SUPREME COURT OF THE STATE OF NEW YORK
COUNTY OF NEW YORK

E. JEAN CARROLL, *Plaintiff*, -against- DONALD J. TRUMP, in his personal capacity, *Defendant*.	Index No. 160694/2019 Hon. Doris Ling-Cohan

PLAINTIFF'S FIRST NOTICE TO SUBMIT TO PHSYICAL EXAMINATION TO DEFENDANT DONALD J. TRUMP

PLEASE TAKE NOTICE THAT, pursuant to CPLR § 3121, Defendant Donald J. Trump is required to submit to a physical examination by LabCorp at its office located at 1145 19th Street NW #601, Washington, D.C. 20036, or at another location convenient for Defendant, on March 2, 2020, at 9 a.m. The examination shall obtain a buccal, blood or skin cell sample from Defendant sufficient for DNA analysis and comparison against unidentified male DNA present on the dress that Plaintiff wore during the sexual assault at issue in this action. *See* Exhibit A.

Dated: New York, New York
January 30, 2020

By: /s/ Roberta A. Kaplan
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Counsel for Plaintiff E. Jean Carroll

EXHIBIT A

Forensic Analytical™ Crime Lab

Laboratory Report[1]

Roberta Kaplan, Esq. Kaplan, Hecker, & Fink LLP 350 Fifth Ave., Ste 7110 New York, NY 10118	Report Date: January 8, 2020 FACL Case #: 20190357 Client #: 21497 Client Case #: 160694/2019

Case Name: E. Jean Carroll v. Donald Trump

Report Type: Physical Evidence Examination and DNA Analysis

Background and Purpose of Examination

The following information is taken from a complaint filed November 4, 2019 with the New York Supreme Court by Roberta Kaplan, counsel for E. Jean Carroll in which it is alleged:

Approximately 23 years ago, E. Jean Carroll visited Bergdorf Goodman, a luxury department store in New York City, to shop. Upon leaving the store, Carroll ran into Donald Trump, with whom she was acquainted. Trump asked Carroll to assist him in purchasing a gift at Bergdorf Goodman for a girl. Carroll agreed and they both entered the store. While browsing the store, Trump suggested visiting the lingerie department. He insisted Carroll try on a see-through bodysuit and maneuvered her into a dressing room, closing the door behind them. At that moment, Trump assaulted Carroll. During the assault, Trump grabbed Carroll's arms, pinned her against the wall, placed his hand under her dress, pulled down her tights, and fondled her vagina with his fingers. He unzipped his pants and forced his penis inside of her. Shortly thereafter, Carroll was able to free herself and ran out of the dressing room and out of the store. The dress and shoes she wore at the time of the assault were kept in her closet until 2019 when Carroll donned them for a photoshoot.

Kaplan requested Forensic Analytical Crime Lab (FACL) examine the dress and shoes to determine if male biology, specifically semen, is present. Additionally, to determine if [redacted], [redacted], [redacted], [redacted], and [redacted] – all individuals

[1] This report was published in full-color and should be read in that form.

who possibly came into contact with the dress at the time of the photoshoot – can be eliminated as contributors to any biology foreign to E. Jean Carroll.

Items of Physical Evidence

The following item of physical evidence was received at FACL from Oliver Farnum of Kaplan, Hecker, & Fink LLP on November 7, 2019 via FedEx courier:

1. A reference buccal specimen from E. Jean Carroll.

The following item of physical evidence was received at FACL from Alina Mogilyanskaya of Mintz Group LLC on November 8, 2019 via FedEx courier:

2. A black dress.

The following item of physical evidence was received at FACL from E. Jean Carroll on November 13, 2019 via FedEx courier:

3. A pair of shoes.

The following items of physical evidence were received at FACL from Oliver Farnum of Kaplan, Hecker, & Fink LLP on December 13, 2019 via FedEx courier:

4. A reference buccal specimen from [redacted].
5. A reference buccal specimen from [redacted].
6. A reference buccal specimen from [redacted].
7. A reference buccal specimen from [redacted].

The following item of physical evidence was received at FACL from Oliver Farnum of Kaplan, Hecker, & Fink LLP on December 19, 2019 via FedEx courier:

8. A reference buccal specimen from [redacted].

Evidence Examination

Reference Specimens

Descriptions and processing of the reference swab specimens for DNA analysis are summarized in Table 1. The external packaging and the reference swabs are shown in Figures 1 through 6.

Table 1. Reference specimen processing summary.

FACL Item No.	Description of Reference Specimen	Total Human DNA recovered, ng	DNA Typing Assay, ng
1	E. Jean Carroll reference buccal swabs (2) – stained light brown, one whole swab consumed for analysis → 1A	~ 1123	~ 0.8
4	[redacted] reference buccal swab (1) – stained light yellow, approximately ½ of swab consumed for analysis → 4A	~ 416	~ 0.8
5	[redacted] reference buccal swab (1) – stained faint yellow, approximately ½ of swab consumed for analysis → 5A	~ 861	~ 0.8
6	[redacted] reference buccal swab (1) – stained light yellow, approximately ½ of swab consumed for analysis → 6A	~ 853	~ 0.8
7	[redacted] reference buccal swab (1) – stained very pale yellow, approximately ½ of swab consumed for analysis → 7A	~ 601	~ 0.8
8	[redacted] reference buccal swab (1) – stained light brown, approximately ½ of swab consumed for analysis → 8A	~ 1289	~ 0.8

Figure 1. E. Jean Carroll reference buccal specimen [#1], packaging and swabs before sampling.

