Collaborative Testing Services, Inc
FORENSIC TESTING PROGRAM

P.O. Box 650820   Sterling, VA 20165-0820
e-mail: forensics@cts-interlab.com
Telephone: +1-571-434-1925
Web site: www.cts-forensics.com

Probabilistic Genotyping Test No. 26-5901/2 Summary Report

Each participant received a sample pack consisting of two known bloodstains and two questioned stains which they were asked to analyze using their existing protocols. Data were returned from 90 participants: 47 for 26-5901 and 43 for 26-5902, and are compiled into the following tables:

Manufacturer's Information

Each sample pack consisted of two known bloodstains provided on either white fabric or FTA™ Micro Cards, and two questioned stains on colored fabric. Participants were asked to analyze these items using their existing protocols.

SAMPLE PREPARATION: Stains from different sources were prepared at separate times and were packaged once they were thoroughly dried into separate envelopes.

SAMPLE PACK ASSEMBLY: One of each item was placed into a pre-labeled sample pack envelope and sealed. The sealed envelopes were then packaged in pre-labeled heat seal envelopes and sealed. Completed sample packs were stored at -20°C until shipment.

VERIFICATION: Predistribution results were consistent with each other and the manufacturer's preparation information. Consistent allelic results were reported for all STR and YSTR loci.

Item	Known/ Questioned	Substrate (Test No.)	Body Fluid	Volume (Mixture Ratio)	Sex	Donor Information
1	Known	White Fabric (5901)/ FTA™ Micro Card (5902)	Blood	50 µL/75 µL	Female	Victim
2	Known	White Fabric (5901)/ FTA™ Micro Card (5902)	Blood	50 µL/75 µL	Male	Suspect
3	Questioned	Tan Fabric	Blood/Blood	50 µL (3:2)	Female/Female	Victim/Additional Female
4	Questioned	Blue Fabric	Blood/Semen/Semen	50 µL (3:2:2)	Female/Male/Male	Victim/Additional Male A/Additional Male B

Manufacturer's Information, continued

Amelogenin and STR Results

Results compiled from predistribution laboratories and a consensus of at least 10 participants.

Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	
1	15.3,18.3	20,24	11.3,14	15,16	11,11	*
	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20	12,13	7,10	15,16	9,9.3	9,11
	16,17	NM	NM	NM	NM	
2	12,17	23,24	14,14	15,16	11,13	11,18
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16,16	11	*	*	2	
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	*
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26	9,12,13	7,10,17,23	14,15,16	7,9,9.3	9,10,11
	15,16,17	NM	NM	NM	NM	
4-Blood	15.3,18.3	20,24	11.3,14	15,16	11,11	*
	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20	12,13	7,10	15,16	9,9.3	9,11
	16,17	NM	NM	NM	NM	
4-Semen	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	*
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11,11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26	9,12	12,15,18,19	23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10,10	*	*	1,2	

* Results were not received by a minimum of 10 participants for the loci indicated.

NM - Non-Male profile, YSTR results not expected.

YSTR Results

Results compiled from predistribution laboratories and a consensus of at least 10 participants.

Item	**DYF387S1**	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
	DYS437	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13	*	17	16	18	23	*	12
4-Semen	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10,10	13,15	12,12
	14,14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11,11	*	17,19	17,20	19.2,22	21,22	*	10,13

* Results were not received by a minimum of 10 participants for the loci indicated.

Summary Comments

This test was designed to allow participants to assess their proficiency in the identification and comparison of dried stains by means of body fluid screening and/or DNA profiling utilizing Probabilistic Genotyping software. Participants were supplied with two known bloodstains (Items 1 and 2) and two questioned stains (Items 3 and 4). Item 1 was created using blood from a female donor. Item 2 was created using blood from a male donor. Item 3 was created by combining three parts blood from the Item 1 female donor and two parts blood from an additional female donor, whose known standard was not provided. Item 4 was created by combining three parts blood from the Item 1 female donor, two parts semen from a male donor whose known standard was not provided, and two parts semen from another male donor whose known standard was not provided. Refer to the Manufacturer's Information for preparation details.

Data were returned by 90 participants.

Screening Test Results
Screening results for body fluids were returned by a total of 76 participants. However, not all of these participants returned screening results for each fluid type for both questioned items.

For Item 3, all participants reported "Positive" for the presence of blood. For the presence of semen, all participants reported "Negative." For the presence of saliva, all participants reported "Negative." For Human Origin Screening, all participants reported "Positive". For Y-Screening, all but one participant reported "Negative." The remaining participant reported "Positive."

For Item 4, all participants reported "Positive" for the presence of blood. For the presence of semen, all participants reported "Positive." For the presence of saliva, all but one participant reported "Negative". The remaining participant reported "Positive". For Human Origin Screening and Y-Screening, all participants reported "Positive."

DNA Analysis
All participants reported DNA results. Only allelic results not containing the minimum expected alleles are highlighted as inconsistent.

For STR results, all participants reported consistent results, with the exception of thirteen participants. Eleven of these participants reported the use of the GlobalFiler™ kit. A majority of inconsistent results were noted for Item 4, including both the unseparated and separated fractions (Item 4, Item 4-Blood, and Item 4-Sperm), in which seven participants were missing an allele attributable to the victim and four participants were missing an allele attributable to additional male A.

For YSTR results, all participants reported consistent results, with the exception of six participants.

DNA Interpretations
For Item 3, all participants included the victim (Item 1) as a possible contributor to the stain. All but one participant excluded the suspect (Item 2) as a possible contributor. The remaining participant reported "Inconclusive." All participants identified the presence of two contributors.

For Item 4, all participants included the victim (Item 1) as a possible contributor to the stain. All but three participants excluded the suspect (Item 2) as a possible contributor to the stain. The remaining participants reported "Inconclusive." All but one participant identified the presence of three contributors in the epithelial fraction. The remaining participant reported the presence of four contributors. For the sperm fraction, thirty-nine participants identified the presence of two contributors, twenty-six participants identified the presence of three contributors, and one participant identified the presence of four contributors. An additional five participants did not perform a differential extraction on this item, but reported the presence of three contributors.

Serology Screening Results

Indicate the results of any screening tests performed on the questioned stains (Items 3 & 4).

TABLE 1a

WebCode - Test	Blood Screening Results Item 3	 Item 4
2U64XP - 5901	Pos LMG, Bluestar OBTI	Pos LMG, Bluestar OBTI
2V3DTT - 5901	Pos KM	Pos KM
3DCVDW - 5902	Pos PTMB	Pos PTMB
3GZ6PJ - 5901	Pos KM, Hematrace	Pos KM, Hematrace
3MLWYX - 5902	Pos PTMB	Pos PTMB
46DPW2 - 5902	Pos KM	Pos KM
6CE2VJ - 5901	Pos Hexagon OBTI Test	Pos Hexagon OBTI Test
6DBH6U - 5902	Pos PTMB	Pos PTMB
6FWJNN - 5901	Pos KM	Pos KM
6GAT2U - 5902	Pos PTMB	Pos PTMB
6H6C3W - 5902	Pos TMB, PHE	Pos TMB, PHE
6UBPYM - 5901	Pos SERATEC HEM	Pos SERATEC HEM
76CCPY - 5901	Pos TMB+ve	Pos TMB+ve
7G4YWE - 5901	Pos KM, Hematrace	Pos KM, Hematrace
7MMEUW - 5901	Pos Hemastix	Pos Hemastix
8FQNHM - 5902	Pos LMG, Hematrace	Pos LMG, Hematrace
8RZL2G - 5901	Pos KM, Hematrace	Pos KM, Hematrace
993KMP - 5902	Pos TMB, PHE	Pos TMB, PHE
9X3XVT - 5902	Pos O-tol	Pos O-tol
AAT7UL - 5901	Pos KM, HT	Pos KM, HT

TABLE 1a

WebCode - Test	Blood Screening Results Item 3	 Item 4
ABPL7H - 5902	Pos	Pos
AQ3XWQ - 5902	Pos PTMB	Pos PTMB
AXW3PR - 5901	Pos KM	Pos KM
AZ3KNM - 5901	Pos visual examination, KM, HT	Pos visual examination, KM, HT
BH4RFU - 5901	Pos TMB, Hematrace	Pos TMB, Hematrace
BUGRCN - 5902	Pos PTMB	Pos PTMB
CRMK7G - 5902	Pos KM	Pos KM
CZXMRH - 5902	Pos KM	Pos KM
DR322B - 5901	Pos TMB	Pos TMB
DZWAKF - 5901	Pos KM	Pos KM
EM2HCG - 5902	Pos Visual exam, KM, HT	Pos Visual exam, KM, HT
ENWXPE - 5901	Pos Hemastix, OBTI	Pos Hemastix, OBTI
EQZU9G - 5902	Pos KM, HT	Pos KM, HT
ERWAKE - 5901	Pos Kastle Meyer	Pos Kastle Meyer
F8HBKN - 5901	Pos Hemastix	Pos Hemastix
FZ8V8M - 5902	Pos PTMB, Hematrace	Pos PTMB
G83CWJ - 5902	Pos PTMB	Pos PTMB
GJRAXG - 5902	Pos PTMB	Pos PTMB
H3M3JE - 5902	Pos KM	Pos KM
H9BPF7 - 5901	Pos human hemoglobin (OBTI)	Pos human hemoglobin (OBTI)
HA79H8 - 5901	Pos KM, Hematrace	Pos KM, Hematrace
HMATHB - 5902	Pos KM	Pos KM

TABLE 1a

WebCode - Test	Blood Screening Results Item 3	Item 4
JJP289 - 5901	Pos O-tol, Hematrace	Pos O-tol, Hematrace
KFMMYA - 5901	Pos KM	Pos KM
KKTFQK - 5902	Pos KM	Pos KM
L6JPQZ - 5901	Pos KM, HemaTrace	Pos KM, HemaTrace
LRURMG - 5902	Pos TMB, PHE	Pos TMB, PHE
MG8BAZ - 5901	Pos Combur 3 test	Pos Seratec
MK7PU6 - 5902	Pos KM	Pos KM
NKKENU - 5902	Pos RSID Blood	Pos RSID Blood
NWDUKX - 5901	Pos KM, Hematrace	Pos KM, Hematrace
PKJZL9 - 5902	Pos PTMB	Pos PTMB
PWCGDV - 5901	Pos KM, Hematrace	Pos KM, Hematrace
QCKU6C - 5901	Pos TMB	Pos TMB
QKVWQD - 5902	Pos KM, Hematrace	Pos KM, Hematrace
QLQFTE - 5902	Pos KM	Pos KM
QY8QPG - 5901	Pos TMB, Hemochromogen	Pos TMB, Hemochromogen
RDVWRB - 5901	Pos KM, HemDirect	Pos KM, HemDirect
RUEQHZ - 5901	Pos KM, HemDirect	Pos KM, HemDirect
TFEBVC - 5902	Pos TMB	Pos TMB
TGAUWD - 5901	Pos TMB, Hematrace	Pos TMB, Hematrace
TKNR4Z - 5902	Pos LMG, Hematrace	Pos LMG, Hematrace
UMRJXY - 5902	Pos KM, HemaTrace	Pos KM, HemaTrace
V6A37P - 5901	Pos KM, Hematrace	Pos KM, Hematrace

TABLE 1a

WebCode - Test	Blood Screening Results Item 3	 Item 4
VBVWBM - 5901	Pos KM	Pos KM
W648ZP - 5901	Pos KM, Hematrace	Pos KM, Hematrace
W883G7 - 5902	Pos KM, Hematrace	Pos KM, Hematrace
WGU2AX - 5901	Pos KM	Pos KM
WP9QBQ - 5901	Pos KM, HemaTrace	Pos KM, HemaTrace
X9G8VV - 5901	Pos KM	Pos KM
XNBWN7 - 5901	Pos TMB	Pos TMB
YMVZW7 - 5901	Pos TMB	Pos TMB
YY83H6 - 5902	Pos TMB, PHE	Pos TMB, PHE
ZBZ72N - 5902	Pos LMG	Pos LMG
ZY36LY - 5902	Pos PTMB	Pos PTMB

Table 1a: Serology Screening Response Summary - Blood

Participants: **75**

This summary table excludes the count of participants who did not report or reported “Not Tested” for Item 3 and/or Item 4. Therefore, participant total may not align with totals shown below.

	Item 3	Item 4
Positive	**75**	**75**
Negative	**0**	**0**
Inconclusive	**0**	**0**

Serology Screening Results

Indicate the results of any screening tests performed on the questioned stains (Items 3 & 4).

TABLE 1b

WebCode - Test	Semen Screening Results Item 3	 Item 4
2U64XP - 5901	Neg PSA	Pos PSA
2V3DTT - 5901	Neg ALS, AP	Pos ALS, AP
3DCVDW - 5902	Neg ALS, AP, PSA	Pos ALS, AP, Micro
3GZ6PJ - 5901	Neg AP	Pos AP, Micro, PSA
3MLWYX - 5902	Neg ALS, AP, PSA	Pos ALS, AP, Micro
46DPW2 - 5902	Neg AP	Pos AP, PSA
6CE2VJ - 5901	Neg RSID Semen	Pos RSID Semen
6DBH6U - 5902	Neg AP, PSA	Pos AP, MICRO
6FWJNN - 5901	Neg ALS, AP	Pos ALS, AP
6GAT2U - 5902	Neg AP P30	Pos AP Micro
6H6C3W - 5902	Neg ALS, AP, P30	Pos ALS, AP, MICRO
6UBPYM - 5901	Neg SERATEC PSA + Micro	Pos SERATEC PSA + Micro
76CCPY - 5901	Neg AP-ve	Pos AP+ve, Micro +ve
7G4YWE - 5901	Neg AP	Pos AP, PSA, Micro
7MMEUW - 5901	Neg PSA and Micro	Pos PSA and Micro
8FQNHM - 5902	Neg AP, Micro	Pos AP, Micro
8RZL2G - 5901	Neg AP	Pos AP, Microscope, PSA
993KMP - 5902	Neg ALS, AP, P30	Pos ALS, AP, Micro
9X3XVT - 5902	Neg AP, PSA, Micro	Pos AP, PSA, Micro
AAT7UL - 5901	Neg ALS, AP	Pos ALS, AP, PSA, Micro
ABPL7H - 5902	Neg	Pos
AQ3XWQ - 5902	Neg ALS, AP	Pos ALS, AP, Micro

TABLE 1b

	Semen Screening Results			
WebCode - Test	**Item 3**		**Item 4**	
AXW3PR - 5901	Neg	AP	Pos	AP, Micro
AZ3KNM - 5901	Neg	visual examination, AP	Pos	visual examination, AP, micro
BH4RFU - 5901	Neg	AP	Pos	AP, PSA, micro
BUGRCN - 5902	Neg	AP, PSA	Pos	AP, Micro
CRMK7G - 5902	Neg	AP, MICRO	Pos	AP, MICRO
CZXMRH - 5902	Neg	AP	Pos	AP, Micro
DR322B - 5901	Neg		Pos	PSA
DZWAKF - 5901	Neg	ALS, AP	Pos	ALS, AP
E6M7KQ - 5901			Pos	Micro
EM2HCG - 5902	Neg	Visual exam, AP	Pos	Visual exam, AP, micro
ENWXPE - 5901	Neg	PSA, PAM	Pos	PSA, PAM
EQZU9G - 5902	Neg	ALS, AP, Micro, PSA	Pos	ALS, AP, Micro
ERWAKE - 5901	Neg	Acid Phosphatase	Pos	Acid Phosphatase
F8HBKN - 5901	Neg	PSA, Micro	Pos	PSA, Micro
FZ8V8M - 5902	Neg	AP	Pos	ALS, AP, Micro, P30
G83CWJ - 5902	Neg	ALS, AP, PSA	Pos	ALS, AP, Micro, PSA
GJRAXG - 5902	Neg	ALS, AP	Pos	ALS, AP, Micro
H3M3JE - 5902	Neg	AP	Pos	AP, micro
H9BPF7 - 5901	Neg	PSA	Pos	PSA
HA79H8 - 5901	Neg	AP	Pos	AP, PSA, Micro
HMATHB - 5902	Neg	AP	Pos	AP, Micro
JJP289 - 5901	Neg	ALS, AP, P30, micro	Pos	ALS, AP, P30, micro
KFMMYA - 5901	Neg	AP, ALS	Pos	AP, ALS

TABLE 1b

	Semen Screening Results	
WebCode - Test	**Item 3**	**Item 4**
KKTFQK - 5902	Neg AP	Pos AP, PSA
L6JPQZ - 5901	Neg AP	Pos AP, Micro, PSA
LRURMG - 5902	Neg P30	Pos P30, Micro
MG8BAZ - 5901	Neg PSA/RSID	Pos RSID
MK7PU6 - 5902	Neg AP, ALS, Micro, PSA	Pos AP, ALS, Micro, PSA
NKKENU - 5902	Neg RSID Semen	Pos AP, RSID Semen, Sperm Hyliter Express
NWDUKX - 5901	Neg AP	Pos AP, PSA, Micro
PKJZL9 - 5902	Neg ALS, P30	Pos ALS, P30, Micro
PWCGDV - 5901	Neg AP	Pos AP, PSA, Micro
QCKU6C - 5901	Neg AP	Pos AP, Micro
QKVWQD - 5902	Neg ALS, AP	Pos ALS, AP, RSID, Micro
QLQFTE - 5902	Neg AP	Pos AP, PSA
QY8QPG - 5901	Neg AP	Pos AP, Micro
RDVWRB - 5901	Neg AP	Pos AP, Micro, PSA
RUEQHZ - 5901	Neg ALS, AP	Pos ALS, AP, micro, PSA
TFEBVC - 5902	Neg AP	Pos Micro, AP
TGAUWD - 5901	Neg AP	Pos AP, PSA, Microscopic
TKNR4Z - 5902	Neg AP, Micro, PSA	Pos AP, Micro, PSA
UMRJXY - 5902	Neg AP, PSA, Micro, ALS	Pos AP, PSA, Micro, ALS
V6A37P - 5901	Neg AP	Pos AP, PSA, Micro
VBVWBM - 5901	Neg AP	Pos AP
W648ZP - 5901	Neg AP	Pos AP, PSA, Micro
W883G7 - 5902	Neg ALS, AP	Pos ALS, AP, RSID, Micro

TABLE 1b

WebCode - Test	Semen Screening Results Item 3		Item 4	
WGU2AX - 5901	Neg	ALS, AP	Pos	ALS, AP, PSA, Micro
WP9QBQ - 5901	Neg	AP	Pos	AP, PSA, Micro
X9G8VV - 5901	Neg	AP, Micro	Pos	AP, Micro
XNBWN7 - 5901	Neg	AP, Micro	Pos	AP, Micro
YMVZW7 - 5901	Neg	AP	Pos	Micro and AP
YY83H6 - 5902	Neg	ALS, P30, AP	Pos	P30, Micro
ZBZ72N - 5902	Neg	AP, ALS, Micro	Pos	AP, ALS, Micro
ZY36LY - 5902	Neg	AP, PSA	Pos	AP, Micro

Table 1b: Serology Screening Response Summary - Semen

Participants: 76

This summary table excludes the count of participants who did not report or reported "Not Tested" for Item 3 and/or Item 4. Therefore, participant total may not align with totals shown below.

	Item 3	Item 4
Positive	**0**	**76**
Negative	**75**	**0**
Inconclusive	**0**	**0**

Serology Screening Results

Indicate the results of any screening tests performed on the questioned stains (Items 3 & 4).

TABLE 1c

WebCode - Test	Saliva Screening Results Item 3		Item 4	
46DPW2 - 5902	Neg	Phadebas	Neg	Phadebas
6CE2VJ - 5901			Pos	RSID Saliva
9X3XVT - 5902	Neg	SERATEC Amylase	Neg	SERATEC Amylase
BH4RFU - 5901	Neg	RSID	Neg	RSID
CRMK7G - 5902	Neg	Phadebas	Neg	Phadebas
CZXMRH - 5902	Neg	Phadebas	Neg	Phadebas
DR322B - 5901	Neg		Neg	
ENWXPE - 5901	Neg	PAM, RSID	Neg	PAM, RSID
ERWAKE - 5901	Neg	Amylase	Neg	Amylase
H3M3JE - 5902	Neg	Phadebas	Neg	Phadebas
H9BPF7 - 5901	Neg	Amylase	Neg	Amylase
HMATHB - 5902	Neg	Phadebas	Neg	Phadebas
JJP289 - 5901	Neg	RSID, micro	Neg	RSID, micro
MG8BAZ - 5901	Neg	RSID Semen	Neg	alfa-amilasi
NKKENU - 5902	Neg	RSID Saliva	Neg	RSID Saliva
QLQFTE - 5902	Neg	Phadebas Press	Neg	Phadebas Press
RUEQHZ - 5901	Neg	Seratec alpha amylase	NT	
TGAUWD - 5901	Neg	RSID Saliva	Neg	RSID Saliva
XNBWN7 - 5901	Neg	RSID	Neg	RSID

Table 1c: Serology Screening Response Summary - Saliva

Participants: **19**

This summary table excludes the count of participants who did not report or reported "Not Tested" for Item 3 and/or Item 4. Therefore, participant total may not align with totals shown below.

	Item 3	Item 4
Positive	**0**	**1**
Negative	**18**	**17**
Inconclusive	**0**	**0**

Serology Screening Results

Indicate the results of any screening tests performed on the questioned stains (Items 3 & 4).

TABLE 1d

	Human Origin Screening Results			
WebCode - Test	**Item 3**		**Item 4**	
2U64XP - 5901	Pos	Quantiplex Prp RGQ, STR	Pos	Quantiplex Prp RGQ, STR
46DPW2 - 5902	Pos	ABA	NT	
6UBPYM - 5901	Pos	Qiagen Investigator Quantiplex pro	Pos	Qiagen Investigator Quantiplex pro
AAT7UL - 5901	Pos	HT	Pos	HT
AXW3PR - 5901	Pos	PowerQuant	Pos	PowerQuant
AZ3KNM - 5901	Pos	HT	Pos	HT
BH4RFU - 5901	Pos	Quant trio, PP21	Pos	Quant trio, PP21
DR322B - 5901	Pos	OBTI	Pos	OBTI
EM2HCG - 5902	Pos	HT	Pos	HT
ENWXPE - 5901	Pos	Quantifiler TRIO	Pos	Quantifiler TRIO
EQZU9G - 5902	Pos	HT	Pos	HT
H9BPF7 - 5901	Pos	PowerQuant RTPCR	Pos	PowerQuant RTPCR
KKTFQK - 5902	Pos	ABAcard HemaTrace	NT	
MG8BAZ - 5901	Pos	Hexagon	Pos	Hexagon
NKKENU - 5902	Pos	Quantifiler Trio	Pos	Quantifiler Trio
QLQFTE - 5902	Pos	ABACard	NT	
RUEQHZ - 5901	Pos	Ouchterlony double immunodiffusion	Pos	Ouchterlony double immunodiffusion
TGAUWD - 5901	Pos	Quantifiler Trio, PP21	Pos	Quantifiler Trio, PP21
VBVWBM - 5901	Pos	RSID	Pos	RSID, MICRO
WGU2AX - 5901	Pos	HemaTrace	Pos	HemaTrace

Table 1d: Serology Screening Response Summary - Human Origin

Participants: **20**

This summary table excludes the count of participants who did not report or reported "Not Tested" for Item 3 and/or Item 4. Therefore, participant total may not align with totals shown below.

	Item 3	Item 4
Positive	**20**	**17**
Negative	**0**	**0**
Inconclusive	**0**	**0**

Serology Screening Results

Indicate the results of any screening tests performed on the questioned stains (Items 3 & 4).

TABLE 1e

	Y Screening Results			
WebCode - Test	**Item 3**		**Item 4**	
2U64XP - 5901	Neg	Quantiplex Prp RGQ, STR	Pos	Quantiplex Prp RGQ, STR, Y-STR
2V3DTT - 5901	Neg	Quant Trio	Pos	Quant Trio
4478ZQ - 5901			Pos	quantifiler trio
46DPW2 - 5902	Neg	Plexor HY	Pos	Plexor HY
6DBH6U - 5902	Neg	MDS & qPCR procedure	Pos	MDS & qPCR procedure
6FWJNN - 5901	Neg	Quantifiler Trio	Pos	Quantiler Trio
6GAT2U - 5902	Neg	MDS & qPCR procedure	Pos	MDS & qPCR procedure
6UBPYM - 5901	Neg	Qiagen Investigator Quantiplex pro	Pos	Qiagen Investigator Quantiplex pro
76CCPY - 5901	Neg	Quantifiler Trio	Pos	Quantifiler Trio
8FQNHM - 5902	Neg	Quant Trio	Pos	Quant Trio
993KMP - 5902	Neg	MDS & qPCR procedure	Pos	MDS & qPCR procedure
AXW3PR - 5901	Neg	PowerQuant, Casework Direct	Pos	PowerQuant, Casework Direct
BH4RFU - 5901	Neg	Quant trio	Pos	Quant trio, YFP
BUGRCN - 5902	Neg	MDS & qPCR procedure	Pos	MDS & qPCR procedure
D2RTLG - 5901			Pos	Quant Trio
DZWAKF - 5901	NT		Pos	Quant Trio
ENWXPE - 5901	Pos	Quantifiler TRIO	Pos	Quantifiler TRIO
H9BPF7 - 5901	Neg	Fusion 6c	Pos	Fusion 6c
H9PEFC - 5901			Pos	Quantifiler Trio
KFMMYA - 5901	Neg	Quant Trio	Pos	Quant Trio
KKTFQK - 5902	Neg	Plexor HY	Pos	Plexor XY
LRURMG - 5902	Neg	MDS & qPCR procedure	Pos	MDS & qPCR procedure
LV8TJ9 - 5901			Pos	Quant Trio

TABLE 1e

WebCode - Test	Y Screening Results: Item 3		Item 4	
NKKENU - 5902	Neg	Quantifiler Trio	Pos	Quantifiler Trio
QKVWQD - 5902	Neg	Quant Trio - Y marker	Pos	Quant Trio - Y marker
QLQFTE - 5902	Neg	Plexor HY	Pos	Plexor HY
TGAUWD - 5901	Neg	Quantifiler Trio	Pos	Quantifiler Trio, YFP
TKNR4Z - 5902	Neg	Quant Trio	Pos	Quant Trio
TLJA72 - 5901			Pos	Quant Trio
W883G7 - 5902	Neg	Y-Quant	Pos	Y-Quant
WGU2AX - 5901	NT		Pos	Quant trio
ZY36LY - 5902	Neg	MDS & qPCR procedure	Pos	MDS & qPCR procedure

Table 1e: Serology Screening Response Summary - Y Screening

Participants: **32**

This summary table excludes the count of participants who did not report or reported “Not Tested” for Item 3 and/or Item 4. Therefore, participant total may not align with totals shown below.

	Item 3	Item 4
Positive	**1**	**32**
Negative	**24**	**0**
Inconclusive	**0**	**0**

Serology Screening Results

Indicate the results of any screening tests performed on the questioned stains (Items 3 & 4).

TABLE 1f

	Other Screening Results					
WebCode - Test	**Item 3**			**Item 4**		
2U64XP - 5901	sperm cells	Neg	Micro	sperm cells	Pos	Micro
H9BPF7 - 5901	PMB-menstrual blood	Neg		PMB-menstrual blood	Neg	

DNA Interpretations

Based on results obtained from DNA analysis, could the Victim (Item 1) and/or the Suspect (Item 2) be a contributor to the questioned stains (Items 3 & 4)?

TABLE 2

WebCode-Test	Victim (Item 1)		Suspect (Item 2)	
	Item 3	Item 4	Item 3	Item 4
2U64XP - 5901	Yes	Yes	No	No
2V3DTT - 5901	Yes	Yes	No	No
3DCVDW - 5902	Yes	Yes	No	No
3GZ6PJ - 5901	Yes	Yes	No	No
3MLWYX - 5902	Yes	Yes	No	No
3P6C3X - 5902	Yes	Yes	No	No
4478ZQ - 5901	Yes	Yes	No	No
46DPW2 - 5902	Yes	Yes	No	No
6CE2VJ - 5901	Yes	Yes	No	No
6DBH6U - 5902	Yes	Yes	No	No
6FWJNN - 5901	Yes	Yes	No	No
6GAT2U - 5902	Yes	Yes	No	Inc
6H6C3W - 5902	Yes	Yes	No	No
6UBPYM - 5901	Yes	Yes	No	No
76CCPY - 5901	Yes	Yes	No	No
7G4YWE - 5901	Yes	Yes	No	No
7MMEUW - 5901	Yes	Yes	No	No
8FQNHM - 5902	Yes	Yes	No	No
8RZL2G - 5901	Yes	Yes	No	No
993KMP - 5902	Yes	Yes	No	No
9X3XVT - 5902	Yes	Yes	No	No
AAT7UL - 5901	Yes	Yes	No	No
ABPL7H - 5902	Yes	Yes	No	No
AQ3XWQ - 5902	Yes	Yes	No	No
AWLZ4T - 5902	Yes	Yes	No	No
AXW3PR - 5901	Yes	Yes	No	Inc
AZ3KNM - 5901	Yes	Yes	No	No
BH4RFU - 5901	Yes	Yes	No	No
BUGRCN - 5902	Yes	Yes	No	No
CRMK7G - 5902	Yes	Yes	No	No
CZXMRH - 5902	Yes	Yes	No	No
D2RTLG - 5901	Yes	Yes	No	No
DR322B - 5901	Yes	Yes	No	No
DZWAKF - 5901	Yes	Yes	No	No
E6M7KQ - 5901	Yes	Yes	No	No
EM2HCG - 5902	Yes	Yes	No	No
ENWXPE - 5901	Yes	Yes	No	No
EQZU9G - 5902	Yes	Yes	No	No
ERWAKE - 5901	Yes	Yes	No	No

TABLE 2

WebCode-Test	Victim (Item 1)		Suspect (Item 2)	
	Item 3	Item 4	Item 3	Item 4
F8HBKN - 5901	Yes	Yes	No	No
FE3CWK - 5902	Yes	Yes	No	No
FYD629 - 5902	Yes	Yes	No	No
FZ8V8M - 5902	Yes	Yes	No	No
G83CWJ - 5902	Yes	Yes	No	No
GJRAXG - 5902	Yes	Yes	No	No
GXDN2G - 5902	Yes	Yes	No	No
H3M3JE - 5902	Yes	Yes	No	No
H9BPF7 - 5901	Yes	Yes	No	No
H9PEFC - 5901	Yes	Yes	No	No
HA79H8 - 5901	Yes	Yes	No	No
HMATHB - 5902	Yes	Yes	No	No
JCRAYE - 5902	Yes	Yes	No	No
JJP289 - 5901	Yes	Yes	No	No
KFMMYA - 5901	Yes	Yes	No	No
KKTFQK - 5902	Yes	Yes	No	No
L6JPQZ - 5901	Yes	Yes	No	No
LBA2Q3 - 5902	Yes	Yes	No	No
LRURMG - 5902	Yes	Yes	No	No
LV8TJ9 - 5901	Yes	Yes	No	No
MG8BAZ - 5901	Yes	Yes	No	No
MK7PU6 - 5902	Yes	Yes	No	No
NKKENU - 5902	Yes	Yes	No	No
NWDUKX - 5901	Yes	Yes	No	No
PKJZL9 - 5902	Yes	Yes	No	No
PWCGDV - 5901	Yes	Yes	No	No
QCKU6C - 5901	Yes	Yes	No	No
QKVWQD - 5902	Yes	Yes	No	No
QLQFTE - 5902	Yes	Yes	No	No
QY8QPG - 5901	Yes	Yes	No	No
R7WA2W - 5902	Yes	Yes	No	No
RDVWRB - 5901	Yes	Yes	No	No
RUEQHZ - 5901	Yes	Yes	No	No
TFEBVC - 5902	Yes	Yes	No	No
TGAUWD - 5901	Yes	Yes	No	No
TKNR4Z - 5902	Yes	Yes	No	No
TLJA72 - 5901	Yes	Yes	No	No
UMRJXY - 5902	Yes	Yes	No	No
V67HG2 - 5901	Yes	Yes	No	No
V6A37P - 5901	Yes	Yes	No	No
VBVWBM - 5901	Yes	Yes	No	No
W648ZP - 5901	Yes	Yes	No	No

TABLE 2

WebCode-Test	Victim (Item 1)		Suspect (Item 2)	
	Item 3	Item 4	Item 3	Item 4
W883G7 - 5902	Yes	Yes	No	No
WGU2AX - 5901	Yes	Yes	No	No
WP9QBQ - 5901	Yes	Yes	No	No
X9G8VV - 5901	Yes	Yes	No	No
XNBWN7 - 5901	Yes	Yes	No	No
YMVZW7 - 5901	Yes	Yes	No	No
YY83H6 - 5902	Yes	Yes	No	No
ZBZ72N - 5902	Yes	Yes	Inc	Inc
ZY36LY - 5902	Yes	Yes	No	No

DNA Interpretation

Response Summary **Participants reporting DNA results: 90**

Based on results obtained from DNA analysis, could the Victim (Item 1) and/or the Suspect (Item 2) be a contributor to the questioned stains (Items 3 & 4)?

