

Multi-omic data
illuminates the placenta's
role as a mediator
between prenatal EDC
exposure and preterm
birth



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Center for Developmental Biology | Seattle Children's Research Institute
Dept. of Pediatrics, Division of Genetic Medicine | University of Washington
Adjunct: Environmental and Occupational Health Sciences

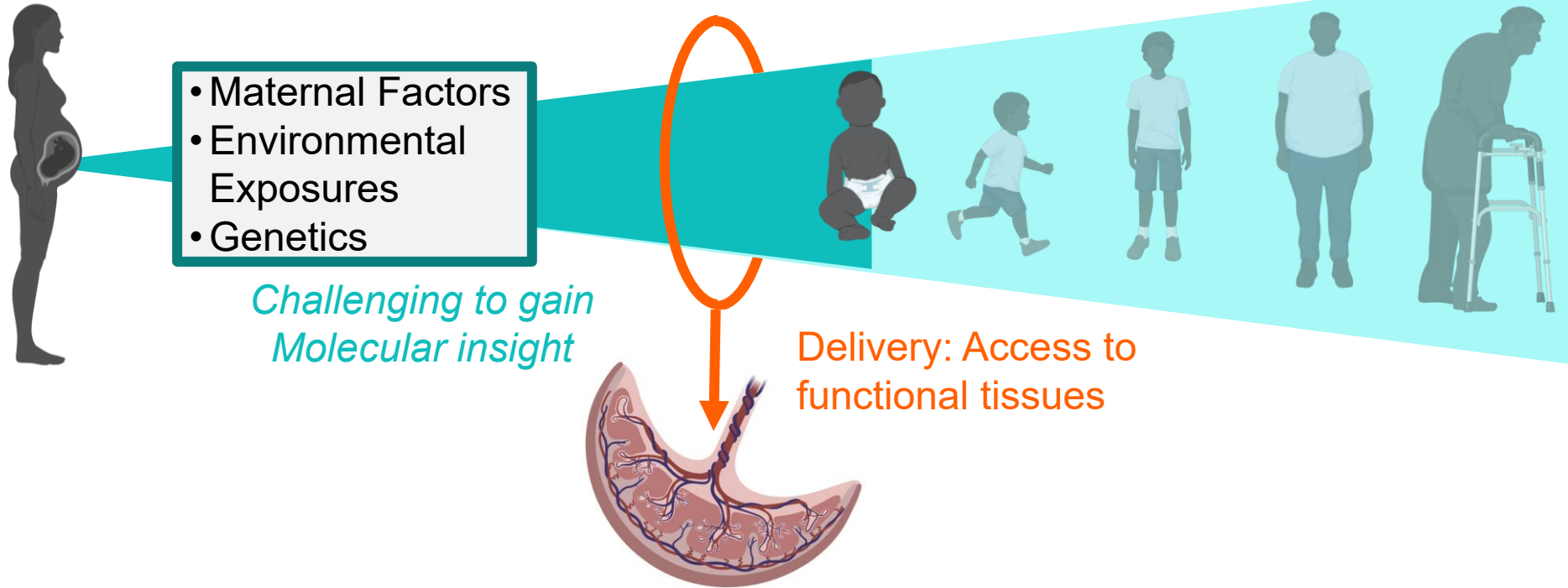


INTERDISCIPLINARY CENTER FOR
EXPOSURES, DISEASES, GENOMICS
AND ENVIRONMENT

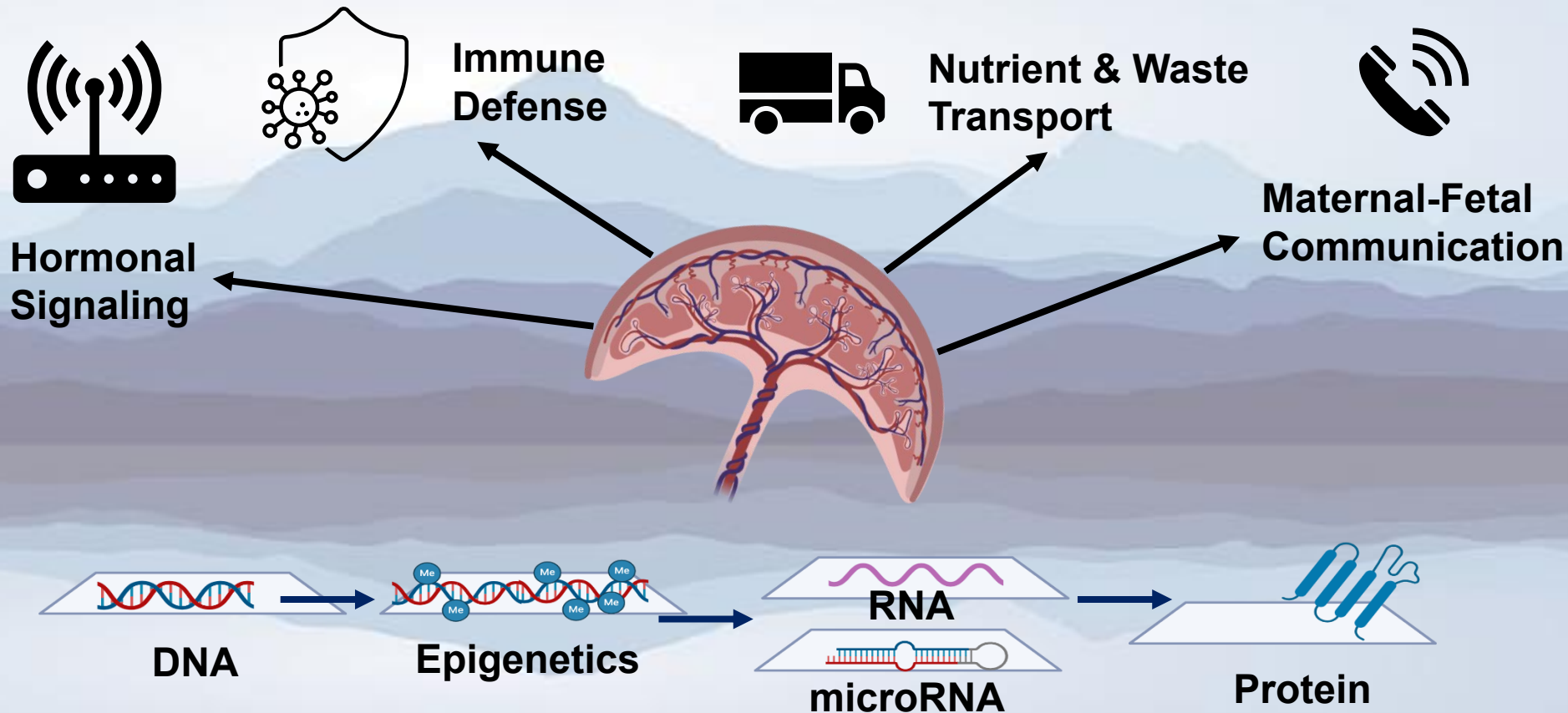


Seattle Children's[®]
HOSPITAL • RESEARCH • FOUNDATION

Research Focus: Using Placental omics data to link the Prenatal Environment and Infant Health

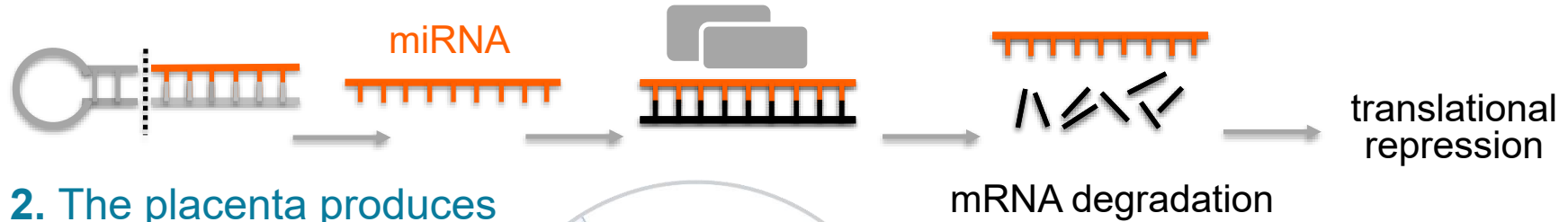


Placental Omics Data: A reflection of molecular processes essential to placental function

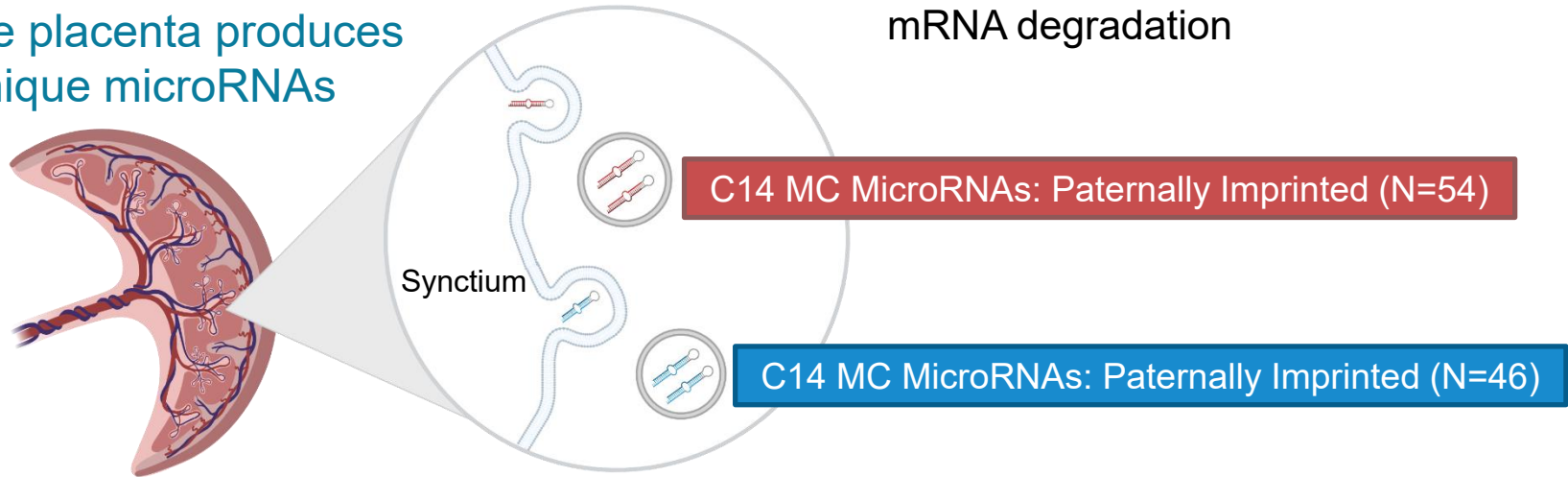


Placental microRNAs are important post transcriptional regulators and signaling molecules

