

# 2014 Rapid DNA Maturity Assessment Results

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CODIS State Administrator Meeting

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Norman, OK

# NIST

**National Institute of  
Standards and Technology**

U.S. Department of Commerce



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- **In no case does such identification imply a recommendation or endorsement by NIST**, nor does it imply that any of the materials, instruments, or equipment identified are necessarily the best available for the purpose.

# Purpose of Maturity Assessment

- To assess the current status of rapid DNA typing technology for the CODIS core loci
  - In support of lab and future external (non-lab-based) Rapid DNA implementation
- Integrated (swab in – allele detection) instruments capable of genotyping the core CODIS 13 STR markers were eligible for the study

# Rapid DNA Instruments

## ANDE (NetBio)



- One biochipset
  - Stored at RT
  - Shelf life  $\approx$  6 months

PowerPlex 16 loci  
 $\approx$ 86 min runtime  
(5 samples)

**ANDE PP16**

## RapidHIT 200 (IntegenX)



- Kit = 4 components
  - Stored between RT-4°C
  - Shelf life  $\approx$  5 months @ 4°C

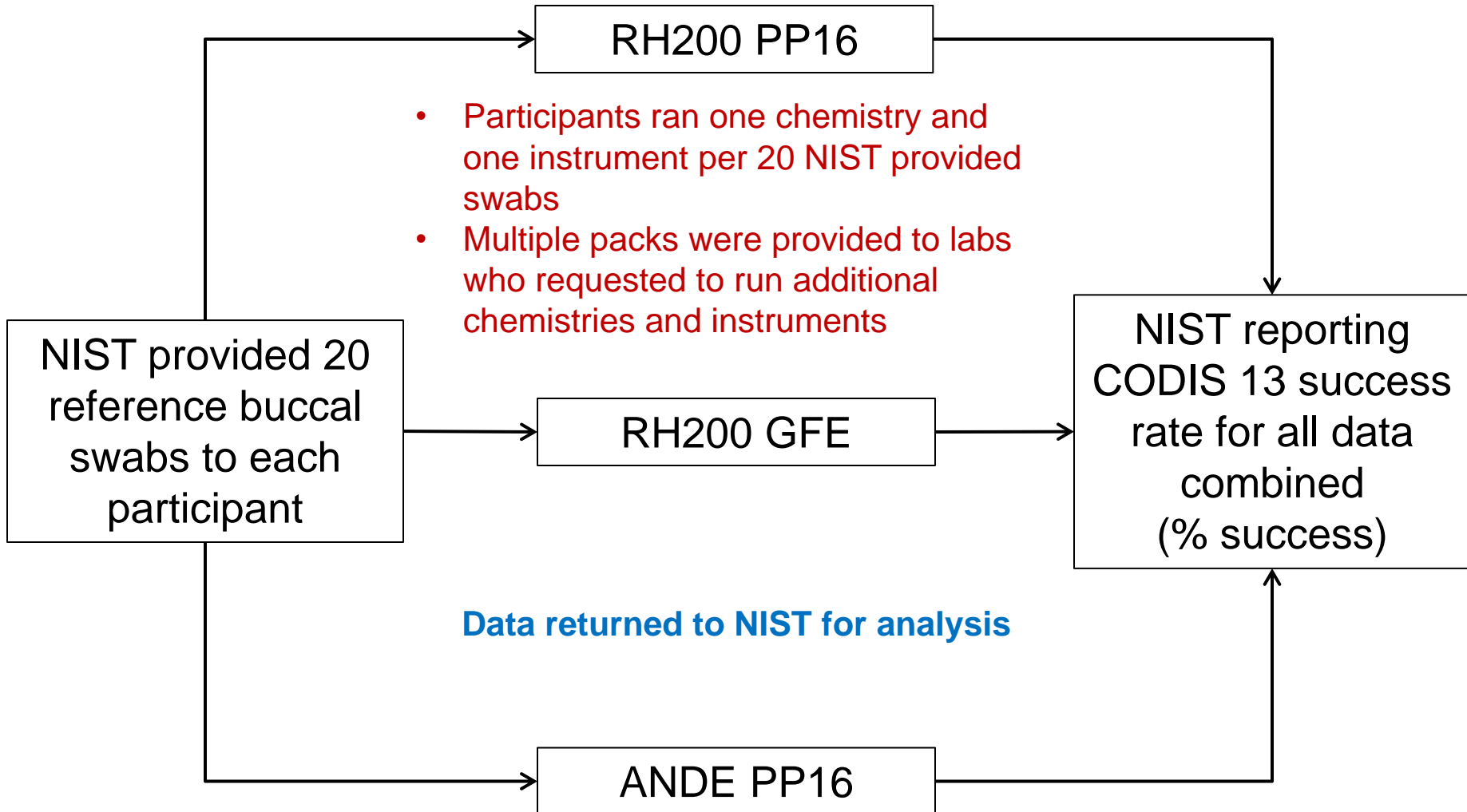
PowerPlex 16 loci  
 $\approx$ 90 min runtime  
(5 samples)

**RH200 PP16**

GlobalFiler Express loci  
 $\approx$ 120 min runtime  
(1-7 samples)

**RH200 GFE**

# R-DNA Maturity Assessment



# Timeline of Maturity Assessment

**January 2014:** Buccal samples collected at NIST and stored at RT



**October 2014:** Samples shipped to participating laboratories



**October-December 2014:** Data electronically returned to NIST



**November 2014 – May 2015:** Data analyzed at NIST

# Maturity Assessment

Participating Laboratories (7)    Instrument Platforms (2)    Independent Instruments (11)    Chemistry    Total Samples Tested (280)

Federal

NetBio ANDE



5

PowerPlex 16

100

State

IntegenX RapidHIT 200



6

PowerPlex 16

60

Private

GlobalFiler Express

120

# NIST Analysis Parameters

- **Rapid DNA Analysis:** Without human intervention
- **Modified Rapid DNA Analysis:** Expert interpretation and analysis of electropherogram  
<http://swgdam.org/docs.html>
- Additional analysis (PHR, Stutter, etc.) of the data performed with GeneMapper IDX v 1.3

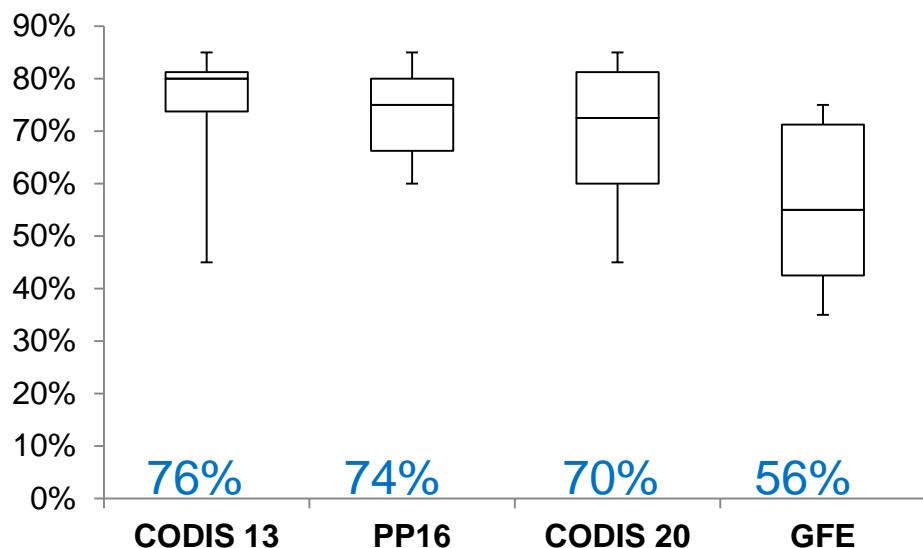




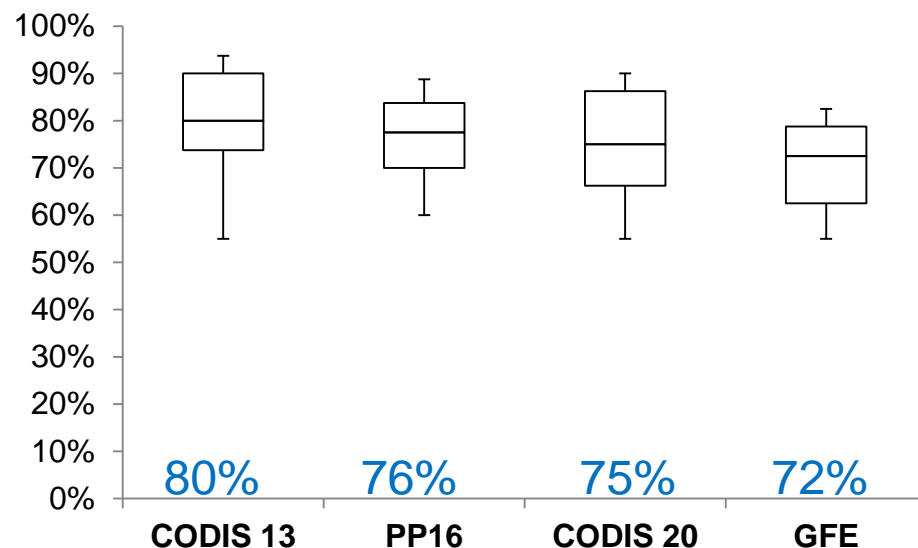


# Overall Success

## Rapid DNA Analysis



## Modified Rapid DNA Analysis



8 samples were passed (for CODIS 13) by performing modified rapid DNA analysis across all platforms (76 → 80%)