	Victim (Item 1)		Suspect (Item 2)	
	Item 3	Item 4	Item 3	Item 4
Yes	**90**	**90**	**0**	**0**
No	**0**	**0**	**89**	**87**
Inc	**0**	**0**	**1**	**3**
No Interpretation	**0**	**0**	**0**	**0**
No Response	**0**	**0**	**0**	**0**

STR Amplification Kit(s) & Results

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
	D1S1656	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
Item	**D7S820**	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	
Item 1 - STR Results						
2U64XP - 5901	PowerPlex® ESX17 Fast- STRMix™ V2.5.11					
	15.3,18.3	20,24	11.3,14	15,16		
1		11,14	14,16	16,23		12,13
	19,20	14,15	27,30	15,16	X,X	
	20,20			15,16	9,9.3	
	16,17					
2V3DTT - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
3DCVDW - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
3GZ6PJ - 5901	GlobalFiler™- STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
3MLWYX - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
3P6C3X - 5902	GlobalFiler™- STRMix™ 2.8.0					
	15.3,18.3	20,24	11.3,14	15,16	11	NT
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20	NT	NT	15,16	9,9.3	9,11
	16,17	NR	NT	NT	NR	

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 1 - STR Results

4478ZQ - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
46DPW2 - 5902	Identifiler® Plus- STRMix™					
		20,24		15,16	11,11	
1	10,11	11,14			11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20				9,9.3	9,11
	16,17					
6CE2VJ - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
6DBH6U - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
6FWJNN - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
6GAT2U - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
6H6C3W - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
Item 1 - STR Results						
6UBPYM - 5901	GlobalFiler™ IQC					
	15.3,18.3	20,24	11.3,14	15,16	11,11	-
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20	-	-	15,16	9,9.3	9,11
	16,17	-	-	-	-	
76CCPY - 5901	PowerPlex® 21					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
7G4YWE - 5901	GlobalFiler™ - STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
7MMEUW - 5901	GlobalFiler™ Express					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
8FQNHM - 5902	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
8RZL2G - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
993KMP - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
Item 1 - STR Results						
9X3XVT - 5902	PowerPlex® Fusion 6C					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20	12,13	7,10	15,16	9,9.3	9,11
	16,17	ND	ND	ND		
AAT7UL - 5901	GlobalFiler™ - STRMix™ v 2.8					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
ABPL7H - 5902	GlobalFiler™ - STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
AQ3XWQ - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
AWLZ4T - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
AXW3PR - 5901	Identifiler® Plus, PowerPlex® Fusion 6C					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20	12,13	7,10	15,16	9,9.3	9,11
	16,17					
AZ3KNM - 5901	GlobalFiler™ - STRMix™ v2.8					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 1 - STR Results

BH4RFU - 5901	PowerPlex® 21- STRMix™ 2.10					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
BUGRCN - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
CRMK7G - 5902	GlobalFiler™- STRMix™ v2.9.1					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
CZXMRH - 5902	GlobalFiler™- STRMix™ v2.9.1					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
D2RTLG - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X,X	12
	20			15,16	9,9.3	9,11
	16,17	NR			NR	
DR322B - 5901	GlobalFiler™ - LR Mix v. 2.1.5 C.E.					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
DZWAKF - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 1 - STR Results

E6M7KQ - 5901	PowerPlex® 21- STRMix™					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
EM2HCG - 5902	GlobalFiler™- STRMix™ 2.8					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
ENWXPE - 5901	GlobalFiler™ - DNAxs, ver. 2.8.11					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
EQZU9G - 5902	GlobalFiler™- STRMix™ v2.8					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X,X	12
	20			15,16	9,9.3	9,11
	16,17					
ERWAKE - 5901	PowerPlex® ESI-17					
	15.3,18.3	20,24	11.3,14	15,16		
1		11,14	14,16	16,23		12,13
	19,20	14,15	27,30	15,16	X,X	
	20,20			15,16	9,9.3	
	16,17					
F8HBKN - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
FE3CWK - 5902	GlobalFiler™- STRMix™ Version 2.8.0					
	15.3,18.3	20,24	11.3,14	15,16	11	NT
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20	NT	NT	15,16	9,9.3	9,11
	16,17	NR	NT	NT	NR	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
Item 1 - STR Results						
FYD629 - 5902	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17	NR			NR	
FZ8V8M - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
G83CWJ - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
GJRAXG - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
GXDN2G - 5902	GlobalFiler™ - STRMix™ 2.8					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
H3M3JE - 5902	GlobalFiler™ - STRMix™ v2.9.1					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
H9BPF7 - 5901	PowerPlex® Fusion 6c					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20	12,13	7,10	15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 1 - STR Results

H9PEFC - 5901	GlobalFiler™					
1	15.3,18.3	20,24	11.3,14	15,16	11,11	
	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
HA79H8 - 5901	GlobalFiler™					
1	15.3,18.3	20,24	11.3,14	15,16	11	
	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
HMATHB - 5902	GlobalFiler™ - STRMix™ v2.9.1					
1	15.3,18.3	20,24	11.3,14	15,16	11	
	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
JCRAYE - 5902	GlobalFiler™ - STRMix™ v2.8					
1	15.3,18.3	20,24	11.3,14	15,16	11	
	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
JJP289 - 5901	PowerPlex® Fusion 6C- STRMix™ v2.9					
1	15.3,18.3	20,24	11.3,14	15,16	11	
	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20	12,13	7,10	15,16	9,9.3	9,11
	16,17					
KFMMYA - 5901	GlobalFiler™					
1	15.3,18.3	20,24	11.3,14	15,16	11	
	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
KKTFQK - 5902	Identifiler® Plus- STRMix™					
1		20,24		15,16	11,11	
	10,11	11,14			11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20				9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
Item	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 1 - STR Results

L6JPQZ - 5901	GlobalFiler™- STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
LBA2Q3 - 5902	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17	NR			NR	
LRURMG - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
LV8TJ9 - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
MG8BAZ - 5901	GlobalFiler™- STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
MK7PU6 - 5902	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
NKKENU - 5902	PowerPlex® Fusion 6C- STRMix™ v2.12					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20	12,13	7,10	15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 1 - STR Results

NWDUKX - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
PKJZL9 - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
PWCGDV - 5901	GlobalFiler™ - STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
QCKU6C - 5901	PowerPlex® 21					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
QKVWQD - 5902	PowerPlex® 21					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
QLQFTE - 5902	Identifiler® ID+					
		20,24		15,16	11,11	
1	10,11	11,14			11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20				9,9.3	9,11
	16,17					
QY8QPG - 5901	Identifiler® plus- STRMix™ v 2.7					
		20,24		15,16	11,11	
1	10,11	11,14			11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20				9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
			Item 1 - STR Results			
R7WA2W - 5902	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17	NR			NR	
RDVWRB - 5901	PowerPlex® Fusion 6C, GlobalFiler™ Express					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20	12,13	7,10	15,16	9,9.3	9,11
	16,17	NID	NID	NID		
RUEQHZ - 5901	Identifiler® plus					
		20,24		15,16	11,11	
1	10,11	11,14			11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20				9,9.3	9,11
	16,17					
TFEBVC - 5902	PowerPlex® 21- STRMix™					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
TGAUWD - 5901	PowerPlex® 21- STRMix™ v.2.10					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
TKNR4Z - 5902	GlobalFiler™- STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
TLJA72 - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 1 - STR Results

UMRJXY - 5902	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
V67HG2 - 5901	GlobalFiler™ - STRMix™ v 2..8					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X,X	12
	20			15,16	9,9.3	9,11
	16,17					
V6A37P - 5901	GlobalFiler™ - STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
VBVWBM - 5901	GlobalFiler™ - EUROFORMIX v4.0.8					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17	-			-	
W648ZP - 5901	GlobalFiler™ - STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
W883G7 - 5902	PowerPlex® 21- STRMix™ 2.10.0					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
WGU2AX - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 1 - STR Results

WP9QBQ - 5901	GlobalFiler™					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20			15,16	9,9.3	9,11
	16,17					
X9G8VV - 5901	GlobalFiler™ - STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
XNBWN7 - 5901	GlobalFiler™ - STRMix™					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
YMVZW7 - 5901	PowerPlex® 21- STRMix™ v2.8.0					
	15.3,18.3	20,24		15,16	11,11	12,17
1	10,11	11,14		16,23	11,11	12,13
	19,20	14,15	27,30		X,X	12,12
	20,20	12,13	7,10		9,9.3	9,11
	16,17					
YY83H6 - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					
ZBZ72N - 5902	PowerPlex® Fusion 6C - DNAxs					
	15.3,18.3	20,24	11.3,14	15,16	11	
1	10,11	11,14	14,16	16,23	11	12,13
	19,20	14,15	27,30	15,16	X	12
	20	12,13	7,10	15,16	9,9.3	9,11
	16,17					
ZY36LY - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,18.3	20,24	11.3,14	15,16	11,11	
1	10,11	11,14	14,16	16,23	11,11	12,13
	19,20	14,15	27,30	15,16	X,X	12,12
	20,20			15,16	9,9.3	9,11
	16,17					

TABLE 3

WebCode - Test	Item	Amplification Kits - Probabilistic Genotyping Software					
		D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
		D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
		D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
		FGA	Penta D	Penta E	SE33	TH01	TPOX
		vWA	DYS391	DYS570	DYS576	Y Indel	
		Item 2 - STR Results					
2U64XP - 5901		PowerPlex® ESX17 Fast- STRMix™ 2.5.11					
	2	12,17	23,24	14,14	15,16		
			14,16	13,14	19,19		10,13
		13,14	13,14	28,31	16,16	X,Y	
		21,26			18,20	7,9	
		16,16					
2V3DTT - 5901		GlobalFiler™					
	2	12,17	23,24	14	15,16	11,13	
		9.3,10	14,16	13,14	19	9,11	10,13
		13,14	13,14	28,31	16	X,Y	10,13
		21,26			18,20	7,9	8,9
		16	11			2	
3DCVDW - 5902		GlobalFiler™- TrueAllele® VUIer Release 2022b					
	2	12,17	23,24	14,14	15,16	11,13	
		9.3,10	14,16	13,14	19,19	9,11	10,13
		13,14	13,14	28,31	16,16	X,Y	10,13
		21,26			18,20	7,9	8,9
		16,16	11			2	
3GZ6PJ - 5901		GlobalFiler™- STRMix™					
	2	12,17	23,24	14	15,16	11,13	
		9.3,10	14,16	13,14	19	9,11	10,13
		13,14	13,14	28,31	16	X,Y	10,13
		21,26			18,20	7,9	8,9
		16	11			2	
3MLWYX - 5902		GlobalFiler™- TrueAllele® VUIer Release 2022b					
	2	12,17	23,24	14,14	15,16	11,13	
		9.3,10	14,16	13,14	19,19	9,11	10,13
		13,14	13,14	28,31	16,16	X,Y	10,13
		21,26			18,20	7,9	8,9
		16,16	11			2	
3P6C3X - 5902		GlobalFiler™- STRMix™ 2.8.0					
	2	12,17	23,24	14	15,16	11,13	NT
		9.3,10	14,16	13,14	19	9,11	10,13
		13,14	13,14	28,31	16	X,Y	10,13
		21,26	NT	NT	18,20	7,9	8,9
		16	11	NT	NT	2	
4478ZQ - 5901		GlobalFiler™					
	2	12,17	23,24	14	15,16	11,13	
		9.3,10	14,16	13,14	19	9,11	10,13
		13,14	13,14	28,31	16	X,Y	10,13
		21,26			18,20	7,9	8,9
		16	11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
	D1S1656	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
Item	**D7S820**	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	
Item 2 - STR Results						
46DPW2 - 5902	Identifiler® Plus- STRMix™					
		23,24		15,16	11,13	
2	9.3,10	14,16			9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26				7,9	8,9
	16,16					
6CE2VJ - 5901	GlobalFiler™					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
6DBH6U - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
6FWJNN - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
6GAT2U - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
6H6C3W - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
6UBPYM - 5901	GlobalFiler™ IQC					
	12,17	23,24	14,14	15,16	11,13	-
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26	-	-	18,20	7,9	8,9
	16,16	11	-	-	2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
Item 2 - STR Results						
76CCPY - 5901	PowerPlex® 21					
2	12,17	23,24		15,16	11,13	11,18
	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					
7G4YWE - 5901	GlobalFiler™ - STRMix™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
7MMEUW - 5901	GlobalFiler™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
8FQNHM - 5902	GlobalFiler™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
8RZL2G - 5901	GlobalFiler™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
993KMP - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
9X3XVT - 5902	PowerPlex® Fusion 6C					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16,16	11	17	16		

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 2 - STR Results

AAT7UL - 5901	GlobalFiler™ - STRMix™ v2.8					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
ABPL7H - 5902	GlobalFiler™ - STRMix™					
2	12,17	23,24	14,15	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
AQ3XWQ - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
AWLZ4T - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
AXW3PR - 5901	Identifiler® Plus, PowerPlex® Fusion 6C					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16	11	17	16		
AZ3KNM - 5901	GlobalFiler™ - STRMix™ v2.8					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
BH4RFU - 5901	PowerPlex® 21- STRMix™ 2.10					
2	12,17	23,24		15,16	11,13	11,18
	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 2 - STR Results

BUGRCN - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
CRMK7G - 5902	GlobalFiler™- STRMix™ v2.9.1					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
CZXMRH - 5902	GlobalFiler™- STRMix™ v2.9.1					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
D2RTLG - 5901	GlobalFiler™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
DR322B - 5901	GlobalFiler™ - LR Mix v. 2.1.5 C.E.					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
DZWAKF - 5901	GlobalFiler™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
E6M7KQ - 5901	PowerPlex® 21- STRMix™					
2	12,17	23,24		15,16	11,13	11,18
	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
Item	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 2 - STR Results

EM2HCG - 5902	GlobalFiler™- STRMix™ 2.8					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
ENWXPE - 5901	GlobalFiler™ - DNAxs, ver. 2.8.11					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11				
EQZU9G - 5902	GlobalFiler™- STRMix™ v2.8					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
ERWAKE - 5901	PowerPlex® esi-17					
	12,17	23,24	14,14	15,16		
2		14,16	13,14	19,19		10,13
	13,14	13,14	28,31	16,16	X,Y	
	21,26			18,20	7,9	
	16,16					
F8HBKN - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
FE3CWK - 5902	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	NT
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26	NT	NT	18,20	7,9	8,9
	16	11	NT	NT	2	
FYD629 - 5902	GlobalFiler™					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 2 - STR Results

FZ8V8M - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
G83CWJ - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
GJRAXG - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
GXDN2G - 5902	GlobalFiler™- STRMix™ 2.8					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
H3M3JE - 5902	GlobalFiler™- STRMix™ v2.9.1					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
H9BPF7 - 5901	PowerPlex® Fusion 6c					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16	11	17	16		
H9PEFC - 5901	GlobalFiler™					
2	12,17	23,24	14,14	15,16	11,13	
	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 2 - STR Results

HA79H8 - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
HMATHB - 5902	GlobalFiler™- STRMix™ v2.9.1					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
JCRAYE - 5902	GlobalFiler™- STRMix™ v2.8					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
JJP289 - 5901	PowerPlex® Fusion 6C- STRMix™ v2.9					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16	11	17	16		
KFMMYA - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
KKTFQK - 5902	Identifiler® Plus- STRMix™					
		23,24		15,16	11,13	
2	9.3,10	14,16			9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26				7,9	8,9
	16,16					
L6JPQZ - 5901	GlobalFiler™- STRMix™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
Item	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
Item 2 - STR Results						
LBA2Q3 - 5902	GlobalFiler™					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
LRURMG - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
LV8TJ9 - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
MG8BAZ - 5901	GlobalFiler™- STRMix™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
MK7PU6 - 5902	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
NKKENU - 5902	PowerPlex® Fusion 6C- STRMix™ v2.12					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16,16	11	17	16		
NWDUKX - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
	Item 2 - STR Results					
PKJZL9 - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
PWCGDV - 5901	GlobalFiler™- STRMix™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
QCKU6C - 5901	PowerPlex® 21					
	12,17	23,24		15,16	11,13	11,18
2	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					
QKVWQD - 5902	PowerPlex® 21					
	12,17	23,24		15,16	11,13	11,18
2	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					
QLQFTE - 5902	Identifiler® ID+					
		23,24		15,16	11,13	
2	9.3,10	14,16			9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26				7,9	8,9
	16,16					
QY8QPG - 5901	Identifiler® plus- STRMix™ v 2.7					
		23,24		15,16	11,13	
2	9.3,10	14,16			9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26				7,9	8,9
	16,16					
R7WA2W - 5902	GlobalFiler™					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 2 - STR Results

RDVWRB - 5901	PowerPlex® Fusion 6C, FlexPlex 27					
2	12,17	23,24	14	15,16	11,13	11,18
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16	11	17	16		
RUEQHZ - 5901	Identifiler® plus					
2		23,24		15,16	11,13	
	9.3,10	14,16			9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26				7,9	8,9
	16,16					
TFEBVC - 5902	PowerPlex® 21- STRMix™					
2	12,17	23,24		15,16	11,13	11,18
	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					
TGAUWD - 5901	PowerPlex® 21- STRMix™ v 2.10					
2	12,17	23,24		15,16	11,13	11,18
	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					
TKNR4Z - 5902	GlobalFiler™- STRMix™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
TLJA72 - 5901	GlobalFiler™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
UMRJXY - 5902	GlobalFiler™					
2	12,17	23,24	14	15,16	11,13	
	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	

TABLE 3

Item 2 - STR Results

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
V67HG2 - 5901	GlobalFiler™- STRMix™ V 2.8					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
V6A37P - 5901	GlobalFiler™- STRMix™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
VBVWBM - 5901	GlobalFiler™ - EUROFORMIX v4.0.8					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
W648ZP - 5901	GlobalFiler™- STRMix™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
W883G7 - 5902	PowerPlex® 21- STRMix™ 2.10.0					
	12,17	23,24		15,16	11,13	11,18
2	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					
WGU2AX - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	
WP9QBQ - 5901	GlobalFiler™					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16	11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 2 - STR Results

X9G8VV - 5901	GlobalFiler™- STRMix™					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
XNBWN7 - 5901	GlobalFiler™- STRMix™					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	
YMVZW7 - 5901	PowerPlex® 21- STRMix™ V2.8.0					
	12,17	23,24		15,16	11,13	11,18
2	9.3,10	14,16		19,19	9,11	10,13
	13,14	13,14	28,31		X,Y	10,13
	21,26	9,14	7,15		7,9	8,9
	16,16					
YY83H6 - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11,11			2	
ZBZ72N - 5902	PowerPlex® Fusion 6C - DNAxs					
	12,17	23,24	14	15,16	11,13	
2	9.3,10	14,16	13,14	19	9,11	10,13
	13,14	13,14	28,31	16	X,Y	10,13
	21,26	9,14	7,15	18,20	7,9	8,9
	16	11	17	16		
ZY36LY - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,17	23,24	14,14	15,16	11,13	
2	9.3,10	14,16	13,14	19,19	9,11	10,13
	13,14	13,14	28,31	16,16	X,Y	10,13
	21,26			18,20	7,9	8,9
	16,16	11			2	

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 3 - STR Results

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
2U64XP - 5901	PowerPlex® ESX17 Fast- STRMix™ V2.5.11					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16		
		11,12,14,15	13,14,15,16	16,19,22,23		9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	
	20,26			14,15,16	7,9,9.3	
	15,16,17					
2V3DTT - 5901	GlobalFiler™- STRMix™ 2.6.1					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
3DCVDW - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
3GZ6PJ - 5901	GlobalFiler™- STRMix™					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	10,11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	13,14,15	27,28,29,30	14,15,16,17	X	12
	19,20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
3MLWYX - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
4478ZQ - 5901	GlobalFiler™- STRMix™ v 2.6					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
46DPW2 - 5902	Identifiler® Plus- STRMix™					
3		17,19,20,24		14,15,16	11,12	
	8,10,11	11,12,14,15			11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X	12
	20,26				7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
	D1S1656	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
Item	**D7S820**	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	
Item 3 - STR Results						
6CE2VJ - 5901	GlobalFiler™					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
6DBH6U - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
6FWJNN - 5901	GlobalFiler™ - STRMix™ 2.6					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
6GAT2U - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
6H6C3W - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
6UBPYM - 5901	GlobalFiler™ IQC- STRMix™ 2.8.0					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	-
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	-	-	14,15,16	7,9,9.3	9,10,11
	15,16,17	-	-	-	-	
76CCPY - 5901	PowerPlex® 21- STRMix™ 2.8					
	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
3	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3 - STR Results

7G4YWE - 5901	GlobalFiler™ - STRMix™					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	10,11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	13,14,15	27,28,29,30	14,15,16,17	X	11,12
	19,20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
7MMEUW - 5901	GlobalFiler™ - STRMix™ v2.7					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
8FQNHM - 5902	GlobalFiler™ - STRMix™					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
8RZL2G - 5901	GlobalFiler™ - STRMix™					
	12,15,15.3,18.3	17,19,20,24	11,11.3,13,14	14,15,16	10,11,12	
3	8,10,11	11,12,13,14,15	13,14,15,16	16,19,22,23	10,11,12,13	9,12,13,15
	12,14,19,20	13,14,15	27,28,29,30	14,15,16,17	X	11,12
	19,20,25,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
993KMP - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
9X3XVT - 5902	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	9,12,13	7,10,17,23	14,15,16	7,9,9.3	9,10,11
	15,16,17	ND	ND	ND		
AAT7UL - 5901	GlobalFiler™ - STRMix™ V2.8					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3 - STR Results

ABPL7H - 5902	GlobalFiler™- STRMix™					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
AQ3XWQ - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
3	12,15,15.3,18.3		11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	17,19,20,24	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
AWLZ4T - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
AXW3PR - 5901	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	9,12,13	7,10,17,23	14,15,16	7,9,9.3	9,10,11
	15,16,17					
AZ3KNM - 5901	GlobalFiler™- STRMix™ v2.8					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
BH4RFU - 5901	PowerPlex® 21- STRMix™ 2.10					
3	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					
BUGRCN - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3 - STR Results

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
CRMK7G - 5902	GlobalFiler™- STRMix™ v2.9.1					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
CZXMRH - 5902	GlobalFiler™- STRMix™ v2.9.1					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
D2RTLG - 5901	GlobalFiler™- STRMix™ V 2.6					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14**,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17	NR			NR	
DR322B - 5901	GlobalFiler™ - LR Mix v. 2.1.5 C.E.					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
DZWAKF - 5901	GlobalFiler™- STRMix™ v. 2.6					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14**,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	10**,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
E6M7KQ - 5901	PowerPlex® 21- STRMix™					
	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
3	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					
EM2HCG - 5902	GlobalFiler™- STRMix™ 2.8					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 3 - STR Results

ENWXPE - 5901	GlobalFiler™ - DNAxs, ver. 2.8.11					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
EQZU9G - 5902	GlobalFiler™- STRMix™ v2.8					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
ERWAKE - 5901	PowerPlex® ESI-17 - LiRa					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16		
		11,12,14,15	13,14,15,16	16,19,22,23		9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	
	20,26			14,15,16	7,9,9.3	
	15,16,17					
F8HBKN - 5901	GlobalFiler™- STRMix™ 2.7					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
FYD629 - 5902	GlobalFiler™- STRMix™ V 2.5.11					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17	NR			NR	
FZ8V8M - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
G83CWJ - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3 - STR Results

GJRAXG - 5902 GlobalFiler™- TrueAllele® VUler Release 2022b

3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

H3M3JE - 5902 GlobalFiler™- STRMix™ v2.9.1

3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

H9BPF7 - 5901 PowerPlex® Fusion 6c - Euroformix 4.2.5

3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	9,12,13	7,10,17,23	14,15,16	7,9,9.3	9,10,11
	15,16,17					

H9PEFC - 5901 GlobalFiler™- STRMix™ V2.6

3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

HA79H8 - 5901 GlobalFiler™- STRMix™

3	12,14,14.3,15,15.3,17.3,18.3	16,17,18,19,20,23,24	10,11,11.3,13,14	13,14,15,16	10,11,12	
	8,9,10,11	10,11,12,13,14,15	12,13,14,15,16	16,19,21,22,23	10,11,12,13	9,12,13,14,15
	11,12,13,14,18,19,20	13,14,15	26,27,28,29,30	13,14,15,16,17	X	11,12
	19,20,25,26			13,14,15,16	7,8,9,9.3	9,10,11
	14,15,16,17					

HMATHB - 5902 GlobalFiler™- STRMix™ v2.9.1

3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

JJP289 - 5901 PowerPlex® Fusion 6C- STRMix™ v2.9

3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	9,12,13	7,10,17,23	14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
	D1S1656	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
Item	**D7S820**	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	
			Item 3 - STR Results			
KFMMYA - 5901	GlobalFiler™- STRMix™ v. 2.6					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
KKTFQK - 5902	Identifiler® Plus- STRMix™					
		17,19,20,24		14,15,16	11,12	
3	8,10,11	11,12,14,15			11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X	12
	20,26				7,9,9.3	9,10,11
	15,16,17					
L6JPQZ - 5901	GlobalFiler™- STRMix™					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	10,11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	10,11,12,13	9,12,13,15
	12,14,19,20	13,14,15	27,28,29,30	14,15,16,17	X	11,12
	19,20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
LBA2Q3 - 5902	GlobalFiler™- STRMix™ v2.5.11					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17	NR			NR	
LRURMG - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
LV8TJ9 - 5901	GlobalFiler™- STRMix™ v. 2.6.1					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
MG8BAZ - 5901	GlobalFiler™- STRMix™					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	
Item 3 - STR Results						
MK7PU6 - 5902	GlobalFiler™- STRMix™ 2.8					
	11,12,14,14.3,15,15.3,17.3,18.3	16,17,18,19,20,23,24	10,10.3,11,11.3,13,14	13,14,15,16	10,11,12	
3	7,8,9,10,11	10,11,12,13,14,15	13,14,15,16	15,16,18,19,21,22,23	10,11,12,13	9,11,12,13,14,15
	12,13,14,18,19,20	13,14,15	26,27,28,29,30	13,14,15,16,17,18	X	11,12
	19,20,25,26			13,13.2,14,14.2,15,15.2,16	6,7,8,8.3,9,9.3	9,10,11
	14,15,16,17					
NKKENU - 5902	PowerPlex® Fusion 6C- STRMix™ v2.12					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	9,12,13	7,10,17,23	14,15,16	7,9,9.3	9,10,11
	15,16,17					
NWDUKX - 5901	GlobalFiler™- STRMix™					
	12,15,15.3,17.3,18.3	17,19,20,23,24	11,11.3,13,14	13,14,15,16	10,11,12	
3	8,9,10,11	10,11,12,13,14,15	12,13,14,15,16	16,19,22,23	10,11,12,13	9,11,12,13,14,15
	12,14,18,19,20	13,14,15	27,28,29,30	14,15,16,17	X	11,12
	19,20,25,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
PKJZL9 - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
PWCGDV - 5901	GlobalFiler™- STRMix™					
	12,14.3,15,15.3,17.3,18.3	17,18,19,20,23,24	10,11,11.3,13,14	13,14,15,16	10,11,12	
3	8,10,11	10,11,12,13,14,15	12,13,14,15,16	16,19,21,22,23	10,11,12,13	9,11,12,13,15
	12,14,18,19,20	13,14,15	26,27,28,29,30	14,15,16,17	X	11,12
	19,20,25,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
QCKU6C - 5901	PowerPlex® 21- STRMix™ V2.8					
	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
3	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X	12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3 - STR Results

