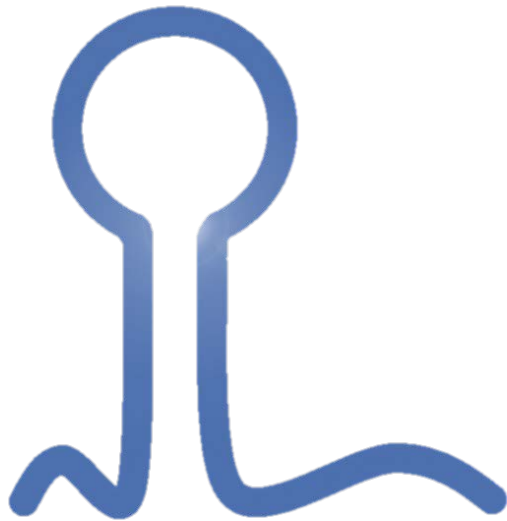


Little Stains, Lots of Problems



**Carrie Mayes, BS; Sarah Seashols-Williams, PhD;
Sheree Hughes-Stamm, PhD**

Department of Forensic Science

Sam Houston State University

Huntsville, TX



VCU

VIRGINIA COMMONWEALTH UNIVERSITY



**Sam Houston
State University**

Role of funding

This study was partially funded by a Graduate Research Fellowship Award #2016-DN-BS-001 (National Institute of Justice, Office of Justice Programs, U.S. Department of Justice). The opinions, findings, conclusions, or recommendations expressed in this presentation are those of the authors and do not necessarily reflect those of the National Institute of Justice.

Statement of the problem

- Body fluid identification (BFID) often undervalued in crime labs
- Current methods either consume or dilute sample
 - Small samples are not being tested for body fluid
- Limited number of body fluids currently being tested
 - Blood, semen, and saliva



Statement of the problem

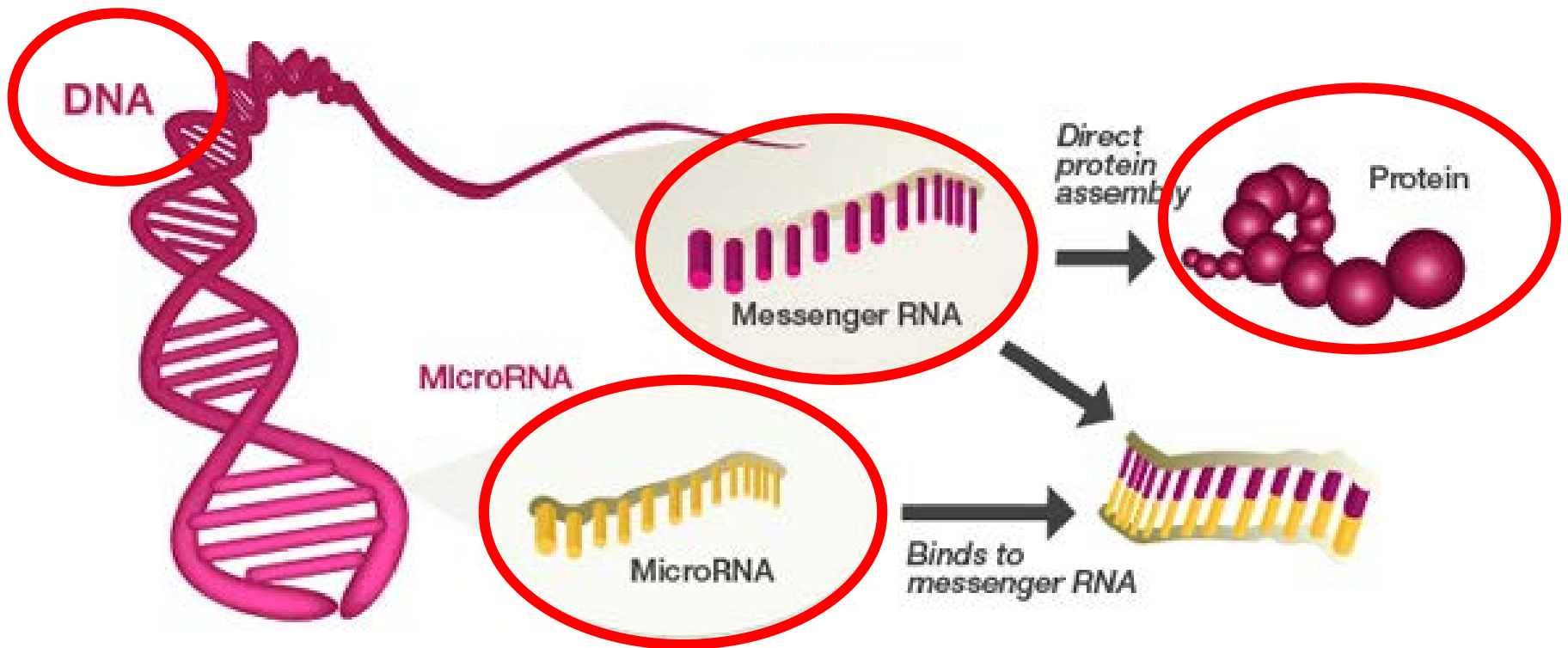
Current Techniques	Problems
Heme-antibody cards	False positives, ambiguous readings, consumption of sample
Luminol, phenolphthalein	Not human specific, not blood specific, dilution of sample
Acid Phosphatase	Not semen specific, susceptible to storage conditions, dilution of sample
P30/PSA cards	Not semen specific, ambiguous readings, consumption of sample
Visualization of Spermatozoa	Oligo/azoospermic individuals, diluted samples

Impromptu game show



Is there a line?

Lines of Research into BFID



mRNA based BFID

- Co-extracted with DNA
- Instrumentation and techniques
- mRNA BFID CE-based assay already implemented (NFI, ESR)
- Persistence
 - Setzer et al. (2008)
 - Zhao et al. (2017)
 - Kulstein & Wiegand (2017)
- SNP analysis



© CL/TALKLEFT.com

A	A	T	A
---	---	---	---



T

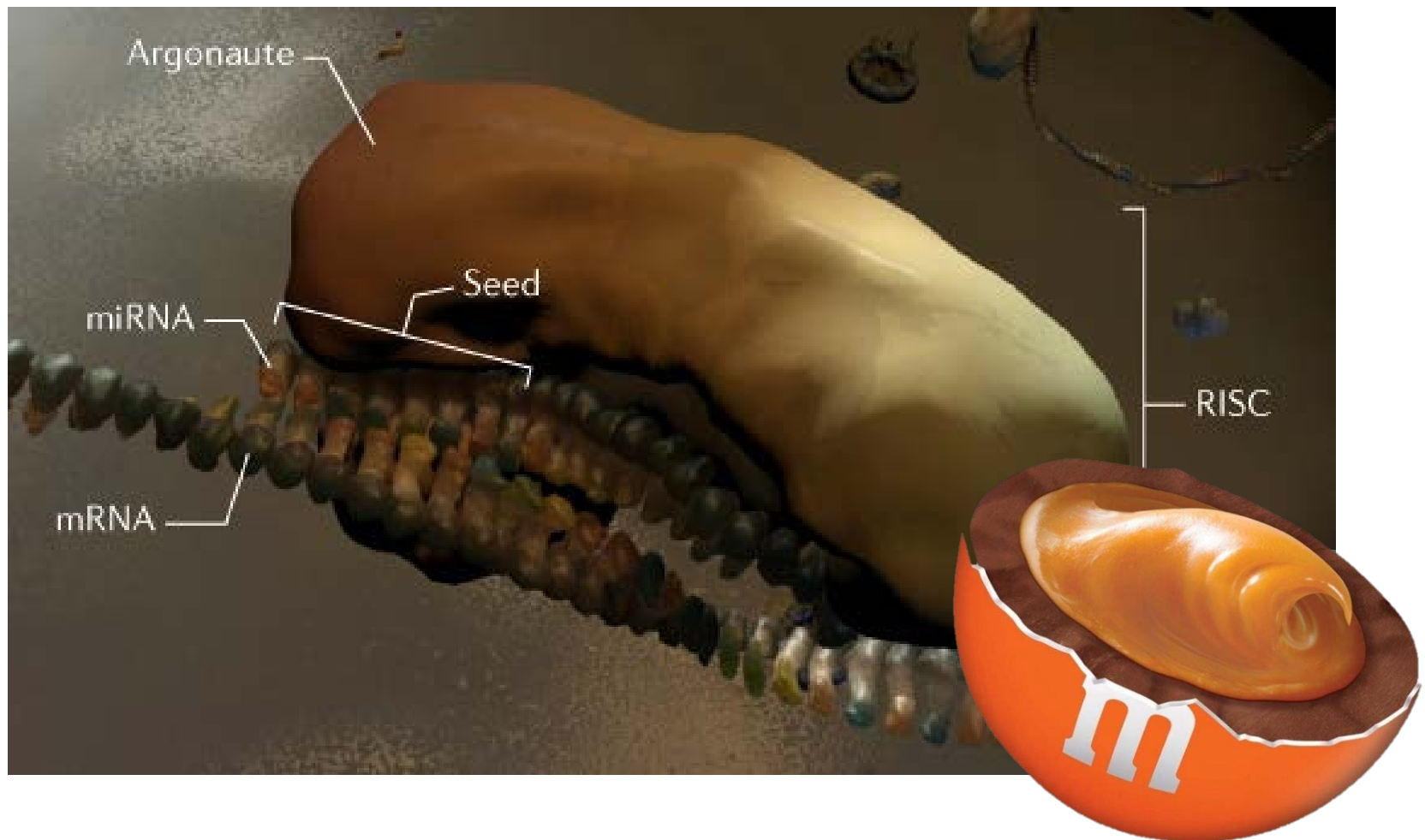


miRNA based BFID

- Co-extracted with DNA
 - Observed in DNA extracts
- Instrumentation
- Similar techniques
- No consensus on markers
- Persistence
 - Grabmüller et al. (2017)
- Stability is theoretical

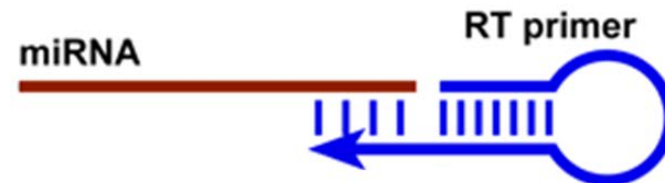


miRNA Stability



Analysis of miRNAs

- Difficult due to their small size (20-25 nucleotides)
- Stem-loop primers or polyadenylation
- Reverse Transcription Quantitative PCR (RT-qPCR)
 - Limited number of miRNAs that can be tested due to instrumentation
- Capillary Electrophoresis
 - Primer dimers



5' ————— AAAA(A)_n 3' Polyadenylation

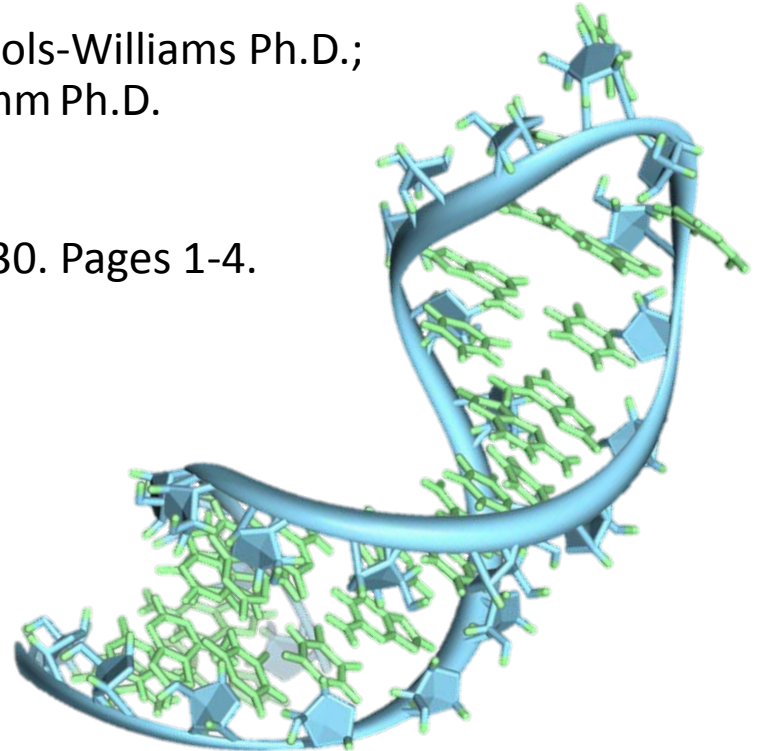
Analysis of miRNAs

- System of linear reverse transcription, specific, and universal primers
 - Paired sequences on reverse transcription and universal primers
 - Developed by Li et al. (2014)
- No primer dimers
- Ability to multiplex
 - Only one dye channel utilized

A capillary electrophoresis method for identifying forensically relevant body fluids using miRNAs

Carrie Mayes B.S.; Sarah Seashols-Williams Ph.D.;
Sheree Hughes-Stamm Ph.D.