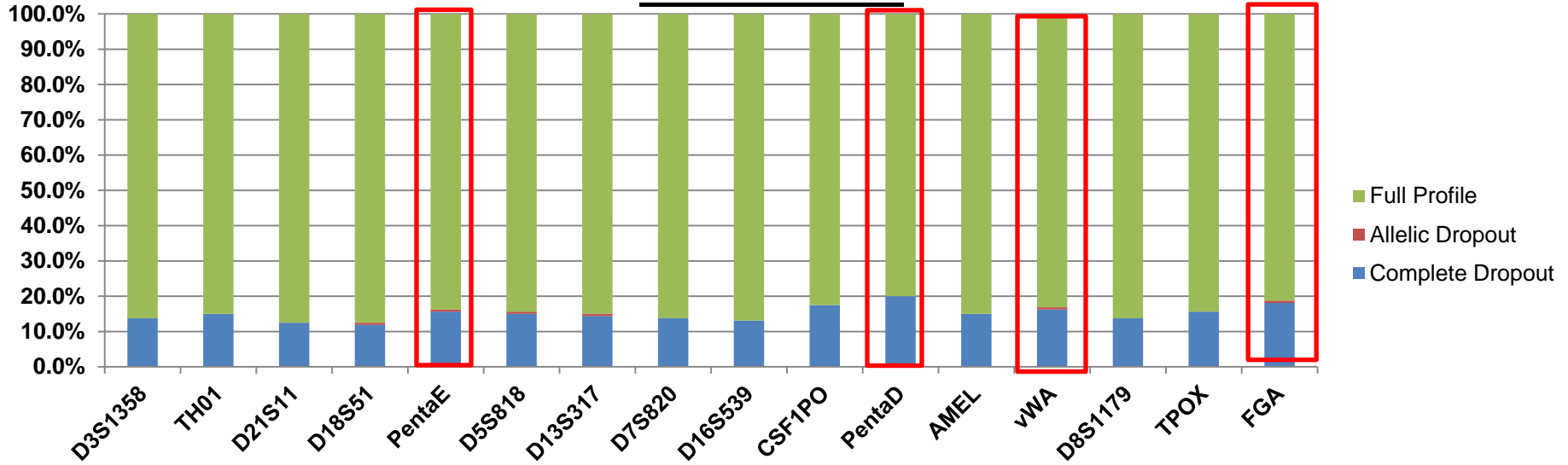
- 2 Samples within the RH200 PP16
- 3 Samples within the RH200 GFE
- 3 Samples within the ANDE PP16

