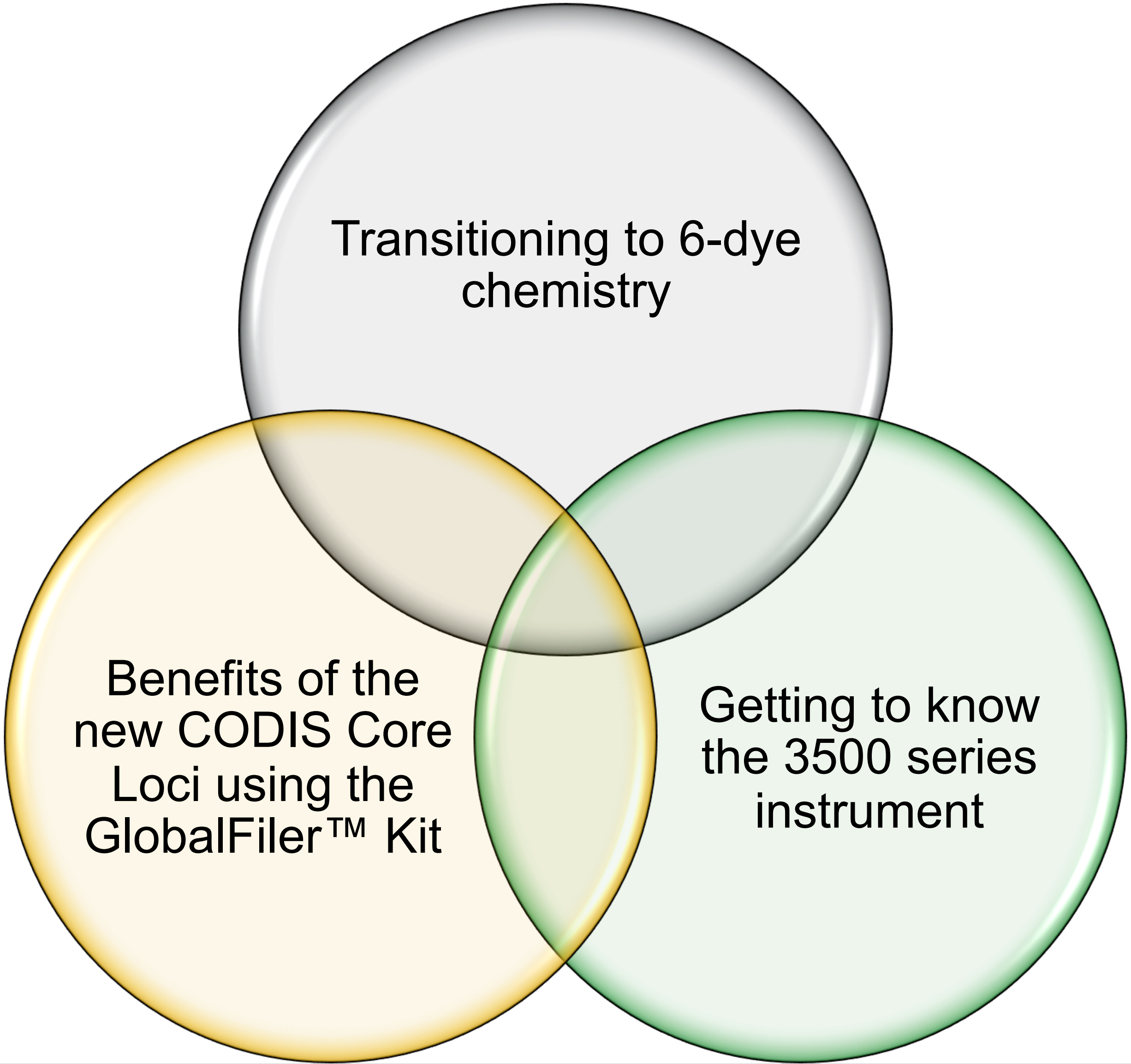
New Core CODIS LOCI implementation

Human Identification Professions Services Tips and Tricks

HID University Seminar Series 2015



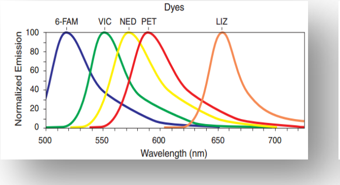
Transitioning to 6-dye chemistry

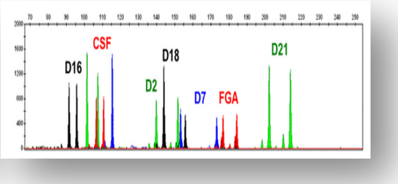
Benefits of the new CODIS Core Loci using the GlobalFiler™ Kit

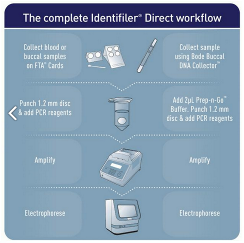
Getting to know the 3500 series instrument

Transitioning to 6-dye chemistry

A History of Innovation







The complete Identifiler® Direct workflow

Collect blood or buccal samples on FTA® Cards

Collect sample using Bode Buccal DNA Collector™

Punch 1.2 mm disc & add PCR reagents

Add 2µL Prep-n-Go™ Buffer. Punch 1.2 mm disc & add PCR reagents

Amplify

Amplify

Electrophorese

Electrophorese

1995
Capillary
Electrophoresis

2001
5-dye Technology
Mobility Modifiers

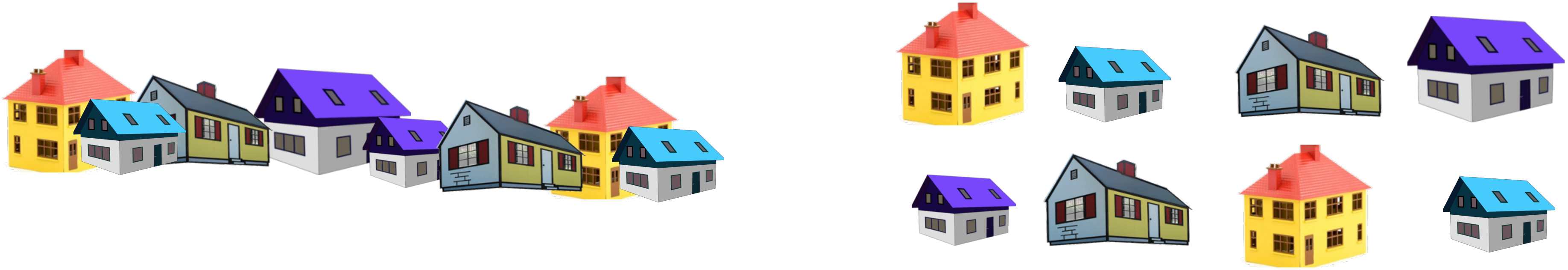
2006
Mini-STR
Technology

2009
Direct PCR
Amplification
Chemistry

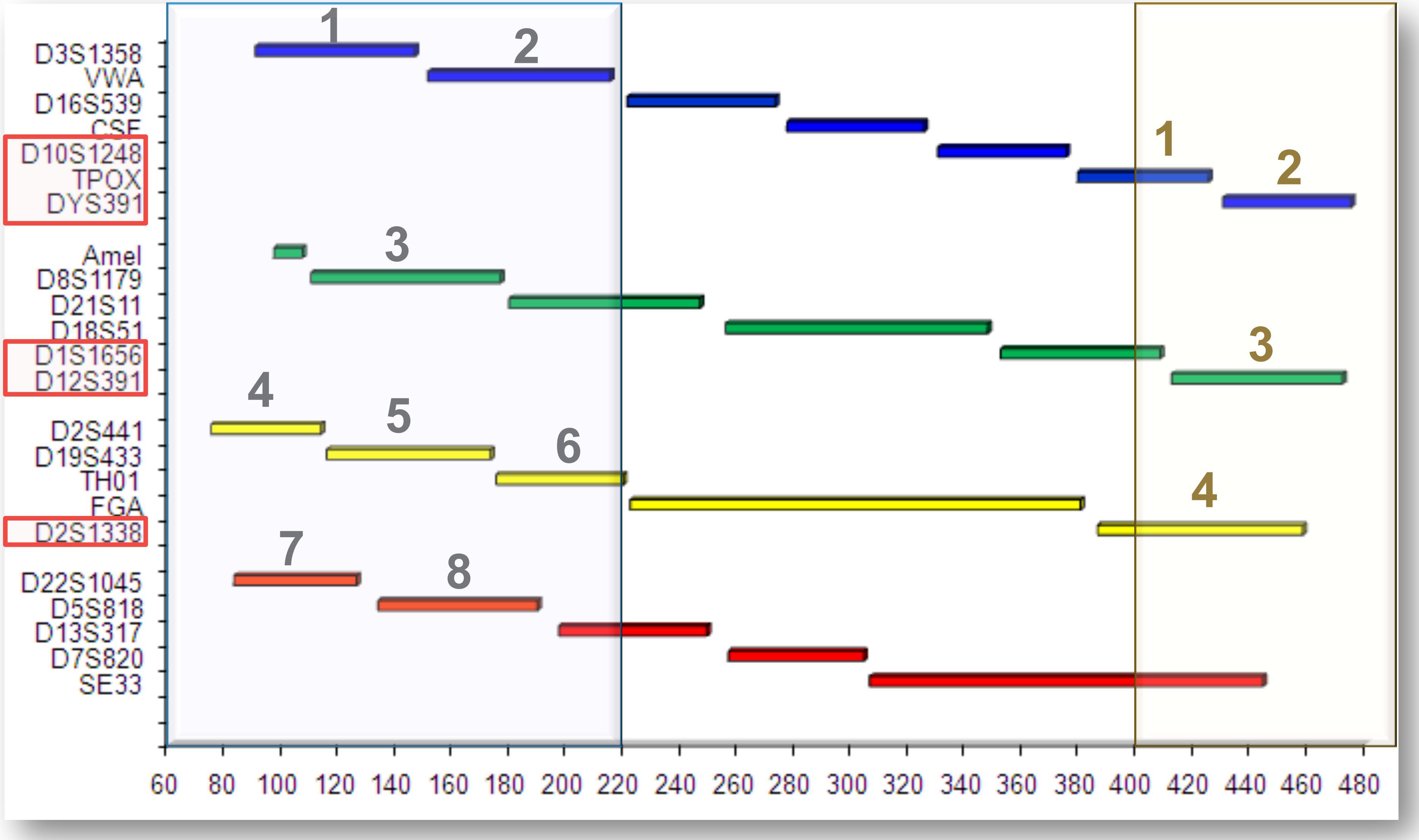
2012
6-Dye
Technology

Why 6-Dye?

- Squeezing all the additional loci into a 5-dye configuration would result in multiple tradeoffs, including:
  - Multiple loci in the high molecular weight size range (>400 bp)
  - Several loci extending almost to 500 bp, which may cause issues with sizing and resolution
  - Fewer miniSTRs (220 bp or smaller)
  - Insufficient spacing between adjacent markers
  - Many loci would require redesigned primer sequences, leading to less concordance with data generated using the original primer sequences



