

# Development of a Highly Sensitive Quantification System for Assessing DNA Quality in Forensic Samples

**SUDHIR K. SINHA, PH.D.**

**CEO**

**INNOGENOMICS TECHNOLOGIES**

[WWW.INNOGENOMICS.COM](http://WWW.INNOGENOMICS.COM)



# QUANTIFICATION

- Several different fluorescence-based quantification assays are currently available.
- Reduced amplicon size has enabled STR analysis of highly compromised samples.
- A system to assess the amount of DNA degradation in forensic samples would be useful in determining which test kit to use.

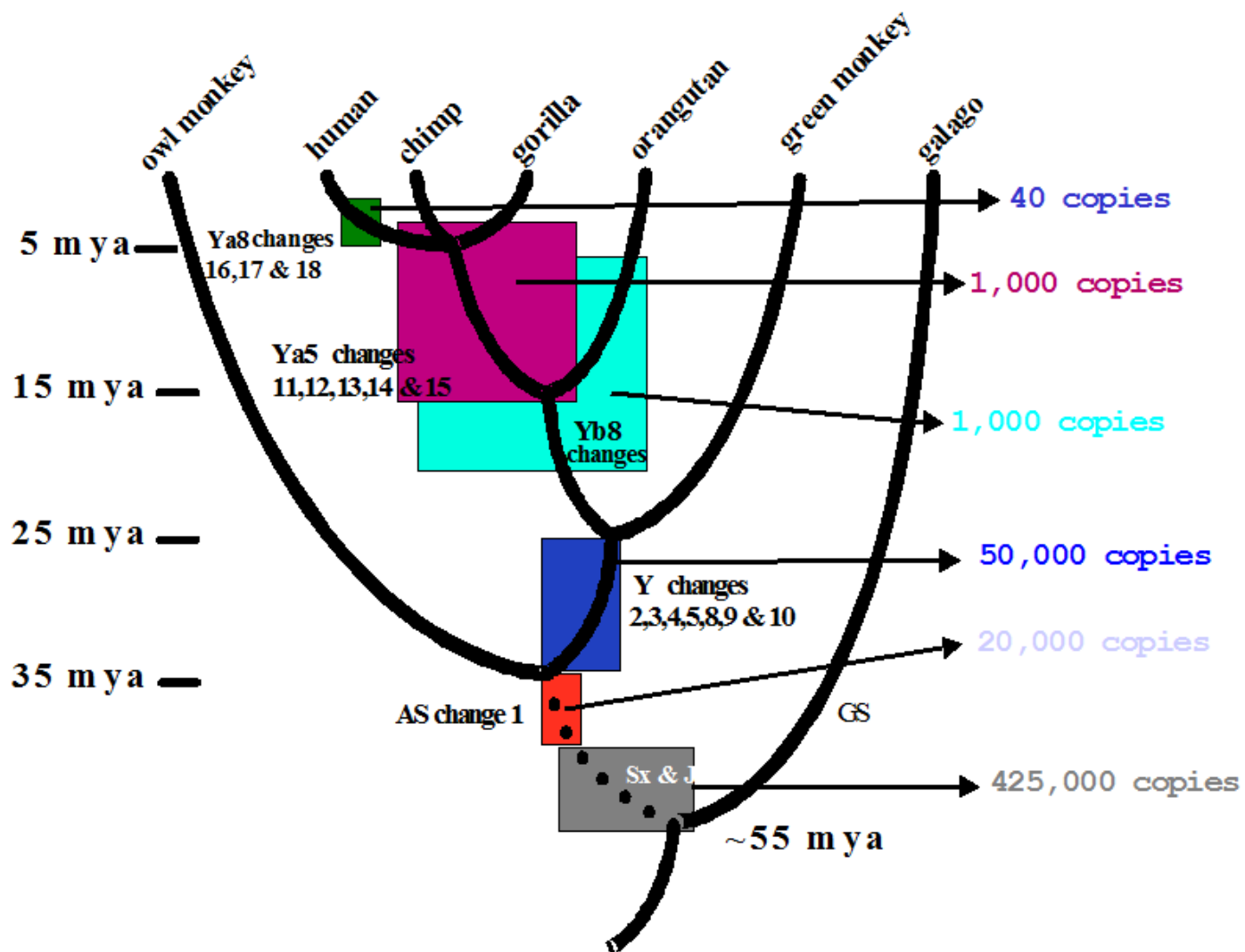


# What are SINEs?

1. Short INterspersed Elements
2. 70 - 300 Base Pairs
3. High Copy Number  
( $>100,000$  Copies/Genome)

# QUANTIFICATION

- A multi-copy, *Alu* based approach, to quantify human specific DNA in forensic samples, has been used previously with high sensitivity.
- Walker et al 2005; Shewale et al 2007; Opel et al 2008; Nicklas JA, 2012



# QUANTIFICATION SYSTEM

Primers and TaqMan® probes for 2 independent *interspersed elements*:

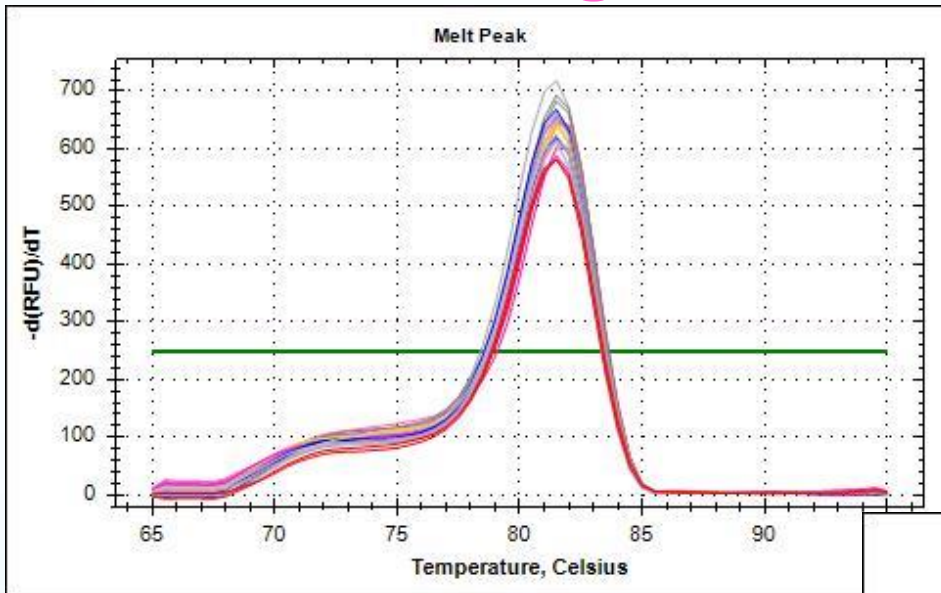
- ~80 bp target sequence labeled with FAM (“short” target)
- ~290 bp target sequence labeled with Cy5 (“long” target)

