



Genomics in formalin-fixed paraffin embedded tissue (FFPE) samples for quantitative risk assessment



Leah C. Wehmas, Ph.D. Genomics Scientist ORD USEPA HESI eSTAR Webinar May 26, 2020





Disclaimer

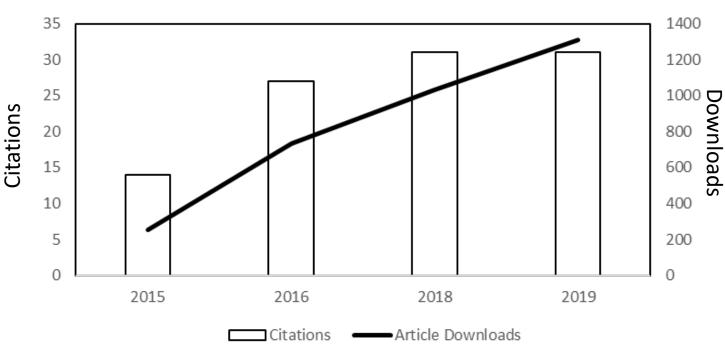
The views presented in this webinar are mine and do not represent the US EPA. Any mention of products does not constitute endorsement.





eSTAR FFPE Workgroup Impact

FFPE Workgroup Publications



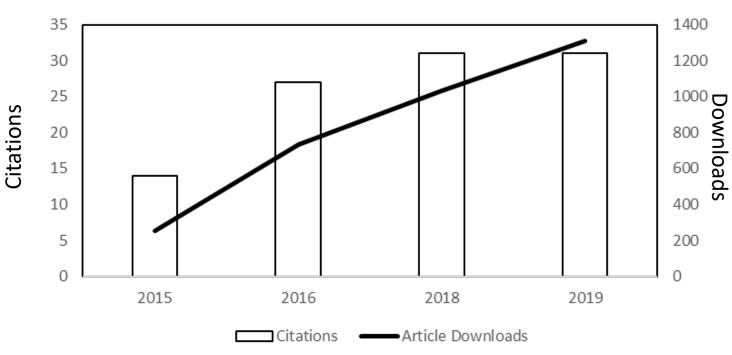
- Mining the Archives: A Cross-Platform Analysis of Gene Expression Profiles in Archival Formalin-Fixed Paraffin-Embedded Tissues. Webster et al. 2015
- Editor's Highlight: Dose-Response Analysis of RNA-Seq Profiles in Archival Formalin-Fixed Paraffin-Embedded Samples. Hester et al. 2016
- Demodifying RNA for Transcriptomic Analyses of Archival Formalin-Fixed Paraffin-Embedded Samples. Wehmas et al. 2018
- Enhanced Quality Metrics for Assessing RNA Derived From Archival Formalin-Fixed Paraffin-Embedded Tissue Samples. Wehmas et al. 2019
- Improving DNA-sequencing Analysis from Formalin-Fixed Paraffin-Embedded Tissue Samples. Wehmas et al. in progress 2020



ILSI Health and Environmental Sciences Institute

Major findings

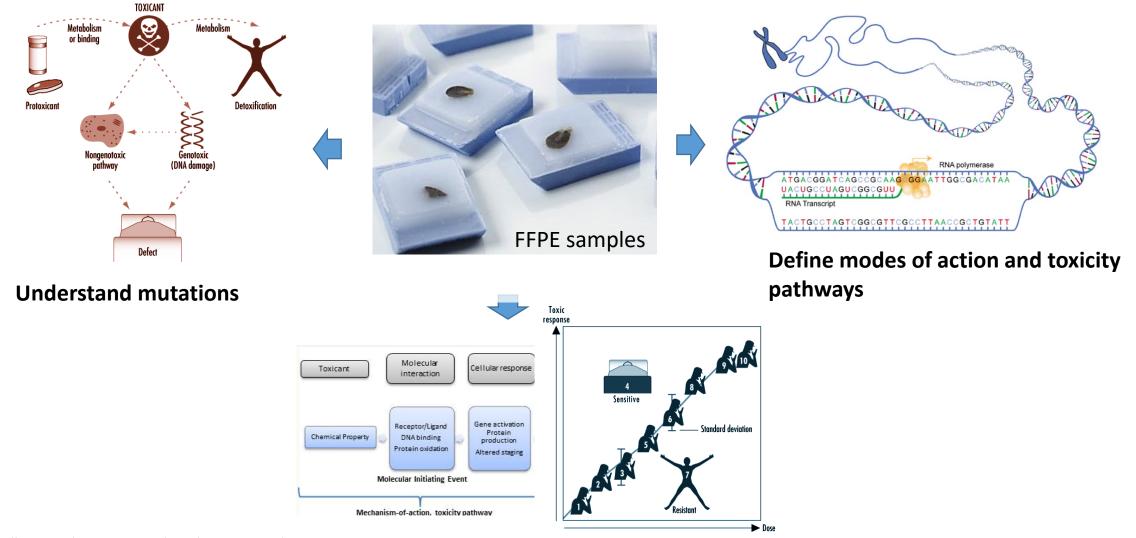




- Applied new technologies
- Characterized major factors impacting FFPE quality
- Identified methods to improve gene expression data
- Developed better metrics for quality assessment
- Translated results to clinical FFPE and improved SNP detection



Archival tissue samples can be repurposed to:

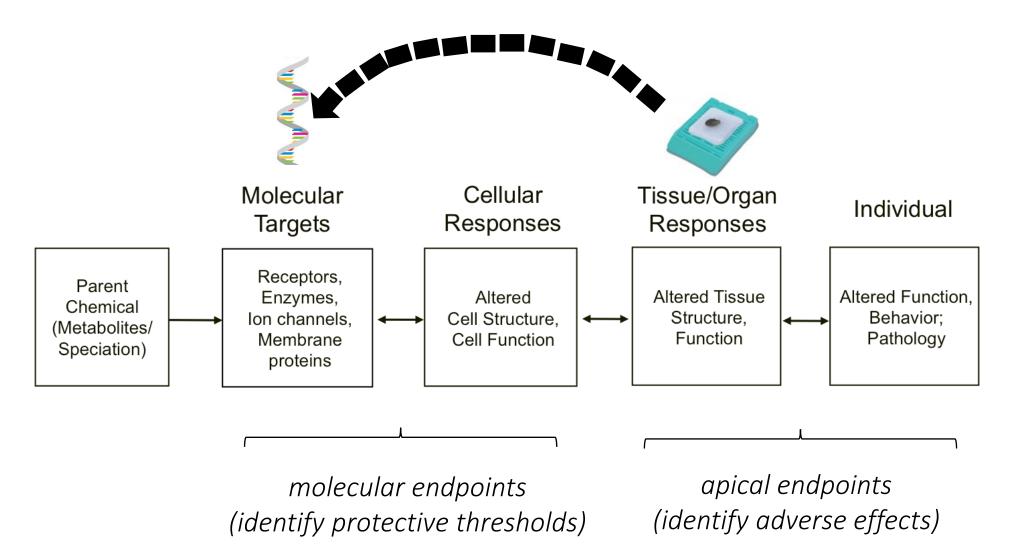


https://opentextbc.ca/anatomyandphysiology/chapter/3-4-protein-synthesis/ http://topcapteam.org/ https://humantoxicologyproject.org/tox-101/pathway-based-toxicology/ http://www.ilocis.org/documents/chpt33e.htm

Quantify and model gene expression



Bridging pathology and pathways





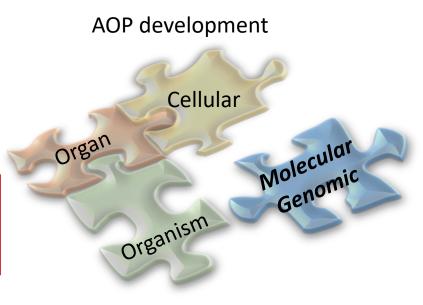
Great potential for adverse outcome pathways

- Billions of archival samples
- Well-characterized pathological data
- Clinically annotated
- Enable rapid assessment of target pathways, dose response, and human health relevance

Important to identify candidate signals of toxicity risk resulting from chemical exposure

