



2391c: PCR-Based DNA Profiling Standard

National Institute of Standards and Technolog Technology Administration, U.S. Department of Commerc

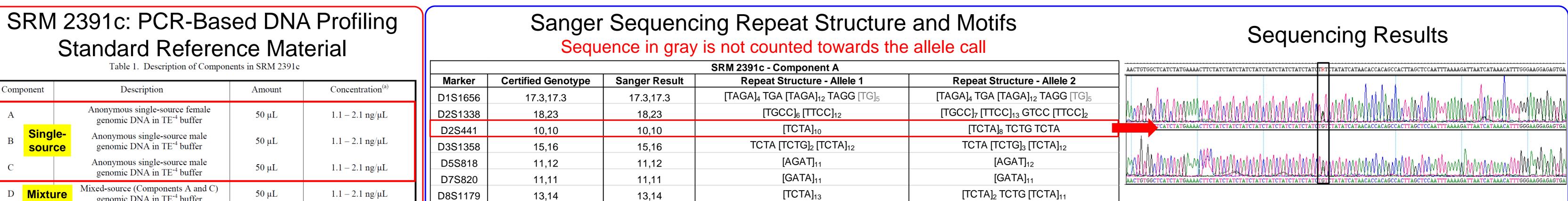


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The NIST Standard Reference Material (SRM) 2391c: PCR-Based DNA Profiling Standard was designed for use in the standardization of forensic and paternity quality assurance procedures for fragment-based typing short tandem repeat (STR) alleles generated by the polymerase chain reaction (PCR). The SRM is intended for law enforcement laboratories, non-clinical research purposes, and for assigning values to in-house control materials. Certified genotypes of the 6 components A-F were assigned for 24 autosomal and 17 Y-STR markers plus Amelogenin using concordance testing between commercial kits. Selected Sanger sequencing characterization was performed for the alleles of 11 STR markers when only one PCR primer set was available for fragment-based typing. Our goal is to characterize the STR loci in components A-C by Sanger sequencing methods for the STR repeat regions and adjacent flanking regions. Core U.S. and European STR autosomal loci were characterized first and will be followed by Y-STRs present in commercial kits, and non-core loci. Additional characterization of the SRM is intended to support the emerging interest in next-generation sequencing technologies for forensic typing applications. Sanger methods have characterized underlying polymorphisms (sequence, insertion-deletion, variation in complex motifs) typically not detected by fragment-based typing. The sequenced regions include the commercial or known PCR binding sites commonly implemented in fragment-based typing.



D	Mixture	genomic DNA in TE ⁻⁴ buffer	50 µL	$1.1 - 2.1 \text{ ng/}\mu\text{L}$
E	Stain	Anonymous single-source female cells spotted on 903 paper	Two 6 mm punches	7.5×10^4 cells per punch
F	Stain	Anonymous single-source male cells spotted on FTA paper	Two 6 mm punches	7.5×10^4 cells per punch

^(a)DNA concentrations and cell counts are nominal values and are not intended for use as quantitative standards.

https://www-s.nist.gov/srmors/view_cert.cfm?srm=2391C

Certified Values

- A NIST certified value is a value for which NIST has the highest confidence in its accuracy in that all known or suspected sources of bias have been investigated or taken into account.
- Below are 41 STR markers plus Amelogenin that have certified genotypes assigned by electrophoretic match to previously sequenced alleles (30) or by direct sequencing (11).
- The remaining 30 markers were Sanger sequenced for Components A-C to further characterize the repeat structure and flanking sequence.

Concordance	with STR Kits	DNA Sequencin	g of Alleles	
Autosomal STR Loc	Y-STR Loci	Autosomal STR Loci	Y-STR Loci	
D2S1338	DYS19	D1S1656	DYS448	
D2S441	DYS385a	D8S1115	DYS456	
D3S1358	DYS385b	D12S391	DYS458	
D5S818	DYS389I			
D7S820	DYS389II	Penta D	DYS635	
D8S1179	DYS390	Penta E	DY-GATA-H4	
D10S1248	DYS391	SE33		
D13S317	DYS392	The genotypes for 41 STR Ma	rkere i Amelegenin s	
D16S539	DYS393	certified; 26% were previous	-	
D18S51	DYS437			
D19S433	DYS438			
D21S11	DYS439			
D22S1045	*Amelogenin		STANDARD REFERENCE MATERIAL®	
CSF1PO			PCR-Based DNA Profiling Standard Components A - P	
FGA			National Institute of Standards and Technology	
TH01 >2	STR Kits were teste	d for concordance	and and a second	
ΤΡΟΧ		Thent &	tent A tent D	
vWA				