Hypothetical 5-Dye Configuration - GlobalFiler™ Kit Loci

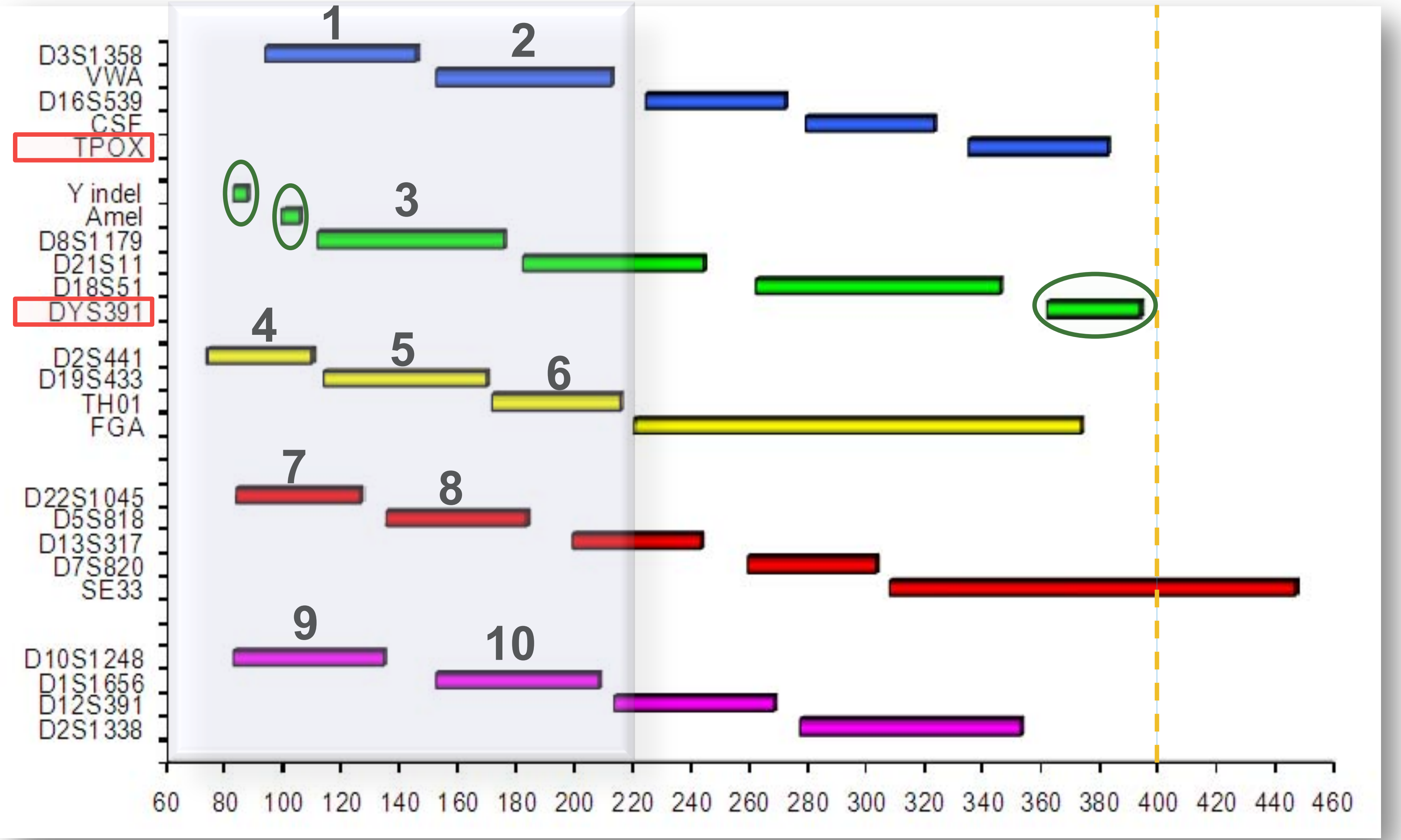


Primer redesign

Fewer mini-STRs

4 loci > 400 bp

6-Dye Configuration – GlobalFiler Kit Loci

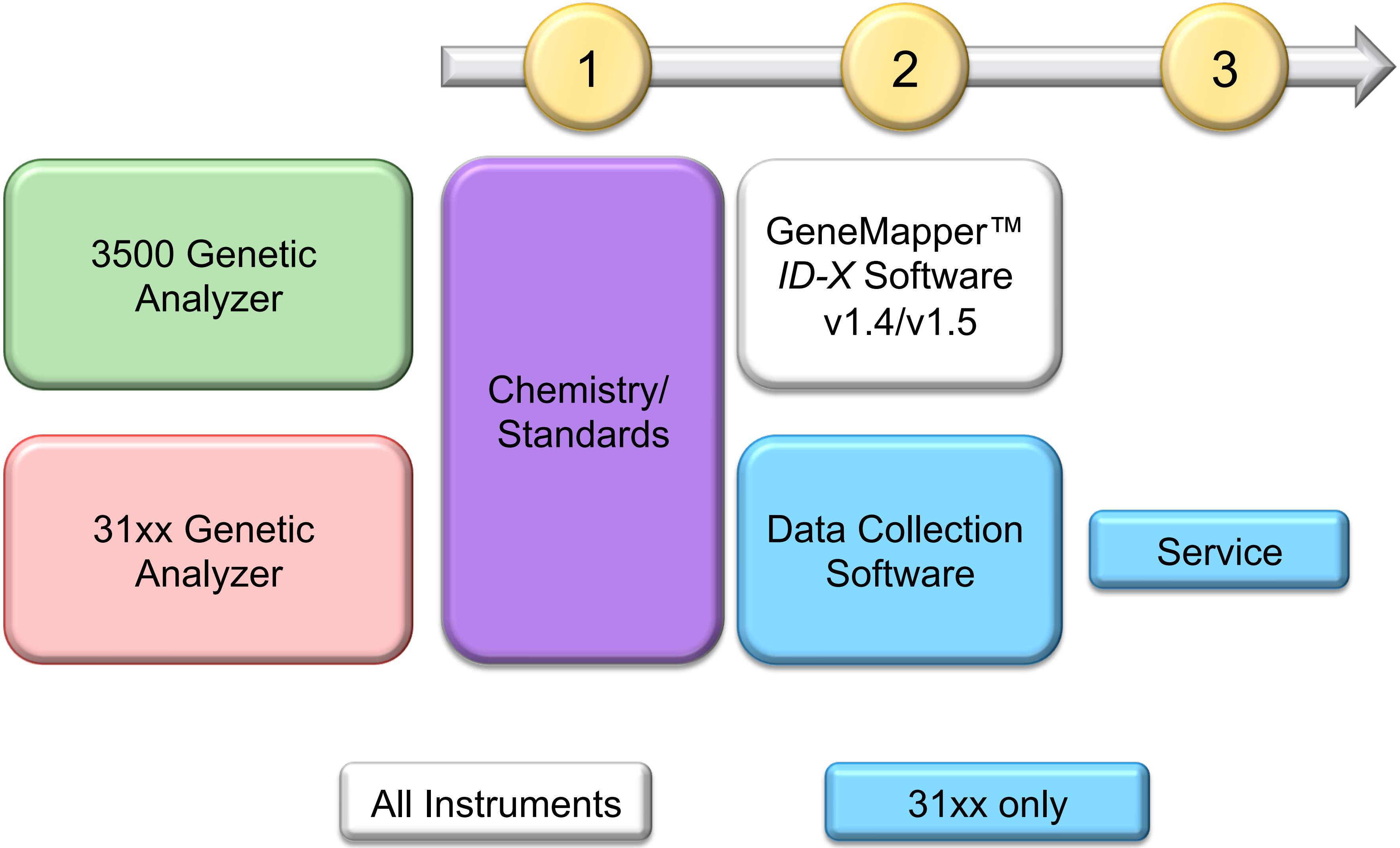


Primer redesign

More mini-STRs

Gender markers

6-Dye Summary



GlobalFiler™ Upgrade Roadmap

Product Type	3500	3130	3100
GeneMapper™ *ID-X* Software v1.4/1.5	✓	✓	✓
Data Collection Software v4.0	N/A	✓	✓
6-dye Data Collection Module	N/A	✓	✓
Service Call/ Computer	N/A	✓	✓
Instrument Upgrade	N/A	N/A	✓

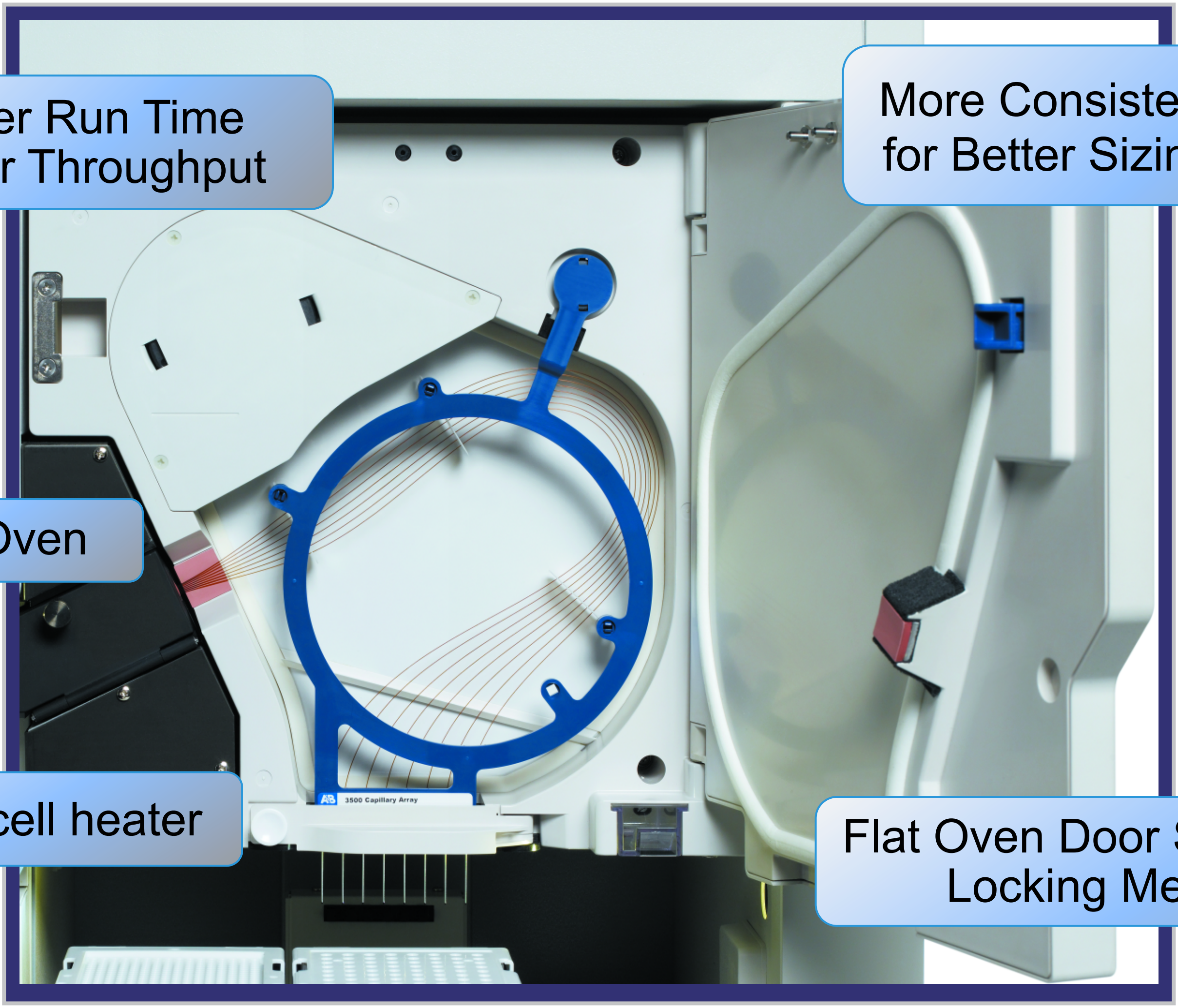
Data Collection Software and Analysis Software

- Data Collection Software
  - 3130/3130xL Genetic Analyzer
    - Data Collection v4
    - 6-dye Data Collection Module
    - Configured computer with Microsoft® Windows® 7 platform
  - 3500/3500xL Genetic Analyzer
    - Data Collection v1, v2, or v3.1

- Software
  - GeneMapper *ID-X* Software v1.4/ v1.5

Getting to know the 3500 series instruments

Improved Data Quality and Sample Throughput



Faster Run Time
Higher Throughput

More Consistent Migration for Better Sizing Precision

Smaller Oven

Detection cell heater

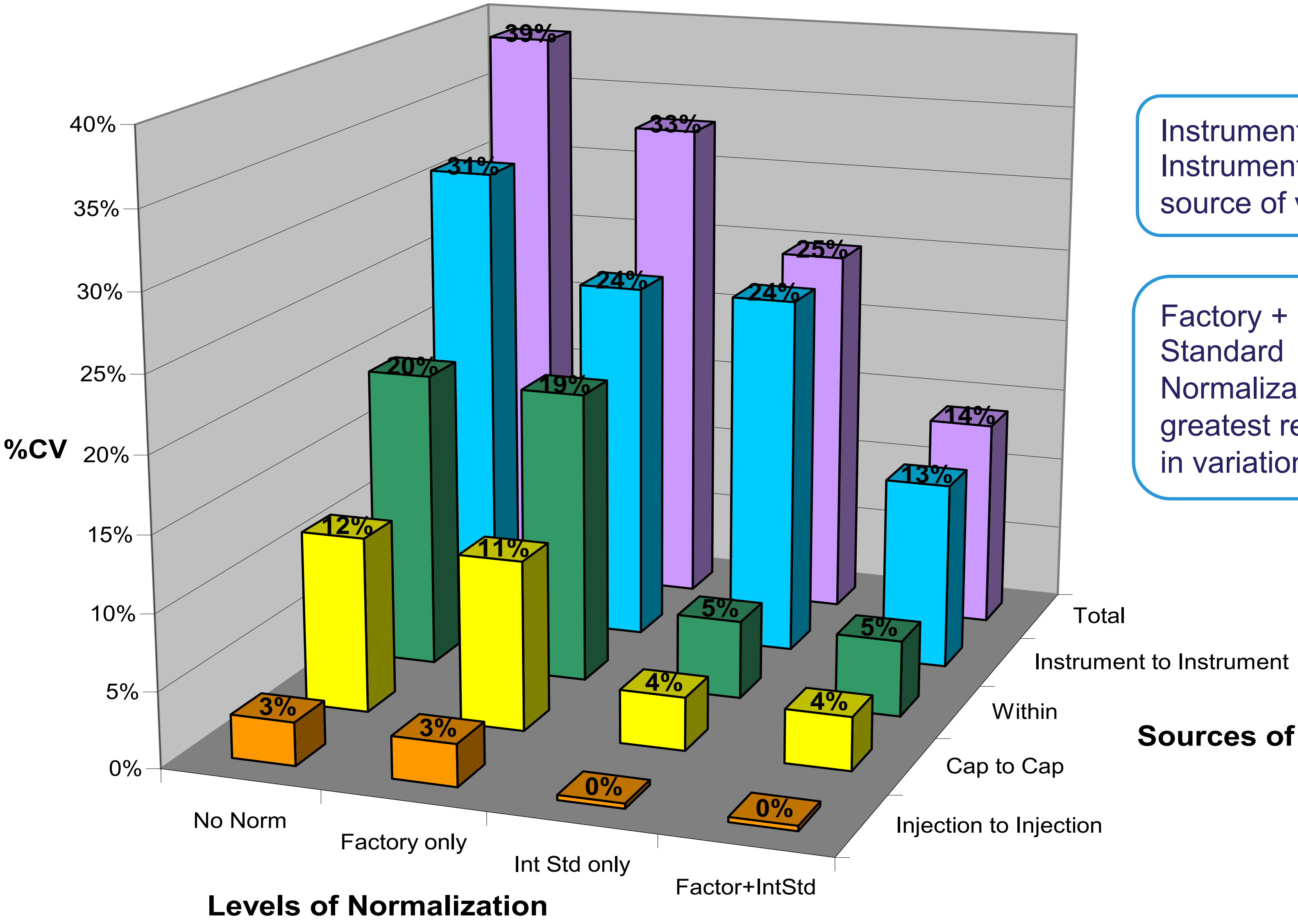
Flat Oven Door Seal and New Locking Mechanism

Instrument Setup and Performance

- Pre-Filled, Quality-Controlled Reagents
- Information Recorded via RFID
  - Lot numbers
  - Part Numbers
  - Serial numbers
  - Dates (expiration and installation)
  - Capacity/Usage
- Per Sample Running Cost

Comp

Sources of Variation by Normalization Method

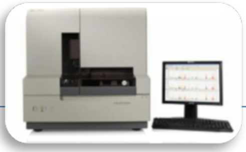


Instrument to Instrument largest source of variation

Factory + Internal Standard Normalization greatest reduction in variation

Sources of Variation

Dynamic Range of the 31xx vs. 3500 Genetic Analyzer



Saturation
(~ ≥ 4 ng)

~8,000

~30,000 – 32,000

3000 RFU

12,000 RFU

Optimal
Target Range
(~1 ng)

RFU

Heterozygote ~1,500

Heterozygote ~6,000

1000 RFU

3000 RFU

Stochastic
Threshold

Peak Height Ratio Imbalance
Low Template DNA (~100 pg)

Peak Height Ratio Imbalance
Low Template DNA (~100 pg)

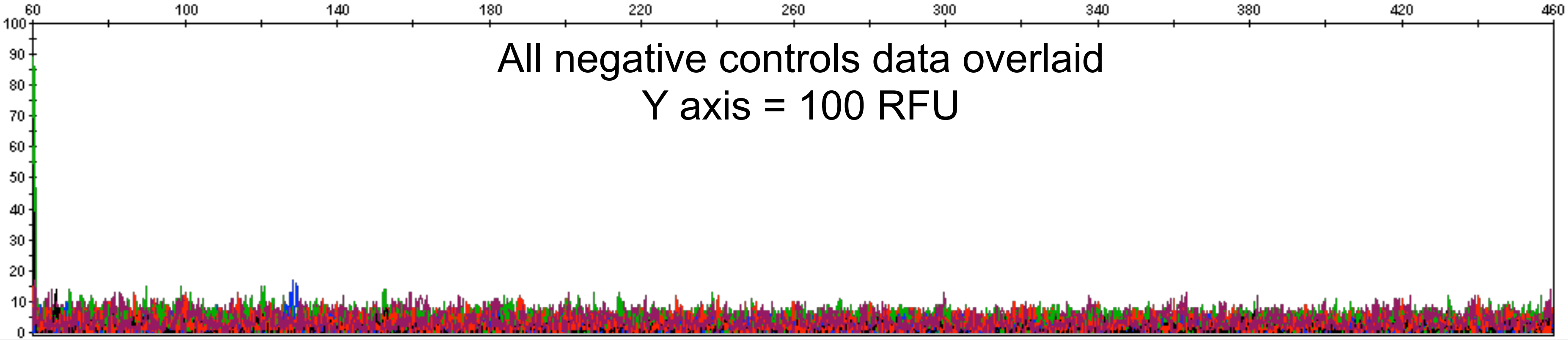
Baseline Noise on a 3500 Series Instrument

- Minimum Threshold
  - Used to determine when a peak has a high enough signal to be differentiated solely from the noise of the instrument and amplification kit
  - Generally negative controls are run throughout the validation and are analyzed to establish the minimum thresholds
    - 1 RFU peak amplitude threshold
    - Between 60 bp and 460 bp
    - Any peaks attributed to artifacts are removed and not used in the calculation
  - Minimum threshold = the Limit of Quantification rounded to the nearest five
    - Provides an upper limit value below which all or nearly all background noise would expect to fall

Baseline Noise on a 3500 Series Instrument

- GlobalFiler™ Kit Minimum Thresholds

Dye Channel	Maximum Peak Height (RFU)	Average Peak Height (RFU)	Standard Deviation	Average + 3 Standard Deviations (LOD)	Average + 10 Standard Deviations (LOQ)	Minimum Threshold (RFU)
Blue (6-FAM™)	17	3.39	1.44	7.72	17.84	20
Green (VIC)	15	5.60	2.05	11.75	26.11	25
Yellow (NED™)	12	2.86	1.20	6.47	14.90	15
Red (TAZ™)	15	4.94	1.89	10.61	23.85	25
Purple (SID™)	14	5.84	2.11	12.16	26.91	25
Orange (LIZ)	33	4.14	2.56	11.81	29.73	30