# Higher success with manual review of GFE

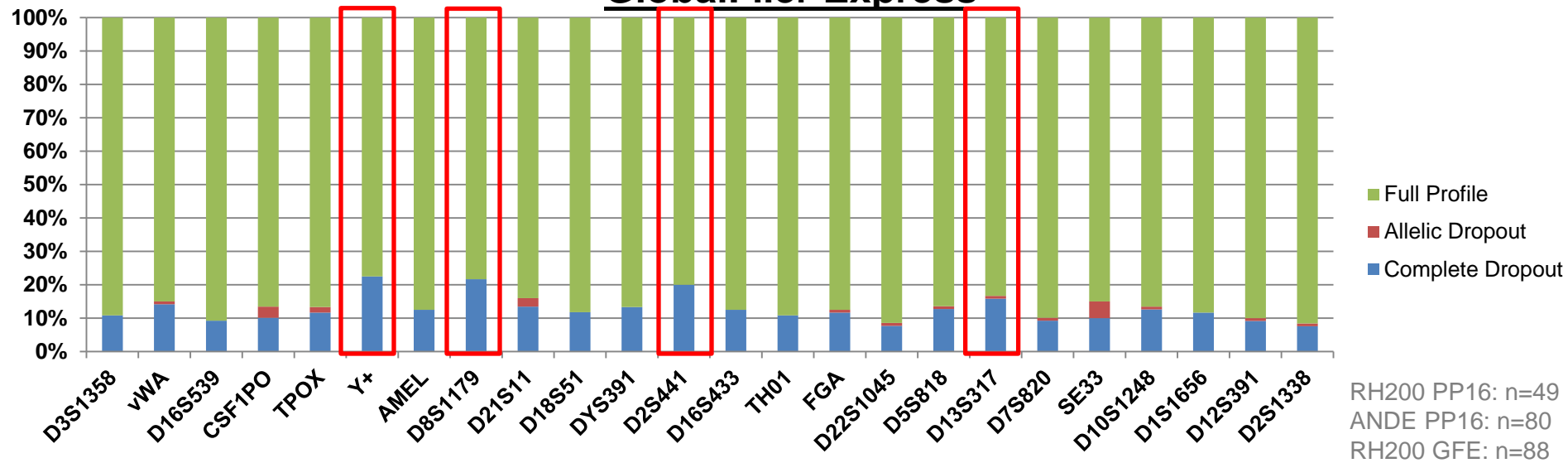


# Locus Success (Rapid Analysis)

## PowerPlex 16

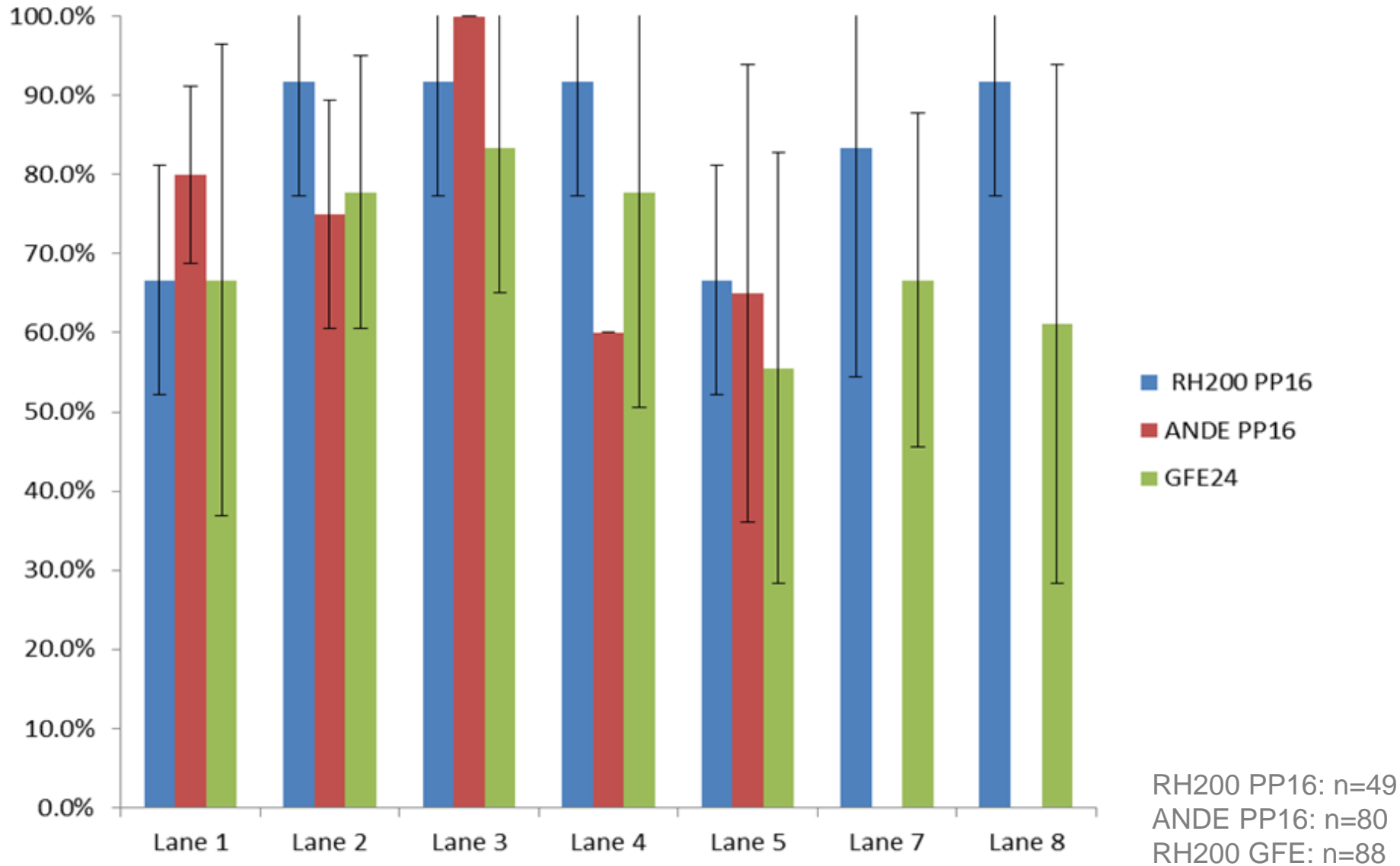


## GlobalFiler Express



RH200 PP16: n=49  
 ANDE PP16: n=80  
 RH200 GFE: n=88

# Lane Success (CODIS 13)

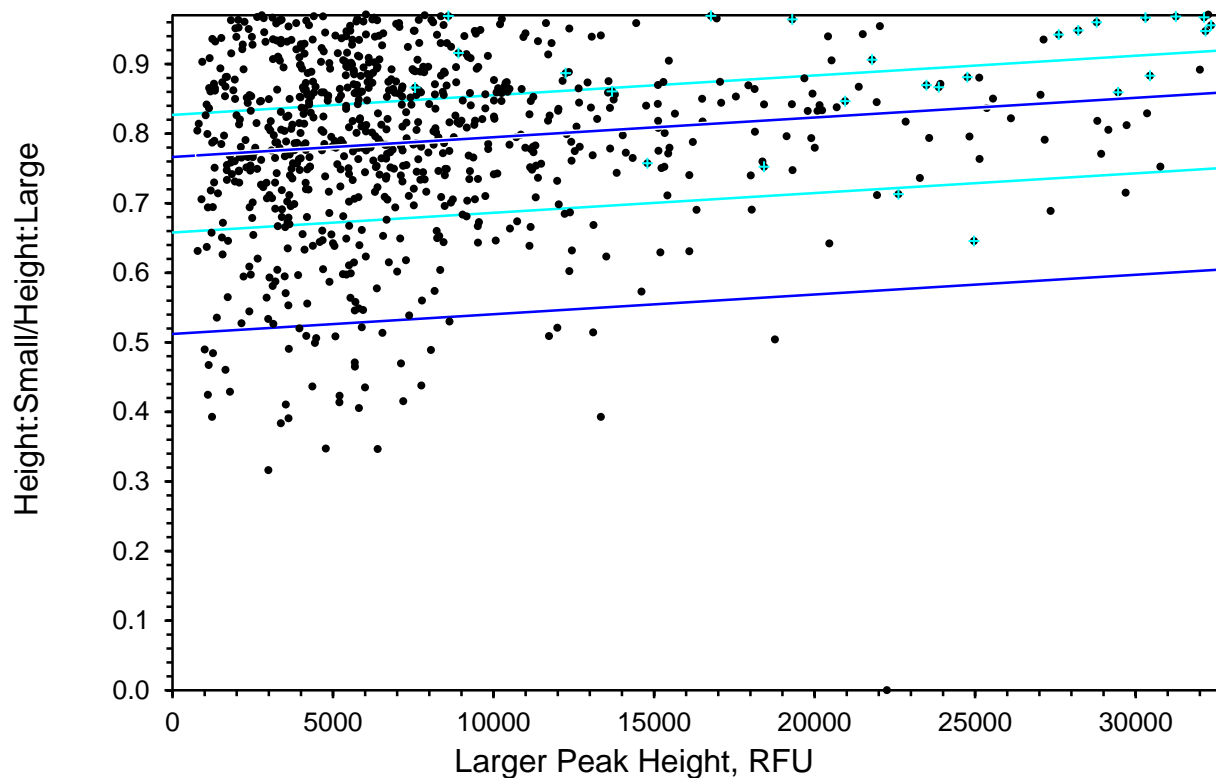


# Peak Height Ratios

## Median PHR for CODIS 13 loci

Locus	#Ratio	Median
D8S1179	55	0.813
D21S11	43	0.825
D18S51	62	0.827
FGA	67	0.829
TPOX	44	0.832
D16S539	52	0.835
vWA	65	0.844
D7S820	47	0.850
D3S1358	61	0.855
D5S818	36	0.863
CSF1PO	61	0.870
D13S317	44	0.871
TH01	28	0.939

Median peak height  
ratio greater than 75%  
for all loci

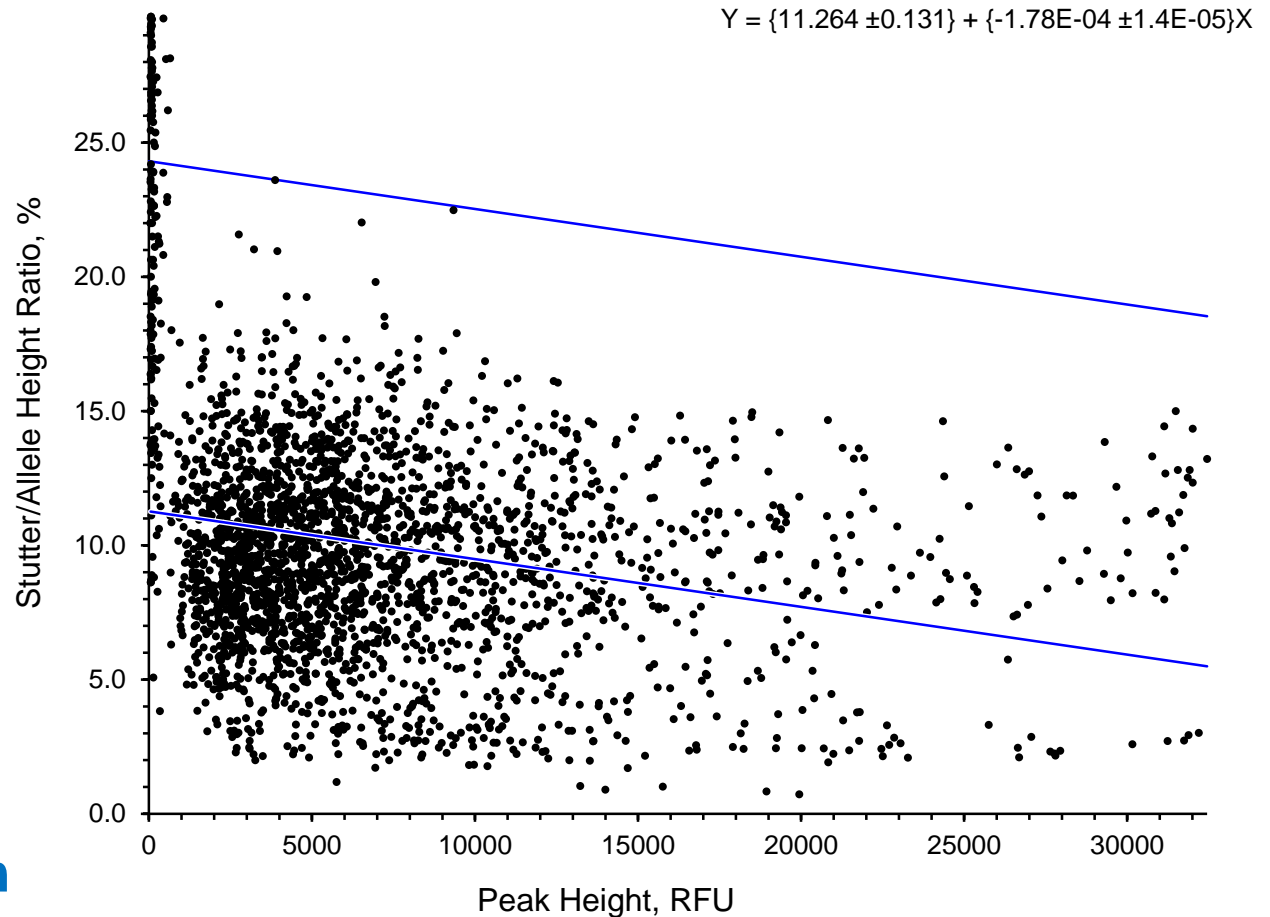


# Stutter Percentage

## Mean stutter for CODIS 13 loci

Locus	Mean	SD
TH01	4.2	4.3
TPOX	5.7	4.4
D7S820	8.1	4.3
D8S1179	9.3	3.2
D18S51	9.7	3.9
D13S317	9.6	3.6
FGA	10.3	4.0
D5S818	10.2	2.4
D16S539	10.5	4.0
vWA	10.7	4.4
CSF1PO	11.3	3.5
D3S1358	13.0	3.1
D21S11	13.9	3.6

Median stutter from  
4.2% to 13.9%





# Thresholds

As described by vendors and currently understood at NIST

- IntegenX employs dynamic thresholding
  - Each run has an independent analytical and stochastic threshold calculated via a programmed algorithm
  - Locus specific dynamic thresholds set within software
- NetBio employs a static threshold applied to all data uniformly

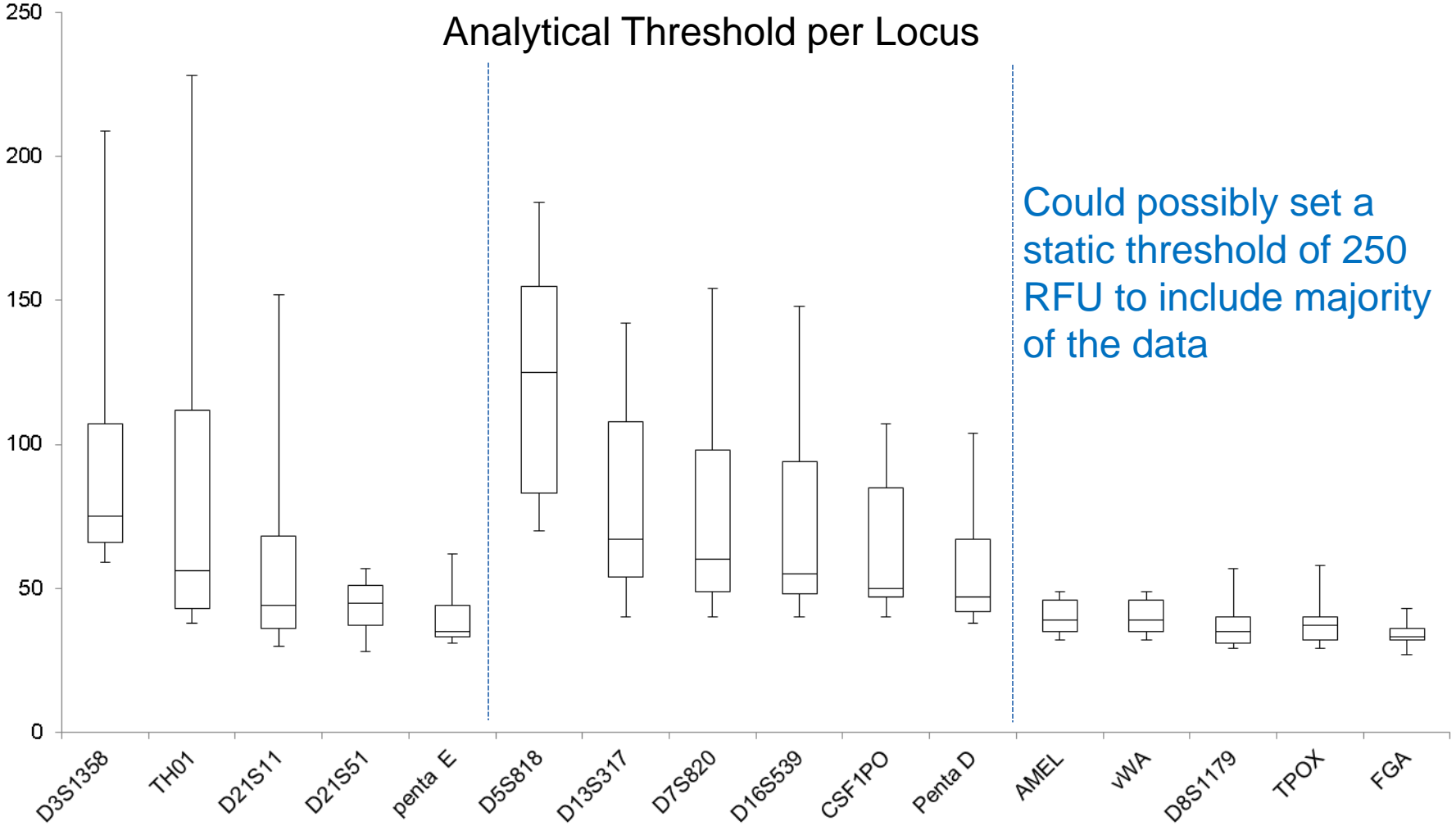
# IntegenX Thresholds

## Analysis Parameters

Locus	Stochastic Threshold	Analytical Threshold
D3S1358	112	56
vWA	49	25
D16S539	37	18
CSF1PO	36	18
TPOX	33	17
Yindel	221	111
AMEL	49	25
D8S1179	100	50
D21S11	75	37
D18S51	66	33
DYS391	77	38
D2S441	419	209
D19S433	224	112
TH01	111	55
FGA	77	39
D22S1045	198	99
D5S818	142	71
D13S317	133	66
D7S820	145	72
SE33	164	82
D10S1248	701	350
D1S1656	422	211
D12S391	270	135
D2S1338	169	84

