	13,16	6,13,14,16	13,16
D12	17.3			18	18,18.3	18.3	18,18.3
D19	†				13.2,15	7,15,16,19.2	13.2,15
FGA	16.1,22.1		†	21		23,†	22,23
D22							15
Method	D	D	E	A	A	A	

Table D12 (cont'd).

Locus	8-6A	8-6B	8-6C	8-7A	8-7B	8-7C	S
Amel	<i>X</i>	<i>X</i>	<i>X</i>				<i>X</i>
D3	18		18	18			18
D1	<i>12,15</i>	<i>12,15</i>	<i>12,15</i>			15	12,15
D2S441	<i>11,11.3</i>	11.3	11.3, <i>14</i>				11,11.3
D10	<i>15</i>	<i>15</i>	<i>15</i>				13,15
D13		<i>12</i>	13		<i>12</i>	<i>12</i>	12,13
Penta E	13	12	12,13				12,13
D16	11	11	11				11
D18	12,16	12	12,16	12		16	12,16
D2S1338	<i>17</i>	<i>17,25</i>		<i>17</i>			17,25
CSF	10	10,11					10,11
Penta D	<i>10,13</i>		10				10,13
THO1	6,9	6,9	6	6,9			6,9
vWA	<i>17,18</i>	<i>16,17,18</i>	<i>17,18</i>	<i>17</i>			17,18
D21	28	28, <i>31</i>	28, <i>29*</i>				28
D7	10	10				10	10
D5	<i>10,12</i>	12					10,12
TPOX			8				8,11
DYS391							N/A
D8	<i>13,16</i>	<i>13,16</i>	†, <i>13,16,19</i>	†			13,16
D12	<i>18,18.3</i>	<i>18,18.3</i>	18.3			†,18.3	18,18.3
D19	15	15	13.2, <i>14</i>	†	†	13.2, <i>18.2</i>	13.2,15
FGA	†	22,23	23,†	†	†	†	22,23
D22	15	15	<i>16</i>		<i>20</i>		15
Method	B	B	B	C	C	C	

Table D13. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer VV during Collection 2.

Locus	10-2A	10-6A	10-6B	10-6C	10-7A	10-7B	10-7C	VV
Amel			X		X	X	Y	X,Y
D3			16			17		14,17
D1					14		14	15,17.3
D2S441			14					11,14
D10					13			12,13
D13								11
Penta E								7,8
D16								12
D18							12	12,16
D2S1338								17,18
CSF	12*					12*		11
Penta D								9,12
THO1					7			9.3
vWA					17	15*		17
D21					32.2			28,32.2
D7						10		10,11
D5			13					11,13
TPOX								11
DYS391								11
D8			8,13*		13*,14			8,12
D12					15			15,25
D19								14,15.2
FGA		32.2,†					27.3	22,23
D22					16*			11,15
Method	D	A	A	A	B	B	B	

Table D14. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer V during Collection 2.

Locus	13-1A	13-1B	13-1C	13-2A	13-2B	13-2C	13-3A	13-3C	V
Amel	X,Y	X,Y	X,Y		X,Y		X,Y		X,Y
D3	14	14	14			16	14		14
D1	17.3	16.3,17.3	16.3				16.3,17.3		16.3,17.3
D2S441	11,11.3		11	11	11,11.3				11,11.3
D10	15,16	15	15,16		15,16		16		15,16
D13	10,12		10						10,12
Penta E	5,14		5,14						5,14
D16	11,12	11,12	12		11,12		11,12	12	11,12
D18	16,17	17	13,16		17		16,17		16,17
D2S1338	20,22		20,22	22			20,22		20,22
CSF	11		10				11		10,11
Penta D	11,12		11	12	12		12		11,12
THO1	9,9.3	9,9.3	6*,9,9.3	3,9	9.3		9,9.3		9,9.3
vWA	16,18	16	16,18		16,17*		16,18	16,18	16,18
D21	28,32.2		28,29		28			36.2	28,32.2
D7	12		11				11		11,12
D5	12	12	12			11			12
TPOX	8	8	8						8
DYS391	11								11
D8	9,12	9	9,12,13*,†	9,12	9,15	†,10	9,12		9,12
D12	21,23	21,23	21,23				21,23		21,23
D19	12,14	11,12,14	14				11,12,14		12,14
FGA	21.2,22	†	22	21.2,41.2	21.2,22		†	†,†	21.2,22
D22	11,16			11			11	†	11,16
Method	B	B	B	C	C	C	D	D	

Table D14 (cont'd).

Locus	13-7A	13-7B	13-7C	V
Amel	X,Y	X,Y	X,Y	X,Y
D3	14,18*	14	14	14
D1	16.3,17.3	16.3,17.3		16.3,17.3
D2S441	11,11.3	11,11.3	11,11.3	11,11.3
D10		15,16	15,16	15,16
D13	10	10,12		10,12
Penta E	5,14	5,14	5,14	5,14
D16	11,12	11,12	12	11,12
D18	17	16,17	16,17	16,17
D2S1338	20,22	20,22	20	20,22
CSF	11	10,11	10	10,11
Penta D	12	11,12	12	11,12
THO1	9,9.3	9,9.3	9,9.3	9,9.3
vWA	16,18	16,18	14,17*,18	16,18
D21	28,32.2	28,32.2	28	28,32.2
D7	12	11,12	11,12	11,12
D5	12	12		12
TPOX		8		8
DYS391	11	11	11	11
D8	9,12	9,12	9,12	9,12
D12	20,21,23	21,23	23	21,23
D19		12	12	12,14
FGA	22	21.2,22	22,23*,32.2	21.2,22
D22		11,16	11,16	11,16
Method	A	A	A	

Table D15. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer HH during Collection 2.

Locus	15-1A	15-1B	15-1C	15-2A	15-2B	15-2C	HH
Amel	X	X			X		X
D3		15					14,18
D1							16,17.3
D2S441							11,14
D10	13						13,15
D13						8	10,11
Penta E	12						10,14
D16	†				11*	11*	9,12
D18	12					15	16
D2S1338						16	17,19
CSF							11,13
Penta D							10
THO1	9.3*		9		9.3*	6	9
vWA							14,16
D21							30,31
D7							11,12
D5	12						9,12
TPOX						11	9,11
DYS391							N/A
D8		10,11	14.1			16	10,13
D12	20					20	20,21
D19						14.2	13,14
FGA					32.2	22	22,25
D22							16
Method	A	A	A	B	B	B	

Table D16. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer L during Collection 2.

Locus	23-2A	23-2B	23-2C	23-3A	23-3B	23-3C	L
Amel	X	X	X	X	X,Y*	X	X
D3	16	16,17		15,16	16	16	16
D1	16,17.3	16,17.3		16,17.3	16	17.3	16,17.3
D2S441	11	11		11	11	11	11
D10		15	14*				13,15
D13	13					12*	13
Penta E	7	7		7			7
D16	11	11	11,12*	11	11	11	11
D18	15,16	15	15		16	16	15,16
D2S1338	17	17			17	17	17
CSF	13		12			12	12,13
Penta D		8.2	9			6	9,11
THO1	8,9.3	8,9.3	3,8,9.3	7,8,9.3	8,9.3	8,9.3	8,9.3
vWA	14	14,18	14	16,18	14,16	14,17*,18	14,18
D21	30	30		30		27,30	27,30
D7	8				10	9,10	8,10
D5					11	12	11,12
TPOX						8	8
DYS391							N/A
D8	13,14	13,14	11,13,14	13		13,14,15,15.1	13,14
D12	20	18,20	18	18	18	18,20,†	18,20
D19		14,15	15	14,15	15	14,15	14,15
FGA	21,23	21,†,†		†	21	21,†	21,23
D22		†,16					15,16
Method	A	A	A	B	B	B	

Table D16 (cont'd).

Locus	23-4A	23-4B	23-4C	23-5A	23-5B	23-5C	L
Amel				<i>X</i>	<i>X</i>	<i>X,Y*</i>	<i>X</i>
D3					16		16
D1		16	15.3,17.3				16,17.3
D2S441							11
D10							13,15
D13							13
Penta E			21				7
D16		11		†,11		11	11
D18					15		15,16
D2S1338							17
CSF							12,13
Penta D							9,11
THO1	9.3		8	9.3		9.3	8,9.3
vWA							14,18
D21							27,30
D7							8,10
D5							11,12
TPOX						8	8
DYS391							N/A
D8				14,19	13,14		13,14
D12					†	18	18,20
D19	15		†,13		14.2	†	14,15
FGA	†			30	†	21	21,23
D22							15,16
Method	C	C	C	D	D	D	

Table D17. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer OO during Collection 2.

Locus	24-3B	24-6A	24-6B	24-6C	24-7A	24-7B	24-7C	OO
Amel			X	Y	X	X	X	X
D3			15					15,18
D1								14,18.3
D2S441								11,14
D10								14,15
D13								9,12
Penta E			12*					10,13
D16			11		8,12		12	12
D18			12*	11,14				11,14
D2S1338		20	20					17,25
CSF								10,11
Penta D			10*					9,12
THO1		6,9	6,7,9,9.3*	6,9.3*		9.3*		6,9
vWA			16				14,17	17,18
D21					29			28,31.2
D7		8	10		10			10
D5								11
TPOX			12*				8	8
DYS391			8					N/A
D8			13,16				16,17	12,17
D12			18*	19,20	19		18*	18.3,20
D19								14,16
FGA	28.2		22					18,24
D22	†							11,15
Method	E	A	A	A	B	B	B	

Table D18. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer T during Collection 2.

Locus	25-3A	25-3B	25-3C	25-4A	25-4B	25-4C	25-5C	25-6A	25-6B	25-6C	25-7C	T
Amel	X				X	X						X
D3	15*		16,18*	16				16				16,17
D1			11		15	17.3						16,17.3
D2S441			14									11,14
D10		14	15*					17				14,17
D13	9*				12*							11
Penta E												11,12
D16	12					11						11,12
D18		13	15	14*	17	15,16		13				13,17
D2S1338												20,24
CSF												10,11
Penta D			12*									8,10
THO1	6,7,9.3	6,8	9.3	6	9*	6						6,7
vWA			15,17*	17*	16,18*							19,20
D21		29		29,34.2								29
D7												8,10
D5			13									12
TPOX			12									8,11
DYS391												N/A
D8			10	14	13,14	11,13,14		13		13		13,14
D12		19,23	22									19,23
D19										11		13,16.2
FGA		24	24					†,†	24			24
D22	11							11				11,18
Method	A	A	A	B	B	B	C	D	D	D	E	

Table D19. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer XX during Collection 2.

Locus	26-4A	26-4B	26-4C	26-5A	26-5B	26-5C	XX
Amel	X	X	X	X	X	X	X
D3	14,15	14,15	14,15	14,15,16	15	14	14,15
D1		14,17.3	14,17.3	17.3	14,17.3		14,17.3
D2S441	14	14	12			12	12,14
D10	14,16	13*,14	14				14,16
D13		11*,12			13	12	12,13
Penta E					12	12	12
D16	11,13	13	11,12*,13	11,13	12*,13	11,13	11,13
D18	17	17,17.2	15,17,18	17,18		17,18	17,18
D2S1338		17	17				17
CSF		10					10,12
Penta D							12
THO1	9,9.3	7,9,9.3	9.3	9,9.3	9,9.3	9	9,9.3
vWA	17,19	17,19	17,19	17,19	17,19	17	17,19
D21			32	29	29	29	29,32
D7			9		9		9,12
D5	10		10			10	10,13
TPOX	12						8,12
DYS391							N/A
D8	10,13	10,13	10,13,17	10,13	10,13	10,13	10,13
D12	18,22	19,22	18,22		22,23	22	18,22
D19	13	14	14	13		13	13,14
FGA	21,23	21.2,23	23	21,†			21,23
D22	6	16,18			16		16,17
Method	A	A	A	B	B	B	

Table D19 (cont'd).

Locus	26-6A	26-6B	26-6C	26-7A	26-7B	26-7C	XX
Amel							X
D3		15			15		14,15
D1		<i>17.3</i>		14			14,17.3
D2S441	11.3			<i>14</i>			12,14
D10							14,16
D13							12,13
Penta E							12
D16	6				13		11,13
D18							17,18
D2S1338				<i>17</i>	16		17
CSF							10,12
Penta D							12
THO1					9		9,9.3
vWA						17	17,19
D21							29,32
D7				<i>12</i>			9,12
D5							10,13
TPOX							8,12
DYS391							N/A
D8			†		<i>10</i>		10,13
D12	18.3				22		18,22
D19				<i>13,14</i>			13,14
FGA	22.2				21		21,23
D22					14		16,17
Method	C	C	C	D	D	D	

Table D20. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer N during Collection 2.

Locus	27-1B	27-1C	27-2B	27-5A	27-5B	27-5C	N
Amel	X			X	X,Y	X,Y	X
D3	16			16	17	14*,17,18	16,17
D1				15.3	14*	15.3,17.3	15.3,17.3
D2S441					11		11
D10						13	13
D13	14				14		12,14
Penta E							13,15
D16				11*,12	12	11*,12	12,13
D18				18*	13,18*	14,16	13,14
D2S1338						20	20,23
CSF							11,12
Penta D	12					12	10,12
TH01	9.3			6,9.3	6,9.3	9.3	6,9.3
vWA	18			16,17,18	17	18	17,18
D21						32.2	30,32.2
D7							11,12
D5						11,13*	12
TPOX							8
DYS391							N/A
D8	13			11,13	13,14	13,15	13
D12	19,21.3			25	17,19	20	19,20
D19	14	†				15.2	13,14
FGA	25.2,29.2	20.3,†	50.2	24	21,46.2		21,25
D22			†	17*		11	11,15
Method	D	D	E	A	A	A	

Table D20 (cont'd).

Locus	27-6A	27-6B	27-6C	27-7B	27-7C	N
Amel	X	X,Y	X	X		X
D3	17	15*,16,17	16			16,17
D1	15	12				15.3,17.3
D2S441		11	16			11
D10						13
D13						12,14
Penta E	12*	12*				13,15
D16	11*,12,13		11*			12,13
D18	12,13,17*	12	12,17*			13,14
D2S1338						20,23
CSF						11,12
Penta D			12			10,12
THO1	6,9*,9.3	6	9*,9.3			6,9.3
vWA	14,16	17,18	17,18			17,18
D21		28				30,32.2
D7		11				11,12
D5	12	12				12
TPOX			8			8
DYS391						N/A
D8	10*,13	13,15	13			13
D12	19		20			19,20
D19			13			13,14
FGA		22,23*				21,25
D22	16*					11,15
Method	B	B	B	C	C	

Table D21. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer B during Collection 2.

Locus	33-1A	33-1B	33-1C	33-2B	33-2C	33-3B	33-3C	B
Amel	X,Y	X,Y	X,Y				Y	X,Y
D3		15	18					16,18
D1	16.3							16.3,17.3
D2S441	10		14					14,15
D10								13,15
D13								10,12
Penta E								7,18
D16		9,13					9	9,13
D18	15	13,15	15					13,15
D2S1338								20,25
CSF	10	10						10,12
Penta D								12,13
THO1	8,9.3	9.3	6,9.3	3				8,9.3
vWA	17,18	17,18	15,17					17,18
D21					31			29,31
D7		9						9,12
D5								11,13
TPOX								8
DYS391								11
D8	8,13		8,11,13,14		8,13	13	8	8,13
D12			23					22,23
D19			15		13,†		14.2	13,15
FGA							22.1	21,23
D22	16	16			†,15			15,16
Method	B	B	B	C	C	D	D	

Table D21 (cont'd).

Locus	33-4B	33-7A	33-7B	33-7C	B
Amel		<i>X,Y</i>	<i>X,Y</i>	<i>X,Y</i>	<i>X,Y</i>
D3	18	16, 17* ,18	16	18	16,18
D1	<i>17.3</i>	16.3, <i>17.3</i>			16.3,17.3
D2S441		<i>14,15</i>		14	14,15
D10	<i>13</i>				13,15
D13		10		10	10,12
Penta E	17.4 ,18			7	7,18
D16		9,13	9, 12* ,13		9,13
D18		15	13,15	13	13,15
D2S1338		25			20,25
CSF		12	12		10,12
Penta D					12,13
THO1	†	8, 9 ,9.3	8,9.3	8	8,9.3
vWA		18	<i>17,18</i>	18	17,18
D21		29			29,31
D7		9		12	9,12
D5		<i>13</i>			11,13
TPOX					8
DYS391					11
D8		8,13	8,13	8,13	8,13
D12	13		22,23		22,23
D19		13, 14*			13,15
FGA	16.1,19.3,23,†,†	31,†			21,23
D22					15,16
Method	E	A	A	A	

Table D22. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer D during Collection 2.

Locus	36-1A	36-1B	36-1C	36-2A	36-2B	36-2C	36-4B	36-4C	D
Amel	X,Y	Y	Y	Y	X	Y		Y	X,Y
D3	17		15				18,18.3,19		17,18
D1				15			14		15
D2S441				11.3*				†,†	11,14
D10									13,14
D13	11								11
Penta E									7,13
D16			12*,13		13		13		13
D18	14				14		†,†		12,14
D2S1338			20	20					17,20
CSF						12		12	11,12
Penta D									9,11
THO1	8,9.3	9*,9.3	9.3	6,9.3		9.3			8,9.3
vWA	15			15				17	15,17
D21							28		28,30
D7									9,12
D5			9						11,12
TPOX									9,11
DYS391									10
D8	8,13	13	9*,13	8,9*,13	9*,12*				8,13
D12	19		18	19,20					15,19
D19	15								14,15
FGA	22.1,†		†				13		21,26
D22	†						18		12,17
Method	A	A	A	B	B	B	D	D	

Table D23. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer WW during Collection 2.

Locus	38-2A	38-2B	38-2C	38-3A	38-3B	38-3C	WW
Amel	X	X,Y	X	X,Y	X	X	X
D3	16,18	16,17*	15,17*	16,17*		16	16,18
D1	11	15		11,15			11,12
D2S441		11,14		11		11	11,14
D10		13*,16	15				15,16
D13	8	11	9	13,14*			8,9
Penta E		7,8		11			11,12
D16	12	12	12	10,11,12	12	12	12
D18	12	12,16,17	14*,15	17	12,15	12,15	12,15
D2S1338		18	18	21		17	17,21
CSF				11			11,12
Penta D		9,12	12				10,12
THO1	9.3	9.3	8,9.3	7,9.3	9.3	8,9.3	9.3
vWA	15,17	15,17		17,18*	17	15,17	15,17
D21	28	28,32.2*		30			28,30
D7		10		10			10,11
D5	13	11					13
TPOX	8	11					8,12
DYS391		11					N/A
D8	10	10,12		10,12	10,12,13*	10,12	10,12
D12	18,19.3	19.3,25		19*	26	17.3,19.3	18,19.3
D19	14	14,15.2	13	13,14	13,14		13,14
FGA		23		20,21*,25*			20,24
D22							16
Method	A	A	A	B	B	B	

Table D23 (cont'd).

Locus	38-4A	38-4B	38-4C	38-5A	WW
Amel	<i>X</i>				<i>X</i>
D3			17*		16,18
D1					11,12
D2S441		11,14	11		11,14
D10		16			15,16
D13					8,9
Penta E					11,12
D16	12	11			12
D18		12			12,15
D2S1338		25		†	17,21
CSF					11,12
Penta D					10,12
THO1					9,3
vWA		15			15,17
D21					28,30
D7					10,11
D5					13
TPOX					8,12
DYS391					N/A
D8		10			10,12
D12		18,21.3			18,19.3
D19					13,14
FGA	†,†			49.2	20,24
D22					16
Method	C	C	C	D	

Table D24. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer SS during Collection 2.

Locus	40-3A	40-3B	40-3C	40-4A	40-4B	40-4C	SS
Amel		X,Y		X			X,Y
D3	14,17*	14,17*		15			14,18
D1		15*,18.3					14,17.3
D2S441	10	11		14*		11	11
D10	13*,14	13*,15					14
D13	11*						10,12
Penta E	7	14					7,19
D16	12	10,12		11	10	12	11,12
D18	10	16				10,12	10,12
D2S1338	22	19				18	17,20
CSF	11,12	12				12	11,12
Penta D	9	9					9,12
THO1	8	7,8		6,8	8		8
vWA	18	15*		15*		16,17	17
D21	29	29,31					29,32.2
D7							12
D5		11*					13
TPOX	8	8					9
DYS391	11						11
D8	†,10,11,13	11,13				12,13,14	12,13
D12	15,20	18	†				15,24
D19		13,14			15		14,15
FGA			23.1				22,24
D22		13					16
Method	A	A	A	B	B	B	

Table D25. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer Y during Collection 2.

Locus	41-4A	41-4B	41-4C	41-5A	41-5B	41-5C	41-6A	41-6B	41-7C	Y
Amel	Y	X,Y	X,Y	X,Y	X,Y	X,Y				X,Y
D3		14	17	17,18	16	17		16		16,17
D1		16.3,17.3*			14	16.3				12,14
D2S441		11.3	14			14		14		14,15
D10	14	15,16			14					14,15
D13		12	9,13	13						13,14
Penta E		5,14								5,14
D16	11	11,12	13	11,12	11	11				11,12
D18	16*	16*,17	17	17	15*,17			17		17
D2S1338		20	17,24		24					17,24
CSF		10								12,14
Penta D		12	8		8					8,13
THO1	6	9,9.3	6,9.3	9.3	9.3	8*,9,9.3		9.3		9,9.3
vWA		16,18*	14	14	16		14			14,16
D21		28,32.2	30.2							29,30.2
D7		11,12	10,12							8,10
D5		12								12
TPOX		8	11							8
DYS391		11								11
D8	10,15	9,12	10,14	10,14	10,14	13*,14		14		10,14
D12		21,23	17,20*	20*,†	17	21		17,24.3		17,21
D19		12,14*	13,15.2	9,16.2				12,13		13,16.2
FGA		21.2,22	20,27						†, 22	22,27
D22		11,16								11,16
Method	A	A	A	B	B	B	C	C	D	

Table D26. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer II during Collection 2.

Locus	50-1C	50-5A	50-5B	50-5C	50-6A	50-6B	50-6C	50-7B	50-7C	II
Amel		X,Y	Y	X,Y	X,Y	X	Y			X,Y
D3		17	17	17	17	17				17
D1		12,15	15,18.3		15	15				15,18.3
D2S441		11,11.3	10,11	10,11			10,11			10,11
D10		15	13	15						13,15
D13		12	11,12	11		11				11,12
Penta E			13,14							13,14
D16		11,12	11,12	11,12	10,12	11,12				12
D18			16	16	17					16,17
D2S1338				19	21			10		19,21
CSF		10	12							12
Penta D						12				9,13
THO1		7,8,9.3	6,8,9,9.3	8	8,9.3	8,9.3	8,9.3			8,9.3
vWA		17,18	15,17	15,17	15,17					15,17
D21		29	31		31					29,31
D7			12							10,12
D5		11	12	12						11,12
TPOX		11	8				8			8
DYS391				11						11
D8		11,13,14,16	11,13	11,13,15,16	11,13	11,13	†,13			11,13
D12	†	18	18,20,†	18,19	18		22			18,20
D19		16.2	14	15.2	13.2,15.2		†,15.2			14,15.2
FGA	22.2	22,23	23,†	21,†	21,†		†			21,23
D22			15,16							15,16
Method	D	A	A	A	B	B	B	C	C	

Table D27. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer W during Collection 3.

Locus	1-1A	1-1B	1-1C	1-2A	1-2B	1-2C	1-3A	1-3B	1-3C	W
Amel	X	X,Y*	X		X	X,Y*				X
D3	14,15*,16		14,16			14				14,16
D1	14									14,15.3
D2S441		11.3	14		14					11.3,14
D10			15							13,15
D13		10,11*					14			10,12
27-7cPenta E			12							12
D16	9*,13	9*,13	11,13							11,13
D18										12
D2S1338		17*								18,22
CSF		10	12							10,12
Penta D										9,11
THO1		6,7,8*,9.3	6,9.3	9.3	6					6,9.3
vWA	15*,16*	16*	15*,17		17			16*		17
D21	30*,32,33.2		28,33.2							28,33.2
D7			9							9,10
D5		13	12,13							12,13
TPOX		12	12							8,12
DYS391										N/A
D8	15	8,10	10,15			15				10,15
D12	18,19*		18,22	17	21		†			18,21
D19	13*,14	13*	7,15							14,15
FGA	†	21	†,18*			22*	†			21,23
D22	10*						6		10*	16
Method	A	A	A	B	B	B	C	C	C	

Table D28. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer W during Collection 3.

