

RapidHIT ID System

Evaluation for Processing of Skeletal Remains

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Research & Innovation



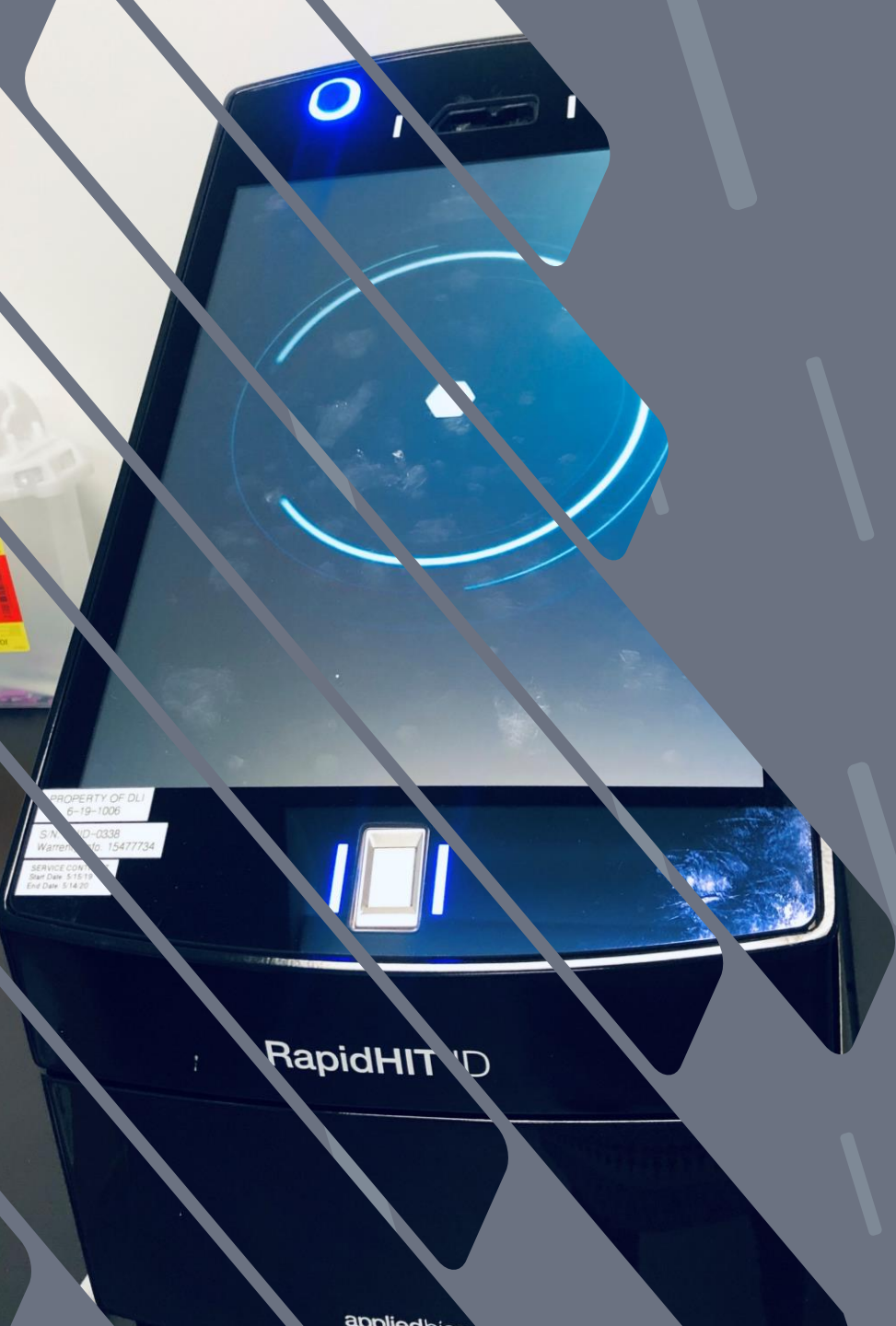
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ISO/IEC 17025:2005 and FBI QAS DNA Laboratory



A Leading Private Forensic DNA Lab
WITH THE NEWEST TECHNOLOGY AVAILABLE

Celebrating 15 Years
PARTNERING ACROSS THE US & CARIBBEAN NATIONS



RapidHIT ID System





RapidHIT ID SYSTEM

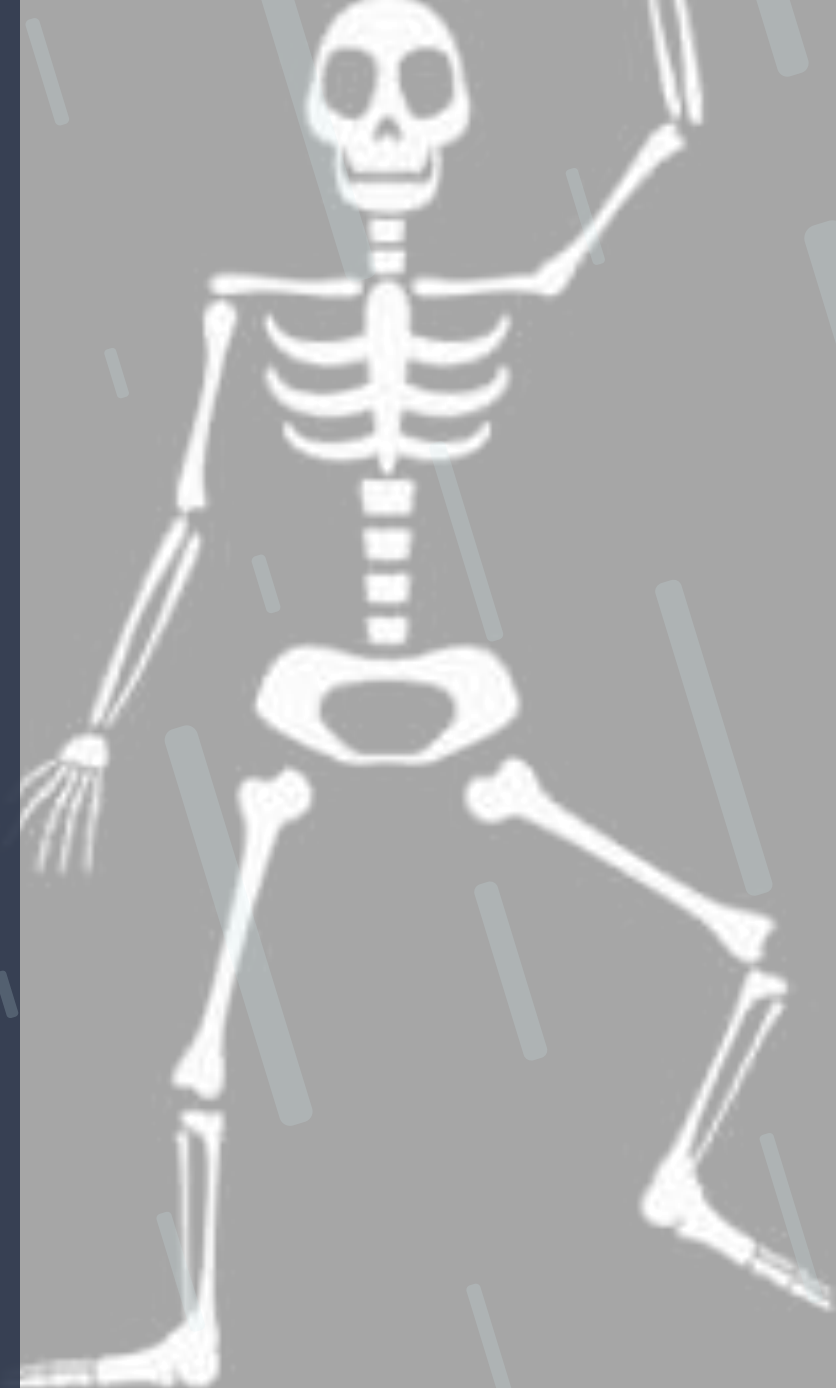
Rapid DNA

- The FBI defines Rapid DNA as “the fully automated (hands free) process of developing a DNA profile from a reference sample buccal (cheek) swab without human intervention”
- Develop a DNA profile in under two hours from a body fluid sample as investigative aid.



WHY TEST BONES USING RAPID?

- Most bone extractions take anywhere from 12 -72 hours
(laboratory dependent)
- Bone extractions are labor intensive.
- Involve extensive bone preparation.
- Require designated screening areas.



*Sensitivity
&
Stochastic Study*



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The image shows two clear plastic test tubes standing upright. Each tube contains several small, white, irregularly shaped bone fragments. The background is dark, making the white samples stand out. A white rounded rectangle with a black border is overlaid on the top left of the image, containing the text 'TESTING SCHEME' next to a double-line icon.

TESTING SCHEME

- Obtained high quality bone samples from a known source.
- Grounded bone sample into small chunk consistency.
- Prepared two sets of bone samples weighing approximately 10mg, 50mg, and 100mg.

Set 1

- 9.9mg
- 50.5mg
- 97mg

Set 2

- 10mg
- 47.3mg
- 93.7mg

- Run samples through Rapid using Intel cartridges.
- Processed raw data for average. heterozygous peak heights and sister allele balances.
- Analyzed in GeneMarker – off instrument.