1. microRNAs: Post transcriptional repression of specific gene targets

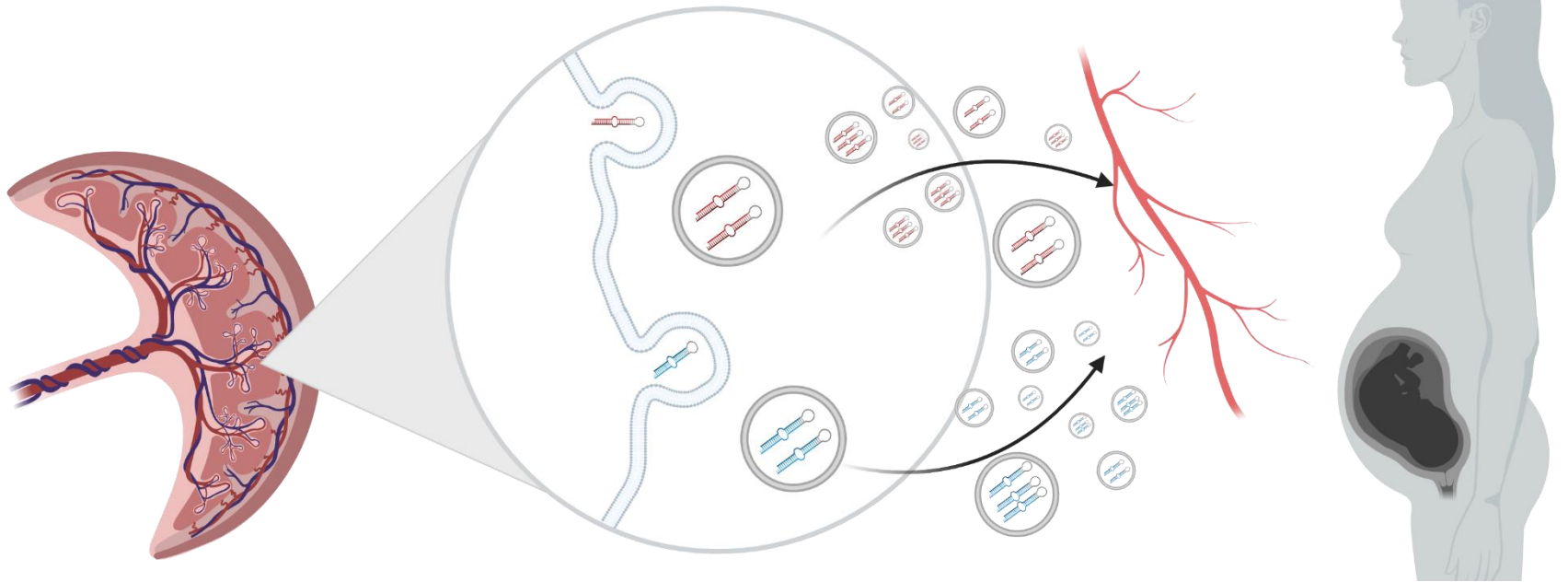


2. The placenta produces unique microRNAs

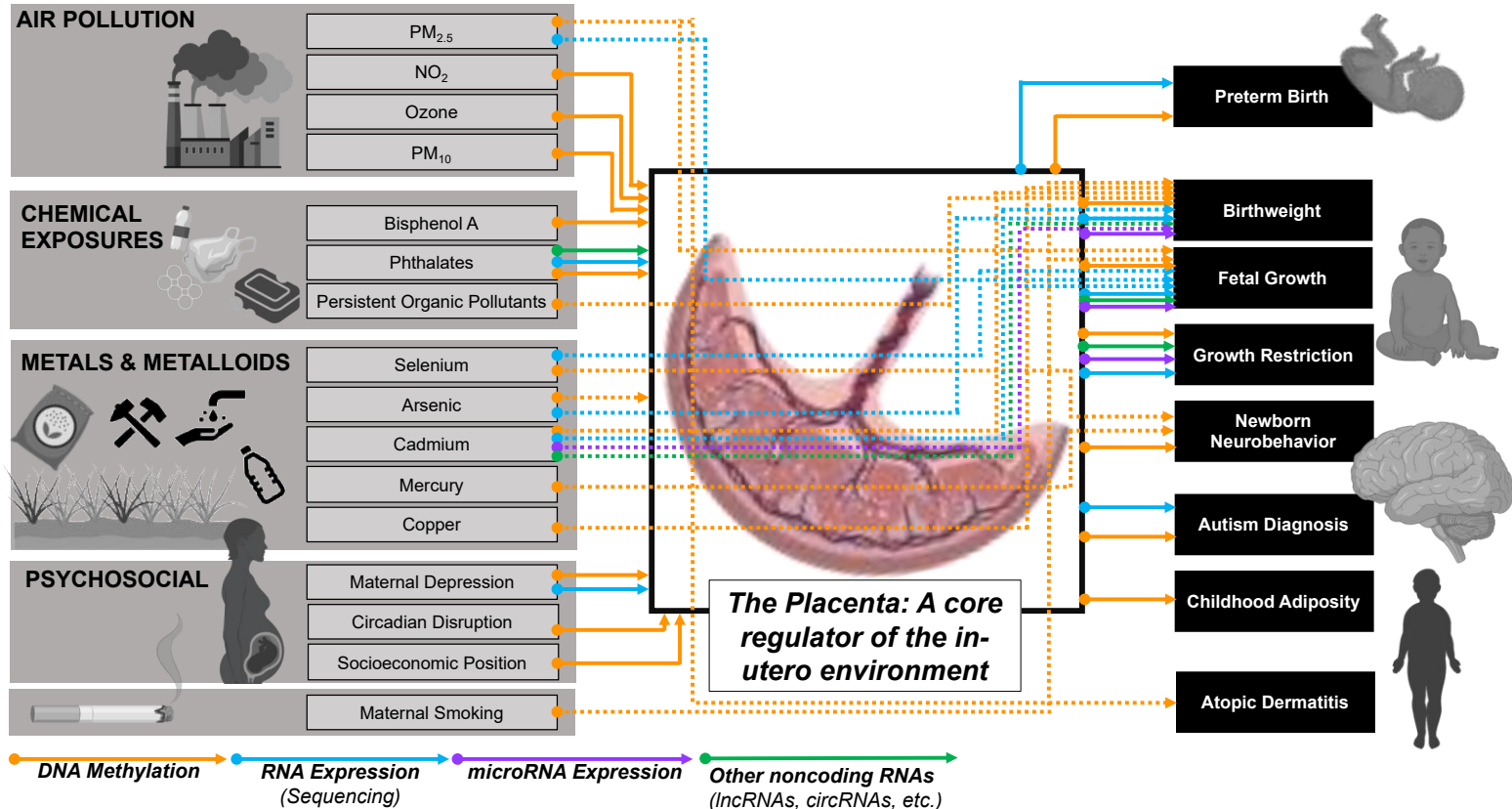


Placental microRNAs are important post transcriptional regulators and signaling molecules

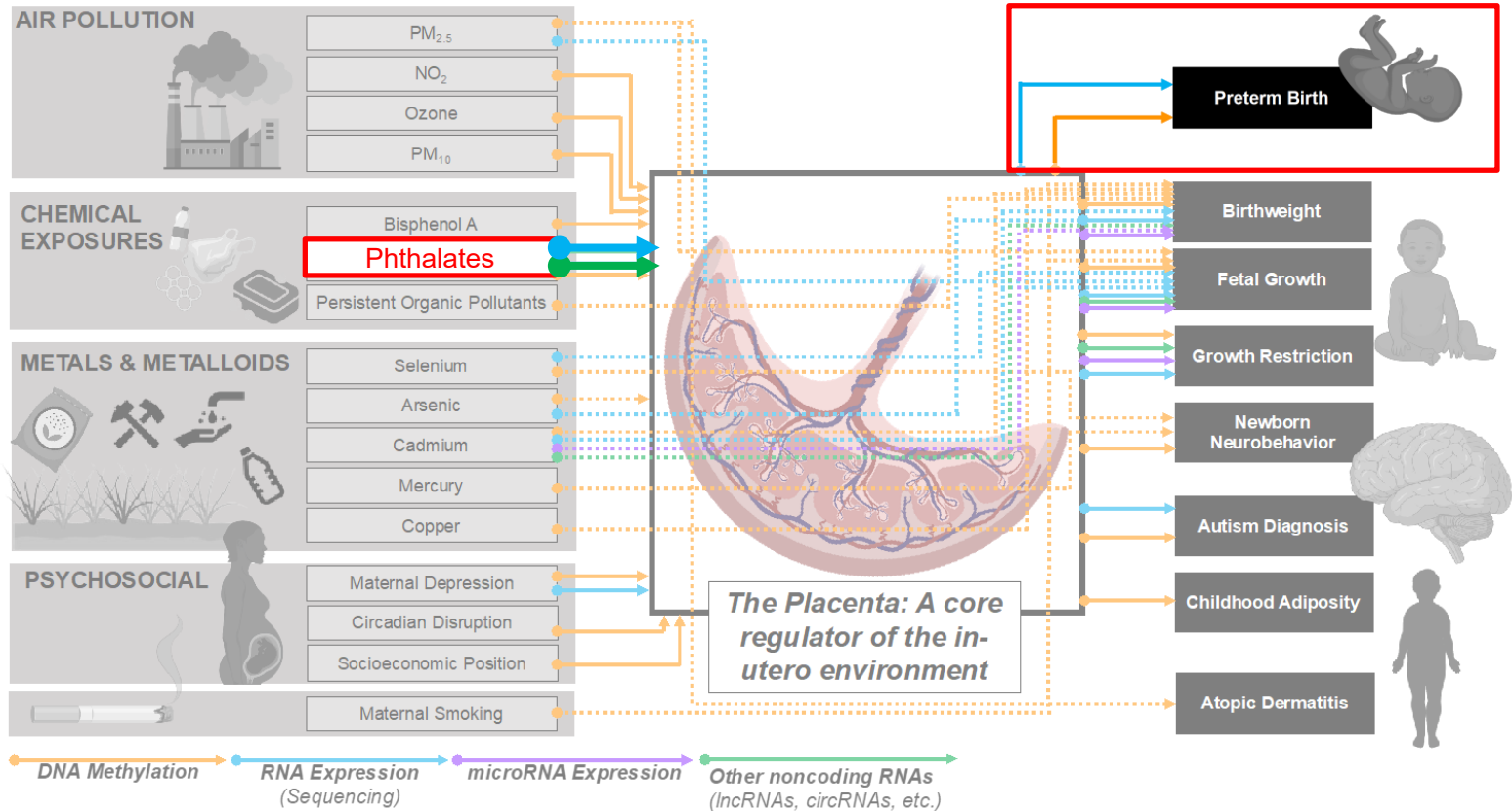
3. C14 and C19 Placental microRNAs are released into maternal and fetal circulation and act as signaling molecules



Summary of Placental 'Omics Studies 2015-2021



Addressing Research Gaps



Preterm Birth: A Major Healthcare Challenge for Infants and Families



PTB is the leading cause of infant mortality: 35.8% of infant deaths are related to prematurity¹

Long term morbidity: developmental delays, vision problems, feeding difficulties, cerebral palsy

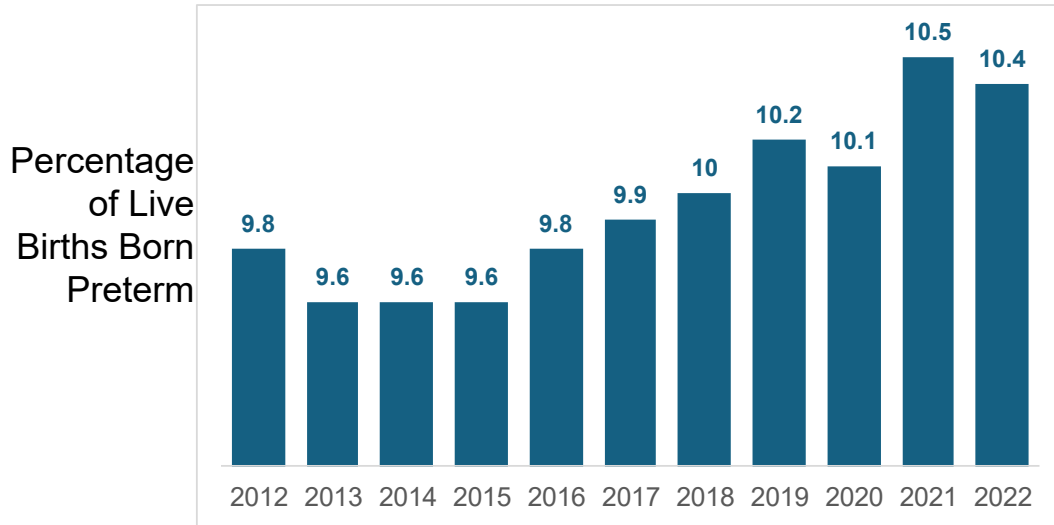
Preterm Infants Require intensive acute and long term care:

- Daily NICU Cost: 3,500\$-20,00\$²
- Limited improvements in long term health outcomes in last 2 decades²

Annual Societal Cost: \$25.2 Billion Dollars (United States)³

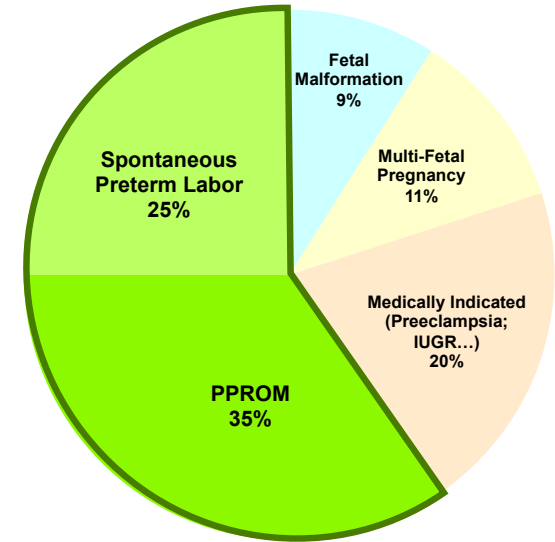
Research Gap: Understanding the Etiology of sPTB

