

My Results are Unintuitive, Now What?

Casework Studies on Unintuitive STRmix™
Results and the Approaches Utilized for
Reporting



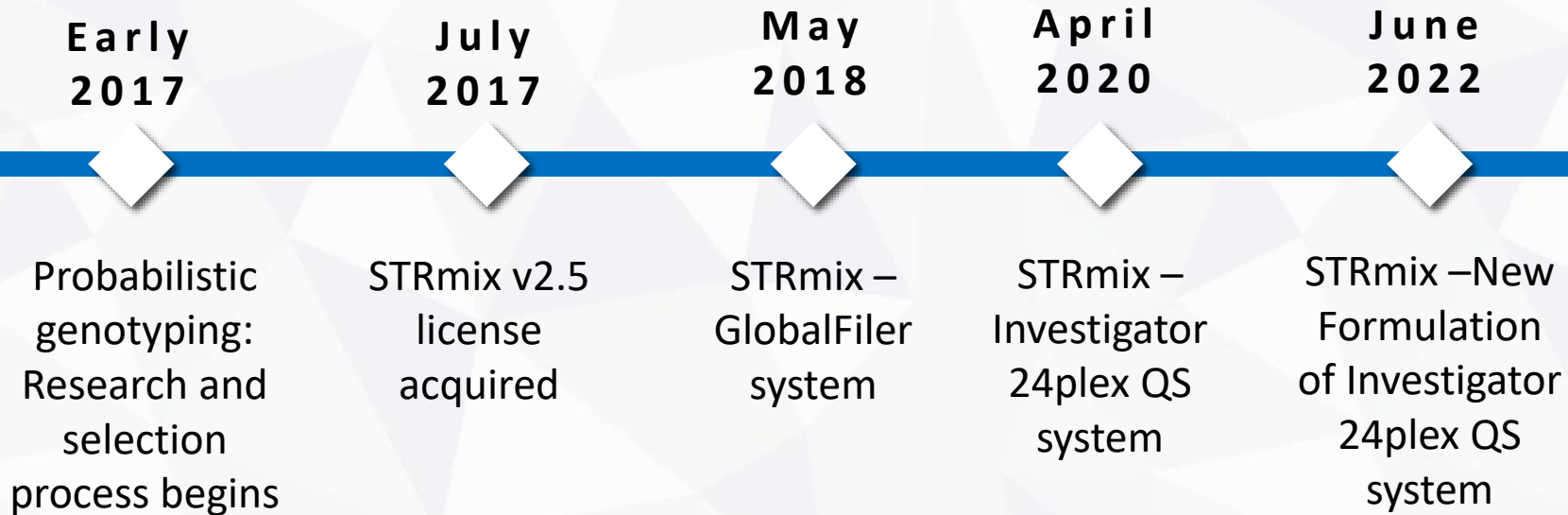
Science Works | AAFS 75th Anniversary Conference

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Signature Science Forensic DNA Laboratory, Austin, TX



Signature Science and Probabilistic Genotyping — A Timeline



**Tune in on Friday for
Samantha Wandzek's
presentation on the
validation and evaluation of
Investigator 24plex QS New
Formulation**

Evaluation Criteria

The Deconvolution Report contains information that will allow the analyst to evaluate if an appropriate deconvolution was performed. The following criteria must be reviewed by both the reporting analyst and the technical reviewer to ensure proper results were obtained through the software.

RUN PARAMETERS

- Number of contributors
- Profiling Kit
- Propositions
- Input file(s)

Deconvolution Report

DETAILS

STRMIX VERSION: STRmix V2.5.11
USER: swandzek
RUN DATE: 11 Feb 2022 14:01:39
TOTAL RUN TIME: 1 min, 33 secs

RUN PARAMETERS

CONTRIBUTORS: 2
PROFILING KIT: Signature_Science_GlobalFiler 24s
SAMPLE FILE: LSS2021-00016P_3.1_BSAJ5.E_C01_CEP-210803-34.hid_EV.csv
KNOWN CONTRIBUTORS UNDER HP: LSS2021-00016P_1.1_BSAJ6_A03_CEP-210803-34.hid_REF.csv

Verify All

EVIDENCE INPUT FILES

LSS2021-00016P_3.1_BSAJ5.E_C01_CEP-210803-34.HID_EV.CSV

LOCUS	ALLELE	HEIGHT	SIZE
D3S1358	13	388	113
	14	7292	117
	15	5924	121
	18	377	133
vWA	16	308	176
	17	5118	180
	19	372	189
	20	4443	193
D16S539	8	219	239
	9	5599	243
	11	319	252
	12	5752	255
CSF1PO	10	258	298
	11	5261	302
	12	5002	306
TPOX	8	4194	350
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REFERENCE FILES

LSS2021-00016P_1.1_BSAJ6_A03_CEP-210803-34.HID_REF.CSV

LOCUS	
D3S1358	14, 15
vWA	17, 20
D16S539	9, 12
CSF1PO	11, 12
TPOX	8, 12
Yindel	
D8S1179	13, 14
D21S11	29, 32.2
D18S51	15, 17
DYS391	
D2S441	11, 11
D19S433	12, 14
TH01	6, 9.3
FGA	19, 26
D22S1045	15, 16
D5S818	12, 12
D13S317	11, 13
D7S820	11, 11
SE33	20, 25.2
D19S1348	14, 14
D15S656	15, 17.3
D12S391	19, 20
D2S1338	23, 24

Evaluation Criteria

RUN SETTINGS

- Majority are default settings defined in SOP (unbolded)
- Ignored Loci
- Burn-in and Post burn-in accepts per chain

SETTINGS

CASE SETTINGS

Case number	LSS2021-00016P
Sample ID	3.1-E_GF
Comments	
Seed	808435
Extended output	N

MCMC SETTINGS

Number of contributors	2
Burn-in accepts per chain	100000
Post burn-in accepts per chain	50000
Use Mix priors	N
Number of chains	8
Random walk SD	0.005
Post burn-in shortlist	9.0
Auto continue on Gelman-Rubin	N

KIT SETTINGS

Ignored loci	Yindel, DYS391
Detection thresholds	D3S1358 125 VWA 125 D16S539 125 CSF1PO 125 TPOX 125 D8S1179 125 D21S11 125 D18S51 125 D2S441 125 D19S433 125 TH01 125 FGA 125 D22S1045 125 D5S818 125 D13S317 125 D7S820 125 SE33 125 D10S1248 125 D1S1656 125 D12S391 125 D2S1338 125
Stutter max	0.3
Forward stutter max	0.15
Saturation	75000
Degradation starts at	-1.0
Degradation max	0.01
Drop-in cap	250
Drop-in frequency	1.0E-4
Drop-in gamma parameters	0.0, 0.0
Allelic variance (α, β)	5.86, 2.49
Stutter variance (α, β)	2.88, 6.38
Min variance factor	0.5
Locus amplification variance	0.014

Evaluation Criteria

The presence of a single sub-optimal diagnostic is not always an indication that rework is required.