Locus	1-1A	1-1B	1-1C	1-2A	1-2B	1-2C	1-3A	1-3B	1-3C	W
Amel	X	X,Y*	X		X	X,Y*				X
D3	14,15*,16		14,16			14				14,16
D1	14									14,15.3
D2S441		11.3	14		14					11.3,14
D10			15							13,15
D13		10,11					14*			10,12
Penta E			12							12
D16	9*,13	9*,13	11,13							11,13
D18										12
D2S1338		17								18,22
CSF		10	12							10,12
Penta D										9,11
THO1		6,7,8,9.3	6,9.3	9.3	6					6,9.3
vWA	15,16*	16*	15,17		17			16*		17
D21	30*,32,33.2		28,33.2							28,33.2
D7			9							9,10
D5		13	12,13							12,13
TPOX		12	12							8,12
DYS391										N/A
D8	15	8,10	10,15			15				10,15
D12	18,19*		18,22	17	21		†			18,21
D19	13*,14	13*	7,15							14,15
FGA	†	21	†,18			22*	†			21,23
D22	10*						6		10*	16
Method	A	A	A	B	B	B	C	C	C	

Table D29. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer QQ during Collection 3.

Locus	6-1A	6-2B	6-2A	6-2C	6-3A	6-3B	6-3C	6-4C	QQ
Amel		Y	X,Y				X		X,Y
D3			16		16	15*	16		16,18
D1		17.3		14	14				16.3,17.3
D2S441			10*				14		14,15
D10			12				14*		13,15
D13			14*						10,12
Penta E							7	7	7,18
D16		9,11	9,12*				11		9,13
D18		12*,15	12*				15		13,15
D2S1338			23*		17			25	20,25
CSF									10,12
Penta D			13						12,13
THO1		8	9,3	8,9,3			8,9,3		8,9,3
vWA	15	16*	15,16*,19*				16*,18	15	17,18
D21			26.2*	27					29,31
D7			8*						9,12
D5			12*				12*		11,13
TPOX						8			8
DYS391									11
D8		13,15	13				13,15	13	8,13
D12			21*				22	21*	22,23
D19		11.1	13				13		13,15
FGA		24	†				23		21,23
D22				16					15,16
Method	D	A	A	A	B	B	B	C	

Table D30. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer P during Collection 3.

Locus	7-3A	7-3B	7-3C	7-4A	7-4B	7-4C	P
Amel		X	X			X,Y	X,Y
D3				16*		14	15,17
D1	11		11	11			11,17.3
D2S441			11.3				11,12
D10		14	13				13,14
D13				12*			8,10
Penta E							11,21
D16			†,11	11			11
D18			16				14,18
D2S1338						19	25,26
CSF							10
Penta D							9,12
THO1		6*,7		9*		9.3	7,9.3
vWA		17			16		16,17
D21							29,32.2
D7							8,11
D5						12	12,13
TPOX							8,11
DYS391							10
D8	12		11,13			†	13,15
D12	17			15,19	20		17,21
D19							13,14
FGA				22*,25			19,21
D22				14			15,17
Method	A	A	A	B	B	B	

Table D31. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by either volunteer P or volunteer Z during Collection 3. Due to miss labeling of bags and minimal STR data, these results could not confidently be associated with a particular volunteer.

Locus	7/18-1A.2	7/18-2B.1	7/18-2C.1	P (coincides w/7)	Z (coincides w/ 18)
Amel	X			X,Y	X
D3		17	15	15,17	15,16
D1				11,17.3	15,18.3
D2S441				11,12	12,14
D10			12,13	13,14	13
D13				8,10	9,11
Penta E				11,21	7,14
D16				11	9,12
D18				14,18	12,15
D2S1338			17*	25,26	19,25
CSF				10	11,13
Penta D			12	9,12	10,14
THO1		7	3	7,9.3	6,9.3
vWA				16,17	18,19
D21		29		29,32.2	30
D7				8,11	10,11
D5				12,13	12,13
TPOX				8,11	8,11
DYS391				10	N/A
D8			15	13,15	11,13
D12				17,21	20
D19				13,14	14
FGA				19,21	21,24
D22				15,17	15
Method	C	D	D		

Table D32. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer P during Collection 3.

Locus	7-3A	7-3B	7-3C	7-4A	7-4B	7-4C	P
Amel		X	X			X,Y	X,Y
D3				16*		14	15,17
D1	11		11	11			11,17.3
D2S441			11.3				11,12
D10		14	13				13,14
D13				12*			8,10
Penta E							11,21
D16			†,11	11			11
D18			16*				14,18
D2S1338						19	25,26
CSF							10
Penta D							9,12
THO1		6*,7		9		9.3	7,9.3
vWA		17			16		16,17
D21							29,32.2
D7							8,11
D5						12	12,13
TPOX							8,11
DYS391							10
D8	12		11,13			†	13,15
D12	17			15,19	20		17,21
D19							13,14
FGA				22,25*			19,21
D22				14			15,17
Method	A	A	A	B	B	B	

Table D33. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by either volunteer P or volunteer Z during Collection 3. Due to miss labeling of bags and minimal STR data, these results could not confidently be associated with a particular volunteer.

Locus	7/18-1A.2	7/18-2B.1	7/18-2C.1	P (coincides w/7)	Z (coincides w/ 18)
Amel	X			X,Y	X
D3		17	15	15,17	15,16
D1				11,17.3	15,18.3
D2S441				11,12	12,14
D10			12,13	13,14	13
D13				8,10	9,11
Penta E				11,21	7,14
D16				11	9,12
D18				14,18	12,15
D2S1338			17	25,26	19,25
CSF				10	11,13
Penta D			12	9,12	10,14
THO1		7	3	7,9.3	6,9.3
vWA				16,17	18,19
D21		29		29,32.2	30
D7				8,11	10,11
D5				12,13	12,13
TPOX				8,11	8,11
DYS391				10	N/A
D8			15	13,15	11,13
D12				17,21	20
D19				13,14	14
FGA				19,21	21,24
D22				15,17	15
Method	C	D	D		

Table D34. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer DD during Collection 3.

Locus	11-1A	11-1B	11-1C	11-2A	11-2B	11-2C	11-3A	11-3C	11-4A	11-4B	11-4C	DD
Amel	Y							X			Y	X,Y
D3			15	16								15,16
D1			11,15*,16							15*		16
D2S441			10,14									10,14
D10			14									13,14
D13			12									12,14
Penta E			14*									7,12
D16			9,12				9			12	9	9,12
D18	18										17	12,17
D2S1338			18									19,23
CSF												12
Penta D												9
THO1			6*,9.3							9	9.3	9.3
vWA			19					15		16		16,19
D21			30					30				26.2,30
D7						9					8	8,9
D5												12
TPOX												8,11
DYS391												11
D8	12,13		11*,14					15				13,14
D12	†			19			17				21	19,21
D19			13							14		13,14
FGA	18						31.2	17				21,22
D22												15
Method	B	B	B	C	C	C	D	D	A	A	A	

Table D35. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer DD during Collection 3.

Locus	11-1A	11-1B	11-1C	11-2A	11-2B	11-2C	11-3A	11-3C	11-4A	11-4B	11-4C	DD
Amel	Y							X			Y	X,Y
D3			15	16								15,16
D1			11,15,16							15		16
D2S441			10,14									10,14
D10			14									13,14
D13			12									12,14
Penta E			14									7,12
D16			9,12				9			12	9	9,12
D18	18										17	12,17
D2S1338			18*									19,23
CSF												12
Penta D												9
THO1			6*,9.3							9	9.3	9.3
vWA			19					15		16		16,19
D21			30					30				26.2,30
D7						9					8	8,9
D5												12
TPOX												8,11
DYS391												11
D8	12,13		11,14					15*				13,14
D12	†			19			17				21	19,21
D19			13							14		13,14
FGA	18						31.2	17				21,22
D22												15
Method	B	B	B	C	C	C	D	D	A	A	A	

Table D36. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer FF during Collection 3.

Locus	12-1A	12-1B	12-1C	12-2A	12-2B	12-2C	12-3A	12-3B	12-3C	12-4B	FF
Amel			X,Y	X	X,Y		X			X	X
D3	18					15	15				15,18
D1	16.3,17.3	17.3									14,17.3
D2S441											10,11
D10											14,17
D13				9							9,11
Penta E											12
D16	10,12		†,11*								10,12
D18			18*				17			17	12,17
D2S1338											17,18
CSF					9						9,10
Penta D											8,16
THO1	6		6,9.3	6			9.3				6,9.3
vWA				16	16					16	16
D21					30					30	30,33.2
D7											10,12
D5			11,12	10							10,12
TPOX											8,11
DYS391											N/A
D8	14	11*	14	15		13*,14,15		6		12,15	14,15
D12		20				23	20		20	18*	20
D19		12	13,13.1			7				14*,15	13,15
FGA			23	20		28.3,†		†			20
D22		12							†		11,16
Method	A	A	A	B	B	B	C	C	C	D	

Table D37. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer FF during Collection 3.

Locus	12-1A	12-1B	12-1C	12-2A	12-2B	12-2C	12-3A	12-3B	12-3C	12-4B	FF
Amel			X,Y*	X	X,Y*		X			X	X
D3	18					15	15				15,18
D1	16.3,17.3	17.3									14,17.3
D2S441											10,11
D10											14,17
D13				9							9,11
Penta E											12
D16	10,12		†,11*								10,12
D18			18*				17			17	12,17
D2S1338											17,18
CSF					9						9,10
Penta D											8,16
THO1	6		6,9.3	6			9.3				6,9.3
vWA				16	16					16	16
D21					30					30	30,33.2
D7											10,12
D5			11,12	10							10,12
TPOX											8,11
DYS391											N/A
D8	14	11	14	15		13*,14,15		6		12,15	14,15
D12		20				23	20		20	18	20
D19		12	13,13.1			7				14*,15	13,15
FGA			23	20		28.3,†		†			20
D22		12							†		11,16
Method	A	A	A	B	B	B	C	C	C	D	

Table D38. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer KK during Collection 3.

Locus	17-1A	17-1C	17-2A	17-2B	17-2C	KK
Amel		<i>Y</i>	<i>X,Y</i>		<i>X</i>	<i>X,Y</i>
D3			15			15,16
D1						17,17.3
D2S441			<i>14</i>	10		10,14
D10			16			14,16
D13						12
Penta E						7,18
D16			11, 13*	9	9,11	9,11
D18				12	16	16,18
D2S1338					23	23,25
CSF						11,12
Penta D			<i>13</i>			12,13
TH01	6		6,7	6,7	6,8*,9.3*	6,7
vWA			15	15	15,17*,18*	15,16
D21						31,32.2
D7			10			10,11
D5						11,12
TPOX						8,10
DYS391						10
D8			<i>13</i>	<i>13,14</i>	14,15	13,14
D12			17	17,19	†, 17	17,23
D19		†			13*	14,15
FGA				25		23,25
D22						11,16
Method	D	D	A	A	A	

Table D38 (cont'd).

Locus	17-3A	17-3B	17-3C	17-4A	17-4B	17-4C	KK
Amel	X,Y	X,Y	X,Y				X,Y
D3	15,16	16	15				15,16
D1	17,17.3						17,17.3
D2S441		14					10,14
D10							14,16
D13	12						12
Penta E			7				7,18
D16	9	9	11				9,11
D18	13*	16,18				15*	16,18
D2S1338				23			23,25
CSF							11,12
Penta D							12,13
THO1		6,7	7				6,7
vWA		15					15,16
D21				32.2			31,32.2
D7			10				10,11
D5							11,12
TPOX							8,10
DYS391							10
D8	14	14	14	†			13,14
D12	17		17,23	†			17,23
D19						12.2	14,15
FGA		25	†	†			23,25
D22						20	11,16
Method	B	B	B	C	C	C	

Table D39. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer Z during Collection 3.

Locus	18-3A	18-3B	18-3C	18-4A	18-4B	18-4C	Z
Amel	X	X,Y	X	X	X		X
D3	15,16	15	15			16	15,16
D1							15,18.3
D2S441	12,14						12,14
D10			13				13
D13							9,11
Penta E		7					7,14
D16	9,11,14	12	10*		†		9,12
D18	18	12,15	12	15			12,15
D2S1338	19	25					19,25
CSF		11					11,13
Penta D		10					10,14
TH01	6,7,9.3	6,9.3	6,9.3	6	9.3	6	6,9.3
vWA	18,19	15				18	18,19
D21	30	29	30	29		30	30
D7	10	10					10,11
D5	10*,12			13			12,13
TPOX	8						8,11
DYS391							N/A
D8	†,11,13	13,15*	13	†	11,13	11	11,13
D12	19.1,20		20		20,25		20
D19	14	14					14
FGA	19.3	21,24			†		21,24
D22							15
Method	A	A	A	B	B	B	

Table D40. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by either volunteer P or volunteer Z during Collection 3. Due to miss labeling of bags and minimal STR data, these results could not confidently be associated with a particular volunteer.

Locus	7/18-1A.1	7/18-1B.1	7/18-1C.1	P (coincides w/7)	Z (coincides w/ 18)
Amel				X,Y	X
D3				15,17	15,16
D1		15		11,17.3	15,18.3
D2S441		11*		11,12	12,14
D10				13,14	13
D13				8,10	9,11
Penta E				11,21	7,14
D16				11	9,12
D18				14,18	12,15
D2S1338		24		25,26	19,25
CSF				10	11,13
Penta D				9,12	10,14
THO1	6			7,9.3	6,9.3
vWA		18		16,17	18,19
D21				29,32.2	30
D7		10		8,11	10,11
D5		12		12,13	12,13
TPOX				8,11	8,11
DYS391				10	N/A
D8	13			13,15	11,13
D12		23		17,21	20
D19				13,14	14
FGA				19,21	21,24
D22				15,17	15
Method	C	C	C		

Table D41. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer Z during Collection 3.

Locus	18-3A	18-3B	18-3C	18-4A	18-4B	18-4C	Z
Amel	X	X,Y	X	X	X		X
D3	15,16	15	15			16	15,16
D1							15,18.3
D2S441	12,14						12,14
D10			13				13
D13							9,11
Penta E		7					7,14
D16	9,11*,14	12	10		†		9,12
D18	18*	12,15	12	15			12,15
D2S1338	19	25					19,25
CSF		11					11,13
Penta D		10					10,14
THO1	6,7,9.3	6,9.3	6,9.3	6	9.3	6	6,9.3
vWA	18,19	15				18	18,19
D21	30	29*	30	29*		30	30
D7	10	10					10,11
D5	10*,12			13			12,13
TPOX	8						8,11
DYS391							N/A
D8	†,11,13	13,15*	13	†	11,13	11	11,13
D12	19.1,20		20		20,25		20
D19	14	14					14
FGA	19.3	21,24*			†		21,24
D22							15
Method	A	A	A	B	B	B	

Table D42. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by either volunteer P or volunteer Z during Collection 3. Due to miss labeling of bags and minimal STR data, these results could not confidently be associated with a particular volunteer.

Locus	7/18-1A.1	7/18-1B.1	7/18-1C.1	P (coincides w/7)	Z (coincides w/ 18)
Amel				X,Y	X
D3				15,17	15,16
D1		15		11,17.3	15,18.3
D2S441		11		11,12	12,14
D10				13,14	13
D13				8,10	9,11
Penta E				11,21	7,14
D16				11	9,12
D18				14,18	12,15
D2S1338		24		25,26	19,25
CSF				10	11,13
Penta D				9,12	10,14
THO1	6			7,9.3	6,9.3
vWA		18		16,17	18,19
D21				29,32.2	30
D7		10		8,11	10,11
D5		12		12,13	12,13
TPOX				8,11	8,11
DYS391				10	N/A
D8	13			13,15	11,13
D12		23		17,21	20
D19				13,14	14
FGA				19,21	21,24
D22				15,17	15
Method	C	C	C		

Table D43. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer PP during Collection 3.

Locus	20-1A	20-1B	20-1C	20-2A	20-2B	20-2C	20-4A	20-4B	20-4C	PP
Amel	X		X	X	X		X	Y*	X,Y*	X
D3	15	14,15	15	15			15			15
D1	12		15.3				12,18.3	17	17.3*	12,15.3
D2S441							13	14	10,14	14
D10										13
D13									12	11
Penta E								7		11,12
D16	11		13		11	11	†,11,13	9,13	9,12	11,13
D18	18		18				18		18,19	16,18
D2S1338	19	19							19,23	17,19
CSF										11,12
Penta D					12				12	10,12
THO1	9,9.3		9.3				9.3	9.3	6,7*,8,9.3	9.3
vWA						16	16	17	16	16,17
D21		28	29					31,32.2	33.2	29,32.2
D7					8			10	10,11*	8,12
D5		11							12	10,12
TPOX									10	8
DYS391										N/A
D8	13	11,13	11,†,14		11,15*	13	11,13	11,13,14,17	13,14	11,13
D12	18	21*					22	17*,†	27	18,22
D19						13.1		14,15		14,15
FGA			24				15	25	22.2,25	22.2,24
D22										16,17
Method	B	B	B	C	C	C	A	A	A	

Table D44. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer PP during Collection 3.

Locus	20-1A	20-1B	20-1C	20-2A	20-2B	20-2C	20-4A	20-4B	20-4C	PP
Amel	X		X	X	X		X	Y*	X,Y*	X
D3	15	14,15	15	15			15			15
D1	12		15.3				12,18.3	17	17.3	12,15.3
D2S441							13	14	10*,14	14
D10										13
D13									12*	11
Penta E								7		11,12
D16	11		13		11	11	†,11,13	9,13	9,12	11,13
D18	18		18				18		18,19	16,18
D2S1338	19	19							19,23	17,19
CSF										11,12
Penta D					12				12	10,12
THO1	9*,9.3		9.3				9.3	9.3	6*,7,8,9.3	9.3
vWA						16	16	17	16	16,17
D21		28	29					31,32.2	33.2	29,32.2
D7					8			10*	10*,11	8,12
D5		11							12	10,12
TPOX									10	8
DYS391										N/A
D8	13	11,13	11,†,14		11,15	13	11,13	11,13,14,17	13,14	11,13
D12	18	21*					22	17,†	27	18,22
D19						13.1		14,15		14,15
FGA			24				15	25	22.2,25	22.2,24
D22										16,17
Method	B	B	B	C	C	C	A	A	A	

Table D45. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer X during Collection 3.

Locus	21-1A	21-1B	21-1C	21-2A	21-2B	21-2C	X
Amel		X,Y	Y	X,Y	X		X,Y
D3	16	15,16	15	15,16	15	15	15,16
D1	11,14	11,14		11	14		11,14
D2S441		14		14	14		14
D10		12,14	14				12,14
D13						11	11,12
Penta E					12,14		12,14
D16	9,11,13	9,13	9	9	9,13	9	9,13
D18	15			15	15		15
D2S1338					17,21		17,21
CSF					11		11
Penta D							12,14
THO1	8,9.3*	8	8	8	8	8	8
vWA	15,16	15,16		15			15,16
D21		27,30		27		26.2*	27,30
D7					9*		10,11
D5					11		11,12
TPOX		8					8,9
DYS391							10
D8	15	13*,15	15	15	15	11,15	15
D12	18	18,19,20.3,23,†	18,21*	20,21*	18,19,23		18,19
D19		13.2	18		12,13		12,13
FGA	18				14,22,30.2		18,22
D22		14			15*		10,14
Method	A	A	A	B	B	B	

Table D45 (cont'd).

Locus	21-3A	21-3B	21-3C	21-4A	X
Amel		<i>Y</i>			X,Y
D3		<i>15,16</i>		<i>15</i>	15,16
D1		11	11,14	17.3	11,14
D2S441			<i>14</i>	11	14
D10		12			12,14
D13					11,12
Penta E					12,14
D16	9,13	13	9,13	11	9,13
D18		15	15		15
D2S1338			17		17,21
CSF					11
Penta D					12,14
THO1	8	8		9	8
vWA		<i>16</i>			15,16
D21			27	30	27,30
D7	11				10,11
D5					11,12
TPOX					8,9
DYS391					10
D8	10,13.2,15	9,15	15		15
D12	†,19	19		18,18.3,†	18,19
D19	16.2				12,13
FGA		†		19	18,22
D22			12	†	10,14
Method	C	C	C	D	

Table D46. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer X during Collection 3.

Locus	21-1A	21-1B	21-1C	21-2A	21-2B	21-2C	X
Amel		X,Y	Y	X,Y	X		X,Y
D3	16	15,16	15	15,16	15	15	15,16
D1	11,14	11,14		11	14		11,14
D2S441		14		14	14		14
D10		12,14	14				12,14
D13						11	11,12
Penta E					12,14		12,14
D16	9,11,13	9,13	9	9	9,13	9	9,13
D18	15			15	15		15
D2S1338					17,21		17,21
CSF					11		11
Penta D							12,14
THO1	8,9.3*	8	8	8	8	8	8
vWA	15,16	15,16		15			15,16
D21		27,30		27		26.2	27,30
D7					9		10,11
D5					11		11,12
TPOX		8					8,9
DYS391							10
D8	15	13*,15	15	15	15	11*,15	15
D12	18	18,19,20.3,23,†	18,21	20*,21	18,19,23		18,19
D19		13.2	18		12,13		12,13
FGA	18				14,22,30.2		18,22
D22		14			15*		10,14
Method	A	A	A	B	B	B	

Table D46 (cont'd).

Locus	21-3A	21-3B	21-3C	21-4A	X
Amel		Y			X,Y
D3		15,16		15	15,16
D1		11	11,14	17.3	11,14
D2S441			14	11	14
D10		12			12,14
D13					11,12
Penta E					12,14
D16	9,13	13	9,13	11	9,13
D18		15	15		15
D2S1338			17		17,21
CSF					11
Penta D					12,14
THO1	8	8		9	8
vWA		16			15,16
D21			27	30	27,30
D7	11				10,11
D5					11,12
TPOX					8,9
DYS391					10
D8	10,13.2,15	9,15	15		15
D12	†,19	19		18,18.3,†	18,19
D19	16.2				12,13
FGA		†		19	18,22
D22			12	†	10,14
Method	C	C	C	D	

Table D47. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer UU during Collection 3.

Locus	35-2A	35-2B	35-2C	35-3A	35-3B	35-3C	UU
Amel	X	X,Y			X		X,Y
D3	14	15*,16,17					16,17
D1		11,12,14,17.3*					12,16.3
D2S441		14*					8,10
D10							13,15
D13		13					11,12
Penta E		13					12
D16	9*,12	11,12	11			11	11
D18		16*,17					13,15
D2S1338	17	17,21					17
CSF							10,12
Penta D							12,13
THO1	9.3	7*,9,9.3			6,9		6,9
vWA	15*,17	14,16*,17,18					14,20
D21		29,30.2					29,30
D7		8,10					10,13
D5						10	10,12
TPOX	11	8					8,11
DYS391							11
D8		10,12,13,14*					13
D12		17*,18			†		18,21
D19		13,14,15*					13.2,14
FGA		14,22	18,30				22
D22		15,16					15,16
Method	A	A	A	B	B	B	

Table D48. Alleles obtained with PowerPlex® Fusion from spent cartridge casings loaded by volunteer UU during Collection 3.

Locus	35-2A	35-2B	35-2C	35-3A	35-3B	35-3C	UU
Amel	X	X,Y			X		X,Y
D3	14	15,16,17					16,17
D1		11,12,14,17.3*					12,16.3
D2S441		14*					8,10
D10							13,15
D13		13					11,12
Penta E		13					12
D16	9*,12	11,12	11			11	11
D18		16,17					13,15
D2S1338	17	17,21					17
CSF							10,12
Penta D							12,13
THO1	9.3*	7,9,9.3*			6,9		6,9
vWA	15,17*	14,16,17*,18*					14,20
D21		29,30.2					29,30
D7		8,10					10,13
D5						10	10,12
TPOX	11	8					8,11
DYS391							11
D8		10,12,13,14					13
D12		17,18			†		18,21
D19		13*,14,15*					13.2,14
FGA		14,22	18,30				22
D22		15,16					15,16
Method	A	A	A	B	B	B	

APPENDIX E. DNA QUANTITIES RECOVERED FROM SPENT CARTRIDGE CASINGS FROM COLLECTION 2

Table E1. Quantitation results for individually swabbed 0.45 casings from Collection 2.