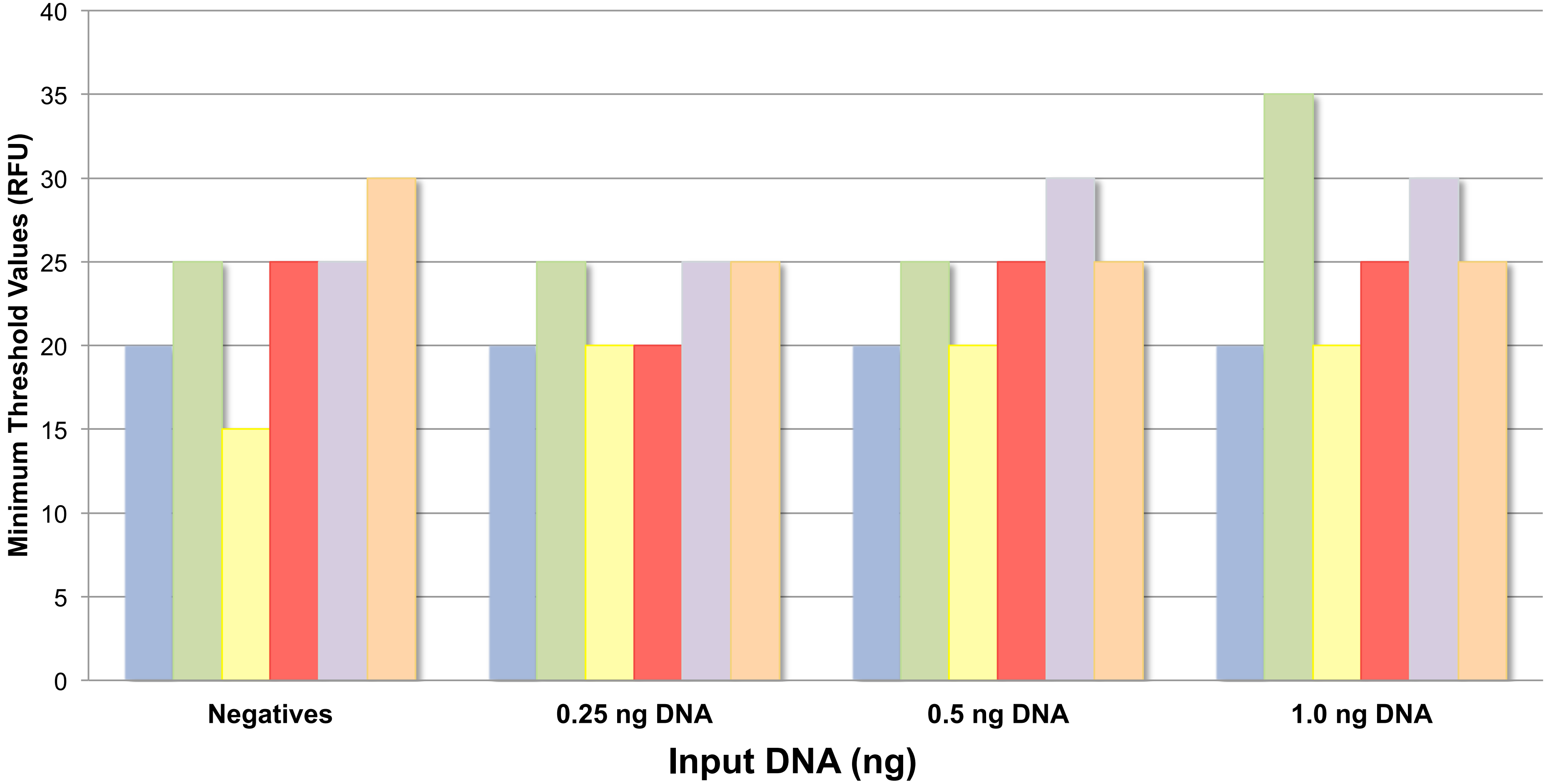


All negative controls data overlaid
Y axis = 100 RFU

Baseline Noise on a 3500 Series Instrument

- Calculated for negative controls and samples containing DNA

Minimum Threshold Values by Dye Channel

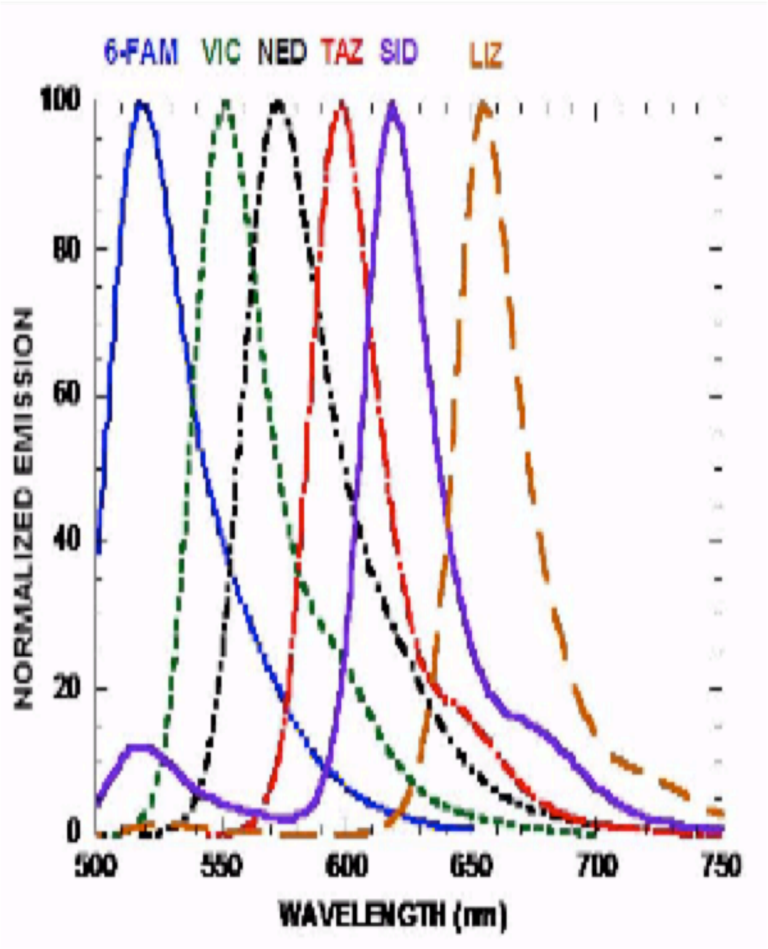


3500 Series Instrument and Pull-up

- Pull-up peaks:
  - Pull-up occurs when the spectral calibration matrix fails to completely separate signal from the different dye colors
  - Pull-up peaks appear at approximately the same base pair size as the source peak
  - Pull-up percentage levels vary among injections, dyes, capillaries, and kits

NOTE: As the peaks for the 3500 series instruments are generally higher as compared to 31xx instruments, pull-up peaks may be more prevalent

Generally, most pull-up peaks are less than 3% of the parent peak



Quick! What’s 3% of 30,000?

3500 Series Instrument and Pull-up

- Implications of pull-up on a 3500 series instrument
  - Consider the following theoretical average peak heights for the indicated DNA input amounts amplified with the GlobalFiler™ Kit on a 3500 instrument

DNA Input	Heterozygote (RFU)	Homozygote (RFU)
250 pg	1250	2500
500 pg	1500	3000
1ng	5000	10000
2 ng	10000	20000

  - If pull-up peaks are generally around 1% and most of the pull-up peaks generally fall below 3%...

DNA Input	1% pull-up		3% pull-up (RFU)	
	Heterozygote (RFU)	Homozygote (RFU)	Heterozygote (RFU)	Homozygote (RFU)
250 pg	12.5	25	37.5	75
500 pg	25	50	75	150
1ng	50	100	150	300
2 ng	100	200	300	600

3500 Series Instrument and Pull-up

- Comparing the minimum threshold values to the pull-up calculations demonstrates that pull-up will be called above the limit of detection in samples with at least 500 pg of DNA

Minimum Threshold (RFU) (negative controls)
20
25
15
25
25

DNA Input	**1% pull-up**		**3% pull-up (RFU)**	
	Heterozygote (RFU)	Homozygote (RFU)	Heterozygote (RFU)	Homozygote (RFU)
250 pg	12.5	**25**	**37.5**	**75**
500 pg	**25**	**50**	**75**	**150**
1ng	**50**	**100**	**150**	**300**
2 ng	**100**	**200**	**300**	**600**

Guideline to Consider

- SWGDAM 2010 Interpretation Guidelines

3.1.1.2. While the application of an analytical threshold may serve to filter out some non-allelic peaks, the analytical threshold should be established based on signal-to-noise considerations (i.e., distinguishing potential allelic peaks from background). The analytical threshold should not be established for purposes of avoiding artifact labeling as such may result in the potential loss of allelic data.

Benefits of the New CODIS Core Loci using the GlobalFiler™ Kit

Benefits of the new CODIS loci


New CODIS Recommendations

Expanded ESSL

Missing Persons Investigations

Why?

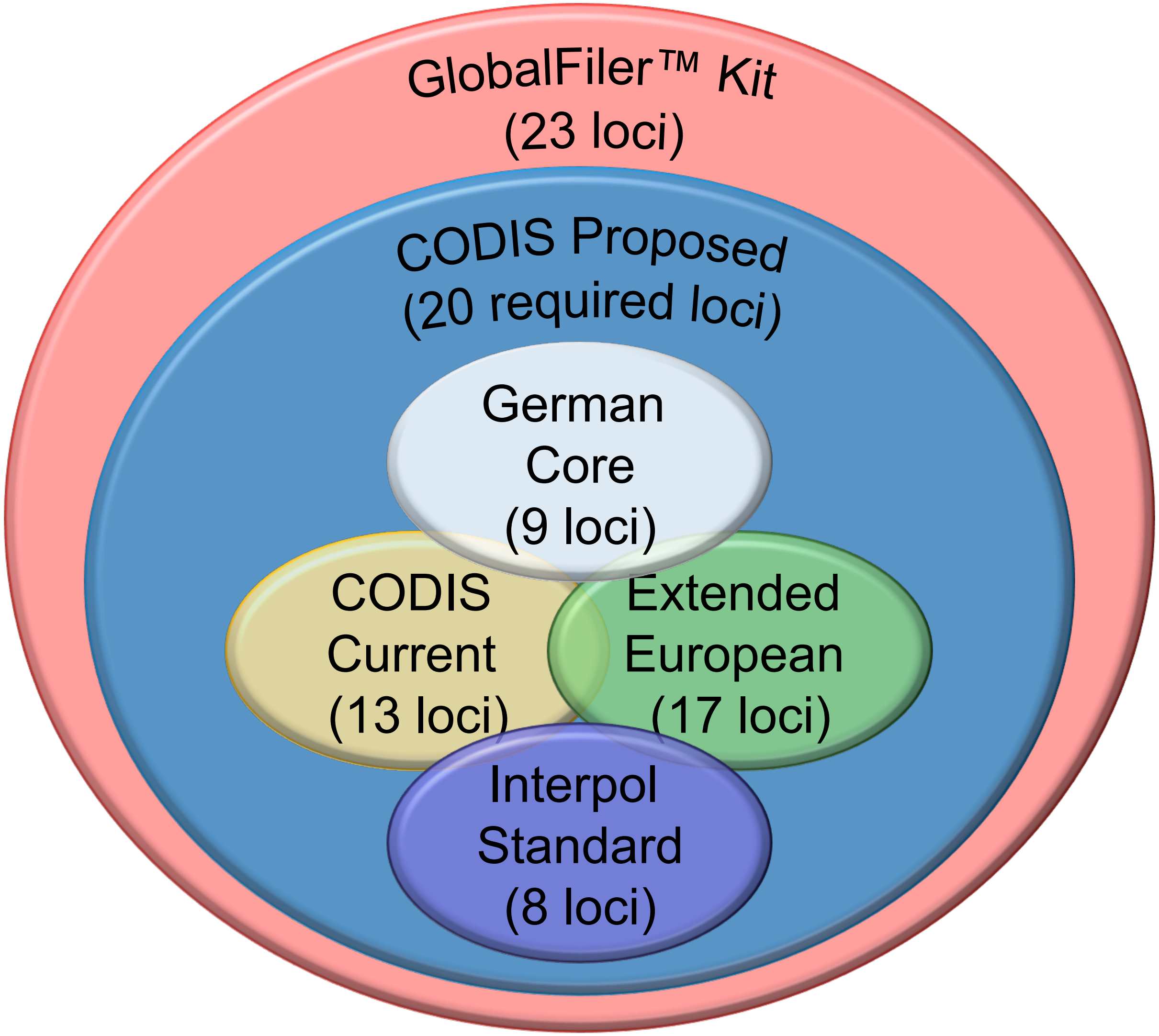
Increase international data compatibility
Increase discrimination power
Reduce the likelihood of adventitious matches

How?

Increase the number of loci

Incorporate loci contained in global databases

Increase International Data Compatibility



What is the GlobalFiler™ Kit?

Locus	CODIS (Current)	Europe	CODIS (Proposed)	GlobalFiler™ Kit
D13S317	X		X	X
D7S820	X		X	X
D5S818	X		X	X
CSF1PO	X		X	X
D1S1656		X	X	X
D12S391		X	X	X
D2S441		X	X	X
D10S1248		X	X	X
D18S51	X	X	X	X
FGA	X	X	X	X
D21S11	X	X	X	X
D8S1179	X	X	X	X
VWA	X	X	X	X
D16S539	X	X	X	X
TH01	X	X	X	X
D3S1358	X	X	X	X
AMEL	X	X	X	X
D2S1338	X	X	X	X
D19S433	X	X	X	X
DYS391			X	X
TPOX	X		X	X
D22S1045		X	X	X
SE33		X	X	X

The GlobalFiler™ Kits are our response to the worldwide expansion of forensic locus sets

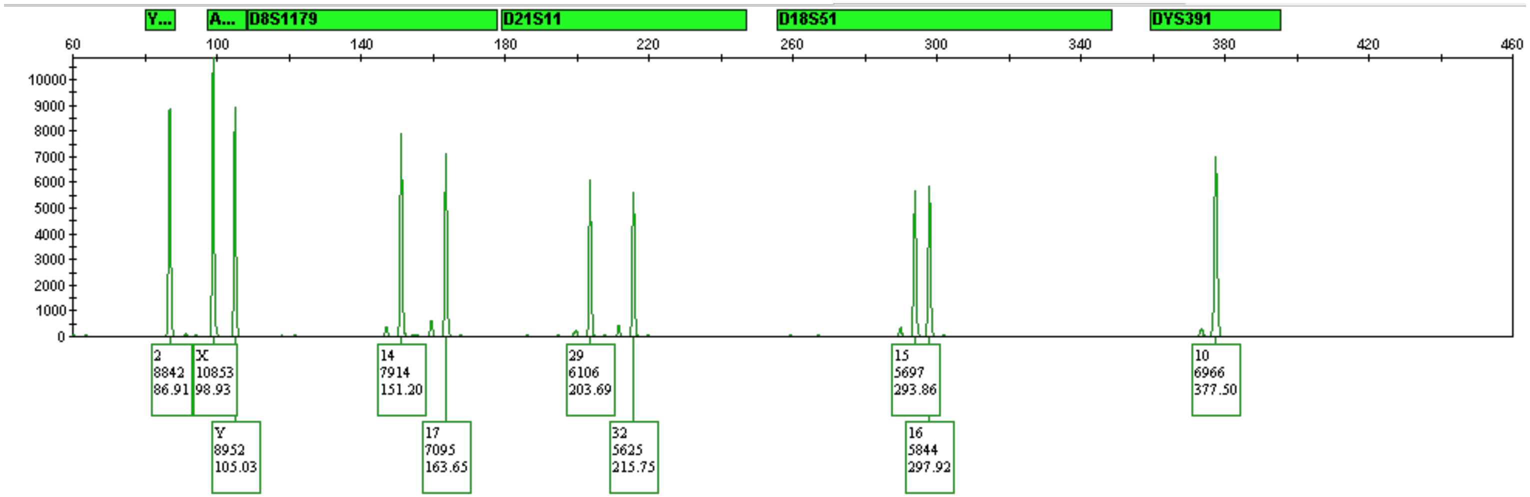
- 20 required loci
- 3 highly recommended

D.R. Hares, Expanding the CODIS core loci in the United States, Forensic Sci. Int. Genet. 6 (2012), e52-e54.