- POST BURN-IN SUMMARY

- Total Iterations – total number of post burn-in iterations that the MCMC has run during its analysis
- Acceptance Rate – Post burn-in accepts/Total Iterations
- Effective Sample Size – number of independent samples the MCMC has taken from the posterior distribution of all parameters
- Gelman-Rubin Convergence Diagnostic – ratio of the stationary distribution and within-chain variances; informs the user whether the MCMC analysis has likely converged
- Log (likelihood) – log of the average likelihood (or probability) value created at each of the post burn-in MCMC iterations
- Allele Variance and Stutter Variance Constants – average value for allele variance and stutter variance constants across the entire post burn-in MCMC analysis

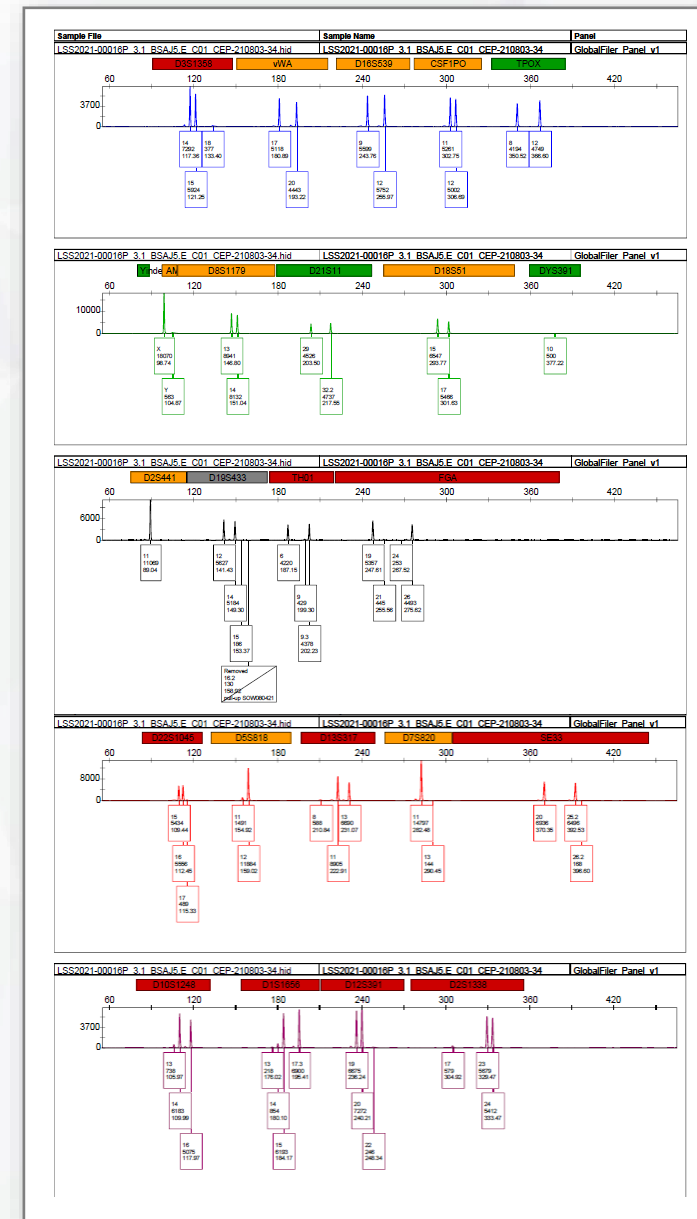
POST BURN-IN SUMMARY

Total iterations	2089102	Acceptance rate	1 in 5.22
Effective sample size	6703.03	log(likelihood)	57.07
Gelman-Rubin convergence diagnostic	1.04		
Allele variance (mode = 12.101)	11.465	Stutter variance (mode = 11.994)	22.34

Mixture Proportions – Is it Intuitive?

SUMMARY OF CONTRIBUTORS

CONTRIBUTORS	1	2
Template (rfu)	6000	306
Mixture Proportion	95%	5%
Degradation starts at 84bp (rfu/bp)	4.272	0.962
CONTRIBUTOR ORDER GIVING HIGHEST LR		
All Populations	LSS2021-00016P_1.1_BSAJ6_A03_CEP-210803-34.hid_REF.csv	Unknown



Component Interpretation – Is it Intuitive?

May also be evaluated against Genotype Probability Distribution

COMPONENT INTERPRETATION

CONTRIBUTOR 1 (95%)