# Internal Synthetic DNA Control

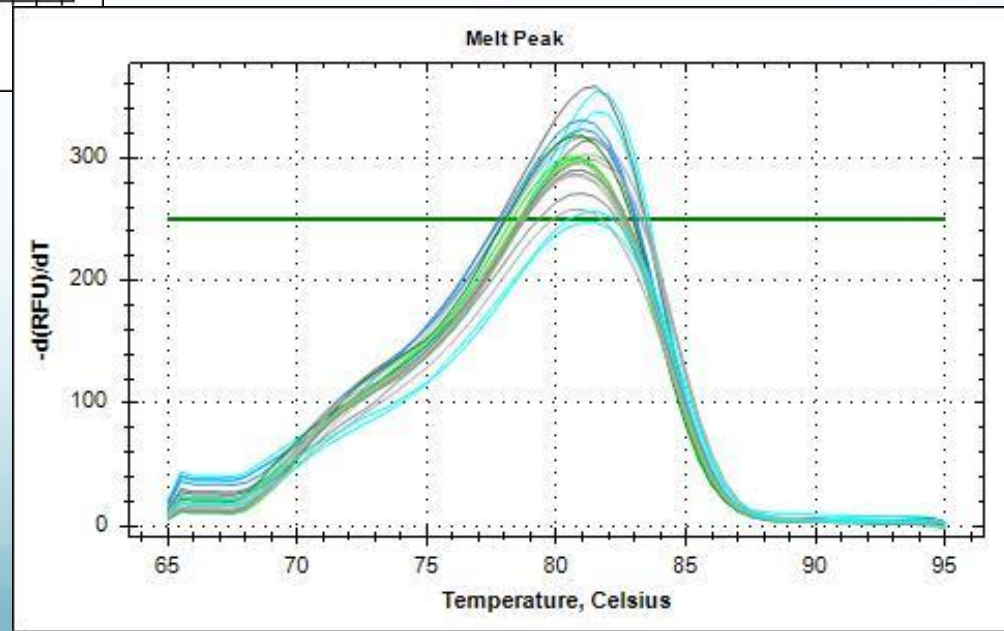
- Cy3 labeled ~90 bp fragment for an Internal Positive Control (IPC)
- IPC assessment for PCR inhibitors