A. Preterm Rate in US (2022): 10.4%



2023 March of Dimes PTB Report Card

B. Causes of Preterm Birth

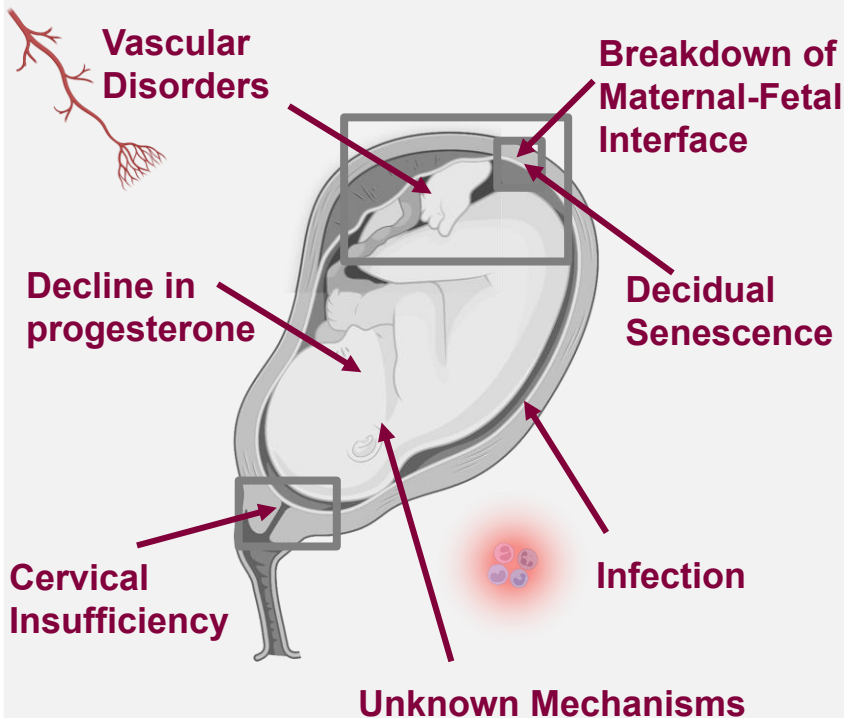


Gracie S et al. BMC Pregn. Childbirth. 2011

Unmet Clinical Needs: Enhanced Diagnostics; Better understanding of causes of spontaneous preterm birth; Better Prevention Strategies; equitable access to care

Causes & Risk factors for Spontaneous Preterm Labor

A. UNDERLYING MECHANISMS



B. RISK FACTORS

Maternal Genetics

- Family History
- GWAS 1: N=43,568; 6 genetic loci (Not fetal)¹
- GWAS 2: N=195,555; 7 loci (fetal and maternal)²
- GWAS 3: N=84,689; 1 locus³

Medical Conditions

- Previous History of sPTB
- Cervical Insufficiency

Behavioral and sociodemographic Factors

- Lower Education
- Geographic Location
- Nutritional Deficiencies
- Smoking, Illicit Drug use
- Maternal Stress

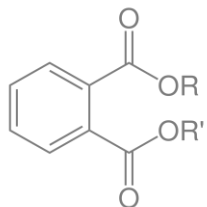
Environmental Exposures

- **Endocrine Disrupting Chemicals**
- Air Pollution

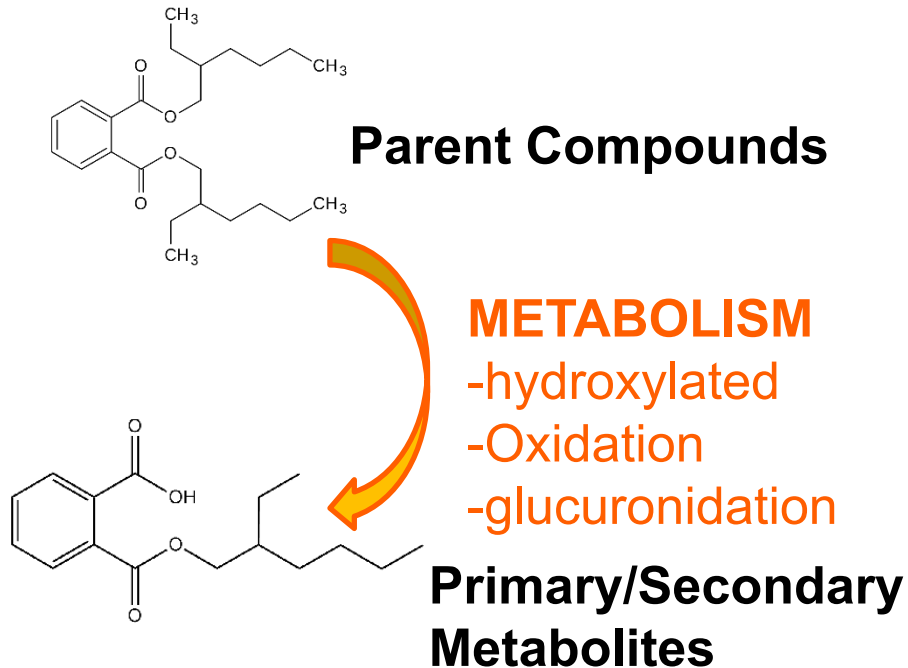
1. Zhang et al, NEJM, 2017 2. Nvais et al, Nature Genetics, 2023; 3. Liu et al, Nature Communications, 2019

Adapted from: Roberto Romero et al. Preterm Labor: One Syndrome Many Causes. Science 2014 ; Sheikh et al, Spontaneous Preterm birth and SNPs: A recent Update, BMC Genomics, 2016

Phthalates are Ubiquitous Chemicals present in a variety of consumer goods and products



Phthalates



Prenatal Phthalate Exposure & Increased risk of sPTB

Original Investigation

ONLINE FIRST

July 11, 2022

Associations Between Prenatal Urinary Biomarkers of Phthalate Exposure and Preterm Birth

A Pooled Study of 16 US Cohorts

Barrett M. Welch, PhD¹; Alexander P. Keil, PhD²; Jessie P. Buckley, PhD³; et al

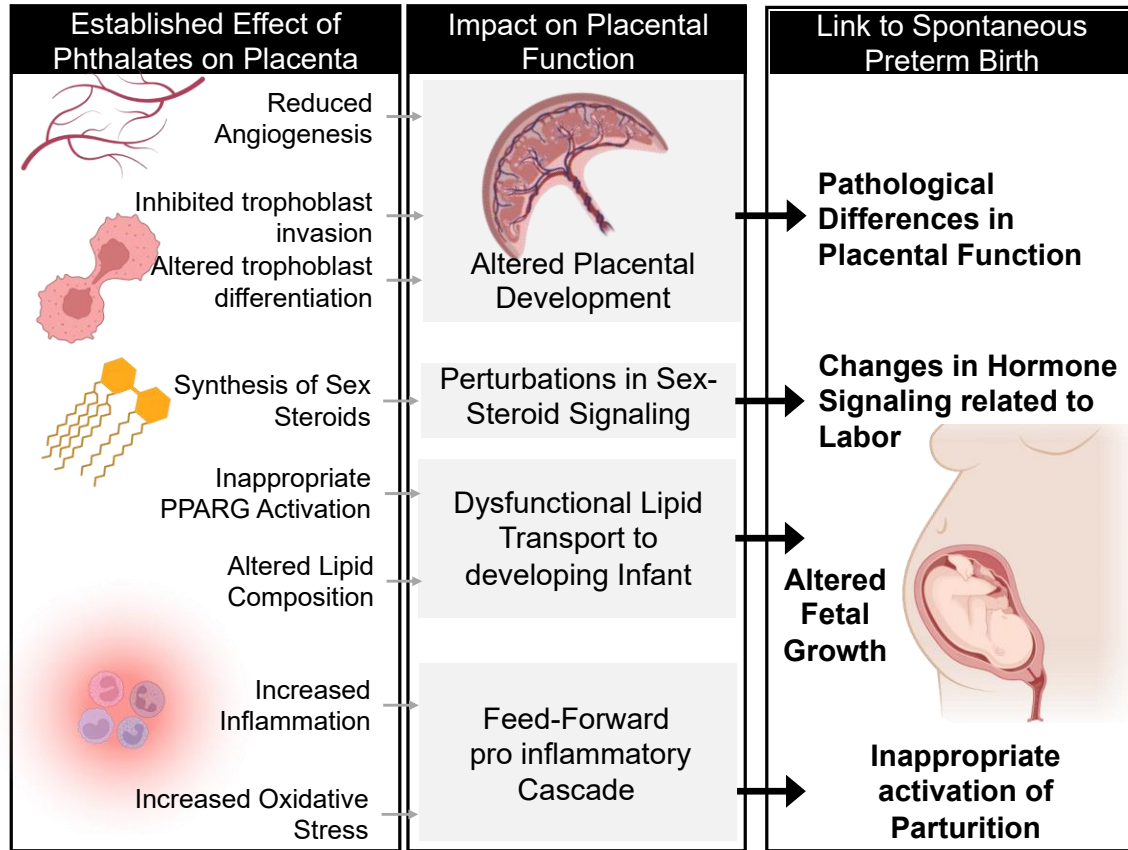
[» Author Affiliations](#) | [Article Information](#)

JAMA Pediatr. Published online July 11, 2022.

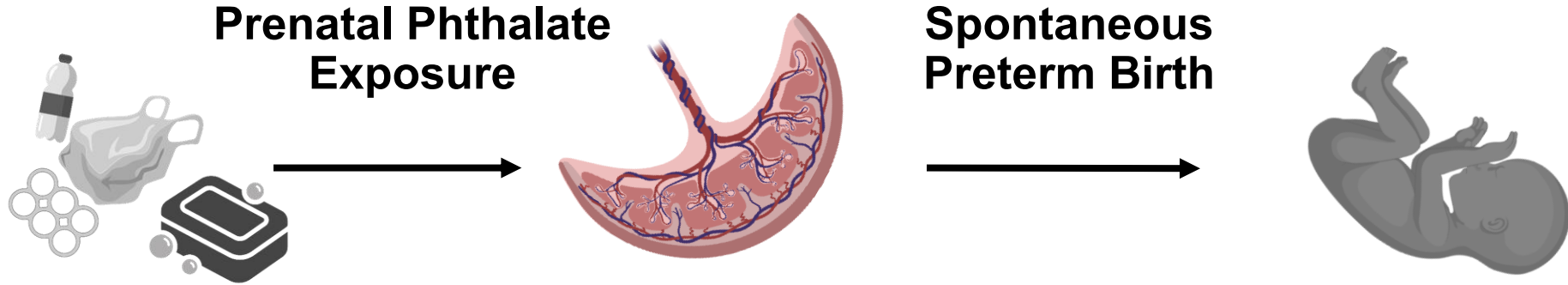
doi:10.1001/jamapediatrics.2022.2252

- 6045 pregnant women across 16 US studies
- Higher concentrations of most phthalate metabolites were associated with slightly higher odds of preterm birth
- Reducing mixture of phthalate metabolite levels by **50%** could prevent preterm births by **12%** on average

Potential Mechanisms



Hypothesis



The placenta is the molecular mediator between prenatal phthalate exposure and spontaneous preterm birth

OVERVIEW OF ECHO PATHWAYS

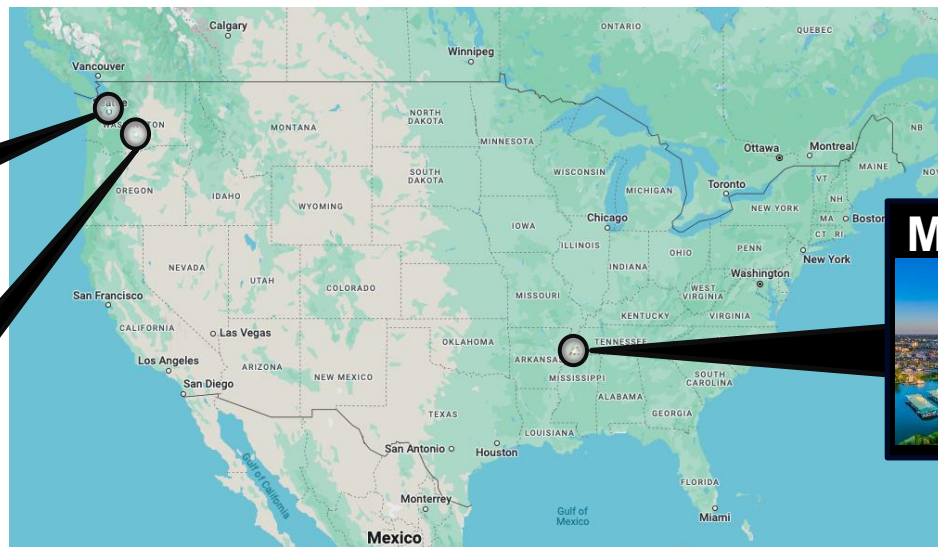


ECHO PATHWAYS: A multi-site, multi-PI consortium

Sheela Sathyanarayana, MD, MPH
Transcriptomics Lead PI



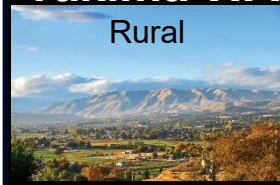
GLOBAL ALLIANCE TO PREVENT
PREMATURITY AND STILLBIRTH



Seattle WA
West Coast



Yakima WA
Rural



Memphis TN
Urban South



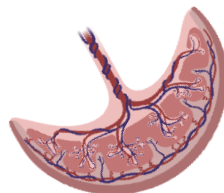
Generating multi-omic data with the UW EDGE center