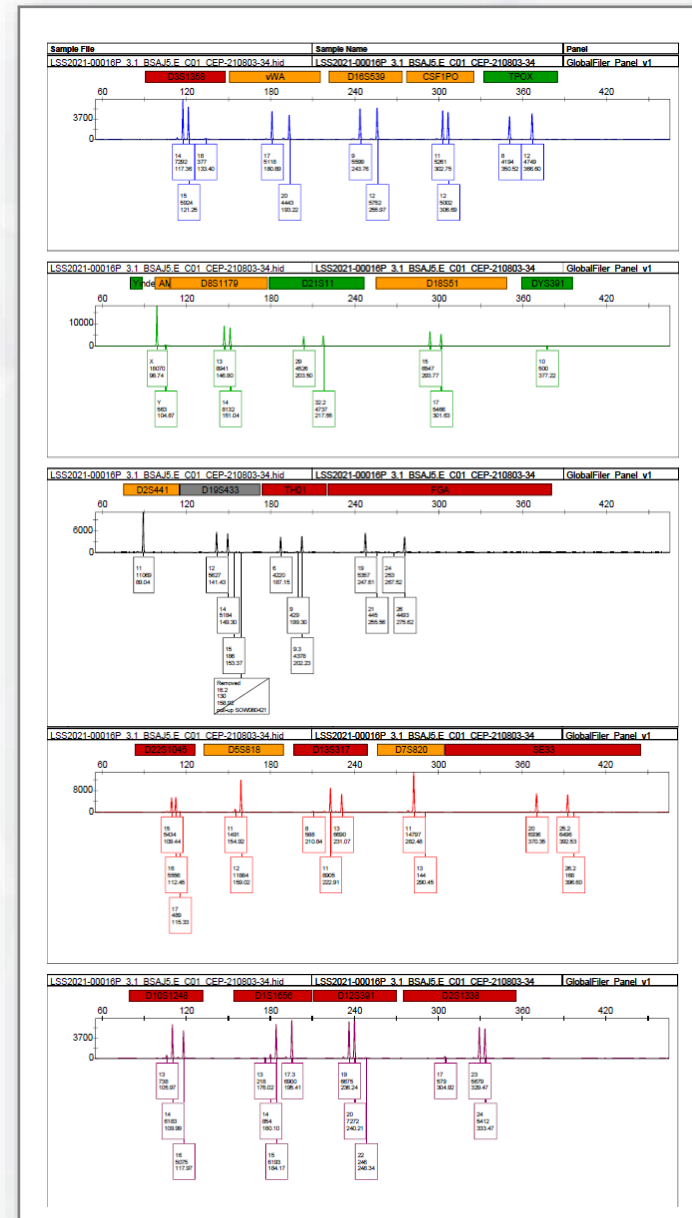
Questioned contributor

LOCUS	GENOTYPE	WEIGHT	COMPONENT ≥ 99%
D3S1358	14, 15	100.00%	14, 15
vWA	17, 20	100.00%	17, 20
D16S539	9, 12	100.00%	9, 12
CSF1PO	11, 12	100.00%	11, 12
TPOX	8, 12	100.00%	8, 12
Yindel			
D8S1179	13, 14	100.00%	13, 14
D21S11	29, 32.2	100.00%	29, 32.2
D18S51	15, 17	100.00%	15, 17
DYS391			
D2S441	11, 11	100.00%	11, 11
D19S433	12, 14	100.00%	12, 14
TH01	6, 9.3	100.00%	6, 9.3
FGA	19, 26	100.00%	19, 26
D22S1045	15, 16	100.00%	15, 16
D5S818	12, 12	100.00%	12, 12
D13S317	11, 13	100.00%	11, 13
D7S820	11, 11	100.00%	11, 11
SE33	20, 25.2	100.00%	20, 25.2
D10S1248	14, 16	100.00%	14, 16
D1S1656	15, 17.3	100.00%	15, 17.3
D12S391	19, 20	100.00%	19, 20
D2S1338	23, 24	100.00%	23, 24

CONTRIBUTOR 2 (5%)

Questioned contributor

LOCUS	GENOTYPE	WEIGHT	COMPONENT ≥ 99%
D3S1358	14, 18	48.61%	18, F
	18, 18	25.17%	
	15, 18	25.06%	
	Q, 18	0.83%	
	13, 18	0.34%	
vWA	17, 17	34.65%	F, F
	17, 20	28.21%	



Contributor Assignment – Is it Intuitive?

- Red flags are observed at one or more loci for the POI
 - Low weights for POI genotypes in component interpretation
 - Contributor assignment is not intuitive when POI is compared to EPG
- Familial component
 - First degree relatives assigned to same contributor with a likelihood ratio supporting inclusion

SUMMARY OF CONTRIBUTORS

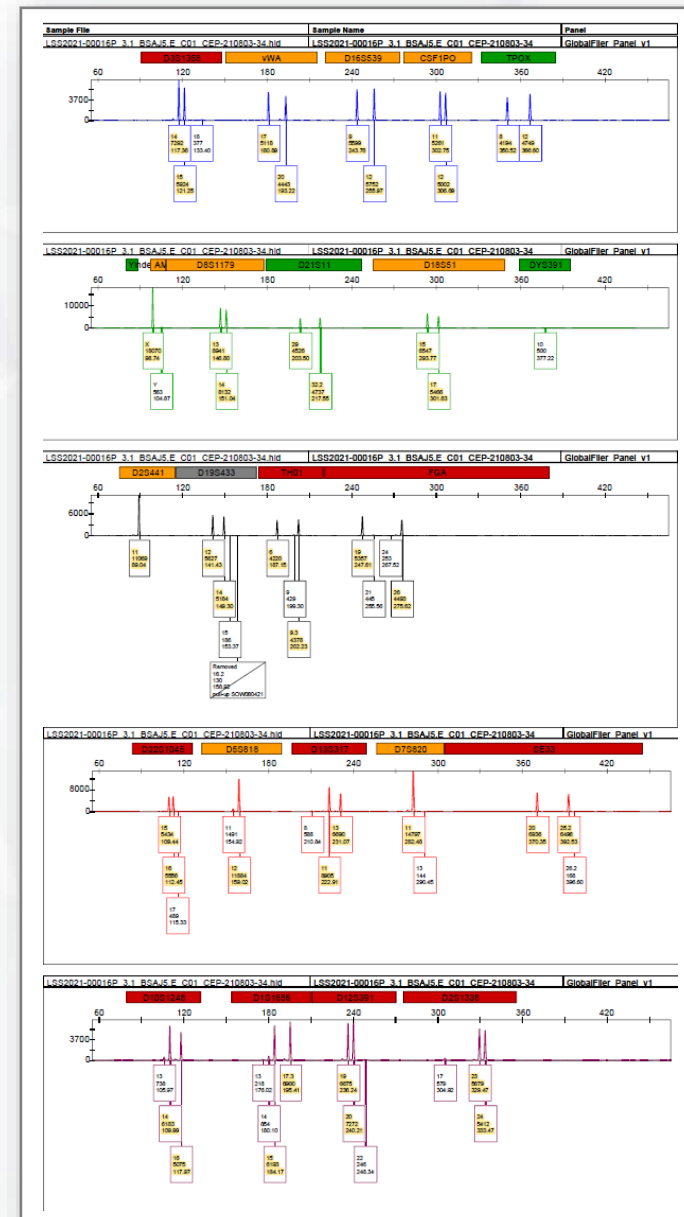
CONTRIBUTORS	1	2
Template (rfu)	6000	306
Mixture Proportion	95%	5%
Degradation starts at 84bp (rfu/bp)	4.272	0.962
CONTRIBUTOR ORDER GIVING HIGHEST LR		
All Populations	LSS2021-00016P_1.1_BSAJ6_A03_CEP-210803-34.hid_REF.csv	Unknown

COMPONENT INTERPRETATION

CONTRIBUTOR 1 (95%)

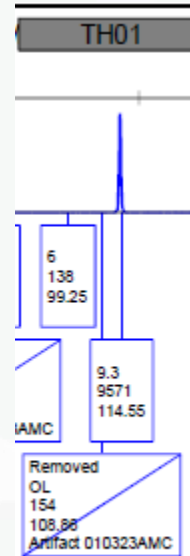
Questioned contributor

LOCUS	GENOTYPE	WEIGHT	COMPONENT ≥ 99%
D3S1358	14, 15	100.00%	14, 15
vWA	17, 20	100.00%	17, 20
D16S539	9, 12	100.00%	9, 12
CSF1PO	11, 12	100.00%	11, 12
TPOX	8, 12	100.00%	8, 12
Yindel			
D8S1179	13, 14	100.00%	13, 14
D21S11	29, 32.2	100.00%	29, 32.2
D18S51	15, 17	100.00%	15, 17
DYS391			
D2S441	11, 11	100.00%	11, 11
D19S433	12, 14	100.00%	12, 14
TH01	6, 9.3	100.00%	6, 9.3
FGA	19, 26	100.00%	19, 26
D22S1045	15, 16	100.00%	15, 16
mtDNA	17, 17	100.00%	17, 17