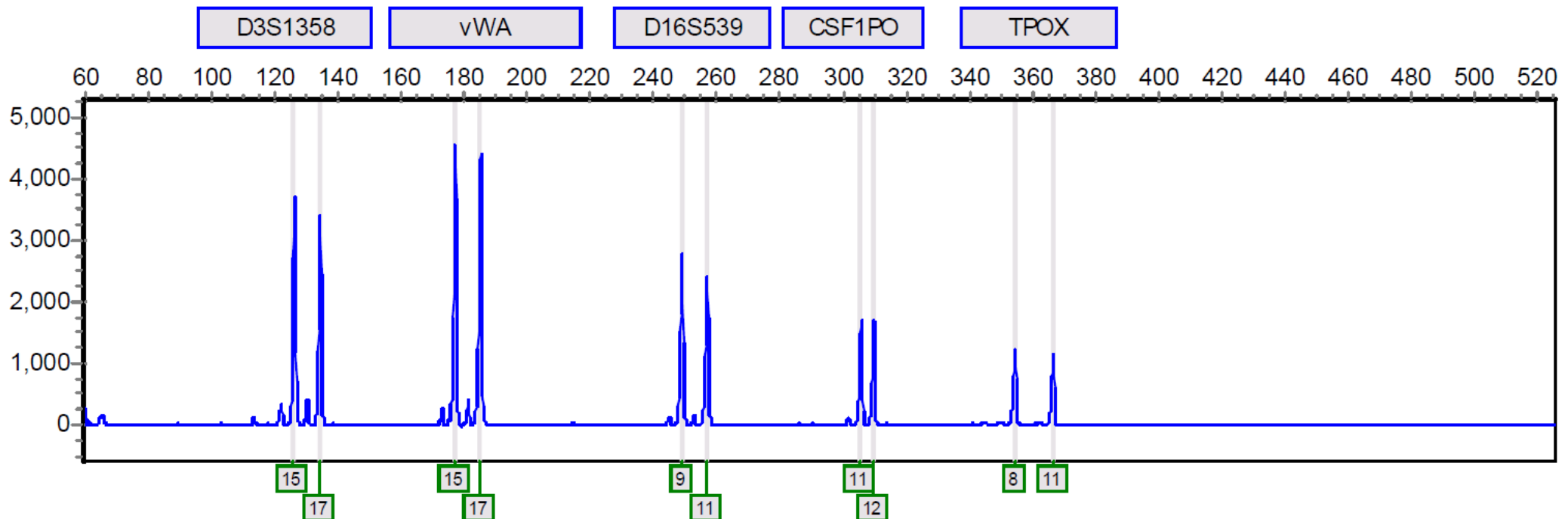


SMALL CHUNK CONSISTENCY

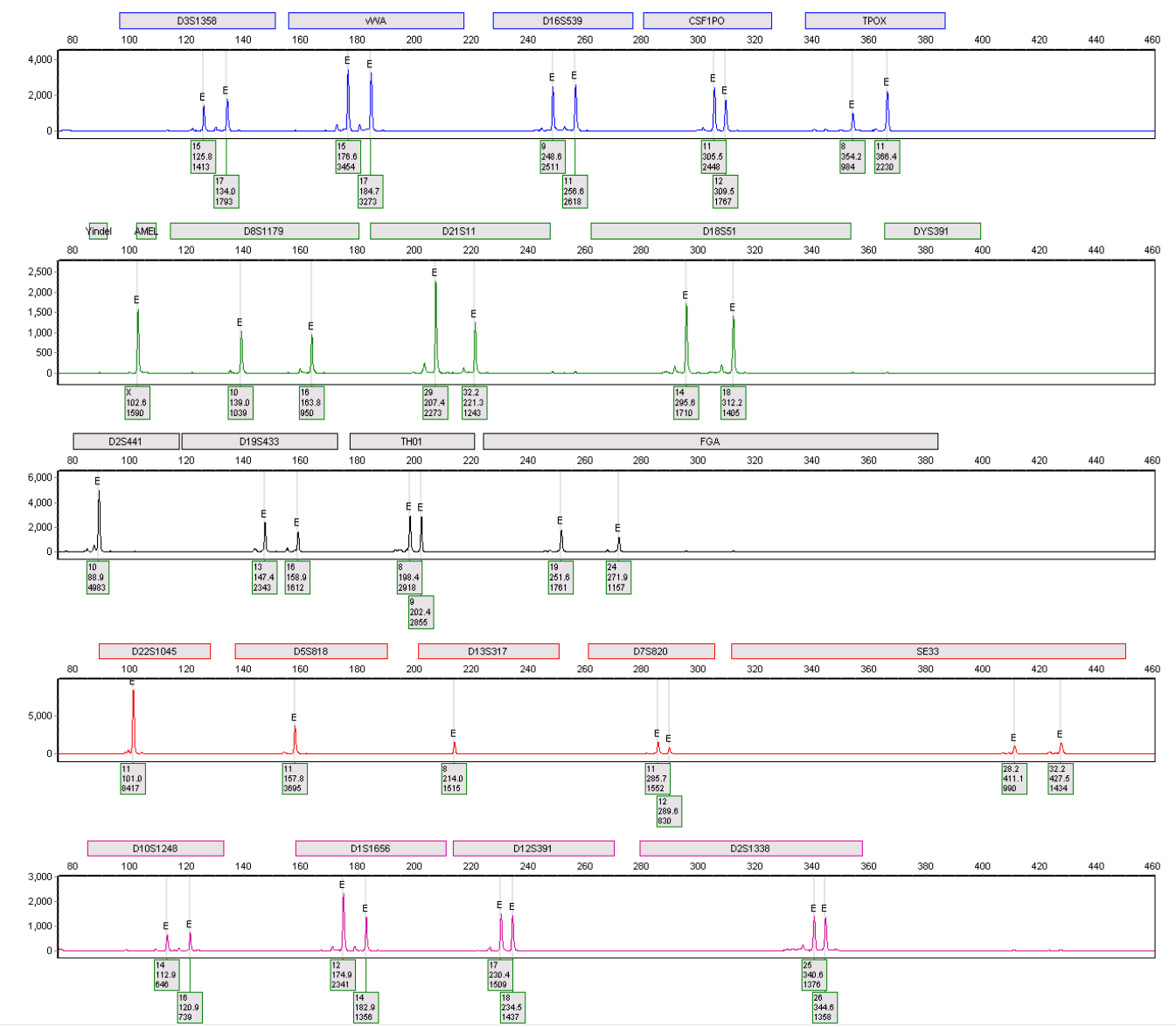
- What does this mean?
- If consistency is too fine will clog the system.
- Think of a sea salt grinder.

SO HOW IS THE DATA?

- High quality bones resulted in full DNA profiles for all amounts tested
 - 10mg, 50mg and 100mg
- High quality: recent remains not exposed to extreme environments (heat, fire, bog, acidic soil).



BONE 1 / 10MG / SET A



- Measured at 9.9mg
- Average Peak Heights:

Blue	2249.10	780.65
Green	1276.25	510.64
Yellow	2203.63	628.05
Red	1843.30	1314.60
Purple	1345.25	518.85
Overall	1807.39	898.25

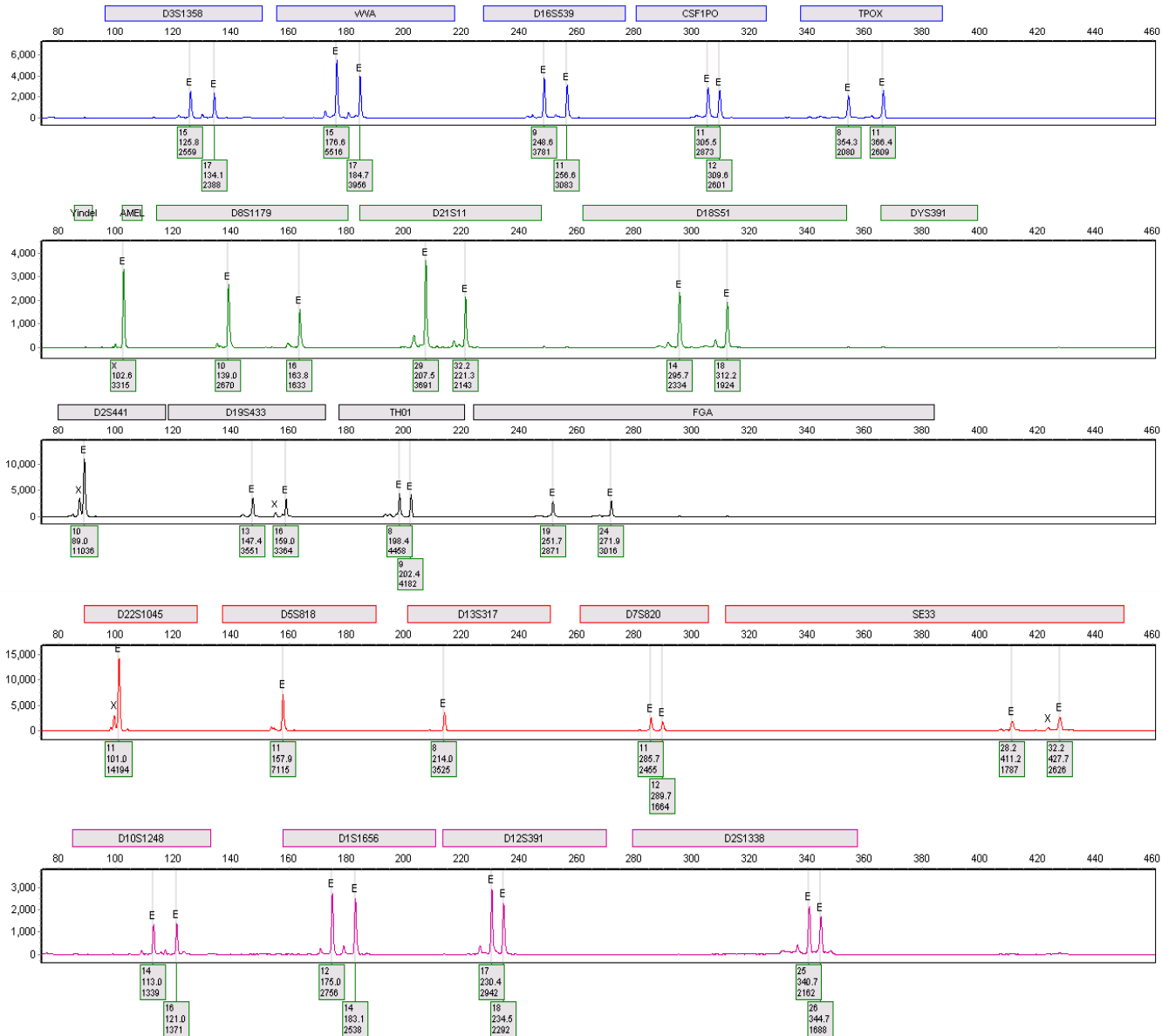
BONE 1 / 10MG /SET B



- Measured at 10.0mg
- Average Peak Heights:

Blue	2781.90	1005.90
Green	1831.38	498.59
Yellow	2965.50	577.45
Red	2417.00	1428.57
Purple	1802.38	615.08
Overall	2381.43	1007.47

BONE 1 / 50MG / SET A

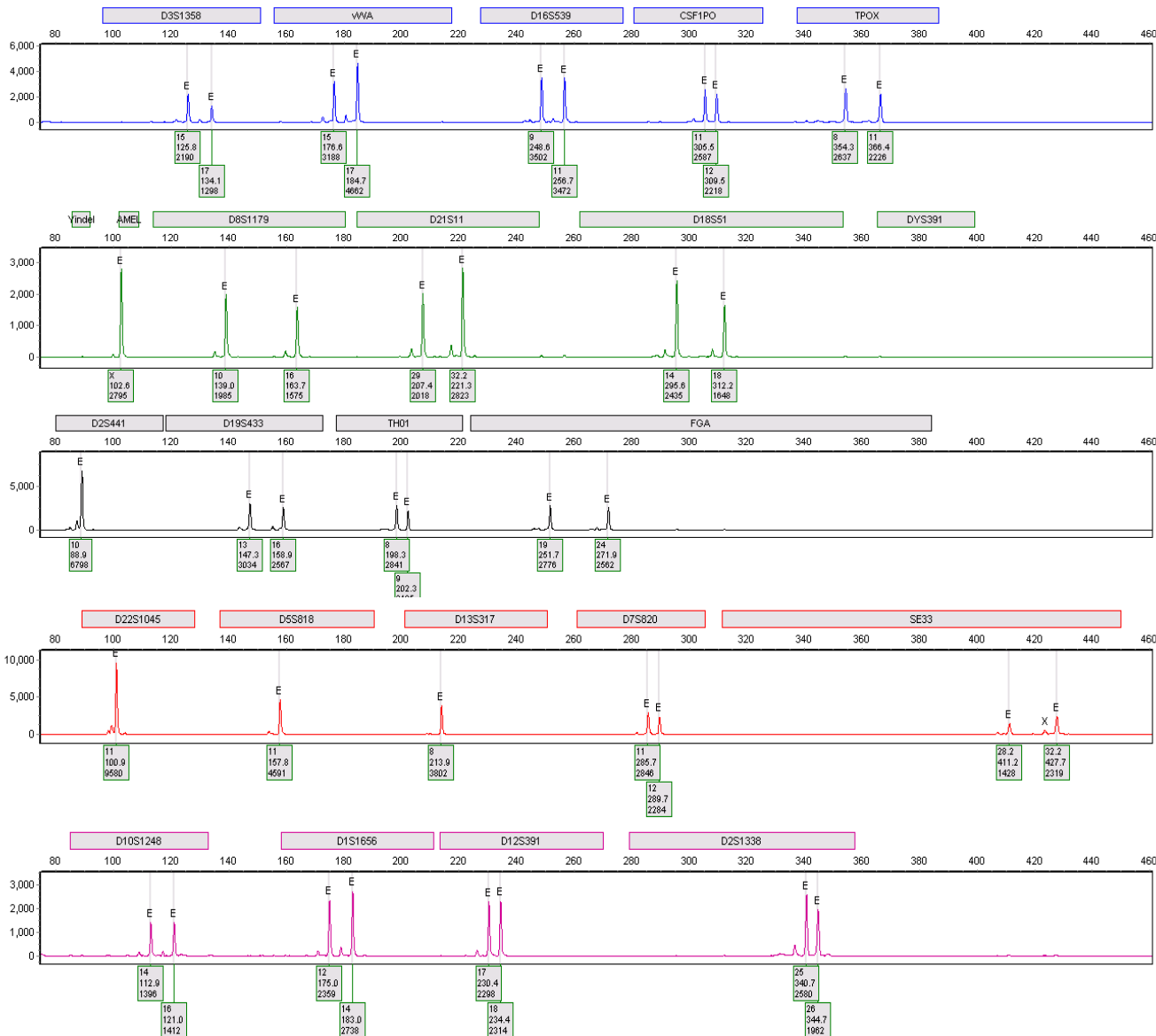


- Measured at 50.5mg

- Average Peak Heights:

Blue	3144.60	1021.74
Green	2213.75	702.03
Yellow	4059.75	1046.90
Red	3336.60	2103.32
Purple	2136.00	614.33
Overall	3002.00	1399.49

