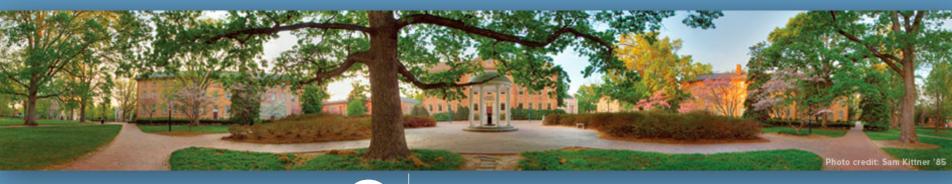
Genome-wide Studies of Toxic Chemical Impacts on Chromatin State

Thursday March 17th, 2016





Grace Chappell

THE UNIVERSITY

of NORTH CAROLINA

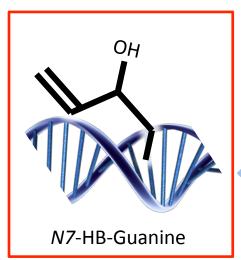
at CHAPEL HILL

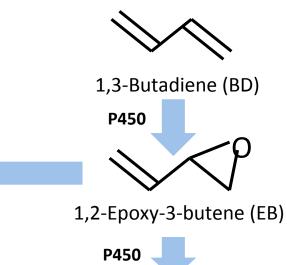
Jennifer Israel
Jeremy Simon
Matt Weiser
Karl Eklund

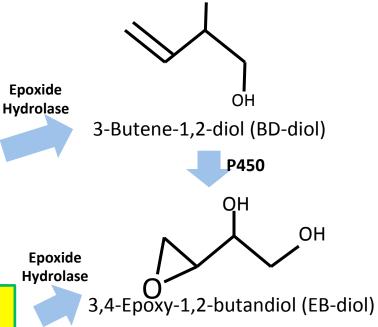


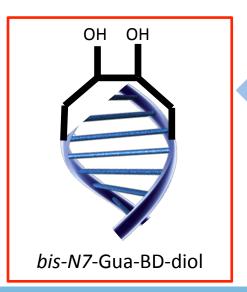
Greg Crawford Alexias Safi

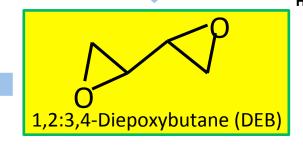
Metabolism of 1,3-butadiene

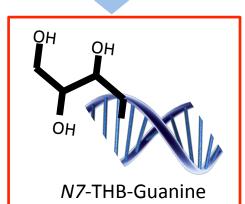










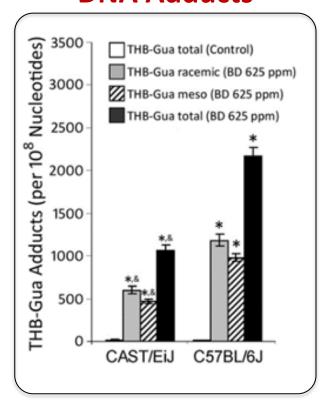






BD induces strain-specific epigenetic effects

DNA Adducts



* Indicates significantly different from controls, ** different between mixtures (p<0.05)

Koturbash et al Tox Sci (2011)

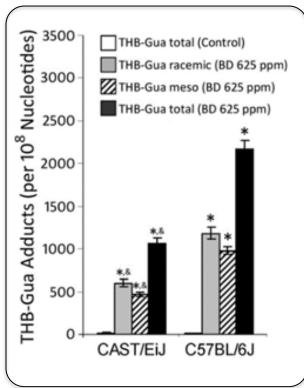




BD induces strain-specific epigenetic effects

DNA hypo-methylation Histone modifications

DNA Adducts



* Indicates significantly different from controls, ** different between mixtures (p<0.05)

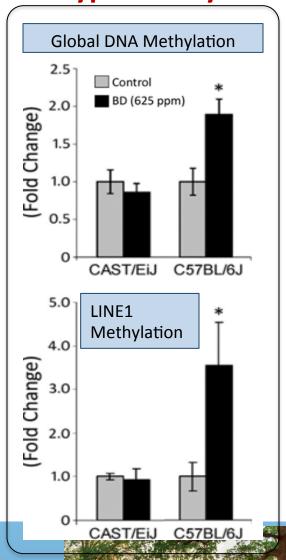
Koturbash et al Tox Sci (2011)