QKVWQD - 5902	PowerPlex® 21- STRMix™ v 2.10.0					
	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
3	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12,12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					
QLQFTE - 5902	Identifiler®					
		17,19,20,24		14,15,16	11,12	
3	8,10,11	11,12,14,15			11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X	12
	20,26				7,9,9.3	9,10,11
	15,16,17					
QY8QPG - 5901	Identifiler® plus- STRMix™ v 2.7					
		17,19,20,23*,24		14,15,16	10*,11,12	
3	8,10,11	10*,11,12,13*,14,15			10*,11,12,13	9,11*,12,13,14*,15
	12,14,18*,19,20	13*,14,15	27,28,29,30		X	11*,12
	19*,20,26				7,9,9.3	9,10,11
	15,16,17					
R7WA2W - 5902	GlobalFiler™- STRMix™ v2.5.11					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17	NR			NR	
RDVWRB - 5901	PowerPlex® Fusion 6C- STRMix™ 2.6.2					
	12,(15),15.3,18.3	17,19,20,24	(11),11.3,14	(14),15,16	11,(12)	
3	8,10,11	11,(12),14,15	13,14,15,16	16,19,22,23	11,(12),(13)	9,12,13,(15)
	(12),(14),19,20	14,15	27,28,29,30	14,15,16,(17)	X	12
	20,(26)	(9),12,13	7,10,(17),(23)	14,15,16	7,9,9.3	9,(10),11
	(15),16,17	NID	NID	NID		
RUEQHZ - 5901	Identifiler® plus - EuroFormix					
		17,19,20,24		14,15,16	11,12	
3	8,10,11	11,12,14,15			11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X	12
	20,26				7,9,9.3	9,10,11
	15,16,17					
TFEBVC - 5902	PowerPlex® 21- STRMix™					
	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
3	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12,12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3 - STR Results

TGAUWD - 5901	PowerPlex® 21- STRMix™ v 2.10					
	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
3	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12,12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					
TKNR4Z - 5902	GlobalFiler™- STRMix™					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
TLJA72 - 5901	GlobalFiler™- STRMix™ v. 2.6					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
UMRJXY - 5902	GlobalFiler™- STRMix™ 2.8					
	11,12,14,14.3,15,15.3,17.3,18.3	16,17,18,19,20,23,24	10,10.3,11,11.3,13,14	13,14,15,16	10,11,12	
3	7,8,9,10,11	10,11,12,13,14,15	13,14,15,16	15,16,19,21,22,23	10,11,12,13	9,11,12,13,14,15
	12,14,18,19,20	13,14,15	26,27,28,29,30	13,14,15,16,17,18	X	11,12
	19,20,21,25,26			13,13.2,14,14.2,15,15.2,16	6,7,8,9,9.3	9,10,11
	14,15,16,17					
V6A37P - 5901	GlobalFiler™- STRMix™					
	12,15,15.3,17.3,18.3	17,19,20,23,24	10,11,11.3,13,14	14,15,16	10,11,12	
3	8,10,11	10,11,12,13,14,15	13,14,15,16	16,19,22,23	10,11,12,13	9,12,13,15
	12,14,18,19,20	13,14,15	27,28,29,30	14,15,16,17	X	11,12
	19,20,25,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
VBVWBM - 5901	GlobalFiler™ - EUROFORMIX v4.0.8					
	12,[15],15.3,18.3	[17],19,20,24	[11],11.3,14	[14],15,[16]	11,[12]	
3	8,10,11	11,12,14,[15]	[13],14,15,16	16,19,[22],23	11,[12],[13]	[9],12,13,15
	[12],[14],19,20	14,15	27,28,29,30	14,15,16,[17]	X	12
	20,[26]			[14],15,16	7,9,9.3	9,10,11
	[15],16,17	-			-	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3 - STR Results

W648ZP - 5901	GlobalFiler™- STRMix™					
3	12,15,15.3,17.3,18.3	17,19,20,23,24	11,11.3,14	14,15,16	10,11,12	
	8,10,11	10,11,12,13,14,15	13,14,15,16	16,19,22,23	10,11,12,13	9,12,13,15
	12,14,18,19,20	13,14,15	27,28,29,30	14,15,16,17	X	11,12
	19,20,25,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
W883G7 - 5902	PowerPlex® 21- STRMix™ 2.10.0					
3	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12,12
		9,12,13	7,10,17,23	20,26	7,9,9.3	9,10,11
	15,16,17					
WGU2AX - 5901	GlobalFiler™- STRMix™ v. 2.6					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,14**,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
WP9QBQ - 5901	GlobalFiler™- STRMix™					
3	12,14,15,15.3,17.3,18.3	17,19,20,23,24	11,11.3,13,14	14,15,16	10,11,12	
	8,10,11	10,11,12,13,14,15	13,14,15,16	16,19,22,23	10,11,12,13	9,11,12,13,14,15
	12,14,18,19,20	13,14,15	27,28,29,30	14,15,16,17	X	11,12
	19,20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
X9G8VV - 5901	GlobalFiler™- STRMix™					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
XNBWN7 - 5901	GlobalFiler™- STRMix™					
3	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
YMVZW7 - 5901	PowerPlex® 21- STRMix™ v2.8.0					
3	12,15,15.3,18.3	17,19,20,24		14,15,16	11,12	11,12,13,17
	8,10,11	11,12,14,15		16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30		X,X	12
	20,26	9,12,13	7,10,17,23		7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 3 - STR Results

YY83H6 - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					
ZBZ72N - 5902	PowerPlex® Fusion 6C - DNAxs					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	9,12,13	7,10,17,23	14,15,16	7,9,9.3	9,10,11
	15,16,17					
ZY36LY - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
3	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12,12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 3e - STR Results

3P6C3X - 5902 GlobalFiler™ - STRMix™ 2.8.0

3e	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	NT
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	NT	NT	14,15,16	7,9,9.3	9,10,11
	15,16,17	NR	NT	NT	NR	

FE3CWK - 5902 GlobalFiler™ - STRMix™ Version 2.8.0

3e	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	NT
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26	NT	NT	14,15,16	7,9,9.3	9,10,11
	15,16,17	NR	NT	NT	NR	

GXDN2G - 5902 GlobalFiler™ - STRMix™ 2.8

3e	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

JCRAYE - 5902 GlobalFiler™ - STRMix™ v2.8

3e	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

V67HG2 - 5901 GlobalFiler™ - STRMix™ V 2.8

3e	12,15,15.3,18.3	17,19,20,24	11,11.3,14	14,15,16	11,12	
	8,10,11	11,12,14,15	13,14,15,16	16,19,22,23	11,12,13	9,12,13,15
	12,14,19,20	14,15	27,28,29,30	14,15,16,17	X,X	12
	20,26			14,15,16	7,9,9.3	9,10,11
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
	D1S1656	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
Item	**D7S820**	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 3sp - STR Results

3P6C3X - 5902	GlobalFiler™- STRMix™ 2.8.0					
	15,18.3	19,20,24	11,11.3,14	14,15,16	11,12	NT
3sp	8,10,11	11,14	14,16	16,22,23	11,12	9,12,15
	14,19,20	14,15	27,30	17	X	12
	20	NT	NT	14,15,16	7,9,9.3	9,10,11
	15,16,17	NR	NT	NT	NR	

FE3CWK - 5902	GlobalFiler™- STRMix™ Version 2.8.0					
	12,15.3,18.3	17,19,20,24	11,11.3,14	15,16	11	NT
3sp	8,11	11,12,13,14,15	14,15	16,19,22,23	12	12
	12,14,20	14,15	28,30	14,15,16	X	12
	20	NT	NT	15,16	7,9,9.3	9,10,11
	15,17	NR	NT	NT	NR	

GXDN2G - 5902	GlobalFiler™- STRMix™ 2.8					
3sp						

JCRAYE - 5902	GlobalFiler™- STRMix™ v2.8					
	15.3	17,20,24	11.3,14	14,15,16	11	
3sp	8,10,11	11,14,15	14,15,16	16,23	11,13	9,12,13
	12,14,19,20	14,15	28,29,30	14,15,16,17	X	12
	20			16	7,9.3	11
	16,17					

V67HG2 - 5901	GlobalFiler™- STRMix™ V 2.8					
3sp						

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4 - STR Results

2U64XP - 5901 PowerPlex® ESX17 Fast- STRMix™ V2.5.11

4	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17		
		11,12,14,15	13,14,15,16	16,18,19,20,23		11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	
	16,17,19,20					

DR322B - 5901 GlobalFiler™ - LR Mix ver. 2.1.5 C.E.

4	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

FYD629 - 5902 GlobalFiler™- STRMix™ V 2.5.11

4	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

H9BPF7 - 5901 PowerPlex® Fusion 6c - Euroformix 4.2.5

4	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19	15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	17,19	17,20		

LBA2Q3 - 5902 GlobalFiler™- STRMix™ v2.5.11

4	15.3,16,17.3,18.3	16,17,19,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

MG8BAZ - 5901 GlobalFiler™- STRMix™

4	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4 - STR Results

R7WA2W - 5902 GlobalFiler™- STRMix™ v2.5.11

	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4	8,9,10,11,12	11,12,14,15	13,14,15,16	18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

2V3DTT - 5901	GlobalFiler™- STRMix™ 2.6.1					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	9,11
	16,17,19	10			1,2	
3DCVDW - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
3GZ6PJ - 5901	GlobalFiler™- STRMix™					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	14,15,16,17	9,10,11,12	
	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	16,18,20,23	8,10,11,12	11,12,13
	14,16,18,19,20	13,14,15,16.2	27,30,31,31.2	14,15,16	X,Y	10,11,12
	19,20,21,22,25,26			14,15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	15,16,17,19	10			2	
3MLWYX - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
3P6C3X - 5902	GlobalFiler™- STRMix™ 2.8.0					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	NT
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26	NT	NT	15,16,23.2,24.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	NT	NT	1,2	
4478ZQ - 5901	GlobalFiler™- STRMix™ v 2.6					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,20	10			1,2	

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

46DPW2 - 5902	Identifiler® Plus- STRMix™					
		17,20,24		15,16,17	11	
4e	9,10,11,12	11,12,14,15			8,11,12	11,12,13
	14,19,20	13,14,15	27,30,31.2		X,Y	10,12
	20				9,9.3	9,11
	16,17,19					
6CE2VJ - 5901	GlobalFiler™					
	15.3,16,17.3,18.3	17,19,20,24	11,11.3,14	15,16,17	9,11	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
6DBH6U - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
4e	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,12
	20,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
6FWJNN - 5901	GlobalFiler™- STRMix™ 2.6					
	15.3,17.3,18.3	16,17,19,20,24	10,11,11.3,14	15,16,17	11,12	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15	27,30,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,26.2	7,9,9.3	8,9,11
	16,17	10			1,2	
6GAT2U - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
6H6C3W - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,12
	20,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

6UBPYM - 5901	GlobalFiler™ IQC- STRMix™ 2.8.0					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	-
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,15.2,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26	-	-	15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	-	-	1,2	
76CCPY - 5901	PowerPlex® 21- STRMix™ 2.8					
4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,20,23	8,10,11,12,13	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					
7G4YWE - 5901	GlobalFiler™- STRMix™					
4e	14.3,15.3,16,16.3,17.3,18.3	16,17,19,20,23,24	10,11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	15,16,17,18,19,20,22,23	8,9,10,11,12	10,11,12,13
	13,14,15,16,18,19,20,21	12,13,14,15,16.2	26,27,29,30,31,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,24,25,26			14,15,16,22.2,23.2,24.2,25.2,26.2	7,8,9,9.3	8,9,10,11
	15,16,17,19,20	10			1,2	
7MMEUW - 5901	GlobalFiler™- STRMix™ v2.7					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31.2	15,16	X,Y	10,11,12
	20,21,22,23,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
8FQNHM - 5902	GlobalFiler™- STRMix™					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
8RZL2G - 5901	GlobalFiler™- STRMix™					
4e	14.3,15.3,16,17.3,18.3	16,17,19,20,23,24	11,11.3,13,14	14,15,16,17	9,10,11,12	
	9,10,11,12	10,11,12,13,14,15	13,14,15,16	16,18,19,20,22,23	8,10,11,12	11,12,13
	14,16,18,19,20,21	13,14,15,16.2	27,29,30,31,31.2	14,15,16	X,Y	10,11,12
	19,20,21,22,24,25,26			14,15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	15,16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4e - STR Results

993KMP - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
4e	15.3,16,17.3,18.3	17,19,20,24	11,11.3,14	15,16,17	9,11	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,12
	20,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
9X3XVT - 5902	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
4e	NT	NT	NT	NT	NT	
	NT	NT	NT	NT	NT	NT
	NT	NT	NT	NT	NT	NT
	NT	NT	NT	NT	NT	NT
	NT	NT	NT	NT		
AAT7UL - 5901	GlobalFiler™- STRMix™ V2.8					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
ABPL7H - 5902	GlobalFiler™- STRMix™					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
AQ3XWQ - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
AWLZ4T - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

AXW3PR - 5901	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
4e		17,20,24		15,16	11	
				16,20,23		11,12,13
	14,19,20	14,15		15,16	X	12
	20,21,22,25				9	
	16,17	10				
AZ3KNM - 5901	GlobalFiler™- STRMix™ v2.8					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
BH4RFU - 5901	PowerPlex® 21- STRMix™ 2.10					
4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					
BUGRCN - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
4e	15.3,16,17.3,18.3	17,19,20,24	11,11.3,14	15,16,17	9,11	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20	13,14,15,16.2	27,30,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
CRMK7G - 5902	GlobalFiler™- STRMix™ v2.9.1					
4e	15.3,17.3,18.3	16,17,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31.2	15,16	X,Y	10,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,20	10			1,2	
CZXMRH - 5902	GlobalFiler™- STRMix™ v2.9.1					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4e - STR Results

D2RTLG - 5901 GlobalFiler™- STRMix™ v 2.6

4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

DZWAKF - 5901 GlobalFiler™- STRMix™ v. 2.6

4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	9,9.3	8,9,11
	16,17,19,20	10			1,2	

E6M7KQ - 5901 PowerPlex® 21- STRMix™

4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,20,23	8,10,11,12	11,12,13,15
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					

EM2HCG - 5902 GlobalFiler™- STRMix™ 2.8

4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

ENWXPE - 5901 GlobalFiler™ - DNAxs, ver. 2.8.11

4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10				

EQZU9G - 5902 GlobalFiler™- STRMix™ v2.8

4e	16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4e - STR Results

ERWAKE - 5901	PowerPlex® ESI-17 - LiRa					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17		
4e		11,12,14,15	13,14,15,16	16,18,19,20,23		11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	
	16,17,19,20					
F8HBKN - 5901	GlobalFiler™ - STRMix™ 2.7					
	15.3,17.3,18.3	16,17,20,24	11,11.3,14	15,16,17	9,11	
4e	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31.2	15,16	X,Y	10,11,12
	20,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
FE3CWK - 5902	GlobalFiler™ - STRMix™ Version 2.8.0					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	NT
4e	9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2,32.2	15,16	X,Y	10,11,12
	20,22,25,26	NT	NT	15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	NT	NT	1,2	
FZ8V8M - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
G83CWJ - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
GJRAXG - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,12
	20,22,25,26			15,16,23.2,24.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4e - STR Results

GXDN2G - 5902	GlobalFiler™ - STRMix™ 2.8					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
H3M3JE - 5902	GlobalFiler™ - STRMix™ v2.9.1					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,22,25,26			15,16,23.2,24.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			2	
H9PEFC - 5901	GlobalFiler™ - STRMix™ V2.6					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
HA79H8 - 5901	GlobalFiler™ - STRMix™					
4e	14.3,15.3,16,16.3,17.3,18.3	16,17,19,20,23,24	10,11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	15,16,17,18,19,20,22,23	8,9,10,11,12	10,11,12,13
	14,16,18,19,20,21	12,13,14,15,16.2	26,27,29,30,31,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,24,25,26			14,15,16,22.2,23.2,24.2,25.2,26.2	7,8,9,9.3	8,9,10,11
	15,16,17,19,20	10			1,2	
HMATHB - 5902	GlobalFiler™ - STRMix™ v2.9.1					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15	27,30,31,31.2	15,16	X,Y	10,11,12
	20,22,25,26			15,16,23.2,24.2,25.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
JCRAYE - 5902	GlobalFiler™ - STRMix™ v2.8					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

JJP289 - 5901	PowerPlex® Fusion 6C- STRMix™ v2.9					
	15.3,16,17.3,18.3	16,17,20,24	11,11.3,14	15,16,17	9,11	
4e	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18	15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	17,19	17,20		
KFMMYA - 5901	GlobalFiler™- STRMix™ v. 2.6					
	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19	10			1,2	
KKTFQK - 5902	Identifiler® Plus- STRMix™					
		17,19,20,24		15,16,17	11	
4e	9,10,11,12	11,12,14,15			8,10,11,12	11,12,13
	14,19,20	13,14,15	27,30,31.2		X,Y	10,12
	20,22				9,9.3	9,11
	16,17					
L6JPQZ - 5901	GlobalFiler™- STRMix™					
	15.3,16,17.3,18.3	16,17,19,20,23,24	10,11,11.3,13,14,15	14,15,16,17	10,11	
4e	8,9,10,11,12	10,11,12,14,15	13,14,15,16	16,18,19,23	8,10,11,12	11,12,13
	14,16,19,20	12,13,14,15,16.2	27,29,30,31,31.2	15,16	X,Y	10,11,12
	19,20,21,22,24,25,26			15,16,23.2,24.2,25.2,26.2	7,8,9,9.3	8,9,11
	16,17	10			2	
LRURMG - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
LV8TJ9 - 5901	GlobalFiler™- STRMix™ v. 2.6.1					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
4e	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,** 21,22,25,26			15,16,23.2,24.2,25.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4e - STR Results

MK7PU6 - 5902	GlobalFiler™- STRMix™ 2.8					
	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	10,11,12	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,23	8,10,11,12	11,12,13
	16,19,20	13,14,15	27,30	15,16	X,Y	11,12
	20,22,25			15,16,23.2,24.2	7,9,9.3	8,9,11
	16,17	10				
NKKENU - 5902	PowerPlex® Fusion 6C- STRMix™ v2.12					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19	15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	17,19	17,20		
NWDUKX - 5901	GlobalFiler™- STRMix™					
	14.3,15.3,16,16.3,17.3,18.3	16,17,19,20,23,24	11,11.3,13,14	14,15,16,17	10,11,12	
4e	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	15,16,17,18,19,20,22,23	8,10,11,12	10,11,12,13
	14,15,16,18,19,20,21	13,14,15,16.2	26,27,29,30,31,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,25,26			14,15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,10,11
	15,16,17,20	10			2	
PKJZL9 - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4e	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
PWCGDV - 5901	GlobalFiler™- STRMix™					
	14.3,15.3,16,16.3,17.3,18.3	16,17,19,20,23,24	10,11,11.3,13,14	14,15,16,17	9,10,11,12	
4e	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	15,16,17,18,19,20,22,23	8,9,10,11,12	10,11,12,13
	14,16,18,19,20,21	13,14,15,16.2	26,27,29,30,31,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,25,26			14,15,16,22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,9,10,11
	15,16,17,19	10			1,2	
QCKU6C - 5901	PowerPlex® 21- STRMix™ V2.8					
	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	11,12	11,12,17,18
4e	8,9,10,11,12	11,12,14,15		16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18		7,9,9.3	8,9,11
	16,17,19,20					

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

QKVWQD - 5902	PowerPlex® 21- STRMix™ v 2.10.0					
4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	9,11	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15		7,9,9.3	8,9,11
	16,17,19,20					
QLQFTE - 5902	Identifiler® ID+- STRMix™					
4e		17,20,24		15,16,17	11	
	8,9,10,11,12	11,12,14,15			10,11,12	11,12,13
	14,16,19,20	13,14,15	27,30,31.2		X	10,11,12
	20				7,9,9.3	8,9,11
	16,17,19					
QY8QPG - 5901	Identifiler® plus- STRMix™ v 2.7					
4e		16,17,19,20,24		14,15,16,17	11	
	9,10,11,12	11,12,14,15			10,11,12	11,12,13
	14,16,19,20	13,14,15	27,29,30,31,31.2		X,Y	10,11,12
	20,21,22,25				7,9,9.3	8,9,11
	16,17					
RDVWRB - 5901	PowerPlex® Fusion 6C- STRMix™ 2.6.2					
4e	15.3,(16),17.3,18.3	(16),17,(19),20,24	(11),11.3,14	15,16,(17)	(9),11,(12)	
	(8),9,10,11,(12)	11,(12),14,(15)	(13),14,(15),16	16,18,(19),(20),23	(8),(10),11,(12)	11,12,13
	(14),(16),19,20,(21)	(13),14,15,(16.2)	27,30,(31),(31.2)	15,16	X,(Y)	(10),(11),12
	20,(21),(22),(25),(26)	(9),12,13	7,10,(12),(15),(18),(19)	15,16,(23.2),(24.2),(25.2),(26.2)	(7),9,9.3	(8),9,11
	16,17,(19),(20)	10	17,(19)	17,(20)		
RUEQHZ - 5901	Identifiler® plus - EuroFormix					
4e		17,19,20,24		15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15			8,10,11,12	11,12,13
	14,16,19,20	13,14,15,16.2	27,30,31.2		X,Y	10,11,12
	20,21,22,25,26				7,9,9.3	8,9,11
	16,17,19,20					
TFEBVC - 5902	PowerPlex® 21- STRMix™					
4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					
TGAUWD - 5901	PowerPlex® 21- STRMix™ v 2.10					
4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	11,11	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15	27,30,31,31.2		X,Y	10,11,12
	20,22,25,26	9,12,13	7,10,12,15		7,9,9.3	8,9,11
	16,17,19					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
TKNR4Z - 5902	GlobalFiler™- STRMix™					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,22,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
TLJA72 - 5901	GlobalFiler™- STRMix™ v. 2.6					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,26.2	7,9,9.3	8,9,11
	16,17	10			1,2	
UMRJXY - 5902	GlobalFiler™- STRMix™ 2.8					
4e	14.3,15.1,15.3,16,16.3,17.3,18.3	16,17,19,20,23,24	10,10.3,11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	15,16,17,18,19,20,22,23	8,10,11,12	10,11,12,13
	14,16,18,19,20,21	12,13,14,15,16.2	26,27,29,30,31,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,24,25,26			14,14.2,15,15.2,16,23.2,24.2,25.2,26.2	7,8,8.3,9,9.3	8,9,10,11
	15,16,17,19,20	10			1,2	
V67HG2 - 5901	GlobalFiler™- STRMix™ V 2.8					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15,16	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
V6A37P - 5901	GlobalFiler™- STRMix™					
4e	14.3,15.3,16,17.3,18.3	16,17,19,20,24	10,11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	16,18,19,20,22,23	8,10,11,12	10,11,12,13
	14,16,18,19,20,21	13,14,15,16.2	27,29,30,31,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,25,26			14,15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	15,16,17,20	10			1,2	
VBVWBM - 5901	GlobalFiler™ - EUROFORMIX v4.0.8					
4e	15.3,[16],[17.3],18.3	[16],17,[19],20,24	[11],11.3,14	15,16,[17]	[9],11,[12]	
	[9],10,11,[12]	11,[12],14,[15]	[13],14,[15],16	16,[18],[19],[22],23	[8],[10],11,[12]	[11],12,13
	[13],[14],[16],19,20	[13],14,15	27,30,[31],[31.2]	15,16	X,[Y]	[10],[11],12
	20,22,[25],[26]			15,[15.2],16,[23.2],[24.2]	9,9.3	[8],9,11
	16,17,[19]	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4e - STR Results

W648ZP - 5901	GlobalFiler™ - STRMix™					
4e	15.3,16,17.3,18.3	16,17,19,20,23,24	11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	16,18,19,22,23	10,11,12	11,12,13
	13,14,16,18,19,20,21	12,13,14,15,16.2	27,29,30,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,25,26			14,15,16,22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	15,16,17,19	10			1,2	
W883G7 - 5902	PowerPlex® 21 - STRMix™ 2.10.0					
4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	9,11	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31.2		X,Y	10,11,12
	20,22,25,26	9,12,13	7,10,12,15,19		7,9,9.3	8,9,11
	16,17,19,20					
WGU2AX - 5901	GlobalFiler™ - STRMix™ v. 2.6					
4e	15.3,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	14,15,16	16,18,19,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,26.2	7,9,9.3	8,9,11
	16,17,19	10			1,2	
WP9QBQ - 5901	GlobalFiler™ - STRMix™					
4e	14.3,15.3,16,16.3,17.3,18.3	16,17,19,20,23,24	11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,10,11,12	10,11,12,13,14,15	13,14,15,16	16,17,18,19,20,22,23	8,10,11,12	11,12,13
	14,16,18,19,20,21	13,14,15,16.2	26,27,29,30,31,31.2	14,15,16,17	X,Y	10,11,12
	19,20,21,22,25,26			14,15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	15,16,17,19,20	10			1,2	
X9G8VV - 5901	GlobalFiler™ - STRMix™					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
XNBWN7 - 5901	GlobalFiler™ - STRMix™					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,26.2	9,9.3	8,11
	16,17,19	10			1,2	

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4e - STR Results

YMVZW7 - 5901	PowerPlex® 21- STRMix™ v2.8.0					
4e	15.3,16,17.3,18.3	16,17,19,20,24		15,16,17	9,11	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20	13,14,15,16.2	27,30,30.2,31,31.2		X,Y	10,11,12
	20,22,25,26	9,12,13	7,10,12,14,15,16,18,19		7,9,9.3	8,9,11
	16,17,19,20					
YY83H6 - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10,10			1,2	
ZBZ72N - 5902	PowerPlex® Fusion 6C - DNAxs					
4e	15.3,16,17.3,18.3	[16],[17],[19],20,24	[11],11.3,14	15,16,[17]	[9],11,[12]	
	[8],[9],10,11,[12]	11,[12],14,[15]	14,[15],16	16,[18],[19],[20],23	[8],[10],11,[12]	11,12,13
	[14],[16],19,20,[21]	[13],14,15,[16.2]	27,30,[31],[31.2]	15,16	X,[Y]	[10],[11],12
	20,[21],[22],[25],[26]	[9],12,13	7,10,[12],[15],[18],[19]	15,16,[23.2],[24.2],[25.2],[26.2]	[7],9,9.3	[8],9,11
	16,17,[19],[20]	[10]	[17],[19]	[17],[20]		
ZY36LY - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
4e	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4sp - STR Results

2V3DTT - 5901	GlobalFiler™- STRMix™ 2.6.1					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
3DCVDW - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	16,17.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,10,12	12,14,15	13,14,15	18,19,20,23	8,10,12	11,13
	14,16,19,20,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
3GZ6PJ - 5901	GlobalFiler™- STRMix™					
	15,16,16.3,17.3	16,17,19	10,11,11.3,14	15,16,17	9,10,11,12	
4sp	8,9,11,12	11,12,13,14,15	13,14,15	17,18,19,20	8,9,10,11,12	10,11
	13,14,16,20,21	12,13,14,15.2,16.2	29,30,31,31.2	15,16	X,Y	10,11,12
	21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,10,11
	16,17,19,20	10			1,2	
3MLWYX - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
4sp						
3P6C3X - 5902	GlobalFiler™- STRMix™ 2.8.0					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	NT
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26	NT	NT	23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10	NT	NT	1,2	
4478ZQ - 5901	GlobalFiler™- STRMix™ v 2.6					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,15.2,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,8**,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

Item 4sp - STR Results

WebCode - Test	Item	Amplification Kits - Probabilistic Genotyping Software					
	Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
		D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
		D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
		FGA	Penta D	Penta E	SE33	TH01	TPOX
		vWA	DYS391	DYS570	DYS576	Y Indel	
46DPW2 - 5902		Identifiler® Plus- STRMix™					
	4sp		16,17,19		15,16,17	9,11,12	
		8,9,12	12,14,15			8,10,12	11
		14,16,20,21	13,14,16.2	30,31,31.2		X,Y	10,11,12
		21,22,25,26				7,9,9.3	8,11
		16,17,19,20					
6CE2VJ - 5901		GlobalFiler™					
	4sp	16,17.3	17,19	11,11.3,14	15,16,17	9,11	
		8,9,12	12,14,15	13,14,15	18,20	8,10,12	11
		14,16,21	13,14,16.2	30,31,31.2	16	X,Y	10,11,12
		21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
		16,17,19,20	10			1,2	
6DBH6U - 5902		GlobalFiler™- TrueAllele® VUIer Release 2022b					
	4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
		8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
		14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
		21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
		16,17,19,20	10			1,2	
6FWJNN - 5901		GlobalFiler™- STRMix™ 2.6					
	4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
		8,9,12	12,14,15	13,14,15	18,19,20	8,10,12,13	11
		14,16,21	13,14,16.2	30,31,31.2,32.2**	15,16	X,Y	10,11,12
		21,22,24,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
		16,17,19,20	10			1,2	
6GAT2U - 5902		GlobalFiler™- TrueAllele® VUIer Release 2022b					
	4sp	15.3,16,17.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
		8,9,11,12	12,14,15	13,14,15	16,18,19,20,23	8,10,12	11,13
		14,16,19,20,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
		20,21,22,25,26			15,23.2,24.2,25.2,26.2	7,9,9.3	8,11
		16,17,19,20	10			1,2	
6H6C3W - 5902		GlobalFiler™- TrueAllele® VUIer Release 2022b					
	4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
		8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11,11
		14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
		21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
		16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4sp - STR Results

6UBPYM - 5901	GlobalFiler™ IQC- STRMix™ 2.8.0					
4sp	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	-
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,15.2,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26	-	-	15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	-	-	1,2	
76CCPY - 5901	PowerPlex® 21- STRMix™ 2.8					
4sp	16,17.3,18.3	16,17,19		15,16,17	9,11,12	11,12,17,18
	8,9,11,12	11,12,14,15		16,18,19,20	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					
7G4YWE - 5901	GlobalFiler™- STRMix™					
4sp	15,16,16.3,17.3	16,17,19	10,11,11.3,14	14,15,16,17	9,10,11,12	
	8,9,12	11,12,14,15	13,14,15	17,18,19,20	8,10,12	10,11
	14,16,21	12,13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,24,25,26			16,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
7MMEUW - 5901	GlobalFiler™- STRMix™ v2.7					
4sp	16,17.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,11,12,13	12,14,15	13,14,15	18,19,20,23	8,10,11,12	11
	14,16,20,21	13,14,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
8FQNHM - 5902	GlobalFiler™- STRMix™					
4sp	15.3,16,17.3,18.3	16,17,19,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
8RZL2G - 5901	GlobalFiler™- STRMix™					
4sp	15,16,16.3,17.3	16,17,19	10,11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,12	11,12,13,14,15	13,14,15	17,18,19,20	8,9,10,11,12	10,11
	13,14,15,16,20,21	12,13,14,16.2	29,30,31,31.2	15,16,17	X,Y	10,11,12
	20,21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4sp - STR Results