1	D8S1179	13,14	13,14	[TCTA] ₁₃	[TCTA] ₂ TCTG [TCTA] ₁₁				
	D8S1179		,	[ATT] ₁₅	[ATT] ₁₆	D2S441, Component A , is a homozygous sample with a (10,10) genotype. This is an unusual example of where each			
	D10S1248	15,16	15,16 15,16	[GGAA] ₁₅	[GGAA] ₁₆				
	D1031248	15,16 18.3,22	18.3,22	AGAT GAT[AGAT] ₉ [AGAC] ₇ AGAT	[AGAT] ₁₃ [AGAC] ₈ AGAT	(10,10) genotype. This is an unusual example of where each			
]	D13S317	8,8	8,8	[TATC] ₈	[TATC] ₈	allele in a homozygote has a different repeat structure. One			
	D16S539	10,11	10,11	[GATA] ₁₀	[GATA] ₁₁	allele has a simple repeat of [TATG] ₁₀ and the other has an			
	D18S51	12,15	12,15	[AGAA] ₁₂	[AGAA] ₁₅	$A \rightarrow G$ SNP, causing the repeat structure to be [TCTA] ₈ TCTG			
	D19S433	13,14	13,14	[AAGG] AAAG [AAGG] TAGG [AAGG] ₁₁	[AAGG] AAAG [AAGG] TAGG [AAGG] ₁₂				ause of the mixture of the A and G
				[TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA	[TCTA] ₅ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA		•		cating that one allele has the A and
	D21S11	28,32.2	28,32.2	[TCTA] ₂ TCCATA} [TCTA] ₁₀	[TCTA] ₂ TCCATA} [TCTA] ₁₂ TA TCTA	the other	r has the G.		
	D22S1045	15,15	15,15	[ATT] ₁₂ ACT [ATT] ₂	[ATT] ₁₂ ACT [ATT] ₂	-	No		anaat Matifa*
	CSF1PO	10,10	10,10			-	INU		epeat Motifs*
	FGA Penta D	21,23 9,13	21,23 9,13	$[TTTC]_3$ TTTT TTCT $[CTTT]_{13}$ CTCC $[TTCC]_2$ [AAAGA] ₉	$[TTTC]_{3} TTTT TTCT [CTTT]_{15} CTCC [TTCC]_{2}$ $[AAAGA]_{13}$	Marker	Component	Allele	Allele Repeat Structure
	Penta E	5,10	9,13 5,10	[AAAGA] ₅	[AAAGA] ₁₀	D8S1179	С	17	[TCTA] ₂ TCTG [TCTA] ₁₄
		0,10	0,10	[AAAG] ₂ AG [AAAG] ₃ AG [AAAG]₁₆ G [AAAG] ₃	[AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₁₈ G	D12S391	A	22	[AGAT] ₁₃ [AGAC] ₈ AGAT
	SE33	16,18	16,18	AG	[AAAG] ₃ AG	D12S391	С	19	[AGAT] ₁₃ [AGAC]₅ AGAT
	TH01	8,9.3	8,9.3	[AATG] ₈	[AATG] ₆ ATG [AATG] ₃	D12S391	С	23	[AGAT] ₁₂ [AGAC] ₁₀ AGAT
	TPOX	8,8	8,8	[AATG] ₈	[AATG] ₈				
	vWA	18,19	18,19	TCTA [TCTG] ₄ [TCTA] ₁₃	TCTA [TCTG] ₄ [TCTA] ₁₄	D21S11	В	32	[TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA
				SRM 2391c - Component B					[TCTA] ₂ TCCATA} [TCTA] ₁₄
	Marker	Certified Genotype	Sanger Result	Repeat Structure - Allele 1	Repeat Structure - Allele 2	-			
	D1S1656	11,14	11,14	[TAGA] ₁₁ [TG] ₅	[TAGA] ₁₄ [TG] ₅	SE33	С	31.2	[AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉
	D2S1338 D2S441	17,17 10,14	17,17	[TGCC] ₆ [TTCC] ₁₁ [TCTA] ₁₀	[TGCC] ₆ [TTCC] ₁₁ [TCTA] ₁₁ TTTA [TCTA] ₂			-	AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG
	D3S1358	15,19	15,19	TCTA [TCTG] ₃ [TCTA] ₁₁	TCTA [TCTG] ₃ [TCTA] ₁₅	DYS389II	В	31	[TCTG] ₆ [TCTA] ₁₂ [TCTG] ₃ [TCTA] ₁₀
	D5S818	12,13	12,13	[AGAT] ₁₂	[AGAT] ₁₃	DYS458	B	17.2	[GAAA] ₁₅ AA [GAAA] ₂
	D7S820	10,10	10,10	[GATA] ₁₀	[GATA] ₁₀	DYS635	B	20	[TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₀
	D8S1179	10,13	10,13	[TCTA] ₁₀	[TCTA] ₁₃	DYS635	C	20	$[TCTA]_4 [TGTA]_2 [TCTA]_2 [TGTA]_2 [TCTA]_{11}$
	D8S1115	15,17	15,17	[ATT] ₁₅	[ATT] ₁₇	L			
	D10S1248	13,13	13,13	[GGAA] ₁₃	[GGAA] ₁₃	· ·			ere not listed in Butler J.M. (2012)
	D12S391 D13S317	19,24 9,12	19,24 9,12	[AGAT] ₁₂ [AGAC] ₆ AGAT [TATC] ₉	[AGAT] ₁₅ [AGAC] ₈ AGAT [TATC] ₁₂	or STRB	ase fact she	eets	
	D135317	9,12	9,12	[GATA] ₁₀	[TATC] ₁₂ [GATA] ₁₃	-1			
	D18S51	13,16	13,16	[AGAA] ₁₃	[AGAA] ₁₆	Sinale	e Nucleo	otide	Polymorphisms (SNPs)
	D19S433	16,16.2	16,16.2	[AAGG] AAAG [AAGG] TAGG [AAGG] ₁₄	[AAGG] AA [AAGG] TAGG [AAGG] ₁₅	Ŭ			
				[TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA	[TCTA] ₅ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA			vehe	at Flanking Regions
	D21S11	32,32.2	32,32.2	[TCTA] ₂ TCCATA} [TCTA] ₁₄	[TCTA] ₂ TCCATA} [TCTA] ₁₂ TA TCTA	Marker C	Component	Allele	Flanking Region Variants
	D22S1045	15,17	15,17			D5S818	A	12	$T \rightarrow C \ 13 \ bp \ us \ of \ the \ repeat$
	CSF1PO	10,11	10,11			D5S818	B	13	$T \rightarrow C$ 13 bp us of the repeat
	FGA	20,23	20,23	$[TTTC]_{3} TTTT TTCT [CTTT]_{12} CTCC [TTCC]_{2}$ $[AAAGA]_{8}$	$[TTTC]_{3} TTTT TTCT [CTTT]_{15} CTCC [TTCC]_{2}$ $[AAAGA]_{12}$	D5S818	B C	13 10	$G \rightarrow T 4$ bp ds of the repeat T $\rightarrow C 13$ bp us of the repeat
	Penta D Penta E	8,12 7,15	8,12 7,15	[AAAGA] ₇	[AAAGA] ₁₂	D5S818	C	11	$T \rightarrow C 13$ bp us of the repeat
		7,10	7,10		[AAAG] ₂ AG [AAAG] ₃ AG [AAAG]₁₈ G [AAAG] ₃	D7S820	С	10	$T \rightarrow G 65 bp ds of the repeat$
	SE33	17,18	17,18	AG	AG	D13S317	C	11	$A \rightarrow C$ 115 bp ds of the repeat
	TH01	6,9.3	6,9.3	[AATG] ₆	[AATG] ₆ ATG [AATG] ₃	D16S539	A	10 10	$A \rightarrow C$ 16 bp ds of the repeat $C \rightarrow A$ 95 bp us of the repeat
	TPOX	8,11	8,11	[AATG] ₈	[AATG] ₁₁	D16S539	A	11	$C \rightarrow A 95$ bp us of the repeat
	VWA	17,18	17,18	$\frac{\text{TCTA} [\text{TCTG}]_4 [\text{TCTA}]_{12}}{\text{TTACAL} \text{TACAL}}$	TCTA [TCTG] ₄ [TCTA] ₁₃	D16S539	B	10	$C \rightarrow A 95$ bp us of the repeat
	DYS19	14	14	[TAGA] ₃ TAGG [TAGA] ₁₁		D16S539 Penta E	C A	10 10	$C \rightarrow A 95$ bp us of the repeat G $\rightarrow A 123$ bp us of the repeat
	DYS385a	13 17	13 17	[GAAA] ₁₃ [GAAA] ₁₇		Penta E	A	10	$A \rightarrow G$ 268 bp us of the repeat
	DYS385b DYS389I	17	17	[TCTG] ₃ [TCTA] ₁₀		Penta E	A	10	$A \rightarrow C$ 280 bp us of the repeat
	DYS389II	31	31	[TCTG] ₆ [TCTA] ₁₂ [TCTG] ₃ [TCTA] ₁₀		Penta E	В	7	$G \rightarrow A 123$ bp us of the repeat
	DYS390	23	23	[TCTG] ₈ [TCTA] ₁₀ TCTG [TCTA] ₄		Penta E Penta E	B	7	$A \rightarrow G$ 268 bp us of the repeat $A \rightarrow C$ 280 bp us of the repeat
	DYS391	10	10	[TCTA] ₁₀		Penta E	B	15	$G \rightarrow A$ 123 bp us of the repeat
	DYS392	11	11	[TAT] ₁₁		Penta E	В	15	$A \rightarrow G$ 268 bp us of the repeat
	DYS393	12	12	[AGAT] ₁₂		Penta E	B	15	$A \rightarrow C 280$ bp us of the repeat
	DYS393 DYS437 DYS438	12 14 10	12 To Be Determined To Be Determined	[AGAT] ₁₂ To Be Determined To Be Determined		TPOX	A	8	$T \rightarrow G$ 148 bp ds of the repeat
	DYS437	14	To Be Determined	To Be Determined		TPOX TPOX	A B	8 8	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat
	DYS437 DYS438	14 10	To Be Determined To Be Determined	To Be Determined To Be Determined		TPOX TPOX Abbreviati	A B ions: bp = b	8 8 ase pair	T \rightarrow G 148 bp ds of the repeat T \rightarrow G 148 bp ds of the repeat T \rightarrow G 148 bp ds of the repeat rs, us = upstream, ds = downstream
	DYS437 DYS438 DYS439	14 10 11	To Be Determined To Be Determined 11	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅		TPOX TPOX Abbreviati Multiple	A B ions: bp = b SNPs were	8 8 ase pair found i	T \rightarrow G 148 bp ds of the repeat T \rightarrow G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS458	14 10 11 20 15 17.2	To Be Determined To Be Determined 11 20 15 17.2	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂		TPOX TPOX Abbreviati Multiple flanking	A B ions: bp = b SNPs were regions. P	8 8 ase pair found i rimers th	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS458 DYS635	14 10 11 20 15 17.2 20	To Be Determined To Be Determined 11 20 15 17.2 20	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀		TPOX TPOX Abbreviati Multiple flanking alleles w	A B ions: bp = b SNPs were regions. P /hen STR ty	8 8 ase pair found i rimers th /ping. N	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat nat bind on SNPs can result in null Note that the variants characterized
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS458	14 10 11 20 15 17.2	To Be Determined To Be Determined 11 20 15 17.2	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂		TPOX TPOX Abbreviati Multiple flanking alleles w in this w	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co	8 ase pair found i rimers th /ping. N nstraine	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat hat bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS458 DYS635 YGATA H4	14 10 11 20 15 17.2 20 11	To Be Determined To Be Determined 11 20 15 17.2 20 11	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C		TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co n generated	8 ase pair found i rimers th ping. N nstraine (Kline e	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat hat bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011).
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS635 YGATA H4 Marker	14 10 11 20 15 17.2 20 11 Certified Genotype	To Be Determined To Be Determined 11 20 15 17.2 20 11 Sanger Result	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1	Repeat Structure - Allele 2	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co n generated	8 ase pair found i rimers th ping. N nstraine (Kline e	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat hat bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS635 OYS635 YGATA H4 Marker D1S1656	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15	To Be Determined To Be Determined 11 20 15 17.2 20 11	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅	[TAGA] ₁₄ TAGG [TG] ₅	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co n generated	8 ase pair found i rimers th ping. N nstraine (Kline e	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat hat bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011).