Legal Medicine. Volume 30. Pages 1-4.



Linear Primer System

Reverse Transcription

miRNA

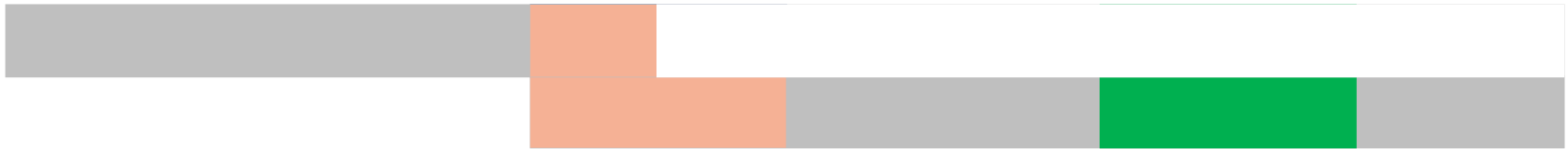


Linear Primer System

PCR

Specific Primer

miRNA



Universal Primer

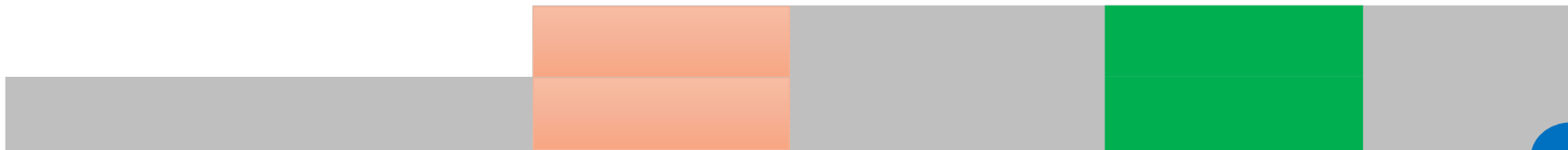
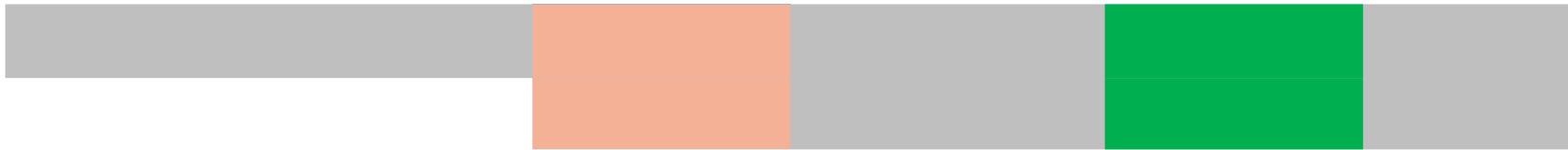


Linear Primer System

PCR

Specific Primer

miRNA



Universal Primer



Linear Primer System



Alter length of specific primer for size based separation



Different paired binding sequences correspond with dye



Body Fluid	Marker	RT Primer	Specific Primer	Universal Primer
Venous Blood	miR-451	GTTCTTGCTGTCAACGATACGCTACGT TTTCTTTTCTTTT-AACTCAGT	GTTCTTCTTTTCTTTTCTTTTCT- AAACCGTTACCATT	FAM'GTTCTTCTTTTCTTTTCT- GCTGTCAACGATACGCTACG
	miR-142-3p	GTTCTTGCTGTCAACGATACGCTACGT TTTCTTTTCTTTT-TCCATAAA	GTTCTTCTTTTCTTTTCTTTTCTTT TTCT-TGTAGTGTTTCTAC	
Ref. Gene	let-7g	GTTCTTGCTGTCAACGATACGCTACGT TTTCTTTTCTTTTAACTGTAC	GTTCTTCTTTTCTTTTCTTTTCTTT TTTCTTTCTTTTGAGGTAGTAGTT	
Menstrual Blood	miR-141-3p	GTTCTT AACTGACTAAACTAGGTGCC TTTTCTTTTCTTTT-CCATCTTT	GTTCTTCTTTTCTTTTCT- TAACACTGTCTGGT	VIC'GTTCTTCTTTTCTTTTCT- AACTGACTAAACTAGGTGCC
	miR-412	GTTCTT AACTGACTAAACTAGGTGCC TTTTCTTTTCTTTT- ACGGCTAG	GTTCTTCTTTTCTTTTCTTTTCTTT TTCT-ACTTCACCTGGTCCA	
Semen	miR-891a	GTTCTT ACGTCGTGAAAGTCTGACAA TTTTCTTTTCTTTT- TCAGTGGC	GTTCTTCTTTTCTTTTCTTTTCTTT TTCTTTT-TGCAACGAACCTGA	NED'GTTCTTCTTTTCTTTTCT- ACGTCGTGAAAGTCTGACAA
	miR-10b	GTTCTT ACGTCGTGAAAGTCTGACAA TTTTCTTTTCTTTT- CACAAATT	GTTCTTCTTTTCTTTTCTTTTCT- ATGGGACATCTCCG	
Saliva	miR-205	GTTCTT GTAAACGACGGCCAG TTTTCTTTTCTTTT- CAGACTCC	GTTCTTCTTTTCTTTTCTTTTCTTT -TCCTTCATTCCACC	PET'GTTCTTCTTTTCTTTTCT- GTAAACGACGGCCAG
	miR-658	GTTCTT GTAAACGACGGCCAG TTTTCTTTTCTTTT- ACCAACGG	GTTCTTCTTTTCTTTT- GGCGGAGGGAAGTAGGT	



Materials and Methods

- Sample Collection
 - Donors (n=5) per body fluid
 - SHSU IRB approval #2015-09-26124
- Venous blood collected through venipuncture, saliva in tubes, menstrual blood on cotton swabs, and semen in specimen containers
- 50 μ L of blood, saliva, and semen or 1 menstrual swab used for extractions

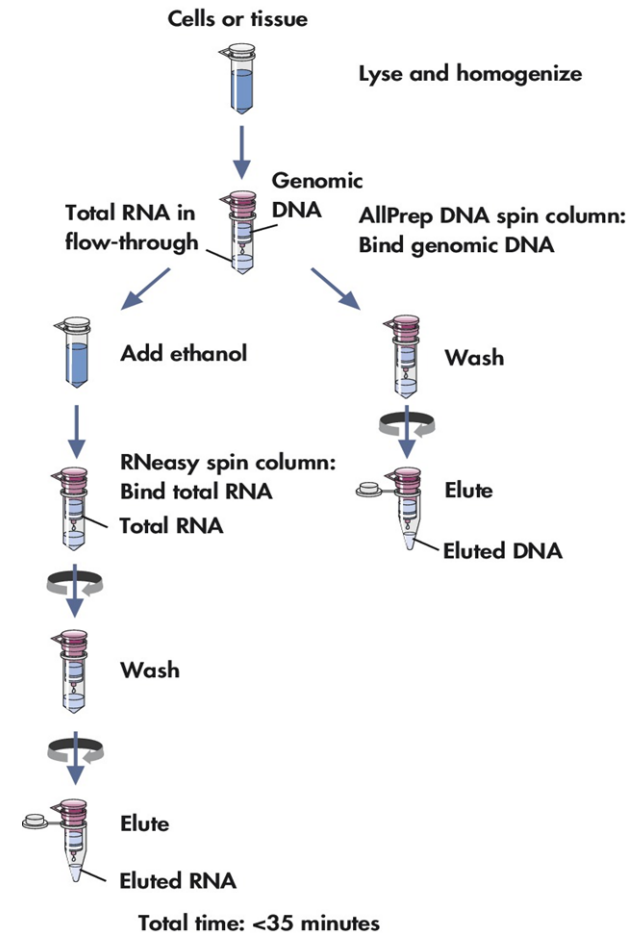
Materials and Methods

Extraction

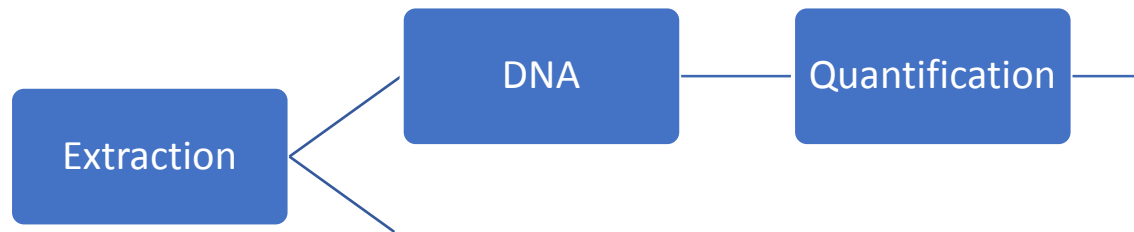
DNA



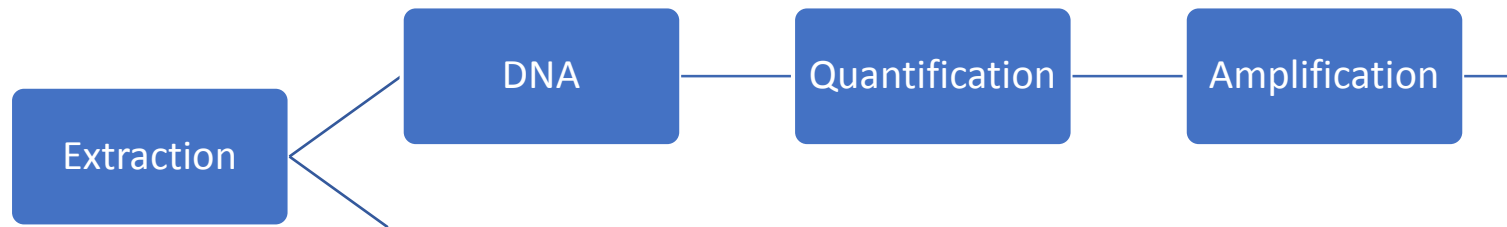
AllPrep DNA/RNA Procedure



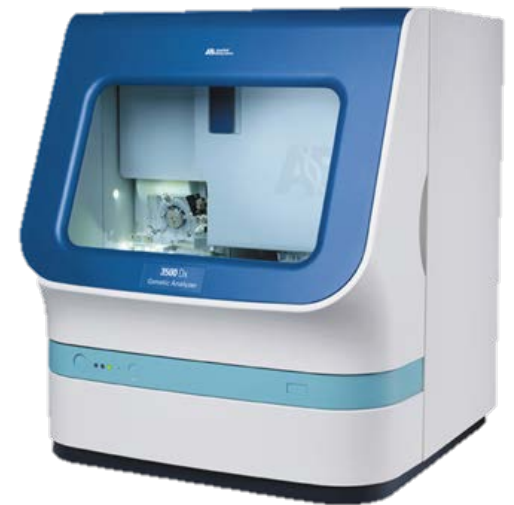
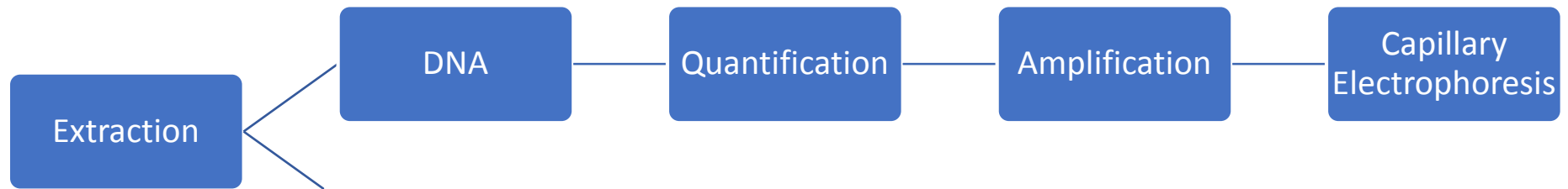
Materials and Methods



