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Forensic Biology/DNA Expert Consultation Report

October 27, 2025

EDS2025-003 Report# 1

Mr. Steven Romines
Romines, Weis & Young, PSC
600 Main Street Suite 100
Louisville, KY 40202

Re: Commonwealth of Kentucky V. Micheal K. McKinney III, Case 25-CR-00223

Lab Case #: 23-C-03889
Agency: Kentucky State Police Post 9
Agency Case #: 09-23-0485

Mr. Steven Romines:
This consultation report includes a review of Reports #1, 2, 4, 5, 8, and 9 only. Any additional reports or materials may be addressed in a supplemental report. We reserve the right to amend or expand our opinions as additional discovery materials become available.

Consultant Qualifications:

Maria Tsocanos is a Forensic DNA Expert with more than fifteen years of experience in forensic biology and DNA analysis. Her professional background includes the examination and interpretation of biological evidence, serological and DNA testing, statistical evaluation, and the preparation of technical and expert reports. Ms. Tsocanos has provided expert testimony in numerous criminal proceedings before the New York State Supreme Court and other local jurisdictions. Her areas of expertise include validation of forensic DNA techniques, evaluation of testing methodologies to ensure accuracy and reliability of results, interpretation of DNA findings within the context of case evidence, and comprehensive review of complex and cold case investigations. As Co-Founder of ExpertDNA Solutions, LLC, Ms. Tsocanos provides forensic case consultation, technical review, and expert testimony for legal counsel. She holds a Bachelor of Science degree in Forensic Science from the City University of New York, John Jay College of Criminal Justice and has held multiple leadership positions within the Northeastern Association of Forensic Scientists, including President and Ethics Chair, and remains actively engaged in professional development and training initiatives within the forensic science community.

Jaime Rodrigues is a Forensic DNA Expert with more than fifteen years of experience in forensic biology and DNA analysis. Her professional background includes the examination and interpretation of biological evidence, serological and DNA testing, statistical evaluation, and the preparation of technical and expert reports. Ms. Rodrigues has provided expert testimony in over forty criminal proceedings before the New York State Supreme Court and has extensive experience in the evaluation and interpretation of forensic DNA results. Her areas of expertise include validation of forensic DNA techniques, development of laboratory protocols and quality assurance measures, and comprehensive review of complex forensic casework. As Co-Founder of ExpertDNA Solutions, LLC, Ms. Rodrigues provides forensic case consultation, technical review, and expert testimony for legal counsel. She holds a Master of Science degree in Forensic Molecular Biology from the State University of New York University at Albany, a Bachelor of Science degree in Biology from the State University of New York College at Geneseo and is an active member of the Northeastern Association of Forensic Scientists and the American Academy of Forensic Sciences.

Laboratory Overview:

Kentucky State Police Division of Forensic Sciences
Forensic Biology/DNA testing conducted at the following laboratory locations:
Central Laboratory Branch, Northern Laboratory Branch

Analysis dates for Reports 1, 2, 4, 5, 8 and 9 range from 09/19/23 to 06/04/25

The following information regarding the ANAB ANSI accreditation was taken directly from the Kentucky State Police website. The accreditation certificate and audits were not part of the discovery material received.

Accreditation:

ANAB ANSI National Accreditation Board Accredited ISO/IEC 17025: 2017
Forensic Testing Laboratory Expiry Date: 30 September 2028 Certificate Number: FT-0345
Central Laboratory Branch
Scope of Accreditation: Discipline: Biology
DNA Profile Determination: Short Tandem Repeat (STR), Y-Short Tandem Repeat (Y-STR)
DNA Profile Determination (Database Samples): Short Tandem Repeat (STR), Y-Short Tandem Repeat (Y-STR)
Individual Characteristic Database: DNA Profile (National DNA Index System)
Physical Comparison: DNA Profile (Software Program)
Qualitative Determination: Body Fluid (Chemical & General Microscopy)
Northern Laboratory Branch
Qualitative Determination: Body Fluid (Chemical & General Microscopy)

FBI Quality Assurance Standards (QAS) audits

The following QAS Audit Documents were received from Kentucky State Police Division of Forensic Sciences for 2021-2025.

Internal Audit May 5-8th, 2025

Findings:
"12.2.7.1 is marked No because multiple Specimen Detail reports were not initialed to confirm the specimen category by the reporting analyst after being moved to that category from the Pending Forensic Index. Initials are required by laboratory policy (Convicted Offender Manual section CO-07, 3.2.4.2)
14.2 and 14.2.b are marked No because KSP Quality Assurance Manual 8.7.1.g notes that the laboratory should monitor the effectiveness of actions taken within 45 days after implementation. The timeline may be extended and the reason for the extension shall be documented in the non-conforming workflow. In Corrective Action noted in NCW 60339 the CA plan was approved by Quality manager 4-22-24, implementation date 4-4-24, and implementation date rework 5-28-24 and on 10-17-24 CA effectiveness was evaluated which is greater than 45 days with no reason for extension was documented in the workflow
17.3, 17.3.3 and 17.3.3.4 are marked No because outsourced casefiles 22-C-07666 and 22-C-08425 did not have the initials from the case analyst or other user on the CODIS Specimen Detail Report to acknowledge the correct final specimen category as per KSP CO manual 3.2.4 and 3.2.4.2 "someone other than the CODIS user who printed the SDR, generally the case analyst, will confirm that the specimen category is correct and initial the SDR""

Taken directly from Audit Document

External Audit May 13-15th, 2024- No Findings

External Audit August 1-3rd, 2023

Findings:

"Standard 14.2.2 is marked No. Notification was not made to the casework CODIS administrator when the nonconformity could impact DNA records entered into CODIS. An analyst was removed from casework resulting from a submission issue with a proficiency test but did review cases that were entered into CODIS during the time period."

Taken directly from Audit Document

External Audit October 24-26th, 2022

Findings:

"6.12.1 and 6.12.1.a No - For one Analyst, three proficiency tests were completed: 05 OCT 20, 06 JAN 21, and 04 OCT 21. Test 2 was completed less than 4 months after test 1 and test 3 was performed more than 8 months after test 2. Analyst was not competency tested prior to completing casework within that cycle.

13.1 No - For one Analyst, three proficiency tests were completed: 05 OCT 20, 06 JAN 21, and 04 OCT 21. Test 2 was completed less than 4 months after test 1 and test 3 was performed more than 8 months after test 2."

Taken directly from Audit Document

External Audit September 14-16th, 2021

Findings:

"10.1 is No because 10.2 is No.
10.2 is marked No because the monthly maintenance for instruments were not completed as per policy. Procedure indicates maintenance shall be performed monthly for both instruments. There is no documentation of maintenance being performed on the EZ1s from October of 2020 to March of 2021. Maintenance was not performed on the 7500s for June of 2021. These instruments were in use during all of the non documented time.
10.4 is marked No because the monthly maintenance for instruments were not completed as per policy. Maintenance was not performed on the EZ1s from October of 2020 to March of 2021. Maintenance was not performed on the 7500s for June of 2021. Procedure indicates maintenance shall be performed monthly for both instruments."

Taken directly from Audit Document

Laboratory Testing Analysts

Forensic Serology analyst (Report #1, 5 and 9):
Erin N. Hildebrandt, Forensic Science Specialist II, Northern Laboratory Branch
Bachelor of Science in Biology, Minor in Neuroscience, Hope College, May 2012
Masters in Forensic Science, University of Florida, 2017

Forensic DNA analyst for STR testing (Report #2, 8):
Elwood D. McCann III (Davey), Forensic Laboratory Supervisor, Central Laboratory Branch
Education: Bachelors of Science in Biology, Minor in Chemistry, Georgetown College, Dec. 2004

Forensic DNA analyst for Y-STR testing (Report #4):
Laura Rauschmayer, Forensic Biologist II, Central Laboratory Branch
Bachelor of Science, Forensic Biology, Minor in Chemistry, Ohio Northern University, 2012

Table 1: Items Received and Reviewed

The following items were received and reviewed by ExpertDNA Solutions, LLC. Although multiple versions of KSP manuals were provided, only the versions in effect at the time of testing or reporting were reviewed. These manuals are not listed in the table below.

File Name	# Pages	Description	Date Received
KSP 26s Report #1.pdf	29	Report #1 - Evidence Submission Documentation	9/2/2025
23-C-03889 Report #1.pdf	2	Report #1 - Serology Report	9/2/2025
Report #1 Analytical notes.pdf	11	Report #1 - Evidence Examination Notes	9/2/2025
23-C-03889 Report #2	4	Report #2 - DNA Report	7/18/2025
23-C-03889 case file Rpt2 *	108	Report #2 - Analytical Case Notes	7/18/2025
E-grams Lab Report 2	56	Report #2 - Electropherograms (includes unedited EPGs and injections not used for interpretation)	7/21/2025
23-C-03889 Report #4	2	Report #4 - Y-STR DNA Report	7/18/2025
23-C-03889 case file Rpt4 *	30	Report #4 - Analytical Case Notes	7/18/2025
E-grams Lab Report 4	14	Report #4 - Electropherograms (includes unedited EPGs and injections not used for interpretation)	7/21/2025
KSP 26s report #5.pdf	3	Report #5 - Evidence Submission Documentation (Item 1)	9/2/2025
KSP 26s report #5-2.pdf	5	Report #5 - Evidence Submission Documentation (Items #22 & #23)	9/2/2025
23-C-03889 Report #5.pdf	2	Report #5 - Serology Report	9/2/2025
Report #5 Analytical notes.pdf	4	Report #5 - Evidence Examination Notes with photographs	9/2/2025
23-C-03889 Report #8.pdf	4	Report #8 - DNA Report	9/2/2025
23-C-03889 case file report #8.pdf	179	Report #8 - Analytical Case Notes	9/2/2025
KSP 26s report #9.pdf	15	Report #9 - Evidence Submission Documentation	9/2/2025
23-C-03889 Report #9.pdf	2	Report #9 - Serology Report	9/2/2025
Serology Photos Report #9.pdf	10	Report #9 - Evidence Photographs	9/2/2025
Report #9 Analytical notes.pdf	15	Report #9 - Evidence Examination Notes	9/2/2025
CSRU documents.pdf	37	Crime Scene Notes (Vehicle & Scene)	9/2/2025
Case Narrative as of 8-18-2025.pdf	42	Case Correspondence as of 081825	9/2/2025
23-C-03889 chain of custody as of 8-18-25.pdf	118	Chain of Custody as of 081825	9/2/2025
Clinical Forensic Institute Report	43	Report from the Institute of Forensic Medicine and Nursing by William S. Smock	9/3/2025

*Duplicate copies of analytical case notes for Report #2 and 4 were received on 9/2/25.