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS635 YGATA H4 Marker	14 10 11 20 15 17.2 20 11 Certified Genotype	To Be Determined To Be Determined 11 20 15 17.2 20 11 Sanger Result	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1	•	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co n generated	8 ase pair found i rimers th ping. N nstraine (Kline e	T->G 148 bp ds of the repeat T->G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized of by the size of the original PCR et al. 2011).
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS635 YGATA H4 Marker D1S1656 D2S1338	14 10 11 20 15 17.2 20 11 20 11 Certified Genotype 11,15 19,19	To Be Determined To Be Determined 11 20 15 17.2 20 11	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co n generated	8 ase pair found i rimers th ping. N nstraine (Kline e	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat Ts, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized of by the size of the original PCR et al. 2011).
	DYS437 DYS438 DYS439 DYS448 DYS456 DYS635 DYS635 DYS635 C DYS635 D DYS635 C D D S S 3 C D S S 3 C C S S 3 C C S S 3 S 3 S S 3 S S S S	14 10 11 20 15 17.2 20 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11	To Be Determined To Be Determined 11 20 15 17.2 20 11 20 11 20 11 10,10 16,18 10,11	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N_{42} [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TGCA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co n generated	8 ase pair found i rimers th ping. N nstraine (Kline e	T->G 148 bp ds of the repeat T->G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized of by the size of the original PCR et al. 2011).
	DYS437 DYS438 DYS439 DYS439 DYS448 DYS456 DYS458 DYS635 YGATA H4 D1S1656 D2S1338 D2S441 D3S1358 D5S818 D7S820	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11 10,12	To Be Determined 11 20 15 17.2 20 11 20 11 20 11 10,10 16,18 10,11 10,12	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N_{42} [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co n generated	8 ase pair found i rimers th ping. N nstraine (Kline e	T->G 148 bp ds of the repeat T->G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized of by the size of the original PCR et al. 2011).
	DYS437 DYS438 DYS439 DYS439 DYS448 DYS456 DYS635 YGATA H4 D1S1656 D2S1338 D2S441 D3S1358 D7S820 D8S1179	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11 10,12 10,17	To Be Determined 11 20 15 17.2 20 11 20 11 20 11 20 11 10,10 16,18 10,11 10,12 10,17	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [TCTA] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. Pr /hen STR ty /ork are constructed	8 8 ase pair found i rimers th ping. N nstraine (Kline e	T->G 148 bp ds of the repeat T->G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized of by the size of the original PCR et al. 2011).
	DYS437 DYS438 DYS439 DYS439 DYS448 DYS456 DYS458 DYS635 YGATA H4 D1S1656 D2S1338 D2S441 D3S1358 D7S820 D8S1179 D8S1115	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9	To Be Determined 11 20 15 17.2 20 11 20 11 20 11 20 11,15 10,10 16,18 10,11 10,12 9,9	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N_{42} [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. Pr /hen STR ty /ork are constructed	8 8 ase pair found i rimers th ping. N nstraine (Kline e	T->G 148 bp ds of the repeat T->G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat hat bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011). TATCTATCTATC
	DYS437 DYS438 DYS439 DYS439 DYS448 DYS456 DYS635 YGATA H4 D1S1656 D2S1338 D2S441 D3S1358 D7S820 D8S1179	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11 10,12 10,17	To Be Determined 11 20 15 17.2 20 11 20 11 20 11 20 11 10,10 16,18 10,11 10,12 10,17	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [TCTA] ₁₀ [TCTA] ₁₀ [AGAT] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon	A B ions: bp = b SNPs were regions. Pr /hen STR ty /ork are constructed	8 8 ase pair found i rimers th ping. N nstraine (Kline e	T->G 148 bp ds of the repeat T->G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat hat bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011). TATCTATCTATC
S	DYS437 DYS438 DYS439 DYS439 DYS448 DYS456 DYS635 DYS635 YGATA H4 D1S1656 D2S1338 D2S441 D3S1358 D7S820 D8S1179 D8S1175 D10S1248	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16	To Be Determined 11 20 15 17.2 20 11 Sanger Result 11,15 19,19 10,10 16,18 10,11 10,12 9,9 12,16	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GGAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC	A B ions: bp = b SNPs were regions. Pr /hen STR ty /ork are conducted	8 8 ase pair found i rimers th ping. N nstraine (Kline e TATCTATCTATCTAT	T->G 148 bp ds of the repeat T->G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat hat bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011). TATCTATCTATC
S	DYS437 DYS438 DYS439 DYS439 DYS448 DYS456 DYS635 DYS635 YGATA H4 D2S1338 D2S441 D3S1358 D7S820 D8S1179 D8S1179 D10S1248 D13S3317 D10S1248 D13S3317	14 10 11 20 15 17.2 20 11 11 10,12 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10	To Be Determined 11 20 15 17.2 20 11 Sanger Result 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GGAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC			T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011).
S	DYS437DYS438DYS438DYS439DYS448DYS456DYS635DYS635YGATA H4D1S1656D2S1338D2S441D3S1358D3S1358D7S820D8S1179D8S1115D10S1248D13S3317D16S539D18S51	14 10 11 20 15 17.2 20 11 11 10,12 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19	To Be Determined 11 20 15 17.2 20 11 Sanger Result 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ NA [GAAA] ₂ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GGAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAT] ₁₀ [GATA] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC			T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011). TATUTATUTATCTATC
S	DYS437 DYS438 DYS439 DYS439 DYS448 DYS456 DYS635 DYS635 YGATA H4 D2S1338 D2S441 D3S1358 D7S820 D8S1179 D8S1179 D10S1248 D13S3317 D10S1248 D13S3317	14 10 11 20 15 17.2 20 11 11 10,12 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10	To Be Determined 11 20 15 17.2 20 11 Sanger Result 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GGAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₆ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄				T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011). TATCTATCTATC
S	DYS437DYS438DYS438DYS439DYS448DYS456DYS635DYS635YGATA H4D1S1656D2S1338D2S441D3S1358D3S1358D7S820D8S1179D8S1115D10S1248D13S3317D16S539D18S51	14 10 11 20 15 17.2 20 11 11 10,12 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13,2,15,2	To Be Determined 11 20 15 17.2 20 11 Sanger Result 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19 13.2,15.2	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ NA [GAAA] ₂ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GGAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAT] ₁₀ [GATA] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉				T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011). TATCTATCTATCT CTATCTATCT CTATCTATCT
S	DYS437DYS438DYS438DYS439DYS448DYS456DYS635YGATA H4D1S1656D2S1338D2S441D3S1358D3S1358D7S820D8S1179D8S1179D10S1248D13S3317D16S5391D18S51D19S433	14 10 11 20 15 17.2 20 11 11 10,12 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19	To Be Determined 11 20 15 17.2 20 11 Sanger Result 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GAAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₆ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₆ [TCTG] ₅ {[TCTA] ₃ TA [TCTA] ₃ TCA		A B ions: bp = b SNPs were regions. P /hen STR ty /ork are connected Interaction Inter		T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat TS, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011).