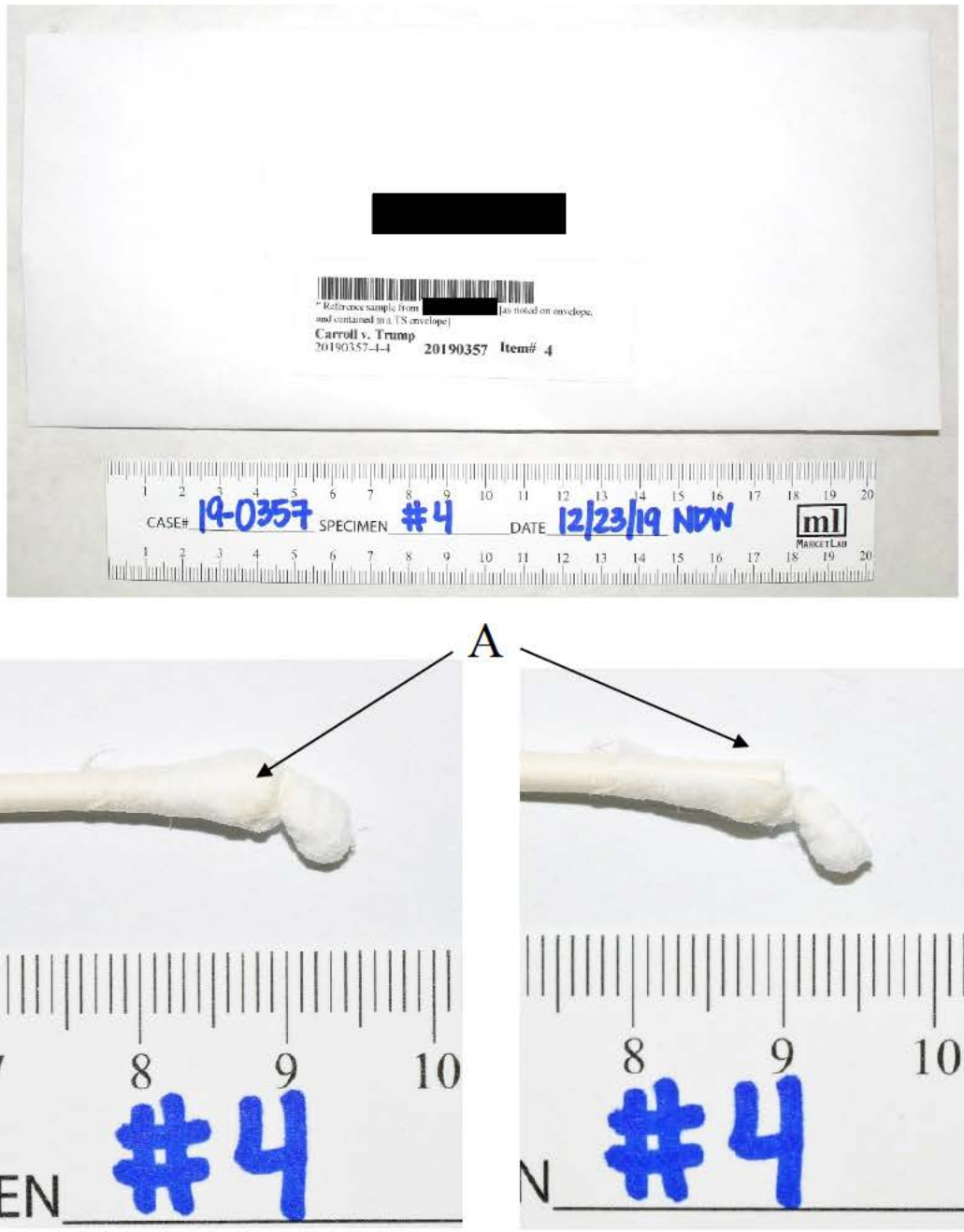

Figure 2. [redacted] reference buccal specimen [#4], packaging and swab before and after sampling.