Unintuitive Mixture Proportions and/or Genotype weights – Case example 1

- Only indication for the minor donor was TH01-6, robust major donor (5K-10K rfu) was noted at all other loci
- STRmix deconvolution
 - Mixture proportions – C1 94% / C2 6%
 - Genotype weights for C1 not intuitive



COMPONENT INTERPRETATION

CONTRIBUTOR 1 (94%)

LOCUS	GENOTYPE	WEIGHT	COMPONENT ≥ 99%
TH01	9,3,9,3	100.00%	9,3,9,3
D3S1358	15,15	100.00%	15,15
vWA	15,17	95.38%	F, F
	15,15	2.45%	
	17,17	2.17%	
D21S11	30,31	95.22%	F, F
	31,31	3.44%	
	30,30	1.34%	
TPOX	11,11	100.00%	11,11
DYS391			
D1S1656	16,17,3	94.13%	F, F
	17,3,17,3	3.53%	
	16,16	2.34%	
D12S391	16,19	94.02%	F, F
	16,16	3.02%	
	19,19	2.96%	
SE33	29,2,31,2	97.16%	F, F
	29,2,29,2	1.79%	
	31,2,31,2	1.04%	
D10S1248	12,15	92.66%	12, F
	12,12	6.74%	
	15,15	0.60%	
D22S1045	15,16	94.05%	F, F
	16,16	3.50%	
	15,15	2.45%	
D19S433	14,15	94.49%	F, F
	14,14	3.13%	
	15,15	2.38%	
D8S1179	10,11	94.59%	F, F
	10,10	3.63%	
	11,11	1.78%	
D2S1338	17,22	91.56%	F, F
	22,22	5.68%	
	17,17	2.76%	
D2S441	10,15	95.41%	F, F
	15,15	3.27%	
	10,10	1.32%	
D18S51	15,17	93.89%	F, F
	17,17	3.95%	
	15,15	2.16%	
FGA	20,26	92.08%	F, F
	26,26	6.09%	
	20,20	1.84%	
D16S539	11,11	100.00%	11,11
CSF1PO	12,12	100.00%	12,12
D13S317	9,12	94.15%	F, F
	12,12	3.58%	
	9,9	2.27%	
D5S818	12,12	100.00%	12,12
D7S820	10,12	91.66%	F, F
	12,12	5.02%	
	10,10	3.32%	

Unintuitive Mixture Proportions and/or Genotype Weights

Case Example 1

- Increased burn-in and post-burn in iterations
 - Default
 - Burn-in accepts per chain – 100,000
 - Post burn-in accepts per chain – 50,000
 - Increased
 - Burn-in accepts per chain – 500,000
 - Post burn-in accepts per chain – 500,000
- STRmix deconvolution
 - Mixture proportions – C1 100% / C2 0%
 - Intuitive genotype weights in comparison to EPG

CONTRIBUTOR 1 (100%)

LOCUS	GENOTYPE	WEIGHT	COMPONENT ≥ 99%
TH01	9,3,9,3	100.00%	9,3,9,3
D3S1358	15,15	100.00%	15,15
vWA	15,17	100.00%	15,17
D21S11	30,31	100.00%	30,31
	30,30	0.00%	
TPOX	11,11	100.00%	11,11
DYS391			
D1S1656	16,17,3	100.00%	16,17,3
D12S391	16,19	100.00%	16,19
SE33	29,2,31,2	100.00%	29,2,31,2
D10S1248	12,15	100.00%	12,15
D22S1045	15,16	100.00%	15,16
D19S433	14,15	100.00%	14,15
D8S1179	10,11	100.00%	10,11
	10,10	0.00%	
D2S1338	17,22	100.00%	17,22
	17,17	0.00%	
D2S441	10,15	100.00%	10,15
D18S51	15,17	100.00%	15,17
FGA	20,26	100.00%	20,26
	20,20	0.00%	
D16S539	11,11	100.00%	11,11
CSF1PO	12,12	100.00%	12,12
D13S317	9,12	100.00%	9,12
D5S818	12,12	100.00%	12,12
D7S820	10,12	100.00%	10,12
	10,10	0.00%	

Reporting –

Results of the unintuitive deconvolution was not reported

- Case record addresses any deconvolutions that are not reported and the reason
 - *“Genotype weightings were unintuitive - data not reported. Re-run with extra burn-in and post burn-in iterations. This data reported”*
- Comparison to POI supported exclusion in both runs

Unintuitive Contributor Assignment

Case Example 2

Homicide

- 3 victims
- Firearm was recovered from suspect flight path
 - Q1: Swabs from rifle
 - Reference standards from S1 and S2
 - No known familial relationship between S1/S2

The partial DNA profile obtained from this item was interpreted as a mixture of four individuals with at least two male contributors.

SUMMARY OF CONTRIBUTORS

CONTRIBUTORS	1	2	3	4
Template (rfu)	1600	297	206	147
Mixture Proportion	71%	13%	9%	7%
Degradation starts at 84bp (rfu/bp)	6.555	1.007	0.506	0.331

S1 AND S2 BOTH ASSIGNED CONTRIBUTOR 1

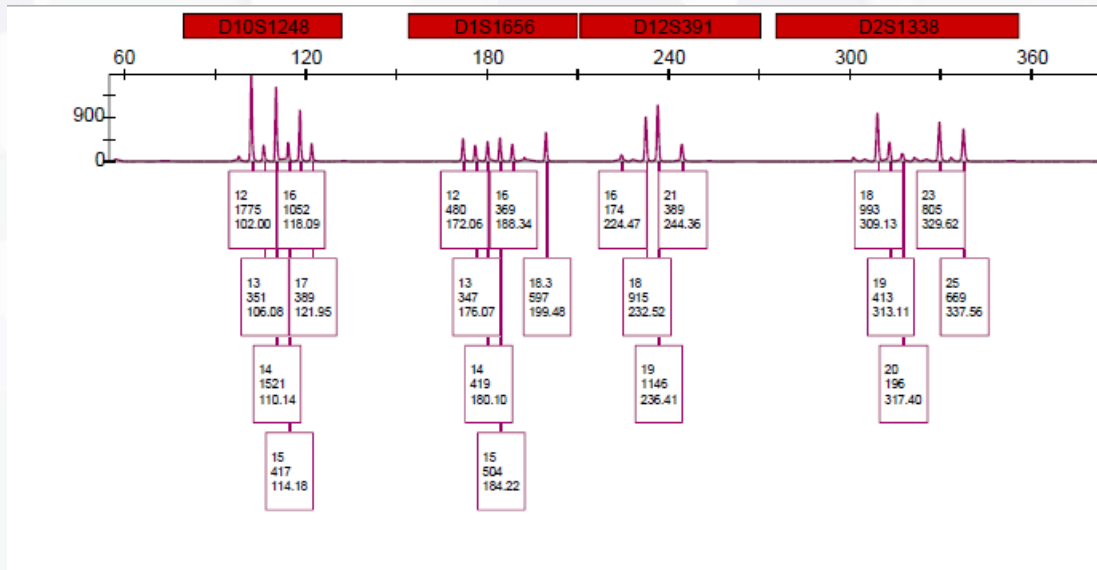
Obtaining this mixture profile is approximately 1.17 quintillion times more likely if the DNA originated from S1 and three unknown, unrelated individuals than if the DNA originated from four unknown, unrelated individuals.