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S	DYS437DYS438DYS439DYS439DYS458DYS635YGATA H4D1S1656D2S1338D2S441D3S1358D7S820D8S1179D8S1179D10S1248D13S3317D13S3317D13S317	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2	To Be Determined 11 20 15 17.2 20 11 20 11.2 20 11. 20 11.2 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 11. 11. 11. 11. 11.15 19,19 10,10 16,18 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19 13.2,15.2 29,30 16,16	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GGAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₆ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTTC] ₃ TTTT TTCT [CTTT] ₁₆ CTCC [TTCC] ₂	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [ATT] ₉ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₆ [TCTG] ₅ {[TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) G [TATC] ₁₂ located	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co generated TGTATTTACAAATACATTATC // // // // // // // // // // // // //	8 8 ase pair found i rimers th ping. N nstraine (Kline e TATCTATCTATCTAT	T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat rs, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null Note that the variants characterized d by the size of the original PCR et al. 2011). TATUTATUTATC
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S	DYS437DYS438DYS439DYS439DYS448DYS456DYS635YGATAH4D1S1656D2S1338D2S441D3S1358D7S818D7S820D8S1179D10S1248D13S3317D13S317D13S317D13S317Panta DD13S317D13S317PD13S317PD13S317PD13S317PD13S317PD13S317PD13S317PD13S317PD13S317PD13S317PD13S317PP<	14 10 11 20 15 17.2 20 11 11 Certified Genotype 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13,2,15,2 29,30 16,16 10,12 24,26 10,12 24,26 10,11 12,13 28,2,31,2 6,8 11,11 12,13	To Be Determined 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 10.10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19 13.2,15.2 29,30 16,16 To Be Determined 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 11,11 16,18 11,11	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391C - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [GATA] ₁₀ [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₆ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTTC] ₃ TTTT TTCT [CTTT] ₁₆ CTCC [TTCC] ₂ [AAAG] ₁₀ [AAAG] ₁₀ [AAAG] ₁₂ [AAAG] ₁₂ [AAAG] ₁₂ [AAAG] ₁₂ [AAAG] ₁₂ [AAAG] ₁₂ [AAAG] ₁₀ AAAAAG [AAAG] ₁₇ G AAGG[AAG] ₁₀ AAAAAG [AAAG] ₁₇ G AAGG[AAAG] ₁₀ AAAAAG [AAAG] ₁₇ G AAGG[AAAG] ₁₀ AAAAAG	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₂ TCCATA] [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂ [AAAGA] ₁₁ [AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈ [AATG] ₈	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC] ₁₂ located most, if STR typi	A B ions: bp = b SNPs were regions. Provenses of the strategions. Provenses of the strategions of the strategion of the	8 8 ase pair found i rimers th ping. N nstraine (Kline e (Kline e (Kline e ATCTATCTATCTAT	T→G 148 bp ds of the repeat T→G 148 bp ds of the repeat TS, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null obte that the variants characterized d by the size of the original PCR et al. 2011).
	DYS437DYS438DYS439DYS448DYS456DYS635DYS635DYS635D1S1656D2S1338D2S441D3S1358D7S820D8S1179D8S1179D13S3317D13S3317D13S33D13S33 <td< td=""><td>14 10 11 20 15 17.2 20 11 11 10 10 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28,2,31,2 6,8 11,11 12,13</td><td>To Be Determined 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 10.10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19 13.2,15.2 29,30 16,16 To Be Determined 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13 </td><td>To Be Determined To Be Determined [AGAT]₁₁ [AGAGAT]₁₂ N₄₂ [AGAGAT]₈ [AGAA]₁₅ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TCTA]₂ [TCTA]₁₀ [TAGA]₁₁ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₂ [AGAT]₁₀ [GATA]₁₀ [GAA]₁₂ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTG]₆ {[TCTA]₃ TA [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [AAGG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTG]₈ {[TCTA]₃ TA [TCTA]₃ TCA [TCTA]₄ [TCTG]₆ {[TCTA]₃ TA [TCTA]₁₁ [AAGG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTG]₆ {[TCCA]₁₂ [AAAGA]₁₀</td><td>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</td><td>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC</td><td>A B ions: bp = b SNPs were regions. Pr /hen STR ty /ork are co generated </td><td>8 8 ase pair found i rimers th ping. N nstraine (Kline e Interaction (Kline e Interaction Active and Active and Stream the prime the prime component ference</td><td>T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat</td></td<>	14 10 11 20 15 17.2 20 11 11 10 10 11,15 19,19 10,10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28,2,31,2 6,8 11,11 12,13	To Be Determined 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 10.10 16,18 10,11 10,12 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19 13.2,15.2 29,30 16,16 To Be Determined 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTG] ₈ {[TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₁₁ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTG] ₆ {[TCCA] ₁₂ [AAAGA] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₂ TCCATA] [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂ [AAAGA] ₁₁ [AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈ [AATG] ₈	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC	A B ions: bp = b SNPs were regions. Pr /hen STR ty /ork are co generated 	8 8 ase pair found i rimers th ping. N nstraine (Kline e Interaction (Kline e Interaction Active and Active and Stream the prime the prime component ference	T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat
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P /hen STR ty /ork are co generated </td><td>8 8 ase pair found i rimers th /ping. N nstraine (Kline e Interactate (Kline e Interactate Active Ac</td><td>T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat Ts, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null vote that the variants characterized d by the size of the original PCR at al. 2011). TATCATCTATE </td></t<></td>	14 10 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 10.12 10,10 16,18 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13 15 12 27 24 11 13 15 12 27 <	To Be Determined 11 20 15 17.2 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12. 13. 15. 12. <t< td=""><td>To Be Determined To Be Determined [AGAT]₁₁ [AGAGAT]₁₂ N₄₂ [AGAGAT]₈ [AGAT]₁₅ [GAAA]₁₅ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TGTA]₂ [TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₈ [TCTA]₁₂ [AGAT]₁₀ [GATA]₁₀ [GAAA]₁₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GAAA]₁₆ [AGAT]₁₀ [AGAT]₁₀ [GAAA]₁₆ [GAAA]₁₆ [GAAA]₁₆ [GAAA]₁₆ [GAAA]₁₆ [AGAT]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₆ [AAAG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTA]₅ [TCTA]₃ TA [TCTA]₃ TCA [TCTA]₄ [TCTG]₆ [TCTA]₃ TA [TCTA]₁₁ [AAAG] AG [AAAG]₃ AG [AAAG]₁₀ [AAAG] AG [AAAG]₃ AG [AAAG]₁₀</td><td>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</td><td>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC ACCCATCTAACGCCTATC ACCCATCTAACGCCTATC ACCCCATCTAACGCCTATC D13S317 (11,11) g [TATC]₁₂ located most, if STR typi • Seque STR typi</td><td>A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co generated </td><td>8 8 ase pair found i rimers th /ping. N nstraine (Kline e Interactate (Kline e Interactate Active Ac</td><td>T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat Ts, us = upstream, ds = downstream In the DNA sequence in the repeat that bind on SNPs can result in null vote that the variants characterized d by the size of the original PCR at al. 2011). TATCATCTATE </td></t<>	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₈ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GAAA] ₁₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GAAA] ₁₆ [AGAT] ₁₀ [AGAT] ₁₀ [GAAA] ₁₆ [GAAA] ₁₆ [GAAA] ₁₆ [GAAA] ₁₆ [GAAA] ₁₆ [AGAT] ₁₀ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₆ [AAAG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTA] ₅ [TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₄ [TCTG] ₆ [TCTA] ₃ TA [TCTA] ₁₁ [AAAG] AG [AAAG] ₃ AG [AAAG] ₁₀ [AAAG] AG [AAAG] ₃ AG [AAAG] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₂ TCCATA] [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂ [AAAGA] ₁₁ [AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈ [AATG] ₈	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC ACCCATCTAACGCCTATC ACCCATCTAACGCCTATC ACCCCATCTAACGCCTATC D13S317 (11,11) g [TATC] ₁₂ located most, if STR typi • Seque STR typi	A B ions: bp = b SNPs were regions. 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S N	DYS437DYS438DYS438DYS438DYS458DYS635YGATA H4D1S635D2S1338D2S441D3S1358D7S820D8S1179D18S1179D18S1179D18S1179D13S337D13S317D13S331D13S333D13S385D13S385D13S385D13S385D13S385D13S383D13S38D13S38D13S38D13S38D13S38D13S38D13S38D13S38D13S38D13S38D13S38	14 10 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 10.12 10,10 16,18 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13 15 12 27 24 11 13 13 14 15 12 <td< td=""><td>To Be Determined 11 20 15 17.2 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12. 