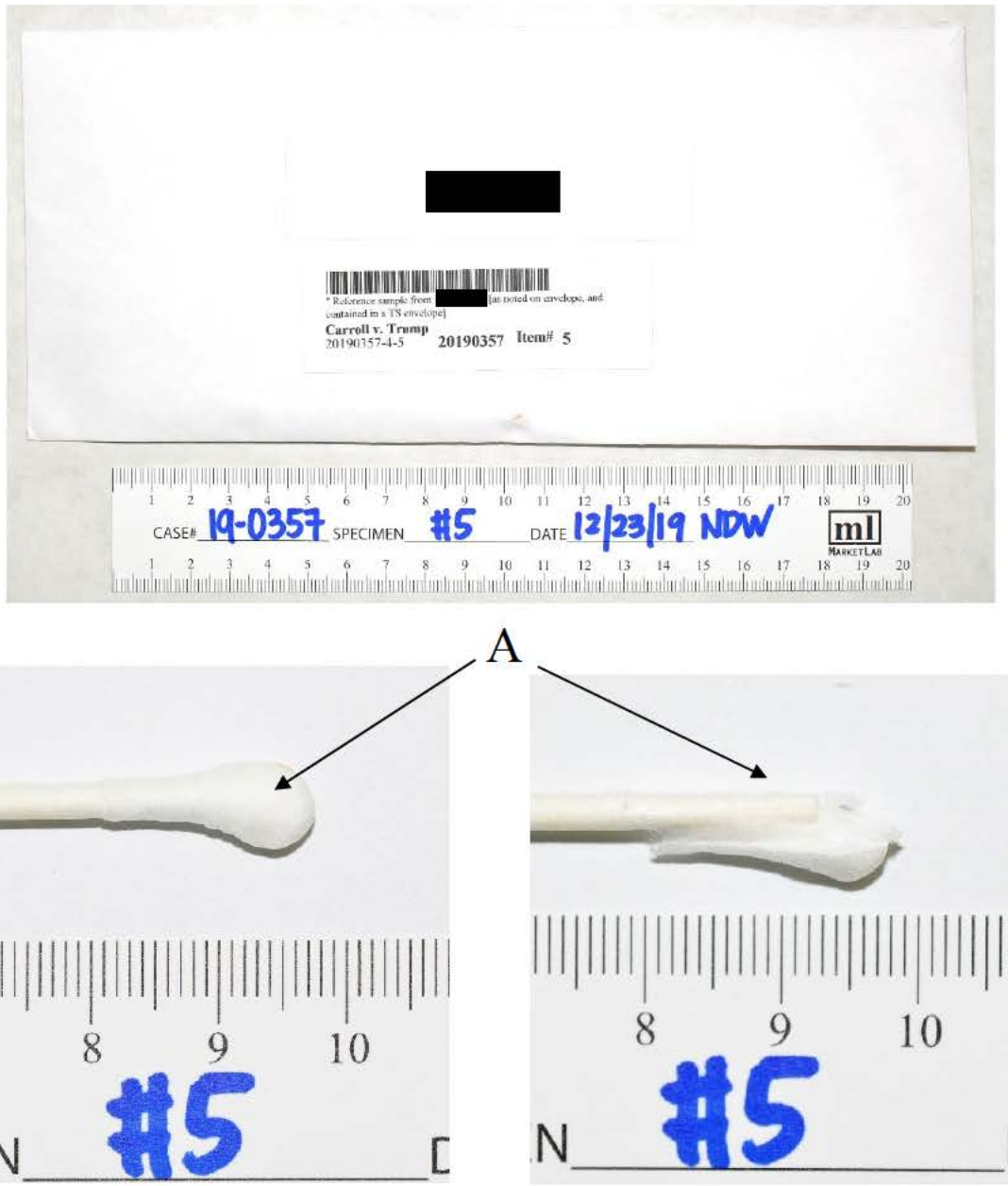

Figure 3. [redacted] reference buccal specimen [#5], packaging and swab before and after sampling.