Sample	Volume (µL)	Concentration (pg/µL)	Yield (pg)
39-4.45a	27.50	4.57E-01	12.57
39-4.45b	34.00	8.16E-01	27.74
39-4.45c	31.80	1.49E+00	47.38
51-2.45a	34.00	2.42E-01	8.23
51-2.45b	26.70	4.08E-01	10.89
51-2.45c	22.00	9.96E-01	21.91
52-3.45a	27.40	1.06E+00	29.04
52-3.45b	30.70	1.71E+00	52.50
52-3.45c	28.60	7.27E-01	20.79
53-4.45a	33.20	2.56E+00	84.99
53-4.45b	25.30	1.67E+00	42.25
53-4.45c	28.50	1.17E+00	33.35
54-3.45a	34.20	2.91E-01	9.95
54-3.45b	31.10	1.57E-01	4.88
54-3.45c	35.00	2.40E-01	8.40
55-1.45a	30.30	2.76E-01	8.36
55-1.45b	30.20	2.79E-01	8.43
55-1.45c	29.20	4.20E-01	12.26
56-4.45a	29.40	2.95E-01	8.67
56-4.45b	29.00	5.00E-02	1.45
56-4.45c	33.80	4.61E-02	1.56
57-1.45a	36.00	4.35E-01	15.66
57-1.45b	31.70	3.48E-01	11.03
57-1.45c	33.00	1.34E-01	4.42
58-3.45a	21.00	1.51E+00	31.71
58-3.45b	28.40	2.05E+00	58.22
58-3.45c	27.20	1.30E+00	35.36
59-2.45a	30.00	8.70E-01	26.10
59-2.45b	30.90	5.77E-01	17.83
59-2.45c	33.30	3.83E-01	12.75
60-4.45a	30.20	8.37E-01	25.28
60-4.45b	31.20	1.07E+00	33.38
60-4.45c	34.80	3.74E+00	130.15
61-4.45a	28.90	1.78E-01	5.14
61-4.45b	29.50	5.13E-01	15.13

Table E1 (cont'd)

61-4.45c	25.50	8.66E-01	22.08
62-3.45a	28.80	3.93E-01	11.32
62-3.45b	27.50	4.24E+00	116.60
62-3.45c	30.50	2.76E+00	84.18
63-2.45a	24.60	1.22E+00	30.01
63-2.45b	34.00	1.12E+00	38.08
63-2.45c	28.40	1.17E+00	33.23
65-2.45a	29.60	4.94E-01	14.62
65-2.45b	26.50	1.37E+00	36.31
65-2.45c	32.50	7.95E-01	25.84
66-1.45a	28.80	1.11E+00	31.97
66-1.45b	31.70	1.02E+00	32.33
66-1.45c	30.70	2.42E-01	7.43
67-1.45a	29.50	1.09E+00	32.16
67-1.45b	34.50	2.09E+00	72.11
67-1.45c	34.20	4.41E-01	15.08
68-1.45a	30.50	9.75E-02	2.97
68-1.45b	36.00	3.60E-01	12.96
68-1.45c	30.00	1.79E-01	5.37
69-2.45a	28.90	3.02E-01	8.73
69-2.45b	30.00	1.43E-01	4.29
69-2.45c	29.80	6.39E-02	1.90
70-3.45a	33.40	4.46E-01	14.90
70-3.45b	33.10	5.57E-01	18.44
70-3.45c	30.30	1.33E+00	40.30

Table E2. Quantitation results of individually swabbed 0.22 casings from Collection 2.

Sample	Volume (μL)	Concentration (pg/μL)	Yield (pg)
39-4.22a	32.80	7.74E-01	25.39
39-4.22b	32.00	4.16E-01	13.31
51-2.22a	32.60	1.46E-01	4.76
51-2.22b	33.60	1.12E-01	3.76
51-2.22c	36.30	1.54E-01	5.59
52-3.22a	27.40	6.34E-02	1.74
52-3.22b	31.50	4.69E-01	14.77
52-3.22c	31.30	2.01E-01	6.29
53-4.22a	33.00	7.32E-01	24.16
53-4.22b	35.50	5.04E-01	17.89
53-4.22c	29.70	2.17E-01	6.44

Table E2 (cont'd)

54-3.22a	31.30	4.69E-01	14.68
54-3.22b	29.60	4.81E-01	14.24
54-3.22c	32.50	2.91E-01	9.46
55-1.22a	33.70	7.07E-01	23.83
55-1.22b	28.30	9.86E-01	27.90
55-1.22c	31.20	1.90E-01	5.93
56-4.22a	32.50	5.92E-01	19.24
56-4.22b	30.10	5.07E-01	15.26
56-4.22c	36.00	6.06E-01	21.82
57-1.22a	29.80	6.60E-02	1.97
57-1.22b	27.70	9.23E-02	2.56
57-1.22c	33.00	4.99E-02	1.65
58-3.22a	30.00	1.24E-01	3.72
58-3.22b	31.80	6.50E-02	2.07
58-3.22c	35.50	3.51E-01	12.46
59-2.22a	26.00	6.27E-01	16.30
59-2.22b	29.50	5.80E-01	17.11
59-2.22c	30.00	4.50E-01	13.50
60-4.22a	29.30	5.20E-01	15.24
60-4.22b	26.50	1.32E+00	34.98
60-4.22c	33.50	1.35E+00	45.23
61-4.22a	29.30	6.95E-02	2.04
61-4.22b	29.00	3.18E-02	0.92
61-4.22c	28.50	4.89E-02	1.39
62-3.22a	31.50	9.92E-01	31.25
62-3.22b	34.00	1.14E+00	38.76
62-3.22c	31.60	3.55E-01	11.22
63-2.22a	30.40	7.72E-01	23.47
63-2.22b	33.20	1.08E+00	35.86
63-2.22c	31.00	1.00E+00	31.00
65-2.22a	28.10	5.23E-01	14.70
65-2.22b	28.70	2.78E-01	7.98
65-2.22c	29.30	3.18E-01	9.32
66-1.22a	34.00	1.70E-01	5.78
66-1.22b	28.40	8.60E-02	2.44
66-1.22c	27.70	5.88E-02	1.63
67-1.22a	30.30	8.63E-01	26.15
67-1.22b	35.80	6.03E-01	21.59
67-1.22c	37.50	5.60E-01	21.00
68-1.22a	28.30	1.48E-01	4.19

Table E2 (cont'd)

68-1.22b	28.40	3.47E-02	0.99
68-1.22c	27.30	1.74E-01	4.75
69-2.22a	31.10	7.13E-02	2.22
69-2.22b	29.20	1.56E-01	4.56
69-2.22c	25.70	8.81E-02	2.26
70-3.22a	28.20	9.74E-01	27.47
70-3.22b	31.80	6.33E-01	20.13
70-3.22c	31.80	8.16E-01	25.95

Table E3. Quantitation results for cumulatively swabbed 0.45 casings from Collection 2.

Sample	Volume (μL)	Concentration (pg/μL)	Yield (pg)
39-1.45	29.70	1.45E+00	43.07
39-2.45	28.60	2.46E+00	70.36
39-3.45	31.70	2.05E+00	64.99
51-1.45	32.20	1.76E-01	5.67
51-3.45	32.50	5.62E-01	18.27
51-4.45	29.60	6.59E-01	19.51
52-1.45	35.40	1.28E+01	453.12
52-2.45	33.10	2.41E+00	79.77
52-4.45	35.30	2.90E+00	102.37
53-1.45	27.80	5.30E+00	147.34
53-2.45	27.70	2.55E+00	70.64
53-3.45	27.60	7.64E+00	210.86
54-1.45	31.30	7.70E+00	241.01
54-2.45	24.80	3.20E+00	79.36
54-4.45	26.60	2.50E+00	66.50
55-2.45	32.80	7.42E-01	24.34
55-3.45	35.20	1.85E+00	65.12
55-4.45	29.80	1.39E+00	41.42
56-1.45	31.50	1.08E+00	34.02
56-2.45	35.00	1.26E+00	44.10
56-3.45	34.10	2.25E+00	76.73
57-2.45	31.70	4.69E+00	148.67
57-3.45	33.50	2.88E-01	9.65
57-4.45	31.00	6.26E-01	19.41
58-1.45	28.20	1.57E+00	44.27
58-2.45	28.70	1.70E+00	48.79
58-4.45	28.30	1.58E+00	44.71
59-1.45	34.80	7.45E-01	25.93

Table E3 (cont'd)

59-3.45	32.30	3.05E-01	9.85
59-4.45	29.00	5.62E-01	16.30
60-1.45	32.80	1.28E+00	41.98
60-2.45	34.70	1.25E+00	43.38
60-3.45	35.70	2.78E+00	99.25
61-1.45	32.50	1.34E+00	43.55
61-2.45	32.50	1.48E+00	48.10
61-3.45	31.80	1.00E+00	31.80
62-1.45	32.00	2.77E+00	88.64
62-2.45	35.00	3.58E+00	125.30
62-4.45	34.00	3.15E+00	107.10
63-1.45	30.50	8.61E-01	26.26
63-3.45	30.30	1.05E+00	31.82
63-4.45	29.00	1.23E+00	35.67
65-1.45	32.40	3.57E+00	115.67
65-3.45	27.80	3.93E+00	109.25
65-4.45	28.50	3.78E+00	107.73
66-2.45	18.20	2.29E+00	41.68
66-3.45	33.50	5.22E+00	174.87
66-4.45	30.30	1.98E+00	59.99
67-2.45	27.50	4.95E-01	13.61
67-3.45	29.70	8.86E-01	26.31
67-4.45	28.50	5.11E+00	145.64
68-2.45	30.70	2.11E+00	64.78
68-3.45	32.00	4.79E-01	15.33
68-4.45	31.50	3.71E-01	11.69
69-1.45	29.40	4.08E-01	12.00
69-3.45	34.10	5.76E-01	19.64
69-4.45	32.20	9.05E-01	29.14
70-1.45	36.20	1.62E+00	58.64
70-2.45	34.50	1.94E+00	66.93
70-4.45	35.10	2.61E+00	91.61

Table E4. Quantitation results for cumulatively swabbed 0.22 casings from Collection 2.

Sample	Volume (µL)	Concentration (pg/µL)	Yield (pg)
39-1.22	30.30	1.51E+00	45.75
39-2.22	28.20	1.37E+00	38.63
39-3.22	33.30	1.42E+00	47.29
51-1.22	28.10	3.11E-01	8.74
51-3.22	26.50	6.58E-01	17.44
51-4.22	32.10	5.16E-01	16.56
52-1.22	32.30	6.61E-01	21.35
52-2.22	30.80	7.13E-01	21.96
52-4.22	29.20	2.59E-01	7.56
53-1.22	30.00	5.70E-01	17.10
53-2.22	32.00	5.15E-01	16.48
53-3.22	32.10	5.83E-01	18.71
54-1.22	29.80	1.86E+00	55.43
54-2.22	28.10	1.49E+00	41.87
54-4.22	29.30	1.16E+00	33.99
55-2.22	31.40	4.68E-01	14.70
55-3.22	33.50	2.99E-01	10.02
55-4.22	28.10	8.02E-02	2.25
56-1.22	31.80	1.20E+00	38.16
56-2.22	27.70	9.37E-01	25.95
56-3.22	31.50	5.69E-01	17.92
57-2.22	30.50	2.11E-02	0.64
57-3.22	30.10	9.34E-02	2.81
57-4.22	29.00	1.59E-01	4.61
58-1.22	33.40	5.43E-01	18.14
58-2.22	32.80	2.54E-01	8.33
58-4.22	33.30	1.92E-01	6.39
59-1.22	30.10	2.61E-02	0.79
59-3.22	32.20	5.33E+00	171.63
59-4.22	28.50	2.96E+00	84.36
60-1.22	29.80	4.92E+00	146.62
60-2.22	28.30	3.91E+00	110.65
60-3.22	34.00	2.76E+00	93.84
61-1.22	34.20	3.78E-01	12.93
61-2.22	33.00	5.04E-01	16.63
61-3.22	32.30	5.69E-01	18.38
62-1.22	26.30	1.64E+00	43.13
62-2.22	30.30	5.73E-01	17.36
62-4.22	34.10	5.39E-01	18.38

Table E4 (cont'd)

63-1.22	31.50	8.06E-01	25.39
63-3.22	33.50	7.29E-01	24.42
63-4.22	27.90	9.01E-01	25.14
65-1.22	31.40	2.97E-01	9.33
65-3.22	31.40	1.77E+00	55.58
65-4.22	32.60	1.25E+00	40.75
66-2.22	27.20	5.62E-01	15.29
66-3.22	32.10	6.28E-01	20.16
66-4.22	31.00	8.11E-02	2.51
67-2.22	33.00	7.89E-01	26.04
67-3.22	35.30	4.08E-01	14.40
67-4.22	35.20	3.11E-01	10.95
68-2.22	26.80	1.53E-01	4.10
68-3.22	34.30	1.65E+00	56.60
68-4.22	34.60	4.77E-01	16.50
69-1.22	34.50	2.52E-01	8.69
69-3.22	34.50	2.92E-01	10.07
69-4.22	29.70	5.01E-01	14.88
70-1.22	32.60	2.16E-01	7.04
70-2.22	28.90	3.74E-01	10.81
70-4.22	20.00	3.69E-01	7.38

APPENDIX F. FUSION STR PROFILES FROM COLLECTION 2

Red font: non-loader allele

**: allele was above the threshold using OSIRIS, but below the threshold using GeneMapper®.*

†: off-ladder allele

Blank cell: no alleles were amplified

N/A: not applicable

Table F1. Fusion profiles generated from spent cartridge casings loaded by individual SSS.

Locus	39-4.45a	39-4.45b	39-4.45c	39-4.22a	39-4.22b	SSS
Amel		X	X		X	X,X
D3	15	15,16		16	15	15,16
D1		18,3	12	12	16,18.3	12,18.3
D2	14	11	11	11,14		11,14
D10	15	14				14,15
D13			11	11		11,12
Penta E						13,17
D16		10,14	12,14	†,12,14	9,14	12,14
D18	12,15	12,21		12		12,12
D2						19,24
CSF	10		10			10,12
Penta D						9,14
THO1	9.3	9.3	9.3	9,9.3	6,9,9.3	9,9.3
vWA	19	19	18	18		18,19
D21	31.2	31.2				31.2
D7						9,10
D5						11,11
TPOX			8			8,8
DYS391						N/A
D8	13,15			13	10,13,15	13,15
D12		17,19				17,19
D19	13	13	13,14			13,14
FGA		25	25			21,25
D22				16		16,16

Table F1 (cont'd)

Locus	39-1.45	39-2.45	39-3.45	39-1.22	39-2.22	39-3.22	SSS
Amel	X	X,Y*	X,Y	X,Y	X	X	X,X
D3	15	15,16	14,15,16	15,16,18	14,15,16	14,15,16	15,16
D1	12	11,12	16.3,17.3	17.3*,18.3	17.3	11	12,18.3
D2	11,14	11,14	11,14	14		11	11,14
D10	14,15	14,15,16	15	14			14,15
D13		11,12	10,12		11,12		11,12
Penta E			14		13	13	13,17
D16	11,12,14	11,14	11,12,14	†,12,14	12	12,14	12,14
D18	12		12,15,16,17	15	12,16,17	-12	12,12
D2	24	19*,24	22		19,24	24	19,24
CSF	10	10	10,11,12	12	10	10	10,12
Penta D	9	14		14	9,14	14	9,14
THO1	7,8,9,9.3	6,9,9.3	9,9.3	9,9.3	6,9,9.3	6,9,9.3	9,9.3
vWA		18,19	18,19	18	17*	17	18,19
D21	31.2	30,31.2	28,31.2	31.2,32	31.2		31.2,31.2
D7	8		10,12		9,10		9,10
D5	11	11	12	11			11,11
TPOX	8	8	8				8,8
DYS391							N/A
D8	13,15	9,10,12,13,15	9,13,15	11,13	13,15,16	10,13,15	13,15
D12	17,19	17,19,20	17,19,25	17,19	17,18.3		17,19
D19	13,15.2	12,13	12,13,14	13,14	14	13	13,14
FGA	21	21,22	21.2,22,25		21	21	21,25
D22		16	11,16	16	16	16	16,16

Table F2. Fusion profiles generated from spent cartridge casings loaded by individual NN.

Locus	51-2.45a	51-2.45b	51-2.45c	51-2.22a	51-2.22b	51-2.22c	NN
Amel	X	X	X,Y		X	X	X,X
D3	16	14	14,16				14,16
D1	16	12	12,16			16	12,16
D2	10,11.3		11	11		10	10,11
D10		14,15	15		14	14	14,15
D13			8				8,12
Penta E							7,21
D16	12		12	12	12		12,12
D18	14.2	12,14	14,14.2				14,14.2
D2	17,23					17,23	17,23
CSF							12,13
Penta D				13			13,13
THO1	9,9.3	6	9.3	6,9		7,9,9.3	9,9.3
vWA	17	17	17		17	17	17,17
D21	29	31.2,33.2	29				29,31.2
D7			11			9	9,11
D5	9		9				9,10
TPOX							8,8
DYS391							N/A
D8	13,14,15	13,14,15	13,15	13	13,15		13,15
D12	18.3		22		18	22	18,22
D19		15.2	14,15.2				14,15.2
FGA							22,26
D22							11,11

Table F2 (cont'd)

Locus	51-1.45	51-3.45	51-4.45	51-1.22	51-3.22	51-4.22	NN
Amel	X	X,Y	X		X	Y	X,X
D3	14,15,16		14,16	18	14	18	14,16
D1	16,17.3	12		12			12,16
D2		11,14				11.3	10,11
D10				14,15			14,15
D13			12				8,12
Penta E		7,21					7,21
D16	11,12	12	12	12	12	12	12,12
D18		14	14,14.2	12	14	18	14,14.2
D2		23	23	17	17,23	17	17,23
CSF					13	12	12,13
Penta D				13	9		13,13
THO1	6,9.3	9	9,9.3	9.3	9	6,9	9,9.3
vWA	16,17	16,17	15	17	18	15,17	17,17
D21		29,31.2			31.2	29	29,31.2
D7		9				9	9,11
D5						9	9,10
TPOX				8			8,8
DYS391							N/A
D8	13,15	9,12,13,15	13			13	13,15
D12	17,18,22	18	18,22				18,22
D19		14	15.2			14	14,15.2
FGA			21.2,22			26	22,26
D22						15	11,11

Table F3. Fusion profiles generated from spent cartridge casings loaded by individual ZZZ.

Locus	52-3.45a	52-3.45b	52-3.45c	52-3.22a	52-3.22b	52-3.22c	ZZZ
Amel	X	X	X		X	X	X,X
D3	14	18	17		18		14,18
D1		15,17.3					15,17.3
D2		10,11	11				10,11
D10		12,14					12,14
D13		12					9,12
Penta E		13			12		9,13
D16	12,16	9,12	9,12	12			9,12
D18	16	10.2,14	16		16	16	16,20
D2	19	19,21	21		20,21		19,21
CSF		12					11,12
Penta D		13					12,13
THO1	6,9.3	9.3	6,9.3		6	6	6,9.3
vWA	17	17		17	17	17	17,17
D21	28.2	28,29					28,29
D7	15	12			12		10,12
D5	11	13			13		11,13
TPOX		8					8,11
DYS391							N/A
D8	10	10,12	10,12		10,12		10,12
D12	24	24,25			24	25	24,25
D19		14	14				13,14
FGA	19						19,26
D22			16				15,16

Table F3 (cont'd)

Locus	52-1.45	52-2.45	52-4.45	52-1.22	52-2.22	52-4.22	ZZZ
Amel	X,Y	X	X	X	X	X	X,X
D3	17	14,17	14,18	14,18	14,18	18	14,18
D1	15,18.3	15	15,17.3		17.3	15	15,17.3
D2	10,11		11	11	10,11	11	10,11
D10	15		14		14		12,14
D13	11,12	9	9,12		9	12	9,12
Penta E	14		13				9,13
D16	12	9,12	9	†,11,12	9	9,12	9,12
D18	16,17	16,20	16,20	16	16,20	16	16,20
D2	19,21,25	19	19		21	21	19,21
CSF	12		12	11			11,12
Penta D	9,13	12	13				12,13
THO1	6,8,9.3	6,9.3	6,9.3	6,9.3	6	6,9.3	6,9.3
vWA	15,17	17	17	17			17,17
D21	29	28,29	28,29	28,29		28	28,29
D7	10,12	12	10	10	12	10,12	10,12
D5	11,12	13	11			13	11,13
TPOX	8	8	11	11			8,11
DYS391	11						N/A
D8	11,12,13	10,12	10,12	10,12	10,12		10,12
D12	18,18.3,20	24	24	24	15,24,25	24	24,25
D19	14,15.2	14	13,14	13,14	13	13	13,14
FGA	21,23	19,26	19,26	26	26	19,25,26	19,26
D22	15,16		16				15,16

Table F4. Fusion profiles generated from spent cartridge casings loaded by individual B.

Locus	53-4.45a	53-4.45b	53-4.45c	53-4.22a	53-4.22b	53-4.22c	B
Amel	X	X				X	X,X
D3	18		18*				18,18
D1	11,12	12					12,15
D2	11.3						11,11.3
D10	15				14		13,15
D13	13	13					12,13
Penta E		12,13					12,13
D16	11	11	11				11,11
D18	16	12,16					12,16
D2	17	25					17,25
CSF				10			10,11
Penta D	13						10,13
THO1	6,9	6	6,9				6,9
vWA	17,18	17,18	17				17,18
D21			28				28,28
D7		10					10,10
D5	12						10,12
TPOX		11					8,11
DYS391							N/A
D8	13,16	13,16	16	9,13			13,16
D12	17,18,18.3	18	18,18.3	18,18.3			18,18.3
D19	15	15					13.2,15
FGA	22	23					22,23
D22							15,15

Table F4 (cont'd)

Locus	53-1.45	53-2.45	53-3.45	53-1.22	53-2.22	53-3.22	B
Amel	X	X	X		X	X	X,X
D3	18	18	18	14	16,18		18,18
D1	12,15,17	12,15	12,15		12	11	12,15
D2	11.3,14	11,11.3	11,11.3			11.3	11,11.3
D10	15	13	13,15				13,15
D13				10,12			12,13
Penta E	12,13,18		12,13				12,13
D16	11	11	11	11	11,12		11,11
D18	12,16	12,16,18	12,16	16,17	12		12,16
D2	23,25	17,25	17,25				17,25
CSF	10,12	10	10,11				10,11
Penta D		10	10,13	12	10		10,13
THO1	6,9	6,9	6,9	6,9		7,9	6,9
vWA	17,18	17,18	17,18			17	17,18
D21	28	28	28	32.2	28		28,28
D7	10	10	10		10		10,10
D5	10,12	10	10	14			10,12
TPOX		8	11				8,11
DYS391							N/A
D8	9,10,13,14,16	13,16	13,16		13	11,15,16	13,16
D12	17,18.3	18,18.3	18,18.3				18,18.3
D19	13.2,15	13.2,15	13.2,15				13.2,15
FGA	22	23	22,23	22		22	22,23
D22		15	15				15,15

Table F5. Fusion profiles generated from spent cartridge casings loaded by individual BBB.