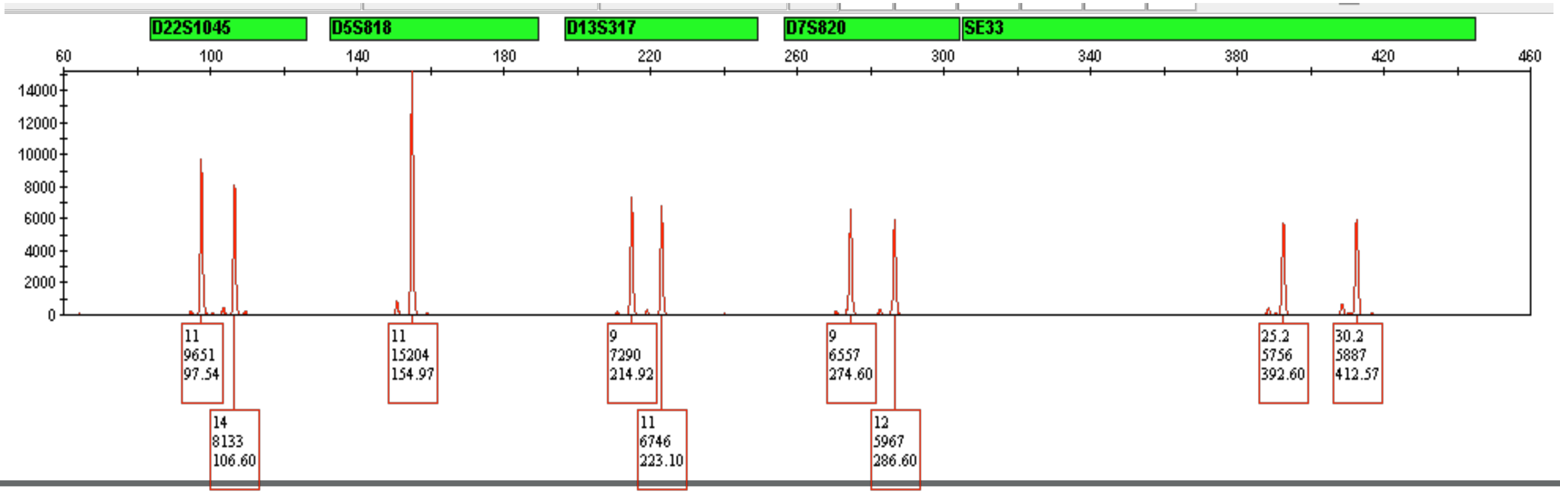
D.R. Hares, Addendum to expanding the CODIS core loci in the United States, Forensic Sci. Int. Genet. 6 (2012), e135.

Getting Familiar with a Few New Markers

- Y markers
  - Y-Indel
  - DYS391

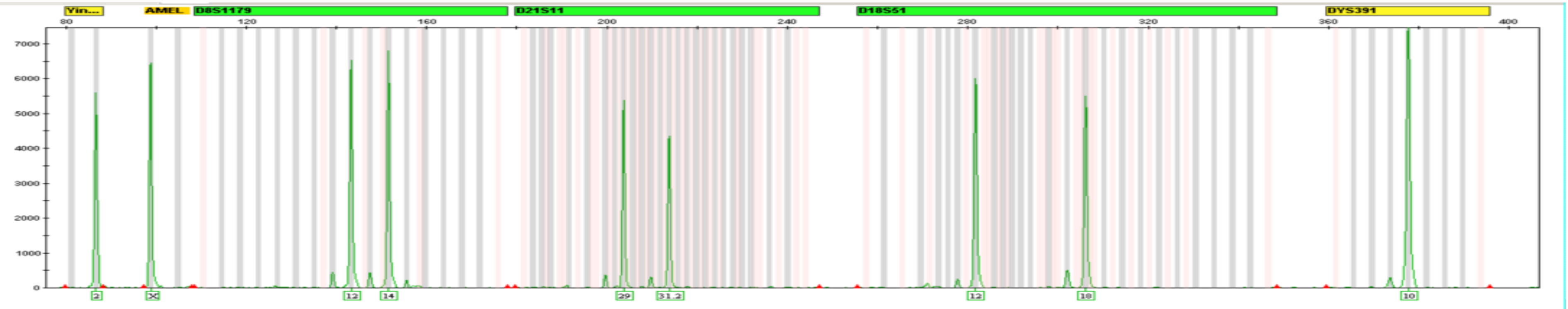


- Autosomal marker
- SE33



Why Include Additional Y Markers?

- Amelogenin Y null alleles occur



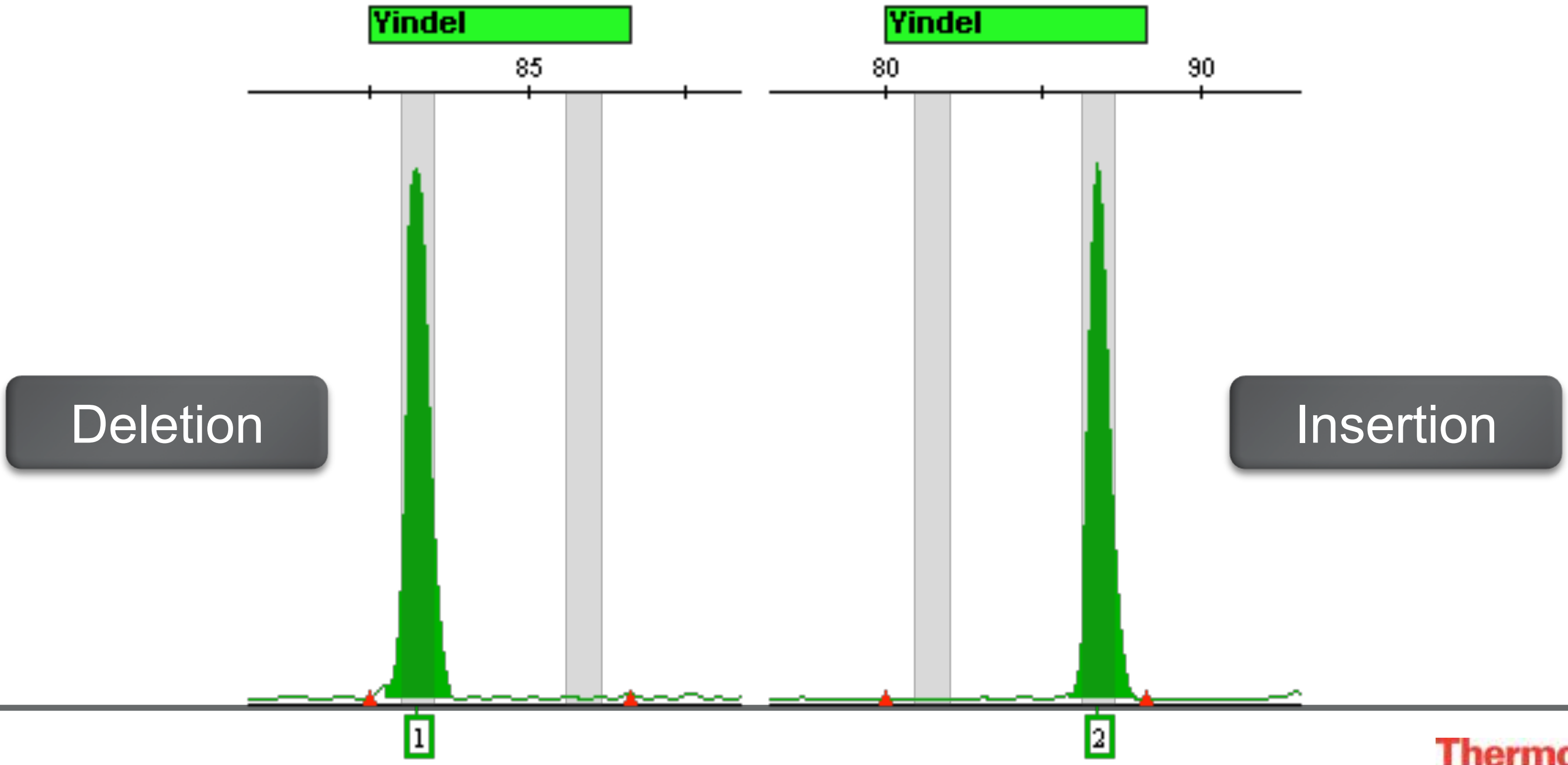
- Additional gender identification markers are on the long arm of the Y chromosome to minimize the risk of a double deletion
- DYS391 is a stable locus with a relatively narrow allele range
- The Y-indel is very short therefore more likely to perform even if DYS391 drops out in degraded samples

Amelogenin

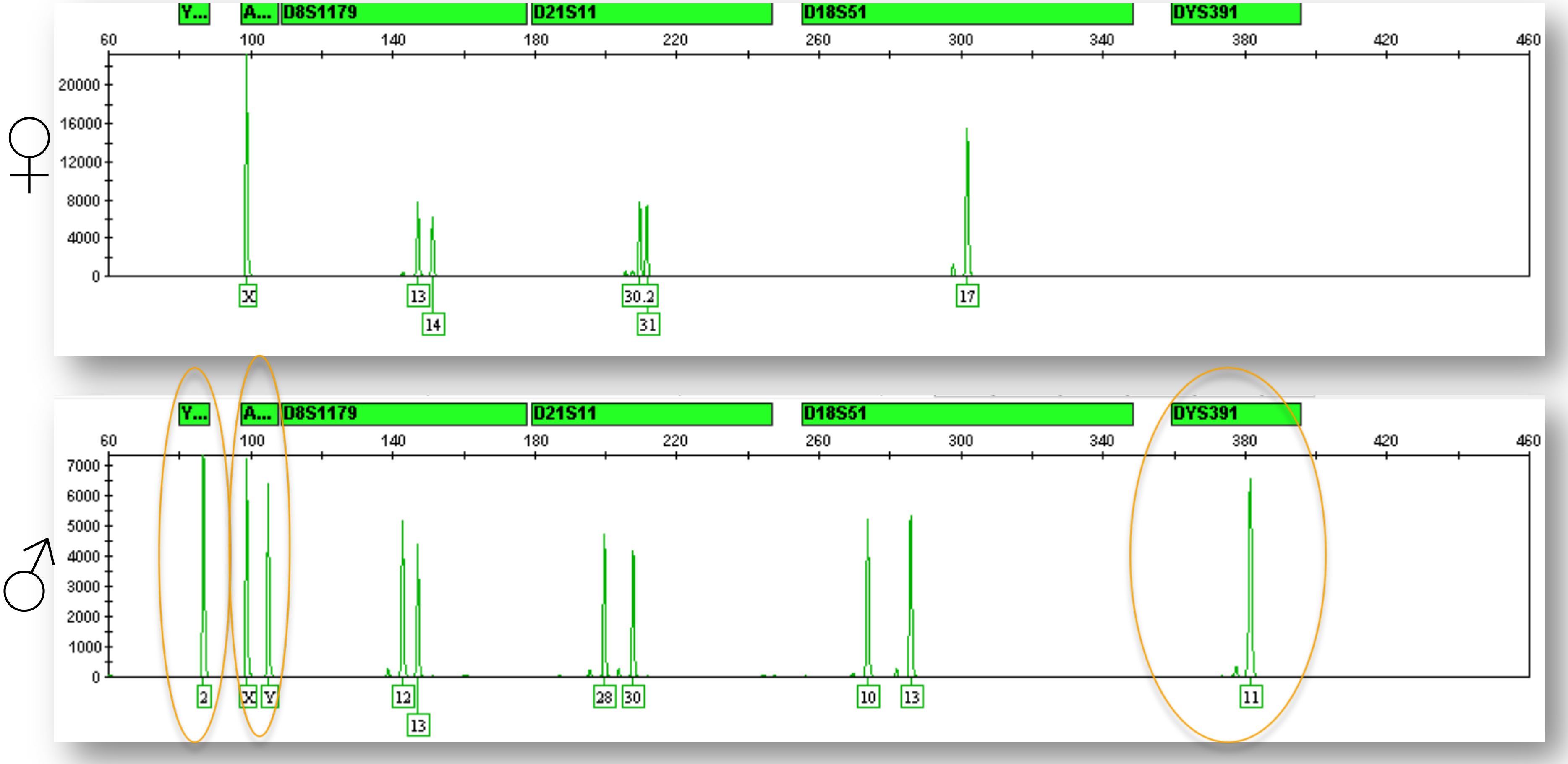
Y-indel/DYS391

What is an Indel?