# Melt Curve Analysis

Short Target



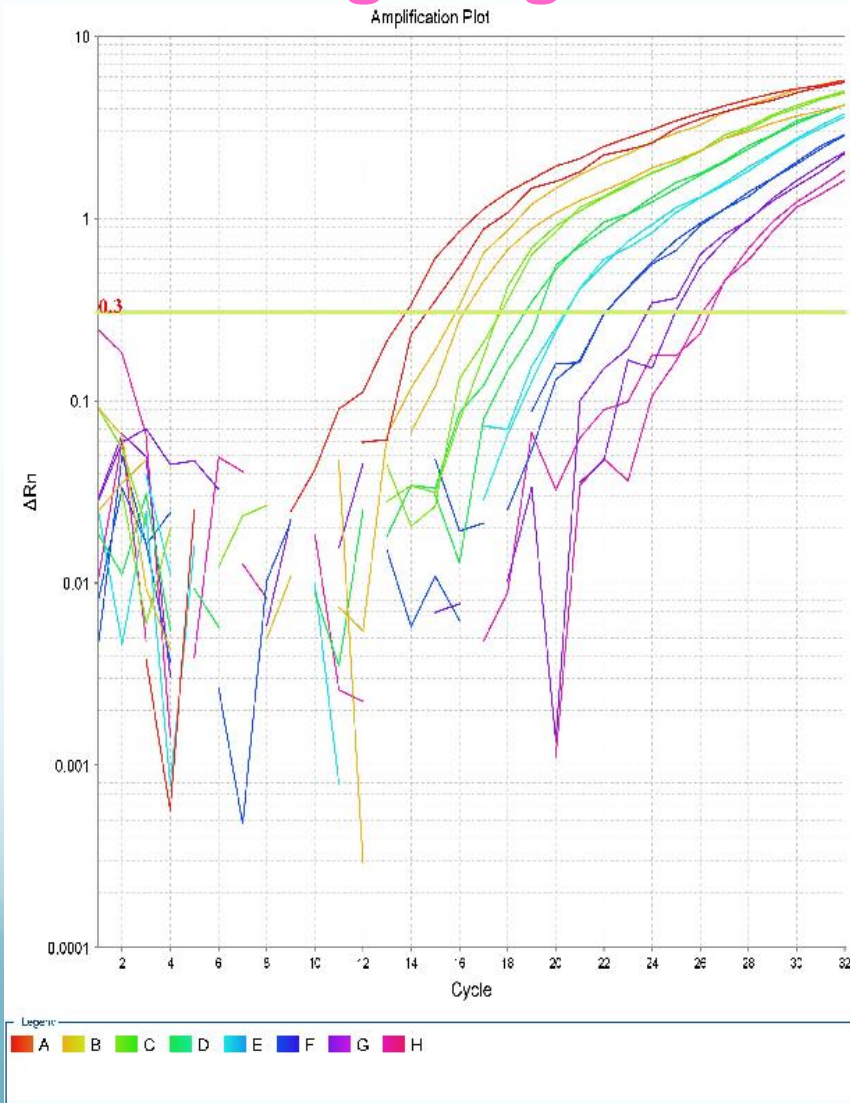
Long Target



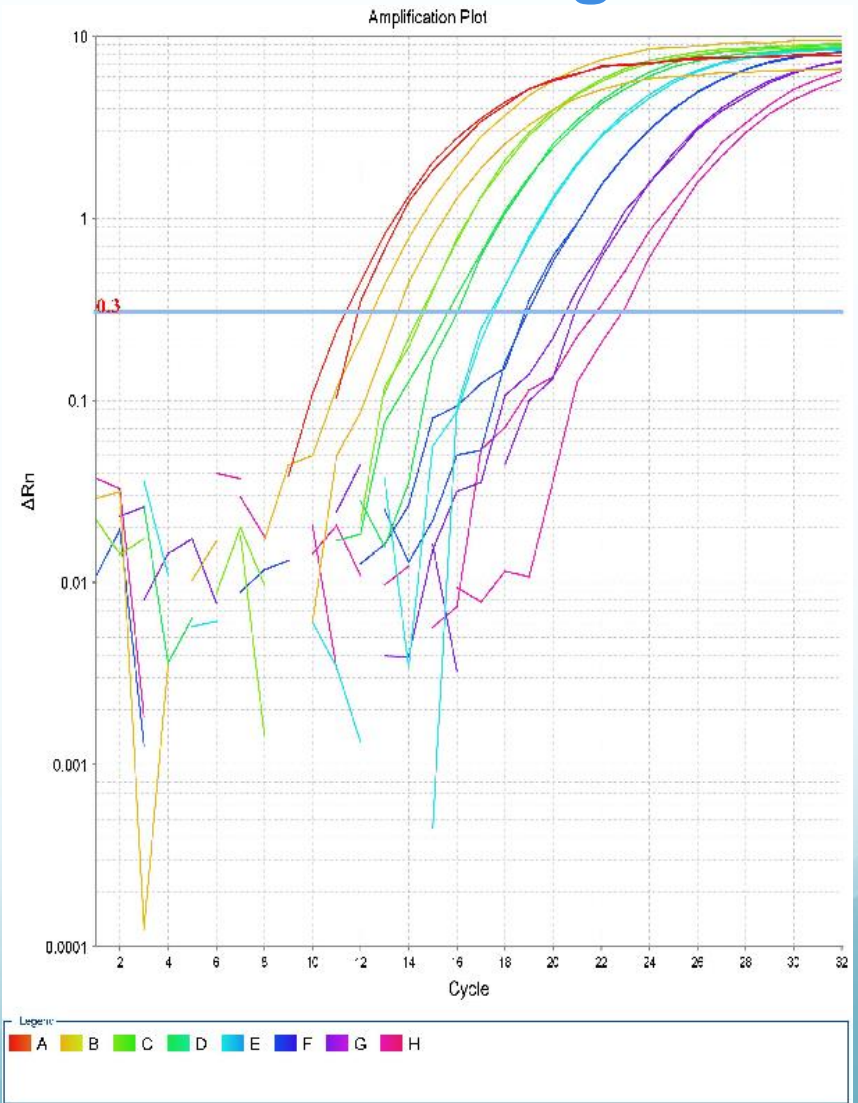


# AB 7500 Amplification Plots

## Long Target



## Short Target

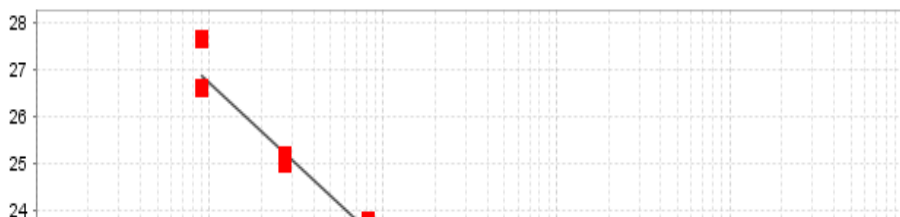


# AB 7500 Standard Curves

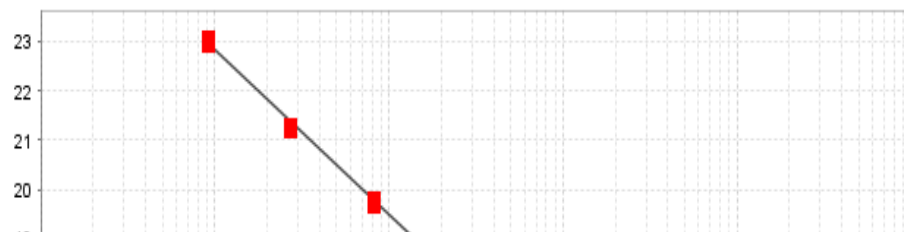
Long Target

Short Target

Standard Curve

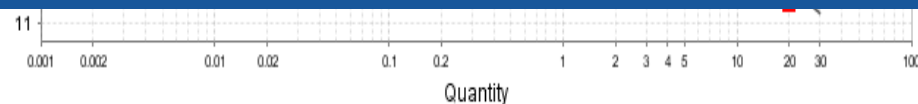
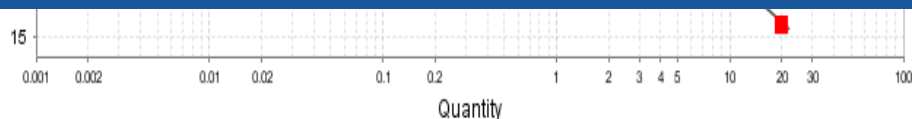


Standard Curve



Long: efficiency = 94.9%,  $R^2=0.992$

Short: efficiency = 98.7%,  $R^2=0.998$



Long

Slope: -3.451 Y-Inter: 19.787  $R^2$ : 0.992 Eff%: 94.882

Legend  
■ Standard ■ Unknown ■ Unknown (Flagged)

Short

Slope: -3.353 Y-Inter: 16.125  $R^2$ : 0.998 Eff%: 98.699

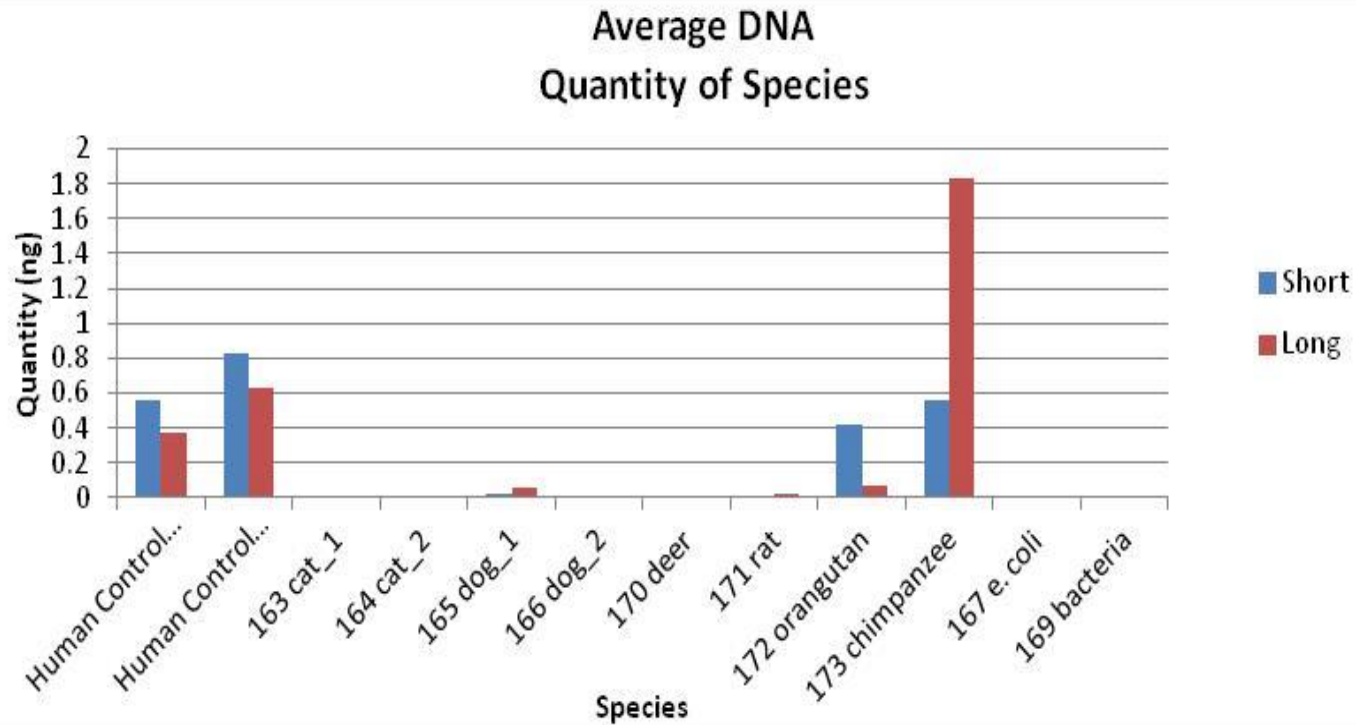
Legend  
■ Standard ■ Unknown ■ Unknown (Flagged)

# REAL TIME PCR METRICS

- Observations from 35 runs
  - Short target:
    - Average efficiency: **95%**, Average R<sup>2</sup> value: **0.994**
  - Long target:
    - Average efficiency: **91%**, Average R<sup>2</sup> value: **0.993**
- Standards dilution scheme ranges from:
  - 20 ng/ul to 0.009 ng/ul.
- Degradation Ratio expressed as a percentage =
  - $(1 - [\text{Long Qty} / \text{Short Qty}]) * 100$