Obtaining this mixture profile is approximately 1.13 trillion times more likely if the DNA originated from S2 and three unknown, unrelated individuals than if the DNA originated from four unknown, unrelated individuals.

Unintuitive Contributor Assignment

Case Example 2

- Concerns for Mixture proportions
- Red flags for contributor assignment
- Complex mixture + Degradation



Mixture Proportions
71%/13%/9%/7%

D21 30,33.2 2.71%
D2S441: 12,13 6.30%

D19 13.2,14 9.33%

D3S1358	16, 17	85.94%	F, F
	17, 17	11.25%	
	16, 16	1.44%	
	15, 17	0.70%	
	15, 16	0.66%	
D21S11	30, 31	54.14%	F, F
	31, 31	31.74%	
	31, 33.2	4.82%	
	29, 31	2.98%	
	30, 33.2	2.71%	
	29, 30	1.64%	
	30, 30	1.36%	
	29, 33.2	0.34%	
	Q, 31	0.12%	
	Q, 30	0.08%	
	Q, 33.2	0.03%	
	Q, 29	0.02%	
	33.2, 33.2	0.01%	
D2S441	11, 12	60.64%	F, F
	11, 14	12.61%	
	12, 14	9.57%	
	11, 13	8.56%	
	12, 13	6.30%	
	13, 14	2.26%	
	11, 11	0.04%	
	12, 12	0.03%	
	14, 14	0.00%	
	13, 13	0.00%	
D19S433	14, 14	90.58%	14, F
	13.2, 14	9.33%	
	14, 15	0.07%	
	13, 14	0.01%	
	13.2, 15	0.01%	
	13.2, 13.2	0.00%	
	13, 13.2	0.00%	
D10S1248	12, 14	72.70%	F, F
	12, 16	13.66%	
	14, 16	12.87%	
	12, 12	0.59%	
	14, 14	0.07%	
	12, 17	0.04%	
	14, 17	0.04%	
	16, 17	0.01%	
	12, 15	0.01%	
	14, 15	0.00%	
	15, 16	0.00%	
	16, 16	0.00%	

Reporting

The partial DNA profile obtained from this item was interpreted as a mixture of three individuals with at least one male contributor.

Obtaining this mixture profile is approximately 1.17 quintillion times more likely if the DNA originated from S1 and three unknown, unrelated individuals than if the DNA originated from four unknown, unrelated individuals. *The statistical calculation for S1 may be overestimated based on the contributor designation assigned by STRmix.*

Obtaining this mixture profile is approximately 1.13 trillion times more likely if the DNA originated from S2 and three unknown, unrelated individuals than if the DNA originated from four unknown, unrelated individuals. *The statistical calculation for S2 may be overestimated based on the contributor designation assigned by STRmix.*

Explaining the Reporting Statement

The statistical calculation for [Name] may be overestimated based on the contributor designation assigned by STRmix. Please contact this laboratory as needed for additional information.

- **“STRmix works in two parts. First, it determines the most likely profiles for contributors in the sample. Then, in comparison to a known sample, it assigns the known sample to a best fit contributor and a statistic is generated. The STRmix results are always evaluated to make sure the results are intuitive.”**
- **“Based on an evaluation of this mixed DNA profile, I believe the statistic for the sample could potentially be falsely elevated. When I evaluated the results in comparison to John Doe there were indications that they may be assigned to the wrong contributor for this sample, which is one of the factors the statistic is based off.”**
- **Case by case basis:**
 - **Issue could be inherent to the complexity of the profile**
 - **Request more information regarding familial relationship**
 - **Request reference standards from first degree relatives if relevant to the case**

Unintuitive Contributor Assignment

Case Example 3

Homicide involving three victims

- V1/V2 were pistol whipped with a gun, V3 (deceased) was shot
- V1 and V2 are mother and daughter
- Gun was recovered from the alleged suspect
 - Q1: Swabs from grips, trigger, slide, magazine release
 - Reference standards from V1, V2, V3 and S1

The partial DNA profile obtained from this item was interpreted as a mixture of three individuals with at least one male contributor.

SUMMARY OF CONTRIBUTORS

CONTRIBUTORS	1	2	3
Template (rfu)	1650	528	209
Mixture Proportion	69%	22%	9%
Degradation starts at 85bp (rfu/bp)	6.703	1.918	0.579

