California Association of Criminalists Fall Meeting
06 November 2012 – San Jose, California

Exploring the Capabilities of Mixture Interpretation using True Allele Software

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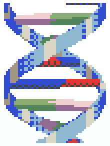
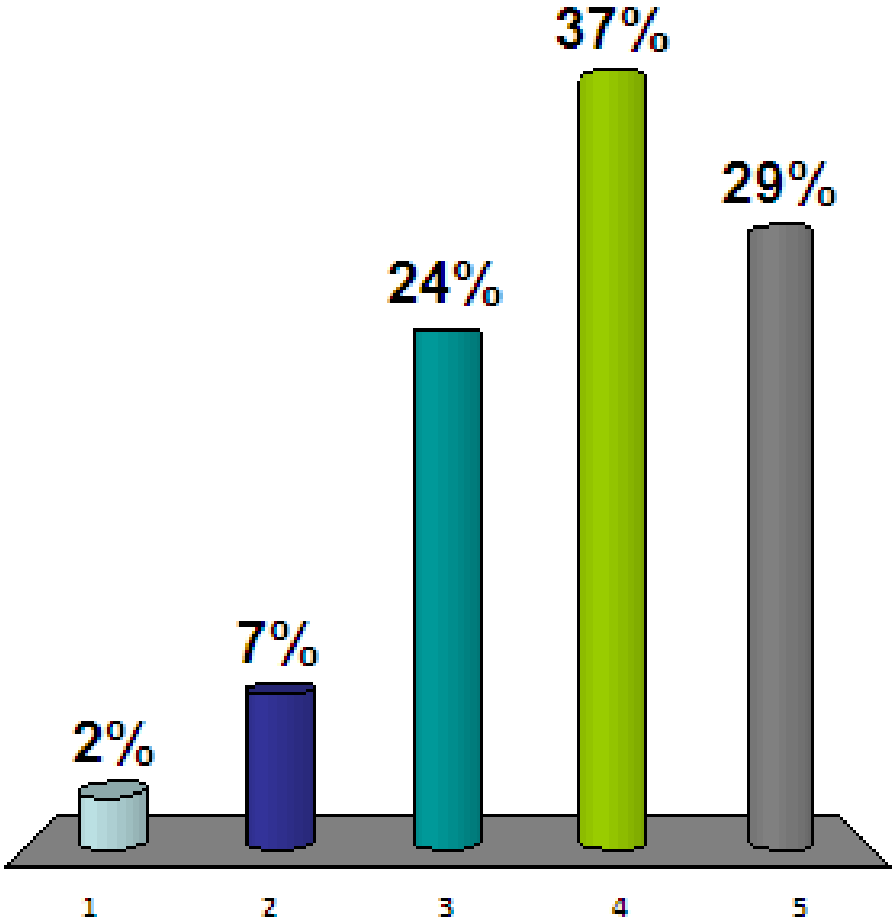


Which of the topics below would be your first choice for additional training?

1. Relevant literature
2. How to validate thresholds
3. How to develop relevant SOPs
4. **Interpretation of low level mixtures**
5. **Statistics**

2/3 want more information on these topics

From one of the regional mixture workshops (Apr – June 2011)



Stats Required for Inclusions

SWGDAM Interpretation Guideline 4.1:

> “**The laboratory must perform statistical analysis in support of any inclusion** that is determined to be relevant in the context of a case, irrespective of the number of alleles detected and the quantitative value of the statistical analysis.”

Buckleton & Curran (2008): “There is a considerable aura to DNA evidence. Because of this aura **it is vital that weak evidence is correctly represented as weak or not presented at all**.”

Buckleton, J. and Curran, J. (2008) A discussion of the merits of random man not excluded and likelihood ratios. *Forensic Sci. Int. Genet.* 2: 343-348.

Statistics

A Tragedy in 400 Quadrillion Acts

http://es.wikipedia.org/wiki/William_Shakespeare

> “Though this be madness,
> yet there is method in't.”
>
> — William Shakespeare, *Hamlet*

Statistical Approaches with Mixtures

See Ladd *et al.* (2001) *Croat Med J.* 42:244-246

“Exclusionary” Approach

Random Man Not Excluded (RMNE)

Combined Prob. of Inclusion (CPI)

Combined Prob. of Exclusion (CPE)

“Allele-centric”

“Inferred Genotype” Approach

Random Match Probability [modified] (mRMP)

Likelihood Ratio (LR)

“Genotype-centric”

FSI GENETICS
Forensic Science International: Genetics 2 (2008) 343–348

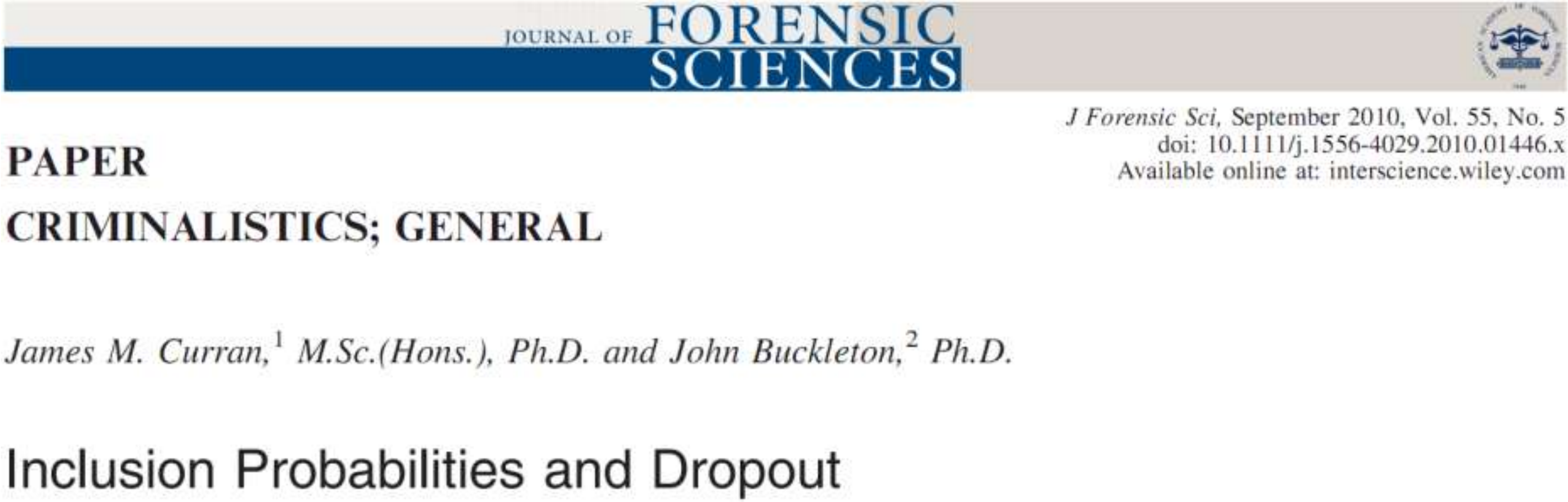
A discussion of the merits of random man not excluded and likelihood ratios

John Buckleton [a,*], James Curran [b]
[a] *ESR, PB 92021, Auckland, New Zealand*
[b] *Department of Statistics, University of Auckland, PB 92019, Auckland, New Zealand*

Received 15 January 2008; received in revised form 29 April 2008; accepted 1 May 2008

We conclude that the two matters that appear to have real force are:
(1) LRs are more difficult to present in court and
(2) the RMNE statistic wastes information that should be utilised.

Curran and Buckleton (2010)



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doi: 10.1111/j.1556-4029.2010.01446.x
Available online at: interscience.wiley.com

PAPER

CRIMINALISTICS; GENERAL

James M. Curran,[1] M.Sc.(Hons.), Ph.D. and John Buckleton,[2] Ph.D.

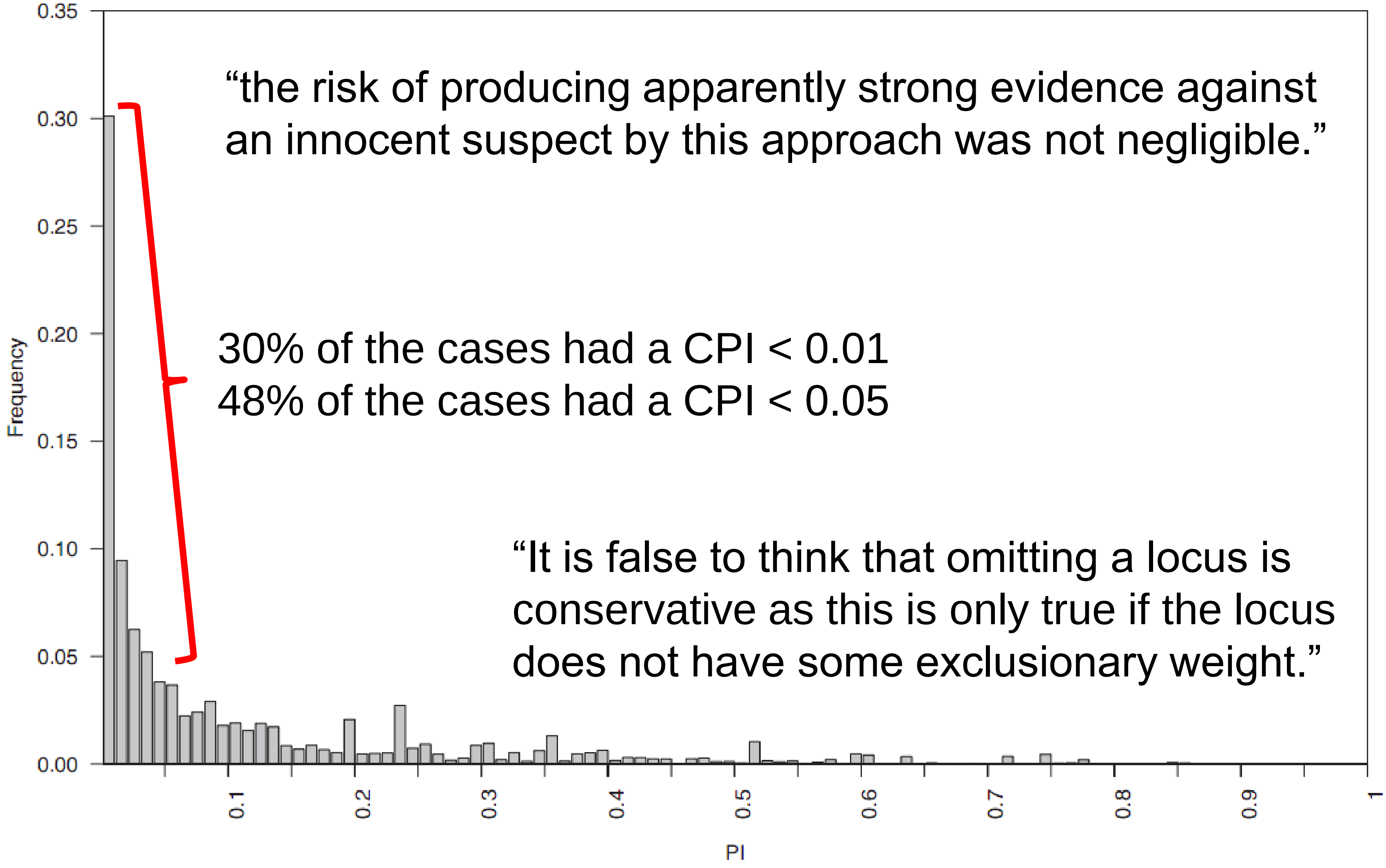
Inclusion Probabilities and Dropout

Created 1000 Two-person Mixtures (Budowle *et al.*1999 AfAm freq.).

Created 10,000 “third person” genotypes.

Compared “third person” to mixture data, calculated PI for included loci, ignored discordant alleles.

Curran and Buckleton (2010)

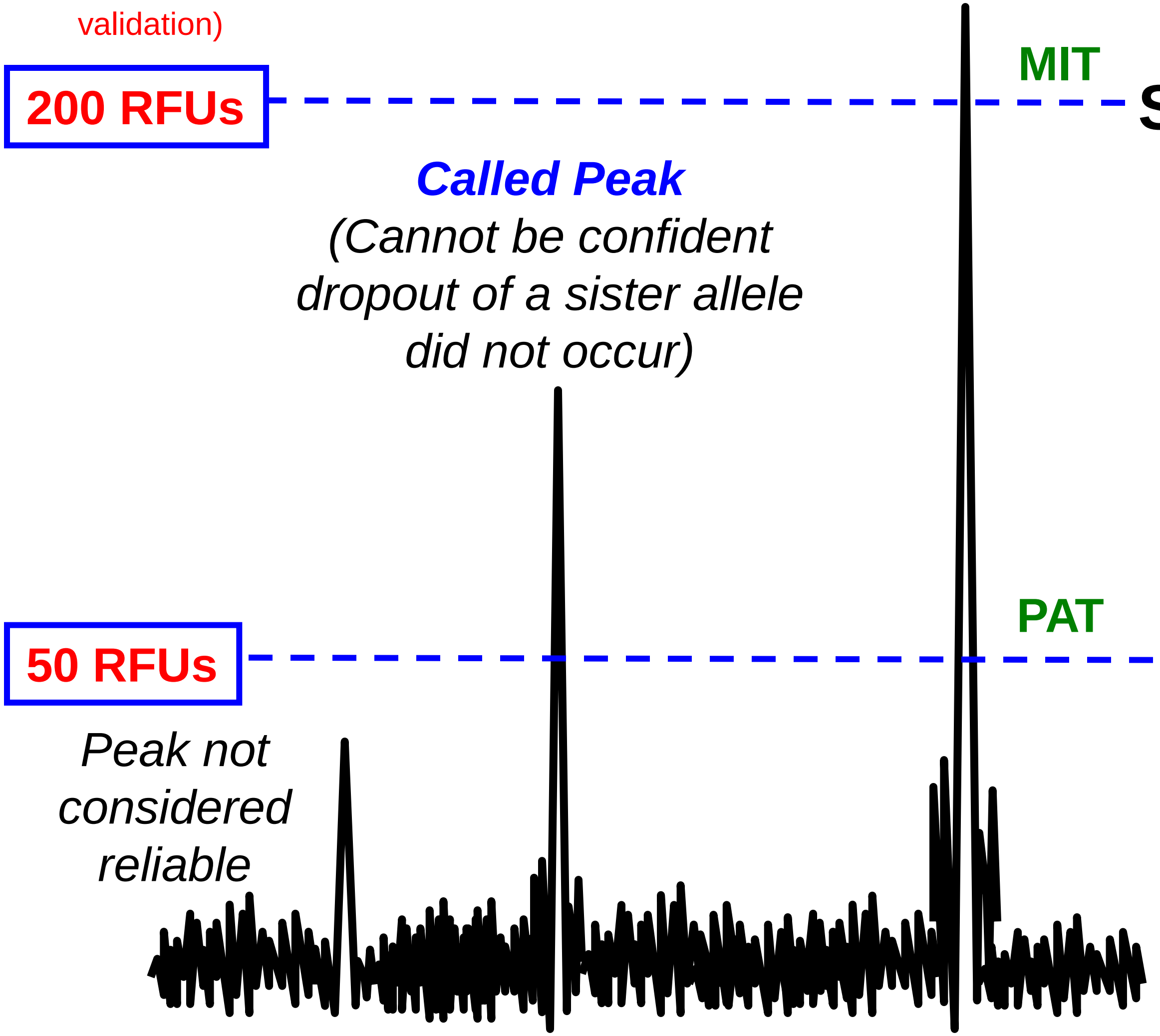


“the risk of producing apparently strong evidence against an innocent suspect by this approach was not negligible.”

30% of the cases had a CPI < 0.01
48% of the cases had a CPI < 0.05

“It is false to think that omitting a locus is conservative as this is only true if the locus does not have some exclusionary weight.”

Review of Two Thresholds



Example values
(empirically determined based on own internal validation)

Called Peak
(Greater confidence a sister allele has not dropped out)

200 RFUs

MIT

Stochastic Threshold

The value above which it is reasonable to assume that allelic dropout of a sister allele has not occurred

Called Peak
(Cannot be confident dropout of a sister allele did not occur)

PAT

50 RFUs

Analytical Threshold

Minimum threshold for data comparison and peak detection in the DNA typing process

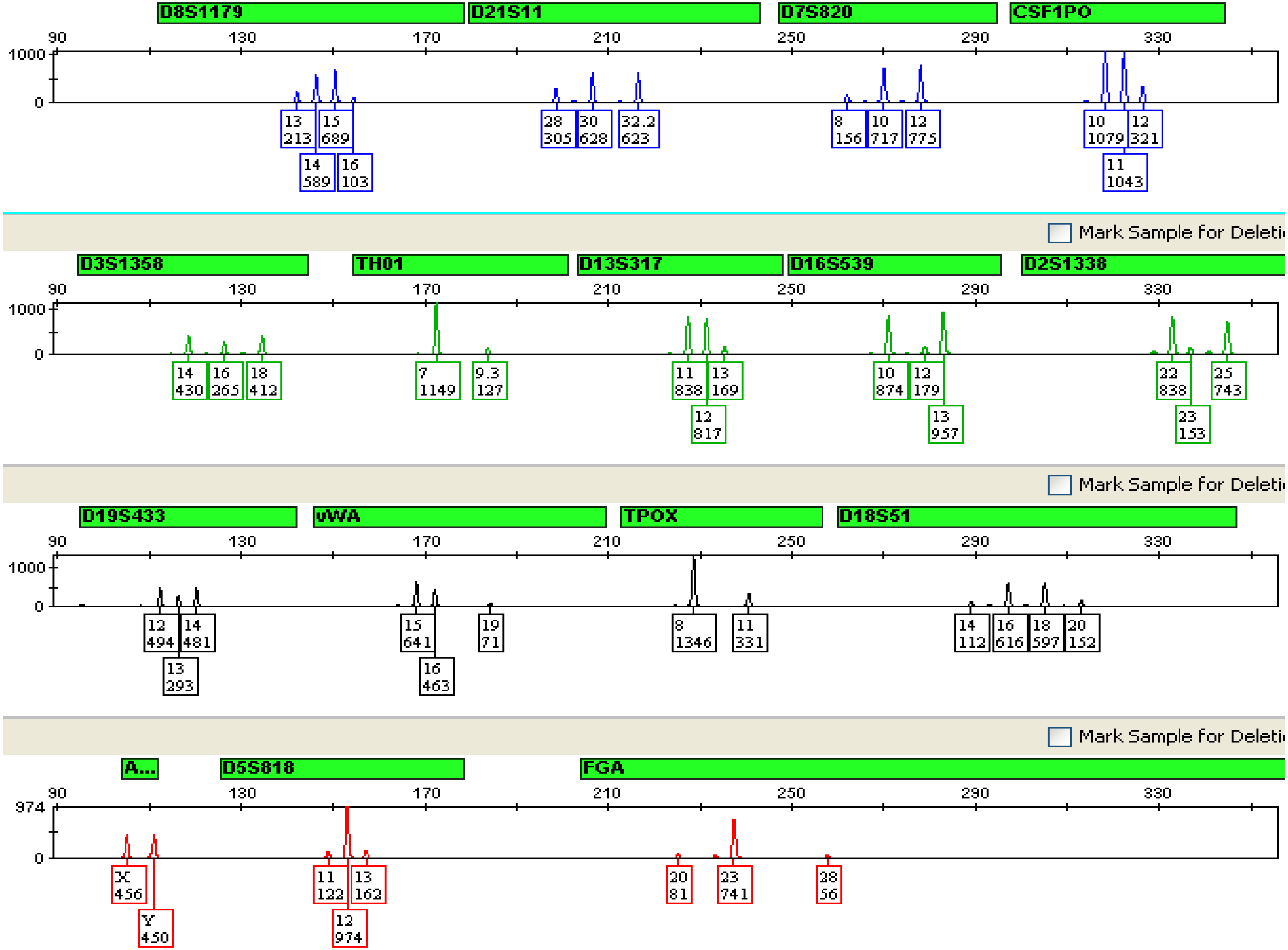
Peak not considered reliable

Noise

Butler, J.M. (2010) *Fundamentals of Forensic DNA Typing*. Elsevier Academic Press: San Diego.

2-person Mixture

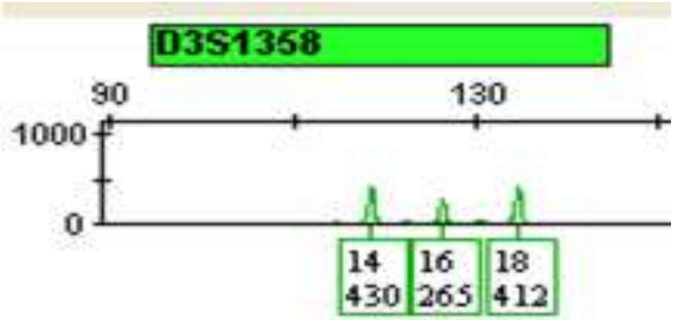
2-Person Mixture

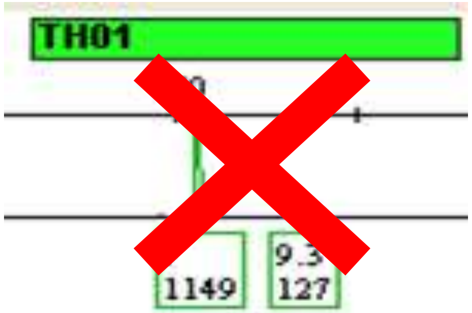


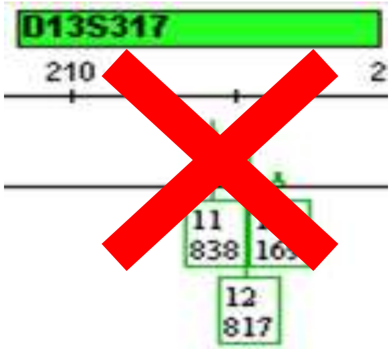
If CPI/CPE Stats are Used

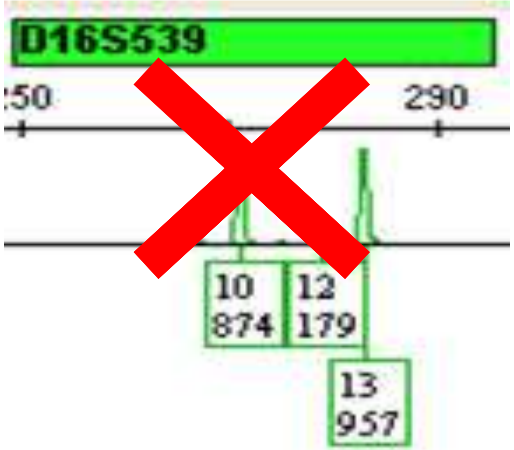
Since exclusionary statistics cannot adjust for the possibility of dropout, and does not take the number of contributors into account, any loci with alleles below the stochastic threshold cannot be used in the CPI statistic.