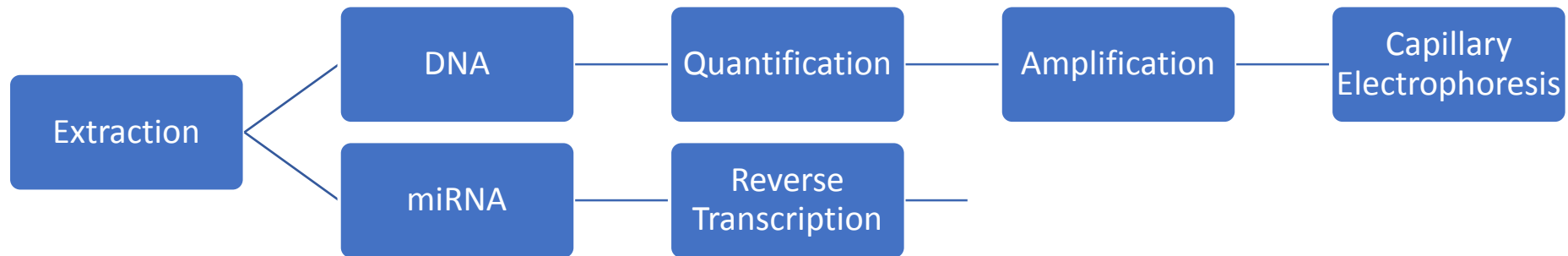
Materials and Methods



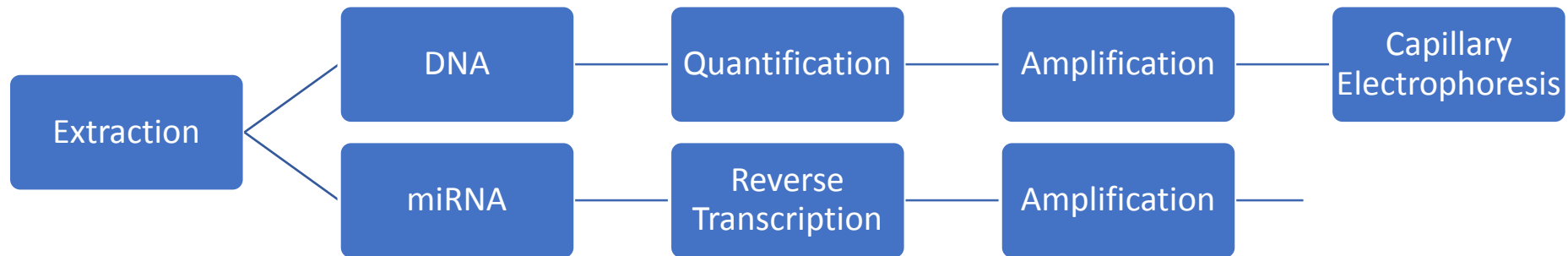
Materials and Methods



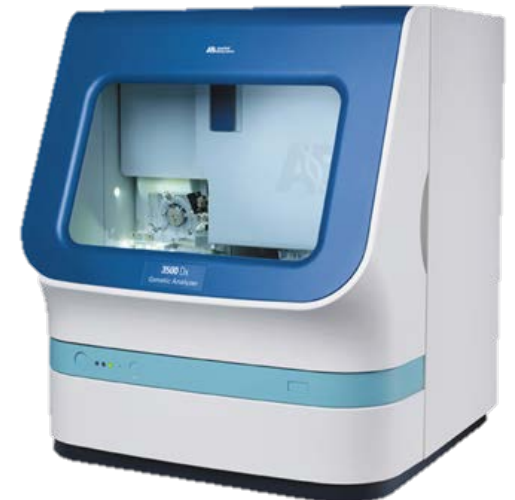
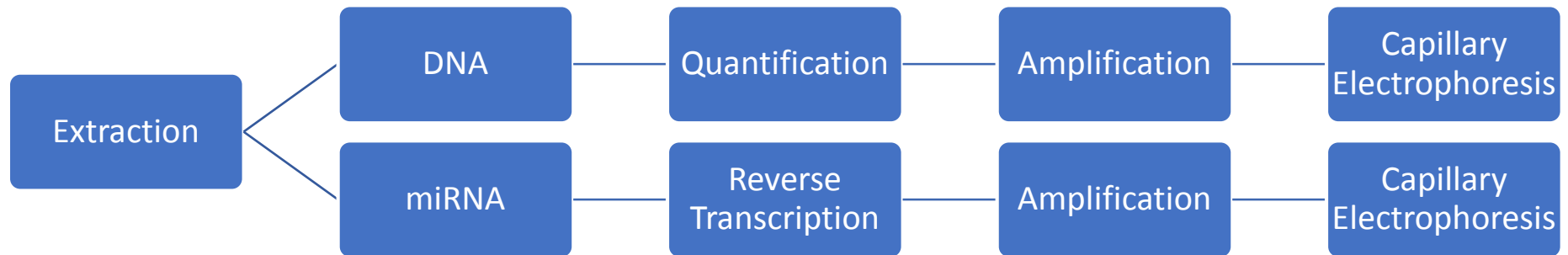
Materials and Methods



Materials and Methods

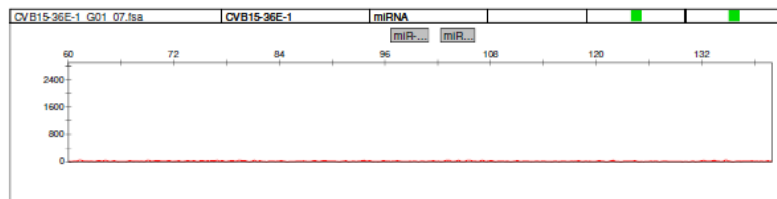
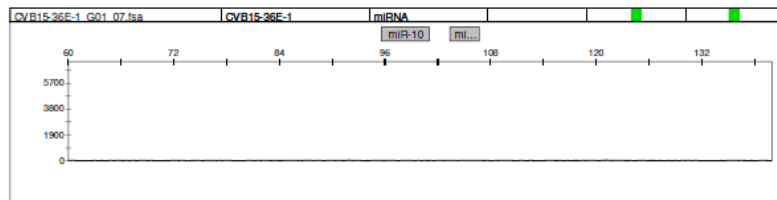
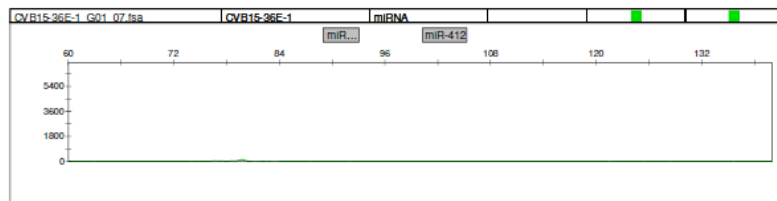
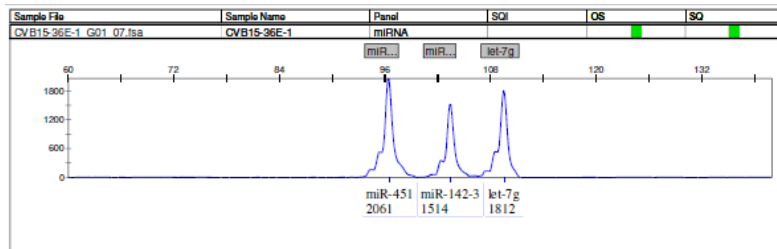


Materials and Methods



miRNA Profiles

VENOUS BLOOD



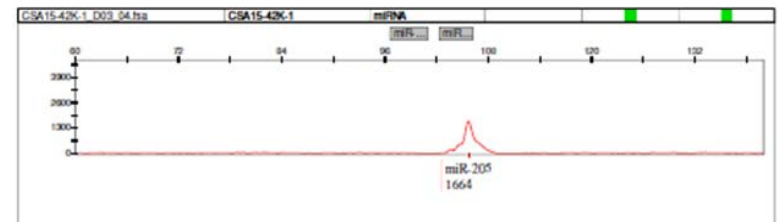
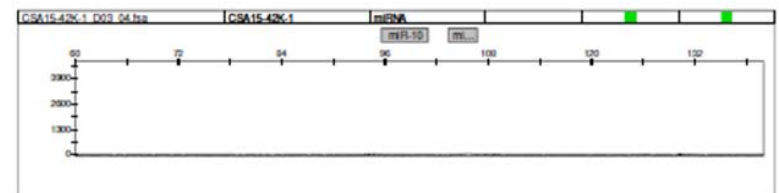
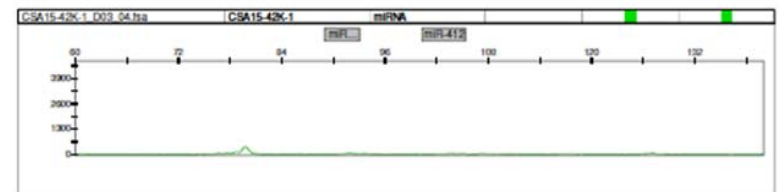
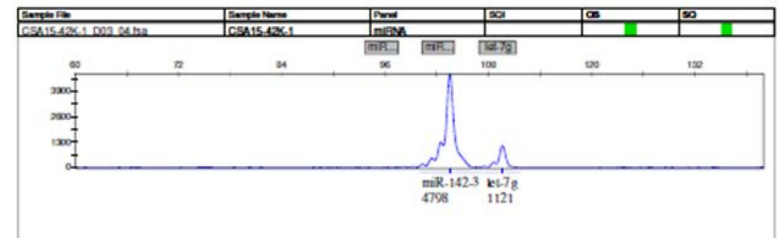
Venous
Blood