993KMP - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

4sp	16,17.3	16,17,19,24	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

9X3XVT - 5902 PowerPlex® Fusion 6C- STRMix™ V2.5.11

4sp	15,15.3,16,16.3,17.3,18.3	15,16,17,18,19,20,24	10,11,11.3,13,14	14,15,16,17	8,9,10,11,12	
	8,9,10,11,12	11,12,13,14,15	12,13,14,15,16	16,17,18,19,20,23	8,9,10,11,12	10,11,12,13
	13,14,15,16,19,20,21	12,13,14,15,15.2,16.2	27,29,30,30.2,31,31.2	14,15,16,17	X,Y	9,10,11,12
	20,21,22,24,25,26	8,9,12,13	7,10,12,14,15,17,18,19	15,16,23.2,24.2,25,25.2,26.2	7,8,9,9.3	8,9,10,11
	15,16,17,18,19,20	10	17,19	17,20		

AAT7UL - 5901 GlobalFiler™- STRMix™ V2.8

4sp	16,17.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,19,20,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

ABPL7H - 5902 GlobalFiler™- STRMix™

4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

AQ3XWQ - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

4sp	16,17.3,18.3	16,17,19,20	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

AWLZ4T - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

4sp	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4sp - STR Results

AXW3PR - 5901	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
4sp	16,17.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15	16,18,19,20	8,10,11,12	11,12,13
	14,16,19,20,21,22	13,14,15,15.2,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26	9,12,13	12,15,18,19	15,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10	17,19	17,20		
AZ3KNM - 5901	GlobalFiler™- STRMix™ v2.8					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
BH4RFU - 5901	PowerPlex® 21- STRMix™ 2.10					
4sp	16,17.3	16,17,19		15,16,17	9,11,12	11,12,18
	8,9,12	12,14,15		18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2		X,Y	10,11,12
	21,22,25,26	9,12	12,15,18,19		7,9,9.3	8,11
	16,17,19,20					
BUGRCN - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11,11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
CRMK7G - 5902	GlobalFiler™- STRMix™ v2.9.1					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
CZXMRH - 5902	GlobalFiler™- STRMix™ v2.9.1					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4sp - STR Results

D2RTLG - 5901	GlobalFiler™ - STRMix™ v 2.6					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,13**,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
DZWAKF - 5901	GlobalFiler™ - STRMix™ v. 2.6					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,10**,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
E6M7KQ - 5901	PowerPlex® 21 - STRMix™					
	16,17.3	16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
4sp	8,9,10,12	12,14,15		18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					
EM2HCG - 5902	GlobalFiler™ - STRMix™ 2.8					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,10,12	11,12,14,15	13,14,15	16,18,19,20	8,10,12	11
	14,16,19,20,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
ENWXPE - 5901	GlobalFiler™ - DNAxs, ver. 2.8.11					
	[15.3],[16],17.3,[18.3]	[16],17,[18],[19],[24]	11,[11.3],14	15,[16],17	[9],11,[12]	
4sp	[8],9,[10],[11],12	12,[14],15,[16]	[13],14,15	[16],18,[19],[20]	[8],10,[11],12	11,[12],[13]
	14,16,[19],[20],[21]	13,14,[15],[15.2],[16.2]	[27],30,[31],31.2	[15],16	X,Y	10,11,[12]
	[20],[21],22,25,[26]			[15],[16],23.2,24.2,[25.2],[26.2]	[7],9,9.3	[8],[9],11
	16,17,[19],[20]	10				
EQZU9G - 5902	GlobalFiler™ - STRMix™ v2.8					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4sp - STR Results

ERWAKE - 5901	PowerPlex® ESI-17 - LiRa					
	16,17.3	16,17,19	11,11.3,14	15,16,17		
4sp		12,14,15	13,14,15	18,19,20		11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	
	16,17,19,20					
F8HBKN - 5901	GlobalFiler™- STRMix™ 2.7					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,11,12	12,14,15	13,14,15	16,18,19,20	8,10,11,12	11
	14,16,19,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
FE3CWK - 5902	GlobalFiler™- STRMix™ Version 2.8.0					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	NT
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26	NT	NT	23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10	NT	NT	1,2	
FZ8V8M - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
G83CWJ - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11,11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
GJRAXG - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11,11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4sp - STR Results

GXDN2G - 5902	GlobalFiler™- STRMix™ 2.8					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
H3M3JE - 5902	GlobalFiler™- STRMix™ v2.9.1					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
H9PEFC - 5901	GlobalFiler™- STRMix™ V2.6					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11,11
	14,16,21	13,14,15.2**,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
HA79H8 - 5901	GlobalFiler™- STRMix™					
4sp	15,16,16.3,17.3,18.3	16,17,19	10,11,11.3,14	14,15,16,17	9,10,11,12	
	8,9,11,12	11,12,14,15	13,14,15	17,18,19,20	8,9,10,11,12	10,11
	13,14,15,16,21	12,13,14,16.2	29,30,31,31.2	15,16,17	X,Y	9,10,11,12
	21,22,24,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,10,11
	16,17,19,20	10			1,2	
HMATHB - 5902	GlobalFiler™- STRMix™ v2.9.1					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
JCRAYE - 5902	GlobalFiler™- STRMix™ v2.8					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	

Item 4sp - STR Results

JJP289 - 5901 PowerPlex® Fusion 6C- STRMix™ v2.9

4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26	9,12	12,15,18,19	23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10	17,19	17,20		

KFMMYA - 5901 GlobalFiler™- STRMix™ v. 2.6

4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,11,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,15.2**,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

KKTFQK - 5902 Identifiler® Plus- STRMix™

4sp		16,17,19		15,16,17	9,11,12	
	8,9,12	12,14,15			8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2		X,Y	10,11,12
	21,22,25,26				7,9,9.3	8,11
	16,17,19,20					

L6JPQZ - 5901 GlobalFiler™- STRMix™

4sp	15,16,16.3,17.3	16,17,19	10,11,11.3,13,14	14,15,16,17	9,10,11,12	
	8,9,11,12	11,12,14,15	13,14,15	17,18,19,20	8,9,10,11,12	10,11
	13,14,15,16,21	12,13,14,16.2	29,30,31,31.2	15,16,17	X,Y	10,11,12
	20,21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,8,9,9.3	8,11
	16,17,19,20	10			1,2	

LRURMG - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

4sp	16,17.3,18.3	16,17,19,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20	8,10,11,12	11,12,13
	14,16,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

LV8TJ9 - 5901 GlobalFiler™- STRMix™ v. 2.6.1

4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test **Amplification Kits - Probabilistic Genotyping Software**

Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	
			Item 4sp - STR Results			
MK7PU6 - 5902	GlobalFiler™- STRMix™ 2.8					
	15,16,16.3,17.3	16,17,19	10,11,11.3,14	14,15,16,17	9,10,11,12	
4sp	8,9,11,12	12,14,15	13,14,15	17,18,19,20	8,9,10,11,12	10,11
	13,14,16,21	12,13,14,15.2,16.2	29,30,31,31.2	15,16,17	X,Y	10,11,12
	20,21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,8,9,9.3	8,10,11
	16,17,19,20	9,10			1,2	
NKKENU - 5902	PowerPlex® Fusion 6C- STRMix™ v2.12					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26	9,12	12,15,18,19	23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10	17,19	17,20		
NWDUKX - 5901	GlobalFiler™- STRMix™					
	15,16,16.3,17.3	16,17,18,19	10,11,11.3,13,14	14,15,16,17	8,9,10,11,12	
4sp	8,9,11,12	11,12,13,14,15	12,13,14,15	16,17,18,19,20	8,9,10,11,12	10,11
	13,14,15,16,20,21,22	12,13,14,16.2	29,30,30.2,31,31.2	14,15,16,17	X,Y	9,10,11,12
	20,21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,10,11
	15,16,17,19,20	10			1,2	
PKJZL9 - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	16,17.3	17,19,20	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,19,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
PWCGDV - 5901	GlobalFiler™- STRMix™					
	15,16,16.3,17.3	15,16,17,19	10,11,11.3,13,14	14,15,16,17	8,9,10,11,12	
4sp	8,9,11,12	11,12,13,14,15	12,13,14,15	17,18,19,20	7,8,9,10,11,12	10,11
	13,14,15,16,17,20,21	12,13,14,15.2,16.2	29,30,30.2,31,31.2	14,15,16,17	X,Y	9,10,11,12
	20,21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,10,11
	15,16,17,18,19,20	10			1,2	
QCKU6C - 5901	PowerPlex® 21- STRMix™ V2.8					
		16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
4sp	8,9,11,12	11,12,14,15		16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					

TABLE 3

WebCode - Test	**Amplification Kits - Probabilistic Genotyping Software**					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4sp - STR Results

QKVWQD - 5902 PowerPlex® 21- STRMix™ v 2.10.0

4sp	16,17.3,18.3	16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
	8,9,10,11,12	11,12,14,15		18,19,20	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,11
	16,17,19,20					

QLQFTE - 5902 Identifiler® ID+- STRMix™

4sp		16,17,19		15,16,17	9,11,12	
	8,9,12	12,14,15			8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2		X,Y	10,11,12
	21,22,25,26				7,9,9.3	8,11
	16,17,19,20					

QY8QPG - 5901 Identifiler® plus- STRMix™ v 2.7

4sp		16,17,19		14*,15,16,17	9,10*,11,12	
	8,9,11*,12	11*,12,14,15			8,9*,10,11*,12	10*,11
	13*,14,15*,16,21	12*,13,14,16.2	29*,30,31,31.2		X,Y	10,11,12
	21,22,24*,25,26				7,8*,9,9.3	8,11
	16,17,19,20					

RDVWRB - 5901 PowerPlex® Fusion 6C- STRMix™ 2.6.2

4sp	(16),17.3	(16),17,(19)	11,(11.3),14	15,(16),17	(9),11,(12)	
	(8),9,12	12,(14),15	(13),14,15	18,(19),(20)	(8),10,12	11
	14,16,(21)	13,14,(16.2)	30,(31),31.2	(15),16	X,Y	10,11,12
	(21),22,25,(26)	9,12	12,15,(18),(19)	23.2,24.2,(25.2),(26.2)	(7),9,9.3	(8),11
	16,17,(19),(20)	10	17,(19)	17,20		

RUEQHZ - 5901 Identifiler® plus - EuroFormix

4sp		16,17,19		15,16,17	9,11,12	
	8,9,12	12,14,15			8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2		X,Y	10,11,12
	21,22,25,26				7,9,9.3	8,11
	16,17,19,20					

TFEBVC - 5902 PowerPlex® 21- STRMix™

4sp	16,17.3,18.3	16,17,19,20		15,16,17	9,11,12	11,12,17,18
	8,9,10,11,12	11,12,14,15		18,19,20,23	8,10,11,12	11,12,13
	14,16,19,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					

TGAUWD - 5901 PowerPlex® 21- STRMix™ v 2.10

4sp	16,17.3	16,17,19		15,16,17	9,11,12	11,12,18
	8,9,12	12,14,15		18,19,20	8,10,12	11,11
	14,16,21	13,14,16.2	30,31,31.2		X,Y	10,11,12
	21,22,25,26	9,12	12,15,18,19		7,9,9.3	8,11
	16,17,19,20					

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4sp - STR Results

TKNR4Z - 5902	GlobalFiler™ - STRMix™					
	15.3,16,17.3,18.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,18,19,20	10			1,2	
TLJA72 - 5901	GlobalFiler™ - STRMix™ v. 2.6					
	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,20,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
UMRJXY - 5902	GlobalFiler™ - STRMix™ 2.8					
	15,16,16.3,17.1,17.3	15,16,17,18,19	10,11,11.3,12,13,14	14,15,16,17	8,9,10,11,12	
4sp	7,8,9,11,12	11,12,13,14,15	12,13,14,15	17,18,19,20	8,9,10,11,12	10,11
	13,14,15,16,20,21	12,13,14,15.2,16.2	29,30,30.2,31,31.2	14,15,16,17	X,Y	9,10,11,12
	20,21,22,23,24,25,26			22.2,23,23.2,24,24.2,25,25.2,26,26.2	6,7,8,8.3,9,9.3	8,10,11
	15,16,17,18,19,20	9,10			1,2	
V67HG2 - 5901	GlobalFiler™ - STRMix™ V 2.8					
	16,17.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
4sp	8,9,10,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,19,20,21	13,14,15,16.2	30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10			1,2	
V6A37P - 5901	GlobalFiler™ - STRMix™					
	16,16.3,17.3	16,17,19	10,11,11.3,14	15,16,17	9,10,11,12	
4sp	8,9,12	11,12,14,15	13,14,15	18,19,20	8,10,11,12	10,11
	14,16,21	12,13,14,16.2	30,31,31.2	15,16,17	X,Y	10,11,12
	21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
VBVWBM - 5901	GlobalFiler™ - EUROFORMIX v4.0.8					
	[15.3],16,17.3,[18.3]	[16],17,[19],[20],[24]	11,[11.3],[14]	15,16,17	[9],11,[12]	
4sp	[8],9,[11],12	[11],12,14,15	[13],14,15,[16]	[16],18,[19],[20],[23]	[8],10,[11],12	11,[12]
	14,16,[19],[20],[21]	13,14,[15],[16.2]	[27],30,[31],31.2	[15],16	X,Y	10,11,12
	[20],[21],22,25,[26]			[16],23.2,24.2,[25.2],[26.2]	7,9,9.3	8,11
	16,17,[19],[20]	10			[1],2	

TABLE 3

Item 4sp - STR Results

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
	FGA	Penta D	Penta E	SE33	TH01	TPOX
	vWA	DYS391	DYS570	DYS576	Y Indel	
W648ZP - 5901	GlobalFiler™ - STRMix™					
4sp	15,16,16.3,17.3	16,17,19	10,11,11.3,14	14,15,16,17	9,10,11,12	
	8,9,11,12	11,12,14,15	13,14,15	17,18,19,20	8,9,10,12	10,11
	13,14,15,16,21	12,13,14,16.2	29,30,31,31.2	15,16,17	X,Y	10,11,12
	21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	15,16,17,19,20	10			1,2	
W883G7 - 5902	PowerPlex® 21 - STRMix™ 2.10.0					
4sp	16,17.3,18.3	16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
	8,9,10,11,12	11,12,14,15		16,18,19,20	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					
WGU2AX - 5901	GlobalFiler™ - STRMix™ v. 2.6					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
WP9QBQ - 5901	GlobalFiler™ - STRMix™					
4sp	15,16,16.3,17.3	16,17,19	10,11,11.3,14	14,15,16,17	9,10,11,12	
	8,9,11,12	12,13,14,15	12,13,14,15,16	17,18,19,20	8,9,10,11,12	10,11
	13,14,15,16,21	13,14,16.2	29,30,31,31.2	15,16,17	X,Y	10,11,12
	20,21,22,24,25,26			22.2,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	15,16,17,19,20	10			1,2	
X9G8VV - 5901	GlobalFiler™ - STRMix™					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	
XNBWN7 - 5901	GlobalFiler™ - STRMix™					
4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,20,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26			23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

TABLE 3

WebCode - Test	Amplification Kits - Probabilistic Genotyping Software					
Item	**D1S1656**	**D2S1338**	**D2S441**	**D3S1358**	**D5S818**	**D6S1043**
	D7S820	**D8S1179**	**D10S1248**	**D12S391**	**D13S317**	**D16S539**
	D18S51	**D19S433**	**D21S11**	**D22S1045**	**Amelogenin**	**CSF1PO**
	FGA	**Penta D**	**Penta E**	**SE33**	**TH01**	**TPOX**
	vWA	**DYS391**	**DYS570**	**DYS576**	**Y Indel**	

Item 4sp - STR Results

YMVZW7 - 5901 PowerPlex® 21- STRMix™ v2.8.0

4sp		16,17,19,20,24		15,16,17	9,11,12	11,12,17,18
	8,9,11,12	11,12,14,15,16		16,18,19,20	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,15,15.2,16.2	27,30,31,31.2		X,Y	10,11,12
	20,21,22,25,26	9,12,13	7,10,12,15,18,19		7,9,9.3	8,9,11
	16,17,19,20					

YY83H6 - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

4sp	15.3,16,17.3	16,17,19,20,24	11,11.3,14	15,16,17	9,11,12	
	8,9,10,11,12	11,12,14,15	13,14,15,16	16,18,19,20,23	8,10,11,12	11,12,13
	14,16,19,20,21	13,14,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,16,23.2,24.2,25.2,26.2	7,9,9.3	8,9,11
	16,17,19,20	10,10			1,2	

ZBZ72N - 5902 PowerPlex® Fusion 6C - DNAxs

4sp	16,17.3	16,17,19	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15	18,19,20	8,10,12	11
	14,16,21	13,14,16.2	30,31,31.2	15,16	X,Y	10,11,12
	21,22,25,26	9,12	12,15,18,19	23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10	17,19	17,20		

ZY36LY - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

4sp	16,17.3	17,19,20	11,11.3,14	15,16,17	9,11,12	
	8,9,12	12,14,15	13,14,15,16	16,18,19,20,23	8,10,12	11,11
	14,16,19,20,21	13,14,16.2	27,30,31,31.2	15,16	X,Y	10,11,12
	20,21,22,25,26			15,23.2,24.2,25.2,26.2	7,9,9.3	8,11
	16,17,19,20	10			1,2	

YSTR Amplification Kit(s) & Results

TABLE 4

Item 2 - YSTR Results

WebCode - Test	Amplification Kit								
Item	**DYF387S1**	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
	DYS437	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
2U64XP - 5901	PowerPlex® Y 23								
2		14	12,14	13	29	24	11	13	13
	15	12	11	19		17	18		22
		13	13	17	16		23	10	12
46DPW2 - 5902	PowerPlex® Y 23								
2		14	12,14	13	29	24	11	13	13
	15	12	11	19		17	18		22
		13	13	17	16		23	10	12
6CE2VJ - 5901									
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
6UBPYM - 5901	Yfiler® Plus								
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13	-	17	16	18	23	-	12
8FQNHM - 5902	Yfiler® Plus								
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
AXW3PR - 5901	Yfiler®								
2		14	12,14	13	29	24	11	13	13
	15	12	11	19		17	18		
							23		12
BH4RFU - 5901	Yfiler® plus								
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
ENWXPE - 5901	Yfiler®								
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
F8HBKN - 5901	Yfiler® Plus								
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
FYD629 - 5902	Yfiler® Plus								
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
KKTFQK - 5902	PowerPlex® Y 23								
2		14	12,14	13	29	24	11	13	13
	15	12	11	19		17	18		22
		13	13	17	16		23	10	12

TABLE 4

WebCode - Test		Amplification Kit							
Item	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 2 - YSTR Results

WebCode - Test		Amplification Kit							
LBA2Q3 - 5902		Yfiler® Plus							
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
MG8BAZ - 5901		Yfiler® Plus							
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
NKKENU - 5902		Yfiler® Plus							
2	35,37	14	12,14	13	13	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
QKVWQD - 5902		Yfiler® Plus							
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
QLQFTE - 5902		PowerPlex® Y							
2		14	12,14	13	29	24	11	13	13
	15	12	11	19		17	18		22
		13	13	17	16		23	10	12
R7WA2W - 5902		Yfiler® Plus							
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
RDVWRB - 5901		PowerPlex® Y 23							
2		14	12,14	13	29	24	11	13	13
	15	12	11	19		17	18		22
		13	13	17	16		23	10	12
RUEQHZ - 5901		Yfiler®							
2		14	12,14	13	29	24	11	13	13
	15	12	11	19		17	18		
							23		12
TGAUWD - 5901		Yfiler® Plus							
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
TKNR4Z - 5902		Yfiler® Plus							
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12
W883G7 - 5902		Yfiler® Plus							
2	35,37	14	12,14	13	29	24	11	13	13
	15	12	11	19	29	17	18	11	22
	37	13		17	16	18	23		12

TABLE 4

WebCode - Test		Amplification Kit							
Item	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 3 - YSTR Results

6CE2VJ - 5901		Yfiler® Plus							
3									

TABLE 4

Item 4 - YSTR Results

WebCode - Test		Amplification Kit							
Item	**DYF387S1**	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
	DYS437	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
2U64XP - 5901		PowerPlex® Y 23							
4		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		24,26
		11	12,13	17,19	17,20		21,22	9,12	10,13
FYD629 - 5902		Yfiler® Plus							
4	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,14,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,18,19	17,20	19.2,22	21,22		10,13
MG8BAZ - 5901		Yfiler® Plus							
4	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,30	19.2,22	21,22		10,13
R7WA2W - 5902		Yfiler® Plus							
4	36,37,40	14,16	12,14,16	12,13	28,29,30	23,25	10	13,14,15	12
	14	10,11	11,12	19,20	28,33	15,16,17	15,16,16.2	10,11	24,26
	36,39,40	11		17,19	17,20	19.2,22,23	21,22		10,13

TABLE 4

Item 4e - YSTR Results

WebCode - Test		Amplification Kit							
Item	**DYF387S1**	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
	DYS437	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
46DPW2 - 5902									
4e		14,16	12,14,16	12,13	29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		24,26
		11	12,13	17,19	17,20		21,22	9	10,13
6CE2VJ - 5901		Yfiler® Plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
6UBPYM - 5901		Yfiler® Plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11	-	17,19	17,20	19.2,22	21,22	-	10,13
7MMEUW - 5901		Yfiler® Plus							
4e									
8FQNHM - 5902		Yfiler® Plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
AXW3PR - 5901		Yfiler®							
4e									
BH4RFU - 5901		Yfiler® plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
ENWXPE - 5901		Yfiler®							
4e	36,37,40	14,15,16	12,14,16	12,13	24,28,29	23,25	8.3,10	13,14,15	12
	14	10,11	11,12	19,20	28,33	15,17,18	16,16.2	10,11	24,26,31
	36,40	11		17,18,19	17,20	19.2,22	21,22		10,13
F8HBKN - 5901		Yfiler® Plus							
4e									
KKTFQK - 5902		PowerPlex® Y 23							
4e		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		24,26
		11	12,13	17,19	17,20		21,22	9,12	10,*
NKKENU - 5902		Yfiler® Plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
QKVWQD - 5902		Yfiler® Plus							
4e	36,37,40	14,[16]	[12,14],16	[12],13	[28],29	[23],25	10	13,[15]	12
	14	[10],11	11,[12]	[19],20	28,[33]	[15],17	[16],16.2	[10],11	24,26
	36,40	11		17,[19]	17,[20]	[19.2],22	21,[22]		10,[13]

TABLE 4

WebCode - Test		Amplification Kit							
Item	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	YGATAH4

Item 4e - YSTR Results

QLQFTE - 5902		PowerPlex® Y 23							
4e		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		17	16,16.2		24,26
		11	12	17,19	17,20		21	9,12	10
RDVWRB - 5901		PowerPlex® Y 23							
4e		14,16	(12),(14),16	(12),13	28,29	23,25	10	13,(15)	12
	14	10,11	11,(12)	19,20		(15),17	16,16.2		24,26
		11	12,13	17,19	17,(20)		21,(22)	9,(12)	10,13
RUEQHZ - 5901		Yfiler®							
4e		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		
							21,22		10,13
TGAUWD - 5901		Yfiler® Plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
TKNR4Z - 5902		Yfiler® Plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
W883G7 - 5902		Yfiler® Plus							
4e	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14,14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13

TABLE 4

Item 4sp - YSTR Results

WebCode - Test		Amplification Kit							
Item	**DYF387S1**	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
	DYS437	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
46DPW2 - 5902									
4sp		14,16	12,14,16	12,13	28,29	23,25	10	13	12
	14	10,11	11,12	19,20		15,17	16.2		24,26
		11	12,13	17,19	17,20		21,22	9,12	10
6CE2VJ - 5901		Yfiler® Plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
6UBPYM - 5901		Yfiler® Plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11	-	17,19	17,20	19.2,22	21,22	-	10,13
7MMEUW - 5901		Yfiler® Plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
8FQNHM - 5902		Yfiler® Plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
AXW3PR - 5901		Yfiler®							
4sp		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		
							21,22		10,13
BH4RFU - 5901		Yfiler® plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
ENWXPE - 5901		Yfiler®							
4sp	36,37,40	14,15,16	12,14,16	12,13	24,28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,18,19	17,20	19.2,22	21,22		10,13
F8HBKN - 5901		Yfiler® Plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
KKTFQK - 5902		PowerPlex® Y 23							
4sp		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		24,26
		11	12,13	17,19	17,20		21,22	9,12	10,13
NKKENU - 5902		Yfiler® Plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
QKVWQD - 5902		Yfiler® Plus							
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	[19],20	28,[33]	[15],17	[16],16.2	[10],11	[24],26
	36,40	11		17,19	17,[20]	19.2,22	21,[22]		10,[13]

TABLE 4

Item 4sp - YSTR Results

WebCode - Test	**Amplification Kit**								
Item	**DYF387S1**	**DYS19**	**DYS385**	**DYS389-I**	**DYS389-II**	**DYS390**	**DYS391**	**DYS392**	**DYS393**
	DYS437	**DYS438**	**DYS439**	**DYS448**	**DYS449**	**DYS456**	**DYS458**	**DYS460**	**DYS481**
	DYS518	**DYS533**	**DYS549**	**DYS570**	**DYS576**	**DYS627**	**DYS635**	**DYS643**	**YGATAH4**
QLQFTE - 5902	PowerPlex® Y 23								
4sp		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		24,26
		11	12,13	17,19	17,20		21,22	9,12	10,13
RDVWRB - 5901	PowerPlex® Y 23								
4sp		14,(16)	(12),(14),16	12,13	28,29	(23),25	10	13,(15)	12
	14	10,11	11,(12)	(19),20		(15),17	(16),16.2		24,26
		11	12,(13)	17,(19)	17,20		21,(22)	9,(12)	10,(13)
RUEQHZ - 5901	Yfiler®								
4sp		14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20		15,17	16,16.2		
							21,22		10,13
TGAUWD - 5901	Yfiler® Plus								
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
TKNR4Z - 5902	Yfiler® Plus								
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13
W883G7 - 5902	Yfiler® Plus								
4sp	36,37,40	14,16	12,14,16	12,13	28,29	23,25	10	13,15	12
	14,14	10,11	11,12	19,20	28,33	15,17	16,16.2	10,11	24,26
	36,40	11		17,19	17,20	19.2,22	21,22		10,13

Additional DNA Results

TABLE 5

Additional DNA results found to be concordant at a pre-existing locus are retained solely within the applicable tables. Non-concordant results and results for loci not found elsewhere will remain in this table.

Locus	WebCode-Test	Item 1	Item 2	Item 3	Item 3e	Item 3sp	Item 4	Item 4e	Item 4sp

No additional DNA results were reported.