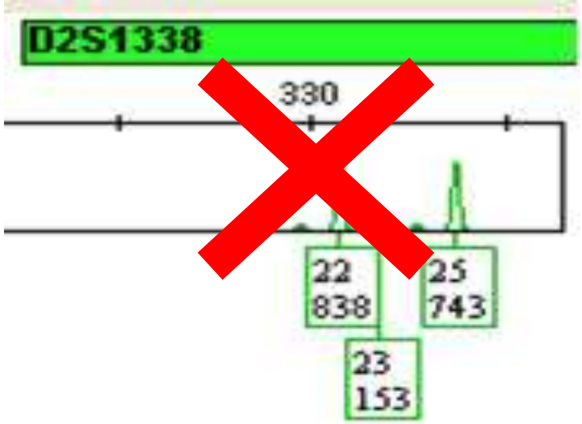
If CPI/CPE Stats are Used
(ST = 200 RFU)











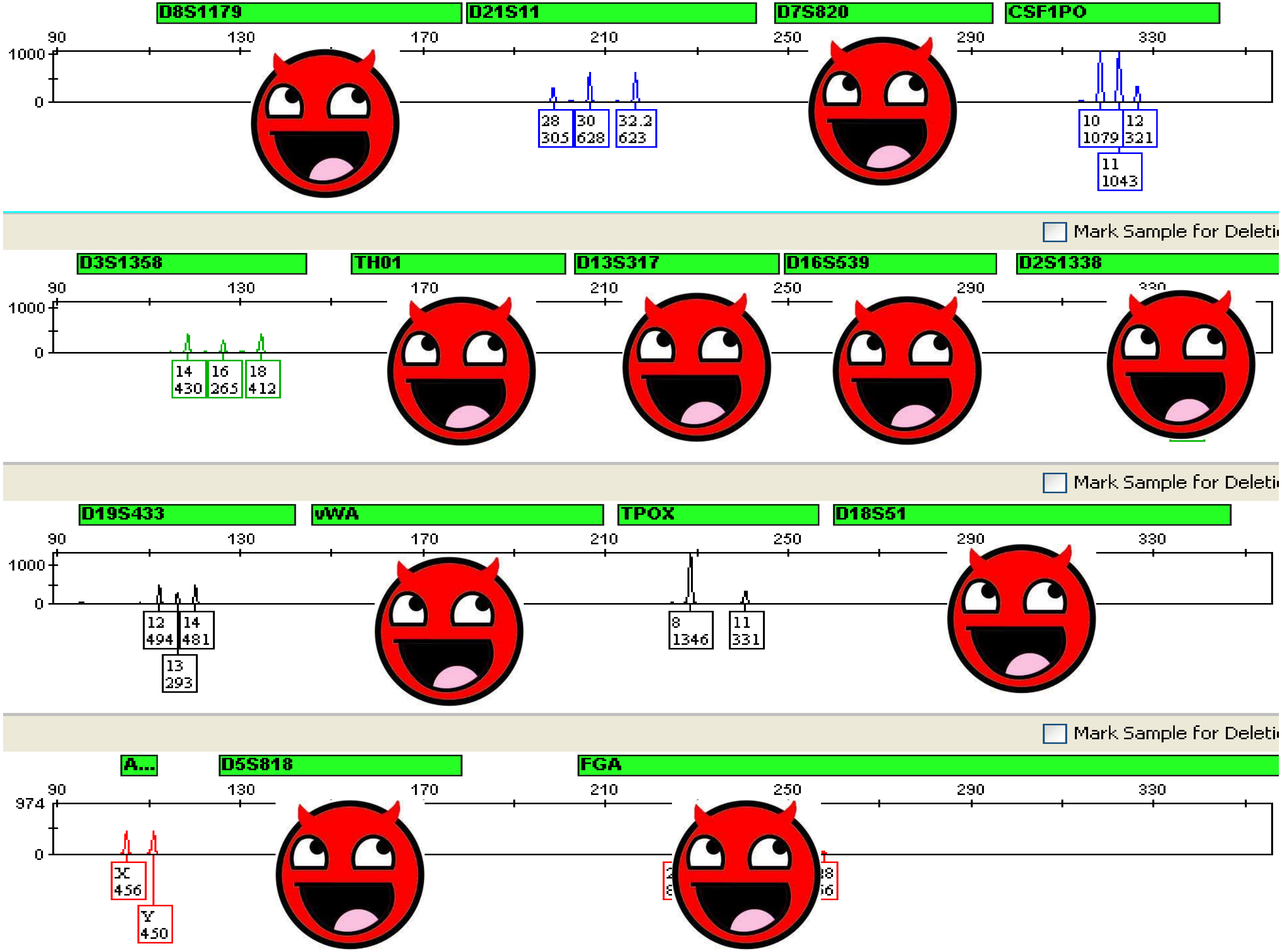
Shakespeare on Allelic Drop-Out

http://es.wikipedia.org/wiki/William_Shakespeare

"Hell is empty and all the devils are here."

— William Shakespeare, *The Tempest*

If CPI/CPE Stats are Used



If CPI/CPE Stats are Used

Can use

D21
CSF
D3
D19
TPOX

Cannot use

D8
D7
TH01
D13
D16
D2
vWA
D18
D5
FGA

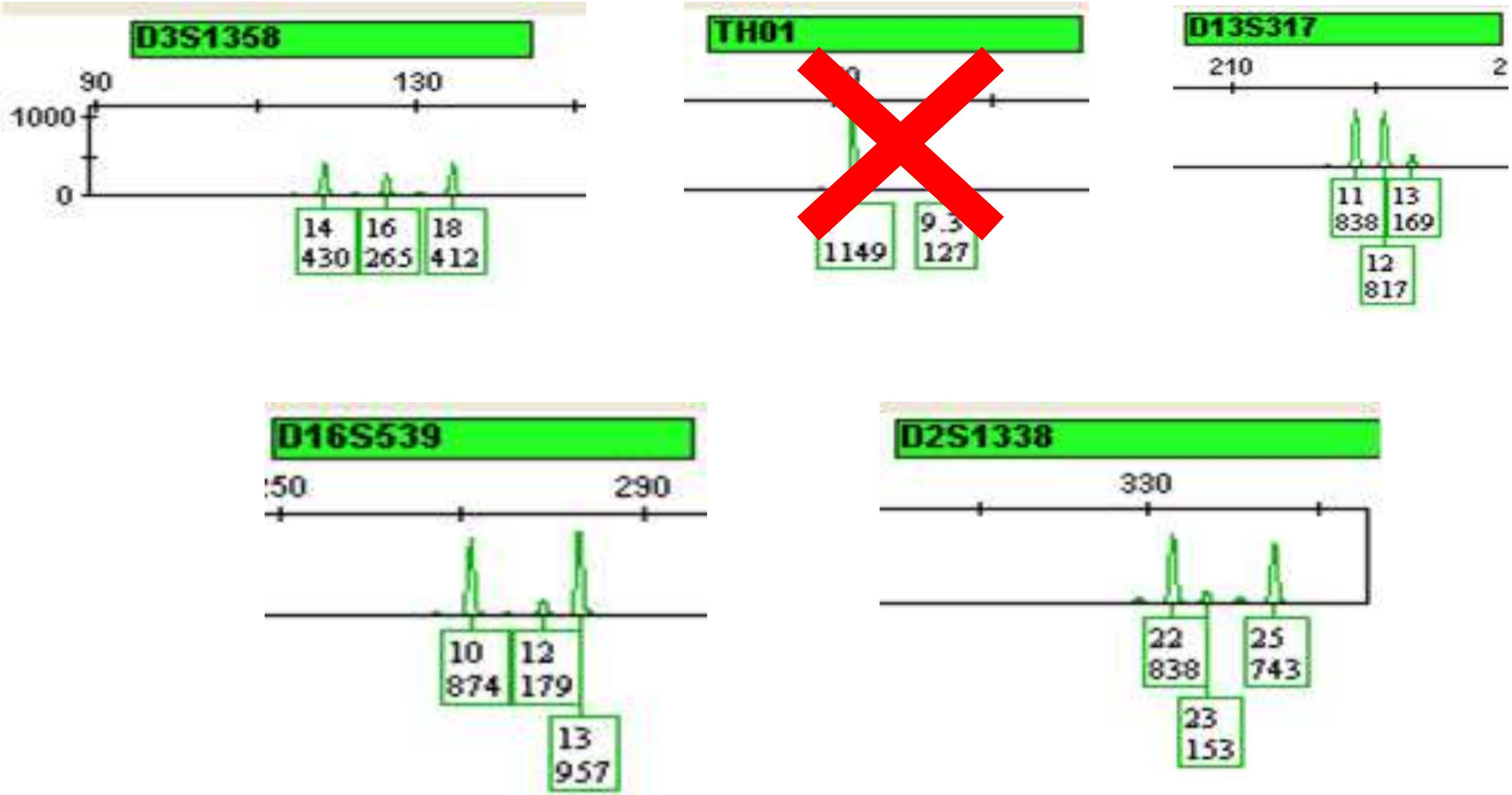
Impact: discarding 2/3 of the data

If CPI/CPE Stats are Used

- CPI statistics using FBI Caucasian Frequencies

- 1 in 71 Caucasians included
- 98.59% Caucasians excluded

If CPI/CPE Stats are Used
(ST = 150 RFU)

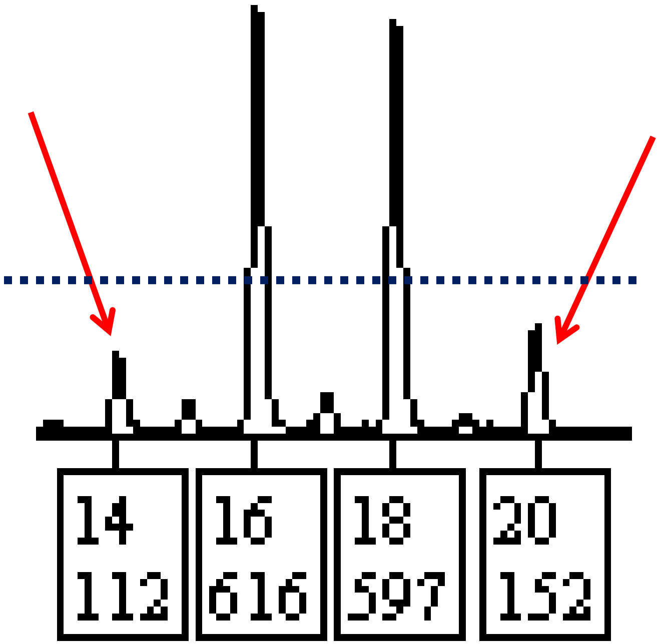


The impact of changing thresholds

If mRMP/LR Stats are Used

- Since there is an assumption to the number of contributors, it is possible to use data that falls below the ST.

mRMP - D18S51



If Assume 2 Contributors….

Major	Minor
16,18	14,20

$$mRMP_{minor} = 2pq$$

$$= 2 \times f(14) \times f(20)$$

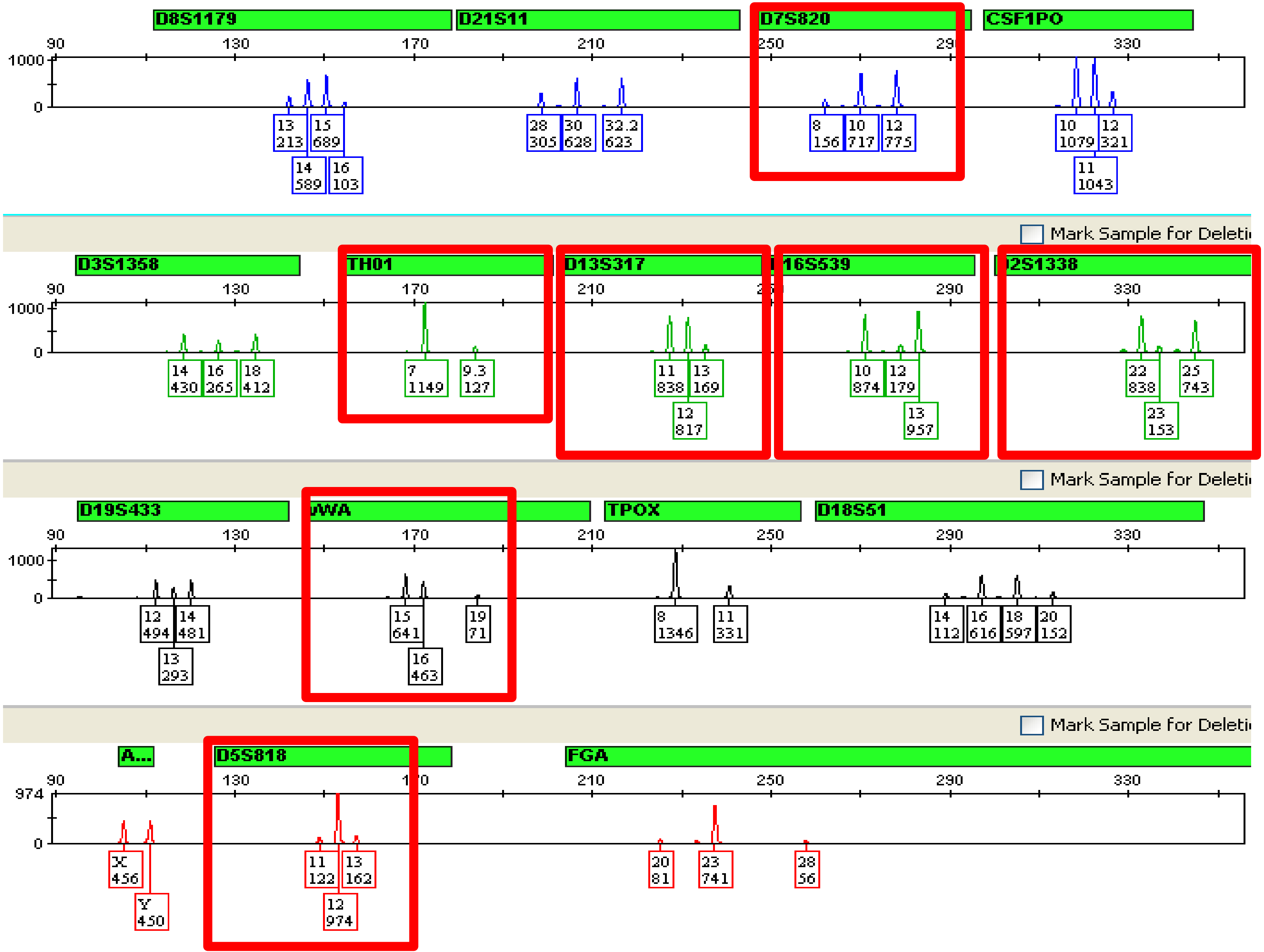
$$= 2 \times (0.1735) \times (0.0255)$$

$$= 0.00884 \quad \text{or 1 in 113}$$

(LR = 113)

mRMP/LR

Potential for Drop-out



If mRMP/LR Stats are Used

Can use

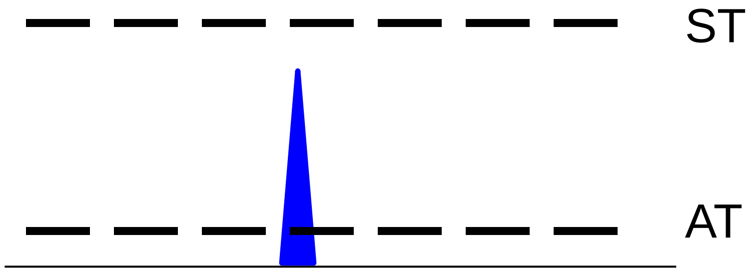
- D8
- D21
- D18
- D3
- D19
- TPOX
- FGA
- CSF

Loci with potential D-out

- D7
- TH01
- D13
- D16
- D2
- vWA
- D5

The “2p” Rule

- The “2p” rule can be used to statistically account for zygosity ambiguity – i.e. is this single peak below the stochastic threshold the result of a homozygous genotype or the result of a heterozygous genotype with allele drop-out of the sister allele?



“2p” or not “2p”… That is the question.

Shakespeare on “2p”

“Drink sir, is a great provoker
of three things….nose painting,
sleep and urine.”

— William Shakespeare, *Macbeth*

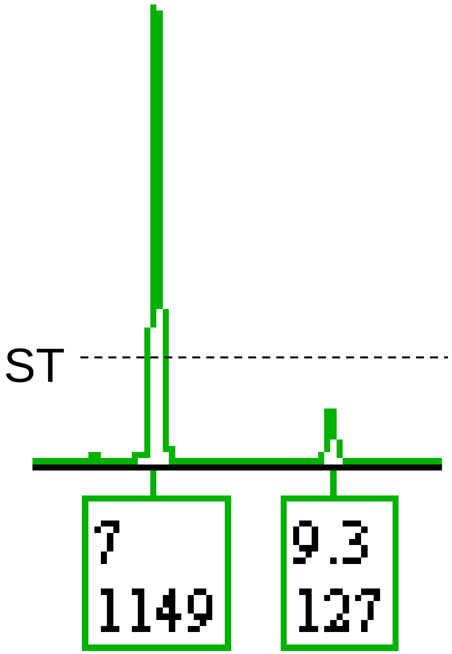
http://es.wikipedia.org/wiki/William_Shakespeare

2p – SWGDAM Guidelines

- 5.2.1.3.1. The formula 2p, as described in recommendation 4.1 of NRCII, may be applied to this result.

- 5.2.1.3.2. Instead of using 2p, the algebraically identical formulae **$2p - p^2$** and **$p^2 + 2p(1-p)$** may be used to address this situation without double-counting the proportion of homozygotes in the population.

Macbeth/Duncan Profile - TH01



Major – 7, 7

Possible Minor Contributors

7, 9.3	(2pq)
9.3, 9.3	p^2
9.3, ?	2p (or $p^2 + 2p(1 – p)$)

Macbeth/Duncan Profile - TH01

$$\frac{P(E|H_1)}{P(E|H_2)} = \frac{V \,\&\, S}{V \,\&\, U} = \frac{\cancel{f_7^{2} + f_7\,(1-f_7)\theta} \;\&\; 1}{\cancel{f_7^{2} + f_7\,(1-f_7)\theta} \;\&\; 2p}$$

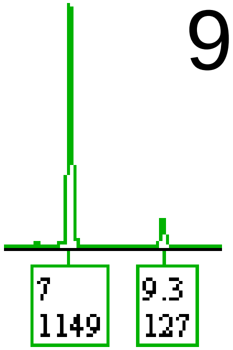
$$p^2 + 2p(1 - p)$$

V = 7, 7

U = 7, 9.3

9.3, 9.3

9.3, ?



$$f_{9.3} = 0.3054$$

$$= \frac{1}{f_{9.3}^{2} + 2f_{9.3}\,(1-f_{9.3})}$$

$$= \; 1 / 0.5175 \; = \boxed{1.93}$$

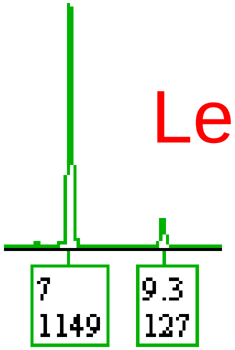
Macbeth/Duncan Profile - TH01

$$\frac{P(E|H_1)}{P(E|H_2)} = \frac{V \,\&\, S}{V \,\&\, U} = \frac{1}{p^2 + p(1-p)\theta + 2pq}$$

V = 7, 7

U = 7, 9.3
9.3, 9.3

$$= \frac{1}{f_{9.3}^2 + f_{9.3}(1-f_{9.3})\theta + 2f_{9.3}f_7}$$



Let ST = 125 RFU

$f_{9.3} = 0.3054$

$f_7 = 0.1724$

$$= 1 / 0.2007 = \boxed{4.98}$$

Macbeth/Duncan Profile - TH01

	LR
ST = 200 (2p is used)	1.93
ST = 125 (2pq is used)	4.98

2p is conservative…

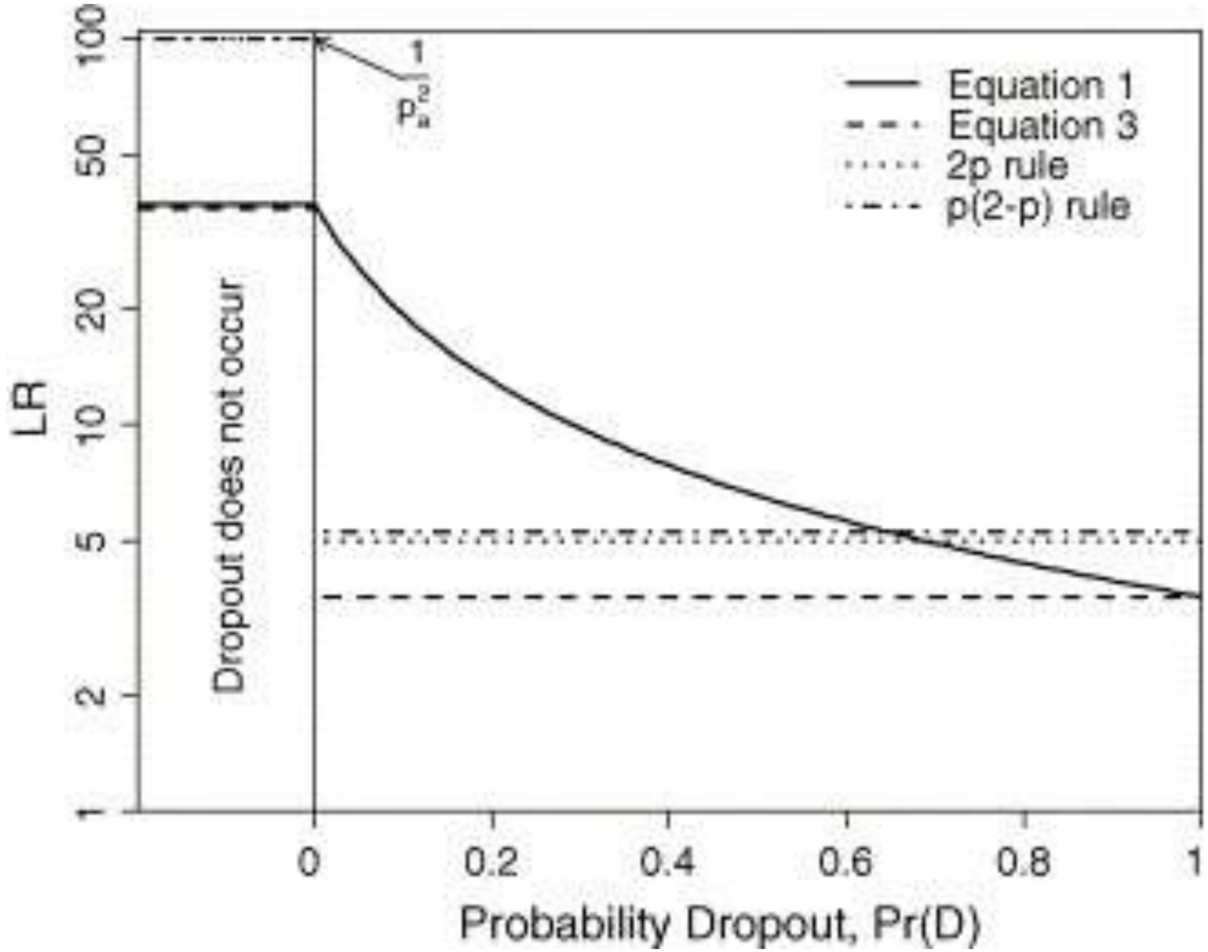
The “2p” Rule

- “This rule arose during the VNTR era. At that time many smaller alleles “ran off the end of the gel” and were not visualised.”

- Buckleton and Triggs (2006)

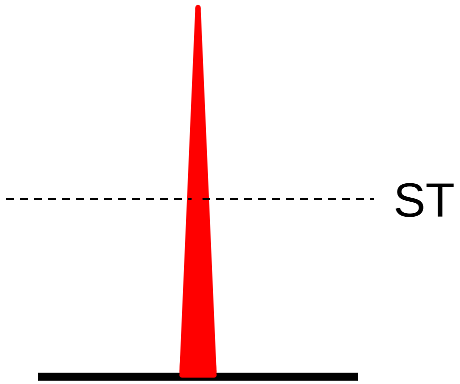
“Is the 2*p* rule always conservative?”