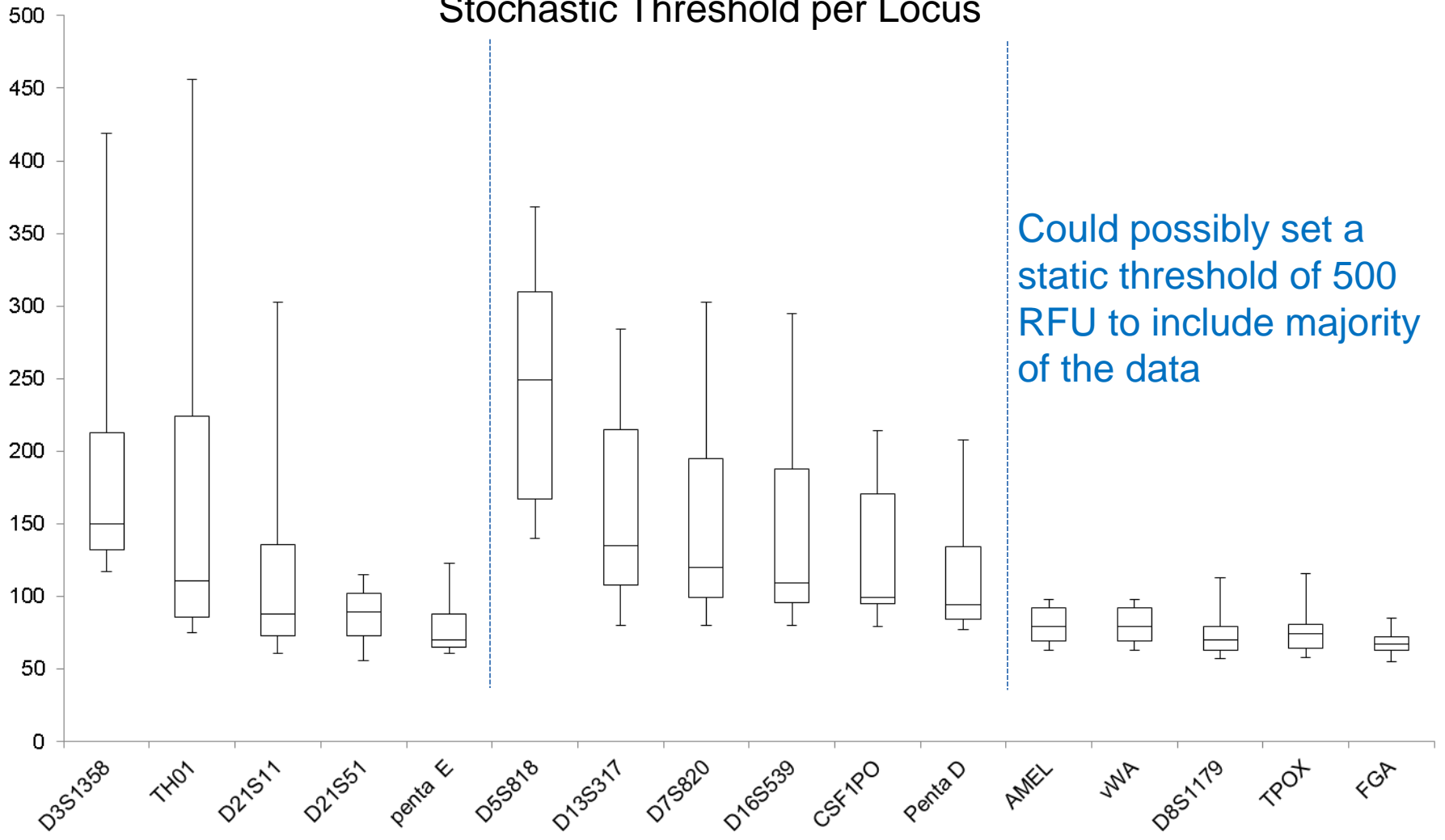
- Can be located in the report file generated per sample
- Table format with PDF report
- Data has been transcribed into an Excel file for analysis