- Indels are short length polymorphisms, consisting of the presence (INsertion) or absence (DELetion) of a short sequence (1-50 nucleotides)
- In the GlobalFiler Kits, an Indel marker on the Y chromosome was incorporated into the multiplex



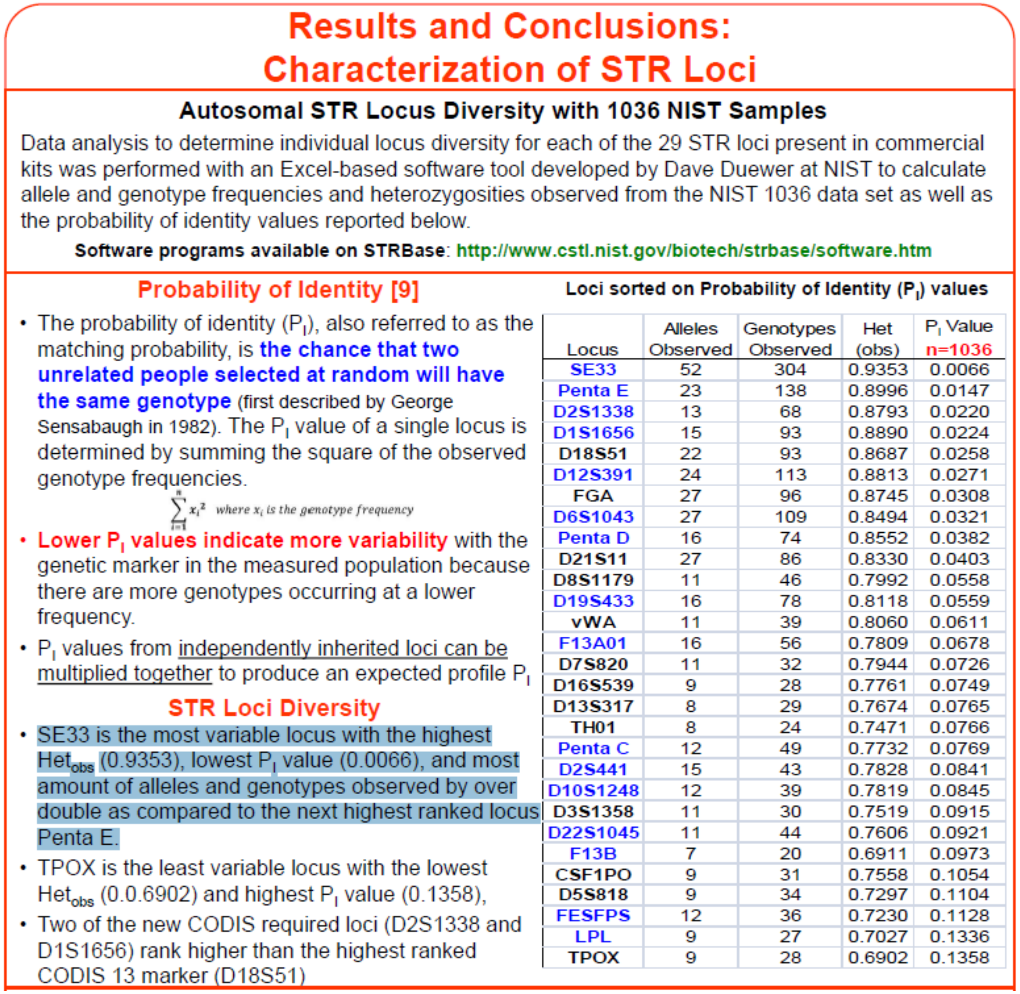
Improved Accuracy of Gender Determination



Y-indel position encourages recovery in degraded samples

Facts about the SE33 Locus

- The most discrimination power of any STR locus in commercial kits
  - highest Het_{obs} (0.9353)
  - lowest P_I value (0.0066)
  - highest amount of alleles and genotypes observed
- Ideal for mixtures
- Widely used in Europe



Results and Conclusions: Characterization of STR Loci

Autosomal STR Locus Diversity with 1036 NIST Samples

Data analysis to determine individual locus diversity for each of the 29 STR loci present in commercial kits was performed with an Excel-based software tool developed by Dave Duewer at NIST to calculate allele and genotype frequencies and heterozygosities observed from the NIST 1036 data set as well as the probability of identity values reported below.

Software programs available on STRBase: http://www.cstl.nist.gov/biotech/strbase/software.htm

Probability of Identity [9]

- The probability of identity (P_I), also referred to as the matching probability, is **the chance that two unrelated people selected at random will have the same genotype** (first described by George Sensabaugh in 1982). The P_I value of a single locus is determined by summing the square of the observed genotype frequencies.

$$\sum_{i=1}^{n} x_i^2 \quad \textit{where } x_i \textit{ is the genotype frequency}$$

- **Lower P_I values indicate more variability** with the genetic marker in the measured population because there are more genotypes occurring at a lower frequency.
- P_I values from independently inherited loci can be multiplied together to produce an expected profile P_I

STR Loci Diversity

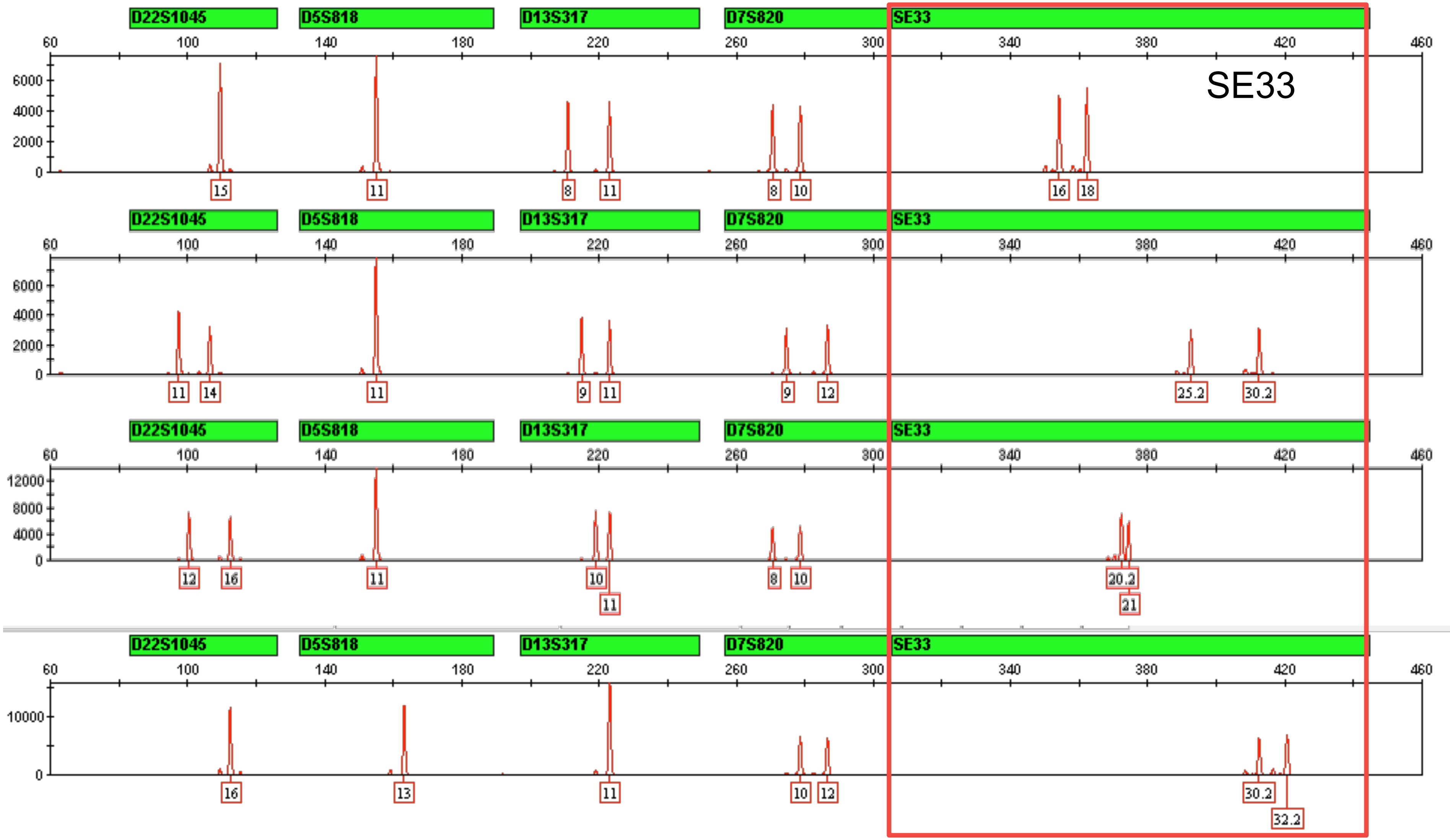
- SE33 is the most variable locus with the highest Het_{obs} (0.9353), lowest P_I value (0.0066), and most amount of alleles and genotypes observed by over double as compared to the next highest ranked locus Penta E.
- TPOX is the least variable locus with the lowest Het_{obs} (0.0.6902) and highest P_I value (0.1358),
- Two of the new CODIS required loci (D2S1338 and D1S1656) rank higher than the highest ranked CODIS 13 marker (D18S51)

Loci sorted on Probability of Identity (P_I) values

Locus	Alleles Observed	Genotypes Observed	Het (obs)	P_I Value n=1036
SE33	52	304	0.9353	0.0066
Penta E	23	138	0.8996	0.0147
D2S1338	13	68	0.8793	0.0220
D1S1656	15	93	0.8890	0.0224
D18S51	22	93	0.8687	0.0258
D12S391	24	113	0.8813	0.0271
FGA	27	96	0.8745	0.0308
D6S1043	27	109	0.8494	0.0321
Penta D	16	74	0.8552	0.0382
D21S11	27	86	0.8330	0.0403
D8S1179	11	46	0.7992	0.0558
D19S433	16	78	0.8118	0.0559
vWA	11	39	0.8060	0.0611
F13A01	16	56	0.7809	0.0678
D7S820	11	32	0.7944	0.0726
D16S539	9	28	0.7761	0.0749
D13S317	8	29	0.7674	0.0765
TH01	8	24	0.7471	0.0766
Penta C	12	49	0.7732	0.0769
D2S441	15	43	0.7828	0.0841
D10S1248	12	39	0.7819	0.0845
D3S1358	11	30	0.7519	0.0915
D22S1045	11	44	0.7606	0.0921
F13B	7	20	0.6911	0.0973
CSF1PO	9	31	0.7558	0.1054
D5S818	9	34	0.7297	0.1104
FESFPS	12	36	0.7230	0.1128
LPL	9	27	0.7027	0.1336
TPOX	9	28	0.6902	0.1358

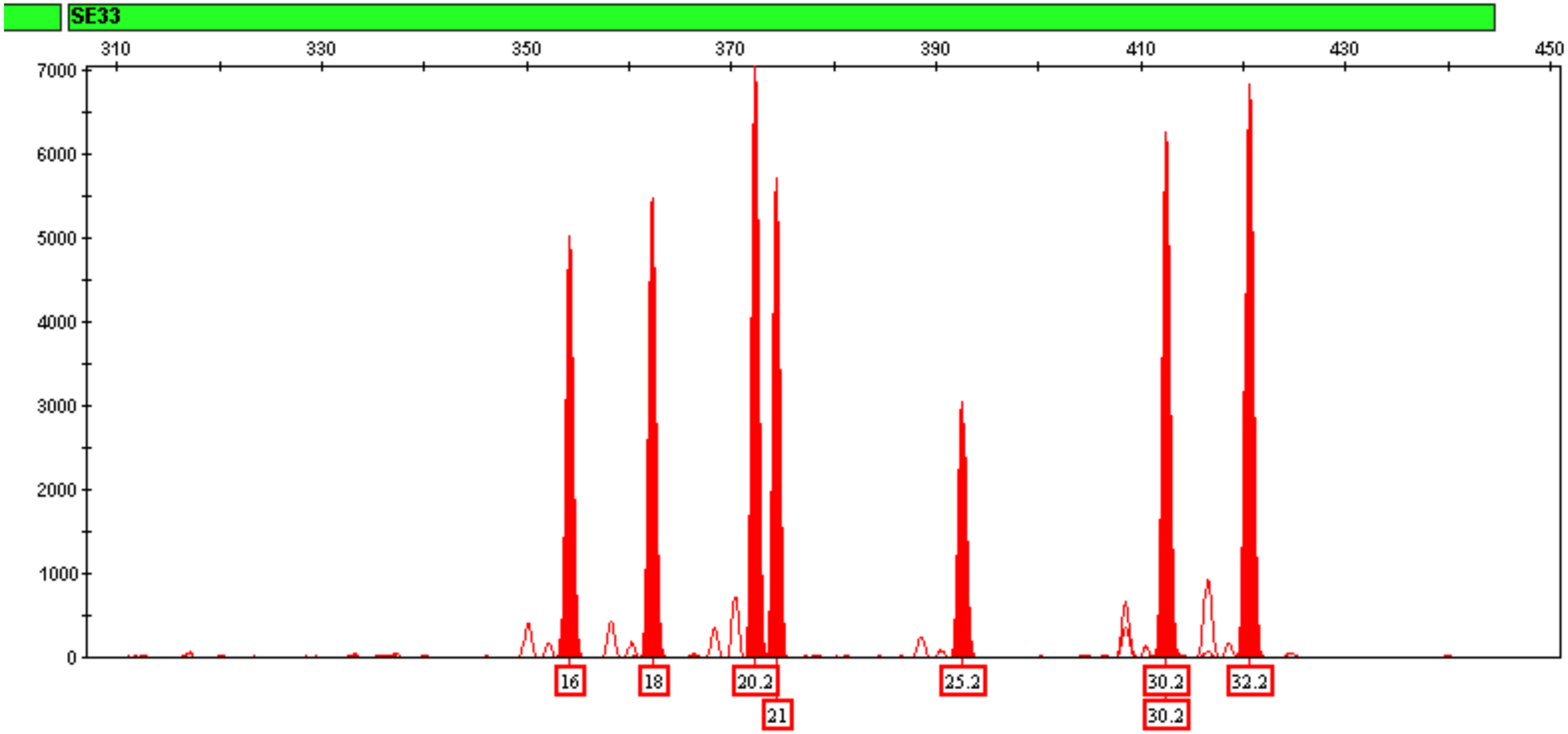
- Hill, B et al, "Population Statistics on the Proposed Expanded U.S. Core Loci", poster at the 23rd International Symposium on Human Identification (ISHI) meeting (Nashville, TN), October 16-17, 2012

