Collaborative Testing Services, Inc
FORENSIC TESTING PROGRAM

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Probabilistic Genotyping Test No. 25-5901/2
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 80 participants and are compiled into the following tables:

This report contains the data received from the participants in this test. Since these participants are located in many countries around the world, and it is their option how the samples are to be used (e.g., training exercise, known or blind proficiency testing, research and development of new techniques, etc.), the results compiled in the Summary Report are not intended to be an overview of the quality of work performed in the profession and cannot be interpreted as such. The Summary Comments are included for the benefit of participants to assist with maintaining or enhancing the quality of their results. These comments are not intended to reflect the general state of the art within the profession.

Participant results are reported using a randomly assigned "WebCode". This code maintains participant's anonymity, provides linking of the various report sections, and will change with every report.

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/Semen	50 µL (1:1:1)	Female/Male/Male	Victim/Suspect/ Additional Male A
4	Questioned	Blue Fabric	Blood/Blood/Blood	50 µL (1:1:1)	Male/Male/Male	Suspect/Additional Male B/Additional Male C

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	11,17.3	17,25	11,11	16,18	10,12	11,11
	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24	9,11	8,11	17,24.2	6,9.3	8,8
	16,16	NM	NM	NM	NM	
2	16,17.3	17,18	14,14	16,16	11,13	12,13
	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7,7	11,14
	15,17	10	*	*	2	
3-Blood	11,16,17.3	17,18,25	11,14	16,18	10,11,12,13	*
	9,10,11,12	10,13,15	13	16,17,18,19	8,12	9,12,14
	14,15,17,19	12,13,15.2	31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,24	9,11,12	5,8,10,11	17,18,24.2,28.2	6,7,9.3	8,11,14
	15,16,17	10	*	*	2	
3-Semen	14,18.3	20,25	11,14	15,18	9,11	12,18
	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2	10,13	8,12	15,28.2	6,9	8,10
	16,17	10	*	*	2	
4	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	10,11,12,13,14
	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14, 15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	*	*	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 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	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12	*	20	17	22	21	*	11
3-Blood	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12	*	20	17	22	21	*	11
3-Semen	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12	*	18	19	20	24	*	12
4	35,36,37,38	13,14,15	11,15,16,17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12	*	17,20	16,17,21	20,22	21,23	*	11,13

* 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 one part blood from the Item 1 female donor, one part blood from the Item 2 male donor, and one part semen from another male donor (Additional Male A) whose known standard was not provided. Item 4 was created by combining equal parts of blood from the Item 2 male donor, and two additional male donors (Additional Male B and Additional Male C), whose known standards were not provided. Refer to the Manufacturer's Information for preparation details.

Data were returned by 80 participants.

Screening Test Results
A total of 74 participants reported screening results for at least one body fluid (blood, semen, saliva), though not all of these participants returned screening results for every fluid across both questioned items.

For Item 3, 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."

For Item 4, 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 but three participants reported "Positive." The remaining participants reported "Negative." For 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 but twenty-four participants reported consistent results for one or more items. The majority of participants were missing alleles for Item 3-Blood (3e), with over half missing one or more alleles at Locus D5S818. The majority of these missing alleles were attributable to the Item 1 female donor.

For YSTR results, all but six participants reported consistent results for one or more items.

DNA Interpretations
For Item 3, all but one participant included the victim (Item 1) as a possible contributor to the stain. The remaining participant reported "Inconclusive." All but one participant included the suspect (Item 2) as a possible contributor to the stain. The remaining participant reported "Inconclusive." All participants identified the presence of three contributors in the epithelial fraction. For the sperm fraction, a consensus was not achieved. A total of 44 participants (68%) identified one contributor, 15 participants (23%) identified two contributors, and six participants (9%) identified three contributors. An additional participant did not perform a differential extraction on this item, but reported the presence of three contributors.

For Item 4, all participants excluded the victim (Item 1) as a possible contributor to the stain. All but one participant included the suspect (Item 2) as a possible contributor. The remaining participant reported "Inconclusive" as to whether the suspect was a contributor. All but one participant identified the presence of three contributors. The remaining participant reported the presence of four contributors.

Key for Screening Tests Used

Participants were asked to use, where possible, the following chart of abbreviated screening test names. This was not an all inclusive list and was not designed to determine what tests should be performed. Participants were advised that tests not on this list may be used for screening.

Test	Abbreviation
Acid Phosphatase	AP
Kastle Meyer	KM
Leucomalachite Green	LMG
Microscopic	Micro
Ortho-tolidine	O-tol
Phenolphthalein-Tetramethyl benzidine	PTMB
Prostate Specific Antigen	PSA
Quantiblot	QB
Quantifiler	QF
Tetramethyl benzidine	TMB

Serology Screening Results

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

TABLE 1a

	Blood Screening Results	
WebCode - Test	**Item 3**	**Item 4**
2QGMC2 - 5902	**Pos** PTMB	**Pos** PTMB
34G3B3 - 5902	**Pos** KM	**Pos** KM
37J2CU - 5901	**Pos** KM	**Pos** KM
3MQZUY - 5902	**Pos** KM	**Pos** KM
3WHFJ3 - 5902	**Pos** KM	**Pos** KM
44PDRD - 5901	**Pos** KM	**Pos** KM
4BEUJW - 5902	**Pos** TMB, Hematrace	**Pos** TMB, Hematrace
4FBJY4 - 5902	**Pos** LMG	**Pos** LMG
4UQG64 - 5901	**Pos** KM, Hematrace	**Pos** KM, Hematrace
4XQRZ4 - 5901	**Pos** KM, Hematrace	**Pos** KM, Hematrace
62K9Q4 - 5901	**Pos** KM, Hematrace	**Pos** KM, Hematrace
63VBC2 - 5901	**Pos** KM, Hematrace	**Pos** KM, Hematrace
6PTH6Y - 5902	**Pos** PTMB	**Pos** PTMB
77A6RY - 5901	**Pos** IR, pth, Hematrace	**Pos** pth
786NUZ - 5901	**Pos** KM, HemeDirect	**Pos** KM, HemeDirect
7H4JRV - 5902	**Pos** PTMB	**Pos** PTMB
8Y8DYV - 5902	**Pos** PTMB	**Pos** PTMB
8YUL9Z - 5901	**Pos** TMB, FOB, Seratec PMB, Luminol	**Pos** TMB, FOB, Seratec PMB, Luminol
9CLYK9 - 5901	**Pos** KM	**Pos** KM
9MBR8Q - 5901	**Pos** TMB	**Pos** TMB
9WLTTR - 5902	**Pos** KM, Hematrace	**Pos** KM, Hematrace
B7W38V - 5901	**Pos** PTH, HEMATRACE, IR	**Pos** PTH
BDR7Z7 - 5901	**Pos** KM, HemDirect	**Pos** KM, HemDIrect
BKHHBU - 5901	**Pos** PTH, IR	**Pos** PTH, HemaTrace
BNGT8U - 5902	**Pos** KM	**Pos** KM
CDTG9M - 5901	**Pos** Hemastix, RSID	**Pos** Hemastix, RSID
CKECAQ - 5902	**Pos** PTMB	**Pos** PTMB
CRBAWU - 5901	**Pos** KM	**Pos** KM
CRVQCW - 5901	**Pos** KM, Hematrace	**Pos** KM, Hemtrace
CXYRCQ - 5902	**Pos** PTMB	**Pos** PTMB
CY6DP6 - 5901	**Pos** KM	**Pos** KM
CZ6EPV - 5901	**Pos** KM, HemaTrace	**Pos** KM, HemaTrace

TABLE 1a

	Blood Screening Results	
WebCode - Test	**Item 3**	**Item 4**
E34ANN - 5902	**Pos** PTMB	**Pos** PTMB
EHXZJK - 5902	**Pos** TMB, Hematrace	**Pos** TMB, Hematrace
ELJJPP - 5902	**Pos** PTMB	**Pos** PTMB
EY6YTN - 5902	**Pos** PTMB	**Pos** PTMB
F7H8UP - 5902	**Pos** KM	**Pos** KM
F8XQDM - 5902	**Pos** TMB,KM	**Pos** TMB,KM
FPXE6L - 5902	**Pos** KM	**Pos** KM
GCH7HK - 5902	**Pos** PTMB	**Pos** PTMB
H484WJ - 5902	**Pos** PTMB	**Pos** PTMB
HEQHYL - 5902	**Pos** PTMB	**Pos** PTMB
HJX7CN - 5901	**Pos** KM	**Pos** KM
J37QNH - 5902	**Pos** Hemastix, Hematrace	**Pos** Hemastix, Hematrace
J772JG - 5902	**Pos** TMB (Hemastix), Hematrace	**Pos** TMB (Hemastix), Hematrace
JHLQHM - 5902	**Pos** Hemastix, OBTI	**Pos** Hemastix, OBTI
JPGUBX - 5901	**Pos** KM	**Pos** KM
K9ECCE - 5902	**Pos** KM, Hematrace	**Pos** KM, Hematrace
KPDQAK - 5902	**Pos** KM	**Pos** KM
L67JVL - 5901	**Pos** KM, Hematrace	**Pos** KM, Hematrace
L8XEJE - 5901	**Pos** TMB	**Pos** TMB
LBAKVF - 5902	**Pos** KM	**Pos** KM; ABAcard
LG3PNJ - 5901	**Pos** LMG	**Pos** LMG
LHUN3H - 5902	**Pos** TMB, PHE	**Pos** TMB, PHE
LUPUWF - 5901	**Pos** KM	**Pos** KM
LYKQJL - 5901	**Pos** KM, HemaTrace	**Pos** KM, HemaTrace
MW99ZF - 5902	**Pos** TMB,PHE	**Pos** TMB,PHE
NWNRKD - 5901	**Pos** KM	**Pos** KM
P3QH3A - 5901	**Pos** TMB	**Pos** TMB
P8KEPF - 5902	**Pos** KM	**Pos** KM
Q99BQE - 5901	**Pos** Seratec HEM	**Pos** Seratec HEM
R3MFPB - 5901	**Pos** KM	**Pos** KM
R9RDYE - 5901	**Pos** KM, Hematrace	**Pos** KM, Hematrace
RCPXZD - 5901	**Pos** KM	**Pos** KM
TMDEV4 - 5902	**Pos** KM	**Pos** KM
TZBZVA - 5901	**Pos** KM	**Pos** KM

TABLE 1a

	Blood Screening Results	
WebCode - Test	**Item 3**	**Item 4**
UNVR99 - 5902	**Pos** PTMB	**Pos** PTMB
VFHZHA - 5902	**Pos** KM	**Pos** KM
VK9834 - 5902	**Pos** RSID Blood	**Pos** RSID Blood
X28843 - 5901	**Pos** TMB	**Pos** TMB
XCU6U9 - 5902	**Pos** LMG	**Pos** LMG
YGJ6L9 - 5901	**Pos** KM, Hematrace	**Pos** KM, Hematrace
YJMUQ3 - 5901	**Pos** O-tol	**Pos** O-tol
Z8LUQ4 - 5902	**Pos** PTMB	**Pos** PTMB

Table 1a: Serology Screening Response Summary - Blood

Participants: **74**

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	**74**	**74**
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

	Semen Screening Results	
WebCode - Test	**Item 3**	**Item 4**
2QGMC2 - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP
34G3B3 - 5902	**Pos** ALS, AP, p30, Micro	**Neg** ALS, AP, p30, Micro
37J2CU - 5901	**Pos** AP, Micro	**Neg** AP
3MQZUY - 5902	**Pos** AP,PSA	**Neg** AP
3WHFJ3 - 5902	**Pos** AP, Micro	**Neg** AP
44PDRD - 5901	**Pos** ALS, AP, Micro	**Neg** ALS, AP
4BEUJW - 5902	**Pos** AP, PSA, Micro	**Neg** AP, PSA
4FBJY4 - 5902	**Pos** AP, Micro	**Neg** AP, micro
4UQG64 - 5901	**Pos** AP, PSA, Micro	**Neg** AP
4XQRZ4 - 5901	**Pos** AP, PSA, Micro	**Neg** AP
62K9Q4 - 5901	**Pos** AP, Micro, PSA	**Neg** AP
63VBC2 - 5901	**Pos** AP, PSA, Micro	**Neg** AP
6PTH6Y - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP
77A6RY - 5901	**Pos** ALS, AP, Micro, PSA	**Neg** AP, Micro
786NUZ - 5901	**Pos** ALS, AP, PSA, Micro	**Neg** ALS, AP, PSA, Micro
7H4JRV - 5902	**Pos** ALS, AP, Micro	**Neg** AP
8Y8DYV - 5902	**Pos** AP, Micro, ALS	**Neg** AP, Micro, ALS
8YUL9Z - 5901	**Pos** ALS, AP, RSID Semen, Seratec PAM	**Neg** ALS, AP, RSID Semen, Seratec PAM
9CLYK9 - 5901	**Pos** ALS, AP	**Neg** ALS, AP
9MBR8Q - 5901	**Pos** AP, Micro	**Neg** AP
9WLTTR - 5902	**Pos** Alternative Light Source, AP, Semenogelin, Microscopy	**Neg** Alternative Light Source, AP
B7W38V - 5901	**Pos** ALS, AP, MICRO, PSA	**Neg** AP
BDR7Z7 - 5901	**Pos** AP, Micro, PSA	**Neg** AP
BKHHBU - 5901	**Pos** AP, PSA, micro, ALS	**Neg** AP, micro
BNGT8U - 5902	**Pos** AP, p30, Micro	**Neg** AP, p30, Micro
CDTG9M - 5901	**Pos** AP, RSID, Micro	**Neg** AP, RSID
CKECAQ - 5902	**Pos** ALS, AP, MICRO	
CRBAWU - 5901	**Pos** AP	**Neg** AP
CRVQCW - 5901	**Pos** AP, PSA, micro	**Neg** AP
CXYRCQ - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP

TABLE 1b

WebCode - Test	Semen Screening Results	
	Item 3	Item 4
CY6DP6 - 5901	**Pos** ALS, AP	**Neg** ALS, AP
CZ6EPV - 5901	**Pos** AP, PSA, Micro	**Neg** AP
E34ANN - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP
EHXZJK - 5902	**Pos** AP, PSA, Micro	**Neg** AP, PSA, Micro
ELJJPP - 5902	**Pos** ALS, AP, Micro, PSA	**Neg** ALS, AP, Micro, PSA
EY6YTN - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP
F7H8UP - 5902	**Pos** AP, MICRO	**Neg** AP, MICRO
F8XQDM - 5902	**Pos** ALS,AP, Micro	**Neg** ALS,AP,Micro
FPXE6L - 5902	**Pos** AP, PSA	**Neg** AP
GCH7HK - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP
H484WJ - 5902	**Pos** ALS, AP, micro	
HEQHYL - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP
HJX7CN - 5901	**Pos** P30	**Neg** P30
J37QNH - 5902	**Pos** AP, PSA, Micro	**Neg** AP
J772JG - 5902	**Pos** AP, Micro, PSA (p30)	**Neg** AP, Micro, PSA (p30)
JHLQHM - 5902	**Pos** PSA	**Neg** PSA
JPGUBX - 5901	**Pos** ALS, AP	**Neg** ALS, AP
K9ECCE - 5902	**Pos** AP, RSID Semen	**Neg** AP
KPDQAK - 5902	**Pos** AP, Micro	**Neg** AP
L67JVL - 5901	**Pos** AP, Micro,PSA	**Neg** AP
L8XEJE - 5901	**Pos** AP	**Neg** AP
LBAKVF - 5902	**Pos** AP, PSA	**Neg** AP
LG3PNJ - 5901	**Pos** PSA	**Neg** PSA
LHUN3H - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP, Micro
LUPUWF - 5901	**Pos** AP, Micro	**Neg** AP
LYKQJL - 5901	**Pos** AP, Micro, PSA	**Neg** AP
MW99ZF - 5902	**Pos** ALS, AP, Micro	**Neg** ALS, AP, Micro
NWNRKD - 5901	**Pos** AP, Micro	**Neg** AP
P3QH3A - 5901	**Pos** Microscopy, AP	**Neg** Microscopy, P30 (PSA), AP
P8KEPF - 5902	**Pos** AP, micro	**Neg** AP
Q99BQE - 5901	**Pos** Seratec PSA + Sperm Tracker	**Neg** Seratec PSA + Sperm Tracker
R3MFPB - 5901	**Pos** AP, micro	**Neg** AP

TABLE 1b

WebCode - Test	Semen Screening Results			
	Item 3		Item 4	
R9RDYE - 5901	Pos	AP, Micro, PSA	Neg	AP
RCPXZD - 5901	Pos	AP, PSA, Micro	Neg	AP
TMDEV4 - 5902	Pos	AP, Micro	Neg	AP
TZBZVA - 5901	Pos	AP, Micro	Neg	AP
UNVR99 - 5902	Pos	ALS, AP, Micro	NT	
VFHZHA - 5902	Pos	AP, micro	Neg	AP
VK9834 - 5902	Pos	Acid phosfatase, RSID Semen, Sperm Hylighter Express	Neg	Acid phosfatase, RSID Semen, Sperm Hylighter Express
X28843 - 5901	Pos	AP, Microscopy	Neg	AP
XCU6U9 - 5902	Pos	p30, sperm search	Neg	p30
YGJ6L9 - 5901	Pos	AP, PSA, Micro	Neg	AP
YJMUQ3 - 5901	Pos	AP, PSA, Micro	Neg	AP, PSA, Micro
Z8LUQ4 - 5902	Pos	ALS, AP, Micro	Neg	ALS, AP

Table 1b: Serology Screening Response Summary - Semen

Participants: **74**

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	**74**	**0**
Negative	**0**	**71**
Inconclusive	**0**	**0**

Serology Screening Results

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

TABLE 1c

Saliva Screening Results				
WebCode - Test	Item 3		Item 4	
3MQZUY - 5902	Neg	Phadebas	Neg	Phadebas
3WHFJ3 - 5902	Neg	Phadebas	Neg	Phadebas
4BEUJW - 5902	Neg	RSID Saliva	Neg	RSID Saliva
77A6RY - 5901	Neg	SALIgAE	NT	
786NUZ - 5901	Neg	Seratec Amalase Test	Neg	Seratec Amalase Test
8YUL9Z - 5901	Neg	ALS, RSID Saliva, Seratec PAM	Neg	ALS, RSID Saliva, Seratec PAM
B7W38V - 5901	Neg	SALIGAE	NT	
BKHHBU - 5901	Neg	SaligAE	NT	
CDTG9M - 5901	Neg	RSID	Neg	RSID
CRBAWU - 5901	Pos	Amylase	Neg	Amylase
EHXZJK - 5902	Neg	RSID saliva	Neg	RSID saliva
F7H8UP - 5902	Neg	PHADEBAS	Neg	PHADEBAS
FPXE6L - 5902	Neg	Phadebas press	Neg	Phadebas press
J37QNH - 5902	NT		Neg	RSID
J772JG - 5902	Neg	RSID saliva	Neg	RSID saliva
JHLQHM - 5902	Neg	RSID Saliva	Neg	RSID Saliva
KPDQAK - 5902	Neg	Phadebas	Neg	Phadebas
LBAKVF - 5902	Neg	Phadebas press	Neg	Phadebas press
LUPUWF - 5901	Neg	Phadebas	Neg	Phadebas
NWNRKD - 5901	Neg	Phadebas	Neg	Phadebas
P8KEPF - 5902	Neg	Phadebas	Neg	Phadebas
R3MFPB - 5901	Neg	Phadebas	Neg	Phadebas
TZBZVA - 5901	Neg	Phadebas	Neg	Phadebas
VFHZHA - 5902	Neg	Phadebas	Neg	Phadebas
VK9834 - 5902	Neg	RSID Saliva	Neg	RSID Saliva
XCU6U9 - 5902	Neg	Amylase	Neg	amylase

Table 1c: Serology Screening Response Summary - Saliva Participants: **26**

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**	**0**
Negative	**24**	**23**
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**
2QGMC2 - 5902	**Pos** HemaTrace, p30	**NT**
3MQZUY - 5902	**Pos** HemaTrace	**Pos** HemaTrace
44PDRD - 5901	**Pos** Hematrace	**Pos** Hematrace
4BEUJW - 5902	**Pos** Quantifiler trio, PP21	**Pos** Quantifiler trio, PP21
6PTH6Y - 5902	**Pos** P30	**Pos** Hematrace
786NUZ - 5901	**Pos** Ouchterlony Double Immunodiffusion	**Pos** Ouchterlony Double Immunodiffusion
7H4JRV - 5902	**Pos** p30	**Pos** Hematrace
8Y8DYV - 5902	**Pos** Hematrace	**Neg** P30
8YUL9Z - 5901	**Pos** FOB, Seratec PMB, RSID Semen, Seratec PAM	**Pos** FOB, Seratec PMB
CDTG9M - 5901	**Pos** RSID-Blood	**Pos** RSID-Blood
CKECAQ - 5902	**Pos** HEMATRACE, P30	
CXYRCQ - 5902	**Pos** P30	**Pos** Hematrace
E34ANN - 5902	**Pos** Hematrace, PSA	**NT**
EHXZJK - 5902	**Pos** Quant trio, PowerPlex 21	**Pos** Quant trio, PowerPlex 21
ELJJPP - 5902	**NT**	**Pos** Hematrace
EY6YTN - 5902	**Pos** PSA	**Pos** Hematrace
F8XQDM - 5902	**Pos** PSA,HemaTrace	**Neg** PSA
FPXE6L - 5902	**Pos** ABACard Hematrace	**NT**
GCH7HK - 5902	**Pos** PSA	**Pos** Hematrace
H484WJ - 5902	**Pos** PSA	**Pos** Hematrace
HEQHYL - 5902	**Pos** Hematrace, P30	**NT**
HJX7CN - 5901	**Pos** Hema Trace ABA Card	**Pos** Hema Trace ABA Card
J37QNH - 5902	**Pos** QT, PP21	**Pos** QT, PP21
J772JG - 5902	**Pos** PowerPlex21, YFilerPlus, Quant Trio	**Pos** PowerPlex21, YFilerPlus, Quant Trio
JHLQHM - 5902	**Pos** OBTI, PSA	**Pos** OBTI, PSA
K9ECCE - 5902	**Pos** Quantifiler Trio	**Pos** Quantifiler Trio
LBAKVF - 5902	**NT**	**Pos** ABAcard
LG3PNJ - 5901	**Pos** Quantiplex Pro RGQ, STR	**Pos** Quantiplex Pro RGQ, STR
LHUN3H - 5902	**NT**	**Neg** P30
LUPUWF - 5901	**Pos** PowerQuant	**Pos** PowerQuant
MW99ZF - 5902	**Pos** p30	**Pos** p30
NWNRKD - 5901	**Pos** PowerQuant	**Pos** PowerQuant
R3MFPB - 5901	**Pos** PowerQuant	**Pos** PowerQuant

TABLE 1d

Human Origin Screening Results		
WebCode - Test	**Item 3**	**Item 4**
TZBZVA - 5901	**Pos** PowerQuant	**Pos** PowerQuant
UNVR99 - 5902	**Pos** Hematrace, P30	NT
VK9834 - 5902	**Pos** Quantifiler Trio	**Pos** Quantifiler Trio
Z8LUQ4 - 5902	**Pos** PSA	**Pos** Hematrace

Table 1d: Serology Screening Response Summary - Human Origin

Participants: **37**

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	**34**	**28**
Negative	**0**	**3**
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	
3MQZUY - 5902	Pos	PlexorHY	Pos	PlexorHY
44PDRD - 5901	Pos	Quant Trio	Pos	Quant Trio
8Y8DYV - 5902	Pos	MDS & qPCR procedure	Pos	MDS & qPCR procedure
9CLYK9 - 5901	Pos	Quant Trio	Pos	Quant Trio
CY6DP6 - 5901	Pos	Quantifiler Trio	Pos	Quantifiler Trio
EHXZJK - 5902	Pos	Quant trio, Yfiler Plus	Pos	Quant trio, Yfiler Plus
F8XQDM - 5902	Pos	MDS & qPCR procedure	Pos	MDS & qPCR procedure
FPXE6L - 5902	Pos	Plexor HY	Pos	Plexor HY
H484WJ - 5902	Pos	MDS&qPCR procedure	Pos	MDS&qPCR procedure
HJX7CN - 5901	Pos	Y-FILER-plus	Pos	Y-FILER-plus
J37QNH - 5902	Pos	QT, PP21	Pos	QT, PP21
J772JG - 5902	Pos	YFilerPlus, Quant Trio	Pos	YFilerPlus, Quant Trio
JHLQHM - 5902	Pos		Pos	
JPGUBX - 5901	Pos	QuantTrio	NT	
K9ECCE - 5902	Pos	Quantifiler Trio	Pos	Quantifiler Trio
LBAKVF - 5902	Pos	Plexor HY	Pos	Plexor HY
LG3PNJ - 5901	Pos	Y-STR	Pos	Y-STR
LUPUWF - 5901	Pos	PowerQuant	Pos	PowerQuant
NWNRKD - 5901	Pos	PowerQuant	Pos	PowerQuant
P8TP7Q - 5901	Pos	Quant Trio	Pos	Quant Trio
R3MFPB - 5901	Pos	PowerQuant	Pos	PowerQuant
TZBZVA - 5901	Pos	PowerQuant	Pos	PowerQuant
VK9834 - 5902	Pos	Quantifiler Trio	Pos	Quantifiler Trio
W2RLKZ - 5901	Pos	Quant Trio	Pos	Quant Trio
WRGKYZ - 5901	Pos	Quantifiler Trio	Pos	Quantifiler Trio
XCU6U9 - 5902	Pos	y-screen	Pos	y-screen