23. 24. <t< td=""><td>To Be Determined To Be Determined [AGAT]₁₁ [AGAGAT]₁₂ N₄₂ [AGAGAT]₈ [AGAA]₁₅ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TGTA]₂ [TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TGCA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₂ [AGAT]₁₀ [GATA]₁₀ [GATA]₁₀ [GAAA]₁₂ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GAAA]₁₆ [AAGG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTA]₆ [TCTA]₃ TA [TCTA]₃ TCA [TCTA]₄ [TCTG]₆ [AGAG]₁₀ [AAAGA]₁₀</td><td>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</td><td>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC]₁₂ located most, if STR typi • Seque STR typi • Seque STR n mixtur • Once Analys • This w seque</td><td>A B ions: bp = b SNPs were regions. 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Delete, the SRM 2391c Certificate of with this new information. gh throughput next generation</td></t<></td></td<>	To Be Determined 11 20 15 17.2 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12. 23. 24. <t< td=""><td>To Be Determined To Be Determined [AGAT]₁₁ [AGAGAT]₁₂ N₄₂ [AGAGAT]₈ [AGAA]₁₅ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TGTA]₂ [TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TGCA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₂ [AGAT]₁₀ [GATA]₁₀ [GATA]₁₀ [GAAA]₁₂ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GAAA]₁₆ [AAGG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTA]₆ [TCTA]₃ TA [TCTA]₃ TCA [TCTA]₄ [TCTG]₆ [AGAG]₁₀ [AAAGA]₁₀</td><td>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</td><td>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC]₁₂ located most, if STR typi • Seque STR typi • Seque STR n mixtur • Once Analys • This w seque</td><td>A B ions: bp = b SNPs were regions. 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Delete, the SRM 2391c Certificate of with this new information. gh throughput next generation</td></t<></td>	14 10 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 10.12 10,10 16,18 10,12 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13 15 12 27 24 11 13 15 12 27 <	To Be Determined 11 20 15 17.2 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12. 13. 15. <t< td=""><td>To Be Determined To Be Determined [AGAT]₁₁ [AGAGAT]₁₂ N₄₂ [AGAGAT]₈ [AGAT]₁₅ [GAAA]₁₅ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TGTA]₂ [TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₈ [TCTA]₁₂ [AGAT]₁₀ [GATA]₁₀ [GAAA]₁₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GAAA]₁₆ [AGAT]₁₀ [AGAT]₁₀ [GAAA]₁₆ [GAAA]₁₆ [GAAA]₁₆ [GAAA]₁₆ [GAAA]₁₆ [AGAT]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₆ [AAAG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTA]₅ [TCTA]₃ TA [TCTA]₃ TCA [TCTA]₄ [TCTG]₆ [TCTA]₃ TA [TCTA]₁₁ [AAAG] AG [AAAG]₃ AG [AAAG]₁₀ [AAAG] AG [AAAG]₃ AG [AAAG]₁₀</td><td>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</td><td>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC]₁₂ located most, if STR typi • Seque STR n mixtur • Once Analys • This w seque applic</td><td>A B ions: bp = b SNPs were regions. 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Delete, the SRM 2391c Certificate of with this new information. gh throughput next generation</td></t<>	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₈ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GAAA] ₁₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GAAA] ₁₆ [AGAT] ₁₀ [AGAT] ₁₀ [GAAA] ₁₆ [GAAA] ₁₆ [GAAA] ₁₆ [GAAA] ₁₆ [GAAA] ₁₆ [AGAT] ₁₀ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₆ [AAAG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTA] ₅ [TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₄ [TCTG] ₆ [TCTA] ₃ TA [TCTA] ₁₁ [AAAG] AG [AAAG] ₃ AG [AAAG] ₁₀ [AAAG] AG [AAAG] ₃ AG [AAAG] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₂ TCCATA] [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂ [AAAGA] ₁₁ [AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈ [AATG] ₈	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC] ₁₂ located most, if STR typi • Seque STR n mixtur • Once Analys • This w seque applic	A B ions: bp = b SNPs were regions. 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S 1 2 2 2 2	DYS437DYS438DYS438DYS458DYS635DYS635YGATA H4D1S1656D2S1338D2S441D3S1358D7S820D8S1179D8S1179D13S317D13S331D13S331D13S33D13S333<	14 10 11 20 15 17.2 20 11 20 11 20 11 20 11 20 11 20 11 10.12 10,10 16,18 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13 15 12 27 24 11 13 16 11 13 16 11 12 </td <td>To Be Determined 11 20 15 17.2 20 17.2 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12.12 13. 14. 15. 12. 13. 13.</td> <td>To Be Determined To Be Determined [AGAT]₁₁ [AGAA]₁₅ AA [GAAA]₂ [[TCTA]₄ [[TGTA]₂ [[TCTA]₂ [[TCTA]₁₀ [TAGA]₁₅ AA [GAAA]₂ [[TCTA]₄ [[TGTA]₂ [[TCTA]₂ [[TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₂ [AGAT]₁₀ [GATA]₁₀ [GATA]₁₀ [GATA]₁₀ [GATA]₁₂ [AGAT]₁₃ [AGAC]₅ AGAT [TACA]₁₂ [GAA]₁₂ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAG] AA [AAGG] TAGG [AAGG]₁₂ [[TCTA]₄ [TCTG]₆ [TCTA]₃ TA [TCTA]₃ TCA [TCTA]₄ [TCTG]₆ [TCTA]₃ TA [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [AAGAG]₁₀ [AAAG]₁₀ [AAAG]₁₀ [AAAGA]₁₀ [AAAG]₁₇ G AAGG[AAAG]₁₀ [AAAAAG [AAAG]₁₇ G AAGG[AAAG]₁₂</td> <td>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</td> <td>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC</td> <td>A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co generated retrattacattacattace // hen STR ty /ork are co generated // hen STR ty /ork are co /ork are co /ork are co /ork are co /or aise all ref /or aise all ref /or</td> <td>8 ase pair found i rimers th /ping. N nstraine (Kline e Interactate Interactate</td> <td>T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat TS, US = Upstream, ds = downstream In the DNA sequence in the repeat hat bind on SNPs can result in null lote that the variants characterized d by the size of the original PCR et al. 2011).</td>	To Be Determined 11 20 15 17.2 20 17.2 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12.12 13. 14. 15. 12. 13. 13.	To Be Determined To Be Determined [AGAT] ₁₁ [AGAA] ₁₅ AA [GAAA] ₂ [[TCTA] ₄ [[TGTA] ₂ [[TCTA] ₂ [[TCTA] ₁₀ [TAGA] ₁₅ AA [GAAA] ₂ [[TCTA] ₄ [[TGTA] ₂ [[TCTA] ₂ [[TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TACA] ₁₂ [GAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAG] AA [AAGG] TAGG [AAGG] ₁₂ [[TCTA] ₄ [TCTG] ₆ [TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₄ [TCTG] ₆ [TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [AAGAG] ₁₀ [AAAG] ₁₀ [AAAG] ₁₀ [AAAGA] ₁₀ [AAAG] ₁₇ G AAGG[AAAG] ₁₀ [AAAAAG [AAAG] ₁₇ G AAGG[AAAG] ₁₂	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₂ TCCATA] [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂ [AAAGA] ₁₁ [AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈ [AATG] ₈	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC	A B ions: bp = b SNPs were regions. P /hen STR ty /ork are co generated retrattacattacattace // hen STR ty /ork are co generated // hen STR ty /ork are co /ork are co /ork are co /ork are co /or aise all ref /or	8 ase pair found i rimers th /ping. N nstraine (Kline e Interactate	T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat TS, US = Upstream, ds = downstream In the DNA sequence in the repeat hat bind on SNPs can result in null lote that the variants characterized d by the size of the original PCR et al. 2011).