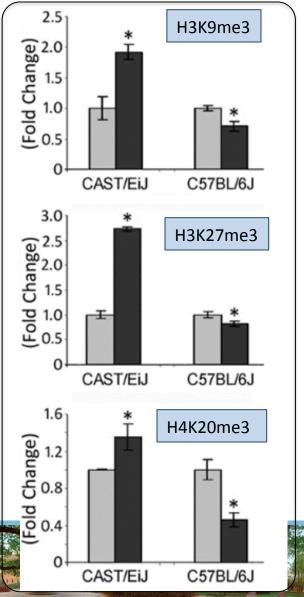


THE UNIVERSITY

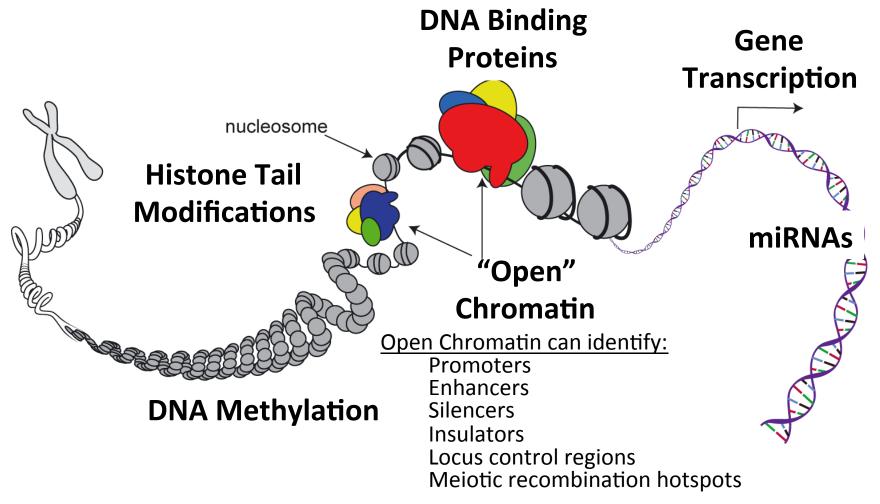
of NORTH CAROLINA

at CHAPEL HILL





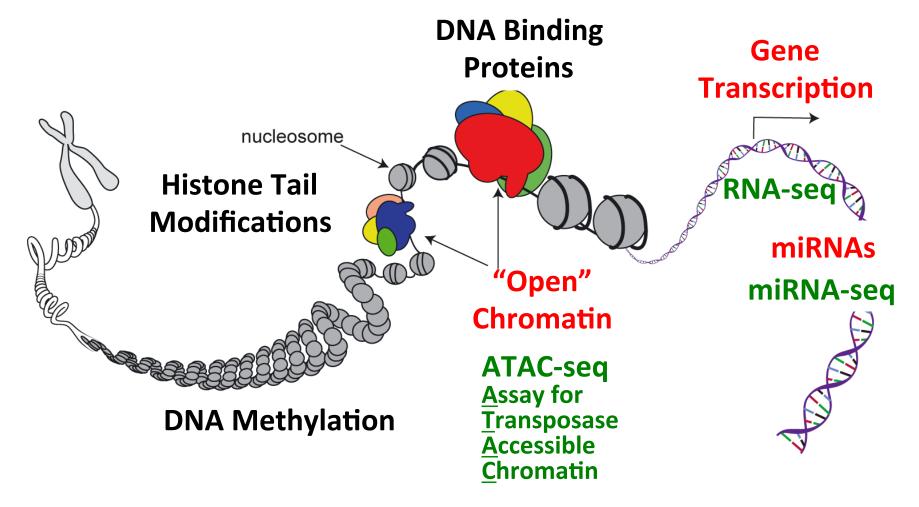
Epigenetics, Regulation and Transcription