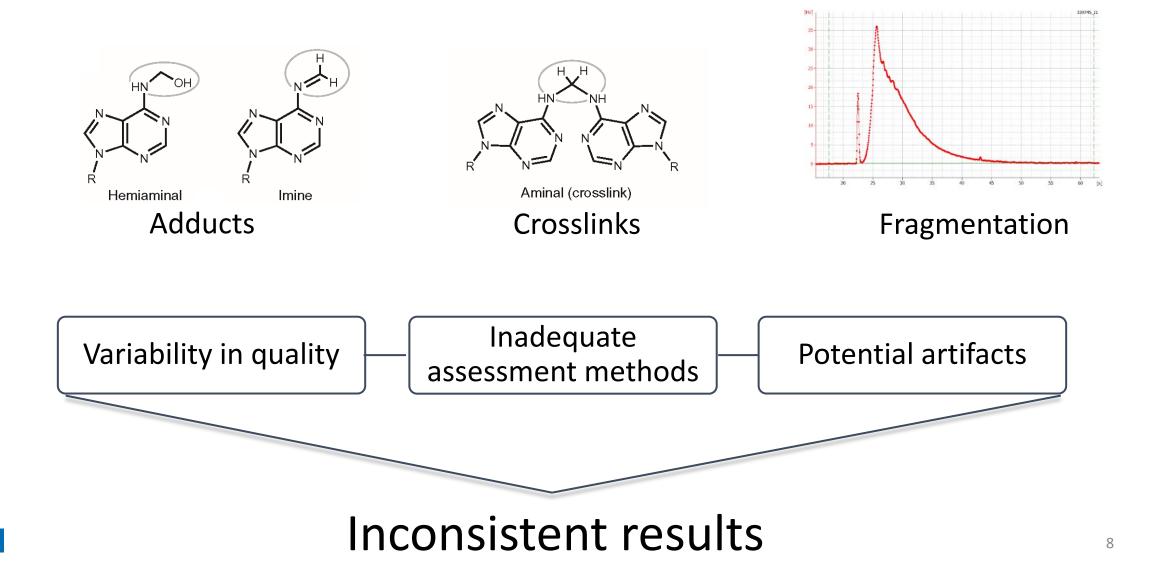


http://topcapteam.org/





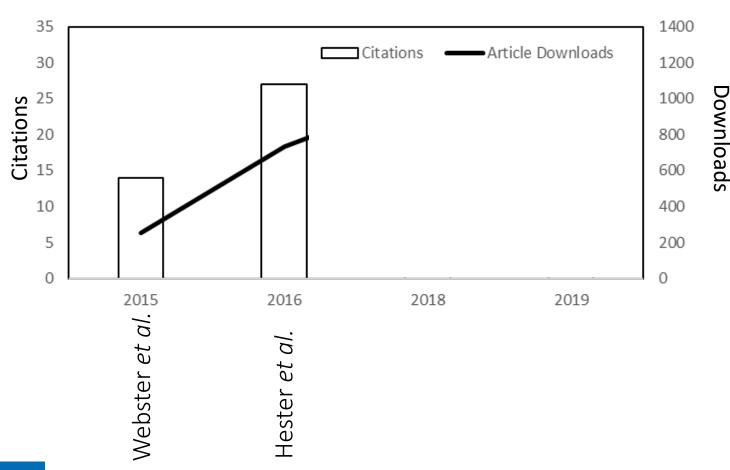
Challenges with FFPE





Objectives

FFPE Workgroup Publications

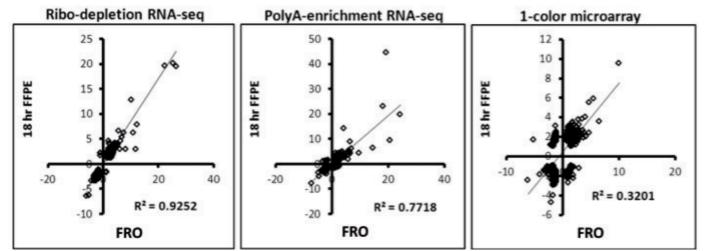




- Apply new technologies
- Characterized major factors
 impacting FFPE quality



Ribo-depletion RNA-sequencing improves gene expression analysis in FFPE



RD SOT Society of Toxicology TOXICOLOGICAL SCIENCES, 148(2), 2015, 460-472

doi: 10.1093/toxsci/kfv195 Advance Access Publication Date: September 10, 2015 Research Article

Mining the Archives: A Cross-Platform Analysis of Gene Expression Profiles in Archival Formalin-Fixed Paraffin-Embedded Tissues

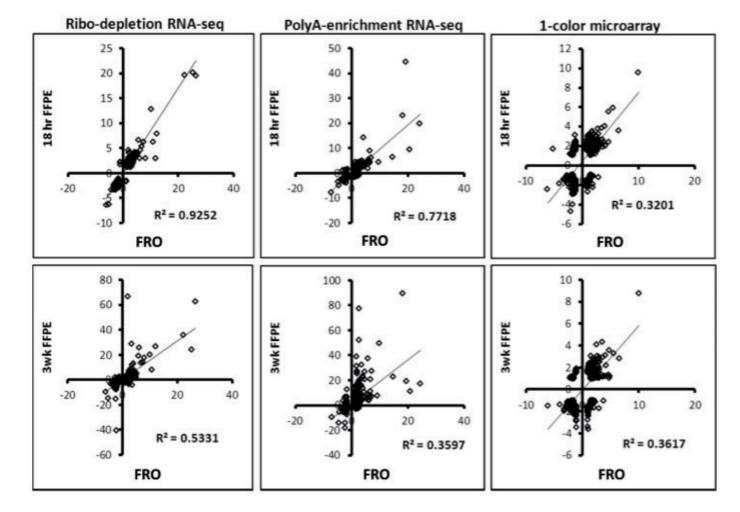
A. Francina Webster^{*,†}, Paul Zumbo[‡], Jennifer Fostel[§], Jorge Gandara[‡], Susan D. Hester[¶], Leslie Recio^{||}, Andrew Williams^{*}, Charles E. Wood[¶], Carole L. Yauk^{*,1,2}, and Christopher E. Mason^{‡,|||,||||,1,2}

Paired liver

- Fresh frozen
- 18 h. FFPE
- 3 wk. FFPE



Time in formalin reduces gene counts





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Paired liver

- Fresh frozen
- 18 h. FFPE
- 3 wk. FFPE

Age in paraffin block influences detection of chemical treatment induced gene response Liver

< 2 yrs. Di-2-ethylhexyl phthalate (DEHP)

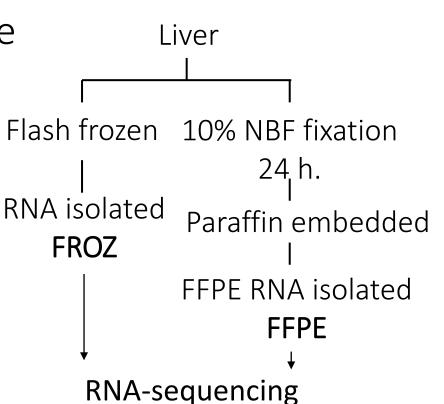
- 4 week-old male B6C3F1 mice
- Doses 0, 1500, 3000 & 6000 ppm in diet
- N=4/dose
- 7 day exposure

>21 yrs. Dichloroacetic acid (DCA)

- 4 week-old male B6C3F1 mice
- Doses 0, 1, 2 & 3.5 g/L in drinking H_2O
- N-6/dose
- 6 day exposure



Volume 154, Issue 2 December 2016

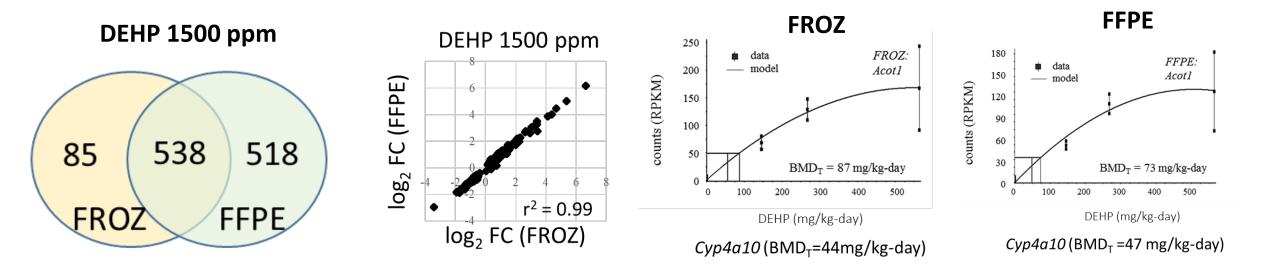


Editor's Highlight: Dose–Response Analysis of RNA-Seq Profiles in Archival Formalin-Fixed Paraffin-Embedded Samples