The “2p” Rule



Stain = AA

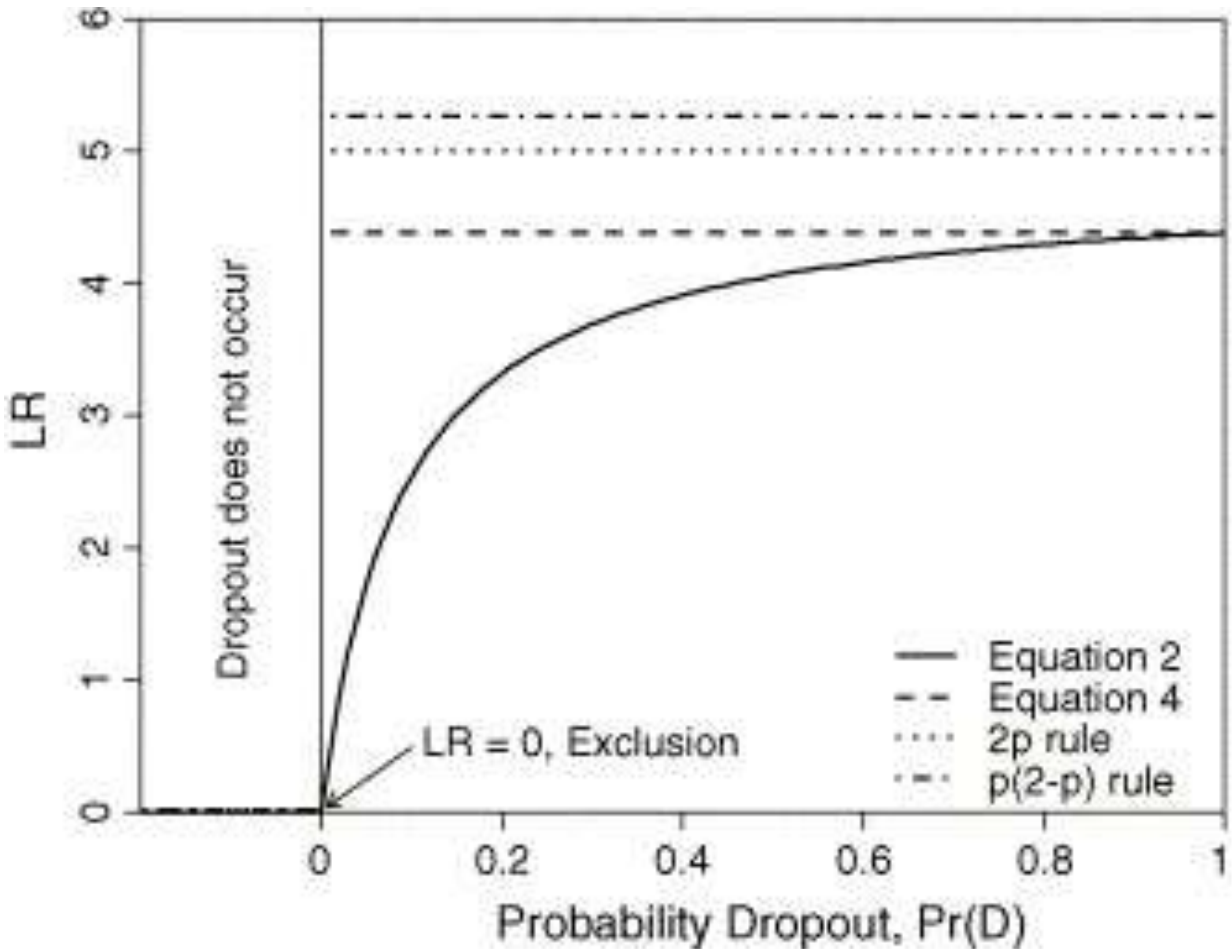
Suspect = AA



LR = 100

f(a) = 0.10 $1/p^2 = 100$ 1/2p = 5

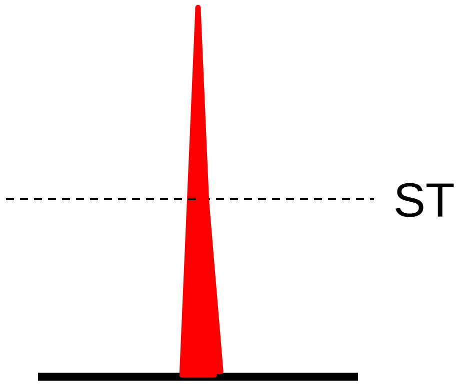
The “2p” Rule



f(a) = 0.10   1/2p = 5

Stain = AA

Suspect = AB



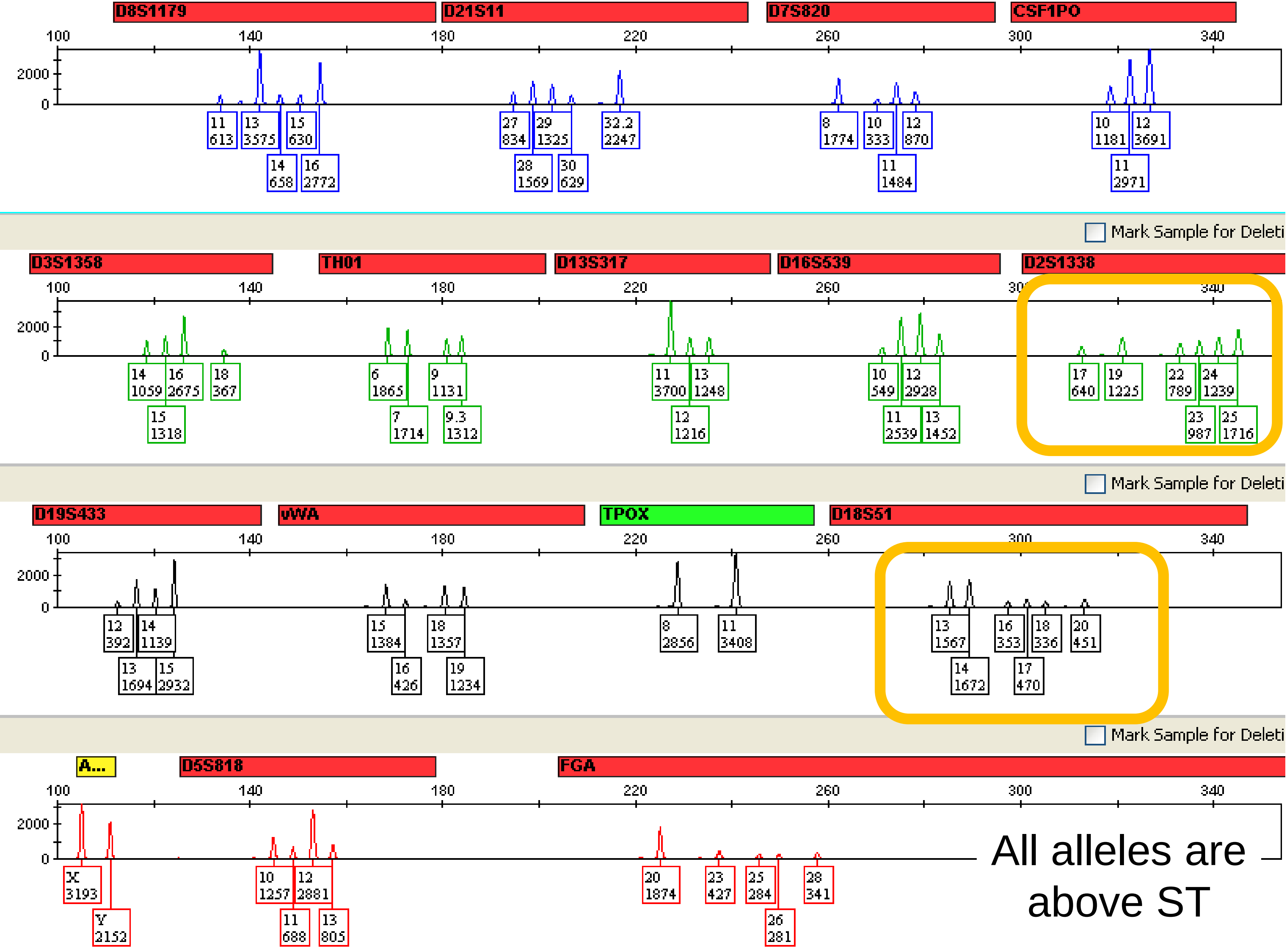
Exclusion

Three Questions

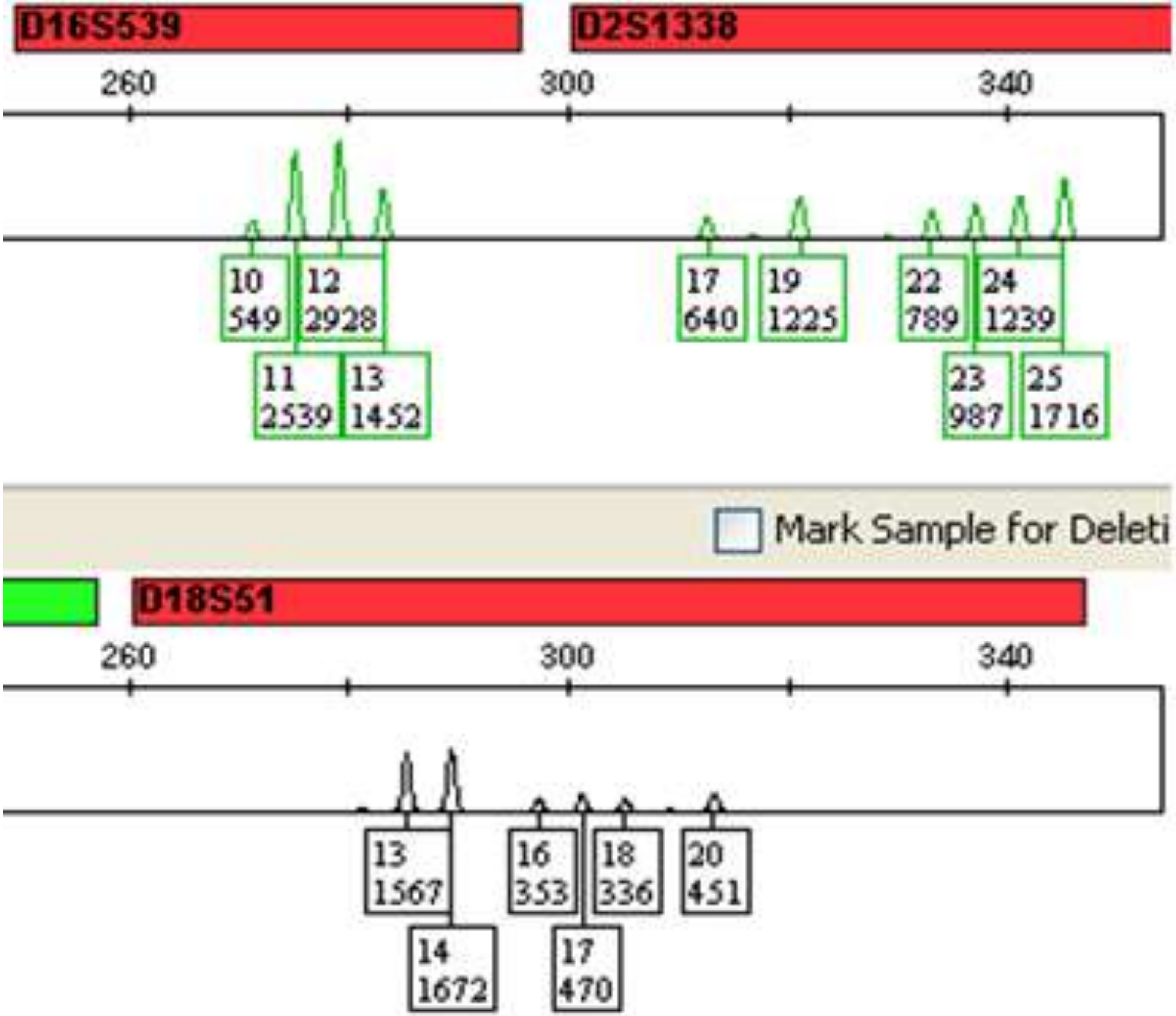
- According to William Shakespeare, what were the last words of Julius Caesar before he died?
- Et tu, Brute?
- What is the capital of Bangladesh?
- Dhaka

Three Questions

- How many people are in this mixture?



All alleles are above ST

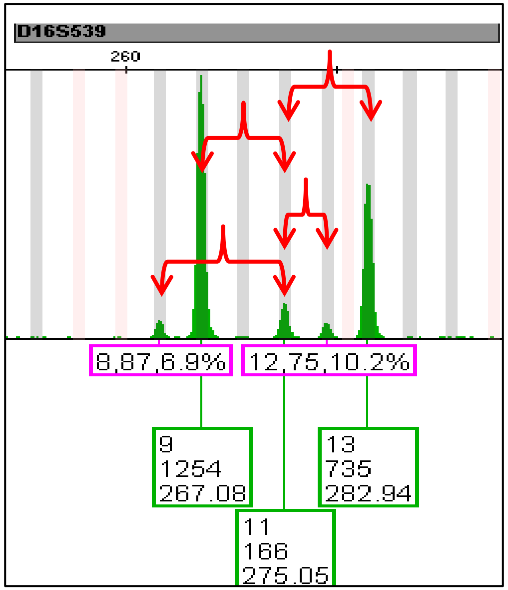

D16S539
D2S1338
260
300
340
10 549
11 2539
12 2928
13 1452
17 640
19 1225
22 789
23 987
24 1239
25 1716
☐ Mark Sample for Deleti
D18S51
260
300
340
13 1567
14 1672
16 353
17 470
18 336
20 451

Do You Have Uncertainty in Your Data?

- **If allele dropout is a possibility** (e.g., in a partial profile), then there is uncertainty in whether or not an allele is present in the sample…and therefore what genotype combinations are possible

- **If different allele combinations are possible** in a mixture, then there is uncertainty in the genotype combinations that are possible…

Possible allele pairing with the 11



Uncertainty and Probability

- “Contrary to what many people think, **uncertainty is present throughout any scientific procedure**.”
  - Dennis V. Lindley, in his foreword to Aitken & Taroni (2004) *Statistics and the Evaluation of Evidence for Forensic Scientists, Second Edition*

- “It is now recognized that **the only tool for handling uncertainty is probability**.”
  - Dennis V. Lindley, in his foreword to Aitken & Taroni (2004) *Statistics and the Evaluation of Evidence for Forensic Scientists, Second Edition*

Is there a way forward?

Next Issue of FSI-Genetics

Forensic Science International: Genetics xxx (2012) xxx–xxx

Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Editorial

Focus issue—Analysis and biostatistical interpretation of complex and low template DNA samples

Article in press…

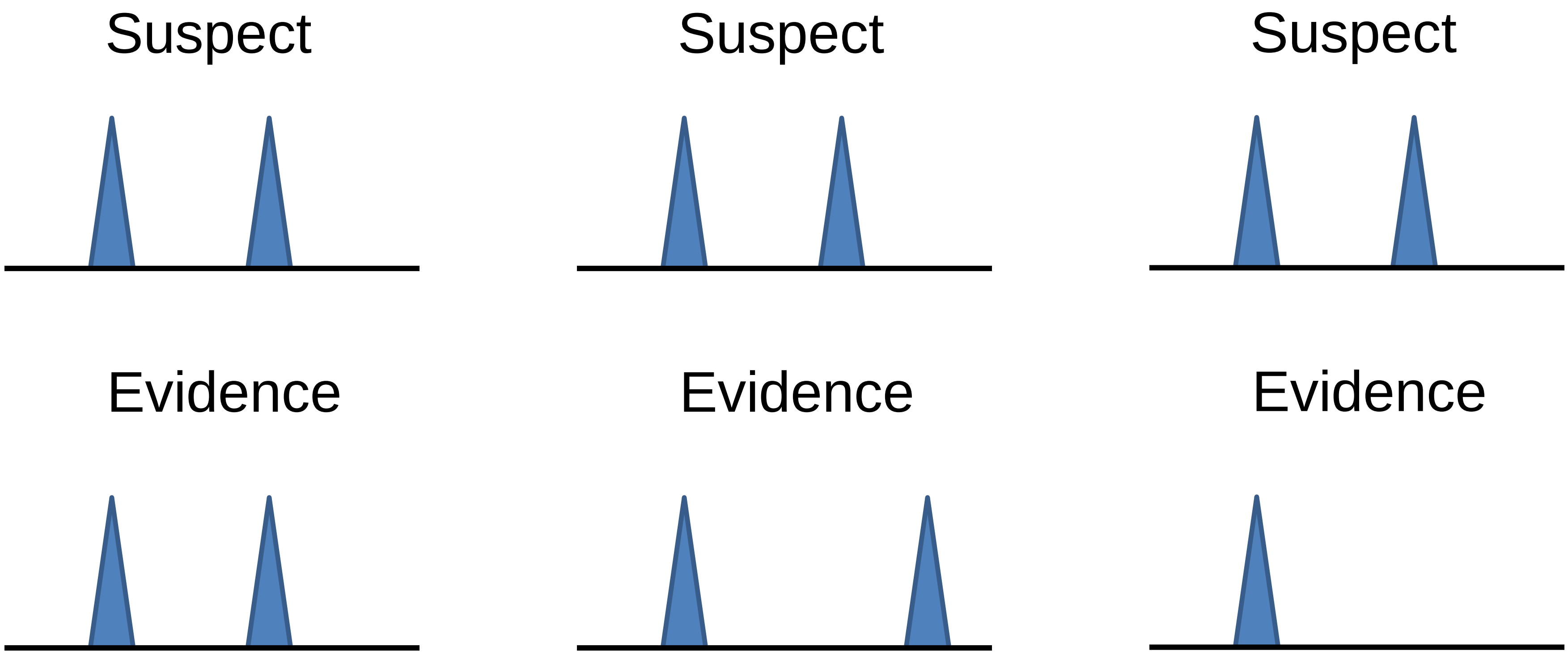
Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods

P. Gill[a,b,*], L. Gusmão[c], H. Haned[d], W.R. Mayr[e], N. Morling[f], W. Parson[g], L. Prieto[h], M. Prinz[i], H. Schneider[j], P.M. Schneider[k], B.S. Weir[l]



$$LR = \frac{1}{2pq}$$

$$LR = \frac{0}{2pq}$$

$$LR = \frac{?}{2pq}$$

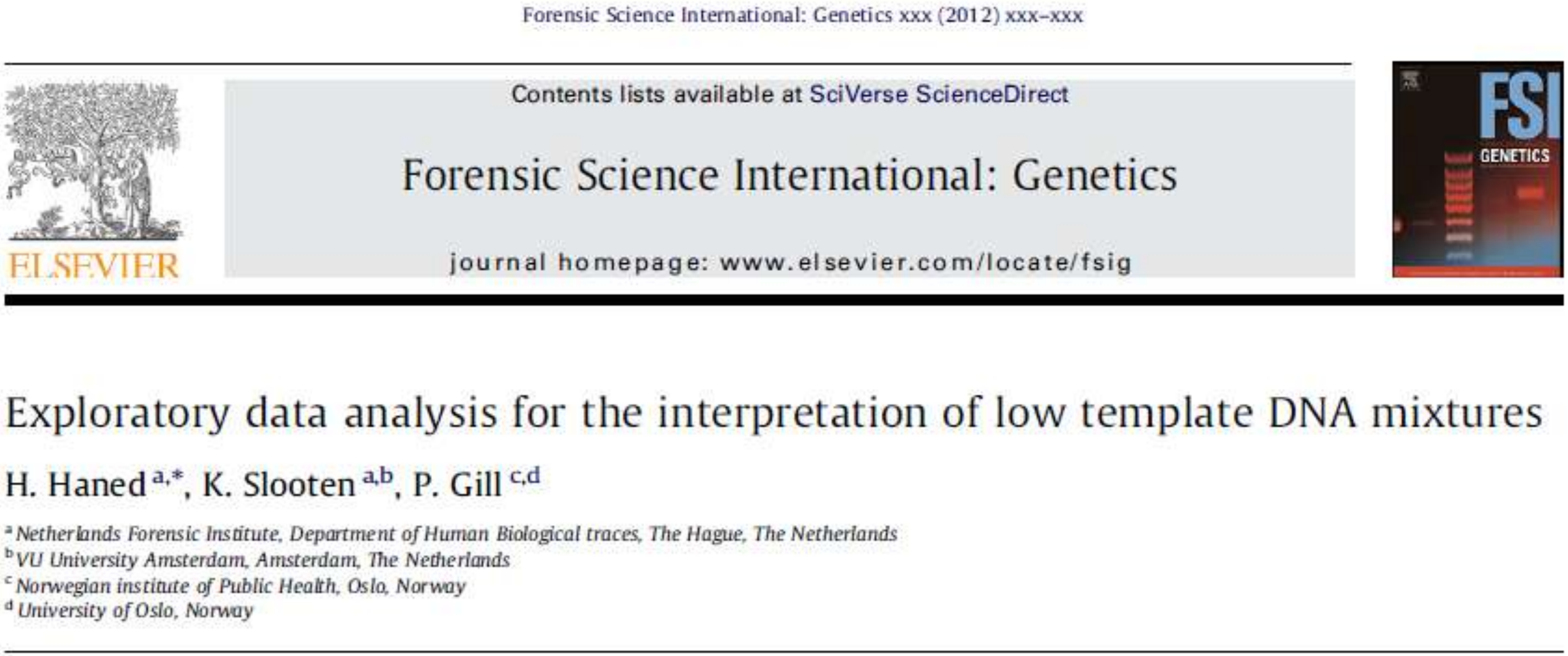
“2p”

$p^2 + 2p(1 - p)$

Whatever way uncertainty is approached, probability is the *only* sound way to think about it.