Epigenetics, Regulation and Transcription

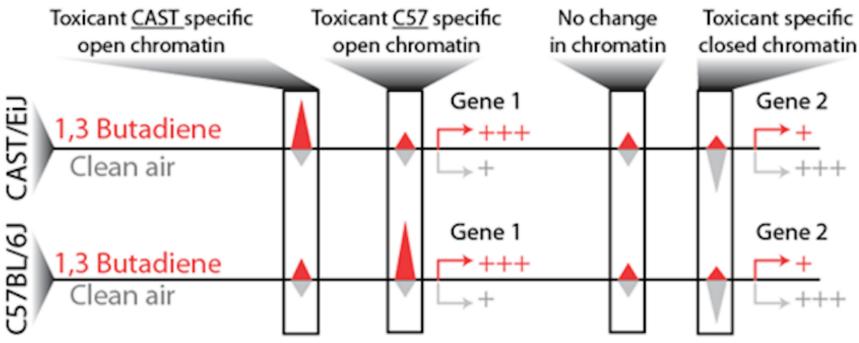






1,3 Butadiene Exposure (TaRGET – NIEHS)

Tissue Strain Exposure Assays C57BL/6 2 week 0 PPM Lung RNA (sensitive) (clean air) exposure Liver miRNA CAST/EiU **625 PPM** Kidney **ATAC** (resistant) 1,3 Butadiene

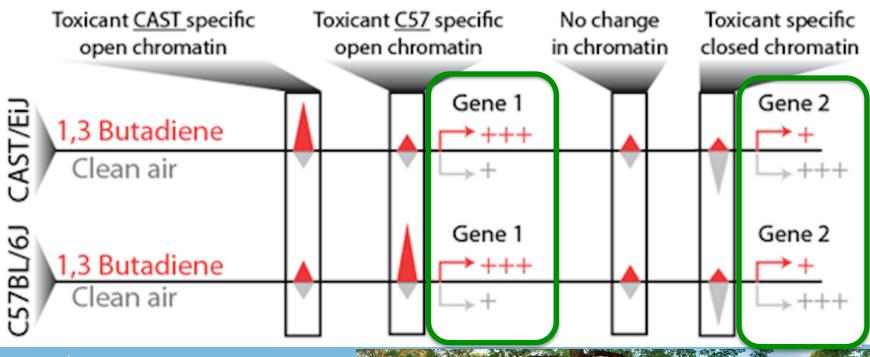






1,3 Butadiene Exposure (TaRGET – NIEHS)

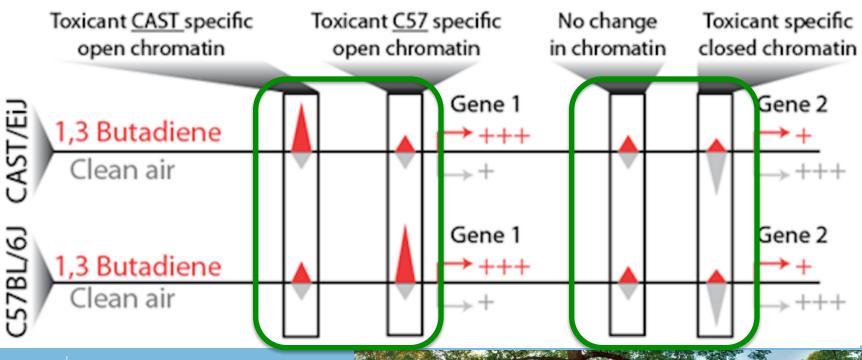
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1,3 Butadiene Exposure (TaRGET – NIEHS)

Strain Tissue Exposure Assays C57BL/6 2 week 0 PPM Lung RNA (sensitive) (clean air) exposure Liver miRNA CAST/EiU **625 PPM** Kidney **ATAC** (resistant) 1,3 Butadiene





BD exposure-induced changes in lung mRNAs

C57BL6 (sensitive)



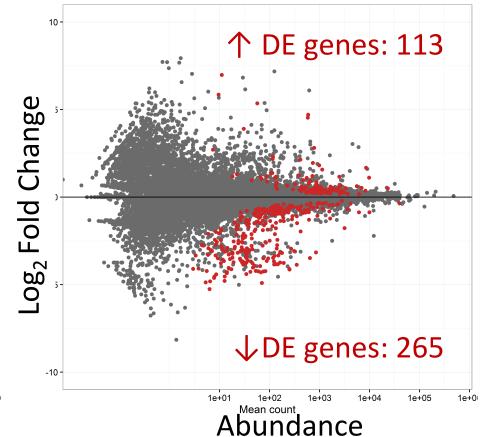
↑ DE genes: 1954

og₂ Fold Change

↓DE genes: 2162

Abundance

CAST (resistant)