Menstrual
Blood

Semen

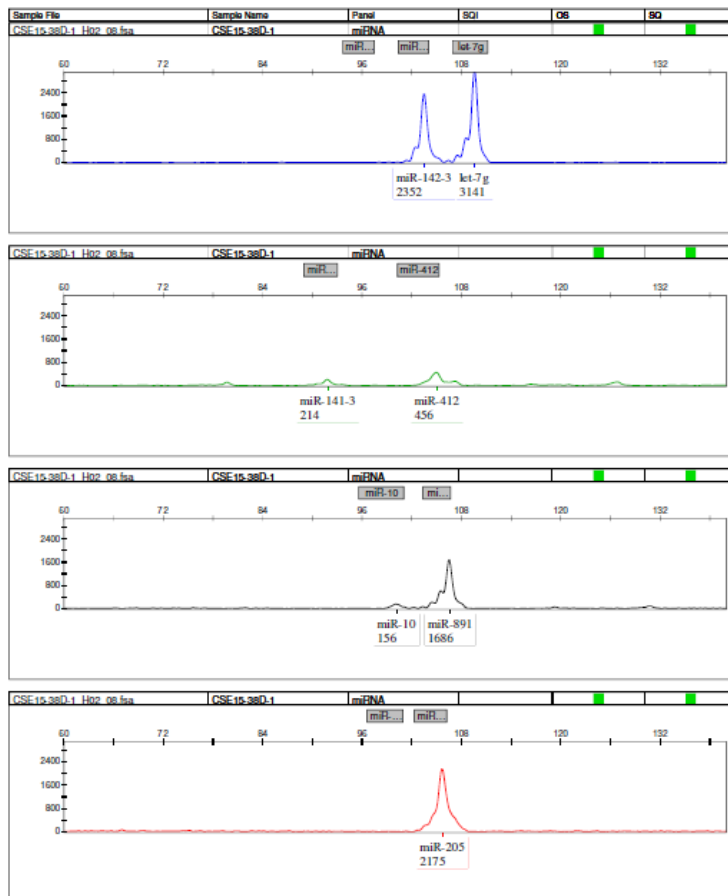
Saliva

SALIVA



miRNA Profiles

SEMEN



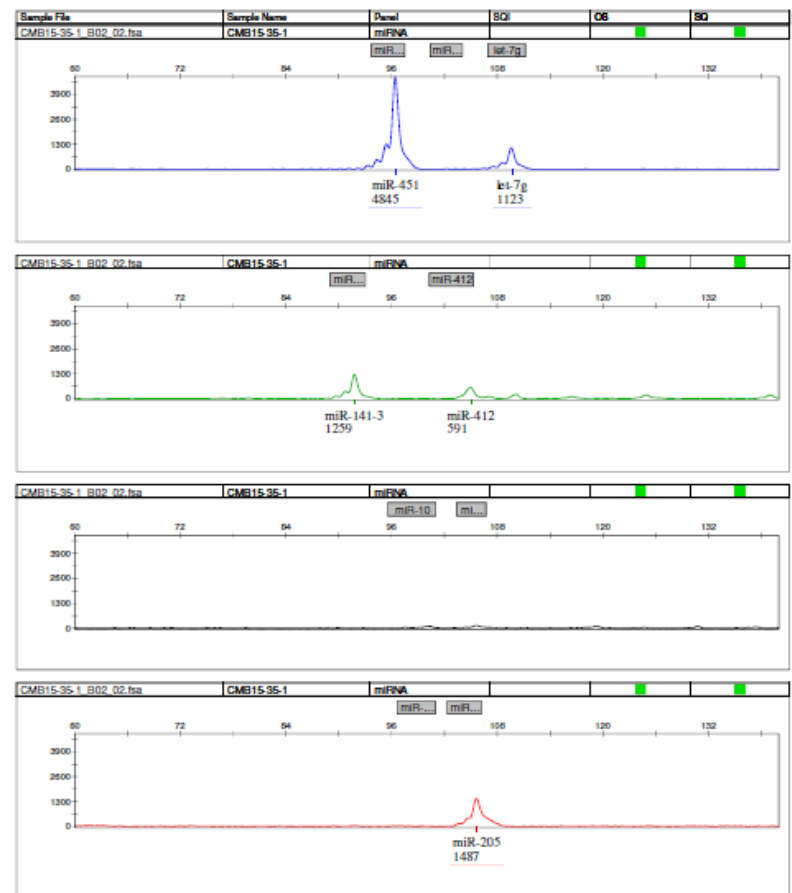
Venous
Blood

Menstrual
Blood

Semen

Saliva

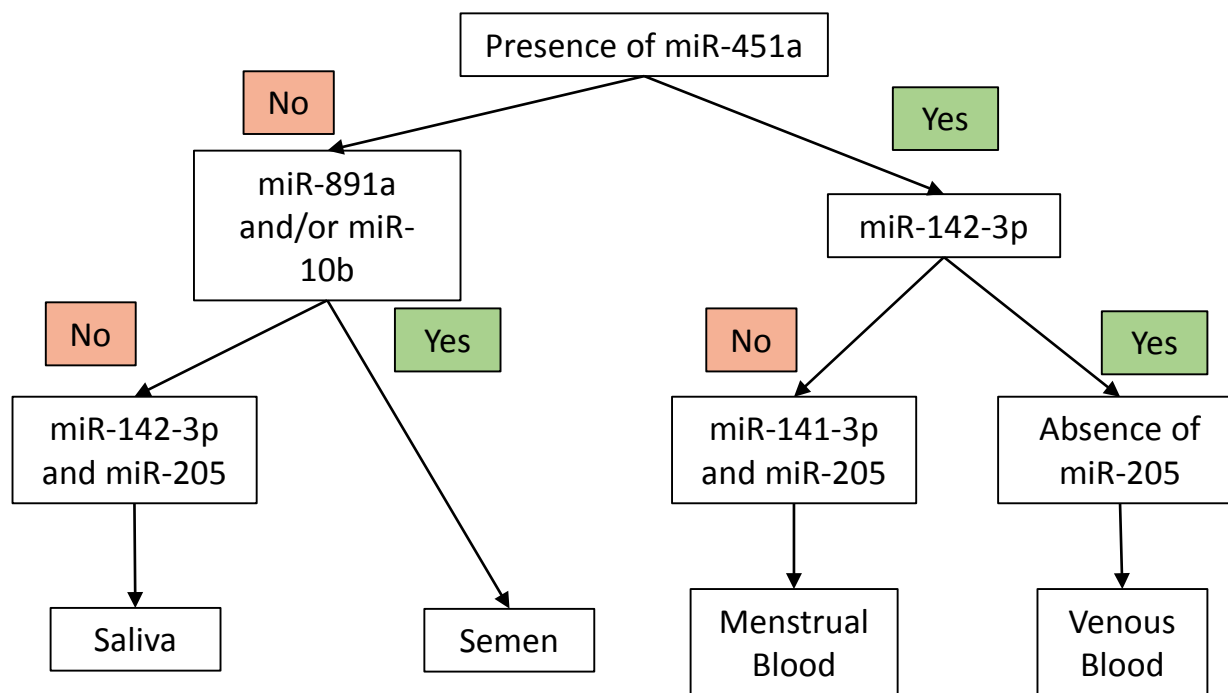
MENSTRUAL BLOOD



Results - Summary

Body Fluid	Reference	Venous Blood		Menstrual Blood		Semen		Saliva
	let-7g	miR-451a	miR-142-3p	miR-141-3p	miR-412-3p	miR-10b	miR-891a	miR-205
Venous Blood	1	1	1	0	0	0	0	0
Menstrual Blood	1	1	0	1	0.6	0	0	1
Semen	1	0	1	0.8	0.8	1	1	1
Saliva	1	0	1	0.2	0.2	0	0	1

- Proportion markers observed in each fluid (n=5)



Decision Tree for BFID Determination

Conclusions

All DNA profiles were concordant



An interpretation strategy was developed based on the presence/absence of markers.



Non-specific amplification was observed in the green channel in menstrual blood and saliva samples.



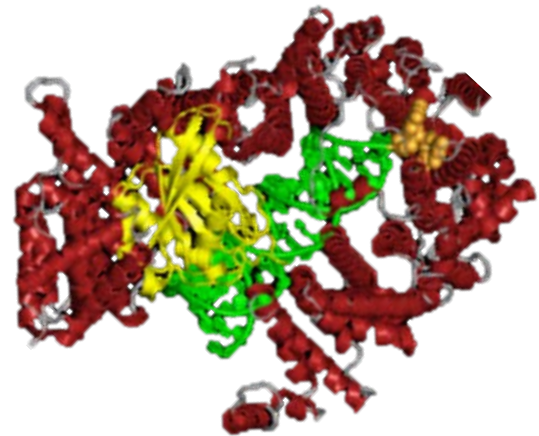
Cross-reactivity of miR-141-3p and miR-412-3p complicates mixture interpretation.

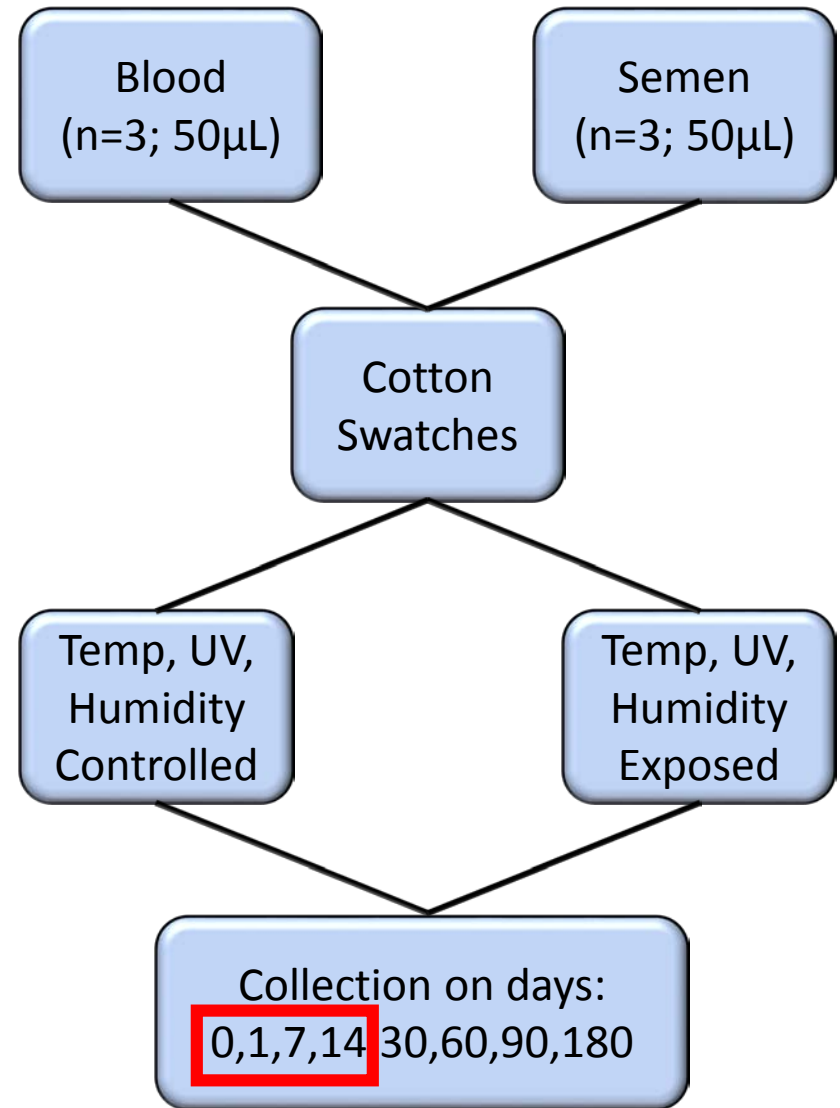


The multiplex was able to distinguish between venous blood, menstrual blood, semen, and saliva.

Comparing the stability and persistence of miRNA and mRNA for body fluid identification in forensic samples

Carrie Mayes B.S.; Sarah Seashols-Williams Ph.D.;
Sheree Hughes-Stamm Ph.D.