-Dennis Lindley

Haned *et al.*



Forensic Science International: Genetics xxx (2012) xxx–xxx

Contents lists available at SciVerse ScienceDirect

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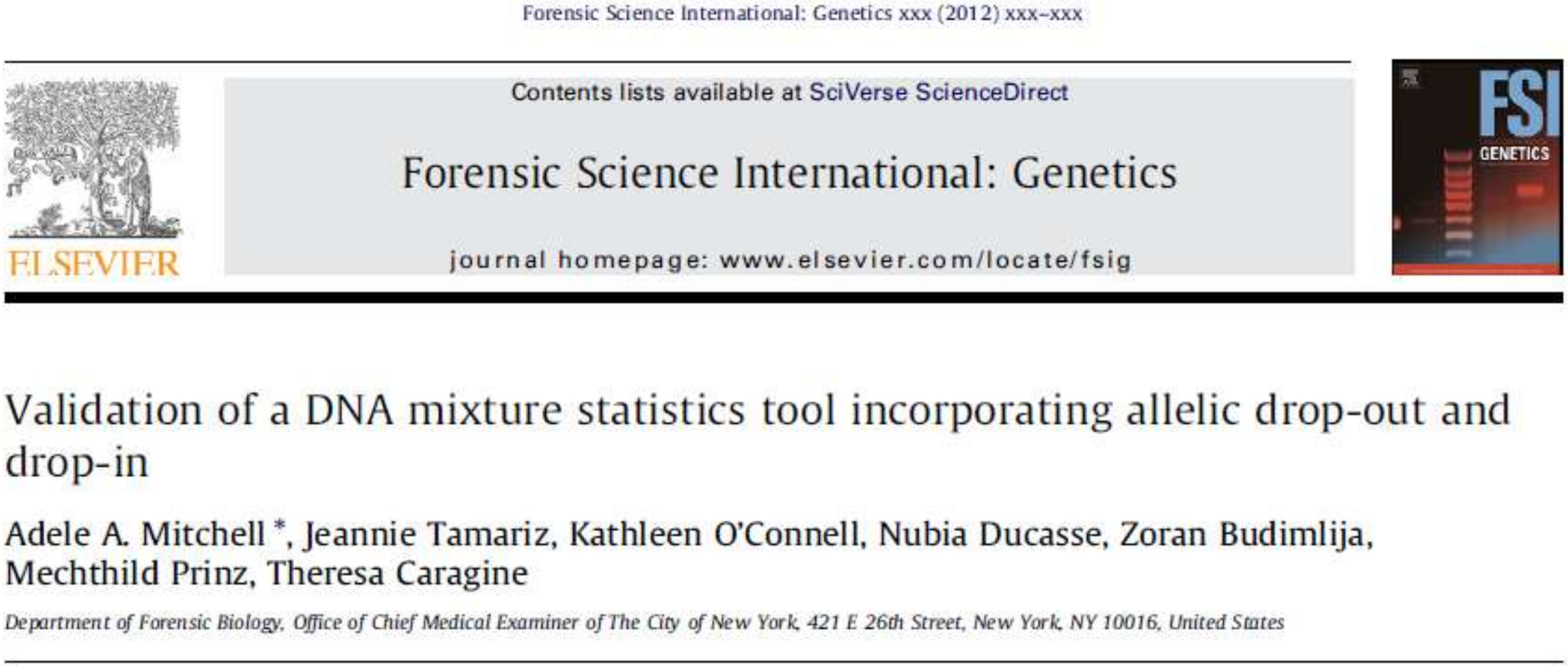
journal homepage: www.elsevier.com/locate/fsig

Exploratory data analysis for the interpretation of low template DNA mixtures

H. Haned [a,*], K. Slooten [a,b], P. Gill [c,d]

[a] Netherlands Forensic Institute, Department of Human Biological traces, The Hague, The Netherlands
[b] VU University Amsterdam, Amsterdam, The Netherlands
[c] Norwegian institute of Public Health, Oslo, Norway
[d] University of Oslo, Norway

Mitchell *et al.*



Forensic Science International: Genetics xxx (2012) xxx–xxx

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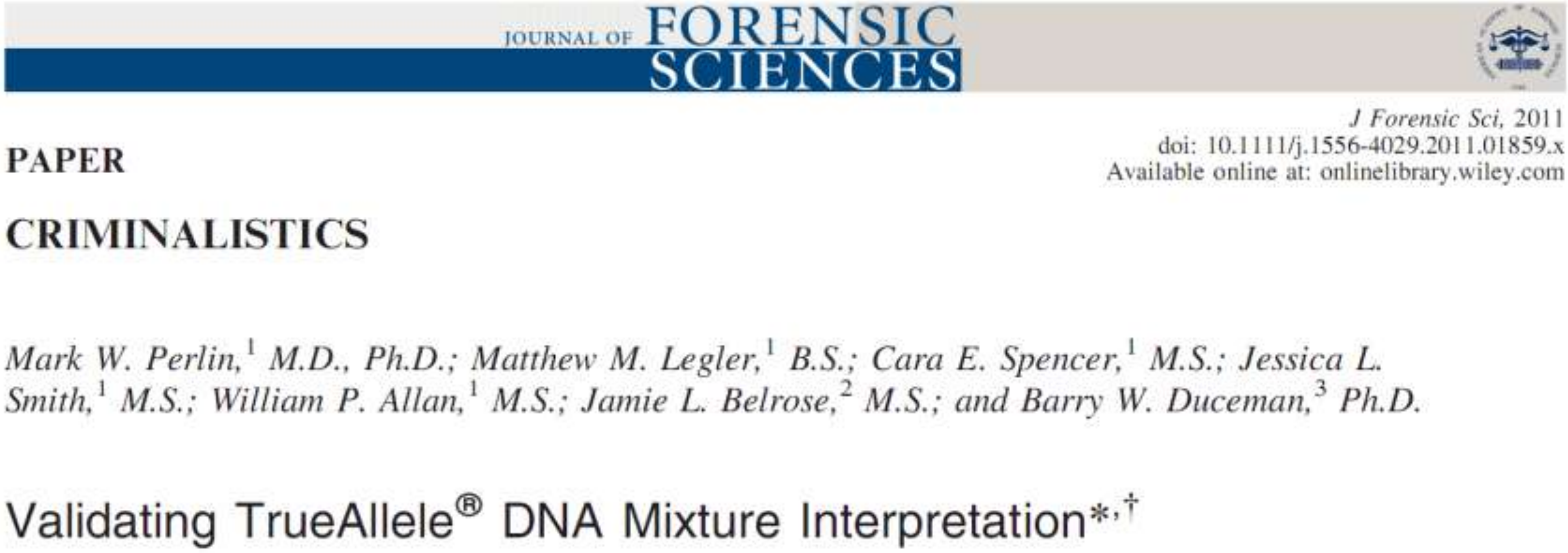
journal homepage: www.elsevier.com/locate/fsig

Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in

Adele A. Mitchell *, Jeannie Tamariz, Kathleen O'Connell, Nubia Ducasse, Zoran Budimlija, Mechthild Prinz, Theresa Caragine

Department of Forensic Biology, Office of Chief Medical Examiner of The City of New York, 421 E 26th Street, New York, NY 10016, United States



JOURNAL OF FORENSIC SCIENCES

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Available online at: onlinelibrary.wiley.com

PAPER

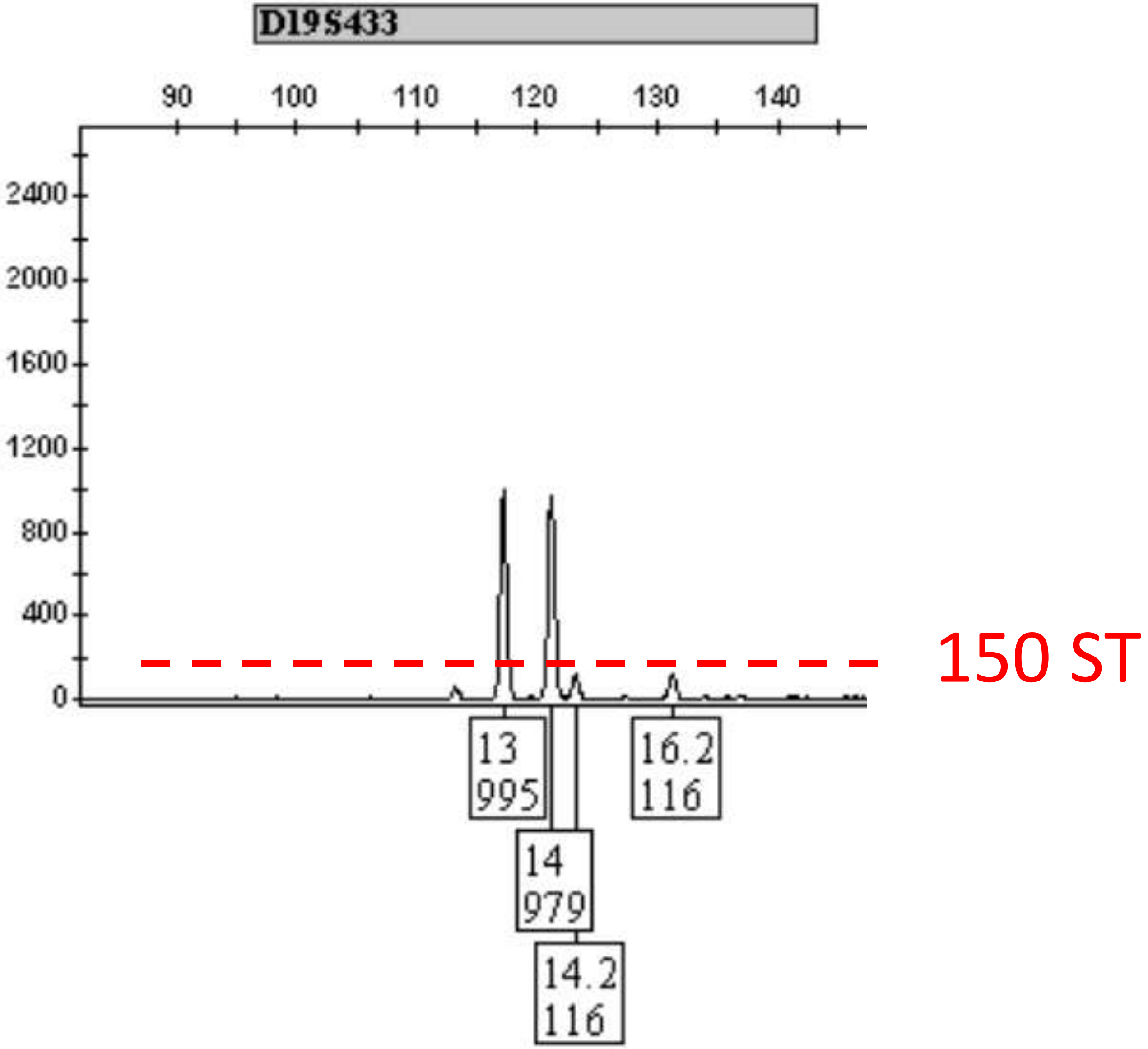
CRIMINALISTICS

Mark W. Perlin,[1] M.D., Ph.D.; Matthew M. Legler,[1] B.S.; Cara E. Spencer,[1] M.S.; Jessica L. Smith,[1] M.S.; William P. Allan,[1] M.S.; Jamie L. Belrose,[2] M.S.; and Barry W. Duceman,[3] Ph.D.

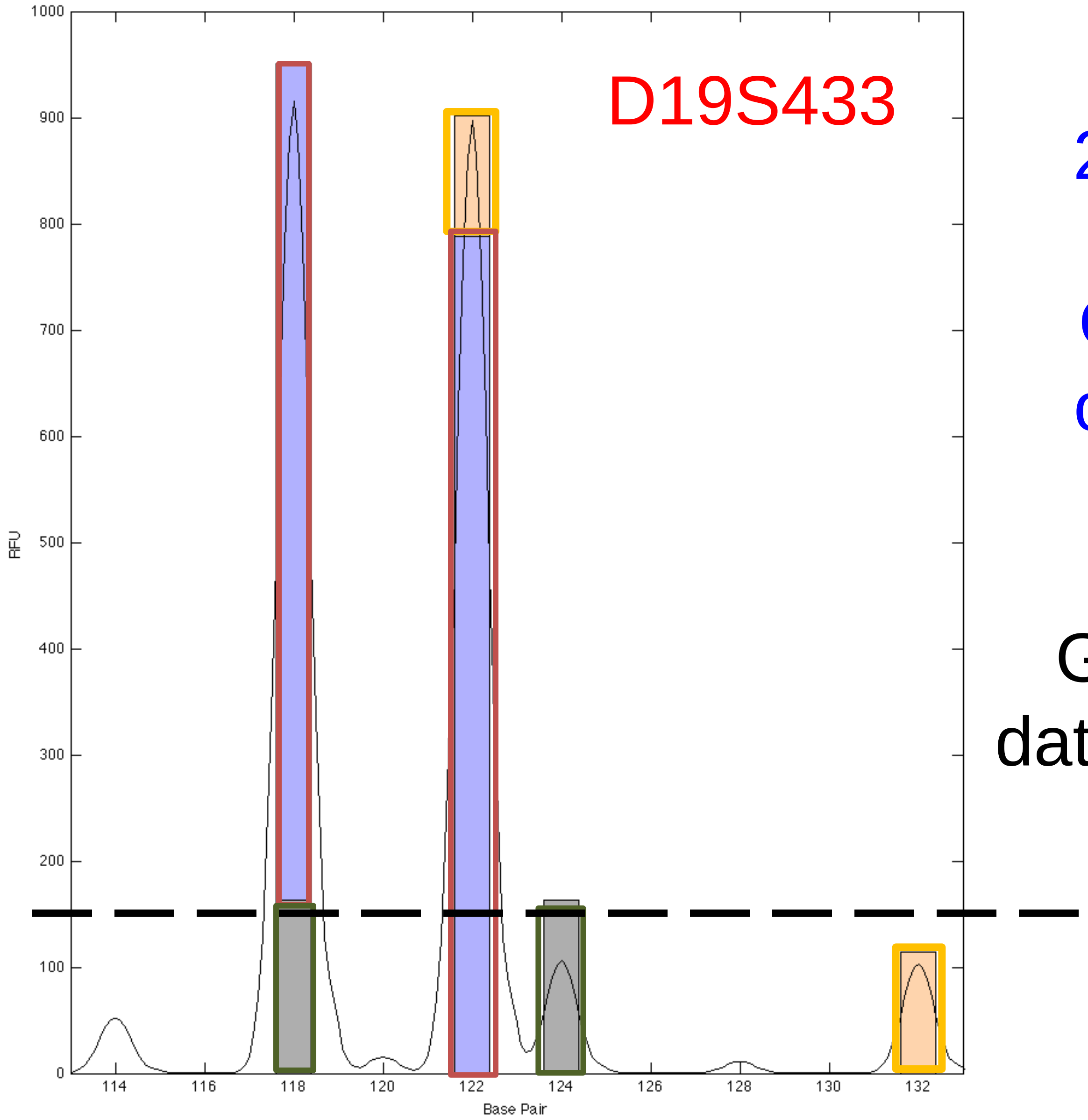
Validating TrueAllele® DNA Mixture Interpretation*,†

- Quantitative computer interpretation using Markov Chain Monte Carlo testing
- Models peak uncertainty and infers possible genotypes
- Results are presented as the Combined LR

3 Person Mixture



Review of One Replicate (of 50K)

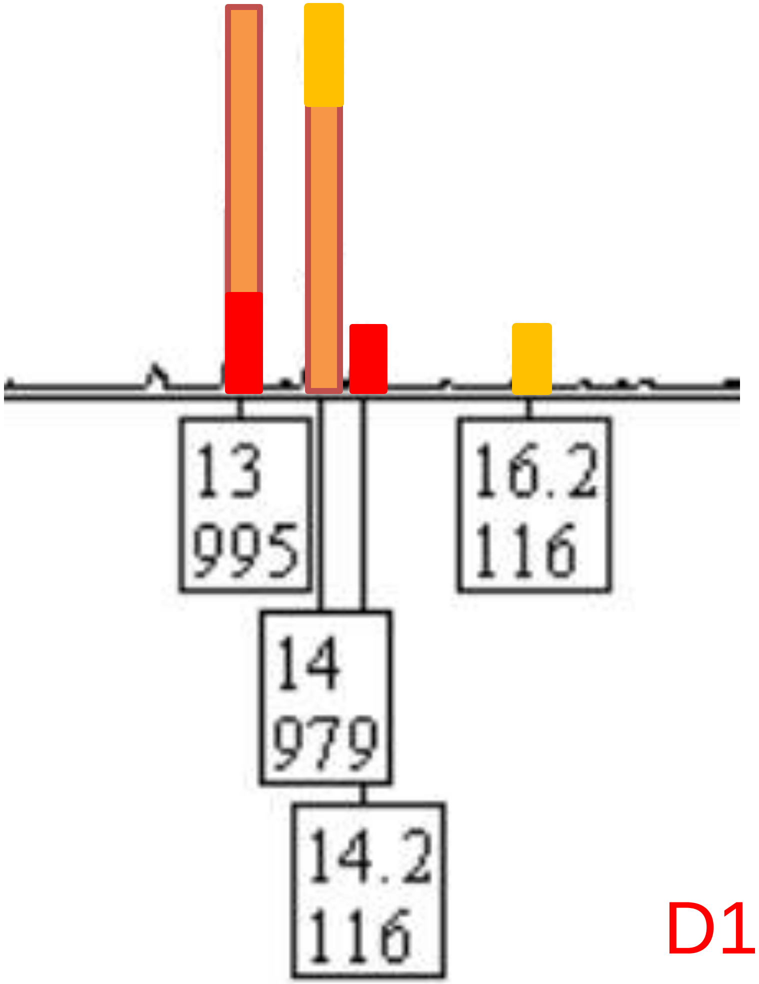


3P mixture,
2 Unknowns,

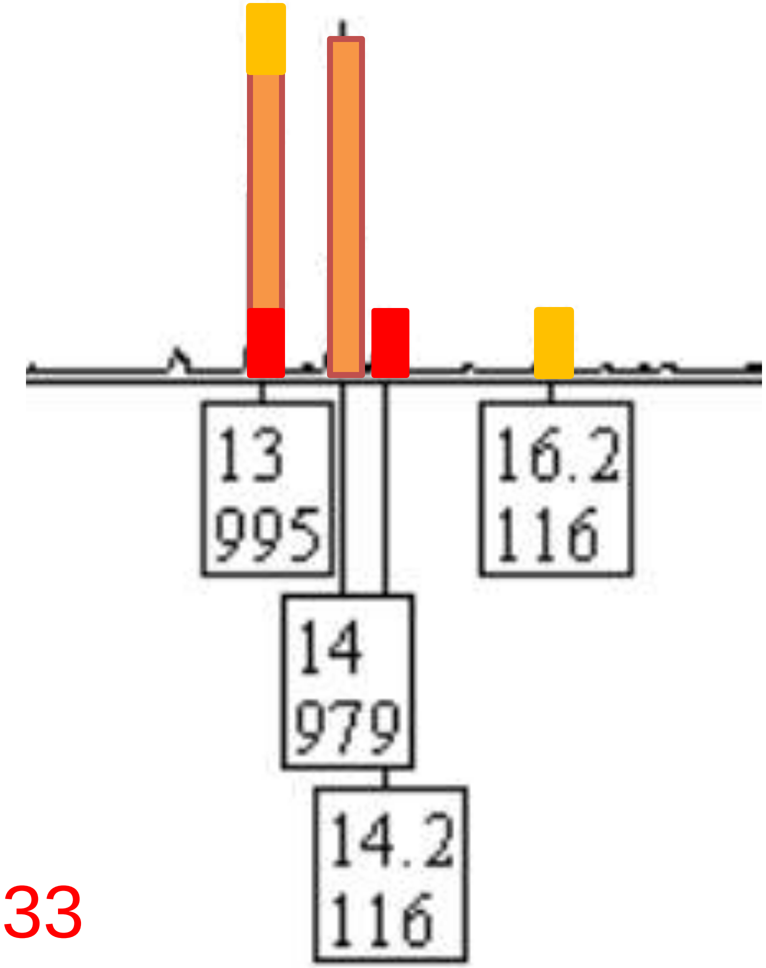
Conditioned
on the Victim
(major)

Good fit of the
data to the model

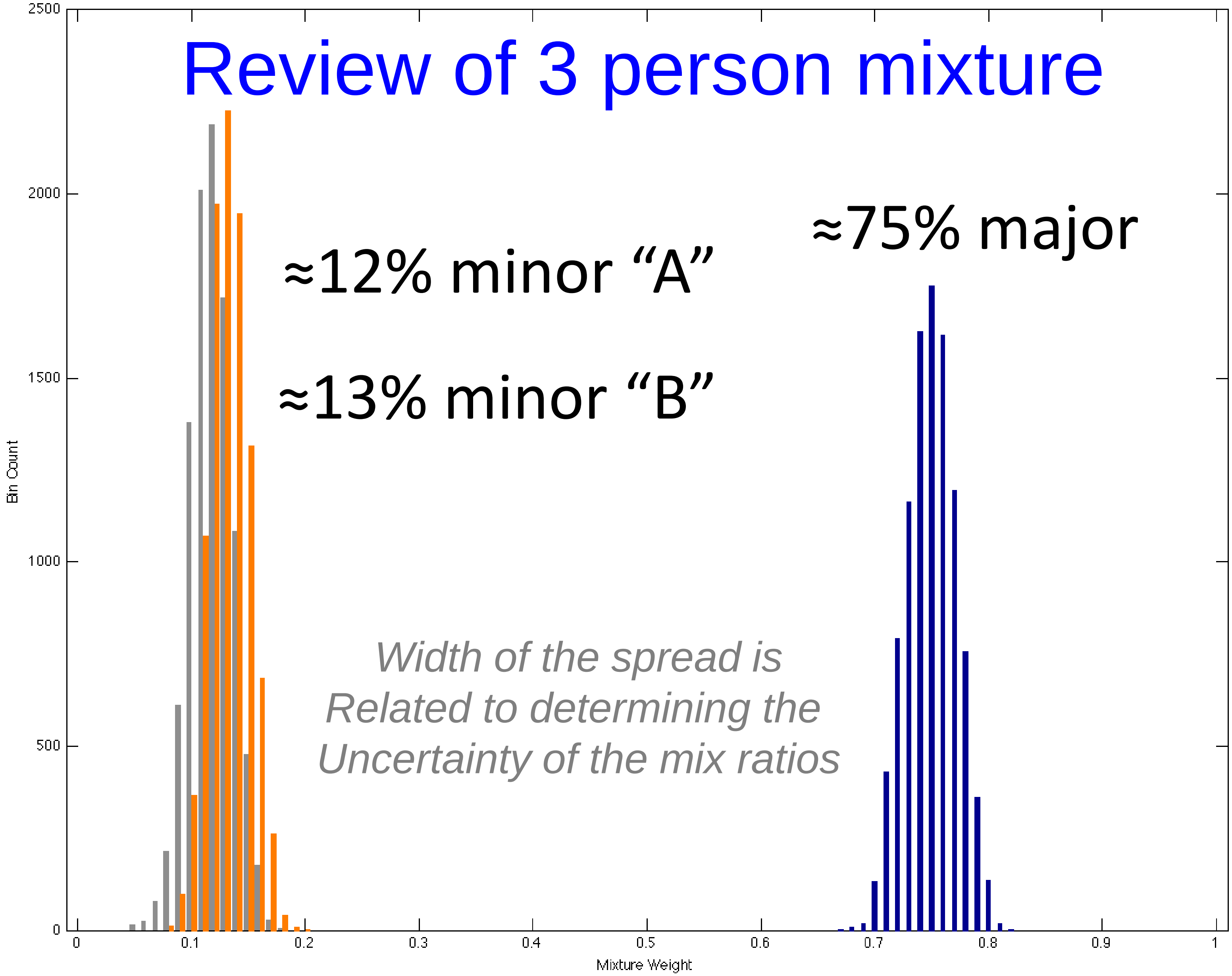
Alternative Explanations of the Data



D19S433



Review of 3 person mixture



≈75% major

≈12% minor “A”

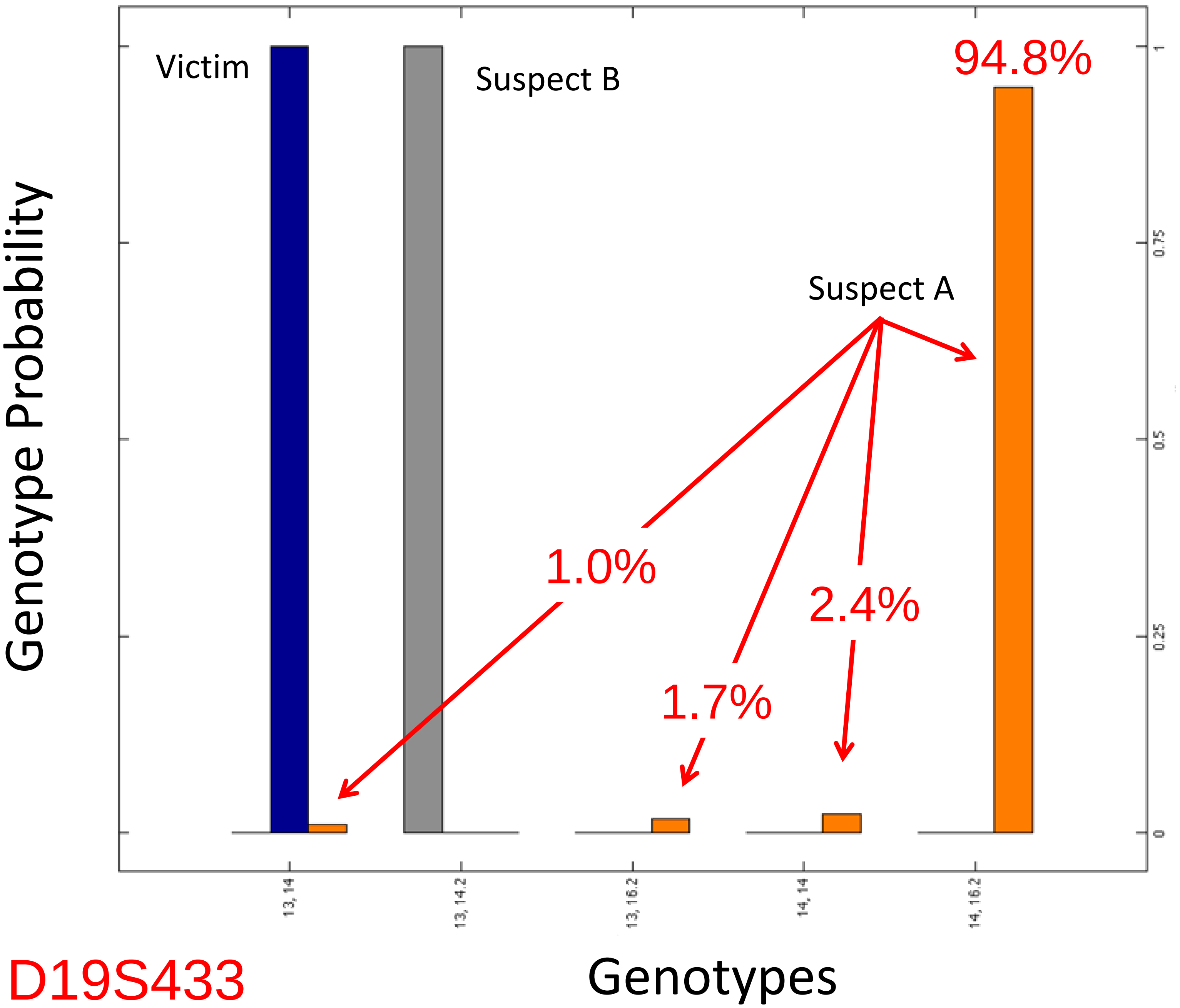
≈13% minor “B”