# IntegenX PP16 Thresholds



# IntegenX PP16 Thresholds

Stochastic Threshold per Locus

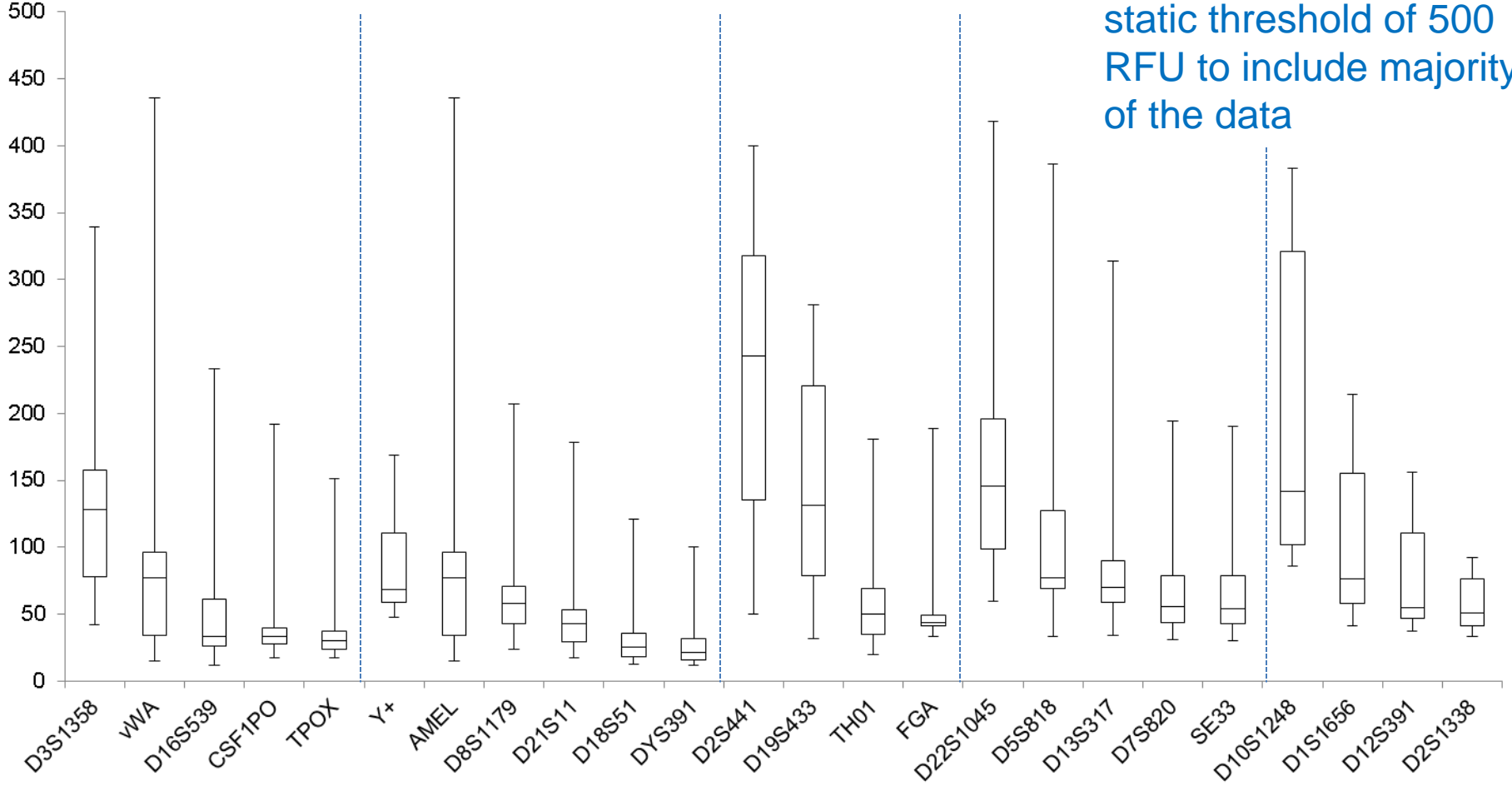


Could possibly set a static threshold of 500 RFU to include majority of the data

# IntegenX GFE Thresholds

Analytical Threshold per Locus

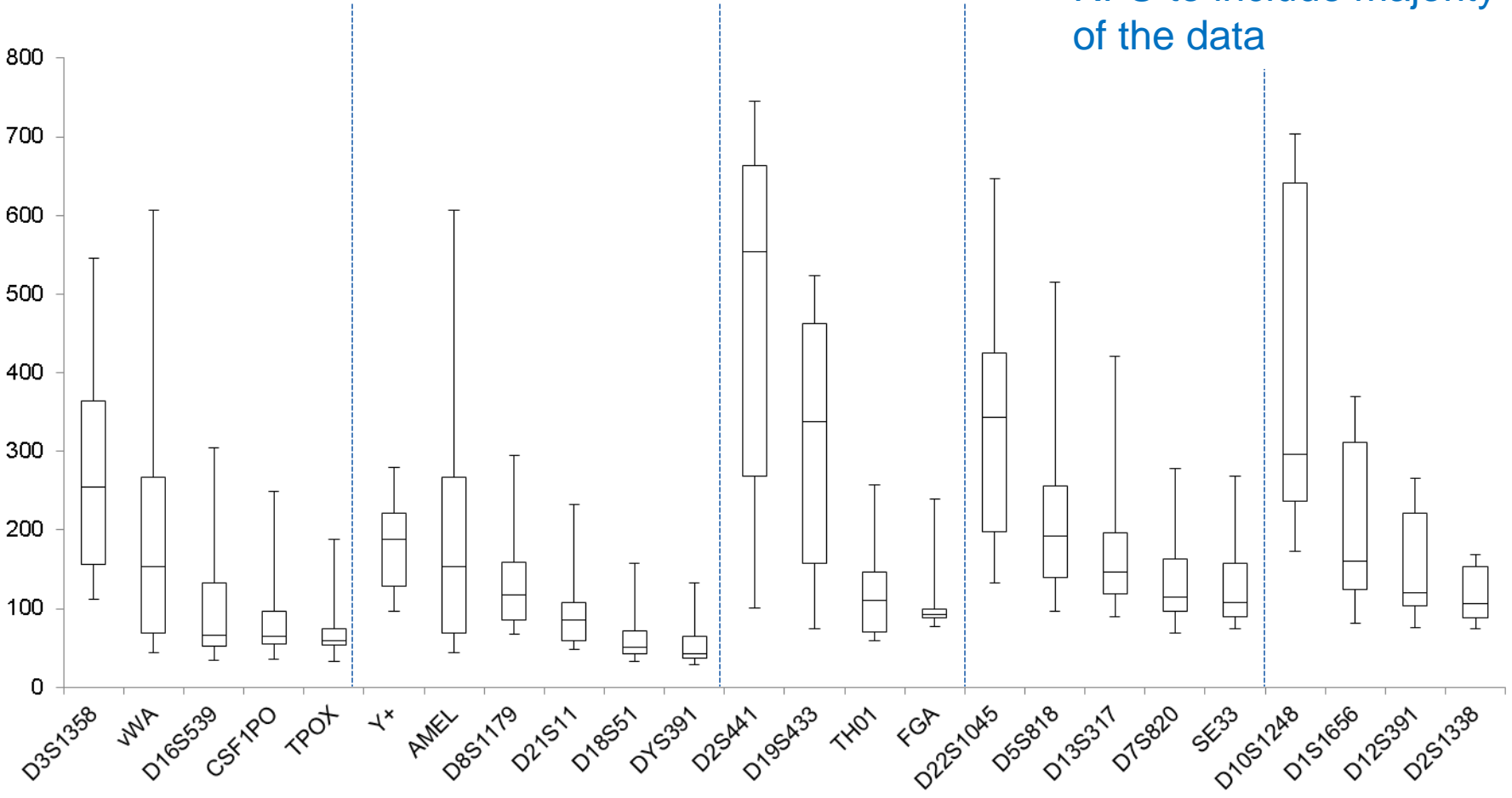
Could possibly set a static threshold of 500 RFU to include majority of the data



# IntegenX GFE Thresholds

Stochastic Threshold per Locus

Could possibly set a static threshold of 800 RFU to include majority of the data



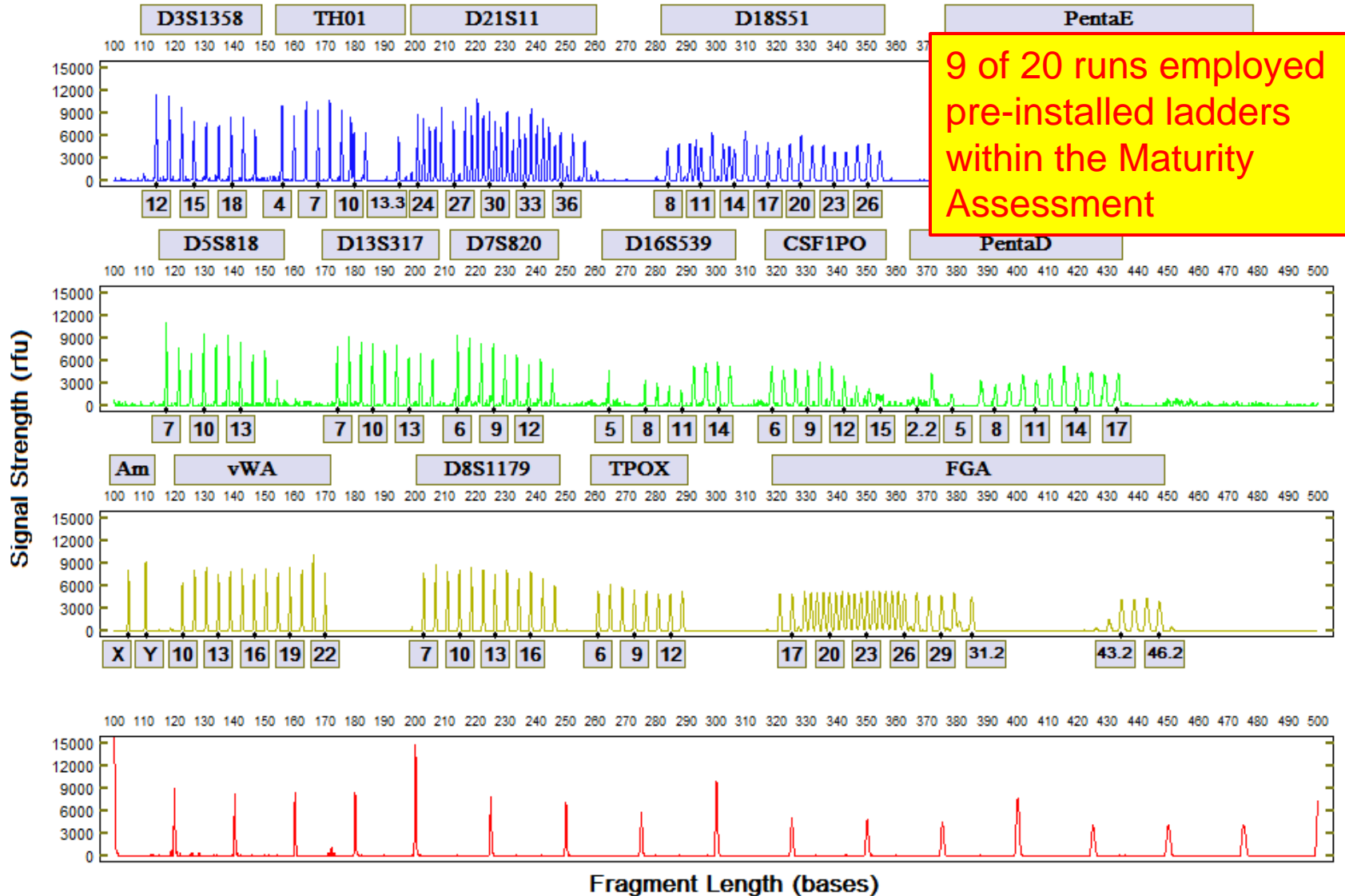
# Ladders

As described by vendors and understood by NIST

- Both instruments contain “onboard” ladders
  - For use if the ladder on the chip fails
- IntegenX
  - “Fit best Ladder” Algorithm
  - Database of ~200 ladders uploaded into each instrument used to find best ladder per sample
    - Uses size standard and algorithm fitting per sample
- ANDE
  - Onboard ladder file saved and applied to data when chip ladder fails

Pre-installed allelic ladder employed to designate sample alleles

9 of 20 runs employed pre-installed ladders within the Maturity Assessment

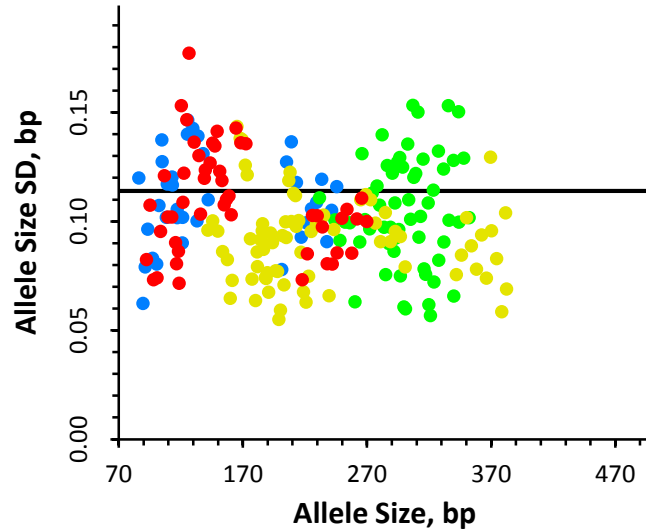






# IntegenX Ladder Precision

## RapidHIT 200: GlobalFiler Express



Allele size SD: 0.114 bp

Peak Height CV: 30.1 %

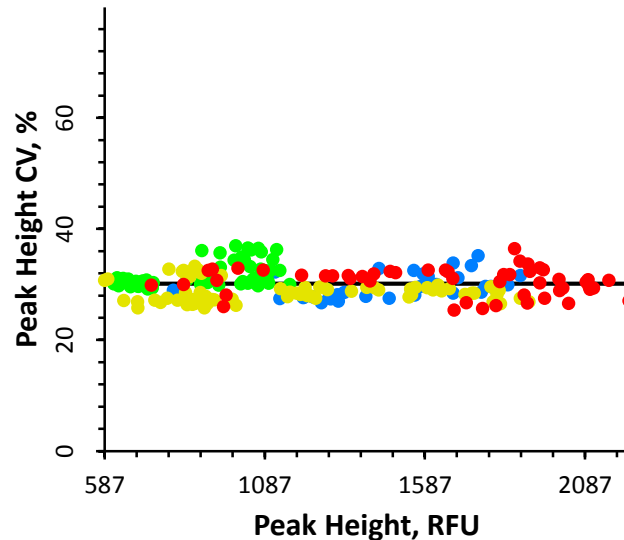
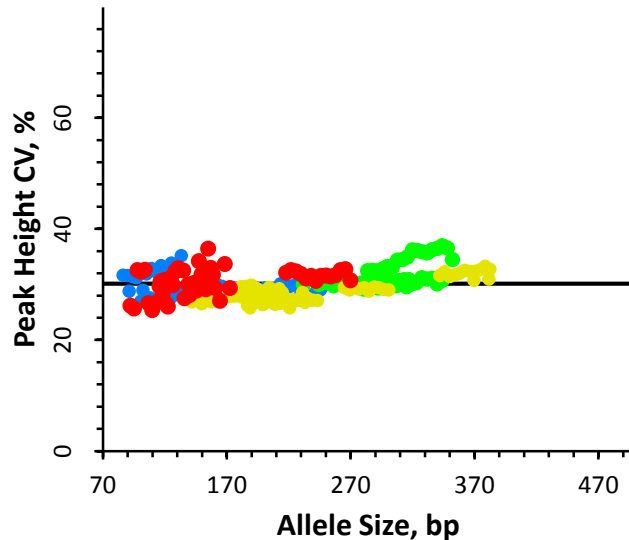
Mean Peak Height: 1251 RFU