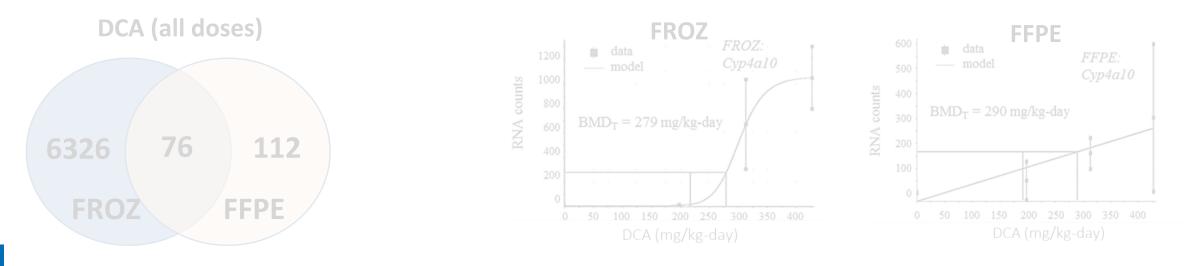
Susan D. Hester, Virunya Bhat, Brian N. Chorley, Gleta Carswell, Wendell Jones, Leah C. Wehmas, Charles E. Wood ∞

Toxicol Sci (2016) 154 (2): 202-213. **DOI:** https://doi.org/10.1093/toxsci/kfw161

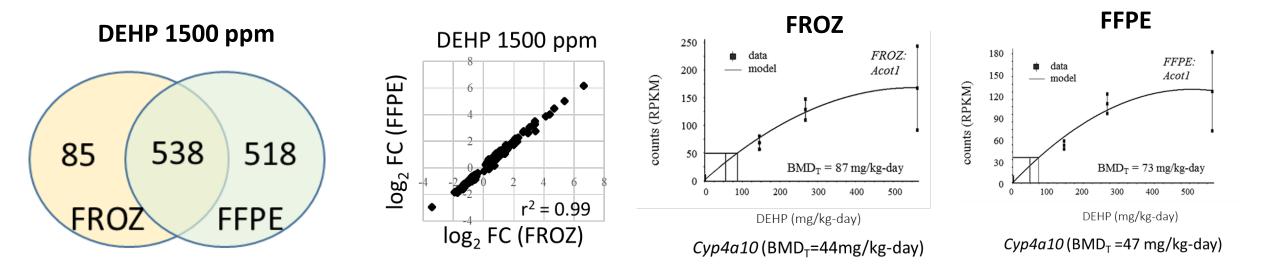
High level of concordance in DEGs across 2 yr. old FFPE samples



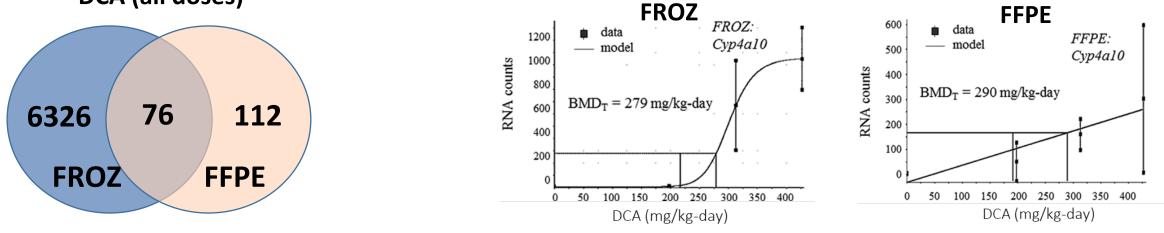
97% reduction in gene counts across >21 yr. FFPE samples



High level of concordance in DEGs across 2 yr. old FFPE samples



97% reduction in gene counts across >21 yr. FFPE samples DCA (all doses)







Major findings

Apply new technologies

- Total RNA-seq outperforms microarray
- Ribodepletion improves gene detection

Characterized major factors impacting FFPE quality

- Time in formalin
- Age in block



Volume 154, Issue 2 December 2016

SORD SOT Society of Toxicolog

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Objectives

35 1400 Citations Article Downloads 30 1200 1000 Downloads 25 Citations 20 15 400 10 5 200 0 0 2015 2016 2019 Wehmas *et al.*800 Webster et al. Hester et al.