DNA Mixture Concentrations and Proportions

TABLE 6

Item 3 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
2U64XP - 5901	2	Unknown Victim	0.5600 0.6900	45.00 55.00
2V3DTT - 5901	2	Unknown Victim		33.00 67.00
3DCVDW - 5902	2	Unknown Victim		
3GZ6PJ - 5901	2	Unknown Victim		44.00 56.00
3MLWYX - 5902	2	Unknown Victim		
4478ZQ - 5901	2	Unknown Victim		36.00 64.00
6CE2VJ - 5901	2	Unknown Victim	0.5420 1.05	34.00 66.00
6DBH6U - 5902	2	Unknown Victim		
6FWJNN - 5901	2	Unknown Victim		36.00 64.00
6GAT2U - 5902	2	Unknown Victim		
6H6C3W - 5902	2	Unknown Victim		
6UBPYM - 5901	2	Unknown Victim	1.78 1.46	54.97 45.03
76CCPY - 5901	2	Unknown Victim		36.11 63.89
7G4YWE - 5901	2	Unknown Victim		33.00 67.00
7MMEUW - 5901	2	Unknown Victim		38.00 61.00
8FQNHM - 5902	2	Unknown Victim		39.56 60.44
8RZL2G - 5901	2	Unknown Victim		35.00 65.00
993KMP - 5902	2	Unknown Victim		
ABPL7H - 5902	2	Unknown Victim	0.2325 0.3911	37.28 62.72

TABLE 6

Item 3 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
AQ3XWQ - 5902	2	Unknown Victim		
AWLZ4T - 5902	2	Unknown Victim		
AXW3PR - 5901	2	Victim		
BH4RFU - 5901	2	Unknown Victim	0.1800 0.1530	54.00 46.00
BUGRCN - 5902	2	Unknown Victim		
CRMK7G - 5902	2	Unknown Victim		35.44 64.56
CZXMRH - 5902	2	Unknown Victim		37.39 62.61
D2RTLG - 5901	2	Unknown Victim		37.00 63.00
DZWAKF - 5901	2	Unknown Victim		34.00 66.00
E6M7KQ - 5901	2	Unknown Victim		30.85 69.15
ENWXPE - 5901	2	Suspect Victim	2.21 2.21	0.00 609.00
ERWAKE - 5901	2			
F8HBKN - 5901	2	Unknown Victim		34.00 65.00
FYD629 - 5902	2	Unknown Victim		42.00 58.00
FZ8V8M - 5902	2	Unknown Victim		
G83CWJ - 5902	2	Unknown Victim		
GJRAXG - 5902	2	Unknown Victim		
H3M3JE - 5902	2	Unknown Victim		36.00 64.00
H9BPF7 - 5901	2	Unknown Victim	1.56 2.07	43.00 57.00
H9PEFC - 5901	2	Unknown Victim		33.00 67.00
HA79H8 - 5901	2	Unknown Victim		33.00 67.00

TABLE 6

Item 3 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
HMATHB - 5902	2	Unknown Victim		32.24 67.76
KFMMYA - 5901	2	Unknown Victim		32.00 68.00
L6JPQZ - 5901	2	Unknown Victim		34.00 66.00
LBA2Q3 - 5902	2	Unknown Victim		43.00 57.00
LRURMG - 5902	2	Unknown Victim		
LV8TJ9 - 5901	2	Unknown Victim		32.00 68.00
MK7PU6 - 5902	2	Unknown Victim		32.55 67.45
NKKENU - 5902	2	Unknown Victim		37.34 62.66
NWDUKX - 5901	2	Unknown Victim		31.00 69.00
PKJZL9 - 5902	2	Unknown Victim		
PWCGDV - 5901	2	Unknown Victim		33.00 67.00
QCKU6C - 5901	2	Unknown Victim		35.75 64.25
QKVWQD - 5902	2	Unknown Victim	1.74 3.15	35.51 64.49
QY8QPG - 5901	2	Unknown Victim		30.67 69.33
R7WA2W - 5902	2	Unknown Victim		46.00 54.00
RDVWRB - 5901	2	Unknown Victim		35.00 65.00
RUEQHZ - 5901	2	Unknown Victim	11.1 14.9	42.65 57.34
TFEBVC - 5902	2	Unknown Victim	1.17 2.21	34.63 65.37
TGAUWD - 5901	2	Unknown Victim	0.6870 0.8070	46.00 54.00
TKNR4Z - 5902	2	Unknown Victim		34.95 65.05

TABLE 6

Item 3 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
TLJA72 - 5901	2	Unknown Victim		35.00 65.00
UMRJXY - 5902	2	Unknown Victim		35.51 64.49
V6A37P - 5901	2	Unknown Victim		43.00 57.00
W648ZP - 5901	2	Unknown Victim		35.00 65.00
W883G7 - 5902	2	Unknown Victim	2.96 5.59	34.57 65.43
WGU2AX - 5901	2	Unknown Victim		33.00 67.00
WP9QBQ - 5901	2	Unknown Victim		35.00 65.00
X9G8VV - 5901	2	Unknown Victim	0.1023 0.1912	34.84 65.16
XNBWN7 - 5901	2	Unknown Victim		31.40 68.60
YMVZW7 - 5901	2	Unknown Victim	0.8662 1.32	39.61 60.39
YY83H6 - 5902	2	Unknown Victim		
ZY36LY - 5902	2	Unknown Victim		

Response Summary: Item 3	
Estimated Number of Contributors	**Percent Reported**
2	**72 (100%)**

TABLE 6

Item 4 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
2U64XP - 5901	3	Unknown Unknown Victim	0.05700 0.02200 0.01600	60.00 23.00 17.00
FYD629 - 5902	3	Unknown Unknown Victim		28.00 66.00 7.00
H9BPF7 - 5901	3	Unknown Unknown Victim	0.06000 0.03200 0.01900	54.00 29.00 17.00
LBA2Q3 - 5902	3	Unknown Unknown Victim		55.00 33.00 12.00
R7WA2W - 5902	3	Unknown Unknown Victim		66.00 21.00 13.00

Response Summary: Item 4	
Estimated Number of Contributors	**Percent Reported**
3	**5 (100%)**

TABLE 6

Item 4e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
2V3DTT - 5901	3	Unknown		10.00
		Unknown		4.00
		Victim		86.00
3DCVDW - 5902	3	Unknown		
		Unknown		
		Victim		
3GZ6PJ - 5901	3	Unknown		12.00
		Unknown		17.00
		Victim		70.00
3MLWYX - 5902	3	Unknown		
		Unknown		
		Victim		
4478ZQ - 5901	3	Unknown		4.00
		Unknown		15.00
		Victim		81.00
6CE2VJ - 5901	3	Unknown	0.08200	20.00
		Unknown	0.1640	40.00
		Victim	0.1640	40.00
6DBH6U - 5902	3	Unknown		
		Unknown		
		Victim		
6FWJNN - 5901	3	Unknown		18.00
		Unknown		5.00
		Victim		77.00
6GAT2U - 5902	3	Unknown		
		Unknown		
		Victim		
6H6C3W - 5902	3	Unknown		
		Unknown		
		Victim		
6UBPYM - 5901	3	Unknown	0.3780	42.88
		Unknown	0.1420	16.09
		Victim	0.3610	41.03
76CCPY - 5901	3	Unknown		47.57
		Unknown		16.13
		Victim		36.30
7G4YWE - 5901	3	Unknown		24.00
		Unknown		8.00
		Victim		68.00
7MMEUW - 5901	3	Unknown		6.00
		Unknown		18.00
		Victim		74.00

TABLE 6

Item 4e Results

WebCode-Test	Number of Contributors	Contributor(s)	DNA Concentration (ng/uL)	DNA Proportion (%)
8FQNHM - 5902	3	Unknown		27.02
		Unknown		49.91
		Victim		23.08
8RZL2G - 5901	3	Unknown		12.00
		Unknown		16.00
		Victim		72.00
993KMP - 5902	3	Unknown		
		Unknown		
		Victim		
ABPL7H - 5902	3	Unknown	0.01910	25.50
		Unknown	0.00540	7.17
		Victim	0.05000	67.33
AQ3XWQ - 5902	3	Unknown		
		Unknown		
		Unknown		
AWLZ4T - 5902	3	Unknown		
		Unknown		
		Victim		
AXW3PR - 5901	3	Victim		
BH4RFU - 5901	3	Unknown	0.01900	18.00
		Unknown	0.05600	54.00
		Victim	0.02900	28.00
BUGRCN - 5902	3	Unknown		
		Unknown		
		Victim		
CRMK7G - 5902	3	Unknown		24.25
		Unknown		8.06
		Victim		67.69
CZXMRH - 5902	3	Unknown		6.23
		Unknown		18.78
		Victim		74.98
D2RTLG - 5901	3	Unknown		5.00
		Unknown		13.00
		Victim		82.00
DZWAKF - 5901	3	Unknown		6.00
		Unknown		11.00
		Victim		82.00
E6M7KQ - 5901	3	Unknown		31.82
		Unknown		7.23
		Victim		60.95
ENWXPE - 5901	3	Suspect	0.1617	0.00
		Unknown	0.1617	56.50
		Victim	0.1617	197.00

TABLE 6

Item 4e Results				
WebCode-Test	Number of Contributors	Contributor(s)	DNA Concentration (ng/uL)	DNA Proportion (%)
ERWAKE - 5901	3			
F8HBKN - 5901	3	Unknown Unknown Victim		5.00 11.00 83.00
FZ8V8M - 5902	3	Unknown Unknown Victim		
G83CWJ - 5902	3	Unknown Unknown Victim		
GJRAXG - 5902	3	Unknown Unknown Victim		
H3M3JE - 5902	3	Unknown Unknown Victim		13.54 5.54 80.92
H9PEFC - 5901	3	Unknown Unknown Victim		6.00 19.00 75.00
HA79H8 - 5901	3	Unknown Unknown Victim		20.00 10.00 70.00
HMATHB - 5902	3	Unknown Unknown Victim		7.10 18.48 74.42
KFMMYA - 5901	3	Unknown Unknown Victim		11.00 4.00 84.00
L6JPQZ - 5901	3	Unknown Unknown Victim		6.00 27.00 66.00
LRURMG - 5902	3	Unknown Unknown Victim		
LV8TJ9 - 5901	3	Unknown Unknown Victim		14.00 5.00 82.00
MK7PU6 - 5902	3	Unknown Unknown Victim		17.50 11.27 71.22
NKKENU - 5902	3	Unknown Unknown Victim		28.46 9.58 61.96

TABLE 6

Item 4e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
NWDUKX - 5901	3	Unknown		23.00
		Unknown		6.00
		Victim		71.00
PKJZL9 - 5902	3	Unknown		
		Unknown		
		Victim		
PWCGDV - 5901	3	Unknown		8.00
		Unknown		26.00
		Victim		66.00
QCKU6C - 5901	3	Unknown		40.82
		Unknown		9.69
		Victim		49.49
QKVWQD - 5902	3	Unknown	0.6000	34.98
		Unknown	0.1800	10.71
		Victim	0.9300	54.31
QY8QPG - 5901	3	Unknown		6.20
		Unknown		32.09
		Victim		61.71
RDVWRB - 5901	3	Unknown		28.00
		Unknown		12.00
		Victim		60.00
RUEQHZ - 5901	3	Unknown	0.00800	8.00
		Unknown	0.03000	29.02
		Victim	0.07000	62.95
TFEBVC - 5902	3	Unknown	0.2695	35.59
		Unknown	0.1100	14.53
		Victim	0.3777	49.88
TGAUWD - 5901	3	Unknown	0.02800	7.00
		Unknown	0.09300	23.00
		Victim	0.2840	70.00
TKNR4Z - 5902	3	Unknown		20.40
		Unknown		48.70
		Victim		30.90
TLJA72 - 5901	3	Unknown		7.00
		Unknown		17.00
		Victim		77.00
UMRJXY - 5902	3	Unknown		20.47
		Unknown		6.16
		Victim		73.37
V6A37P - 5901	3	Unknown		14.00
		Unknown		20.00
		Victim		66.00
W648ZP - 5901	3	Unknown		21.00
		Unknown		4.00
		Victim		74.00

TABLE 6

Item 4e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
W883G7 - 5902	3	Unknown Unknown Victim	0.3700 1.01 2.13	10.62 28.73 60.65
WGU2AX - 5901	3	Unknown Unknown Victim		4.00 13.00 83.00
WP9QBQ - 5901	3	Unknown Unknown Victim		20.00 10.00 70.00
X9G8VV - 5901	3	Unknown Unknown Victim	0.08140 0.03134 0.1849	27.37 10.53 62.11
XNBWN7 - 5901	3	Unknown Unknown Victim		51.70 17.96 30.34
YMVZW7 - 5901	4	Unknown Unknown Unknown Victim	0.09840 0.02380 0.00370 0.1839	31.76 7.67 1.21 59.36
YY83H6 - 5902	3	Unknown Unknown Victim		
ZY36LY - 5902	3	Unknown Unknown Victim		

Response Summary: Item 4e	
Estimated Number of Contributors	**Percent Reported**
3	66 (99%)
4	1 (1%)

TABLE 6

Item 4sp Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
2V3DTT - 5901	2	Unknown Unknown		61.00 39.00
3DCVDW - 5902	3	Unknown Unknown Unknown		
3GZ6PJ - 5901	2	Unknown Unknown		31.00 69.00
4478ZQ - 5901	2	Unknown Unknown		58.00 42.00
6CE2VJ - 5901	2	Unknown Unknown	0.8050 3.22	20.00 80.00
6DBH6U - 5902	2	Unknown Unknown		
6FWJNN - 5901	3	Unknown Unknown Unknown		38.00 1.00 61.00
6GAT2U - 5902	3	Unknown Unknown Unknown		
6H6C3W - 5902	2	Unknown Unknown		
6UBPYM - 5901	3	Unknown Unknown Victim	3.67 1.60 0.2390	66.57 29.09 4.34
76CCPY - 5901	3	Unknown Unknown Victim		36.92 62.26 0.82
7G4YWE - 5901	3	Unknown Unknown Victim		33.00 67.00 0.00
7MMEUW - 5901	3	Unknown Unknown Victim		39.00 59.00
8FQNHM - 5902	3	Unknown Unknown Victim		28.52 66.12 5.36
8RZL2G - 5901	2	Unknown Unknown		35.00 65.00
993KMP - 5902	2	Unknown Unknown		
ABPL7H - 5902	2	Unknown Unknown	0.2896 0.5033	36.52 63.48

TABLE 6

Item 4sp Results				
WebCode-Test	Number of Contributors	Contributor(s)	DNA Concentration (ng/uL)	DNA Proportion (%)
AQ3XWQ - 5902	3	Unknown Unknown Victim		
AWLZ4T - 5902	3	Unknown Unknown Victim		
AXW3PR - 5901	3	Unknown		
BH4RFU - 5901	2	Unknown Unknown	0.1550 0.3300	32.00 68.00
BUGRCN - 5902	2	Unknown Unknown		
CRMK7G - 5902	2	Unknown Unknown		40.32 59.68
CZXMRH - 5902	2	Unknown Unknown		32.36 67.64
D2RTLG - 5901	2	Unknown Unknown		71.00 29.00
DZWAKF - 5901	2	Unknown Unknown		39.00 61.00
E6M7KQ - 5901	3	Unknown Unknown Victim		37.17 58.92 3.91
ENWXPE - 5901	3	Suspect Unknown Victim	0.4406 0.4406 0.4406	0.00 74.90 41.00
ERWAKE - 5901	2			
F8HBKN - 5901	3	Unknown Unknown Victim		36.00 59.00 3.00
FZ8V8M - 5902	2	Unknown Unknown		
G83CWJ - 5902	2	Unknown Unknown		
GJRAXG - 5902	2	Unknown Unknown		
H3M3JE - 5902	2	Unknown Unknown		41.68 58.32
H9PEFC - 5901	2	Unknown Unknown		38.00 62.00
HA79H8 - 5901	2	Unknown Unknown		35.00 65.00

TABLE 6

Item 4sp Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
HMATHB - 5902	2	Unknown Unknown		61.37 38.63
KFMMYA - 5901	2	Unknown Unknown		33.00 67.00
L6JPQZ - 5901	2	Unknown Unknown		31.00 69.00
LRURMG - 5902	3	Unknown Unknown Unknown		
LV8TJ9 - 5901	2	Unknown Unknown		37.00 63.00
MK7PU6 - 5902	3	Unknown Unknown Unknown		39.12 59.68 1.21
NKKENU - 5902	2	Unknown Unknown		30.89 69.11
NWDUKX - 5901	3	Unknown Unknown Unknown		63.00 0.00 37.00
PKJZL9 - 5902	3	Unknown Unknown Unknown		
PWCGDV - 5901	2	Unknown Unknown		65.00 35.00
QCKU6C - 5901	3	Unknown Unknown Victim		41.83 54.58 3.59
QKVWQD - 5902	3	Unknown Unknown Victim	5.76 11.9 3.86	26.73 55.37 17.90
QY8QPG - 5901	2	Unknown Unknown		34.60 65.40
RDVWRB - 5901	2	Unknown Unknown		73.00 27.00
RUEQHZ - 5901	2	Unknown Unknown	0.02700 0.05200	34.49 65.50
TFEBVC - 5902	3	Unknown Unknown Victim	0.9542 0.6484 0.06590	57.19 38.86 3.95
TGAUWD - 5901	2	Unknown Unknown	0.4560 0.2450	65.00 35.00

TABLE 6

Item 4sp Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
TKNR4Z - 5902	3	Unknown Unknown Victim		31.87 57.32 10.80
TLJA72 - 5901	2	Unknown Unknown		62.00 38.00
UMRJXY - 5902	2	Unknown Unknown		66.96 33.04
V6A37P - 5901	2	Unknown Unknown		35.00 65.00
W648ZP - 5901	2	Unknown Unknown		68.00 32.00
W883G7 - 5902	3	Unknown Unknown Victim	6.26 11.5 1.92	31.84 58.40 9.76
WGU2AX - 5901	2	Unknown Unknown		36.00 64.00
WP9QBQ - 5901	3	Unknown Unknown Victim		39.00 61.00 0.00
X9G8VV - 5901	2	Unknown Unknown	0.8263 1.66	33.21 66.79
XNBWN7 - 5901	2	Unknown Unknown		23.82 76.18
YMVZW7 - 5901	4	Unknown Unknown Unknown Victim	0.01270 0.3336 0.1524 0.04840	2.32 60.98 27.86 8.84
YY83H6 - 5902	3	Unknown Unknown Victim		
ZY36LY - 5902	3	Unknown Unknown Unknown		

Response Summary: Item 4sp	
Estimated Number of Contributors	**Percent Reported**
2	**39 (59%)**
3	**26 (39%)**
4	**1 (2%)**

Statistical Analysis for Item 3

TABLE 7

WebCode-Test	Item 3 Methods & Results
2U64XP - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Known contributors under Hp: victim and unknown. Known contributors under Hd: two unknowns. LR (total): 1,9E17. **Database(s) Used:** [Location Identifying Database]
2V3DTT - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item was interpreted as a mixture of two individuals. The DNA results are approximately 945 septillion times more likely if they originated from the "Known blood from the female victim" and an unknown, unrelated individual than if they originated from two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the “Known blood from the female victim" is a contributor to the DNA from this item. The "Known blood from the male suspect" is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
3DCVDW - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The "...dress..." (item 3) contained a mixture of DNA from two individuals. A DNA match was identified between the data obtained from the "...dress..." (item 3) and the victim. A match between the data obtained from the "...dress..." (item 3) and the victim is approximately 40 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the "...dress..." (item 3) and the suspect is approximately 400 undecillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the "...dress..." (item 3). **Database(s) Used:** The National Institute of Standards and Technology’s 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
3GZ6PJ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is approximately 323 trillion times more likely if it originated from Female Victim (K1) and an unknown individual than if it originated from two unknown individuals. This analysis provides very strong support for inclusion. Male Suspect (K2) is excluded as a contributor to this profile based on a LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
3MLWYX - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the stain from dress (item 3) and Victim. A match between the data obtained from the stain from dress (item 3) and Victim is approximately 700 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the stain from dress (item 3) and Suspect is approximately 100 decillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the stain from dress (item 3). **Database(s) Used:** The National Institute of Standards and Technology’s 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

TABLE 7

WebCode-Test	Item 3 Methods & Results
3P6C3X - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The results are consistent with the DNA profile from item #003-001-01A being a mixture of two contributors. Assuming two contributors, the DNA profile from item #003-001-01A is at least 1 trillion times more likely to occur if it originated from female victim and one unknown individual than if it originated from two unknown individuals. The results are consistent with the DNA profile from item #003-001-01B being a mixture of two contributors. Assuming two contributors, the DNA profile from item #003-001-01B is at least 1 trillion times more likely to occur if it originated from female victim and one unknown individual than if it originated from two unknown individuals. **Database(s) Used:** FBI Extended AfAmBahJam; FBI Extended Cauc; FBI Extended SE Hisp
4478ZQ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item was interpreted as a mixture of two individuals. The DNA results are approximately 56.9 septillion times more likely if they originated from the female victim and an unknown, unrelated individual than if they originated from two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the female victim is a contributor to the DNA from this item. The male suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
46DPW2 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** CONCLUSIONS: 1. VICTIM (item 1-1) cannot be excluded as a contributor to Mixture 1 (see Testing Summary) from a portion of blood from a dress (item 3-1) from near VICTIM's body. The STR DNA results are estimated to be greater that one trillion times more likely if they originate from VICTIM and one unknown person than if they originate from two unknown people unrelated to VICTIM. SUSPECT (item 2-1) is excluded as a contributor to Mixture 1. **Database(s) Used:** NIST Asian, NIST African American, NIST Caucasian Srivastava et al. (2019) South Asian, [Location Identifying Database]
6CE2VJ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Hp: The mixture contains the DNA of the victim and an unknown person. Hd: The mixture contains the DNA of two unknown people. LR=Hp/Hd= 5,93*10 exp15> 1.000.000 (extremely strong support for Hp). **Database(s) Used:** [Location Identifying Database]
6DBH6U - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the stain from dress (item 3) and the victim. A match between the data obtained from the stain from dress (item 3) and the victim is approximately 100 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the stain from dress (item 3) and the suspect is approximately 100 undecillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the stain from dress (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
6FWJNN - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item was interpreted as a mixture of two individuals with the female victim as an assumed contributor. The male suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017

TABLE 7

WebCode-Test	Item 3 Methods & Results
6GAT2U - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from dress found near victim's body (tan) (item 3) and the female victim. A match between the data obtained from the questioned stain from dress found near victim's body (tan) (item 3) and the female victim is approximately 3 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress found near victim's body (tan) (item 3) and the male suspect is approximately 300 decillion times less probable than a coincidental match to an unrelated person in the population. The male suspect is excluded from the data obtained from the questioned stain from dress found near victim's body (tan) (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
6H6C3W - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the stain from dress (item 3) and the victim. A match between the data obtained from the stain from dress (item 3) and victim is approximately five hundred sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the stain from dress (item 3) and the suspect is approximately thirty undecillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the stain from dress (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
6UBPYM - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** LRmix studio 2.1.3-community edition, caucasian population, theta = 0.01 used. The victim's contribution in the mixture is calculated according to the following hypothesis : Hp = the mixture belongs to the Victim and 1 unknown person. Hd = the mixture belongs to 2 unknown people. LR = 9.2928E13. **Database(s) Used:** caucasian population from Globalfiler IQC kit used.

TABLE 7

WebCode-Test	Item 3 Methods & Results
76CCPY - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** This item/sample provided a DNA profile that indicated the presence of DNA from two contributors. Some or all of the components of the DNA profile from the associated barcode (Item 1) sent with this exhibit report are represented within this mixed DNA profile. This DNA profile is greater than 100 billion times more likely to have occurred if the barcode sent with this exhibit report has contributed to this DNA profile, rather than two unknown, unrelated individuals. The statistical interpretation shows that the associated barcode (Item 2) sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile. The associated barcode/unknown designation sent with this exhibit report is consistent with this partially deconvoluted DNA profile (UKF1) and is therefore a possible contributor to this mixed DNA profile. For ease of reference, this partially deconvoluted DNA profile has been assigned a sub-sample barcode number. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on [Location Identifying Database] (as per the [Location Identifying Database] matching rules). Any subsequent profiles that are loaded to [Location Identifying Database] will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. **Database(s) Used:** [Location Identifying Database]
7G4YWE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 3A-2PT: The evidence DNA profile is approximately 2 quadrillion times more likely if it originated from Female Victim (K1) and 1 unknown individual than if it originated from 2 unknown individuals. This provides very strong support for inclusion. Male suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
7MMEUW - 5901	**Method(s)**: Random Match Probability **Stats Analysis:** The DNA profile from Item 3 indicates a mixture of 2 individuals. A DNA profile estimated to account for 61% of the DNA matches the DNA profile from Victim. This would not be expected to occur more than once among unrelated individuals in the world's population. This statistic is based on 18 of 21 loci. The DNA profile does not match the DNA profile obtained from Suspect. **Database(s) Used:** NIST 1036 Revised 2017
8FQNHM - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixture of DNA is 7.25 x 10^25 times more likely if it had originated from the Victim and an unknown, unrelated individual than if it had originated from two unknown, unrelated individuals. This is support that the Victim can be included as a contributor to the mixture of DNA. **Database(s) Used:** Caucasian, African American, Southeast Hispanic, and Southwest Hispanic population groups from the 2015 FBI Population Data for the Expanded CODIS Core STR Loci.
8RZL2G - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is approximately 15 quadrillion times more likely if it originated from Female victim (K1) and one unknown individual than if it originated from two unknown individuals. This provides very strong support for the inclusion of Female Victim (K1). Male Suspect (K2) is excluded based on an LR of 0. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 7

WebCode-Test	Item 3 Methods & Results
993KMP - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from dress (Item 3) and the victim. A match between the data obtained from the questioned stain from dress (Item 3) and the victim is approximately 70 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress (Item 3) and the suspect is approximately 2 nonillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the questioned stain from dress (Item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
9X3XVT - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming two contributors, the DNA typing results were interpreted using probabilistic genotyping software. The DNA typing results are 36.3 octillion times more likely to be observed if they originated from the "female victim" (Item 1) and one unknown, unrelated individual, rather than if they originated from two unknown, unrelated individuals. The results provide very strong support for the proposition that the "female victim" (Item 1) is a contributor to the DNA obtained from Item 3 rather than the alternate proposition. The "male suspect" (Item 2) is excluded as a contributor to this mixture. **Database(s) Used:** NIST 1036 (2017)
AAT7UL - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile was interpreted as a mixture of two individuals. The DNA profile is at least 1 trillion times more likely if it originated from the Victim (1) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of the Victim (1). The Suspect (2) is excluded as a possible contributor to the mixed DNA profile. **Database(s) Used:** FBI Extended CODIS core alleles frequencies - Caucasian, African American, and Southwest Hispanic
ABPL7H - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** nest_cauc
AQ3XWQ - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from dress (item 3) and the victim. A match between the data obtained from the questioned stain from dress (item 3) and the victim is approximately thirty septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress (item 3) and the suspect is approximately five undecillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the questioned stain from dress (item 3). **Database(s) Used:** All evidence genotypes were compared with all reference genotypes to compute likelihood ratio (LR) DNA match statistics. The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

TABLE 7

WebCode-Test	Item 3 Methods & Results
AWLZ4T - 5902	Method(s): Likelihood Ratio Stats Analysis: A DNA match was identified between the data obtained from the questioned stain from dress… (item #3) and the female victim (item #1). A match between the data obtained from the questioned stain from dress… (item #3) and the female victim (item #1) is approximately 100 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress… (item #3) and the male suspect (item #2) is approximately 8 decillion times less probable than a coincidental match to an unrelated person in the population. The male suspect (item #2) is excluded from the data obtained from the questioned stain from dress… (item #3). Database(s) Used: The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
AXW3PR - 5901	Method(s): Likelihood Ratio Stats Analysis: For the possible involvement of the female victim, the LR value calculated was 2.61E19 to 1, which means it is about 2.61E19 times more likely that the observed DNA profile being a mixture originating from the female victim and an unknown individual than if it originating from two unrelated individuals selected at random from the local [Population]. Database(s) Used: [Location Identifying Database]
AZ3KNM - 5901	Method(s): Likelihood Ratio Stats Analysis: The DNA profile was interpreted as a mixture of two individuals including unknown female individual A. The DNA profile is at least 1 trillion times more likely if it originated from Female Victim (1) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. Database(s) Used: FBI extended CODIS core allele frequencies - Caucasian, African American and Southwest Hispanic
BH4RFU - 5901	Method(s): Likelihood Ratio Stats Analysis: Victim - not excluded (LR = 100 billion). Suspect - excluded. Database(s) Used: [Location Identifying Database]
BUGRCN - 5902	Method(s): Likelihood Ratio Stats Analysis: A DNA match was identified between the data obtained from the questioned stain from dress (Item 3) and Victim. A match between the data obtained from the questioned stain from dress (Item 3) and Victim is approximately 900 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress (Item 3) and Suspect is approximately 3 duodecillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the questioned stain from dress (Item 3). Database(s) Used: The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
CRMK7G - 5902	Method(s): Likelihood Ratio Stats Analysis: (H1): The evidence originated from victim and one unknown, unrelated individual. (H2): The evidence originated from two unknown, unrelated individuals. The DNA profile obtained from Item 3 is approximately 670 septillion times more likely if it originated from victim and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals. Database(s) Used: NIST revised: African American, Asian, Caucasian, Hispanic

TABLE 7

WebCode-Test	Item 3 Methods & Results
CZXMRH - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from Victim and one unknown, unrelated individual. H2: The evidence originated from two unknown, unrelated individuals. The DNA profile obtained is approximately 2.2 octillion times more likely if it originated from Victim and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic.
D2RTLG - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from this item was interpreted as a mixture of two individuals. The DNA results are approximately 324 septillion times more likely if they originated from The Victim and an unknown, unrelated individual than if they originated from two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that The Victim is a contributor to the DNA from this item. The Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
DR322B - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** LR=2.90046E014 (2.9*10^14) in this two contributors mix, our LR is the ratio between Hp= a mix that consists of ITEM 1+ 1 Unknown, while Hd= a mix that consists of 2 Unknowns. **Database(s) Used:** "caucasian poulation frequencies" provided by Promega
DZWAKF - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** The DNA profile(s) from this item(s) was interpreted as a mixture of two individuals with Female Victim as an assumed contributor. Male Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** [Participant did not return a database used.]
E6M7KQ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Mixed DNA profile. Two contributors. The DNA profile is greater than 100 billion times more likely if the Victim is a contributor. The suspect is excluded. **Database(s) Used:** The LR is a population stratified calculation using the [Location Identifying Database].
EM2HCG - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile was interpreted as a mixture of two individuals including unknown female A. The DNA profile is at least 1 trillion times more likely if it originated from Female Victim (1) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, Southwest Hispanic
ENWXPE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** It is 2,1e22 times more likely to observe the DNA profile if the mixed stain on the dress (ITEM 3) originates from ITEM 1 (Victim) and one unknown person, than if it originated from two unknown persons, unrelated to ITEM 1 (Victim). Theta is 0.01 and probability of drop-in is 0.05. We did not detect the suspect’s biological traces (ITEM 2) in the disputed trace (ITEM 3). **Database(s) Used:** For statistical analysis we used internal [Population] statistics. Rare allele frequency is 0.0007.

TABLE 7

WebCode-Test	Item 3 Methods & Results
EQZU9G - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile was interpreted as a mixture of two individuals including unknown female individual A. The DNA profile is at least 1 trillion times more likely if it originated from female victim (1) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of female victim (1). Male suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS Core Allele Frequencies- Caucasian, African American, and Southwest Hispanics
ERWAKE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** I have calculated the mixed DNA profile to be one billion times more likely if it comprised DNA from the V and an unknown unrelated individual rather than if it originated from two unknown unrelated individuals. **Database(s) Used:** [Location Identifying Database]
F8HBKN - 5901	**Method(s)**: RMP **Stats Analysis:** DNA profile from Item 3 indicates a mixture of 2 individuals. DNA profile estimated to account for 65% of the DNA matches the DNA profile of the Victim. This DNA profile would not be expected to occur more than once among unrelated individuals in the world's population. This statistic is based on 19 of 21 loci. **Database(s) Used:** NIST 1036 revised 2017
FE3CWK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The results are consistent with the DNA profile from item #003-001-01A being a mixture of two contributors. Assuming two contributors, the DNA profile from item #003-001-01A is at least 1 trillion times more likely to occur if it originated from Female Victim and one unknown individual than if it originated from two unknown individuals. The results are consistent with the DNA profile from item #003-001-01B being a mixture of three contributors. Assuming three contributors, the DNA profile from item #003-001-01B is at least 460 million times more likely to occur if it originated from Female Victim and two unknown individuals than if it originated from three unknown individuals.1. **Database(s) Used:** FBI Extended AfAmBahJam; FBI Extended Cauc; FBI Extended SE Hisp
FYD629 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile is 2.24638E24 times more likely if it originated from Item 1 (victim) and 1 unknown individual than if it had originated from 2 unknown individuals. The statistical analysis does not support the proposition that Item 2 (suspect) is a contributor to the mixture DNA profile. **Database(s) Used:** NIST1036 Caucasian
FZ8V8M - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from dress (item 3) and the victim. A match between the data obtained from the questioned stain from dress (item 3) and the victim is approximately 200 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress (item 3) and the suspect is approximately 300 undecillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the questioned stain from dress (item 3). **Database(s) Used:** The National Institute of Standards and Technology’s 1036 Revised [Location Identifying Database] was used to generate DNA match statistics.