W INTERDISCIPLINARY CENTER FOR EXPOSURES, DISEASES, GENOMICS AND ENVIRONMENT

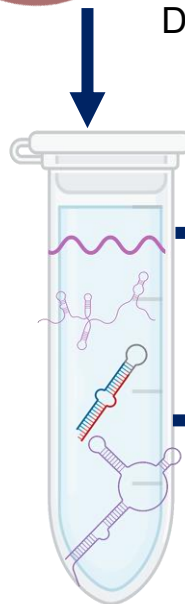


Theo Bammler, PhD

Manager: Genomics, Bioinformatics & Biostatistics,
Microphysiological Systems Facility Core



Qiagen: AllPrep
DNA/RNA Micro Kit



ECHO PATHWAYS (UH/UG3OD023271)
mRNA (N=784 CANDLE; 465 GAPPS)
Sequenced 2016-2023

NIEHS ONES (R01ES033785)
microRNA (N=769 CANDLE)
Sequenced 2022-2024

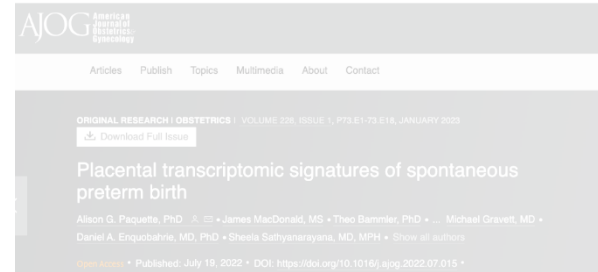
Transcriptomic Signatures of Prenatal Phthalate Exposure

Vol. 129, No. 9 | Research

A Comprehensive Assessment of Associations between Prenatal Phthalate Exposure and the Placental Transcriptomic Landscape

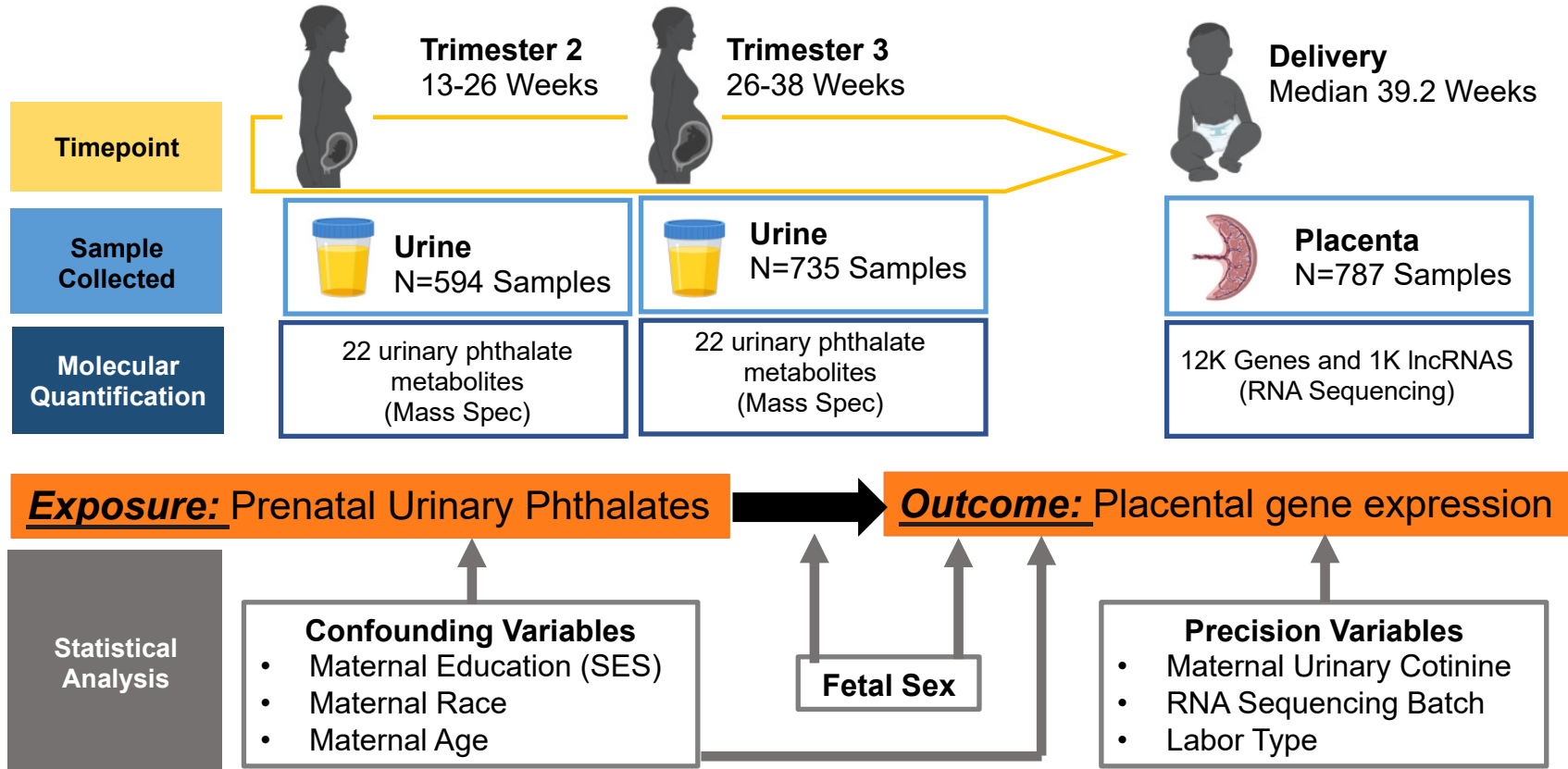
Alison G. Paquette, James MacDonald, Samantha Lapehn, Theo Bammler, Laken Kruger, Drew B. Day, Nathan D. Price, Christine Loftus, Kurunthachalam Kannan, Carmen Marsit, W. Alex Mason, Nicole R. Bush, Kaja Z. LeWinn, Daniel A. Enquobahrie, ... [See all authors](#) ✓

Published: 3 September 2021 | CID: 097003 | <https://doi.org/10.1289/EHP8973>



The placenta is the molecular mediator between prenatal phthalate exposure and spontaneous preterm birth

Analysis Strategy

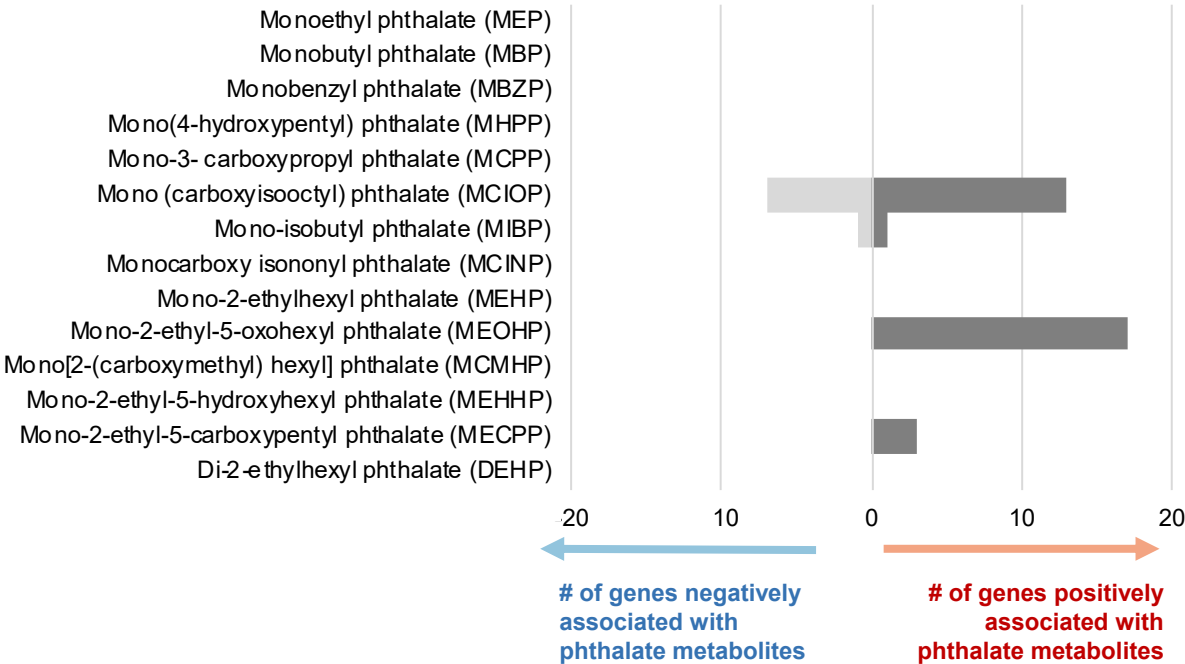


Differentially Expressed Genes (DEGs) and microRNAs (DE miRNAs)