Table 2: Summary of Serological Results

The table below summarizes the serological results reported by the Kentucky State Police Laboratory (Central and Northern branches, as applicable). For complete details, refer to Case Reports #1, 2, 5, and 9 from Case File 23-C-03889.

Item #	PD Item #	Description of item	Date tested	PHE result	Hematrace® result	Serology conclusions as reported	Sent for DNA analysis
1	1	Knife blade	8/7/2024			Presumptive* testing for blood was positive on item	
1.1		Swabs from knife blade	8/7/2024	Positive	QNS		Yes
5	14	Swabs from sink in bathroom A	9/19/2023	Negative		No blood	
6	15	Boots from bathroom A (Tecovas brand brown boots)	9/29/2023			Presumptive* testing for blood was positive on item	
6.1		Swab from left boot	9/29/2023	Positive	QNS		Yes
6.2		Swabs from boots	9/29/2023	N/A	N/A	N/A	Yes
6.3		Swab from right boot	9/29/2023	Positive	QNS		Yes
7	16	Shoes from bathroom A (ON brand, blue grey and white shoes)	9/29/2023	Negative		No blood	
8	17	Shoes from bathroom A (ON brand, navy blue and white shoes)	10/12/2023	Negative		No blood	
9	18	Swabs from sink in bathroom D	9/19/2023	Negative		No blood	
10	19	Towel from bathroom D closet (Martha Stewart brand, blue towel.)	10/13/2023	Negative		No blood	
11	20	Towel from bathroom D closet (Hotel Collection brand, off white towel)	10/24/2023			Presumptive* testing for blood was positive on item	
11.1		Cutting from towel from bathroom D closet	10/24/2023	Positive	QNS		Yes
12	21	Swabs from basement bathroom F doorframe	9/19/2023	Positive	QNS	Presumptive* testing for blood was positive on item	Yes
13	22	Swabs from bathroom F drain	9/19/2023	Negative		No blood	
14	23	Swabs from kitchen sink B	9/19/2023	Positive	QNS	Presumptive* testing for blood was positive on item	Yes
15	24	Swabs from sink in laundry room G	9/19/2023	Positive	QNS	Presumptive* testing for blood was positive on item	Yes
16	25	Shirt from Roy Kidd (Navy Yard brand, size XL, black shirt)	10/24/2023			Item contains blood. Presumptive* testing for human origin was positive.	
16.1		Cutting from shirt from Roy Kidd	10/24/2023	Positive	Positive		Yes

Table 2: Summary of Serological Results (continued)

Item #	PD Item #	Description of item	Date tested	PHE result	Hematrace® result	Serology conclusions as reported	Sent for DNA analysis
17	26	Belt from Roy Kidd (American Eagle Outfitters brand, brown belt with metal buckle)	10/24/2023			Item contains blood. Presumptive* testing for human origin was positive.	
17.1		Swabs from belt from Roy Kidd	10/24/2023	Positive	Positive		Yes
18	27	Fingernail clippings from right hand of Amber Spradlin and clippers	Start date 1/30/24				
18.1		Swabs from right hand fingernail clippings from Amber Spradlin	swabbing taken	N/A	N/A	N/A	Yes
19	28	Fingernail clippings from left hand of Amber Spradlin	Start date 1/30/24				
19.1		Swabs from left hand fingernail clippings from Amber Spradlin	swabbing taken	N/A	N/A	N/A	Yes
20	29	Head hair standard from Amber Spradlin		N/A	N/A	N/A	
21	30	Blood standard from Amber Spradlin		N/A	N/A	N/A	Yes
22	31	Knife from couch	8/7/2024			Presumptive* testing for blood was positive on item	
22.1		Swabs from blade of knife from couch	8/7/2024	Positive	QNS		Yes
22.2		Swabs from handle of knife from couch	8/7/2024	N/A	N/A	N/A	Yes
23	32	Piece of plastic from Amber Spradlin	8/7/2024			Item contains blood. Presumptive* testing for human origin was positive.	
23.1		Swabs from piece of plastic from Amber Spradlin	8/7/2024	Positive	Positive		Yes
24	33	Buccal standard from Michael McKinney II		N/A	N/A	N/A	Yes
25	34	Buccal standard from Joshua Mullins		N/A	N/A	N/A	Yes
26	35	Buccal standard from Loren Carlson		N/A	N/A	N/A	Yes
27	36	Buccal standard from Roy Kidd		N/A	N/A	N/A	Yes
28	37	Swabs from cut under Roy Kidd's chin	1/30/2024	Positive	Positive	Item contains blood. Presumptive* testing for human origin was positive.	Yes
29	38	Buccal standard from Michael McKinney III		N/A	N/A	N/A	Yes
30	39	Swab(s) from right arm of Michael McKinney III	N/A			No analysis was performed on item	

Table 2: Summary of Serological Results (continued)

Item #	PD Item #	Description of item	Date tested	PHE result	Hematrace® result	Serology conclusions as reported	Sent for DNA analysis
31	40	Swab(s) from left arm of Michael McKinney III	N/A			No analysis was performed on item	
32	41	Control swab(s) from Michael McKinney III	N/A			No analysis was performed on item	
33	44	T-shirt (Love Sick brand, size 3, red, green, white, and black tie-dyed t-shirt) from Amber Spradlin	3/28/2025			Item contains blood. Presumptive* testing for human origin was positive.	
33.1		Cutting from t-shirt from Amber Spradlin	3/28/2025	Positive	Positive		Yes
33.2		Cutting from t-shirt from Amber Spradlin	3/28/2025	Positive	Positive		Yes
33.3		Cutting from t-shirt from Amber Spradlin	3/28/2025	Positive	Positive		Yes
34	45	Bra (Cacique brand, size 46G, black bra) from Amber Spradlin	3/28/2025			Item contains blood. Presumptive* testing for human origin was positive.	
34.1		Cutting from bra from Amber Spradlin	3/28/2025	Positive	positive		Yes
34.2		Cutting from bra from Amber Spradlin	3/28/2025	Positive	positive		Yes
35	46	Pants (m jeans by Maurices brand, size 22W X-short, blue jeans) from Amber Spradlin	4/23/2025			Item contains blood. Presumptive* testing for human origin was positive.	
35.1		Cutting from pants from Amber Spradlin	4/23/2025	Positive	Positive		Yes
35.2		Cutting from pants from Amber Spradlin	4/23/2025	Positive	Negative		Yes
35.3		Cutting from pants from Amber Spradlin	4/23/2025	Positive	Negative		Yes
36	47	Belt (3XL black belt with silver colored buckle) from Amber Spradlin	4/23/2025			Presumptive* testing for blood was positive on item	
36.1		Swabs from belt from Amber Spradlin	4/23/2025	Positive	QNS		Yes
37	48	Socks (No nonsense white socks) from Amber Spradlin	4/23/2025			See items 37.1 and 37.2 for results	
37.1		Cutting from sock from Amber Spradlin	4/23/2025	Positive	Positive	Item contains blood. Presumptive* testing for human origin was positive.	Yes
37.2		Cutting from sock from Amber Spradlin	4/23/2025	Positive	Negative	Presumptive* testing for blood was positive on item	Yes
38	49	Pants (BKE brand, size 34x34, blue jeans)	4/30/2025			Item contains blood. Presumptive* testing for human origin was positive.	
38.1		Cutting from pants	4/30/2025	Positive	Positive		Yes
38.2		Cutting from pants	4/30/2025	Positive	QNS		Yes

Table 2: Summary of Serological Results (continued)

Item #	PD Item #	Description of item	Date tested	PHE result	Hematrace® result	Serology conclusions as reported	Sent for DNA analysis
38.3		Swabs from pants	4/30/2025	N/A	N/A		Yes
39	50	Shirt (Travis Mathew brand, size XL, dark blueish-grey shirt)	4/30/2025			Item contains blood. Presumptive* testing for human origin was positive.	
39.1		Cutting from shirt	4/30/2025	Positive	Positive		Yes
39.2		Swabs from shirt	4/30/2025	N/A	N/A	N/A	Yes
40	51	Belt (Johnston & Murphy brand, size 42, brown leather belt with black backing)	4/30/2025			Presumptive* testing for blood was positive on item	
40.1		Swab from belt	4/30/2025	Positive	N/A		Yes
40.2		Swabs from belt	4/30/2025	N/A	N/A	N/A	Yes
41	52	Shorts (American Eagle, size 31, tan shorts) from bedroom floor	4/10/2025			Item contains blood. Presumptive* testing for human origin was positive.	
41.1		Cutting from shorts from bedroom floor	4/10/2025	Positive	Positive		Yes
41.2		Swabs from shorts from bedroom floor	4/10/2025	N/A	N/A	N/A	Yes
42	53	Towel (All Clad brand, blue towel) from countertop in kitchen B3	3/28/2025			Item contains blood. Presumptive* testing for human origin was positive.	
42.1		Cutting from towel from countertop in kitchen B3	3/28/2025	Positive	Positive		Yes
43	54	Swabs from shower drain in bathroom D4	3/21/2025	Negative		No blood	
44	55	Swabs from shower drain in hallway bathroom C1	3/21/2025	Negative		No blood	
45	56	Swabs from shower drain in bathroom A5	3/21/2025	Negative		No blood	
46	57	Swabs from tub drain in bathroom A6	3/21/2025	Negative		No blood	
47	58	Swabs from shower drain in bathroom F3	3/21/2025	Negative		No blood	

QNS = Quantity Not Sufficient
PHE= Phenolphthalein Test
*Presumptive tests do not confirm the presence of bodily fluids or human origin
Please note: Known standards were not subjected to serology testing

Table 3: Summary of DNA Quantitation Results
The table below summarizes the DNA Quantitation results reported by the Kentucky State Police Central Laboratory branch. For complete details, refer to Case Reports # 2,4 and 8 from Case File 23-C-03889.