Table 1e: Serology Screening Response Summary - Y Screening Participants: **26**

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	**26**	**25**
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 1f

WebCode - Test	Other Screening Results					
	Item 3			Item 4		
8YUL9Z - 5901	Menstrual blood	Neg	Seratec PMB	Menstrual blood	Neg	Seratec PMB
K9ECCE - 5902	Spermatozoa	Pos	Microscopy			
LG3PNJ - 5901	sperm cells	Pos	Micro	sperm cells	Neg	Micro

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
2QGMC2 - 5902	Yes	No	Yes	Yes
34G3B3 - 5902	Yes	No	Yes	Yes
37J2CU - 5901	Yes	No	Yes	Yes
3MQZUY - 5902	Yes	No	Yes	Yes
3WHFJ3 - 5902	Yes	No	Yes	Yes
44PDRD - 5901	Yes	No	Yes	Yes
4BEUJW - 5902	Yes	No	Yes	Yes
4FBJY4 - 5902	Yes	No	Yes	Yes
4UQG64 - 5901	Yes	No	Yes	Yes
4XQRZ4 - 5901	Yes	No	Yes	Yes
62K9Q4 - 5901	Yes	No	Yes	Yes
63VBC2 - 5901	Yes	No	Yes	Yes
6PTH6Y - 5902	Yes	No	Yes	Yes
77A6RY - 5901	Yes	No	Yes	Yes
786NUZ - 5901	Yes	No	Yes	Yes
7H4JRV - 5902	Yes	No	Yes	Yes
8DDAHX - 5901	Yes	No	Yes	Yes
8Y8DYV - 5902	Yes	No	Yes	Yes
8YUL9Z - 5901	Yes	No	Yes	Yes
9CLYK9 - 5901	Yes	No	Yes	Yes
9MBR8Q - 5901	Yes	No	Yes	Yes
9WLTTR - 5902	Yes	No	Yes	Yes
B7W38V - 5901	Yes	No	Yes	Yes
BDR7Z7 - 5901	Yes	No	Yes	Yes
BKHHBU - 5901	Yes	No	Yes	Yes
BNGT8U - 5902	Yes	No	Yes	Yes
CDTG9M - 5901	Yes	No	Yes	Yes
CKECAQ - 5902	Yes	No	Yes	Yes
CRBAWU - 5901	Yes	No	Yes	Yes
CRVQCW - 5901	Yes	No	Yes	Yes
CXYRCQ - 5902	Yes	No	Yes	Yes
CY6DP6 - 5901	Yes	No	Yes	Yes
CZ6EPV - 5901	Yes	No	Yes	Yes
E34ANN - 5902	Yes	No	Yes	Yes
EHXZJK - 5902	Yes	No	Yes	Yes
ELJJPP - 5902	Yes	No	Yes	Yes
EY6YTN - 5902	Yes	No	Yes	Yes
F7H8UP - 5902	Yes	No	Yes	Yes
F8XQDM - 5902	Yes	No	Yes	Yes

TABLE 2

WebCode-Test	Victim (Item 1)		Suspect (Item 2)	
	Item 3	Item 4	Item 3	Item 4
FPXE6L - 5902	Yes	No	Yes	Yes
GCH7HK - 5902	Yes	No	Yes	Yes
H484WJ - 5902	Yes	No	Yes	Yes
HEQHYL - 5902	Inc	No	Yes	Yes
HJX7CN - 5901	Yes	No	Yes	Yes
J37QNH - 5902	Yes	No	Yes	Yes
J772JG - 5902	Yes	No	Yes	Yes
JHLQHM - 5902	Yes	No	Yes	Yes
JPGUBX - 5901	Yes	No	Yes	Yes
K9ECCE - 5902	Yes	No	Yes	Yes
KPDQAK - 5902	Yes	No	Yes	Yes
L67JVL - 5901	Yes	No	Yes	Yes
L8XEJE - 5901	Yes	No	Yes	Yes
LBAKVF - 5902	Yes	No	Yes	Yes
LG3PNJ - 5901	Yes	No	Yes	Yes
LHUN3H - 5902	Yes	No	Yes	Yes
LUPUWF - 5901	Yes	No	Yes	Yes
LYKQJL - 5901	Yes	No	Yes	Yes
MW99ZF - 5902	Yes	No	Yes	Yes
NWNRKD - 5901	Yes	No	Yes	Yes
P3QH3A - 5901	Yes	No	Yes	Yes
P8KEPF - 5902	Yes	No	Yes	Yes
P8TP7Q - 5901	Yes	No	Yes	Yes
PD88ZF - 5902	Yes	No	Yes	Yes
Q99BQE - 5901	Yes	No	Yes	Yes
R3MFPB - 5901	Yes	No	Yes	Yes
R9RDYE - 5901	Yes	No	Yes	Yes
RCPXZD - 5901	Yes	No	Yes	Yes
TMDEV4 - 5902	Yes	No	Yes	Yes
TZBZVA - 5901	Yes	No	Yes	Yes
UNVR99 - 5902	Yes	No	Yes	Yes
VFHZHA - 5902	Yes	No	Yes	Yes
VK9834 - 5902	Yes	No	Yes	Yes
W2RLKZ - 5901	Yes	No	Yes	Yes
WRGKYZ - 5901	Yes	No	Yes	Yes
WU8M28 - 5901	Yes	No	Yes	Yes
X28843 - 5901	Yes	No	Yes	Yes
XCU6U9 - 5902	No Interp	No Interp	Inc	Inc
YGJ6L9 - 5901	Yes	No	Yes	Yes
YJMUQ3 - 5901	Yes	No	Yes	Yes
Z8LUQ4 - 5902	Yes	No	Yes	Yes

DNA Interpretation

Response Summary

Participants reporting DNA results: 80

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	**78**	**0**	**79**	**79**
No	**0**	**79**	**0**	**0**
Inc	**1**	**0**	**1**	**1**
No Interpretation	**1**	**1**	**0**	**0**
No Response	**0**	**0**	**0**	**0**

STR Amplification Kit(s) & Results

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

2QGMC2 - 5902	GlobalFiler™ Express- TrueAllele® "VUler Release 2022b					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					
34G3B3 - 5902	GlobalFiler™					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					
37J2CU - 5901	GlobalFiler™- STRMix™					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					
3MQZUY - 5902	Identifiler® Plus					
		17,25		16,18	10,12	
1	10,12	13,15			8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24				6,9.3	8,8
	16,16					
3WHFJ3 - 5902	GlobalFiler™- STRMix™ V2.9.1					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					
44PDRD - 5901	GlobalFiler™					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

4BEUJW - 5902 PowerPlex® 21- STRMix™ 2.10.0

	11,17.3	17,25		16,18	10,12	11,11
1	10,12	13,15		16,17	8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24	9,11	8,11		6,9.3	8,8
	16,16					

4FBJY4 - 5902 PowerPlex® Fusion 6C - DNAxs

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24	9,11	8,11	17,24.2	6,9.3	8,8
	16,16					

4UQG64 - 5901 GlobalFiler™- STRMix™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

4XQRZ4 - 5901 GlobalFiler™- STRMix™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

62K9Q4 - 5901 GlobalFiler™- STRMix™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

63VBC2 - 5901 GlobalFiler™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

6PTH6Y - 5902 GlobalFiler™ Express- TrueAllele® VUIer Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

77A6RY - 5901	GlobalFiler™					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					
786NUZ - 5901	Identifiler® Plus - EuroForMix					
		17,25		16,18	10,12	
1	10,12	13,15			8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24				6,9.3	8,8
	16,16					
7H4JRV - 5902	GlobalFiler™ Express- TrueAllele® VUIer Release 2022b					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					
8DDAHX - 5901	GlobalFiler™- STRMix™ 2.8					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					
8Y8DYV - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					
8YUL9Z - 5901	PowerPlex® Fusion 6C, NGM Detect - LRmix					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24	9,11	8,11	17,24.2	6,9.3	8,8
	16,16	-	-	-	-	
9CLYK9 - 5901	GlobalFiler™- STRMix™					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16	NR			NR	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

9MBR8Q - 5901	PowerPlex® 21					
	11,17.3	17,25		16,18	10,12	11,11
1	10,12	13,15		16,17	8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24	9,11	8,11		6,9.3	8,8
	16,16					
9WLTTR - 5902	PowerPlex® 21					
	11,17.3	17,25		16,18	10,12	11,11
1	10,12	13,15		16,17	8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24	9,11	8,11		6,9.3	8,8
	16,16					
B7W38V - 5901	GlobalFiler™					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					
BDR7Z7 - 5901	PowerPlex® Fusion 6C, GlobalFiler™ Express					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24	9,11	8,11	17,24.2	6,9.3	8
	16					
BKHHBU - 5901	GlobalFiler™					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					
BNGT8U - 5902	GlobalFiler™					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					
CDTG9M - 5901	GlobalFiler™					
	11,17.3	17,25	11,11	16,18	10,12	-
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24	-	-	17,24.2	6,9.3	8,8
	16,16	-	-	-	-	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

CKECAQ - 5902 GlobalFiler™ Express- TrueAllele® VUIer Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

CRBAWU - 5901 PowerPlex® ESI-17 Fast - LiRa v3.0

	11,17.3	17,25	11,11	16,18		
1		13,15	13,13	16,17		9,12
	14,17	12,13	31.2,32.2	11,12	X,X	
	21,24			17,24.2	6,9.3	
	16,16					

CRVQCW - 5901 GlobalFiler™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

CXYRCQ - 5902 GlobalFiler™ Express

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

CY6DP6 - 5901 GlobalFiler™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

CZ6EPV - 5901 GlobalFiler™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

E34ANN - 5902 GlobalFiler™ Express- TrueAllele® VUIer Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

EHXZJK - 5902 PowerPlex® 21- STRMix™ 2.10

	11,17.3	17,25		16,18	10,12	11,11
1	10,12	13,15		16,17	8,12	9,12
	14,17	12,23	31.2,32.2		X,X	10,11
	21,24	9,11	8,11		6,9.3	8,8
	16,16					

ELJJPP - 5902 GlobalFiler™ Express- TrueAllele® VUIer Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

EY6YTN - 5902 GlobalFiler™ Express- TrueAllele® VUIer Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

F7H8UP - 5902 GlobalFiler™- STRMix™ v2.9.1

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

F8XQDM - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

FPXE6L - 5902 Identifiler® Plus

		17,25		16,18	10,12	
1	10,12	13,15			8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24				6,9.3	8,8
	16,16					

GCH7HK - 5902 GlobalFiler™ Express- TrueAllele® VUIer Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

H484WJ - 5902		GlobalFiler™ Express- TrueAllele® VUIer Release 2022b					
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
HEQHYL - 5902		GlobalFiler™ Express- TrueAllele® VUIer Release 2022b					
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
HJX7CN - 5901		GlobalFiler™ IQC					
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
J37QNH - 5902		PowerPlex® 21- STRMix™ v2.10.0					
	11,17.3	17,25		16,18	10,12	11,11	
1	10,12	13,15		16,17	8,12	9,12	
	14,17	12,13	31.2,32.2		X,X	10,11	
	21,24	9,11	8,11		6,9.3	8,8	
	16,16						
J772JG - 5902		PowerPlex® 21- STRMix™ 2.10					
	11,17.3	17,25		16,18	10,12	11,11	
1	10,12	13,15		16,17	8,12	9,12	
	14,17	12,13	31.2,32.2		X,X	10,11	
	21,24	9,11	8,11		6,9.3	8,8	
	16,16						
JHLQHM - 5902		GlobalFiler™ - DNAxs					
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
JPGUBX - 5901		GlobalFiler™					
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

K9ECCE - 5902	PowerPlex® 21					
	11,17.3	17,25		16,18	10,12	11,11
1	10,12	13,15		16,17	8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24	9,11	8,11		6,9.3	8,8
	16,16					
KPDQAK - 5902	GlobalFiler™- STRMix™ v2.9.1					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					
L67JVL - 5901	GlobalFiler™- STRMix™					
	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					
L8XEJE - 5901	PowerPlex® 21					
	11,17.3	17,25		16,18	10,12	11,11
1	10,12	13,15		16,17	8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24	9,11	8,11		6,9.3	8,8
	16,16					
LBAKVF - 5902	Identifiler® Plus					
		17,25		16,18	10,12	
1	10,12	13,15			8,12	9,12
	14,17	12,13	31.2,32.2		X,X	10,11
	21,24				6,9.3	8,8
	16,16					
LG3PNJ - 5901	PowerPlex® ESX17 Fast System- STRMix™ V2.5.11					
	11,17.3	17,25	11,11	16,18		
1		13,15	13,13	16,17		9,12
	14,17	12,13	31.2,32.2	11,12	X,X	
	21,24			17,24.2	6,9.3	
	16,16					
LHUN3H - 5902	GlobalFiler™ Express- TrueAllele® VUIer Release 2022b					
	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

LUPUWF - 5901	Identifiler® Plus, PowerPlex® Fusion 6C, Minifiler						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24	9,11	8,11	17,24.2	6,9.3	8	
	16						
LYKQJL - 5901	GlobalFiler™ - STRMix™						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						
MW99ZF - 5902	GlobalFiler™ Express- TrueAllele® VUIer Release 2022b						
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
NWNRKD - 5901	Identifiler® Plus, PowerPlex® Fusion 6C, MiniFiler						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24	9,11	8,11	17,24.2	6,9.3	8	
	16						
P3QH3A - 5901	PowerPlex® 21- STRMix™ 2.8						
	11,17.3	17,25		16,18	10,12	11,11	
1	10,12	13,15		16,17	8,12	9,12	
	14,17	12,13	31.2,32.2		X,X	10,11	
	21,24	9,11	8,11		6,9.3	8,8	
	16,16						
P8KEPF - 5902	GlobalFiler™ - STRMix™						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						
P8TP7Q - 5901	GlobalFiler™						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

PD88ZF - 5902		GlobalFiler™ - STRMix™ v2.8					
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						
Q99BQE - 5901		GlobalFiler™ IQC					
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
R3MFPB - 5901		Identifiler® Plus, PowerPlex® Fusion 6C, Minifiler					
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24	9,11	8,11	17,24.2	6,9.3	8	
	16						
R9RDYE - 5901		GlobalFiler™					
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						
RCPXZD - 5901		Investigator® 24plex QS					
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16	-					
TMDEV4 - 5902		GlobalFiler™ Express					
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13,13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
TZBZVA - 5901		Identifiler® Plus, PowerPlex® Fusion 6C, MiniFiler™					
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24	9,11	8,11	17,24.2	6,9.3	8	
	16						

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

UNVR99 - 5902	GlobalFiler™ Express- TrueAllele® VUIer Release 2022b						
	11,17.3	17,25	11,11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X,X	10,11	
	21,24			17,24.2	6,9.3	8,8	
	16,16						
VFHZHA - 5902	GlobalFiler™- STRMix™ v2.9.1						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						
VK9834 - 5902	PowerPlex® Fusion 6C- STRMix™ v2.10						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24	9,11	8,11	17,24.2	6,9.3	8	
	16						
W2RLKZ - 5901	GlobalFiler™						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16	NR			NR		
WRGKYZ - 5901	GlobalFiler™						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						
WU8M28 - 5901	GlobalFiler™- STRMix™ 2.8						
	11,17.3	17,25	11	16,18	10,12		
1	10,12	13,15	13	16,17	8,12	9,12	
	14,17	12,13	31.2,32.2	11,12	X	10,11	
	21,24			17,24.2	6,9.3	8	
	16						
X28843 - 5901	PowerPlex® 21- STRMix™ V2.8.0						
	11,17.3	17,25		16,18	10,12	11,11	
1	10,12	13,15		16,17	8,12	9,12	
	14,17	12,13	31.2,32.2		X,X	10,11	
	21,24	9,11	8,11		6,9.3	8,8	
	16,16						

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

YGJ6L9 - 5901 GlobalFiler™ - STRMix™

	11,17.3	17,25	11	16,18	10,12	
1	10,12	13,15	13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X	10,11
	21,24			17,24.2	6,9.3	8
	16					

YJMUQ3 - 5901 PowerPlex® Fusion 6C

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24	9,11	8,11	17,24.2	6,9.3	8,8
	16,16	ND	ND	ND		

Z8LUQ4 - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	11,17.3	17,25	11,11	16,18	10,12	
1	10,12	13,15	13,13	16,17	8,12	9,12
	14,17	12,13	31.2,32.2	11,12	X,X	10,11
	21,24			17,24.2	6,9.3	8,8
	16,16					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

2QGMC2 - 5902	GlobalFiler™ Express- TrueAllele® "VUler Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
34G3B3 - 5902	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
37J2CU - 5901	GlobalFiler™- STRMix™					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
3MQZUY - 5902	Identifiler® Plus					
		17,18		16,16	11,13	
2	9,11	10,13			12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23				7,7	11,14
	15,17					
3WHFJ3 - 5902	GlobalFiler™- STRMix™ V2.9.1					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
44PDRD - 5901	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
4BEUJW - 5902	PowerPlex® 21- STRMix™ 2.10.0					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

4FBJY4 - 5902	PowerPlex® Fusion 6C - DNAxs					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7,7	11,14
	15,17	10,10	20,20	17,17		
4UQG64 - 5901	GlobalFiler™ - STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
4XQRZ4 - 5901	GlobalFiler™ - STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
62K9Q4 - 5901	GlobalFiler™ - STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
63VBC2 - 5901	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
6PTH6Y - 5902	GlobalFiler™ - TrueAllele® VUier Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
77A6RY - 5901	GlobalFiler™					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

786NUZ - 5901	Identifiler® Plus - EuroForMix					
		17,18		16,16	11,13	
2	9,11	10,13			12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23				7,7	11,14
	15,17					
7H4JRV - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	16,17.3	17,18	14,14	16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
8DDAHX - 5901	GlobalFiler™- STRMix™ 2.8					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
8Y8DYV - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
8YUL9Z - 5901	PowerPlex® Fusion 6C, NGM Detect - LRmix					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7,7	11,14
	15,17	10	20	17	2	
9CLYK9 - 5901	GlobalFiler™- STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
9MBR8Q - 5901	PowerPlex® 21					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

9WLTTR - 5902	PowerPlex® 21					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					
B7W38V - 5901	GlobalFiler™					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
BDR7Z7 - 5901	PowerPlex® Fusion 6C, FlexPlex 27					
	16,17.3	17,18	14	16	11,13	12,13
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7	11,14
	15,17	10	20	17		
BKHHBU - 5901	GlobalFiler™					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
BNGT8U - 5902	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
CDTG9M - 5901	GlobalFiler™					
	16,17.3	17,18	14,14	16,16	11,13	-
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	-	-	18,28.2	7,7	11,14
	15,17	10	-	-	2	
CKECAQ - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

CRBAWU - 5901		PowerPlex® ESI-17 Fast					
	16,17.3	17,18	14,14	16,16			
2		10,13	13,13	18,19			9,14
	15,19	12,15.2	33,33.2	14,15	X,Y		
	20,23			18,28.2	7,7		
	15,17						
CRVQCW - 5901		GlobalFiler™					
	16,17.3	17,18	14	16	11,13		
2	9,11	10,13	13	18,19	12		9,14
	15,19	12,15.2	33,33.2	14,15	X,Y		10,12
	20,23			18,28.2	7		11,14
	15,17	10			2		
CXYRCQ - 5902		GlobalFiler™					
	16,17.3	17,18	14,14	16,16	11,13		
2	9,11	10,13	13,13	18,19	12,12		9,14
	15,19	12,15.2	33,33.2	14,15	X,Y		10,12
	20,23			18,28.2	7,7		11,14
	15,17	10			2		
CY6DP6 - 5901		GlobalFiler™					
	16,17.3	17,18	14	16	11,13		
2	9,11	10,13	13	18,19	12		9,14
	15,19	12,15.2	33,33.2	14,15	X,Y		10,12
	20,23			18,28.2	7		11,14
	15,17	10			2		
CZ6EPV - 5901		GlobalFiler™					
	16,17.3	17,18	14	16	11,13		
2	9,11	10,13	13	18,19	12		9,14
	15,19	12,15.2	33,33.2	14,15	X,Y		10,12
	20,23			18,28.2	7		11,14
	15,17	10			2		
E34ANN - 5902		GlobalFiler™ Express- TrueAllele® VUIer Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13		
2	9,11	10,13	13,13	18,19	12,12		9,14
	15,19	12,15.2	33,33.2	14,15	X,Y		10,12
	20,23			18,28.2	7,7		11,14
	15,17	10			2		
EHXZJK - 5902		PowerPlex® 21- STRMix™ 2.10					
	16,17.3	17,18		16,16	11,13		12,13
2	9,11	10,13		18,19	12,12		9,14
	15,19	12,15.2	33,33.2		X,Y		10,12
	20,23	9,12	5,10		7,7		11,14
	15,17						

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

ELJJPP - 5902	GlobalFiler™- TrueAllele® VUier Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
EY6YTN - 5902	GlobalFiler™ Express- TrueAllele® VUier Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
F7H8UP - 5902	GlobalFiler™- STRMix™ v2.9.1					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
F8XQDM - 5902	GlobalFiler™- TrueAllele® VUier Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
FPXE6L - 5902	Identifiler® Plus					
		17,18		16,16	11,13	
2	9,11	10,13			12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23				7,7	11,14
	15,17					
GCH7HK - 5902	GlobalFiler™- TrueAllele® VUier Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
H484WJ - 5902	GlobalFiler™- TrueAllele® VUier Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

HEQHYL - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
HJX7CN - 5901	GlobalFiler™ IQC					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
J37QNH - 5902	PowerPlex® 21- STRMix™ v2.10.0					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					
J772JG - 5902	PowerPlex® 21- STRMix™ 2.10					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					
JHLQHM - 5902	GlobalFiler™ - DNAxs					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
JPGUBX - 5901	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
K9ECCE - 5902	PowerPlex® 21					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

KPDQAK - 5902	GlobalFiler™- STRMix™ v2.9.1					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
L67JVL - 5901	GlobalFiler™- STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
L8XEJE - 5901	PowerPlex® 21					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					
LBAKVF - 5902	Identifiler® Plus					
		17,18		16,16	11,13	
2	9,11	10,13			12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23				7,7	11,14
	15,17					
LG3PNJ - 5901	PowerPlex® ESX17 Fast System- STRMix™ V2.5.11					
	16,17.3	17,18	14,14	16,16		
2		10,13	13,13	18,19		9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	
	20,23			18,28.2	7,7	
	15,17					
LHUN3H - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
LUPUWF - 5901	Identifiler® Plus, PowerPlex® Fusion 6C, Minifiler					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7	11,14
	15,17	10	20	17		

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

LYKQJL - 5901	GlobalFiler™- STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
MW99ZF - 5902	GlobalFiler™ Express- TrueAllele® VUIer Release 2022b					
	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	
NWNRKD - 5901	Identifiler® Plus, PowerPlex® Fusion 6C, MiniFiler					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7	11,14
	15,17	10	20	17		
P3QH3A - 5901	PowerPlex® 21- STRMix™ 2.8					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					
P8KEPF - 5902	GlobalFiler™- STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
P8TP7Q - 5901	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
PD88ZF - 5902	GlobalFiler™- STRMix™ v2.8					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

Q99BQE - 5901	GlobalFiler™ IQC						
	16,17.3	17,18	14,14	16,16	11,13		
2	9,11	10,13	13,13	18,19	12,12	9,14	
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12	
	20,23			18,28.2	7,7	11,14	
	15,17	10			2		
R3MFPB - 5901	Identifiler® Plus, PowerPlex® Fusion 6C, Minifiler						
	16,17.3	17,18	14	16	11,13		
2	9,11	10,13	13	18,19	12	9,14	
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12	
	20,23	9,12	5,10	18,28.2	7	11,14	
	15,17	10	20	17			
R9RDYE - 5901	GlobalFiler™						
	16,17.3	17,18	14	16	11,13		
2	9,11	10,13	13	18,19	12	9,14	
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12	
	20,23			18,28.2	7	11,14	
	15,17	10			2		
RCPXZD - 5901	Investigator® 24plex QS						
	16,17.3	17,18	14,14	16,16	11,13		
2	9,11	10,13	13,13	18,19	12,12	9,14	
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12	
	20,23			18,28.2	7,7	11,14	
	15,17	10					
TMDEV4 - 5902	GlobalFiler™ Express						
	16,17.3	17,18	14,14	16,16	11,13		
2	9,11	10,13	13,13	18,19	12,12	9,14	
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12	
	20,23			18,28.2	7,7	11,14	
	15,17	10			2		
TZBZVA - 5901	Identifiler® Plus, PowerPlex® Fusion 6C, MiniFiler™						
	16,17.3	17,18	14	16	11,13		
2	9,11	10,13	13	18,19	12	9,14	
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12	
	20,23	9,12	5,10	18,28.2	7	11,14	
	15,17	10	20	17			
UNVR99 - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b						
	16,17.3	17,18	14,14	16,16	11,13		
2	9,11	10,13	13,13	18,19	12,12	9,14	
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12	
	20,23			18,28.2	7,7	11,14	
	15,17	10			2		