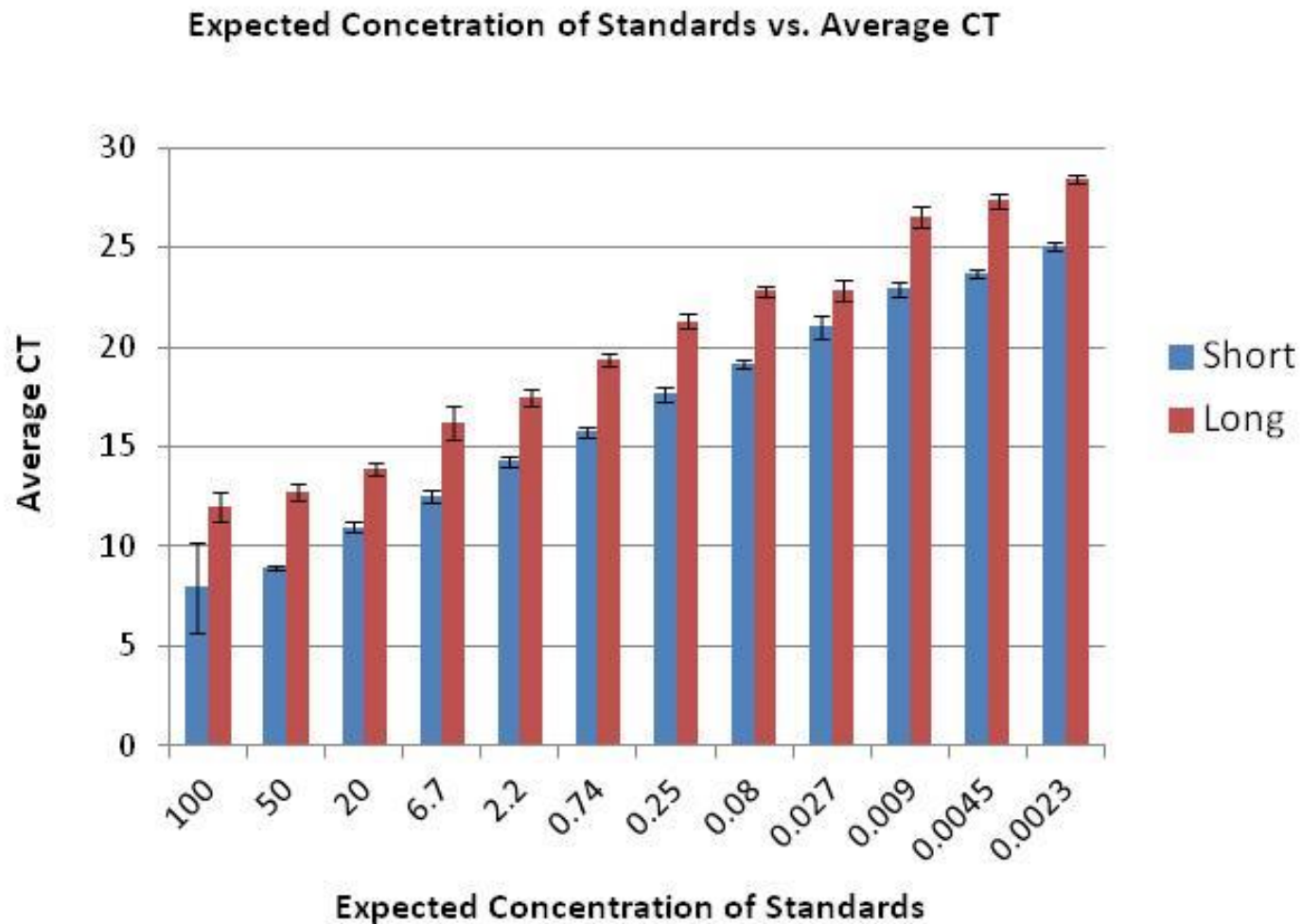
# SPECIES STUDY



# CONCORDANCE STUDY

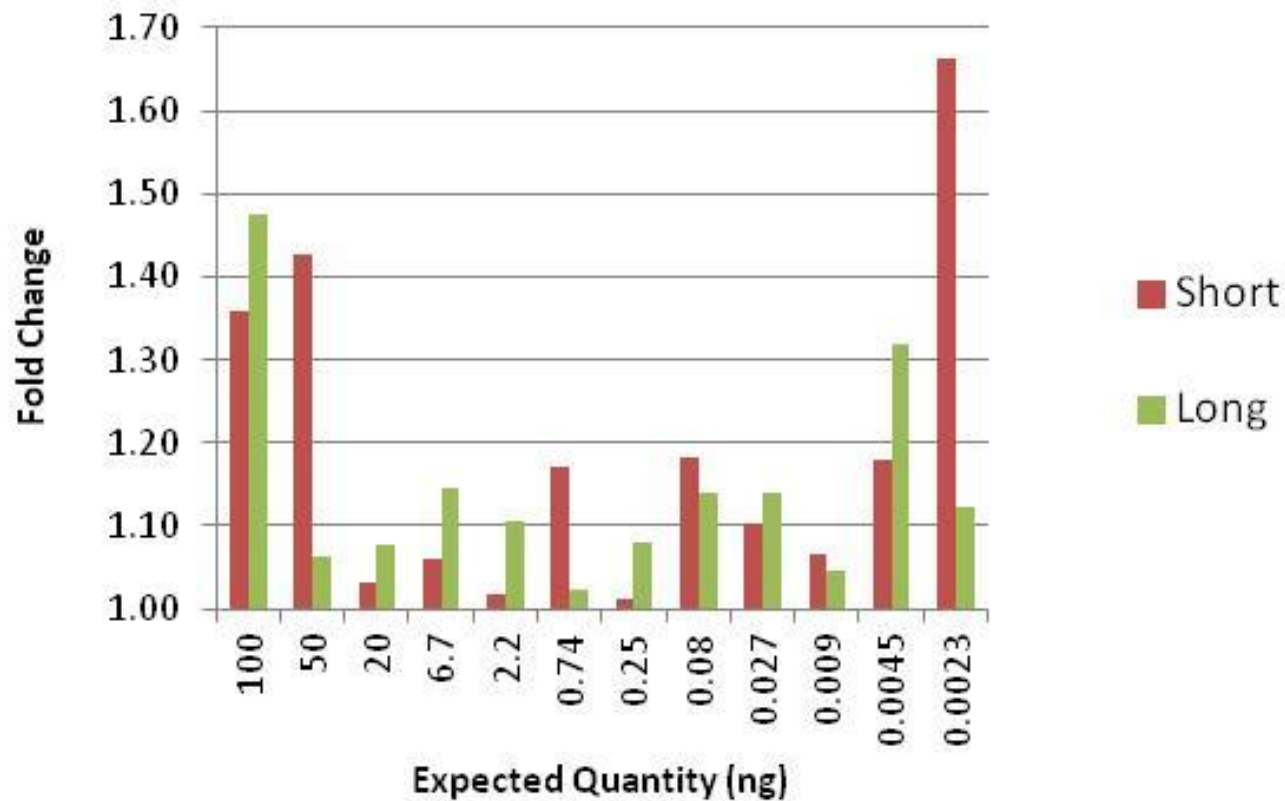
- 19 samples quantified using Degradation Assay and Quantifiler® Human
- Quantifiler® human DNA concentrations averaged 140% of those calculated using the short target of this dual target assay
- If differences were observed, in all instances, Quantifiler® human values were higher than dual target assay values
- Differences are attributed to differences in the DNA standards and differences in amplicon length (62 bp vs. 80 bp)

# SENSITIVITY STUDY



# REPRODUCIBILITY STUDY

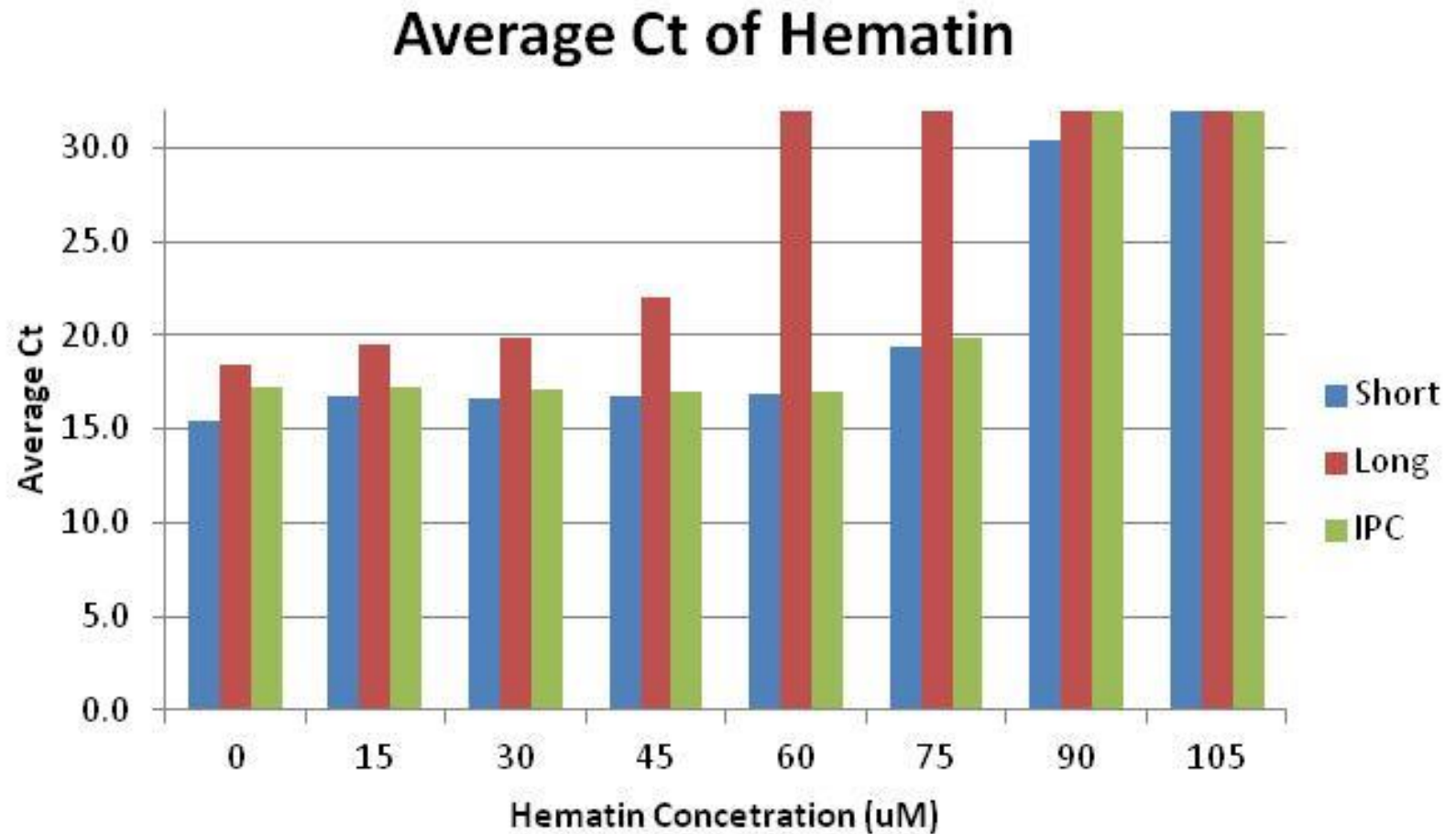
Average Quantity vs. Fold Change Standards