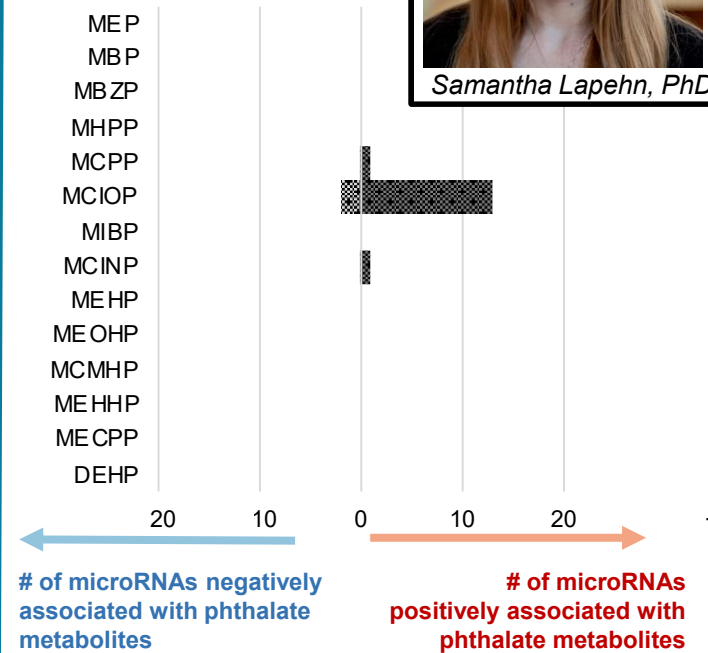
associated with Phthalate Metabolites



Differentially Expressed Genes *Paquette et al, EHP, 2021* FDR<0.05

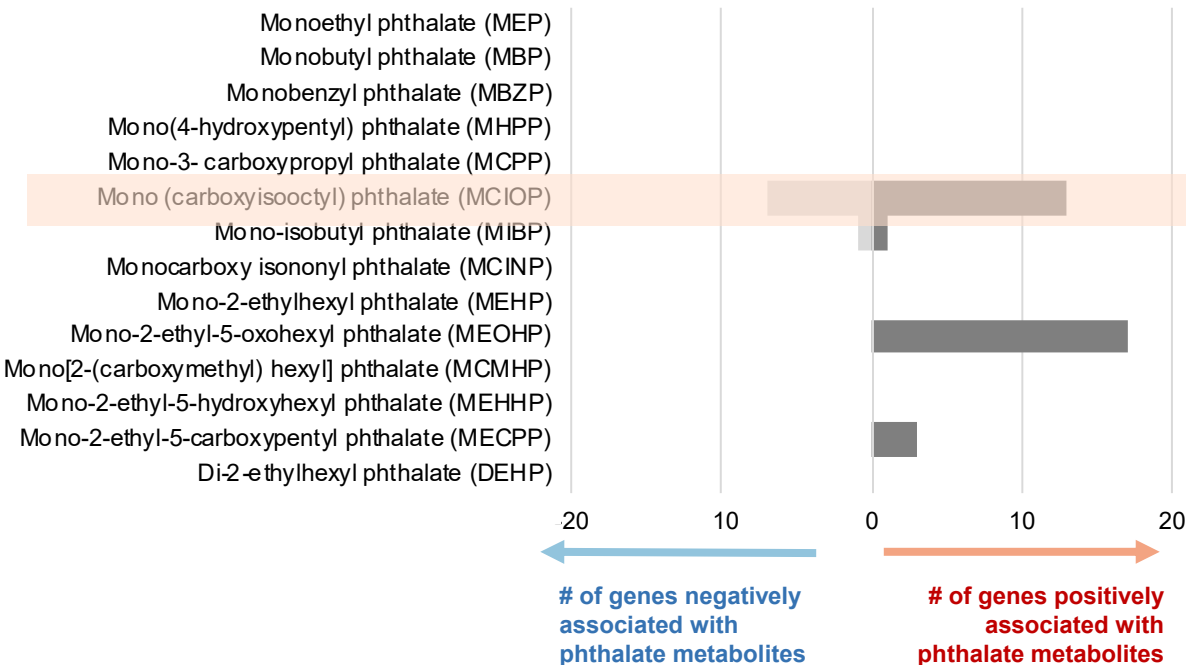


DE microRNAs FDR<0.1

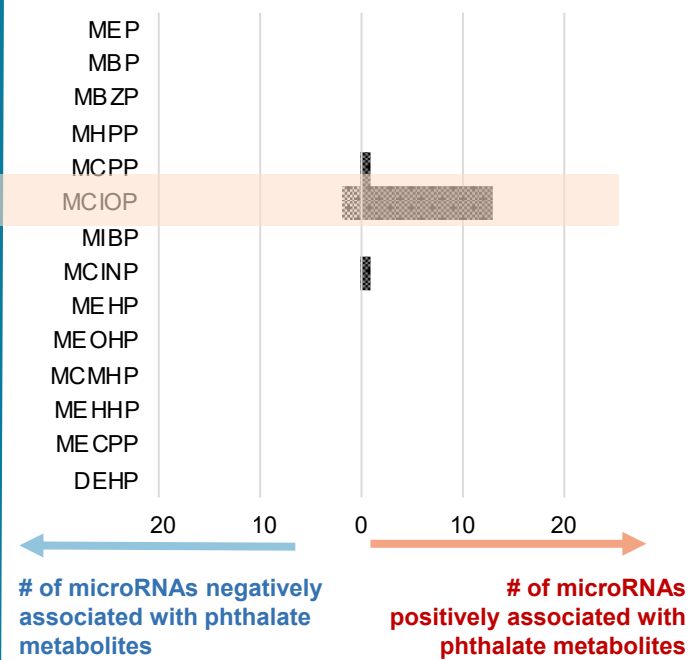


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Differentially Expressed Genes *Paquette et al, EHP, 2021* FDR<0.05

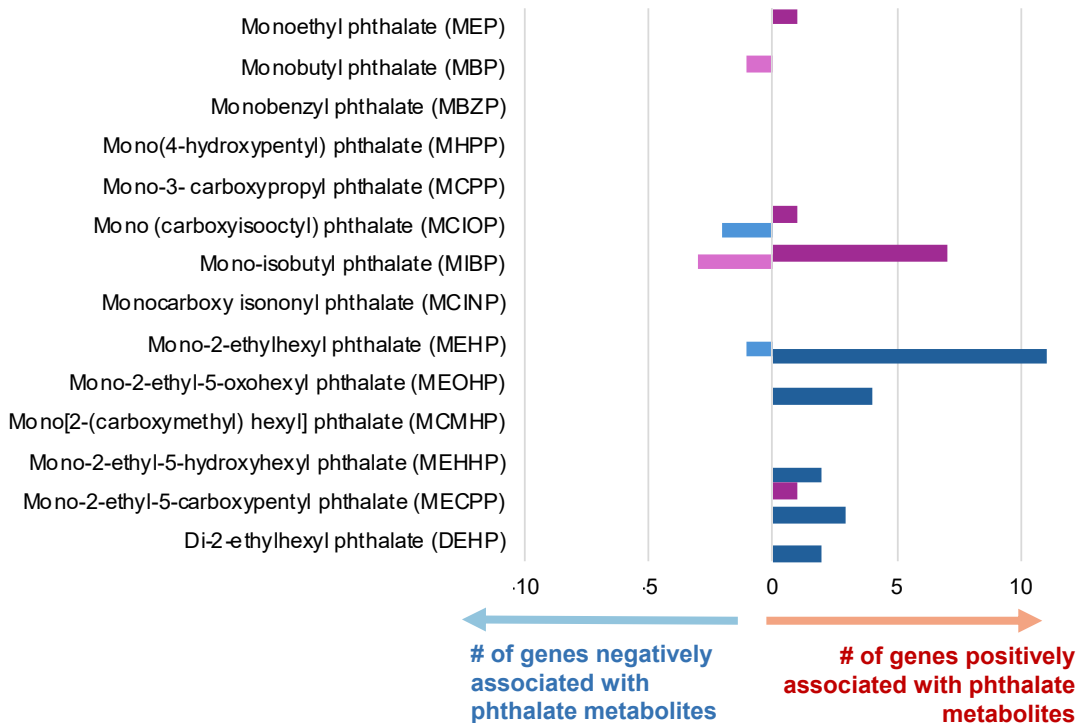


DE microRNAs FDR<0.1

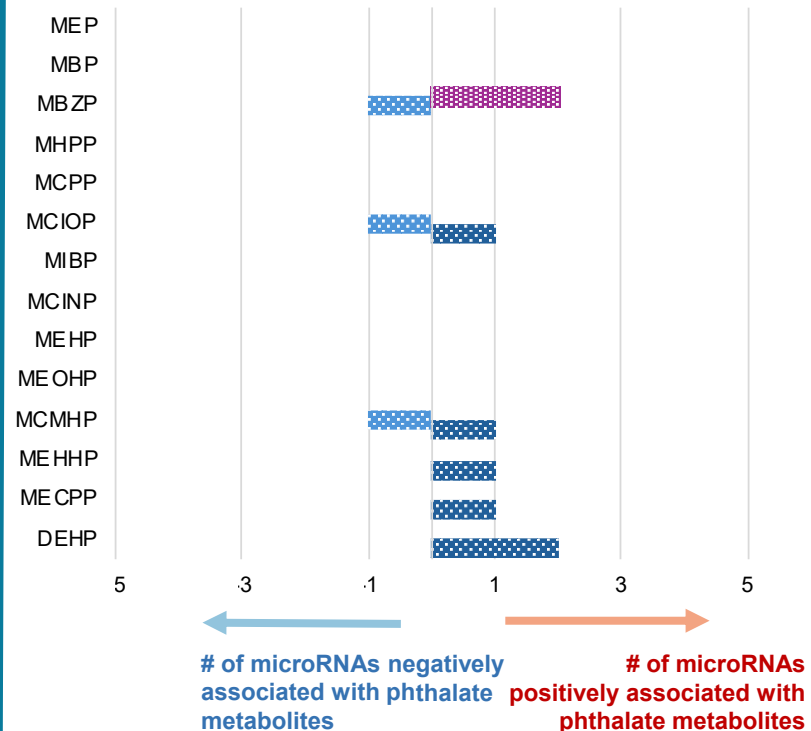


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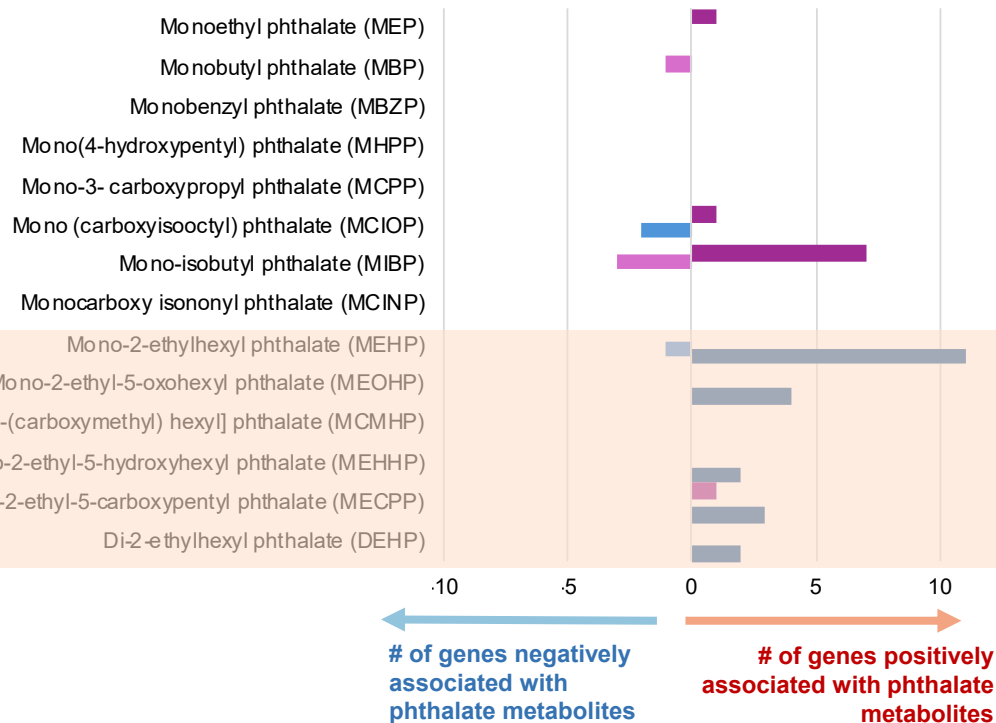


DE microRNAs FDR<0.1

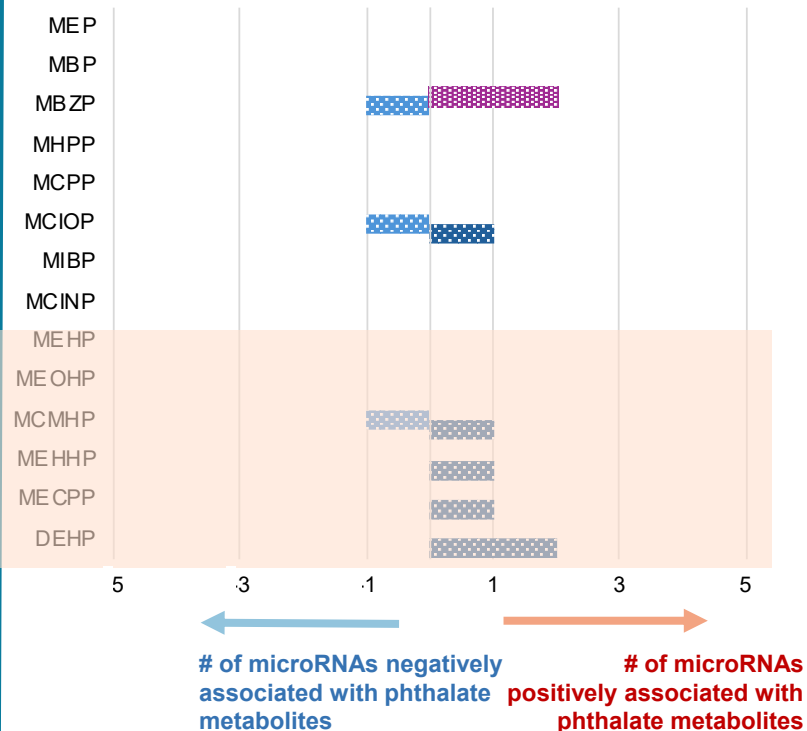


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Differentially Expressed Genes *Paquette et al, EHP, 2021* FDR<0.05



DE microRNAs FDR<0.1



Biological Pathways Significantly Associated With Phthalate Metabolites

SIGNAL TRANSDUCTION PATHWAYS

Wnt signaling pathway
 TGF-beta signaling pathway
 Notch signaling pathway
 mTOR signaling pathway
 Hedgehog signaling pathway
 FoxO signaling pathway
 AMPK signaling pathway

ORGANISMAL SYSTEM PATHWAYS

- Endocrine
- Excretory
- Digestive

Vasopressin-regulated water reabsorption
 Proximal tubule bicarbonate reclamation
 Neurotrophin signaling pathway
 Mineral absorption
 Growth hormone synthesis, secretion and action
 Dopaminergic synapse
 Cortisol synthesis and secretion
 Cholinergic synapse