Locus	54-3.45a	54-3.45b	54-3.45c	54-3.22a	54-3.22b	54-3.22c	BBB
Amel	X		X	X	X	X	X,X
D3	16	16			16,17	15	15,16
D1	12	12	12				11,12
D2	11	14					11,14
D10				13			14,14
D13			12		11		11,12
Penta E							13,16
D16	11,12,13	†,13	12		12	†,12	12,13
D18	14,16	14				14	14,16
D2	24			24		24	24,24
CSF	10	10					10,10
Penta D	9		9				9,9
THO1	8,9	8		9	9		8,9
vWA	17		17	17	18		17,17
D21		28	28		29		29,30
D7							7,8
D5				9			9,11
TPOX							8,8
DYS391							N/A
D8	14	14	8,9	14		14	14,14
D12	21	20	21	20		19	20,21
D19							12,13
FGA	22						20,22
D22							11,16

Table F5 (cont'd)

Locus	54-1.45	54-2.45	54-4.45	54-1.22	54-2.22	54-4.22	BBB = 54
Amel	X	X	X	X	X	X	X,X
D3	15,16	15,16	15,16	15	15,16	15	15,16
D1	11,12	11	11,12	12,15.3	11,12	12	11,12
D2	11,14	11	11.3	11,11.3	11		11,14
D10	14	14	14			14	14,14
D13	11,12		11	10		12	11,12
Penta E	13	16	13,14				13,16
D16	12,13	12,13	11,12	12,13*	12,13	12,13	12,13
D18	14,16	14,16	12,14,16,17	16		16	14,16
D2	19,21,24	24	24	18	24	22	24,24
CSF	10		10*	12	10		10,10
Penta D	9					9	9,9
THO1	8,9	8	8,9,9.3	6,9,9.3	8,9,9.3	7,8	8,9
vWA	17	17	17	17	17	17	17,17
D21	29	30	29,30	28,33.2			29,30
D7	7,8	6.3,7,9	7,8	10	7,8	8	7,8
D5	9,11	11	11	12	8,11	11,12	9,11
TPOX	8	8	8	12	8		8,8
DYS391							N/A
D8	14	14	14	13,14	13,14	14	14,14
D12	20,21		20,23	17,20	20	19.3,20,21	20,21
D19	12,13	13	12	12	13	12	12,13
FGA	20,22		22	21	20,22		20,22
D22	11						11,16

Table F6. Fusion profiles generated from spent cartridge casings loaded by individual C.

Locus	55-1.45a	55-1.45b	55-1.45c	55-1.22a	55-1.22b	55-1.22c	C
Amel			X				X,X
D3	18			15,18			15,18
D1							14,16
D2				10			11,11
D10		14					14,15
D13			12				11,12
Penta E							11,13
D16			†	11			11,12
D18				16,17			11,17
D2							17,25
CSF		10					10,11
Penta D							9,10
THO1		6				8	6,6
vWA							11,14
D21							28,29
D7							9,13
D5							11,12
TPOX				8			12,12
DYS391							N/A
D8		13,14					13,14
D12							17,19
D19							13,14
FGA							20,24
D22							15,17

Table F6 (cont'd)

Locus	55-2.45	55-3.45	55-4.45	55-2.22	55-3.22	55-4.22	C
Amel	X	X	X	X	X,Y	X,Y	X,X
D3	15,16	15,17,18	14,18	15			15,18
D1	11,12	14,15,15.3		11,14,15.3,16	14		14,16
D2		11	11				11,11
D10		15	15			15	14,15
D13		11,12	12				11,12
Penta E		7,11	5,14				11,13
D16	12,13	11,12	11,12	8.3*	12,14	11	11,12
D18	11,14,17	11	11	12,18			11,17
D2		17					17,25
CSF		10	10				10,11
Penta D		10	12				9,10
THO1	6	6	6	3,9,9.3	6	9.3	6,6
vWA		14,18	14,17	14,17		18	11,14
D21		28,29		29			28,29
D7		9	13	10			9,13
D5							11,12
TPOX		8,12				12	12,12
DYS391			11				N/A
D8	13,14	10,13,14	13,14	13,15	13,14	13,14	13,14
D12	17,19.3	17,18,19,19.3,20	17,19,21	15,20	20	19,21	17,19
D19	8.2,14	13,14	12,13	13			13,14
FGA		18,24		20			20,24
D22		15,17					15,17

Table F7. Fusion profiles generated from spent cartridge casings loaded by individual AA.

Locus	56-4.45a	56-4.45b	56-4.45c	56-4.22a	56-4.22b	56-4.22c	AA
Amel	Y			X		X	X,Y
D3			9,17				15,15
D1		19.3					18.3,19.3
D2							11,11.3
D10							13,14
D13							9,12
Penta E							5,5
D16							9,12
D18			13				13,14
D2							19,21
CSF							10,11
Penta D							11,14
THO1	9.3						6,9.3
vWA							15,17
D21			28				28,30.2
D7	9						9,9
D5							12,13
TPOX							8,11
DYS391							10
D8		15					12,15
D12						20	19,22
D19					15	15	13,15
FGA							18,21
D22							11,17

Table F7 (cont'd)

Locus	56-1.45	56-2.45	56-3.45	56-1.22	56-2.22	56-3.22	AA
Amel	X	X,Y		X		X,Y	X,Y
D3	15	14,15	16	14		15	15,15
D1	18.3,19.3			14	15		18.3,19.3
D2	11.3	14				11	11,11.3
D10	13,16					14	13,14
D13	9		12				9,12
Penta E		15					5,5
D16	9	9	9,11	11,12	13	9	9,12
D18	14	11,17	14,16	16	14,15	13	13,14
D2		17		20		20	19,21
CSF					11		10,11
Penta D							11,14
THO1	6	7,9	7,9.3		8	6	6,9.3
vWA	15,17		14			18	15,17
D21			28	28*			28,30.2
D7							9,9
D5	11,13		13	11			12,13
TPOX	11		11	8			8,11
DYS391							10
D8	12	10	10,13	9,12	12	12	12,15
D12	22	21,23	17,22	21,23		18	19,22
D19		16.2	13		13.2		13,15
FGA	21		20,21	20			18,21
D22							11,17

Table F8. Fusion profiles generated from spent cartridge casings loaded by individual A.

Locus	57-1.45a	57-1.45b	57-1.45c	57-1.22a	57-1.22b	57-1.22c	A
Amel				X		X	X,X
D3	15						15,16
D1					14		11,14
D2							14,16
D10							15,16
D13	12						13,14
Penta E							7,12
D16	11,12	9					11,11
D18					11		12,17
D2					18		17,25
CSF					10		10,12
Penta D							12,12
THO1	7	6					7,9,3
vWA	16	15	17				17,18
D21	32.2						28,30
D7				10			10,12
D5						11	9,12
TPOX							8,11
DYS391							N/A
D8		9,15				13	12,15
D12	18.3				20		18,24
D19	19						13,15.2
FGA							23,24
D22					16		15,16

Table F8 (cont'd)

Locus	57-2.45	57-3.45	57-4.45	57-2.22	57-3.22	57-4.22	A
Amel	X	X	X		X	Y	X,X
D3	15,16	16	18	16	18		15,16
D1	11,14		14		14	12,17.3	11,14
D2	14,16						14,16
D10	15,16						15,16
D13	13,14		14				13,14
Penta E	7,12						7,12
D16	11	11	11		11		11,11
D18	12,17	17	12			17	12,17
D2	17,25		17,25				17,25
CSF	10,12		12			10	10,12
Penta D	12						12,12
THO1	7,9.3	7,9.3	7	6	6	8	7,9.3
vWA	17,18	16	18	14	18		17,18
D21	28,30,31		30	28			28,30
D7	10,12		10				10,12
D5	9,12		12				9,12
TPOX	8,11						8,11
DYS391							N/A
D8	12,15		13	12		13,14	12,15
D12	18,24	15	18,19.3,24		20		18,24
D19	13,15.2						13,15.2
FGA	23,24						23,24
D22	15,16						15,16

Table F9. Fusion profiles generated from spent cartridge casings loaded by individual J.

Locus	58-3.45a	58-3.45b	58-3.45c	58-3.22a	58-3.22b	58-3.22c	J
Amel		Y	X	X			X,Y
D3	15,16	16,18		16			15,16
D1		17.3					13,13
D2						13	11.3,13
D10							13,14
D13							11,11
Penta E		7				16	11,16
D16	12	†,9,11	9	13	11,12		12,13
D18	10	16					10,18
D2				18			17,18
CSF		12					
Penta D							8,9
THO1	6,8	9	10	6,7	6		6,8
vWA	18	15,17					18,18
D21		31	28				30.2,31.2
D7							12,12
D5							10,12
TPOX		10					8,10
DYS391							10
D8	12,13	10,13,14	11,12,13,16				11,12
D12		17,23			17,18		18,18
D19		14,15					14,15
FGA							20,22
D22							16,16

Table F9 (cont'd)

Locus	58-1.45	58-2.45	58-4.45	58-1.22	58-2.22	58-4.22	J
Amel	X,Y	X,Y	X,Y	X	X,Y	X	X,Y
D3		16,18	14,15,16		16	15,16,17	15,16
D1	12,13,15	11	11	14,17.3		12	13,13
D2		11.3					11.3,13
D10	13,15	13		14	14	14	13,14
D13	10	11	12	11			11,11
Penta E				12	16		11,16
D16	12,13	9,12,13	11,12,13	11		11,12,13,14	12,13
D18	16,18	10,12,14,18	10	17		10	10,18
D2	18			17		19	17,18
CSF		10			10	11	
Penta D	13				8		8,9
THO1	6,9,9.3	6,7,8	6,8,9.3	6,9.3	8	6,9,9.3	6,8
vWA	15,17,18	18	18,19	15		17,18	18,18
D21	28						30.2,31.2
D7			12				12,12
D5		10		12		12	10,12
TPOX						10,11	8,10
DYS391							10
D8	15	11,12,13	11,13	14	11,12	8,9,11,12,13,15	11,12
D12	18,18.3,21	18,18.3	18,20	18		17,18,18.3,21	18,18
D19	13,13.2,14	15	14			13	14,15
FGA	21	20		23		20,24	20,22
D22	14,15			15			16,16

Table F10. Fusion profiles generated from spent cartridge casings loaded by individual KKK.

Locus	59-2.45a	59-2.45b	59-2.45c	59-2.22a	59-2.22b	59-2.22c	KKK
Amel	Y		X,Y	Y		X,Y	X,Y
D3			15	15		15	15,16
D1	17			11	15,16,18.3	16	11,16
D2	10	14		14	14	10	10,14
D10	15			14			14,18
D13							10,10
Penta E							5,7
D16	12	11,12	9,11	†,9,11	9	9	9,11
D18				18	14,18		16,18
D2							18,19
CSF	10						10,14
Penta D							9,14
THO1	6	8,9.3	8,9.3	8,9.3	8	8,9.3	8,9.3
vWA	15		17	14,17		14	14,17
D21	29			30		30	30,30
D7				10		8	8,10
D5		10			10		10,13
TPOX							8,8
DYS391							9
D8		13,14	11,14	11,12,13,14,16	14	14,16	14,16
D12	15	15,20	20	15	15*,20	15,20	15,20
D19		13,15.2		13			13,14
FGA	23				18,21,22	24	21,24
D22							14,15

Table F10 (cont'd)

Locus	59-1.45	59-3.45	59-4.45	59-1.22	59-3.22	59-4.22	KKK
Amel	Y	X,Y		X,Y	X,Y	X,Y	X,Y
D3	15,18	16	15	16	15,16	15,16	15,16
D1	11,12,15	16	11,15,16	11,17.3	11,16	11	11,16
D2	11	14		14	14	10	10,14
D10	14,18				14,18	18	14,18
D13	12			10	10	10	10,10
Penta E	13			7	7,12		5,7
D16	9,11	9,13	9,11	11	9,11	9,11	9,11
D18	18			18	16,18	16,18	16,18
D2	18,20	18		19	18	18,19	18,19
CSF	10	14	10		10,14	14	10,14
Penta D	9,14	14			9,14	8	9,14
THO1	8	9.3	9.3	8,9.3	8,9.3	6,8,9,9.3	8,9.3
vWA	14,17		14	14	14,17	14,17	14,17
D21	28,29,30	28,29			30	30,31.2	30,30
D7			10		8,10	8	8,10
D5	10			13	10,13	10,13	10,13
TPOX					8	8	8,8
DYS391				9	9		9
D8	13,14,16	16	13,16	13,14,16	14,16	14,16	14,16
D12	15,17,19,20	20	15,19,20	20	15,18,20	15	15,20
D19					13,14	13	13,14
FGA	24				21,24	21	21,24
D22			14		14,15		14,15

Table F11. Fusion profiles generated from spent cartridge casings loaded by individual JJJ.

Locus	60-4.45a	60-4.45b	60-4.45c	60-4.22a	60-4.22b	60-4.22c	JJJ
Amel	X		X	X	X,Y	X	X,Y
D3	16,18		18		18	16	16,18
D1	16.3	16.3*	12,14,16.3	12	12,16.3	12	12,16.3
D2			11	11	11	11,11.3	11,11
D10	13,16		13				13,13
D13	12						12,12
Penta E			17	7			7,17
D16	12	12	12	12	12	12	12,12
D18	17		17		17	17	17,17
D2	19		20				20,22
CSF		10	12				10,12
Penta D	10						10,11
THO1	9,9.3	9	9,9.3	6,7,9,9.3	6,9,9.3	9,9.3	9,9.3
vWA	18	14,18	14,18	14,18		14,18	14,18
D21	28,30		29,30	30	30,30.2		30,30.2
D7			9,11	11	9		9,11
D5							12,13
TPOX		8					8,8
DYS391			10				10
D8	10,14	14	10,14	10,14	10	14	10,14
D12	20		19.3,20	20		19.3,20	19.3,20
D19		15.2	12			15.2	12,15.2
FGA	20	18	18		18,20		18,20
D22	11						11,15

Table F11 (cont'd)

Locus	60-1.45	60-2.45	60-3.45	60-1.22	60-2.22	60-3.22	JJJ
Amel	X,Y	X	X,Y	X,Y	X,Y	X,Y	X,Y
D3		16,17	15,18	16,18	16,18	16,17,18	16,18
D1	12,16.3	16.3	12,16.3	12,16.3	12	12,14,16.3	12,16.3
D2	11	11	11	11	11	11	11,11
D10			13	13	13		13,13
D13	12	12	12	12	12	12	12,12
Penta E	17		5,7,17	7,17	7	17	7,17
D16	†,12,13	12	12	12	12	12	12,12
D18		17	15,17	17	17	17	17,17
D2	20,22	20	19,20,21,22	20,22	22	20,22	20,22
CSF	10		10	10,12		10	10,12
Penta D	11	9,11	10	10,11	10		10,11
THO1	7,9,9.3	7,8,9,9.3	9,9.3	9,9.3	9,9.3	6,7,9,9.3	9,9.3
vWA	14,18	14,17,18	14,17,18	14,18	14,18	14,18	14,18
D21	30.2	28,30.2	30,30.2	30,30.2	30.2	29.2,30.2	30,30.2
D7			9,11	9,11	9,11		9,11
D5			12	12,13	12,13	13	12,13
TPOX			8	8		8	8,8
DYS391		10	10	10	10		10,10
D8	10,12,14	10,13,14	10,12,14,15	10,14	10,14	10,14	10,14
D12	19.3,20	19.3,21	19.3,20,22	19.3,20	20,21	19.3,20	19.3,20
D19		12,15.2	12,15.2	12,15.2	12,15.2	12	12,15.2
FGA	18,20	18	20,21,22	18,20	20		18,20
D22		16	15	11,15	11,15		11,15

Table F12. Fusion profiles generated from spent cartridge casings loaded by individual I.

Locus	61-4.45a	61-4.45b	61-4.45c	61-4.22a	61-4.22b	61-4.2c	I
Amel	X	X	X				X,X
D3	15			14*		16	16,16
D1							16,17.3
D2			11	11			11,11
D10	15						13,15
D13		12					13,13
Penta E							7,7
D16	4	9,11,13	11				11,11
D18	12,15	13		15			15,16
D2			17				17,17
CSF		11					12,13
Penta D							9,11
THO1	5,11	6,9.3	6,8		9.3		8,9.3
vWA	14,15,18,19			16			14,18
D21				27			27,30
D7							8,10
D5		13					11,12
TPOX					10		8,8
DYS391							N/A
D8	13	12,13		10		13,14,15	13,14
D12		22					18,20
D19		13,15,15.2	15		15	14	14,15
FGA							21,23
D22							15,16

Table F12 (cont'd)

Locus	61-1.45	61-2.45	61-3.45	61-1.22	61-2.22	61-3.22	I
Amel		X	X	X	X	X	X,X
D3			16			16	16,16
D1	15,17.3			15	17.3		16,17.3
D2	11	11					11,11
D10	13						13,15
D13							13,13
Penta E	9						7,7
D16	9	11,13	11				11,11
D18			15	15			15,16
D2	17	17	17		17		17,17
CSF			13				12,13
Penta D							9,11
THO1	6,9.3	8,9.3	8,9.3				8,9.3
vWA	14,18	16	17	18			14,18
D21	29	29,30	30		30		27,30
D7	12				8	9	8,10
D5	11						11,12
TPOX	8				8		8,8
DYS391							N/A
D8	11,13	13,14	13,14	13		10	13,14
D12	24,25		18			18	18,20
D19			13.2,14,15	13.2			14,15
FGA		21,23					21,23
D22							15,16

Table F13. Fusion profiles generated from spent cartridge casings loaded by individual YYY.

Locus	62-3.45a	62-3.45b	62-3.45c	62-3.22a	62-3.22b	62-3.22c	YYY
Amel		X	X	X	X	X	X,X
D3		17,18		16,17			17,18
D1	15,15.3	15,19.3	15.3	14			14,15
D2		10	10	10	10		10,10
D10		16	16				16,16
D13				9	13	12	9,13
Penta E				5			5,10
D16		13	13	12,14		13	13,14
D18		13,15	13,15	13	15	13,18	13,15
D2		20		21	18		18,20
CSF							11,12
Penta D							9,11
THO1	6,7	6,7	7,9.3	9,9.3	6,7,9.3	6,7	6,7
vWA	18	14	18	14*	14	14	14,18
D21	27	30	27			30	27,30
D7		10,12	12	9			10,12
D5			11	12			11,12
TPOX							8,11
DYS391				10			N/A
D8		13	13		13	13	13,13
D12	18	18,21	18,21	19	18,21		18,21
D19		15.2		13			14,15.2
FGA		24		21		24,26	20,24
D22				11			11,11

Table F13 (cont'd)

Locus	62-1.45	62-2.45	62-4.45	62-1.22	62-2.22	62-4.22	YYY
Amel	X	X		X	X	X	X,X
D3	17	15,17,18	17,18			17,18	17,18
D1	14,15	12,14,15	14,15,16			14	14,15
D2	10	10					10,10
D10	16	16	13,15				16,16
D13		9,13					9,13
Penta E	5,10	5,10	5				5,10
D16	13,14	13,14	12,13,14	13	13	†,14	13,14
D18	13,15	13,15	13,14,15			13	13,15
D2		18	18		18		18,20
CSF	11	12				11	11,12
Penta D		11					9,11
THO1	6,7	6,7	6,7,9.3	6	6	6,7	6,7
vWA	14,18	14,18	14,18			18	14,18
D21	27	27	27,30			27	27,30
D7	10,12	10			10	12	10,12
D5	12	12	10				11,12
TPOX	11	8,11	8				8,11
DYS391							N/A
D8	13	13	13	13	12,13	13	13,13
D12	18,21	17,18,21	18,21			18	18,21
D19	14,15.2	13,14,15.2	14,15.2		15.2	14	14,15.2
FGA	20,23*	20,24					20,24
D22	11						11,11

Table F14. Fusion profiles generated from spent cartridge casings loaded by individual EE.

Locus	63-2.45a	63-2.45b	63-2.45c	63-2.22a	63-2.22b	63-2.22c	EE
Amel			X			X	X,Y
D3			16				16,18
D1							16.3,17.3
D2	11						14,15
D10	13						13,15
D13							10,12
Penta E							7,18
D16	11,13		9				9,13
D18		16	14				13,15
D2							20,25
CSF							10,12
Penta D							12,13
THO1	9.3	8	9				8,9.3
vWA					18		17,18
D21	30.2		31.2			32.2	29,31
D7							9,12
D5							11,13
TPOX							8,8
DYS391							11,11
D8	8	8	8	16		8	8,13
D12							22,23
D19			15				13,15
FGA							21,23
D22	11						15,16

Table F14 (cont'd)

Locus	63-1.45	63-3.45	63-4.45	63-1.22	63-3.22	63-4.22	EE
Amel	X	X,Y	X,Y	X		X,Y	X,Y
D3	14,16	16,17				16,17	16,18
D1	11	16.3				17.3	16.3,17.3
D2		11.3,15		11,14,15		15	14,15
D10							13,15
D13	12		13				10,12
Penta E							7,18
D16	12,13	11,14		12		9	9,13
D18	12,13,15,17					13	13,15
D2				17,20		18	20,25
CSF			11			10	10,12
Penta D							12,13
THO1	7,8	9,9.3	6,8,9.3			8	8,9.3
vWA		18					17,18
D21	28					29	29,31
D7		10					9,12
D5							11,13
TPOX							8,8
DYS391							11,11
D8	8,9,13		10,13,14	8,9,15,16	8,10,13,16	13	8,13
D12	19.3	20,21	15			22	22,23
D19		13		13,15	13,15		13,15
FGA	21.2	21		21			21,23
D22							15,16

Table F15. Fusion profiles generated from spent cartridge casings loaded by individual JJ.

Locus	65-2.45a	65-2.45b	65-2.45c	65-2.22a	65-2.22b	65-2.22c	JJ
Amel	X	X			X	X	X
D3	14,17	17				16	14,17
D1		12,16				16	12,16
D2				11		14	11,14
D10	13						14,14
D13							11,12
Penta E	18					11	10,11
D16	10,11	11		12	11	11,12,13	11,11
D18		14,19			14		14,19
D2	18,19						18,19
CSF		11			11		11,13
Penta D							11,14
THO1	5,11	8,9,3		9	9	9.3	9,9,3
vWA	16	11,14		13,14		18	11,15
D21	31	29			30.2		30.2,31.2
D7					9	10	9,10
D5		11					12,13
TPOX	8						8,8
DYS391						10	N/A
D8	13	13	13	13		13	13,13
D12	20	16,21		15,20,21	19	15	15,20
D19							11,13.2
FGA	20						22,24
D22		14					11,14

Table F15 (cont'd)

Locus	65-1.45	65-3.45	65-4.45	65-1.22	65-3.22	65-4.22	JJ
Amel	X	X	X		X	X	X,X
D3	14,17,18	14,17	14,16,17,18	18	16,17	17	14,17
D1		12,16	12	12		16	12,16
D2	11,14	11,14	11,14		14	14	11,14
D10	14	14	14		14	14	14,14
D13		11,12	11,12				11,12
Penta E		10,11	10,12				10,11
D16	11	11	11	11	12	11	11,11
D18	14,17	14,19	16,19	14	19		14,19
D2	19	18,19	18,19		18		18,19
CSF		11,13		13	10,11,13		11,13
Penta D		11,14					11,14
THO1	9,9.3	9,9.3	6,9,9.3	6,9	9,9.3	9,9.3	9,9.3
vWA	14,18	14,18	14,15,17,18	18	14,18	14	11,15
D21	30.2,31.2	30.2,31.2	28,30.2,31.2	30.2			30.2,31.2
D7	10	9,10					9,10
D5	11,12	11,12	11		11		12,13
TPOX		8					8,8
DYS391							N/A
D8	13	13	12,13,15	13	13	13	13,13
D12	15,20	15,20	15,18,20	20		21	15,20
D19	11,13.2	11,13.2	14,15				11,13.2
FGA		22,24					22,24
D22		11,14					11,14

Table F16. Fusion profiles generated from spent cartridge casings loaded by individual DDD.