# INHIBITION STUDY

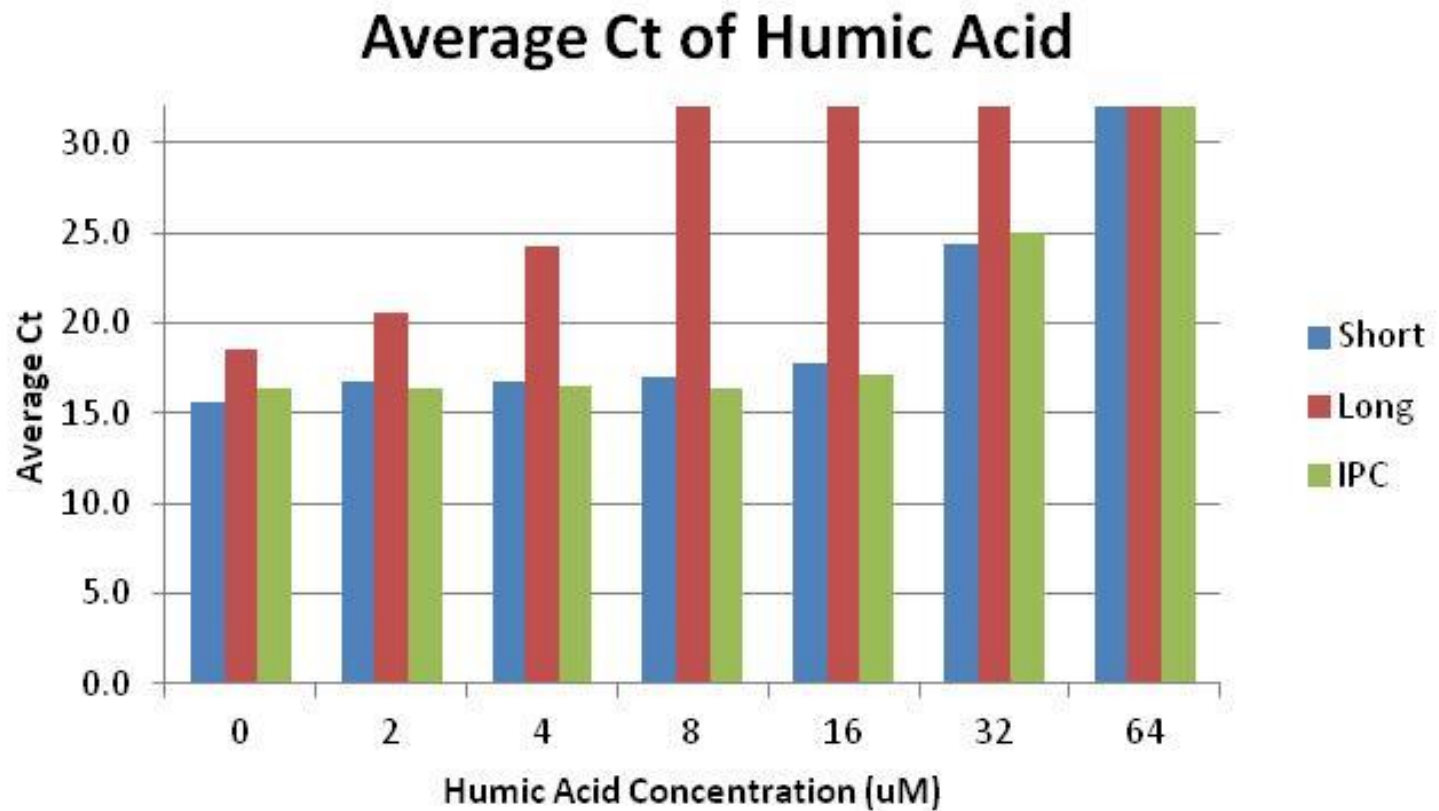
## HEMATIN





# INHIBITION STUDY

## HUMIC ACID



# DEGRADATION STUDIES

- Sonication
  - Mixture sample
  - Single source sample
- DNase-I
  - Mixture sample
  - Single source sample
- Environmental Degradation
- Targeted 3 concentrations of total DNA for Identifiler Plus Amplifications: 1 ng, 500 pg, and 200 pg
  - 28 cycles for IDP