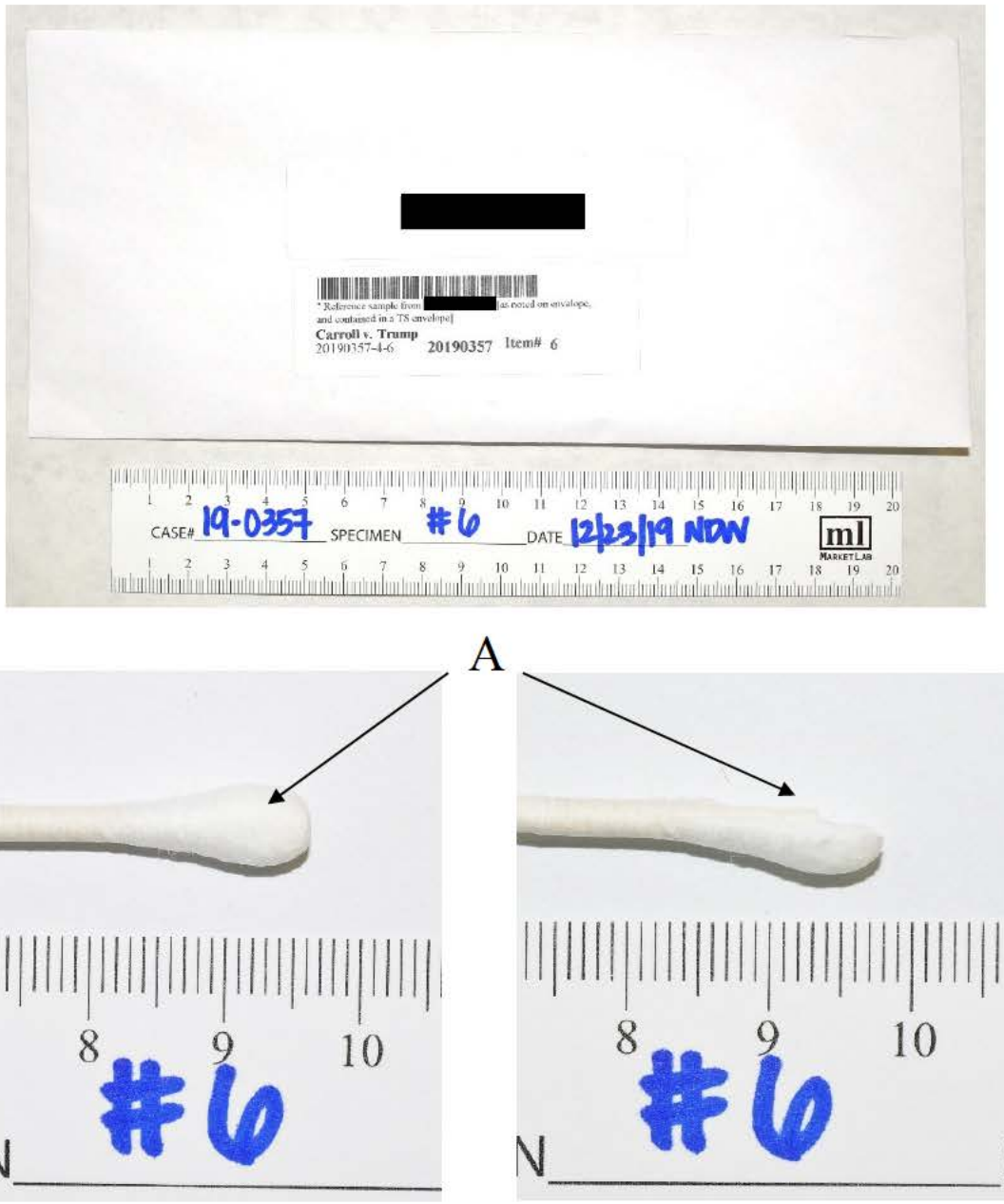

Figure 4. [redacted] reference buccal specimen [#6], packaging and swab before and after sampling.