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S 1 2 2 2 7	DYS433DYS438DYS438DYS448DYS458DYS458DYS635DYS635DYS635D1S1656D2S1338D7S820D3S1358D7S820D3S1179D8S1179D10S1248D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S317D13S311D13S311D13S311D13S311D13S311D13S311D13S311D13S314D13S314D13S314D13S385 <td>14 10 11 20 15 17.2 20 11 20 11 20 11 20 11 20 11 20 11 10,12 10,10 16,18 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 12 27 24 11 13 14 13 14 15 12 27 24 11</td> <td>To Be Determined 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12. 29.30 116.16 To Be Determined 24.26 10.11 12. 27 24 12 27</td> <td>To Be Determined To Be Determined [AGAT]₁₁ [AGAGAT]₁₂ N₄₂ [AGAGAT]₈ [GAAA]₁₅ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TCTA]₄ [TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₄ [TCTA]₄ [TCTA]₁₀ [TGCA]₁₁ [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₄ [TCTA]₂ [TCTA]₁₂ [AGAT]₁₀ [GAA]₁₂ [AGAT]₁₃ [GGAA]₁₂ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GAA]₁₆ [AAGG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTA]₂ [TCTA]₃ TA [TCTA]₄ [TCTA]₅ [TCTA]₁₁ [AAGG] AA [AAGG] TAGG [AAGG]₁₂ [TCTA]₄ [TCTA]₅ [CTCA]₃ [A [TATC]₁₂ CCATA [TCTA]₁₁ [TATC]₁₃ ACT [ATT]₂ To Be Determined [TTTC]₃ TTT TTCT [CTT]₁₆ CTCC [TTCC]₂ [AAAG]₁₄ G AAGG[AAG]₁₀ [AAAG]₁₅ G AAGG[AAG]₂ AG [AAAG]₁₄ G AAGG[AAG]₂ AG</td> <td>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</td> <td>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC]₁₂ located most, if STR typi • Seque remain loci to certifie • Seque sTR typi</td> <td>A B ions: bp = b SNPs were regions. P then STR ty ork are con generated totattacatacatacatacatacatacatacatacatac</td> <td>8 8 ase pair found i rimers th /ping. N nstraine (Kline e interation (Kline e interation (Kline e interation interation interation interation istream istream istream istream istream istream istream istream istream istream istream istream istream istream</td> <td>T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat 's, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null vote that the variants characterized d by the size of the original PCR et al. 2011).</td>	14 10 11 20 15 17.2 20 11 20 11 20 11 20 11 20 11 20 11 10,12 10,10 16,18 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 12 27 24 11 13 14 13 14 15 12 27 24 11	To Be Determined 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 12. 29.30 116.16 To Be Determined 24.26 10.11 12. 27 24 12 27	To Be Determined To Be Determined [AGAT] ₁₁ [AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TCTA] ₄ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₄ [TCTA] ₄ [TCTA] ₁₀ [TGCA] ₁₁ [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₄ [TCTA] ₂ [TCTA] ₁₂ [AGAT] ₁₀ [GAA] ₁₂ [AGAT] ₁₃ [GGAA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GAA] ₁₆ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTA] ₂ [TCTA] ₃ TA [TCTA] ₄ [TCTA] ₅ [TCTA] ₁₁ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TCTA] ₄ [TCTA] ₅ [CTCA] ₃ [A [TATC] ₁₂ CCATA [TCTA] ₁₁ [TATC] ₁₃ ACT [ATT] ₂ To Be Determined [TTTC] ₃ TTT TTCT [CTT] ₁₆ CTCC [TTCC] ₂ [AAAG] ₁₄ G AAGG[AAG] ₁₀ [AAAG] ₁₅ G AAGG[AAG] ₂ AG [AAAG] ₁₄ G AAGG[AAG] ₂ AG	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₂ TCCATA] [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂ [AAAGA] ₁₁ [AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈ [AATG] ₈	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC] ₁₂ located most, if STR typi • Seque remain loci to certifie • Seque sTR typi	A B ions: bp = b SNPs were regions. P then STR ty ork are con generated totattacatacatacatacatacatacatacatacatac	8 8 ase pair found i rimers th /ping. N nstraine (Kline e interation (Kline e interation (Kline e interation interation interation interation istream istream istream istream istream istream istream istream istream istream istream istream istream istream	T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat 's, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null vote that the variants characterized d by the size of the original PCR et al. 2011).
S 2 2 2 2 2 2 2 2 2 2 2 2 2	DYS433DYS438DYS438DYS438DYS448DYS458DYS635YARKERD1S1656D2S1338D2S441D3S1358D7S8200D8S1179D16S5391D13S317D13S389D13S389D13S389D13S389D13S389D13S389D13S389D13S389D13S389D13S389D13S389D13S389D13S38 <th>14 10 11 20 15 17.2 20 11 20 11 20 11 20 11 20 11 20 11 10,12 10,10 16,18 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13 15 13 15 13 15 12 27 24 11 13 16 11</th> <th>To Be Determined 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 11. 11. 11. 11. 11. 11. 10.10 16,18 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19 13.2,15.2 29,30 16,16 To Be Determined 12 28.2,31.2 6,8 11.1 16,18 15 12 27 24 11 13 13. 15 <</th> <th>To Be Determined [AGAT]₁₁ [AGAAT]₁₂ N₄₂ [AGAGAT]₈ [AGAT]₁₅ [GAAA]₁₅ AA [GAAA]₂ [TCTA]₄ [TGTA]₂ [TCTA]₂ [TGTA]₂ [TCTA]₁₀ [TAGA]₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA]₁₁ TG]₅ [TGCC]₇ [TTCC]₁₂ [TGCA]₁₀ [TCTA]₁₀ [TGCA]₁₁ TG]₅ [TGCA]₁₀ [TCTA]₁₂ [AGAT]₁₀ [GATA]₁₀ [GATA]₁₀ [GATA]₁₂ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAT]₁₃ [AGAC]₅ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAG] AA [AAGG] TAGG [AAGG]₁₂ [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AAGG] AA [AAGG] TAGG [AAGG]₁₂ [TATC]₁₂ CCATA} [TCTA]₃ TA [TCTA]₃ TCA [TCTA]₄ [TCTA]₆ [TCTA]₁₄ [TCTA]₁₄ [AAAG]₁₀ [AAAG]₁₀ [AAAG]₁₀ [AAAG]₁₀</th> <th>[TAGA]₁₄ TAGG [TG]₅ [TGCC]₇ [TTCC]₁₂ [TCTA]₈ TCTG TCTA TCTA [TCTG]₃ [TCTA]₁₄ [AGAT]₁₁ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [TCTA]₂ TCTG [TCTA]₁₄ [GATA]₁₂ [GGAA]₁₆ [AGAT]₁₂ [AGAC]₁₀ AGAT [TATC]₁₂ del [ATCA] 6 bp ds [GATA]₁₀ [AGAA]₁₉ [AAGG] AA [AAGG] TAGG [AAGG]₁₄ [TCTA]₂ TCCATA] [TCTA]₃ TCA [TCTA]₂ TCCATA} [TCTA]₁₁ [ATT]₁₃ ACT [ATT]₂ To Be Determined [TTC]₃ TTTT TTCT [CTTT]₁₈ CTCC [TTCC]₂ [AAAGA]₁₁ [AAAG]₂ AG [AAAG]₃ AG [AAAG]₉ AAAAAG [AAAG]₂₁ G AAGG[AAAG]₂ AG [AATG]₈ [AATG]₈</th> <th>TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC]₁₂ located most, if STR typi • Seque remain loci to certifie • Seque sTR typi • Seque amixtur • Once Analys • This w seque applic • SRM 2</th> <th>A B ions: bp = b SNPs were regions. P then STR ty vork are co generated totattacattacattace for a generated for a transfor repeats. 6 bp down not all, of t ing kits. 6 bp down not all, of t ing kits. 7, Compon genotype. H repeats. 6 bp down not all, of t ing kits. F encing of Co ning autoso raise all ref ed level. encing will a markers for re of Compo sequencing sis will be u vork suppor encing techn ations. 2391c has s is project was s a set of compo set of compo set</th> <th>8 8 ase pair found i rimers th /ping. N nstraine (Kline e ///////////////////////////////////</th> <th>T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat Ts, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null vote that the variants characterized d by the size of the original PCR et al. 2011).</th>	14 10 11 20 15 17.2 20 11 20 11 20 11 20 11 20 11 20 11 10,12 10,10 16,18 10,17 9,9 12,16 19,23 11,11 10,10 16,19 13.2,15.2 29,30 16,16 10,12 24,26 10,11 12,13 28.2,31.2 6,8 11,11 16,18 15 13 15 13 15 13 15 12 27 24 11 13 16 11	To Be Determined 11 20 15 17.2 20 11 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 20 11. 11. 11. 11. 11. 11. 11. 10.10 16,18 10,17 9,9 12,16 19,23 (12,12)* 10,10 16,19 13.2,15.2 29,30 16,16 To Be Determined 12 28.2,31.2 6,8 11.1 16,18 15 12 27 24 11 13 13. 15 <	To Be Determined [AGAT] ₁₁ [AGAAT] ₁₂ N ₄₂ [AGAGAT] ₈ [AGAT] ₁₅ [GAAA] ₁₅ AA [GAAA] ₂ [TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₀ [TAGA] ₁₁ SRM 2391c - Component C Repeat Structure - Allele 1 [TAGA] ₁₁ TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TGCA] ₁₀ [TCTA] ₁₀ [TGCA] ₁₁ TG] ₅ [TGCA] ₁₀ [TCTA] ₁₂ [AGAT] ₁₀ [GATA] ₁₀ [GATA] ₁₀ [GATA] ₁₂ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAT] ₁₃ [AGAC] ₅ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAG] AA [AAGG] TAGG [AAGG] ₁₂ [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AAGG] AA [AAGG] TAGG [AAGG] ₁₂ [TATC] ₁₂ CCATA} [TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₄ [TCTA] ₆ [TCTA] ₁₄ [TCTA] ₁₄ [AAAG] ₁₀ [AAAG] ₁₀ [AAAG] ₁₀ [AAAG] ₁₀	[TAGA] ₁₄ TAGG [TG] ₅ [TGCC] ₇ [TTCC] ₁₂ [TCTA] ₈ TCTG TCTA TCTA [TCTG] ₃ [TCTA] ₁₄ [AGAT] ₁₁ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [TCTA] ₂ TCTG [TCTA] ₁₄ [GATA] ₁₂ [GGAA] ₁₆ [AGAT] ₁₂ [AGAC] ₁₀ AGAT [TATC] ₁₂ del [ATCA] 6 bp ds [GATA] ₁₀ [AGAA] ₁₉ [AAGG] AA [AAGG] TAGG [AAGG] ₁₄ [TCTA] ₂ TCCATA] [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₁ [ATT] ₁₃ ACT [ATT] ₂ To Be Determined [TTC] ₃ TTTT TTCT [CTTT] ₁₈ CTCC [TTCC] ₂ [AAAGA] ₁₁ [AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈ [AATG] ₈	TPOX TPOX Abbreviati Multiple flanking alleles w in this w amplicon GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC GACCCATCTAACGCCTATC D13S317 (11,11) g [TATC] ₁₂ located most, if STR typi • Seque remain loci to certifie • Seque sTR typi • Seque amixtur • Once Analys • This w seque applic • SRM 2	A B ions: bp = b SNPs were regions. P then STR ty vork are co generated totattacattacattace for a generated for a transfor repeats. 6 bp down not all, of t ing kits. 6 bp down not all, of t ing kits. 7, Compon genotype. H repeats. 6 bp down not all, of t ing kits. F encing of Co ning autoso raise all ref ed level. encing will a markers for re of Compo sequencing sis will be u vork suppor encing techn ations. 2391c has s is project was s a set of compo set	8 8 ase pair found i rimers th /ping. N nstraine (Kline e ///////////////////////////////////	T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat T-G 148 bp ds of the repeat Ts, us = upstream, ds = downstream in the DNA sequence in the repeat that bind on SNPs can result in null vote that the variants characterized d by the size of the original PCR et al. 2011).