FFPE Workgroup Publications

Apply new technologies

• Characterized major factors

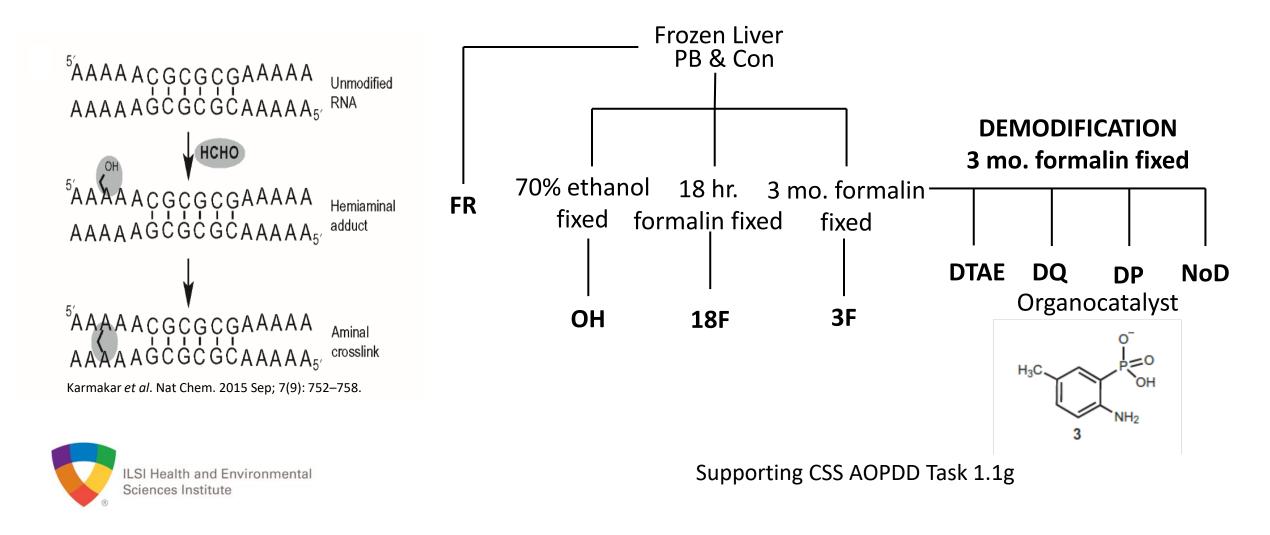
impacting FFPE quality

• Identified methods to improve gene expression data

Developed better metrics for quality assessment

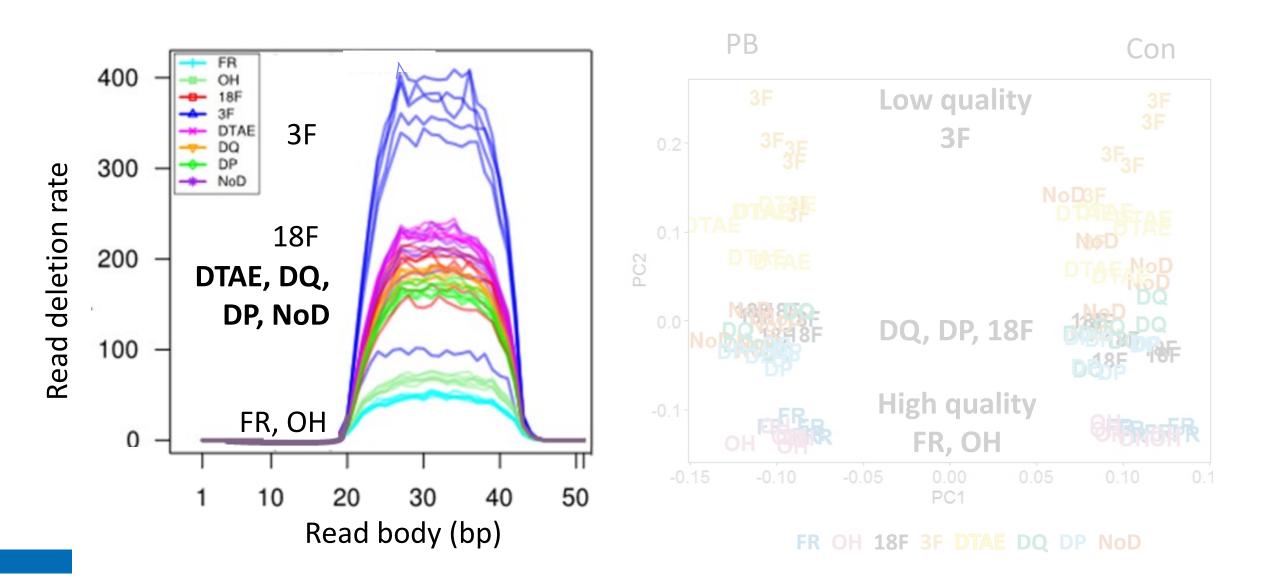


Improving quality of FFPE RNA



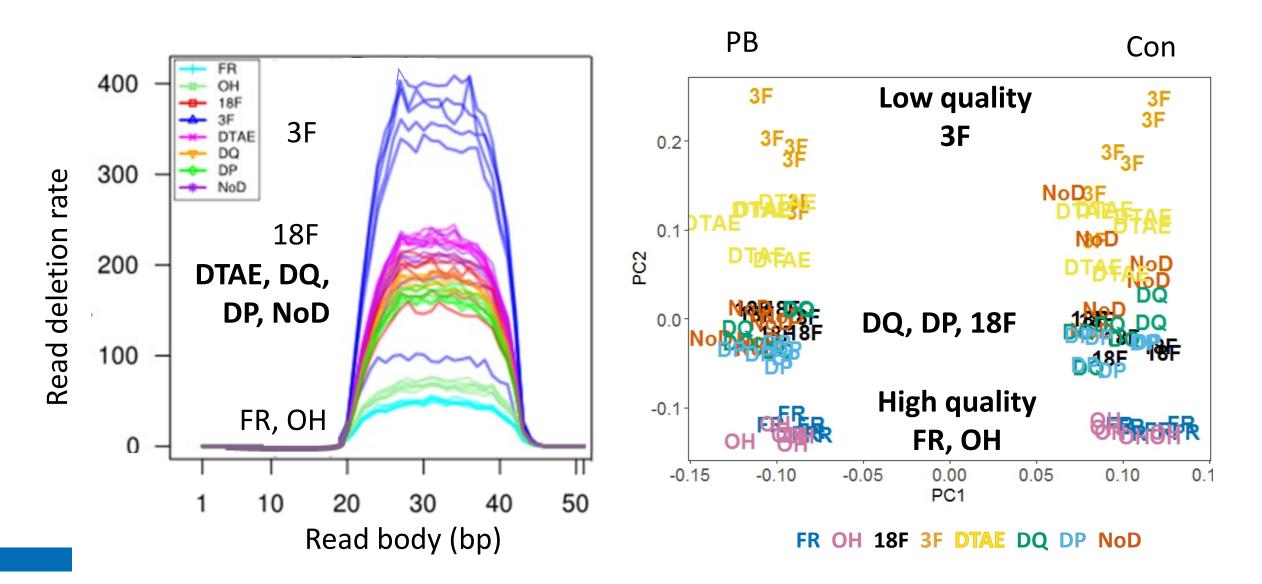


Demodification improves FFPE RNA





Organocatalyst improves FFPE RNA and gene detection





Identifying methods to better evaluate FFPE RNA quality

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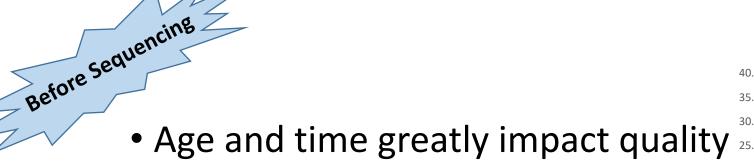
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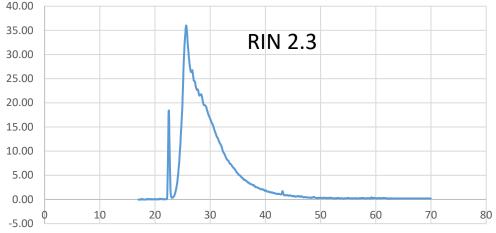
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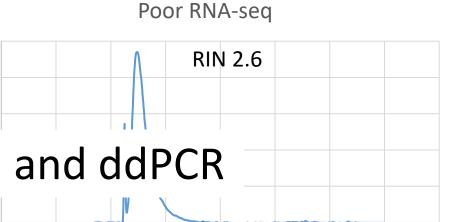
Good RNA-seq



- Better characterize FFPE RNA quality
- Better indicate sequencing success
- Adequately reflect experiment dependent response







40

₆₀ 20

50

70

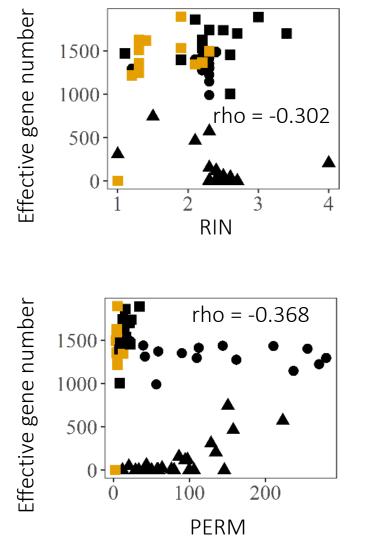
80



RIN and PERM perform poorly with FFPE

Age in block and time in formalin

- RIN performs poorly
- PERM performs poorly
- DV200 shows improvement
- DV100 and ddPCR perform best



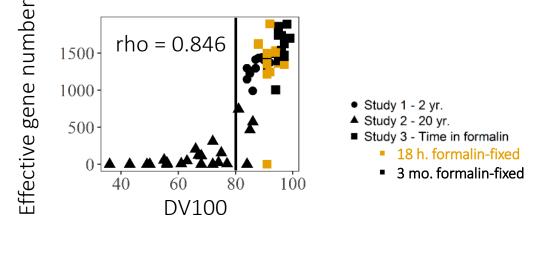
- Study 1 2 yr.
 ▲ Study 2 20 yr.
- Study 3 Time in formalin
 - 18 h. formalin-fixed
 - 3 mo. formalin-fixed

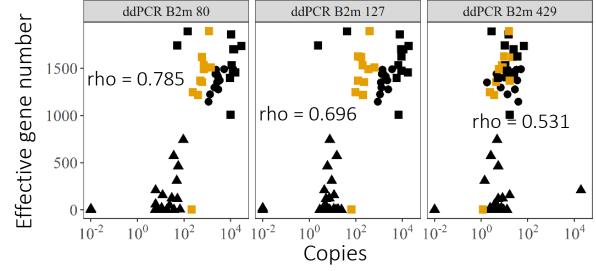


DV100 and ddPCR best distinguishes FFPE RNA quality

Age in block and time in formalin

- RIN performs poorly
- PERM performs poorly
- DV200 shows improvement
- DV100 and ddPCR perform best
- DV100>80 distinguishes high and low quality FFPE

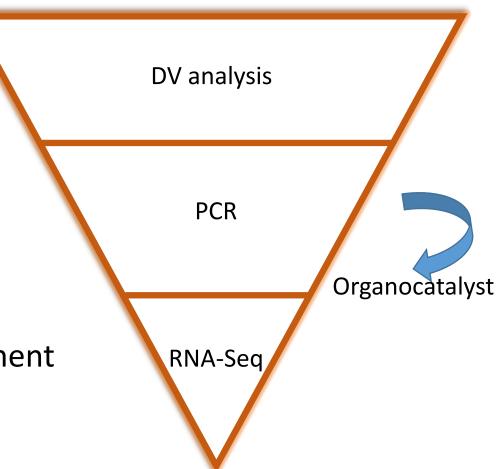






Major findings: Strategy for sequencing FFPE samples

- 1. Evaluate DV100
- 2. If DV100 > 80%, sequence
- 3. If DV100 is near 80%, run qRT-PCR
- 4. Use 80-100 nt amplicon size
- 5. If >500 copies of housekeeping gene detected, sequence
- 6. If <500 copies, try organocatalyst treatment