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WebCode-Test	Item 3 Methods & Results
G83CWJ - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the dress (item 3) and the victim. A match between the data obtained from the dress (item 3) and the victim is approximately 10 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the dress (item 3) and the suspect is approximately 1 duodecillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the dress (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
GJRAXG - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from dress (Item 3) and the victim. A match between the data obtained from the questioned stain from dress (Item 3) and the victim is approximately 8 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress (Item 3) and the suspect is approximately 100 decillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the questioned stain from dress (Item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
GXDN2G - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Due to an insufficient amount of male DNA detected during quantitation, Short Tandem Repeat (STR) analysis was not performed on sperm fraction. The DNA profile obtained from the epithelial fraction was interpreted as a mixture of two individuals. Assuming Female Victim (1) as a contributor, the mixture contains unknown female A. Male Suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended Caucasian, FBI Extended South West Hispanic, FBI Extended African American
H3M3JE - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from Victim and one unknown, unrelated individual. H2: The evidence originated from two unknown, unrelated individuals. The DNA profile obtained from Item 3 is 380 septillion times more likely if it originated from Victim and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
H9BPF7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The likelihood of observing the given trace under the hypothesis of the donorship of the victim and one unknown subject is 10^19 more likely than observing the given trace under the hypothesis of the contribution of two unknowns. **Database(s) Used:** Hill et al. Forensic Science International: Genetics 7 (2013) e82–e83. NIST 1036 Revised [Population] Dataset (July 2017)

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WebCode-Test	Item 3 Methods & Results
H9PEFC - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3.1 (Portion of "Questioned stain from dress found near victim's body"): The DNA profile from this item was interpreted as a mixture of two individuals. The DNA results are approximately 880 septillion times more likely if they originated from Female Victim and an unknown, unrelated individual than if they originated from two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that Female Victim is a contributor to the DNA from this item. Male Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036
HA79H8 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is approximately 2 quadrillion times more likely if it originated from Female Victim (K1) and one unknown individual than if it originated from two unknown individuals. This analysis provides very strong support for the proposition that Female Victim (K1) is included as a contributor to the DNA obtained from this sub-item. Male Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
HMATHB - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Hypothesis 1 (H1): The evidence originated from Victim and one unknown, unrelated individual. Hypothesis 2 (H2): The evidence originated from two unknown, unrelated individuals. The DNA profile obtained from Item 3 is approximately 190 septillion times more likely if it originated from Victim and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
JCRAYE - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile of the sperm fraction was interpreted as a mixture of two individuals. The DNA profile is at least 1 trillion times more likely if it originated from female victim (1) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of female victim (1). Due to the limited data obtained, no conclusions can be drawn for contributor 2. Male suspect (2) is excluded from the interpretable contributor in the DNA mixture. The DNA profile of the epithelial fraction was interpreted as a mixture of two individuals including an unknown female A. The DNA profile is at least 1 trillion times more likely if it originated from female victim (1) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of female victim (1). Male suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanics
JJP289 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixture is at least 91 octillion (10^27) times more likely if it originated from Victim and an unknown, unrelated individual, than if it originated from two unknown, unrelated individuals. This analysis provides very strong support for the proposition that Victim is a contributor to the mixture. **Database(s) Used:** NIST_1036

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WebCode-Test	Item 3 Methods & Results
KFMMYA - 5901	**Method(s):** Likelihood Ratio **Stats Analysis:** The DNA profile from this item was interpreted as a mixture of two individuals. The DNA results are approximately 1.50 octillion times more likely if they originated from the Female Victim and an unknown, unrelated individual than if they originated from two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the Female Victim is a contributor to the DNA from this item. The Male Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
KKTFQK - 5902	**Method(s):** Likelihood Ratio **Stats Analysis:** Victim (item Q1-1) cannot be excluded as a contributor to Mixture 1 (see Testing Summary) from blood on the dress from the hotel room (item Q03-1). The STR DNA results are estimated to be greater than one trillion times more likely if they originate from the victim and one unknown person than if they originate from two unknown people unrelated to the victim. **Database(s) Used:** NIST Asian, NIST African American, NIST Caucasian, Srivastava et al (2019) South Asian, [Location Identifying Database].
L6JPQZ - 5901	**Method(s):** Likelihood Ratio **Stats Analysis:** Assuming Female Victim (K1), the evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) and Male Suspect (K2) than if it originated from Female Victim (K1) and an unknown individual. Male Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
LBA2Q3 - 5902	**Method(s):** Likelihood Ratio **Stats Analysis:** A DNA profile consistent with a mixture of 2 individuals, neither of whom are male, with contributors in roughly 60:40 proportion was obtained for sample 26-5902_ LBA2Q3-Item 3 and analyzed in STRmix. 26-5902_ LBA2Q3-Item 1 (Victim) is included as a possible contributor to the mixture DNA profile obtained from 26-5902_ LBA2Q3-Item 3. The mixed DNA profile is 5.23025E21 times more likely if it originated from 26-5902_ LBA2Q3-Item 1 (Victim) and 1 unknown individual than if it had originated from 2 unknown individuals. Therefore, it is expected that one person in 5.23025E21 random individuals would provide an equal or greater likelihood ratio based on the scenario above. A DNA profile consistent with a mixture of 2 individuals, neither of whom are male, with contributors in roughly 60:40 proportion was obtained for sample 26-5902_LBA2Q3-Item 3. The statistical analysis does not support the proposition that 26-5902_LBA2Q3-Item 2 (Suspect) is a contributor to the mixture DNA profile. **Database(s) Used:** NIST1036 Caucasian
LRURMG - 5902	**Method(s):** Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from dress found near victim's body (Item 3) and Victim. A match between the data obtained from the questioned stain from dress found near victim's body (Item 3) and Victim is approximately 700 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress found near victim's body (Item 3) and Suspect is approximately 3 duodecillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the questioned stain from dress found near victim's body (Item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

TABLE 7

WebCode-Test	Item 3 Methods & Results
LV8TJ9 - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** The DNA profile from this item was interpreted as a mixture of two individuals with the female victim as an assumed contributor. The male suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
MG8BAZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Inclusion: item1 (victim); Log10=15 (LRmix Studio v. 2.1.5) and Log10=19 (EuroForMix v. 4.2.5). **Database(s) Used:** STRidER V.3/R.4 /[Country]
MK7PU6 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming two contributors, the DNA mixture is 1.9 octillion times more likely to be observed if Victim and an unknown person are the contributors than if two unknown people are the contributors. This provides very strong support that Victim is a contributor to the DNA mixture detected for the apparent bloodstain from the tan dress found near the victim's body (item 3). Assuming Victim and one additional contributor, the suspect is excluded from the DNA mixture detected on the apparent bloodstain from the tan dress found near the victim's body. **Database(s) Used:** LRs were calculated across the three major [Population] groups (African American, Caucasian, and Hispanic) with the lowest LR being reported for each pair of propositions. NIST Databases - Forensic Sci. Int.: Genetics 31 (2017) e36–e40
NKKENU - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The DNA on Item 3 came from the victim and an unknown, unrelated person. H2: The DNA on Item 3 came from two unknown, unrelated persons. LR= 1.84E+30. H1: The DNA on Item 3 came from the suspect and an unknown, unrelated person. H2: The DNA on Item 3 came from two unknown, unrelated persons. LR= 0. **Database(s) Used:** [Location Identifying Database]
NWDUKX - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence profile is approximately 6 quadrillion times more likely if it originated from Female Victim (K1) and an unknown individual than if it originated from two unknown individuals. This analysis provides very strong support for the proposition that Female Victim (K1) is a contributor to the DNA obtained from this sub-item. Male Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
PKJZL9 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from dress (item 3) and Victim. A match between the data obtained from the questioned stain from dress (item 3) and Victim is approximately thirty septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from dress (item 3) and Suspect is approximately ten duodecillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the questioned stain from dress (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

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WebCode-Test	**Item 3 Methods & Results**
PWCGDV - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 3: The evidence DNA profile is approximately 9 quadrillion times more likely if it originated from Female Victim (K1) and one unknown individual than if it originated from two unknown individuals. This analysis provides very strong support for the proposition that Female Victim (K1) is a contributor to the DNA obtained from this sub-item. Based on a likelihood ratio if 0, Male Suspect (K2) is excluded as a contributor to the evidence DNA profile. **Database(s) Used:** 2015 FBI expanded population database
QCKU6C - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1 - support for contribution >100 billion; Item 2 - Excluded; Resolved Unknown Female profile. **Database(s) Used:** The LR is a population stratified calculation using the following sub-population datasets: [Location Identifying Database]
QKVWQD - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA evidence is greater than 100 billion times more likely if the victim is a contributor. The suspect is excluded as a contributor. **Database(s) Used:** [Location Identifying Database]
QLQFTE - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** VICTIM (Q01-1) cannot be excluded as a contributor to Mixture 1 (see Testing Summary) from the stain on the dress (Q03-1) from the hotel room found near VICTIM. The STR DNA results are estimated to be greater than one trillion times more likely if they originate from VICTIM and one unknown person than if it originates from two unknown people unrelated to her. **Database(s) Used:** i. NIST Asian; ii. NIST African American; iii. NIST Caucasian; iv. Srivastava et al. (2019) South Asian; v. [Location Identifying Database]
QY8QPG - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA typing profile obtained from exhibit ITEM 3 (stain from dress, area AA: near centre) is of mixed origin consistent with having originated from two individuals. This profile is suitable for comparison, which provided the following results: Reference sample Likelihood Ratio (LR) Level of support; Exhibit ITEM 1 - VICTIM: 17 quadrillion; Very strong support for inclusion. Exhibit ITEM 2 - SUSPECT: n/a; Exclusion. a. The DNA evidence is LR times more likely to be observed if it originated from reference sample and one unknown, unrelated individual rather than if it originated from two unknown, unrelated individuals selected at random. b. The profile of an unknown individual was obtained and is consistent with being female. This profile has been personally designated as Female 1. See Remark 1. **Database(s) Used:** [Location Identifying Database]
R7WA2W - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile is 3.02437E16 times more likely if it originated from 26-5902_Item 1 (Victim) and 1 unknown individual than if it had originated from 2 unknown individuals. The statistical analysis does not support the proposition that 26-5902_Item 2 (Suspect) is a contributor to the mixture DNA profile. **Database(s) Used:** NIST1036_Cauc
RDVWRB - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** A. Proposition: Explanation 1: The DNA profile obtained originated from the Female Victim (Item 1) and an unknown, unrelated individual. Explanation 2: The DNA profile obtained originated from two unknown, unrelated individuals. The DNA profile obtained is approximately 4E29 times more likely (very strong support) if it originated from the Female Victim (Item 1) and an unknown, unrelated individual than if the DNA profile obtained originated from two unknown, unrelated individuals. **Database(s) Used:** NIST1036 (revised 2017) - Caucasian, African American, Hispanic

TABLE 7

WebCode-Test	Item 3 Methods & Results
RUEQHZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA obtained form item # 3 is a mixture of at least two individuals. Following set of hypotheses were evaluated: Hypothesis A: Hp; item #1 plus one unknown, Hd; two unknown, LR (MLE) = 90e^9. Hypothesis B: Hp; item # 1 plus item # 2, Hd; item #1 plus one unknown, LR (MLE) = 8.6e^-60. **Database(s) Used:** NIST Caucasian database 2017 with theta co-ancestry coefficient = 0.03
TFEBVC - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile obtained from this sample indicates the presence of DNA from two contributors. As such, an assumption of two contributors has been made for statistical analysis. Each of the reference DNA profiles associated to this case has been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA. Based on statistical analysis, it is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if the donor of Item 1 had contributed DNA, rather than if she had not. The donor of Item 2 has been excluded as a contributor. **Database(s) Used:** PP21 [Location Identifying Database].
TGAUWD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Victim: Not Excluded, LR = 100 billion. Suspect: Excluded. **Database(s) Used:** [Location Identifying Database] (PP21)
TKNR4Z - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixture of DNA is 8.32 x 10^23 times more likely if it had originated from the Victim and an unknown, unrelated individual than if it had originated from two unknown, unrelated individuals. This is support that the Victim can be included as a contributor to the mixture of DNA. **Database(s) Used:** Caucasian, African American, Southeast Hispanic, and Southwest Hispanic population groups from the 2015 FBI Population Data for the Expanded CODIS Core STR Loci
TLJA72 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3.1 (Portion of "Questioned stain from dress found near victim's body"): The DNA profile(s) from this item(s) was interpreted as a mixture of two individuals with the Female Victim as an assumed contributor. Based on the likelihood ratio result, the Male Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
UMRJXY - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming two contributors, the evidence profile is 950 septillion times more likely to be observed if the victim and one unknown are the contributors than if two unknowns are the contributors. **Database(s) Used:** NIST Databases - Forensic Sci. Int.: Genetics 31 (2017) e36–e40
V67HG2 - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** Due to an insufficient amount of male DNA detected during quantitation, Short Tandem Repeat (STR) analysis was not performed on the sperm fraction. The DNA profile of the epithelial fraction was interpreted as a mixture of two individuals, including unknown female individual A. The DNA profile is at least 1 trillion times more likely if it originated from Female Victim (1) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanic

TABLE 7

WebCode-Test	Item 3 Methods & Results
V6A37P - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA mixture is approximately 7 quadrillion times more likely if it originated from Female Victim (K1) and one unknown individual than if it originated from two unknown individuals. This analysis provides very strong support for the proposition that Female Victim (K1) is included as a contributor to the DNA obtained from this sub-item. Male Suspect (K2) is excluded as a contributor to the DNA obtained from this sub-item. **Database(s) Used:** 2015 Expanded FBI STR database
VBVWBM - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from item #03 is a mixture consistent with contributions from two individuals. Statistical analysis indicates that the DNA profile is approximately 1.92 × 10^45 times more likely if the contributors are the victim (item #01) and an unknown female, rather than two unknown, unrelated individuals. This provides extremely strong support for the inclusion of the victim as a contributor to the DNA mixture, with the second contributor being an unknown female. The DNA profile of the suspect (item #02) is not supported as a contributor to this mixture and is therefore excluded. **Database(s) Used:** NIST 1036 STR DNA DATABASE 2017
W648ZP - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming Female Victim (K1), the evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) and Male Suspect (K2) than if it originated from Female Victim (K1) and an unknown individual. Male Suspect (K2) is excluded based on a LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
W883G7 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A mixed DNA profile consistent with originating from two individuals was recovered. A contributor identified within this mixed DNA profile matched Victim. The DNA evidence is greater than 100 billion times more likely if Victim is a contributor. A further contributor identified within this mixed DNA profile was designated Unknown Female 1. Suspect is excluded as a contributor. **Database(s) Used:** [Location Identifying Database]
WGU2AX - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** The DNA profile from this item was interpreted as a mixture of two individuals with the female victim as an assumed contributor. The male suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
WP9QBQ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is approximately 15 quadrillion times more likely if it originated from Female victim (K1) and an unknown individual than if it originated from two unknown individuals. This analysis provides very strong support for the proposition that Female victim (K1) is a contributor to this mixture. Male suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
X9G8VV - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** NIST- CAUC
XNBWN7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence is at least 100 BILLION times more likely if the victim is one of two contributors to the mixed DNA profile than if the profile originated from two unknown individuals, unrelated to the victim, selected at random from the [Population]. **Database(s) Used:** [Location Identifying Database]

TABLE 7

WebCode-Test	**Item 3 Methods & Results**
YMVZW7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3: A DNA profile was obtained which appears to originate from two individuals. The DNA profile from the evidence is >100 billion times more likely if the victim is a contributor to the DNA along with an unknown unrelated individual, rather than two unknown unrelated individuals. The suspect is excluded as a contributor to the DNA profile. **Database(s) Used:** [Location Identifying Database]
YY83H6 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the stain from dress (Item 3) and victim. A match between the data obtained from the stain from dress (Item 3) and victim is approximately 7 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the stain from dress (Item 3) and subject is approximately 2 undecillion times less probable than a coincidental match to an unrelated person in the population. Subject is excluded from the data obtained from the stain from dress (Item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
ZBZ72N - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1 (Victim): 2.168e+22. **Database(s) Used:** [Location Identifying Database]
ZY36LY - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from the dress (item 3) and the female victim. A match between the data obtained from the questioned stain from the dress (item 3) and the female victim is approximately 400 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the questioned stain from the dress (item 3) and the male suspect is approximately 3 undecillion times less probable than a coincidental match to an unrelated person in the population. The male suspect is excluded from the data obtained from the questioned stain from the dress (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

Statistical Analysis for Item 4

TABLE 8

WebCode-Test	**Item 4 Methods & Results**
2U64XP - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Known contributors under Hp: victim and two unknowns. Known contributors under Hd: three unknowns. LR (total): 5,1E14. **Database(s) Used:** [Location Identifying Database]
2V3DTT - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** Item 4.2 (Portion of "Questioned stain from hotel bedsheet"- Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals, with at least two male contributors and with the "Known blood from female victim" as an assumed contributor. The "Known blood from the male suspect" is excluded as a possible contributor to the DNA from this item. Item 4.2 (Portion of "Questioned stain from hotel bedsheet"- Fraction 1): The DNA profile from this item was interpreted as a mixture of two individuals with at least two male contributors. The "Known blood from female victim" and the "Known blood from the male suspect" are excluded as possible contributors to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
3DCVDW - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The first fraction of the "...hotel bedsheet..." (item 4) contained a mixture of DNA from three individuals. A DNA match was identified between the data obtained from the first fraction of the "...hotel bedsheet..." (item 4) and the victim. A match between the data obtained from the first fraction of the "...hotel bedsheet..." (item 4) and the victim is approximately 400 trillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction of the "...hotel bedsheet..." (item 4) and the suspect is approximately 3 sextillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction of the "...hotel bedsheet..." (item 4). The second fraction of the "...hotel bedsheet..." (item 4) contained a mixture of DNA from at least three individuals. A DNA match between the data obtained from the second fraction of the "...hotel bedsheet..." (item 4) and the victim is approximately 7 nonillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the second fraction of the "...hotel bedsheet..." (item 4). A DNA match between the data obtained from the second fraction of the "...hotel bedsheet..." (item 4) and the suspect is approximately 5 septillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction of the "...hotel bedsheet..." (item 4). Due to limited data, no conclusive determination can be made as to the most minor evidence genotype from the data obtained from the second fraction of the "...hotel bedsheet..." (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
3GZ6PJ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 4e: The evidence DNA profile is approximately 7 quadrillion times more likely if it originated from Female Victim (K1) and two unknown individuals than if it originated from three unknown individuals. This analysis provides very strong support for inclusion. Male Suspect (K2) is excluded as a contributor to this profile based on a LR of zero. 4SP: Female Victim (K1) is excluded as a contributor to this profile based on a LR of zero. Male Suspect (K2) is excluded as a contributor to this profile based on a LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 8

WebCode-Test	Item 4 Methods & Results
3MLWYX - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the stain from hotel bedsheet (item 4) and Victim. A match between the data obtained from the first fraction from the stain from hotel bedsheet (item 4) and Victim is approximately 20 billion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the stain from hotel bedsheet (item 4) and Suspect is approximately 300 quintillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the first fraction from the stain from hotel bedsheet (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
3P6C3X - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The results are consistent with the DNA profile from item #004-001-01A being a mixture of three contributors with at least two of them being male. Assuming three contributors, the DNA profile from item #004-001-01A is at least 1 trillion times more likely to occur if it originated from female victim and two unknown individuals than if it originated from three unknown individuals. The results do not support the hypothesis that male suspect is a contributor to this profile. Assuming three contributors, male suspect is eliminated as a contributor to the DNA profile from item #004-001-01A. The results are consistent with the DNA profile from item #004-001-01B being a mixture of two male contributors. The results do not support the hypothesis that female victim is a contributor to this profile. Assuming two contributors, female victim is eliminated as a contributor to the DNA profile from item #004-001-01B. The results do not support the hypothesis that male suspect is a contributor to this profile. Assuming two contributors, male suspect is eliminated as a contributor to the DNA profile from item #004-001-01B. **Database(s) Used:** FBI Extended AfAmBahJam; FBI Extended Cauc; FBI Extended SE Hisp
4478ZQ - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from hotel bedsheet" – Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals with at least two male contributors and with the female victim as an assumed contributor. The male suspect is excluded as a possible contributor to the DNA from this item. Item 4.1 (Portion of "Questioned stain from hotel bedsheet" – Fraction 1): The DNA profile from this item was interpreted as a mixture of two individuals with at least two male contributors. The female victim and the male suspect are excluded as possible contributors to the DNA from this item. **Database(s) Used:** [Participant did not report a database used.]
46DPW2 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** 2. VICTIM (item 1-1) cannot be excluded as a contributor to Mixture 2 (see Testing Summary) from a portion of blood and semen from a hotel bedsheet (item 4-1E). The STR DNA results are estimated to be greater that one trillion times more likely if they originate from VICTIM and two unknown people than if they originate from three unknown people unrelated to VICTIM. SUSPECT (item 2-1) is excluded as a contributor to Mixture 2. 3. VICTIM (item 1-1) cannot be excluded as a contributor to Mixture 3 (see Testing Summary) from a portion of blood and semen from a hotel bedsheet (item 4-1S). The STR DNA results are estimated to be equally likely if they originate from VICTIM and two unknown people than if they originate from three unknown people unrelated to VICTIM. SUSPECT (item 2-1) is excluded as a contributor to Mixture 3. **Database(s) Used:** NIST Asian, NIST African American, NIST Caucasian Srivastava et al. (2019) South Asian, [Location Identifying Database]

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WebCode-Test	**Item 4 Methods & Results**
6CE2VJ - 5901	Method(s): Likelihood Ratio Stats Analysis: Hp: The mixture contains the DNA of the victim and two unknown people. Hd: The mixture contains the DNA of three unknown people. LR=Hp/Hd= 3,87*10 exp11> 1.000.000 (extremely strong support for Hp). Database(s) Used: [Location Identifying Database]
6DBH6U - 5902	Method(s): Likelihood Ratio Stats Analysis: A DNA match was identified between the data obtained from the first fraction of the stain from hotel bedsheet (item 4) and the victim. A match between the data obtained from the first fraction of the stain from hotel bedsheet (item 4) and the victim is approximately 1 octillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction of the stain from hotel bedsheet (item 4) and the suspect is approximately 4 quintillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction of the stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction of the stain from hotel bedsheet (item 4) and the victim is approximately 300 septillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the second fraction of the stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction of the stain from hotel bedsheet (item 4) and the suspect is approximately 2 octillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction of the stain from hotel bedsheet (item 4). Database(s) Used: The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
6FWJNN - 5901	Method(s): Likelihood Ratio Stats Analysis: Item 4.1 (Portion of "Questioned stain from hotel bedsheet" - Fraction 1): The DNA profile from this item was interpreted as a mixture of three individuals with at least two male contributors. Based on the likelihood ratio result, the female victim and the male suspect are excluded as possible contributors to the DNA from this item. Item 4.1 (Portion of "Questioned stain from hotel bedsheet" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals with at least two male contributors and with the female victim as an assumed contributor. Based on the likelihood ratio result, the male suspect is excluded as a possible contributor to the DNA from this item. Database(s) Used: NIST 1036 July 2017

TABLE 8

WebCode-Test	**Item 4 Methods & Results**
6GAT2U - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet (blue) (item 4) and the female victim. A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (blue) (item 4) and the female victim is approximately 400 million times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (blue) (item 4) and the male suspect is approximately 200 quintillion times less probable than a coincidental match to an unrelated person in the population. The male suspect is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet (blue) (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (blue) (item 4) and the female victim is approximately 100 nonillion times less probable than a coincidental match to an unrelated person in the population. The female victim is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (blue) (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (blue) (item 4) and the male suspect is approximately 200 octillion less probable than a coincidental match to an unrelated person in the population. The male suspect is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (blue) (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
6H6C3W - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction of the stain from hotel bedsheet (item 4) and the victim. A match between the data obtained from the first fraction of the stain from hotel bedsheet (item 4) and victim is approximately twenty septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction of the stain from hotel bedsheet (item 4) and the suspect is approximately thirty quintillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction of the stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction of the stain from hotel bedsheet (item 4) and the suspect is approximately ten septillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction of the stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction of the stain from hotel bedsheet (item 4) and the victim is approximately twenty septillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the second fraction of the stain from hotel bedsheet (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
6UBPYM - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** LRmix studio 2.1.3-community edition, caucasian population, theta = 0.01 used. The victim's contribution in the mixture is calculated according to the following hypothesis : Hp = the mixture belongs to the Victim and 2 unknown people. Hd = the mixture belongs to 3 unknown people. LR = 5.43915E8. **Database(s) Used:** caucasian population from Globalfiler IQC kit used.

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WebCode-Test	Item 4 Methods & Results
76CCPY - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Epithelial Fraction: This item/sample provided a DNA profile that indicated the presence of three contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode (Item 1) has contributed to this mixed DNA profile. The statistical interpretation shows that the associated barcode (Item 2) sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to [Location Identifying Database]. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to [Location Identifying Database] for intelligence purposes. This partially deconvoluted DNA profile is consistent with associated barcode (UKM1) and is therefore a possible contributor to this mixed DNA profile. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to [Location Identifying Database]. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to [Location Identifying Database] for intelligence purposes. This partially deconvoluted DNA profile is consistent with associated barcode (UKP1) and is therefore a possible contributor to this mixed DNA profile. Spermatozoa Fraction: This item/sample provided a DNA profile that indicated the presence of three contributors. Based on information provided to the laboratory, it has been assumed that the associated barcode (Item 1) has contributed to this mixed DNA profile. The statistical interpretation shows that the associated barcode (Item 2) sent with this exhibit report has been compared, and can be excluded as having contributed to this mixed DNA profile. This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to [Location Identifying Database]. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to [Location Identifying Database] for intelligence purposes. This partially deconvoluted DNA profile is consistent with associated barcode (UKM1) and is therefore a possible contributor to this mixed DNA profile. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on [Location Identifying Database] (as per the [Location Identifying Database] matching rules). Any subsequent profiles that are loaded to [Location Identifying Database] will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. This item/sample provided a DNA profile that indicated the presence of three contributors. When conditioning on the assumed known contributor, a remaining contribution has been separated. This remaining contribution is a mixed DNA profile which has been deconvoluted in order to resolve any DNA profiles suitable for loading to [Location Identifying Database]. In this instance, the analysis resulted in a partially deconvoluted DNA profile able to be loaded to [Location Identifying Database] for intelligence purposes. This partially deconvoluted DNA profile is consistent with associated barcode (UKP1) and is therefore a possible contributor to this mixed DNA profile. The partially deconvoluted DNA profile will be searched against any DNA profiles already held on [Location Identifying Database] (as per the [Location Identifying Database] matching rules). Any subsequent profiles that are loaded to [Location Identifying Database] will be searched against this DNA profile. It is important to note that this process has been performed for intelligence purposes only, and that any reference samples subsequently received will be compared with the entire mixed DNA profile, with the result reported as a likelihood ratio. Depending on the nature of the mixed DNA profile, the strength of the support for contribution will vary. **Database(s) Used:** [Location Identifying Database]

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WebCode-Test	Item 4 Methods & Results
7G4YWE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 4A-3PT_NS: Assuming Female Victim (K1), Male suspect (K2) is excluded based on the LR of zero. 4A-3PT_SP: The evidence DNA profile is approximately 4 times more likely if it originated from Female Victim (K1) and 2 unknown individuals than if it originated from 3 unknown individuals. This provides limited support for inclusion. Coincidental matching to random individuals and exclusions of true donors have been observed for samples associated with likelihood ratios in the limited support range. The evidence DNA profile is approximately 208 times more likely if it originated from 3 unknown individuals than if it originated from Male Suspect (K2) and 2 unknown individuals. This provides moderate support for exclusion. **Database(s) Used:** 2015 FBI Expanded Population Database
7MMEUW - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile from fraction 1 of Item 4 indicates a mixture of 3 individuals. Victim is expected to be present in the mixture (estimated to account for 74% of the DNA). Assuming the presence of Victim, the DNA profile from Suspect was compared to the mixture. An LR of zero was calculated for this comparison. Suspect is excluded as being a contributor to this DNA mixture. **Database(s) Used:** NIST 1036 Revised 2017
8FQNHM - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Epithelial Fraction: The mixture of DNA is 9.20 x 10^16 times more likely if it had originated from the Victim and two unknown, unrelated individuals than if it had originated from three unknown, unrelated individuals. This is support that the Victim can be included as a contributor to the mixture of DNA. Sperm Fraction: The mixture of DNA is 1.10 x 10^15 times more likely if it had originated from the Victim and two unknown, unrelated individuals than if it had originated from three unknown, unrelated individuals. This is support that the Victim can be included as a contributor to the mixture of DNA. **Database(s) Used:** Caucasian, African American, Southeast Hispanic, and Southwest Hispanic population groups from the 2015 FBI Population Data for the Expanded CODIS Core STR Loci.
8RZL2G - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** for 4e:Assuming Female Victim (K1), Male Suspect (K2) is excluded based on an LR of 0. for 4sp: Female Victim (K1) and Male Suspect (K2) are excluded based on LR of 0. **Database(s) Used:** 2015 FBI Expanded Population Database

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WebCode-Test	**Item 4 Methods & Results**
993KMP - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and the victim. A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and the victim is approximately 5 octillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and the suspect is approximately 400 million times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4). There is a 5.36% chance of a false exclusion. A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) and the victim is approximately 8 nonillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) and the suspect is approximately 30 octillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
9X3XVT - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming three contributors, including at least two males, the DNA typing results were interpreted using probabilistic genotyping software. The DNA typing results are 161 quintillion times more likely to be observed if they originated from the "female victim" (Item 1) and two unknown, unrelated individuals, rather than if they originated from three unknown, unrelated individuals. The results provide very strong support for the proposition that the "female victim" (Item 1) is a contributor to the DNA obtained from Item 4 SF rather than the alternate proposition. The "male suspect" (Item 2) is excluded as a contributor to this mixture. **Database(s) Used:** NIST 1036 (2017)
AAT7UL - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from the sperm fraction was interpreted as a mixture of three individuals, including unknown male individual A and unknown male individual B. Due to the limited data obtained, no conclusions can be drawn for contributor(s) three. The Victim (1) and Suspect (2) are excluded from the interpretable contributors to the DNA mixture. The DNA profile obtained from the epithelial fraction was interpreted as a mixture of three individuals. The DNA profile is at least 1 trillion times more likely if it originated from the Victim (1) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of the Victim (1). The Suspect (2) is excluded from the mixed DNA profile. **Database(s) Used:** FBI Extended CODIS core alleles frequencies - Caucasian, African American, and Southwest Hispanic
ABPL7H - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** nest_cauc