Item #	Human Quant Value (ng/µl)	Male Quant Value (ng/µl)	Item concentrated	Total input DNA (ng)
1.1	0.383	0.0038		0.5
6.1	0.0157	0.0164	yes	0.5264
6.2	0.0487	0.0445		0.5
6.3	0.7757	0.6709		0.5
11.1	0.0125	0.0089	yes	0.4191
12	0.1333	0.1184		0.5
14	0.0997	0.012		0.5
15	1.3934	0		0.5
16.1	37.0531	32.4036		0.5
17.1	2.9616	2.5902		0.5
18.1 (1st extraction on 02/06/24)	2.1121	0.0049		0.5
18.1* (2nd extraction on 04/25/24)	1.0941	0.0032	yes	0.1216 Total input male DNA (ng)
19.1 (1st extraction on 02/06/24)	0.471	0.0019		0.5
19.1*(2nd extraction on 04/25/24)	0.4954	0.0001	N/A	See Table 5 below
22.1	0.7641	0.0003		0.5
22.2	0.0058	0.0024	yes	0.1945
23.1	2.3307	0		0.5
28	84.2872	68.8944		0.5

(ng/µl) = nanograms per microliter. It's the concentration of the DNA sample
ng= nanograms

*Samples re-extracted for Y-STR analysis only. See Table 5 below for additional results.

The following samples were concentrated prior to amplification:
Item 6.1 (Swab from left boot)
Item 11.1(Cutting from towel from bathroom D closet)
Item 18.1, 2nd extraction (Swabs from right hand fingernail clippings from Amber Spradlin)
Item 22.2 (Swabs from handle of knife from couch)

In DNA analysis, concentration is used for low-level samples that contain less DNA than the amplification kit manufacturer's recommended target input.

On average, a diploid human cell contains 6.6 pg (0.0066 ng) of DNA. [18]
Total Cells = Total DNA (ng) ÷ DNA per Cell (ng)

The following items were consumed during DNA analysis:
18.1 (Swabs from right hand fingernail clippings from Amber Spradlin)
19.1 (Swabs from left hand fingernail clippings from Amber Spradlin)

Table 4: Summary of DNA STR Results.
The table below summarizes the autosomal STR results reported by the Kentucky State Police Central Laboratory branch. For complete details, refer to Case Reports # 2, and 8 from Case File 23-C-03889.

Item #	NOC as Reported	DNA Conclusions as Reported	Statistics (RMP & LR)
1.1	1	Very strong support for the proposition that Amber Spradlin is a contributor to this profile	LR- 70 octillion
6.1	4	Due to the complexity of this mixture, no meaningful comparisons can be made.	
6.2	3	Michael McKinney II can be included as a contributor to the major component	RMP- 1 in 140 octillion
6.3	1	Male profile matches Roy Kidd	RMP- 1 in 7.2 nonillion
11.1	3	All known profiles excluded	
12	1	Male profile matches Roy Kidd	RMP- 1 in 7.2 nonillion
14	2	Major profile matches Amber Spradlin	RMP- 1 in 8.7 nonillion
15	1	Female profile matches Amber Spradlin	RMP- 1 in 8.7 nonillion
16.1	1	Male profile matches Roy Kidd	RMP- 1 in 7.2 nonillion
17.1	1	Male profile matches Roy Kidd	RMP- 1 in 7.2 nonillion
18.1		No DNA foreign to Amber Spradlin was found on item	No statistics conducted
19.1		DNA foreign to Amber Spradlin was found on item but was too limited for meaningful comparison	No statistics conducted
22.1	1	Very strong support for the proposition that Amber Spradlin is a contributor to this profile	LR- 70 octillion
22.2*	3	Very strong support for the proposition that Michael McKinney II is a contributor to this profile	LR- 50 billion
23.1	1	Very strong support for the proposition that Amber Spradlin is a contributor to this profile	LR- 70 octillion
28		No DNA foreign to Roy Kidd was found on item	No statistics conducted

NOC= Number of Contributors
RMP= Random Match Probability.
Random Match Probability is the probability of randomly selecting an unrelated individual in the population with the same DNA profile as the evidence in question.
LR= Likelihood Ratio
The likelihood ratio (LR) assesses the probability of the evidence (E) given two alternate, mutually exclusive propositions.

***** For this sample, only results with a likelihood ratio (LR) indicating strong support or greater for inclusion or exclusion are listed. Refer to Report #8 for additional results.

Table 5: Summary of DNA Y-STR Results
The table below summarizes the Y-STR results reported by the Kentucky State Police Central Laboratory branch. For complete details, refer to Case Report # 4 from Case File 23-C-03889.

Item #	NOC as Reported	DNA Conclusions as Reported	Statistics
18.1 (2nd extraction)	2	The major profile matches Michael McKinney II and Michael McKinney III (and their paternal relatives)	Utilizing a subset of the YHRD United States database and assuming a single source profile, the match is estimated to be 463 times more likely to occur if Michael McKinney II and Michael McKinney III (and their paternal relatives) is a contributor of the Y-STR profile than if the source is a randomly selected male individual from the United States population.
19.1 (2nd extraction)	N/A	Male quant was insufficient for conclusions.	

Observations:

Observation #1- Reagent Blank Contamination
The Reagent Blank B(U)1-02-06-24, associated with all samples included in Report #2, was contaminated. According to KSP laboratory policies and procedures, this extraction subset should have been deemed uninterpretable, as there was only one reagent blank for that subset and it showed contamination.

Review of pages 16–18 and 20 of the Case File from Report #2 indicates that all samples associated with B(U)1-02-06-24 had remaining material available, meaning they could have been recut and re-extracted. Instead, a Reagent Blank from a different extraction subset was used to interpret the data. This decision appears to be in direct conflict with the KSP laboratory standard operating procedures (SOP) and established best practices.
The purpose of an Extraction Reagent Blank is to verify that the entire DNA process (extraction, quantitation, amplification, and detection) was performed properly and that the resulting data are valid.

For complete details and supporting documentation, refer to Appendix.

Observation #2- Potential Carryover/Contamination of Y-STR results
Referring to the Case File from Report #4, Item 18.1 and BU3-2-04-25-24 were set up manually and run on 3500 CE instrument #1 on 6/13/24 in wells C01 and D01, respectively. The known samples for this case, Items 24, 25, 27, 29 and 29dup, were also manually set up and run on the same instrument and date in wells E01, F01, G01, H01, and A02, respectively.

It appears that both the unknown and known samples were processed on the same plate, creating the potential for cross-contamination or carryover, either during the manual plate setup or during injection by the instrument. The proximity of Item 24 (Michael McKinney II) to Item 18.1 (swabs from the right-hand fingernail clippings of Amber Spradlin) increases the potential for carryover/contamination and deviates from best laboratory practices. Furthermore, as noted in Observation #1, similar carryover/contamination has already been documented in this case.

For complete details and supporting documentation, refer to Appendix.

Observation #3- Consumption of Swabs from Nail Clippings (Items 18.1 & 19.1) Preventing Further Testing
Items 18.1 (swabs from right-hand fingernail clippings from Amber Spradlin) and 19.1 (swabs from left-hand fingernail clippings from Amber Spradlin) were consumed during the Y-STR analysis, eliminating the possibility of conducting additional testing. This raises concern, as it appears the laboratory did not comply with its protocol pertaining to extraction subset preparation. According to the KSP DNA Casework Analytical Manual, *"Two or more blanks should be prepared for each extraction subset to allow for secondary analyses using alternative amplification systems, as one blank may be consumed during analysis by the first amplification system."*

Items 18.1 and 19.1 were reextracted for Y-STR analysis because the original extracts could not be used because of contamination and consumption of the Reagent Blank(s). Refer to Observation #1.

For complete details and supporting documentation, refer to Appendix.

Observation #4- Miscalculation of Y-STR statistics
The Y-STR profile generated for Item 18.1 (2nd extraction, swabs from right-hand fingernail clippings from Amber Spradlin) is a mixture indicating a minimum of 2 male donors. The KSP laboratory conducted a mixture separation and the major profile matched Michael McKinney II and Michael McKinney III (and their patrilineal relatives). While we agree with the separation of the mixture and its resulting major profile, based on their "*Y-STR mixture interpretation sheet*", comparisons (and therefore statistics) should not have been conducted on locus DYS385.

Applying that reasoning, we conducted an independent search of the Y-Chromosome Haplotype Reference Database (YHRD) using the same dataset, kit, database and release version (Release R69 valid as per 2024-03-07 20:22:41 UTC). The updated corrected match probability is 1 in 451. When this Y-STR profile was searched in the United States Database (Overall) 2 matches were found in 29,207 haplotypes.

Y-STR analysis targets male-specific loci on the Y-chromosome, which is passed unchanged from father to son except for rare mutations. Consequently, males who share a common paternal ancestor (e.g., father, son, brother, uncle, cousin) will exhibit the same Y-STR profile. Therefore, it is not possible to distinguish which specific male relative contributed to a Y-STR profile within a shared paternal lineage.

Because of this inheritance pattern, Y-STR statistical evaluation differs fundamentally from that used for autosomal STRs. The Y-chromosome is inherited as a single unit, meaning that its loci are not independent. To account for this, the forensic community applies the counting method for statistical interpretation. Using this method, the sample is searched and the number of times the profile is observed in a database is reported. The YHRD database also calculates a Theta-corrected Match Probability which is what was reported in 23-C-03889 Report# 4.

For complete details and supporting documentation, refer to Appendix.

Observation #5- Limited testing of Roy Kidd's shirt (Item 16) and belt (Item 17)
With respect to Item 16, the analyst noted reddish brown staining near the neck area and tested multiple stains with Phenolphthalein (PHE), all of which yielded positive results. A separate stain was then selected, which tested positive for both PHE and Hematrace®. This stain was then cut and designated as Item 16.1, representing the only portion of Item 16 forwarded for DNA analysis.

Upon review of the Analytical Notes from Report #1, it was observed that only a single photograph of the item was taken. This image did not capture the entirety of the item, nor was there a photograph of the back of the item. In forensic investigations, it is essential to thoroughly document and photograph each item, clearly indicating where testing was conducted to preserve context and support interpretation.