RNA Extraction:
miRNeasy Kit

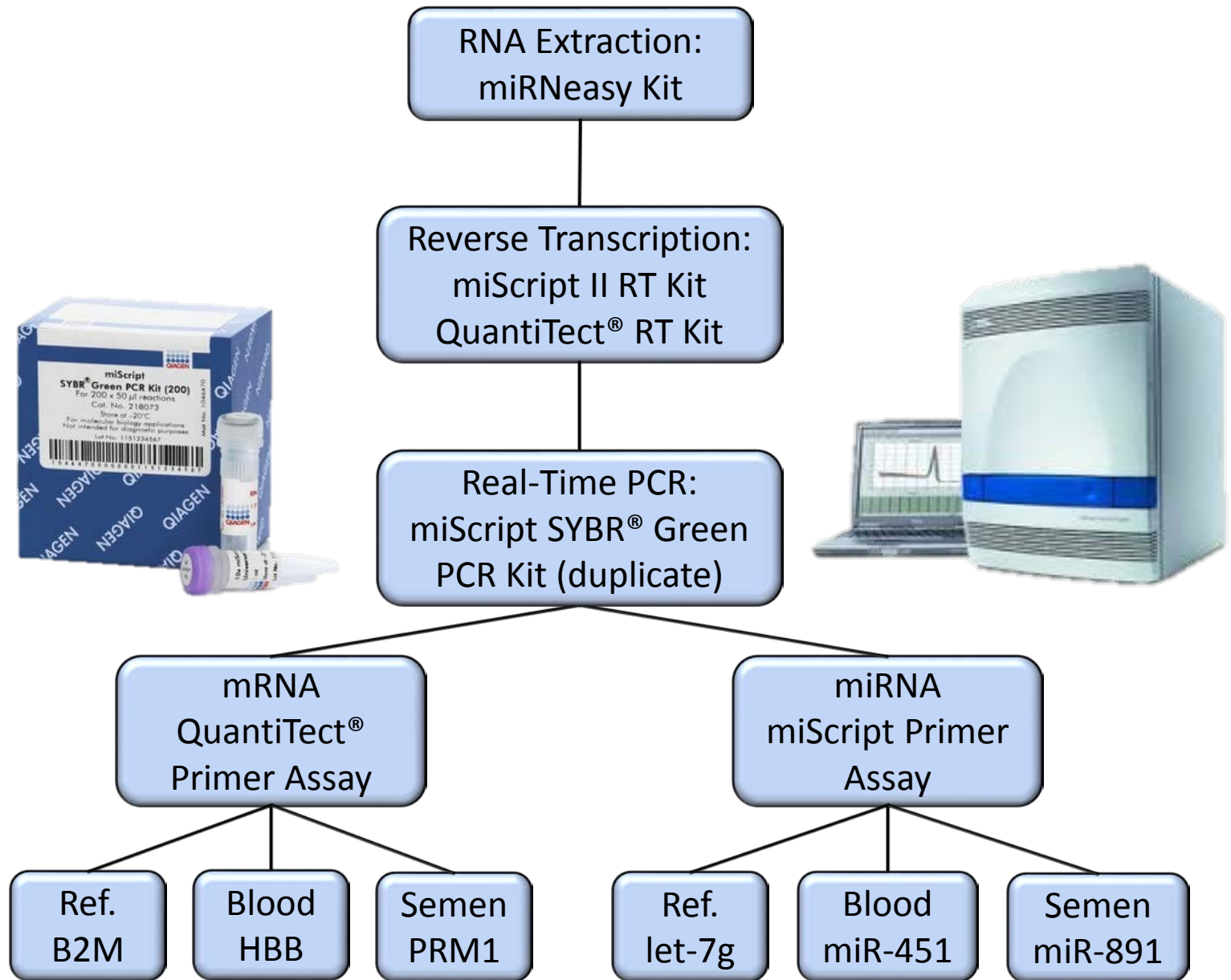


RNA Extraction:
miRNeasy Kit



Reverse Transcription:
miScript II RT Kit
QuantiTect® RT Kit



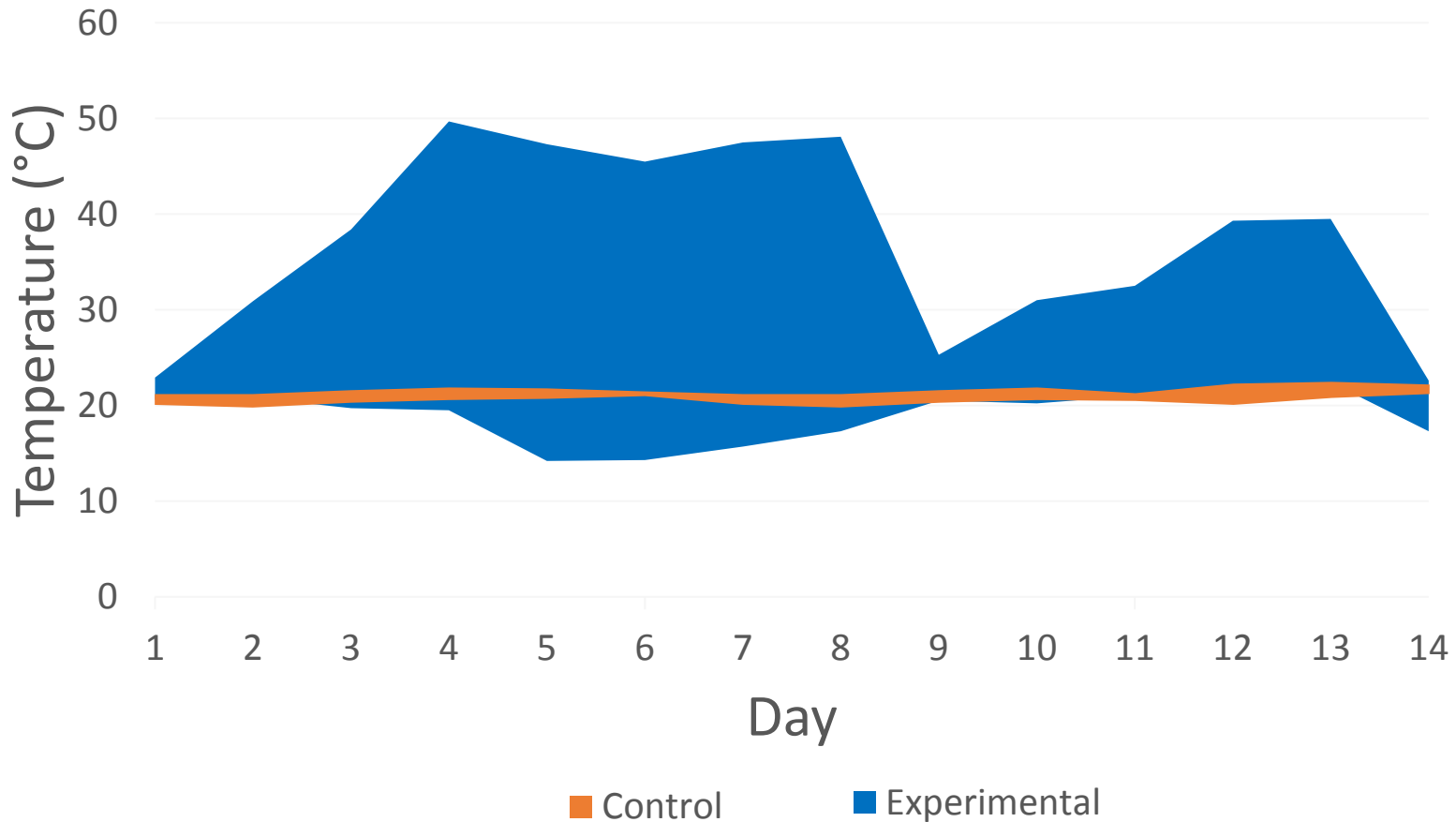


Data Interpretation

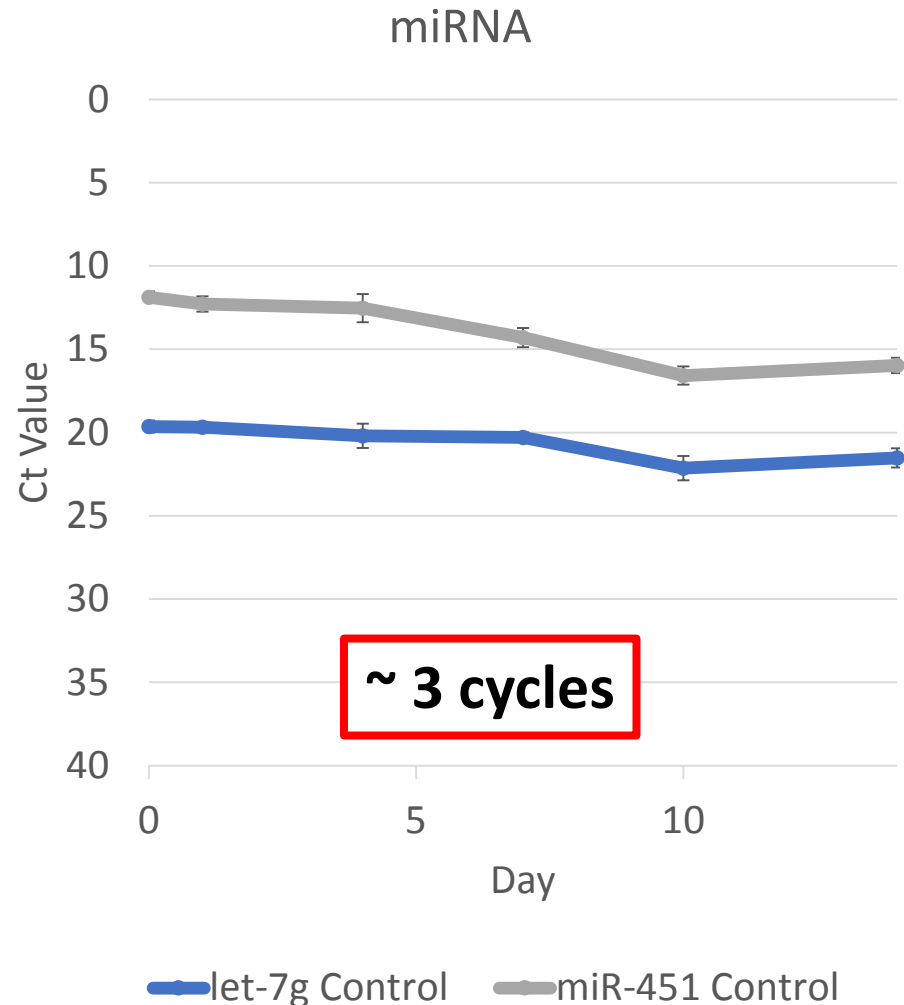
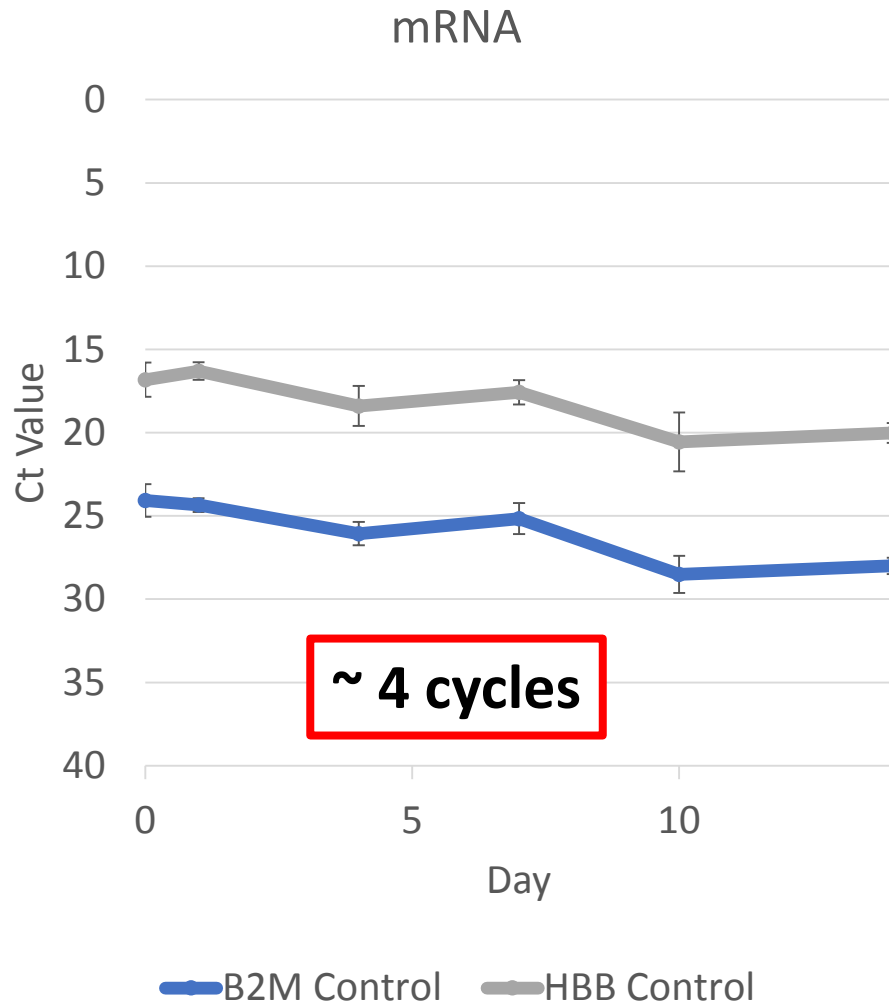
- Primer validation
 - Amplification efficiencies
 - Melt curve
 - Comparable scale between mRNA and miRNA assays
- $\Delta\Delta C_t$
- Drop in cycle number over time

Fluid	Marker	Efficiency	R ²
Blood	let-7g	87.3%	0.999
	miR-451	89.2%	0.999
	B2M	95.3%	0.994
	HBB	93.2%	0.998
Semen	let-7g	96.6%	0.994
	miR-891	95.5%	0.988
	B2M	96.9%	1.000
	PRM1	98.0%	0.999