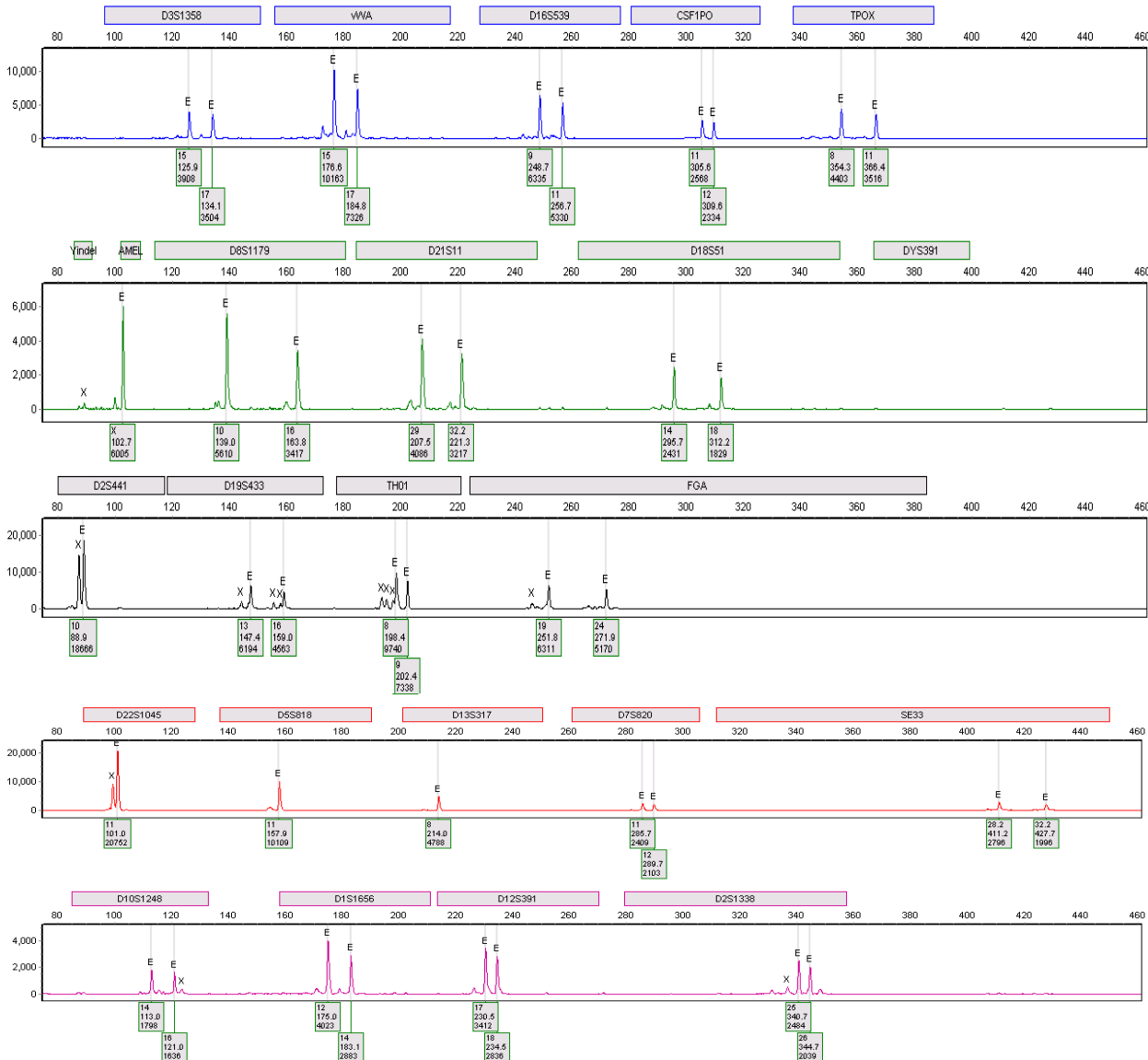
BONE 1 / 50MG / SET B



- Measured at 47.3mg
- Average Peak Heights:

Blue	2798.00	938.69
Green	1909.88	511.67
Yellow	2846.63	419.89
Red	2685.00	1168.83
Purple	2132.38	502.73
Overall	2498.66	850.72

BONE 1 / 100MG / SET A



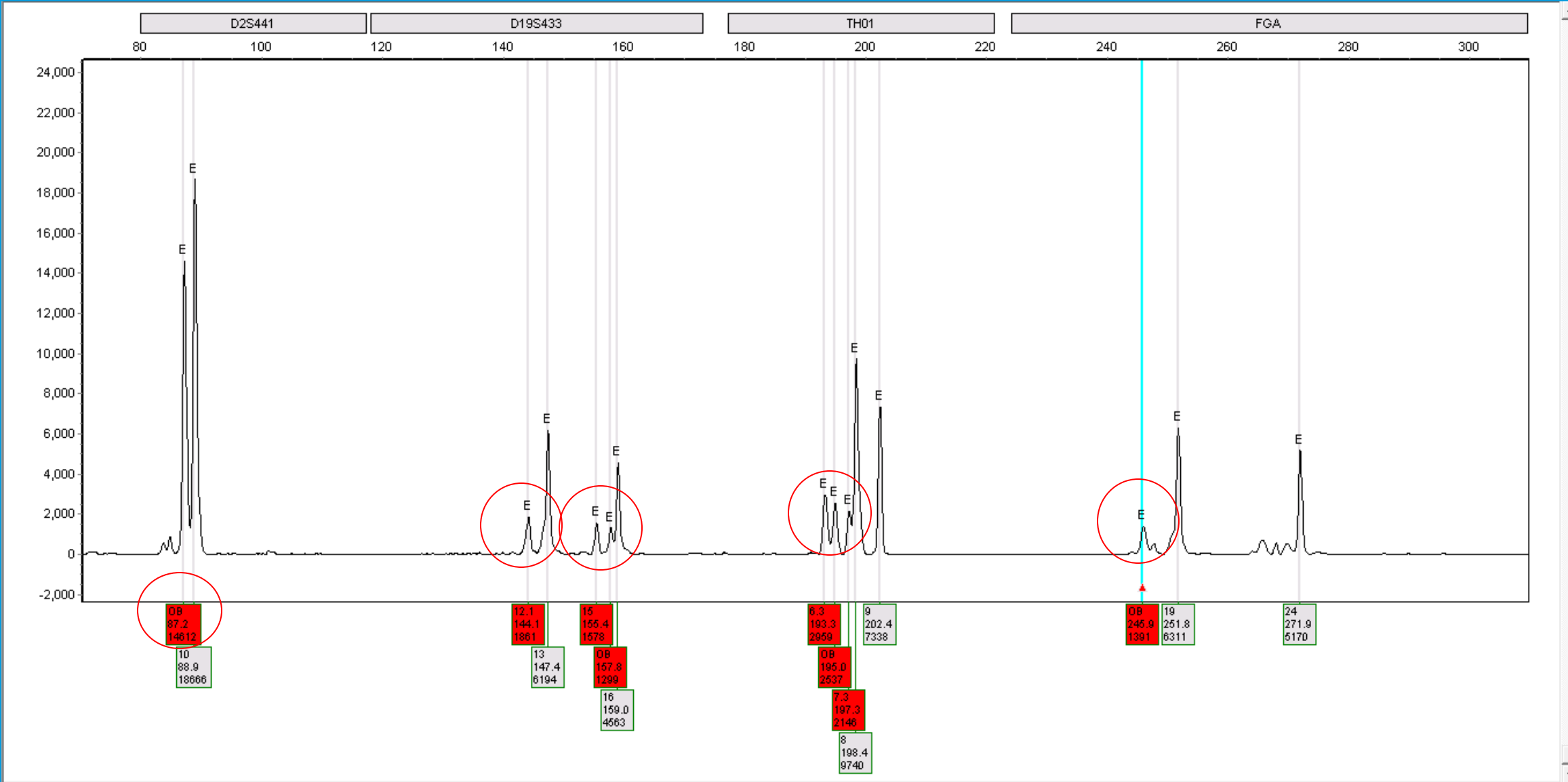
- Measured at 97.0mg

- Average Peak Heights:

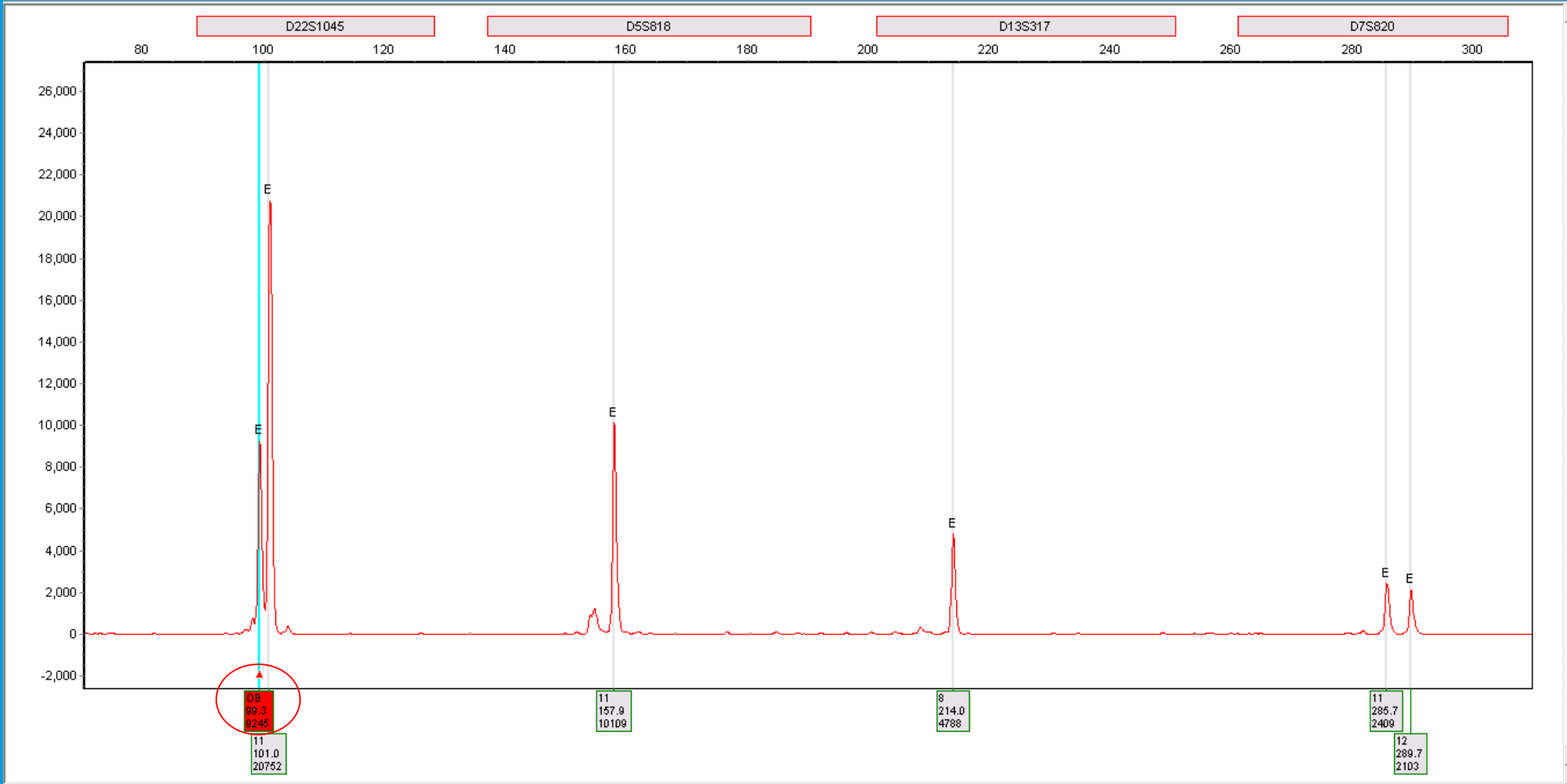
Blue	4938.70	2425.14
Green	3324.38	1138.03
Yellow	7247.75	2015.26
Red	4495.30	3296.99
Purple	2638.88	820.16
Overall	4546.09	2614.65