With regards to Item 17, the analyst noted the presence of reddish brown staining throughout the item, which tested positive for PHE. The analyst then documented, swabbing the stain showing the "most transfer" and testing it with both PHE and Hematrace®, designating this sample as Item 17.1.

In our opinion, a more representative sampling of the reddish brown staining from items belonging to Roy Kidd (Items 16 &17) should have been tested for blood and forwarded for DNA analysis, where appropriate. In cases where multiple individuals may have been bleeding, it is critical to sample adequately across the entire item. For items with multiple stains, samples should be taken from distinct areas to allow for comprehensive DNA testing if needed.

Observation #6- Incorrect Number of Contributors for Swabs from basement bathroom F doorframe (Item 12)
Item 12 was reported to match Roy Kidd, indicating that the sample was interpreted as a single source profile. However, upon review of the DNA profile from Item 12, three loci contain extraneous alleles, consistent with a mixture from at least two contributors. On the electropherogram used for interpretation, the DNA analyst drew boxes around these extraneous alleles and annotated them as "*additional peaks too limited for meaningful comparisons*" (see pages 60-61 of the Report #2 Analytical Case Notes).

The sample should have been interpreted as a mixture. Reporting the profile as single source does not accurately reflect the data observed in the electropherogram and is in direct conflict of the KSP Laboratory DNA Casework Analytical Manual.

For complete details and supporting documentation, refer to Appendix.

Observation #7- Interpretation of Swabs from boots (Item 6.2) using ArmedXpert
During the initial data interpretation of Item 6.2, the 8-second injection from the Capillary Electrophoresis (CE) instrument was used. This injection contained less information and indicated at least two contributors. Following peer review, the 15-second injection was selected for final interpretation and the sample was interpreted as a mixture with a minimum of three contributors.

In the statistical calculation section of ArmedXpert documentation (see page 44 of the Report #2 Analytical Case Notes), the number of contributors (NOC) was entered as two instead of three. This incorrect entry may have resulted in an inaccurate deconvolution and/or an erroneous statistical calculation.

For complete details and supporting documentation, refer to Appendix.

Observation #8- Handling of Test items/ Chain of Custody
According to the KSP Forensic Laboratory Quality Assurance Manual, Section 7.4.1.1(a) Internal Evidence Handling, Storage, and Preparation, *"All evidence that is not in process of examination shall be stored in a secure location."*. Furthermore, Section 7.4.1.1(a) specifies that "*Evidence shall not remain in "process" of examination for more than 90 days. If the process of examination exceeds 90 days as denoted by the start and complete date, then the evidence shall either:*

-Be electronically scanned into a personal locker in which an analyst has ownership
-Noted in the narrative that the evidence is locked in a personal locker"

<u>The following items remained in the analyst's custody for more than 90 days.</u>

- Items 6.1, 6.2, 6.3, 11.1, 12, 14, 15, 16.1, 17.1, 18-21, 24-29 were in the custody of Davey McCann from 01/30/24 until the printing of the chain of custody received (as of 08/18/25). These items are contained within Report# 2.

- Item 1.1, 22.1, 22.2, 23.1 were in the custody of Davey McCann from 08/23/24 until the printing of the chain of custody received (as of 08/18/25). These items were contained within Report #8.

- Item 700.1 was in the custody of Davey McCann from 04/9/25 until the printing of the chain of custody received (as of 08/18/25). These items were contained within Report #8.

- Item 1 remained in the custody of Timothy Evans (Forensic Latent Print Analyst III) from 06/20/23 to 06/06/24.

- Item 33-47 were in the custody of Erin N. Hildebrandt from 10/30/24 until 6/4/25. These items are contained within Report# 9.

Observation #8- Handling of Test items/ Chain of Custody (continued)
The chain of custody description for Item 700.1 lists "*dried extracts from Items 1.1, 22.1, 22.2, and 23.1*." However, the extract from Item 22.2 was consumed during analysis on 09/18/24. Therefore, only extracts from Items 1.1, 22.1, and 23.1 were dried to form Item 700.1, and the chain of custody entry incorrectly includes Item 22.2. See Report # 8 Disposition of evidence.

For complete details and supporting documentation, refer to Appendix.

Discussion/Conclusions

It is essential that the laboratory adhere to its standard operating procedures (SOPs) to maintain confidence in the quality, reliability, and integrity of its work product. Any deviation from established SOPs or procedural drift, is a cause for concern. While there may be circumstances that justify exceptions to standard procedures, such deviations should be clearly documented in contemporaneous case notes, that include the reasoning and justification for the decision.
An additional way to ensure the quality and reliability of the results is by having the report undergo a thorough technical review. The primary purpose of a technical review is to verify that laboratory SOPs were properly followed during analysis, interpretation, and reporting; to identify and correct any errors; and to confirm that the reviewing analyst agrees with the scientific interpretations and conclusions reported.

It is our opinion that the samples associated with Reagent Blank B(U)1-02-06-24 should have been classified as uninterpretable, in accordance with the KSP laboratory DNA casework analytical manual [2] and standard practices [5,6,8]. It is inappropriate to disregard a contamination event and substitute a different reagent blank from another instrument that shows no contamination. According to the case narrative, the contamination appears to have originated from another casework sample.

An independent assessment of the potential source of this contamination was not performed because the electropherograms and raw data for the controls in this case were not provided in discovery. Additionally, although a log of unanticipated results, contamination events, and carryover was requested for expert review, these documents were not received. Instead, a document was provided stating "*Currently there are no nonconformities for the reports completed*" [3]. As a result, it cannot be determined whether a quality issue investigation was initiated or resolved in response to this contamination event. Proper documentation of all quality issues is essential to assess whether a systemic problem exists within analytical procedures.
As stated in the Expert Working Group on Human Factors in Forensic DNA Interpretation document *"Contamination events, and the reasons identified for each, should be regularly reviewed to identify trends, with procedures and training updated as necessary."* [15].

Advancements in DNA technology have greatly increased the sensitivity of forensic DNA analysis, allowing interpretation of samples containing only small amounts of DNA. While this heightened sensitivity enables analysts to obtain results from samples that would previously have been uninterpretable, it also introduces new challenges, particularly the potential detection of background DNA that may have been deposited through everyday activities. Therefore, it is important to recognize that not all DNA results are relevant in the same way.

"*The sensitivity of DNA analysis has progressed to the point that trace levels of DNA, originating from only a few cells, can generate informative profiles. This means that virtually any item or surface can be sampled with a reasonable chance of obtaining a DNA profile*" [17]. Due to this increased sensitivity, it is vitally important to implement rigorous methods that minimize the possibility of inadvertent contamination during crime scene processing, evidence handling, and DNA analysis. This is accomplished through the proper collection, handling, preservation, and storage of evidence.

Even when strict QA/QC procedures are followed, contamination can still occur during the DNA process. Human factors inevitably play a role, as mistakes can happen [15]. To minimize such risks, it is best practice to keep known and unknown samples separated by time and/or space [4, 5, 15]. It is also recommended to "*incorporate robotics to reduce human contamination*." [5]

In this case, during the Capillary Electrophoresis (CE) setup for Y-STRs, the known and unknown samples appear to have been placed on the same plate in consecutive wells. There is no indication that a robotic system was used for loading; instead, manual pipetting appears to have been performed, as supported by the witness statement noting that "*well locations were verified and maintained*." These factors raise concerns about the potential for contamination.

DNA Transfer, Persistence, Prevalence, and Recovery (DNA-TPPR)

Locard's Exchange Principle states that "*every contact leaves a trace*" [9]. Therefore, whenever two objects come into contact there is a potential transfer of material. This foundational concept underlies all trace evidence disciplines, including forensic DNA analysis.

Understanding the principles of DNA Transfer, Persistence, Prevalence, and Recovery (DNA-TPPR) is therefore essential. Transfer refers to the movement of DNA from one object to another, which can occur directly (e.g., person-to-person or person-to-object) or indirectly, where "*there is no direct contact of the original source of the DNA with the location or surface on which it is ultimately found*" [10]. Persistence describes how long DNA remains detectable on an object or surface after deposition. Prevalence refers to background or preexisting DNA present on an item prior to the event in question. Recovery pertains to the ability to collect and detect DNA from an item, which depends on the collection and analysis methods.

It is well established that DNA can be transferred in a variety of ways. Humans are continually shedding skin cells into their surrounding environment, and the rate at which an individual sheds exists on a continuum [16]. Research has demonstrated that areas of habitual activity (such as living spaces, offices, or other frequently occupied environments) tend to accumulate a baseline level of DNA originating from the individuals who regularly inhabit them [11]. Similarly, it is expected that a homeowner's DNA will be present throughout their residence, as they have frequent and direct contact with the objects and surfaces within that environment.

DNA transfer can occur in various ways and through a range of substrates. The type of substrate can influence the amount of DNA transferred or recovered. As demonstrated in one study, *"indirect DNA transfer without contact is possible when a relatively gentle agitation was applied to used everyday items. Importantly, detectable levels of DNA were transferred and in most instances were sufficient to provide informative profiles."* [12] This highlights that DNA can transfer in unexpected ways, reinforcing the importance of considering substrate type and handling conditions.

Although we can never know with certainty how DNA came to be deposited on a piece of evidence (since we can never know the ground truth of the case) it is important to recognize that DNA can be transferred either directly or indirectly, and sometimes in highly variable or unexpected ways. In some instances, it is only after an unexpected DNA result is obtained that the possibility of transfer becomes apparent.

A recent 2025 publication reported a case involving indirect DNA transfer [19]. Although the authors could not determine the precise vector, they concluded that the transfer likely occurred via a blanket from a police station. The blanket had been used by an individual who was later erroneously implicated in the crime and was subsequently given to the victim while she provided her statement to police. Because the victim personally knew the actual perpetrator, the database hit implicating the unrelated individual was called into question, prompting further investigation into

the mechanism of transfer.

This case underscores the importance of the trier of fact to interpret the DNA results within the full context of the case, including the location from which the sample was collected and the potential for background or unrelated DNA that may have preexisted on the surface and is unrelated to the incident under investigation [14 ,19].

DNA Limitations

Even though we are beginning to understand the mechanism of how DNA can transfer from one object to another, this knowledge should not be used to directly infer how a DNA profile came to be on an object in a case. "*DNA analysts cannot provide any information on how or when DNA was deposited in a particular case, based on a report considering only the source of the DNA*". [15] The STR results that are reported in forensic DNA reports are only evaluating who may have potentially contributed to the DNA in the evidence profile. The how or when questions can never be answered because we do not know the ground truth of the case.