Width of the spread is
Related to determining the
Uncertainty of the mix ratios

Bin Count

Mixture Weight

D19S433



14,16.2	**(94.8)**
14,14	**(2.4)**
13,16.2	**(1.7)**
13,14	**(1.0)**

Determining the LR for D19S433

Suspect A = 14, 16.2

$H_P = 0.967$

Allele Pair	Probability Before Conditioning
→ 14, 16.2	$\boxed{0.967}$
14, 14	0.003
13, 16.2	0.026
13, 14	0.001

$$LR = \frac{0.967}{}$$

Determining the LR for D19S433

Suspect A = 14, 16.2

$H_P = 0.967$

Allele Pair	Probability Before Conditioning	Genotype Frequency	Probability * Genotype Freq
14, 16.2	0.967	0.0120	0.01164
14, 14	0.003	0.0498	0.00013
13, 16.2	0.026	0.0131	0.00034
13, 14	0.001	0.1082	0.00009
		sum	**0.0122**

$$LR = \frac{0.967}{0.0122} = 79.26$$

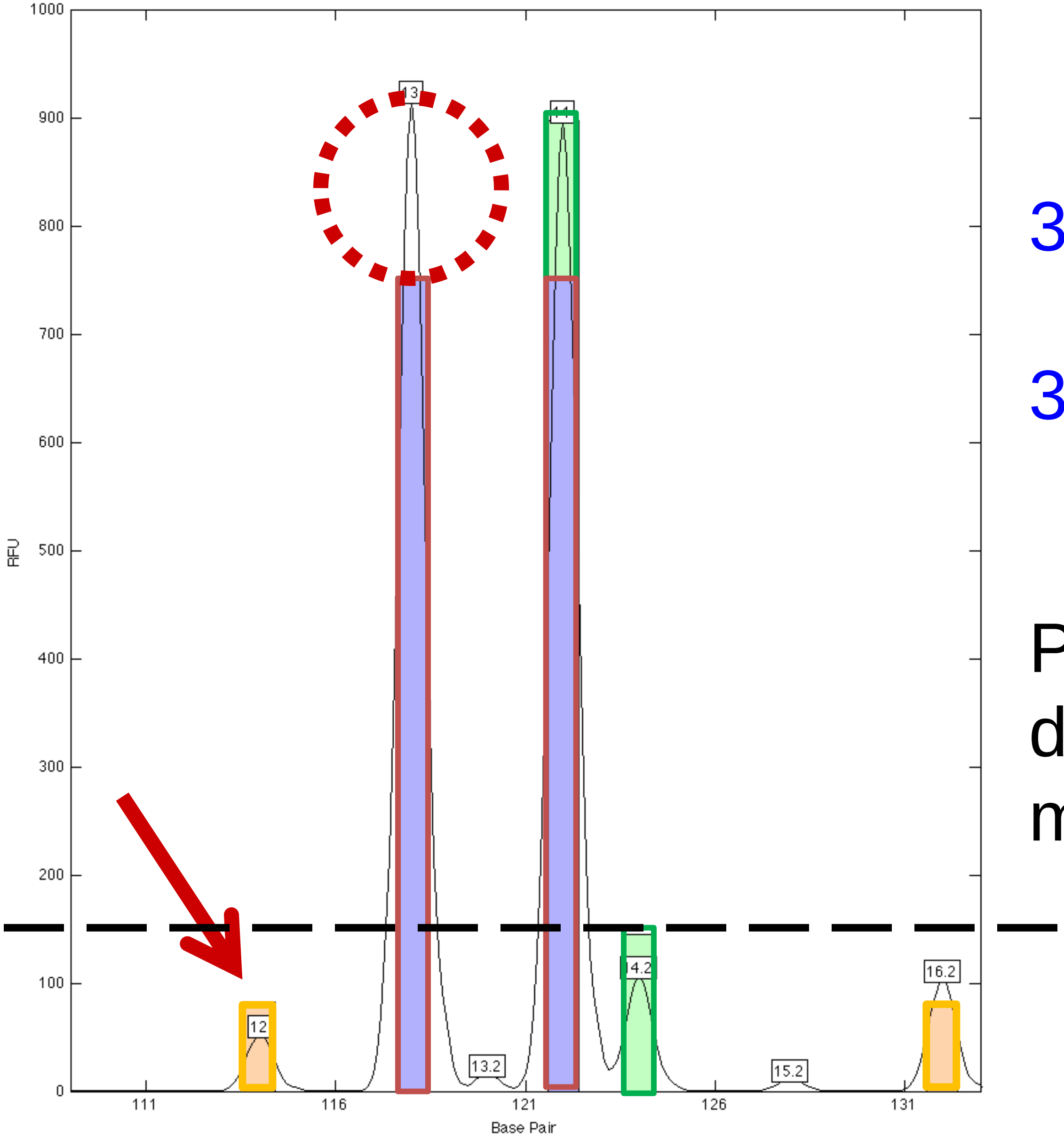
H_D

Combined LR = 5.6 Quintillion

			Genotype Probability Distribution			Weighted Likelihood		Likelihood Ratio	
	allele pair	Likelihood	Questioned	Reference	Suspect	Numerator	Denominator	LR	log(LR)
locus	x	l(x)	q(x)	r(x)	s(x)	l(x)*s(x)	l(x)*r(x)		
CSF1PO	11, 12	0.686	0.778	0.1448	1	0.68615	0.1292	5.31	0.725
D13S317	9, 12	1	1	0.0291	1	0.99952	0.02913	34.301	1.535
D16S539	9, 11	0.985	0.995	0.1238	1	0.98451	0.12188	8.036	0.905
D18S51	13, 17	0.999	1	0.0154	1	0.99915	0.01543	64.677	1.811
D19S433	14, 16.2	0.967	0.948	0.012	1	0.96715	0.01222	79.143	1.898
D21S11	28, 30	0.968	0.98	0.0872	1	0.96809	0.08648	11.194	1.049
D2S1338	23, 24	0.998	1	0.0179	1	0.99831	0.01787	55.866	1.747
D3S1358	15, 17	0.988	0.994	0.1224	1	0.98759	0.12084	8.14	0.911
D5S818	11, 11	0.451	0.394	0.0537	1	0.45103	0.07309	6.17	0.79
D7S820	11, 12	0.984	0.978	0.0356	1	0.98383	0.03617	27.198	1.435
D8S1179	13, 14	0.203	0.9	0.1293	1	0.20267	0.02993	6.771	0.831
FGA	21, 25	0.32	0.356	0.028	1	0.31986	0.01906	16.783	1.225
TH01	7, 7	0.887	0.985	0.1739	1	0.88661	0.15588	5.687	0.755
TPOX	8, 8	1	1	0.1375	1	1	0.13746	7.275	0.862
vWA	15, 20	0.998	0.996	0.0057	1	0.99808	0.00569	174.834	2.243

Review of One Replicate (of 50K)

D19S433



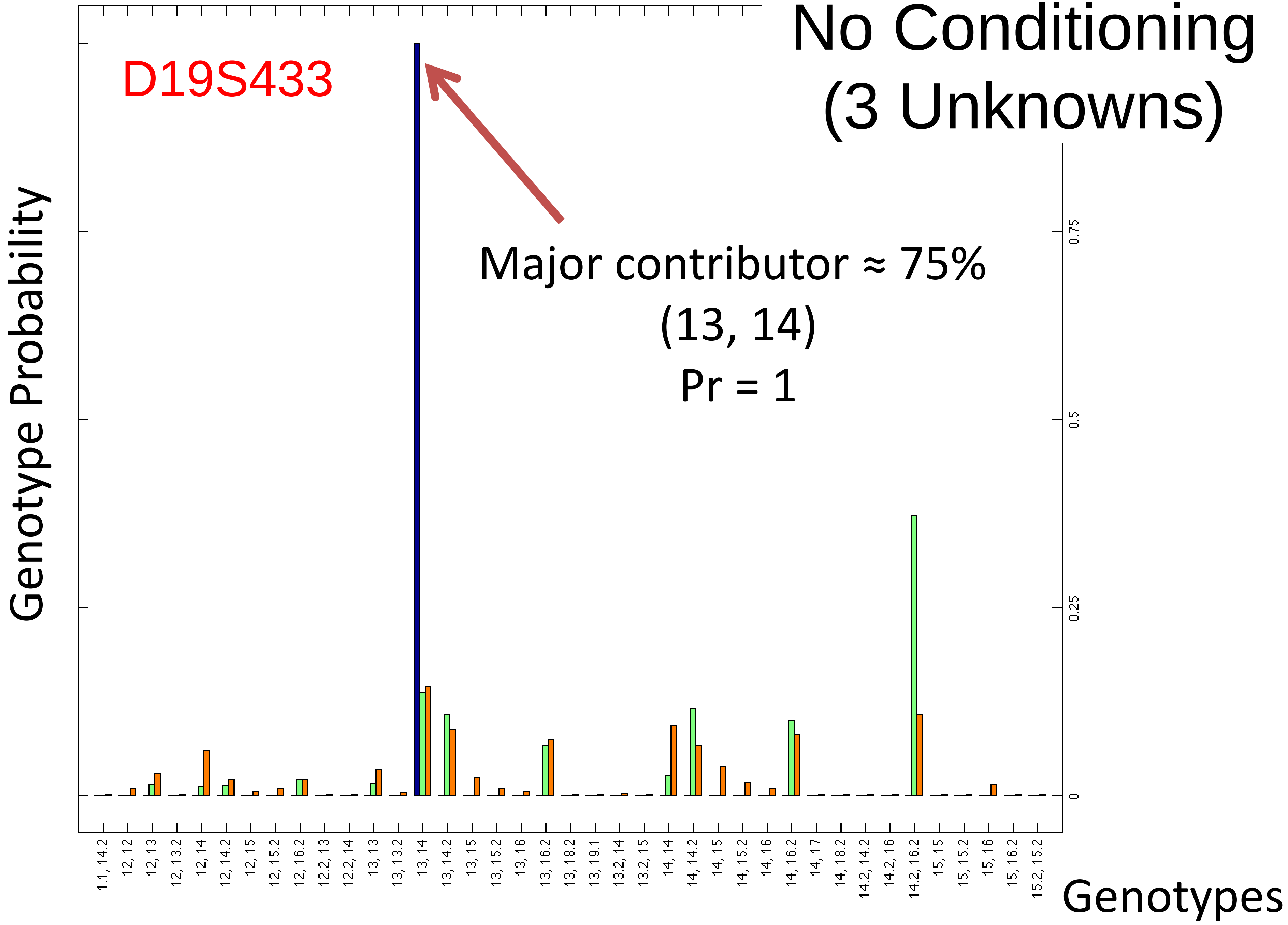
150 RFU

3P mixture,

3 Unknowns

Poor fit of the data to the model

No Conditioning (3 Unknowns)



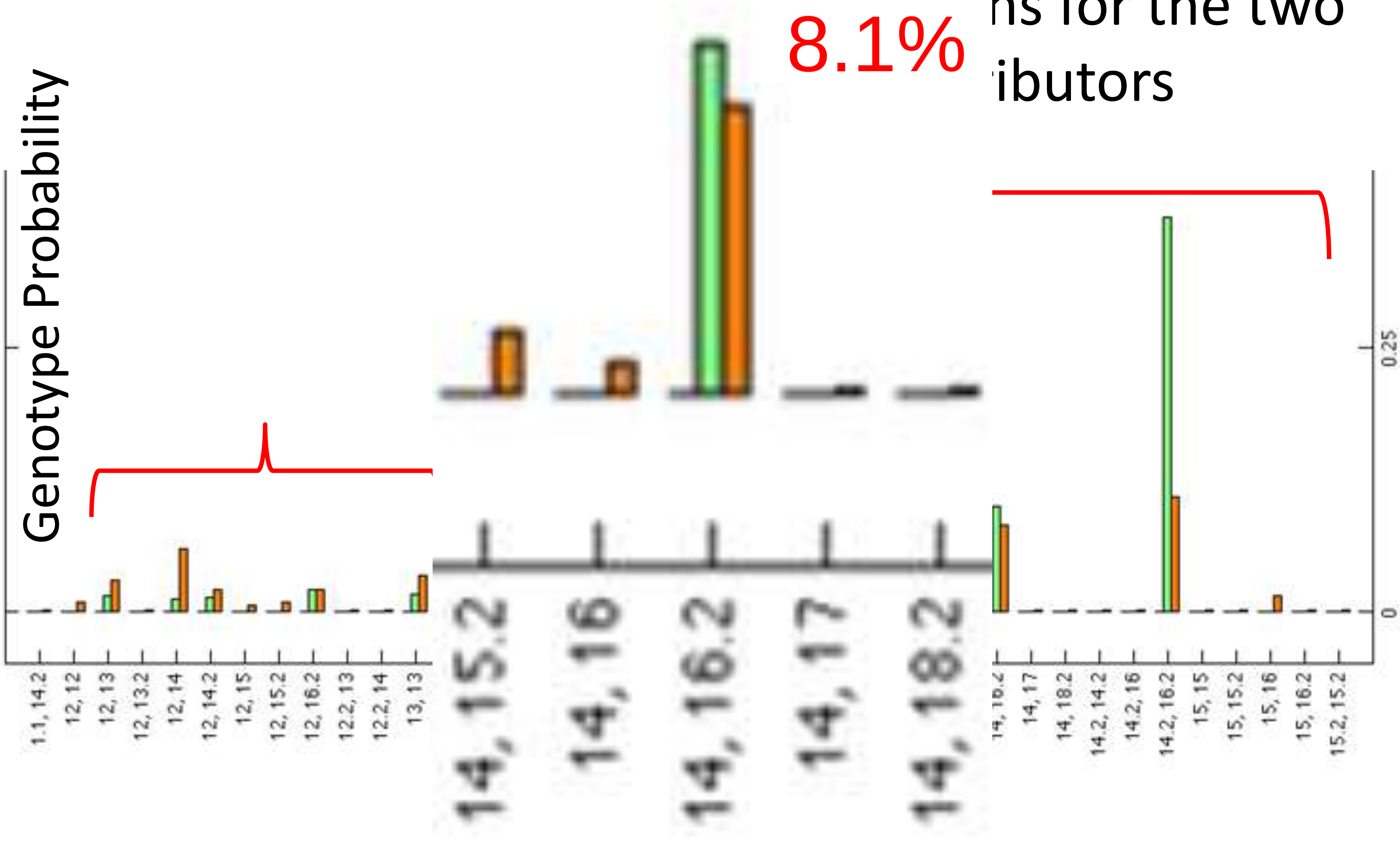
Major contributor ≈ 75%
(13, 14)
Pr = 1

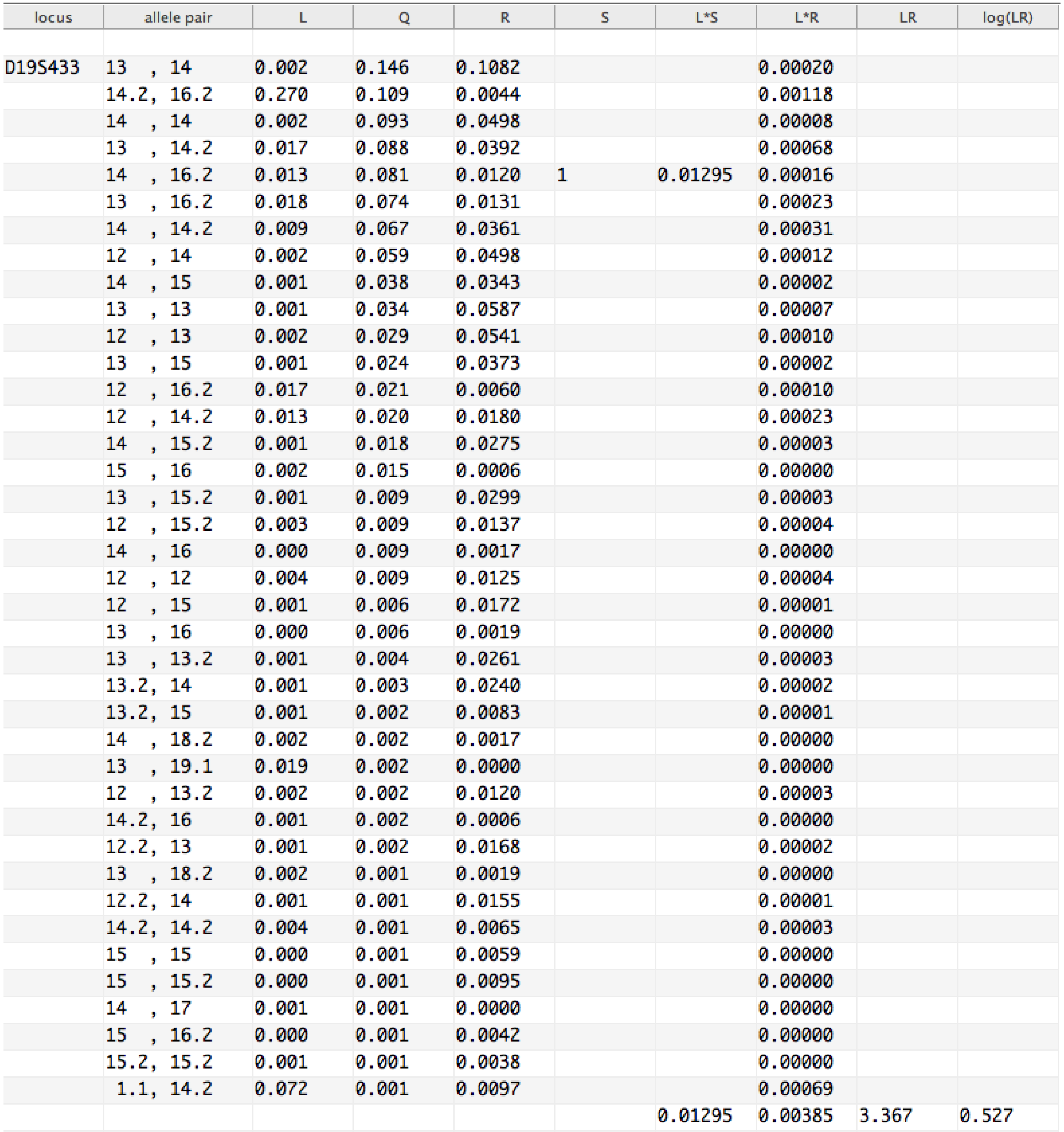
No Conditioning (3 Unknowns)

D19S433

ns for the two
ibutors

8.1%





locus	allele pair	L	Q	R	S	L*S	L*R	LR	log(LR)
D19S433	13 , 14	0.002	0.146	0.1082			0.00020		
	14.2, 16.2	0.270	0.109	0.0044			0.00118		
	14 , 14	0.002	0.093	0.0498			0.00008		
	13 , 14.2	0.017	0.088	0.0392			0.00068		
	14 , 16.2	0.013	0.081	0.0120	1	0.01295	0.00016		
	13 , 16.2	0.018	0.074	0.0131			0.00023		
	14 , 14.2	0.009	0.067	0.0361			0.00031		
	12 , 14	0.002	0.059	0.0498			0.00012		
	14 , 15	0.001	0.038	0.0343			0.00002		
	13 , 13	0.001	0.034	0.0587			0.00007		
	12 , 13	0.002	0.029	0.0541			0.00010		
	13 , 15	0.001	0.024	0.0373			0.00002		
	12 , 16.2	0.017	0.021	0.0060			0.00010		
	12 , 14.2	0.013	0.020	0.0180			0.00023		
	14 , 15.2	0.001	0.018	0.0275			0.00003		
	15 , 16	0.002	0.015	0.0006			0.00000		
	13 , 15.2	0.001	0.009	0.0299			0.00003		
	12 , 15.2	0.003	0.009	0.0137			0.00004		
	14 , 16	0.000	0.009	0.0017			0.00000		
	12 , 12	0.004	0.009	0.0125			0.00004		
	12 , 15	0.001	0.006	0.0172			0.00001		
	13 , 16	0.000	0.006	0.0019			0.00000		
	13 , 13.2	0.001	0.004	0.0261			0.00003		
	13.2, 14	0.001	0.003	0.0240			0.00002		
	13.2, 15	0.001	0.002	0.0083			0.00001		
	14 , 18.2	0.002	0.002	0.0017			0.00000		
	13 , 19.1	0.019	0.002	0.0000			0.00000		
	12 , 13.2	0.002	0.002	0.0120			0.00003		
	14.2, 16	0.001	0.002	0.0006			0.00000		
	12.2, 13	0.001	0.002	0.0168			0.00002		
	13 , 18.2	0.002	0.001	0.0019			0.00000		
	12.2, 14	0.001	0.001	0.0155			0.00001		
	14.2, 14.2	0.004	0.001	0.0065			0.00003		
	15 , 15	0.000	0.001	0.0059			0.00000		
	15 , 15.2	0.000	0.001	0.0095			0.00000		
	14 , 17	0.001	0.001	0.0000			0.00000		
	15 , 16.2	0.000	0.001	0.0042			0.00000		
	15.2, 15.2	0.001	0.001	0.0038			0.00000		
	1.1, 14.2	0.072	0.001	0.0097			0.00069		
						0.01295	0.00385	3.367	0.527

Suspect "A" Genotype

39 probable genotypes

D19S433

Suspect A = 14, 16.2 $H_P = 0.013$

Allele Pair	Probability	Genotype Frequency	Prob * GenFreq
13,14	0.002	0.1082	0.00020
14.2, 16.2	0.270	0.0044	0.00118
14, 14	0.002	0.0498	0.00008
13, 14.2	0.017	0.0392	0.00068
14, 16.2	0.013	0.0120	0.00016
13, 16.2	0.018	0.0131	0.00023
etc…	etc…	etc…	etc…
		Sum	**0.00385**