Locus	66-1.45a	66-1.45b	66-1.45c	66-1.22a	66-1.22b	66-1.22c	DDD
Amel	X,Y	X,Y	X	X	X	X	X,Y
D3	14	14,18	18	18			14,18
D1	14,17.3	14					14,17.3
D2	11			11			11,11
D10		14					14,14
D13							10,12
Penta E				19			7,19
D16	†,11,12	7				12	11,12
D18	12	17	10				10,12
D2	20						17,20
CSF							11,12
Penta D		9					9,12
THO1	8	8	8				8,8
vWA	17	17	16,17	17,18		17	17,17
D21							29,32.2
D7							12,12
D5	10						13,13
TPOX							9,9
DYS391							11
D8	12,13	12,13	13	16	12,14		12,13
D12	15,23,24	15		24		24	15,24
D19	13*,14	14		14,15			14,15
FGA	22	22		24			22,24
D22							16,16

Table F16 (cont'd)

Locus	66-2.45	66-3.45	66-4.45	66-2.22	66-3.22	66-4.22	DDD
Amel	X,Y	X,Y	X		Y		X,Y
D3	14,16,17,18	14,18	14	14,18	14	14	14,18
D1	14	14,17.3		14	17.3		14,17.3
D2		11	11,11.3	11	11		11,11
D10		14		14			14,14
D13	10	10,12					10,12
Penta E	7,13	7,19		7			7,19
D16	11,12	11,12	11,12		11,12		11,12
D18	12	10,12	10	10	10		10,12
D2	20	17,20		20			17,20
CSF	11	11,12		12			11,12
Penta D		12					9,12
THO1	8,9	8	6,7,8,9.3	6,8,9.3	7		8,8
vWA	14,17	17	16,17	17	14		17,17
D21	28,32.2	29,32.2			29		29,32.2
D7	12	12					12,12
D5	13	13			13		13,13
TPOX	9	9	9				9,9
DYS391	11	11					11
D8	12,13	12,13	11,12,13,14, 15,16			13	12,13
D12		15,24	15,18,23		15,21	15	15,24
D19	13,15	14,15		14,15	13.2		14,15
FGA	24	22,24					22,24
D22	16	16		16			16,16

Table F17. Fusion profiles generated from spent cartridge casings loaded by individual VVV.

Locus	67-1.45a	67-1.45b	67-1.45c	67-1.22a	67-1.22b	67-1.22c	VVV
Amel			X		X	X,Y	X,Y
D3		14	14,15			15	14,17
D1				17.3			15,17.3
D2			11				11,14
D10							12,13
D13	12		11				11,11
Penta E							7,8
D16					12		12,12
D18	12			17			12,16
D2							17,18
CSF							11,11
Penta D							9,12
THO1			9.3				9.3,9.3
vWA							17,17
D21							28,32.2
D7							10,11
D5							11,13
TPOX							11,11
DYS391							11
D8	8		16				8,12
D12		18.3	15		15	15,18.3	15,25
D19		15					14,15.2
FGA				21.2			22,23
D22							11,15

Table F17 (cont'd)

Locus	67-2.45	67-3.45	67-4.45	67-2.22	67-3.22	67-4.22	VVV
Amel	Y		X	X			X,Y
D3		17	15,17	16	15		14,17
D1	17.3		16,16.3,17.3				15,17.3
D2			11				11,14
D10			13	14			12,13
D13			9,12				11,11
Penta E			12,21				7,8
D16		12	11,13	11,12			12,12
D18	17		14,16				12,16
D2			17,24	19			17,18
CSF			10				11,11
Penta D			9,11	9			9,12
THO1	9.3		7,9.3	9		9,9.3	9.3,9.3
vWA		17	14,16				17,17
D21			30,30.2	28			28,32.2
D7			12		10		10,11
D5			13				11,13
TPOX			8,11				11,11
DYS391							11
D8	11,16		14	10	9,11,12		8,12
D12	23		17,22	15,18,18.3		18	15,25
D19			13,15,15.2			14	14,15.2
FGA			22,23		23	21	22,23
D22							11,15

Table F18. Fusion profiles generated from spent cartridge casings loaded by individual XXX.

Locus	68-1.45a	68-1.45b	68-1.45c	68-1.22a	68-1.22b	68-1.22c	XXX
Amel	X	X		X		Y	X,Y
D3							14,16
D1		15.3		17.3			12,16
D2	11						11.3,14
D10		11				14	14,16
D13							9,12
Penta E				14			7,7
D16	13	†*,13	13	†,14			12,13
D18				25		18	14,16
D2				20			18,25
CSF							10,12
Penta D						10	9,11
THO1				13.3			7,9.3
vWA		23					18,18
D21	28.2		30				28,30
D7		5					10,10
D5			11,12				11,11
TPOX				8			8,8
DYS391							10
D8	14	15		9,15		10,16	14,15
D12				21			19,21
D19				14		15	14,15
FGA						23	23.2,25
D22	16						14,16

Table F18 (cont'd)

Locus	68-2.45	68-3.45	68-4.45	68-2.22	68-3.22	68-4.22	XXX
Amel	X	X	X				X,Y
D3	14,18*	18			15	18	14,16
D1		16	12,16,17.3		17	12,17	12,16
D2	11*	11				11	11.3,14
D10					14	16	14,16
D13					12		9,12
Penta E							7,7
D16	9,13	12	13		9,13		12,13
D18	16,20		14			12	14,16
D2	18		17		25	25	18,25
CSF		10					10,12
Penta D		13	11				9,11
THO1	6,7,9		7	9.3	6	7,9.3	7,9.3
vWA	18		18		15,16		18,18
D21				30.2	32.2		28,30
D7		10					10,10
D5		12					11,11
TPOX						8	8,8
DYS391							10
D8	11,12,13		13,14		13,14	10,16	14,15
D12					17,23		19,21
D19		15			14		14,15
FGA				22	25		23.2,25
D22					16		14,16

Table F19. Fusion profiles generated from spent cartridge casings loaded by individual R.

Locus	69-2.45a	69-2.45b	69-2.45c	69-2.22a	69-2.22b	69-2.22c	R
Amel	X	X			X	X	X,X
D3		16					16,17
D1	15	15				12	12,18.3
D2							11,11
D10							13,14
D13							12,12
Penta E							10,14
D16	9,11,16						12,14
D18					18		17,18
D2							20,23
CSF							10,13
Penta D							12,13
THO1	9	6			9	9.3	6,9
vWA		17			15		15,17
D21				29			30,30.2
D7	11						10,10
D5							10,11
TPOX							8,11
DYS391							N/A
D8	7,11		13,16	13	10		10,12
D12	19				20		18,21
D19	13					14	14,15.2
FGA							21,25
D22							15,15

Table F19 (cont'd)

Locus	69-1.45	69-3.45	69-4.45	69-1.22	69-3.22	69-4.22	R
Amel	X		X	X		X	X,X
D3		16	16				16,17
D1			12		17.3		12,18.3
D2		11		11.3			11,11
D10							13,14
D13							12,12
Penta E						14	10,14
D16							12,14
D18		17					17,18
D2							20,23
CSF						10	10,13
Penta D							12,13
THO1	6	6,9	6	9	8		6,9
vWA	18				17		15,17
D21							30,30.2
D7							10,10
D5				11			10,11
TPOX						11	8,11
DYS391							N/A
D8	10		12	10	10	10	10,12
D12					19		18,21
D19	14				15		14,15.2
FGA							21,25
D22							15,15

Table F20. Fusion profiles generated from spent cartridge casings loaded by individual OOO.

Locus	70-3.45a	70-3.45b	70-3.45c	70-3.22a	70-3.22b	70-3.22c	OOO
Amel		Y	X	X			X,Y
D3	14		14	14			14,14
D1							16.3,17.3
D2							11,11.3
D10			15	16			15,16
D13	12		12	10			10,12
Penta E							5,14
D16			12				11,12
D18							16,17
D2			20				20,22
CSF							10,11
Penta D							11,12
THO1	9		9,9.3,11	9	9.3		9,9.3
vWA	16				20	12	16,18
D21	32.2						28,32.2
D7	11		12				11,12
D5							12,12
TPOX							8,8
DYS391							11
D8			12,13	9			9,12
D12			21				21,23
D19							12,14
FGA		22		22			21.2,22
D22							11,16

Table F20 (cont'd)

Locus	70-1.45	70-2.45	70-4.45	70-1.22	70-2.22	70-4.22	OOO
Amel	X,Y	Y	X,Y	X	Y	X	X,Y
D3		14,16	14,17			14	14,14
D1	11,16.3	16.3,17.3	16.3,17.3				16.3,17.3
D2	10	11,11.3	11,11.3				11,11.3
D10	16		16				15,16
D13	10	10					10,12
Penta E	5,14						5,14
D16	9,11	11,12,13	11,12			11,12	11,12
D18	16	16,17	17			16	16,17
D2		20	20		22		20,22
CSF		10,11	11				10,11
Penta D					12		11,12
THO1	9.3	9,9.3	9,9.3		9	9.3	9,9.3
vWA	16,18	16,18	15,16,18		16	18	16,18
D21		28,32.2	32.2				28,32.2
D7	12	12					11,12
D5		12	12				12,12
TPOX			8				8,8
DYS391		11	11				11
D8	12	9,12	9,12	9	12	12,13,16	9,12
D12	23	23	21,22,23	21		21,23	21,23
D19	12,15		12		12,13		12,14
FGA	21.2	21.2	21.2,22		22		21.2,22
D22	16						11,16

APPENDIX G. MTDNA PROFILES GENERATED FROM SPENT CARTRIDGE CASINGS

Red font: polymorphism not consistent with handler

Blank: no polymorphisms

A: adenine

T: thymine

C: cytosine

G: guanine

Y: mixture between cytosine and thymine

R: mixture between adenine and guanine

M: mixture between adenine and cytosine

S: mixture between cytosine and guanine

Table G1. MtDNA profiles generated from spent cartridge casings loaded by individual NN.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
NN	16293G,16311T	195C, 263G, 309.1C, 315.1C	-----	-----
51-1.45	16293G, 16311T	(73 not sequenced) 195C, 263G, 309.1C, 315.1C	Consistent	Low
51-4.22	16069T, 16126C, 16160G	73G, 185A, 263G, 295T, 315.1C, 462T	Inconsistent	Medium

Table G2. MtDNA profiles generated from spent cartridge casings loaded by individual ZZZ.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
ZZZ	16126C, 16294T, 16296T, 16304C	73G, 263G, 315.1C	-----	-----
52-1.45	16256T	204C, 263G, 315.1C	Inconsistent	High
52-3.22a	16126C, 16294T, 16296T, 16304C	73G, 263G, 315.1C	Consistent	Low
52-3.22b	16185T, 16223T, 16355A, 16362C	73G, 263G, 315.1C	Inconsistent	Medium
52-3.45b	16126C, 16294T, 16296T, 16304C	73G, 263G, 315.1C	Consistent	High
52-3.45c	16126C, 16294T, 16296T, 16304C	73R, 263G (315.1 not sequenced)	Mixed-Consistent	Medium

Table G3. MtDNA profiles generated from spent cartridge casings loaded by individual B.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
B	16069T, 16126C, 16160G, 16222T	73G, 185A, 263G, 295T, 315.1C, 462T	-----	-----
53-1.22	16069Y, 16126Y, 16160R, 16222Y	73G, 185A, 263G, 295T, 315.1C, 462T	Mixed-Consistent	Medium
53-1.45	16069Y, 16126C, 16160R, 16222Y	73G, 185A, 263G, 295T, 315.1C, 462T	Mixed-Consistent	High
53-3.45	16069T, 16126C, 16160G, 16222T	73G, 185A, 263G, 295T, 315.1C, 462T	Consistent	High
53-4.45a	16069T, 16126C, 16160G, 16222T	73G, 185A, 263G, 295T, 315.1C, 462T	Consistent	High
53-4.45b	16069T, 16126C, 16160G, 16222T	73G, 185A, 263G, 295T, 315.1C (462 not sequenced)	Consistent	High

Table G4. MtDNA profiles generated from spent cartridge casings loaded by individual BBB.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
BBB		66T, 152C, 263G, 315.1C	-----	-----
54-1.22		263G, 315.1C	Inconsistent	High
54-1.45		66T, 152C, 263G, 315.1C	Consistent	High
54-3.22a		66T, 152C, 263G, 315.1C	Consistent	Medium
54-3.22c		66T, 152C, 263G, 315.1C	Consistent	Medium
54-3.45b		66T, 152C, 263G, 315.1C	Consistent	Low

Table G5. MtDNA profiles generated from spent cartridge casings loaded by individual C.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
C	16192T, 16256T, 16270T	73G, 263G, 315.1C	-----	-----
55-1.22b		263G, 315.1C	Inconsistent	High
55-3.45	16192T, 16256T, 16270T	(73 not sequenced) 263G, 315.1C	Consistent	Medium
55-4.22		263G, 315.1C	Inconsistent	Low

Table G6. MtDNA profiles generated from spent cartridge casings loaded by individual AA.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
AA	16104T, 16126C, 16294T, 16304C	73G, 152C, 263G, 315.1C	-----	-----
56-3.22	16104Y, 16126Y, 16294Y, 16304Y	73G, 152Y, 263G, 315.1C	Mixed-Consistent	Medium
56-4.45b	16069Y, 16126Y, 16160R, 16222Y	73G, 152C, 263G, 315.1C	Mixed-Inconsistent	Low
56-4.45c	16104T, 16126C, 16294T, 16304C	73G, 152C, 263G, 315.1C	Consistent	Low

Table G7. MtDNA profiles generated from spent cartridge casings loaded by individual A.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
A	16051G, 16129C, 16183C, 16189C	73G, 152C, 217C, 263G, 315.1C	-----	-----
57-1.22a	16051G, 16162G	263G, 315.1C	Inconsistent	Low
57-1.22c	16093C, 16189C	73G, 263G (<i>315 not sequenced</i>)	Inconsistent	Low
57-1.45c	16051R, 16126Y, 16129S, 16183M, 16189Y, 16294Y, 16296Y	73G, 152Y, 217Y, 263G, 315.1C	Mixed-Consistent	Low
57-2.22	16051R, 16126Y, 16129S, 16183M, 16189C, 16294Y, 16296Y	73G, 152C, 217Y, 263G, 315.1C	Mixed-Consistent	Low
57-2.45	16051G, 16129C, 16183C, 16189C	73G, 152C, 217C, 263G, 315.1C	Consistent	High
57-3.22	16051R, 16126Y, 16129S, 16183M, 16189Y, 16294Y, 16296Y	73G, 185R, 263G, 295Y, 315.1C	Mixed-Consistent	Low
57-3.45	16051G, 16126Y, 16129S, 16183C, 16189Y	73G, 152C, 263G, 315.1C	Mixed-Consistent	Low
57-4.22	16051R, 16126Y, 16129S, 16183M, 16189Y, 16294Y, 16296Y	73G, 152Y, 217Y, 263G, 315.1C	Mixed-Consistent	Low

Table G8. MtDNA profiles generated from spent cartridge casings loaded by individual J.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
J		263G, 309.2C, 315.1C	-----	-----
58-1.22		263G (309, 315 not sequenced)	Consistent	Medium
58-1.45	16069Y, 16126Y, 16160R, 16222Y	73R, 185R, 263G (309, 315 not sequenced)	Mixed-Consistent	Medium
58-2.45	16126Y, 16222Y	263G, 309.2C, 315.1C	Mixed-Consistent	Medium
58-3.22b		263G, 309.2C, 315.1C	Consistent	Low
58-3.22c		not sequenced	Consistent	Medium
58-3.45b		263G (309, 315 not sequenced)	Consistent	High
58-4.22		73G, 185A, 263G, 295T, 315.1C, 462T	Inconsistent	Low
58-4.45		73R, 152Y, 263G (309, 315 not sequenced)	Mixed-Consistent	Medium

Table G9. MtDNA profiles generated from spent cartridge casings loaded by individual KKK.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
KKK	16311C	93G, 263G, 315.1C	-----	-----
59-1.22	16311C	93R, 263G, 315.1C	Mixed-Consistent	Low
59-2.22c	16311C	93G, 263G, 315.1C	Consistent	Medium
59-2.45b	16311C	73R, 93R, 263G, 315.1C	Mixed-Consistent	Medium
59-3.22	16311C	93G, 263G, 315.1C	Consistent	High
59-3.45	16311C	73R, 93R, 263G, 295Y, 315.1C	Mixed-Consistent	Low
59-4.22	16311C	93G, 263G, 315.1C	Consistent	High
59-4.45	16311C	73R, 93R, 263G, 315.1C	Mixed-Consistent	Low

Table G10. MtDNA profiles generated from spent cartridge casings loaded by individual JJJ.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
JJJ	16126C, 16294T, 16296T	73G, 263G, 315.1C	-----	-----
60-1.22	16126C, 16294T, 16296T	73G, 263G, 315.1C	Consistent	High
60-2.22	16126C, 16294T, 16296T	73G, 263G, 315.1C	Consistent	High
60-3.22	16126C, 16294T, 16296T	73G, 263G, 315.1C	Consistent	High
60-4.22b	16126C, 16294T, 16296T	73G, 263G, 315.1C	Consistent	High
60-4.22c	16126C, 16294T, 16296T	73G, 263G, 315.1C	Consistent	High
60-4.45c	16126C, 16294T, 16296T	73G, 263G, 315.1C	Consistent	High

Table G11. MtDNA profiles generated from spent cartridge casings loaded by individual I.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
I	16192T, 16256T, 16270T, 16291T	73G, 263G, 315.1C	-----	-----
61-2.45	16192T, 16256T, 16270T, 16291T	73G, 263G, 315.1C	Consistent	Medium
61-3.22	16192T, 16246T, 16270T, 16291T	73G, 263G, 315.1C	Consistent	Medium
61-4.22c	16192T, 16256T, 16270T, 16291T	73G, 263G, 315.1C	Consistent	Low
61-4.45a	16192T, 16256T, 16270T, 16291T	73G, 263G, 315.1C	Consistent	Low
61-4.45b	16104Y, 16126Y, 16192Y, 16256Y, 16270Y, 16291Y, 16294Y, 16304Y	73G, 263G, 315.1C	Mixed-Consistent	Medium

Table G12. MtDNA profiles generated from spent cartridge casings loaded by individual YYY.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
YYY	16126C, 16294T, 16296T, 16304C	73G, 263G, 309.1C, 315.1C, 458T	-----	-----
62-2.22	16069Y, 16126Y, 16160R, 16162R, 16222Y, 16294T, 16296T, 16304C	73G, 263G, 309.1C, 315.1C, 458T	Mixed-Consistent	Medium
62-3.22a	16093C, 16104T, 16126C, 16294T	73G, 152C, 263G, 315.1C	Inconsistent	High
62-3.22b	16126C, 16294T, 16296T, 16304C	73G, 263G, 309.1C, 315.1C, 458T	Consistent	High
62-3.22c	16126C, 16294T, 16296T, 16304C	73G, 263G, 309.1C, 315.1C, 458T	Consistent	Medium
62-3.45b	16126C, 16294T, 16296T, 16304C	73G, 263G, 309.1C, 315.1C, 458T	Consistent	High
62-3.45c	16051R, 16126Y, 16126R, 16294T, 16296T, 16304C	73G, 263G, 309.1C, 315.1C, 458T	Mixed-Consistent	High
62-4.22	16093C, 16192T, 16294T, 16296T, 16304C	73G, 263G, 315.1C	Inconsistent	Medium

Table G13. MtDNA profiles generated from spent cartridge casings loaded by individual EE.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
EE	16126C, 16189C, 16294T, 16296T, 16298C	73G, 195C, 263G, 315.1C	-----	-----
63-2.22b	16126Y, 16189Y, 16294Y, 16296Y, 16304Y	73R, 195Y, 263G (315 not sequenced)	Mixed-Consistent	High
63-2.22c	16126Y, 16294Y, 16296Y	73R, 263G, 315.1C	Mixed-Inconsistent	High

Table G14. MtDNA profiles generated from spent cartridge casings loaded by individual JJ.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
JJ	16147T	263G, 309.2C, 315.1C	-----	-----
65-2.22c	16147T	263G (309, 315 not sequenced)	Consistent	Medium
65-2.45a	16126Y, 16222Y	73G, 242Y, 263G, 295Y, 315.1C	Mixed-Inconsistent	Medium
65-2.45c	16147T	263G, 309.2C, 315.1C	Consistent	Medium
65-3.22	16126Y, 16147Y, 16294Y	73R, 263G, 309.1Y, 315.1C	Mixed-Consistent	High
65-3.45	16147T	263G, 309.2C, 315.1C	Consistent	High

Table G15. MtDNA profiles generated from spent cartridge casings loaded by individual DDD.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
DDD	16051G, 16162G	73G, 263G, 315.1C	-----	-----
66-1.22c	16051G, 16162G	73G, 263G, 315.1C	Consistent	Low
66-2.22	16051G, 16162G	73G, 263G, 315.1C	Consistent	Medium
66-3.45	16051G, 16162G,	73G, 263G, 315.1C	Consistent	High
66-4.22	16051G, 16162G	73R, 263G, 315.1C	Mixed-Consistent	Low

Table G16. MtDNA profiles generated from spent cartridge casings loaded by individual VVV.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
VVV	16189C	73G, 150T, 263G, 315.1C	-----	-----
67-1.45b	16189C	73G, 150T, 263G, 315.1C	Consistent	High
67-2.45	16189Y	73G, 150Y, 242Y, 263G, 295Y, 315.1C	Mixed-Consistent	Low
67-4.45	16179T, 16242T	73G, 150T, 195Y, 263G, 315.1C	Inconsistent	High

Table G17. MtDNA profiles generated from spent cartridge casings loaded by individual XXX.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
XXX	16093C, 16189C	263G, 315.1C	-----	-----
68-1.45a	16093C, 16189C	263G, 315.1C	Consistent	Low
68-1.22b	16051G, 16129C, 16183C, 16189C,	73G, 152C, 217C, 263G, 315.1C	Inconsistent	Low
68-2.22	16093T/Y, 16189T/Y	263G, 315.1C	Mixed-Consistent	Low
68-3.22		263G, 315.1C	Inconsistent	High
68-3.45	16069T, 16126C, 16160G, 16222T	73G, 185A, 263G, 295T, 315.1C, 462T	Inconsistent	Low
68-4.45	16093Y, 16189Y	263G, 315.1C	Mixed-Consistent	Low

Table G18. MtDNA profiles generated from spent cartridge casings loaded by individual R.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
R	16093C, 16192T, 16256T, 16270T, 16291T	73G, 263G, 315.1C	-----	-----
69-1.45	16104T, 16126C, 16294T, 16304C	73G, 152C, 263G, 315.1C	Inconsistent	Low
69-2.45b	16093C, 16192T, 16256T, 16270T, 16291T	73G, 263G, 315.1C	Consistent	Low
69-2.45c	16256Y	73G, 152C, 195C, 263G, 309.1C, 315.1C	Inconsistent	Low

Table G19. MtDNA profiles generated from spent cartridge casings loaded by individual OOO.

Sample	HV1	HV2	mtDNA Classification	Quantification Level
OOO		263G, 309.1C, 315.1C	-----	-----
70-1.45		263G, 309.1C, 315.1C	Consistent	Medium
70-2.45		263G, 309.1C, 315.1C	Consistent	Medium
70-3.22a		263G, 309.1C, 315.1C	Consistent	High
70-3.45b	16051G, 16129C, 16183C, 16189C	73G, 152C, 217C, 263G, 315.1C	Inconsistent	Medium

APPENDIX H. COMPARISON OF HANDLER AND NON-HANDLER ALLELES AMPLIFIED WITH FUSION AND MTDNA PROFILE CLASSIFICATIONS

Table H1. Number of alleles both consistent with (H) and not consistent with (NH) the handler and the corresponding mtDNA profile result.