Marker	Component	Allele	Allele Repeat Structure
D8S1179	С	17	[TCTA] ₂ TCTG [TCTA] ₁₄
D12S391	А	22	[AGAT] ₁₃ [AGAC] ₈ AGAT
D12S391	С	19	[AGAT] ₁₃ [AGAC] ₅ AGAT
D12S391	С	23	[AGAT] ₁₂ [AGAC] ₁₀ AGAT
D21S11	В	32	[TCTA] ₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA [TCTA] ₂ TCCATA} [TCTA] ₁₄
SE33	С	31.2	[AAAG] ₂ AG [AAAG] ₃ AG [AAAG] ₉ AAAAAG [AAAG] ₂₁ G AAGG[AAAG] ₂ AG
DYS389II	В	31	[TCTG] ₆ [TCTA] ₁₂ [TCTG] ₃ [TCTA] ₁₀
DYS458	В	17.2	[GAAA] ₁₅ AA [GAAA] ₂
DYS635	В	20	$[TCTA]_4 [TGTA]_2 [TCTA]_2 [TGTA]_2 [TCTA]_{10}$
DYS635	С	21	$[TCTA]_4 [TGTA]_2 [TCTA]_2 [TGTA]_2 [TCTA]_{11}$

D21S11	32,32.2	32,32.2			Marker Component Allele Flanking Region Variants
D22S1045	15,17	15,17			D5S818 A 12 $T \rightarrow C$ 13 bp us of the repeat
CSF1PO	10,11	10,11	[AGAT] ₁₀	[AGAT] ₁₁	D5S818 B 13 $T \rightarrow C$ 13 bp us of the repeat
FGA	20,23	20,23	$[TTTC]_3 TTTT TTCT [CTTT]_{12} CTCC [TTCC]_2$	$[TTTC]_3$ TTTT TTCT $[CTTT]_{15}$ CTCC $[TTCC]_2$	D5S818 B 13 $G \rightarrow T4$ bp ds of the repeat
Penta D	8,12	8,12	[AAAGA] ₈	[AAAGA] ₁₂	D5S818 C 10 $T \rightarrow C$ 13 bp us of the repeat
Penta E	7,15	7,15	[AAAGA] ₇	[AAAGA] ₁₅	D5S818 C 11 $T \rightarrow C$ 13 bp us of the repeat
			$[AAAG]_2 AG [AAAG]_3 AG [AAAG]_{17} G [AAAG]_3$	$[AAAG]_2 AG [AAAG]_3 AG [AAAG]_{18} G [AAAG]_3$	D7S820 C 10 $T \rightarrow G 65 \text{ bp ds of the repeat}$
SE33	17,18	17,18	AG	AG	D13S317C11 $A \rightarrow C$ 115 bp ds of the repeatD16S539A10 $A \rightarrow C$ 16 bp ds of the repeat
TH01	6,9.3	6,9.3	[AATG] ₆	[AATG] ₆ ATG [AATG] ₃	$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$
ТРОХ	8,11	8,11	[AATG] ₈	[AATG] ₁₁	$\begin{bmatrix} D 103539 \\ D 16S539 \end{bmatrix} A = \begin{bmatrix} 10 \\ 11 \end{bmatrix} C \rightarrow A 95 bp us of the repeat$
√WA	17,18	17,18	TCTA [TCTG] ₄ [TCTA] ₁₂	TCTA [TCTG] ₄ [TCTA] ₁₃	D16S539 B 10 $C \rightarrow A 95 bp us of the repeat$
DYS19	14	14	[TAGA] ₃ TAGG [TAGA] ₁₁		D16S539 C 10 $C \rightarrow A 95$ bp us of the repeat
DYS385a	13	13	[GAAA] ₁₃		Penta EA10 $G \rightarrow A 123$ bp us of the repeat
DYS385b	17	17	[GAAA] ₁₇		Penta EA10 $A \rightarrow G 268$ bp us of the repeat
			[TCTG] ₃ [TCTA] ₁₀		Penta E A 10 $A \rightarrow C 280$ bp us of the repeat
DYS3891	13	13			Penta E B 7 $G \rightarrow A 123$ bp us of the repeat
DYS389II	31	31	$[TCTG]_{6} [TCTA]_{12} [TCTG]_{3} [TCTA]_{10}$		Penta EB7 $A \rightarrow G 268$ bp us of the repeat
DYS390	23	23			Penta EB7 $A \rightarrow C 280$ bp us of the repeat
DYS391	10	10			Penta EB15 $G \rightarrow A 123$ bp us of the repeat
DYS392	11	11	[TAT] ₁₁		Penta EB15 $A \rightarrow G 268$ bp us of the repeat
DYS393	12	12 To Do Dotominad	[AGAT] ₁₂		Penta EB15 $A \rightarrow C$ 280 bp us of the repeatTDOX(ACCC
DYS437	14	To Be Determined	To Be Determined		TPOXA8 $T \rightarrow G 148$ bp ds of the repeat
DYS438	10	To Be Determined	To Be Determined		TPOXB8T \rightarrow G 148 bp ds of the repeat
DYS439	11	11	[AGAT] ₁₁		Abbreviations: bp = base pairs, us = upstream, ds = downstrear
DYS448	20	20	[AGAGAT] ₁₂ N ₄₂ [AGAGAT] ₈		Multiple SNPs were found in the DNA sequence in the repea
DYS456	15	15			flanking regions. Primers that bind on SNPs can result in nu
DYS458	17.2	17.2	$[GAAA]_{15}AA [GAAA]_2$		
DYS635	20	20	$[TCTA]_4 [TGTA]_2 [TCTA]_2 [TGTA]_2 [TCTA]_{10}$		alleles when STR typing. Note that the variants characterized
YGATA H4	11	11	[TAGA] ₁₁		in this work are constrained by the size of the original PCF
			SRM 2391c - Component C		amplicon generated (Kline et al. 2011).
Marker	Certified Genotype	Sanger Result	Repeat Structure - Allele 1	Repeat Structure - Allele 2	GACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATC
D1S1656	11,15	11,15	[TAGA] ₁₁ [TG] ₅	[TAGA] ₁₄ TAGG [TG] ₅	
D2S1338	19,19	19,19	[TGCC] ₇ [TTCC] ₁₂	[TGCC] ₇ [TTCC] ₁₂	I all a set a second of the second se
D2S441	10,10	10,10	[TCTA] ₈ TCTG TCTA	[TCTA] ₈ TCTG TCTA	
D3S1358	16,18	16,18	TCTA [TCTG] ₃ [TCTA] ₁₂	TCTA [TCTG] ₃ [TCTA] ₁₄	GACCCATCTAACGCCTATCTGTATTTACAAATACATTATCTATC
D5S818	10,11	10,11	[AGAT] ₁₀	[AGAT] ₁₁	
D7S820	10,12	10,12	[GATA] ₁₀	[GATA] ₁₂	L MIYAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
D8S1179	10,17	10,17	[TCTA] ₁₀	[TCTA] ₂ TCTG [TCTA] ₁₄	
D8S1115	9,9	9,9	[ATT] ₉	[ATT] ₉	
D10S1248	12,16	12,16	[GGAA] ₁₂	[GGAA] ₁₆	
	19,23	19,23	[AGAT] ₁₃ [AGAC] ₅ AGAT	[AGAT] ₁₂ [AGAC] ₁₀ AGAT	T MYYNYYN ARABAN ANNANANANANANANANANANANANANANANANAN
D12S391 D13S317	11,11	(12,12)*	[TATC] ₁₂ del [ATCA] 6 bp ds	[TATC] ₁₂ del [ATCA] 6 bp ds	
D16S539	10,10	10,10	[GATA] ₁₀	[GATA] ₁₀	
D18S51	16,19	16,19	[AGAA] ₁₆	[AGAA] ₁₉	1. a a fille for a first a star a fille a fi
D19S433	13.2,15.2	13.2,15.2	[AAGG] AA [AAGG] TAGG [AAGG] ₁₂	[AAGG] AA [AAGG] TAGG [AAGG] ₁₄	
	· · · · · · · · · · · · · · · · · · ·		[TCTA]₄ [TCTG] ₆ {[TCTA] ₃ TA [TCTA] ₃ TCA	$[TCTA]_6 [TCTG]_5 {[TCTA]_3 TA [TCTA]_3 TCA}$	
D21S11	29,30	29,30	[TCTA] ₂ TCCATA} [TCTA] ₁₁	[TCTA] ₂ TCCATA} [TCTA] ₁₁	D13S317, Component C , is a homozygous sample with ar
D22S1045	16,16	16,16	[ATT] ₁₃ ACT [ATT] ₂	[ATT] ₁₃ ACT [ATT] ₂	(11,11) genotype. However, it is sequencing as a (12,12) with
CSF1PO	10,10	To Be Determined	To Be Determined	To Be Determined	[TATC] ₁₂ repeats. The cause is a 4 bp [ATCA] deletion (del
FGA	24,26	24,26			located 6 bp downstream (ds) of the repeat, that is within
Penta D			[AAAGA] ₁₀	[AAAGA] ₁₁	most, if not all, of the primer sequences used in commercia
	10,11	10,11			
Penta E				STR typing kits.	
SE33	28.2,31.2	28.2,31.2	$[AAAG]_{17} G AAGG[AAAG]_2 AG$	[AAAG] ₂₁ G AAGG[AAAG] ₂ AG	Future Directions
			[AAAG] ₁₇ G AAGG[AAAG] ₂ AG [AATG] ₆	[AAAG] ₂₁ G AAGG[AAAG] ₂ AG [AATG] ₈	
TH01	6,8	6,8			 Sequencing of Components A-C will be completed for all
TPOX	11,11	11,11			remaining autosomal and Y-STR loci, including non-core
WA	16,18	16,18	TCTA [TCTG] ₄ [TCTA] ₁₁	TCTA [TCTG] ₄ [TCTA] ₁₃	loci to raise all reference and informational genotypes to a
DYS19	15	15	[TAGA] ₃ TAGG [TAGA] ₁₂		certified level.
DYS385a	13	13	[GAAA] ₁₃		 Sequencing will also be completed for all autosomal and Y-
DYS385b	15	15			STR markers for Components E and F (Component D is a
DYS3891	12	12			mixture of Components A and C).
DYS389II	27	27	$[TCTG]_{5} [TCTA]_{10} [TCTG]_{3} [TCTA]_{9}$		i ,
DYS390	24	24			 Once sequencing is complete, the SRM 2391c Certificate of Analysis will be undeted with this new information
DYS391	11	11	[TCTA] ₁₁		Analysis will be updated with this new information.
DYS392	13	13			 This work supports the high throughput next generation
DYS393	13	13	[AGAT] ₁₃		sequencing technologies at NIST for forensic typing
DYS437 DYS438	<u> </u>	To Be Determined	To Be Determined To Be Determined		applications.
DYS439	12	12	[AGAT] ₁₂		 SRM 2391c has superseded SRM 2395 for Y-STR typing.
DYS448	12	12	[AGAGAT] ₁₁ N ₄₂ [AGAGAT] ₈		
DYS456	19	19	[AGAT] ₁₅		Funding This project was supported by an interagency agreement between NIJ and
DYS456 DYS458	15	15	[GAAA] ₁₇		the NIST Law Enforcement Standards Office. Points of view in this document are
DYS635	21	21	[TCTA] ₄ [TGTA] ₂ [TCTA] ₂ [TGTA] ₂ [TCTA] ₁₁		those of the authors and do not necessarily represent the official position or policies
			[TAGA] ₁₁		of the US Department of Justice. Certain commercial equipment, instruments and materials are identified in order to specify experimental procedures as completely as
YGATA H4	11	11]	possible. In no case does such identification imply a recommendation or
	la decimentione :	lood bara war	a dariwad from Dutlar IM (201	a) Advanced Tenice in	

