Mixture Interpretation Consistency Training Initiative

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Outline

- Initiative to improve consistency of mixture interpretation
- Improvements made to mixture interpretation procedure lead by an internal mixture working group
- Training of new analysts coupled with retraining of existing experts
- Use in extensive examples in training and in manuals
- All analysts interpret the same complex 3 person mixtures
- Examine performance and seek opportunities for improvement

Mixture Training and Procedures

- Examples to cover the gamut of issues
- Thirty-three page interpretation procedure
- Locus by locus approach
- Pictorial along with calculations and rationale
- Include case specific common scenarios to include victim, suspect and other relevant possibilities
- Highlight and resolve common issues through training

D8S1179

✓150

ST = 170

10	16
134.55	159.37
336	1194

13
146.99
621
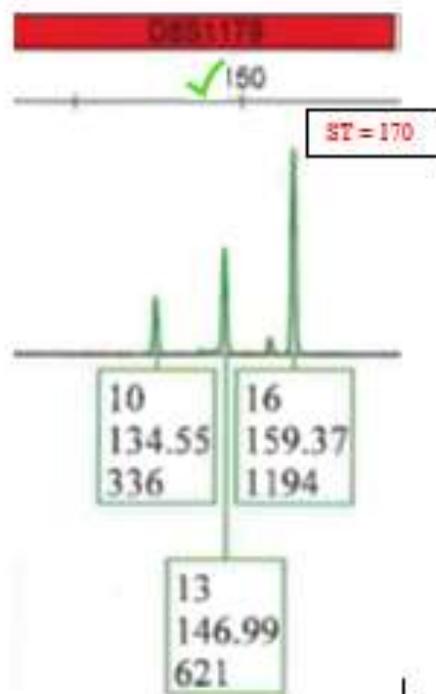
Example 1

All detected alleles are greater than the ST and allelic drop-out was not documented or presumed for this locus. Therefore, all detected alleles are suitable for potential inclusions.

1° & 2° Donor Alleles = 10, 13, & 16

However, to account for the possibility of detected alleles and filtered stutter masking lower level alleles, inconclusive genotypes must still be considered.

Preceding the comparison, a list of inconclusive genotypes can be characterized:

(10, UND), (13, UND), (16, UND), & (STT, -)

Preceding the comparison, a list of potentially included genotypes can be characterized:

(10, 10), (10, 13), (10, 16), (13, 13), (13, 16), & (16, 16)

Assume the Victim and Suspect were submitted for comparison. Based on the interpretation of the entire profile, both are included as a donor to this mixture.
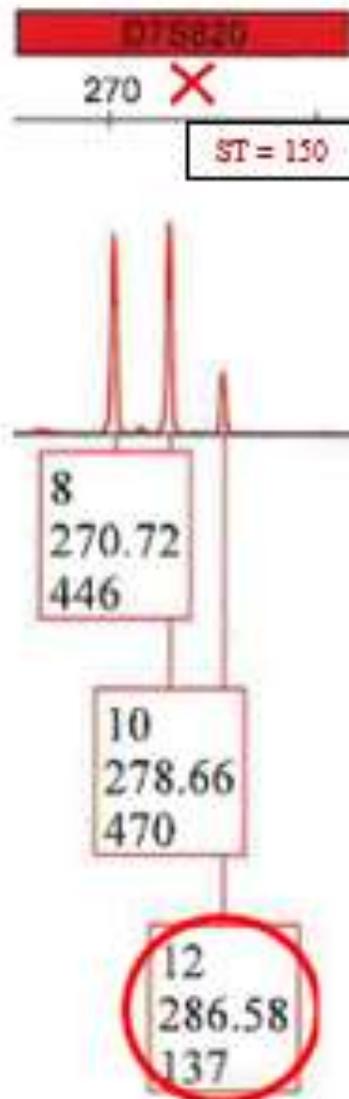
Victim: (13, 16)
Suspect: (10, 16)

At this locus, the information interpreted as suitable for potential inclusions is consistent with the Victim and the Suspect.

UND = Undetected Allele
STT = Stutter

Interpretation of STR DNA Profiles (GlobalFiler®)

Class:	Procedure		Effective Date:	04/06/2018
ID:	Version 5		Page:	24 of 33

D7S820

270 ✗

ST = 150

8
270.72
446

10
278.66
470

12
286.58
137

Example 2

The 12 is less than the ST; therefore, defined as inconclusive.