This distinction is so critical that leading research and standards organizations, including the National Institute of Standards and Technology (NIST) and the Organization of Scientific Area Committees for Forensic Science (OSAC), have emphasized the need to clearly state these limitations within forensic DNA reports. [8, 15] Including such language helps ensure that readers understand the scope of the findings and do not misinterpret or overstate the significance of the DNA results.

Chain of Custody

The chain of custody is a critical component of any forensic investigation. It begins with the collection and preservation of evidence at the crime scene by law enforcement or investigators. To ensure admissibility in court, the integrity and authenticity of the evidence must remain intact and the chain of custody must remain unbroken. Any break or lapse in this process can compromise the integrity of the evidence and jeopardize its admissibility in legal proceedings.

Once evidence is submitted to a forensic laboratory, the responsibility for maintaining the chain of custody transfers to the laboratory. It is essential that the lab uphold the integrity of all evidence through proper documentation, secure handling, and controlled transfers within the system.

Each forensic laboratory abides by standards that are set forth by it's accrediting body and are detailed in the laboratory's quality assurance manual. The Quality Assurance Standards state the laboratory "*shall have and follow procedures that address handling and preserving the integrity of evidence and work product designed to minimize loss, contamination, and/or deleterious change; shall have and follow a policy or procedure for securing evidence and work product in progress and shall have and follow a policy or procedure for properly sealing evidence.*" [4]. Any violation of these procedures can place the admissibility of the evidence at risk.

During our review, it was identified that 40 items remained in analysts' custody for more than 90 days, in violation of the KSP laboratory quality assurance procedure stating that "*evidence shall not remain in process of examination for more than 90 days.*" [1]. Additionally, these items were not electronically scanned into a personal locker under the analyst's ownership, further deviating from the laboratory's evidence handling protocols [1].

Respectfully submitted,

Digitally signed by Maria Tsocanos
Date: 2025.10.27 11:22:34 -04'00'

Maria Tsocanos
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Digitally signed by Jaime Rodrigues
Date: 2025.10.27 11:27:29 -04'00'

Jaime L. Rodrigues
Forensic DNA Consultant
ExpertDNA Solutions, LLC

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[20] KSP Forensic Biology Quality Assurance Manual Effective Date: 02/27/24

Appendix
Supporting Documentation of Observations

Observation #1- Reagent Blank Contamination

Detailed Notes

Samples that were extracted on 02/06/24 EZ1XL-9 (this includes Items 6.1,6.2,6.3,11.1,12,14,15,16.1,17.1,18.1 and 19.1) had an associated Reagent Blank B(U)1-02-06-24. B(U)1-02-06-24 was concentrated to 17ul and 15ul was amplified on 02/07/24. B(U)1-02-06-24 was injected on 02/08/24EDM for 15sec and 24sec. Each time there were peaks called above threshold in the blank, an single peak for the 15 sec and three peaks over analytical threshold. On 02/12/24EDM, B(U)2-02-06-24 was injected for 15 sec and 2 peaks were observed above threshold. There is a comment to "*amp BU2*" on the 3500 analysis worksheet.

B(U)2-02-06-24 was amplified on 02/13/24. The sample was concentrated to 15ul and 15ul was amplified. This blank produced satisfactory results.

Case Narrative:

On 02/22/24 @ 12:02pm, Davey McCann sent an email to Amy Smith and Megan May indicating "*there is a low level contamination in B(U)1-02-06-24*". He indicates "*Source appears to be from Item 23-C-03889-6.1. These items were concentrated together at the same time*." On 03/13/24 @ 9:18pm, Davey McCann emails Amy Smith and Megan May to follow up on his previous email. He indicates "*I have my PT in this set along with a couple of other RUSH cases*." See page 14 of 42 from Case narrative as of 8-18-25.

On 03/14/24 Megan May replies to Davey McCann asking for him to send his workbook/amp sheet. She then also asks if BU2 was concentrated. "*I looked at your amp sheet and through your project and it looks like the peaks present in your B(U)1-02-06-24 are more consistent with 24-C-00710. This case is the case immediately before your blanks, so this makes sense and since that specific case was not concentrated the contamination likely did not happen during concentration. I looked through the rest of your unknown samples to make sure no other samples were affected by this profile and that doesn't appear to be the case. Your BU2-02-06-24 was clean and did not show any peak above or below threshold, so it is okay to use for interpreting that unknown set.*" See page 12-4 of 42 from Case narrative as of 8-18-25.

Figure 1: Extraction Log of samples extracted on 02/06/24.
Figure copied from Page 21 of Report #2.

23-C-03889 EDM

Extraction Log

Reagents			
Extraction Date: 02/06/24			
Dilute ATL LN: n/a	ProK LN: 172039319	MTL Buffer LN: 175018744	cRNA LN: 12/18/23 LMB
EZ1 cartridge LN: 175028460	Wash G2 LN: n/a	Lysis DTT LN: n/a	Lysis G2 LN: 172038727
ATL Buffer LN: n/a			

LAB # ITEM #	Unknown 1	
22-C-07872-6,1	56° Thermomixer#:	17
23-C-03889-6.1	EZ1 XL #:	9
23-C-03889-6.2	EZ1 Protocol:	Large Volume
23-C-03889-6.3		
23-C-03889-11,1		
23-C-03889-12		
23-C-03889-14		
23-C-03889-15		
23-C-03889-16.1		
23-C-03889-17,1		
23-C-03889-18.1		
23-C-03889-19.1		
23-C-03889-28		
B(U)1-02-06-24		

LAB # ITEM #	Unknown 2	
23-C-04677-1,2	56° Thermomixer#:	17
23-C-04677-1.3	EZ1 XL #:	10
24-C-00710-3	EZ1 Protocol:	Large Volume
24-C-00710-4		
B(U)2-02-06-24		
LC7-02-06-24		

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KSP Forensic Biology Quality Assurance Manual Effective Date: 02/27/24

"5.12.1.1 A match found between cases within an extraction batch/amplification plate will be investigated (e.g. review of case histories). Confirmation of results as appropriate to the circumstances may be undertaken, including additional analysis."

KSP DNA Casework Analytical Manual Effective date: 09/14/23

GUIDELINES FOR ANALYTICAL REAGENT BLANK CONTROLS
"1.3 When multiple sets of the same type are run within a single extraction batch, blanks of the same type but from different subsets will be numerically labeled to differentiate between them (e.g. BU1-1, BU2-1, or other designations if defined)."

"2.2. Two or more blanks should be prepared for each extraction subset to allow for secondary analyses using alternative amplification systems, as one blank may be consumed during analysis by the first amplification system. Multiple blanks of the same type are aliquots of the same reagent blank."

"2.4. An extraction subset or set processed robotically may be run within a single instrument or across two instruments; the associated blanks may be run either together on one of the instruments or split between the two instruments"

DEFINITIONS
"Extraction Batch – all casework samples extracted in a similar time period to be extracted, quantified, amplified, or electrophoresed together. This may include differential extractions, non- differential extractions, hairs, knowns and/or direct amplification samples.

Extraction Set – all casework samples extracted using the same method in a batch (i.e. differential, non-differential, known or direct amplification buccal)

Extraction Subset – all casework samples associated with the same reagent blanks within an extraction set. For example, a batch may have extraction sets including differentials, non-differentials, and knowns, and each of these sets may include subsets which each have their own pair of reagent blanks."

CASEWORK AUTOSOMAL STR DATA INTERPRETATION GUIDELINES
"3. Evaluation of controls
3.1. The applicable laboratory control, associated blank, amplification positive and negative controls will be amplified in all STR systems used for a sample set, and produce the expected results.
3.2. A negative control or blank within an amplification set should show no typeable peaks, and background peaks, exclusive of artifact peaks, should be less than 100 RFU (3500xl).
3.2.1. If a reagent blank shows a typeable contaminant, it should be reamplified in the pertinent system if appropriate.
3.2.2. If negative controls show a reproducible contaminant profile, the associated amplification set or subset as applicable shall be uninterpretable.
3.2.2.1. If any associated samples are of limited quantity and cannot be reanalyzed, or if circumstance excludes reanalysis, those samples may be interpreted with caution at the discretion of the technical leader
3.2.3. If two reagent blanks are made for a subset and one blank shows a contaminant profile, but the

Appendix
Supporting Documentation of Observations

second blank is clean, and if there are no other indications of contamination in the subset, the subset may be interpreted with Technical Leader approval.
3.2.4. If a contaminant profile occurs in both blanks or in a subset with only a single blank, the associated samples shall be uninterpretable except as for 3.2.2.1.
3.2.5. A single peak in a reagent blank or negative control may be considered a drop-in event, and the associated samples may be acceptable for interpretation."

QUALITY ASSURANCE STANDARDS FOR FORENSIC DNA TESTING LABORATORIES effective July 1, 2020

"9.5.1 Reagent blank controls associated with each extraction set being analyzed shall be:
"Forensic Standard 9.5.1 A laboratory must associate at least one reagent blank control with each extraction set or batch of samples, as defined by the laboratory."
9.5.1.1 Extracted concurrently and treated with the most sensitive conditions as the samples;
Forensic Standard 9.5.1.1 The reagent blank(s) are extracted concurrently with the set or batch of samples, as defined by the laboratory. The extractions must be occurring at the same time to be considered concurrent.
9.5.1.2 Amplified utilizing the same typing test kit, instrument model, and sensitivity conditions as required by the sample(s) containing the least amount of DNA; and

9.5.1.3 Typed utilizing the same instrument model, injection conditions and most sensitive volume conditions of the extraction set."

SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories – APPROVED 01/12/2017 Rev 07/13/2021

"IV. (1.3) The laboratory shall establish criteria for evaluation of controls.
The results of the analysis controls [i.e., reagent blank(s), positive amplification control(s), and negative amplification control(s)] are evaluated. If the reagent blank(s), positive amplification control(s), and negative amplification control(s) yield results that are within their prescribed specifications, the DNA analyst interprets the DNA typing results from each sample."