Sample	Quantitation Level	mtDNA Result	#H Alleles	#NH Alleles
52-1.45	High	Inconsistent	24	20
54-1.45	High	Consistent	35	4
53-3.45	High	Consistent	36	2
53-1.45	High	Mixed-Consistent	27	9
66-3.45	High	Consistent	38	0
67-4.45	High	Inconsistent	14	27
57-2.45	High	Consistent	43	1
65-3.45	High	Consistent	39	2
59-3.22	High	Consistent	41	4
60-1.22	High	Consistent	41	0
60-2.22	High	Consistent	31	2
59-4.22	High	Consistent	30	4
60-3.22	High	Consistent	26	5
54-1.22	High	Inconsistent	11	17
65-3.22	High	Mixed-Consistent	11	8
68-3.22	High	Inconsistent	8	11
62-3.45b	High	Consistent	21	3
60-4.45c	High	Consistent	25	4
62-3.45c	High	Mixed-Consistent	13	3
53-4.45a	High	Consistent	21	3
67-1.45b	High	Consistent	1	3
58-3.45b	High	Consistent	5	17
52-3.45b	High	Consistent	28	2
53-4.45b	High	Consistent	20	4
60-4.22c	High	Consistent	14	3
60-4.22b	High	Consistent	17	1
62-3.22b	High	Consistent	11	2
63-2.22b	High	Mixed-Consistent	1	3
63-2.22c	High	Mixed-Inconsistent	2	3
62-3.22a	High	Inconsistent	11	10
55-1.22b	High	Inconsistent	2	4
70-3.22a	High	Consistent	7	1
70-2.45	Medium	Consistent	27	2

Table H1 (cont'd)

55-3.45	Medium	Consistent	30	14
58-2.45	Medium	Mixed-Consistent	19	9
70-1.45	Medium	Consistent	18	4
58-4.45	Medium	Mixed-Consistent	14	10
58-1.45	Medium	Mixed-Consistent	12	19
61-2.45	Medium	Consistent	11	5
39-1.45	Medium	Consistent	24	5
62-2.22	Medium	Mixed-Consistent	7	1
53-1.22	Medium	Mixed-Consistent	6	7
56-3.22	Medium	Mixed-Consistent	9	3
61-3.22	Medium	Consistent	3	3
66-2.22	Medium	Consistent	14	2
58-1.22	Medium	Consistent	7	10
62-4.22	Medium	Inconsistent	15	2
51-4.22	Medium	Inconsistent	13	6
39-4.45b	Medium	Consistent	15	5
65-2.45c	Medium	Consistent	0	4
52-3.45c	Medium	Mixed-Consistent	12	3
59-2.45b	Medium	Mixed-Consistent	9	3
70-3.45b	Medium	Inconsistent	2	1
61-4.45b	Medium	Mixed-Consistent	5	12
65-2.45a	Medium	Mixed-Inconsistent	9	9
39-4.45a	Medium	Consistent	11	2
52-3.22b	Medium	Inconsistent	11	3
54-3.22a	Medium	Consistent	7	2
59-2.22c	Medium	Consistent	16	0
39-4.22b	Medium	Consistent	8	4
62-3.22c	Medium	Consistent	9	4
58-3.22c	Medium	Consistent	2	3
65-2.22c	Medium	Consistent	9	5
54-3.22c	Medium	Consistent	6	5
59-4.45	Low	Mixed-Consistent	12	3
67-2.45	Low	Mixed-Consistent	3	5
68-3.45	Low	Inconsistent	6	7
69-1.45	Low	Inconsistent	4	3
68-4.45	Low	Mixed-Consistent	9	5
59-3.45	Low	Mixed-Consistent	12	6
57-3.45	Low	Mixed-Consistent	6	2
51-1.45	Low	Consistent	11	7

Table H1 (cont'd)

58-4.22	Low	Inconsistent	15	19
57-4.22	Low	Mixed-Consistent	2	8
68-2.22	Low	Mixed-Consistent	1	2
57-3.22	Low	Mixed-Consistent	4	4
66-4.22	Low	Mixed-Consistent	3	4
55-4.22	Low	Inconsistent	7	4
59-1.22	Low	Mixed-Consistent	18	4
57-2.22	Low	Mixed-Consistent	3	3
61-4.45a	Low	Consistent	6	11
54-3.45b	Low	Consistent	9	7
69-2.45b	Low	Mixed-Consistent	4	2
57-1.45c	Low	Consistent	1	6
68-1.45a	Low	Consistent	4	5
69-2.45c	Low	Inconsistent	0	5
56-4.45b	Low	Mixed-Inconsistent	2	2
56-4.45c	Low	Consistent	2	5
57-1.22a	Low	Inconsistent	2	3
58-3.22b	Low	Consistent	3	2
52-3.22a	Low	Consistent	2	3
66-1.22c	Low	Consistent	4	2
57-1.22c	Low	Inconsistent	1	8
61-4.22c	Low	Consistent	4	2
68-1.22b	Low	Inconsistent	0	2
61-4.22b	Low	Consistent	2	5

APPENDIX I. DNA QUANTITIES RECOVERED FROM SPENT CARTRIDGE CASINGS FROM COLLECTION 1

Table I1. Quantitation results of casings fumed at MSU from Collection 1.

Sample	Extract Volume (μL)	DNA Concentration (pg/μL)	DNA Yield (pg)
2-2a	27.00	1.01E+00	27.27
2-2b	24.20	1.05E+00	25.41
2-2c	22.50	1.12E+01	252.00
3-3a	23.50	6.76E-01	15.89
3-3b	25.50	6.10E-01	15.56
3-3c	27.00	5.79E-01	15.63
8-4a	26.00	1.58E+00	41.08
8-4b	19.40	5.61E-01	10.88
8-4c	21.00	7.21E-01	15.14
10-5a	26.50	3.10E-02	0.82
10-5b	23.80	1.42E-01	3.38
10-5c	21.60	7.33E-02	1.58
13-6a	24.80	4.18E+00	103.66
13-6b	22.50	4.81E+00	108.23
13-6c	24.00	2.18E+00	52.32
15-7a	26.60	1.83E-01	4.87
15-7b	26.40	3.14E-01	8.29
15-7c	21.00	1.25E+00	26.25
23-1a	22.00	1.05E+00	23.10
23-1b	25.50	3.17E-01	8.08
23-1c	27.00	1.04E+00	28.08
24-5a	24.00	6.20E-01	14.88
24-5b	26.40	1.90E-01	5.02
24-5c	27.00	1.45E-01	3.92
25-2a	27.20	2.71E-02	0.74
25-2b	22.50	1.06E-01	2.39
25-2c	26.00	2.14E-02	0.56
26-3a	27.20	1.31E+00	35.63
26-3b	27.50	8.69E-01	23.90
26-3c	23.00	6.36E+00	146.28
27-4a	21.70	2.88E-01	6.25
27-4b	20.50	3.83E+00	78.52
27-4c	23.00	2.05E+00	47.15
33-6a	26.20	1.61E+00	42.18

Table I1 (cont'd)

33-6b	27.00	5.26E+01	1420.20
33-6c	25.50	4.94E-01	12.60
36-7a	30.00	4.85E-02	1.46
36-7b	27.50	1.11E-01	3.05
36-7c	26.70	1.48E-02	0.40
38-1a	22.80	4.37E-01	9.96
38-1b	24.20	4.12E-01	9.97
38-1c	22.80	1.49E+00	33.97
40-2a	27.80	7.25E-02	2.02
40-2b	29.70	8.56E-02	2.54
40-2c	25.00	3.57E-01	8.93
41-3a	25.50	2.05E-01	5.23
41-3b	24.00	2.34E-01	5.62
41-3c	25.80	6.21E-01	16.02
50-4a	7.00	8.61E-01	6.03
50-4b	24.00	2.68E-01	6.43
50-4c	20.40	5.65E-01	11.53

Table I2. Quantitation results of casings fumed at MSP from Collection 1.

Sample	Extract Volume (μL)	DNA Concentration (pg/μL)	DNA Yield (pg)
2-1a	29.30	1.32E-01	3.87
2-1b	30.00	7.02E-03	0.21
2-1c	27.00	8.43E-01	22.76
3-2a	20.00	2.61E-07	0.00
3-2b	26.30	4.29E-04	0.01
3-3c	28.60	5.18E-03	0.15
8-3a	28.40	6.72E-01	19.08
8-3b	27.80	7.99E-01	22.21
8-3c	25.00	4.14E-01	10.35
10-4a	26.70	2.85E-03	0.08
10-4b	28.80	2.61E-01	7.52
10-4c	26.00	2.46E-01	6.40
13-5a	29.20	5.63E-01	16.44
13-5b	30.30	1.31E+00	39.69
13-5c	26.00	1.89E+00	49.14
15-6a	26.00	3.60E-02	0.94
15-6b	26.70	5.55E-02	1.48
15-6c	24.40	4.52E-04	0.01
23-7a	32.00	1.28E+00	40.96

Table I2 (cont'd)

23-7b	29.80	3.34E+00	99.53
23-7c	26.30	1.18E-01	3.10
24-4a	25.70	8.07E-03	0.21
24-4b	27.50	7.81E-01	21.48
24-4c	27.40	2.92E-02	0.80
25-1a	27.00	2.48E-01	6.70
25-1b	28.40	1.00E-01	2.84
25-1c	22.20	7.15E-02	1.59
26-2a	26.50	7.83E-01	20.75
26-2b	22.60	4.56E-01	10.31
26-2c	22.10	1.07E+00	23.65
27-3a	28.20	1.18E-01	3.33
27-3b	23.20	1.09E-01	2.53
27-3c	27.30	1.45E-01	3.96
33-5a	27.60	6.95E-02	1.92
33-5b	23.00	2.15E-01	4.95
33-5c	27.80	5.15E-01	14.32
36-6a	30.00	6.87E-02	2.06
36-6b	27.50	4.01E-01	11.03
36-6c	26.70	3.72E-01	9.93
38-7a	25.80	1.72E-01	4.44
38-7b	27.00	1.87E-01	5.05
38-7c	25.00	6.57E-02	1.64
40-1a	27.80	1.77E-01	4.92
40-1b	29.70	7.88E-02	2.34
40-1c	25.00	1.27E-01	3.18
41-2a	27.80	4.95E-01	13.76
41-2b	29.00	5.45E-01	15.81
41-2c	26.50	5.83E-01	15.45
50-3a	28.50	8.62E-01	24.57
50-3b	29.00	1.77E-01	5.13
50-3c	28.80	8.98E-02	2.59

Table I3. Quantitation results of non-fumed casings from Collection 1.

Sample	Extract Volume (μL)	DNA Concentration (pg/μL)	DNA Yield (pg)
2-3a	28.80	2.21E+00	63.65
2-3b	33.00	5.19E-01	17.13
2-3c	26.00	8.25E-01	21.45
3-4a	29.00	2.42E+00	70.18
3-4b	26.00	5.35E-01	13.91
3-4c	24.00	3.40E-01	8.16
8-5a	27.00	9.57E-01	25.84
8-5b	25.00	1.66E+00	41.50
8-5c	29.00	1.97E+00	57.13
10-6a	26.20	2.59E-01	6.79
10-6b	27.80	3.14E-01	8.73
10-6c	28.40	2.28E-01	6.48
13-7a	25.20	3.69E+00	92.99
13-7b	24.00	1.61E+01	386.40
13-7c	27.50	2.93E+00	80.58
15-1a	25.20	1.74E-01	4.38
15-1b	30.80	3.67E-01	11.30
15-1c	27.60	3.81E-01	10.52
23-2a	25.60	5.14E+00	131.58
23-2b	24.00	4.15E+00	99.60
23-2c	25.20	1.38E+00	34.78
24-6a	26.80	1.24E-01	3.32
24-6b	27.00	4.73E-01	12.77
24-6c	27.40	3.06E-01	8.38
25-3a	26.80	2.95E-01	7.91
25-3b	24.80	3.54E-01	8.78
25-3c	24.00	4.79E-01	11.50
26-4a	24.50	1.70E+00	41.65
26-4b	26.80	1.78E+00	47.70
26-4c	27.00	1.38E+00	37.26
27-5a	21.20	1.38E+00	29.26
27-5b	18.80	1.39E+00	26.13
27-5c	24.50	1.31E+00	32.10
33-7a	24.50	2.16E+00	52.92
33-7b	24.40	2.65E+00	64.66
33-7c	25.60	1.19E+00	30.46
36-1a	22.20	9.91E-01	22.00
36-1b	25.00	5.80E-01	14.50
36-1c	28.00	8.94E-01	25.03

Table I3 (cont'd)

38-2a	26.20	9.87E-01	25.86
38-2b	27.20	1.55E+00	42.16
38-2c	26.00	7.87E-01	20.46
40-3a	27.00	6.83E-01	18.44
40-3b	28.80	1.83E+00	52.70
40-3c	27.20	3.53E-01	9.60
41-4a	24.00	5.42E-01	13.01
41-4b	29.30	4.04E+00	118.37
41-4c	25.50	7.36E-01	18.77
50-5a	25.70	1.94E+00	49.86
50-5b	25.50	3.68E+00	93.84
50-5c	27.40	9.58E-01	26.25

APPENDIX J. COMPARISON OF FUSION AND MINIFILER™ STR PROFILES

Red font: non-loader allele

**: allele was above the threshold using OSIRIS, but below the threshold using GeneMapper®.*

†: off-ladder allele

Blank cell: no alleles were amplified

Gray cell: locus not amplified

N/A: not applicable

Table J1. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual U.

Locus	2-1c (Fusion)	2-1c (MiniFiler™)	2-2a (Fusion)	2-2a (MiniFiler™)	U
Amel			X		X,X
D3			15		15,15
D1			15.3,16.3		11,17.3
D2					10,15
D10					12,14
D13	13		9		9,13
Penta E			12		12,15
D16	11,13		6		11,13
D18	14,15	14			14,15
D2		17	17		17,25
CSF					10,12
Penta D			11		10,11
THO1	6		9,9.3		6,7
vWA	14,20		18		14,20
D21					28,30
D7			11		11,11
D5	11				11,11
TPOX					8,11
DYS391					N/A
D8	12		†,†,13,15		12,12
D12	17,23				17,23
D19	15				13,13
FGA					24,25
D22			16		16,16
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J1 (cont'd)

Locus	2-2c (Fusion)	2-2c (MiniFiler™)	2-3a (MiniFiler™)	2-3a (Fusion)	U
Amel	X	X	X	X	X,X
D3	14,15,18		15		15,15
D1	14,17.3		11,17.3		11,17.3
D2	10,11,11.3		10,15		10,15
D10	12,14		12		12,14
D13	10,11	9,10,11		9	9,13
Penta E	12				12,15
D16	10,12		11,13	11	11,13
D18	12,17	12,17	13,14,15	14,15	14,15
D2	17,18,25	17,18	25	17,25	17,25
CSF	10	9,10	12	12	10,12
Penta D	16		10		10,11
THO1	6,7,9.3		6,7		6,7
vWA	16		14		14,20
D21	30,33.2	28,30,33.2	28,30,31	28,30	28,30
D7	10,12			11	11,11
D5	12		11		11,11
TPOX	8,11		8,11		8,11
DYS391					N/A
D8	12,14,15		12		12,12
D12	20		23		17,23
D19	13,15		13		13,13
FGA	20	20,†	17.2,24,25	24,†,†,†	24,25
D22	11,16		16		16,16
Fuming Method	MSU-Fumed	MSU-Fumed	Non-Fumed	Non-Fumed	Buccal

Table J2. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual MM.

Locus	3-3b (Fusion)	3-3b (MiniFiler™)	3-4a (Fusion)	3-4a (MiniFiler™)	MM
Amel	X		Y		X,X
D3			18		14,16
D1	12				12,16
D2	14				10,11
D10					14,15
D13					8,12
Penta E	12				7,21
D16	11,12		12		12,12
D18	13.2,16	12			14,14.2
D2	17,18,22	17,23			17,23
CSF		12		†	12,13
Penta D	11				13,13
THO1	9.3				9,9.3
vWA					17,17
D21					29,31.2
D7					9,11
D5					9,10
TPOX	12				8,8
DYS391					N/A
D8	10,15,15.1,†,†				13,15
D12			22		18,22
D19	13				14,15.2
FGA	23.2	22,25,26.2	17.2	47.2,†,†,†	22,26
D22	16				11,12
Fuming Method	MSU-Fumed	MSU-Fumed	Non-Fumed	Non-Fumed	Buccal

Table J3. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual S.

Locus	8-3a (Fusion)	8-3a (MiniFiler™)	8-3b (Fusion)	8-3b (MiniFiler™)	S
Amel	Y				X,X
D3	18				18,18
D1					12,15
D2	16				11,11.3
D10					13,15
D13	13	13	14		12,13
Penta E					12,13
D16	11		11		11,11
D18	12,17			12,16	12,16
D2	17,25	17,25		17	17,25
CSF					10,11
Penta D	12				10,13
THO1	6,9.3				6,9
vWA	15,17				17,18
D21	28,30	28	28		28,28
D7	10,12				10,10
D5					10,12
TPOX	11				8,11
DYS391					N/A
D8	12,15		13		13,16
D12	18,18.3		18		18,18.3
D19	14,15				13.2,15
FGA	23,24		22*		22,23
D22					15,15
Fuming Method	MSP-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Buccal

Table J3 (cont'd)

Locus	8-3c (Fusion)	8-3c (MiniFiler™)	8-4a (Fusion)	8-4a (MiniFiler™)	S
Amel	X		XY		X,X
D3			16		18,18
D1	12				12,15
D2	11,11.3				11,11.3
D10	15		13		13,15
D13	12		10,13	13	12,13
Penta E					12,13
D16	11		9,11,13	†	11,11
D18					12,16
D2	17		18		17,25
CSF				6	10,11
Penta D					10,13
THO1	6		6,7		6,9
vWA	17		17		17,18
D21	28			28	28,28
D7	10				10,10
D5					10,12
TPOX			8		8,11
DYS391					N/A
D8	13,16		10,13,15,16		13,16
D12			17,18		18,18.3
D19	13.2				13.2,15
FGA					22,23
D22					15,15
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J4. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual VV.

Locus	10-4b (Fusion)	10-4b (MiniFiler™)	VV
Amel	X		X,Y
D3	15,18		14,17
D1	12,14,15,16.3		15,17.3
D2			11,14
D10	14		12,13
D13	9,11	12	11,11
Penta E			7,8
D16	12,13		12,12
D18	13,16	14	12,16
D2		17	17,18
CSF	10,12		11,11
Penta D	12		9,12
THO1	6,9.3		9.3,9.3
vWA	15,18		17,17
D21	29,30.2,32.2		28,32.2
D7			10,11
D5			11,13
TPOX	8		11,11
DYS391			11
D8	8,10		8,12
D12	23		15,25
D19	14		14,15.2
FGA	24		22,23
D22			11,15
Fuming Method	MSP-Fumed	MSP-Fumed	Buccal

Table J5. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual V.

Locus	13-5a (Fusion)	13-5a (MiniFiler™)	13-5b (Fusion)	13-5b (MiniFiler™)	V
Amel	XY		XY		X,Y
D3	14		14		14,14
D1	16,16.3		15,16,16.3, 17.3		16.3,17.3
D2	11		11,11.3		11,11.3
D10	15		13,15		15,16
D13	12	†	10,12		10,12
Penta E			14		5,14
D16	12		11,12,13		11,12
D18	16	16	14		16,17
D2	†	20			20,22
CSF	11				10,11
Penta D			12		11,12
THO1	9,9.3		9,9.3		9,9.3
vWA	16		16,18		16,18
D21					28,32.2
D7			12		11,12
D5	12		12		12,12
TPOX	8		8		8,8
DYS391	11		11		11
D8	12		9,12		9,12
D12	23		21,23		21,23
D19	12		12,16		12,14
FGA	21.2,22.2	21.2			21.2,22
D22	11		11		11,16
Fuming Method	MSP-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Buccal

Table J5 (cont'd)

Locus	13-5c (Fusion)	13-5c (MiniFiler™)	13-6a (Fusion)	13-6a (MiniFiler™)	V
Amel	Y		XY		X,Y
D3			14		14,14
D1			16.3,17.3		16.3,17.3
D2	11.3		11		11,11.3
D10	16		15,16		15,16
D13	10,12	10,12	10,12	10,12	10,12
Penta E					5,14
D16			11,12		11,12
D18		16	16,17	16,17	16,17
D2	20	20,22	20,22	20,22	20,22
CSF	10	10,11	11	10	10,11
Penta D	11				11,12
THO1	9,9.3		9,9.3		9,9.3
vWA	16		16,18		16,18
D21		32.2	32.2	28,33.2	28,32.2
D7			11,12		11,12
D5			12		12,12
TPOX			8		8,8
DYS391	11				11
D8	9,12		9,12		9,12
D12	23		21,23		21,23
D19	12		12,14		12,14
FGA	21.2,22	21.2	21.2,22,22.2	16.2,21.2,22	21.2,22
D22	11				11,16
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J5 (cont'd)

Locus	13-6b (Fusion)	13-6b (MiniFiler™)	13-6c (Fusion)	13-6c (MiniFiler™)	V
Amel	XY		XY		X,Y
D3	14		14,15		14,14
D1	15.3,16.3, 17.3		14,17.3		16.3,17.3
D2	11,11.3				11,11.3
D10	15		13,16		15,16
D13	10,12	10,12	12	10	10,12
Penta E	5,14				5,14
D16	11,12	11,12	11,13		11,12
D18	16,17	16,17,18	12		16,17
D2	20,22	20,22,23	23.3	17,20,22	20,22
CSF	11	10,11	12	10,12	10,11
Penta D	11,12				11,12
THO1	7,9, 9.3		9		9,9.3
vWA	17,18		17		16,18
D21	28,32.2	28,33.2			28,32.2
D7	11,12		9,11		11,12
D5	12				12,12
TPOX			7		8,8
DYS391					11
D8	9,10,11,12		12,14,15		9,12
D12	17,21,23		21, 23		21,23
D19	12,14		14		12,14
FGA	22,23	21,22,23	17	20,22	21.2,22
D22	11				11,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J5 (cont'd)

Locus	13-7a (Fusion)	13-7a (MiniFiler™)	13-7b (Fusion)	13-7b (MiniFiler™)	V
Amel	X,Y		X,Y	X,Y	X,Y
D3	14,18		14		14,14
D1	16.3,17.3		16.3,17.3		16.3,17.3
D2	11,11.3		11,11.3		11,11.3
D10			15,16		15,16
D13	10	12	10,12	10,12	10,12
Penta E	5,14		5,14		5,14
D16	11,12	11,12	11,12	11,12	11,12
D18	17	16	16,17	16,17	16,17
D2	20,22	17,20,22, 25	20,22	20,22	20,22
CSF	11	†	10,11	10,11	10,11
Penta D	12		11,12		11,12
THO1	9,9.3		9,9.3		9,9.3
vWA	16,18		16,18		16,18
D21	28,32.2	32.2	28,32.2	28,32.2	28,32.2
D7	12		11,12	11	11,12
D5	12		12		12,12
TPOX			8		8,8
DYS391	11		11		11
D8	9,12		9,12		9,12
D12	20,21,23		21,23		21,23
D19			12		12,14
FGA	22	21.2,31.2,†,†	21.2,22	21.2,22,†	21.2,22
D22			11,16		11,16
Fuming Method	Non-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table J5 (cont'd)

Locus	13-7c (Fusion)	13-7c (MiniFiler™)	V
Amel	X,Y		X,Y
D3	14		14,14
D1			16.3,17.3
D2	11,11.3		11,11.3
D10	15,16		15,16
D13		12	10,12
Penta E	5,14		5,14
D16	12	11,12	11,12
D18	16,17	16	16,17
D2	20	20,22	20,22
CSF	10	10,11	10,11
Penta D	12		11,12
THO1	9,9.3		9,9.3
vWA	14,17,18		16,18
D21	28	28	28,32.2
D7	11,12	11	11,12
D5			12,12
TPOX			8,8
DYS391	11		11
D8	9,12		9,12
D12	23		21,23
D19	12		12,14
FGA	22,23,32.2	21.2,†,†	21.2,22
D22	11,16		11,16
Fuming Method	Non-Fumed	Non-Fumed	Buccal

Table J6. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual HH.

Locus	15-7c (Fusion)	15-7c (MiniFiler™)	HH
Amel			X,X
D3	14		14,18
D1	15.3		16,17.3
D2			11,14
D10			13,15
D13	†		10,11
Penta E			10,14
D16			9,12
D18	12, †		16,16
D2		17,18,19	17,19
CSF	†		11,13
Penta D	†		10,10
THO1	6,7		9,9
vWA			14,16
D21			30,31
D7	11		11,12
D5			9,12
TPOX			9,11
DYS391			N/A
D8	10*,15*		10,13
D12	18*		20,21
D19	14		13,14
FGA		20	22,25
D22			16,16
Fuming Method	MSU-Fumed	MSU-Fumed	Buccal

Table J7. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual L.