Based on a resolvability threshold of 4:1, the 8 and the 10 were determined to be unresolved from the 12 allele and therefore, also inconclusive.
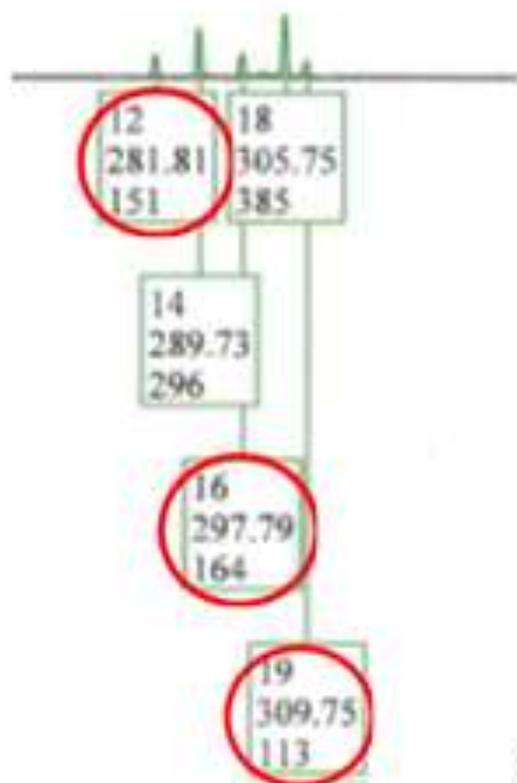
$$\frac{446}{137} = 3.26$$

$$\frac{470}{446} = 1.05$$

Therefore, all detected alleles and the resulting genotypes at this locus are inconclusive.

1° & 2° Donor Alleles = N/A

Preceding the comparison, a list of inconclusive genotypes can be characterized:

(8, -), (10, -), (12, -), & (STT, -)

This locus cannot be used in support of an inclusion or be used to increase the statistical rarity of the profile. The data detected at this locus may only be used to characterize inconclusive genotypes or, if applicable, used for exclusionary determinations.

D18S51

270   X   330

ST = 170

12	18
281.81	305.75
151	385

| 14 |
| 289.73 |
| 296 |

| 16 |
| 297.79 |
| 164 |

| 19 |
| 309.75 |
| 113 |

Example 3

The 12, 16, and 19 are less than the ST; therefore, defined as inconclusive.

Based on a resolvability threshold of 4:1, the 14 and the 18 were determined to be unresolved from the 12, 16, and 19 alleles and therefore, also inconclusive.

$$\frac{296}{164} = 1.80$$

$$\frac{385}{296} = 1.30$$

Therefore, all detected alleles and the resulting genotypes at this locus are inconclusive.

$$1°, 2°, \& 3° \text{ Donor Alleles} = NA$$

Preceding the comparison, a list of inconclusive genotypes can be characterized:

$$(12, -), (14, -), (16, -), (18, -), (19, -), \& (STT, -)$$

This locus cannot be used in support of an inclusion or be used to increase the statistical rarity of the profile. The data detected at this locus may only be used to characterize inconclusive genotypes or, if applicable, used for exclusionary determinations.

D1S1656

175 ✓

ST = 160

12
172.09
344

13
176.26
253

16
188.35
428

16.3
191.44
211
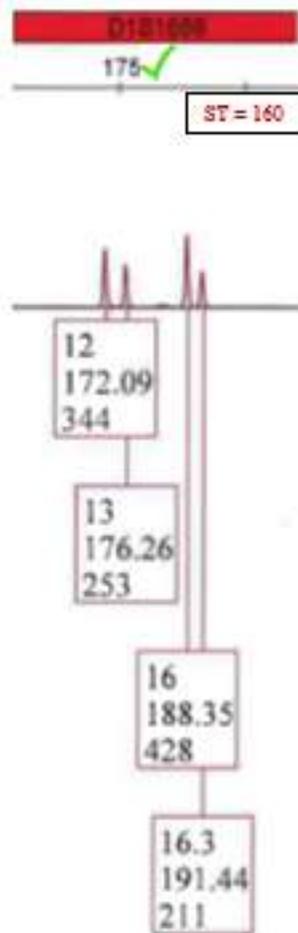
Example 5

All detected alleles are greater than the ST and allelic drop-out was not documented or presumed for this locus. Based on a resolvability threshold of 4:1, all detected alleles are unresolved from one another.

$$\frac{253}{211} = 1.20$$

$$\frac{344}{253} = 1.36$$

$$\frac{428}{344} = 1.24$$

However, based on the number of alleles detected, a minimum of two donors were detected at this locus. Since, the number of donors is less than three, all detected alleles at this locus are suitable for potential inclusions.