SE33 Locus – Ideal for Mixtures



Four randomly selected single source samples

Overlay of SE33 Data from Four Individuals

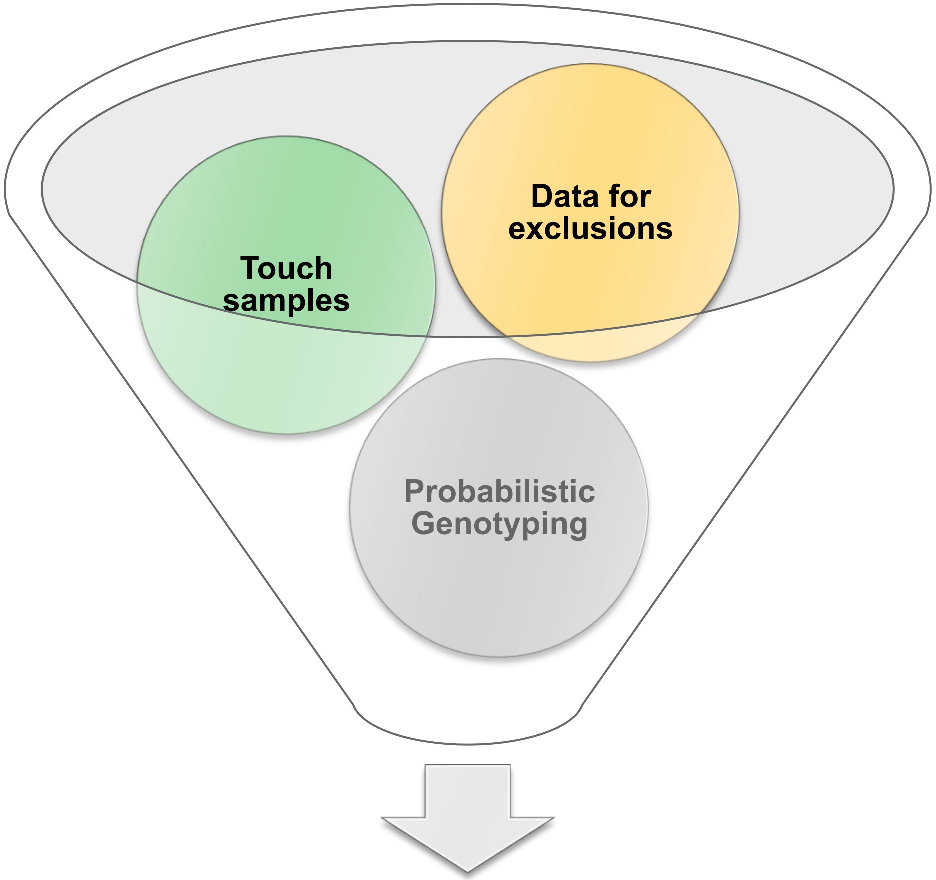


The previous four single-source samples were overlaid in GeneMapper™ *ID-X*

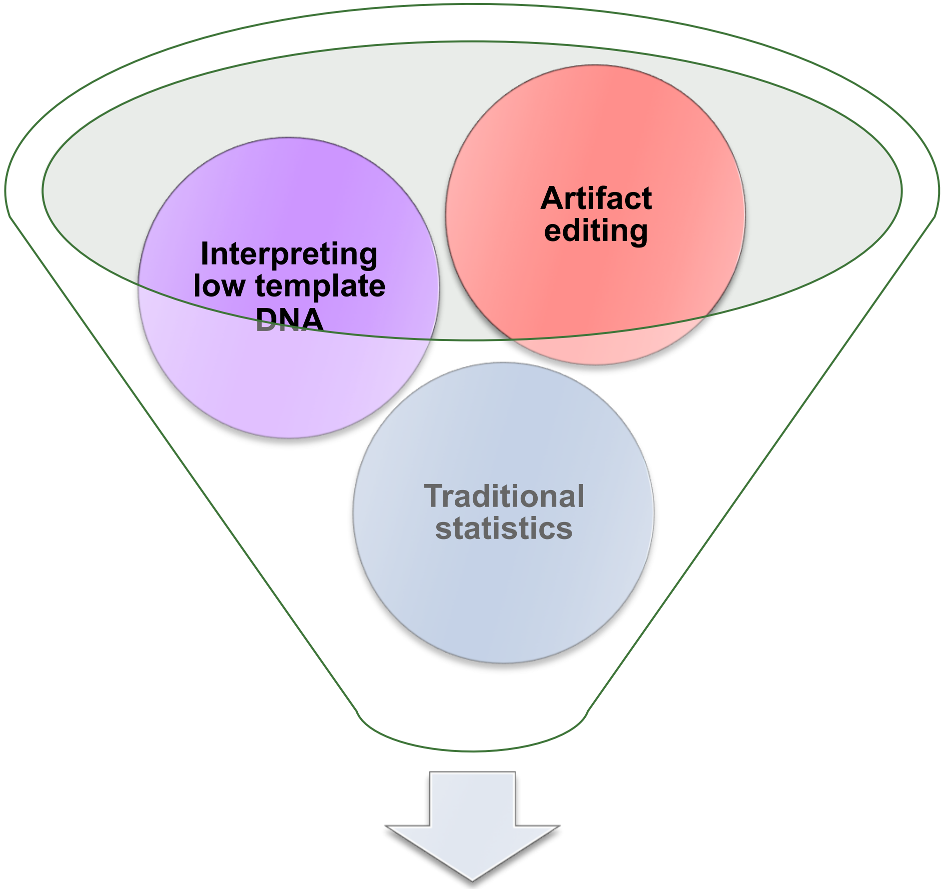
Seven total peaks generated from four donors

SE33 is extremely valuable for mixture interpretation

GlobalFiler™ Kit and 3500 Series Sensitivity



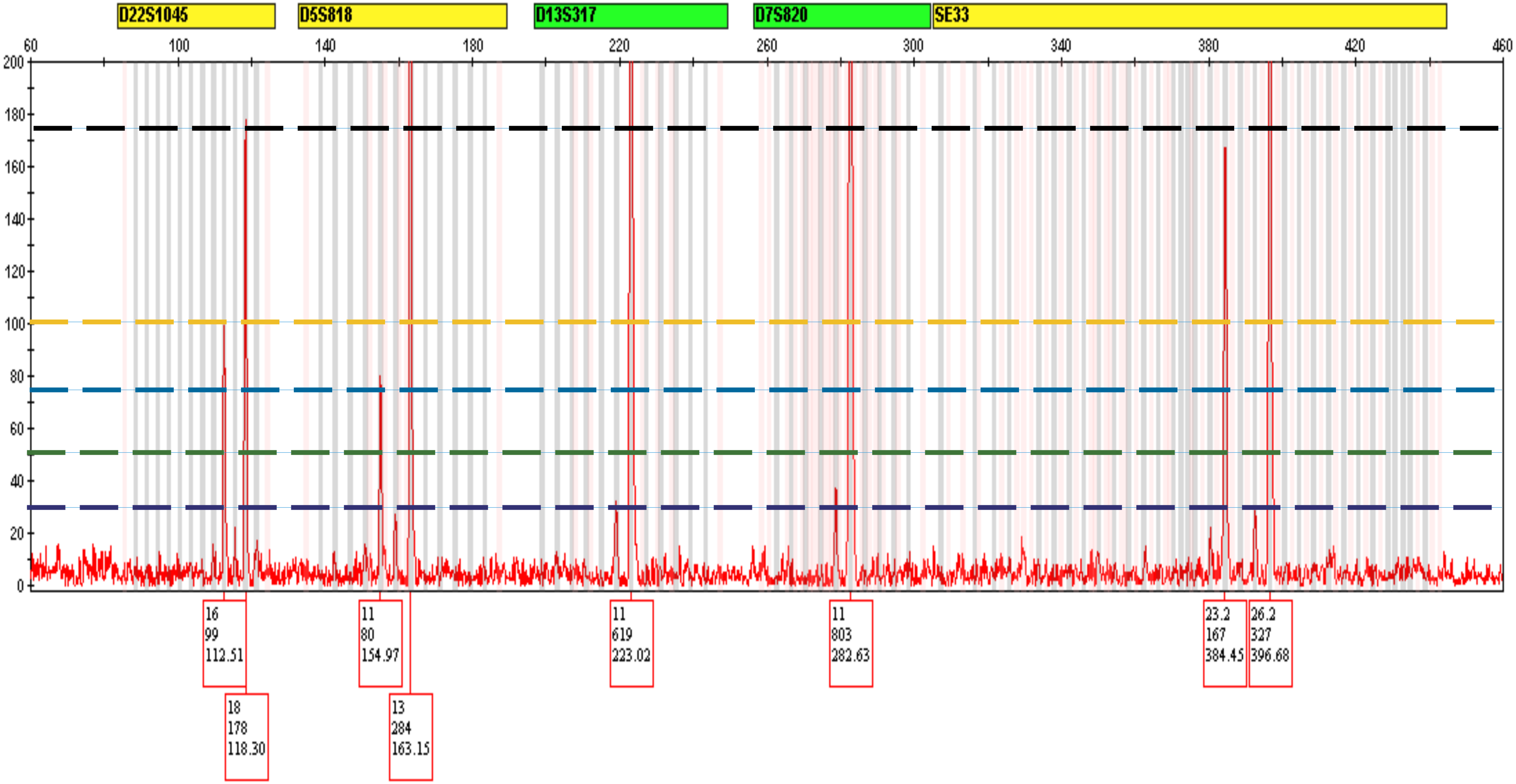
Sensitivity is GREAT!



Sensitivity is CHALLENGING

A look at different analytical thresholds

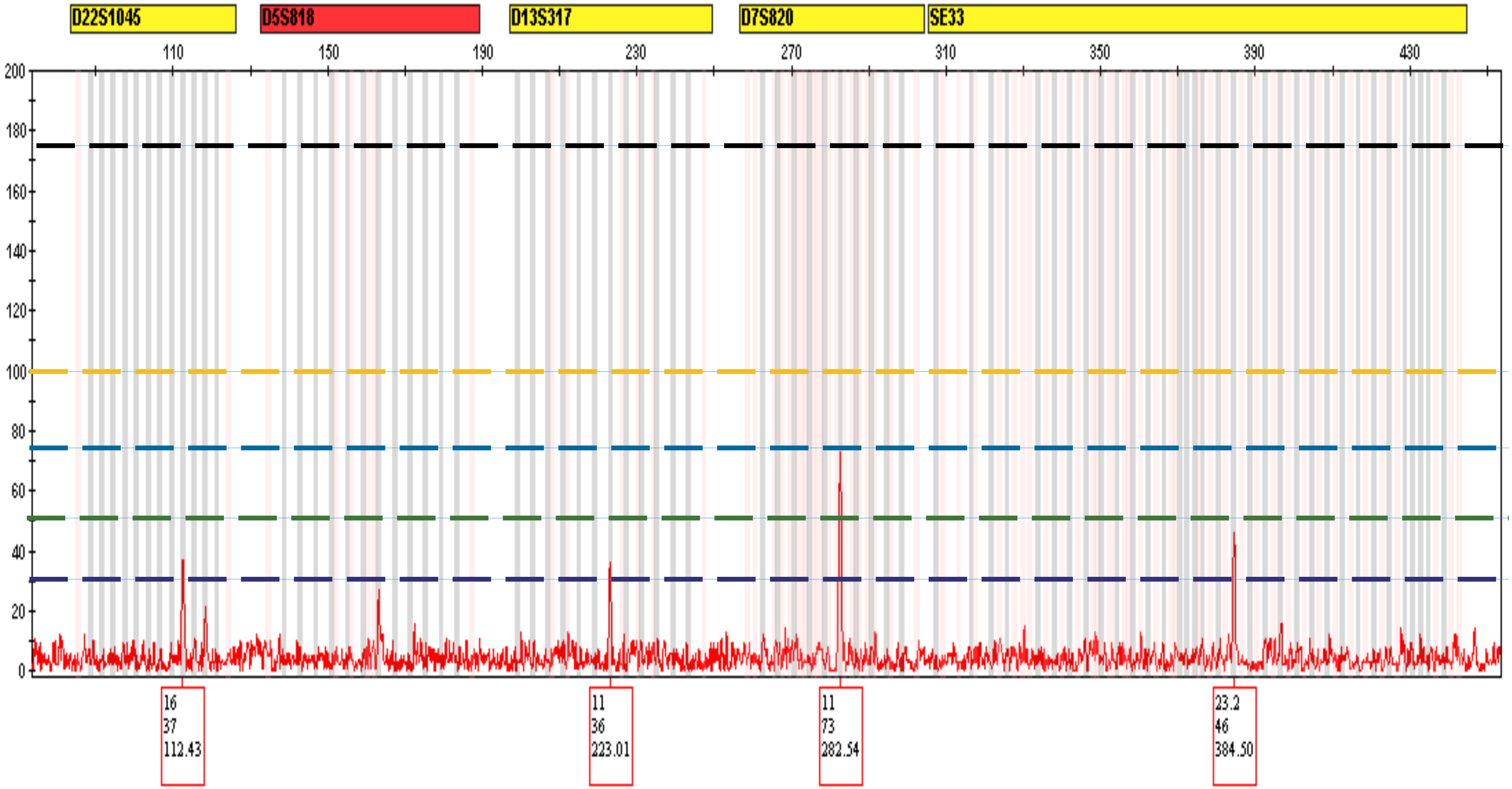
62 pg single source sample



May want to consider how much DNA you are comfortable with typing when assessing thresholds

A look at different analytical thresholds

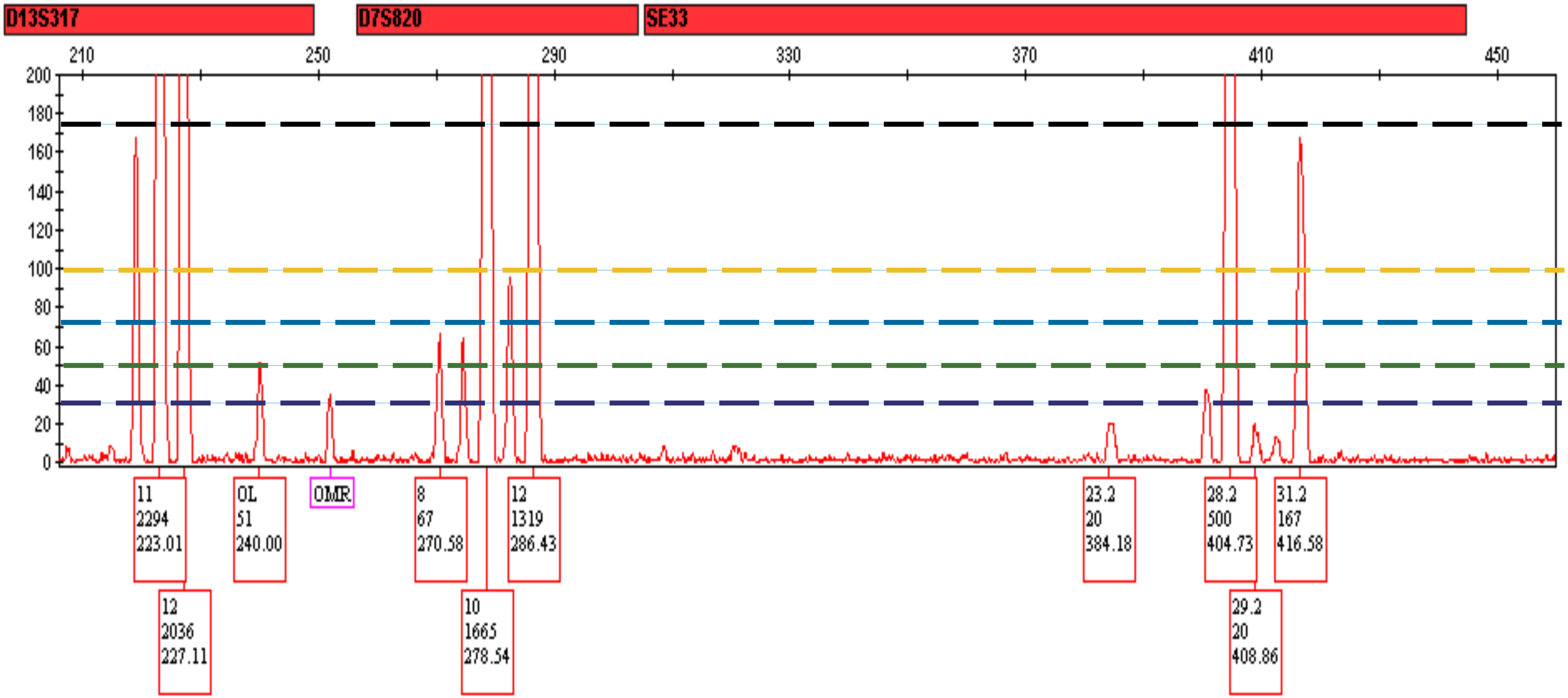
31 pg single source sample

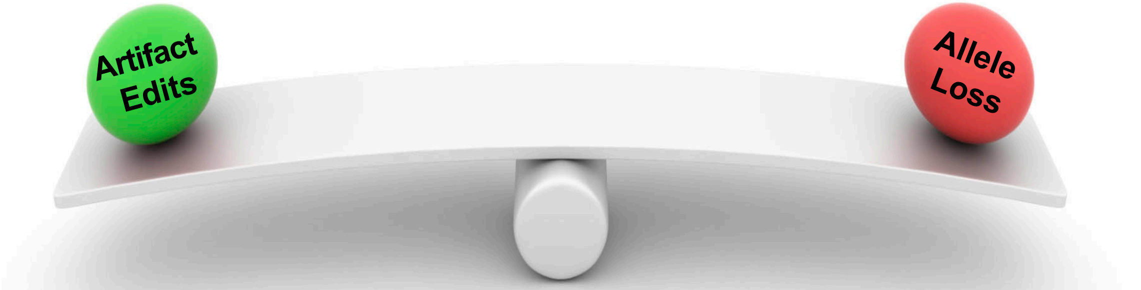


May want to consider how much DNA you are comfortable with typing when assessing thresholds

A look at different analytical thresholds

Tooth
Degradation Index = 5





Watch the magic!

- HPS uses a data macro to increase efficiency and minimize errors
  - Let me show you!
    - Source of DNA
      - NIGMS Human Genetic Cell Repository at the Coriell Institute for Medical Research
      - **NA07057 (7057)**
    - Serial dilution from 4 ng to 16 pg total DNA input run in triplicate
    - Analyzed at two thresholds
      - 35 RFU (minimum threshold)
      - 100 RFU

Watch the magic!