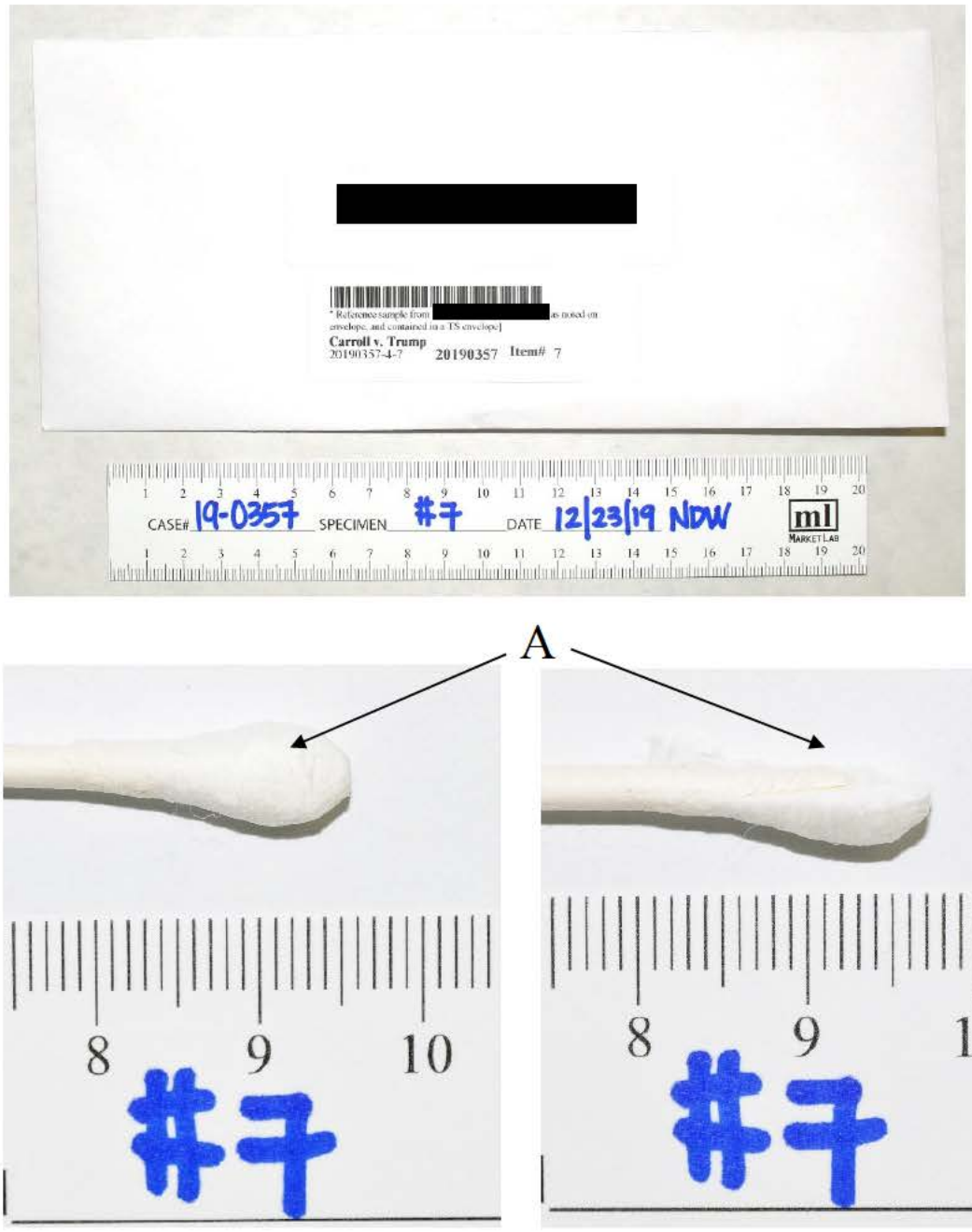

Figure 5. [redacted] reference buccal specimen [#7], packaging and swab before and after sampling.

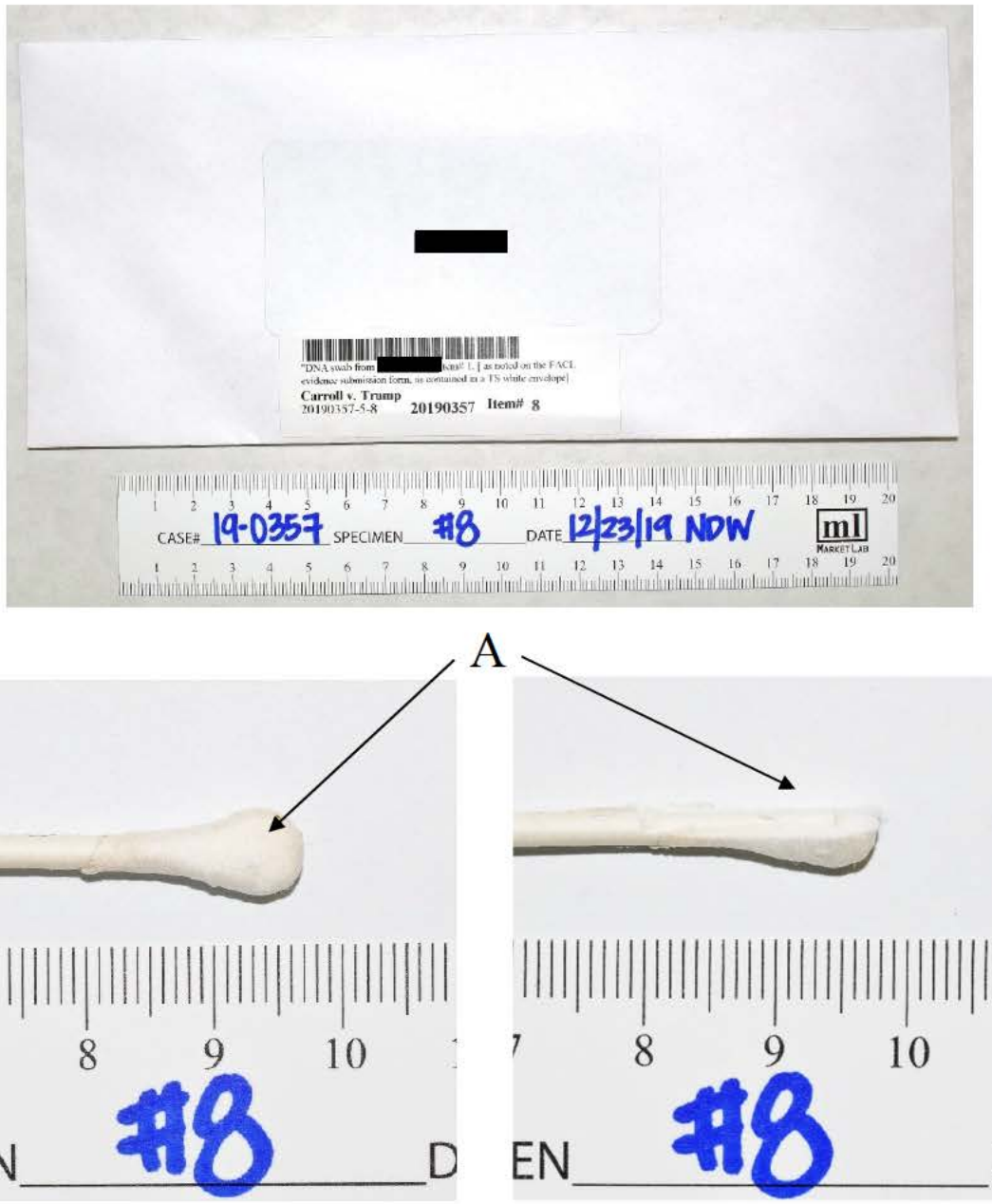

Figure 6. [redacted] reference buccal specimen [#8], packaging and swab before and after sampling.