1° & 2° Donor Alleles = 12, 13, 16, & 16.3

Preceding the comparison, a list of inconclusive genotypes can be characterized:

(12, UND), (13, UND), (16, UND), (16.3, UND), & (STT, -)

Preceding the comparison, a list of potentially included genotypes can be characterized:

=(12, 12), (12, 13), (12, 16), (12, 16.3), (13, 13), (13, 16), (13, 16.3), (16, 16), (16, 16.3), & (16.3, 16.3)

Assume the Victim and Suspect were submitted for comparison. Based on the interpretation of the entire profile, both are included as a donor to this mixture.

Victim: (12, 16)
Suspect: (13, 16.3)

At this locus, the information interpreted as suitable for potential inclusions is consistent with the Victim and the Suspect.

Procedures and Training

- Provide a visual
- Use of data and demonstration
- Provide rationale and logic
- Colorful examples to demonstrate gamut of possibilities
- Marry examples to procedures
- Evaluation of procedures though use of a challenge set

Challenge set of 3 complex mixtures

- Three mixtures provided to staff and group of trainees

- Each are 3 person mixtures

- One mixture expected result is use of all loci for statistic, one mixture no loci used for statistic, one mixture with some but not all loci used for statistic

- Permits an evaluation of staff capability

- Evaluates our current protocols

- Provides opportunity for improvement on an individual and group level

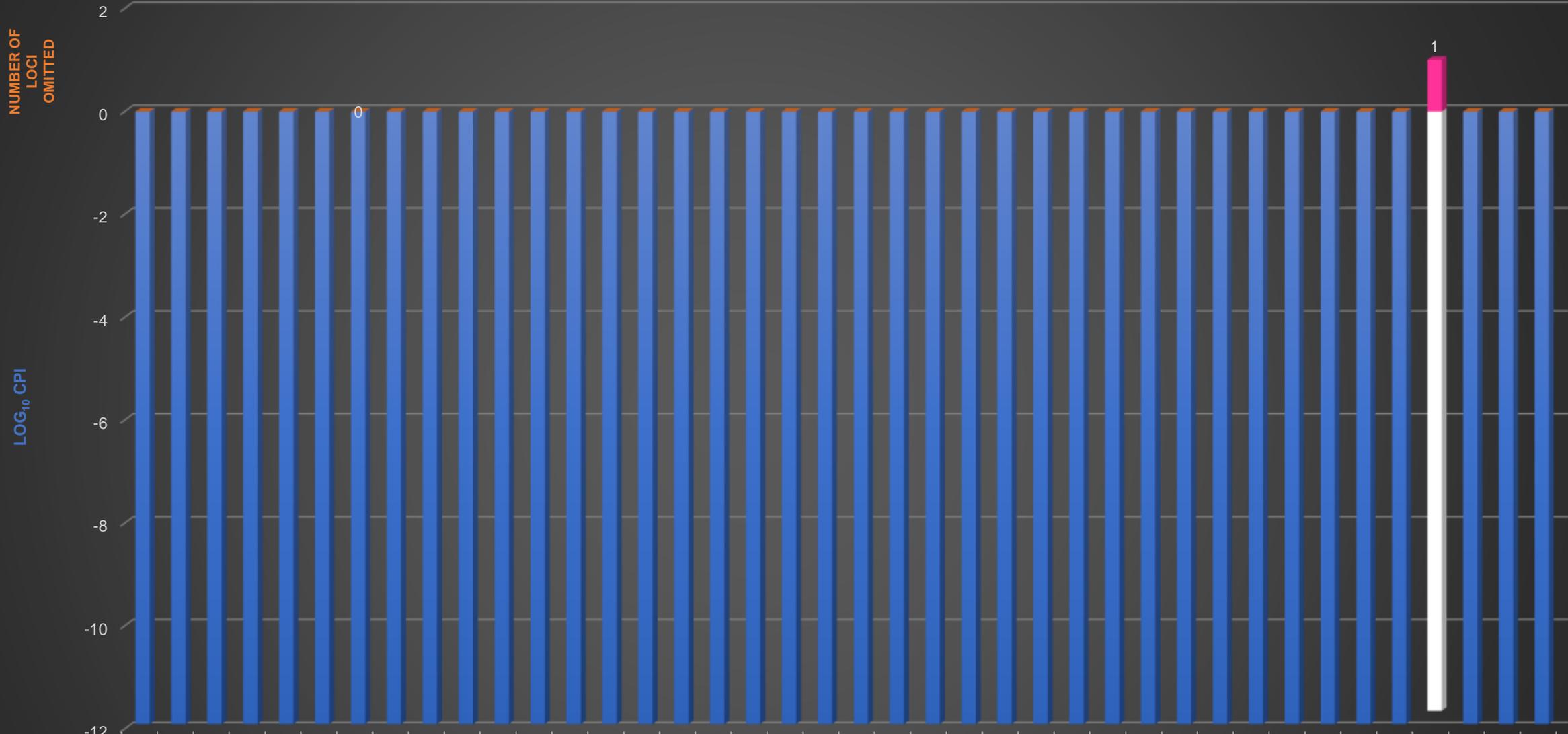# Q1 Concatenated Log$_{10}$ CPI Valuations & Number of Loci Omitted
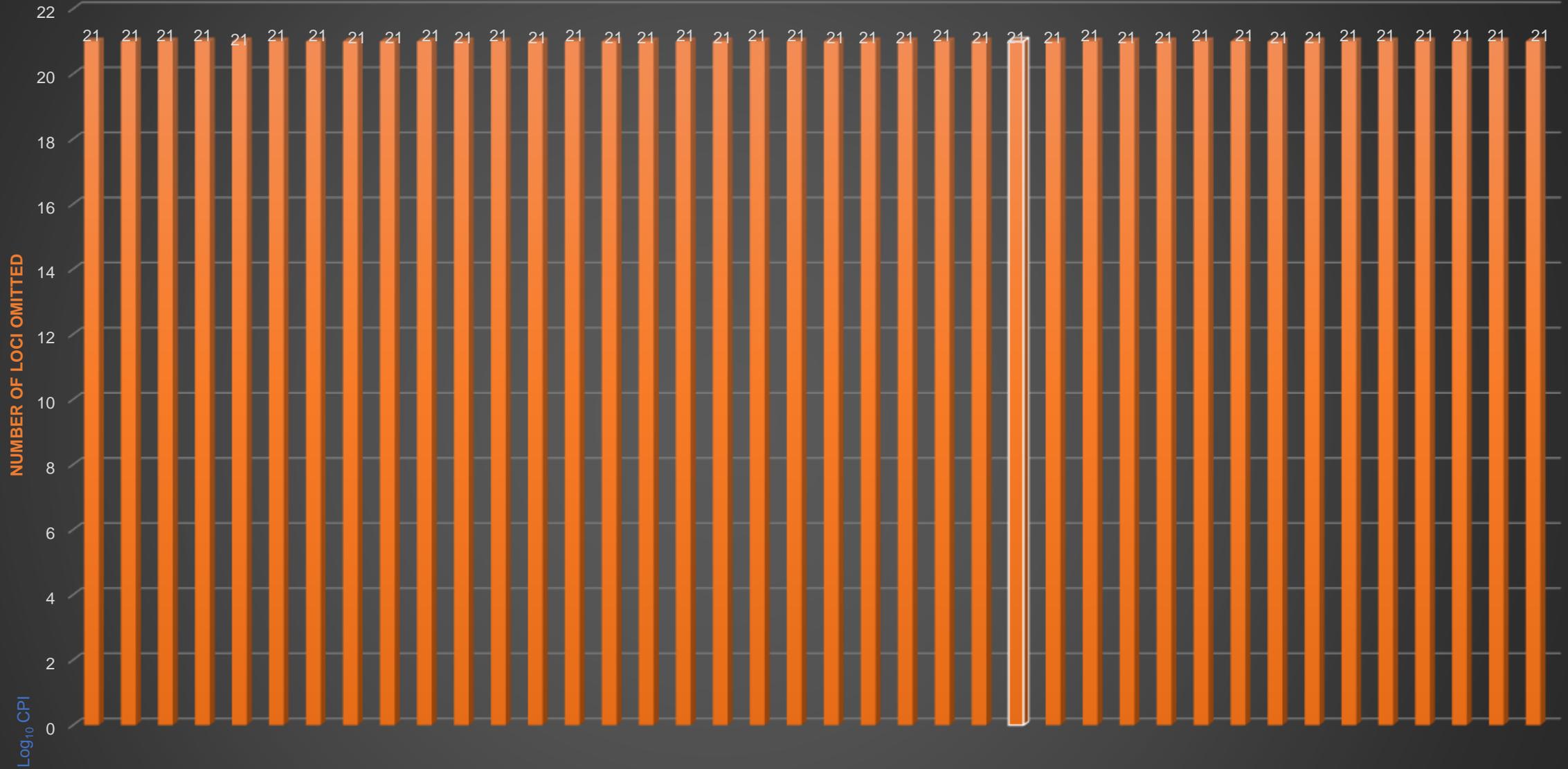
	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12	A13	A14	A15	A16	A17	A18	T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11	C1	C2	C3	S1	S2	S3	S4	S5	S6	S7	S8
■ Number of Loci Omitted	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
■ Log10 CPI Question 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