- Increased artefactual peaks / edits

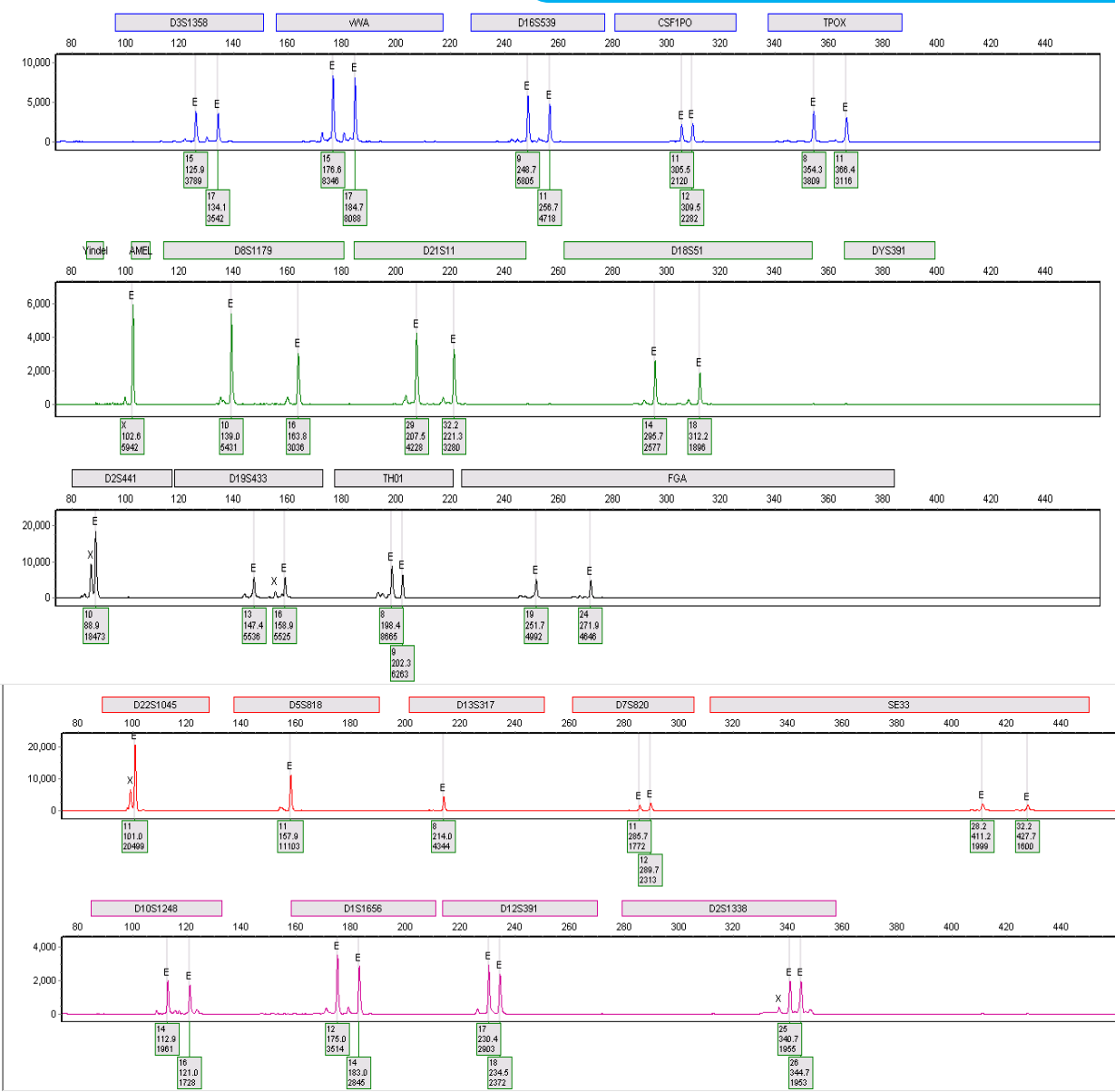
BONE 1 / 100MG / SET A



BONE 1 / 100MG / SET A



BONE 1 / 100MG / SET B

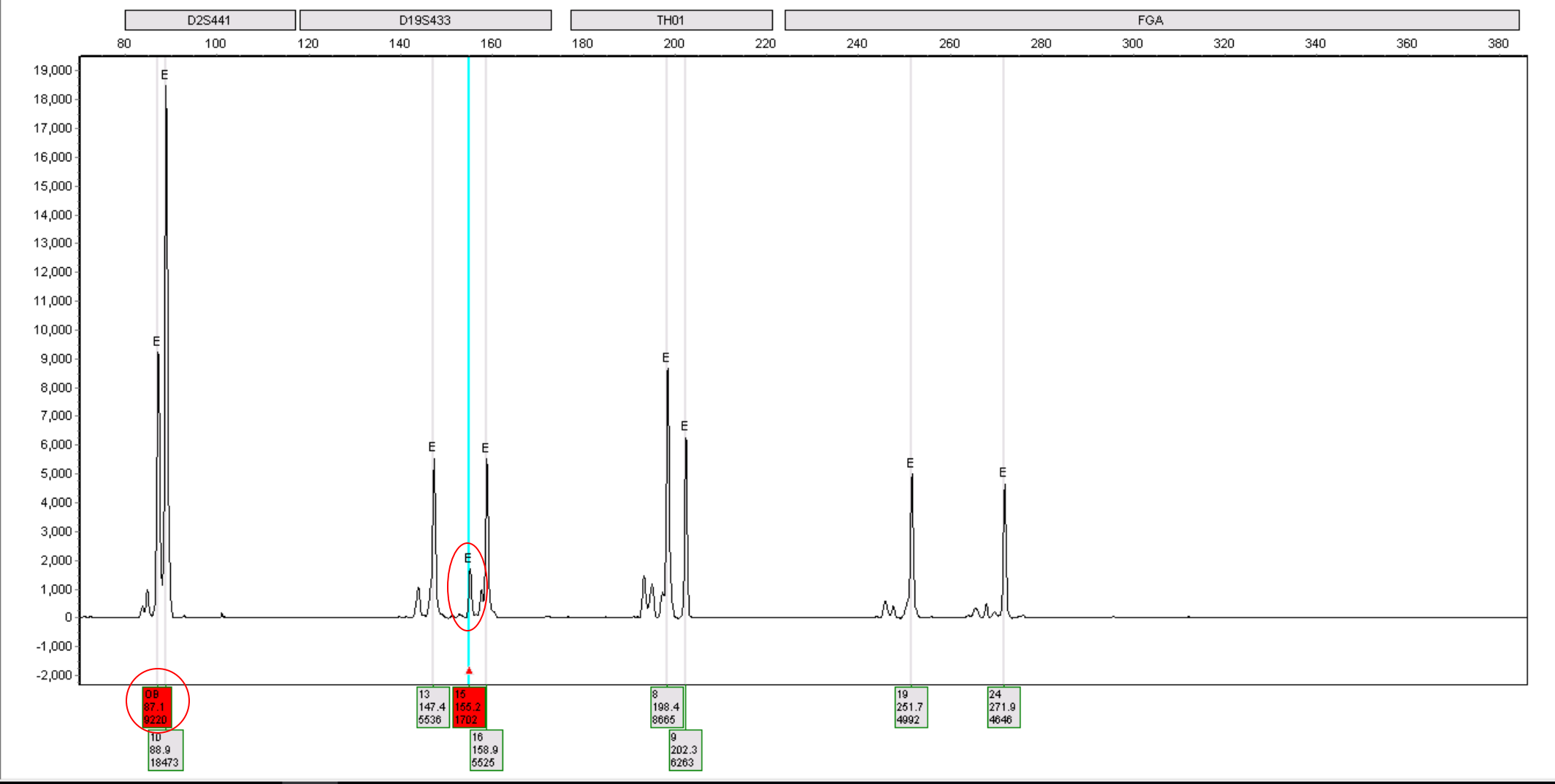


- Measured at 93.7mg
- Average Peak Heights:

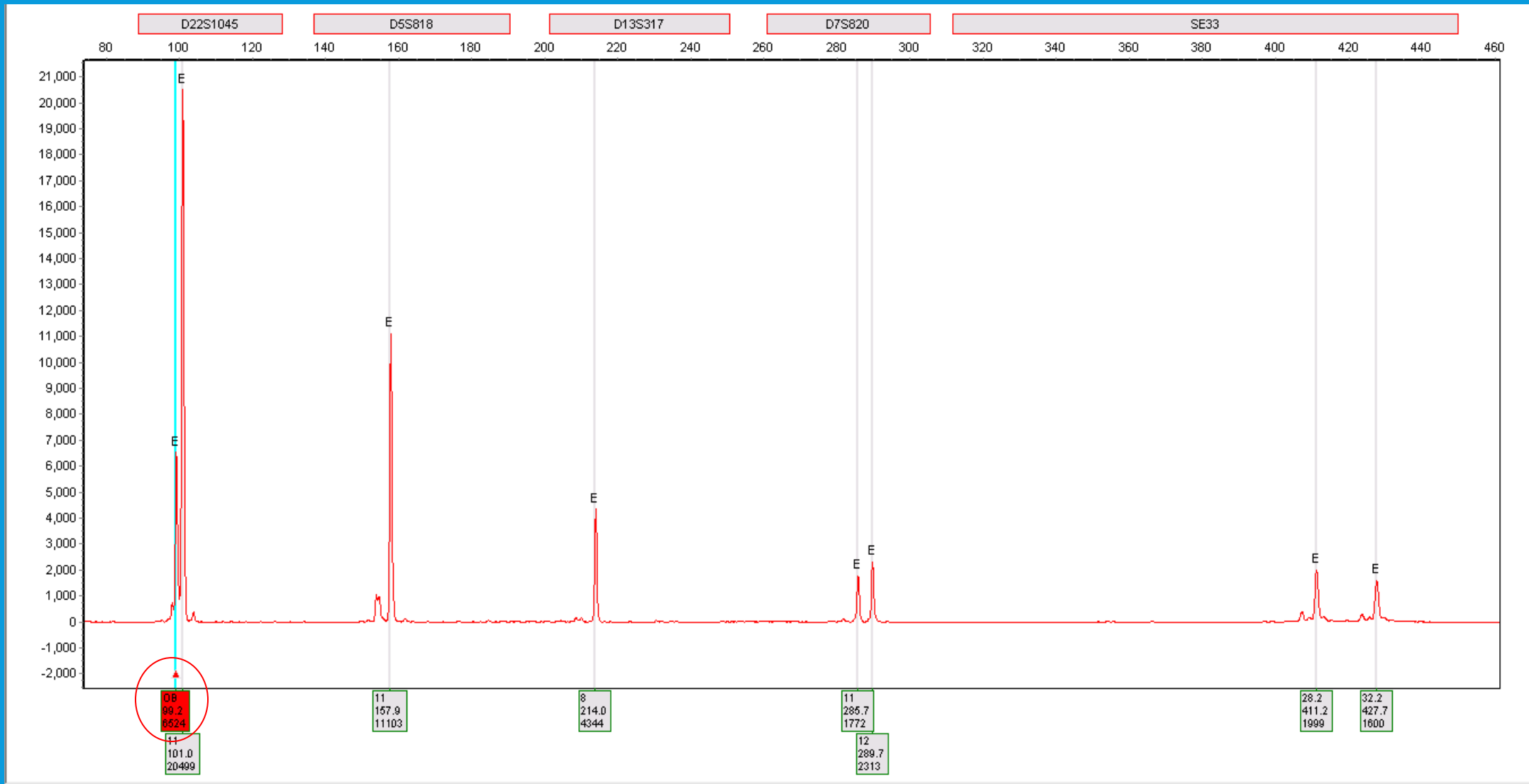
Blue	4561.50	2205.51
Green	3298.75	1081.19
Yellow	6762.50	1955.22
Red	4363.00	3429.71
Purple	2403.88	625.05
Overall	4294.68	2521.25