Methods for Sanger Sequencing

- NIST DNA sequencing procedures and all sequencing primers were published in 2011 (see S1)
- Note: alternative primers were designed for D19S433

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Forensic Science International: Genetics

F

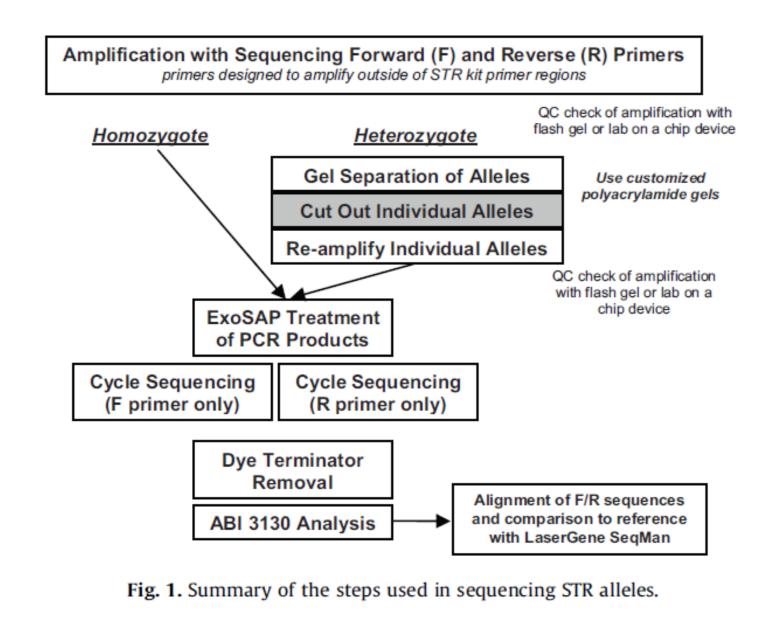
Short communication

STR sequence analysis for characterizing normal, variant, and null alleles

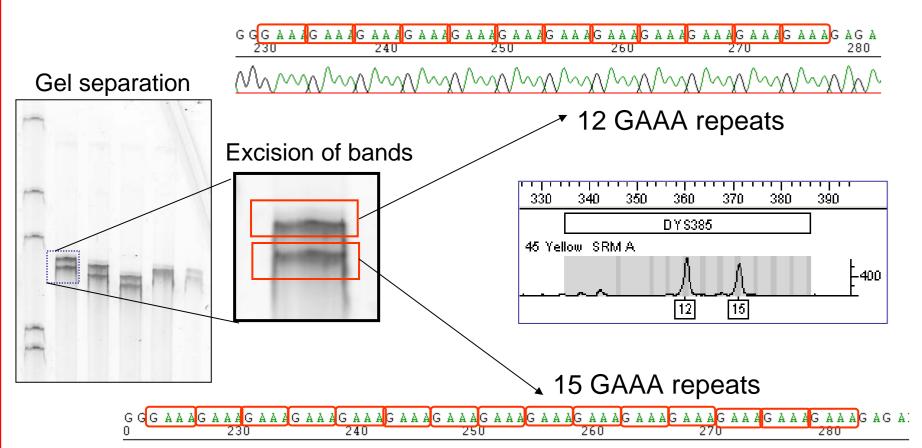
Margaret C. Kline^{*}, Carolyn R. Hill, Amy E. Decker¹, John M. Butler

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Sanger Sequencing Flow Chart



Sequencing Individual Heterozygous Alleles



Kline, M.C., Hill, C.R., Decker, A.E., Butler, J.M. (2011) STR sequence analysis for characterizing normal, variant, and null alleles. Forensic Sci. Int. Genet. 5(4): 329-332

GenBank Reference Sequences

The GenBank Accession numbers and reference alleles were obtained were based on the May 2004 assembly of the human genome, build 35.

	GenBank		GenBank		GenBank		GenBank
Marker	Accession	Marker	Accession	Marker	Accession	Marker	Accession
	Number		Number		Number		Number
D1S1656	G07820	D13S317	AL353628.2	SE33	V00481	DYS393	AC006152
D2S1338	AC010136	D16S539	AC024591.3	TH01	D00269	DYS437	AC002992
D2S441	AC079112	D18S51	AP001534	TPOX	M68651	DYS438	AC002992
D3S1358	AC099539	D19S433	AC008507.6	vWA	M25858	DYS439	AC002992
D5S818	AC008512	D21S11	AP000433	DYS19	AC017019	DYS448	AC025227
D7S820	AC004848	D22S1045	AL022314	DYS385	AC022486	DYS456	AC010106.2
D8S1179	AF216671	CSF1PO	X14720	DYS389	AF140635	DYS458	AC010902
D8S1115	AC090739	FGA	M64982	DYS390	AC011289	DYS635	AC004772
D10S1248	AL391869	Penta D	AP001752	DYS391	AC011302	Y GATA H4	AC011751
D12S391	G08921	Penta E	AC027004	DYS392	AC06152		

Sequences were aligned de novo using LaserGene SeqMan software and compared to SeqBuilder maps based on the listed GenBank reference sequences.

The allele designations used here were derived from Butler, J.M. (2012) Advanced Topics in Forensic DNA Typing: Methodology. Elsevier Academic Press:

San Diego [textbook: third edition, volume 2] and STRBase fact sheets. The information on this poster is not certified until an updated Certificate of Analysis for SRM 2391c is released.

possible. In no case does such identification imply a recommendation or endorsement by the National Institute of Standards and Technology nor does it imply that any of the materials, instruments or equipment identified are necessarily the best available for the purpose.

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