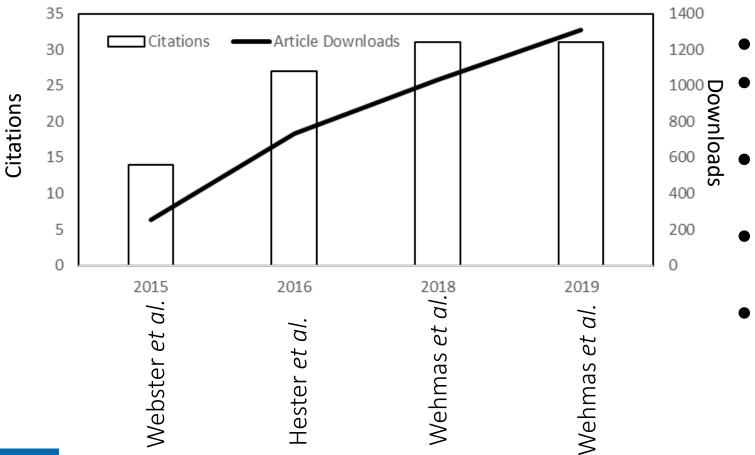






Objectives

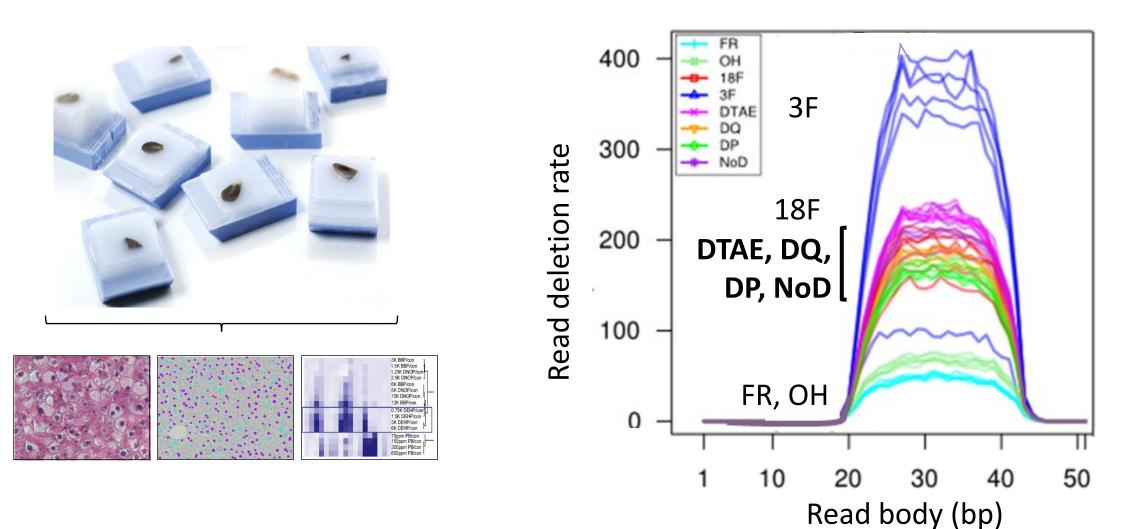
FFPE Workgroup Publications



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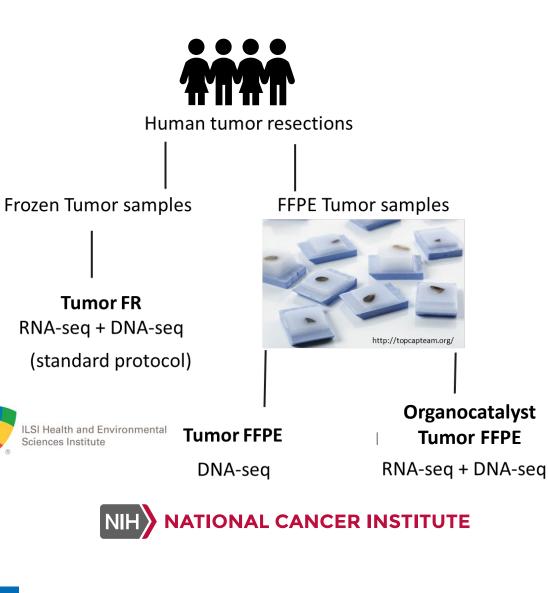


Organocatalyst reduces RNA deletion rates, what about DNA?



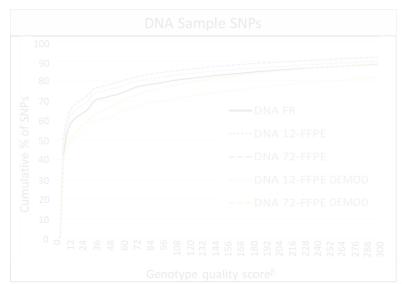


Organocatalyst increases confidence in variant calls



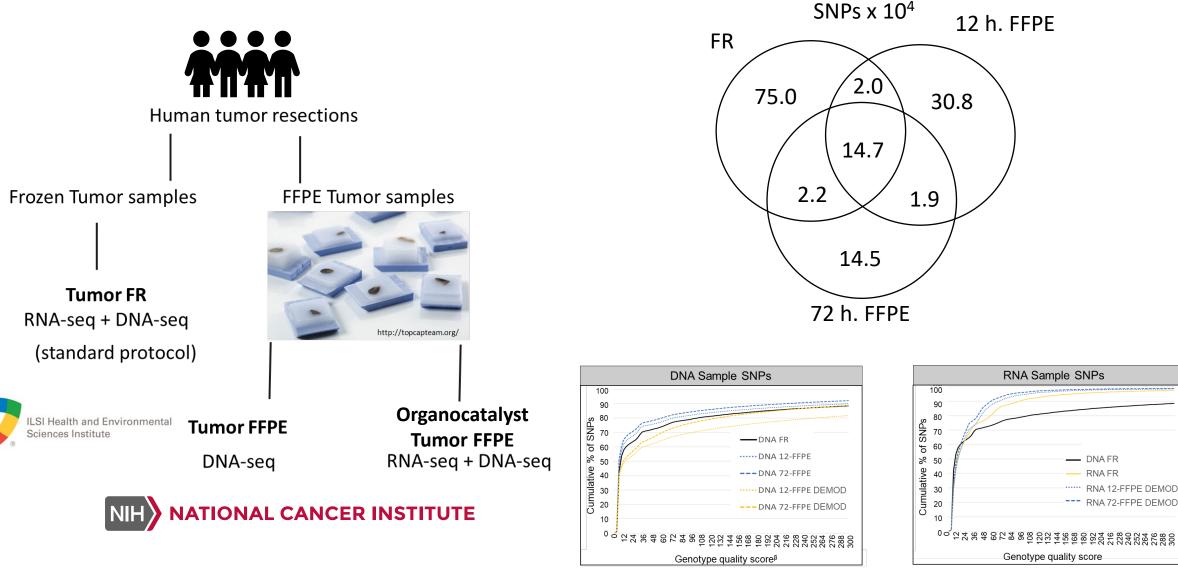
Wehmas et al. 2020 in preparation







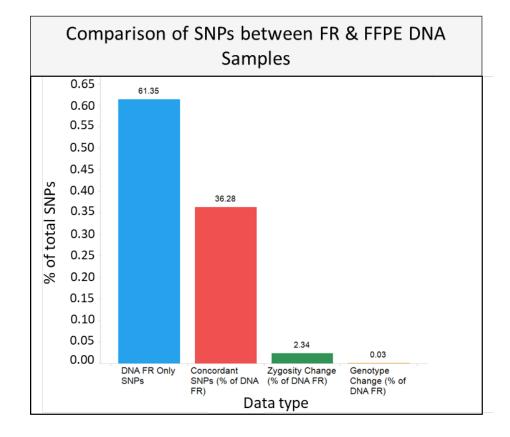
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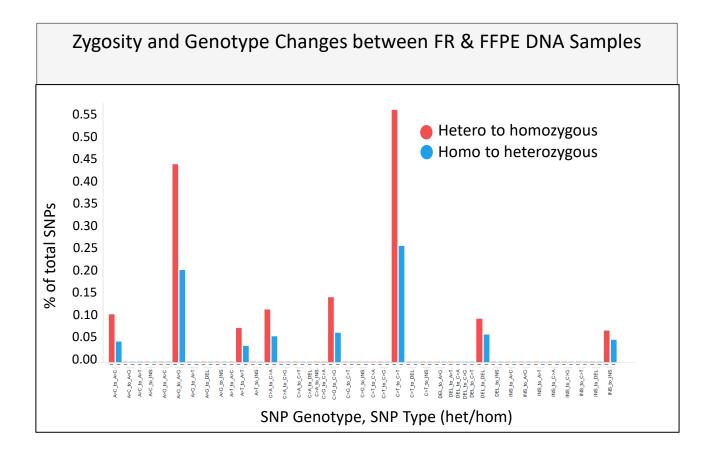


^B The Genotype quality score represents the Phred-scaled confidence that the genotype assignment is correct