Locus	23-1a (Fusion)	23-1a (MiniFiler™)	23-7a (Fusion)	23-7a (MiniFiler™)	L
Amel	X		X	X	X,X
D3	17				16,16
D1	15.3				16,17.3
D2	11		11		11,11
D10	13		13,15		13,15
D13		12,13	13	13	13,13
Penta E			7		7,7
D16	11		11	11	11,11
D18	12,16	12	15,16	19	15,16
D2		16,17,18,19, 24	17	17	17,17
CSF	12	11,12			12,13
Penta D	10,14				9,11
THO1	9,9.3		8,9.3		8,9.3
vWA	17,19		14,17,18		14,18
D21	29	31.2	24,30		27,30
D7	8		10		8,10
D5			11		11,12
TPOX					8,8
DYS391	10				N/A
D8			13,14		13,14
D12	21		18*		18,20
D19			15		14,15
FGA		23,25	21,23	23	21,23
D22	16				15,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	Buccal

Table J7 (cont'd)

Locus	23-7b (Fusion)	23-7b (MiniFiler™)	23-7c (Fusion)	23-7c (MiniFiler™)	L
Amel	X		X		X,X
D3	16		16		16,16
D1	16				16,17.3
D2	11				11,11
D10	13				13,15
D13	13	13			13,13
Penta E	7				7,7
D16	11		11		11,11
D18	16				15,16
D2	17,23	17			17,17
CSF		12			12,13
Penta D					9,11
THO1	8,9.3				8,9.3
vWA	14,18		14		14,18
D21	30	30	27		27,30
D7	8,10		12		8,10
D5	12		11,12		11,12
TPOX					8,8
DYS391					N/A
D8	11,13,14		13,14		13,14
D12	18,20		20		18,20
D19	15				14,15
FGA		23			21,23
D22					15,16
Fuming Method	MSP-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Buccal

Table J7 (cont'd)

Locus	23-2a (Fusion)	23-2a (MiniFiler™)	23-2b (Fusion)	23-2b (MiniFiler™)	L
Amel	X	X	X	X	X,X
D3	16		16,17		16,16
D1	16,17.3		16,17.3		16,17.3
D2	11		11		11,11
D10			15		13,15
D13	13	13		13	13,13
Penta E	7		7		7,7
D16	11	11	11	11	11,11
D18	15,16	15,16	15	15,16	15,16
D2	17	17	17	17,19	17,17
CSF	13	12,13,†,†		12,13,†,†	12,13
Penta D			8.2		9,11
THO1	8,9.3		8,9.3		8,9.3
vWA	14		14,18		14,18
D21	30	27,30	30		27,30
D7	8	8,10			8,10
D5					11,12
TPOX					8,8
DYS391					N/A
D8	13,14		13,14		13,14
D12	20		18,20		18,20
D19			14,15		14,15
FGA	21,23	23.2,30,†,†,†	21,†,†	21,23	21,23
D22			†,16		15,16
Fuming Method	Non-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table J8. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual OO.

Locus	24-4b (Fusion)	24-4b (MiniFiler™)	24-5a (Fusion)	24-5a (MiniFiler™)	OO
Amel			X		X,X
D3	14,16		15		15,18
D1	15.3				14,18.3
D2	11.3,14				11,14
D10					14,15
D13	10			11,12	9,12
Penta E	12				10,13
D16	13		11	13	12,12
D18	12		12	†	11,14
D2	22	22,25			17,25
CSF	10,12			10	10,11
Penta D	11				9,12
THO1	9.3		6		6,9
vWA	17		17		17,18
D21	28,33.2				28,31.2
D7	10				10,10
D5	12,13		†		11,11
TPOX	12		8		8,8
DYS391					N/A
D8	10		14*,15		12,17
D12	18,21				18.3,20
D19	14,15		14		14,16
FGA	21,23		21,23	20,†	18,24
D22	16				11,15
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccals

Table J9. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual XX.

Locus	26-2a (Fusion)	26-2a (MiniFiler™)	26-2b (Fusion)	26-2b (MiniFiler™)	XX
Amel			X		X,X
D3	15		14,15,16,18		14,15
D1	12		14,17.3		14,17.3
D2					12,14
D10					14,16
D13	10		13	13	12,13
Penta E			12		12,12
D16	13		13		11,13
D18			12,17	18	17,18
D2	16				17,17
CSF		10,12	10	10,12	10,12
Penta D					12,12
THO1	9,9.3		9.3		9,9.3
vWA			17		17,19
D21	29				29,32
D7	12		12		9,12
D5			10		10,13
TPOX	8				8,12
DYS391					N/A
D8	10,13		10		10,13
D12	18,21		20		18,22
D19	14				13,14
FGA	23				21,23
D22					16,17
Fuming Method	MSP-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Buccal

Table J9 (cont'd)

Locus	26-2c (Fusion)	26-2c (MiniFiler™)	26-3a (Fusion)	26-3a (MiniFiler™)	XX
Amel	X		X		X,X
D3	14,15		†,16		14,15
D1	15.3,17.3		15,15.3		14,17.3
D2	12,14		11		12,14
D10					14,16
D13			12		12,13
Penta E			7		12,12
D16	OL5.1,11,13		11		11,13
D18	17		12,15,16	13,24,†	17,18
D2	17	17	20,24		17,17
CSF	10,12				10,12
Penta D			3.2,10,11		12,12
THO1	7,9.3		8,9.3		9,9.3
vWA	17,19		17		17,19
D21	30			30	29,32
D7	9,12		9		9,12
D5	9,13		10		10,13
TPOX	8		8		8,12
DYS391					N/A
D8	10,13,15		13,14		10,13
D12	18,22				18,22
D19			15		13,14
FGA	23,24		21		21,23
D22	16		15		16,17
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J9 (cont'd)

Locus	26-3c (Fusion)	26-3c (MiniFiler™)	XX
Amel	XY	X	X,X
D3	15,16,17		14,15
D1	11		14,17.3
D2	10,11		12,14
D10	13,15		14,16
D13	10	10,11,12,13	12,13
Penta E	5,14		12,12
D16	9,11,11.3	9,11	11,13
D18	17,21	15,17,21	17,18
D2	20,24	17,20,24	17,17
CSF	10,12,13	10	10,12
Penta D	9,11		12,12
THO1	9		9,9.3
vWA	14,16,18		17,19
D21	31,32.2	31,33.2	29,32
D7	8,9,11		9,12
D5	7		10,13
TPOX	11,12		8,12
DYS391	10		N/A
D8	10,12,13,14, 16		10,13
D12	18,21		18,22
D19	14.2,15		13,14
FGA	20,22,24	21,22,23	21,23
D22	15,16		16,17
Fuming Method	MSU-Fumed	MSU-Fumed	Buccal

Table J10. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual N.

Locus	27-4b (Fusion)	27-4b (MiniFiler™)	27-4c (Fusion)	27-4c (MiniFiler™)	N
Amel	X		X		X,X
D3	15,17,18				16,17
D1	12,17.3				15.3,17.3
D2	11,11.3				11,11
D10	13,15				13,13
D13	11,13				12,14
Penta E	13				13,15
D16	11		10		12,13
D18	12,16				13,14
D2	17,25	17,25			20,23
CSF	10	11			11,12
Penta D	10				10,12
THO1	6,9,9.3				6,9.3
vWA	17,18				17,18
D21	28	28			30,32.2
D7	10				11,12
D5	10,12				12,12
TPOX	8				8,8
DYS391					N/A
D8	12,13		13		13,13
D12	18,18.3				19,20
D19	13.2,15				13,14
FGA	22,29.1				21,25
D22	15				11,15
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J11. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual B.

Locus	33-5c (Fusion)	33-5c (MiniFiler™)	33-6a (Fusion)	33-6a (MiniFiler™)	B
Amel			X		X,Y
D3	14,16		18		16,18
D1	14,16.3				16.3,17.3
D2			11.3,14		14,15
D10	16		15		13,15
D13			10	10	10,12
Penta E					7,18
D16	9,11,12		11,12,13		9,13
D18			12,13,19.2		13,15
D2	17		22	20,22	20,25
CSF	10,12	12	12		10,12
Penta D					12,13
THO1	8		6,8,9.3		8,9,3
vWA	16,17,18		17,18		17,18
D21	28,29,30		31		29,31
D7	10				9,12
D5	13		12,13		11,13
TPOX	12		8,12		8,8
DYS391					11
D8	8,13		8,13		8,13
D12	23		21		22,23
D19	14,15				13,15
FGA					21,23
D22	16				15,16
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J11 (cont'd)

Locus	33-6b (Fusion)	33-6b (MiniFiler™)	33-6c (Fusion)	33-6c (MiniFiler™)	B
Amel	X				X,Y
D3	14,16,18		18		16,18
D1	14,15.3,16.3,17.3		15.3,16.3		16.3,17.3
D2	11.3,14,15				14,15
D10	15				13,15
D13	10,12	10,12			10,12
Penta E	7,12				7,18
D16	11,13		9,13		9,13
D18	12	12	16,18		13,15
D2	18,22,25	18,20,22,25		22,25	20,25
CSF	10,12	12	12		10,12
Penta D	9,11,12,13				12,13
THO1	6,9.3		9.3		8,9.3
vWA	17		17		17,18
D21	28,29,31,33.2	28,29,32,33.2	32.2		29,31
D7	9,10,12		12		9,12
D5	11,12,13				11,13
TPOX	8,12		8		8,8
DYS391	11				11
D8	8,10,15		8,13		8,13
D12	18,21,23		22		22,23
D19	13,14,15				13,15
FGA	21,23	21,23		19.2	21,23
D22	15,16		17		15,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU- Fumed	MSU-Fumed	Buccal

Table J11 (cont'd)

Locus	33-7a (Fusion)	33-7a (MiniFiler™)	33-7b (Fusion)	33-7b (MiniFiler™)	B
Amel	X,Y		X,Y		X,Y
D3	16, 17 ,18		16		16,18
D1	16.3,17.3				16.3,17.3
D2	14,15				14,15
D10					13,15
D13	10	12		10,12	10,12
Penta E					7,18
D16	9,13		9,12 ,13	9,13	9,13
D18	15	15	13,15	13,15	13,15
D2	25			20	20,25
CSF	12	10,†	12	10,12,†,†	10,12
Penta D					12,13
THO1	8,9 ,9.3		8,9.3		8,9.3
vWA	18		17,18		17,18
D21	29	29		29	29,31
D7	9				9,12
D5	13				11,13
TPOX					8,8
DYS391					11
D8	8,13		8,13		8,13
D12			22,23		22,23
D19	13,14				13,15
FGA	31,†	20.2,23,†,†		21,23,48.2	21,23
D22					15,16
Fuming Method	Non-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table J12. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual WW.

Locus	38-1b (Fusion)	38-1b (MiniFiler™)	38-1c (Fusion)	38-1c (MiniFiler™)	WW
Amel	X		X		X,X
D3	16				16,18
D1	15				11,12
D2					11,14
D10	15,16				15,16
D13		12	10,12		8,9
Penta E					11,12
D16	†,11,12,13				12,12
D18	12				12,15
D2	18	18		18	17,21
CSF	11,12		†		11,12
Penta D					10,12
THO1	7,9.1,9.3		6		9.3,9.3
vWA	16,17				15,17
D21					28,30
D7					10,11
D5					13,13
TPOX					8,12
DYS391					N/A
D8	10				10,12
D12	18,23		17*,21		18,19.3
D19	15		14		13,14
FGA	23		21		20,24
D22			16		16,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J13. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual SS.

Locus	40-1a (Fusion)	40-1a (MiniFiler™)	SS
Amel			X,Y
D3			14,18
D1	12,17.3		14,17.3
D2	10		11,11
D10			14,14
D13			10,12
Penta E			7,19
D16			11,12
D18			10,12
D2	20		17,20
CSF			11,12
Penta D			9,12
THO1			8,8
vWA	15,17		17,17
D21	29,32.2		29,32.2
D7			12,12
D5			13,13
TPOX	8		9,9
DYS391	11		11
D8	13		12,13
D12	15		15,24
D19			14,15
FGA			22,24
D22	18		16,16
Fuming Method	MSP-Fumed	MSP-Fumed	Buccal

Table J14. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual Y.

Locus	41-2c (Fusion)	41-2c (MiniFiler™)	41-3c (Fusion)	41-3c (MiniFiler™)	Y
Amel	X		X		X,Y
D3	14,16,17				16,17
D1	14		14,15		12,14
D2	14				14,15
D10	14				14,15
D13	11				13,14
Penta E	14,18				5,14
D16	11		10	11	11,12
D18	17		12,20,2		17,17
D2	17	17			17,24
CSF			12,14		OL,12,14
Penta D					8,13
THO1			9,3		9,9,3
vWA	14		14,18		14,16
D21	30.2				29,30.2
D7	8		8		8,10
D5					12,12
TPOX	8				8,8
DYS391					11
D8			†,10,13		10,14
D12	21		20,21		17,21
D19	13		14		13,16.2
FGA	21,27			22	22,27
D22					11,16
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J14 (cont'd)

Locus	41-4b (Fusion)	41-4b (MiniFiler™)	Y
Amel	X,Y		X,Y
D3	14		16,17
D1	16.3,17.3		12,14
D2	11.3		14,15
D10	15,16		14,15
D13	12		13,14
Penta E	5,14		5,14
D16	11,12	11,12	11,12
D18	16,17	16,17	17,17
D2	20	20,22	17,24
CSF	10	7,10,11	OL,12,14
Penta D	12		8,13
THO1	9,9.3		9,9.3
vWA	16,18		14,16
D21	28,32.2	28,32.2	29,30.2
D7	11,12	11,12	8,10
D5	12		12,12
TPOX	8		8,8
DYS391	11		11
D8	9,12		10,14
D12	21,23		17,21
D19	12,14		13,16.2
FGA	21.2,22	25.2,†,†	22,27
D22	11,16		11,16
Fuming Method	Non-Fumed	Non-Fumed	Buccal

Table J15. Fusion and MiniFiler™ profiles generated from spent cartridge casings loaded by individual II.

Locus	50-3a (Fusion)	50-3a (MiniFiler™)	50-4c (Fusion)	50-4c (MiniFiler™)	II
Amel	X		X		X,Y
D3	15		16		17,17
D1					15,18.3
D2	14		11.3		10,11
D10			15		13,15
D13	12	12			11,12
Penta E					13,14
D16	11				12,12
D18	13	13		17	16,17
D2			23		19,21
CSF		10		11	12,12
Penta D					9,13
THO1	7,8,9.3				8,9.3
vWA	17		15		15,17
D21		31,31.2			29,31
D7					10,12
D5	12		12		11,12
TPOX	11				8,8
DYS391					11
D8	14				11,13
D12	20		18,20		18,20
D19	14		14		14,15.2
FGA		50.2			21,23
D22	17*		12		15,16
Fuming Method	MSP-Fumed	MSP-Fumed	MSU-Fumed	MSU-Fumed	Buccal

Table J15 (cont'd)

Locus	50-5b (Fusion)	50-5b (MiniFiler™)	II
Amel	Y	Y	X,Y
D3	17		17,17
D1	15,18.3		15,18.3
D2	10,11		10,11
D10	13		13,15
D13	11,12	12	11,12
Penta E	13,14		13,14
D16	11,12	12	12,12
D18	16	16,17	16,17
D2		19,21	19,21
CSF	12	12	12,12
Penta D			9,13
THO1	6,8,9,9.3		8,9.3
vWA	15,17		15,17
D21	31	29	29,31
D7	12	10	10,12
D5	12		11,12
TPOX	8		8,8
DYS391			11
D8	11,13		11,13
D12	18,20,†		18,20
D19	14		14,15.2
FGA	23,†	20,21,23,25.2,†,†,†,†, †	21,23
D22	15,16		15,16
Fuming Method	Non-Fumed	Non-Fumed	Buccal

APPENDIX K. FUSION STR PROFILES FROM COLLECTION 1.

Red font: non-loader allele

**: allele was above the threshold using OSIRIS, but below the threshold using GeneMapper®.*

†: off-ladder allele

Blank cell: no alleles were amplified

N/A: not applicable

Table K1. Fusion profiles generated from spent cartridge casings loaded by individual U.

Locus	2-2a	2-2b	2-2c	2-1a	2-1b	2-1c	2-3a	2-3b	2-3c	U
Amel	X	X	X		X		X	X,Y	X	X,X
D3	15		14,15,18				15	15	15	15,15
D1	15.3,16.3		14,17.3				11,17.3	11	17.3	11,17.3
D2			10,11, 11.3				10,15	15		10,15
D10			12,14				12	12	14	12,14
D13	9	11	10,11		12	13				9,13
Penta E	12		12					15		12,15
D16	6		10,12	13		11,13	11,13		11,13	11,13
D18			12,17		14	14,15	13,14,15		14,15	14,15
D2	17		17,18,25		19		25	17,25		17,25
CSF			10	10			12	10		10,12
Penta D	11		16				10			10,11
THO1	9,9.3	6	6,7,9.3	6,7	7	6	6,7	6,7	7	6,7
vWA	18		16	14		14,20	14	14	15	14,20
D21			30,33.2	30			28,30,31			28,30
D7	11		10,12	11						11,11
D5			12		11	11	11	11		11,11
TPOX			8,11				8,11	11		8,11
DYS391										N/A
D8	13,15,††	12	12,14,15		12	12	12	12	12,13,15	12,12
D12		18	20		17	17,23	23		17	17,23
D19			13,15			15	13	13		13,13
FGA			20				17.2,24, 25			24,25
D22	16		11,16				16			16,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K2. Fusion profiles generated from spent cartridge casings loaded by individual MM.

Locus	3-3a	3-3b	3-3c	3-2a	3-2b	3-2c	3-4a	3-4b	3-4c	MM
Amel		X	X	Y			Y		X	X,X
D3							18			14,16
D1		12	11		16					12,16
D2		14							11	10,11
D10										14,15
D13			14						8	8,12
Penta E		12								7,21
D16		11,12	12,13		12		12	11		12,12
D18		13,2,16	16			14.2			15,17	14,14.2
D2		17,18,22								17,23
CSF			12							12,13
Penta D		11							13	13,13
THO1		9.3		6				9.3	6,9,9.3	9,9.3
vWA			17							17,17
D21										29,31.2
D7								8		9,11
D5									11	9,10
TPOX		12				8				8,8
DYS391										N/A
D8		10,15, 15.1,††			13			12	†,13,15	13,15
D12				22			22		18	18,22
D19		13								14,15.2
FGA		23.2					17.2			22,26
D22		16	16							11,12
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K3. Fusion profiles generated from spent cartridge casings loaded by individual S.

Locus	8-4a	8-4c	8-3a	8-3b	8-3c	8-5a	8-5b	8-5c	S
Amel	XY	X	Y		X	X	X	X	X,X
D3	16	14,16	18			18	18	18	18,18
D1		14,15,3			12	11,15	12,15		12,15
D2		11,3	16		11,11.3			11	11,11.3
D10	13	13			15	15		15	13,15
D13	10,13	10,12	13	14	12	13	13		12,13
Penta E		12					13		12,13
D16	9,11,13	11,13	11	11	11	11	11	11	11,11
D18		12	12,17			12	12	12	12,16
D2	18	20,25	17,25		17			17	17,25
CSF		10,12				11	13		10,11
Penta D		11	12						10,13
THO1	6,7	6,9,9.3	6,9.3		6	7,9	6,9		6,9
vWA	17	17,18	15,17		17		18		17,18
D21		28,33.2	28,30	28	28	29,34			28,28
D7		9,10,11	10,12		10	12	10	10	10,10
D5		13					12	10	10,12
TPOX	8	12	11			8	11		8,11
DYS391									N/A
D8	10,13,15,16	10,13,15	12,15	13	13,16	10,13,16	13,16	6,13,14,16	13,16
D12	17,18	17	18,18.3	18		18	18,18.3	18.3	18,18.3
D19		14,15,17	14,15		13.2		13.2,15	7,15,16,19.2	13.2,15
FGA		21,23,†††	23,24	22*		21		23,†	22,23
D22		16,†							15,15
Fuming Method	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K4. Fusion profiles generated from spent cartridge casings loaded by individual VV.

Locus	10-5a	10-5b	10-5c	10-4a	10-4b	10-4c	10-6a	10-6b	10-6c	VV
Amel			X	X	X			X		X,Y
D3			12		15,18			16		14,17
D1					12,14,15, 16.3					15,17.3
D2								14		11,14
D10					14					12,13
D13				12	9,11					11,11
Penta E			13							7,8
D16			11	12	12,13					12,12
D18			10,17		13,16					12,16
D2										17,18
CSF					10,12					11,11
Penta D				10	12					9,12
THO1		8	6	9,9.3	6,9.3					9.3,9.3
vWA				15,18	15,18					17,17
D21		28			29,30.2, 32.2					28,32.2
D7		9								10,11
D5		12						13		11,13
TPOX					8					11,11
DYS391										11
D8		14	10	11	8,10			8,13		8,12
D12		18,22		24	23					15,25
D19			14		14					14,15.2
FGA					24		32.2,†			22,23
D22										11,15
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K5. Fusion profiles generated from spent cartridge casings loaded by individual V.

Locus	13-6a	13-6b	13-6c	13-5a	13-5b	13-5c	13-7a	13-7b	13-7c	V
Amel	XY	XY	XY	XY	XY	Y	X,Y	X,Y	X,Y	X,Y
D3	14	14	14,15	14	14		14,18	14	14	14,14
D1	16.3,17.3	15.3,16.3,17.3	14,17.3	16,16.3	15,16,16.3,17.3		16.3,17.3	16.3,17.3		16.3,17.3
D2	11	11,11.3		11	11,11.3	11.3	11,11.3	11,11.3	11,11.3	11,11.3
D10	15,16	15	13,16	15	13,15	16		15,16	15,16	15,16
D13	10,12	10,12	12	12	10,12	10,12	10	10,12		10,12
Penta E		5,14			14		5,14	5,14	5,14	5,14
D16	11,12	11,12	11,13	12	11,12,13		11,12	11,12	12	11,12
D18	16,17	16,17	12	16	14		17	16,17	16,17	16,17
D2	20,22	20,22	23.3	†		20	20,22	20,22	20	20,22
CSF	11	11	12	11		10	11	10,11	10	10,11
Penta D		11,12			12	11	12	11,12	12	11,12
THO1	9,9.3	7,9, 9.3	9	9,9.3	9,9.3	9,9.3	9,9.3	9,9.3	9,9.3	9,9.3
vWA	16,18	17,18	17	16	16,18	16	16,18	16,18	14,17,18	16,18
D21	32.2	28,32.2					28,32.2	28,32.2	28	28,32.2
D7	11,12	11,12	9,11		12		12	11,12	11,12	11,12
D5	12	12		12	12		12	12		12,12
TPOX	8		7	8	8			8		8,8
DYS391				11	11	11	11	11	11	11
D8	9,12	9,10,11,12	12,14,15	12	9,12	9,12	9,12	9,12	9,12	9,12
D12	21,23	17,21,23	21, 23	23	21,23	23	20,21,23	21,23	23	21,23
D19	12,14	12,14	14	12	12,16	12		12	12	12,14
FGA	21.2,22,22.2	22,23	17	21.2,22.2		21.2,22	22	21.2,22	22,23,32.2	21.2,22
D22		11		11	11	11		11,16	11,16	11,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K6. Fusion profiles generated from spent cartridge casings loaded by individual HH.

Locus	15-7a	15-7b	15-7c	15-6a	15-6b	15-6c	15-1a	15-1b	15-1c	HH
Amel		X					X	X		X,X
D3		16	14					15		14,18
D1		11,14	15.3							16,17.3
D2	11.3	11,11.3, 14		14						11,14
D10	15						13			13,15
D13		10,12	†							10,11
Penta E							12			10,14
D16		9,13			11		†			9,12
D18		12,17	12,†		13		12			16,16
D2										17,19
CSF			†							11,13
Penta D		11,13	†							10,10
THO1		6,7,9.3	6,7		8		9.3		9	9,9
vWA		17								14,16
D21										30,31
D7			11		10					11,12
D5							12			9,12
TPOX	8	12								9,11
DYS391										N/A
D8		10,13	10*,15*	12,13	13			10,11	14.1	10,13
D12		18,20	18*		22,23		20			20,21
D19	15	15	14							13,14
FGA		24		21	23					22,25
D22		16								16,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K7. Fusion profiles generated from spent cartridge casings loaded by individual L.