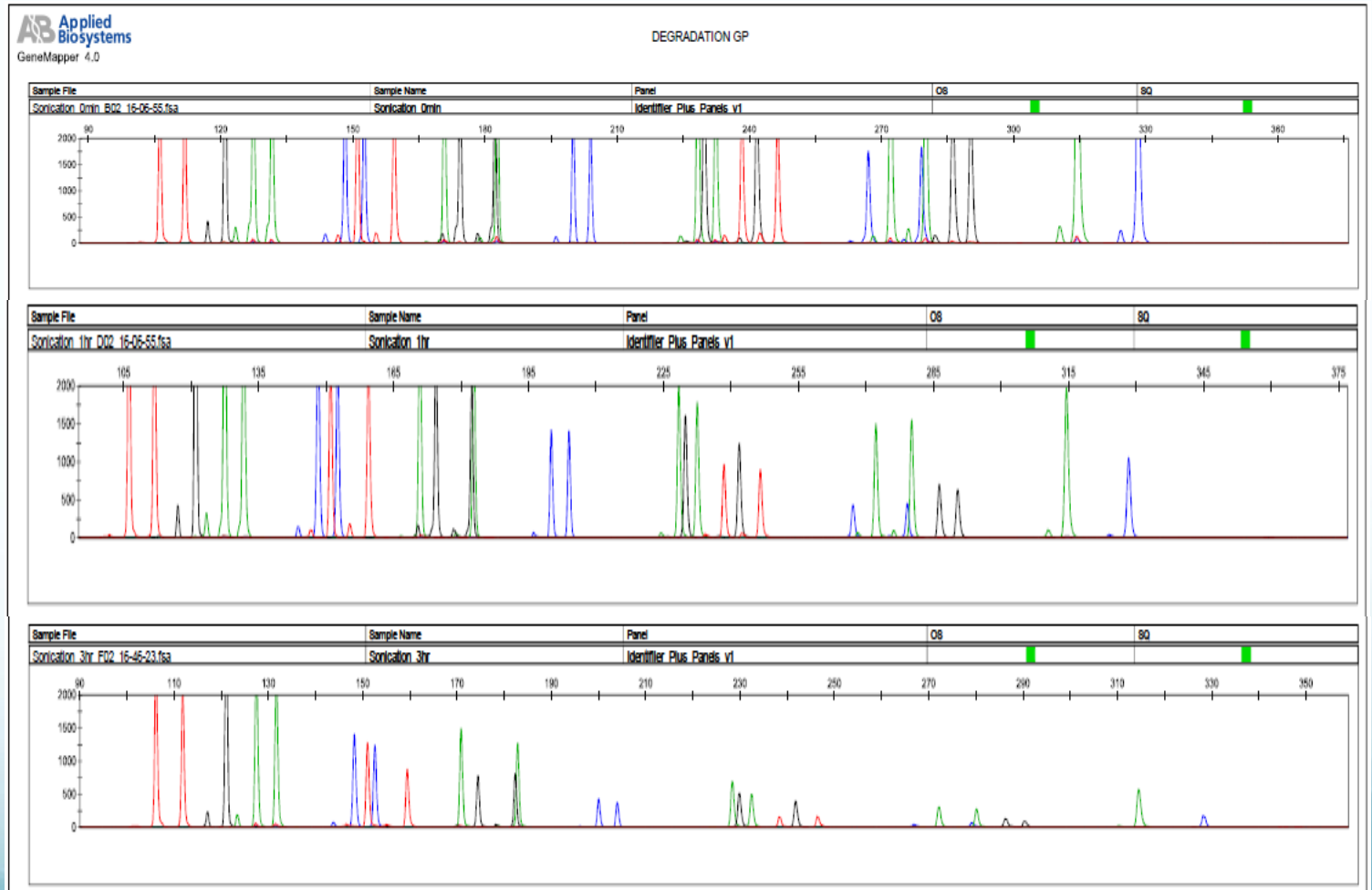
# DEGRADATION STUDY: SONICATION

## 1 NG INPUT [DNA]

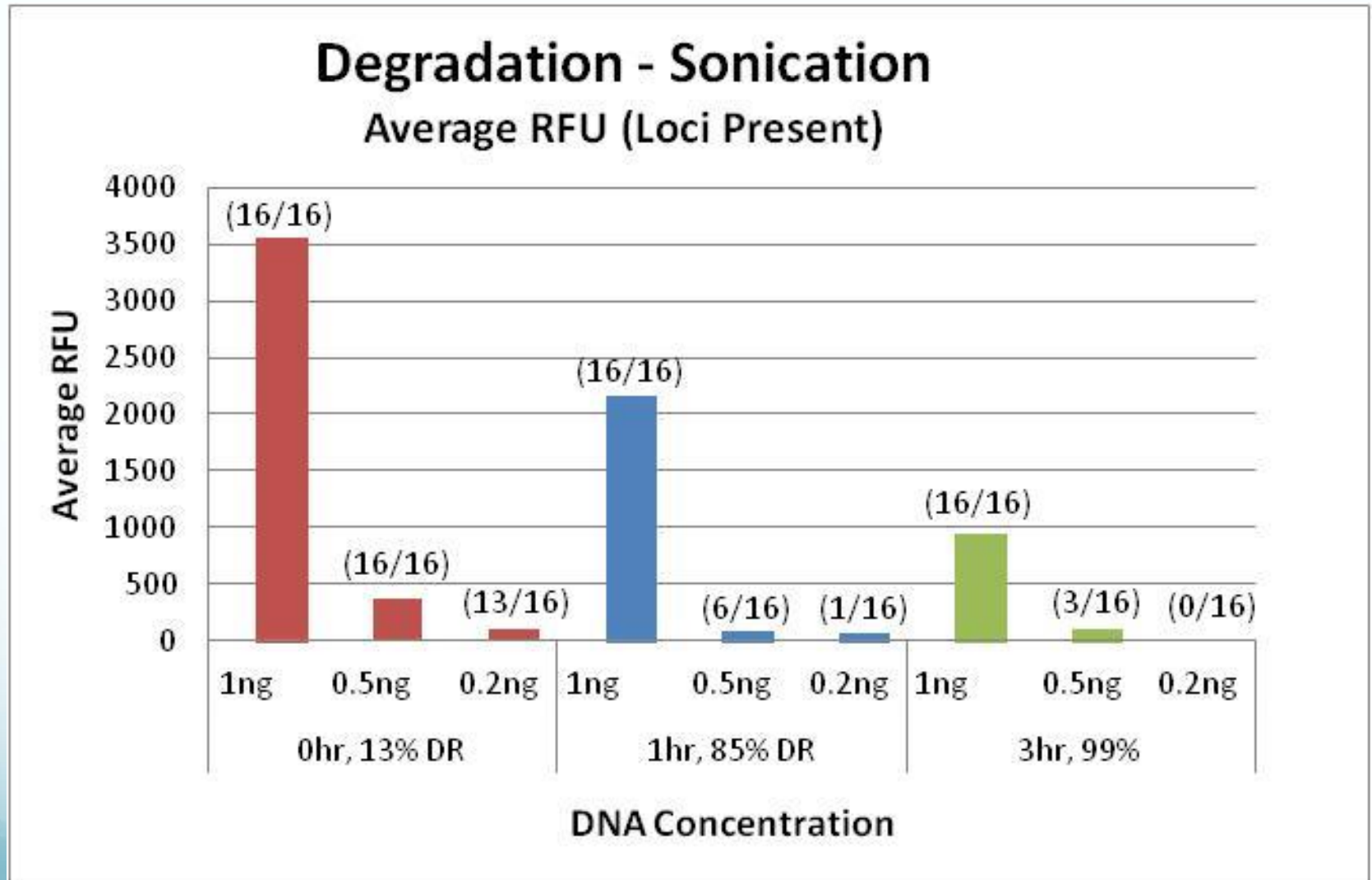
Control-  
13% DR

1 hour-  
85% DR

3 hour-  
99% DR



# DEGRADATION STUDY: SONICATION



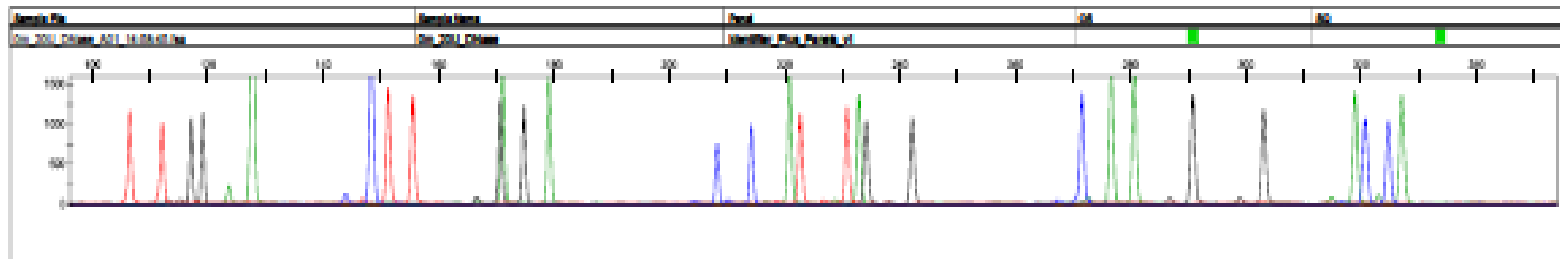
# DEGRADATION STUDY: DNASE I

## 1 NG INPUT [DNA]

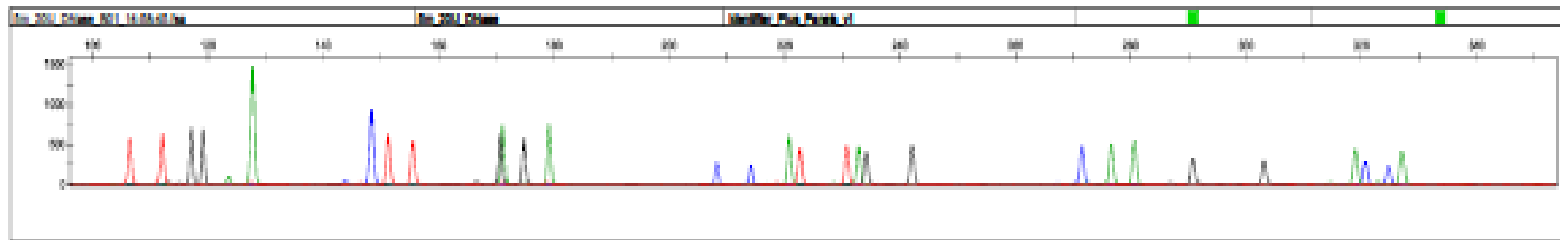
Applied  
Biosystems  
GenMapper 4.0

Degradation\_Validation\_001.d

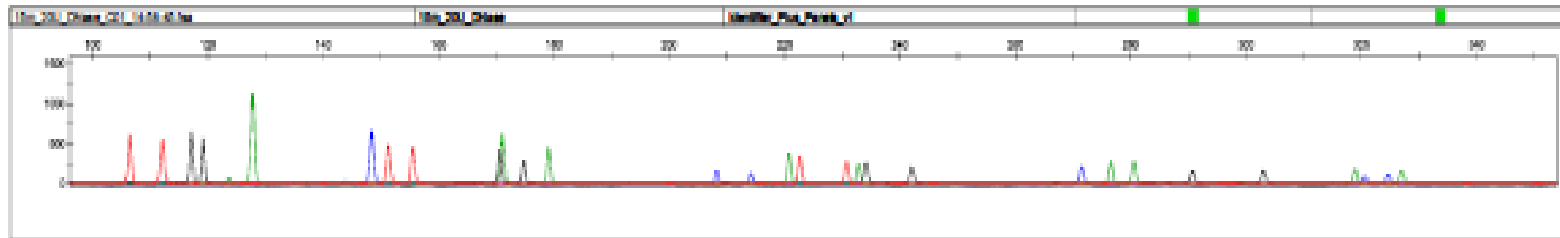
Control-  
13% DR



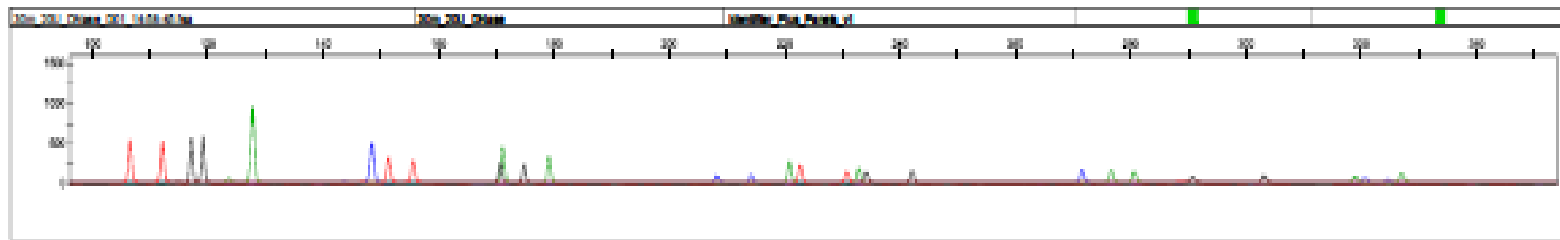
5 min  
25% DR



15 min  
81% DR



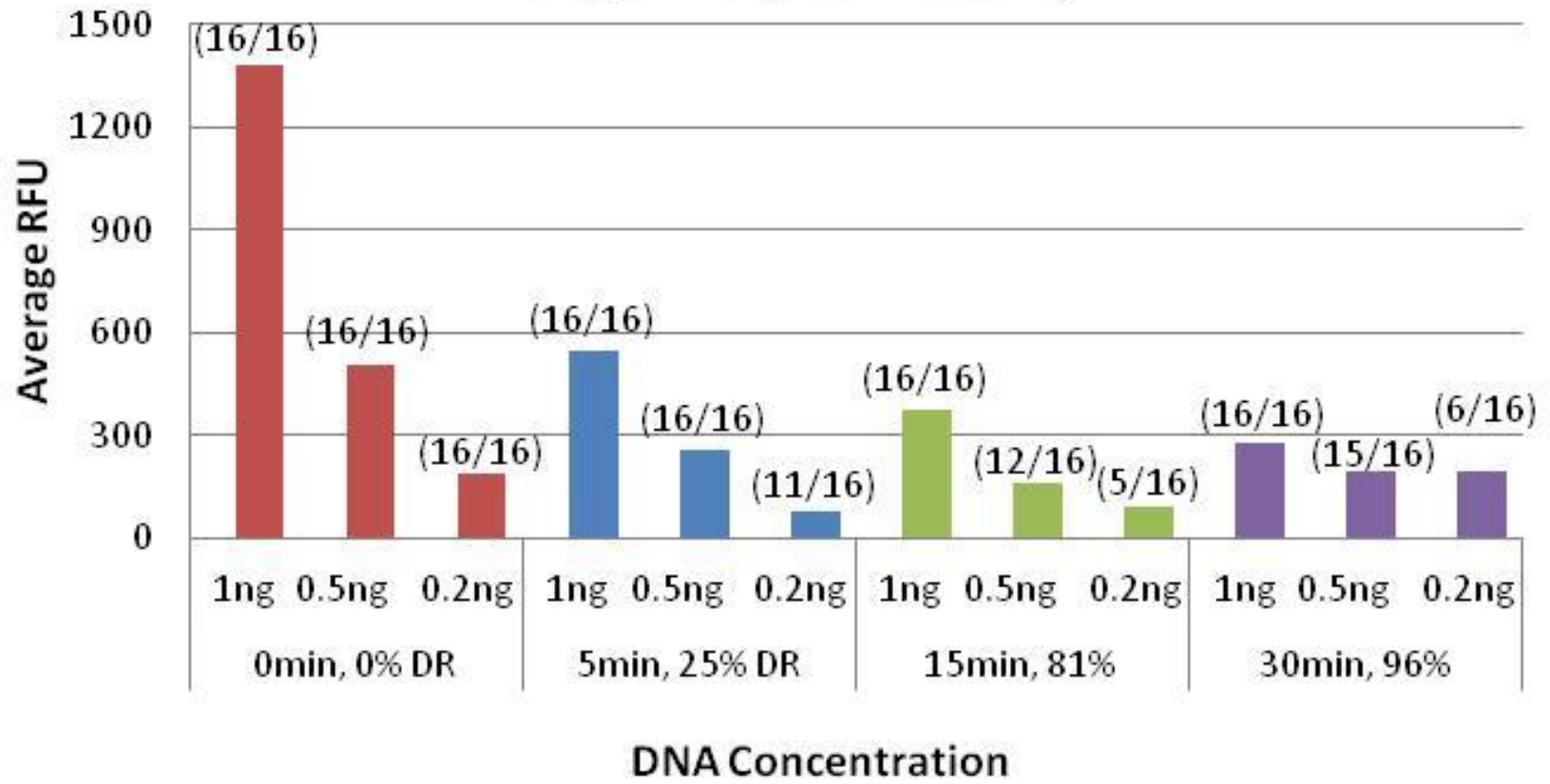
30 min  