METABOLIC PATHWAYS

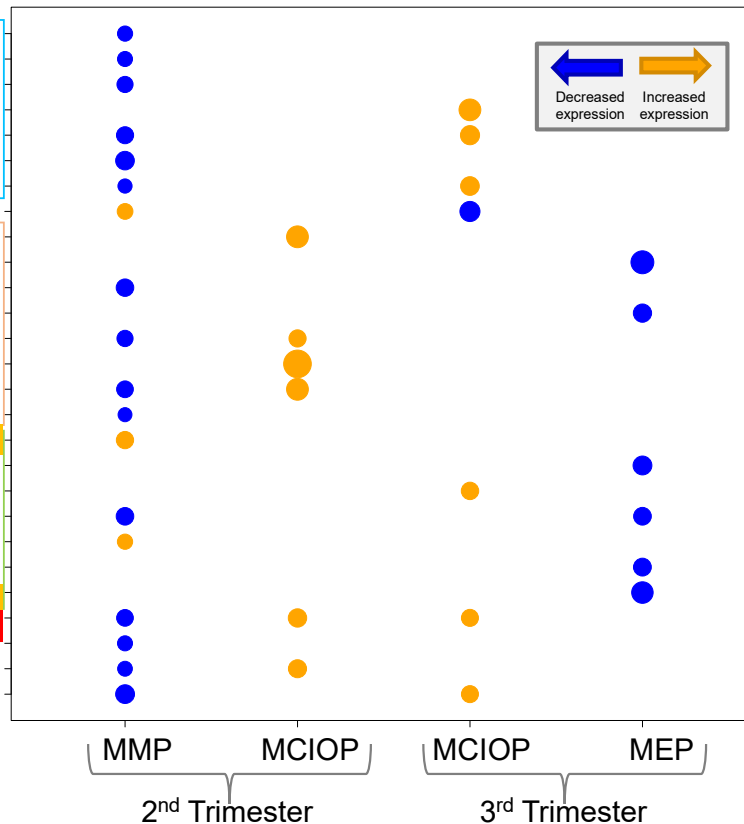
STEROID BIOSYNTHESIS

Starch and sucrose metabolism
 Sphingolipid signaling pathway
 Other types of O-glycan biosynthesis
 Lipoic acid metabolism
 Heparin Glycosaminoglycan biosynthesis

FATTY ACID BIOSYNTHESIS

ADHERENS JUNCTION

Apoptosis
 Longevity regulating pathway multiple species
 Longevity regulating pathway



Self contained gene-set testing: **FDR adjusted P<0.2**

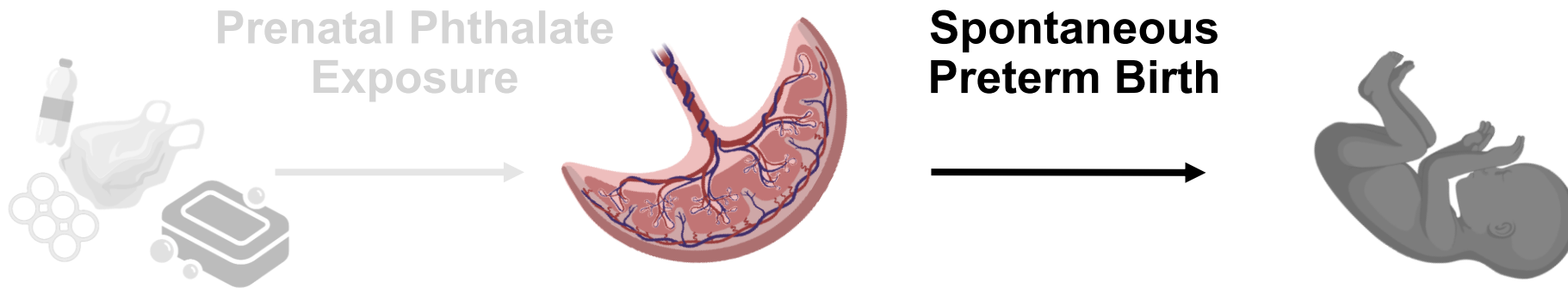
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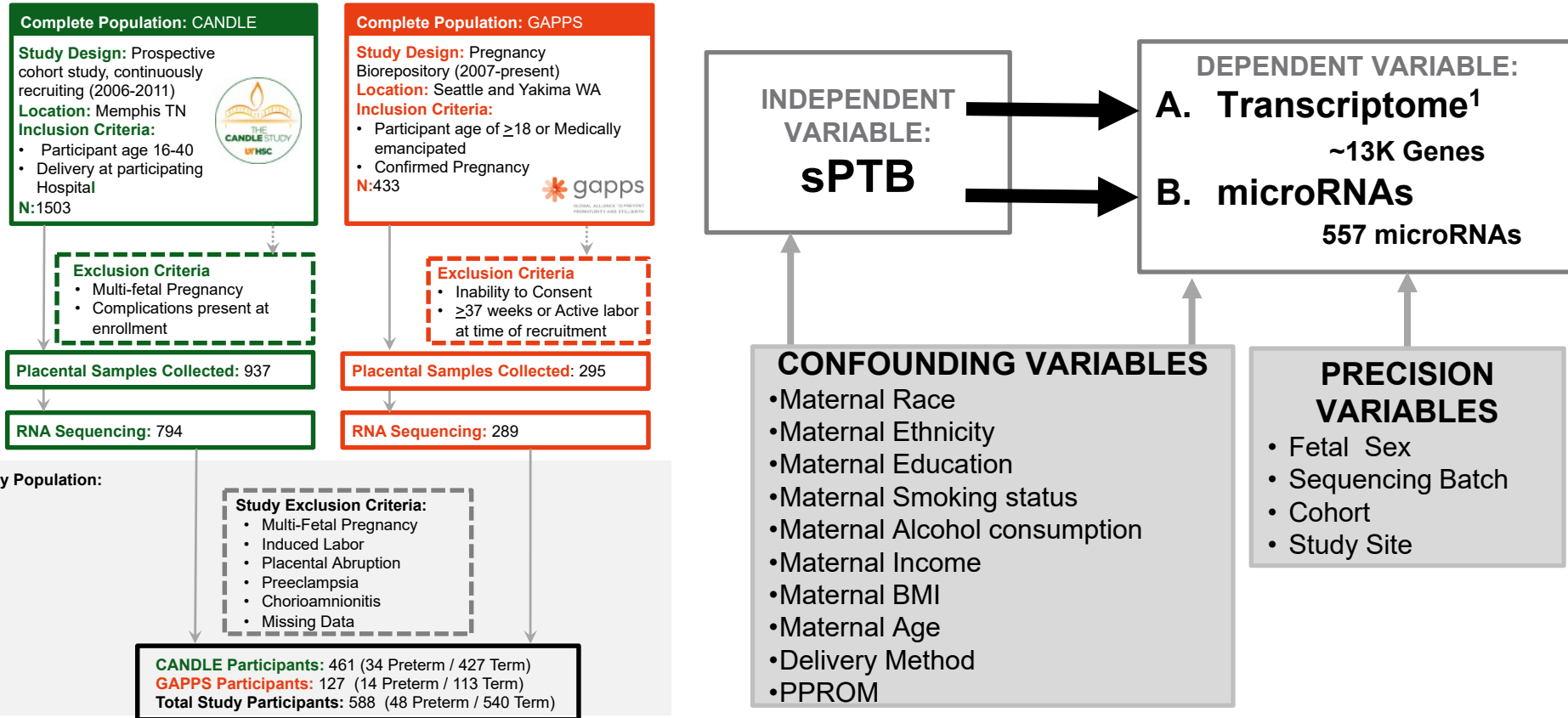
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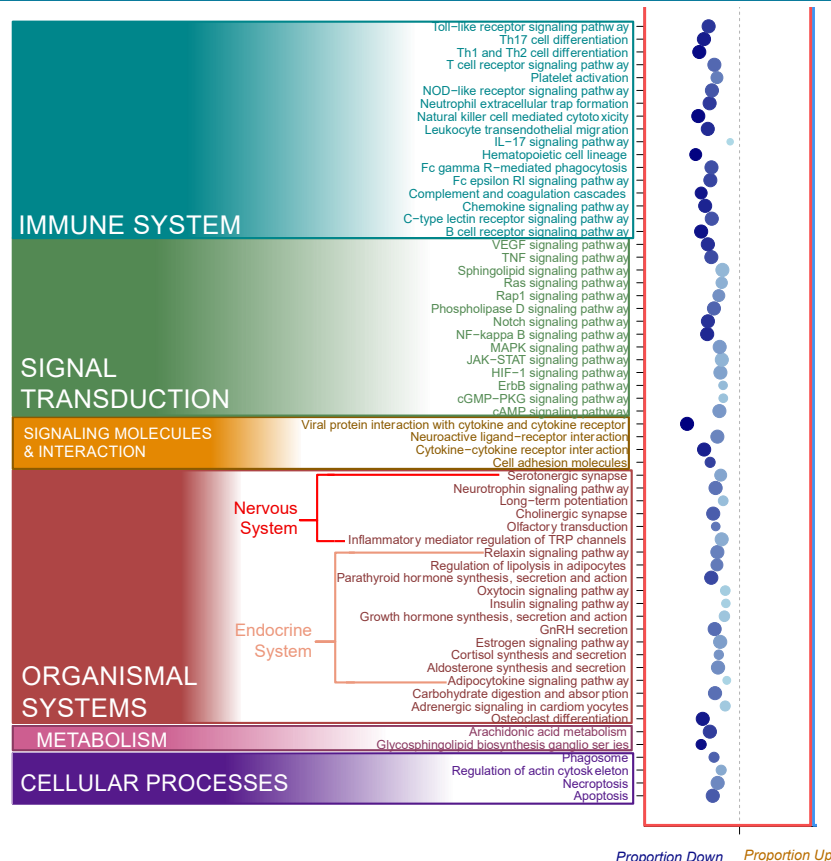
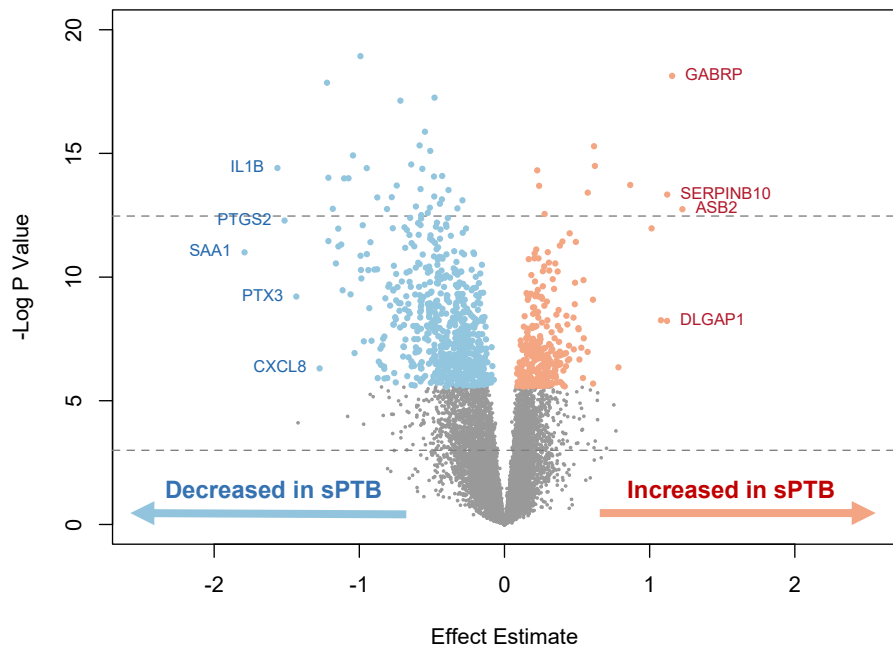