Mean Peak Area: 6909 RFU × bp

Peak Area CV: 30.1 %

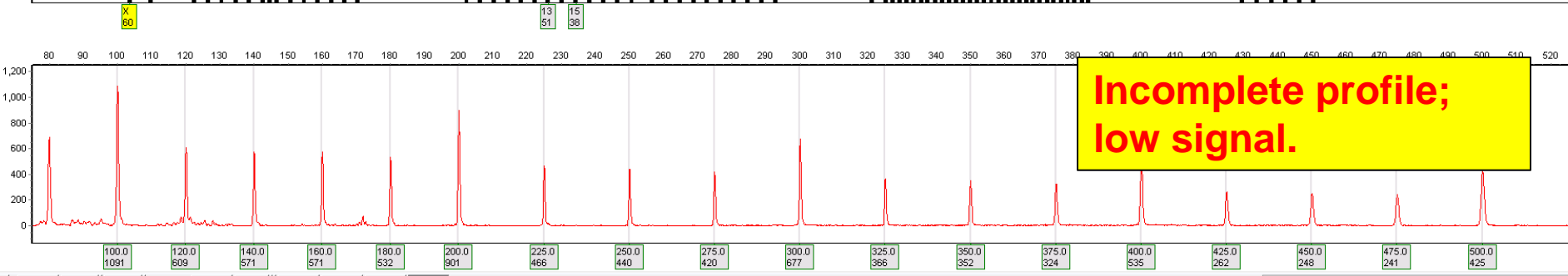
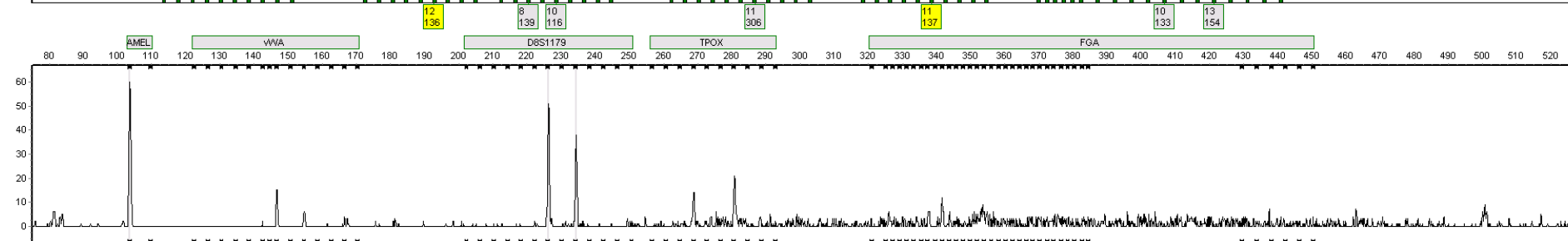
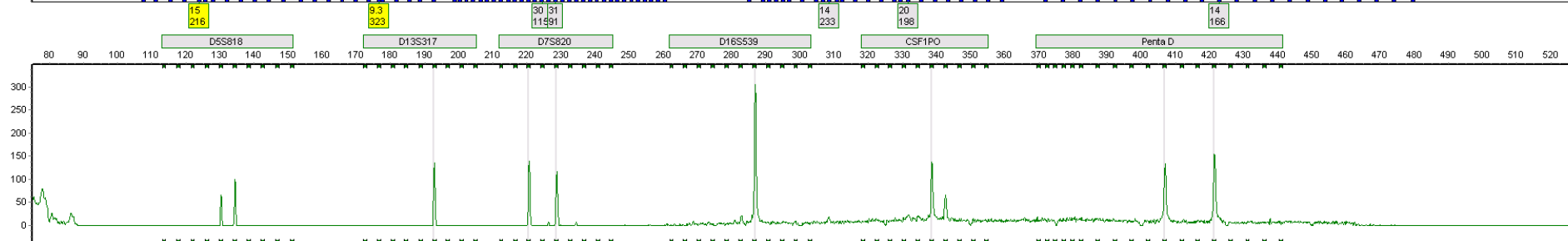
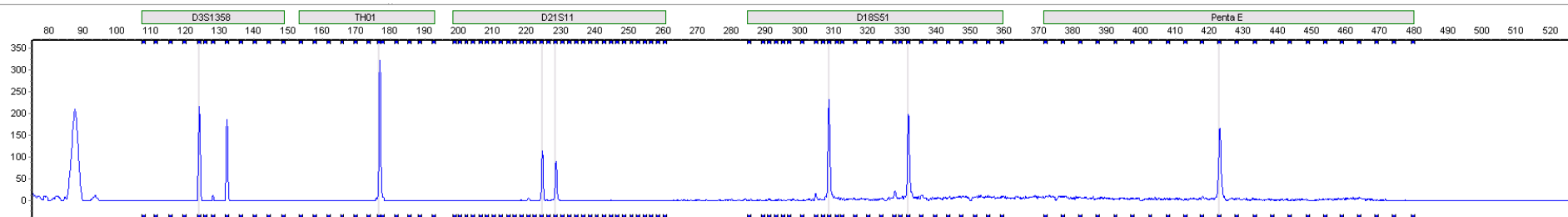
Mean Peak Width: 5.4 bp

Slope {CV(Area),CV(Height)}: 0.998

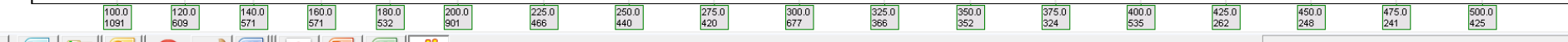


# Examination of the remaining ~20% samples that were not successful

Examples observed between at  
least 2 individual datasets within  
the Maturity Assessment Data

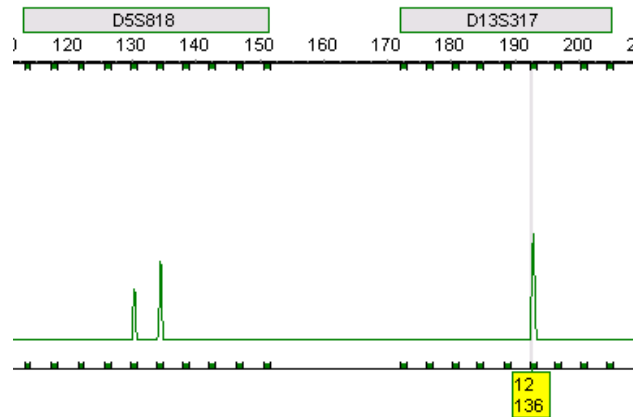
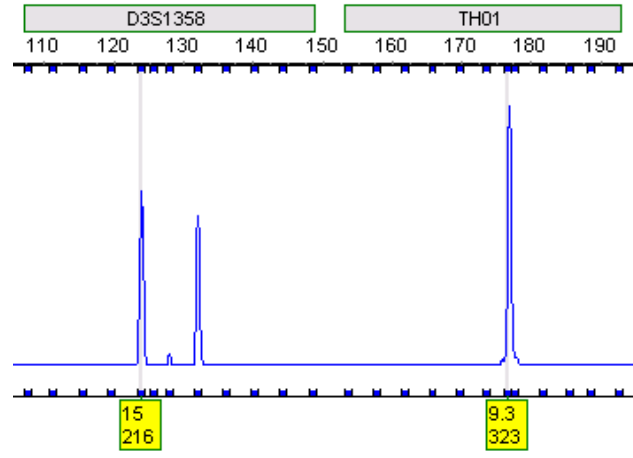