Item #2 Dress

A black "Donna Karan" brand jacket dress [#2] was submitted to FACL for examination. The packaging for this specimen is shown in Figure 7. The outside and inside surfaces of the dress are shown in Figures 8 through 11. The dress is size 6 and appeared minimally worn. Some apparent animal hairs were noted on the dress. Several scuff/wear marks and/or stains were observed on the outer surface of the dress, most notably the backs of the sleeves. Numerous fluorescent deposits were revealed on the dress with high intensity filtered (450 nm) light. Acid phosphatase activity, a presumptive indication of the presence of semen, was not detected in any of thirty-three fluorescent stains tested on the dress. Various surface areas of the dress were swabbed to collect biological material. Descriptions and processing of the sample swabs taken from the dress are summarized in Table 2. The surface areas swabbed are illustrated in Figures 8 through 10. The sample swabs are shown in Figures 12 through 17. All the swabs were consumed for analysis. The results of these analyses are described below.

Figure 7. Dress [#2], external and nested packaging.

Figure 8. Dress [#2], outside front showing approximate sample areas A, B, C, D, and E.

Figure 9. Dress [#2], outside back showing approximate sample areas A, B, C, and D.

Figure 10. Dress [#2], inside front showing approximate sample area F.

Figure 11. Dress [#2], inside back.

Table 2. Summary of dress swab processing for DNA analysis.

FACL Item #	Area of Dress swabbed	Microscopy Results	Total Human DNA recovered, ng	Total Male DNA recovered, ng	DNA Typing Assay, ng
2A	Outside left shoulder/front neck area (1 swab)	moderate amount of skin cells	~ 0.54	~ 0.03	All, combined as 2AB (Yfiler)
2B	Outside right shoulder/front neck area (1 swab)	numerous skin cells	~ 0.65	~ 0.09	
2C	Outside left sleeve (2 swabs)	moderate amount of skin cells	~ 0.76	~ 0.07	All (Inv. 24plex)
2D	Outside right sleeve (2 swabs)	numerous skin cells, low NECs[2]	~ 1.01	~ 0.53	All (Inv. 24plex)
2E	Outside front skirt area (1 swab)	moderate amount of skin cells	~ 0.88	~ 0.07	All, combined as 2EF (Yfiler)
2F	Inside front skirt area (1 swab)	low number of skin cells and NECs	~ 0.16	~ 0.02	

[2] NECs = nucleated epithelial cells

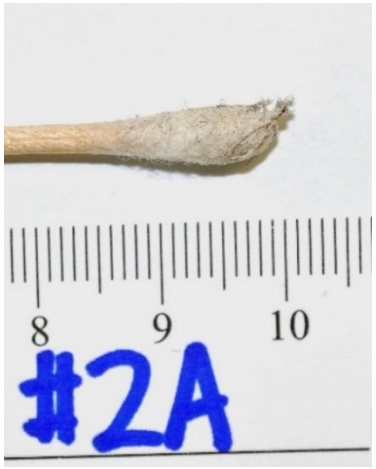

Figure 12. Dress outside left shoulder/front neck area swab.

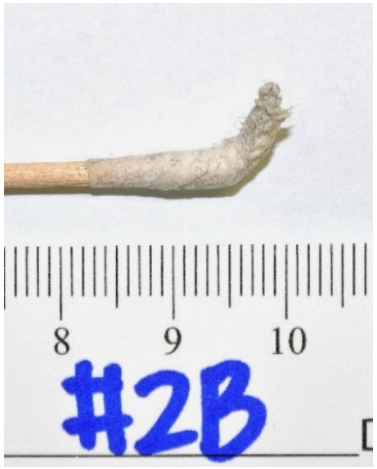

Figure 13. Dress outside right shoulder/front neck area swab.

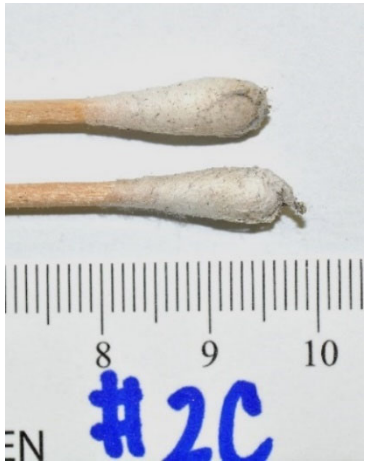

Figure 14. Dress outside left sleeve swabs.

Figure 15. Dress outside right sleeve swabs.

Figure 16. Dress outside front skirt area swab.

Figure 17. Dress inside front skirt area swab.