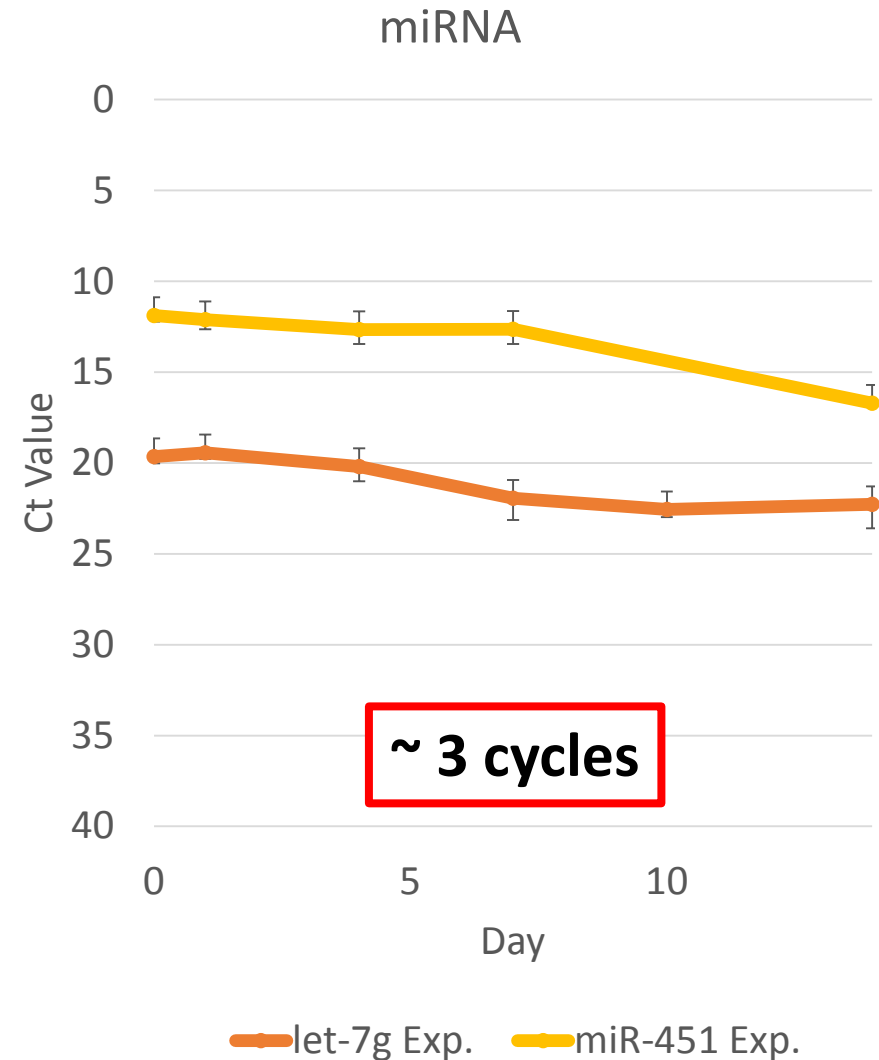
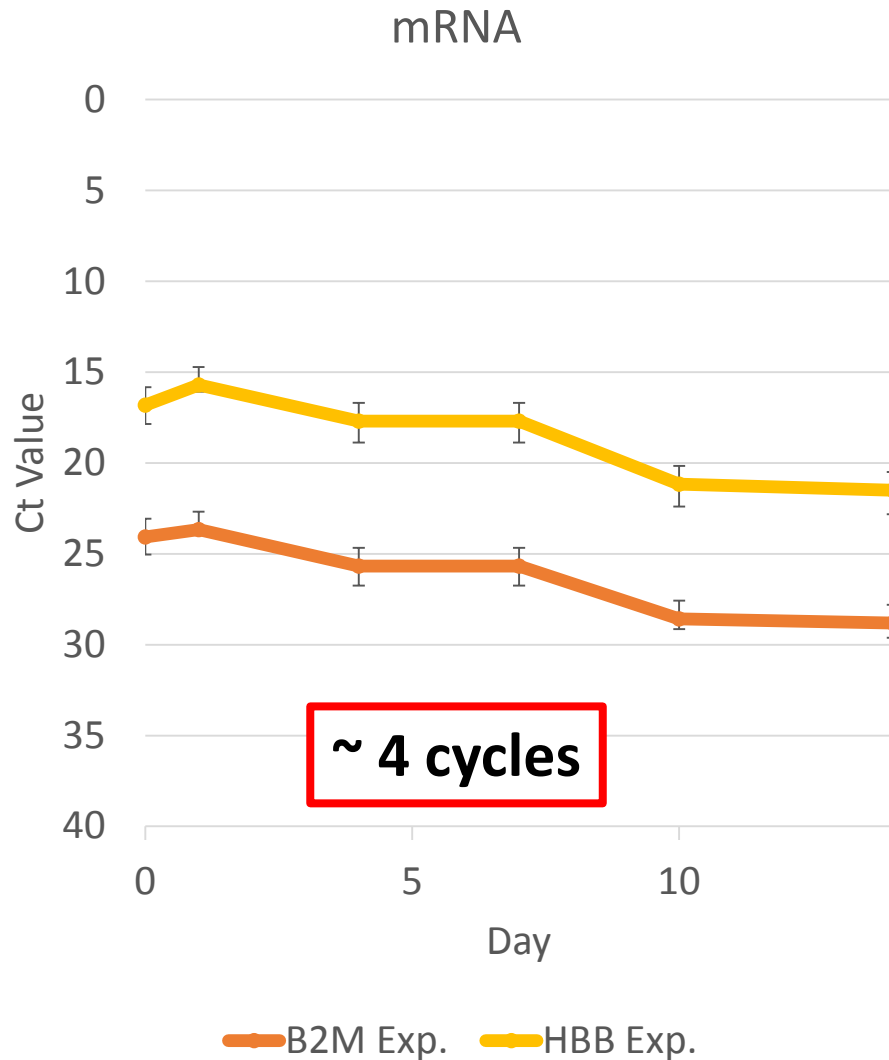
Temperature



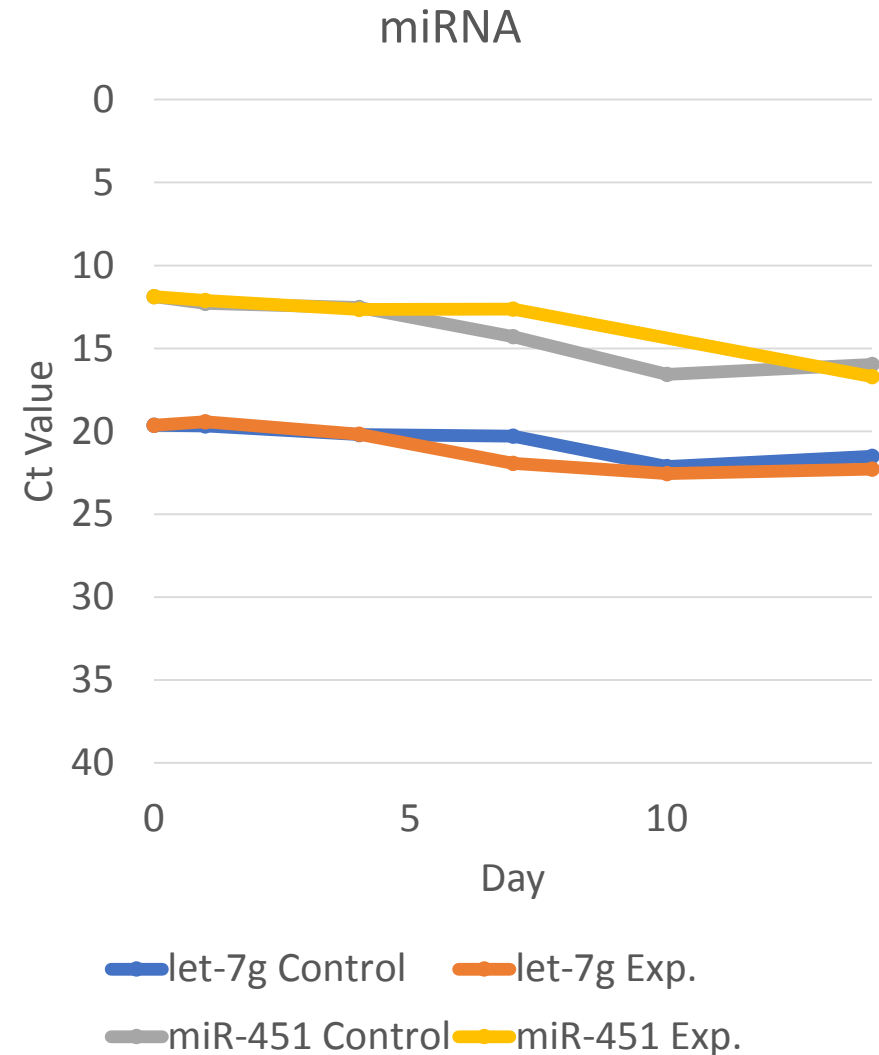
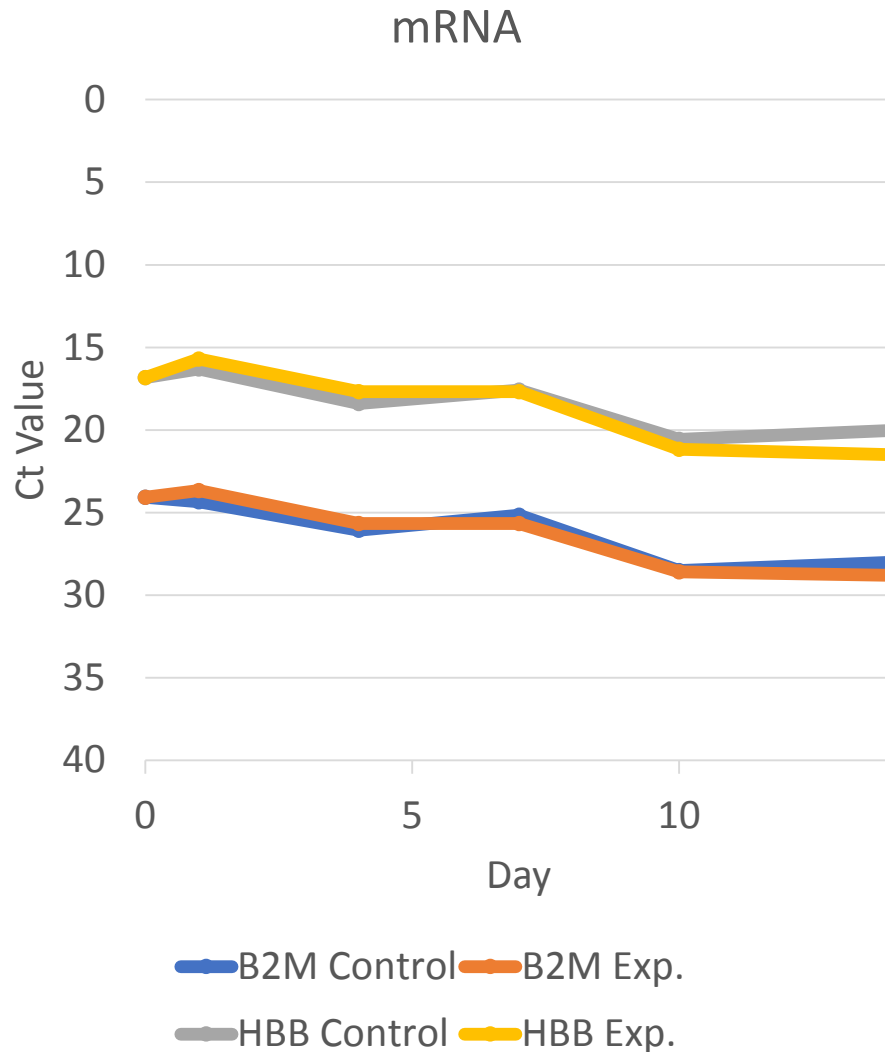
Blood – Controlled Conditions