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WebCode-Test	**Item 4 Methods & Results**
AQ3XWQ - 5902	Method(s): Likelihood Ratio Stats Analysis: A DNA match between the data obtained from the first fraction obtained from the questioned stain from hotel bedsheet (item 4) and the victim is approximately twenty sextillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the first fraction obtained from the questioned stain from hotel bedsheet (item 4). A DNA match between the data obtained from the first fraction obtained from the questioned stain from hotel bedsheet (item 4) and the suspect is approximately ninety sextillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction obtained from the questioned stain from hotel bedsheet (item 4). Due to limited data, no conclusive determination can be made as to the most minor evidence genotype from the data obtained from the first fraction obtained from the questioned stain from hotel bedsheet (item 4). A DNA match was identified between the data obtained from the second fraction obtained from the questioned stain from hotel bedsheet (item 4) and the victim. A match between the data obtained from the second fraction obtained from the questioned stain from hotel bedsheet (item 4) and the victim is approximately forty thousand times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the second fraction obtained from the questioned stain from hotel bedsheet (item 4) and the suspect is approximately nine hundred trillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction obtained from the questioned stain from hotel bedsheet (item 4). There is a 5.36% chance of a false exclusion. Database(s) Used: All evidence genotypes were compared with all reference genotypes to compute likelihood ratio (LR) DNA match statistics. The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
AWLZ4T - 5902	Method(s): Likelihood Ratio Stats Analysis: A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet… (item #4) and the female victim (item #1). A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet… (item #4) and the female victim (item #1) is approximately 20 quadrillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet… (item #4) and the male suspect (item #2) is approximately 200 septillion times less probable than a coincidental match to an unrelated person in the population. The male suspect (item #2) is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet… (item #4). A DNA match was identified between the data obtained from the second fraction from the questioned stain from hotel bedsheet… (item #4) and the female victim (item #1). A match between the data obtained from the second fraction from the questioned stain from hotel bedsheet… (item #4) and the female victim (item #1) is approximately 1 million times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet… (item #4) and the male suspect (item #2) is approximately 10 trillion times less probable than a coincidental match to an unrelated person in the population. The male suspect (item #2) is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet… (item #4). There is a 5.36% chance of a false exclusion. Database(s) Used: The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

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WebCode-Test	Item 4 Methods & Results
AXW3PR - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For the possible involvement of the female victim in the sperm fraction of item 4, the LR value calculated was 1.93E14 to 1, which means it is about 1.93E14 times more likely that the observed DNA profile being a mixture originating from the female victim and two unknown individuals than if it originating from three unrelated individuals selected at random from the local [Population]. For the possible involvement of the female victim in the epithelial fraction of item 4, the LR value calculated was 6.82E7 to 1, which means it is about 6.82E7 times more likely that the observed DNA profile being a mixture originating from the female victim and two unknown individuals than if it originating from three unrelated individuals selected at random from the local [Population]. **Database(s) Used:** [Location Identifying Database]
AZ3KNM - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from the sperm fraction was interpreted as a mixture of two individuals including unknown male individual B and unknown male individual C. Female Victim (1) and Male Suspect (2) are excluded as contributors to the DNA profile. The DNA profile obtained from the epithelial fraction was interpreted as a mixture of three individuals including unknown male individual B. The DNA profile is at least 1 trillion times more likely if it originated from Female Victim (1) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI extended CODIS core allele frequencies - Caucasian, African American and Southwest Hispanic
BH4RFU - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Sperm fraction: Victim - excluded. Suspect - excluded. Non-Sperm fraction: Victim - not excluded (LR = 100 billion). Suspect - excluded. **Database(s) Used:** [Location Identifying Database]
BUGRCN - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and Victim. A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and Victim is approximately 10 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and Suspect is approximately 100 quintillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) and Victim is approximately 1 nonillion times less probable than a coincidental match to an unrelated person in the population. Victim is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) and Suspect is approximately 30 octillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

TABLE 8

WebCode-Test	Item 4 Methods & Results
CRMK7G - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** (H1): The evidence originated from victim and two unknown, unrelated individuals. (H2): The evidence originated from three unknown, unrelated individuals. The DNA profile obtained from Item 4 NSF is approximately 20 septillion times more likely if it originated from victim and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
CZXMRH - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from Victim and two unknown, unrelated individuals. H2: The evidence originated from three unknown, unrelated individuals. The DNA profile obtained is approximately 20 septillion times more likely if it originated from Victim and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic.
D2RTLG - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from hotel bedsheet" - Fraction 1 and Fraction 2): A contamination event occurred. No results will be reported for this item. Please see Quality Report 2026-011 for additional information [Report not included]. Item 4.2 (Portion of "Questioned stain from hotel bedsheet" - Fraction 1): The DNA profile from this item was interpreted as a mixture of two individuals with at least two male contributors. The Victim and The Suspect are excluded as possible contributors to the DNA from this item. Item 4.2 (Portion of "Questioned stain from hotel bedsheet" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals with at least two male contributors and with The Victim as an assumed contributor. Based on the likelihood ratio result, The Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
DR322B - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** LR=3.96106E009 (3.96*10^9) in this three contributors mix, our LR is the ratio between Hp= a mix that consists of ITEM 1+ 2 Unknown, while Hd= a mix that consists of 3 Unknowns. **Database(s) Used:** "caucasian poulation frequencies" provided by Promega
DZWAKF - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** Fraction 1- The DNA profile(s) from this item(s) was interpreted as a mixture of two individuals with at least two male contributors. Female Victim and Male Suspect are excluded as possible contributors to the DNA from this item. Fraction 2- The DNA profile(s) from this item(s) was interpreted as a mixture of three individuals with at least two male contributors and with Female Victim as an assumed contributor. Male Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** [Participant did not report a database used.]
E6M7KQ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Fraction 1 - Mixed DNA profile. Three contributors. The DNA profile is approximately 254 million times more likely if the Victim is a contributor. The suspect is excluded. Fraction 2 - Mixed DNA profile. Three contributors. The DNA profile is greater than 100 billion times more likely if the Victim is a contributor. The suspect is excluded. **Database(s) Used:** The LR is a population stratified calculation using the [Location Identifying Database].

TABLE 8

WebCode-Test	Item 4 Methods & Results
EM2HCG - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile of the sperm fraction was interpreted as a mixture of three individuals including unknown male B and unknown male C. Due to the limited data obtained, no conclusions can be drawn for contributor three. Female Victim (1) and Male Suspect (2) are excluded from the interpretable contributors in the DNA mixture. The DNA profile of the epithelial fraction was interpreted as a mixture of three individuals including unknown male B. The DNA profile is at least 1 trillion times more likely if it originated from Female Victim (1) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, Southwest Hispanic
ENWXPE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** It is 1,6e13 times more likely to observe the DNA profile if the mixed stain on the hotel bedsheet (ITEM 4 - epitel) originates from ITEM 1 (Victim) and two unknown persons, than if it originated from three unknown persons, unrelated to ITEM 1 (Victim). Theta is 0.01 and probability of drop-in is 0.05. We did not detect the suspect's biological traces (ITEM 2) in the disputed trace (ITEM 4 - epitel). It is 4,6e9 times more likely to observe the DNA profile if the mixed stain on the hotel bedsheet (ITEM 4 - sperm) originates from ITEM 1 (Victim) and two unknown persons, than if it originated from three unknown persons, unrelated to ITEM 1 (Victim). Theta is 0.01 and probability of drop-in is 0.05. We did not detect the suspect's biological traces (ITEM 2) in the disputed trace (ITEM 4 - sperm). **Database(s) Used:** For statistical analysis we used internal [Population] statistics. Rare allele frequency is 0.0007.
EQZU9G - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile of the sperm fraction was interpreted as a mixture of two individuals including unknown male A and unknown male B. Female victim (1) and male suspect (2) are excluded as contributors to the DNA profile. The DNA profile of the epithelial fraction was interpreted as a mixture of three individuals. The DNA profile is at least 1 trillion times more likely if it originated from female victim (1) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of female victim (1). Male suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS Core Allele Frequencies- Caucasian, African American, and Southwest Hispanics
ERWAKE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** I have calculated the mixed DNA profile to be around 200 times more likely if it comprised DNA from the V and two unknown unrelated individuals rather than if it originated from three unknown unrelated individuals. **Database(s) Used:** [Location Identifying Database]

TABLE 8

WebCode-Test	Item 4 Methods & Results
F8HBKN - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** DNA profile from Fraction 1 of Item 4 indicates a mixture of 3 individuals. The Victim is expected to be present in the mixture (estimated to account for 83% of the DNA). Assuming the presence of Victim, the DNA profile from Suspect was compared to the mixture. An LR of zero was calculated for this comparison. Suspect is excluded as being a contributor to this DNA mixture. DNA profile from Fraction 2 of Item 4 indicates a mixture of 3 individuals. The DNA profile from Victim was compared to the mixture. This mixture is approximately 20 times more likely (limited support) to be observed if it originated from Victim and 2 unknown, unrelated individuals than if it originated from 3 unknown, unrelated individuals. The DNA profile from Suspect was compared to the mixture. This mixture is approximately 6,000 times more likely (moderate support) to be observed if it originated from 3 unknown, unrelated individuals than if it originated from Suspect and 2 unknown, unrelated individuals. **Database(s) Used:** NIST 1036 Revised 2017
FE3CWK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The results are consistent with the DNA profile from item #004-001-01A being a mixture of three contributors with two of them being male. Assuming three contributors, the DNA profile from item #004-001-01A is at least 1 trillion times more likely to occur if it originated from Female Victim and two unknown individuals than if it originated from three unknown individuals. **Database(s) Used:** FBI Extended AfAmBahJam; FBI Extended Cauc; FBI Extended SE Hisp
FYD629 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile is 3.76922E21 times more likely if it originated from Item 1 (victim) and 2 unknown individual than if it had originated from 3 unknown individuals. The statistical analysis does not support the proposition that Item 2 (suspect) is a contributor to the mixture DNA profile. **Database(s) Used:** NIST1036 Caucasian
FZ8V8M - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4) and the victim. A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4) and the victim is approximately 20 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4) and the suspect is approximately 1 septillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4) and the victim is approximately 2 nonillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4) and the suspect is approximately 600 septillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics.

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WebCode-Test	Item 4 Methods & Results
G83CWJ - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the bedsheet (item 4) and the victim. A match between the data obtained from the first fraction from the bedsheet (item 4) and the victim is approximately 500 quadrillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the bedsheet (item 4) and the suspect is approximately 100 sextillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction from the bedsheet (item 4). A DNA match between the data obtained from the second fraction from the bedsheet (item 4) and the victim is approximately 1 decillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the second fraction from the bedsheet (item 4). A DNA match between the data obtained from the second fraction from the bedsheet (item 4) and the suspect is approximately 5 nonillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction from the bedsheet (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
GJRAXG - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and the victim. A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and the victim is approximately 2 octillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and the suspect is approximately 10 octillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4). Due to limited data, no conclusive determination can be made as to the most minor evidence genotype(s) from the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) and the victim is approximately 200 nonillion times less probable than a coincidental match to an unrelated person in the population. The victim is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) and the suspect is approximately 1 nonillion times less probable than a coincidental match to an unrelated person in the population. The suspect is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

TABLE 8

WebCode-Test	Item 4 Methods & Results
GXDN2G - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from the sperm fraction was interpreted as a mixture of two individuals consisting of unknown male individual A and unknown male individual B. Female Victim (1) and Male Suspect (2) are excluded as contributors to the DNA profile. The DNA profile obtained from the epithelial fraction was interpreted as a mixture of three individuals, including unknown male individual A. The DNA profile is at least 1 trillion times more likely if it originated from Female Victim (1) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended Caucasian, FBI Extended South West Hispanic, FBI Extended African American
H3M3JE - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from Victim and two unknown, unrelated individuals. H2: The evidence originated from three unknown, unrelated individuals. The DNA profile obtained from the non-sperm cell fraction of Item 4 is 2.6 octillion times more likely if it originated from Victim and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
H9BPF7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The likelihood of observing the given trace under the hypothesis of the donorship of the victim and two unknowns subject is 10^16 more likely than observing the given trace under the hypothesis of the contribution of three unknowns. **Database(s) Used:** Hill et al. Forensic Science International: Genetics 7 (2013) e82–e83. NIST 1036 Revised [Population] Dataset (July 2017)
H9PEFC - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from hotel bedsheet" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals with at least two male contributors and with Female Victim as an assumed contributor. Male Suspect is excluded as a possible contributor to the DNA from this item. Item 4.1 (Portion of "Questioned stain from hotel bedsheet" - Fraction 1): The DNA profile from this item was interpreted as a mixture of two individuals with at least two male contributors. Female Victim and Male Suspect are excluded as possible contributors to the DNA from this item. **Database(s) Used:** STRmix V2.6
HA79H8 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 4e: Assuming Female Victim (K1), Male Suspect (K2) is excluded based on the LR of zero. For 4sp: Female Victim (K1) is excluded based on the LR of zero. Male Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
JCRAYE - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile of the sperm fraction was interpreted as a mixture of two unknown individuals including unknown male B and unknown male C. An additional allele was detected from which no conclusion can be drawn due to insufficient sample data. Female victim (1) and male suspect (2) are excluded as contributors to the DNA profile. The DNA profile of the epithelial fraction was interpreted as a mixture of three individuals including unknown male B. Female victim (1) was assumed as a contributor. Male suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanics

TABLE 8

WebCode-Test	Item 4 Methods & Results
JJP289 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixture is at least 710 octillion (10^27) times more likely if it originated from Victim and two unknown, unrelated individuals, than if it originated from three unknown, unrelated individuals. This analysis provides very strong support for the proposition that Victim is a contributor to the mixture. **Database(s) Used:** NIST_1036
KFMMYA - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 4sp: The DNA profile from this item was interpreted as a mixture of two individuals with at least two male contributors. The Female Victim and the Male Suspect are excluded as possible contributors to the DNA from this item. 4e: The DNA profile from this item was interpreted as a mixture of three individuals with at least two male contributors. The DNA results are approximately 8.22 octillion times more likely if they originated from the Female Victim and two unknown, unrelated individuals than if they originated from three unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the Female Victim is a contributor to the DNA from this item. The Male Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
KKTFQK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Victim (item Q1-1) cannot be excluded as a contributor to Mixture 2 (see Testing Summary) from blood and semen stain on the bedsheet from the hotel room (item Q04-1). The STR DNA results are estimated to be greater than one trillion times more likely if they originate from the victim and two unknown people than if they originate from three unknown people unrelated to the victim. **Database(s) Used:** NIST Asian, NIST African American, NIST Caucasian, Srivastava et al (2019) South Asian, [Location Identifying Database].
L6JPQZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4e: Assuming Female Victim (K1), the evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1), Male Suspect (K2), and an unknown individual than if it originated from Female Victim (K1) and 2 unknown individuals. Male Suspect (K2) is excluded based on the LR of zero. Item 4sp: The evidence DNA profile is approximately 0 times more likely if it originated from the person of interest and an unknown individual than if it originated from 2 unknown individuals. Female Victim (K1) and Male Suspect (K2) are both excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
LBA2Q3 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA profile consistent with a mixture of 3 individuals, at least 2 of whom are male, with contributors in roughly 5:3:1 proportion was obtained for sample 26-5902_ LBA2Q3-Item 4 and analyzed in STRmix. 26-5902_ LBA2Q3-Item 1 (Victim) is included as a possible contributor to the mixture DNA profile obtained from 26-5902_ LBA2Q3-Item 4. The mixed DNA profile is 1.30675E22 times more likely if it originated from 26-5902_ LBA2Q3-Item 1 (Victim) and 2 unknown individuals than if it had originated from 3 unknown individuals. Therefore, it is expected that one person in 1.30675E22 random individuals would provide an equal or greater likelihood ratio based on the scenario above. A DNA profile consistent with a mixture of 3 individuals, at least 2 of whom are male, with contributors in roughly 5:3:1 proportion was obtained for sample 26-5902_ LBA2Q3-Item 4 and analyzed in STRmix. The statistical analysis does not support the proposition that 26-5902_ LBA2Q3-Item 2 (Suspect) is a contributor to the mixture DNA profile. **Database(s) Used:** NIST1036 Caucasian

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WebCode-Test	**Item 4 Methods & Results**
LRURMG - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and Victim. A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and Victim is approximately 200 billion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4) and Suspect is approximately 5 sextillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet (Item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) and Suspect is approximately 200 million times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4). There is a 5.36% chance of a false exclusion. **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
LV8TJ9 - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** 4e: The DNA profile from this item was interpreted as a mixture of three individuals, with at least two male contributors and with the female victim as an assumed contributor. The male suspect is excluded as a possible contributor to the DNA from this item. 4sp: The DNA profile from this item was interpreted as a mixture of two individuals with at least two male contributors. The female victim and the male suspect are excluded as possible contributors to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
MG8BAZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Inclusion: item1 (victim); Log10=9 (LRmix Studio v. 2.1.5) and Log10=12 (EuroForMix v. 4.2.5). **Database(s) Used:** STRidER V.3/R.4 /[Country]

TABLE 8

WebCode-Test	**Item 4 Methods & Results**
MK7PU6 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming three contributors, the DNA mixture is forty times more likely to be observed if three unknown people are the contributors than if Victim and two unknown people are the contributors. This provides limited support that Victim is not a contributor to the DNA mixture detected for the sperm fraction of the semen/apparent bloodstain from the blue hotel bedsheet (item 4). Assuming three contributors, the DNA mixture is 1,800 times more likely to be observed if three unknown people are the contributors than if Suspect and two unknown people are the contributors. This provides moderate support that Suspect is not a contributor to the DNA mixture detected for the sperm fraction of the semen/apparent bloodstain from the blue hotel bedsheet. Assuming three contributors, the DNA mixture is 160 septillion times more likely to be observed if Victim and two unknown people are the contributors than if three unknown people are the contributors. This provides very strong support that Victim is a contributor to the DNA mixture detected for the non-sperm fraction of the semen/apparent bloodstain from the blue hotel bedsheet (item 4). Assuming Victim and two additional contributors, the DNA mixture is 40 trillion times more likely to be observed if Victim and two unknown people are the contributors than if Suspect, Victim and an unknown person are the contributors. This provides very strong support that Suspect is not a contributor to the DNA mixture detected for the non-sperm fraction of the semen/apparent bloodstain from the blue hotel bedsheet. **Database(s) Used:** LRs were calculated across the three major [Population] groups (African American, Caucasian, and Hispanic) with the lowest LR being reported for each pair of propositions. NIST Databases - Forensic Sci. Int.: Genetics 31 (2017) e36–e40
NKKENU - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The DNA in the epithelial fraction of Item 4 came from the victim and two unknown, unrelated person. H2: The DNA in the epithelial fraction of Item 4 came from three unknown, unrelated persons. LR= 1.35E+30. H1: The DNA in the epithelial fraction of Item 4 came from the suspect and two unknown, unrelated person. H2: The DNA in the epithelial fraction of Item 4 came from three unknown, unrelated persons. LR= 0. H1: The DNA in the sperm fraction of Item 4 came from the victim and an unknown, unrelated person. H2: The DNA in the sperm fraction of Item 4 came from two unknown, unrelated persons. LR= 0. H1: The DNA in the sperm fraction of Item 4 came from the suspect and an unknown, unrelated person. H2: The DNA in the sperm fraction of Item 4 came from two unknown, unrelated persons. LR= 0. **Database(s) Used:** [Location Identifying Database]
NWDUKX - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 4e: Assuming Female Victim (K1), Male Suspect (K2) is excluded based on the LR of zero. For 4sp: The evidence profile is approximately 3 times more likely if it originated from three unknown individuals than if it originated from Female Victim (K1) and two unknown individuals. This analysis provides limited support for the proposition that Female Victim (K1) is excluded as a contributor to the DNA obtained from this sub-item. Male Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 8

WebCode-Test	Item 4 Methods & Results
PKJZL9 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4) and Victim. A match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4) and Victim is approximately five hundred billion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4) and Suspect is approximately one sextillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the first fraction from the questioned stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4) and Victim is approximately one decillion times less probable than a coincidental match to an unrelated person in the population. Victim is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4) and Suspect is approximately two octillion times less probable than a coincidental match to an unrelated person in the population. Suspect is excluded from the data obtained from the second fraction from the questioned stain from hotel bedsheet (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
PWCGDV - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 4e: The evidence DNA profile is approximately 42 quadrillion times more likely if it originated from Female Victim (K1) and two unknown individuals than if it originated from three unknown individuals. This analysis provides very strong support for the proposition that Female Victim (K1) is a contributor to the DNA obtained from this sub-item. Based on a likelihood ratio if 0, Male Suspect (K2) is excluded as a contributor to the evidence DNA profile. 4sp: Based on a likelihood ratio if 0, Female Victim (K1) and Male Suspect (K2) are excluded as contributors to the evidence DNA profile. **Database(s) Used:** 2015 FBI expanded population database
QCKU6C - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Spermatozoa Fraction: Item 1 - support for contribution >100 billion; Item 2 - Excluded; Unresolved Unknown Contributor; Unresolved Unknown Contributor. Epithelial Fraction: Item 1 - support for contribution >100 billion; Item 2 - Excluded; Resolved Unknown Contributor; Unresolved Unknown Contributor. **Database(s) Used:** The LR is a population stratified calculation using the following sub-population datasets: [Location Identifying Database]
QKVWQD - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Epithelial Fraction: The DNA evidence is greater than 100 billion times more likely if the victim is a contributor. The DNA evidence is more likely if the suspect is not a contributor. Sperm Fraction: The DNA evidence is 4.4 million times more likely if the victim is a contributor. The DNA evidence is more likely if the suspect is not a contributor. **Database(s) Used:** [Location Identifying Database]

TABLE 8

WebCode-Test	**Item 4 Methods & Results**
QY8QPG - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA typing results obtained from exhibit ITEM 4 (stain from bedsheet, area AA: near centre) are of mixed origin, consistent with having originated from three individuals, at least one of whom is male. a. The DNA typing profile obtained from fraction one of these results is of mixed origin, consistent with having originated from three individuals, at least one of whom is male. The donor of the known sample, exhibit ITEM 1 (VICTIM), is assumed to be a contributor to this profile. This profile is suitable for comparison. i. The donor of the known sample, exhibit ITEM 2 (SUSPECT), is excluded from this mixed profile. ii. The donor of the Female 1 profile is excluded from this mixed profile. b. The DNA typing profile obtained from fraction two of these results is of mixed origin, consistent with having originated from two individuals, at least one of whom is male. This profile is suitable for comparison. See remark 1. i. The donors of the known samples, exhibits ITEM 1 (VICTIM 1) and ITEM 2 (SUSPECT), are excluded from this mixed profile. ii. The donor of the Female 1 profile is excluded from this mixed profile. **Database(s) Used:** [Location Identifying Database]
R7WA2W - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The mixed DNA profile is 3.64508E17 times more likely if it originated from 26-5902_Item 1 (Victim) and 2 unknown individuals than if it had originated from 3 unknown individuals. The statistical analysis does not support the proposition that 26-5902_Item 2 (Suspect) is a contributor to the mixture DNA profile. **Database(s) Used:** NIST1036_Cauc
RDVWRB - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Fraction 1: a. Proposition: Explanation 1: The DNA profile obtained originated from the Female Victim (Item 1) and two unknown, unrelated individuals. Explanation 2: The DNA profile obtained originated from three unknown, unrelated individuals. The DNA profile obtained is approximately 2E29 times more likely (very strong support) if it originated from the Female Victim (Item 1) and two unknown, unrelated individuals than if the DNA profile obtained originated from three unknown, unrelated individuals. **Database(s) Used:** NIST1036 (revised 2017) - Caucasian, African American, Hispanic
RUEQHZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 4EF: The DNA profile obtained from epithelial fraction of item # 4 is a mixture of at least three individuals. Following set of hypotheses were evaluated: Hypothesis A: HP; item # 1 plus two unknown, HD; 3 unknown, LR (MLE) = 17.9+e^15. Hypothesis B: HP; item #1 plus item # 2 plus unknown, HD; item #1 plus 2 unknown, LR (MLE) = 1.3 e^-10. 4SF: The DNA profile obtained from sperm fraction of item # 4 is a mixture of at least two individuals. Following set of hypotheses were evaluated: Hypothesis A: HP; item #1 plus unknown, HD: two unknown, LR (MLE) = 3.4e^-18. Hypothesis B: HP; item #2 plus unknown, HD: two unknown, LR (MLE) = 5.3e^-14. **Database(s) Used:** NIST Caucasian database 2017 with theta co-ancestry coefficient = 0.03

TABLE 8

WebCode-Test	Item 4 Methods & Results
TFEBVC - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4 e: The mixed DNA profile obtained from this fraction indicates the presence of DNA from three contributors. As such, an assumption of three contributors has been made for statistical analysis. Each of the reference DNA profiles associated to this case has been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA. Based on statistical analysis, it is estimated that the mixed DNA profile obtained is greater than 100 billion times more likely to have occurred if the donor of Item 1 had contributed DNA, rather than if she had not. The donor of Item 2 has been excluded as a contributor. 4 sp: The mixed DNA profile obtained form this fraction indicates the presence of DNA from three contributors. As such, an assumption of three contributors has been made for statitical analysis. Each of the reference DNA profiles associated to this case has been compared with this mixed DNA profile separately, in order to assess whether or not either of them may have contributed DNA. Based on statistical analysis, it is estimated that the mixed DNA profile obtained is approximately 1.8 million times more likely to have occurred if the donor of Item 1 had contributed DNA, rather than if she had not. The donor of Item 2 has been excluded as a contributor. **Database(s) Used:** PP21 [Location Identifying Database].
TGAUWD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Sperm fraction (Organic 2): Victim: Excluded. Suspect: Excluded. Non-sperm fraction (Organic 2): Victim: Not Excluded, LR = 100 billion. Suspect: Supports Exclusion, LR < 1. **Database(s) Used:** [Location Identifying Database] (PP21)
TKNR4Z - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Epithelial Fraction: The mixture of DNA is 2.01 x 10^14 times more likely if it had originated from the Victim and two unknown, unrelated individuals than if it had originated from three unknown, unrelated individuals. This is support that the Victim can be included as a contributor to the mixture of DNA. Sperm Fraction: The mixture of DNA is 8.75 x 10^22 times more likely if it had originated from the Victim and two unknown, unrelated individuals than if it had originated from three unknown, unrelated individuals. This is support that the Victim can be included as a contributor to the mixture of DNA. **Database(s) Used:** Caucasian, African American, Southeast Hispanic, and Southwest Hispanic population groups from the 2015 FBI Population Data for the Expanded CODIS Core STR Loci
TLJA72 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from hotel bedsheet" Fraction 1): The DNA profile(s) from this item(s) was interpreted as a mixture of two individuals with two male contributors. Based on the likelihood ratio result, the Female Victim and the Male Suspect are excluded as possible contributors to the DNA from this item. Item 4.1 (Portion of "Questioned stain from hotel bedsheet" - Fraction 2): The DNA profile(s) from this item(s) was interpreted as a mixture of three individuals with at least two male contributors and with the Female Victim as an assumed contributor. Based on the likelihood ratio result, the Male Suspect is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
UMRJXY - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming three contributors, the evidence profile (non-sperm fraction) is 3.6 octillion times more likely to be observed if the victim and two unknowns are the contributors than if three unknowns are the contributors. **Database(s) Used:** NIST Databases - Forensic Sci. Int.: Genetics 31 (2017) e36–e40

TABLE 8

WebCode-Test	Item 4 Methods & Results
V67HG2 - 5901	**Method(s)**: [Participant did not report a method.] **Stats Analysis:** The DNA profile of the sperm fraction was interpreted as a mixture of three individuals, including unknown male individual A and unknown male individual B. The DNA profile is 1.2 billion times more likely if it originated from Female Victim (1) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. The DNA profile of the epithelial fraction was interpreted as a mixture of three individuals, including unknown male individual B. The DNA profile is at least 1 trillion times more likely if it originated from Female Victim (1) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Female Victim (1). Male Suspect (2) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanic
V6A37P - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Sub-item 4A-2PT_NS (Cutting of center, fraction 1): Assuming Female Victim (K1), Male Suspect (K2) is excluded as a contributor to the DNA obtained from this sub-item. Sub-item 4A-2PT_SP (Cutting of center, fraction 2): Female Victim (K1) is excluded as a contributor to the DNA obtained from this sub-item. Male Suspect (K2) is excluded as a contributor to the DNA obtained from this sub-item. **Database(s) Used:** 2015 Expanded FBI STR database
VBVWBM - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from the epithelial fraction of item #04 is a mixture consistent with contributions from three individuals. Statistical analysis indicates that the DNA profile is approximately 9.29 × 10^50 times more likely if the contributors are the victim (item #01) and two unknown male individuals, rather than three unknown, unrelated individuals. This provides extremely strong support for the inclusion of the victim as a contributor to the DNA mixture, with the remaining contributors being two unknown males. The DNA profile of the suspect (item #02) is not supported as a contributor to this mixture and is therefore excluded. The DNA profile obtained from the sperm fraction of item #04 is a mixture consistent with contributions from three individuals. Statistical analysis indicates that the DNA profile is approximately 1.32 × 10^23 times more likely if the contributors are the victim (item #01) and two unknown male individuals, rather than three unknown, unrelated individuals. This provides extremely strong support for the inclusion of the victim as a contributor to the DNA mixture, with the remaining contributors being two unknown males. The DNA profile of the suspect (item #02) is not supported as a contributor to this mixture and is therefore excluded. **Database(s) Used:** NIST 1036 STR DNA DATABASE 2017
W648ZP - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4E: Assuming Female Victim (K1), the evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1), Male Suspect (K2) and an unknown individual than if it originated from Female Victim (K1) and two unknown individuals. Male Suspect (K2) is excluded based on a LR of zero. Item 4SP: The evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) and an unknown individual than if it originated from two unknown individuals. Female Victim (K1) is excluded based on a LR of zero. The evidence DNA profile is approximately 0 times more likely if it originated from Male Suspect (K2) and an unknown individual than if it originated from two unknown individuals. Male Suspect (K2) is excluded based on a LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 8