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

VFHZHA - 5902	GlobalFiler™- STRMix™ v2.9.1					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
VK9834 - 5902	PowerPlex® Fusion 6C- STRMix™ v2.10					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7	11,14
	15,17	10	20	17		
W2RLKZ - 5901	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
WRGKYZ - 5901	GlobalFiler™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
WU8M28 - 5901	GlobalFiler™- STRMix™ 2.8					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	
X28843 - 5901	PowerPlex® 21- STRMix™ V2.8.0					
	16,17.3	17,18		16,16	11,13	12,13
2	9,11	10,13		18,19	12,12	9,14
	15,19	12,15.2	33,33.2		X,Y	10,12
	20,23	9,12	5,10		7,7	11,14
	15,17					
YGJ6L9 - 5901	GlobalFiler™- STRMix™					
	16,17.3	17,18	14	16	11,13	
2	9,11	10,13	13	18,19	12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7	11,14
	15,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

YJMUQ3 - 5901 PowerPlex® Fusion 6C

	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23	9,12	5,10	18,28.2	7,7	11,14
	15,17	10	20	17		

Z8LUQ4 - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	16,17.3	17,18	14,14	16,16	11,13	
2	9,11	10,13	13,13	18,19	12,12	9,14
	15,19	12,15.2	33,33.2	14,15	X,Y	10,12
	20,23			18,28.2	7,7	11,14
	15,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

8YUL9Z - 5901 PowerPlex® Fusion 6C, NGM Detect - LRmix

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12	15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10	18,20	17,19	2	

LG3PNJ - 5901 PowerPlex® ESX17 Fast System- STRMix™ V2.5.11

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18		
3		10,13,15	13,14	16,17,18,19,21		8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

2QGMC2 - 5902 GlobalFiler™- TrueAllele® "VUIer Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

34G3B3 - 5902 GlobalFiler™- STRMix™ 2.8

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14,15	14,15,16,17,18	8,9,10,11,12,13	
3e	8,9,10,11,12	9,10,12,13,14,15	12,13,14	16,17,18,19,20,21	8,10,11,12	7,8,9,11,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	29,30,30.2,31.2,32,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	19,20,21,22,22.2,23,23.2,24			14,14.2,15,16,16.2,17,17.2,18,23.2,24.2,27.2,28,28.2,29.2	5,6,7,8,9,9.3	8,10,11,13,14
	14,15,16,17	9,10			2	

37J2CU - 5901 GlobalFiler™- STRMix™

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

3MQZUY - 5902 Identifiler® Plus- STRMix™

		17,18,20,25		15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15			8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24				6,7,9,9.3	8,10,11,14
	15,16,17					

3WHFJ3 - 5902 GlobalFiler™- STRMix™ V2.9.1

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

44PDRD - 5901 GlobalFiler™- STRMix™

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

4BEUJW - 5902 PowerPlex® 21- STRMix™ 2.10.0

	11,14,16,17.3,18.3	17,18,25		15,16,18	10,11,12,13	12,13
3e	9,11	10,13,15		16,18,19	11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,12
	20,24	9,10,11,12,13	5,10		6,7,9.3	8,11,14
	15,16,17					

4FBJY4 - 5902 PowerPlex® Fusion 6C - DNAxs

	11	17,18,20,25	14,16,17.3,18.3	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	11,14	16,17,18,19,21	13,14	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12	15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10	18,20	17,19		

4UQG64 - 5901 GlobalFiler™ - STRMix™

	11,14,15,16,17.3,18.3	17,18,20,24,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,15	12,13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,27.2,28.2,29.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

4XQRZ4 - 5901 GlobalFiler™ - STRMix™

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14	14,15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,20,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	30,31.2,32.2,33,33.2	11,12,13,14,15,16	X,Y	10,11,12
	19,20,21,22,22.2,23,23.2,24			14,15,16,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

62K9Q4 - 5901 GlobalFiler™ - STRMix™

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14	14,15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	30,30.2,31.2,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	19,20,21,23,23.2,24			14,15,16,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

63VBC2 - 5901 GlobalFiler™ - STRMix™

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14	15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,15.2	30,30.2,31.2,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	20,21,22.2,23,23.2,24			14,15,16,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

6PTH6Y - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

77A6RY - 5901 GlobalFiler™ - STRMix™

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14	15,16,17,18	9,10,11,12,13	
3e	8,9,10,11,12	9,10,12,13,14,15	12,13,14	16,17,18,19,20,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	30,30.2,31.2,32,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	19,20,21,22,22.2,23,23.2,24			14,15,16,17,18,24.2,27.2,28,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	9,10			2	

786NUZ - 5901 Identifiler® Plus - EuroForMix

		17,18,20,25		15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15			8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24				6,7,9,9.3	8,10,11,14
	15,16,17					

7H4JRV - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

8DDAHX - 5901 GlobalFiler™ - STRMix™ 2.8

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

8Y8DYV - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
9CLYK9 - 5901	GlobalFiler™ - STRMix™					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,14**,15	13,14	17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32**,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
9MBR8Q - 5901	PowerPlex® 21 - STRMix™ 2.8.0					
	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,15		16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,14
	15,16,17					
9WLTTR - 5902	PowerPlex® 21 - STRMix™ 2.10.0					
	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,14,15		16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,14
	15,16,17					
B7W38V - 5901	GlobalFiler™ - STRMix™					
	11,13,14,15,16,16.3,17.3,18.3	16,17,18,20,24,25	10,11,13,14	15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,15.2	30,31.2,32.2,33,33.2	11,12,13,14,15	X,Y	9,10,11,12
	19,20,21,23,23.2,24			15,16,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	9,10			2	
BDR7Z7 - 5901	PowerPlex® Fusion 6C - STRMix™ 2.6.2					
	(11),14,(16),17.3,(18.3)	17,(18),20,25	11,14	(15),16,(18)	9,(10),11,(12),13	
3e	9,(10),11,(12)	(10),13,(15)	13,(14)	(16),(17),18,19,(20),(21)	(8),(11),12	8,9,(12),13,14
	14,15,17,18,19	12,(13),(15.2)	30,31.2,(32.2),33,33.2	(11),(12),(14),15	X,Y	10,(11),(12)
	20,(21),(23),(23.2),(24)	9,(10),(12),(13)	(5),8,(10),11,12	(15),(17),(18),(24.2),28.2	6,7,(9),(9.3)	8,10,(11),14
	(15),16,17	10	(18),20	17,19		

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

BKHHBU - 5901 GlobalFiler™- STRMix™

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14	14,15,16,17,18	8,9,10,11,12,13	
3e	8,9,10,11,12	9,10,12,13,14,15	12,13,14	16,17,18,19,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	29,30,30.2,31.2,32,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	19,20,21,22,23,23.2,24			14,15,16,17,17.2,18,23.2,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	14,15,16,17	9,10			2	

BNGT8U - 5902 GlobalFiler™- STRMix™ 2.8

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14,15	14,15,16,17,18	8,9,10,11,12,13	
3e	8,9,10,11,12	9,10,12,13,14,15	12,13,14	16,17,18,19,20,21	8,10,11,12,13	8,9,11,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	29,30,30.2,31.2,32,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	19,20,21,22,22.2,23,23.2,24			14,14.2,15,16,16.2,17,17.2,18,23.2,24.2,27.2,28,28.2,29.2	5,6,7,8,9,9.3	8,10,11,14
	14,15,16,17	9,10			2	

CDTG9M - 5901 GlobalFiler™

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	-
3e	9,10,11,12	10,13,15	13,14	16,17,18,19	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24	-	-	15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10	-	-	2	

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

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

CRBAWU - 5901 PowerPlex® ESI-17 Fast - LiRa v3.0

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18		
3e		10,13,15	13,14	16,17,18,19,21		8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

CRVQCW - 5901 GlobalFiler™ - STRMix™

	11,14,16,17.3,18.3	16,17,18,19,20,25	10,11,13,14	15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15,16	12,13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	11,12,13,14.2,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	19,20,21,22,23,23.2,24			15,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

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

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

CY6DP6 - 5901 GlobalFiler™ - STRMix™

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10,11**			2	

CZ6EPV - 5901 GlobalFiler™ - STRMix™

	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14	15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	30,30.2,31.2,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	19,20,21,23,23.2,24			14,15,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

E34ANN - 5902 GlobalFiler™ - TrueAllele® VUIer Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,13	
3e	9,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

EHXZJK - 5902 PowerPlex® 21 - STRMix™ 2.10

	11,14,16,17.3	17,18,20,25		16,18	9,10,11,12,13	11,12,13
3e	9,10,11,12	10,13,15		16,17,18,19	8,12	9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33.2,33		X,Y	10,11,12
	20,21,23,23.2,24	9,11,12	5,8,10,11		6,7,9,9.3	8,10,11,14
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

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

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

EY6YTN - 5902 GlobalFiler™- TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

F7H8UP - 5902 GlobalFiler™- STRMix™ v2.9.1

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

F8XQDM - 5902 GlobalFiler™- TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

FPXE6L - 5902 Identifiler® Plus- STRMix™

		17,18,20,25		15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15			8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24				6,7,9,9.3	8,10,11,14
	15,16,17					

GCH7HK - 5902 GlobalFiler™- TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

H484WJ - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

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

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

HJX7CN - 5901 GlobalFiler™ IQC

	(11),14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	(9,10),11,(12,13)	
3e	9,(10),11,(12)	(10),13,15	13,(14)	(16,17),18,19,21	(8,11),12	8,9,(12),13,14
	(14),15,17,18,19	12,13,(15.2)	30,31.2,(32.2),33,33.2	(11,12,14),15	X,Y	10,11,(12)
	20,(21,23),23.2,(24)			15,(17),18,(24.2),28.2	6,7,9,(9.3)	8,10,11,14
	(15),16,17	10			2	

J37QNH - 5902 PowerPlex® 21 - STRMix™ 2.10.0

	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,15		16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,13,14
	15,16,17					

J772JG - 5902 PowerPlex® 21 - STRMix™ 2.10

	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,15		18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,12		6,7,9,9.3	8,10,11,14
	15,16,17					

JHLQHM - 5902 GlobalFiler™ - DNAxs

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,14,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

JPGUBX - 5901	GlobalFiler™ - STRMix™					
	11,14,16,17.3,18.3	17,18,20,24,25	11,14	16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13	16,18,19,21	8,11,12	9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,23,23.2,24			15,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10,11			2	
K9ECCE - 5902	PowerPlex® 21 - STRMix™ 2.10					
	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,15		16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,14
	15,16,17					
KPDQAK - 5902	GlobalFiler™ - STRMix™ v2.9.1					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
L67JVL - 5901	GlobalFiler™ - STRMix™					
	11,13,14,16,16.3,17.3,18.3	16,17,18,20,24,25	10,11,13,14	15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	9,10,11,12
	19,20,21,22,22.2,23,23.2,24			15,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
L8XEJE - 5901	PowerPlex® 21 - STRMix™ v2.8.0					
	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,15		16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,14
	15,16,17					
LBAKVF - 5902	Identifiler® Plus - STRMix™ 2.7.0					
		17,18,20,25		15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15			8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24				6,7,9,9.3	8,10,11,14
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

LHUN3H - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

LUPUWF - 5901 PowerPlex® Fusion 6C- STRMix™ STRmix V2.5.11

	11,16,17.3,18.3	17,18,20,25	11,14	15,16,18	10,11,12,13	
3e	9,10,11,12	10,13,15	13	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,14,15	X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11	15,17,18,24.2,28.2	6,7,9,9.3	8,11,14
	15,16,17	10	18,20	17,19		

LYKQJL - 5901 GlobalFiler™ - STRMix™

	11,13,14,15,16,16.3,17.3,18.3	17,18,19,20,24,25	10,11,13,14	14,15,16,17,18	9,10,11,12,13	
3e	8,9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15,16	X,Y	10,11,12
	19,20,21,23,23.2,24			14,15,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

MW99ZF - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

NWNRKD - 5901 PowerPlex® Fusion 6C- STRMix™ V2.5.11

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,13	
3e	9,11	10,13,15	13,14	16,17,18,19,21	11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	14,15	X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,12	15,17,18,28.2	6,7,9	8,10,11,14
	15,16,17	10	18,20	17,19		

P3QH3A - 5901 PowerPlex® 21- STRMix™ 2.8

	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,15		16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,14
	15,16,17					

TABLE 3

Item 3e - STR Results

WebCode - Test	Amplification Kits - Probablistic 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	
P8KEPF - 5902	GlobalFiler™- STRMix™					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
P8TP7Q - 5901	GlobalFiler™- STRMix™					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
PD88ZF - 5902	GlobalFiler™- STRMix™ v2.8					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
Q99BQE - 5901	GlobalFiler™ IQC- STRMix™ 2.8.0					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
R3MFPB - 5901	PowerPlex® Fusion 6C- STRMix™ STRmix v2.5.11					
	11,14,16,17.3,18.3	17,18,20,25	11,14	16,18	10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12	5,8,10,11	15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10	18,20	17		
R9RDYE - 5901	GlobalFiler™- STRMix™ STRmix					
	11,13,14,15,16,16.3,17.3,18.3	16,17,18,19,20,24,25	10,11,13,14	14,15,16,17,18	9,10,11,12,13	
3e	8,9,10,11,12	10,12,13,14,15,16	12,13,14	16,17,18,19,20,21	8,10,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,14.2,15.2	30,31.2,32,32.2,33,33.2	11,12,13,14,15,16	X,Y	9,10,11,12
	19,20,21,22.2,23,23.2,24			14,15,17,18,24.2,27.2,28.2,29.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TABLE 3

Item 3e - STR Results

WebCode - Test	Amplification Kits - Probablistic 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	

RCPXZD - 5901 Investigator® 24plex QS - EuroForMix

	[11],14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,[10],11,[12]	10,13,15	13,[14]	16,17,18,19,21	[8],11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	[11,12,14],15	X,Y	10,11,12
	20,[21],23,23.2,[24]			15,17,18,24.2,28.2	6,7,9,[9.3]	8,10,11,14
	[15],16,17	10				

TMDEV4 - 5902 GlobalFiler™

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TZBZVA - 5901 PowerPlex® Fusion 6C- STRMix™ V2.5.11

	14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,11	10,13,15	13,14	16,17,18,19,21	11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	14,15	X,Y	10,11,12
	20,21,23,23.2,24	9,10,12,13	5,8,10,12	15,18,28.2	6,7,9	8,10,11,14
	15,16,17	10	18,20	17,19		

UNVR99 - 5902 GlobalFiler™- TrueAllele® VUier Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

VFHZHA - 5902 GlobalFiler™- STRMix™ v2.9.1

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

VK9834 - 5902 PowerPlex® Fusion 6C- STRMix™ v2.10

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,22.2,23,23.2,24	9,10,11,12,13	5,8,10,11,12	15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10	18,20	17,19		

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

W2RLKZ - 5901	GlobalFiler™ - STRMix™					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
WRGKYZ - 5901	GlobalFiler™ - STRMix™					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
WU8M28 - 5901	GlobalFiler™ - STRMix™ 2.8					
	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
X28843 - 5901	PowerPlex® 21- STRMix™ V2.8.0					
	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3e	9,10,11,12	10,13,15		16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,14
	15,16,17					
YGJ6L9 - 5901	GlobalFiler™ - STRMix™					
	11,14,16,17.3,18.3	17,18,19,20,24,25	10,11,13,14	15,16,17,18	9,10,11,12,13	
3e	9,10,11,12	10,12,13,14,15	12,13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,16,17,18,19	11,12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	19,20,21,22,22.2,23,23.2,24			15,17,18,24.2,27.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	
YJMUQ3 - 5901	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
	16,17.3	17,18,20	11,14	15,16	10,11	
3e	ND	10,13,15	13	18,19	12	9
	15,17,19	12,15.2	ND	ND	Y	10
	ND	12	5,8	17	ND	8
	15,16	ND	ND	ND		

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

Z8LUQ4 - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3e	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24			15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

2QGMC2 - 5902 GlobalFiler™- TrueAllele® "VUIer Release 2022b

	14,18.3	17,20,24,25	11,14	15,16	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,27.2,28.2	6,9	8,10
	16,17	10			2	

34G3B3 - 5902 GlobalFiler™- STRMix™ 2.8

	13,13.2,14,17.3,18.1,18.3	19,20,21,24,25,26	10,11,12,13,14,15	14,15,16,17,18	8,9,10,11,12	
3sp	8,9,10,11,12	12,13,14,15,16	12,13,14	18,19,20,21	10,11,12,13	7,8,12,13,14
	16,17,18,19	11,12,13	29,30,30.2,31,31.2	13,14,15,16	X,Y	9,10,11,12
	19,20,21,21.2,22.2,23.2,24.2			14,14.2,15,16,26.2,27.2,28,28.2,29.2	5,6,8,9	7,8,9,10
	15,16,17,18	9,10			2	

37J2CU - 5901 GlobalFiler™- STRMix™

	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

3MQZUY - 5902 Identifiler® Plus- STRMix™

		20,25		15,18	9,11	
3sp	9,11	13,15			11,12	8,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23.2				6,9	8,10
	16,17					

3WHFJ3 - 5902 GlobalFiler™- STRMix™ V2.9.1

	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

44PDRD - 5901 GlobalFiler™- STRMix™

	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2,24.2**			15,28.2	6,9	8,10
	16,17	10			2	

4BEUJW - 5902 PowerPlex® 21- STRMix™ 2.10.0

	14,18.3	20,25		15,18	9,11	12,18
3sp	9,11	13,15		19,21	11,12	8,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23.2	10,13	8,12		6,9	8,10
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

4FBJY4 - 5902	PowerPlex® Fusion 6C - DNAxs					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,21.2	15	X,Y	10,11
	20,23.2	10,13	8,12	15,28.2	6,9	8,10
	16,17	10	18	19		
4UQG64 - 5901	GlobalFiler™ - STRMix™					
	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,15,27.2,28.2	6,9	8,10
	15,16,17	10			2	
4XQRZ4 - 5901	GlobalFiler™ - STRMix™					
	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,15,27.2,28.2	6,9	8,10
	15,16,17	10			2	
62K9Q4 - 5901	GlobalFiler™ - STRMix™					
	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2,24.2			14,15,27.2,28.2,29.2	6,9	8,10
	15,16,17	10			2	
63VBC2 - 5901	GlobalFiler™ - STRMix™					
	13,14,15,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13
	16,17,18	11,12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11,12
	19,20,22.2,23.2,24.2			14,15,27.2,28.2,29.2	6,9	8,10
	15,16,17	10			2	
6PTH6Y - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

77A6RY - 5901	GlobalFiler™ - STRMix™					
	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	7,8,12,13
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,14.2,15,27.2,28,28.2	6,9	8,10
	15,16,17	9,10			2	
786NUZ - 5901	Identifiler® Plus - EuroForMix					
		17,18,20,25		15,16,18	9,10,11,12,13	
3sp	9,10,11,12	10,13,15			8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,21,23,23.2,24				6,7,9,9.3	8,10,11,14
	15,16,17					
7H4JRV - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	8,11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
8DDAHX - 5901	GlobalFiler™ - STRMix™ 2.8					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
8Y8DYV - 5902	GlobalFiler™ - TrueAllele® VUIer Release 2022b					
3sp						
9CLYK9 - 5901	GlobalFiler™ - STRMix™					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

9MBR8Q - 5901 PowerPlex® 21- STRMix™ 2.8.0

	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,10,11,12,13	11,12,13,18
3sp	9,10,11,12	10,13,15		17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,23,23.2,24	9,10,12,13	5,8,10,11,12		6,7,9,9.3	8,10,11,14
	15,16,17					

9WLTTR - 5902 PowerPlex® 21- STRMix™ 2.10.0

	11,14,16,17.3,18.3	17,18,20,25		15,16,18	9,11,12,13	12,18
3sp	9,10,11,12	10,13,15		16,17,19,21	11,12	8,9,13
	14,15,17,18,19	12,13,15.2	30,31.2,32.2		X,Y	10,11
	20,23,23.2	9,10,13	8,10,11,12		6,7,9	8,10,14
	16,17					

B7W38V - 5901 GlobalFiler™- STRMix™

	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,14.2,15,27.2,28,28.2	6,9	8,10
	15,16,17	9,10			2	

BDR7Z7 - 5901 PowerPlex® Fusion 6C- STRMix™ 2.6.2

	14,18.3	(18),20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	(16),19,21	11,12	8,13
	17,18	12,13	30,31.2,(33.2)	15	X,Y	10,11
	20,23.2	10,13	8,(10),12	15,(17),28.2	6,9	8,10
	16,17	10	18	19		

BKHHBU - 5901 GlobalFiler™- STRMix™

	13,13.2,14,17.3,18.1,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15,16	12,13,14	18,19,20,21	10,11,12	7,8,12,13,14
	16,17,18	11,12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2,24.2			14,14.2,15,16,27.2,28,28.2	6,9	8,10
	15,16,17	9,10			2	

BNGT8U - 5902 GlobalFiler™- STRMix™ 2.8

	13,13.2,14,17.3,18.1,18.3	19,20,24,25	10,11,12,13,14,15	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12,13	7,8,12,13
	16,17,18	11,12,13	29,30,30.2,31.2	13,14,15,16	X,Y	9,10,11
	19,20,22.2,23.2,24.2			14,14.2,15,16,27.2,28,28.2,29.2	5,6,8,9	7,8,9,10
	15,16,17	9,10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

CDTG9M - 5901	GlobalFiler™					
	14,18.3	20,25	11,14	15,18	9,11	-
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2	-	-	15,28.2	6,9	8,10
	16,17	10	-	-	2	
CKECAQ - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
CRBAWU - 5901	PowerPlex® ESI-17 Fast - LiRa v3.0					
	14,18.3	20,25	11,14	15,18		
3sp		13,15	13,14	19,21		8,13
	17,18	12,13	30,31.2	15,15	X,Y	
	20,23.2			15,28.2	6,9	
	16,17					
CRVQCW - 5901	GlobalFiler™- STRMix™					
	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13,14
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,15,27.2,28.2	6,9	8,10
	15,16,17	10			2	
CXYRCQ - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
CY6DP6 - 5901	GlobalFiler™- STRMix™					
	14,18.3	20,21**,25	11,14	15,18,19**	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2,24.2**			15,28.2	6,9	8,10
	16,17	10			2	
CZ6EPV - 5901	GlobalFiler™- STRMix™					
	13,14,17.3,18.3,19.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,15,16,27.2,28.2,29.2	6,9	8,10
	15,16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

E34ANN - 5902 GlobalFiler™- TrueAllele® VUier Release 2022b

	14,18.3	20,25	11,14	15,16,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	15,16,17	10			2	

EHXZJK - 5902 PowerPlex® 21- STRMix™ 2.10

	14,18.3	20,25		15,18	9,11	12,18
3sp	9,11	13,15		19,21	11,12	8,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23.2	10,13	8,12		6,9	8,10
	16,17					

ELJJPP - 5902 GlobalFiler™- TrueAllele® VUier Release 2022b

	11,14,18.3	20,25	11,14	15,16,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,9,12,13,14
	14,17,18	12,13,15.2	30,31.2,33.2	11,15	X,Y	10,11,12
	20,23.2			15,17,28.2	6,9	8,10,14
	16,17	10			2	

EY6YTN - 5902 GlobalFiler™- TrueAllele® VUier Release 2022b

	11,14,18.3	17,18,20,25	11,14	15,16,18	9,11,12,13	
3sp	9,10,11	13,15	13,14	16,17,19,21	8,11,12	8,9,13
	14,17,18,19	12,13,15.2	30,31.2,33,33.2	15	X,Y	10,11
	20,21,23.2			15,28.2	6,7,9	8,10
	16,17	10			2	

F7H8UP - 5902 GlobalFiler™- STRMix™ v2.9.1

	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

F8XQDM - 5902 GlobalFiler™- TrueAllele® VUier Release 2022b

	14,18.3	18,20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

FPXE6L - 5902 Identifiler® Plus- STRMix™

		20,25		15,18	9,11	
3sp	9,11	13,15			11,12	8,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23.2				6,9	8,10
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

GCH7HK - 5902	GlobalFiler™ - TrueAllele® VUier Release 2022b					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
H484WJ - 5902	GlobalFiler™ - TrueAllele® VUier Release 2022b					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,7,9	8,10
	16,17	10			2	
HEQHYL - 5902	GlobalFiler™ - TrueAllele® VUier Release 2022b					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
HJX7CN - 5901	GlobalFiler™ IQC					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
J37QNH - 5902	PowerPlex® 21 - STRMix™ 2.10.0					
	14,18.3	20,25		15,18	9,11	12,18
3sp	9,11	13,15		19,21	11,12	8,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23.2	10,13	8,12		6,9,9.3	8,10
	16,17					
J772JG - 5902	PowerPlex® 21 - STRMix™ 2.10					
	14,18.3	20,25		15,18	9,11	12,18
3sp	9,11	13,15		19,21	11,12	8,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23.2	10,13	8,12		6,9	8,10
	16,17					
JHLQHM - 5902	GlobalFiler™ - DNAxs					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