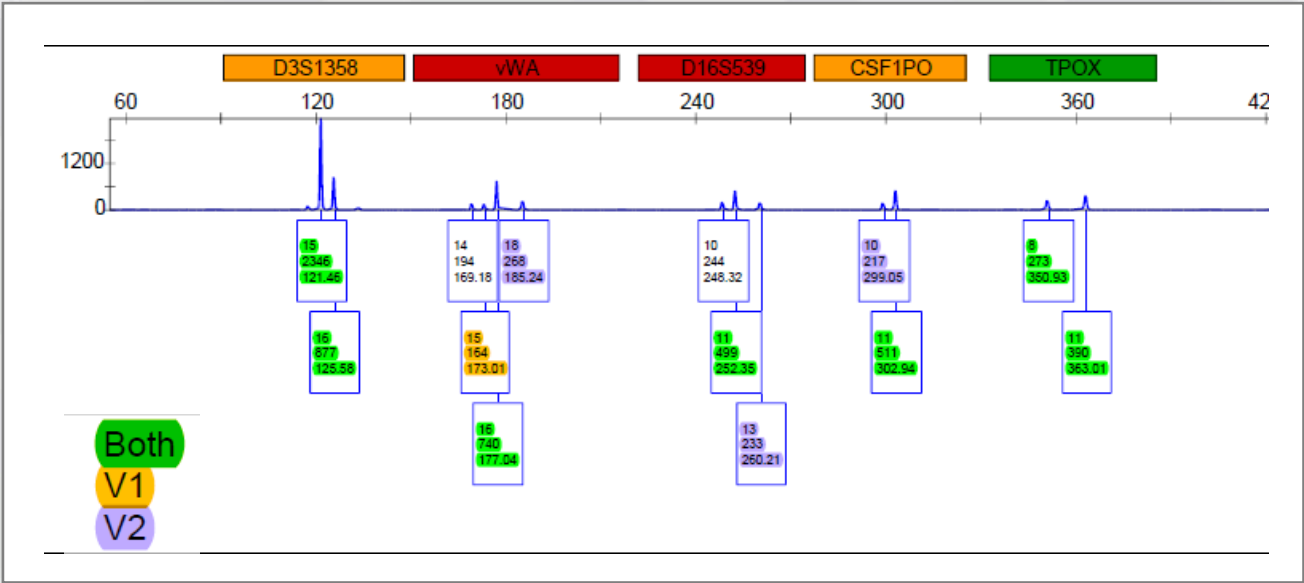
MOTHER (V1) AND DAUGHTER (V2) BOTH ASSIGNED CONTRIBUTOR 1

Obtaining this mixture profile is approximately 6.83 quadrillion times more likely if the DNA originated from V1 and two unknown, unrelated individuals than if the DNA originated from three unknown, unrelated individuals.

Obtaining this mixture profile is approximately 8.52 trillion times more likely if the DNA originated from V2 and two unknown, unrelated individuals than if the DNA originated from three unknown, unrelated individuals

Unintuitive Contributor Assignment

Case Example 3 - Blue Channel



Mixture Proportions
69%/22%/9%

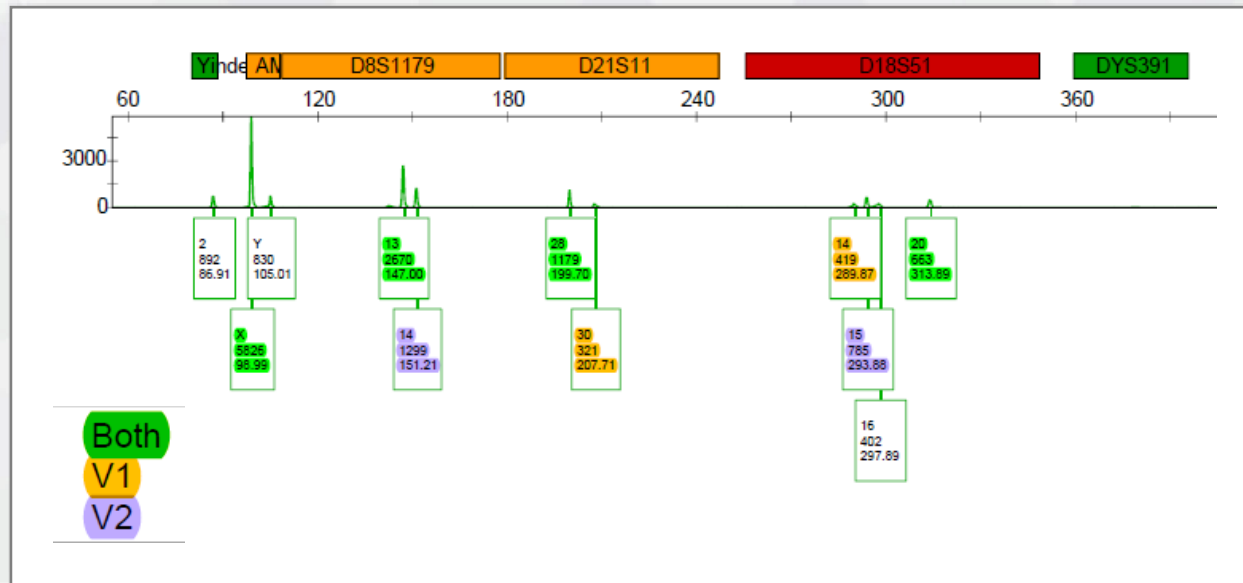
vWA: V1 15,16 1.32%

COMPONENT INTERPRETATION			
CONTRIBUTOR 1 (69%)			
Questioned contributor			
LOCUS	GENOTYPE		
D3S1358	15, 15	66.19%	15, F
	15, 16	33.62%	
vWA	16, 16	0.18%	
	16, 18	50.99%	F, F
	16, 16	41.53%	
	14, 16	4.26%	
	15, 16	1.32%	
	14, 18	1.19%	
	15, 18	0.40%	
	14, 15	0.19%	
	18, 18	0.08%	
	Q, 16	0.02%	
	Q, 18	0.01%	
	Q, 15	0.01%	
	Q, 14	0.00%	
	14, 14	0.00%	
D16S539	11, 13	37.59%	F, F
	10, 11	24.90%	
	11, 11	21.47%	
	10, 13	12.46%	
	13, 13	1.50%	
	Q, 11	0.79%	
	10, 10	0.52%	
	Q, 13	0.42%	
	Q, 10	0.35%	
	Q, Q	0.02%	
CSF1PO	11, 11	50.08%	F, F
	10, 11	36.80%	
	Q, 11	5.37%	
	10, 10	4.08%	
	Q, 10	3.17%	
TPOX	Q, Q	0.51%	
	8, 11	41.24%	F, F
	11, 11	29.40%	
	8, 8	15.21%	
	Q, 11	6.75%	
	Q, 8	6.10%	
	Q, Q	1.30%	

V1 is highlighted in yellow
V2 is highlighted in blue
If weights are highlighted, both share the same genotype