WebCode-Test	**Item 4 Methods & Results**
W883G7 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Sperm Fraction PP21 results: A mixed DNA profile consistent with originating from three individuals was recovered. A contributor identified within this mixed DNA profile was designated Unknown Male 1. The DNA evidence is 36 million times more likely if Victim is a contributor. Suspect is excluded as a contributor. Sperm Fraction YFiler Plus results: A mixed Y-chromosome DNA profile consistent with originating from two male individuals was recovered. This mixed Y-chromosome DNA profile could be separated into major and minor components. The partial major component Y-chromosome DNA profile was designated Unknown Y-chromosome Profile 1. The partial minor component Y-chromosome DNA profile was designated Unknown Y-chromosome Profile 2. Suspect is excluded from being a contributor. Epithelial Fraction PP21 results: A mixed DNA profile consistent with originating from three individuals was recovered. A contributor identified within this mixed DNA profile matched Victim. The DNA evidence is greater than 100 billion times more likely if Victim is a contributor. The DNA evidence is more likely if Suspect is not a contributor. Epithelial Fraction YFiler Plus results: A mixed Y-chromosome DNA profile consistent with originating from two male individuals was recovered. This mixed Y-chromosome DNA profile could be separated into major and minor components. The partial major component Y-chromosome DNA profile was designated Unknown Y-chromosome Profile 1. The partial minor component Y-chromosome DNA profile was designated Unknown Y-chromosome Profile 2. Suspect is excluded from being a contributor. **Database(s) Used:** PP21: [Location Identifying Database]; YFiler Plus: [Location Identifying Database]
WGU2AX - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4.2 (Portion of "Questioned stain from hotel bedsheet" - Fraction 1/SF): The DNA profile from this item was interpreted as a mixture of two individuals with at least two male contributors. The female victim and male suspect are excluded as possible contributors to the DNA from this item. Item 4.2 (Portion of "Questioned stain from hotel bedsheet" - Fraction 2/EF): The DNA profile from this item was interpreted as a mixture of three individuals with at least two male contributors. The male suspect is excluded as a possible contributor to the DNA from this item. The DNA results are approximately 20.8 octillion times more likely if they originated from the female victim and two unknown, unrelated individuals than if they originated from three unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the female victim is a contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
WP9QBQ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 4e: Assuming the Female victim (K1), the Male suspect (K2) is excluded based on the LR of zero. For 4sp: Assuming the Female victim (K1), the Male suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
X9G8VV - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** NIST- CAUC
XNBWN7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Ep fraction. The evidence is at least 100 BILLION times more likely if the victim is one of three contributors to the mixed DNA profile than if the profile originated from three unknown individuals, unrelated to the victim, selected at random from the [Population]. **Database(s) Used:** [Location Identifying Database]

TABLE 8

WebCode-Test	**Item 4 Methods & Results**
YMVZW7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4: Sperm fraction: A DNA profile was obtained which appears to originate from four individuals. The DNA profile from the evidence is approximately 392 million times more likely if the victim is a contributor to the DNA along with three unknown unrelated individuals, rather than four unknown unrelated individuals. The DNA profile from the evidence is approximately 4 times more likely if it originates from four unknown unrelated individuals, rather than if it originates from the suspect and three unknown unrelated individuals. Item 4: Epithelial fraction: A DNA profile was obtained which appears to originate from four individuals. The DNA profile from the evidence is >100 billion times more likely if the victim is a contributor to the DNA along with three unknown unrelated individuals, rather than four unknown unrelated individuals. The DNA profile from the evidence is approximately 2609 times more likely if it originates from four unknown unrelated individuals, rather than if it originates from the suspect and three unknown unrelated individuals. **Database(s) Used:** [Location Identifying Database]
YY83H6 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the hotel bedsheet (Item 4) and victim. A match between the data obtained from the first fraction from the hotel bedsheet (Item 4) and victim is approximately 20 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the hotel bedsheet (Item 4) and subject is approximately 10 septillion times less probable than a coincidental match to an unrelated person in the population. Subject is excluded from the data obtained from the first fraction from the hotel bedsheet (Item 4). A DNA match was identified between the data obtained from the second fraction from the hotel bedsheet (Item 4) and victim. A match between the data obtained from the second fraction from the hotel bedsheet (Item 4) and victim is approximately 200 billion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the second fraction from the hotel bedsheet (Item 4) and subject is approximately 20 quadrillion times less probable than a coincidental match to an unrelated person in the population. Subject is excluded from the data obtained from the second fraction from the hotel bedsheet (Item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.
ZBZ72N - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Epithelial extraction Item 1 (Victim): 4.935e+27. **Database(s) Used:** [Location Identifying Database]

TABLE 8

WebCode-Test	**Item 4 Methods & Results**
ZY36LY - 5902	Method(s): Likelihood Ratio Stats Analysis: A DNA match was identified between the data obtained from the first fraction from the questioned stain from the hotel bedsheet (item 4) and the female victim. A match between the data obtained from the first fraction from the questioned stain from the hotel bedsheet (item 4) and the female victim is approximately 20 billion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the first fraction from the questioned stain from the hotel bedsheet (item 4) and the male suspect is approximately 2 sextillion times less probable than a coincidental match to an unrelated person in the population. The male suspect is excluded from the data obtained from the first fraction from the questioned stain from the hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from the hotel bedsheet (item 4) and the female victim is approximately 400 nonillion times less probable than a coincidental match to an unrelated person in the population. The female victim is excluded from the data obtained from the second fraction from the questioned stain from the hotel bedsheet (item 4). A DNA match between the data obtained from the second fraction from the questioned stain from the hotel bedsheet (item 4) and the male suspect is approximately 4 nonillion times less probable than a coincidental match to an unrelated person in the population. The male suspect is excluded from the data obtained from the second fraction from the questioned stain from the hotel bedsheet (item 4). Database(s) Used: The National Institute of Standards and Technology's 1036 Revised [Location Identifying Database] was used to generate DNA match statistics. The combined population database contains African American, Caucasian, Hispanic and Asian populations. Identical siblings will have identical DNA data and DNA match statistics.

Additional Comments

TABLE 9

WebCode-Test	Additional Comments
3MLWYX - 5902	For the sperm fraction of item 4, the quantification value I obtained fell below the validated threshold that is listed in our policies. We use the Applied Biosystems Quantifiler Trio on the QuantStudio 5. Our threshold is greater than or equal to 0.0063ng/ul and my value obtained was 0.0059ng/ul. It is not within our policies to re-extract samples if this scenario occurs. Therefore, item 4 was not re-extracted and I assessed the results obtained from the epithelial fraction only. This is why the places associated with any DNA results from the sperm fraction were left blank. I also followed our sampling policy appropriately when determining how much to sample during the extraction.
3P6C3X - 5902	NR = No results. NT = Not tested. Per laboratory policy, number of contributors is assessed/determined during analysis. Upon comparison to known samples, first a visual comparison is conducted. A manual elimination without the use of probabilistic genotyping software can be done. The assuming of individuals of items of evidence where their presence is expected and non-probative is also permitted. In assessing number of contributors, the following was determined: Item 3-1-1A: 2 contributors with 0 being male, Item 3-1-1B: 2 contributors with 0 being male, Item 4-1-1A: 3 contributors with 2 being male, Item 4-1-1B: 2 male contributors. Male suspect (Item 2) was eliminated by analyst as a contributor to the DNA profiles from items 3-1-1A and 3-1-1B. The likelihood ratios calculated by STRmix are included in the statistical analysis section. The laboratory has a ceiling value of 1 trillion for reporting likelihood ratios.
4478ZQ - 5901	** = possible stutter
6FWJNN - 5901	** = possible elevated stutter
76CCPY - 5901	Item 4 epithelial fraction - an unresolved peak at D1 (15.3) was observed in one amplification. Please note all LRs reported are Stratified LR as per our laboratory's standard operating procedures
8FQNHM - 5902	Item 4 - The combined stutter in the YFP sample at DYS392 were higher than what is typically observed. Our laboratory protocols do not have us calculate the DNA concentration per contributor. Our STRmix reports have the DNA proportion (%) for each contributor. While working through the pre-distribution of this test there was a discrepancy between the color of Items 3 and 4 from the CTS Portal and the physical evidence. This was brought to CTS's attention and the discrepancy was resolved and the CTS Portal was updated.
9X3XVT - 5902	No DNA was detected for the epithelial cell fraction of Item 4; therefore, DNA analysis/STRmix deconvolution was not conducted on this sample. ND = Not Detected. NT = Not Tested. All potential alleles considered by STRmix during deconvolution have been reported.
AXW3PR - 5901	Item 4 was subjected to differential extraction twice, yet the extraction results of both trials remained unsatisfactory. Epithelial fraction could not receive any DNA for the first attempt and minute amount of DNA was obtained in the second attempt. Partial DNA profile could only be received in the second attempt. It seemed that the DNA originated from the female victim was highly degraded in the item 4 and thereby full profiling could not be attained. Based on the partial profile, conclusive conclusion could not be obtained when comparing the DNA results with those of the male suspect. Our lab has purchased three of the tests yet the other two did not receive any DNA from the epithelial fractions neither after differential extraction.
BH4RFU - 5901	Item 4 proved to be very problematic in terms of obtaining a DNA profile. Specifically, the non-spem fraction did not produce an interpretable profile until the fourth attempt. For interpretation purposes in this report, both the sperm and non-sperm fraction results from this fourth attempt were used.

TABLE 9

WebCode-Test	Additional Comments
D2RTLG - 5901	**=possible elevated stutter
DR322B - 5901	According both on autosomal markers results and our SOP, haplotype analysis wasn’t performed for any sample.
DZWAKF - 5901	**= possible elevated stutter
ENWXPE - 5901	Based on the DNA results (electropherograms), we determined that in sample ITEM 4 there are biological traces of the victim (ITEM 1) and at least two male individuals. Based on the results of the preliminary tests and the DNA analysis, the findings are consistent with the presence of seminal fluid and blood. The seminal fluid may originate from both male individuals, while the blood is likely from the victim; however, it is also possible that the blood originates from one or both of the male individuals. In ITEM 3, we detected a mixture of biological traces from at least three female individuals. The donor of one component in the mixture of biological traces is Victim (ITEM 1).
ERWAKE - 5901	Item 3: KM positive, AP negative, Amylase negative. No odour of urine/faeces – no chemical tests for faeces or urine. Two person mix - all female. Includes V – unable to attribute to blood. LR = 1 billion (V+U/2U). Given lack of information in submission cannot sensibly draw anything other than a source-level conclusion. Conclusion - DNA matching V present in bloodstained area that was targeted. Item 4: KM positive, AP positive, Amylase negative. SpermTrap = 3+H. No odour of urine/faeces – no chemical tests. SF = two person mix but excludes S. Able to determine most of profile of a major donor and much of the profile of a minor DNA – both suitable for search of NDNAD and IMO attributable to semen. CF = three person mix and appears to include two males above plus V. Able to determine most of profile of a major donor and much of the profile of a minor DNA – both suitable for search of NDNAD. V DNA probably attributable to blood. LR = 200 (V+2U/3U). Problem with one of PCR replicates is depressing the LR. If use one replicate get LR = billion but if add the second replicate where inputs were increased to detect minor contributions, it crashes the LR. Given lack of information in submission cannot sensibly draw anything other than a source-level conclusion. Conclusion = no semen from S evident in stain.
FE3CWK - 5902	NR = No Result. NT = Not Tested. The laboratory has a ceiling value of 1 trillion for reporting likelihood ratios. Per laboratory policy, number of contributors is assessed/determined during analysis. Upon comparison to known samples, first a visual comparison is conducted. A manual elimination without the use of probabilistic genotyping software can be done. The assuming of individuals of items of evidence where their presence is expected and non-probative is also permitted. In assessing number of contributors, the following was determined: - Item 3e: 2 contributors. - Item 3sp: 3 contributors. - Female victim (item 1) was included as a contributor to the DNA profile from 3e and 3sp. The likelihood ratios calculated by STRmix are included in the statistical analysis section. Male suspect (item 2) was eliminated by the analyst as a contributor. - Item 4e: 3 contributors with 2 being male. - Item 4sp: 2 male contributors. - Female victim (item 1) was included as a contributor to the DNA profile from 4e. The likelihood ratios calculated by STRmix are included in the statistical analysis section. Male suspect (item 2) was eliminated by the analyst as a contributor - Female victim (item 1) and Male suspect (item 2) were eliminated by the analyst as contributors to the DNA profile from 4sp.
FYD629 - 5902	This laboratory does not report DNA Concentration (ng/uL) for Mixture Sample Analysis.
H9PEFC - 5901	**possible elevated stutter

TABLE 9

WebCode-Test	Additional Comments
JJP289 - 5901	The blood/semen mixture (item 4) does not work with Tween for digestion for the NS fraction.The item was sampled 4 times. The first, second, and third extractions yielded ~.040ng-0.050ng. The 4th time I was able to use SEB instead of Tween and was able to obtain usable results (~130ng). Its possible that there is something treated on the fabric that interferes with Tween.
KFMMYA - 5901	** = possible stutter
KKTFQK - 5902	Allele drop out observed at Y GATA H4 locus in item 4e (indicated as *).
LBA2Q3 - 5902	YSTR analysis not performed on mixtures. Laboratory does not report DNA concentration.
LRURMG - 5902	The comparison between Victim and the data obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4) is inconclusive because meaningful match statistics were not obtained. Therefore, no conclusions will be offered regarding Victim as a possible contributor to the DNA mixture obtained from the second fraction from the questioned stain from hotel bedsheet (Item 4).
LV8TJ9 - 5901	** = possible stutter
MK7PU6 - 5902	For items 3 and 4, the results include all detected alleles along with the associated stutter peaks. This reflects the data that is imported into STRmix in order to perform probabilistic genotyping.
PKJZL9 - 5902	The most minor contributor obtained in the second ("sperm") fraction from item 4 is inconclusive and not suitable for comparison. It fell below the validated 4% contribution threshold to be used.
QCKU6C - 5901	Item 4 Spermatozoa Fraction: As per standard laboratory procedure, the D1S1656 locus was ignored for analysis due to an unresolved peak, in the 15.3 position, above the laboratory's drop-in threshold. As a result, no information has been entered at the D1 locus for this sample.
R7WA2W - 5902	In Section IV, Mixture Sample Analysis [Table 6: DNA Mixture Concentrations and Proportions], no DNA concentrations are reported as the laboratory does not report DNA concentrations.
RDVWRB - 5901	1. DNA concentration for contributor position is not reported. 2. NID = No interpretable data. 3. Inclusions and exclusions were conducted by the analyst outside of the STRmix software program. STRmix was used, however, to calculate a likelihood ratio for Item 3 and Item 4f1: Item 3: 1sU_UU; Item 4f1: 1sUU_UUU. 4. Item 4f2 was run through STRmix for deconvolution purposes only; no statistical analysis was conducted. 5. Item 2 run on ANDE system with a result of 17/27; will report alleles from PowerPlex Fusion 6C. 6. Y-STR analysis was conducted on Item 4f1; no major was able to be pulled out and the overall haplotype was deemed unsuitable for comparisons. Met interpretation guidelines per TL. 7. Y-STR analysis was conducted on Item 4f2; major was pulled out, however the FBU does not interpret minor contributors and is deemed unsuitable for comparisons. Met interpretation guidelines per TL.
TGAUWD - 5901	The DNA processing of item 4 for this proficiency test experienced some difficulties. Item 3 (blood detected) yielded DNA results using the standard DNA IQ method. Item 4 (blood and semen detected) specifically the non-seprm fraction, produced unexpected very partial / limited DNA profiling results using the differential method. Three subsequent attempts using an organic differential method were undertaken with the last attempt (Organic 2) yielding DNA results for both the sperm and non-sperm fractions. The DNA results of the Organic 2 samples were reported in this proficiency.
TKNR4Z - 5902	No DNA Concentration per contributor values were entered due to our lab not reporting those out.

TABLE 9

WebCode-Test	Additional Comments
UMRJXY - 5902	The original predistribution case scenario described Item 3 as blue and Item 4 as tan; however the envelope labeled "Item 3" contained a tan swatch of fabric and the envelope labeled "Item 4" contained a blue swatch of fabric. The current scenario item descriptions match what was originally observed. For Items 3 and 4, the results include all detected alleles along with the associated stutter peaks. This reflects the data that is imported into STRmix in order to perform probabilistic genotyping.
WGU2AX - 5901	** = possible stutter
XNBWN7 - 5901	LR truncated to 100 billion.
YMVZW7 - 5901	Item 4 - Sperm fraction: The DNA profile had an unresolved peak at locus D1 (15.3) > 80fru the laboratory's analytical threshold and therefore this locus was ignored in the STRmix interpretation.

-End of Report-
(Appendix may follow)

Test No. 26-5901: Probabilistic Genotyping

DATA MUST BE SUBMITTED BY **April 13, 2026, 11:59 p.m. EDT** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A WebCode: 3KYGDG

The Accreditation Release section can be accessed by using the "Continue to Final Submission" button above. This information can be entered at any time prior to submitting to CTS.

Scenario:

Police are investigating a homicide case involving a female victim and male suspect. According to police, the victim was believed to have been sexually assaulted, as her body was found unclothed lying on a bed in a hotel room. The suspect, who was the registered guest of the hotel room, has been apprehended by police. Police are submitting a stain from a dress found near the victim's body (Item 3) and a stain from the hotel bedsheet on which the victim's body was found (Item 4). Also provided are known standards from the female victim (Item 1) and male suspect (Item 2).

Items Submitted (Sample Pack G1 - Cloth Swatches):

Item 1: Known blood from the female victim
Item 2: Known blood from the male suspect
Item 3: Questioned stain from dress found near victim's body (tan)
Item 4: Questioned stain from hotel bedsheet (blue)

Part I: SCREENING TESTS

Note: Laboratories submitting their results for ASCLD/LAB or NATA accreditation MUST identify any screening tests performed and report the test results.

Indicate the results of any screening tests performed on the questioned stains (Items 3 & 4).

Please use the abbreviations listed in this response key to fill in the Screening Test tables on this tab. This is not an all inclusive list of tests, and should not be used to determine what tests should be performed.

TESTS NOT ON THIS LIST MAY BE USED FOR SCREENING.

Test	Abbreviation	Test	Abbreviation
Acid Phosphatase	AP	Alternate Light Source	ALS
Kastle Meyer	KM	Leucomalachite Green	LMG
Microscopic	Micro	Ortho-tolidine	O-tol
Phenolphthalein-Tetramethyl benzidine	PTMB	Prostate Specific Antigen	PSA
Rapid Stain Identification	RSID	Tetramethyl benzidine	TMB

Example:	Positive	Negative	Inconclusive	Not Tested	Test(s) Performed
Blood	●	○	○	○	KM, O-tol, PTMB
Semen	○	●	○	○	PSA
Saliva	○	○	○	●	
Human Origin	○	○	○	●	
Y-Screening (male DNA)	○	○	○	●	
Other Specified Body Fluid	○	○	○	○	

Please indicate the Test(s) Performed on the corresponding line for each type of screening.

Screening data not reported. ☐

Item 3:	Positive	Negative	Inconclusive	Not Tested	Test(s) Performed
Blood	○	○	○	○	
Semen	○	○	○	○	
Saliva	○	○	○	○	
Human Origin	○	○	○	○	
Y-Screening (male DNA)	○	○	○	○	
Other:	○	○	○	○	

Item 4:	Positive	Negative	Inconclusive	Not Tested	Test(s) Performed
Blood	○	○	○	○	
Semen	○	○	○	○	
Saliva	○	○	○	○	
Human Origin	○	○	○	○	
Y-Screening (male DNA)	○	○	○	○	
Other:	○	○	○	○	

Part II: DNA INTERPRETATION

Based on results obtained from DNA analysis, could the Victim (Item 1) and/or the Suspect (Item 2) be a contributor to the questioned stains (Items 3 & 4)?

	Victim (Item 1)			Suspect (Item 2)	
	Item 3	Item 4		Item 3	Item 4
Yes	○	○	Yes	○	○
No	○	○	No	○	○
Inconclusive	○	○	Inconclusive	○	○
No Interpretation	○	○	No Interpretation	○	○

Participant Code: U1234A
WebCode: 3KYGDG

Part III: DNA Results for Known Item 1

- Report alleles in numerical order, separated by a comma.
- Follow your laboratory procedures for reporting homozygotes (i.e. X,X or X) and null responses.
- If your laboratory policy is to indicate minor or weaker alleles, please enclose them within brackets [ ].

STR Amplification Kit(s) Used: Please check all the brands that apply for this item and record only additional kit specific information in the blank provided (i.e. 16, Plus, Direct, HS, Fusion, etc.).

☐ Identifiler® ☐ GlobalFiler™ ☐ Investigator® 24plex

☐ PowerPlex® Other

Report the Probabilistic Genotyping Software Used:

☐ STRmix ☐ TrueAllele Other

Alleles below are sorted in **Default** *order.*

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
1						
ITEM	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
1						
ITEM	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
1						
ITEM	FGA	Penta D	Penta E	SE33	TH01	TPOX
1						
ITEM	vWA	DYS391	DYS570	DYS576	Y Indel	
1						

Part III (continued): DNA Results for Known Item 2

- Report alleles in numerical order, separated by a comma.
- Follow your laboratory procedures for reporting homozygotes (i.e. X,X or X) and null responses.
- If your laboratory policy is to indicate minor or weaker alleles, please enclose them within brackets [ ].

STR Amplification Kit(s) Used: Please check all the brands that apply for this item and record only additional kit specific information in the blank provided (i.e. 16, Plus, Direct, HS, Fusion, etc.).

☐ Identifiler® ☐ GlobalFiler™ ☐ Investigator® 24plex
☐ PowerPlex® Other

Report the Probabilistic Genotyping Software Used:

☐ STRmix ☐ TrueAllele Other

Alleles below are sorted in **Default** *order.*

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
2						
ITEM	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
2						
ITEM	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
2						
ITEM	FGA	Penta D	Penta E	SE33	TH01	TPOX
2						
ITEM	vWA	DYS391	DYS570	DYS576	Y Indel	
2						

YSTR Amplification Kit(s) Used: Please check all the brands that apply for this item and record only additional kit specific information in the blank provided (i.e. Plus, 23, etc.).

☐ YFiler™ ☐ PowerPlex® Y Other

Alleles below are sorted in **Default** *order.*

ITEM	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
2									
ITEM	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
2									
ITEM	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y GATA H4
2									

Part III (continued): DNA Results for Questioned Item 3

- Report alleles in numerical order, separated by a comma.
- Follow your laboratory procedures for reporting homozygotes (i.e. X,X or X) and null responses.
- If your laboratory policy is to indicate minor or weaker alleles, please enclose them within brackets [ ].

STR Amplification Kit(s) Used: Please check all the brands that apply for this item and record only additional kit specific information in the blank provided (i.e. 16, Plus, Direct, HS, Fusion, etc.).

☐ Identifiler® ☐ GlobalFiler™ ☐ Investigator® 24plex

☐ PowerPlex® Other

Report the Probabilistic Genotyping Software Used:

☐ STRmix ☐ TrueAllele Other

Did you perform a differential extraction of Item 3? **YES** ○ **NO** ○

Alleles below are sorted in **Default** *order.*

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
3						
3 e						
3 sp						
ITEM	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
3						
3 e						
3 sp						
ITEM	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
3						
3 e						
3 sp						
ITEM	FGA	Penta D	Penta E	SE33	TH01	TPOX
3						
3 e						
3 sp						
ITEM	vWA	DYS391	DYS570	DYS576	Y Indel	
3						
3 e						
3 sp						

YSTR Amplification Kit(s) Used: Please check all the brands that apply for this item and record only additional kit specific information in the blank provided (i.e. Plus, 23, etc.).

☐ YFiler™ ☐ PowerPlex® Y Other

Did you perform a differential extraction of Item 3? **YES** ○ **NO** ○

Alleles below are sorted in **Default** *order.*

ITEM	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
3									
3 e									
3 sp									
ITEM	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
3									
3 e									
3 sp									
ITEM	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y GATA H4
3									
3 e									
3 sp									

Part III (continued): DNA Results for Questioned Item 4

- Report alleles in numerical order, separated by a comma.
- Follow your laboratory procedures for reporting homozygotes (i.e. X,X or X) and null responses.
- If your laboratory policy is to indicate minor or weaker alleles, please enclose them within brackets [ ].

STR Amplification Kit(s) Used: Please check all the brands that apply for this item and record only additional kit specific information in the blank provided (i.e. 16, Plus, Direct, HS, Fusion, etc.).

☐ Identifiler® ☐ GlobalFiler™ ☐ Investigator® 24plex

☐ PowerPlex® Other

Report the Probabilistic Genotyping Software Used:

☐ STRmix ☐ TrueAllele Other

Did you perform a differential extraction of Item 4? YES ○ NO ○

Alleles below are sorted in **Default** *order.*

ITEM	D1S1656	D2S1338	D2S441	D3S1358	D5S818	D6S1043
4						
4 e						
4 sp						
ITEM	D7S820	D8S1179	D10S1248	D12S391	D13S317	D16S539
4						
4 e						
4 sp						
ITEM	D18S51	D19S433	D21S11	D22S1045	Amelogenin	CSF1PO
4						
4 e						
4 sp						
ITEM	FGA	Penta D	Penta E	SE33	TH01	TPOX
4						
4 e						
4 sp						
ITEM	vWA	DYS391	DYS570	DYS576	Y Indel	
4						
4 e						
4 sp						

YSTR Amplification Kit(s) Used: Please check all the brands that apply for this item and record only additional kit specific information in the blank provided (i.e. Plus, 23, etc.).

☐ YFiler™ ☐ PowerPlex® Y Other

Did you perform a differential extraction of Item 4? YES ○ NO ○

Alleles below are sorted in **Default** *order.*

ITEM	DYF387S1	DYS19	DYS385	DYS389-I	DYS389-II	DYS390	DYS391	DYS392	DYS393
4									
4 e									
4 sp									
ITEM	DYS437	DYS438	DYS439	DYS448	DYS449	DYS456	DYS458	DYS460	DYS481
4									
4 e									
4 sp									
ITEM	DYS518	DYS533	DYS549	DYS570	DYS576	DYS627	DYS635	DYS643	Y GATA H4
4									
4 e									
4 sp									

Part III (continued): DNA Analysis - Additional DNA

- Use this section to report results for loci not currently listed in other sections of the data sheet.
- Report alleles in numerical order, separated by a comma.
- If your laboratory policy is to indicate minor or weaker alleles, please enclose them within brackets [ ].
- Click "Add Row" to show another row of boxes for entry.

Did you perform a differential extraction of Item 3? Yes ○ No ○

Did you perform a differential extraction of Item 4? Yes ○ No ○

Locus	Item 1	Item 2	Item 3	Item 3e	Item 3sp	Item 4	Item 4e	Item 4sp

Part IV: Mixture Sample Analysis

NOTE: To allow functionality of this page please select an answer to differential extraction questions on previous tabs for Item 3 and Item 4.

For each item, select the Estimated Number of Contributors and Contributor Identification (Victim, Suspect, or Unknown Individual). Calculate the DNA Concentration and DNA Proportion for each contributor using your laboratory’s protocols. For Unknown Individual(s), report the contributor determined to have the highest concentration of DNA first and remaining in descending order. Enter "DNA Concentration" in ng/uL and "DNA Proportion" in percentage.

Concentration and proportion data not reported. ☐

Item 3:

Estimated number of contributors:

		DNA Concentration (ng/uL)	**DNA Proportion (%)**
Contributor 1			

Item 4:

Estimated number of contributors:

		DNA Concentration (ng/uL)	**DNA Proportion (%)**
Contributor 1			

Part V: DNA Statistical Analysis

Item 3:

1) Statistical Analysis of Item 3 DNA Typing Results:

Select the statistical method(s) used by marking the associated box and report these results in the space below:

☐ Likelihood Ratio (LR)

Other ☐

Note: *Please use appropriate punctuation to indicate the end of sentences, sections, and statements in the free-form space below. Extra spacing and returns used for separation within your text will not transfer and may cause your information to be illegible in the Summary Report. The use of lists and tabular formats to deliver information is also cautioned against, as these do not transfer.*

2) Please list any databases used in the statistical analysis of Item 3 below.

Item 4:

1) Statistical Analysis of Item 4 DNA Typing Results:

Select the statistical method(s) used by marking the associated box and report these results in the space below:

☐ Likelihood Ratio (LR)

Other ☐

Note: *Please use appropriate punctuation to indicate the end of sentences, sections, and statements in the free-form space below. Extra spacing and returns used for separation within your text will not transfer and may cause your information to be illegible in the Summary Report. The use of lists and tabular formats to deliver information is also cautioned against, as these do not transfer.*

2) Please list any databases used in the statistical analysis of Item 4 below.

Part VI: ADDITIONAL COMMENTS

- Use this section to report comments regarding any part of this test.
- Written conclusions (including statistical information) for DNA analysis are not required.
- Note: Laboratories submitting their results for accreditation are asked to report any additional information that will assist in the review of their results. This includes an explanation of any deviations from a full completion of the test and/or unique findings such as elevated stutter.

Note: *Please use appropriate punctuation to indicate the end of sentences, sections, and statements in the free-form space below. Extra spacing and returns used for separation within your text will not transfer and may cause your information to be illegible in the Summary Report. The use of lists and tabular formats to deliver information is also cautioned against, as these do not transfer.*

RELEASE OF DATA TO ACCREDITATION BODIES

The Accreditation Release is accessed by pressing the "Continue to Final Submission" button online and can be completed at any time prior to submission to CTS.

CTS submits external proficiency test data directly to ANAB and/or A2LA. Please select one of the following statements to ensure your data is handled appropriately.

○ This participant's data is intended for submission to ANAB and/or A2LA. (Accreditation Release section below must be completed.)
○ This participant's data is **not** intended for submission to ANAB and/or A2LA.

Have the laboratory's designated individual complete the following steps
only if your laboratory is accredited in this testing/calibration discipline
by one or more of the following Accreditation Bodies.

Step 1: Provide the applicable Accreditation Certificate Number(s) for your laboratory

ANAB Certificate No. ☐

A2LA Certificate No. ☐

Step 2: Complete the Laboratory Identifying Information in its entirety

Authorized Contact Person and Title

☐

Laboratory Name

☐

Location (City/State)

☐