JPGUBX - 5901	GlobalFiler™ - STRMix™					
	14,16,18.3	17,18,20,25	11,14	15,16,18	9,11	
3sp	9,11	10,13,15	13,14	19,21	11,12	8,13
	17,18	12,13,15.2	30,31.2	15	X,Y	10,11
	20,23.2			15,18,28.2	6,9	8,10
	16,17	10			2	
K9ECCE - 5902	PowerPlex® 21 - STRMix™ 2.10					
	14,16,18.3	17,18,20,25		15,16,18	9,11	12,18
3sp	9,11	13,14,15		17,19,21	11,12	8,12,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23,23.2	9,10,13	8,12		6,9	8,10
	16,17					
KPDQAK - 5902	GlobalFiler™ - STRMix™ v2.9.1					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
L67JVL - 5901	GlobalFiler™ - STRMix™					
	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,16,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	7,8,12,13
	16,17,18	11,12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,15,27.2,28.2	6,8,9	8,10
	15,16,17	10			2	
L8XEJE - 5901	PowerPlex® 21 - STRMix™ v2.8.0					
	14,16,18.3	20,25		15,16,18	9,11,12	12,13,18
3sp	9,11	13,14,15		16,19,21	8,11,12,13	8,13,14
	17,18,19	12,13	30,31.2,32.2,33,33.2		X,Y	10,11,12
	20,23.2,24.2	9,10,11,13	8,12		6,9	8,10
	16,17,18					
LBAKVF - 5902	Identifiler® Plus - STRMix™ 2.7.0					
		20,25		15,18	9,11	
3sp	9,11	13,15			11,12	8,13
	17,18	12,13	30,31.2		X,Y	10,11
	20,23.2				6,9	8,10
	16,17					
LHUN3H - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	14,18.3	20,25	11,14	15,16,18	9,11	
3sp	9,11	10,13,15	13,14	19,21	11,12	8,12,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

LUPUWF - 5901 PowerPlex® Fusion 6C- STRMix™ STRmix V2.5.11

	14,18.3	17,18,20,25	11,14	15,16,18	9,11,12	
3sp	9,11	10,13,15	13,14	16,18,19,21	11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2	11,15	X,Y	10,11,12
	20,23.2	9,10,11,12,13	8,12	15,17,18,28.2	6,7,9	8,10
	16,17	10	18,20	17,19		

LYKQJL - 5901 GlobalFiler™- STRMix™

	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12,13	7,8,12,13
	16,17,18	12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,21,22.2,23.2			14,15,27.2,28.2	6,8,9	8,10
	15,16,17	10			2	

MW99ZF - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

	11,14,16,18.3	17,18,20,25	11,14	15,18	9,11,13	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13,15.2	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

NWNRKD - 5901 PowerPlex® Fusion 6C- STRMix™ V2.5.11

	14,18.3	18,20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,9,12,13,14
	17,18	12,13	30,31.2	15	X,Y	10,11,12
	20,23.2	9,10,12,13	8,12	15,28.2	6,9	8,10
	16,17	10	18	19		

P3QH3A - 5901 PowerPlex® 21- STRMix™ 2.8

	14,16,17.3,18.3	17,18,20,25		15,16,18	9,11,13	11,12,13,18
3sp	9,11	10,13,15		16,17,18,19,21	8,11,12	8,9,13,14
	14,15,17,18	12,13	30,31.2,32.2,33,33.2		X,Y	10,11
	20,21,23,23.2,24	9,10,13	5,8,10,12		6,9	8,10,11,14
	16,17					

P8KEPF - 5902 GlobalFiler™- STRMix™

	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

P8TP7Q - 5901 GlobalFiler™- STRMix™

	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11,12**	13,14**,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

PD88ZF - 5902	GlobalFiler™- STRMix™ v2.8					
	14,18.3	17,20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,21,23,23.2			15,28.2	6,7,9	8,10
	16,17	10			2	
Q99BQE - 5901	GlobalFiler™ IQC- STRMix™ 2.8.0					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
R3MFPB - 5901	PowerPlex® Fusion 6C- STRMix™ STRmix v2.5.11					
	14,17.3,18.3	17,18,20,25	11,14	15,16,18	9,11,13	
3sp	9,11	13,15	13,14	18,19,21	11,12	8,9,13,14
	15,17,18,19	12,13,15.2	30,31.2	11,15	X,Y	10,11,12
	20,23.2	9,10,12,13	8,12	15,18,28.2	6,7,9	8,10
	16,17	10	18,20	17,19		
R9RDYE - 5901	GlobalFiler™- STRMix™ STRmix					
	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18	8,9,10,11	
3sp	9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	8,12,13
	16,17,18	11,12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2,24.2			14,15,27.2,28.2	6,9	8,10
	15,16,17	10			2	
RCPXZD - 5901	Investigator® 24plex QS - EuroForMix					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10				
TMDEV4 - 5902	GlobalFiler™					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15,15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
TZBZVA - 5901	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11,12
	20,23.2	10,13	8,12	15,28.2	6,9	8,10
	16,17	10	18	19		

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

UNVR99 - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	11,14,16,18.3	17,20,25	11,14	15,16,18	9,11	
3sp	9,11	10,13,15	13,14	17,19,21	11,12	8,13,14
	17,18	12,13	30,31.2,33	15,15	X,Y	10,11
	20,23,23.2			15,28.2	6,7,9	8,10,11,14
	16,17	10			2	
VFHZHA - 5902	GlobalFiler™- STRMix™ v2.9.1					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
VK9834 - 5902	PowerPlex® Fusion 6C- STRMix™ v2.10					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2	10,13	8,12	15,28.2	6,9	8,10
	16,17	10	18	19		
W2RLKZ - 5901	GlobalFiler™- STRMix™					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15,16**	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2,24.2**			15,28.2	6,9	8,10
	16,17,18**	10,11**			2	
WRGKYZ - 5901	GlobalFiler™- STRMix™					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,14**,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2,24.2**			15,28.2	6,9	8,10
	16,17	10			2	
WU8M28 - 5901	GlobalFiler™- STRMix™ 2.8					
	14,18.3	20,25	11,14	15,18	9,11	
3sp	9,11	13,15	13,14	19,21	11,12	8,13
	17,18	12,13	30,31.2	15	X,Y	10,11
	20,23.2			15,28.2	6,9	8,10
	16,17	10			2	
X28843 - 5901	PowerPlex® 21- STRMix™ V2.8.0					
	11,14,17.3,18.3	20,25		15,18	9,11,12,13	12,18
3sp	9,11	13,15		19,21	11,12	8,13,14
	17,18,19	12,13	30,31.2,33		X,Y	10,11
	20,23.2,24.2	9,10,13	5,8,10,12		6,9	8,10
	16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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 3sp - STR Results

YGJ6L9 - 5901 GlobalFiler™ - STRMix™

	13,14,17.3,18.3	19,20,24,25	10,11,13,14	14,15,17,18,19	8,9,10,11	
3sp	8,9,10,11	12,13,14,15	12,13,14	18,19,20,21	10,11,12	7,8,12,13
	16,17,18	11,12,13	29,30,30.2,31.2	14,15,16	X,Y	9,10,11
	19,20,22.2,23.2			14,15,27.2,28.2	6,8,9	8,10
	15,16,17	10			2	

YJMUQ3 - 5901 PowerPlex® Fusion 6C- STRMix™ V2.5.11

	11,14,16,17.3,18.3	17,18,20,25	11,14	15,16,18	9,10,11,12,13	
3sp	9,10,11,12	10,13,15	13,14	16,17,18,19,21	8,11,12	8,9,12,13,14
	14,15,17,18,19	12,13,15.2	30,31.2,32.2,33,33.2	11,12,14,15	X,Y	10,11,12
	20,21,23,23.2,24	9,10,11,12,13	5,8,10,11,12	15,17,18,24.2,28.2	6,7,9,9.3	8,10,11,14
	15,16,17	10	18,20	17,19		

Z8LUQ4 - 5902 GlobalFiler™ - TrueAllele® VUler Release 2022b

	14,18.3	17,18,20,25	11,14	15,18	9,11,13	
3sp	9,11,12	10,13,15	13,14	19,21	11,12	8,9,12,13
	17,18	12,13	30,31.2	11,15	X,Y	10,11
	20,23.2			15,28.2	6,7,9	8,10
	16,17	10			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

2QGMC2 - 5902 GlobalFiler™- TrueAllele® "VUIer Release 2022b

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

34G3B3 - 5902 GlobalFiler™- STRMix™ 2.8

	11,15,15.2,16,16.3,17.1,17.3	16,17,18,22,23,24,25	9,10,13,14,15	13,14,15,16	10,11,12,13	
4	7,8,9,10,11,12	9,10,12,13,14,15,16	12,13,14,15	17,18,19,20,21	8,9,10,11,12,13	8,9,10,11,12,13,14
	13,14,15,16,17,18,19	11,12,12.2,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,13,14,15,16,17	X,Y	9,10,11,12,13
	19,20,21,22,23,25,26,27			13,13.2,14,17,17.2,18,22.2,23.2,25.2,26.2,27.2,28,28.2	6,7,9.3	8,10,11,13,14
	14,15,16,17	9,10,11			2	

37J2CU - 5901 GlobalFiler™- STRMix™

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

3MQZUY - 5902 Identifiler® Plus- STRMix™

		17,18,23,24,25		14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16			8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26				7,9.3	8,11,14
	15,16,17					

3WHFJ3 - 5902 GlobalFiler™- STRMix™ V2.9.1

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

44PDRD - 5901 GlobalFiler™- STRMix™

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

4BEUJW - 5902	PowerPlex® 21- STRMix™ 2.10.0					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					
4FBJY4 - 5902	PowerPlex® Fusion 6C - DNAxs					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	17,20	16,17,21		
4UQG64 - 5901	GlobalFiler™ - STRMix™					
	11,15,16,17.3	16,17,18,23,24,25	9,10,13,14	13,14,15,16	10,11,12,13	
4	8,9,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,20,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,17,18,19	12,12.2,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,13,14,15,16	X,Y	10,11,12,13
	19,20,21,22,23,25,26			14,17,18,23.2,25.2,26.2,27.2,28.2	6,7,9.3	8,11,14
	15,16,17	10,11			2	
4XQRZ4 - 5901	GlobalFiler™ - STRMix™					
	11,16,17.3	16,17,18,23,24,25	9,10,13,14	14,15,16	11,12,13	
4	8,9,11,12	10,12,13,14,16	12,13,14,15	18,19,21	8,10,11,12,13	9,11,12,13,14
	13,15,17,18,19	12,12.2,13,13.2,14,14.2,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	19,20,21,22,23,25,26			14,17,18,23.2,26.2,28.2	6,7,9.3	8,11,14
	15,16,17	10,11			2	
62K9Q4 - 5901	GlobalFiler™ - STRMix™					
	10,11,15,16,16.3,17.3	16,17,18,23,24,25	9,10,13,14	14,15,16	10,11,12,13	
4	8,9,10,11,12	9,10,12,13,14,15,16	12,13,14,15	17,18,19,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,17,18,19	11,12,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,13,14,15,16	X,Y	9,10,11,12,13
	19,20,21,22,23,25,26			14,17,18,23.2,26.2,27.2,28.2	6,7,9.3	8,10,11,14
	14,15,16,17	10,11			2	
63VBC2 - 5901	GlobalFiler™ - STRMix™					
	11,15,16,16.3,17.3	16,17,18,23,24,25	9,10,13,14	14,15,16	10,11,12,13	
4	8,9,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,20,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,16,17,18,19	12,12.2,13,13.2,14,15.2	28,29,30,32,33,33.2	11,13,14,15,16	X,Y	9,10,11,12,13
	20,21,22,23,25,26			14,17,18,23.2,26.2,27.2,28.2	6,7,9.3	8,10,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

6PTH6Y - 5902 GlobalFiler™ - TrueAllele® VUIer Release 2022b

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

77A6RY - 5901 GlobalFiler™ - STRMix™

	11,15,16,16.3,17.3	16,17,18,22,23,24,25	9,10,13,14	13,14,15,16	10,11,12,13	
4	8,9,10,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,20,21	8,10,11,12,13	9,10,11,12,13,14
	13,14,15,16,17,18,19	11,12,12.2,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,13,14,15,16	X,Y	9,10,11,12,13
	19,20,21,22,23,25,26			14,17,17.2,18,22.2,23.2,25.2,26.2,27.2,28,28.2	6,7,9.3	8,10,11,13,14
	14,15,16,17	9,10,11			2	

786NUZ - 5901 Identifiler® Plus - EruoForMix

		17,18,23,24,25		14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16			8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26				7,9.3	8,11,14
	15,16,17					

7H4JRV - 5902 GlobalFiler™ - TrueAllele® VUIer Release 2022b

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

8Y8DYV - 5902 GlobalFiler™ - TrueAllele® VUIer Release 2022b

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

8YUL9Z - 5901 PowerPlex® Fusion 6C, NGM Detect - LRmix

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	17,20	16,17,21	2	

TABLE 3

Item 4 - STR Results

WebCode - Test	Amplification Kits - Probablistic 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	
9CLYK9 - 5901	GlobalFiler™ - STRMix™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
9MBR8Q - 5901	PowerPlex® 21 - STRMix™ 2.8.0					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					
9WLTTR - 5902	PowerPlex® 21 - STRMix™ 2.10.0					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					
B7W38V - 5901	GlobalFiler™ - STRMix™					
	11,15,16,16.3,17.3	16,17,18,23,24,25	10,13,14	14,15,16	10,11,12,13	
4	8,9,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,20,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,17,18,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,13,14,15,16	X,Y	10,11,12,13
	20,21,23,25,26			14,17,18,23.2,26.2,27.2,28.2	7,9.3	8,11,14
	15,16,17	9,10,11			2	
BDR7Z7 - 5901	PowerPlex® Fusion 6C - STRMix™ 2.6.2					
	(11),16,17.3	17,18,(24),(25)	(10),14	(14),(15),16	11,(12),13	
4	(8),9,11,(12)	10,13,(14),(16)	13,(14),(15)	18,19,(21)	(8),(10),12,(13)	9,(11),(12),(13),14
	(13),15,(17),19	12,(13),(13.2),(14),15.2	(28),(29),(30),33,33.2	(11),14,15,(16)	X,Y	10,(11),12,(13)
	20,(21),23,(26)	9,(10),(11),12,(15)	5,10,(11),(12),(14)	(14),18,(23.2),(26.2),28.2	7,(9.3)	(8),11,(13),14
	15,(16),17	10,(11)	(17),20	(16),17,(21)		
BKHHBU - 5901	GlobalFiler™ - STRMix™					
	11,15,16,16.3,17.3	16,17,18,22,23,24,25	9,10,13,14	13,14,15,16	10,11,12,13	
4	7,8,9,10,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,20,21	8,10,11,12,13	9,10,11,12,13,14
	13,14,15,16,17,18,19	11,12,12.2,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,13,14,15,16	X,Y	9,10,11,12,13
	19,20,21,22,23,25,26			13,13.2,14,17,18,23.2,25.2,26.2,27.2,28.2	6,7,9.3	8,10,11,14
	14,15,16,17	9,10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

BNGT8U - 5902 GlobalFiler™ - STRMix™ 2.8

	11,15,15.2,16,16.3,17.1,17.3	16,17,18,22,23,24,25	9,10,13,14	13,14,15,16	10,11,12,13,14	
4	7,8,9,10,11,12	9,10,12,13,14,15,16	12,13,14,15	17,18,19,20,21	8,9,10,11,12,13	8,9,10,11,12,13,14
	13,14,15,16,17,18,19	11,12,12.2,13,13.2,14,14.2,15.2	27,28,29,30,32,32.2,33,33.2	11,13,14,15,16,17	X,Y	9,10,11,12,13
	19,20,21,22,23,24,25,26			13,14,17,17.2,18,22.2,23.2,25.2,26.2,27.2,28,28.2	6,7,9.3	8,10,11,13,14
	14,15,16,17	9,10,11			2	

CDTG9M - 5901 GlobalFiler™

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	-
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	-	-	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	-	-	2	

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

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

CRBAWU - 5901 PowerPlex® ESI-17 Fast - LiRa v3.0

	11,16,17.3	17,18,23,24,25	10,14	14,15,16		
4		10,13,14,16	13,14,15	18,19,21		9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15	28,29,30,33,33.2	11,14,15,16	X,Y	
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	
	15,16,17					

CRVQCW - 5901 GlobalFiler™ - STRMix™

	11,15,16,16.3,17.3	17,18,23,24,25	9,10,13,14	13,14,15,16	10,11,12,13	
4	8,9,10,11,12	9,10,12,13,14,16	12,13,14,15	18,19,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,17,18,19	12,12.2,13,13.2,14,14.2,15.2	28,29,30,32.2,33,33.2	11,14,15,16	X,Y	10,11,12,13
	19,20,21,22,23,25,26			14,17,18,23.2,26.2,27.2,28.2	6,7,9.3	8,11,14
	15,16,17	10,11			2	

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

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

Item 4 - STR Results

WebCode - Test	Amplification Kits - Probablistic 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	
CY6DP6 - 5901	GlobalFiler™ - STRMix™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
CZ6EPV - 5901	GlobalFiler™ - STRMix™					
	11,15,16,16.3,17.3	16,17,18,22,23,24,25	9,10,13,14,15	13,14,15,16	10,11,12,13	
4	8,9,10,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,21	8,9,10,11,12,13	9,10,11,12,13,14
	13,14,15,17,18,19	11,12,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,13,14,15,16	X,Y	9,10,11,12,13
	19,20,21,22,23,25,26			13,14,17,18,22.2,23.2,25.2,26.2,27.2,28.2	6,7,9.3	8,10,11,14
	14,15,16,17	10,11			2	
E34ANN - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
EHXZJK - 5902	PowerPlex® 21 - STRMix™ 2.10					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					
ELJJPP - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
EY6YTN - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

F7H8UP - 5902	GlobalFiler™ - STRMix™ v2.9.1					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	
F8XQDM - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	
FPXE6L - 5902	Identifiler® Plus - STRMix™					
		17,18,23,24,25		14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16			8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26				7,9.3	8,11,14
	15,16,17					
GCH7HK - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	
H484WJ - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	
HEQHYL - 5902	GlobalFiler™ - TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

HJX7CN - 5901	GlobalFiler™ IQC					
	(11),16,17.3	17,18,(23,24,25)	(10),14	(14),15,16	11,(12),13	
4	8,9,11,(12)	10,13,(14,16)	13,(14,15)	18,(19,21)	(8,10),12,(13)	9,11,(12,13),14
	(13),15,(17),19	12,13,13.2,(14),15.2	(28),29,(30,32),33,33.2	(11),14,15,(16)	X,Y	10,11,12,(13)
	20,(21),23,26			(14),18,(23.2,26.2),28.2	7,(9.3)	(8),11,14
	15,16,17	10,(11)			2	
J37QNH - 5902	PowerPlex® 21- STRMix™ 2.10.0					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,13,14
	15,16,17					
J772JG - 5902	PowerPlex® 21- STRMix™ 2.10					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					
JHLQHM - 5902	GlobalFiler™ - DNAxs					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
JPGUBX - 5901	GlobalFiler™- STRMix™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,27.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
K9ECCE - 5902	PowerPlex® 21- STRMix™ 2.10					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

KPDQAK - 5902 GlobalFiler™- STRMix™ v2.9.1

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

L67JVL - 5901 GlobalFiler™- STRMix™

	11,16,16.3,17.3	16,17,18,23,24,25	9,10,13,14	14,15,16	11,12,13	
4	8,9,11,12	9,10,12,13,14,16	12,13,14,15	18,19,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,17,18,19	11,12,13,13.2,14,14.2,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	19,20,21,22,23,24,25,26			14,17,18,23.2,26.2,27.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

L8XEJE - 5901 PowerPlex® 21- STRMix™ v 2.8.0

	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14,15
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					

LBAKVF - 5902 Identifiler® Plus- STRMix™ 2.7.0

		17,18,23,24,25		14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16			8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26				7,9.3	8,11,14
	15,16,17					

LG3PNJ - 5901 PowerPlex® ESX17 Fast System- STRMix™ V2.5.11

	11,16,17.3	17,18,23,24,25	10,14	14,15,16		
4		10,13,14,16	13,14,15	18,19,21		9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	
	15,16,17					

LHUN3H - 5902 GlobalFiler™- TrueAllele® VUIer Release 2022b

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

LUPUWF - 5901	PowerPlex® Fusion 6C- STRMix™ STRmix V2.5.11					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,32,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,14,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	17,20	16,17,21		
LYKQJL - 5901	GlobalFiler™- STRMix™					
	11,15,16,16.3,17.3	16,17,18,23,24,25	9,10,13,14	13,14,15,16	10,11,12,13	
4	8,9,10,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,20,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,17,18,19	11,12,12.2,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,13,14,15,16	X,Y	9,10,11,12,13
	19,20,21,22,23,25,26			13,14,17,18,23.2,25.2,26.2,27.2,28.2	6,7,9.3	8,10,11,14
	15,16,17	10,11			2	
MW99ZF - 5902	GlobalFiler™- TrueAllele® VUIer Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
NWNRKD - 5901	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	17,20	16,17,21		
P3QH3A - 5901	PowerPlex® 21- STRMix™ 2.8					
	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					
P8KEPF - 5902	GlobalFiler™- STRMix™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

Item 4 - STR Results

WebCode - Test	Amplification Kits - Probablistic 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	
P8TP7Q - 5901	GlobalFiler™ - STRMix™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
Q99BQE - 5901	GlobalFiler™ IQC- STRMix™ 2.8.0					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
R3MFPB - 5901	PowerPlex® Fusion 6C- STRMix™ STRmix v2.5.11					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	17,19,20	16,17,21		
R9RDYE - 5901	GlobalFiler™ - STRMix™ STRmix					
	11,15,16,16.3,17.3	16,17,18,23,24,25	9,10,13,14	14,15,16	10,11,12,13	
4	8,9,10,11,12	9,10,12,13,14,16	12,13,14,15	17,18,19,20,21	8,10,11,12,13	9,11,12,13,14
	13,14,15,17,18,19	12,13,13.2,14,14.2,15.2	28,29,30,32,32.2,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,22,23,25,26			14,17,18,23.2,26.2,27.2,28.2	7,9.3	8,10,11,14
	15,16,17	10,11			2	
RCPXZD - 5901	Investigator® 24plex QS - EuroForMix					
	[11],16,17.3	17,[18,23,24,25]	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,[14,16]	13,[14,15]	18,[19],21	8,10,12,13	9,11,12,13,14
	[13],15,[17],19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,[21],23,26			14,18,23.2,26.2,28.2	7,9.3	[8],11,[14]
	15,16,17	10,[11]				
TMDEV4 - 5902	GlobalFiler™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

TZBZVA - 5901	PowerPlex® Fusion 6C- STRMix™ V2.5.11					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	17,20	16,17,21		
UNVR99 - 5902	GlobalFiler™- TrueAllele® VUler Release 2022b					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
VFHZHA - 5902	GlobalFiler™- STRMix™ v2.9.1					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
VK9834 - 5902	PowerPlex® Fusion 6C- STRMix™ v2.10					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,12,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,12.2,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11	17,20	16,17,21		
W2RLKZ - 5901	GlobalFiler™- STRMix™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,32,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	
WRGKYZ - 5901	GlobalFiler™- STRMix™					
	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28.2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

X28843 - 5901 PowerPlex® 21- STRMix™ V2.8.0

	11,16,17.3	17,18,23,24,25		14,15,16	11,12,13	10,11,12,13,14
4	8,9,11,12	10,13,14,16		18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2		X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14		7,9.3	8,11,14
	15,16,17					

YGJ6L9 - 5901 GlobalFiler™- STRMix™

	11,15,16,17.3	17,18,23,24,25	9,10,13,14	14,15,16	10,11,12,13	
4	8,9,11,12	10,12,13,14,16	12,13,14,15	18,19,21	8,10,11,12,13	9,11,12,13,14
	13,15,17,18,19	11,12,12.2,13,13.2 ,14,14.2,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,22,23,25,26			14,17,18,23.2,26.2 ,27.2,28.2	6,7,9.3	8,11,14
	15,16,17	10,11			2	

YJMUQ3 - 5901 PowerPlex® Fusion 6C- STRMix™ V2.5.11

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26	9,10,11,12,15	5,10,11,12,14	14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11	17,20	16,17,21		

Z8LUQ4 - 5902 GlobalFiler™- TrueAllele® VUler Release 2022b

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

8DDAHX - 5901 GlobalFiler™- STRMix™ 2.8

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4e	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	

PD88ZF - 5902 GlobalFiler™- STRMix™ v2.8

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4e	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	

WU8M28 - 5901 GlobalFiler™- STRMix™ 2.8

	11,16,17.3	17,18,23,24,25	10,14	14,15,16	11,12,13	
4e	8,9,11,12	10,13,14,16	13,14,15	18,19,21	8,10,12,13	9,11,12,13,14
	13,15,17,19	12,13,13.2,14,15.2	28,29,30,33,33.2	11,14,15,16	X,Y	10,11,12,13
	20,21,23,26			14,18,23.2,26.2,28 .2	7,9.3	8,11,14
	15,16,17	10,11			2	

TABLE 3

WebCode - Test	Amplification Kits - Probablistic 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

8DDAHX - 5901 GlobalFiler™- STRMix™ 2.8

4sp						

PD88ZF - 5902 GlobalFiler™- STRMix™ v2.8

	11,16,17.3	17,18,19,23,24,25	10,14	15,16	11,12,13	
4sp	8,9,11	10,13,14,16	13,14,15	18,19,21	10,12,13	9,11,14
	13,15,17,19	12,13.2,15.2	28,29,33,33.2	11,14,15,16	X,Y	10,11
	20,23,26			14,18,23.2	7,9.3	8,11,14
	15,16,17	10			2	

WU8M28 - 5901 GlobalFiler™- STRMix™ 2.8

	11,16,17.3	17,18,24,25	10,14	14,15,16	11,13	
4sp	8,9,11,12	10,13,14	13,15	18,19,21	10,12,13	9,11,14
	17,19	12,13,13.2,15.2	30,33,33.2	11,14,15,16	X,Y	10,11,12
	20,23,26			14,18,26.2,28.2	7,9.3	11
	15,16,17	10			2	