- Increased artefactual peaks / edits

BONE 1 / 100MG / SET B

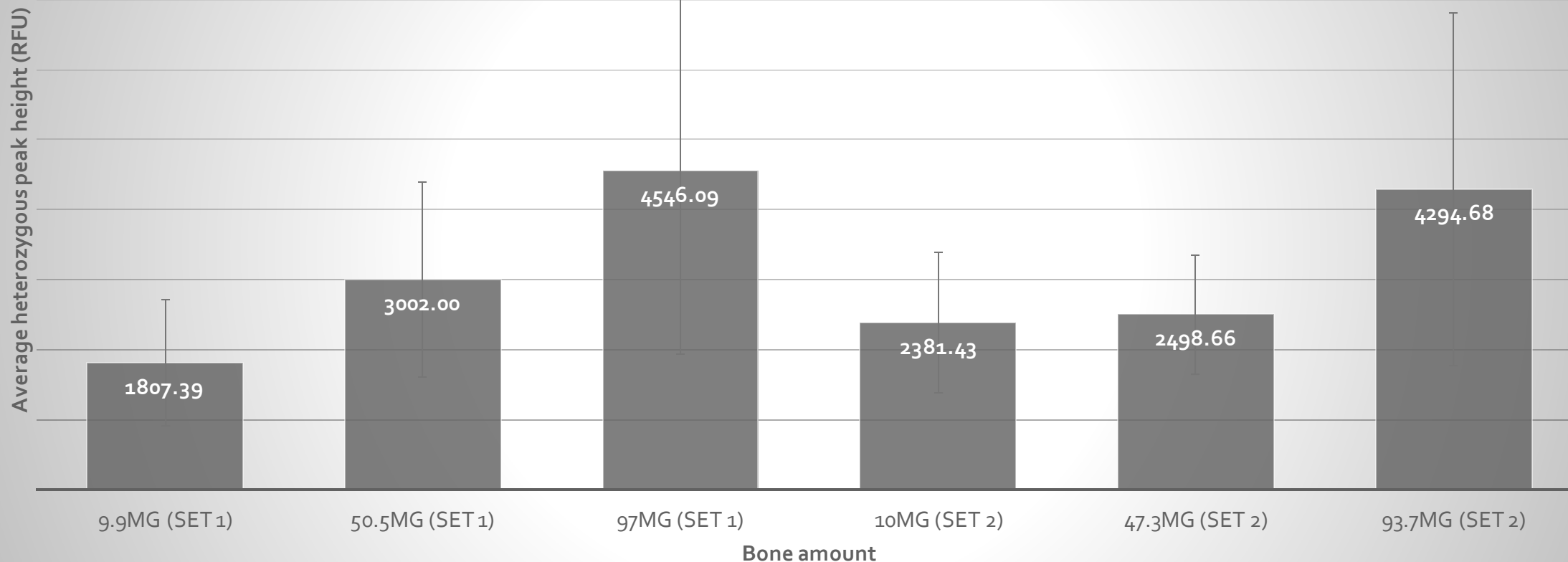


BONE 1 / 100MG / SET B

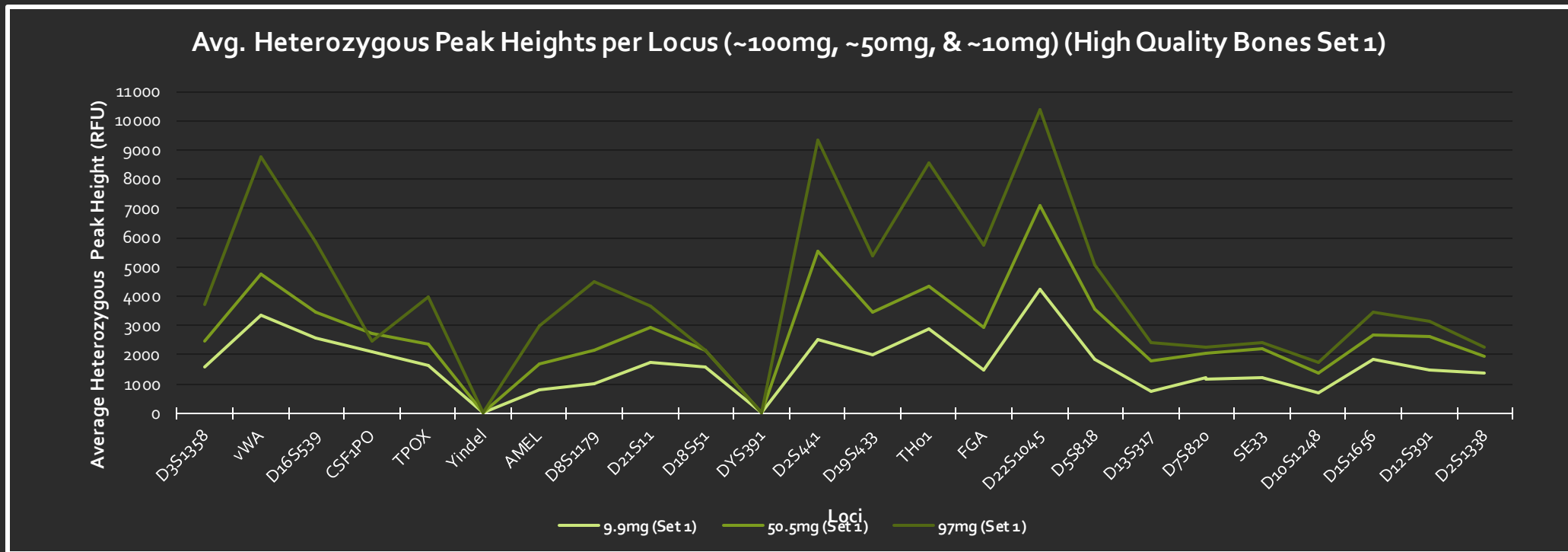




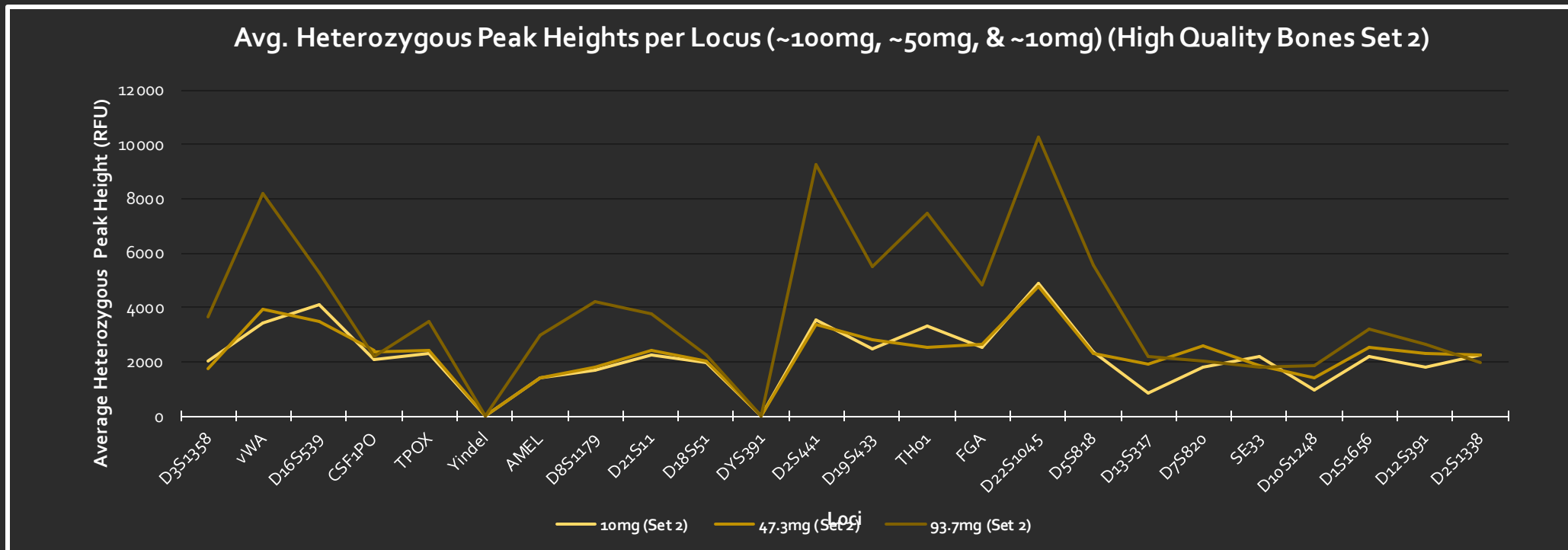
AVERAGE PEAK HEIGHTS vs BONE AMOUNT



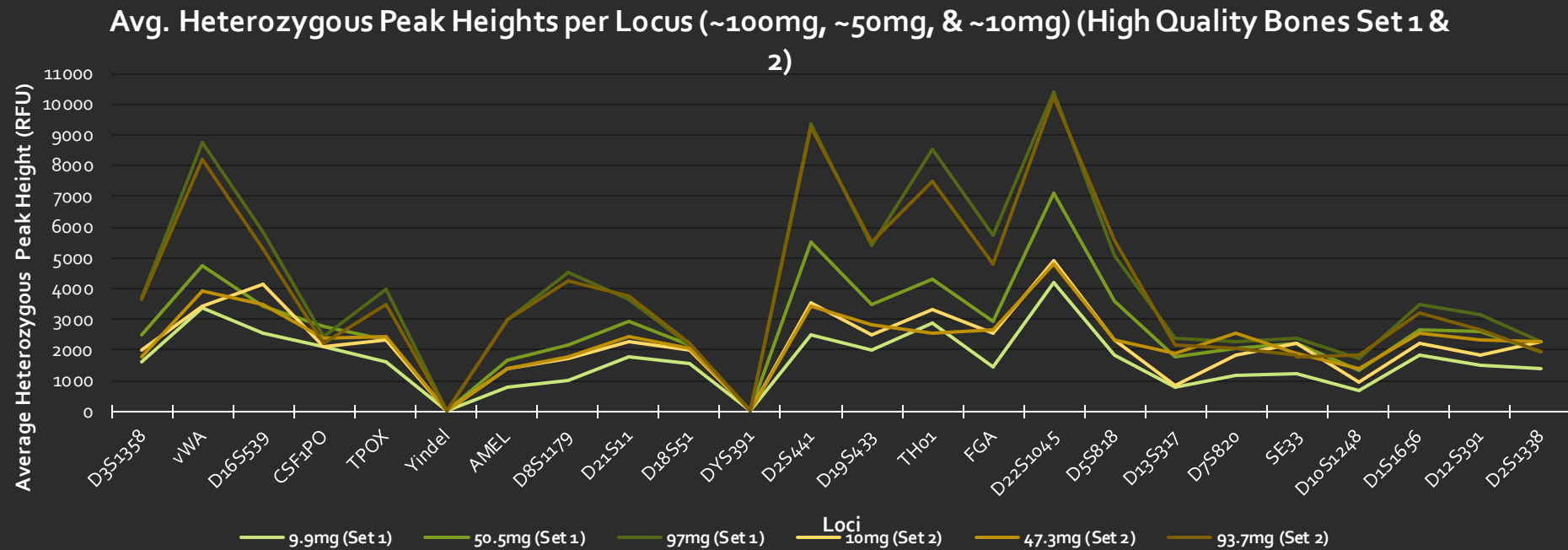
APH BY LOCUS VERSUS BONE INPUT (SET 1)



APH BY LOCUS VERSUS BONE INPUT (SET 2)



APH BY LOCUS VERSUS BONE INPUT (SETS 1 & 2)