Unintuitive Contributor Assignment

Case Example 3 - Green Channel



Mixture Proportions
69%/22%/9%

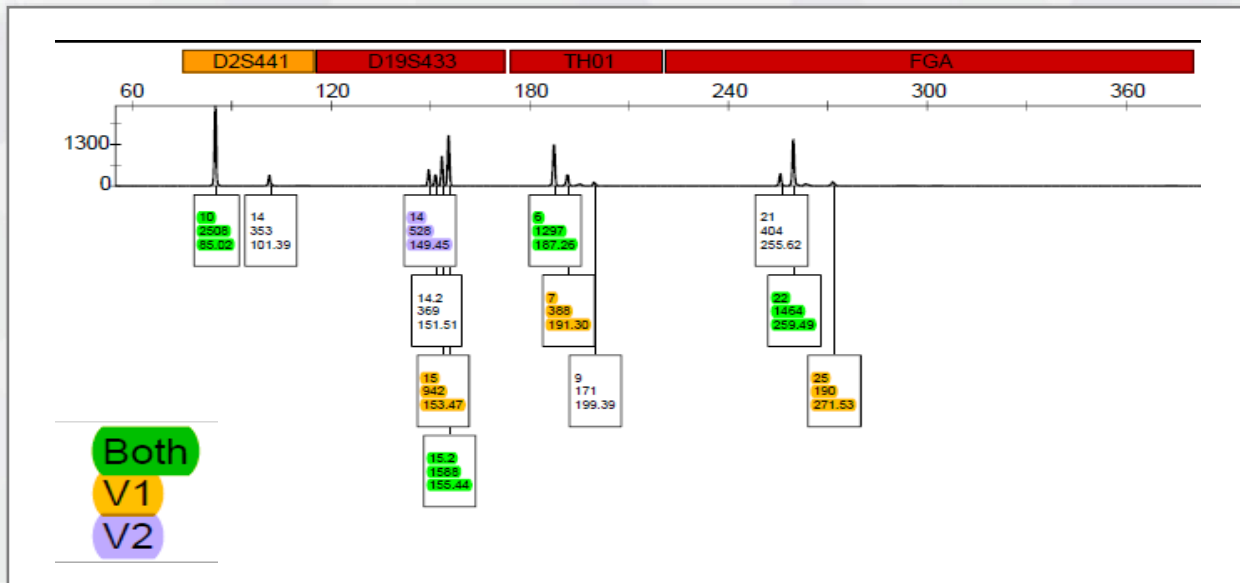
D18: V1 14,20 10.34%

V1 is highlighted in yellow
V2 is highlighted in blue
If weights are highlighted, both share the same genotype

Marker	Genotype	Weight	Assignment
Yindel			
D8S1179	13, 14	52.54%	13, F
	13, 13	47.04%	
	14, 14	0.42%	
D21S11	28, 28	73.65%	28, F
	28, 30	25.99%	
	30, 30	0.26%	
	Q, 28	0.08%	
	Q, 30	0.02%	
D18S51	15, 20	29.95%	F, F
	15, 16	16.02%	
	16, 20	13.08%	
	14, 15	12.73%	
	14, 20	10.34%	
	14, 16	8.30%	
	15, 15	4.59%	
	20, 20	3.81%	
	16, 16	0.64%	
	14, 14	0.37%	
	Q, 15	0.05%	
	Q, 20	0.04%	

Unintuitive Contributor Assignment

Case Example 3 - Yellow Channel



Mixture Proportions
69%/22%/9%

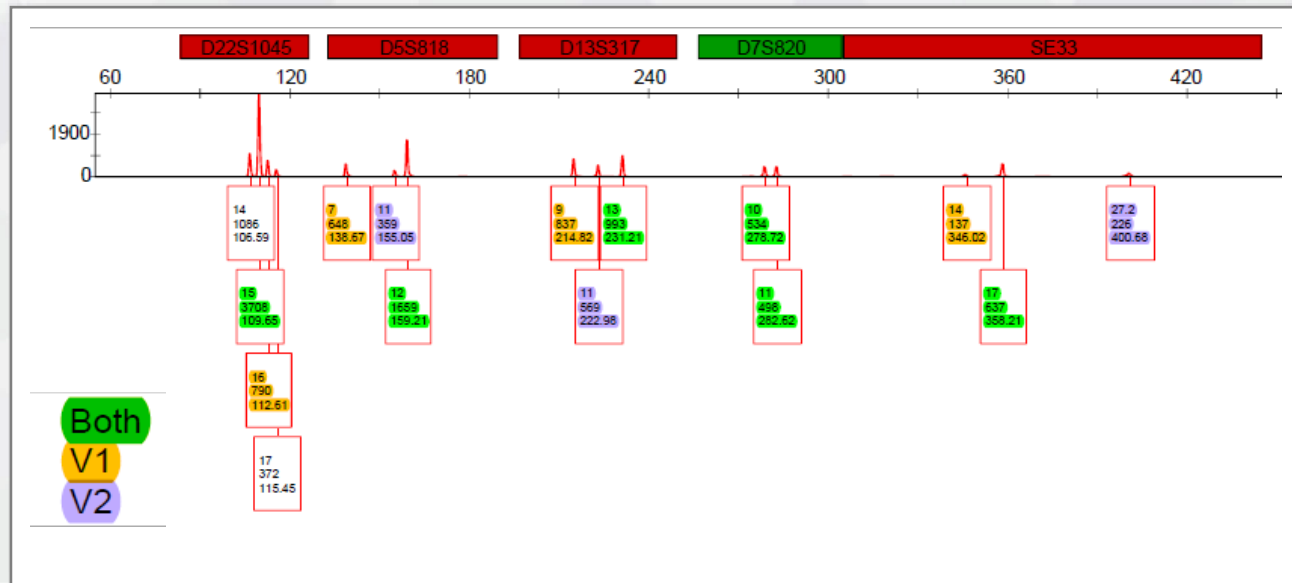
D19: V2 14,15.2 2.45%
FGA: V1 22,25 7.84%

V1 is highlighted in yellow
V2 is highlighted in blue
If weights are highlighted, both share the same genotype

D2S441	10, 10	98.98%	10, F
	10, 14	1.02%	
D19S433	15, 15.2	81.62%	F, F
	15.2, 15.2	13.96%	
	14, 15.2	2.45%	
	14, 15	1.47%	
	15, 15	0.20%	
	14.2, 15.2	0.19%	
	14.2, 15	0.09%	
	14, 14.2	0.02%	
TH01	6, 6	73.20%	6, F
	6, 7	24.32%	
	6, 9	1.77%	
	7, 9	0.59%	
	7, 7	0.09%	
	Q, 6	0.03%	
	Q, 7	0.00%	
	Q, 9	0.00%	
FGA	22, 22	72.41%	F, F
	21, 22	16.19%	
	22, 25	7.84%	
	21, 25	2.78%	
	21, 21	0.37%	
	25, 25	0.13%	
	Q, 22	0.13%	
	Q, 21	0.08%	
	Q, 25	0.06%	
	Q, Q	0.00%	