RESPONDENTS

Mixture 1

- Expected outcome: Mixture profile is too complex for inclusionary purposes
- None of the 40 participants calculated a statistic for this mixture
- A single examiner in training, wrongly interpreted the presence of a major contributor to this mixture
- Provides a teachable moment
- Evaluate training
- Improve understanding
- Produce better, more consistent analysts

Q2 Concatenated Log₁₀ CPI Valuations & Number of Loci Omitted 2

$$\text{Q2 Concatenated Log}_{10}\text{ CPI Valuations \& Number of Loci Omitted 2}$$

	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12	A13	A14	A15	A16	A17	A18	T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11	C1	C2	C3	S1	S2	S3	S4	S5	S6	S7	S8
■ Number of Loci Omitted	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
■ Log10 CPI Question 2	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12

RESPONDENTS

■ Log10 CPI Question 2   ■ Number of Loci Omitted
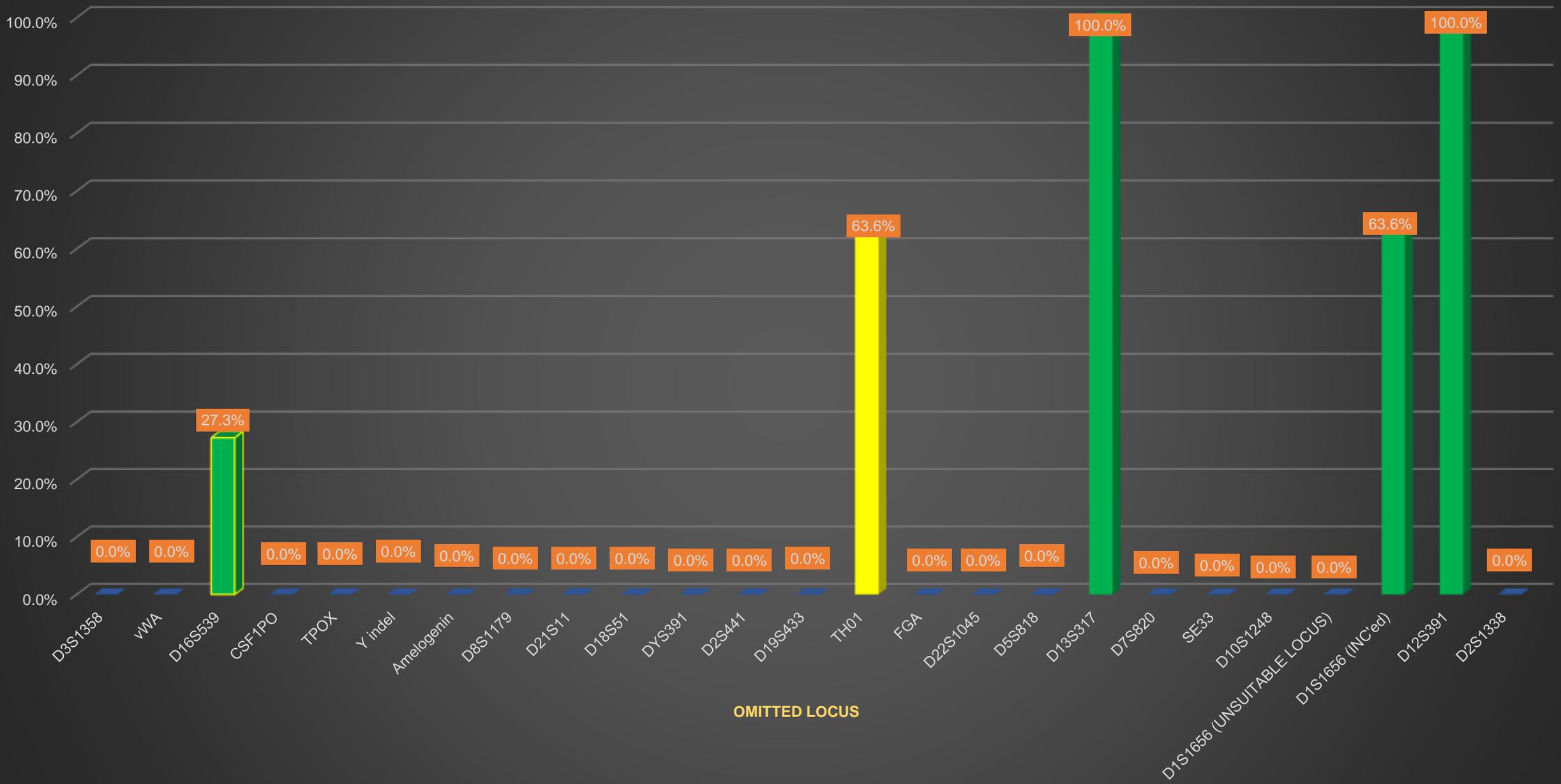
NUMBER OF LOCI OMITTED