- Peak height ratio map at 35 RFU threshold

Input DNA	Rep	D3S1358	vWA	D16S539	CSF1PO	AMEL	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D2S1338
4	1	99%	87%	96%	95%	81%	99%	98%	95%	93%	94%	94%	92%	95%	89%	99%	81%	91%	98%	95%
	2	88%	98%	100%	81%	67%	85%	99%	94%	97%	98%	90%	92%	99%	94%	93%	88%	92%	93%	98%
	3	96%	99%	92%	88%	74%	97%	94%	97%	94%	89%	94%	96%	87%	99%	93%	96%	97%	93%	89%
2	1	98%	91%	88%	96%	87%	91%	96%	91%	88%	87%	96%	91%	91%	90%	77%	94%	95%	95%	96%
	2	89%	88%	95%	98%	61%	85%	78%	85%	98%	98%	81%	96%	89%	100%	85%	100%	92%	95%	92%
	3	95%	98%	98%	92%	87%	94%	96%	87%	98%	97%	92%	87%	90%	94%	91%	96%	96%	92%	92%
1	1	98%	99%	97%	90%	68%	99%	88%	99%	88%	89%	97%	81%	96%	89%	88%	91%	98%	91%	94%
	2	83%	90%	99%	90%	90%	96%	96%	96%	96%	86%	94%	87%	84%	74%	88%	84%	96%	88%	77%
	3	93%	73%	84%	94%	72%	93%	87%	100%	91%	94%	84%	95%	83%	91%	96%	80%	81%	83%	74%
0.5	1	88%	93%	88%	90%	73%	84%	64%	88%	98%	95%	99%	80%	81%	69%	100%	100%	82%	99%	90%
	2	78%	82%	88%	77%	78%	86%	66%	92%	91%	81%	73%	92%	90%	78%	83%	96%	94%	97%	79%
	3	92%	82%	88%	93%	68%	93%	82%	86%	80%	72%	76%	90%	67%	82%	95%	62%	90%	96%	99%
0.25	1	85%	90%	71%	95%	100%	88%	81%	87%	75%	52%	89%	92%	95%	97%	65%	94%	76%	70%	95%
	2	83%	64%	83%	84%	62%	70%	94%	96%	91%	89%	95%	77%	82%	82%	89%	93%	87%	94%	70%
	3	85%	90%	59%	84%	59%	65%	90%	76%	87%	74%	89%	80%	90%	71%	69%	75%	93%	90%	69%
0.125	1	72%	99%	86%	54%	82%	97%	66%	66%	100%	91%	53%	62%	87%	80%	68%	77%	90%	91%	76%
	2	75%	61%	65%	98%	50%	76%	88%	91%	97%	58%	46%	63%	68%	48%	89%	33%	72%	85%	75%
	3	63%	99%	53%	71%	38%	82%	59%	73%	68%	91%	81%	89%	68%	73%	61%	63%	98%	93%	96%
0.063	1	30%	54%	72%	84%	29%	55%	83%	69%	52%	74%	91%	73%	63%	67%	97%	96%	49%	56%	78%
	2	64%	61%	30%	34%	56%	87%	58%	40%	45%	36%	88%	42%	44%	72%	70%	13%	22%	85%	48%
	3	39%	78%	95%	88%	69%	28%	84%	37%	53%	91%	78%	93%	92%	55%	15%	70%	31%	86%	64%
0.031	1	74%	63%	18%	42%		53%	31%	58%		42%	84%		100%	50%	80%	91%	99%	63%	42%
	2	79%	55%	29%	44%	38%	35%	72%	45%	92%	94%		81%	58%	57%		99%	56%	56%	60%
	3	50%	73%		39%	86%	92%	41%	46%	70%	34%		71%		57%	72%	70%	83%	98%	31%
0.016	1	71%	24%	41%		38%	60%	81%		69%		34%	43%	59%	40%	93%	33%	68%	92%	89%
	2	88%	66%	80%	37%	26%	35%		54%	34%	89%	45%		78%		75%		60%	99%	49%
	3		46%	27%	76%		90%		29%	20%		32%		47%	51%	24%		96%	27%	41%

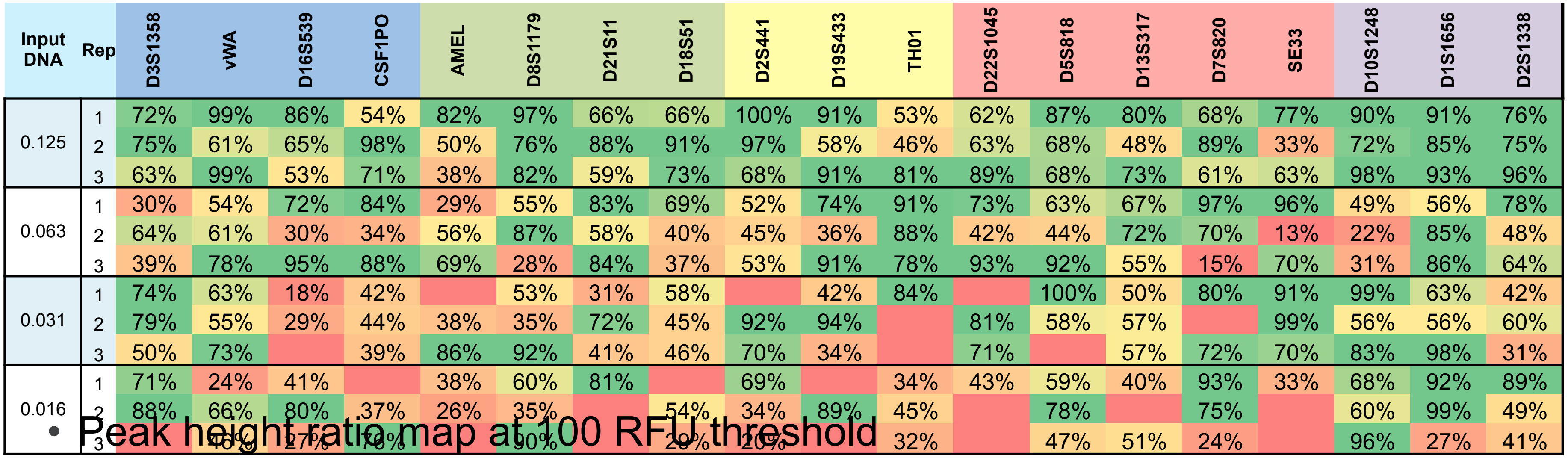
Watch the magic!

- Peak height ratio map at 100 RFU threshold

Input DNA	Rep	D3S1358	vWA	D16S539	CSF1PO	AMEL	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D2S1338
4	1	99%	87%	96%	95%	81%	99%	98%	95%	93%	94%	94%	92%	95%	89%	99%	81%	91%	98%	95%
	2	88%	98%	100%	81%	67%	85%	99%	94%	97%	98%	90%	92%	99%	94%	93%	88%	92%	93%	98%
	3	96%	99%	92%	88%	74%	97%	94%	97%	94%	89%	94%	96%	87%	99%	93%	96%	97%	93%	89%
2	1	98%	91%	88%	96%	87%	91%	96%	91%	88%	87%	96%	91%	91%	90%	77%	94%	95%	95%	96%
	2	89%	88%	95%	98%	61%	85%	78%	85%	98%	98%	81%	96%	89%	100%	85%	100%	92%	95%	92%
	3	95%	98%	98%	92%	87%	94%	96%	87%	98%	97%	92%	87%	90%	94%	91%	96%	96%	92%	92%
1	1	98%	99%	97%	90%	68%	99%	88%	99%	88%	89%	97%	81%	96%	89%	88%	91%	98%	91%	94%
	2	83%	90%	99%	90%	90%	96%	96%	96%	96%	86%	94%	87%	84%	74%	88%	84%	96%	88%	77%
	3	93%	73%	84%	94%	72%	93%	87%	100%	91%	94%	84%	95%	83%	91%	96%	80%	81%	83%	74%
0.5	1	88%	93%	88%	90%	73%	84%	64%	88%	98%	95%	99%	80%	81%	69%	100%	100%	82%	99%	90%
	2	78%	82%	88%	77%	78%	86%	66%	92%	91%	81%	73%	92%	90%	78%	83%	96%	94%	97%	79%
	3	92%	82%	88%	93%	68%	93%	82%	86%	80%	72%	76%	90%	67%	82%	95%	62%	90%	96%	99%
0.25	1	85%	90%	71%	95%	100%	88%	81%	87%	75%	52%	89%	92%	95%	97%	65%	94%	76%	70%	95%
	2	83%	64%	83%	84%	62%	70%	94%	96%	91%	89%	95%	77%	82%	82%	89%	93%	87%	94%	70%
	3	85%	90%	59%	84%	59%	65%	90%	76%	87%	74%	89%	80%	90%	71%	69%	75%	93%	90%	69%
0.125	1	72%	99%	86%	54%	82%	97%	66%	66%	100%	91%	53%	62%	87%	80%	68%	77%	90%	91%	76%
	2	75%	61%	65%	98%	50%	76%	88%	91%	97%	58%	46%	63%	68%	48%	89%	33%	72%	85%	75%
	3	63%	99%	53%	71%	38%	82%	59%	73%	68%	91%	81%	89%	68%	73%	61%	63%	98%	93%	96%
0.063	1	30%	54%	72%	84%	29%	55%	83%	69%	52%	74%	91%	73%	63%	67%	97%	96%	49%	56%	78%
	2	64%	61%	30%	34%	56%	87%	58%	40%	45%	36%	88%	42%	44%	72%	70%			85%	48%
	3	39%	78%	95%	88%	69%	28%	84%	37%	53%	91%	78%	93%	92%	55%	15%	70%	31%	86%	64%
0.031	1	74%	63%		42%		53%	31%	58%		42%	84%		100%	50%	80%	91%	99%	63%	42%
	2	79%	55%		44%	38%	35%	72%	45%	92%	94%		81%	58%	57%		99%		56%	60%
	3		73%			86%	92%	41%	46%	70%	34%		71%		57%	72%	70%	83%	98%	
0.016	1	71%					60%	81%		69%						93%			92%	89%
	2		66%								89%			78%		75%			99%	49%
	3		46%				90%							47%	51%			96%		41%

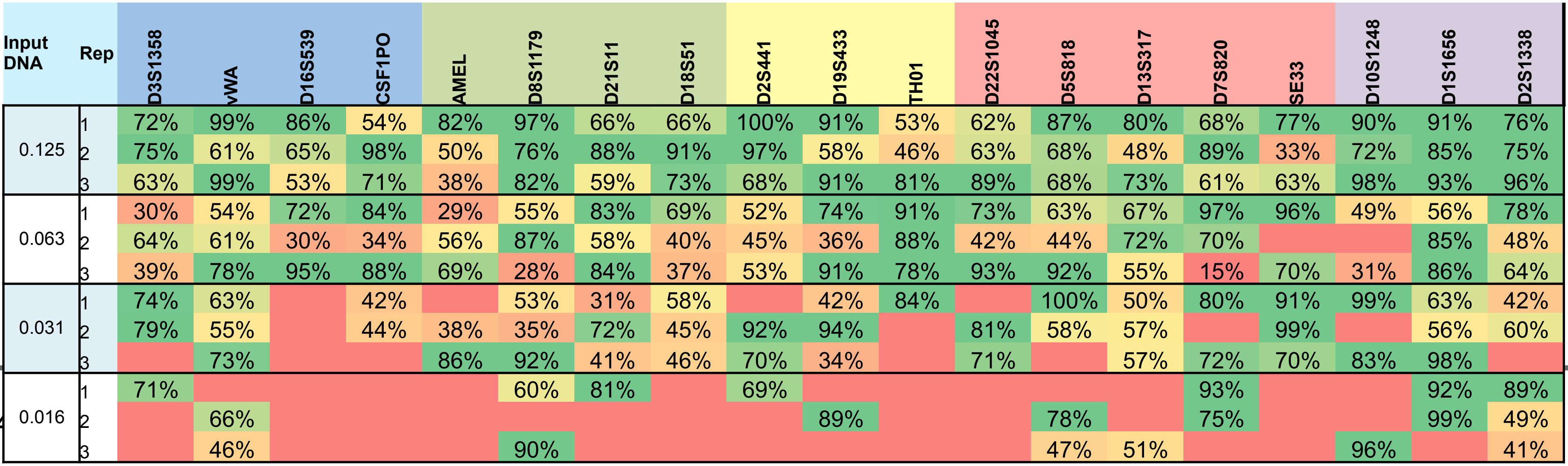
Peak height ratio heat map at with two thresholds

- Peak height ratio map at 35 RFU threshold



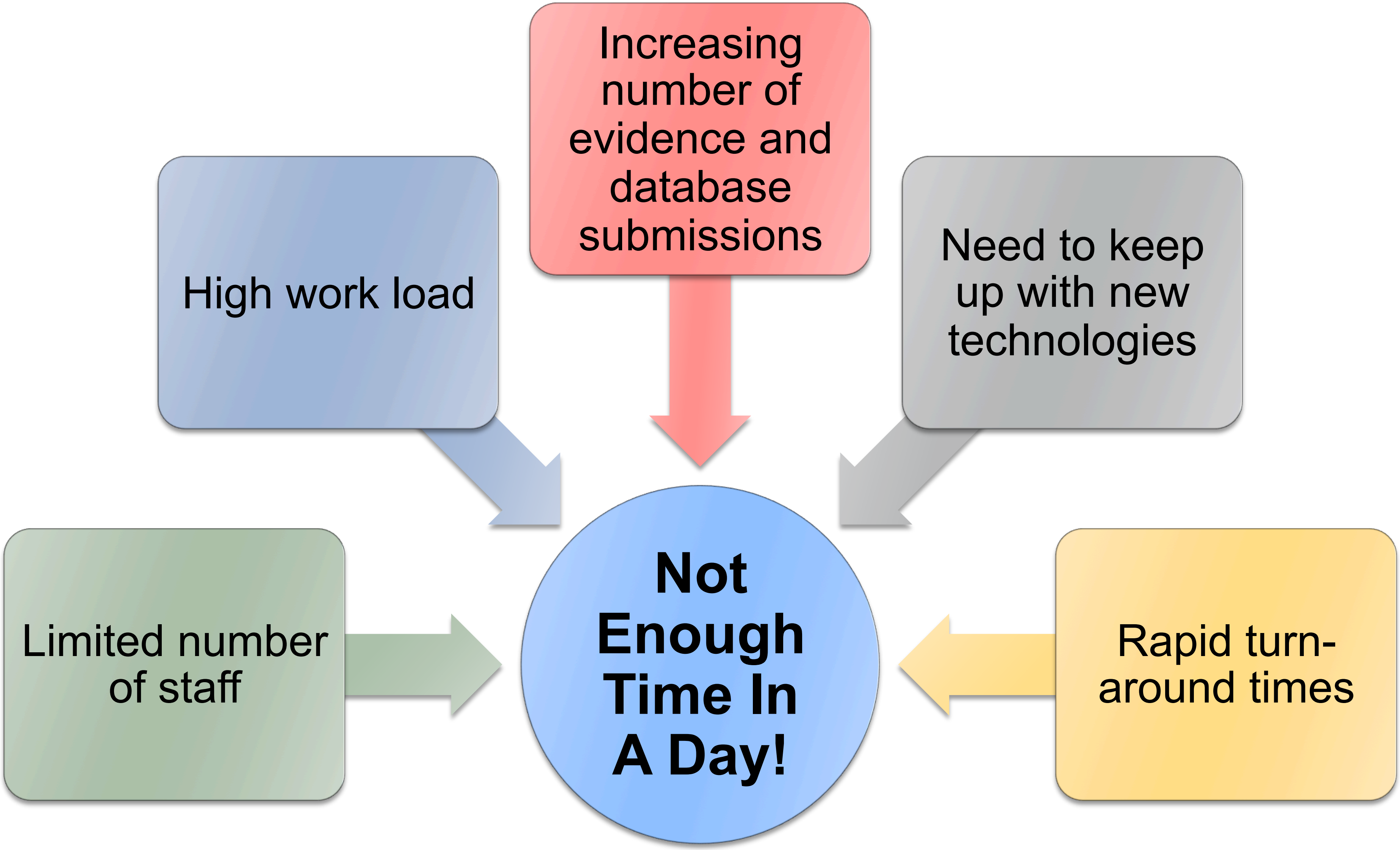
Input DNA	Rep	D3S1358	vWA	D16S539	CSF1PO	AMEL	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D2S1338
0.125	1	72%	99%	86%	54%	82%	97%	66%	66%	100%	91%	53%	62%	87%	80%	68%	77%	90%	91%	76%
	2	75%	61%	65%	98%	50%	76%	88%	91%	97%	58%	46%	63%	68%	48%	89%	33%	72%	85%	75%
	3	63%	99%	53%	71%	38%	82%	59%	73%	68%	91%	81%	89%	68%	73%	61%	63%	98%	93%	96%
0.063	1	30%	54%	72%	84%	29%	55%	83%	69%	52%	74%	91%	73%	63%	67%	97%	96%	49%	56%	78%
	2	64%	61%	30%	34%	56%	87%	58%	40%	45%	36%	88%	42%	44%	72%	70%	13%	22%	85%	48%
	3	39%	78%	95%	88%	69%	28%	84%	37%	53%	91%	78%	93%	92%	55%	15%	70%	31%	86%	64%
0.031	1	74%	63%	18%	42%		53%	31%	58%		42%	84%		100%	50%	80%	91%	99%	63%	42%
	2	79%	55%	29%	44%	38%	35%	72%	45%	92%	94%		81%	58%	57%		99%	56%	56%	60%
	3	50%	73%		39%	86%	92%	41%	46%	70%	34%		71%		57%	72%	70%	83%	98%	31%
0.016	1	71%	24%	41%		38%	60%	81%		69%		34%	43%	59%	40%	93%	33%	68%	92%	89%
	2	88%	66%	80%	37%	26%	35%		54%	34%	89%	45%		78%		75%		60%	99%	49%
	3		46%	27%	76%		90%		29%	20%		32%		47%	51%	24%		96%	27%	41%