YSTR Amplification Kit(s) & Results

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									
3MQZUY - 5902		PowerPlex® Y 23							
2		13	16,17	13	30	24	10	11	13
	14	10	11	19		17	15		22
		12	13	20	17		21	12	11
786NUZ - 5901		Yfiler®							
2		13	16,17	13	30	24	10	11	13
	14	10	11	19		17	15		
							21		11
8DDAHX - 5901		Yfiler® Plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11
8YUL9Z - 5901		Yfiler® Plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11
9WLTTR - 5902		Yfiler® Plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11
EHXZJK - 5902		Yfiler® Plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11
FPXE6L - 5902		PowerPlex® Y 23							
2		13	16,17	13	30	24	10	11	13
	14	10	11	19		17	15		22
		12	13	20	17		21	12	11
HJX7CN - 5901		Yfiler® plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11
J772JG - 5902		Yfiler® Plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11
JHLQHM - 5902		Yfiler® plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11
K9ECCE - 5902		Yfiler® Plus							
2	35,37	13	16,17	13	30	24	10	11	13
	14	10	11	19	32	17	15	9	22
	40	12		20	17	22	21		11

TABLE 4

Item 2 - YSTR Results

WebCode - Test / Item	Amplification Kit	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
LBAKVF - 5902	PowerPlex® Y 23									
2			13	16,17	13	30	24	10	11	13
		14	10	11	19		17	15		22
			12	13	20	17		21	12	11
LG3PNJ - 5901	PowerPlex® Y 23									
2			13	16,17	13	30	24	10	11	13
		14	10	11	19		17	15		22
			12	13	20	17		21	12	11
LUPUWF - 5901	Yfiler®									
2			13	16,17	13	30	24	10	11	13
		14	10	11	19		17	15		
								21		11
NWNRKD - 5901	Yfiler®									
2			13	16,17	13	30	24	10	11	13
		14	10	11	19		17	15		
								21		11
PD88ZF - 5902	Yfiler® Plus									
2	35,37		13	16,17	13	30	24	10	11	13
		14	10	11	19	32	17	15	9	22
		40	12		20	17	22	21		11
Q99BQE - 5901	Yfiler® Plus									
2	35,37		13	16,17	13	30	24	10	11	13
		14	10	11	19	32	17	15	9	22
		40	12		20	17	22	21		11
R3MFPB - 5901	Yfiler®									
2			13	16,17	13	30	24	10	11	13
		14	10	11	19		17	15		
								21		11
RCPXZD - 5901	Yfiler® Plus									
2	35,37		13	16,17	13	30	24	10	11	13
		14	10	11	19	32	17	15	9	22
		40	12		20	17	22	21		11
TZBZVA - 5901	Yfiler®									
2			13	16,17	13	30	24	10	11	13
		14	10	11	19		17	15		
								21		11
VK9834 - 5902	Yfiler® Plus									
2	35,37		13	16,17	13	30	24	10	11	13
		14	10	11	19	32	17	15	9	22
		40	12		20	17	22	21		11
WU8M28 - 5901	Yfiler® Plus									
2	35,37		13	16,17	13	30	24	10	11	13
		14	10	11	19	32	17	15	9	22
		40	12		20	17	22	21		11
XCU6U9 - 5902	Yfiler® Plus									
2	35,37		13	16,17	13	30	24	10	11	13
		14	10	11	19	32	17	15	9	22
		40	12		20	17	22	21		11

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									
8YUL9Z - 5901		Yfiler® Plus							
3	35,36,37	13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
LG3PNJ - 5901		PowerPlex® Y 23							
3		13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19		14,17	15,17		22
		12	13	18,20	17,19		21,24	10,12	11,12

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 3e - YSTR Results									
3MQZUY - 5902		PowerPlex® Y 23							
3e		13,14	11,13,16,17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19		14,17	15,17		22
		12	13	18,20	17,19		21,24	10,12	11,12
786NUZ - 5901		Yfiler®							
3e		13,14	11,13,16,17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19		14,17	15,17		
							21,24		11,12
8DDAHX - 5901		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16,17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
9WLTTR - 5902		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16,17	13,14	30,30	24	10	11,12,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
EHXZJK - 5902		Yfiler® Plus							
3e	35,37	13,14	11,13,16,17	13,14	30	24	10	11,13	13
	14,15	10	11,12	19	29,32	14,17	15,17	9	22
	40	12		18,20	17,19	20,22	21,24		11
FPXE6L - 5902		PowerPlex® Y 23							
3e		13,14	11,13,16,17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19		14,17	15,17		22
		12	13	18,20	17,19		21,24	10,12	11,12
HJX7CN - 5901		Yfiler® plus							
3e	35,36,37	13,14	11,13,16,17	13,14	30	24,24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
J772JG - 5902		Yfiler® Plus							
3e	35	13,14	17	13,14		24	10		13
	14	10			29,32	14	15	9	22
		12		18,20	17	22	21,24		11
JHLQHM - 5902		Yfiler® plus							
3e	35,36,37	13,14	11,13,16,17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
K9ECCE - 5902		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16,17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12

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 3e - YSTR Results									
LBAKVF - 5902		PowerPlex® Y 23							
3e		13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19		14,17	15,17		22
		12	13	18,20	17,19		21,24	10,12	11,12
PD88ZF - 5902		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
Q99BQE - 5901		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
VK9834 - 5902		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
WU8M28 - 5901		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12
XCU6U9 - 5902		Yfiler® Plus							
3e	35,36,37	13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12

TABLE 4

Item 3sp - 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
3MQZUY - 5902		PowerPlex® Y 23							
3sp		14	11,13	14	30	24	10	13	13
	15	12	12	19		14	17		22
		12	13	18	19		24	10	12
786NUZ - 5901		Yfiler®							
3sp		13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19		14,17	15,17		
							21,24		11,12
8DDAHX - 5901		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
9WLTTR - 5902		Yfiler® Plus							
3sp	35,36	13,14	11,13	13,14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		11,12
EHXZJK - 5902		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
FPXE6L - 5902		PowerPlex® Y 23							
3sp		14	11,13	14	30	24	10	13	13
	15	12	12	19		14	17		22
		12	13	18	19		24	10	12
HJX7CN - 5901		Yfiler® plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
J772JG - 5902		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
JHLQHM - 5902		Yfiler® plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
K9ECCE - 5902		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
LBAKVF - 5902		PowerPlex® Y 23							
3sp		14	11,13	14	30	24	10	13	13
	15	12	12	19		14	17		22
		12	13	18	19		24	10	12
PD88ZF - 5902		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	15,17	11	22
	38	12		18	19	20,22	24		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 3sp - YSTR Results									
Q99BQE - 5901		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
VK9834 - 5902		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
WU8M28 - 5901		Yfiler® Plus							
3sp	35,36	14	11,13	14	30	24	10	13	13
	15	12	12	19	29	14	17	11	22
	38	12		18	19	20	24		12
XCU6U9 - 5902		Yfiler® Plus							
3sp	35,36,37	13,14	11,13,16, 17	13,14	30	24	10	11,13	13
	14,15	10,12	11,12	19	29,32	14,17	15,17	9,11	22
	38,40	12		18,20	17,19	20,22	21,24		11,12

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 4 - YSTR Results									
3MQZUY - 5902		PowerPlex® Y 23							
4		13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11	13,14
	14,15,16	10,12	11,12	19,21		14,16,17	15,18,19		20,22,23
		10,12	12,13	17,20	16,17,21		21,23	10,11,12	11,13
786NUZ - 5901		Yfiler®							
4		13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21		14,16,17	15,18,19		
							21,23		11,13
8YUL9Z - 5901		Yfiler® Plus							
4	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
9WLTTR - 5902		Yfiler® Plus							
4	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
EHXZJK - 5902		Yfiler® Plus							
4	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
FPXE6L - 5902		PowerPlex® Y 23							
4		13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21		14,16,17	15,18,19		20,22,23
		10,12	12,13	17,20	16,17,21		21,23	10,11,12	11,13
HJX7CN - 5901		Yfiler® plus							
4	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
J772JG - 5902		Yfiler® Plus							
4	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10	10,11,14	13
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
JHLQHM - 5902		Yfiler® plus							
4	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
K9ECCE - 5902		Yfiler® Plus							
4	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13

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
LBAKVF - 5902		PowerPlex® Y 23							
4		13,14,15	11,15,16,17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21		14,16,17	15,18,19		20,22,23
		10,12	12,13	17,20	16,17,21		21,23	10,11,12	11,13
LG3PNJ - 5901		PowerPlex® Y 23							
4		13,14,15	11,15,16,17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21		14,16,17	15,18,19		20,22,23
		10,12	12,13	17,20	16,17,21		21,23	10,11,12	11,13
Q99BQE - 5901		Yfiler® Plus							
4	35,36,37,3	13,14,15	11,15,16,17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	-,-	21,23		11,13
VK9834 - 5902		Yfiler® Plus							
4	35,37,38	13,14,15	11,15,16,17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
XCU6U9 - 5902		Yfiler® Plus							
4	35,36,37,3	13,14,15	11,15,16,17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,29,30,3	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13

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									
8DDAHX - 5901	Yfiler® Plus								
4e	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
PD88ZF - 5902	Yfiler® Plus								
4e	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13
WU8M28 - 5901	Yfiler® Plus								
4e	35,36,37,3	13,14,15	11,15,16, 17	12,13	28,29,30	22,24	10,11	10,11,14	13,14
	14,15,16	10,12	11,12	19,21	28,30,32	14,16,17	15,18,19	9,10,11	20,22,23
	37,38,40	10,12		17,20	16,17,21	20,22	21,23		11,13

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 4sp - YSTR Results									
8DDAHX - 5901		Yfiler® Plus							
4sp									
						22			
PD88ZF - 5902		Yfiler® Plus							
4sp	35,37	13				24		10,11	13
				19			19	9,11	
		10		20		22	21,23		11
WU8M28 - 5901		Yfiler® Plus							
4sp	35,36,37,3	13	15,16,17	13			10		13
	14	10	11,12	19	28,32	17	15,18,19	9	23
	40	12		17,20	16,17	20,22	21		11

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 (%)**
LG3PNJ - 5901	3	Suspect	208	39.00
		Unknown	235	44.00
		Victim	91.0	17.00

Response Summary: Item 3	
Estimated Number of Contributors	**Percent Reported**
3	**1 (100%)**

TABLE 6

Item 3e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
2QGMC2 - 5902	3	Suspect Unknown Victim		
34G3B3 - 5902	3	Suspect Unknown Victim		34.73 46.61 18.67
37J2CU - 5901	3	Suspect Unknown Victim	0.3410 0.1840 0.1350	51.66 27.89 20.46
3WHFJ3 - 5902	3	Suspect Unknown Victim		35.93 40.95 23.12
44PDRD - 5901	3	Suspect Unknown Victim		33.00 50.00 17.00
4BEUJW - 5902	3	Suspect Unknown Victim	0.00210 0.00130 0.00160	42.00 26.00 32.00
4FBJY4 - 5902	3	Suspect Unknown Victim	46.0 27.0 25.0	471.00 282.00 258.00
4UQG64 - 5901	3	Suspect Unknown Victim		41.00 36.00 23.00
4XQRZ4 - 5901	3	Suspect Unknown Victim		39.00 45.00 16.00
62K9Q4 - 5901	3	Suspect Unknown Victim		36.00 42.00 22.00
63VBC2 - 5901	3	Suspect Unknown Victim		35.00 43.00 21.00
6PTH6Y - 5902	3	Suspect Unknown Victim		
77A6RY - 5901	3			
786NUZ - 5901	3	Suspect Unknown Victim	0.09490 0.04450 0.03440	54.56 25.60 19.80

TABLE 6

Item 3e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
7H4JRV - 5902	3	Suspect Unknown Victim		
8Y8DYV - 5902	3	Suspect Unknown Victim		
9CLYK9 - 5901	3	Suspect Unknown Victim		73.00 18.00 9.00
9MBR8Q - 5901	3	Suspect Unknown Victim	0.07000 0.09000 0.04000	37.38 43.24 19.38
9WLTTR - 5902	3	Suspect Unknown Victim	4.70 3.59 2.27	44.54 33.97 21.49
B7W38V - 5901	3			
BDR7Z7 - 5901	3	Suspect Unknown Victim		34.00 47.00 19.00
BKHHBU - 5901	3			
BNGT8U - 5902	3	Suspect Unknown Victim		37.00 42.00 21.00
CDTG9M - 5901	3	Suspect Unknown Victim	0.2983 0.1120 0.1397	54.23 20.36 25.40
CKECAQ - 5902	3	Suspect Unknown Victim		
CRBAWU - 5901	3	Suspect Unknown Victim		43.30 33.30 23.30
CRVQCW - 5901	3	Suspect Unknown Victim		45.00 36.00 19.00
CXYRCQ - 5902	3	Suspect Unknown Victim		

TABLE 6

Item 3e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
CY6DP6 - 5901	3	Suspect Unknown Victim		38.00 43.00 19.00
CZ6EPV - 5901	3	Suspect Unknown Victim		33.00 47.00 20.00
E34ANN - 5902	3	Suspect Unknown Victim		
EHXZJK - 5902	3	Suspect Unknown Victim	0.2260 0.01290 0.08400	70.00 4.00 26.00
ELJJPP - 5902	3	Suspect Unknown Victim		
EY6YTN - 5902	3	Suspect Unknown Victim		
F7H8UP - 5902	3	Suspect Unknown Victim		49.16 33.13 17.71
F8XQDM - 5902	3	Suspect Unknown Victim		
GCH7HK - 5902	3	Suspect Unknown Victim		
H484WJ - 5902	3	Suspect Unknown Victim		
HEQHYL - 5902	3	Suspect Unknown Unknown		
HJX7CN - 5901	3	Suspect Unknown Victim	0.3600 0.3600 0.3600	39.00 45.00 16.00
J37QNH - 5902	3	Suspect Unknown Victim	0.2210 0.08300 0.05800	61.00 23.00 16.00
J772JG - 5902	3	Suspect Unknown Victim	0.01504 0.00896 0.00800	47.00 28.00 25.00

TABLE 6

Item 3e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
JHLQHM - 5902	3	Suspect Unknown Victim	236 4.00 122	31.00 53.00 16.00
JPGUBX - 5901	3	Suspect Unknown Victim		93.00 4.00 3.00
K9ECCE - 5902	3	Suspect Unknown Victim	6.65 5.14 3.37	43.88 33.90 22.22
KPDQAK - 5902	3	Suspect Unknown Victim		41.54 35.82 22.64
L67JVL - 5901	3	Suspect Unknown Victim		37.00 43.00 20.00
L8XEJE - 5901	3	Unknown Unknown Victim		32.78 48.58 18.64
LHUN3H - 5902	3	Suspect Unknown Victim		
LYKQJL - 5901	3	Suspect Unknown Victim		33.00 40.00 26.00
MW99ZF - 5902	3	Suspect Unknown Victim		
P3QH3A - 5901	3	Suspect Unknown Victim		41.09 36.09 22.82
P8KEPF - 5902	3	Suspect Unknown Victim		42.11 36.32 21.57
P8TP7Q - 5901	3	Suspect Unknown Victim		33.00 43.00 24.00
Q99BQE - 5901	3	Suspect Unknown Victim	0.1400 0.1140 0.04800	46.45 37.76 15.79
R9RDYE - 5901	3	Suspect Unknown Victim		34.00 40.00 26.00

TABLE 6

Item 3e Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
RCPXZD - 5901	3	Suspect	0.1600	40.00
		Unknown	0.1640	41.00
		Victim	0.07600	19.00
TMDEV4 - 5902	3	Suspect	1.28	42.64
		Unknown	1.12	37.26
		Victim	0.6030	20.10
UNVR99 - 5902	3	Suspect		
		Unknown		
		Victim		
VFHZHA - 5902	3	Suspect		35.98
		Unknown		42.13
		Victim		21.89
VK9834 - 5902	3	Suspect	1.89	43.08
		Unknown	1.43	32.57
		Victim	1.07	24.35
W2RLKZ - 5901	3	Suspect		34.00
		Unknown		48.00
		Victim		18.00
WRGKYZ - 5901	3	Suspect		37.00
		Unknown		44.00
		Victim		18.00
X28843 - 5901	3	Suspect	0.4683	37.54
		Unknown	0.5301	42.53
		Victim	0.2486	19.93
YGJ6L9 - 5901	3	Suspect		37.00
		Unknown		45.00
		Victim		18.00
Z8LUQ4 - 5902	3	Suspect		
		Unknown		
		Victim		

Response Summary: Item 3e	
Estimated Number of Contributors	**Percent Reported**
3	**66 (100%)**

TABLE 6

Item 3sp Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
2QGMC2 - 5902	2	Unknown Unknown		
34G3B3 - 5902	1	Unknown		100.00
37J2CU - 5901	1	Unknown	0.4412	100.00
3WHFJ3 - 5902	1	Unknown		100.00
44PDRD - 5901	1	Unknown		100.00
4BEUJW - 5902	1	Unknown	0.02800	100.00
4FBJY4 - 5902	1	Unknown	257	100.00
4UQG64 - 5901	1	Unknown		100.00
4XQRZ4 - 5901	1	Unknown		100.00
62K9Q4 - 5901	1	Unknown		100.00
63VBC2 - 5901	1	Unknown		100.00
6PTH6Y - 5902	1	Unknown		
77A6RY - 5901	1			
786NUZ - 5901	3	Suspect Unknown Victim	0.9440 1.24 0.4210	36.20 47.64 16.14
7H4JRV - 5902	2	Unknown Unknown		
9CLYK9 - 5901	1	Unknown		100.00
9MBR8Q - 5901	3	Suspect Unknown Victim	0.03000 0.3400 0.02000	8.38 85.69 5.93
9WLTTR - 5902	3	Suspect Unknown Victim	0.5800 7.08 0.3500	7.28 88.34 4.37
B7W38V - 5901	1			
BDR7Z7 - 5901	2	Unknown Unknown		1.00 99.00
BKHHBU - 5901	1			

TABLE 6

Item 3sp Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
BNGT8U - 5902	1	Unknown		100.00
CDTG9M - 5901	1	Unknown	0.09200	100.00
CKECAQ - 5902	1	Unknown		
CRBAWU - 5901	1	Unknown		100.00
CRVQCW - 5901	1	Unknown		100.00
CXYRCQ - 5902	1	Unknown		
CY6DP6 - 5901	1	Unknown		100.00
CZ6EPV - 5901	1	Unknown		100.00
E34ANN - 5902	2	Suspect Unknown		
EHXZJK - 5902	1	Unknown	0.3180	100.00
ELJJPP - 5902	2	Unknown Unknown		
EY6YTN - 5902	2	Unknown Unknown		
F7H8UP - 5902	1	Suspect		100.00
F8XQDM - 5902	2	Unknown Unknown		
GCH7HK - 5902	1	Unknown		
H484WJ - 5902	2	Unknown Unknown		
HEQHYL - 5902	1	Unknown		
HJX7CN - 5901	1	Unknown	0.7100	100.00
J37QNH - 5902	2	Unknown Victim	0.7460 0.01500	98.00 2.00
J772JG - 5902	1	Unknown	0.06700	100.00
JHLQHM - 5902	1	Unknown	417	100.00
JPGUBX - 5901	2	Suspect Unknown		1.00 99.00

TABLE 6

Item 3sp Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
K9ECCE - 5902	2	Suspect Unknown	0.2000 9.19	2.16 97.84
KPDQAK - 5902	1	Unknown		100.00
L67JVL - 5901	1	Unknown		100.00
L8XEJE - 5901	3	Unknown Unknown Victim		97.84 1.43 0.73
LHUN3H - 5902	2	Unknown Unknown		
LYKQJL - 5901	1	Unknown		100.00
MW99ZF - 5902	2	Unknown Unknown		
P3QH3A - 5901	3	Suspect Unknown Victim		2.64 95.24 2.12
P8KEPF - 5902	1	Unknown		100.00
P8TP7Q - 5901	1	Unknown		100.00
Q99BQE - 5901	1	Unknown	0.9950	100.00
R9RDYE - 5901	1	Unknown		100.00
RCPXZD - 5901	1	Unknown	0.1000	100.00
TMDEV4 - 5902	1	Unknown	2.65	100.00
UNVR99 - 5902	3	Unknown Unknown Unknown		
VFHZHA - 5902	1	Unknown		100.00
VK9834 - 5902	1	Unknown	0.6970	100.00
W2RLKZ - 5901	1	Unknown		100.00
WRGKYZ - 5901	1	Unknown		100.00
X28843 - 5901	2	Unknown Unknown	0.01240 0.7702	1.59 98.41

TABLE 6

Item 3sp Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
YGJ6L9 - 5901	1	Unknown		100.00
Z8LUQ4 - 5902	2	Unknown Unknown		

Response Summary: Item 3sp	
Estimated Number of Contributors	**Percent Reported**
1	**44 (68%)**
2	**15 (23%)**
3	**6 (9%)**

TABLE 6

Item 4 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
2QGMC2 - 5902	3	Suspect Unknown Unknown		
34G3B3 - 5902	3	Suspect Unknown Unknown		51.72 31.81 16.47
37J2CU - 5901	3	Suspect Unknown Victim	2.13 1.10 0.7110	54.12 27.82 18.05
3WHFJ3 - 5902	3	Suspect Unknown Unknown		37.85 49.16 12.99
44PDRD - 5901	3	Suspect Unknown Unknown		51.00 22.00 28.00
4BEUJW - 5902	3	Suspect Unknown Unknown	1.09 0.6698 0.3349	52.00 32.00 16.00
4FBJY4 - 5902	3	Suspect Unknown Unknown	166 184 65.0	40.00 444.00 156.00
4UQG64 - 5901	3	Suspect Unknown Unknown		50.00 30.00 20.00
4XQRZ4 - 5901	3	Suspect Unknown Unknown		42.00 33.00 25.00
62K9Q4 - 5901	3	Suspect Unknown Unknown		52.00 27.00 20.00
63VBC2 - 5901	3	Suspect Unknown Unknown		40.00 46.00 14.00
6PTH6Y - 5902	3	Suspect Unknown Unknown		
77A6RY - 5901	3			
786NUZ - 5901	3	Suspect Unknown Unknown	0.1010 0.03300 0.03300	60.33 19.83 19.83

TABLE 6

Item 4 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
7H4JRV - 5902	3	Suspect Unknown Unknown		
8Y8DYV - 5902	3	Suspect Unknown Unknown		
9CLYK9 - 5901	3	Suspect Unknown Unknown		51.00 34.00 16.00
9MBR8Q - 5901	3	Suspect Unknown Unknown	10.4 7.27 4.37	47.27 32.93 19.80
9WLTTR - 5902	3	Suspect Unknown Unknown	4.48 1.84 2.36	51.61 21.22 27.16
B7W38V - 5901	3			
BDR7Z7 - 5901	3	Suspect Unknown Unknown		80.00 8.00 11.00
BKHHBU - 5901	3			
BNGT8U - 5902	3	Suspect Unknown Unknown		55.00 17.00 28.00
CDTG9M - 5901	3	Suspect Unknown Unknown	0.8702 0.3478 0.4959	50.77 20.29 28.93
CKECAQ - 5902	3	Suspect Unknown Unknown		
CRBAWU - 5901	3	Suspect Unknown Unknown		48.30 18.30 33.30
CRVQCW - 5901	3	Suspect Unknown Unknown		46.00 30.00 24.00
CXYRCQ - 5902	3	Suspect Unknown Unknown		

TABLE 6

Item 4 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
CY6DP6 - 5901	3	Suspect Unknown Unknown		40.00 26.00 34.00
CZ6EPV - 5901	3	Suspect Unknown Unknown		46.00 32.00 23.00
E34ANN - 5902	3	Suspect Unknown Unknown		
EHXZJK - 5902	3	Suspect Unknown Unknown	1.35 0.4060 0.9200	50.00 15.00 34.00
ELJJPP - 5902	3	Suspect Unknown Unknown		
EY6YTN - 5902	3	Suspect Unknown Unknown		
F7H8UP - 5902	3	Suspect Unknown Unknown		52.16 31.53 16.31
F8XQDM - 5902	3	Suspect Unknown Unknown		
GCH7HK - 5902	3	Suspect Unknown Unknown		
H484WJ - 5902	3	Suspect Unknown Unknown		
HEQHYL - 5902	3	Suspect Unknown Unknown		
HJX7CN - 5901	4	Suspect Unknown Unknown Unknown	0.7700 0.7700 0.7700 0.7700	
J37QNH - 5902	3	Suspect Unknown Unknown	4.31 2.73 1.76	49.00 31.00 20.00
J772JG - 5902	3	Suspect Unknown Unknown	1.37 0.4323 0.7375	54.00 17.00 29.00

TABLE 6

Item 4 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
JHLQHM - 5902	3	Suspect	964	57.00
		Unknown	364	215.00
		Unknown	364	215.00
JPGUBX - 5901	3	Suspect		47.00
		Unknown		13.00
		Unknown		40.00
K9ECCE - 5902	3	Suspect	7.31	53.16
		Unknown	3.65	26.52
		Unknown	2.79	20.32
KPDQAK - 5902	3	Suspect		53.13
		Unknown		26.73
		Unknown		20.14
L67JVL - 5901	3	Suspect		57.00
		Unknown		27.00
		Unknown		16.00
L8XEJE - 5901	3	Unknown		15.18
		Unknown		25.73
		Unknown		59.09
LG3PNJ - 5901	3	Suspect	95.0	55.00
		Unknown	29.0	17.00
		Unknown	48.0	28.00
LHUN3H - 5902	3	Suspect		
		Unknown		
		Unknown		
LYKQJL - 5901	3	Suspect		49.00
		Unknown		35.00
		Victim		16.00
MW99ZF - 5902	3	Suspect		
		Unknown		
		Unknown		
P3QH3A - 5901	3	Suspect		53.67
		Unknown		17.37
		Unknown		28.96
P8KEPF - 5902	3	Suspect		51.50
		Unknown		18.24
		Unknown		30.27
P8TP7Q - 5901	3	Suspect		45.00
		Unknown		37.00
		Unknown		18.00
Q99BQE - 5901	3	Suspect	1.01	5,021.00
		Unknown	0.3460	17.20
		Unknown	0.6550	32.59