Locus	23-1a	23-1b	23-1c	23-7a	23-7b	23-7c	23-2a	23-2b	23-2c	L
Amel	X	X		X	X	X	X	X	X	X,X
D3	17	14,16	16		16	16	16	16,17		16,16
D1	15.3	12,14	14		16		16,17.3	16,17.3		16,17.3
D2	11			11	11		11	11		11,11
D10	13	16		13,15	13			15	14	13,15
D13			8,10	13	13		13			13,13
Penta E				7	7		7	7		7,7
D16	11		12	11	11	11	11	11	11,12	11,11
D18	12,16	12		15,16	16		15,16	15	15	15,16
D2		23		17	17,23		17	17		17,17
CSF	12	10,12					13		12	12,13
Penta D	10,14		12,13					8.2	9	9,11
THO1	9,9.3	6,7	6,9.3	8,9.3	8,9.3		8,9.3	8,9.3	3,8,9.3	8,9.3
vWA	17,19	17	16	14,17,18	14,18	14	14	14,18	14	14,18
D21	29			24,30	30	27	30	30		27,30
D7	8			10	8,10	12	8			8,10
D5				11	12	11,12				11,12
TPOX										8,8
DYS391	10	10								N/A
D8		10,13,15	13	13,14	11,13,14	13,14	13,14	13,14	11,13,14	13,14
D12	21	21		18*	18,20	20	20	18,20	18	18,20
D19		14	15	15	15			14,15	15	14,15
FGA				21,23			21,23	21,†,†		21,23
D22	16							†,16		15,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K8. Fusion profiles generated from spent cartridge casings loaded by individual OO.

Locus	24-5a	24-5b	24-5c	24-4a	24-4b	24-4c	24-6a	24-6b	24-6c	OO
Amel	X							X	Y	X,X
D3	15			16	14,16			15		15,18
D1			14		15.3					14,18.3
D2		15			11.3,14					11,14
D10										14,15
D13		12	12		10					9,12
Penta E			12		12			12		10,13
D16	11	12	8,13		13	9,11		11		12,12
D18	12				12			12	11,14	11,14
D2					22		20	20		17,25
CSF			10		10,12					10,11
Penta D					11			10		9,12
THO1	6		7		9.3	6	6,9	6,7,9,9.3	6,9.3	6,9
vWA	17		15		17	17		16		17,18
D21			28,33.2		28,33.2					28,31.2
D7		9,10			10		8	10		10,10
D5	†				12,13					11,11
TPOX	8		8		12			12		8,8
DYS391								8		N/A
D8	14*,15		9,10		10	10		13,16		12,17
D12					18,21			18	19,20	18.3,20
D19	14				14,15					14,16
FGA	21,23				21,23			22		18,24
D22		16			16					11,15
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K9. Fusion profiles generated from spent cartridge casings loaded by individual T.

Locus	25-2a	25-2b	25-2c	25-1a	25-1b	25-1c	25-3a	25-3b	25-3c	T
Amel						X	X			X,X
D3							15		16,18	16,17
D1	14								11	16,17.3
D2									14	11,14
D10								14	15	14,17
D13		12			11		9			11,11
Penta E										11,12
D16		9,11					12			11,12
D18		12				13		13	15	13,17
D2										20,24
CSF			12							10,11
Penta D									12	8,10
THO1		8,9			6	6	6,7,9.3	6,8	9.3	6,7
vWA			18	18		15			15,17	19,20
D21	32.2							29		29,29
D7										8,10
D5		12							13	12,12
TPOX		8							12	8,11
DYS391										N/A
D8									10	13,14
D12								19,23	22	19,23
D19										13,16.2
FGA		21			24			24	24	24,24
D22							11			11,18
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K10. Fusion profiles generated from spent cartridge casings loaded by individual XX.

Locus	26-3a	26-3b	26-3c	26-2a	26-2b	26-2c	26-4b	26-4b	26-4c	XX
Amel	X		XY		X	X	X	X	X	X,X
D3	16,†	†	15,16,17	15	14,15,16, 18	14,15	14,15	14,15	14,15	14,15
D1	15,15.3		11	12	14,17.3	15.3,17.3		14,17.3	14,17.3	14,17.3
D2	11	10	10,11			12,14	14	14	12	12,14
D10		15	13,15				14,16	13,14	14	14,16
D13	12		10	10	13			11,12		12,13
Penta E	7		5,14		12					12,12
D16	11	10,11,†	9,11,11.3	13	13	11,13, †	11,13	13	11,12,13	11,13
D18	12,15,16	16	17,21		12,17	17	17	17,17.2	15,17,18	17,18
D2	20,24		20,24	16		17		17	17	17,17
CSF			10,12,13		10	10,12		10		10,12
Penta D	3.2,10,11		9,11							12,12
THO1	8,9.3	8,9,9.3	9	9,9.3	9.3	7,9.3	9,9.3	7,9,9.3	9.3	9,9.3
vWA	17	14,15	14,16,18		17	17,19	17,19	17,19	17,19	17,19
D21			31,32.2	29		30			32	29,32
D7	9	8	8,9,11	12	12	9,12			9	9,12
D5	10		7		10	9,13	10		10	10,13
TPOX	8		11,12	8		8	12			8,12
DYS391			10							N/A
D8	13,14		10,12,13, 14,16	10,13	10	10,13,15	10,13	10,13	10,13,17	10,13
D12		17	18,21	18,21	20	18,22	18,22	19,22	18,22	18,22
D19	15	14	14.2,15	14			13	14	14	13,14
FGA	21		20,22,24	23		23,24	21,23	21.2,23	23	21,23
D22	15	11	15,16			16	6	16,18		16,17
Fuming Method	MSU- Fumed	MSU- Fumed	MSU- Fumed	MSP- Fumed	MSP- Fumed	MSP- Fumed	Non- Fumed	Non- Fumed	Non- Fumed	Buccal

Table K11. Fusion profiles generated from spent cartridge casings loaded by individual N.

Locus	27-4a	27-4b	27-4c	27-3a	27-3b	27-3c	27-5a	27-5b	27-5c	N
Amel		X	X	X	X		X	X,Y	X,Y	X,X
D3		15,17,18					16	17	14,17,18	16,17
D1		12,17.3					15.3	14	15.3,17.3	15.3,17.3
D2		11,11.3						11		11,11
D10		13,15							13	13,13
D13		11,13						14		12,14
Penta E		13			18					13,15
D16	14	11	10		13		11,12	12	11,12	12,13
D18	16,19.2	12,16		17	14		18	13,18	14,16	13,14
D2		17,25							20	20,23
CSF		10								11,12
Penta D		10		8					12	10,12
THO1	6,†	6,9,9.3			6,9.3	4	6,9.3	6,9.3	9.3	6,9.3
vWA	†	17,18			16		16,17,18	17	18	17,18
D21	30.1,34.1	28		28					32.2	30,32.2
D7		10								11,12
D5		10,12		10					11,13	12,12
TPOX		8								8,8
DYS391										N/A
D8	13	12,13	13		13		11,13	13,14	13,15	13,13
D12	20	18,18.3					25	17,19	20	19,20
D19		13.2,15			15.2				15.2	13,14
FGA		22,29.1					24	21,46.2		21,25
D22	19	15					17		11	11,15
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K12. Fusion profiles generated from spent cartridge casings loaded by individual B.

Locus	33-6a	33-6b	33-6c	33-5a	33-5b	33-5c	33-7a	33-7b	33-7c	B
Amel	X	X		X	X		X,Y	X,Y	X,Y	X,Y
D3	18	14,16,18	18		16	14,16	16,17,18	16	18	16,18
D1		14,15.3, 16.3,17.3	15.3,16.3			14,16.3	16.3,17.3			16.3,17.3
D2	11.3,14	11.3,14,15		11			14,15		14	14,15
D10	15	15				16				13,15
D13	10	10,12					10		10	10,12
Penta E		7,12							7	7,18
D16	11,12,13	11,13	9,13	9		9,11,12	9,13	9,12,13		9,13
D18	12,13, 19.2	12	16,18	17			15	13,15	13	13,15
D2	22	18,22,25			17	17	25			20,25
CSF	12	10,12	12			10,12	12	12		10,12
Penta D		9,11,12,13								12,13
THO1	6,8,9.3	6,9.3	9.3		8,9,9.3,†	8	8,9,9.3	8,9.3	8	8,9.3
vWA	17,18	17	17			16,17,18	18	17,18	18	17,18
D21	31	28,29,31, 33.2	32.2	31		28,29,30	29			29,31
D7		9,10,12	12			10	9		12	9,12
D5	12,13	11,12,13				13	13			11,13
TPOX	8,12	8,12	8			12				8,8
DYS391		11								11
D8	8,13	8,10,15	8,13	8	13,†,†	8,13	8,13	8,13	8,13	8,13
D12	21	18,21,23	22			23		22,23		22,23
D19		13,14,15		15		14,15	13,14			13,15
FGA		21,23					31,†			21,23
D22		15,16	17	11		16				15,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K13. Fusion profiles generated from spent cartridge casings loaded by individual D.

Locus	36-7a	36-7b	36-7c	36-6a	36-6b	36-6c	36-1a	36-1b	36-1c	D
Amel	X	X				X	X,Y	Y	Y	X,Y
D3		15	16	16			17		15	17,18
D1	17.3									15,15
D2										11,14
D10		13								13,14
D13							11			11,11
Penta E										7,13
D16		5,8,13		13		10,12,13			12,13	13,13
D18		12				14	14			12,14
D2			17			16			20	17,20
CSF										11,12
Penta D										9,11
THO1	9			9	8	8,9.3	8,9.3	9,9.3	9.3	8,9.3
vWA		17	16		15		15			15,17
D21										28,30
D7		9,10	12							9,12
D5									9	11,12
TPOX		9								9,11
DYS391										10
D8	15	8,15		13	8,16,18		8,13	13	9,13	8,13
D12			24				19		18	15,19
D19					18		15			14,15
FGA							22.1,†		†	21,26
D22							†			12,17
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K14. Fusion profiles generated from spent cartridge casings loaded by individual WW.

Locus	38-1a	38-1b	38-1c	38-7a	38-7b	38-7c	38-2a	38-2b	38-2c	WW
Amel	Y	X	X				X	X,Y	X	X,X
D3	14,16	16					16,18	16,17	15,17	16,18
D1	11,14, 17.3	15		11			11	15		11,12
D2	11,14			14				11,14		11,14
D10		15,16						13,16	15	15,16
D13			10,12				8	11	9	8,9
Penta E	12			10				7,8		11,12
D16	12	11,12,13, †		12			12	12	12	12,12
D18		12		15	15		12	12,16,17	14,15	12,15
D2		18						18	18	17,21
CSF		11,12	†							11,12
Penta D								9,12	12	10,12
THO1	6,9.3	7,9.1,9.3	6	6,9.3	8,9.3		9.3	9.3	8,9.3	9.3,9.3
vWA		16,17			17*,18*		15,17	15,17		15,17
D21							28	28,32.2		28,30
D7				11				10		10,11
D5							13	11		13,13
TPOX							8	11		8,12
DYS391								11		N/A
D8	17	10			10,12,14	10	10	10,12		10,12
D12	21	18,23	17*,21		18	23	18,19.3	19.3,25		18,19.3
D19		15	14	14			14	14,15.2	13	13,14
FGA		23	21					23		20,24
D22			16							16,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K15. Fusion profiles generated from spent cartridge casings loaded by individual SS.

Locus	40-2a	40-2b		40-1a	40-1b	40-1c	40-3a	40-3b	40-3c	SS
Amel	Y							X,Y		X,Y
D3						16	14,17	14,17		14,18
D1	17.3			12,17.3				15,18.3		14,17.3
D2		11		10			10	11		11,11
D10							13,14	13,15		14,14
D13							11			10,12
Penta E							7	14		7,19
D16							12	10,12		11,12
D18							10	16		10,12
D2		17		20			22	19		17,20
CSF							11,12	12		11,12
Penta D							9	9		9,12
THO1							8	7,8		8,8
vWA		17		15,17			18	15		17,17
D21				29,32.2		29	29	29,31		29,32.2
D7										12,12
D5		13						11		13,13
TPOX				8			8	8		9,9
DYS391				11			11			11
D8		12		13			†,10,11, 13	11,13		12,13
D12	15	15,23		15			15,20	18	†	15,24
D19						14		13,14		14,15
FGA									23.1	22,24
D22		16		18				13		16,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K16. Fusion profiles generated from spent cartridge casings loaded by individual Y.

Locus	41-3a	41-3b	41-3c	41-2a	41-2b	41-2c	41-4a	41-4b	41-4c	Y
Amel	XY		X			X	Y	X,Y	X,Y	X,Y
D3		15,17				14,16,17		14	17	16,17
D1			14,15			14		16.3,17.3		12,14
D2					11	14		11.3	14	14,15
D10		15				14	14	15,16		14,15
D13						11		12	9,13	13,14
Penta E		7				14,18		5,14		5,14
D16			10			11	11	11,12	13	11,12
D18			12,20.2			17	16	16,17	17	17,17
D2	17					17		20	17,24	17,24
CSF			12,14		12			10		OL,12,14
Penta D								12	8	8,13
THO1	9.3		9.3		9.3		6	9,9.3	6,9.3	9,9.3
vWA	14	17	14,18		17	14		16,18	14	14,16
D21					33.3*	30.2		28,32.2	30.2	29,30.2
D7			8	10	10	8		11,12	10,12	8,10
D5				12				12		12,12
TPOX		8				8		8	11	8,8
DYS391								11		11
D8	12	12,13,15,19	10,13,†		13		10,15	9,12	10,14	10,14
D12		24	20,21			21		21,23	17,20	17,21
D19			14			13		12,14	13,15.2	13,16.2
FGA		23,24				21,27		21.2,22	20,27	22,27
D22								11,16		11,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

Table K17. Fusion profiles generated from spent cartridge casings loaded by individual II.

Locus	50-4a	50-4b	50-4c	50-3a	50-3b	50-3c	50-5a	50-5b	50-5c	II
Amel		X	X	X	XY	XY	X,Y	Y	X,Y	X,Y
D3			16	15	15		17	17	17	17,17
D1		15,18.3					12,15	15,18.3		15,18.3
D2			11.3	14			11,11.3	10,11	10,11	10,11
D10			15				15	13	15	13,15
D13				12			12	11,12	11	11,12
Penta E								13,14		13,14
D16		12		11	12		11,12	11,12	11,12	12,12
D18				13				16	16	16,17
D2			23		25				19	19,21
CSF							10	12		12,12
Penta D										9,13
THO1		6,7,8		7,8,9.3			7,8,9.3	6,8,9,9.3	8	8,9.3
vWA		15	15	17		17	17,18	15,17	15,17	15,17
D21		29			31		29	31		29,31
D7								12		10,12
D5			12	12			11	12	12	11,12
TPOX				11			11	8		8,8
DYS391									11	11
D8		11		14	13	11,13	11,13,14,16	11,13	11,13,15,16	11,13
D12			18,20	20		23	18	18,20,†	18,19	18,20
D19			14	14	13,14		16.2	14	15.2	14,15.2
FGA		23			25		22,23	23,†	21,†	21,23
D22			12	17*		15		15,16		15,16
Fuming Method	MSU-Fumed	MSU-Fumed	MSU-Fumed	MSP-Fumed	MSP-Fumed	MSP-Fumed	Non-Fumed	Non-Fumed	Non-Fumed	Buccal

APPENDIX L. HANDLER AND NON-HANDLER ALLELES AMPLIFIED WITH FUSION FROM COLLECTION 1

Table L1. Summary of the number of handler (H) alleles, non-handler (NH) alleles, and percent profile produced using Fusion for all samples in Collection 1.

Sample	Treatment	Fusion % Profile	# H alleles (Fusion)	# NH alleles (Fusion)
2-1a	Fumed at MSP	17.9%	7	0
2-1b	Fumed at MSP	15.4%	6	2
2-1c	Fumed at MSP	30.8%	12	1
2-2a	Fumed at MSU	20.5%	8	10
2-2b	Fumed at MSU	7.7%	3	2
2-2c	Fumed at MSU	46.2%	18	25
2-3a	Non-Fumed	71.8%	28	3
2-3b	Non-Fumed	41.0%	16	1
2-3c	Non-Fumed	28.2%	11	3
3-2a	Fumed at MSP	2.4%	1	2
3-2b	Fumed at MSP	7.3%	3	0
3-2c	Fumed at MSP	4.9%	2	0
3-3a	Fumed at MSU	0.0%	0	0
3-3a	Fumed at MSU	9.8%	4	5
3-3b	Fumed at MSU	14.6%	6	16
3-4a	Non-Fumed	4.9%	2	3
3-4b	Non-Fumed	2.4%	1	3
3-4c	Non-Fumed	21.9%	9	4
8-3a	Fumed at MSP	37.5%	15	12
8-3b	Fumed at MSP	12.5%	5	1
8-3c	Fumed at MSP	37.5%	15	0
8-4a	Fumed at MSU	25.0%	10	10
8-4b	Fumed at MSU	-	-	-
8-4c	Fumed at MSU	45.0%	18	26
8-5a	Non-Fumed	31.7%	13	7
8-5b	Non-Fumed	48.8%	20	1
8-5c	Non-Fumed	34.1%	14	5
10-4a	Fumed at MSP	9.8%	4	6
10-4b	Fumed at MSP	24.4%	10	20
10-4c	Fumed at MSP	-	-	-
10-5a	Fumed at MSU	0.0%	0	0
10-5b	Fumed at MSU	2.4%	1	6
10-5c	Fumed at MSU	4.9%	2	7

Table L1 (cont'd)

10-6a	Non-Fumed	0.0%	0	1
10-6b	Non-Fumed	9.7%	4	2
10-6c	Non-Fumed	0.0%	0	0
13-5a	Fumed at MSP	47.7%	21	3
13-5b	Fumed at MSP	63.6%	28	6
13-5c	Fumed at MSP	43.2%	19	0
13-6a	Fumed at MSU	77.3%	34	1
13-6b	Fumed at MSU	84.1%	37	7
13-6c	Fumed at MSU	34.1%	15	11
13-7a	Non-Fumed	70.4%	31	2
13-7b	Non-Fumed	97.7%	43	0
13-7c	Non-Fumed	65.9%	29	4
15-1a	Non-Fumed	9.7%	4	3
15-1b	Non-Fumed	4.9%	2	2
15-1c	Non-Fumed	2.4%	1	1
15-6a	Fumed at MSP	4.9%	2	2
15-6b	Fumed at MSP	2.4%	1	7
15-6c	Fumed at MSP	0.0%	0	0
15-7a	Fumed at MSU	2.4%	1	3
15-7b	Fumed at MSU	22.0%	9	18
15-7c	Fumed at MSU	9.8%	4	10
23-1a	Fumed at MSU	23.7%	9	11
23-1a	Fumed at MSU	10.5%	4	8
23-1b	Fumed at MSU	13.2%	5	14
23-2a	Non-Fumed	57.9%	22	0
23-2b	Non-Fumed	60.5%	23	2
23-2c	Non-Fumed	31.6%	12	4
23-7a	Fumed at MSP	60.5%	23	2
23-7b	Fumed at MSP	60.5%	23	2
23-7c	Fumed at MSP	26.3%	10	1
24-4a	Fumed at MSP	0.0%	0	1
24-4b	Fumed at MSP	14.6%	6	23
24-4c	Fumed at MSP	4.9%	2	3
24-5a	Fumed at MSU	14.6%	6	7
24-5b	Fumed at MSU	7.3%	3	3
24-5c	Fumed at MSU	12.2%	5	8
24-6a	Non-Fumed	2.4%	1	2
24-6b	Non-Fumed	1220.0%	5	14
24-6c	Non-Fumed	12.2%	5	2
25-1a	Fumed at MSP	0.0%	0	1

Table L1 (cont'd)

25-1b	Fumed at MSP	7.3%	3	0
25-1c	Fumed at MSP	7.3%	3	1
25-2a	Fumed at MSU	0.0%	0	2
25-2b	Fumed at MSU	7.3%	3	6
25-2c	Fumed at MSU	0.0%	0	2
25-3a	Non-Fumed	12.2%	5	3
25-3b	Non-Fumed	17.1%	7	1
25-3c	Non-Fumed	7.3%	3	12
26-2a	Fumed at MSP	28.6%	12	4
26-2b	Fumed at MSP	35.7%	15	4
26-2c	Fumed at MSP	59.5%	25	7
26-3a	Fumed at MSU	23.8%	10	18
26-3b	Fumed at MSU	9.5%	4	12
26-3c	Fumed at MSU	31.0%	13	39
26-4a	Non-Fumed	52.4%	22	1
26-4b	Non-Fumed	52.4%	22	7
26-4c	Non-Fumed	57.1%	24	3
27-3a	Fumed at MSP	2.5%	1	4
27-3b	Fumed at MSP	15.0%	6	3
27-3c	Fumed at MSP	0.0%	0	1
27-4a	Fumed at MSU	7.5%	3	8
27-4b	Fumed at MSU	37.5%	15	24
27-4c	Fumed at MSU	5.0%	2	1
27-5a	Non-Fumed	22.5%	9	7
27-5b	Non-Fumed	30.0%	12	6
27-5c	Non-Fumed	37.5%	15	9
33-5a	Fumed at MSP	10.9%	5	3
33-5b	Fumed at MSP	10.9%	5	6
33-5c	Fumed at MSP	32.6%	15	11
33-6a	Fumed at MSU	30.4%	14	13
33-6b	Fumed at MSU	76.1%	35	21
33-6c	Fumed at MSU	26.1%	12	5
33-7a	Non-Fumed	50.0%	23	4
33-7b	Non-Fumed	34.8%	16	1
33-7c	Non-Fumed	26.1%	12	0
36-1a	Non-Fumed	27.3%	12	1
36-1b	Non-Fumed	6.8%	3	1
36-1c	Non-Fumed	11.4%	5	5
36-6a	Fumed at MSP	4.5%	2	2
36-6b	Fumed at MSP	6.8%	3	3

Table L1 (cont'd)

36-6c	Fumed at MSP	11.4%	5	3
36-7a	Fumed at MSU	2.3%	1	3
36-7b	Fumed at MSU	18.2%	8	5
36-7c	Fumed at MSU	4.5%	2	3
38-1a	Fumed at MSU	17.1%	7	7
38-1b	Fumed at MSU	29.3%	12	11
38-1c	Fumed at MSU	7.3%	3	7
38-2a	Non-Fumed	41.5%	17	0
38-2b	Non-Fumed	41.5%	17	18
38-2c	Non-Fumed	21.9%	9	4
38-7a	Fumed at MSP	17.1%	7	2
38-7b	Fumed at MSP	14.6%	6	3
38-7c	Fumed at MSP	2.4%	1	1
40-1a	Fumed at MSP	20.5%	8	6
40-1b	Fumed at MSP	0.0%	0	0
40-1c	Fumed at MSP	5.1%	2	1
40-2a	Fumed at MSU	7.7%	3	0
40-2b	Fumed at MSU	17.9%	7	1
40-2c	Fumed at MSU	-	-	-
40-3a	Non-Fumed	33.3%	13	10
40-3b	Non-Fumed	30.8%	12	18
40-3c	Non-Fumed	0.0%	0	1
41-2a	Fumed at MSP	4.5%	2	0
41-2b	Fumed at MSP	7.1%	3	4
41-2c	Fumed at MSP	40.5%	17	4
41-3a	Fumed at MSU	11.4%	5	1
41-3b	Fumed at MSU	6.8%	3	10
41-3c	Fumed at MSU	20.5%	9	9
41-4a	Non-Fumed	9.1%	4	3
41-4b	Non-Fumed	40.9%	18	21
41-4c	Non-Fumed	40.9%	18	8
50-3a	Fumed at MSP	18.6%	8	8
50-3b	Fumed at MSP	14.0%	6	4
50-3c	Fumed at MSP	14.0%	6	1
50-4a	Fumed at MSU	0.0%	0	0
50-4b	Fumed at MSU	20.9%	9	2
50-4c	Fumed at MSU	16.3%	7	4
50-5a	Non-Fumed	39.5%	17	11
50-5b	Non-Fumed	69.8%	30	4
50-5c	Non-Fumed	46.5%	20	4