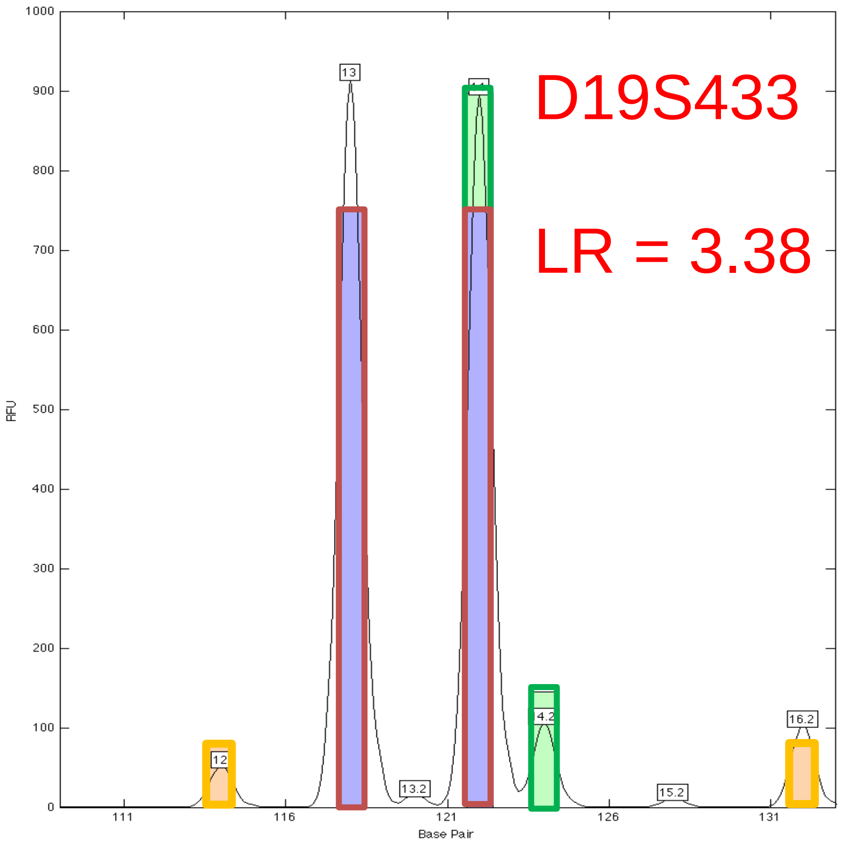
H_D

$$LR = \frac{0.013}{0.00385} = 3.38$$

D19S433

No Conditioning (3 Unknowns)

No Conditioning



D19S433

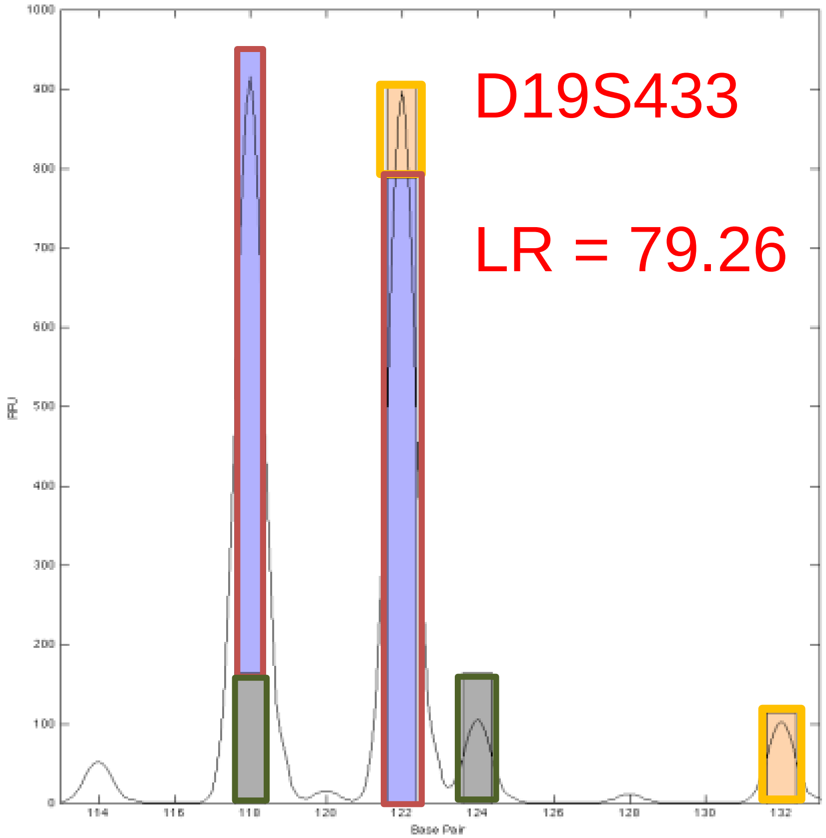
LR = 3.38

Profile - Combined log(LR)

Suspect A log(LR) = 8.03

Suspect B log(LR) = 7.84

Conditioned on Victim



D19S433

LR = 79.26

Profile - Combined log(LR)

Suspect A log(LR) = 18.72

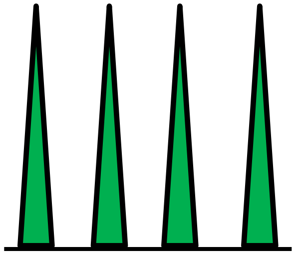
Suspect B log(LR) = 19.45

Mixture Data Set

- Mixtures of pristine male and female DNA amplified at a total concentration of 1.0 ng/μL using Identifiler (standard conditions).
- Mixture ratios ranged from 90:10, 80:20, 70:30 60:40, 50:50, 40:60, 30:70, 20:80, and 10:90
- Each sample was amplified twice.

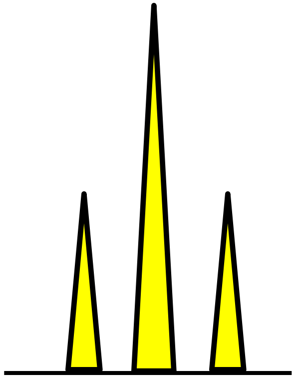
Mixture Data Set

- Three different combinations:



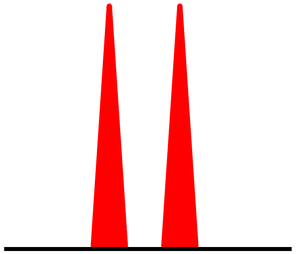
“Low” Sharing

4 alleles – 10 loci
3 alleles – 5 loci
2 alleles – 0 loci
1 allele – 0 loci



“Medium” Sharing

4 alleles – 3 loci
3 alleles – 8 loci
2 alleles – 4 loci
1 allele – 0 loci

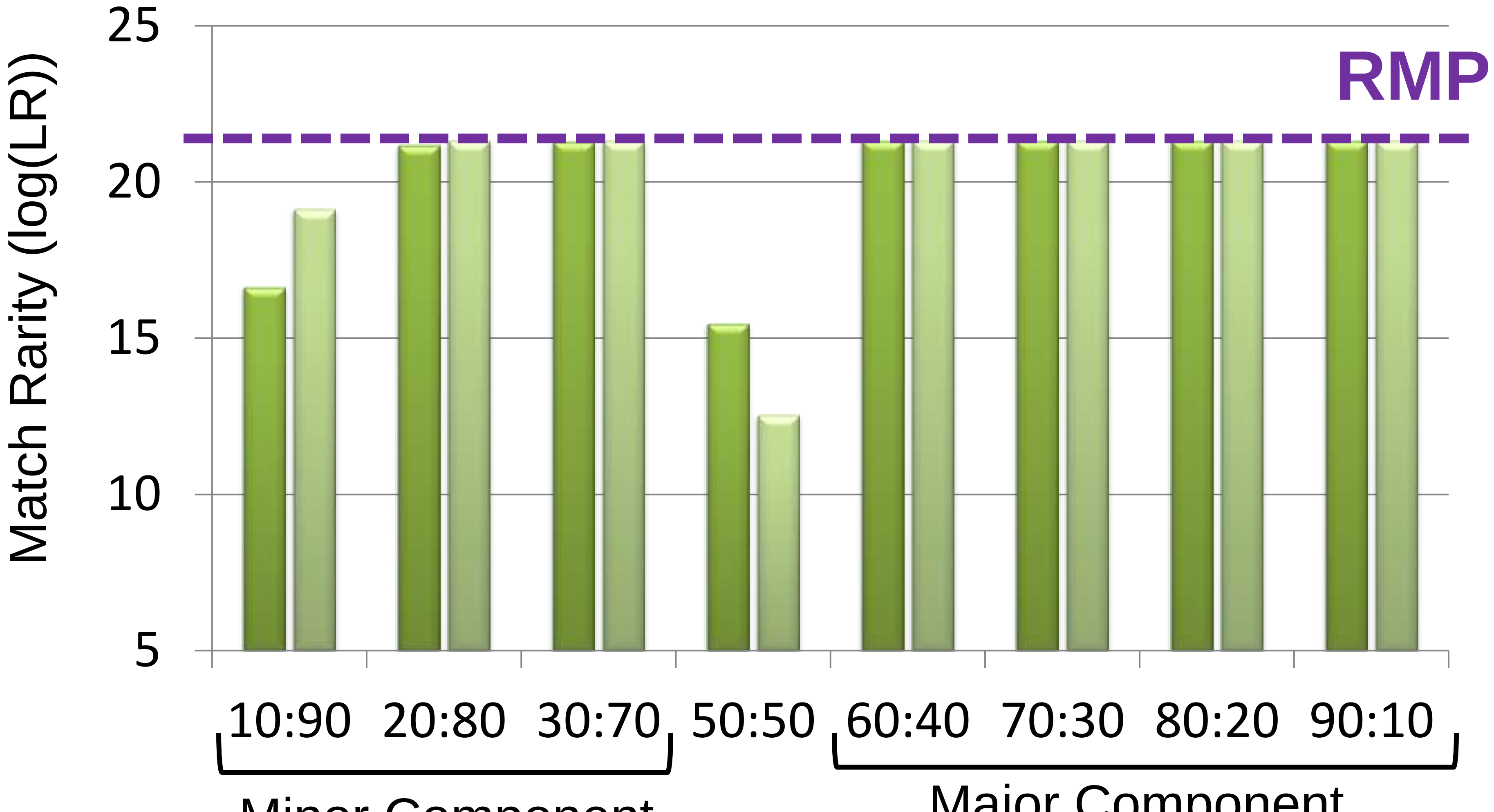


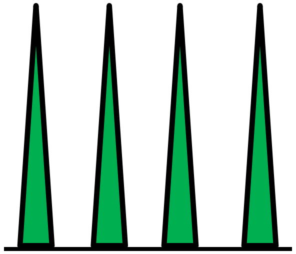
“High” Sharing

4 alleles – 0 loci
3 alleles – 6 loci
2 alleles – 8 loci
1 allele – 1 loci

Virtual MixtureMaker - http://www.cstl.nist.gov/strbase/software.htm

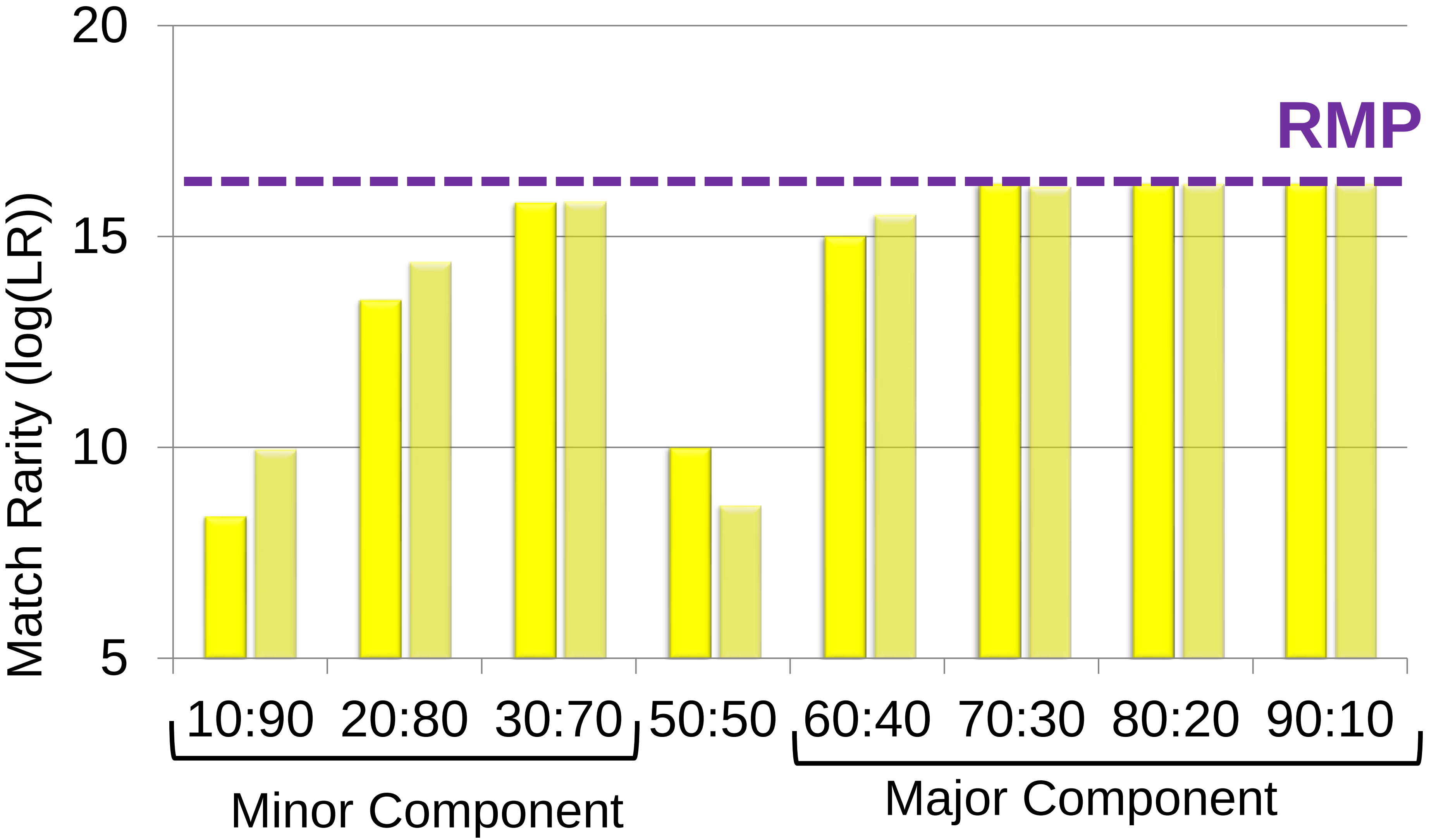
Match Score in Duplicate Runs

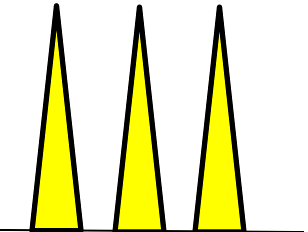




"Easy" for Deconvolution

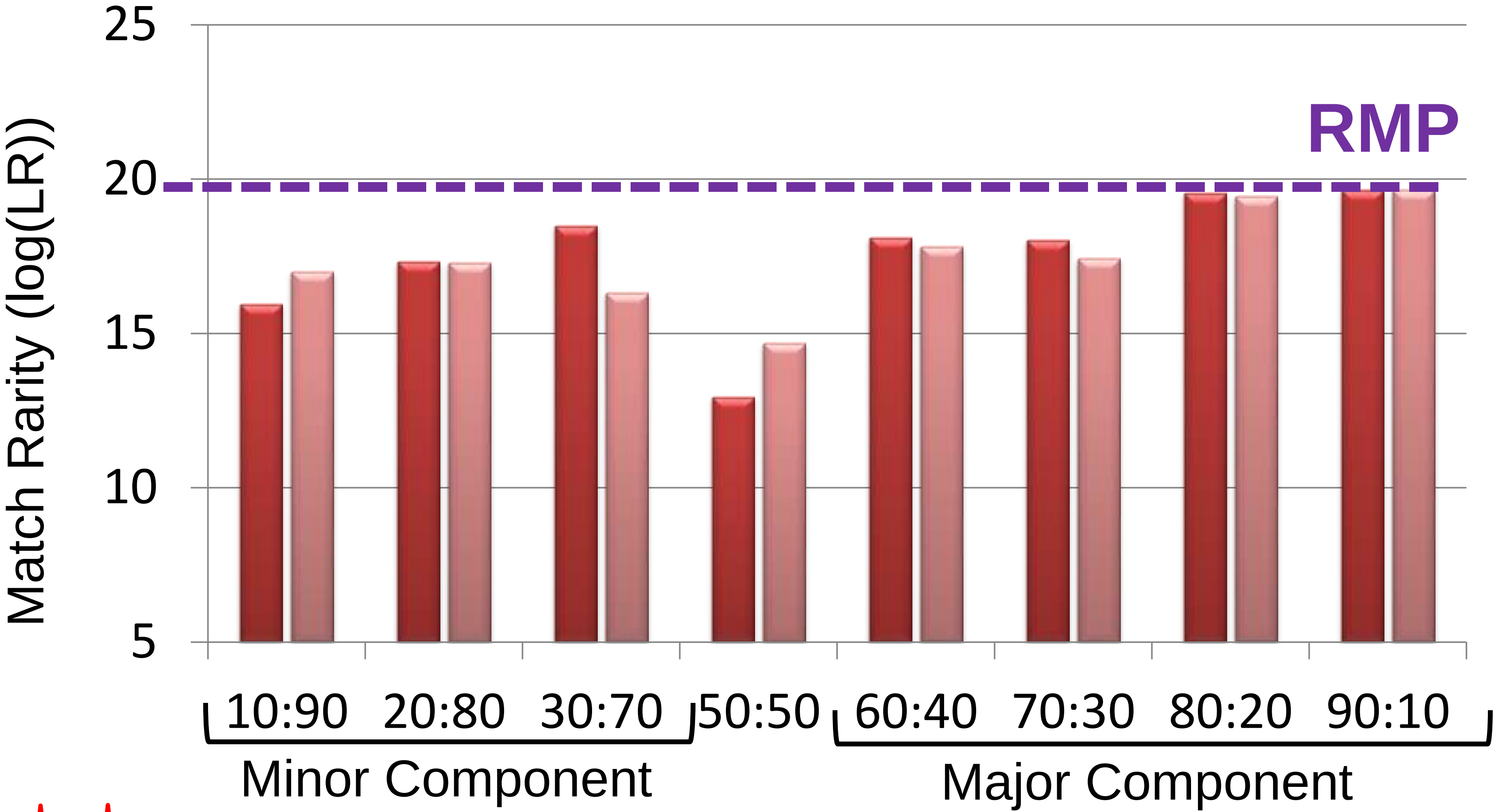
Match Score in Duplicate Runs

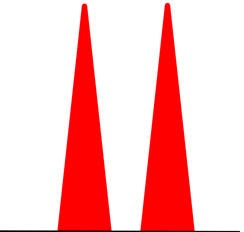




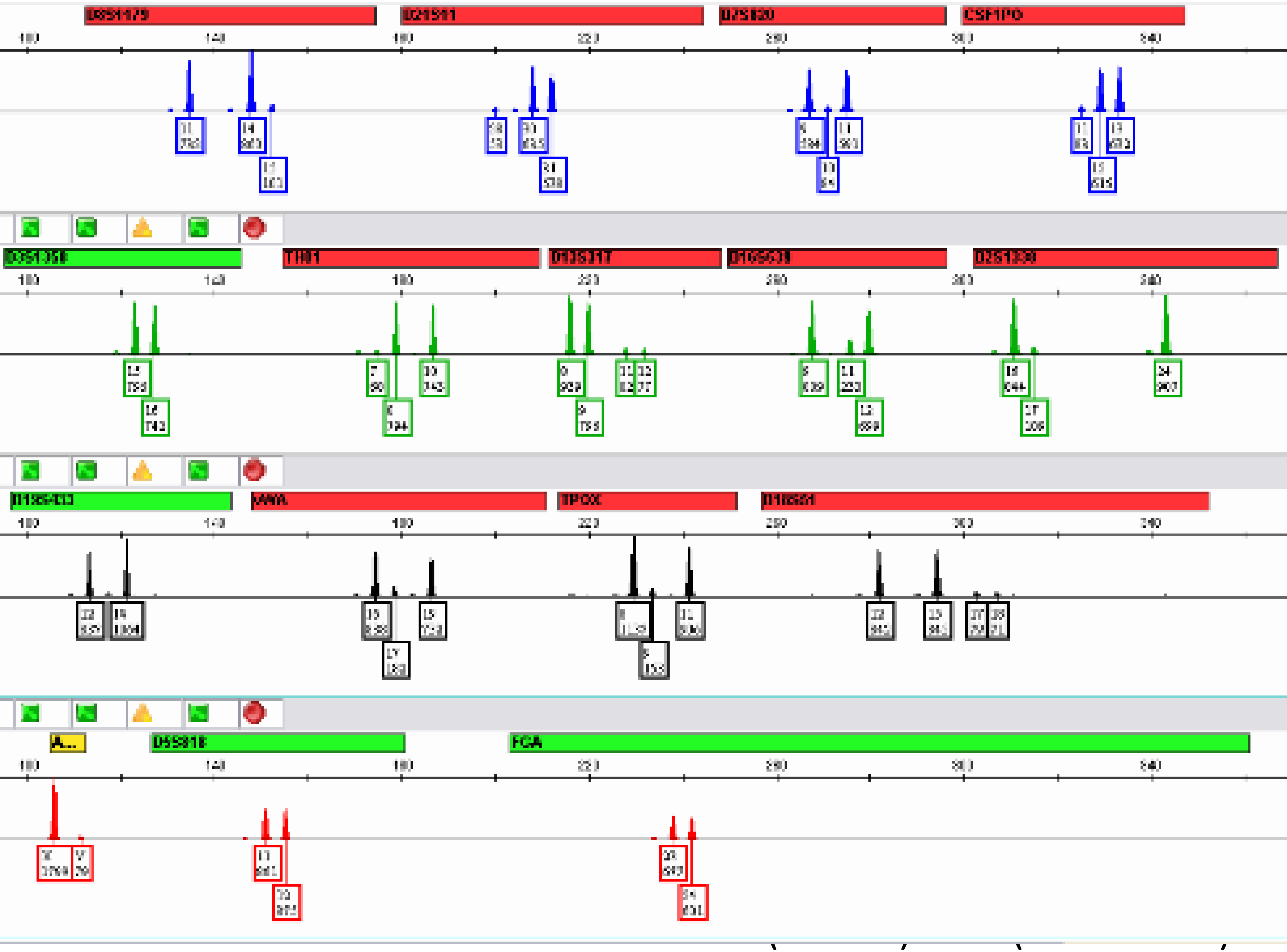
“Challenging” for Deconvolution

Match Score in Duplicate Runs

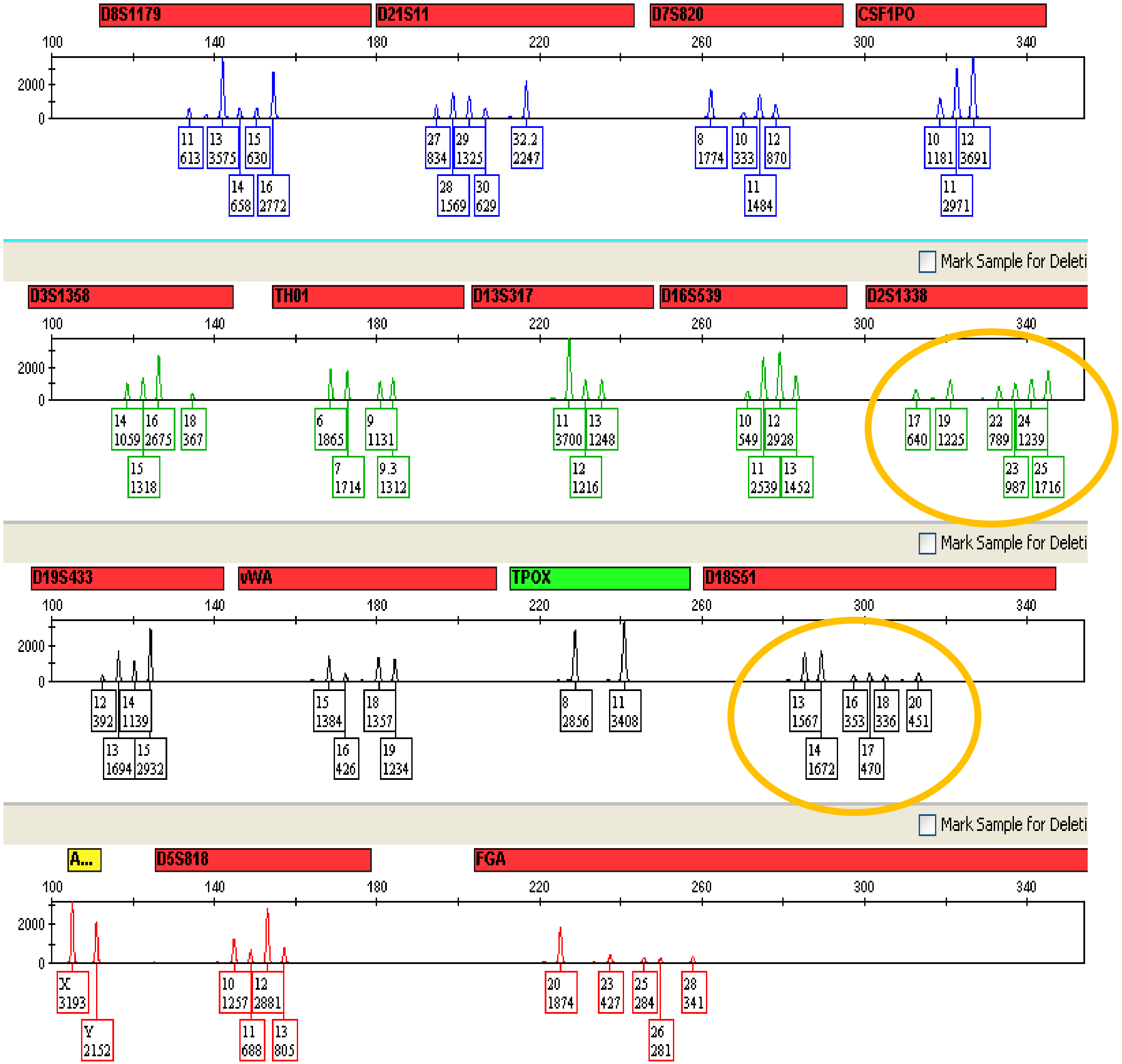




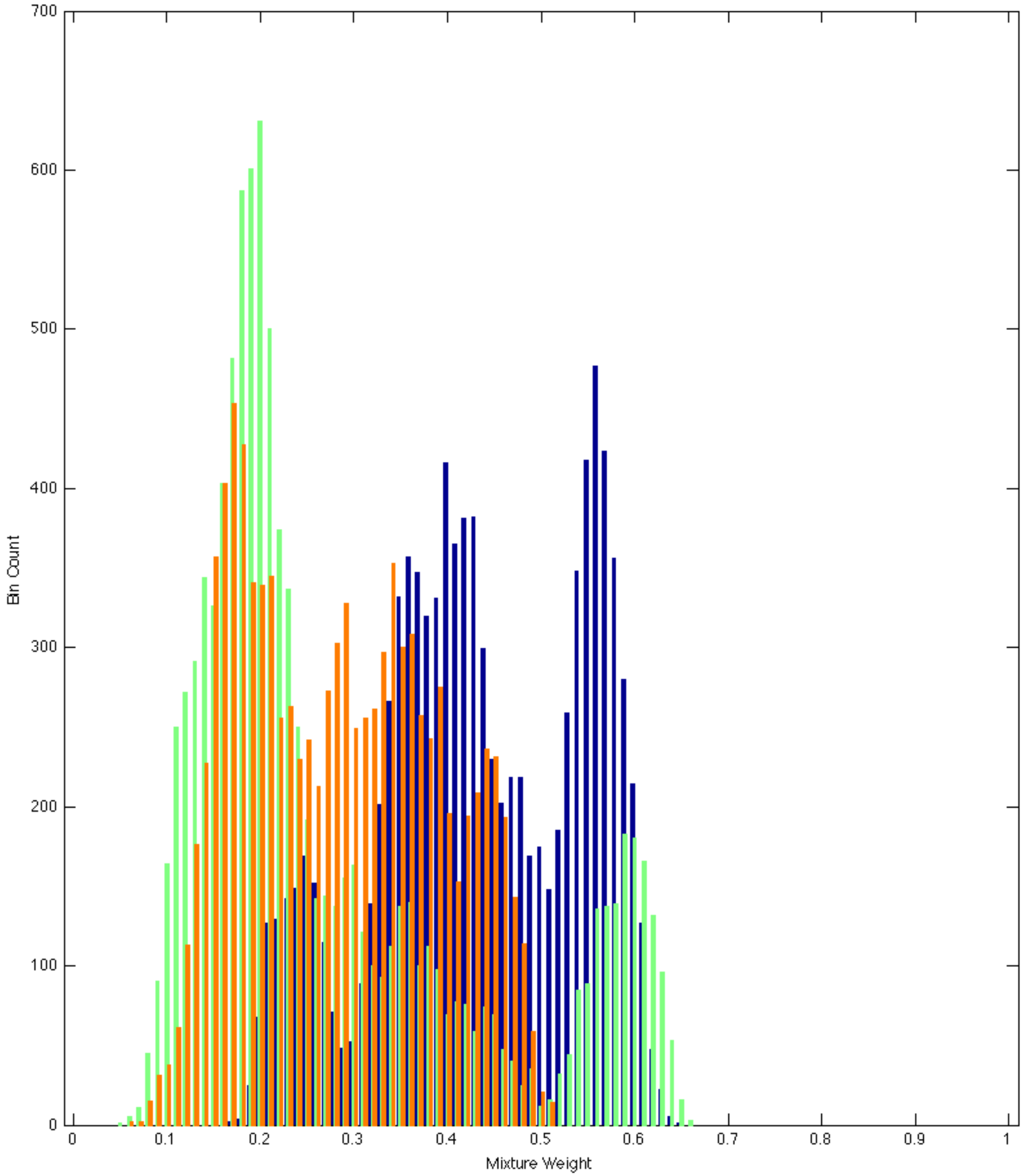
"Difficult" for Deconvolution


D8S1179
D21S11
D7S820
CSF1PO
D3S1358
TH01
D13S317
D16S539
D2S1338
D19S433
vWA
TPOX
D18S51
A...
D5S818
FGA
100
140
180
220
260
300
340

Complex Mixture



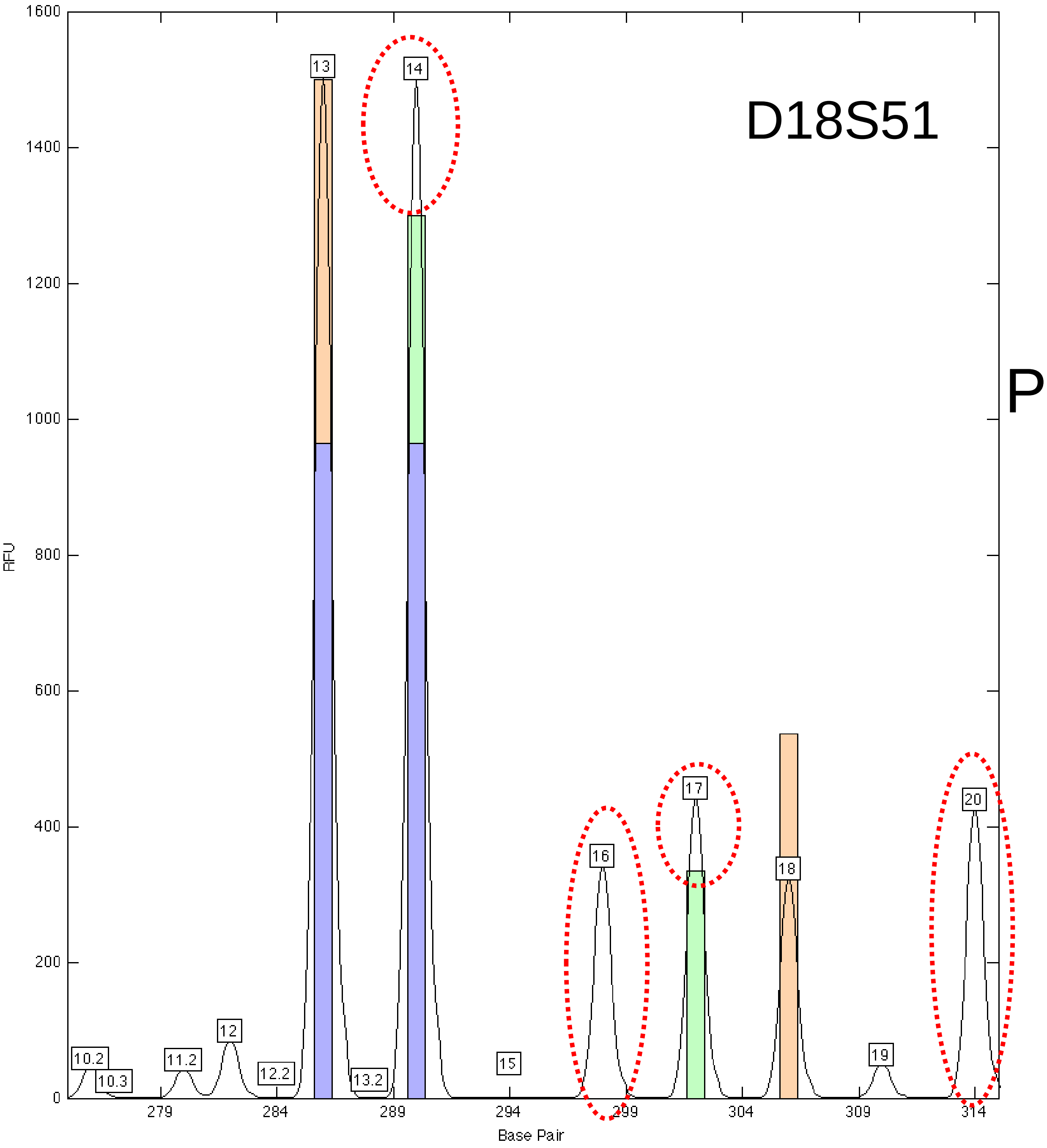
True Allele Results – 3 person mixture



100K examinations
3 unknowns
(no conditioning)

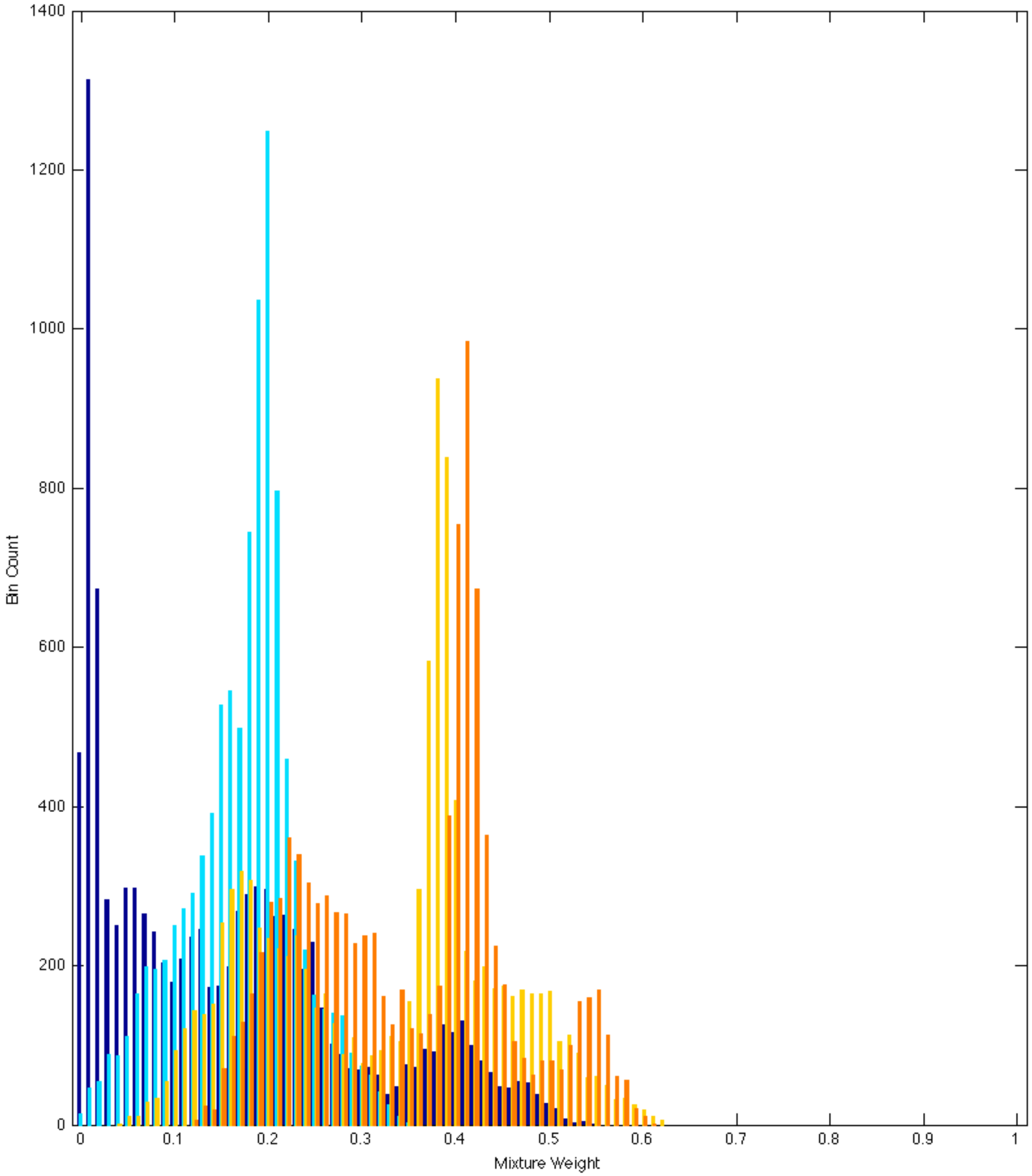
No clear separation

Mix ratio (green)
10-60%



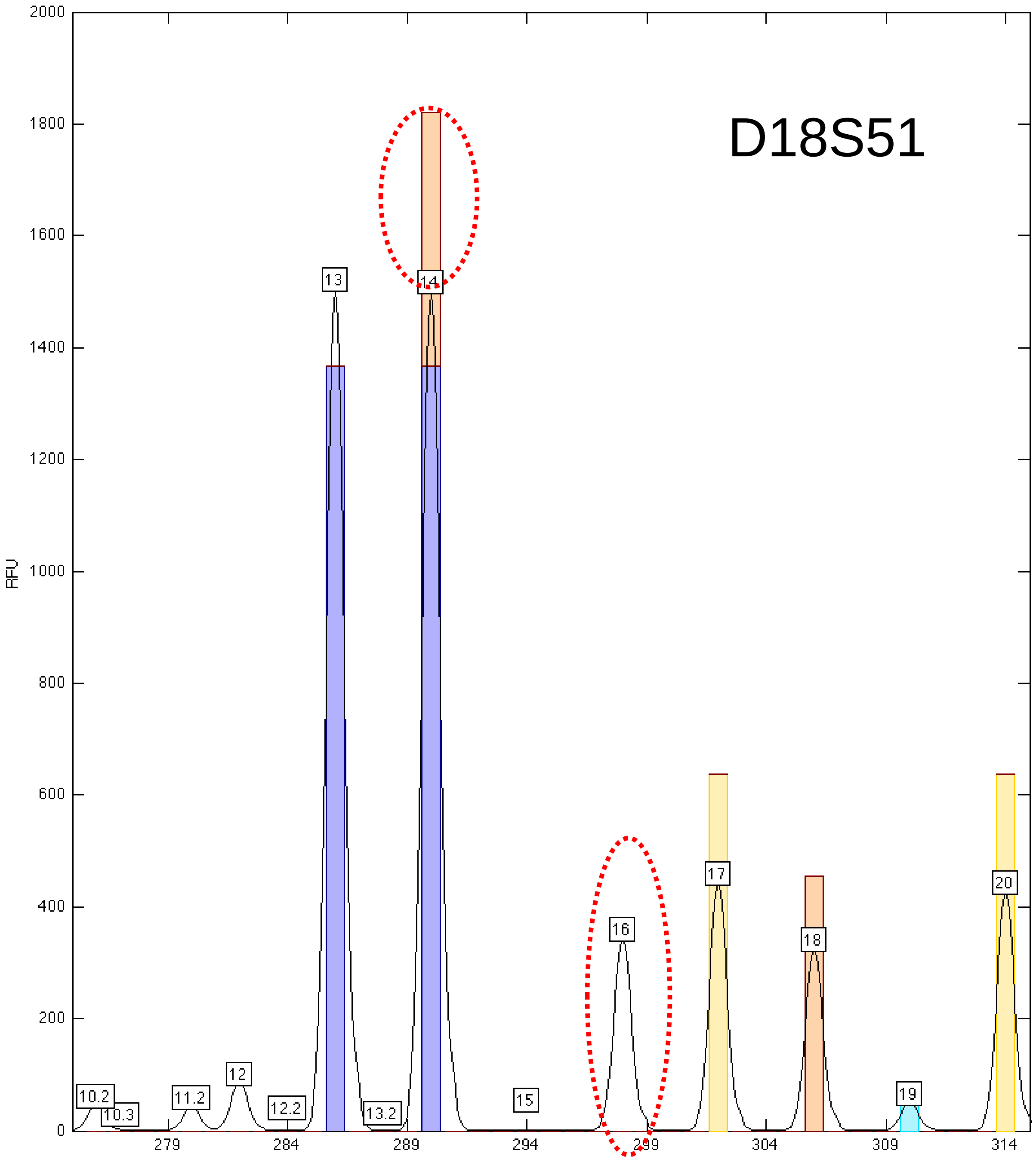
VERY
Poor fit of the data
to the model

True Allele Results – 4 person mixture

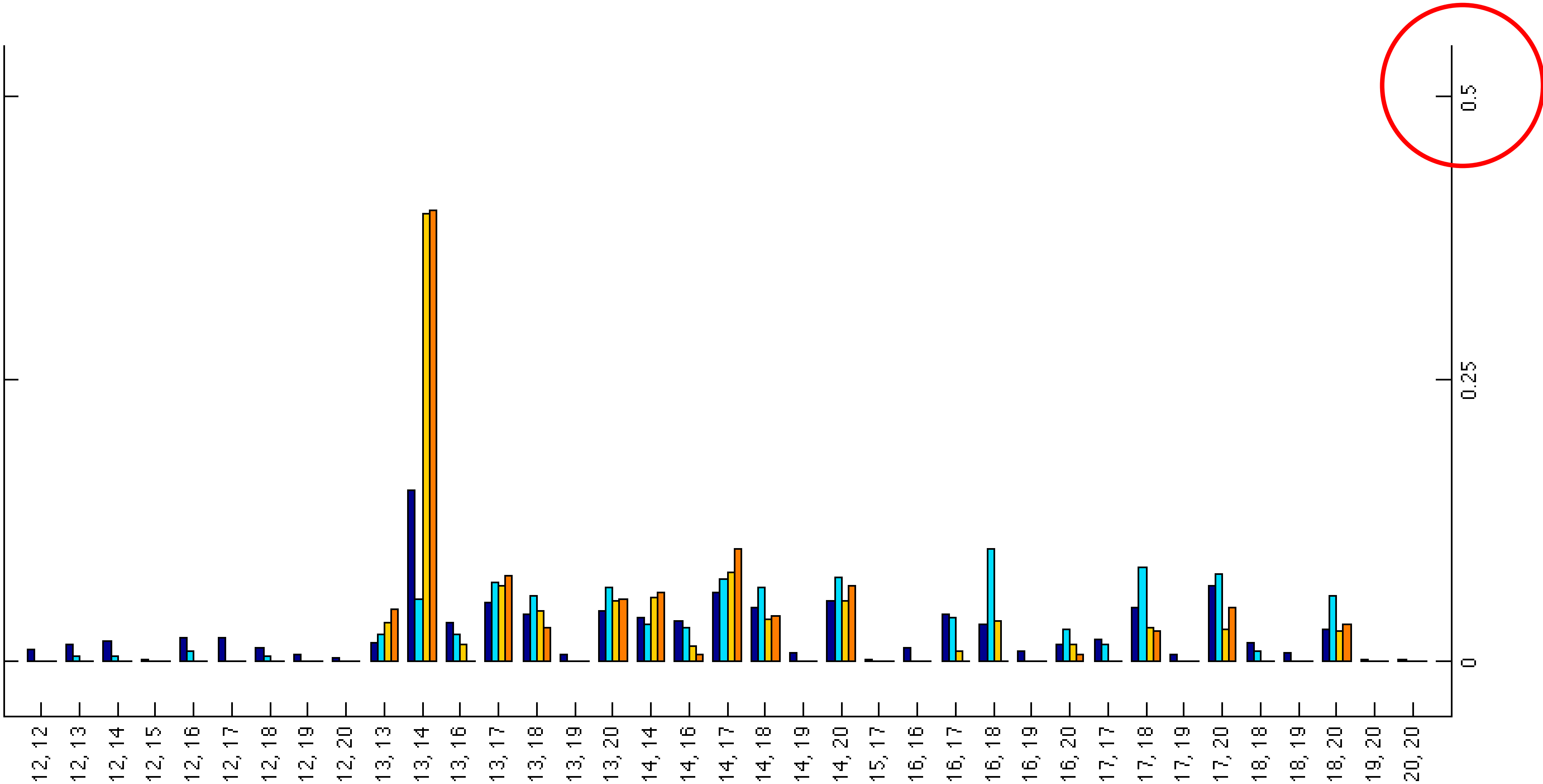


100K examinations
4 unknowns
(no conditioning)

Better separation,
Still uncertainty.

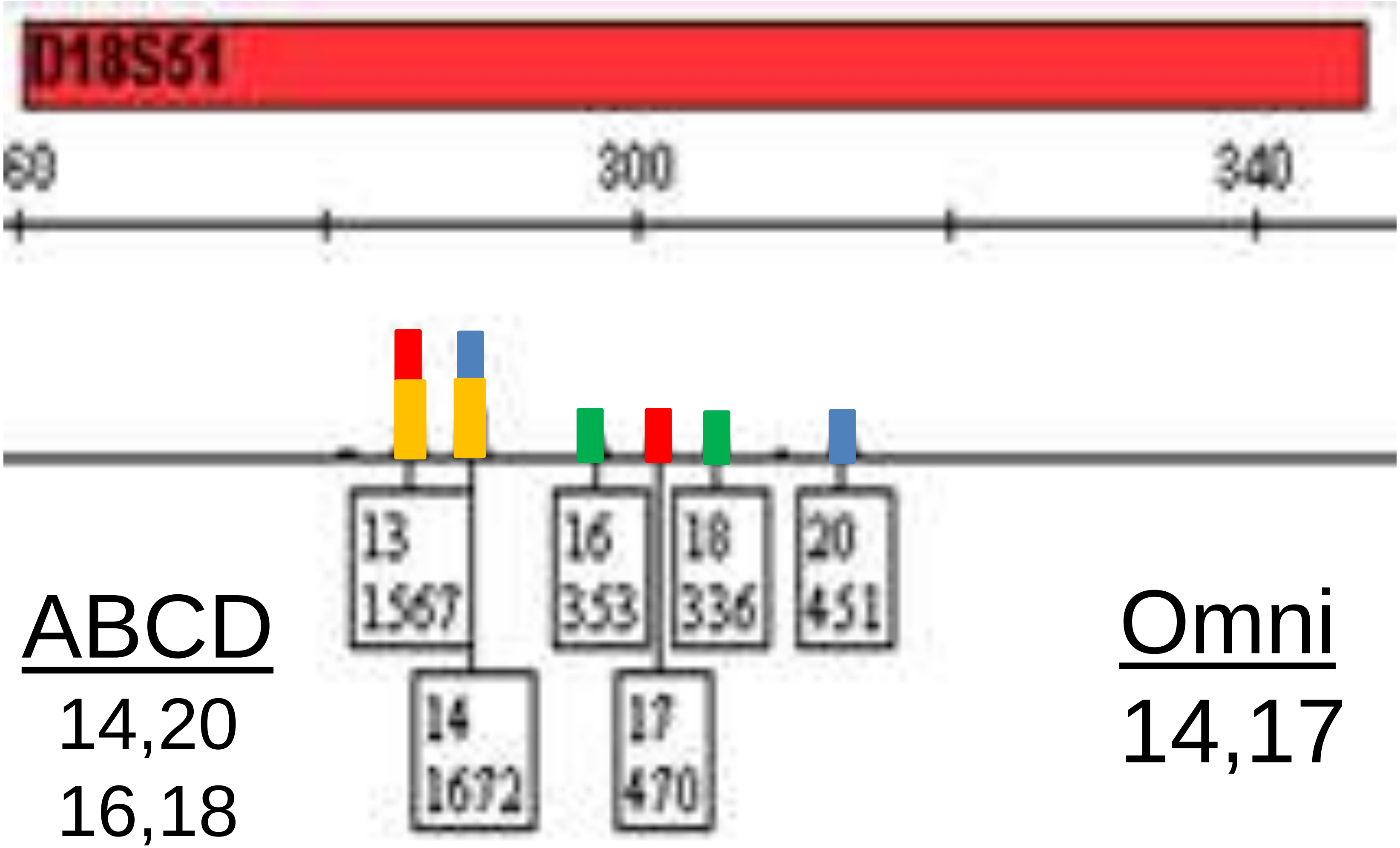


Still a poor fit of the data to the model


0
0.25
0.5
12, 12
12, 13
12, 14
12, 15
12, 16
12, 17
12, 18
12, 19
12, 20
13, 13
13, 14
13, 16
13, 17
13, 18
13, 19
13, 20
14, 14
14, 16
14, 17
14, 18
14, 19
14, 20
15, 17
16, 16
16, 17
16, 18
16, 19
16, 20
17, 17
17, 18
17, 19
17, 20
18, 18
18, 19
18, 20
19, 20
20, 20

Potential Suspects

- A, B, C and D are the four individuals in the mixture.
- John Butler is also a suspect (The Butler did it).
- “Omni man” is also a possible suspect.