TABLE 6

Item 4 Results				
WebCode-Test	**Number of Contributors**	**Contributor(s)**	**DNA Concentration (ng/uL)**	**DNA Proportion (%)**
R9RDYE - 5901	3	Suspect Unknown Unknown		51.00 18.00 31.00
RCPXZD - 5901	3	Suspect Unknown Unknown	1.23 0.8700 0.9000	41.00 29.00 30.00
TMDEV4 - 5902	3	Suspect Unknown Unknown	1.35 0.6265 0.4264	56.16 26.08 17.75
UNVR99 - 5902	3	Suspect Unknown Unknown		
VFHZHA - 5902	3	Suspect Unknown Unknown		49.39 22.24 28.38
VK9834 - 5902	3	Suspect Unknown Unknown	8.96 3.14 4.76	53.14 18.63 28.22
W2RLKZ - 5901	3	Suspect Unknown Unknown		46.00 16.00 39.00
WRGKYZ - 5901	3	Suspect Unknown Unknown		55.00 16.00 29.00
X28843 - 5901	3	Suspect Unknown Unknown	2.03 1.34 0.5646	51.59 34.08 14.33
YGJ6L9 - 5901	3	Suspect Unknown Unknown		44.00 33.00 22.00
Z8LUQ4 - 5902	3	Suspect Unknown Unknown		

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

Statistical Analysis for Item 3

TABLE 7

WebCode-Test	Item 3 Methods & Results
2QGMC2 - 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 victim's underwear (item 3) and the male suspect. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and the male suspect is approximately fifty quadrillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and the female victim. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and the female victim is approximately nine hundred trillion 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 victim's underwear (item 3) and the suspect is approximately three 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 second fraction from the questioned stain from victim's underwear (item 3). A DNA match between the data obtained from the second fraction from the questioned stain from victim's underwear (item 3) and the victim is approximately seven octillion 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 victim's underwear (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database
34G3B3 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming three contributors to the non-sperm fraction of item 3, the evidence profile is 1.2E+24 times more likely to be observed if Female Victim and two unknown individuals are the contributors than if three unknown individuals are the contributors. Assuming three contributors to the non-sperm fraction of item 3, the evidence profile is 2.0E+27 times more likely to be observed if Female Victim, Male Suspect, and one unknown individual are the contributors than if Female Victim and two unknown individuals are the contributors. **Database(s) Used:** NIST Databases - Forensic Sci Int.: Genetics 31 (2017) e36-e40
37J2CU - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** [Location Identifying Database]
3MQZUY - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** 3. The SUSPECT (item 2-1) cannot be excluded as a contributor to Mixture 1 (see Testing Summary) from the VICTIM's underwear (item 3-1). The STR DNA results are estimated to be greater than one trillion times more likely if they originate from the VICTIM, SUSPECT and one unknown person than if they originate from the VICTIM and two unknown people unrelated to the SUSPECT. 5. The SUSPECT (item 2-1) also cannot be excluded as the source of a male-specific DNA profile (Y-STR Profile B; see Testing Summary) from the VICTIM's underwear (item 3-1) The Y-STR DNA results are further estimated to be 2000 times more likely if it originates from the SUSPECT than if it originates from an unknown male, unrelated to him. Note: Close paternal male relatives of SUSPECT may also not be excluded. **Database(s) Used:** i. NIST Asian, ii. NIST African American, iii. NIST Caucasian, iv. Srivastava et al. (2019) South Asian, v. [Location Identifying Database]

TABLE 7

WebCode-Test	Item 3 Methods & Results
3WHFJ3 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from the Known Female, Known Male, and one unknown, unrelated individual. H2: The evidence originated from the Known Female and two unknown, unrelated individuals. The DNA profile obtained from Item 3 is approximately 320 quintillion times more likely if it originated from the Known Female, Known Male and one unknown, unrelated individual than if it originated from the Known Female and two unknown, unrelated individuals. There is evidentiary support for the inclusion of the Known Male as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
44PDRD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals, with at least one male contributor and with FEMALE VICTIM as an assumed contributor. The DNA results are approximately 74.8 quintillion times more likely if they originated from MALE SUSPECT, FEMALE VICTIM and an unknown, unrelated individual than if they originated from FEMALE VICTIM and two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that MALE SUSPECT is a contributor to the DNA from this item. Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 1): The male DNA profile from this item was interpreted as a single-source profile. FEMALE VICTIM and MALE SUSPECT are excluded as possible contributors to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
4BEUJW - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Sperm fraction: The Victim (Item 1) is Excluded as being the source of the DNA in this sample. The Suspect (Item 2) is Excluded as being the source of the DNA in this sample. Non-sperm fraction/Epithelial: Victim (Item 1): Assumed contributor Suspect (Item 2): The DNA evidence is estimated to be 100 billion times more likely to occur if the DNA originated from the victim and the suspect and one unknown, unrelated person selected randomly from the [Population], than if it originated from the victim and two unknown and unrelated people selected randomly from the [Population]. **Database(s) Used:** [Location Identifying Database]
4FBJY4 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1: 5.754e+11. Item 2: 4.377e+22. Unknown male from sperm fraction: 8.087e+11. **Database(s) Used:** [Location Identifying Database]
4UQG64 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming Female Victim (K1), the evidence profile 3A-3PTNS is approximately 130 trillion 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. This provides very strong support for inclusion of Male Suspect (K2). The evidence DNA profile 3A-3PTSP is approximately 0 times more likely if it originated from Female Victim (K1) than if it originated from an unknown individual. This provides support for exclusion of Female Victim (K1). The evidence DNA profile 3A-3SP is approximately 0 times more likely if it originated from Male Suspect (K2) than if it originated from an unknown individual. This provides support for exclusion of Male Suspect (K2). **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 7

WebCode-Test	Item 3 Methods & Results
4XQRZ4 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 3 e: Assuming Female Victim(K1), the evidence profile is approximately 234 trillion 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. This analysis provides very strong support that Male Suspect (K2) is a contributor to the DNA obtained from this sub-item. For 3 sp: 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
62K9Q4 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 3A-3NS: Assuming (K1), the evidence profile is approximately 115 trillion 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. This analysis provides very strong support for the proposition that Male Suspect (K2) is a contributor to the DNA obtained from this sub-item. For 3A-3SP: The evidence profile is approximately 0 times more likely if it originated from Female Victim (K1) than if it originated from an unknown individual. Female Victim (K1) is excluded based on the LR of zero. The evidence profile is approximately 0 times more likely if it originated from Male Suspect (K2) than if it originated from an unknown individual. Male Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population
63VBC2 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 3e: Assuming Female Victim (K1), the evidence profile is approximately 2 trillion times more likely if it originated from Female Victim (K1), Male Suspect (K2), and one unknown individual than if it originated from Female Victim (K1) and two unknown individuals. This analysis provides very strong support for the proposition that Male Suspect (K2) is included as a contributor to this DNA mixture. For 3sp: The evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) than if it originated from one unknown individual. The evidence DNA profile is approximately 0 times more likely if it originated from Male Suspect (K2) than if it originated from one unknown individual. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 7

WebCode-Test	Item 3 Methods & Results
6PTH6Y - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The first fraction from the victim's underwear from item 3 contained a mixture of DNA from at least three individuals. A DNA match was identified between the data obtained from the first fraction from the victim's underwear from item 3 and the victim. A match between the data obtained from the first fraction from the victim's underwear from item 3 and the victim is approximately one sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the victim's underwear from item 3 and the suspect. A match between the data obtained from the first fraction from the victim's underwear from item 3 and the suspect is approximately eighty quadrillion times more probable than a coincidental match to an unrelated person in the population. The DNA obtained from the second fraction from the victim's underwear from item 3 contained the genotype of one individual. A DNA match between the data obtained from the second fraction from the victim's underwear from item 3 and the victim is approximately four 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 victim's underwear from item 3. A DNA match between the data obtained from the second fraction from the victim's underwear from item 3 and the suspect is approximately six hundred 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 second fraction from the victim's underwear from item 3. **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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.
77A6RY - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 3.0457E19 **Database(s) Used:** The FBI's extended database for African Americans was used.
786NUZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from epithelial fraction of item # 3 is a mixture of at least 3 individuals. Following set of hypotheses were evaluated: A) Hp; item No. 1+2 unknown, Hd; 3 unknown, LR (MLE) =30555. B) HP; Item No. 1+item No. 2 + 1 unknown, Hd; Item No. 1+ 2 Unknown, LR (MLE)= 1.373 e +18. C) Hp; Item No. 1+ Item No. 2+ 1 unknown, Hd; Item No. 1+ item No. 2 +1 unknown LR(MLE)=6.307 e +14 The DNA profile obtained from sperm fraction of item #3 is a mixture of at least 3 individuals. Following set of hypotheses were evaluated: A) Hp; item No. 1+2 unknown, Hd; 3 unknown, LR (MLE) = 1.421 e +8. B) Hp; item No.1+ item No. 2 + 1 unknown, Hd; Item #1 +2 unknown, LR (MLE) = 7.638 e +12. C) Hp; Item No. 1+ Item No. 2+ 1 unknown, Hd; Item No. 1+ item No. 2 +1 unknown LR(MLE)=2.150 e +18 **Database(s) Used:** NIST Caucasian database 2017 with theta co-ancestry coefficient = 0.03

TABLE 7

WebCode-Test	Item 3 Methods & Results
7H4JRV - 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 victim's underwear (item 3) and the victim. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and victim is approximately twenty trillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and the subject. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and subject is approximately seven hundred trillion 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 victim's underwear (item 3) and the victim is approximately four 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 victim's underwear (item 3). A DNA match between the data obtained from the second fraction from the questioned stain from victim's underwear (item 3) and the suspect is approximately six hundred 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 second fraction from the questioned stain from victim's underwear (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database
8DDAHX - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile of the sperm fraction was interpreted as originating from a single unknown male A. The DNA profile of the epithelial fraction was interpreted as a mixture of three individuals. Known Female Victim (1) was assumed as a contributor. The DNA profile is at least 1 trillion times more likely if it originated from Known Female Victim (1), Known Male Suspect (2), and one unknown individual than if it had originated from Known Female Victim (1) and two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Known Male Suspect (2). **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanic
8Y8DYV - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the "questioned stain…underwear…" (item #3) and the male suspect (item #2). A match between the data obtained from the "questioned stain…underwear…" (item #3) and the male suspect (item #2) is approximately 2 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the "questioned stain…underwear…" (item #3) and the female victim (item #1). A match between the data obtained from the "questioned stain…underwear…" (item #3) and the female victim (item #1) is approximately 40 thousand times more probable than a coincidental match to an unrelated person in the population. **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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
8YUL9Z - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** A likelihood ratio (LR) analysis was performed using the LRmix Studio software, using allele frequency data specific to the [Population]- based on own laboratory reference population database consisting of 5,000 genotypes from [Country]. The LR values for mixed DNA profiles were calculated with consideration for both drop-in and drop-out phenomena. The analysis assumed a drop-in probability of 0.05 and applied a minimum allele frequency threshold of 0.001. A subpopulation correction factor of 0.01 was also incorporated into the calculations. The resulting LR values were interpreted in terms of their probative value. The evaluated hypotheses included: Prosecution Hypothesis (Hp): The DNA mixture includes the genetic profiles of item1, item2, and one unknown, untested individual from the population. Alternative Hypothesis (Hd): The DNA mixture includes the genetic profile of item1 and two unknown, untested individuals from the population. The comparison of these hypotheses was used to assess the strength of the genetic evidence in the context of the case. Likelihood ratio on this sample is: 1.4024E12. Y-STR: Given the Haplotypes above and that there is 1 additional unknown contributor, the likelihood of observing the given trace under the hypothesis of the donorship of the suspect is approx. 135,377 times more likely than observing the given trace under the hypothesis of the non-donorship. This calculation is based on 298,405 haplotypes (Y17) in the worldwide database YHRD R69. **Database(s) Used:** STR laboratory population base of [Country]
9CLYK9 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3.1 (Portion of "Questioned stain from victim's underwear" -Fraction 1): The male DNA profile from this item was interpreted as a single-source profile. The female victim and the male suspect are excluded as possible contributors to the DNA from this item. Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals, with at least one male contributor and with the female victim as an assumed contributor. The DNA results are approximately 2.32 nonillion times more likely if they originated from the female victim, the male suspect, and an unknown, unrelated individual than if they originated from the female victim and two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the male suspect is a contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
9MBR8Q - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** sp fraction - Item 1 (complainant) - Assumed contributor. Item 2 (known suspect) - >100 billion in favour of H1 (favouring contribution). e fraction - Item 1 (complainant) - Assumed contributor. Item 2 (known suspect) - >100 billion in favour of H1 (favouring contribution). **Database(s) Used:** [Location Identifying Database]
9WLTTR - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** 3e: The DNA evidence is 30 billion times more likely if the suspect is a contributor. The DNA evidence is 4.9 billion times more likely if the victim is a contributor. 3sp: The DNA evidence is 3600 times more likely if the suspect is a contributor. The DNA evidence is 440 times more likely if the victim is a contributor. **Database(s) Used:** [Location Identifying Database]
B7W38V - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 1.2896E18 **Database(s) Used:** FBI Extended African American

TABLE 7

WebCode-Test	Item 3 Methods & Results
BDR7Z7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Fraction 1 of differential: Explanation 1: The DNA profile obtained originated from item 1 (1C), item 2 (1D), and an unknown, unrelated individual. Explanation 2: The DNA profile obtained originated from item 1 (1C) and two unknown, unrelated individuals. The DNA profile obtained is approximately 2E18 times more likely (very strong support) if it originated from the item 1 (1C), item 2 (1D), and an unknown, unrelated individual than if the DNA profile obtained originated from item 1 (1C) and two unknown, unrelated individuals. Fraction 2 of differential: No LR reported. Item 1 (1C) and item 2 (1D) were excluded. Ran STRmix for prob gen proportions only. **Database(s) Used:** Nist1036 (revised 2017)_Caucasian, Nist1036 (revised 2017)_African American, Nist1036 (revised 2017)_Hispanic
BKHHBU - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 1.7158e27 **Database(s) Used:** FBI Extended African American
BNGT8U - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming 3 contributors for the non-sperm fraction of item 3, the evidence profile is 5.8 x 10^25 times more likely to be observed if the victim and two unknowns are the contributors than if three unknowns are the contributors. Assuming 3 contributors for the non-sperm fraction of item 3, the evidence profile is 6.2 x 10^20 times more likely to be observed if the suspect, victim, and one unknown are the contributors than if the victim and two unknowns are the contributors. **Database(s) Used:** NIST Databases - Forensic Sci. Int.: Genetics 31 (2017) e36–e40
CDTG9M - 5901	**Method(s)**: Likelihood Ratio, STRmix **Stats Analysis:** Epithelial Fraction Propositions for contributor 1: The propositions considered for ITEM 3 were: P1: The SUSPECT is one of three contributors to the mixed DNA profile obtained. P2: The SUSPECT is NOT a contributor to the mixed DNA profile obtained. Three unknown individuals, unrelated to the SUSPECT, are the contributors. For this calculation, it was assumed that three individuals have contributed to the DNA profile obtained. Likelihood Ratio: The evidence is at least 100 BILLION (2.9563E20) times more likely if the SUSPECT is one of three contributors to the mixed DNA profile than if the profile originated from three unknown individuals, unrelated to the SUSPECT, selected at random from the [Population]. Propositions for contributor 2: The propositions considered for ITEM 3 were: P1: The VICTIM is one of three contributors to the mixed DNA profile obtained. P2: The VICTIM is NOT a contributor to the mixed DNA profile obtained. Three unknown individuals, unrelated to the VICTIM, are the contributors. For this calculation, it was assumed that three individuals have contributed to the DNA profile obtained. Likelihood Ratio: The evidence is at least 9 BILLION (9.2033E9) 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 7

WebCode-Test	Item 3 Methods & Results
CKECAQ - 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 victim's underwear (Item 3) and the Victim. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and the Victim is approximately 60 quadrillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and the Subject. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and the Subject 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 second fraction from the questioned stain from victim's underwear (Item 3) and the Subject is approximately 600 undecillion times less probable than a coincidental match to an unrelated person in the population. The Subject is excluded from the data obtained from the second fraction from the questioned stain from victim's underwear (Item 3). A DNA match between the data obtained from the second fraction from the questioned stain from victim's underwear (Item 3) and the Victim is approximately 400 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 victim's underwear (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 U.S. combined population 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.
CRBAWU - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA evidence is at least one billion times more likely if the mixture of DNA originated from the Victim, the Suspect and an unknown unrelated individual rather than if it originated from the Victim, and two unknown, unrelated males **Database(s) Used:** [Location Identifying Database]
CRVQCW - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 3A-1PT NS: Assuming Female Victim (K1), the evidence profile is 196 Trillion 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. This provides very strong support for inclusion. 3A-1PT SP: Male Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 7

WebCode-Test	Item 3 Methods & Results
CXYRCQ - 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 victim's underwear (Item 3) and Suspect. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and Suspect is approximately fifty quadrillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and Victim. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and Victim is approximately two trillion 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 victim's underwear (Item 3) and Victim is approximately four 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 victim's underwear (Item 3). A DNA match between the data obtained from the second fraction from the questioned stain from victim's underwear (Item 3) and Suspect is approximately six hundred undecillion 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 victim's underwear (Item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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.
CY6DP6 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Fraction 1: The male DNA profile from this item was interpreted as a single-source profile. The female victim and the male suspect are excluded as possible contributors to this DNA profile. Fraction 2: The DNA profile from this item was interpreted as a mixture of three individuals, with at least one male contributor and with the female victim as an assumed contributor. The DNA results are approximately 27.4 quintillion times more likely if they originated from the female victim, the male suspect, and an unknown, unrelated individual than if they originated from the female victim, and two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the male suspect is a contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
CZ6EPV - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3e: Assuming Female Victim (K1), the evidence profile is approximately 359 Trillion times more likely if it originated from the female victim (K1), male suspect (K2), and one unknown individual than if it originated from the female victim (K1) and two unknown individuals. This analysis provides very strong support for the proposition that the Male Suspect (K2) is a contributor to this mixture. Item 3sp: 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

TABLE 7

WebCode-Test	Item 3 Methods & Results
E34ANN - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the stain from underwear (item 3) and Victim. A match between the data obtained from the first fraction from the stain from underwear (item 3) and Victim is approximately 5 billion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the stain from underwear (item 3) and Suspect. A match between the data obtained from the first fraction from the stain from underwear (item 3) and Suspect is approximately 10 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the second fraction from the stain from underwear (item 3) and Suspect. A match between the data obtained from the second fraction from the stain from underwear (item 3) and Suspect is approximately 100 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 from the stain from underwear (item 3) and Victim is approximately 100 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 stain from underwear (item 3). **Database(s) Used:** NIST1036
EHXZJK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Sp: PP21 Item 1: Excluded. Item 2: Excluded. YFP Item 2: Excluded. E: PP21 Item 1: Assumed contributor. Item 2: Not excluded (LR = 100 billion). YFP Item 2: Not excluded (LR = 13,000). **Database(s) Used:** [Location Identifying Database]
ELJJPP - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction of the stain from victim's underwear (item 3) and the male suspect (item 2). A match between the data obtained from the first fraction of the stain from victim's underwear (item 3) and the male suspect (item 2) is approximately 900 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction of the stain from victim's underwear (item 3) and the female victim (item 1). A match between the data obtained from the first fraction of the stain from victim's underwear (item 3) and the female victim (item 1) is approximately 2 quadrillion 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 of the stain from victim's underwear (item 3) and the male suspect (item 2) is approximately 30 undecillion 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 of the stain from victim's underwear (item 3). A DNA match between the data obtained from the second fraction of the stain from victim's underwear (item 3) and the female victim (item 1) is approximately 2 nonillion times less probable than a coincidental match to an unrelated person in the population. The female victim (item 1) is excluded from the data obtained from the second fraction of the stain from victim's underwear (item 3). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population database

TABLE 7

WebCode-Test	Item 3 Methods & Results
EY6YTN - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The first fraction of the "…victim's underwear" (item 3) contained a mixture of DNA from at least three individuals. A DNA match was identified between the data obtained from the first fraction of the "…victim's underwear" (item 3) and the suspect. A match between the data obtained from the first fraction of the "…victim's underwear" (item 3) and the suspect is approximately 10 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction of the "…victim's underwear" (item 3) and the victim. A match between the data obtained from the first fraction of the "…victim's underwear" (item 3) and the victim is approximately 5 quadrillion times more probable than a coincidental match to an unrelated person in the population. The second fraction of the "…victim's underwear" (item 3) contained a mixture of DNA from at least two individuals. A DNA match between the data obtained from the second fraction of the "…victim's underwear" (item 3) and the suspect is approximately 1 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 second fraction of the "…victim's underwear" (item 3). A DNA match between the data obtained from the second fraction of the "…victim's underwear" (item 3) and the victim is approximately 20 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 "…victim's underwear" (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database was used to generate DNA match statistics.
F7H8UP - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from the victim, suspect and one unknown, unrelated individual. H2: The evidence originated from victim and two unknown, unrelated individuals. The DNA profile obtained from the non-sperm cell fraction from the victim's underwear is approximately 1.3 septillion times more likely if it originated from the victim, suspect and one unknown, unrelated individual than if it originated from the victim and two unknown, unrelated individuals. There is evidentiary support for the inclusion of the suspect as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
F8XQDM - 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 victim's underwear (item 3) and Victim. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and Victim is approximately 100 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and Suspect. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and Suspect 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 second fraction from the questioned stain from victim's underwear (item 3) and Victim is approximately 400 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 victim's underwear (item 3). A DNA match between the data obtained from the second fraction from the questioned stain from victim's underwear (item 3) and Suspect is approximately 600 undecillion 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 victim's underwear (item 3). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population database

TABLE 7

WebCode-Test	Item 3 Methods & Results
FPXE6L - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** 1. The SUSPECT (item Q02-01) cannot be excluded as a contributor to the following (see Testing Summary): • Mixture 1 and Y-STR Profile B from a blood and semen stained area on the underwear (item Q03-1) from the VICTIM. The STR DNA results for Mixture 1 are estimated to be greater than one trillion times more likely if they originate from the VICTIM, the SUSPECT and the donor of STR Profile 1 than if they originate from the VICTIM, the donor of STR Profile 1 and one unknown person unrelated to the SUSPECT. Note: A supplementary statistic can be calculated for the male-specific Y-STR profile that adds further weight to the association reported. **Database(s) Used:** i. NIST Asian, ii. NIST African American, iii. NIST Caucasian, iv. Srivastava et al. (2019) South Asian, v. [Location Identifying Database]
GCH7HK - 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 victim's underwear (item 3) and the victim. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and the victim is approximately 50 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and the suspect. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (item 3) and the suspect 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 second fraction from the questioned stain from victim's underwear (item 3) and the victim is approximately 400 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 victim's underwear (item 3). A DNA match between the data obtained from the second fraction from the questioned stain from victim's underwear (item 3) and the suspect is approximately 600 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 second fraction from the questioned stain from victim's underwear (item 3). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population
H484WJ - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the tan fabric (item 3) and the male subject. A match between the data obtained from the first fraction from the tan fabric (item 3) and the male subject is approximately 100 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the tan fabric (item 3) and the female victim. A match between the data obtained from the first fraction from the tan fabric (item 3) and the female victim is approximately 7 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 tan fabric (item 3) 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 tan fabric (item 3). A DNA match between the data obtained from the second fraction from the tan fabric (item 3) and the male subject is approximately 100 undecillion times less probable than a coincidental match to an unrelated person in the population. The male subject is excluded from the data obtained from the second fraction from the tan fabric (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database was used to generate DNA match statistics.