≡ Buccal Swabs

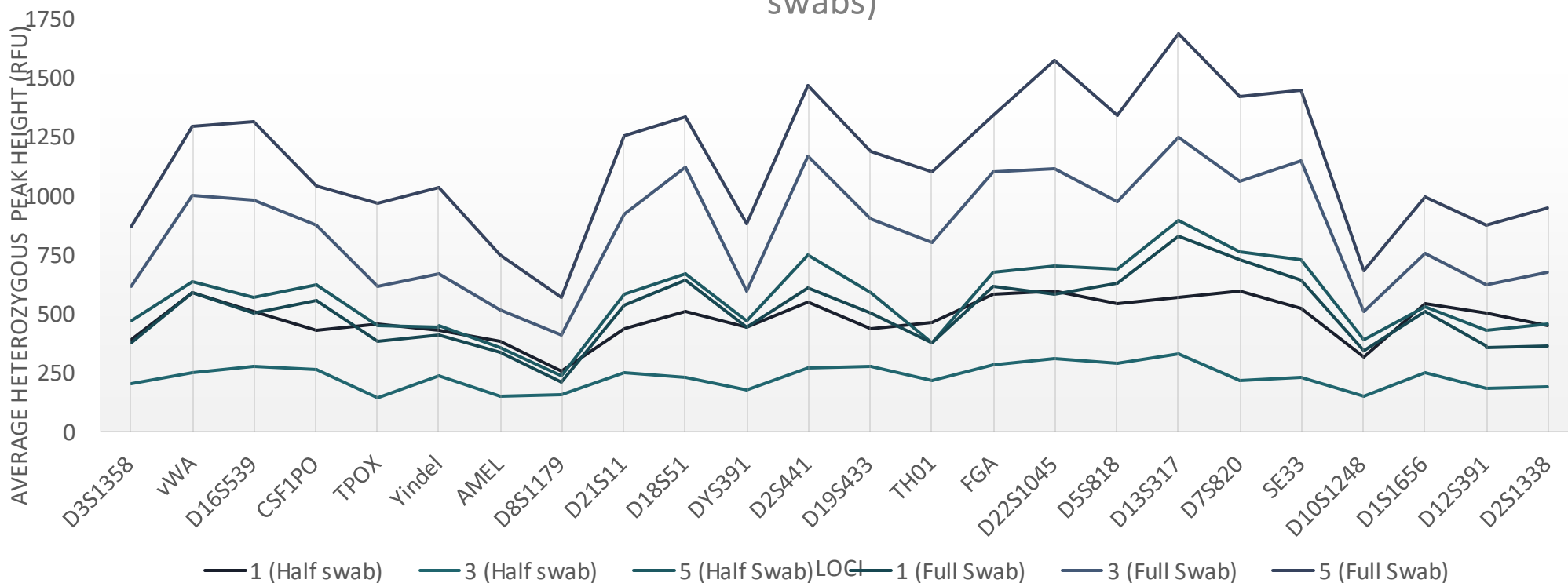
Average Peak Height vs. # of Swipes
Half and Full Buccal Swabs





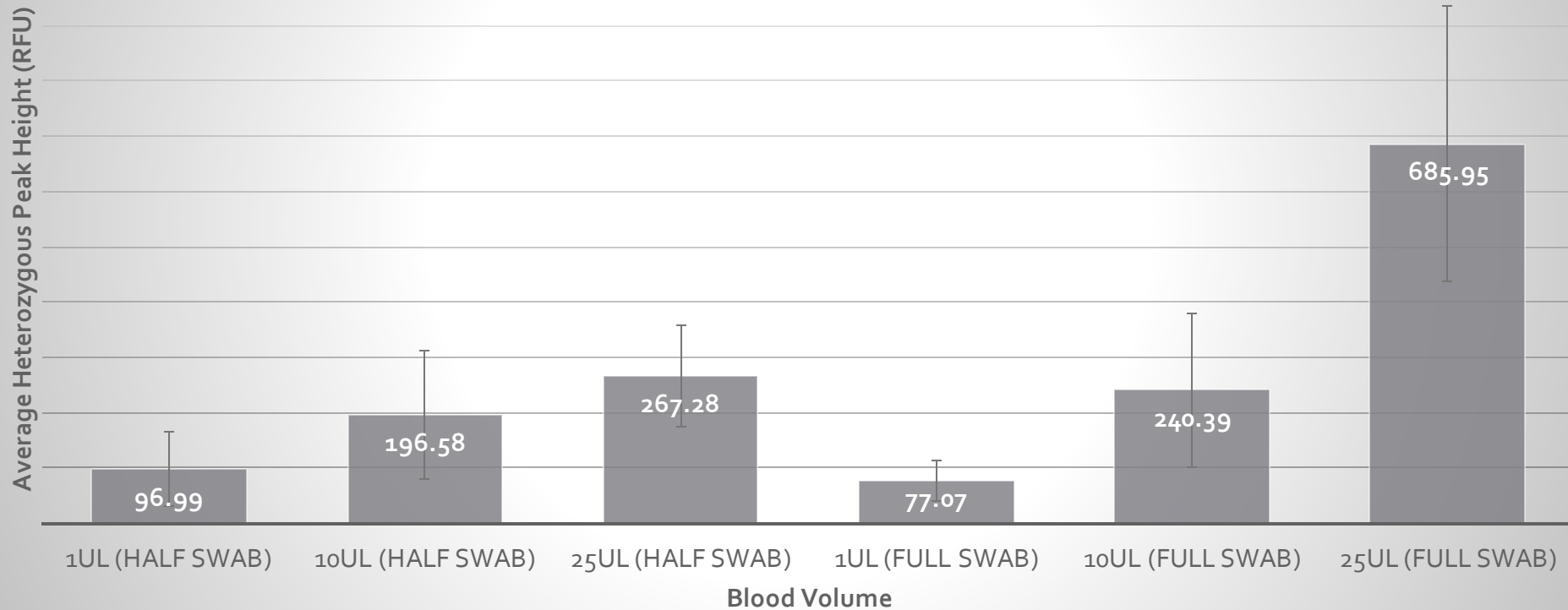
AVERAGE PEAK HEIGHT BY LOCUS VERSUS BUCCAL SWAB INPUT

Avg. Heterozygous Peak Heights per Locus (5, 3, & 1 Swipes) (Half and Full swabs)



≡ BLOOD SWABS

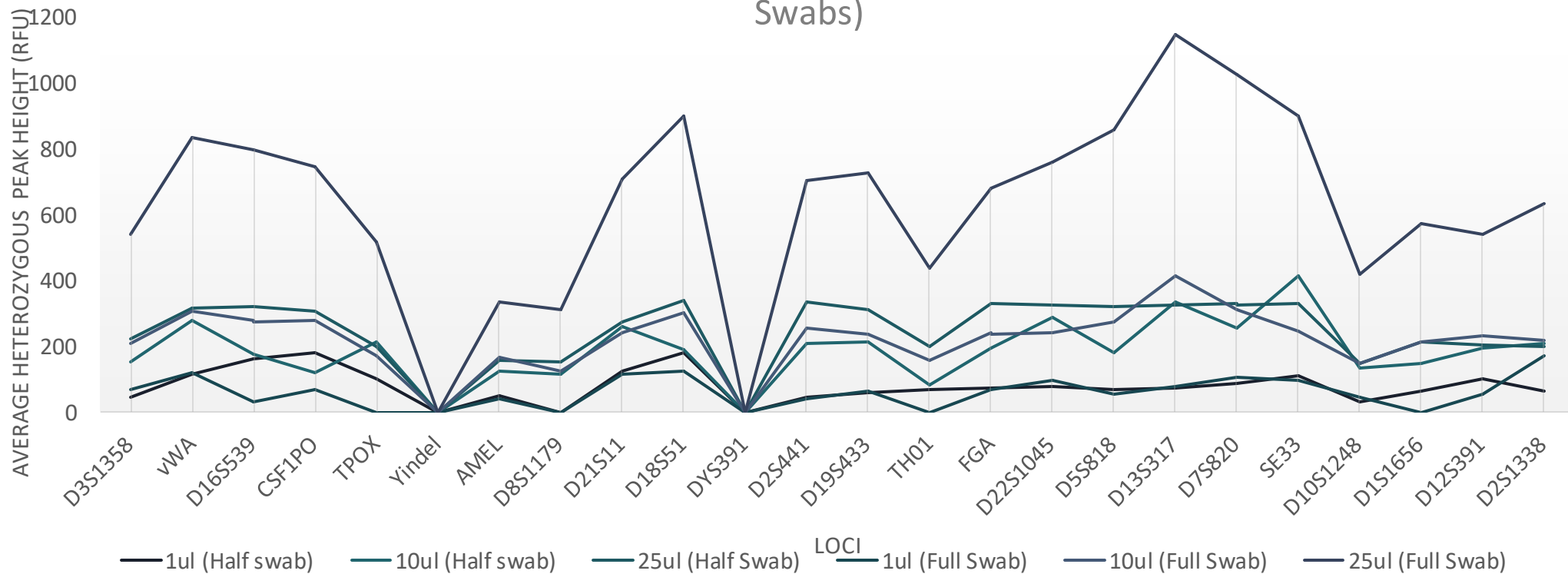
Average Peak Height vs. Blood Volume – Half and Full Swabs





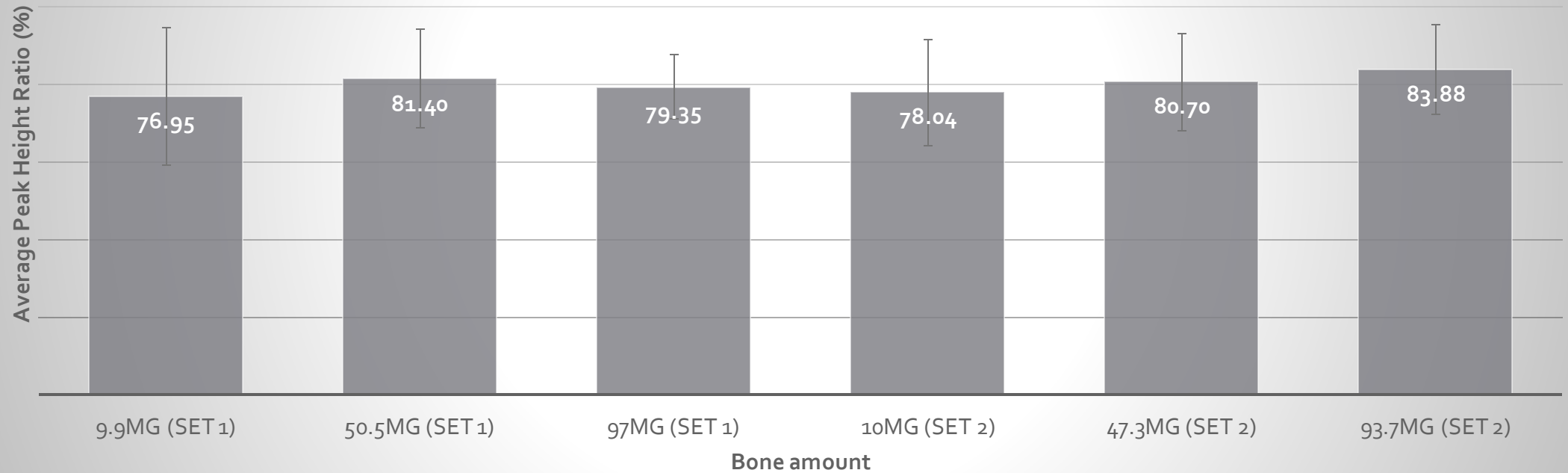
AVERAGE PEAK HEIGHT BY LOCUS VERSUS BLOOD SWAB INPUT

Avg. Heterozygous Peak Heights per Locus (25ul, 10ul, & 1ul) (Full and Half Swabs)