**Incomplete profile;  
low signal.**

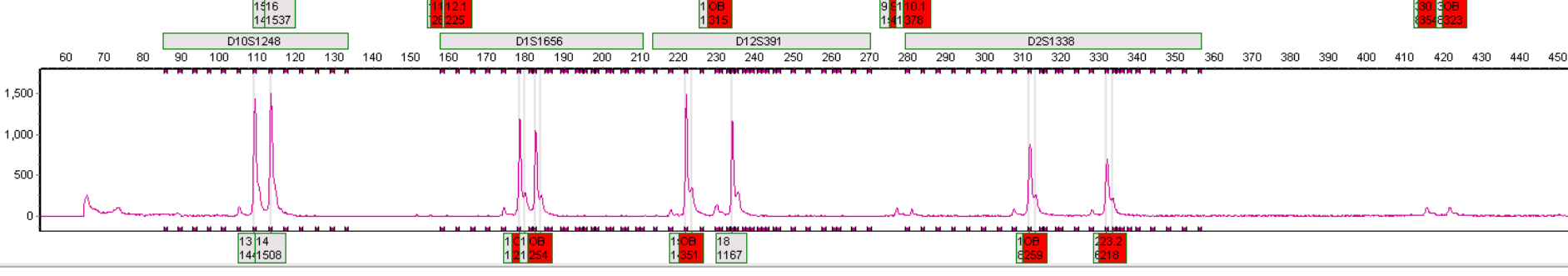
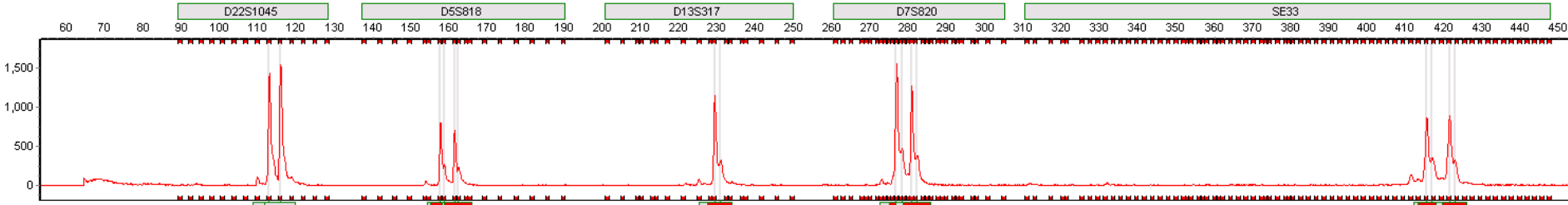
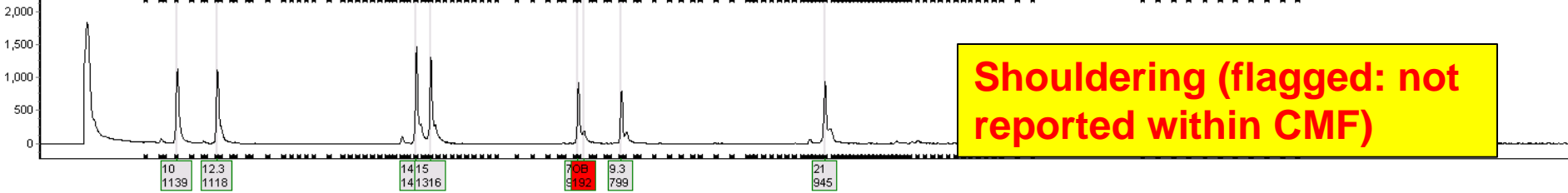
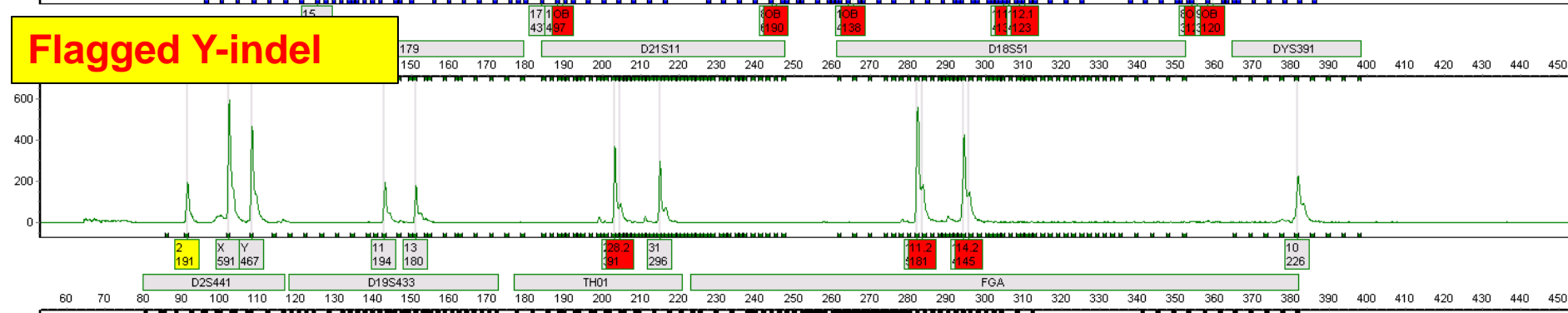
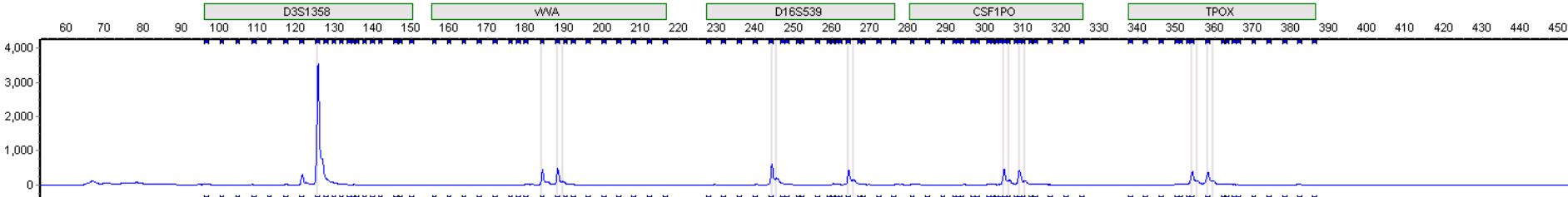


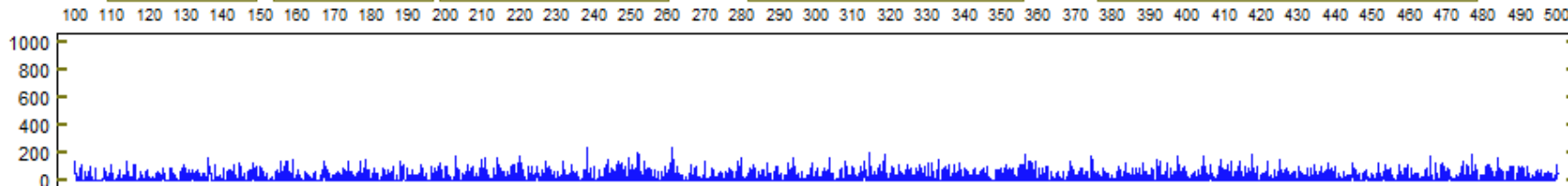
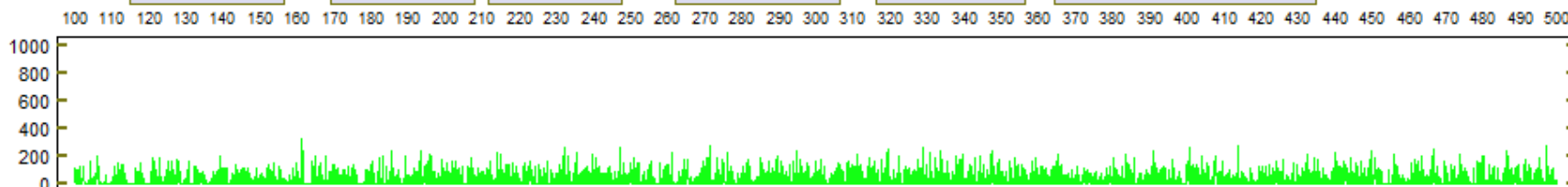
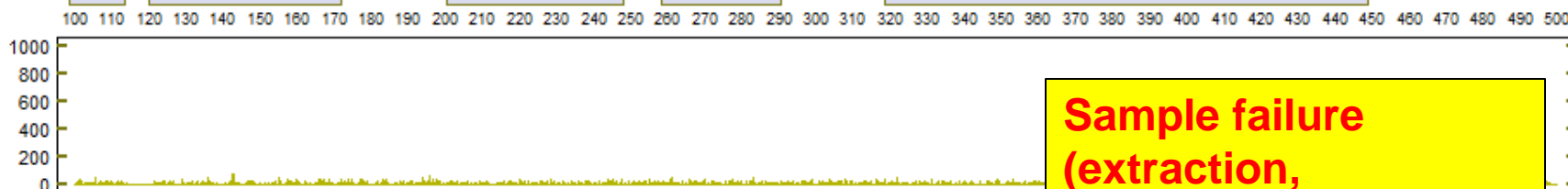
# Report for Previous Sample

Loci	5. LabC_NN_5
D3S1358	15,
TH01	9.3,
D21S11	30, 31,
D18S51	14, 20,
Penta E	14,
D5S818	
D13S317	12,
D7S820	8, 10,
D16S539	11,
CSF1PO	11,
Penta D	10, 13,
AMEL	X,
vWA	
D8S1179	13, 15,
TPOX	
FGA	