TABLE 7

WebCode-Test	Item 3 Methods & Results
HEQHYL - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the victim's underwear (item 3) and the suspect. A match between the data obtained from the first fraction from the victim's underwear (item 3) and the suspect is approximately 3 sextillion times more probable than a coincidental match to an unrelated person in the population. The comparison between the victim and the data obtained from the first fraction from the victim's underwear (item 3) is inconclusive because reproducible match statistics were not obtained. Therefore, no conclusions will be offered regarding the victim as a possible contributor to the DNA mixture obtained from the first fraction from the victim's underwear (item 3). A DNA match between the data obtained from the second fraction from the victim's underwear (item 3) and the suspect is approximately 600 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 second fraction from the victim's underwear (item 3). A DNA match between the data obtained from the second fraction from the victim's underwear (item 3) and the victim is approximately 400 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 victim's underwear (item 3). **Database(s) Used:** Revised NIST 1036
HJX7CN - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** OVERALL LR=9.2694E11 BY ANALYSIS WITH LRmixStudio **Database(s) Used:** [Location Identifying Database]
J37QNH - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1 (complainant) Assumed contributor for both FF and MF (minor contributor). Item 2 (suspect) and FF. Not Excluded LR = 100 billion item 2 (suspect) and MF. Excluded **Database(s) Used:** [Location Identifying Database]
J772JG - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** PP21 MF/SP fraction: COMP (Item 1) Excluded; SUS (Item 2) Excluded. YFP MF/SP fraction: SUS (Item 2): Excluded. PP21 FF/E fraction: COMP (Item 1) Assumed Contributor, SUS (Item 2) Not Excluded (LR=100 billion). YFP FF/E fraction: SUS (Item 2) Not Excluded (LR can't be calculated as unresolved mixture). **Database(s) Used:** [Location Identifying Database]
JHLQHM - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** It is 4,3e18 times more likely to observe the DNA profile if the mixed stain on the underwear (ITEM 3) originates from ITEM 2 (Suspect) and two unknown persons, than if it originated from three unknown persons, unrelated to ITEM 2 (Suspect). Theta is 0.01 and probability of drop-in is 0.05. It is 1,8e13 times more likely to observe the DNA profile if the mixed stain on the underwear (ITEM 3) 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. It is 7,8e21 times more likely to observe the DNA profile if the mixed stain on the underwear (ITEM 3) originates from unknown sperm donor (in sperm fraction) and two unknown persons, than if it originated from three unknown persons, unrelated to unknown sperm donor. Theta is 0.01 and probability of drop-in is 0.05. **Database(s) Used:** [Location Identifying Database]. Rare allele frequency is 0.0007

TABLE 7

WebCode-Test	Item 3 Methods & Results
JPGUBX - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3e: 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 DNA results are approximately 2.60 nonillion times more likely if they originated from the female victim, the male suspect and an unknown, unrelated individual than if they originated from the female victim and two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the male suspect is a contributor to the DNA from this item. Item 3sp: The DNA profile from this item was interpreted as a mixture of two individuals with at least one male contributor. The DNA results are approximately 46.5 quadrillion times more likely if they originated from two unknown, unrelated individuals than if they originated from the female victim and an unknown, unrelated individual. Based on the likelihood ratio, this provides very strong support that the female victim is not a contributor to the DNA from this item. The DNA results are approximately 2.66 million times more likely if they originated from the male suspect 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 male suspect is a contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
K9ECCE - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3 - Sperm Fraction: The DNA evidence is 14 times more likely if Item 2 (Suspect) is a contributor. The DNA evidence is more likely if Item 1 (Victim) is not a contributor. Item 3 - Epithelial Fraction: The DNA evidence is 630 million times more likely if Item 2 (Suspect) is a contributor. The DNA evidence is 15 billion times more likely if Item 1 (Victim) is a contributor. **Database(s) Used:** [Location Identifying Database]
KPDQAK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** NSF: H1 = The evidence originated from Victim, Suspect, and one unknown, unrelated individual. H2 = The evidence originated from Victim and two unknown, unrelated individuals. The DNA profile obtained from the non-sperm cell fraction of the underwear stain is approximately 1.4 quintillion times more likely if it originated from Victim, Suspect, and one unknown, unrelated individual than if it originated from Victim and two unknown, unrelated individuals. There is evidentiary support for the inclusion of Suspect as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
L67JVL - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 3e: Assuming Female Victim (K1), the evidence profile is approximately 272 trillion 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. This analysis provides very strong support for inclusion. 3sp: Female Victim (K1) is excluded based on the LR of zero. Suspect (K2) is excluded based on the LR of zero. **Database(s) Used:** Allele frequencies from the 2015 FBI Expanded Population Database were used for STR statistical calculations.
L8XEJE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Sperm Fraction: Item 1 - Assumed contributor, Item 2 - LR = 3.281E2 (320 support for contribution). Epithelial Fraction: Item 1 - Assumed contributor, Item 2 - LR = 4.4071E19 (>100 billion support for contribution). **Database(s) Used:** [Participant did not return a database used.]

TABLE 7

WebCode-Test	Item 3 Methods & Results
LBAKVF - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** SUSPECT (Q02-1) cannot be excluded as a contributor to Mixture 1 from the underwear (Q03-1E) from the VICTIM. The STR DNA results are estimated to be greater than a trillion times more likely if they originate from VICTIM, SUSPECT and one unknown person than they originate from VICTIM and two unknown people, unrelated to SUSPECT. **Database(s) Used:** i. NIST Asian, ii. NIST African American, iii. NIST Caucasian, iv. Srivastava et al. (2019) South Asian, v.[Location Identifying Database]
LG3PNJ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Known contributors under Hp: victim and suspect. Known contributors under Hd: victim LR (total): 2,7E13. **Database(s) Used:** [Location Identifying Database]
LHUN3H - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the stain from victim's underwear (Item 3) and Suspect. A match between the data obtained from the first fraction from the stain from victim's underwear (Item 3) and Suspect is approximately 9 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the stain from victim's underwear (Item 3) and Victim. A match between the data obtained from the first fraction from the stain from victim's underwear (Item 3) and Victim is approximately 100 quadrillion 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 stain from victim's underwear (Item 3) and Suspect is approximately 400 undecillion 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 stain from victim's underwear (Item 3). A DNA match between the data obtained from the second fraction from the stain from victim's underwear (Item 3) and Victim is approximately 300 octillion 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 stain from victim's underwear (Item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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
LUPUWF - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For the epithelial fraction: The LR value regarding the possible involvement of the female victim was calculated to be 2.52 x 10^15 to 1, which means it is about 2.52 x 10^15 to 1 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]. The LR value regarding the possible involvement of the male suspect was calculated to be 2.14 x 10^30 to 1, which means it is about 2.14 x 10^30 to 1 times more likely that the observed DNA profile being a mixture originating from the male suspect and two unknown individuals than if it originating from three unrelated individuals selected at random from the local [Population]. For the sperm fraction: The LR value regarding the possible involvement of the female victim was calculated to be 1.36 x 10^3 to 1, which means it is about 1.36 x 10^3 to 1 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]. The LR value regarding the possible involvement of the male suspect was calculated to be 1.22 x 10^6 to 1, which means it is about 1.22 x 10^6 to 1 times more likely that the observed DNA profile being a mixture originating from the male suspect 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]
LYKQJL - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Non-sperm Fraction: Assuming Female Victim (K1), the evidence DNA profile is approximately 26 trillion times more likely if it originated from Female Victim (K1), Male Suspect (K2), and an unknown individual (Hypothesis 1) than if it originated from Female Victim (K1) and two unknown individuals (Hypothesis 2). This analysis provides very strong support for the proposition that Male Suspect (K2) is a contributor to the DNA obtained from this sub-item. Sperm Fraction: The evidence DNA profile is approximately 0 times more likely if it originated from Male Suspect (K2) (Hypothesis 1) than if it originated from an unknown individual (Hypothesis 2). This analysis provides an exclusion for the proposition that Male Suspect (K2) is a contributor to the DNA obtained from this sub-item. **Database(s) Used:** 2015 FBI Expanded Population Database
MW99ZF - 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 victim's underwear (Item 3) and suspect. A match between the data obtained from the first fraction from the questioned stain from the victim's underwear (Item 3) and suspect is approximately 4 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from the victim's underwear (Item 3) and victim. A match between the data obtained from the first fraction from the questioned stain from the victim's underwear (Item 3) and victim is approximately 6 trillion 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 the victim's underwear (Item 3) and suspect is approximately 6 undecillion 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 the victim's underwear (Item 3). A DNA match between the data obtained from the second fraction from the questioned stain from the victim's underwear (Item 3) and victim is approximately 400 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 the victim's underwear (Item 3). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population database.

TABLE 7

WebCode-Test	Item 3 Methods & Results
NWNRKD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For the epithelial (e) fraction: The calculated LR value for the possible involvement of the victim in this mixture was 1.27E+7 to 1. This means it is about 1.27E+7 times more likely that the observed DNA profile being a mixture originating from the victim and two unknown persons than if it originating from three unrelated persons selected at random from the local [Population]. The calculated LR value for the possible involvement of the suspect in this mixture was 1.97E+15 to 1. This means it is about 1.97E+15 times more likely that the observed DNA profile being a mixture originating from the suspect and two unknown persons than if it originating from three unrelated persons selected at random from the local [Population]. **Database(s) Used:** [Location Identifying Database]
P3QH3A - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3e: Item 1 - conditioned on. Item 2 - support for contribution greater than 100 billion (8.29E17). Unresolved unknown contributor. Item 3sp: Item 1 - conditioned on. Item 2 - support for contribution greater than 100 billion (2.21E15). Resolved unknown male profile. **Database(s) Used:** [Location Identifying Database]
P8KEPF - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1:The evidence originated from Victim, suspect, and one unknown, unrelated individual. H2: The evidence originated from Victim and two unknown, unrelated individuals. The DNA profile obtained from the non-sperm cell fraction of Item 3 is approximately 15 quintillion times more likely if it originated from Victim, Suspect and one unknown, unrelated individual than if it originated from the Victim and two unknown, unrelated individuals. There is evidentiary support for the inclusion of Suspect as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
P8TP7Q - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals, with at least one male contributor and with the female victim as an assumed contributor. The DNA results are approximately 2.81 quintillion times more likely if they originated from the female victim, the male suspect, and an unknown, unrelated individual than if they originated from the female victim and two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that the male suspect is a contributor to the DNA from this item. Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 1): The male DNA profile from this item was interpreted as a single-source profile. 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
PD88ZF - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from the sperm fraction was interpreted as a mixture of two individuals. The DNA profile is 27 times more likely if it originated from the Suspect (2) and one unknown individual than if it had originated from two unknown, unrelated individuals. Statistical analysis provides limited support for the inclusion of the Suspect (2). The Victim (1) is excluded as a contributor to the DNA profile. The DNA profile obtained from the epithelial fraction was interpreted as a mixture of three individuals. The Victim (1) was assumed as a contributor. The DNA profile is at least 1 trillion times more likely if it originated from the Victim (1), the Suspect (2), and one unknown individual than if it had originated from the Victim (1) and two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of the Suspect (2). **Database(s) Used:** The FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanics

TABLE 7

WebCode-Test	Item 3 Methods & Results
Q99BQE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** STRMIX 2.8.0 used Knowing the underwear belongs to the victim, the suspect's contribution in the mixture is calculated according to the following hypothesis : Hp : the mixture belongs to the victim, the suspect and 1 unknown person. Hd : the mixture belongs to the victim and 2 unknown people. LR = 7.0273E24.
R3MFPB - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For the epithelial fraction: The LR value for the involvement of female victim is 6.75E+20 to 1, which means it is about 6.75E+20 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]. The LR value for the involvement of male suspect is 2.02E+31 to 1, which means it is about 2.02E+31 times more likely that the observed DNA profile being a mixture originating from the male suspect and two unknown individuals than if it originating from three unrelated individuals selected at random from the local [Population]. For the sperm fraction: The LR value for the involvement of female victim is 5.67E-1 to 1 which is uninformative. Hence, no conclusion could be made as to whether or not the female victim is a possible source of the DNA profile. The LR value for the involvement of male suspect is 7.22E+12 to 1, which means it is about 7.22E+12 times more likely that the observed DNA profile being a mixture originating from the male suspect 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]
R9RDYE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 3e: Assuming Female Victim (K1), the evidence profile is approximately 229 Trillion 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. This provides very strong support for the inclusion of Male Suspect (K2). For 3SP: The evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) than if it originated from an unknown individual. Female Victim (K1) is excluded. For 3SP: The evidence DNA profile is approximately 0 times more likely if it originated from Male Suspect (K2) than if it originated from an unknown individual. Male Suspect (K2) is excluded. **Database(s) Used:** 2015 FBI Expanded Population Database.
RCPXZD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** LR was calculated for the epithelial fraction of Item 3, assuming the mixture is comprised of three contributors. We assumed the presence of the victim on her own underwear is not in question. The DNA profile is approximately 5*10^17 (500 billiard) times more likely if it originated from the Victim, the Suspect and an unknown individual than if it originated from the Victim and two unknown individuals. **Database(s) Used:** [Location Identifying Database]
TMDEV4 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** FBI_EXTENDED_CAUC **Database(s) Used:** [Participant did not return a database used.]

TABLE 7

WebCode-Test	Item 3 Methods & Results
TZBZVA - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For the epithelial(e) fraction: The LR value calculated for the possible involvement of the female victim was 2.18E7 to 1, which means it is about 2.18E7 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]. The LR value calculated for the possible involvement of the male suspect was 4.93E18 to 1, which means it is about 4.93E18 times more likely that the observed DNA profile being a mixture originating from the male suspect 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]
UNVR99 - 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 victim's underwear (Item 3) and victim. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and victim is approximately 600 million times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and suspect. A match between the data obtained from the first fraction from the questioned stain from victim's underwear (Item 3) and suspect is approximately 300 quintillion times more probable than a coincidental match to an unrelated person in the population. Due to the complexity of the mixture, no conclusive determination can be made as to the evidence genotypes from the data obtained from the second fraction from the questioned stain from victim's underwear (Item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database.
VFHZHA - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Hypothesis 1 (H1): The evidence originated from Victim, Suspect and one unknown, unrelated individual. Hypothesis 2 (H2): The evidence originated from Victim and two unknown, unrelated individuals. The DNA profile obtained from the non-sperm cell fraction of the underwear is approximately 66 quintillion times more likely if it originated from Victim, Suspect, and one unknown, unrelated individual than if it originated from Victim and two unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic.
VK9834 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Semen fraction: H1: The DNA on Item 3 (Semen fraction) came from the suspect. H2: The DNA on Item 3 (Semen fraction) came from an unknown, unrelated person. LR= 0. H1: The DNA on Item 3 (Semen fraction) came from the victim. H2: The DNA on Item 3 (Semen fraction) came from an unknown, unrelated person. LR= 0. Epithelial fraction: H1: The DNA on Item 3 (Epithelial fraction) came from the suspect and two unknown, unrelated persons. H2: The DNA on Item 3 (Epithelial fraction) came from three unknown, unrelated persons. LR= 2.0093E17. H1: The DNA on Item 3 (Epithelial fraction) came from the victim and two unknown, unrelated persons. H2: The DNA on Item 3 (Epithelial fraction) came from three unknown, unrelated persons. LR= 2.2010E15. H1: The DNA on Item 3 (Epithelial fraction) came from the male contributor to the semen fraction of item 3 and two unknown, unrelated persons. H2: The DNA on Item 3 (Epithelial fraction) came from three unknown, unrelated persons. LR= 3.5888E12 **Database(s) Used:** [Location Identifying Database]

TABLE 7

WebCode-Test	Item 3 Methods & Results
W2RLKZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 1): The male DNA profile from this item was interpreted as a single-source profile. The Female Victim and The Male Suspect are excluded as possible contributors to this DNA profile. Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals with at least one male contributor and with The Female Victim as an assumed contributor. The DNA results are approximately 3.97 sextillion times more likely if they originated from The Female Victim, The Male Suspect and an unknown, unrelated individual than if they originated from The Female Victim and two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that The Male Suspect is a contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
WRGKYZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 2): The DNA profile from this item was interpreted as a mixture of three individuals, with at least one male contributor and with Female Victim as an assumed contributor. The DNA results are approximately 42.4 quintillion times more likely if they originated from Male Suspect, Female Victim and an unknown, unrelated individual than if they originated from Female Victim and two unknown, unrelated individuals. Based on the likelihood ratio, this provides very strong support that Male Suspect is a contributor to the DNA from this item. Item 3.1 (Portion of "Questioned stain from victim's underwear" - Fraction 1): The male DNA profile from this item was interpreted as a single-source profile. Female Victim and Male Suspect are excluded as possible contributors to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
WU8M28 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from the sperm fraction was interpreted as originating from a single unknown male individual A. The DNA profile obtained from the epithelial fraction was interpreted as a mixture of three individuals. Assuming female victim (1) and the corresponding sperm fraction as contributors, the mixture contains one unknown individual. The DNA profile is at least 1 trillion times more likely if it originated from female victim (1), male suspect (2), and one unknown individual than if it had originated from female victim (1) and two unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of male suspect (2). **Database(s) Used:** FBI Extended CODIS Core Allele Frequencies- Caucasian, African American, and Southwest Hispanics
X28843 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Spermatozoa Fraction: Item 1 - approximately 830 million supporting non-contribution; Item 2 - approximately 3500 supporting non-contribution. Epithelial Fraction: Item 1 - assumed contributor; Item 2 - greater than 100 billion supporting contribution. **Database(s) Used:** [Location Identifying Database]
YGJ6L9 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 3e - Assuming the victim (item 1), the evidence profile is approximately 247 trillion times more likely if it originated from the victim (item 1), suspect (item 2), and one unknown individual than if it originated from the victim (item 1) and two unknown individuals. This provides very strong support for inclusion of suspect (item 2). For 3s - Victim (item 1) is excluded with a likelihood ratio of 0. Suspect (item 2) is excluded with a likelihood ratio of 0. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 7

WebCode-Test	Item 3 Methods & Results
YJMUQ3 - 5901	**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 Victim (Item 1) is assumed to be a contributor to this mixture. The DNA typing results are 29.6 nonillion times more likely to be observed if they originated from the Victim (Item 1), the Suspect (Item 2), and one unknown, unrelated individual, rather than if they originated from the Victim (Item 1) and two unknown, unrelated individuals. This analysis provides very strong support for the proposition that includes the Suspect (Item 2) as one of the contributors to this mixture. **Database(s) Used:** NIST 1036 (2017)
Z8LUQ4 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the first fraction from the cutting from the tan fabric (item 3) and the subject. A match between the data obtained from the first fraction from the cutting from the tan fabric (item 3) and the subject is approximately 600 septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match was identified between the data obtained from first fraction from the cutting from the tan fabric (item 3) and the victim. A match between the data obtained from first fraction from the cutting from the tan fabric (item 3) and the victim is approximately 600 quadrillion 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 cutting from the tan fabric (item 3) and the victim is approximately 400 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 cutting from the tan fabric (item 3). A DNA match between the data obtained from the second fraction from the cutting from the tan fabric (item 3) and the subject is approximately 600 undecillion times less probable than a coincidental match to an unrelated person in the population. The subject is excluded from the data obtained from the second fraction from the cutting from the tan fabric (item 3). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database

Statistical Analysis for Item 4

TABLE 8

WebCode-Test	Item 4 Methods & Results
2QGMC2 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (item 4) and the male suspect. A match between the data obtained from the questioned stain from victim's pants (item 4) and the male suspect is approximately one 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 victim's pants (item 4) and the victim is approximately two hundred 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 questioned stain from victim's pants (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database
34G3B3 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming three contributors, Female Victim is excluded (LR=0) as being a contributor to the mixture detected for this item. Assuming three contributors, the evidence profile is 1.3E+24 times more likely to be observed if Male Suspect and two unknown individuals are the contributors than if three unknown individuals are the contributors. **Database(s) Used:** NIST Databases - Forensic Sci Int.: Genetics 31 (2017) e36-e40
37J2CU - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** [Location Identifying Database]
3MQZUY - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** 4. The SUSPECT (item 2-1) cannot be excluded as a contributor to Mixture 2 (see Testing Summary) from the VICTIMS pants (item 4-1) The STR DNA results are estimated to be greater than one trillion times more likely if they originate from the SUSPECT and two unknown people than if they originate from three unknown people unrelated to the SUSPECT. **Database(s) Used:** i. NIST Asian, ii. NIST African American, iii. NIST Caucasian, iv. Srivastava et al. (2019) South Asian, v. [Location Identifying Database]
3WHFJ3 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from the Known Male and two unknown, unrelated individuals. H2: The evidence originated from three unknown, unrelated individuals. The DNA profile obtained from Item 4 is approximately 520 quadrillion times more likely if it originated from the Known Male and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals. There is evidentiary support for the inclusion of the Known Male as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
44PDRD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from victim's pants"): 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 106 sextillion times more likely if they originated from MALE SUSPECT 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 MALE SUSPECT is a contributor to the DNA from this item. FEMALE VICTIM 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
4BEUJW - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Victim (Item 1): Excluded as being a contributor to the DNA in this sample. Suspect (Item 2): The DNA evidence is estimated to be 100 billion times more likely to occur if the DNA originated from the suspect and and two unknown, unrelated people selected randomly from the [Population], than if it originated from three unknown and unrelated people selected randomly from the [Population]. **Database(s) Used:** [Location Identifying Database]
4FBJY4 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1: no statistical calculation performed due to number of missmatches. Item 2: 4.524e+15. Unknown male from sperm fraction: no statistical calculation performed due to number of missmatches. **Database(s) Used:** [Location Identifying Database]
4UQG64 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile 4A-2PT is approximately 0 times more likely if it originated from Female Victim (K1) and two unknown individuals than if it originated from three unknown individuals. This provides support for exclusion of Female Victim (K1). The evidence DNA profile 4A-2PT is approximately 572 trillion times more likely if it originated from Male Suspect (K2) and two unknown individuals than if it originated from three unknown individuals. This provides very strong support for inclusion of Male Suspect (K2). **Database(s) Used:** 2015 FBI Expanded Population Database
4XQRZ4 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Female Victim (K1) is excluded based on the LR of zero. The evidence profile is approximately 25 trillion times more likely if it originated from Male Suspect (K2) and two unknown individuals than if it originated from three unknown individuals. This analysis provides very strong support that Male Suspect (K2) is a contributor to the DNA obtained from this sub-item **Database(s) Used:** 2015 FBI Expanded Population Database
62K9Q4 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** For 4A-2: The evidence profile is approximately 0 times more likely if it originated from Female Victim (K1) and two unknown individuals than if it originated from three unknown individuals. Female Victim (K1) is excluded based on the LR of zero. The evidence profile is approximately 3 quadrillion times more likely if it originated from Male Suspect (K2) and two unknown individuals than if it originated from three unknown individuals. This analysis provides very strong support for the proposition that Male Suspect (K2) is a contributor to the DNA obtained from this sub-item. **Database(s) Used:** 2015 FBI Expanded Population
63VBC2 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) and two unknown individuals than if it originated from three unknown individuals. The evidence DNA profile is approximately 12 trillion times more likely if it originated from Male Suspect (K2) and two unknown individuals than if it originated from three unknown individuals. This analysis provides very strong support for the proposition that Male Suspect (K2) is included as a contributor to this DNA mixture. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 8

WebCode-Test	Item 4 Methods & Results
6PTH6Y - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The victim's pants from item 4 contained a mixture of DNA from at least three individuals. A DNA match was identified between the data obtained from the victim's pants from item 4 and the suspect. A match between the data obtained from the victim's pants from item 4 and the suspect is approximately one septillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the victim's pants from item 4 and the victim is approximately two 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 victim's pants from item 4. **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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.
77A6RY - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 2.9365E26 **Database(s) Used:** The FBI's extended database for African Americans was used.
786NUZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from item # 4 is a mixture of at least 3 individuals, following set of hypotheses were evaluated: A) Hp; item No. 1+ 2 unknown, Hd; 3 unknown, LR (MLE)= 1.698 e -5. B) Hp; item No. 2+ 2 unknown, Hd; 3 unknown, LR (MLE) = 3.627 e +17 **Database(s) Used:** NIST Caucasian database 2017 with theta co-ancestry coefficient = 0.03
7H4JRV - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (item 4) and the subject. A match between the data obtained from the questioned stain from victim's pants (item 4) and subject is approximately one hundred quadrillion 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 victim's pants (item 4) and the victim is approximately two hundred 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 questioned stain from victim's pants (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database
8DDAHX - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 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 Known Male Suspect (2) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of Known Male Suspect (2). Known Female Victim (1) is excluded as a contributor to the DNA profile. Due to an insufficient amount of male DNA detected during quantitation, autosomal Short Tandem Repeat (STR) analysis was not performed on the sperm fraction. **Database(s) Used:** FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanic

TABLE 8

WebCode-Test	Item 4 Methods & Results
8Y8DYV - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the "questioned stain…pants…" (item #4) and the male suspect (item #2). A match between the data obtained from the "questioned stain…pants…" (item #4) and the male suspect (item #2) is approximately 1 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…pants…" (item #4) and the female victim (item #1) is approximately 500 quintillion times less probable than a coincidental match to an unrelated person in the population. The female victim (item #1) is excluded from the data obtained from the "questioned stain…pants…" (item #4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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.
8YUL9Z - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** A likelihood ratio (LR) analysis was performed using the LRmix Studio software, using allele frequency data specific to the [Population]- based on own laboratory reference population database consisting of 5,000 genotypes from [Country]. The LR values for mixed DNA profiles were calculated with consideration for both drop-in and drop-out phenomena. The analysis assumed a drop-in probability of 0.05 and applied a minimum allele frequency threshold of 0.001. A subpopulation correction factor of 0.01 was also incorporated into the calculations. The resulting LR values were interpreted in terms of their probative value. The evaluated hypotheses included: Prosecution Hypothesis (Hp): The DNA mixture includes the genetic profiles of item2, and two unknown, untested individual from the population. Alternative Hypothesis (Hd): The DNA mixture includes the genetic profile of three unknown, untested individuals from the population. The comparison of these hypotheses was used to assess the strength of the genetic evidence in the context of the case. Likelihood ratio on this sample is: 4.6942E10. Y-STR: Given the Haplotypes above and that there is 1 additional unknown contributor, the likelihood of observing the given trace under the hypothesis of the donorship of the suspect is approx. 5,786 times more likely than observing the given trace under the hypothesis of the non-donorship. This calculation is based on 298,405 haplotypes (Y17) in the worldwide database YHRD R69. **Database(s) Used:** STR laboratory population base of [Country]
9CLYK9 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from victim's pants"): 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 is excluded as a possible contributor to the DNA from this item. The DNA results are approximately 35.1 sextillion times more likely if they originated from the male suspect 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 male victim is a contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
9MBR8Q - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1 (complainant) - Excluded. Item 2 (known suspect) - >100 billion in favour of H1 (favouring contribution). **Database(s) Used:** [Location Identifying Database]
9WLTTR - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA evidence is greater than 100 billion times more likely if the suspect is a contributor. The victim is excluded as a contributor. **Database(s) Used:** [Location Identifying Database]