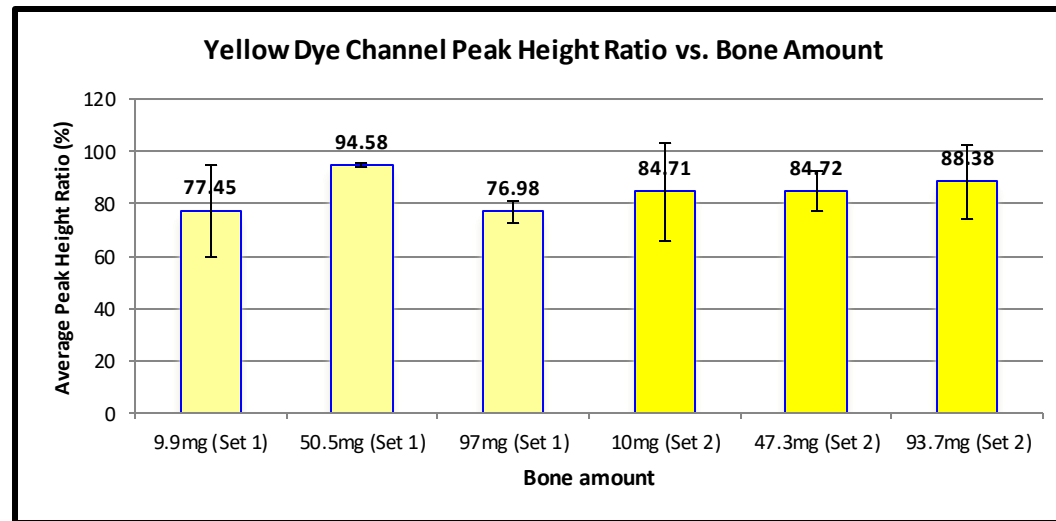
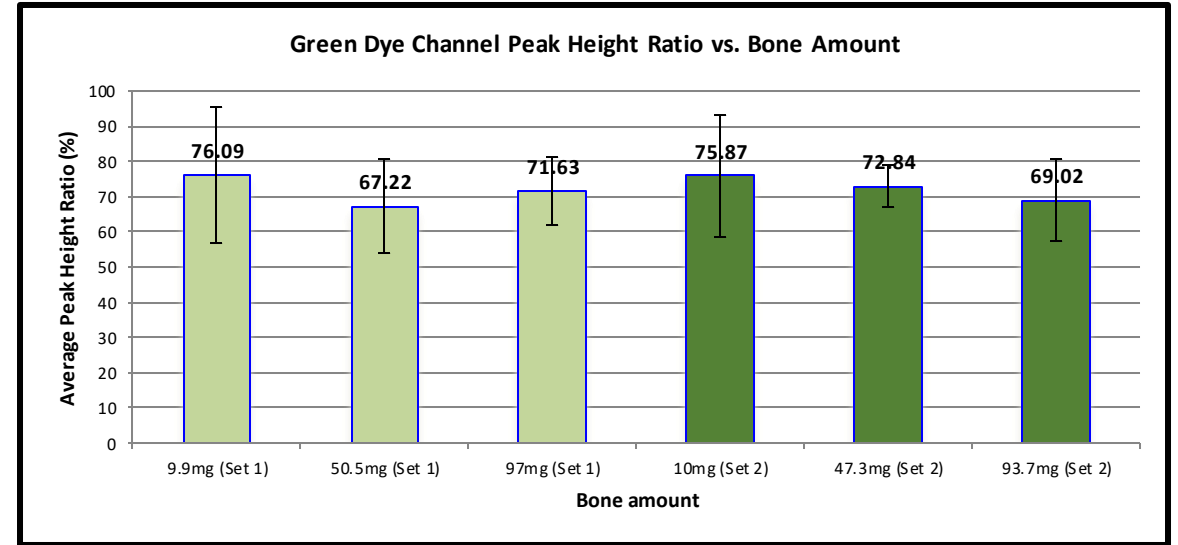
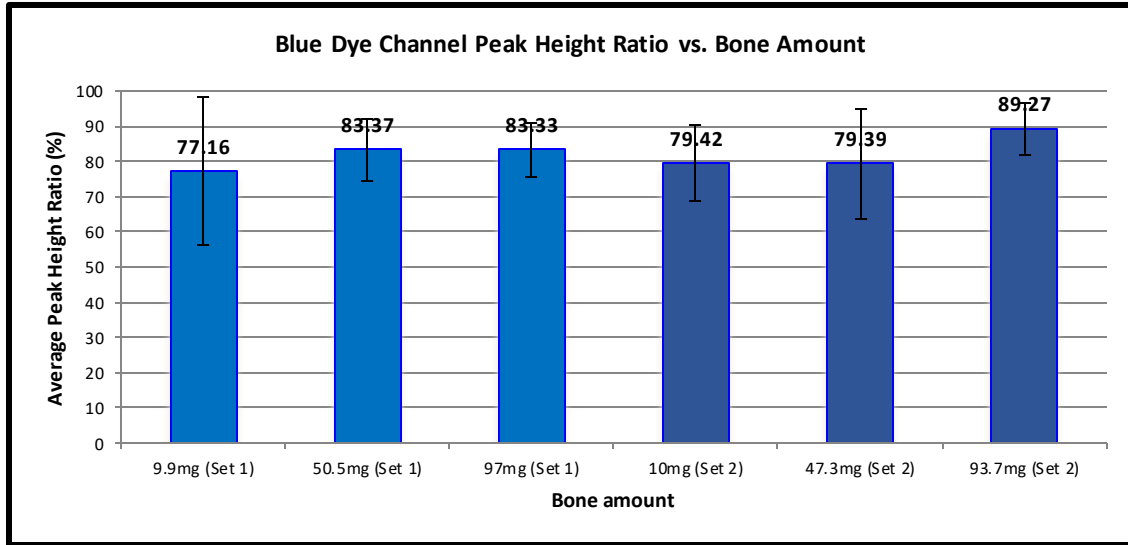
≡ PEAK HEIGHT RATIOS

Overall Peak Height Ratio vs. Bone Amount





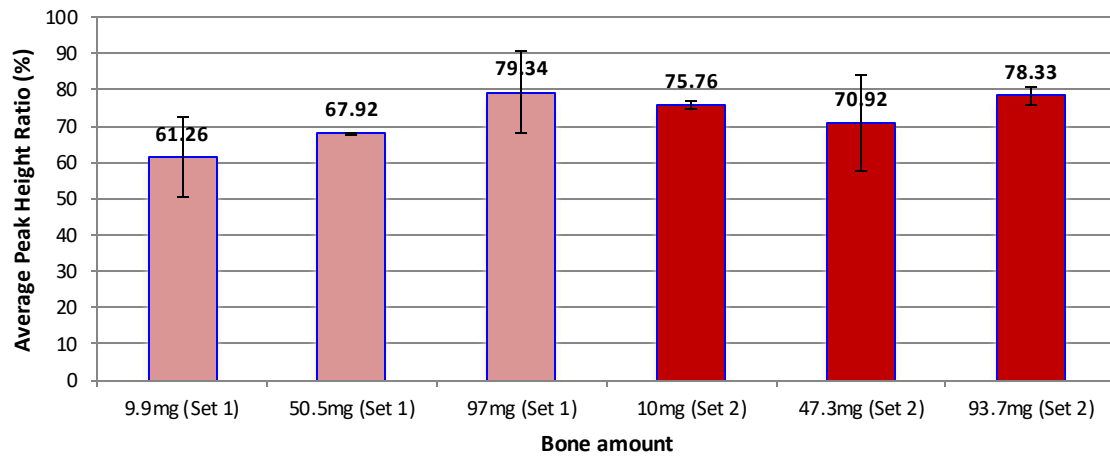
DYE CHANNEL PHR vs BONE INPUT



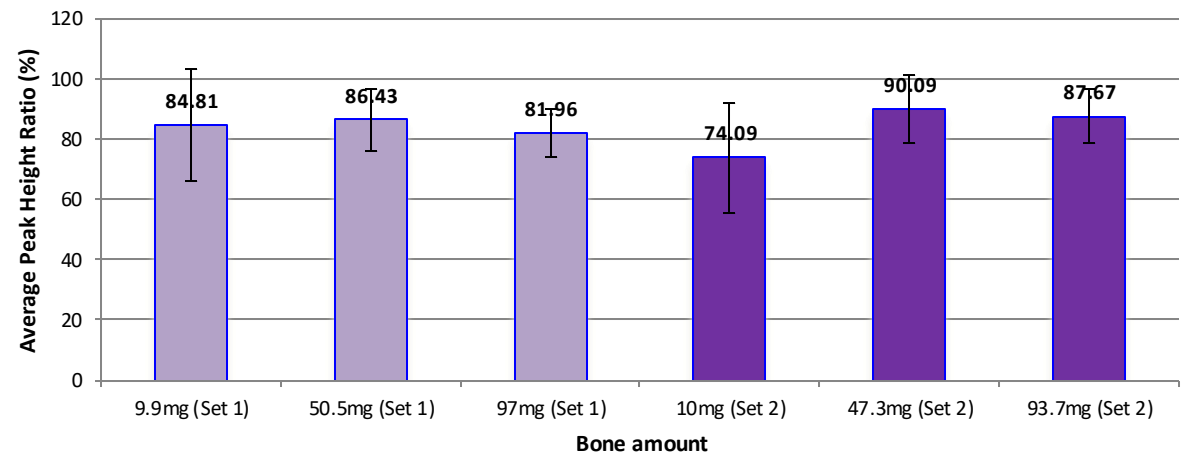


DYE CHANNEL PHR vs BONE INPUT

Red Dye Channel Peak Height Ratio vs. Bone Amount



Purple Dye Channel Peak Height Ratio vs. Bone Amount





COMPARISON TO CURRENT METHODS

Demineralization Bone Extraction Method

- Overnight incubation
- Hands on time ~3 hours
- Additional processing to obtain a fine powder
- Multiple tubes often required
- Two PCIA washes to remove inhibitors

Large Volume Extraction Method

- Overnight incubation
- Hands on time ~3 hours
- Additional Processing to obtain a fine powder
- May require more than one PCIA washes to remove inhibitors



COMPARISON TO CURRENT METHODS

TOTAL DNA RECOVERED

Current Bone Extraction Method

- 0.0112ng (170.5mg)
- 8.1732ng (453.5mg)
- 1.9880ng (544.0mg)
- 4.1636ng (644.6mg)

Large Volume Extraction Method

- 0.0350ng (160.2mg)
- 10.1466ng (450.0mg)
- 3.5760ng (496.6mg)
- 6.3350ng (679.3mg)



COMPARISON TO CURRENT METHODS

TOTAL DNA RECOVERED

Current Bone Extraction Method

Average ~0.006ng/mg of bone

Large Volume Protocol Method

Average ~0.009ng/mg of bone

RapidHIT Inputs Tested

- 10mg, ~0.06ng to 0.09ng
- 50mg, ~0.3ng to 0.45ng
- 100mg, ~0.6ng to 0.9ng



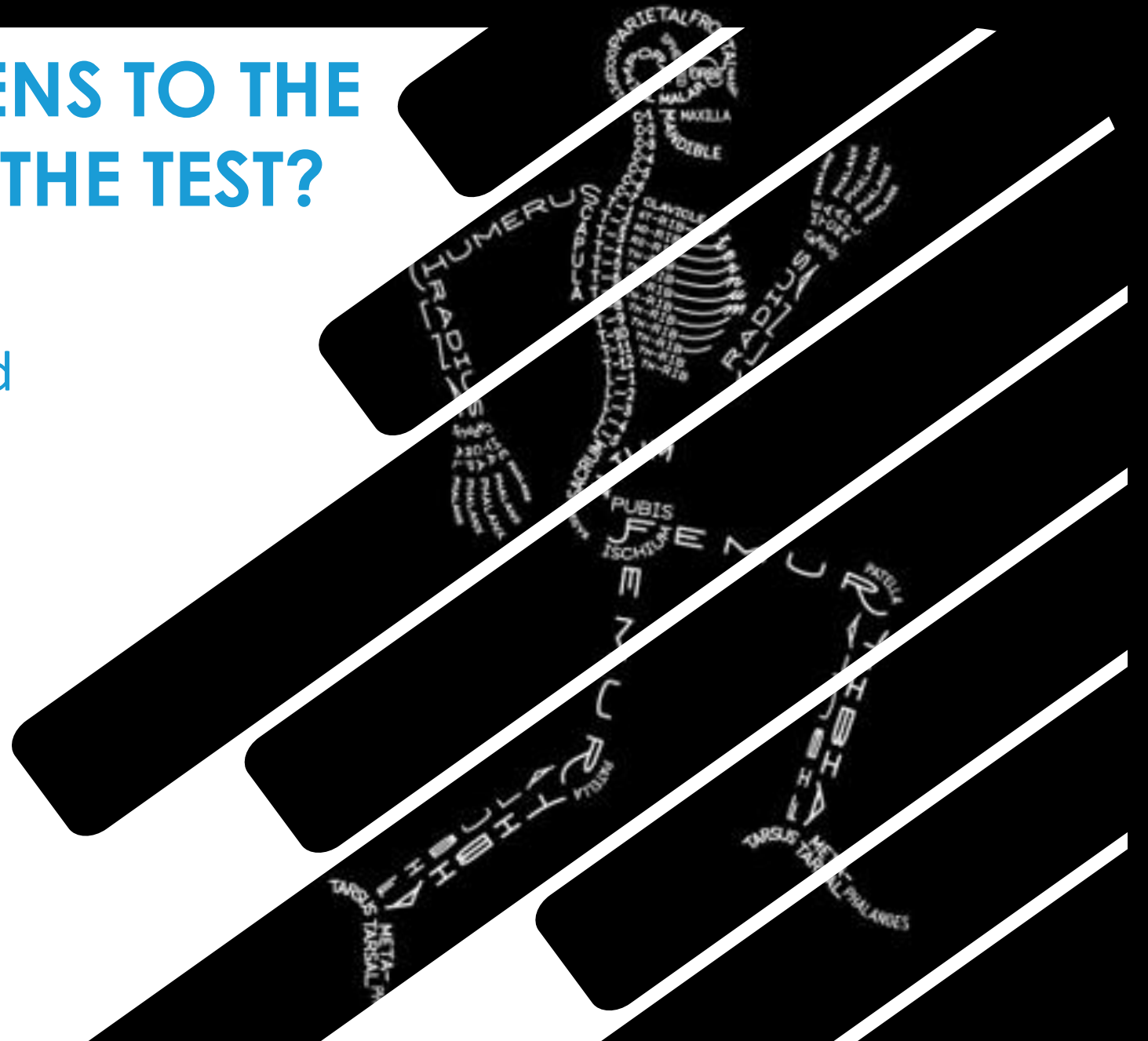
WHAT ABOUT QUALITY?