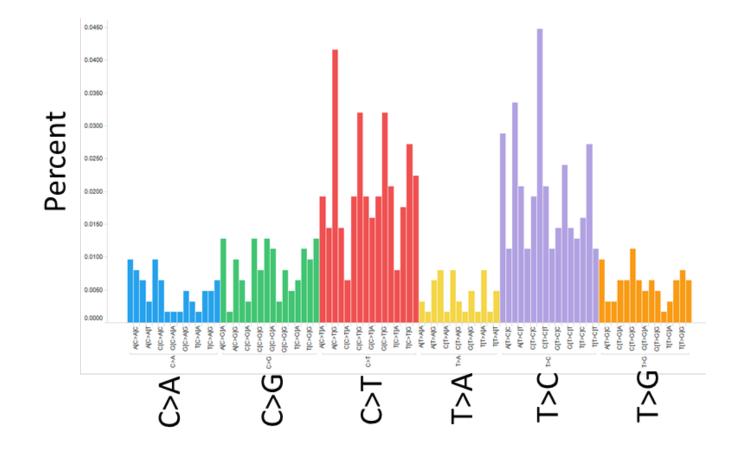
Fixation results mainly in zygosity changes for variant calls





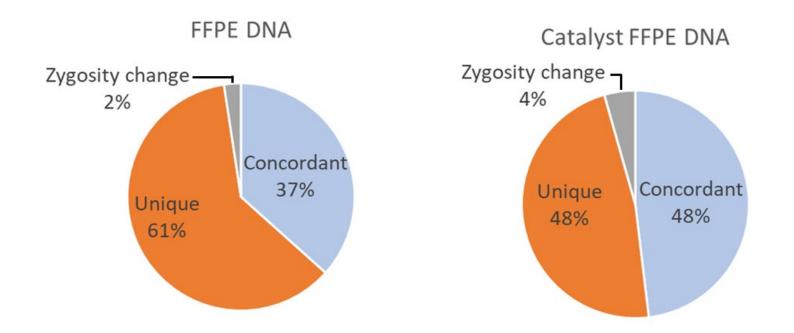


FFPE damage more likely to cause changes of C>T and T>C with < 1% = "Genotype Changes"





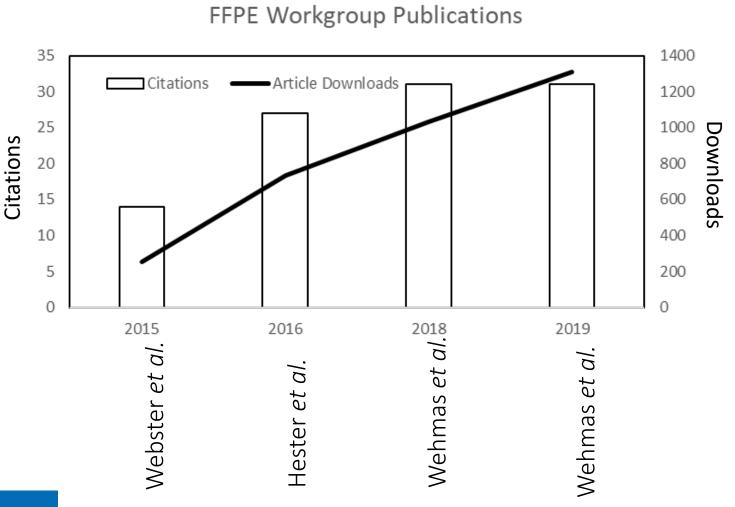
Organocatalyst treatment improves concordance in mutation calls by 11.5%







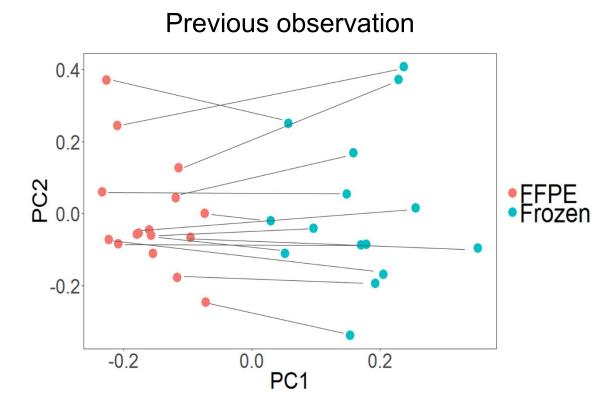
Major findings and unanswered questions



- Applied new technologies
- Characterized major factors impacting FFPE quality
- Identified methods to improve gene expression data
- Developed better metrics for quality assessment;
- Translated results to clinical FFPE and improved SNP detection
- FFPE artifacts?
- Age limitations?

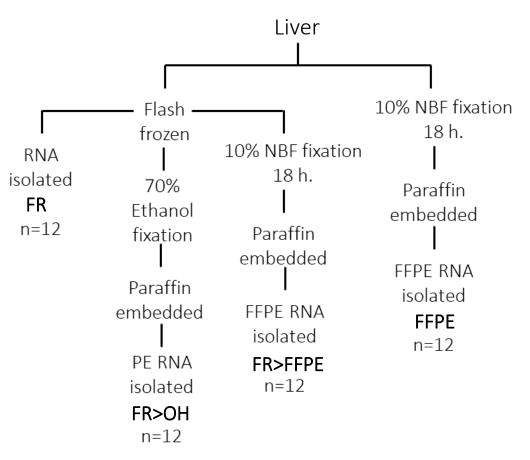


Formalin fixation causes shift in gene response



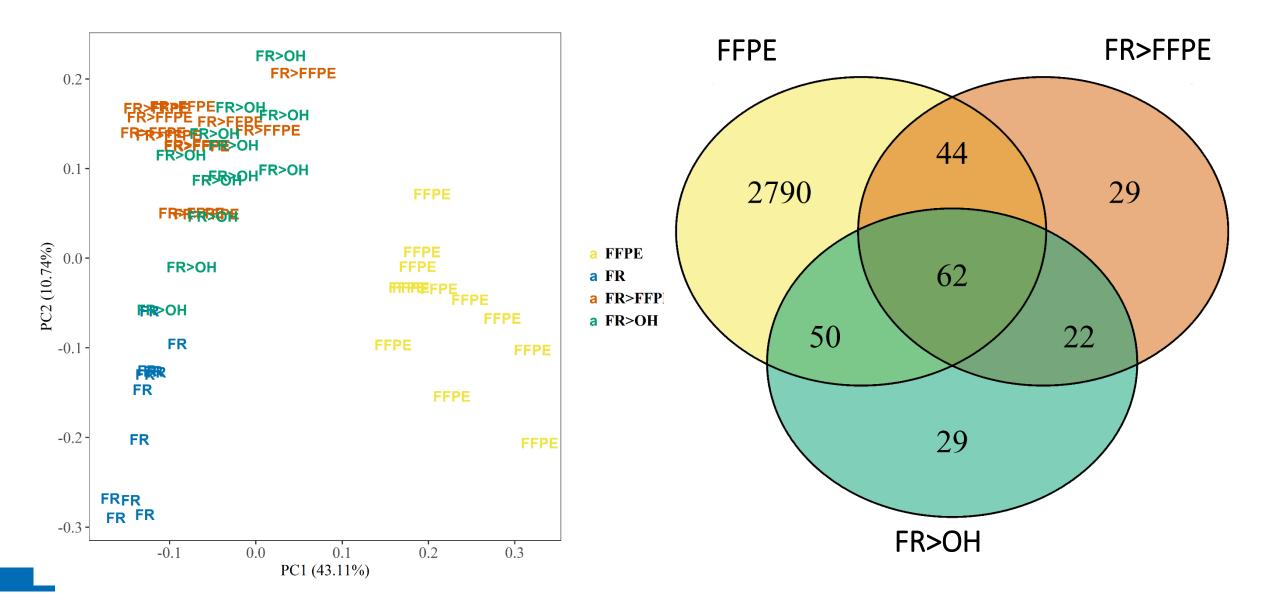
Wehmas, L. C., et al. (2020). "Formalin fixation has wide spread genomic effects in preserved tissue samples". Submitted.