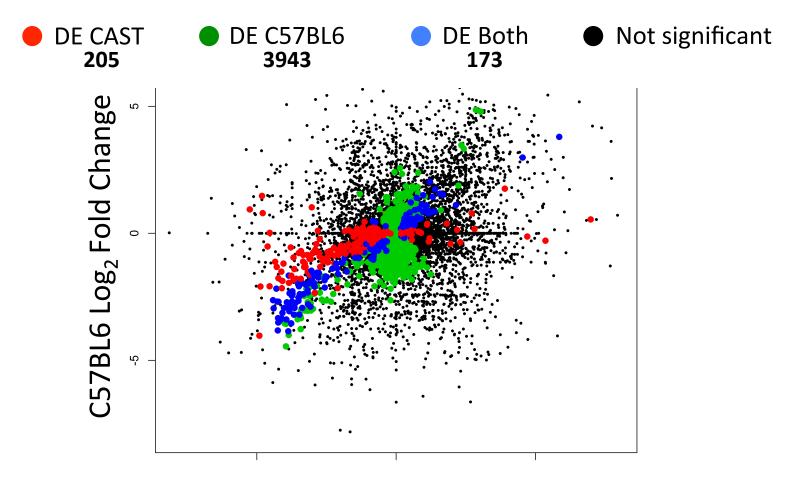


- Differentially expressed (q < 0.1; DESeq)
- Not significant





C57BL6 vs CAST mRNA changes



CAST Log₂ Fold Change





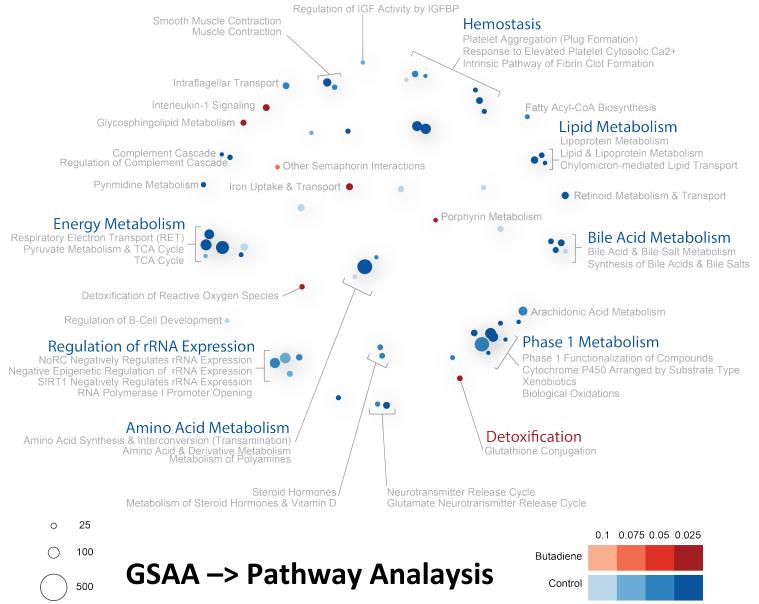
Mitochondrial Translation Initiation Mitochondrial Translation Elongation **C57BL6** Mitochondrial Translation Termination Toll-like Signaling T-cell Signaling TRAF6-mediated Inudction of NFkB & MAPK upon TLR7,8, or 9 Activation TCR Signaling CO-stimulation by the CD28 Family Activated TAK1 Mediates P38 MAPK Activation TLR Cascades [TLR2, TLR3, TLR4, TLR1:TLR2, TLR6:TLR2, TLR7/8] PD-1 Signaling SRP-dependent Co-translational Protein Targeting to Membrane PI3K Signaling PI3K/AKT Activation PI3K Events in ERBB2 and ERBB4 Signaling PI3K Cascade [FGFR1, FGFR2, FGFR3, FGFR4] **DNA Damage Response** Regulation of Mitotic Cell Cycle Regulation of Apoptosis Interferon Signaling Stabilization of P53 P53-Independent DNA Damage Response Cytokine Signaling in Immune System Hemostasis G1/S DNA Damage Checkpoints Intrinsic Pathway of Fibrin Clot Formation Interferon Signaling **DNA** Replication Interferon y Signaling GPVI-mediated Activation Cascade Platelet Activation, Signaling, & Aggregation Activation of the pre-Replicative Complex • Signal Transduction DNA Strand Elongation • G Beta: Gamma Signaling through PI3K Gamma GPCR Downstream Signaling Activation of ATR in Response to Replication Stress • G Alpha (Q) Signaling Events Detoxification Glutathione Conjugation Phase II Conjugation **Nucleotide Excision Repair Energy Metabolism** Nucleotide Excision Repair Respiratory Electron Transport (RET) 25 TCA Cycle & RET Transcription-coupled NER 0.1 0.075 0.05 0.025 100 Butadiene **GSAA** -> Pathway Analaysis Control 500