Differentially Expressed Genes (DEGs) and Pathways associated with sPTB

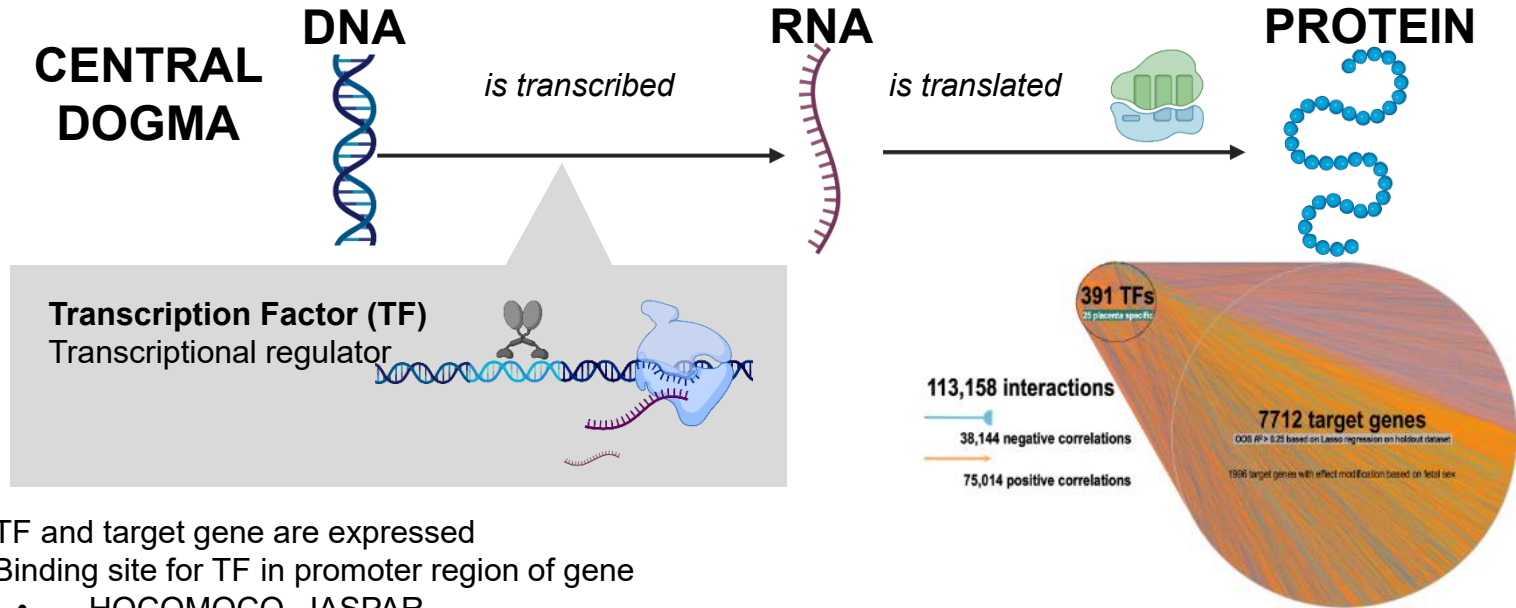
961 Differentially Expressed Genes

Paquette et al, AJOG, 2023

FDR<0.05



Pre and Post-transcriptional Regulation of Gene Expression



1. TF and target gene are expressed
2. Binding site for TF in promoter region of gene
 - HOCOMOCO, JASPAR
3. TF and target gene are correlated
 - **Negatively correlated**- repressor
 - **Positively correlated**-activator
4. TF predicts gene expression in an independent dataset

SCIENCE ADVANCES | RESEARCH ARTICLE

DEVELOPMENTAL BIOLOGY

A genome scale transcriptional regulatory model of the human placenta

Alison Paquette^{1,2*}, Kylla Ahuna³, Yeon Mi Hwang⁴, Jocelynn Pearl⁵, Hanna Liao¹, Paul Shannon⁶, Leena Kadam⁷, Samantha Lapehn², Matthew Bucher⁸, Ryan Roper⁹, Cory Funk¹⁰, James MacDonald¹, Theo Bammler¹¹, Priyanka Baloni¹², Heather Brockway¹³, W. Alex Mason⁷, Nicole Bush⁸, Kaja Z. Lewinn⁸, Catherine J. Karr⁹, John Stamatoyannopoulos¹³, Louis J. Muglia^{14,15}, Helen Jones¹², Yoel Sadovsky^{13,14}, Leslie Myatt², Sheela Sathyanarayana^{1,2}, Nathan D. Price^{1,15}

ECHO OIF: 0035
2019-2021

TRN Web Tool: A resource for ECHO Investigators

1. Identify the TFs of a given target gene

2. Identify the target genes of a given TF

3. Perform TF Enrichment Analysis for a list of target genes

Placental TRN

Home Instructions **TRN Tools** Model Construction Information FAQ Acknowledgements

Gene Selection:
Type in a target gene or scroll to find and select

A1BG

Filter by:
 Correlation P-value
 Q-value

Download Results

R² value: 0.278

Transcription Factor	Correlation	P-value	Q-value
1 E2F6	-0.337	4.38e-14	5.06e-14
2 FOXO1	0.400	1.21e-19	1.85e-19
3 HIC1	0.344	1.25e-14	1.48e-14
4 IKZF1	0.294	6.29e-11	6.56e-11
5 KLF12	0.334	8.26e-14	9.44e-14

Placental TRN

Home Instructions **TRN Tools** Model Construction Information FAQ Acknowledgements

Transcription Factor Selection:
Type in a TF or scroll to find and select

AHR

Filter by:
 Correlation P-value
 Q-value R²

Download Results

Show 10 entries

Search results for target gene:

Target Gene	Correlation	P-value	Q-value	R ²
1 LNPEP	0.783	1.25e-99	9.65e-97	0.870
2 MAN1A2	0.764	5.59e-92	2.44e-89	0.773
3 NIPAL1	0.743	1.18e-84	3.14e-82	0.753
4 MICU3	0.741	6.70e-84	1.70e-81	0.786
5 AZIN1	0.740	2.20e-83	5.37e-81	0.814
6 VGLL3	0.737	1.95e-82	4.38e-80	0.905

Placental TRN

Home Instructions **TRN Tools** Model Construction Information FAQ Acknowledgements

Upload Gene List

Browse... Example_Data_1

Upload complete

Module Min: 10

Module Max: 1000

Min Significant Genes: 5

Download Enrichment Results

Show 10 entries

Search results for transcription factor:

Transcription Factor	Num Targets	Significant Genes	Fisher Test	Fisher Adj P-value
1 BCL6B	121	6	0.0157	0.70
2 THAP5	754	20	0.0250	0.70
3 AHR	967	23	0.0499	0.73
4 ARID5B	127	5	0.0614	0.73
5 TBX5	170	6	0.0652	0.73
6 NFE2L2	229	7	0.0889	0.83
7 ARNT	278	7	0.1837	1.00
8 ARNT2	214	5	0.2878	1.00

Placental TRN

Home Instructions **TRN Tools** Model Construction Information FAQ Acknowledgements

Target Gene Search

Purpose: This tool allows the user to ascertain a list of transcription factors that influence their target gene of interest.

Instructions: There are 2 ways to search for your target gene. You can either use the "drag and drop" option on the left side of the screen to select your gene, or you can use the Search tool on the right side of the column to search your gene.

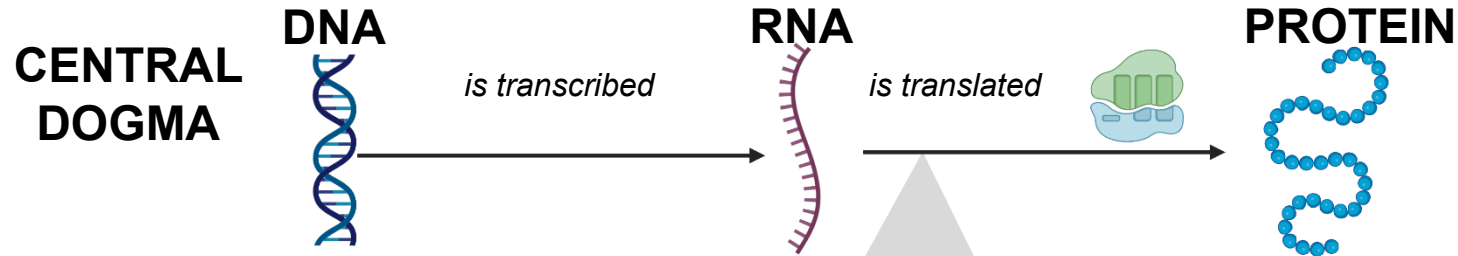
91 TFs
113,158 interactions
23,946 regulatory connections
7,712 Target Genes

Output Information	Column Description
Transcription Factor	These are the top 15 TFs that regulate your gene of interest.
Correlation	Pearson correlation coefficient between the TF and target gene
P-value	P value from Pearson correlation
Q-value	P value adjusted for multiple comparison (i.e. total # of correlations made in TRN)
R2	Overall out of sample R2 value (listed in table header)

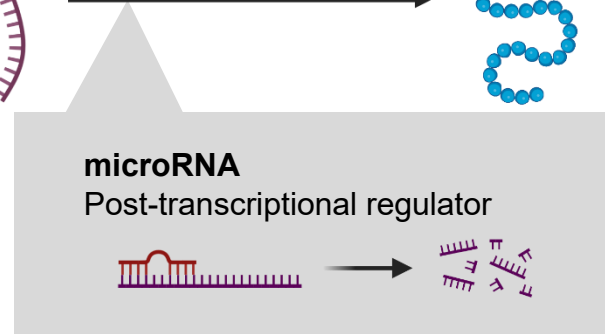
-instructions
-model construction information
-frequently asked questions



Pre and Post-transcriptional Regulation of Gene Expression

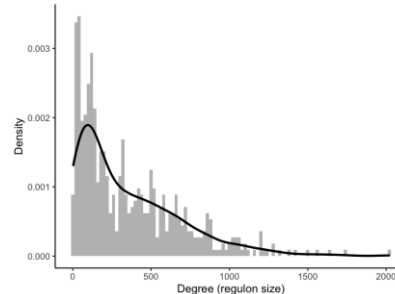


1. microRNA and target gene are expressed
2. microRNA binds to target gene
 - Targetscan, mirDB
3. TF and target gene are negatively correlated

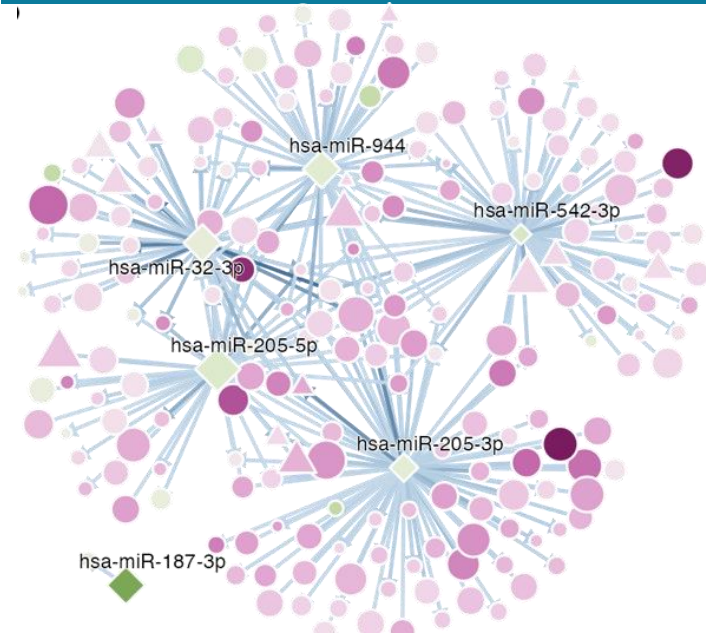


Placental microRNA Regulatory Network

- 563 miRNA
- 11,771 target genes
- 199,188 miRNA–mRNA interactions (FDR<0.05)
- *Shiny app: Coming soon!*



Placental microRNAs provide insight into Perturbed Pathways

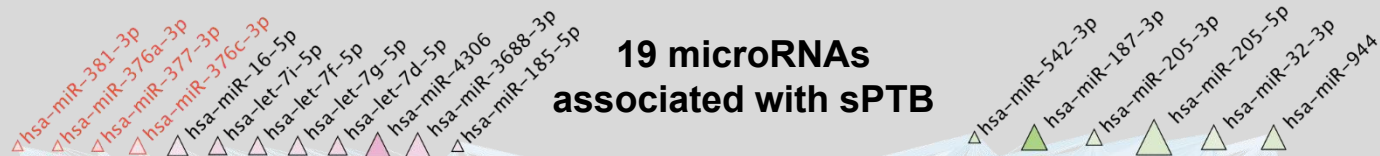


Gene set over-
representation analysis
(FDR<0.1)

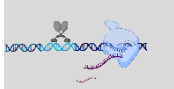
Pathways	FDR	sPTB Genes /Target Genes
Th17 cell differentiation	0.0334	8/74
B cell receptor signaling pathway	0.0555	7/67
Fc epsilon RI signaling pathway	0.0851	7/85
Hematopoietic cell lineage	0.0851	5/47
Natural killer cell mediated cytotoxicity	0.0851	6/73
Intestinal immune network for IgA production	0.0851	4/25
Fc gamma R-mediated phagocytosis	0.0851	5/51
Antigen processing and presentation	0.0851	5/46
TNF signaling pathway	0.0825	8/99
VEGF signaling pathway	0.0851	5/48
cAMP signaling pathway	0.0851	8/125
Neuroactive ligand-receptor interaction	0.0851	7/99
Osteoclast differentiation	0.0851	8/111