96% DR



# DEGRADATION STUDY: DNase I

## Degradation - DNase I

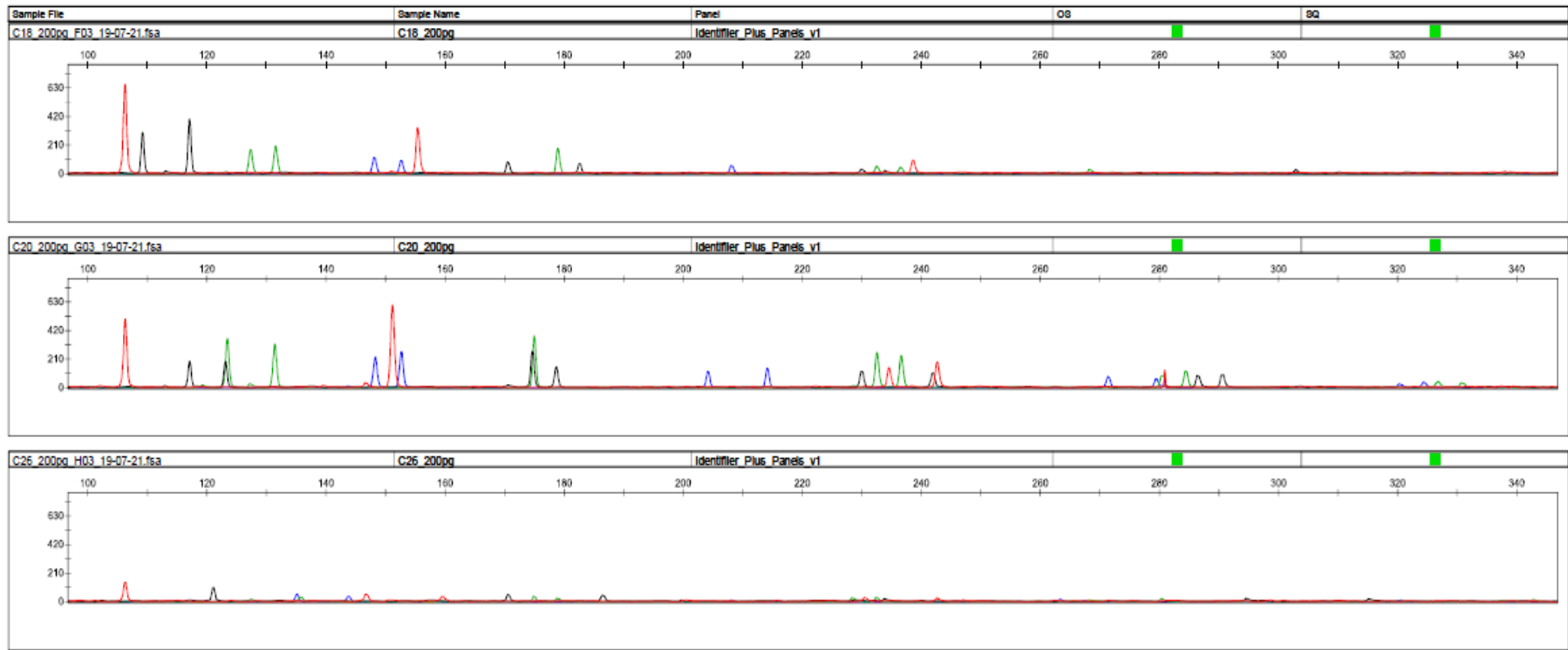
Average RFU (Loci Present)



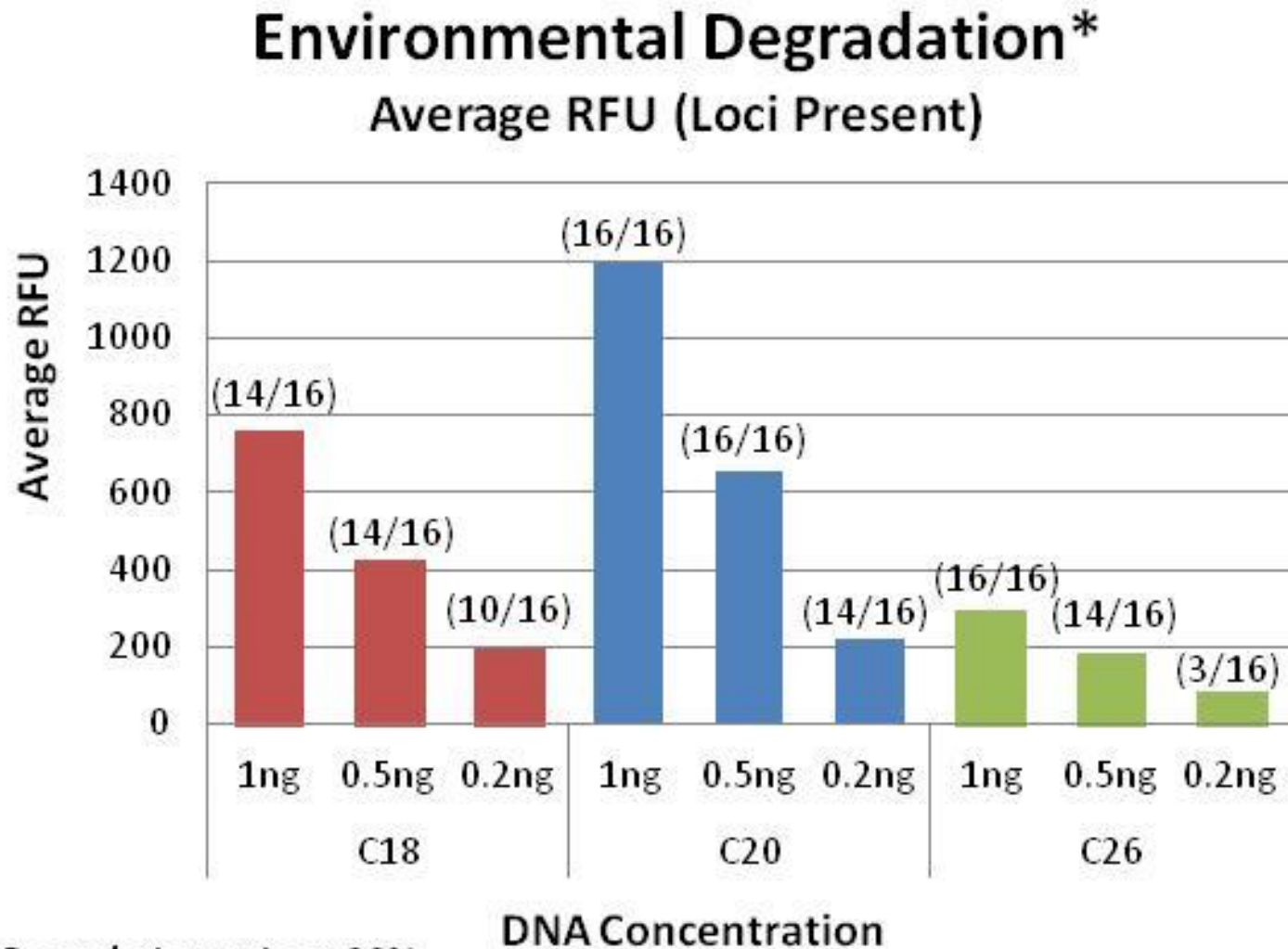
# DEGRADATION STUDY: ENVIRONMENTAL DEGRADATION: 200 PG INPUT [DNA]

AB Applied  
Biosystems  
GeneMapper 4.0

DEGRADATION GP



# ENVIRONMENTAL DEGRADATION



\* Degradation ratios > 99%



# CONCLUSION

- A dual target human qualitative / quantitative / inhibition assessment system has been developed
- Extremely sensitive:  $\sim 9$  picograms/ $\mu$ l
- Accurately predicts degradation ratio of a biological sample
- Valuable tool for deciding which DNA test kit to utilize and how much input DNA to use when processing forensically compromised samples



# Acknowledgements

Robyn Thompson  
Tess Cherlin

Anne Montgomery  
Gina Pineda  
Sid Sinha

*This material is based upon work supported by the National Science Foundation, Award Number: 1230352. Any opinions, findings, and conclusions or recommendations expressed in this publication are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.*



# Q&A

## Contact Info:

Sudhir K. Sinha, Ph.D.

[ssinha@innogenomics.com](mailto:ssinha@innogenomics.com)

#504-573-6443 office

Thank you for your time