- Male B6C3F1 mice
- PB exposed 0 or 600 ppm
- n =6/dose



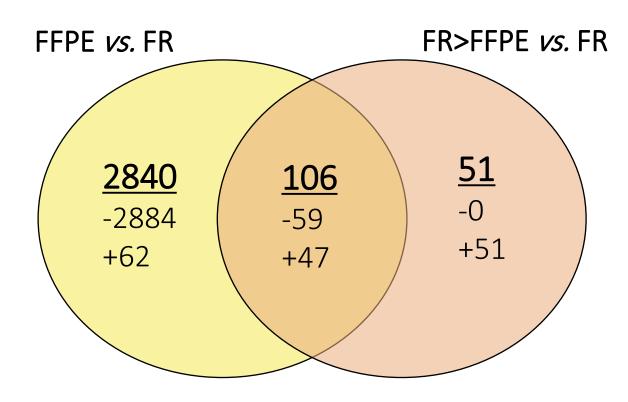


Direct formalin fixation significantly impacts gene expression





Direct formalin fixation impacts cell metabolism and transcription

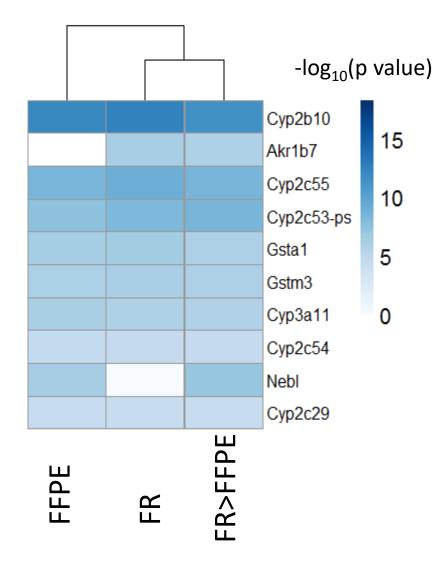


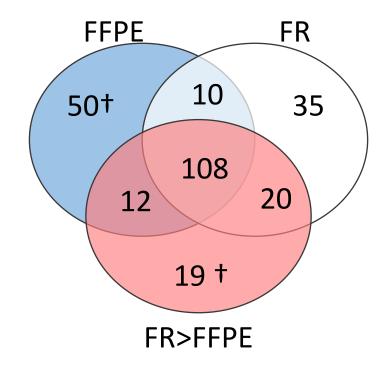
| FFPE vs. FR Canonical pathways | |
|--|--------|
| -log ₁₀ (p | value) |
| Oxidative Phosphorylation | 40 |
| Mitochondrial Dysfunction | |
| EIF2 Signaling | 30 |
| LXR/RXR Activation | |
| Protein Ubiquitination Pathway EXR/RXR Activation | |
| Superpathway of Cholesterol Biosynthesis | 20 |
| Coagulation System | |
| Extrinsic Prothrombin Activation Pathway | 10 |
| Acute Phase Response Signaling | |
| Phagosome Maturation | |
| Superpathway of Melatonin Degradation | |
| Melatonin Degradation I | |
| Complement System | |
| Serotonin Degradation | |
| tRNA Charging | |
| Nicotine Degradation III | |
| Nicotine Degradation II | |
| Glutathione-mediated Detoxification | |
| LPS/IL-1 Mediated inhibition of RXR Function | |

Study 2 Study 1 Present Study



Biomarkers of PB exposure are detected across all groups

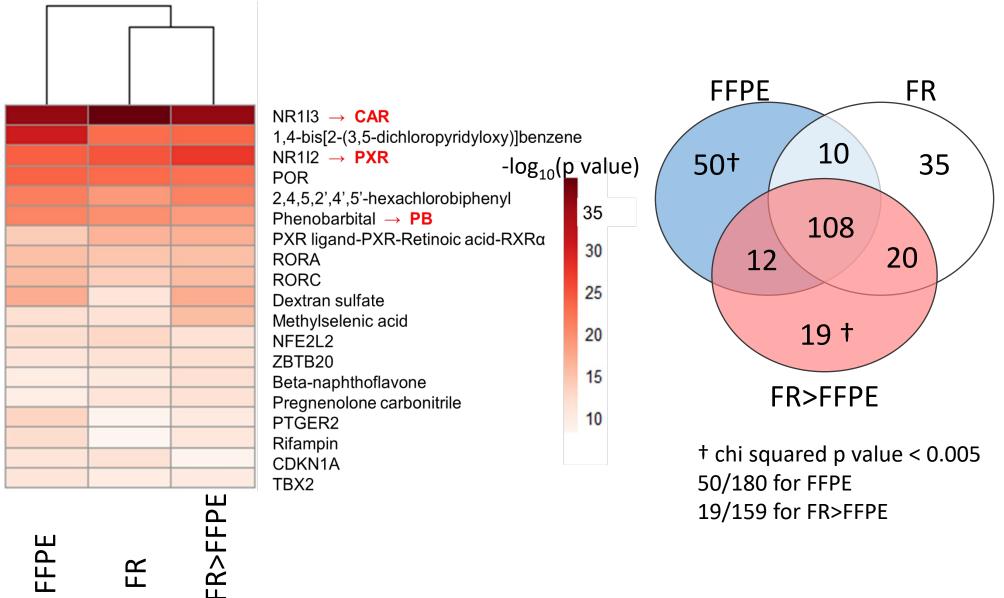




+ chi squared p value < 0.00550/180 for FFPE19/159 for FR>FFPE



Chemical (PB) response remains detectable



FR



>21 yrs. FFPE results in 97% reduction in gene counts

1200

1000

800

600

400

200

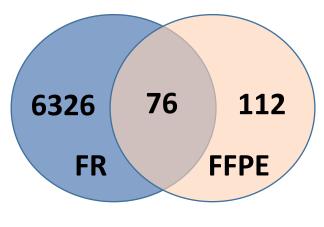
0

RNA counts

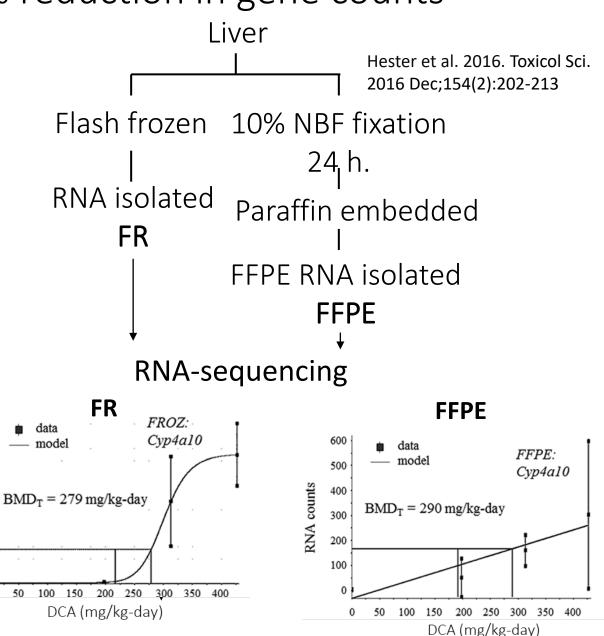
>21 yrs. Dichloroacetic acid (DCA)

- 4 week-old male B6C3F1 mice
- Doses 0, 1, 2 & 3.5 g/L in drinking H_2O
- N-6/dose
- 6 day exposure

DCA (all doses)









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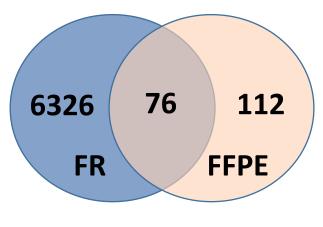
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RNA counts

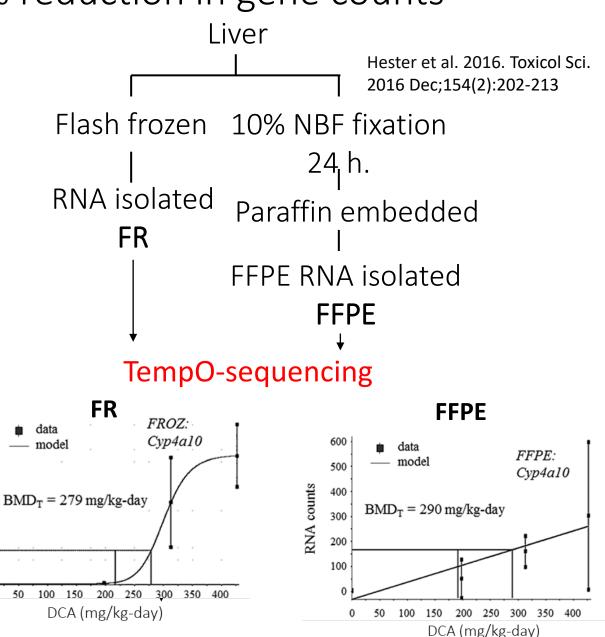
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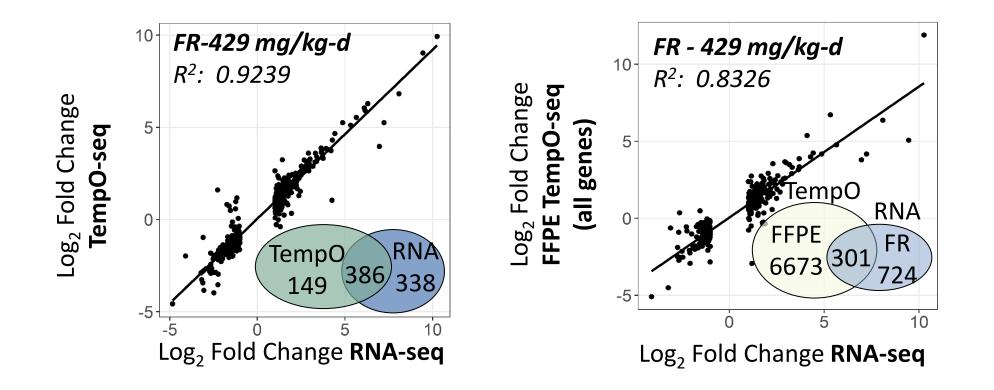