LOG₁₀ CPI

Mixture 2

- Expected outcome: All loci and detected alleles suitable for potential inclusions and statistical estimation purposes (if applicable)
- All 40 participants included and excluded the correct individuals and calculated the stat as expected with an exception of a single participant that omitted one locus
- One examiner, an experienced examiner, chose not to include a locus
- Opportunity to gather information on reasoning and make an appropriate correction
- Notice by the graph there is one "nail" sticking up that needs to be tapped down (or at least evaluated)

Q3 Omitted Loci from CPI - Trainees/Analysts < 6 months

Chart showing omitted locus percentages:

- D3S1358: 0.0%
- vWA: 0.0%
- D16S539: 27.3%
- CSF1PO: 0.0%
- TPOX: 0.0%
- Y indel: 0.0%
- Amelogenin: 0.0%
- D8S1179: 0.0%
- D21S11: 0.0%
- D18S51: 0.0%
- DYS391: 0.0%
- D2S441: 0.0%
- D19S433: 0.0%
- TH01: 63.6%
- FGA: 0.0%
- D22S1045: 0.0%
- D5S818: 0.0%
- D13S317: 100.0%
- D7S820: 0.0%
- SE33: 0.0%
- D10S1248: 0.0%
- D1S1656 (UNSUITABLE LOCUS): 0.0%
- D1S1656 (INC'ed): 63.6%
- D12S391: 100.0%
- D2S1338: 0.0%

OMITTED LOCUS

Mixture 3 - Trainees

- Complex mixture containing multiple major contributors suitable for restricted interpretation

- Variation seen among group of trainees, albeit within a generally accepted range

- In the last graph D13 & D2 should have been omitted from being used for potential inclusionary and statistical estimation purposes….D1S should have as well however only 63.6% of the trainees omitted this locus.

- D16 and TH01 were variable (due to potentially low level baseline level activity); either using the locus or omitting it (with appropriate and proper documentation) from the being used for potential inclusionary and statistical estimation purposes was determined to be acceptable

- More documentation needed to describe reason for loci omissions for interpretation and statistic estimation purposes

Take home messages

- Training to include overview, ground truth samples, procedures, good visual case relevant examples, locus by locus demonstration with logic

- Use variation of mixtures to evaluate and improve staff

- Continuous improvement means this is a moving target, not a snapshot in time

- Be open to change and improvement

Questions?

Thank-you for your kind attention

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