Blood – Experimental

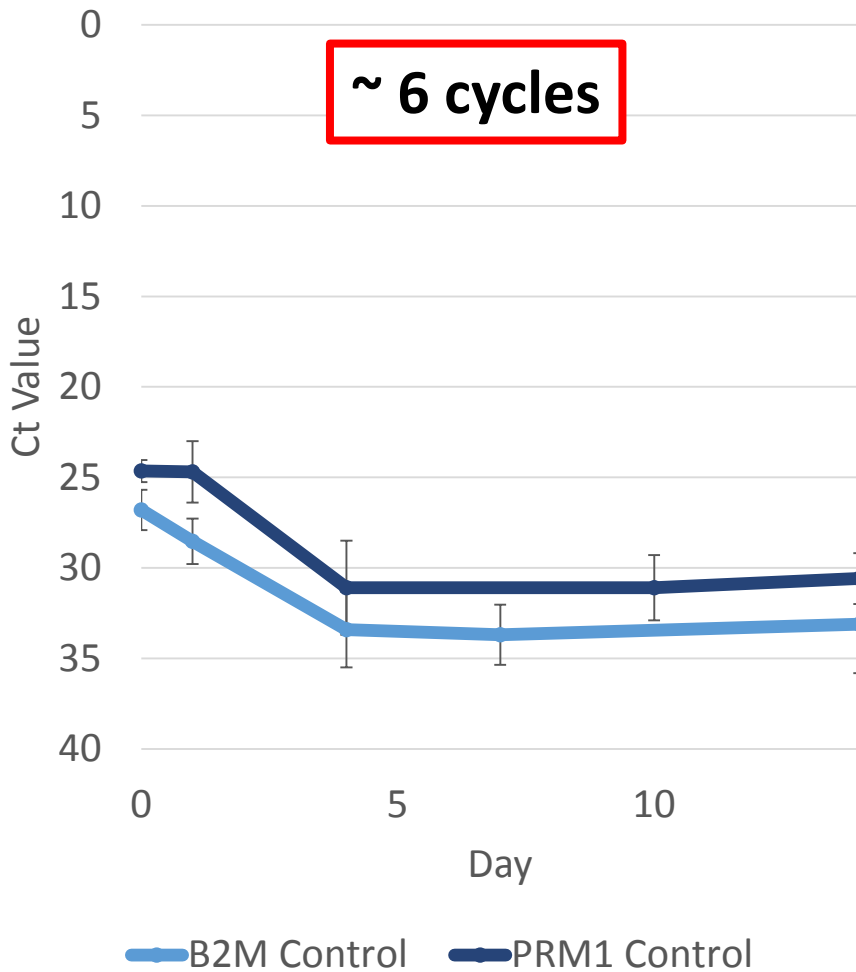


Blood – Overall

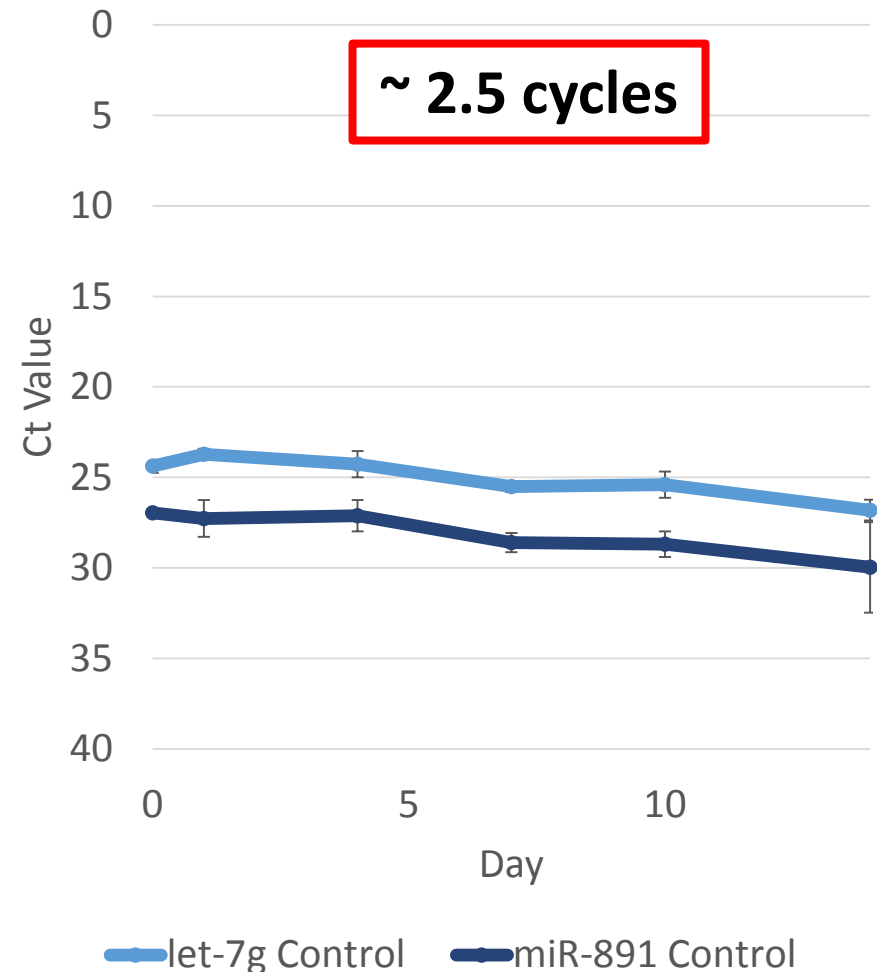


Semen – Controlled Conditions

mRNA

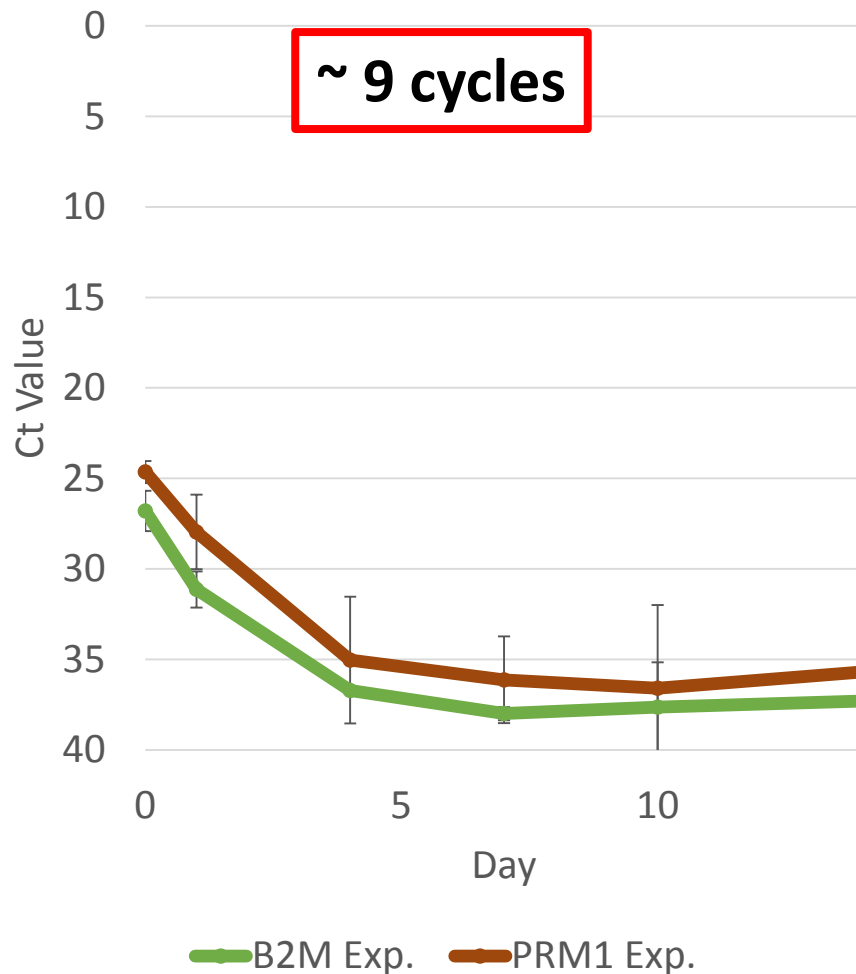


miRNA

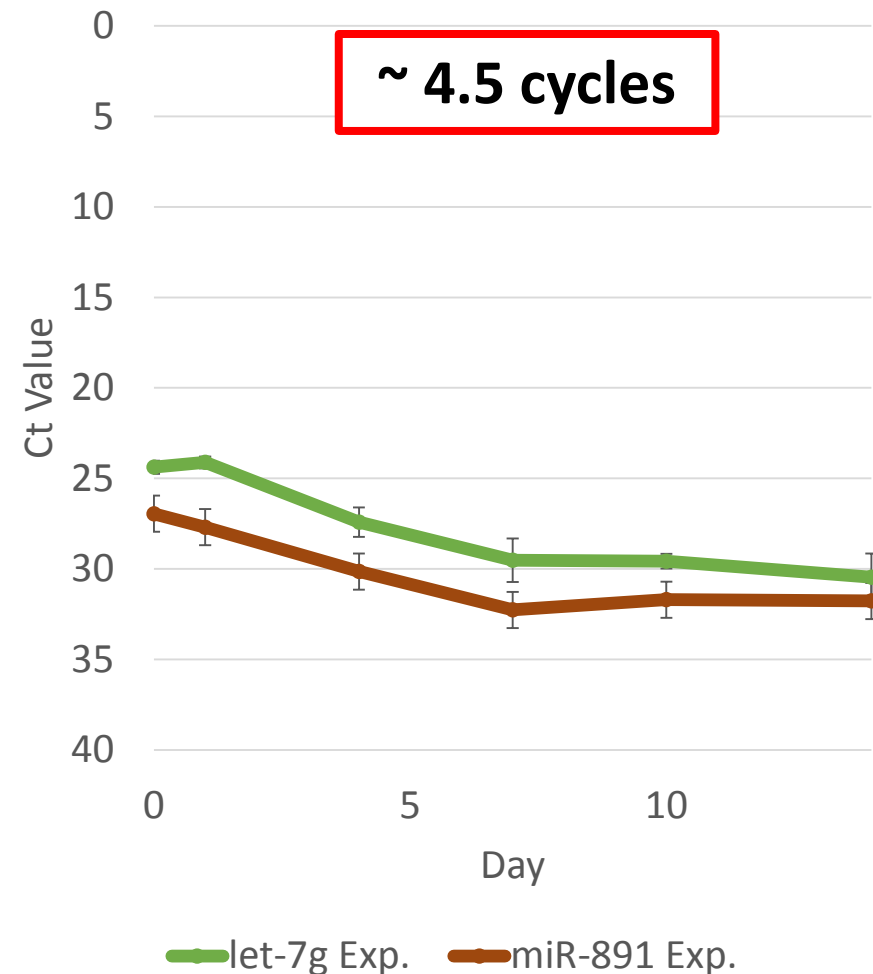


Semen – Experimental

mRNA

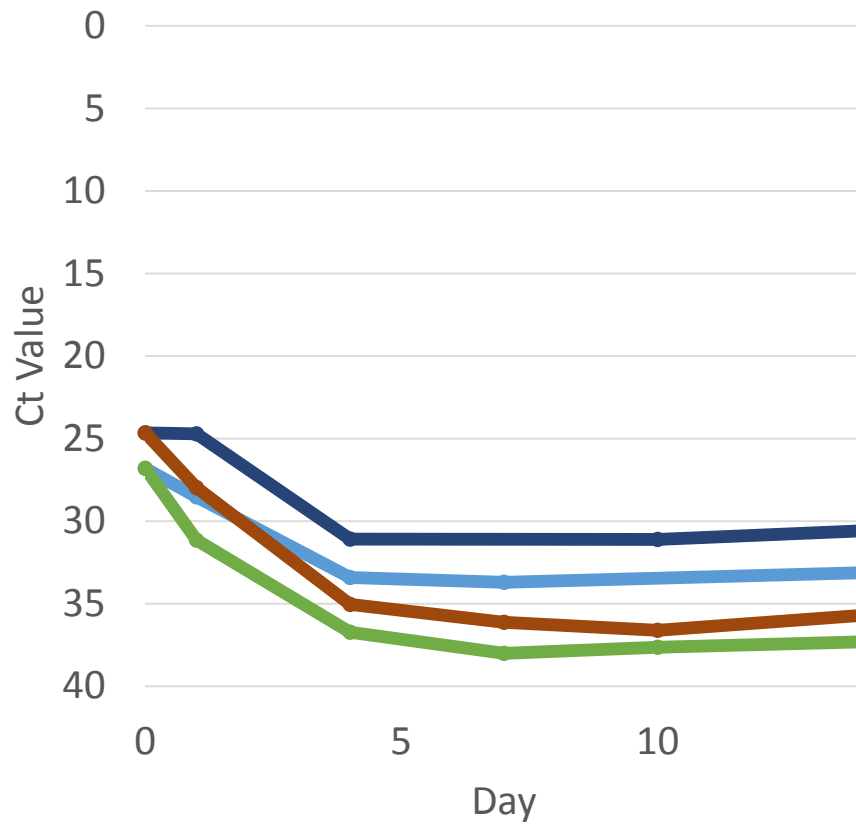


miRNA



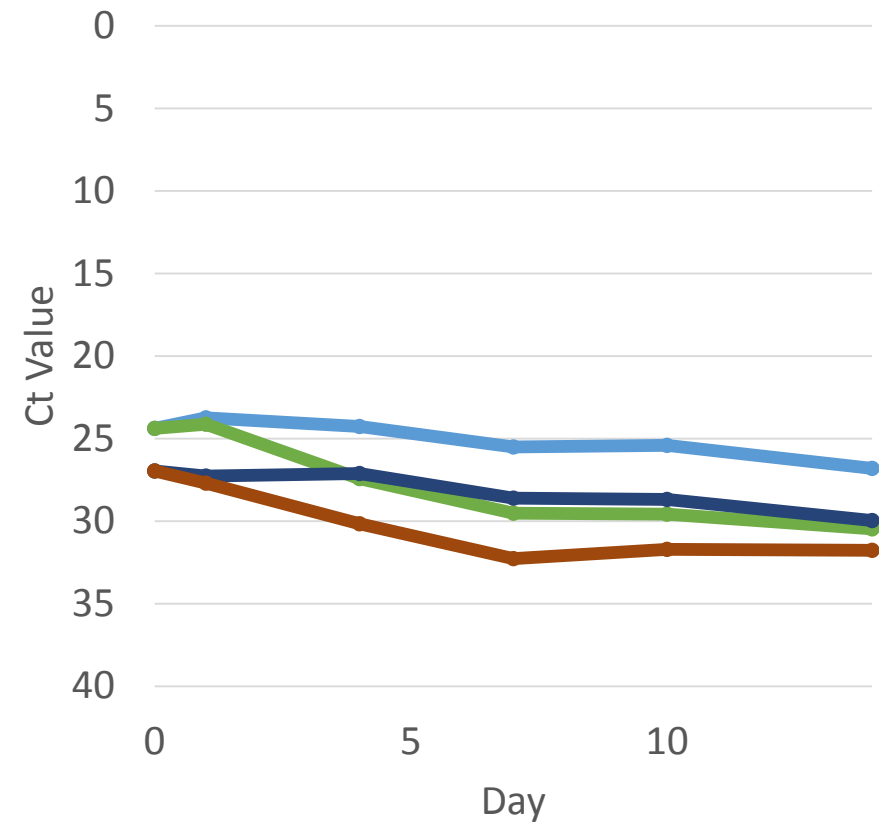
Semen – Controlled Conditions

mRNA



— B2M Control — B2M Exp.
— PRM1 Control — PRM1 Exp.

miRNA



— let-7g Control — let-7g Exp.
— miR-891 Control — miR-891 Exp.