"1.3 Controls are required to assess analytical procedures.
1.3.1 The laboratory must establish criteria for evaluation of the following controls, including but not limited to: reagent blank and positive and negative amplification controls.
1.3.2 The laboratory must develop criteria for the interpretation and documentation of results in the event that the controls do not perform as expected."

SWGDAM Contamination Prevention and Detection Guidelines for Forensic DNA Laboratories APPROVED 01/12/2017

"*3.1 Controls*
Positive, negative and reagent blank controls are critical for detecting contamination.
3.1.1 Negative and reagent blank controls
3.1.1.1 Any detectable peaks or sequence data in negative and reagent blank controls may indicate contamination. Refer to Appendix 1 for examples regarding acceptability of associated data."

Appendix
Supporting Documentation of Observations

Observation #2- Potential Carryover/Contamination of Y-STR results

KSP DNA Casework Analytical Manual Effective Date: 03/14/2024

In section "*SAMPLE PREPARATION FOR ELECTROPHORESIS*"
"Manual preparation of samples in formamide/size standard solution for electrophoresis"
"*Note: When unknown and direct amplification samples are added to the same plate for CE, the direct amp samples should be set up in a separate set of 24 wells on 3500xl (starting at A1, A4, A7 or A10) from any regularly processed samples*."

Figure 2: 3500 YSTR Analysis Sheet for Unknowns from the Case File for Report #4, page 12.

23-C-03889 LER

3500 Analysis Sheet

tTechnician: SP
LER 6/24/24

Yfiler Plus	DYS576	DYS389I	DYS635	DYS389II	DYS627	DYS460	DYS458	DYS19	YGATAH4	DYS448	DYS391	DYS456	DYS390	DYS438	DYS392	DYS518
Pos 007	19	13	24	29	21	11	17	15	13	19	11	15	24	12	13	37
LC7	18	13	23	29	21	11	17	14	12	19	11	15	24	12	13	36

Yfiler Plus	DYS570	DYS437	DYS385	DYS449	DYS393	DYS439	DYS481	DYF387S1	DYS533
Pos 007	17	15	11,14	30	13	12	22	35,37	13
LC7	15	15	11,15	28	13	14	22	35,36	12

HT:	
8sec	200rfu
15sec	200rfu
24sec	300rfu

Project Name: 06-13-24sp **Instrument #:** 1 **Qiagility #:** n/a

Well	Sample Name	06-13-24sp_YU Injection Time	Comments	pr pk	Egram	Reviewer: MDM
C01	23-C-03889-18.1	YFP 15s 1.2kv	injected higher			✓
D01	BU3-2-04-25-24	YFP 15s 1.2kv	ok	X		✓
E02	Pos_06-13-24	YFP 15s 1.2kv	ok			✓
F02	Neg_06-13-24	YFP 15s 1.2kv	ok	X		✓
G02	Ladder	YFP 15s 1.2kv	ok			✓
H02	Ladder	YFP 15s 1.2kv	ok			✓

Well	Sample Name	06-13-24sp_YU Injection Time	Comments	pr pk	Egram	
C01	23-C-03889-18.1	YFP 24s 1.2kv	ok		X	✓
D01	BU3-2-04-25-24	YFP 24s 1.2kv	ok	X		✓

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Supporting Documentation of Observations

Figure 3: 3500 YSTR Analysis Sheet for Knowns from the Case File for Report #4, page 13.

23-C-03889 LER

Direct 3500 Analysis Sheet

Technician: SP
LER 6/24/24

Yfiler Plus	DYS576	DYS389I	DYS635	DYS389II	DYS627	DYS460	DYS458	DYS19	YGATAH4	DYS448	DYS391	DYS456	DYS390	DYS438	DYS392	DYS518
Pos 007	19	13	24	29	21	11	17	15	13	19	11	15	24	12	13	37
LC5	17	14	22	31	22	9	17	13	11	20	10	16	23	10	11	40
LC7	18	13	23	29	21	11	17	14	12	19	11	15	24	12	13	36

Yfiler Plus	DYS570	DYS437	DYS385	DYS449	DYS393	DYS439	DYS481	DYF387S1	DYS533
Pos 007	17	15	11,14	30	13	12	22	35,37	13
LC5	19	14	16,17	31	13	12	22	35,38	12
LC7	15	15	11,15	28	13	14	22	35,36	12

HT:	8sec	170rfu
27 cycles	15sec	170rfu
	24sec	170rfu

HT:	8sec	190rfu
28 cycles	15sec	190rfu
	24sec	190rfu

Project Name: 06-13-24sp **Instrument #:** 1

Well	Sample Name	06-13-24sp_YK Injection Time	Comments	pr pk	Egram	Reviewer: MDM
E01	23-C-03889-24	YFP 24s 1.2kv	ok		X	✓
F01	23-C-03889-25	YFP 24s 1.2kv	ok		X	✓
G01	23-C-03889-27	YFP 24s 1.2kv	ok		X	✓
H01	23-C-03889-29	YFP 24s 1.2kv	ok		X	✓
A02	23-C-03889-29dup	YFP 24s 1.2kv	matches 29			✓
B02	BSS-02-07-24	YFP 24s 1.2kv	ok	X		✓
H02	Ladder	YFP 24s 1.2kv	ok			✓
B03	Pos_06-13-24	YFP 24s 1.2kv	ok			✓
C03	Neg_06-13-24	YFP 24s 1.2kv	ok	X		✓
D03	LC5_06-13-24	YFP 24s 1.2kv	ok			✓
E03	Ladder	YFP 24s 1.2kv	ok			✓

Verified well locations maintained MDM
Reviewer Initials
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Supporting Documentation of Observations

Observation #3- Consumption of Swabs from Nail Clippings (Items 18.1 & 19.1) Preventing Further Testing

DNA Casework Analytical Manual Effective date: 09/14/23

GUIDELINES FOR ANALYTICAL REAGENT BLANK CONTROLS

"1.3 When multiple sets of the same type are run within a single extraction batch, blanks of the same type but from different subsets will be numerically labeled to differentiate between them (e.g. BU1-1, BU2-1, or other designations if defined)."

"2.2. Two or more blanks should be prepared for each extraction subset to allow for secondary analyses using alternative amplification systems, as one blank may be consumed during analysis by the first amplification system. Multiple blanks of the same type are aliquots of the same reagent blank."

Observation #4- Miscalculation of Y-STR statistics

Figure 4: YSTR Mixture Interpretation from 23-C-03889 Case File Report 4 Page 18

Y-STR Mixture Interpretation Sheet

page added 6/25/24 LER

Sample File	Marker	Allele 1	Height 1	Allele 2	Height 2	Allele 3	Height 3	Allele 4	Height 4	MEC	ADO	Total RFU	Major RFU	Major P	major
C01_23-C-03889-18.1(2).hid	DYS576	**16**	610	**18**	75							685	610	89	16
C01_23-C-03889-18.1(2).hid	DYS389I	**13**	412									412	412	100	13
C01_23-C-03889-18.1(2).hid	DYS635	**23**	102	**25**	462							564	462	82	25
C01_23-C-03889-18.1(2).hid	DYS389II	**29**	64												
C01_23-C-03889-18.1(2).hid	DYS627	**23**	143												
C01_23-C-03889-18.1(2).hid	DYS460	**11**	912									912	912	100	11
C01_23-C-03889-18.1(2).hid	DYS458	**17**	1256									1256	1256	100	17
C01_23-C-03889-18.1(2).hid	DYS19	**14**	149												
C01_23-C-03889-18.1(2).hid	YGATAH4	**12**	208												
C01_23-C-03889-18.1(2).hid	DYS448	**19**	175												
C01_23-C-03889-18.1(2).hid	DYS391	**10**	110												
C01_23-C-03889-18.1(2).hid	DYS456	**15**	457									457	457	100	15
C01_23-C-03889-18.1(2).hid	DYS390	**24**	495									495	495	100	24
C01_23-C-03889-18.1(2).hid	DYS438	**13**	273												
C01_23-C-03889-18.1(2).hid	DYS392	**13**	183												
C01_23-C-03889-18.1(2).hid	DYS518	**41**	114												
C01_23-C-03889-18.1(2).hid	DYS570	**17**	539									539	539	100	17
C01_23-C-03889-18.1(2).hid	DYS437	**15**	594									594	594	100	15
C01_23-C-03889-18.1(2).hid	DYS385	**11**	269	**15**	310							579	see below		11,15
C01_23-C-03889-18.1(2).hid	DYS449	**28**	112												
C01_23-C-03889-18.1(2).hid	DYS393	**13**	407									407	407	100	13
C01_23-C-03889-18.1(2).hid	DYS439	**11**	640	**13**	64							704	640	91	11
C01_23-C-03889-18.1(2).hid	DYS481	**22**	763									763	763	100	22
C01_23-C-03889-18.1(2).hid	DYF387S1	**36**	445									445	see below		36,36
C01_23-C-03889-18.1(2).hid	DYS533	**12**	89												

Item description: swab from fingernail clippings from right hand of A Spradlin
Injection parameter: 24s/300RFU
Number of contributors? at least two

Results:
no comparisons with all loci below 300 RFUs
M McKinney II and M McKinney III included as contributor to major. R Kidd and J Mullins excluded
no meaningful comparisons to remainder due to possibility of undetected genetic information

DYS385 Major Allele(s)

Allele	Height	Allele	Height
11	269	15	310
Major RFU	579		
Major P	100		
Major PHR	87		