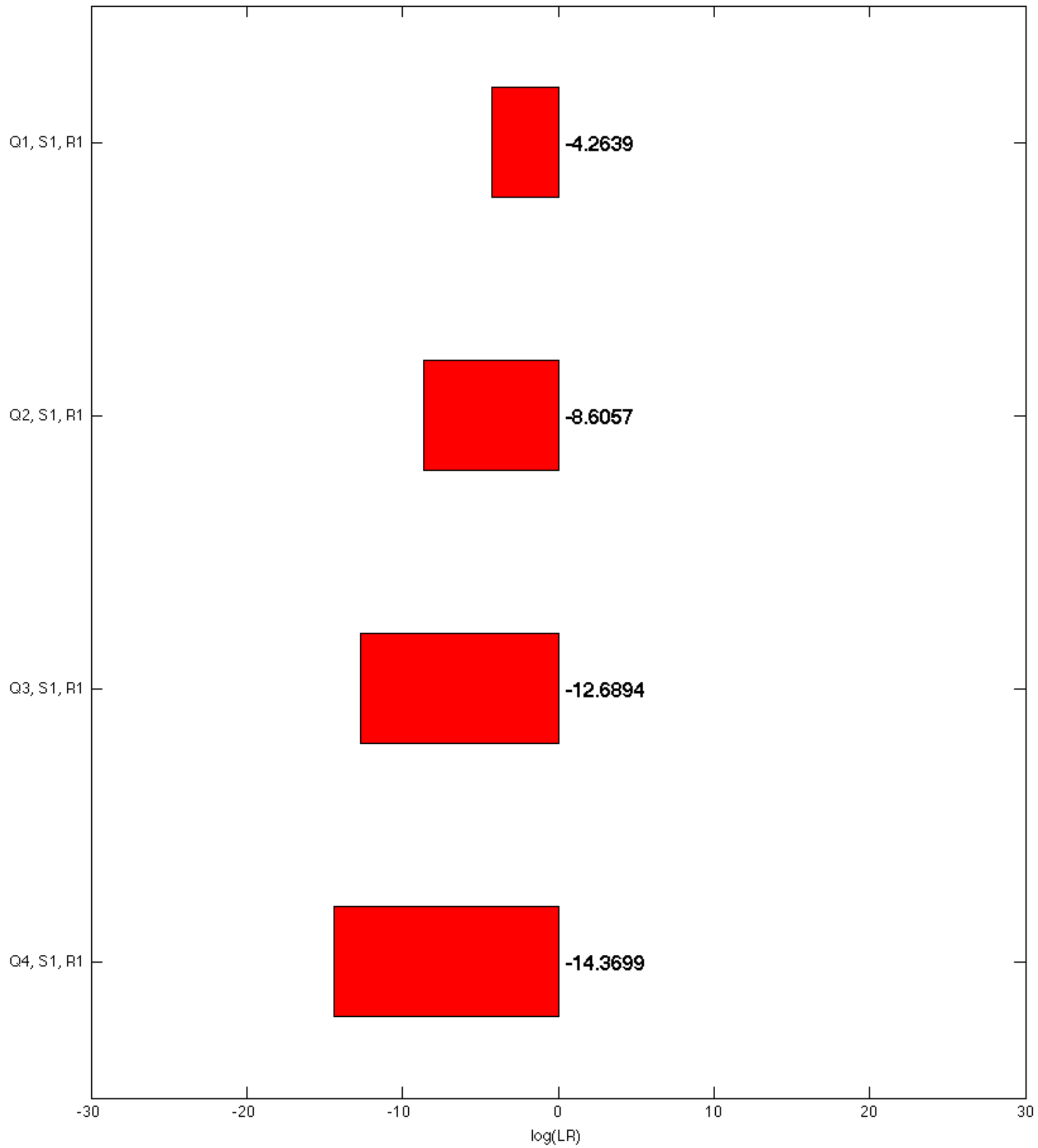
ABCD

14,20
16,18
13,17
13,14

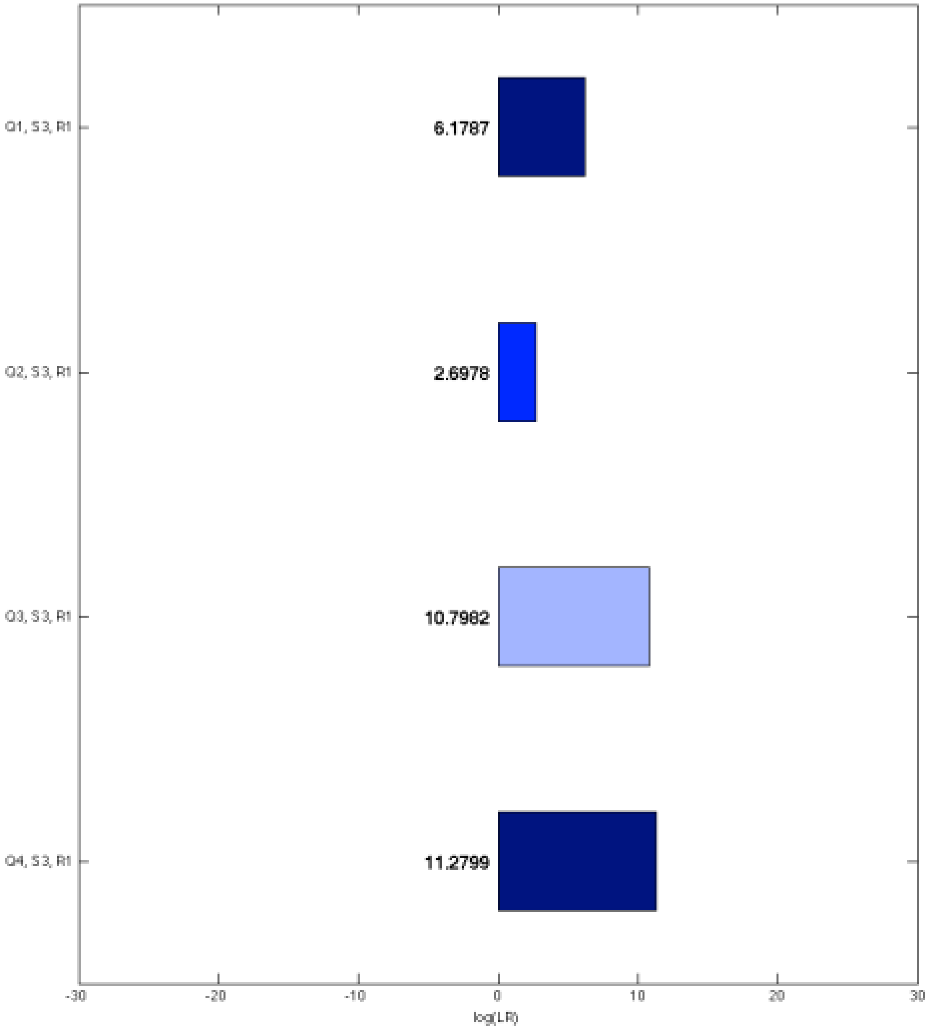
Omni

14,17

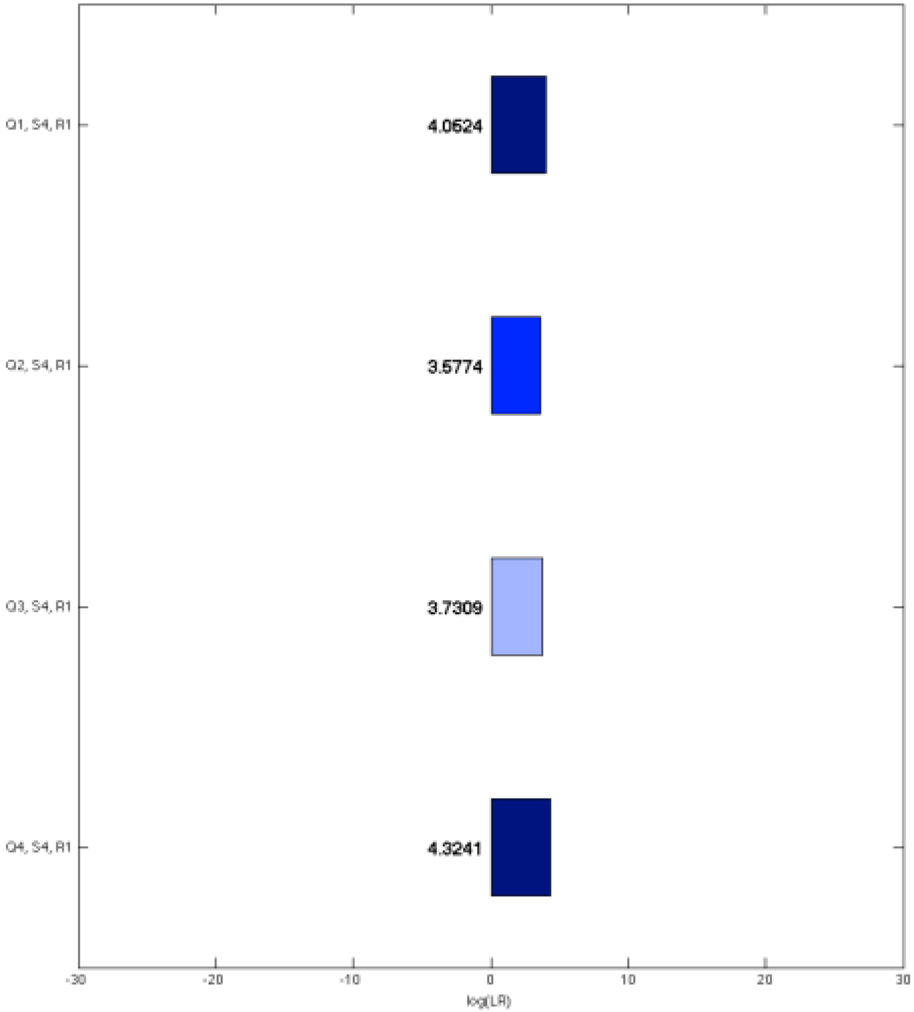
“The Butler”


Q1, S1, R1
-4.2639
Q2, S1, R1
-8.6057
Q3, S1, R1
-12.6894
Q4, S1, R1
-14.3699
-30
-20
-10
0
10
20
30
log(LR)

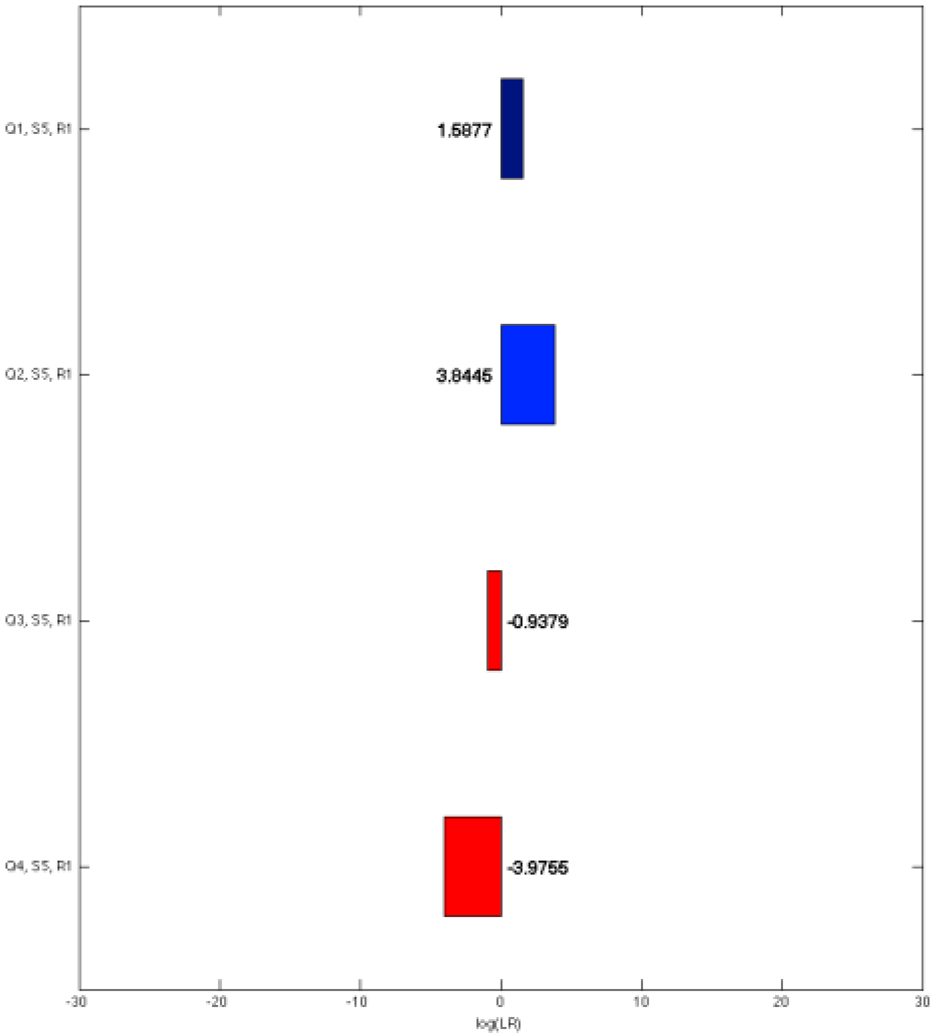
Suspect A



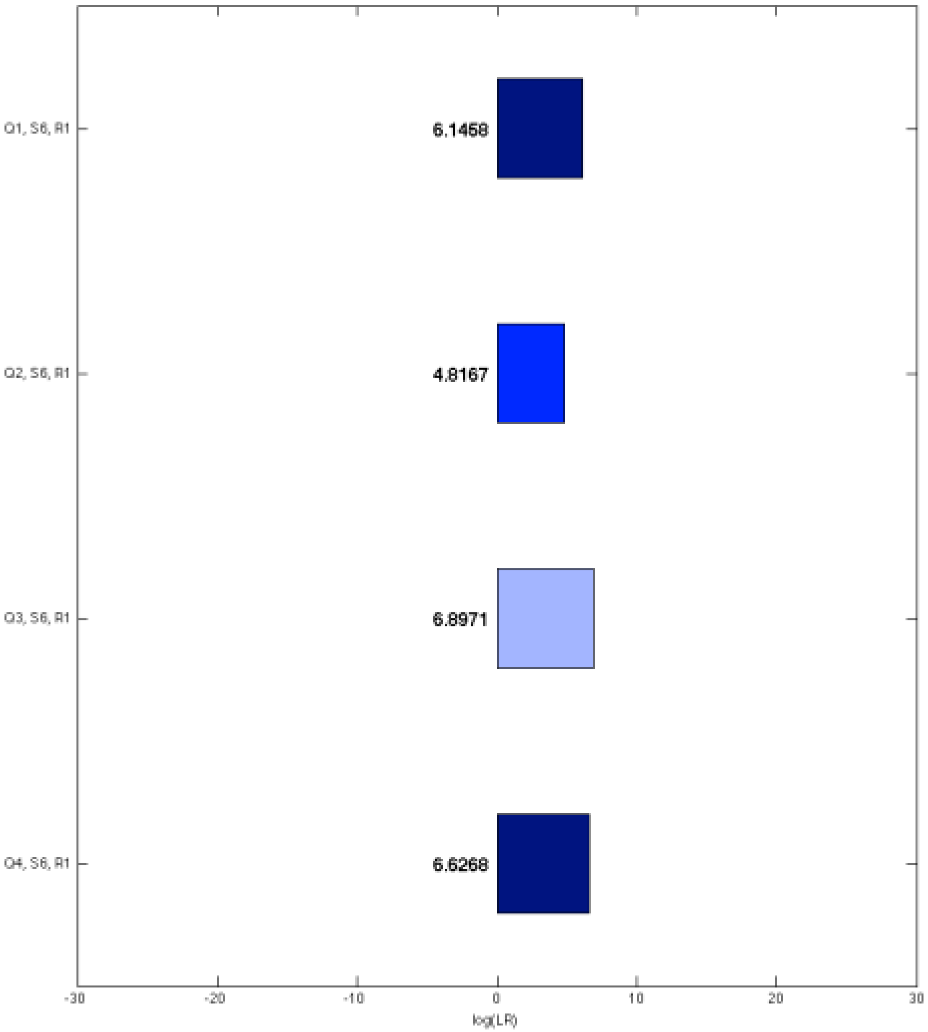
Suspect B



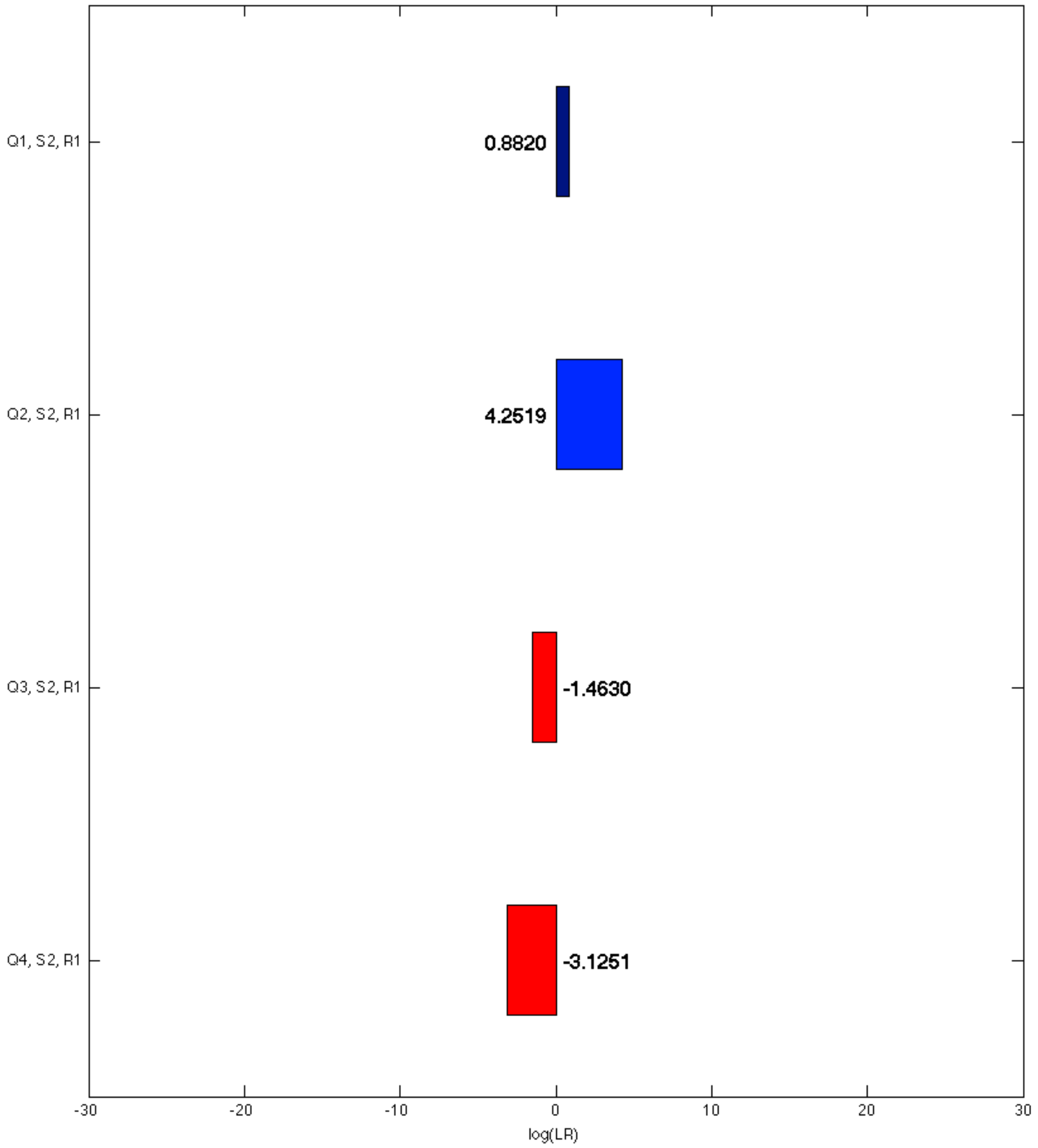
Suspect C



Suspect D



Omni Man


Q1, S2, R1
Q2, S2, R1
Q3, S2, R1
Q4, S2, R1
0.8820
4.2519
-1.4630
-3.1251
-30
-20
-10
0
10
20
30
log(LR)

Strategies

- Conditioning will help…
- This may not be possible.
- Multiple replicates will be necessary.
- There is a need to determine an appropriate method for an inclusion log(LR).

Summary of the Issues

- We need to move away from the interpretation of mixtures from an “allele-centric” point of view.
- Methods to incorporate probability will be necessary as we make this transition and confront the issues of low-level profiles with drop-out.

- “Just as logic is reasoning applied to truth and falsity, probability is reasoning with uncertainty”

-Dennis Lindley

Summary of the Issues

- The LR is the preferred method to evaluate low-level, complex mixture evidence with drop-out. ISFG recommendations are in press.
- This will require (obviously) software solutions… however, we need to better understand and be able to explain the statistics as a community.
- “But, for my own part, it was Greek to me”

  — William Shakespeare, *Julius Caesar*
- “We know what we are, but know not what we may be.” — William Shakespeare, *Hamlet*

Summary of the Issues

- Extensive training will be necessary – and a single 8 hour workshop will once a year will not suffice.

- “Do, or do not. There is no try.”
  — Yoda

Thank You

- “I can no other answer make but thanks, and thanks.” - William Shakespeare, *Twelfth Night*

http://es.wikipedia.org/wiki/William_Shakespeare

California Association of Criminalists
Dr. Steve Lee (SJSU) and Students!
CyberGenetics

Dr. Robin Cotton
Dr. Catherine Grgicak
Dr. Charlotte Word
Dr. John Butler

NIJ

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