TABLE 8

WebCode-Test	Item 4 Methods & Results
B7W38V - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 1.3551E21 **Database(s) Used:** FBI Extended African American
BDR7Z7 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Explanation 1: The DNA profile obtained originated from item 2 (1D), and two unknown, unrelated individuals. Explanation 2: The DNA profile obtained originated from three unknown, unrelated individuals. The DNA profile obtained is approximately 1E33 times more likely (very strong support) if it originated from the item 2 (1D) and two unknown, unrelated individuals than if the DNA profile obtained originated from three unknown, unrelated individuals. **Database(s) Used:** Nist1036 (revised 2017)_Caucasian, Nist1036 (revised 2017)_African American, Nist1036 (revised 2017)_Hispanic
BKHHBU - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 2.8651e24 **Database(s) Used:** FBI Extended African American
BNGT8U - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The LR calculations exclude the victim as being a contributor to the DNA mixture detected for item 4. Assuming 3 contributors for item 4, the evidence profile is 9.9 x 10^26 times more likely to be observed if the suspect 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
CDTG9M - 5901	**Method(s)**: Likelihood Ratio, STRmix **Stats Analysis:** Propositions for contributor 1: The propositions considered for ITEM 4 were: P1: The SUSPECT is one of three contributors to the mixed DNA profile obtained. P2: The SUSPECT is NOT a contributor to the mixed DNA profile obtained. Three unknown individuals, unrelated to the SUSPECT, are the contributors. For this calculation, it was assumed that three individuals have contributed to the DNA profile obtained. Likelihood Ratio: The evidence is at least 100 BILLION (5.5762E22) times more likely if the SUSPECT is one of three contributors to the mixed DNA profile than if the profile originated from three unknown individuals, unrelated to the SUSPECT, selected at random from the [Population]. **Database(s) Used:** [Location Identifying Database]
CKECAQ - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (Item 4) and the Subject. A match between the data obtained from the questioned stain from victim's pants (Item 4) and the Subject is approximately 900 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 victim's pants (Item 4) and the Victim is approximately 90 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 questioned stain from victim's pants (Item 4). **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 U.S. combined population 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
CRBAWU - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA evidence is at least one billion times more likely if the mixture of DNA originated from the Suspect and two unknown unrelated individuals rather than if it originated from three unknown, unrelated individuals **Database(s) Used:** [Location Identifying Database]
CRVQCW - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is 95 Trillion times more likely if it originated from Male Suspect (K2) and two unknown individuals than if it originated from three unknown individuals. This provides very strong support for inclusion. Female Victim (K1) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database
CXYRCQ - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (Item 4) and Suspect. A match between the data obtained from the questioned stain from victim's pants (Item 4) and Suspect 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 questioned stain from victim's pants (Item 4) and Victim is approximately twenty sextillion times less probable than a coincidental match to an unrelated person in the population. Victim is excluded from the data obtained from the questioned stain from victim's pants (Item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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.
CY6DP6 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 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 2.98 quadrillion times more likely if they originated from the male suspect 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 male suspect is a contributor to the DNA from this item. Based on the likelihood ratio result, the female victim is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
CZ6EPV - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4: The evidence DNA profile is approximately 82 Trillion times more likely if it originated from the male suspect (K2) and two unknown individuals than if it originated from three unknown individuals. This analysis provides very strong support for the proposition that the male suspect (K2) is a contributor to this DNA mixture. Female victim (K1) is excluded based on the LR of zero. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 8

WebCode-Test	Item 4 Methods & Results
E34ANN - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the stain from pants (item 4) and Suspect. A match between the data obtained from the stain from pants (item 4) and Suspect is approximately 1 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 pants (item 4) and Victim is approximately 600 sextillion times less probable than a coincidental match to an unrelated person in the population. Victim is excluded from the data obtained from the stain from pants (item 4). **Database(s) Used:** NIST 1036
EHXZJK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** PP21 Item 1: Excluded. Item 2: Not excluded (LR = 100 billion). YFP Item 2: Unable to be compared as mixture unresolvable. **Database(s) Used:** [Location Identifying Database]
ELJJPP - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the stain from victim's pants (item 4) and the male suspect (item 2). A match between the data obtained from the stain from victim's pants (item 4) and the male suspect (item 2) is approximately 10 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 victim's pants (item 4) and the female victim (item 1) is approximately 500 quintillion times less probable than a coincidental match to an unrelated person in the population. The female victim (item 1) is excluded from the data obtained from the stain from victim's pants (item 4). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population database
EY6YTN - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The "…victim's pants" (item 4) contained a mixture of DNA from at least three individuals. A DNA match was identified between the data obtained from the "…victim's pants" (item 4) and the suspect. A match between the data obtained from the "…victim's pants" (item 4) and the suspect 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 from the "…victim's pants" (item 4) and the victim is approximately 20 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 "…victim's pants" (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database was used to generate DNA match statistics.
F7H8UP - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The evidence originated from the suspect and two unknown, unrelated individual. H2: The evidence originated from three unknown, unrelated individuals. The DNA profile obtained from the pants stain is approximately 580 sextillion times more likely if it originated from the suspect and two unknown, unrelated individual than if it originated from three unknown, unrelated individuals. There is evidentiary support for the inclusion of the suspect as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic

TABLE 8

WebCode-Test	Item 4 Methods & Results
F8XQDM - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (item 4) and Suspect. A match between the data obtained from the questioned stain from victim's pants (item 4) and Suspect is approximately 30 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 victim's pants (item 4) and Victim is approximately 300 quintillion times less probable than a coincidental match to an unrelated person in the population. Victim is excluded from the data obtained from the questioned stain from victim's pants (item 4). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population database
FPXE6L - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** The SUSPECT (item Q02-01) cannot be excluded as a contributor to the following: • Mixture 2 from a bloodstained area on the pants (item Q04-1) from the VICTIM. The STR DNA results are estimated to be greater than one trillion times more likely if they originate from the SUSPECT and two unknown people than if they originate from three unknown people unrelated to the SUSPECT. **Database(s) Used:** i. NIST Asian, ii. NIST African American, iii. NIST Caucasian, iv. Srivastava et al. (2019) South Asian, v. [Location Identifying Database]
GCH7HK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (item 4) and the suspect. A match between the data obtained from the questioned stain from victim's pants (item 4) and the suspect is approximately 10 octillion 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 victim's pants (item 4) and the victim is approximately 10 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 questioned stain from victim's pants (item 4). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population
H484WJ - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the blue fabric (item 4) and the male subject. A match between the data obtained from the blue fabric (item 4) and the male subject is approximately 10 quintillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the blue fabric (item 4) and the female victim is approximately 90 octillion 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 blue fabric (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database was used to generate DNA match statistics.
HEQHYL - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the victim's pants (item 4) and the suspect. A match between the data obtained from the victim's pants (item 4) and the suspect 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 victim's pants (item 4) and the victim is approximately 20 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 victim's pants (item 4). **Database(s) Used:** Revised NIST 1036

TABLE 8

WebCode-Test	Item 4 Methods & Results
HJX7CN - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** LR= 7.1650E12 BY ANALYSIS WITH LRmixStudio **Database(s) Used:** [Location Identifying Database]
J37QNH - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1 (complainant) Excluded. Item 2 (suspect) Not Exlcuded. LR = 100 billion. **Database(s) Used:** [Location Identifying Database]
J772JG - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** PP21: COMP (Item 1) Excluded, SUS (Item 2) Not Excluded (LR=100 billion). YFP: SUS (Item 2) Not Excluded (LR can't be calculated as unresolved mixture). **Database(s) Used:** [Location Identifying Database]
JHLQHM - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** It is 4,4e26 times more likely to observe the DNA profile if the mixed stain on the victim's pants (ITEM 4) originates from ITEM 2 (Suspect) and two unknown persons, than if it originated from three unknown persons, unrelated to ITEM 2 (Suspect). Theta is 0.01 and probability of drop-in is 0.05. **Database(s) Used:** [Location Identifying Database]. Rare allele frequency is 0.0007
JPGUBX - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** 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 168 quadrillion times more likely if they originated from the male suspect 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 male suspect is a contributor to the DNA from this item. Based on the likelihood ratio result, the female victim is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
K9ECCE - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4 - The DNA evidence is greater than 100 billion times more likely if Item 2 (Suspect) is a contributor. Item 1 (Victim) is excluded as a contributor. **Database(s) Used:** [Location Identifying Database]
KPDQAK - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1 = The evidence originated from Suspect and two unknown, unrelated individuals. H2 = The evidence originated from three unknown, unrelated individuals. The DNA profile obtained from the pants stain is approximately 16 septillion times more likely if it originated from Suspect and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals. There is evidentiary support for the inclusion of Suspect as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
L67JVL - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Female Victim (K1) is excluded based on the LR of zero. The evidence DNA profile is approximately 2 quadrillion times more likely if it originated from Male Suspect (K2), and two unknown individuals than if it originated from three unknown individuals. This analysis provides very strong support for inclusion. **Database(s) Used:** allele frequencies from the 2015 FBI Expanded Population Database were used for STR statistical calculations.

TABLE 8

WebCode-Test	Item 4 Methods & Results
L8XEJE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1 - 0 (excluded). Item 2 - LR = 1.4556E21 (>100 billion support for contribution). **Database(s) Used:** [Participant did not return database used.]
LBAKVF - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** SUSPECT (Q02-1) cannot be excluded as a contributor to Mixture 2 from the pants (Q04-1) from the VICTIM. The STR DNA results are estimated to be 1.8 billion times more likely if they originate from SUSPECT and two unknown people than they originate from three unknown people, unrelated to SUSPECT. **Database(s) Used:** i. NIST Asian, ii. NIST African American, iii. NIST Caucasian, iv. Srivastava et al. (2019) South Asian, v. [Location Identifying Database]
LG3PNJ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Known contributors under Hp: suspect. Known contributors under Hd: - LR (total): 8,9E19. **Database(s) Used:** [Location Identifying Database]
LHUN3H - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the stain from victim's pants (Item 4) and Suspect. A match between the data obtained from the stain from victim's pants (Item 4) and Suspect 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 stain from victim's pants (Item 4) and Victim is approximately 300 quintillion times less probable than a coincidental match to an unrelated person in the population. Victim is excluded from the data obtained from the stain from victim's pants (Item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population 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.
LUPUWF - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The LR value regarding the possible involvement of the male suspect was calculated to be 1.39 x 10^17 to 1, which means it is about 1.39 x 10^17 to 1 times more likely that the observed DNA profile being a mixture originating from the male suspect 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]
LYKQJL - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is approximately 142 trillion times more likely if it originated from Male Suspect (K2) and two unknown individuals than if it originated from 3 unknown individuals. This analysis provides very strong support for the proposition that Male Suspect (K2) is a contributor to the DNA obtained from this sub-item. The evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) (Hypothesis 1) than if it originated from an unknown individual (Hypothesis 2). This analysis provides an exclusion for the proposition that Female Victim (K1) is a contributor to the DNA obtained from this sub-item. **Database(s) Used:** 2015 FBI Expanded Population Database

TABLE 8

WebCode-Test	Item 4 Methods & Results
MW99ZF - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (Item 4) and suspect. A match between the data obtained from the questioned stain from victim's pants (Item 4) and suspect is approximately 500 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 victim's pants (Item 4) and victim is approximately 7 sextillion times less probable than a coincidental match to an unrelated person in the population. Victim is excluded from the data obtained from the questioned stain from victim's pants (Item 4). **Database(s) Used:** National Institute of Standards and Technology's 1036 Revised U.S. combined population database.
NWNRKD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The calculated LR value for the possible involvement of the suspect in this mixture was 4.25E+24 to 1. This means it is about 4.25E+24 times more likely that the observed DNA profile being a mixture originating from the suspect and two unknown persons than if it originating from three unrelated persons selected at random from the local [Population]. **Database(s) Used:** [Location Identifying Database]
P3QH3A - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4: Item 1 - excluded. Item 2 - support for contribution greater than 100 billion (2.81E17). Unresolved unknown contributor. Unresolved unknown contributor. **Database(s) Used:** [Location Identifying Database]
P8KEPF - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1:The evidence originated from Suspect, and two unknown, unrelated individuals. H2: The evidence originated from three unknown, unrelated individuals. The DNA profile obtained from Item 4 is approximately 110 sextillion times more likely if it originated from Suspect and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals. There is evidentiary support for the inclusion of Suspect as a possible contributor to the DNA profile obtained as compared with the alternate explanation of the evidence. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic
P8TP7Q - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from victim's pants"): The DNA profile from this item was interpreted as a mixture of three individuals, with at least one male contributor. The DNA results are approximately 10.8 quintillion times more likely if they originated from the male suspect 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 male suspect is a contributor to the DNA from this item. Based on the likelihood ratio result, the female victim is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
PD88ZF - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** 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 Suspect (2) 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 Suspect (2). The victim (1) is excluded as a contributor to the DNA profile. **Database(s) Used:** The FBI Extended CODIS core allele frequencies - Caucasian, African American, and Southwest Hispanics

TABLE 8

WebCode-Test	Item 4 Methods & Results
Q99BQE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** STRMIX 2.8.0 used The pants belongs to the victim. The victim (item 1) is not contributor to the questioned stain, but the suspect (item 2) is contributor to the questioned stain. The suspect's contribution in the mixture is calculated according to the following hypothesis : Hp : the mixture belongs to the suspect and 2 unknown people. Hd : the mixture belongs to 3 unknow people. LR = 2.7357E25.
R3MFPB - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The LR value for the involvement of male suspect is 8.65E+22 to 1, which means it is about 8.65E+22 times more likely that the observed DNA profile being a mixture originating from the male suspect 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]
R9RDYE - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The evidence DNA profile is approximately 0 times more likely if it originated from Female Victim (K1) and two unknown individuals than if it originated from three unknown individuals. Female Victim (K1) is excluded. The evidence DNA profile is approximately 1 Quadrillion times more likely if it originated from Male Suspect and two unknown individuals than if it originated from three unknown individuals. This provides very strong support for the inclusion of Male Suspect (K2). **Database(s) Used:** 2015 FBI Expanded Population Database.
RCPXZD - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** LR was calculated assuming the mixture is comprised of three contributors. The DNA profile is approximately 8*10^15 (8 billiard) times more likely if it originated from the Suspect and two unknown individuals than if it originated from the three unknown individuals. **Database(s) Used:** [Location Identifying Database]
TMDEV4 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** [Participant did not return statistical analysis.] **Database(s) Used:** FBI_EXTENDED_CAUC
TZBZVA - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The LR value calculated for the possible involvement of the male suspect was 3.87E25 to 1, which means it is about 3.87E25 times more likely that the observed DNA profile being a mixture originating from the male suspect 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]
UNVR99 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the questioned stain from victim's pants (Item 4) and suspect. A match between the data obtained from the questioned stain from victim's pants (Item 4) and suspect is approximately 600 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 victim's pants (Item 4) and victim is approximately 2 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 questioned stain from victim's pants (Item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database.

TABLE 8

WebCode-Test	Item 4 Methods & Results
VFHZHA - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** Hypothesis 1 (H1): The evidence originated from Suspect and two unknown, unrelated individuals. Hypothesis 2 (H2): The evidence originated from three unknown, unrelated individuals. The DNA profile obtained from the stain from the victim's pants is approximately 1.6 septillion times more likely if it originated from Suspect and two unknown, unrelated individuals than if it originated from three unknown, unrelated individuals. **Database(s) Used:** NIST revised: African American, Asian, Caucasian, Hispanic.
VK9834 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** H1: The DNA on Item 4 came from suspect and two unknown, unrelated persons. H2: The DNA on Item 4 came from three unknown, unrelated persons. LR= 3.4804E24. H1: The DNA on Item 4 came from victim and two unknown, unrelated persons. H2: The DNA on Item 4 came from three unknown, unrelated persons. LR= 0 **Database(s) Used:** [Location Identifying Database]
W2RLKZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** tem 4.1 (Portion of "Questioned stain from victim's pants"): 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 113 quintillion times more likely if they originated from The Male Suspect 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 Male Suspect is a contributor to the DNA from this item. Based on the likelihood ratio, The Female Victim is excluded as a possible contributor to this DNA profile **Database(s) Used:** NIST 1036 July 2017
WRGKYZ - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 4.1 (Portion of "Questioned stain from victim's pants"): 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 1.02 octillion times more likely if they originated from Male Suspect 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 Male Suspect is a contributor to the DNA from this item. Female Victim is excluded as a possible contributor to the DNA from this item. **Database(s) Used:** NIST 1036 July 2017
WU8M28 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** The DNA profile obtained from the sperm fraction is a mixture. No further conclusions can be drawn due to an insufficient amount of DNA for interpretation. 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 male suspect (2) and two unknown individuals than if it had originated from three unknown, unrelated individuals. Statistical analysis provides very strong support for the inclusion of male suspect (2). Female victim (1) is excluded as a contributor to the DNA profile. **Database(s) Used:** FBI Extended CODIS Core Allele Frequencies- Caucasian, African American, and Southwest Hispanics
X28843 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Item 1 - excluded as a contributor of DNA. Item 2 - greater than 100 billion supporting contribution. **Database(s) Used:** [Location Identifying Database]

TABLE 8

WebCode-Test	Item 4 Methods & Results
YGJ6L9 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Victim (item 1) is excluded with a likelihood ratio of 0. The evidence DNA profile is approximately 56 trillion times more likely if it originated from the suspect (item 2) and 2 unknown individuals than if it originated from 3 unknown individuals. This provides very strong support for inclusion of suspect (item 2). **Database(s) Used:** 2015 FBI Expanded Population Database
YJMUQ3 - 5901	**Method(s)**: Likelihood Ratio **Stats Analysis:** Assuming three contributors, including at least three males, the DNA typing results were interpreted using probabilistic genotyping software. The DNA typing results are 552 sextillion times more likely to be observed if they originated from the Suspect (Item 2), and two unknown, unrelated individuals, rather than if they originated from three unknown, unrelated individuals. This analysis provides very strong support for the proposition that includes the Suspect (Item 2) as one of the contributors to this mixture. The Victim (Item 1) is excluded as a contributor to this mixture. **Database(s) Used:** NIST 1036 (2017)
Z8LUQ4 - 5902	**Method(s)**: Likelihood Ratio **Stats Analysis:** A DNA match was identified between the data obtained from the cutting from the blue fabric (item 4) and the subject. A match between the data obtained from the cutting from the blue fabric (item 4) and the subject is approximately 800 sextillion times more probable than a coincidental match to an unrelated person in the population. A DNA match between the data obtained from the cutting from the blue fabric (item 4) and the victim is approximately 2 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 cutting from the blue fabric (item 4). **Database(s) Used:** The National Institute of Standards and Technology's 1036 Revised U.S. combined population database

Additional Comments

TABLE 9

WebCode-Test	Additional Comments
2QGMC2 - 5902	Two peaks in the second fraction of item 3 (3 sp) were identified as possible elevated stutter; however, neither peak could be confirmed with re-amplification due to lower level data during the re-amp. The peaks are 27.2 at SE33 and 24 at D2S1338.
34G3B3 - 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.
44PDRD - 5901	** Possible Stutter
4BEUJW - 5902	The results obtained and presented in this report were generated following lab procedures, however I am not authorised to report the following in casework: Y Profiling/YSTR testing. I can only determine if a Y quant has been detected. The quality of the DNA may not have been ideal in this test. The DNA results for Item 3 (epithelial/non-sperm fraction) had low levels of DNA (0.005ng/ul), requiring re-amp. In case work, I may have considered taking a second sample, however the very narrow time frame allowed for this test did not allow time for resampling.
77A6RY - 5901	Reported/listed alleles for evidence samples include stutter peaks. Our laboratory does not report DNA concentration or DNA proportions.
786NUZ - 5901	DNA mixture concentration and proportions: DNA mixture proportions are reported as computed by probabilistic genotyping software (EuroForMIX). DNA concentrations (ng/ul) for each contributor is reported as concentration of item obtained by real time PCR analysis multiplied by mixture proportion of that contributor, divided by 100.
8Y8DYV - 5902	PCR amplification procedures were not performed on the second fraction from the "questioned stain...underwear..." (item 3) due to an insufficient amount of DNA detected using the Quantifiler Trio DNA Quantification Kit on the Applied Biosystems 7500 real-time PCR system.
9CLYK9 - 5901	NR=No results. **= Possible elevated stutter.
9MBR8Q - 5901	Item 3 - S#. Resolved contributor (C2) - Designated Unknown Male 1. Resolved contributor (C3) - Item 2 (known suspect).
9WLTTR - 5902	This laboratory truncates likelihood ratios favouring contribution at 100 billion. For reporting purposes any figure greater than is reported as 'greater than 100 billion'.
B7W38V - 5901	Reported/listed alleles for evidence samples include stutter peaks. Our laboratory does not report DNA concentration or proportion.
BDR7Z7 - 5901	DNA concentration for contributor positions is not reported. Reported 99% 1-sided Lower HPD for statistical analysis. Reported lowest HPD of the three databases used. Reported verbal scale endorsed by the Scientific Working Group on DNA Analysis Methods. NID= No Interpretable Data. No LR stat reported for fraction 2 of item 3 (1Af2) due to exclusions for item 1 and item 2. Carry over from f1 fraction (Penta E, D2S1338, D21, D12, and SE33) at 5 markers. Trace contributor (contributor 2) was unsuitable for comparison.
BKHHBU - 5901	Reported/listed alleles for evidence samples include stutter peaks. Our laboratory does not report DNA concentration or proportion.
BNGT8U - 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.
CXYRCQ - 5902	Item 1 was tested using the RapidHIT ID System in accordance with internal approved policies. Note that per internal validated protocol, partial information was obtained at Amelogenin but is approved for use for comparison purposes and at D10S1248 which was marked as inconclusive and not suitable for comparison.

TABLE 9

WebCode-Test	Additional Comments
CY6DP6 - 5901	** = possible elevated stutter
HJX7CN - 5901	Item 4 : we reach to total 4 contributor (inclusive of sperm contributor) based upon the estimate of the DNA proportion concentration percentage.
LHUN3H - 5902	A "partial" profile was obtained for item 1 due to the homozygous allele at D10S1248 being below the stochastic threshold.
P3QH3A - 5901	Please note: DNA Proportions are obtained from the STRmix output file. [Laboratory] does not use the DNA proportions to calculate the DNA concentrations of each contributor.
P8TP7Q - 5901	** = possible elevated stutter.
PD88ZF - 5902	Y-STR DNA profiles of indistinguishable mixtures of two or more individuals are not interpreted per our laboratory procedures.
Q99BQE - 5901	Although the item 4 is supposed to be victim's pants, the genetic profil of the female victim (item 1) is not found in the mixture obtained from item 4. The unknown contributor of item 3 sp is not found in the mixutre of item 4.
UNVR99 - 5902	The second (sperm) faction is inconclusive due to the complexity of the mixture. The mixture weights of two concordant runs did not reflect the data. The data had a major contributor with some minor alleles. Review of the data in TrueAllele showed five alleles at SE33 making it an at least three person mixture. Two concordant runs in TrueAllele had mixture weights of ~52,46,2 and ~50,49,1 which, as stated above, is not reflective of the data. Item 4 was run on the RapidHIT system (twice). The allele at D10S1248 did not meet our stochastic threshold; therefore, it was not used for comparison or statistical calculations.
W2RLKZ - 5901	NR: No results. **: Possible Stutter peak.
WRGKYZ - 5901	** = Possible Elevated Stutter
XCU6U9 - 5902	Inconclusive Y-STR DNA results were obtained from the following item(s). These results are not suitable for comparison purposes due to the poor quality or complexity of the data. Item 1.3F1 - The results are best described as an indistinguishable mixture of 2 male individuals and no assumptions can be made. Item 1.3F2 - The results are best described as an indistinguishable mixture of 2 male individuals and no assumptions can be made. Item 1.4 - The results are best described as a mixture of >2 male individuals.
YJMUQ3 - 5901	The number of contributors could not be determined for the epithelial cell fraction of Item 3 due to low-level results. STRmix deconvolution was not conducted on this sample. ND = Not Detected. All potential alleles considered during deconvolution have been reported.

-End of Report-
(Appendix may follow)

Collaborative Testing Services ~ Forensic Testing Program

Test No. 25-5901: Probabilistic Genotyping

DATA MUST BE SUBMITTED BY **April 14, 2025, 11:59 p.m. EDT** TO BE INCLUDED IN THE REPORT

Participant Code: U1234A WebCode: MCZ9PU

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 sexual assault involving a female victim and male suspect. The victim reported to police that her boyfriend and several of his friends assaulted her when she was drunk. Her boyfriend, the male suspect, has been apprehended by police. The other men have not yet been identified. Police are submitting a stain from the underwear (Item 3) and a stain from the pants (Item 4) the victim was wearing at the time of the assault. 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 victim's underwear (tan)
Item 4: Questioned stain from victim's pants (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	○	○

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)