Network Biology Approaches Yield Additional Insight into the Etiology of sPTB


Post Transcriptional
regulation


**19 microRNAs
associated with sPTB**

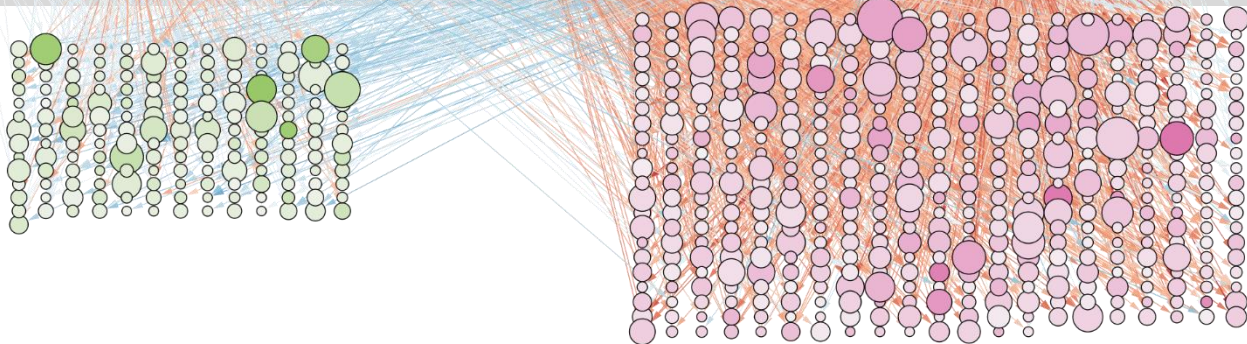
- hsa-miR-381-3p
- hsa-miR-376a-3p
- hsa-miR-377-3p
- hsa-miR-376c-3p
- hsa-miR-16-5p
- hsa-let-7f-5p
- hsa-let-7f-5p
- hsa-let-7g-5p
- hsa-let-7d-5p
- hsa-miR-4306
- hsa-miR-3688-3p
- hsa-miR-185-5p
- hsa-miR-542-3p
- hsa-miR-187-3p
- hsa-miR-205-3p
- hsa-miR-205-5p
- hsa-miR-32-3p
- hsa-miR-944


Transcriptional
Regulation


**35 TFs
associated
with sPTB**

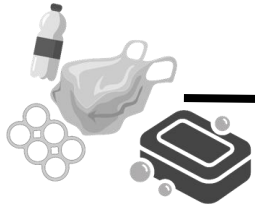
- BHLHE41
- E2F7
- HOXB4
- ELF5
- SIX4
- PBX1
- RFY7
- RELA
- KLF10
- HSF1
- HIC2
- ARID3A
- ELF3
- E4F1
- KLF16
- IRF9
- ETS2
- OVOL1
- GATA3
- FOXP1
- RUNX1
- JDP2
- RXR
- DLX3
- ELF4
- NFE2
- RARA
- CEBPBD
- HEY1
- TFAP2A
- ARID3A
- ZBTB16
- FOSL2
- SPTL
- KLF9

- microRNAs regulate 33% of sPTB DEGs
- microRNAs regulate 22 TFs
- microRNA/TF networks regulate **67%** of sPTB Genes (625/961)

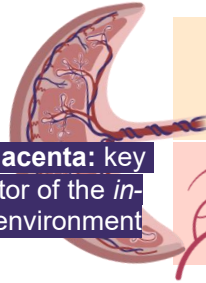


Integrating Signatures to Identify Shared Mechanisms

Prenatal Phthalate Exposure



The Placenta: key regulator of the *in-utero* environment



Placental Gene Expression

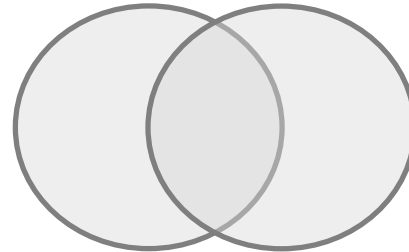
Biological Functions of the Placenta

Spontaneous Preterm Birth



Meet in the Middle Strategy:

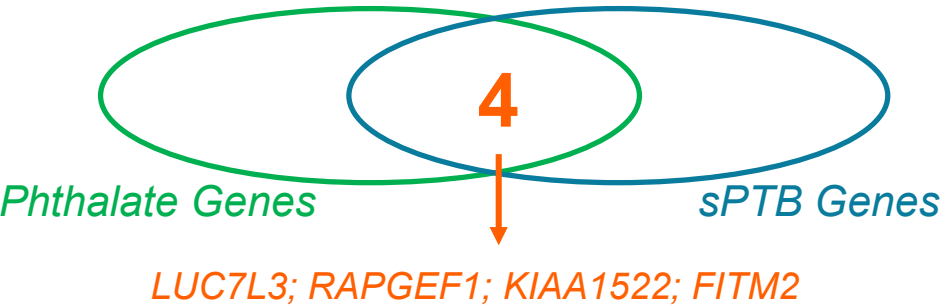
Genes and Pathways associated with phthalates



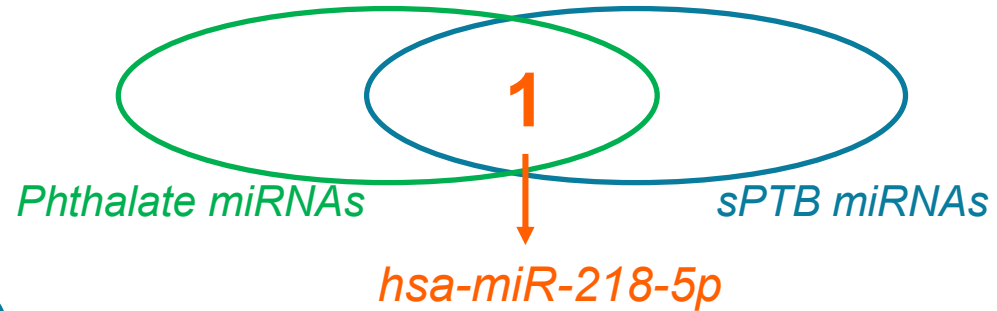
Genes and Pathways associated with sPTB

Meet in the Middle Results

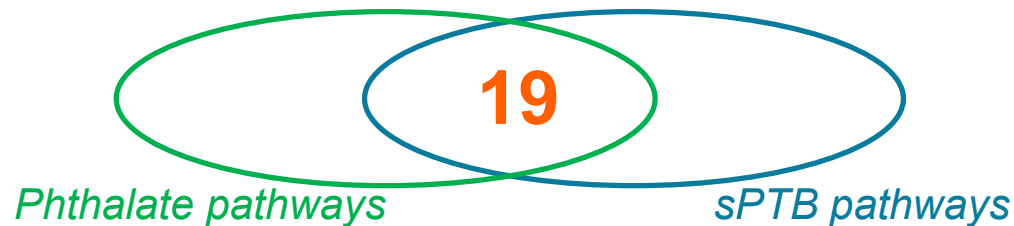
1. Genes



2. microRNAs



3. Pathways



Prenatal Phthalate Exposure and sPTB: Overlapping Pathway Signatures

KEGG Pathways Associated with Prenatal Phthalate Exposure (Paquette et al, EHP, 2021)



KEGG Pathways Associated with Prematurity

	Metabolite	Phthalate Analysis			sPTB Analysis		
		Trimester Collected	FDR Adjusted P	Direction	Preterm Birth Group	FDR Adjusted P	Direction
METABOLISM	Sphingolipid signaling pathway	MCIOP Trimester 2	0.125	Up	Preterm vs. Term	Down	3.01E-05
		MCIOP Trimester 3	0.177	Up	Early Preterm vs. Full	Down	1.35E-03
	Steroid biosynthesis	MMP Trimester 2	0.160	Up	Late Preterm vs. Full	Down	1.82E-03
SIGNAL TRANSDUCTION	Other types of O-glycan biosynthesis	MEP Trimester 3	0.160	Down	Preterm vs. Term	Down	2.52E-03
	Notch signaling pathway	MMP Trimester 2	0.160	Down	Early Preterm vs. Full	Down	1.44E-04
	AMPK signaling pathway	MCIOP Trimester 3	0.177	Up	Preterm vs. Term	Down	3.01E-05
	FoxO signaling pathway	MMP Trimester 2	0.160	Down	Early Preterm vs. Full	Down	5.06E-05
	Wnt signaling pathway	MCIOP Trimester 3	0.177	Up	Late Preterm vs. Full	Down	4.14E-03
	mTOR signaling pathway	MMP Trimester 2	0.160	Down	Preterm vs. Term	Down	5.48E-03
	TGF-beta signaling pathway	MCIOP Trimester 3	0.177	Up	Late Preterm vs. Full	Down	4.31E-02
CELLULAR PROCESSES	Fanconi anemia pathway	MMP Trimester 2	0.160	Down	Preterm vs. Term	Down	3.77E-03
	Adherens junction	MCIOP Trimester 3	0.177	Up	Early Preterm vs. Full	Down	2.19E-04
	Longevity regulating pathway	MCIOP Trimester 2	0.160	Down	Preterm vs. Term	Down	7.29E-03
	Vasopressin-regulated water reabsorption	MCIOP Trimester 3	0.177	Up	Early Preterm vs. Full	Down	1.12E-04
	Dopaminergic synapse	MCIOP Trimester 2	0.047	Up	Preterm vs. Term	Down	2.46E-02
ENDOCRINE SYSTEMS	Growth hormone synthesis, secretion and action	MCIOP Trimester 2	0.125	Up	Early Preterm vs. Full	Down	4.43E-04
	Cortisol synthesis and secretion	MMP Trimester 2	0.160	Down	Preterm vs. Term	Down	3.02E-02
	Neurotrophin signaling pathway	MCIOP Trimester 3	0.177	Up	Early Preterm vs. Full	Down	1.48E-03
	Cholinergic synapse	MCIOP Trimester 2	0.125	Up	Preterm vs. Term	Down	4.81E-03
		MMP Trimester 2	0.183	Down	Early Preterm vs. Full	Down	2.64E-02

Hormones Involved in Parturition

↑ **Steroid Biosynthesis**

↓ **Cortisol synthesis & secretion**

Signaling for Placental Growth & development

↓ **TGF Beta Signaling**

↓ **Notch Signaling**

Oxidative Stress

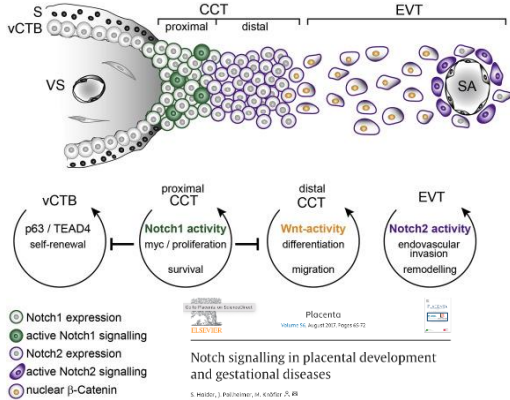
↓ **FOXO1 Signaling**

Key Take Aways

1. Developmental Origins of Health and Disease (**DOHAD**): The prenatal environment is regulated by the **placenta** and shapes infant & childhood health outcomes
2. Prenatal **phthalate exposure** is associated with placental dysfunction and **sPTB** in epidemiological studies
3. We have identified changes in placental gene and microRNA expression attributable to phthalate exposure
4. We have identified a substantial number of transcriptomic differences related to **sPTB**. We have used network tools to map these genes to selected TFs and microRNAs
5. We identified **19 pathways** with shared transcriptional disruption related to prenatal phthalate exposure & sPTB, including **metabolic**, **immune signaling**, and **endocrine** pathways

How can Placental Omics data inform regulatory decisions and promote precision environmental health?

Novel insight into molecular mechanisms underlying toxicity

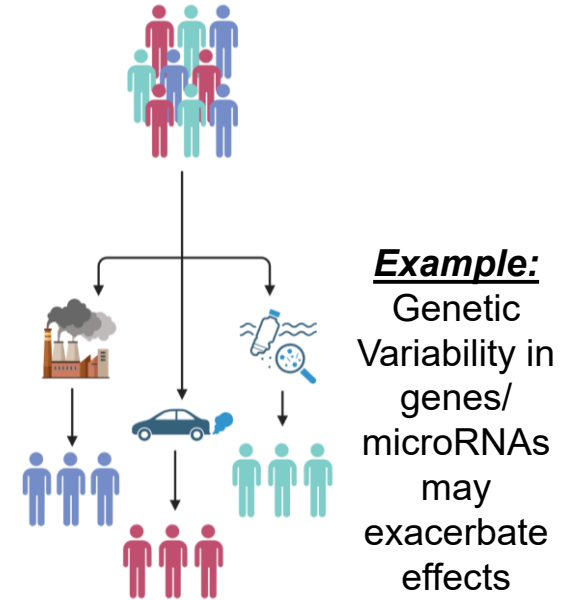


Example: Notch Signaling and Placental Function

Chemical screening to evaluate effects on pregnancy



Informing Precision Environmental Health approaches



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