Unintuitive Contributor Assignment

Case Example 3 - Red Channel



Mixture Proportions
69%/22%/9%

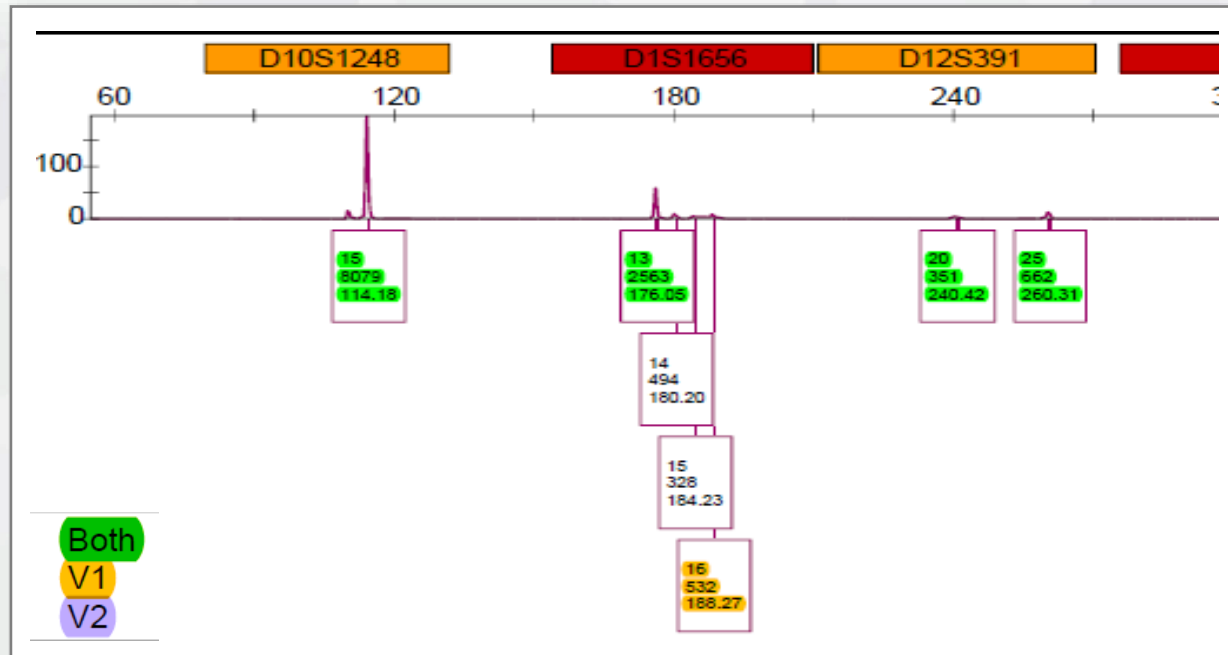
D22: V1 15,16 2.20%
D5: V2 11,12 0.94%

V1 is highlighted in yellow
V2 is highlighted in blue
If weights are highlighted, both share the same genotype

D22S1045	15, 15	95.07%	15, F
	14, 15	2.38%	
	15, 16	2.20%	
	14, 16	0.17%	
	15, 17	0.15%	
	14, 17	0.02%	
	16, 17	0.01%	
	16, 16	0.00%	
D5S818	12, 12	79.11%	12, F
	7, 12	19.51%	
	11, 12	0.94%	
	7, 11	0.38%	
	7, 7	0.06%	
D13S317	9, 13	46.99%	F, F
	11, 13	23.43%	
	9, 11	17.98%	
	13, 13	9.35%	
	9, 9	1.89%	
	11, 11	0.34%	
	Q, 13	0.01%	
	Q, 11	0.01%	
	Q, 9	0.01%	
D7S820	10, 11	54.82%	F, F
	11, 11	21.64%	
	10, 10	20.82%	
	Q, 11	1.34%	
	Q, 10	1.31%	
	Q, Q	0.08%	
SE33	17, 27.2	30.01%	F, F
	17, 17	25.48%	
	14, 17	16.28%	
	14, 27.2	12.47%	
	27.2, 27.2	7.80%	
	Q, 17	2.60%	
	Q, 27.2	2.08%	
	Q, 14	1.82%	
	14, 14	1.19%	
	Q, Q	0.27%	

Unintuitive Contributor Assignment

Case Example 3 - Purple Channel



Mixture Proportions
69%/22%/9%

D1: V1 13,16 6.54%

V1 is highlighted in yellow
V2 is highlighted in blue
If weights are highlighted, both share the same genotype

D10S1248	15,15	100.00%	15,15
D1S1656	13,13	89.58%	13,F
	13,16	6.54%	
	13,14	2.96%	
	13,15	0.40%	
	14,16	0.40%	
	15,16	0.09%	
	14,15	0.04%	
D12S391	25,25	52.96%	F,F
	20,25	42.87%	
	20,20	2.85%	
	Q,25	0.75%	
	Q,20	0.53%	
	Q,Q	0.03%	
D2S1338	23,23	32.98%	F,F
	19,23	23.99%	
	17,23	22.56%	
	17,19	14.35%	
	19,19	2.14%	
	17,17	1.59%	
	Q,23	0.93%	
	Q,17	0.76%	
	Q,19	0.65%	
	Q,Q	0.05%	

Run	Most Conservative Total LR	Contributor 1	Contributor 2	Contributor 3
3p (V1)	8.52 trillion	69%	22%	9%
3p (V2)	6.83 quadrillion	69%	22%	9%
3p (V1 assuming V2)	8.42 billion	62% (V2)	31% (V1)	7%
3p (V2 assuming V1)	1.05 trillion	59% (V1)	33% (V2)	8%

Due to the known familial relationship, additional propositions were considered in order to explore the contributor assignment

By assuming one and running LR for the other, genotype weights for C2 assignment were more intuitive

Reporting

The partial DNA profile obtained from this item was interpreted as a mixture of three individuals with at least one male contributor.

Obtaining this mixture profile is approximately 6.83 quadrillion times more likely if the DNA originated from V1 and two unknown, unrelated individuals than if the DNA originated from three unknown, unrelated individuals. *The statistical calculation for V1 may be overestimated based on the contributor designation assigned by STRmix.*

Obtaining this mixture profile is approximately 8.52 trillion times more likely if the DNA originated from V2 and two unknown, unrelated individuals than if the DNA originated from three unknown, unrelated individuals. *The statistical calculation for V2 may be overestimated based on the contributor designation assigned by STRmix.*

Reporting

The partial DNA profile obtained from this item was also interpreted as a mixture of three individuals with at least one male contributor and with V1 as an assumed contributor. Obtaining this mixture profile is approximately 8.42 billion times more likely if the DNA originated from V1, V2, and one unknown, unrelated individual than if the DNA originated from V1 and two unknown, unrelated individuals.

The partial DNA profile obtained from this item was also interpreted as a mixture of three individuals with at least one male contributor and with V2 as an assumed contributor. Obtaining this mixture profile is approximately 1.05 trillion times more likely if the DNA originated from V2, V1, and one unknown, unrelated individual than if the DNA originated from V2 and two unknown, unrelated individuals.

Final Thoughts

Evaluate all information as a whole when considering whether results are unintuitive.

Low genotype weights can be observed in:

- Complex Mixtures
- High molecular weight loci in degraded samples
- Equal contributors to a mixture

Caution: May be inherent to the profile rather than a red flag for contributor assignment

Propositions explored for likelihood ratios should take into consideration case information

QUESTIONS?

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