Item #3 Shoes

A pair of Barney's New York brand patent leather high heels [#3] were submitted to FACL for examination. The packaging for this specimen is shown in Figure 18. The shoes, shown in Figures 19 through 21, are size 40 and appeared well-worn. Scuff marks and various stains were observed about the shoes. Multiple areas fluoresced when visualized with high intensity filtered light. Acid phosphatase activity was not detected in three fluorescent stains tested on the shoes. The shoes were not pursued further.

Figure 18. Shoes [#3], packaging.

Figure 19. Shoes [#3], top surface.

Figure 20. Right shoe [#3], outer and inner surfaces.

Figure 21. Left shoe [#3], outer and inner surfaces.

Genetic Analysis of DNA

In this case several loci, or genetic markers, were amplified using the polymerase chain reaction [PCR] and subsequently typed using the **Investigator 24plex QS** genotyping system. The STR loci typed with 24plex are known as **TH01**, **D3S1358**, **vWA**, **D21S11**, **TPOX**, **DYS391**, **D1S1656**, **D12S391**, **SE33**, **D10S1248**, **D22S1045**, **D19S433**, **D8S1179**, **D2S1338**, **D2S441**, **D18S51**, **FGA**, **D16S539**, **CSF1PO**, **D13S317**, **D5S818**, **D7S820**, and amelogenin, a gene for sex determination. This system also includes one Y-STR marker, **DYS391**, to aid in determining the number of males in a mixed result.

TH01, D3S1358, vWA, D21S11, TPOX, DYS391, D1S1656, D12S391, SE33, D10S1248, D22S1045, D19S433, D8S1179, D2S1338, D2S441, D18S51, FGA, D16S539, CSF1PO, D13S317, D5S818, D7S820 are short tandem repeat [STR] loci. These loci are composed of core segments of DNA three to four bases in length repeated in tandem. Autosomal loci have two alleles per locus where the difference between alleles is the number of repeated core segments within each allele. An individual who is heterozygous at any given locus possesses alleles that have a different number of repeated core segments. An individual who is homozygous at any given locus possesses alleles with the same number of repeated core segments. The primers that recognize these STR loci are labeled with a fluorescent dye so that they can be detected and quantitatively assessed after electrophoresis.

Male specific Y chromosome genetic markers can be employed to examine male-only traits in male/female mixtures. Male specific Y chromosome genetic markers can also be employed to count the number of males in male/male mixtures. All individuals related to one another through the male line of inheritance share the same Y chromosome genetic markers. Since the Y chromosome markers are inherited together as a group, the group of Y chromosome markers is considered as one type called a haplotype. The frequency of occurrence of a haplotype can only be determined by counting the proportion of a population possessing that haplotype. For some evidence samples in this case we utilized the **Yfiler** typing system. The seventeen Y-STR genes included in this system are **DYS456, DYS389i, DYS390, DYS389ii**, **DYS458, DYS19, DYS385**

a,b[3], **DYS393**, **DYS391**, **DYS439**, **DYS635**, **DYS392**, **Y GATA H4, DYS437, DYS438,** and **DYS448**.

Genetic analysis of the specimens in this case involved the following essential steps:

1. Evidence and reference samples were digested with SDS and proteinase K.
2. DNA was extracted from sample digests with the EZ1 Advanced XL robot. Evidence sample DNA extracts were concentrated using Microcon molecular filters.
3. The various genes described above were amplified using the Polymerase Chain Reaction [PCR].
4. The STR genes and amelogenin were typed using capillary electrophoresis.

Interpretation of the following evidence profiles was assisted/supplemented with STRmix™ probabilistic genotyping software. STRmix™ uses laboratory specific parameters (STR kit, amplification protocols and capillary electrophoresis platform) and the quantitative allele peak data from an electropherogram in a Markov Chain Monte Carlo (MCMC) analysis to interpret contributor profiles in a DNA result. During MCMC analysis the likely genotypes of the individual contributors to a DNA profile are determined and given a weight of probability. The more likely genotypes of the contributors to a DNA profile, as determined by this analysis, will have higher weights.

Comparison of a reference profile to an interpreted (or deconvoluted) evidence profile is performed using a likelihood ratio (LR), which assesses the probability of two alternative hypotheses. Typically, the hypothesis of the prosecution (H_p) includes the person of interest (POI) whereas the alternative hypothesis (H_d) attempts to explain the data in the absence of the POI as a contributor. The LR of any given proposition will indicate which hypothesis has more support.[4] In general, a LR > 1 favors H_p and a LR < 1 favors H_d.

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[3] The DYS385 locus is duplicated on the Y chromosome such that one set of primers amplifies the DYS385a locus as well as the DYS385b locus. Each of these loci has acquired genetic variation over time as a consequence of mutation. The typing analysis itself is not able to determine which of the two alleles detected by the DYS385 primers originates from the "a" locus or the "b" locus. Typically, most other Y STR loci produce only one allele per male because there is only one copy of these genes per individual.