- All samples had the correct profiles obtained.
- Multiple replicates of same bone source produced consistent profiles.
- No signs of contamination.



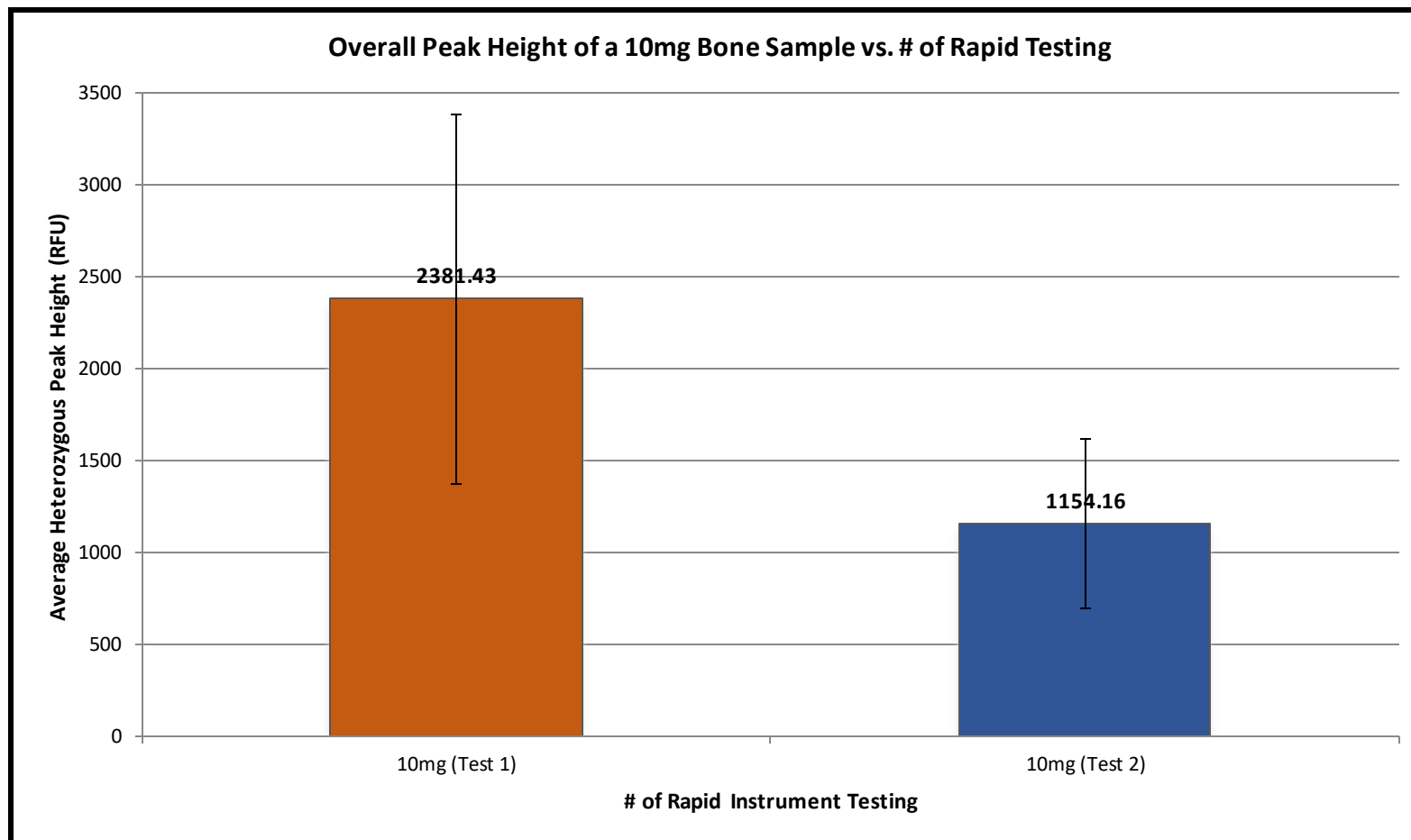
WHAT HAPPENS TO THE BONE AFTER THE TEST?

- Bone can be removed from the cartridge after testing.
- Bone can be reanalyzed in a new cartridge.



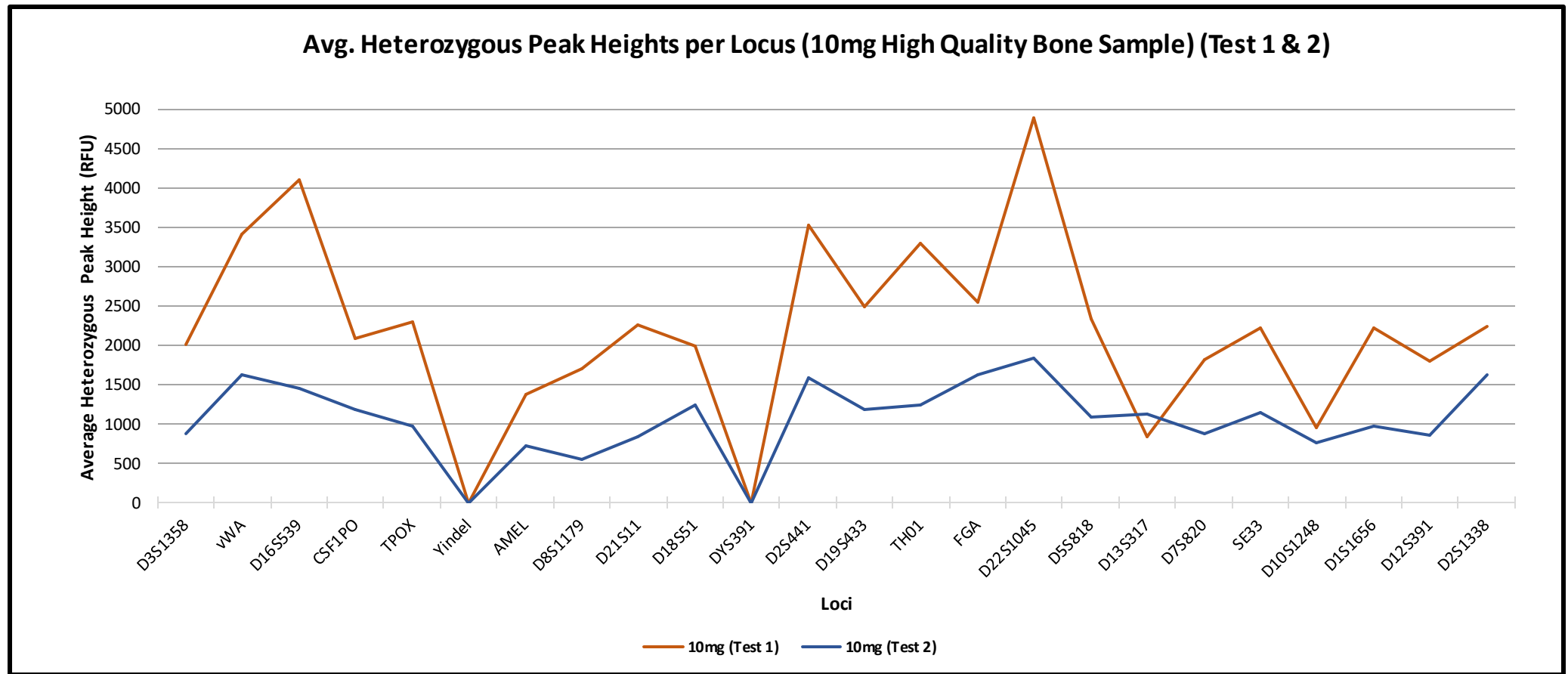


MULTIPLE TESTING OF A BONE SAMPLE THROUGH RAPIDHIT ID SYSTEM USING INTEL CARTRIDGES





MULTIPLE TESTING OF A BONE SAMPLE THROUGH RAPIDHIT ID SYSTEM USING INTEL CARTRIDGES





OTHER OPTIONS

**Comparable Results
Obtained for High Quality
Bones From:**

- **Bone Extract**
- **Partially digested
(demineralization buffer)
bone chunks.**





ADDITIONAL TESTING

Low Quality Bones

- Evaluate bone chunks vs partially digested bone chunks vs bone extract



*Uses for Rapid
Testing of Bones*



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REASSOCIATION

Statistical analysis of:

- Highly fragmented remains
- Disaster Human Identification
- Rush Cases



≡ Kinship Analysis

Statistical analysis of:

- Parent/Child
- Siblings
- Half-Sibling Relationships



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Snapshot: S&T's Rapid DNA Technology Identified Victims of California Wildfire

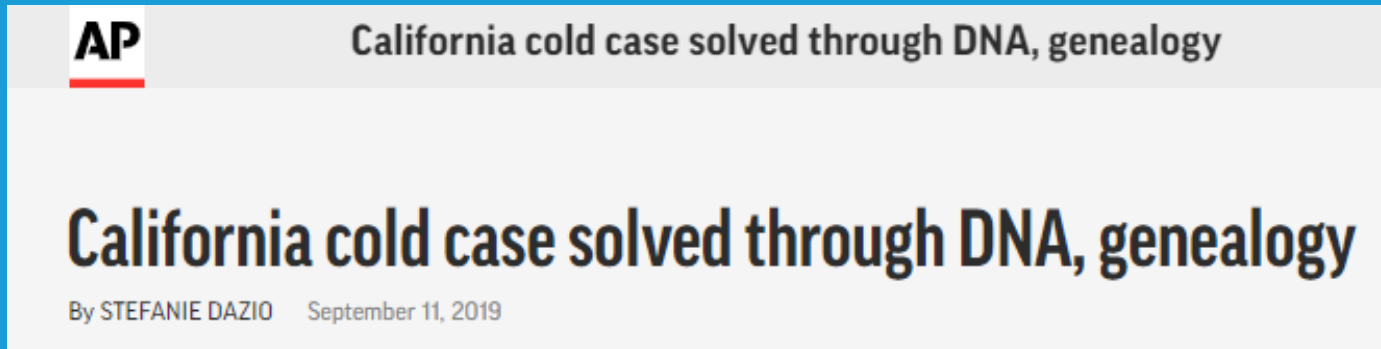


Release Date: April 23, 2019

- Fall of 2018
- 85 victims to Camp Fire Wildfire
- Funded in part by the Department of Homeland Security Science and Technology Directorate
- 85% of the victims successfully identified using Rapid technology
- Only 2 victims unaccounted for as of February 2019
- Two phases
 - Test samples from remains
 - Test samples from potential family members

<https://www.dhs.gov/science-and-technology/news/2019/04/23/snapshot-st-rapid-dna-technology-identified-victims>

POTENTIAL APPLICATION?



- 1972 Homicide of 11-year old
 - Suspect linked through genealogy, died in 2003
- Body exhumed for direct comparison to DNA results

With new investigative avenues for cold cases may see an increased need to process skeletal remains for direct comparisons

<https://www.apnews.com/1e499329875a42c09055b6511103dadc>

Thank You!

Special thanks to
Thermo Fisher
& the team at
DNA Labs International

Send all inquires to:
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