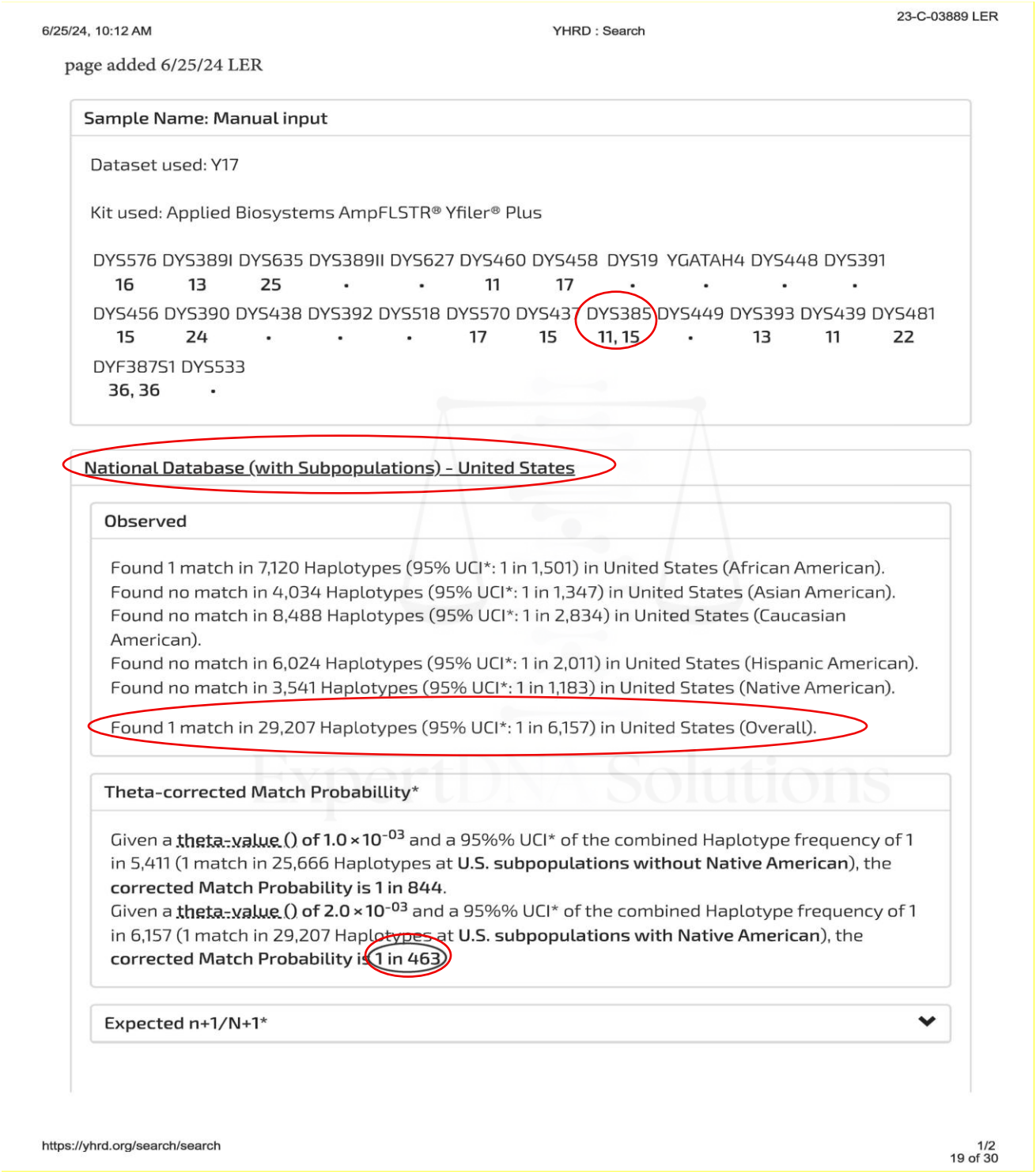
DYF387S1 Major Allele(s)

Allele	Height	Allele	Height
36	445		
Major RFU	445		
Major P	100		
Major PHR	100		

On the YSTR Mixture Interpretation Sheet, DYS385 allele 11 is under 300 RFU. According to the sheet, the locus should not be used for comparisons. Therefore, statistics should not have been conducted at this locus.

Appendix
Supporting Documentation of Observations

Figure 5: Screen shot from Report #4 - Analytical Case Notes, pages 19-20.
Red highlighted areas were added for illustrative purposes.



23-C-03889 LER

6/25/24, 10:12 AM YHRD : Search

page added 6/25/24 LER

Sample Name: Manual input

Dataset used: Y17

Kit used: Applied Biosystems AmpFLSTR® Yfiler® Plus

DYS576	DYS389I	DYS635	DYS389II	DYS627	DYS460	DYS458	DYS19	YGATAH4	DYS448	DYS391
16	13	25	·	·	11	17	·	·	·	·

DYS456	DYS390	DYS438	DYS392	DYS518	DYS570	DYS437	DYS385	DYS449	DYS393	DYS439	DYS481
15	24	·	·	·	17	15	11, 15	·	13	11	22

DYF387S1	DYS533
36, 36	·

National Database (with Subpopulations) - United States

Observed

Found 1 match in 7,120 Haplotypes (95% UCI*: 1 in 1,501) in United States (African American).
Found no match in 4,034 Haplotypes (95% UCI*: 1 in 1,347) in United States (Asian American).
Found no match in 8,488 Haplotypes (95% UCI*: 1 in 2,834) in United States (Caucasian American).
Found no match in 6,024 Haplotypes (95% UCI*: 1 in 2,011) in United States (Hispanic American).
Found no match in 3,541 Haplotypes (95% UCI*: 1 in 1,183) in United States (Native American).

Found 1 match in 29,207 Haplotypes (95% UCI*: 1 in 6,157) in United States (Overall).

Theta-corrected Match Probabillity*

Given a theta-value () of 1.0×10^{-03} and a 95%% UCI* of the combined Haplotype frequency of 1 in 5,411 (1 match in 25,666 Haplotypes at **U.S. subpopulations without Native American**), the **corrected Match Probability is 1 in 844**.
Given a theta-value () of 2.0×10^{-03} and a 95%% UCI* of the combined Haplotype frequency of 1 in 6,157 (1 match in 29,207 Haplotypes at **U.S. subpopulations with Native American**), the **corrected Match Probability is 1 in 463**

Expected n+1/N+1*

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Figure 5 (continued): Screen shot from Report #4 - Analytical Case Notes, pages 19-20.
Red highlighted areas were added for illustrative purposes

page added 6/25/24 LER

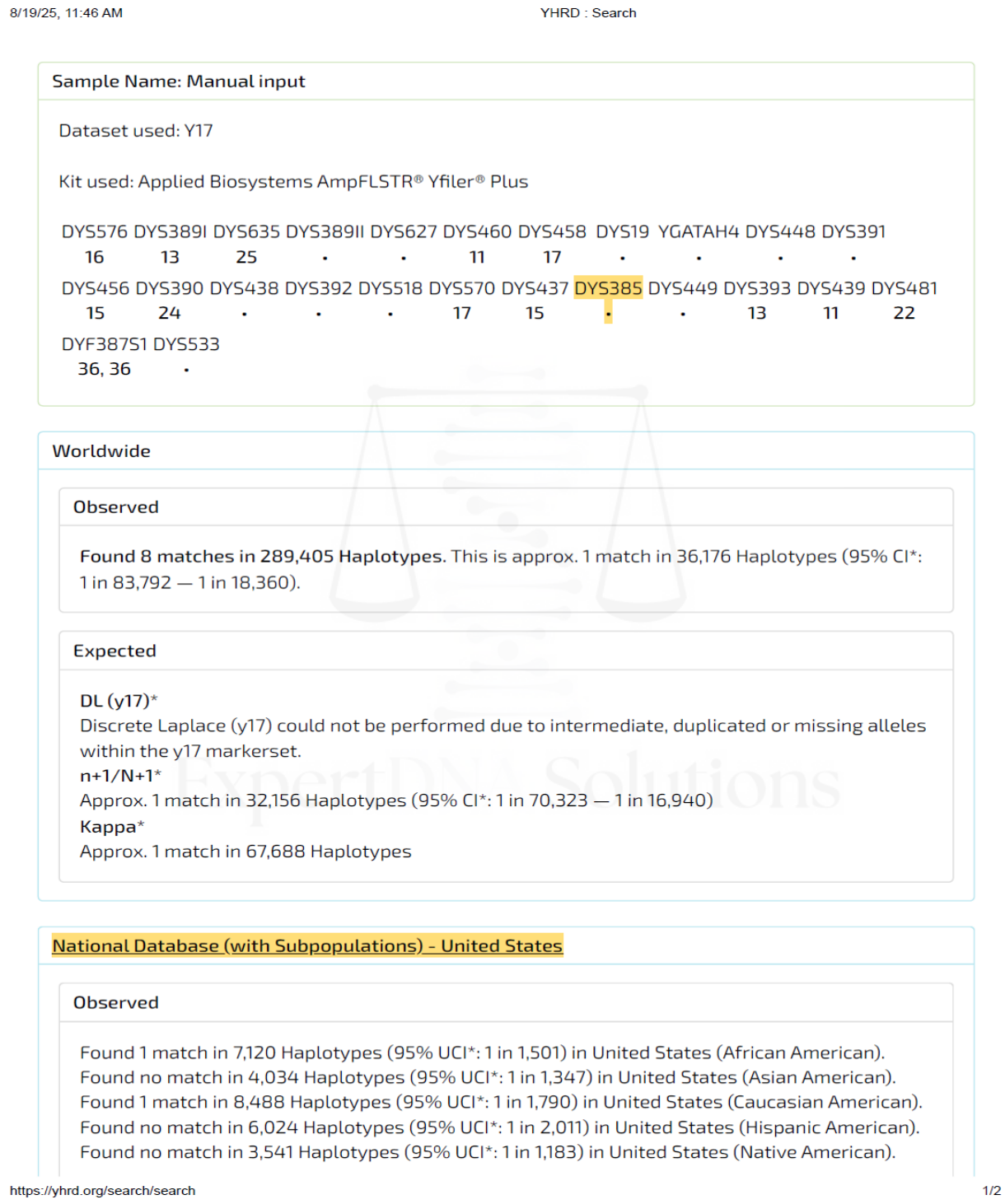
Expected Kappa*

Results are based upon Release **R69** valid as per 2024-03-07 20:22:41 UTC. This query was sent at 2024-06-25 14:05:46 UTC.

* See FAQ/Glossary (http://yhrd.org/pages/faq) for further explanations of abbreviated terms used here

Appendix
Supporting Documentation of Observations

Figure 6: EDS generated Updated YHRD Calculations.
Orange areas indicate updated information.