[4] The FBI expanded CODIS core STR loci frequency data for the populations used in the LR calculations at FACL, provided with STRmix™, is described in: Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States. *Forensic Science International: Genetics* 25 (2016) 175-181. The ABI STR loci frequency data used for LR calculations at FACL is from the Applied Biosystems GlobalFiler™ PCR Amplification Kit User Guide, Publication Number 4477604, Revision E.

FACL likelihood ratio range:

Likelihood ratio	Verbal equivalent
≥ 1 million	Very strong support for POI inclusion
10,000 to 999,999	Strong support for POI inclusion
1000 to 9,999	Moderate support for POI inclusion
2 to 999	Limited support for POI inclusion
1	Uninformative
> 0.001 to < 1 (1/LR = 2 to 999)	Limited support for POI exclusion
0 to ≤ 0.001 (1/LR ≥ 1000)	POI is excluded

Results

#2D Dress outside right sleeve swabs

1. The DNA recovered from the dress outside right sleeve swabs [#2D] was determined to be a mixture of at least four contributors: three significant contributors, of whom at least one is male, and at least one minor/trace-level contributor.
2. The #2D dress outside right sleeve swabs typing result was analyzed with STRmix assuming four contributors. E. Jean Carroll was then compared to this result as a potential contributor.
3. The DNA result from the dress outside right sleeve swabs is approximately 3 million times more likely if the DNA originated from E. Jean Carroll and three unknown individuals than if the DNA originated from four unknown individuals. This likelihood ratio provides very strong support that E. Jean Carroll is a significant contributor to this result.
4. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll as a contributor. [redacted] was then compared to this result as a potential contributor.
5. The DNA result from the dress outside right sleeve swabs is approximately 1 quadrillion times more likely if the DNA originated from E. Jean Carroll, [redacted], and two unknown individuals than if the DNA originated from E. Jean Carroll and three unknown individuals. This likelihood ratio provides very strong support that [redacted] is a significant contributor to this result.

6. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll and [redacted] as contributors. [redacted], [redacted], [redacted], and [redacted] were then compared to this result as potential contributors.
7. [redacted] (1/LR >> 1000), [redacted] (LR = 0), [redacted] (LR = 0), and [redacted] (LR = 0) are all eliminated as potential contributors to the mixture of DNA from the dress outside right sleeve swabs.

#2C Dress outside left sleeve swabs

8. The DNA recovered from the dress outside left sleeve swabs [#2C] was determined to be a mixture of at least four contributors: two significant contributors and at least two minor/trace-level contributors, of whom at least one is male.
9. The #2C dress outside left sleeve swabs typing result was analyzed with STRmix assuming four contributors. E. Jean Carroll was then compared to this result as a potential contributor.
10. The DNA result from the dress outside left sleeve swabs is approximately 10 trillion times more likely if the DNA originated from E. Jean Carroll and three unknown individuals than if the DNA originated from four unknown individuals. This likelihood ratio provides very strong support that E. Jean Carroll is a significant contributor to this result.
11. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll as a contributor. [redacted] was then compared to this result as a potential contributor.
12. The DNA result from the dress outside left sleeve swabs is approximately 70 trillion times more likely if the DNA originated from E. Jean Carroll, [redacted], and two unknown individuals than if the DNA originated from E. Jean Carroll and three unknown individuals. This likelihood ratio provides very strong support that [redacted] is a significant contributor to this result.
13. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll and [redacted] as contributors. [redacted], [redacted], [redacted], and [redacted] were then compared to this result as potential contributors.
14. [redacted] (1/LR >> 1000), [redacted] (1/LR >> 1000), [redacted] (1/LR >> 1000), and [redacted] (LR = 0) are all eliminated as potential contributors to the mixture of DNA from the dress outside left sleeve swabs.

#2AB Combined DNA extracts from dress shoulder/neck area swabs

#2EF Combined DNA extracts from dress front skirt swabs

15. The Y-chromosome STR analyses of the male DNA recovered from the combined DNA extracts from the dress shoulder/neck area swabs [#2AB] and the front skirt swabs [#2EF] revealed a low-level mixture of at least three contributors. Due to the complexity of each mixture, elucidation of individual Y-STR haplotypes is not feasible.

Additional reference specimens may be submitted for comparison to the DNA typing results from the combined DNA extracts from the dress shoulder/neck area swabs [#2AB], and the dress outside left [#2C] and outside right [#2D] sleeve swabs. The electropherograms documenting the Investigator 24plex and Yfiler analysis results are provided in Appendix 1.

Disposition of Evidence

All evidence items will be returned to the submitter.

Prepared by:

Nancy Wilson, M.S., Forensic Scientist [5]

Reviewed by:

Alan Keel, Senior Forensic Scientist [6]

The testing described and documented herein was completed in compliance with the accreditation requirements of the current ISO/IEC 17025 standard, ANSI National Accreditation Board (ANAB), and FBI Quality Assurance Standards as defined by the ANAB Forensic Testing Certificate and Scope of Accreditation (AT-1641).

[5] Lab analyses conducted by and report written by Nancy Wilson.

[6] Report reviewed by and technical review of lab analyses by Alan Keel.