- Peak height ratio map at 100 RFU threshold



Input DNA	Rep	D3S1358	vWA	D16S539	CSF1PO	AMEL	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D2S1338
0.125	1	72%	99%	86%	54%	82%	97%	66%	66%	100%	91%	53%	62%	87%	80%	68%	77%	90%	91%	76%
	2	75%	61%	65%	98%	50%	76%	88%	91%	97%	58%	46%	63%	68%	48%	89%	33%	72%	85%	75%
	3	63%	99%	53%	71%	38%	82%	59%	73%	68%	91%	81%	89%	68%	73%	61%	63%	98%	93%	96%
0.063	1	30%	54%	72%	84%	29%	55%	83%	69%	52%	74%	91%	73%	63%	67%	97%	96%	49%	56%	78%
	2	64%	61%	30%	34%	56%	87%	58%	40%	45%	36%	88%	42%	44%	72%	70%			85%	48%
	3	39%	78%	95%	88%	69%	28%	84%	37%	53%	91%	78%	93%	92%	55%	15%	70%	31%	86%	64%
0.031	1	74%	63%		42%		53%	31%	58%		42%	84%		100%	50%	80%	91%	99%	63%	42%
	2	79%	55%		44%	38%	35%	72%	45%	92%	94%		81%	58%	57%		99%		56%	60%
	3		73%			86%	92%	41%	46%	70%	34%		71%		57%	72%	70%	83%	98%	
0.016	1	71%					60%	81%		69%						93%			92%	89%
	2		66%								89%			78%		75%			99%	49%
	3		46%				90%							47%	51%			96%		41%

Feeling Overwhelmed?



Increasing number of evidence and database submissions

High work load

Need to keep up with new technologies

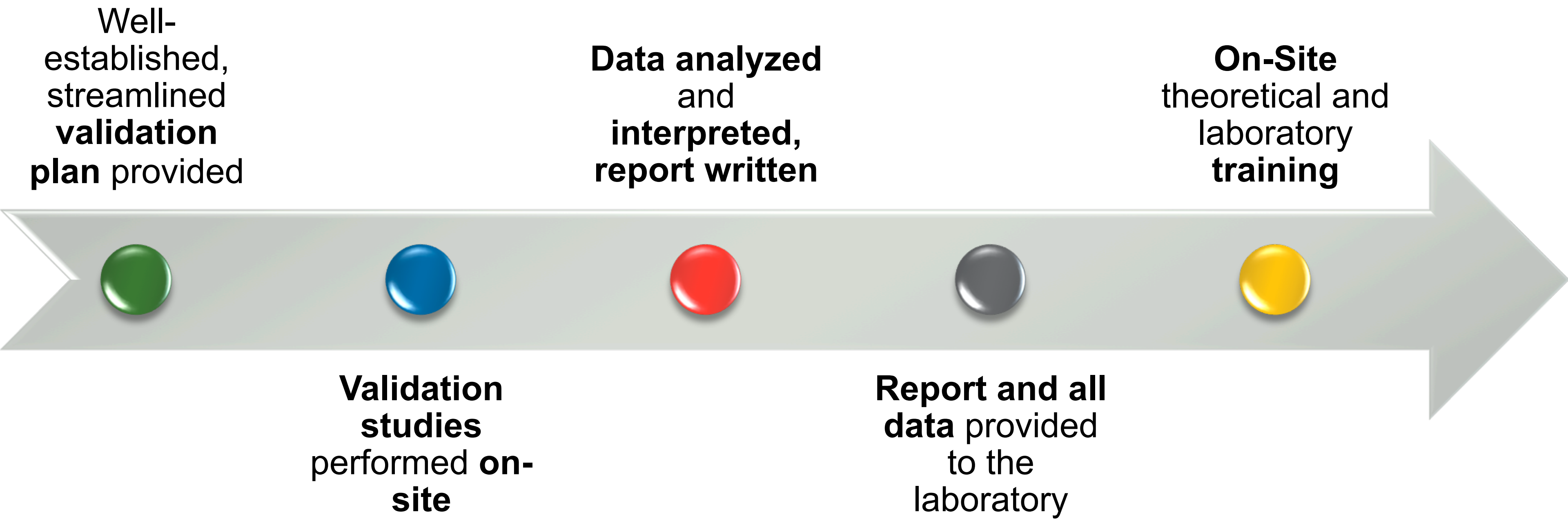
Limited number of staff

Not Enough Time In A Day!

Rapid turn-around times

We Can Help!

- HID Professional Services (HPS)
  - Expeditious and thorough validation solutions
  - Decades of experience in the forensic community
  - Continued assistance after completion of validation



Well-established, streamlined **validation plan** provided

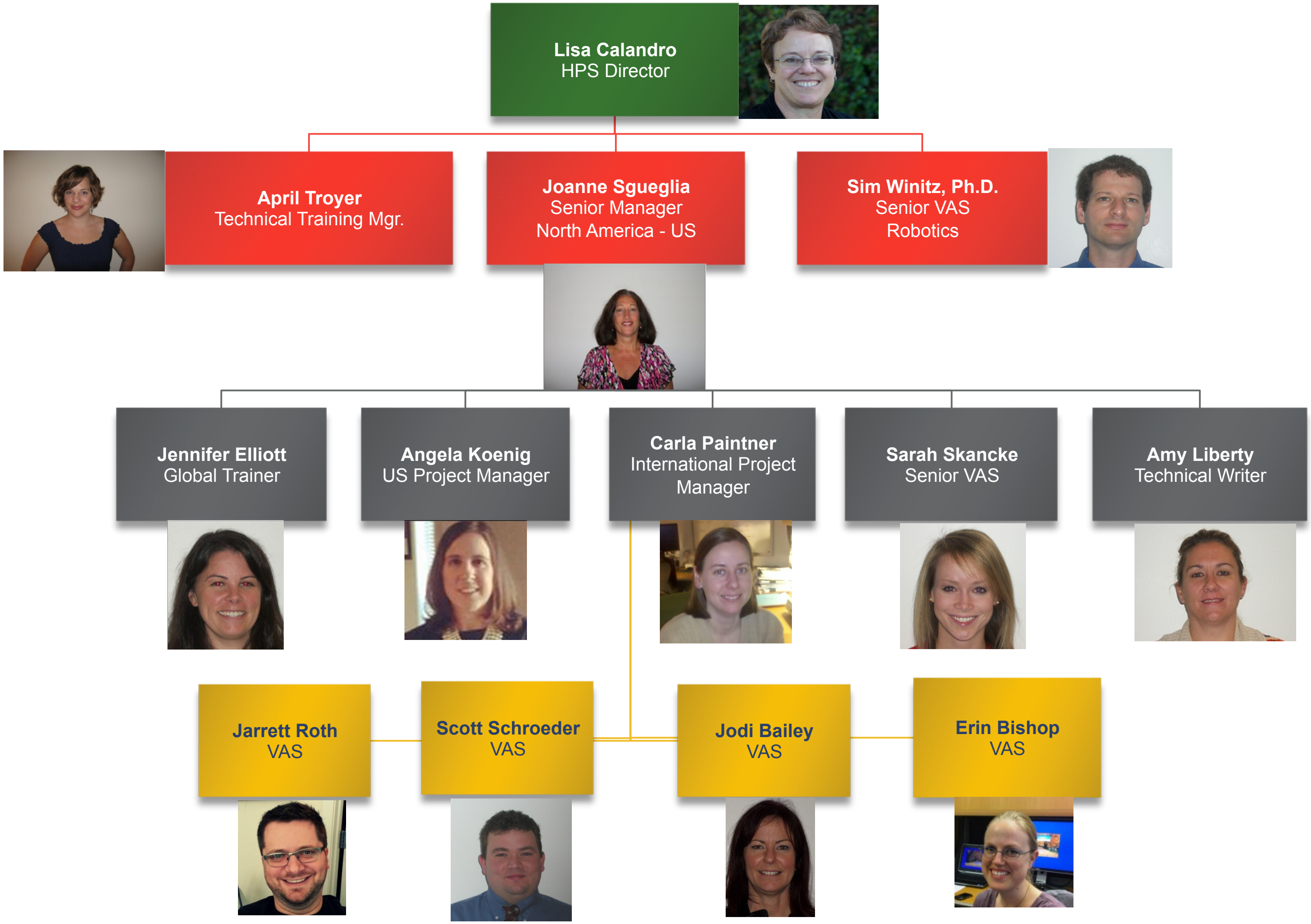
Validation studies performed **on-site**

Data analyzed and **interpreted, report written**

Report and all data provided to the laboratory

On-Site theoretical and laboratory **training**

North America HID Professional Services Team



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Technical Training Mgr.

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Senior VAS
Robotics

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International Project Manager

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Senior VAS

Amy Liberty
Technical Writer

Jarrett Roth
VAS

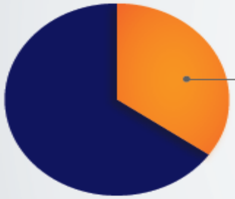
Scott Schroeder
VAS

Jodi Bailey
VAS

Erin Bishop
VAS

What Our Customers Are Saying

98% More than 98% of surveyed customers said they would recommend the HPS team to a colleague.



Over 35% of customers have used the services of the HPS team more than once.

"The validation was well worth the cost. I would have it no other way. The presentation you receive after your validation is unbelievable. Great! It's already in the format for auditing."

—Technical leader, state crime lab, US

"I was extremely pleased with how the validation, training, and teachback were conducted. The process was well organized and pertinent to our needs. This validation has saved us considerable analysis time, yet we still have as much understanding of the data as if we had done the work ourselves."

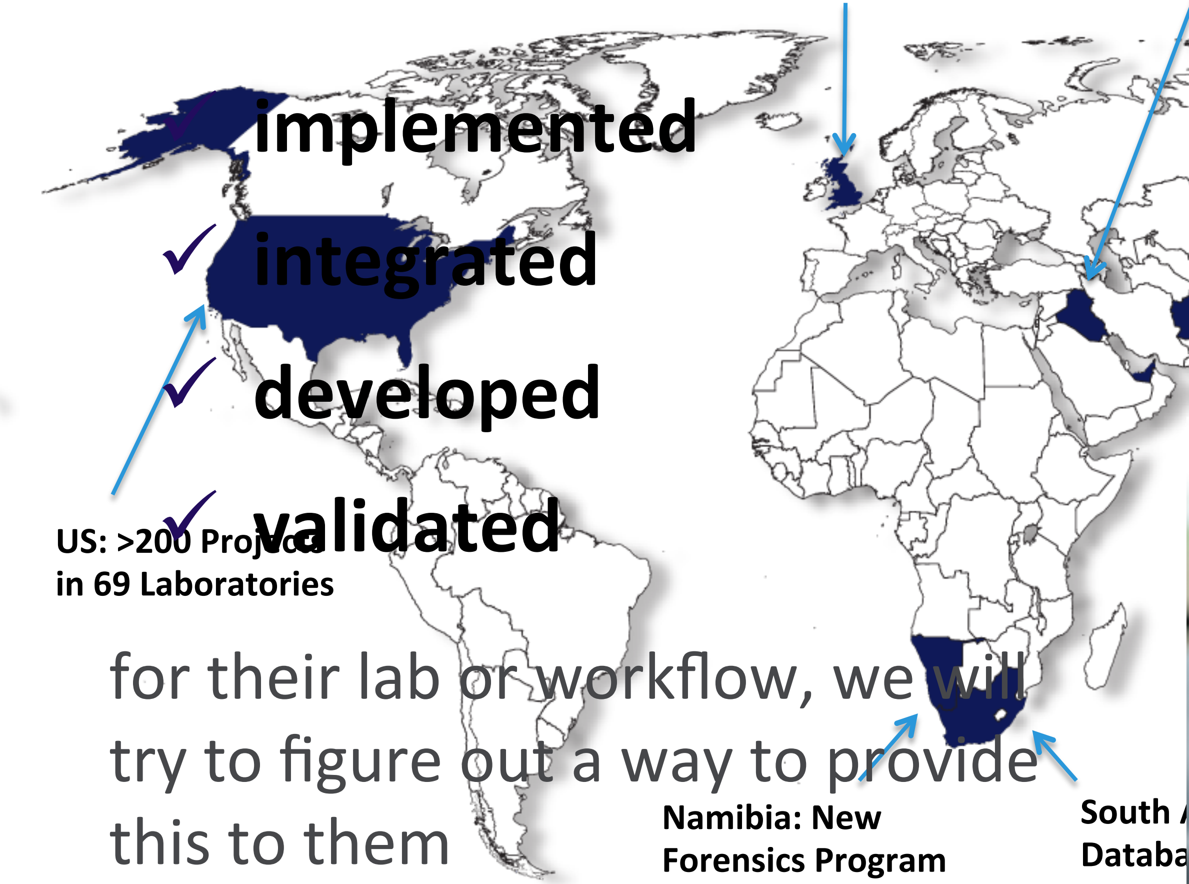
—Technical leader, county crime lab, US

HID Professional Services Guiding Principle

If an HID customer needs something

- ✓ **implemented**
- ✓ **integrated**
- ✓ **developed**
- ✓ **validated**

for their lab or workflow, we will try to figure out a way to provide this to them



THANK YOU!!

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