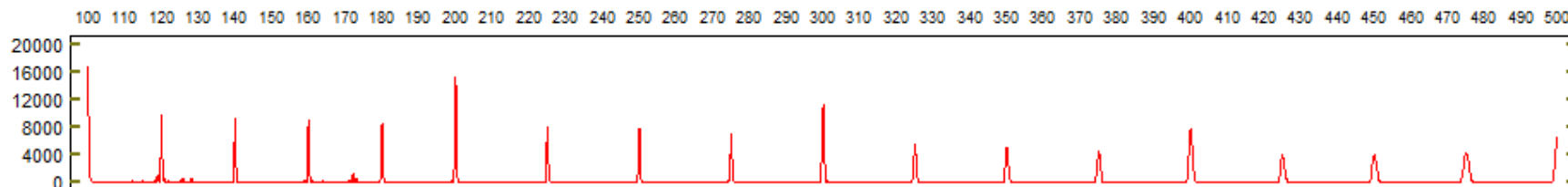


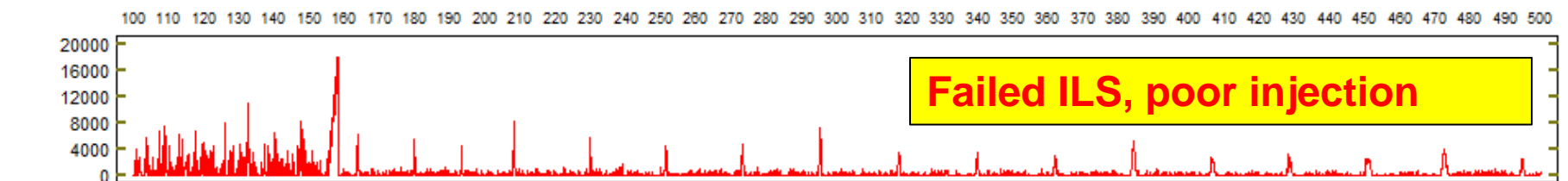
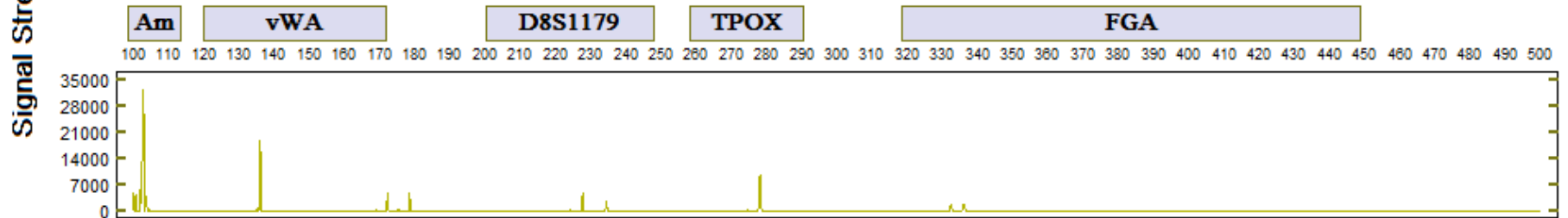
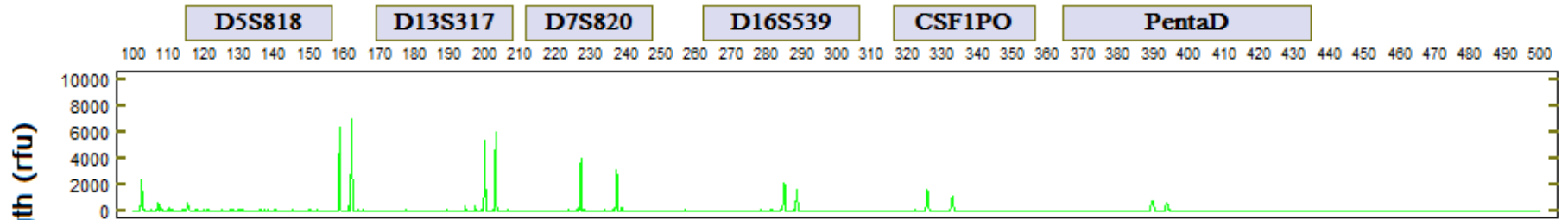
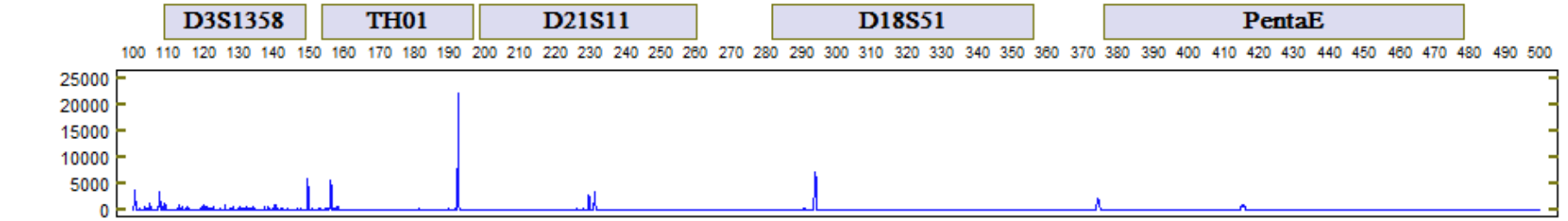
**Incomplete profiles reported (in xml file)**



**D3S1358****TH01****D21S11****D18S51****PentaE****D5S818****D13S317****D7S820****D16S539****CSF1PO****PentaD****Am****vWA****D8S1179****TPOX****FGA**

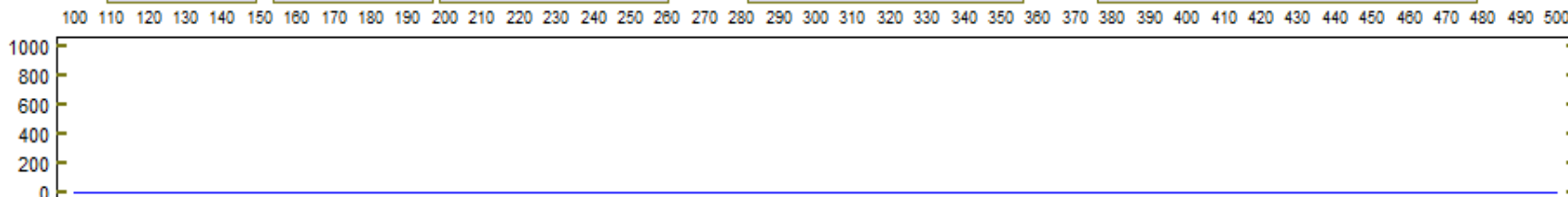
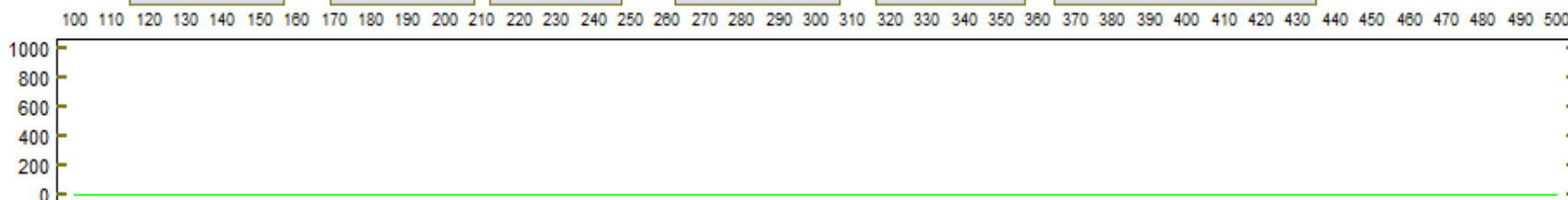
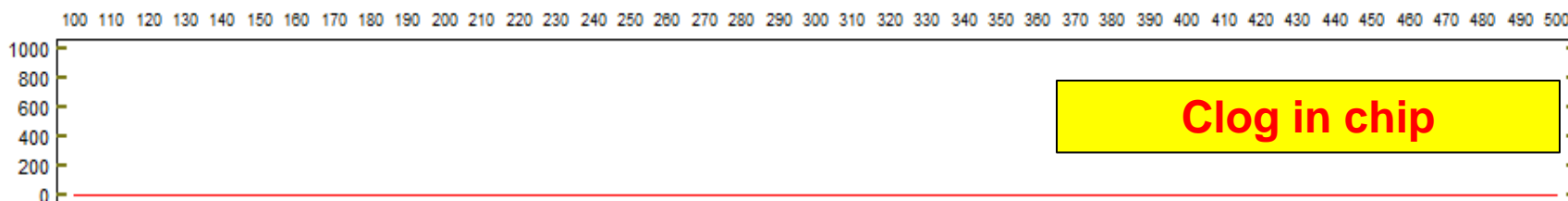
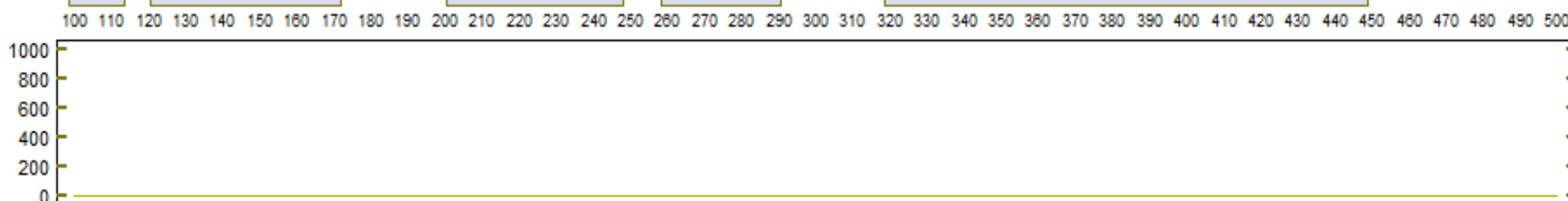
**Sample failure  
(extraction,  
amplification?)**

**Fragment Length (bases)**



**Failed ILS, poor injection**



**D3S1358****TH01****D21S11****D18S51****PentaE****D5S818****D13S317****D7S820****D16S539****CSF1PO****PentaD****Am****vWA****D8S1179****TPOX****FGA****Fragment Length (bases)**

# Improvements Since R-DNA MA

- Problems with IXI GFE cartridge manufacturing Summer/Fall of 2014 (during this study)
  - Leaking buffer cartridges
  - Leaking PCR mastermix during injection of pogos

Chips were redesigned in January 2015
- Bad lot of polymer (exposed to extreme heat in AZ and began to break down)
- New RH200 software version (2.0)
  - Added kinship function (pair-wise comparisons)
  - Rapid DNA Process mode (complete expert mode)
    - GlobalFiler Express with GeneMarker HID 2.7

# Summary

- 2014 R-DNA Maturity Assessment exhibited a 76% success rate for the CODIS 13 Core Loci using Rapid DNA Analysis
  - Success ranged from 45% to 85% across laboratories, chemistries, and instruments
- Precision is within 0.114 bp on average for RH200 GFE
- Continuing to run R-DNA platforms with newer chemistries and upgrades
  - GFE with the RapidHIT200
  - 27plex 6-dye chemistry with ANDE

# Final Results

Rapid DNA Instrument Platforms	Number of Participating Labs	Total Instruments	Samples Attempted	Core CODIS Success (Rapid DNA Analysis)	Core CODIS Success (Modified Rapid DNA Analysis)
2	7	11	280	76.1%	80.0%

Overall success for the R-DNA maturity assessment will be reported:

[http://www.nist.gov/mml/bmd/genetics/dna\\_biometrics.cfm](http://www.nist.gov/mml/bmd/genetics/dna_biometrics.cfm)

This data will be made available to the public.

# Thank you for your attention!

Thanks to David Duewer and Sanae Lembirik for assistance with data analysis

Contact Info:

[erica.romsos@nist.gov](mailto:erica.romsos@nist.gov)

301-975-5107

## Funding

**DHS** – Rapid DNA  
Prototype and Kinship  
Performance Evaluation

**FBI** - the Evaluation of  
Forensic DNA Typing as  
a Biometric Tool