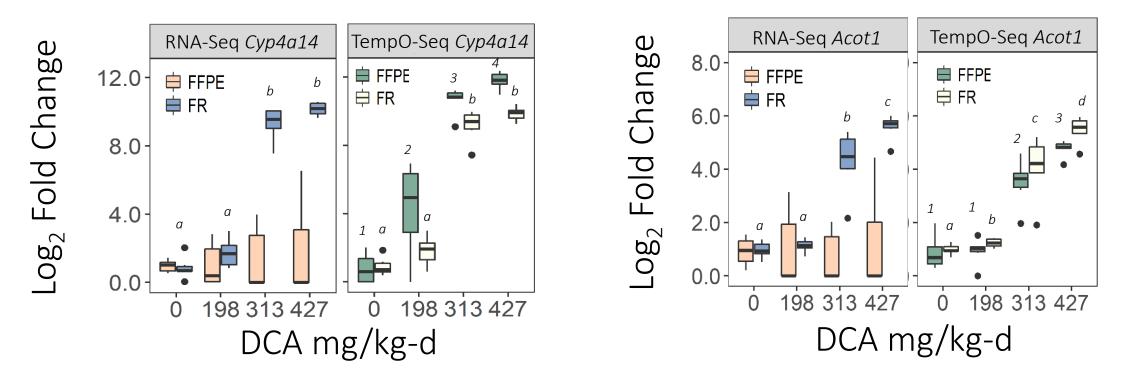


TempO-seq significant genes concordant with RNA-seq





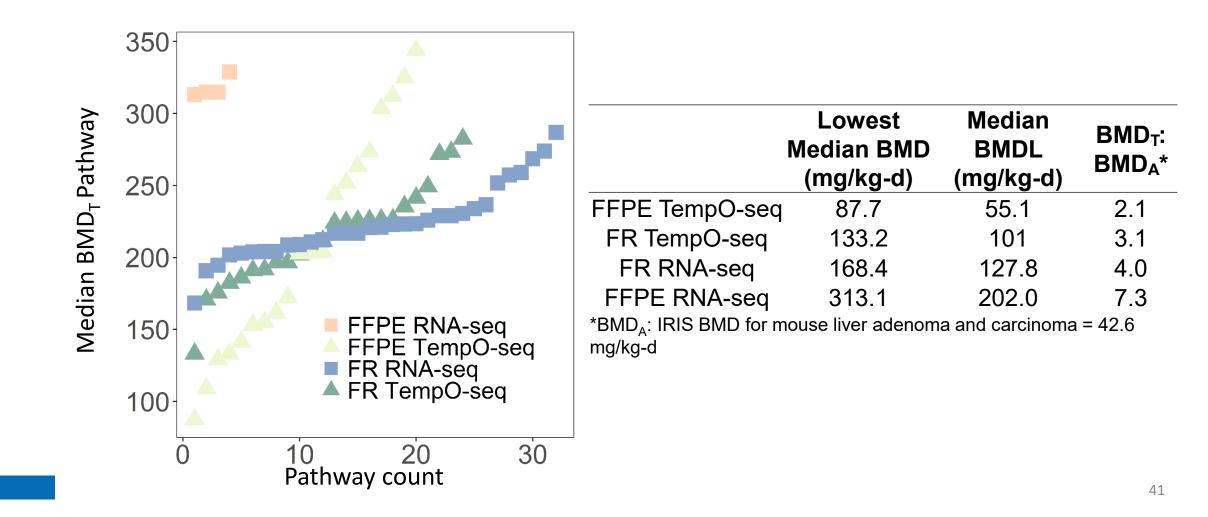
TempO-seq FFPE more consistent with frozen marker genes



a, b, c, and d: FR significant difference (p-value <0.05) between dose groups. 1, 2, 3, and 4: FFPE significant difference (p-value <0.05) between dose groups.



TempO-seq gene response BMD within 2.1-3.1 fold of traditional value

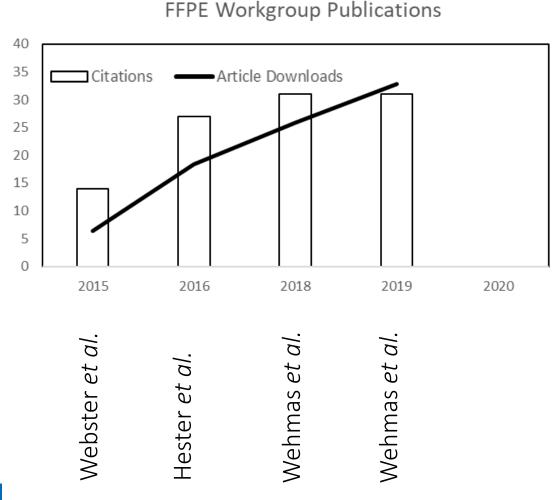




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Major findings





• Applied new technologies

1600

1400

1200

1000

800

600

400

200

Ω

Downloads

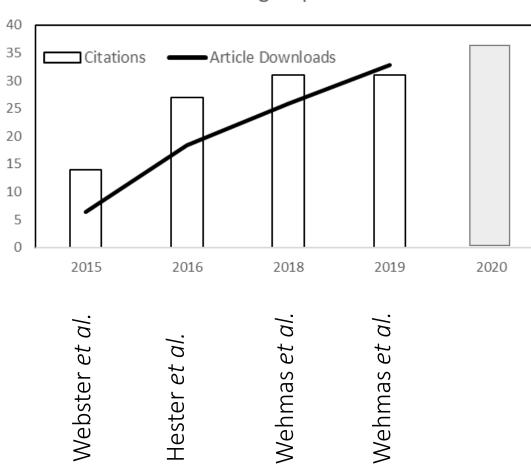
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- Identified artifacts and importance of controls
- Improved transcriptomic benchmark dose analysis for >21 yr. old FFPE





Major findings





FFPE Workgroup Publications

1600

1400

1200

1000

800

600

400

200

Ω

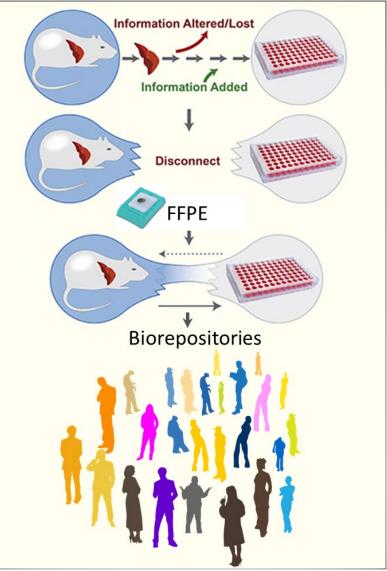
Downloads

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Archival tissue samples can be repurposed to:

- Quantify gene expression
- Understand chemical mode of action
- Expand toxicity pathways
- Bridge molecular and traditional toxicology data
- Save resources and time
- Aid translation to humans



https://doi.org/10.1124/jpet.117.245019



Biorepository resources

- Specimen Resource Locator https://specimens.cancer.gov/
- Biorepositories & Biospecimen Research Branch (BBRB) -<u>https://biospecimens.cancer.gov/default.asp</u>
- Mayo Clinic Biorepositories program <u>https://www.mayo.edu/research/centers-programs/mayo-clinic-biobank/overview</u>
- Specialized Programs of Research Excellence (SPORE)https://www.cancer.gov/about-nci/budget/fact-book/extramuralprograms/spores
- National Toxicology Program Archives-<u>https://ntp.niehs.nih.gov/data/archives/index.html</u>
- National Gene Vector Biorespository <u>https://www.ngvbcc.org/Home.action</u>



Acknowledgments



<u>EPA</u>

Charles Wood, DVM, PhD (now BI) Susan Hester, PhD Gail Nelson Judy Schmidt AOP task members

<u>NCI</u>

Ping Guan Helen Moore

Quintiles

(Q2-Solutions, Durham, NC) RNA-Seq processing



NATIONAL CANCER INSTITUTE

Funding: US EPA CSS Program

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Supplemental-Direct formalin fixation effect does not confound chemical treatment response