8/19/25, 11:46 AM YHRD : Search

Sample Name: Manual input

Dataset used: Y17

Kit used: Applied Biosystems AmpFLSTR® Yfiler® Plus

DYS576	DYS389I	DYS635	DYS389II	DYS627	DYS460	DYS458	DYS19	YGATAH4	DYS448	DYS391
16	13	25	·	·	11	17	·	·	·	·

DYS456	DYS390	DYS438	DYS392	DYS518	DYS570	DYS437	DYS385	DYS449	DYS393	DYS439	DYS481
15	24	·	·	·	17	15	·	·	13	11	22

DYF387S1	DYS533
36, 36	·

Worldwide

Observed

Found 8 matches in 289,405 Haplotypes. This is approx. 1 match in 36,176 Haplotypes (95% CI*: 1 in 83,792 — 1 in 18,360).

Expected

DL (y17)*
Discrete Laplace (y17) could not be performed due to intermediate, duplicated or missing alleles within the y17 markerset.
n+1/N+1*
Approx. 1 match in 32,156 Haplotypes (95% CI*: 1 in 70,323 — 1 in 16,940)
Kappa*
Approx. 1 match in 67,688 Haplotypes

National Database (with Subpopulations) - United States

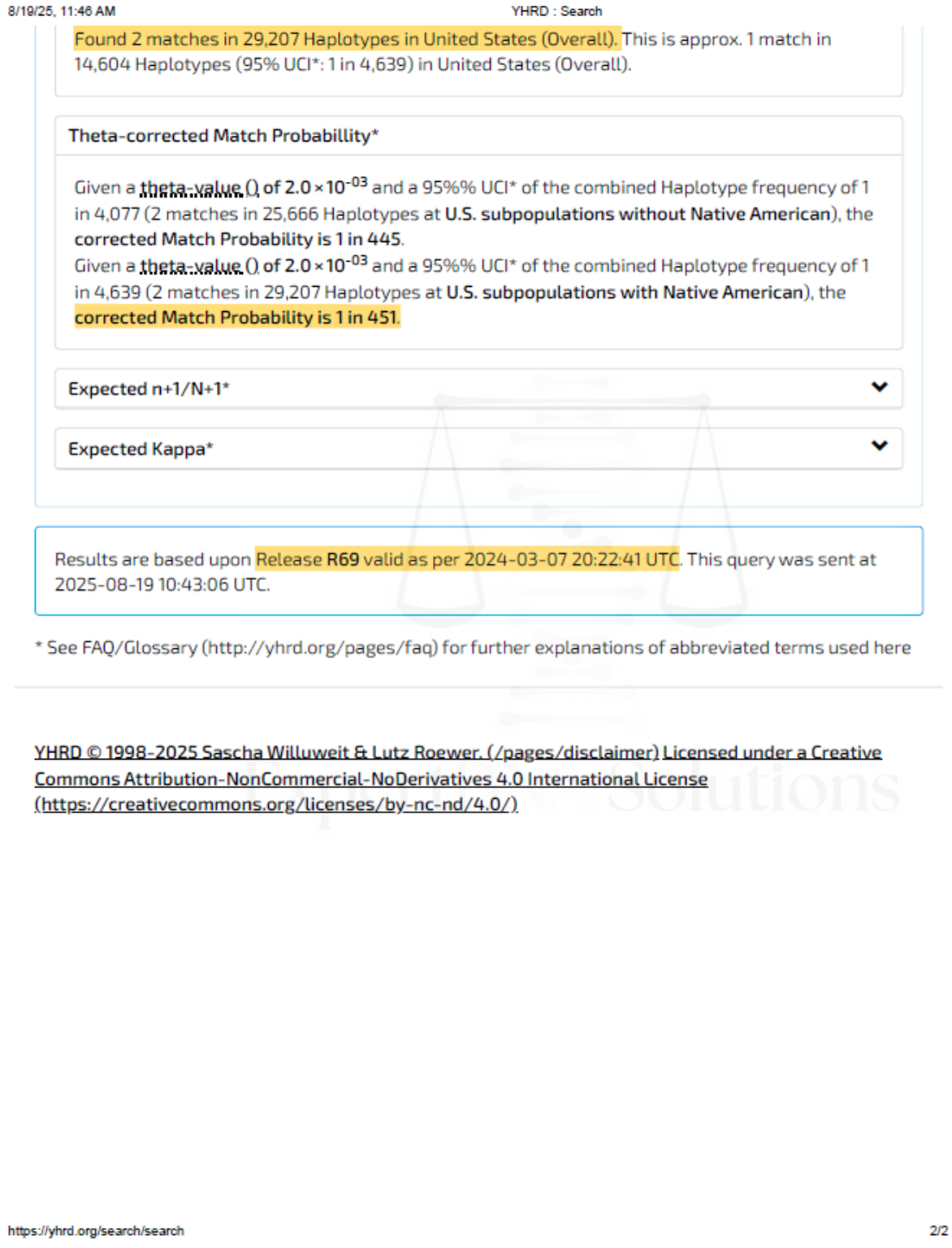
Observed

Found 1 match in 7,120 Haplotypes (95% UCI*: 1 in 1,501) in United States (African American).
Found no match in 4,034 Haplotypes (95% UCI*: 1 in 1,347) in United States (Asian American).
Found 1 match in 8,488 Haplotypes (95% UCI*: 1 in 1,790) in United States (Caucasian American).
Found no match in 6,024 Haplotypes (95% UCI*: 1 in 2,011) in United States (Hispanic American).
Found no match in 3,541 Haplotypes (95% UCI*: 1 in 1,183) in United States (Native American).

https://yhrd.org/search/search 1/2

Appendix
Supporting Documentation of Observations

Figure 6 (continued): EDS generated Updated YHRD Calculations.
Orange areas indicate updated information.



8/19/25, 11:46 AM YHRD : Search

Found 2 matches in 29,207 Haplotypes in United States (Overall). This is approx. 1 match in 14,604 Haplotypes (95% UCI*: 1 in 4,639) in United States (Overall).

Theta-corrected Match Probabillity*

Given a theta-value () of 2.0×10^{-03} and a 95%% UCI* of the combined Haplotype frequency of 1 in 4,077 (2 matches in 25,666 Haplotypes at **U.S. subpopulations without Native American**), the **corrected Match Probability is 1 in 445**.
Given a theta-value () of 2.0×10^{-03} and a 95%% UCI* of the combined Haplotype frequency of 1 in 4,639 (2 matches in 29,207 Haplotypes at **U.S. subpopulations with Native American**), the **corrected Match Probability is 1 in 451**.

Expected n+1/N+1*

Expected Kappa*

Results are based upon Release **R69** valid as per 2024-03-07 20:22:41 UTC. This query was sent at 2025-08-19 10:43:06 UTC.

* See FAQ/Glossary (http://yhrd.org/pages/faq) for further explanations of abbreviated terms used here

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https://yhrd.org/search/search 2/2

(https://yhrd.org) “Willuweit S. and Roewer L. (2015), ‘The new Y Chromosome Haplotype Reference Database.’, Forensic Sci Int Genet 15:43-8”

Appendix
Supporting Documentation of Observations

Observation #6- Incorrect Number of Contributors for Swabs from basement bathroom F doorframe (Item 12)

DNA Casework Analytical Manual Effective date: 03/14/24

In CASEWORK AUTOSOMAL STR DATA INTERPRETATION GUIDELINES Section:
"8.4. A sample is considered to be from a single source when the observed number of alleles and the peak height ratios are consistent with a profile from a single contributor."

"8.6. Samples should be evaluated for the possible presence of a mixture. The presence of a mixture may be indicated by:
8.6.1. The presence of more than two alleles at one locus.
8.6.2. The presence at one or more loci of a peak in stutter position with a height significantly greater than would be expected for a stutter peak.
8.6.3. The presence of allele imbalance in a heterozygous allele pair. Allele peak height ratios greater than the expected stutter and less than 70% may indicate a mixture."

Observation #7- Interpretation of Swabs from boots (Item 6.2) using ArmedXpert

DNA Casework Analytical Manual Effective date: 03/14/24

In MIXTURE INTERPRETATION AND STATISTICAL ANALYSIS WITH ARMEDXPERT SOFTWARE Section:
"4.4. Verify the number of contributors is correct at the bottom of the window. Review the allele combinations and statistical methods used for each locus on the statistical analysis page. If necessary, modify the allele combinations to achieve the appropriate calculations. A locus can also be removed from the calculations by double clicking its name."

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Observation #8- Handling of Test items/ Chain of Custody

KSP Forensic Laboratory Quality Assurance Manual Effective Dates: 07/07/23 and 07/09/24

In Section 7.4.1.1 (a) Internal Evidence Handling, Storage, and Preparation
"*1. Evidence shall remain properly sealed from the time of receipt into the laboratory until the time of release or disposal, unless actively being analyzed.*

- *Submitting agencies are encouraged to initial seals before sending to the laboratory.*
- *Analysts must properly seal evidence that has been opened and re-sealed prior to release.*
- *Unopened evidence that was sealed but not initialed by submitting agency upon receipt must be properly sealed and dated by analyst prior to release.*
- *Evidence which is properly sealed and appropriately marked can be placed in an unsealed bulk container for the purpose of grouping items, transfer, or transport or for the convenience of carrying, as long as the storage of the bulk container follows laboratory security measures.*

2. All evidence that is not in process of examination shall be stored in a secure location. Evidence shall not remain in "process" of examination for more than 90 days.

- *If the process of examination exceeds 90 days as denoted by the start and complete date, then the evidence shall either:*
  - *Be electronically scanned into a personal locker in which an analyst has ownership*
  - *Noted in the narrative that the evidence is locked in a personal locker*
  - *Noted in the narrative that the evidence was resealed following examination/sampling*

3. Analyst's handwritten initials and container or item barcode(s) bearing the unique laboratory number shall be attached to all containers. That barcode(s) connects evidence to the appropriate casefile and offers constant traceability.

- *Item Marking*

Individual items shall be marked with the item number, the laboratory number, and the analyst's initials.

- *The laboratory number does not need to be computer generated for inner packages.*
- *If an item cannot be directly marked, either the next layer of packaging may be marked or a tag may be attached that shall provide the unique identifiers.*
- *Whenever possible analysts should refrain from marking items of intrinsic value in obvious defacing areas.*

4. One-hundred percent (100%) evidence inventory shall be conducted and documented twice a year (January and July) by the analyst, the analyst's Supervisor, or designee.
One-hundred percent (100%) evidence inventory shall be conducted when an analyst (or evidence custodian) is no longer employed by the Kentucky State Police Forensic Laboratory (for whatever reason)."