Preliminary Degradation Results

- Blood appears more stable
 - Anti-coagulant in venipuncture tubes
- mRNA drop-off between day 1 and day 4 in all semen samples
 - Similar trend observed in miRNA experimental samples
- Greater change in cycle number for mRNA
 - Suggests miRNA may be more stable
- Looking forward to later dates

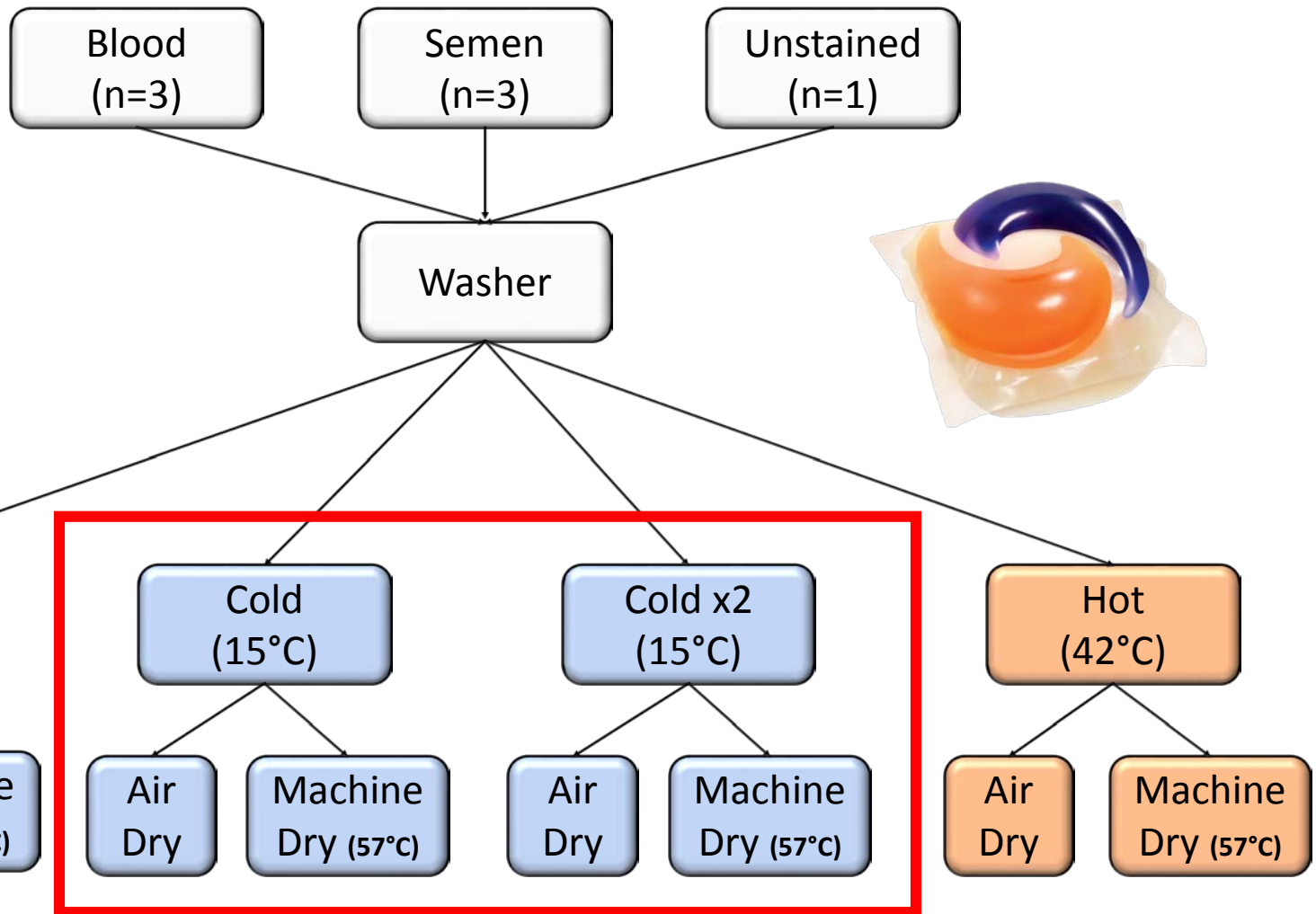


Laundered Items

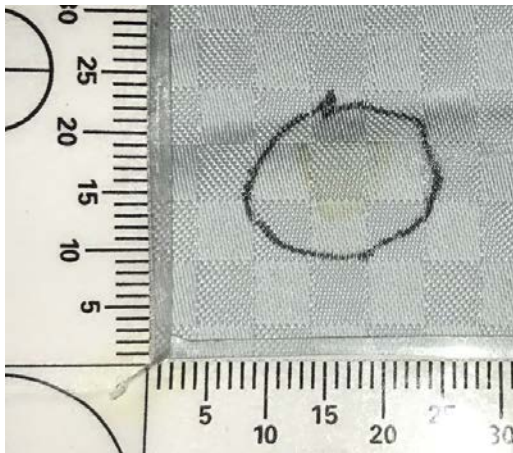
- Transferred DNA has been observed in laundered items
 - Voskoboinik et al. (2017), Brayley-Mills et al. (2017).
- Conventional BFID techniques
 - Kulstein and Wiegand (2017), Edler et al. (2017)
- Spermatozoa identified post-laundry
 - Noel et al. (2016)



Laundered



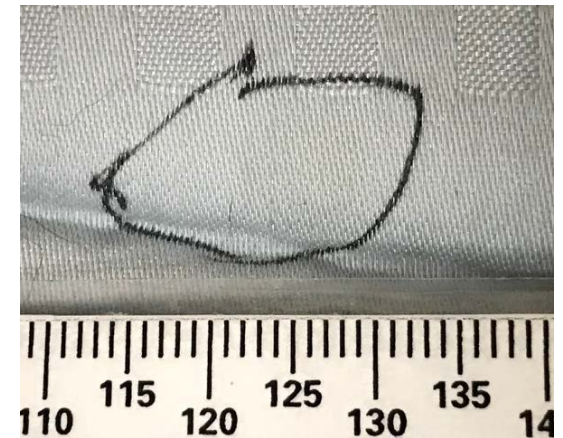
Rethinking my detergent...



Cold Wash
Air Dry

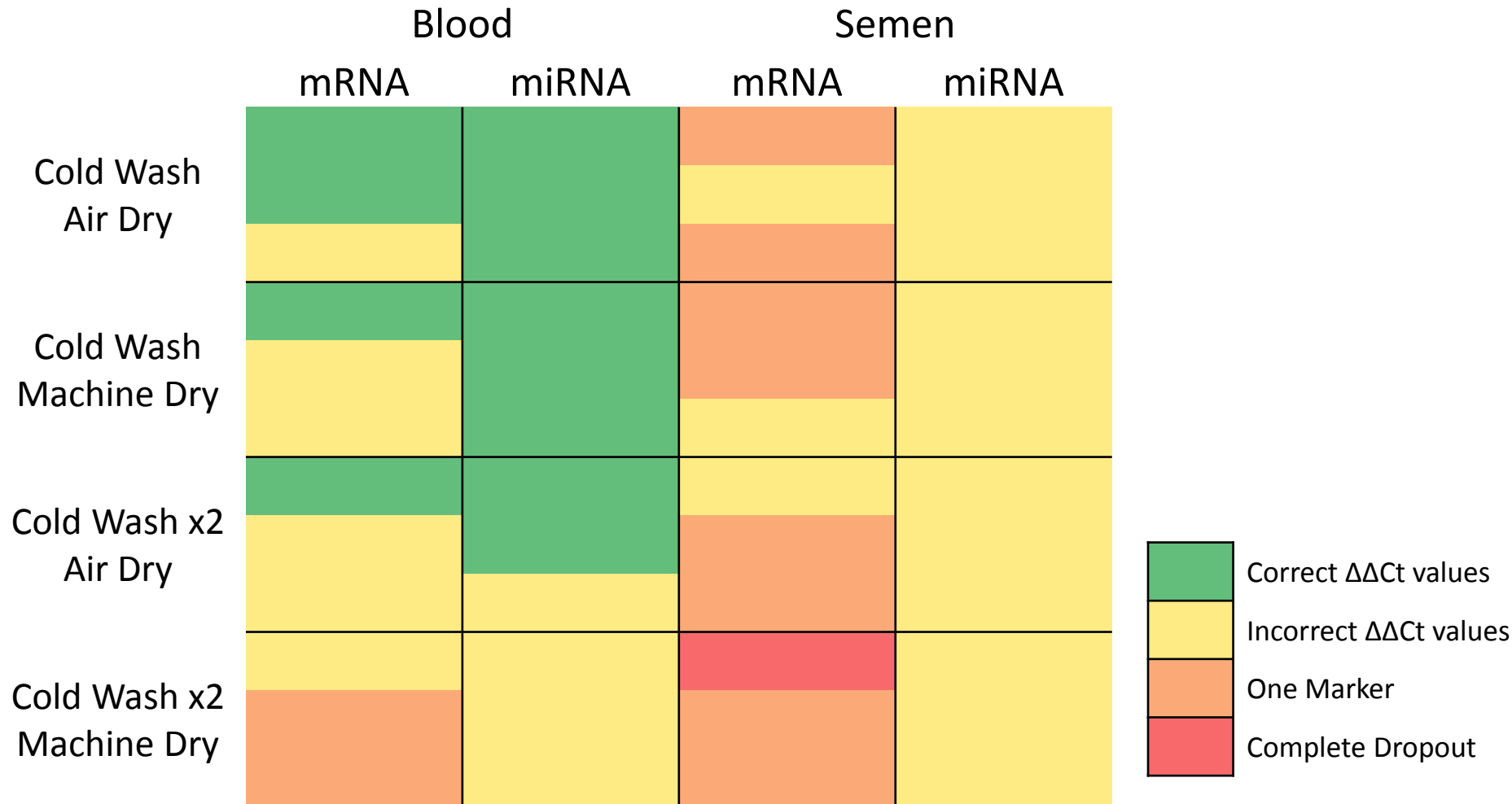


Cold Wash x2
Air Dry



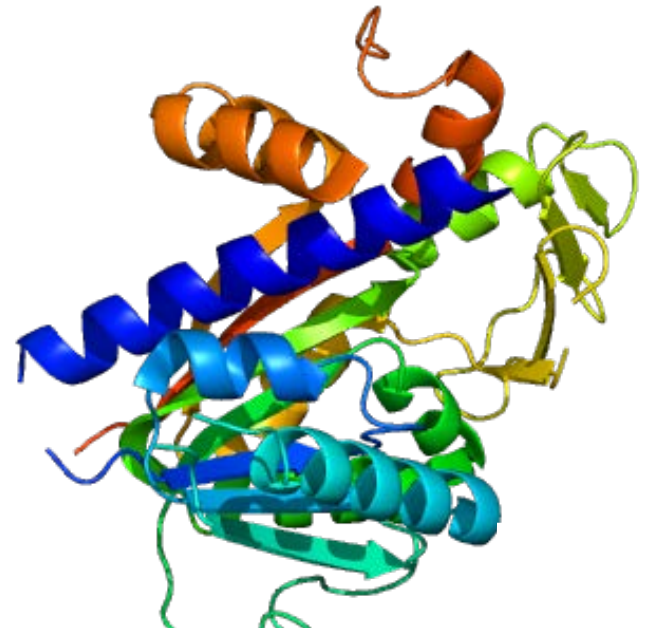
Cold Wash
Machine Dry

Laundered Samples



**COMING
SOON!**

Evaluating the utility of massively parallel
sequencing for mRNA for body fluid
identification in challenging samples



Acknowledgements

- Qiagen
 - Dr. Meredith Turnbough
 - Bryan Davis
- Sam Houston State University
- NIJ GRF #2016-DN-BS-001
- Dr. Sheree Hughes-Stamm
- Dr. Rachel Houston
- Team DNA



Questions?

Carrie Mayes

cam115@shsu.edu



Extractimus Prime



Sam Houston
State University