Mitochondrial Translation





CAST



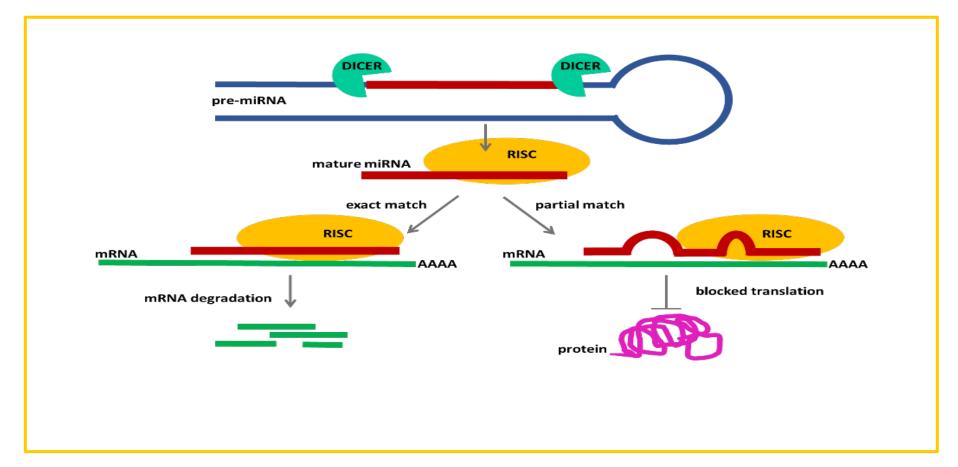




What is controlling this differential expression?



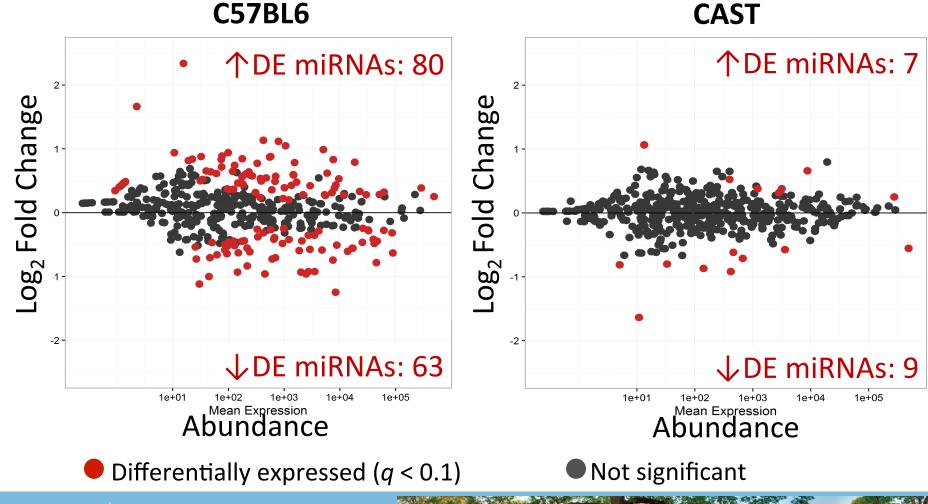
miRNAs block translation of target mRNAs or mark target mRNAs for degradation







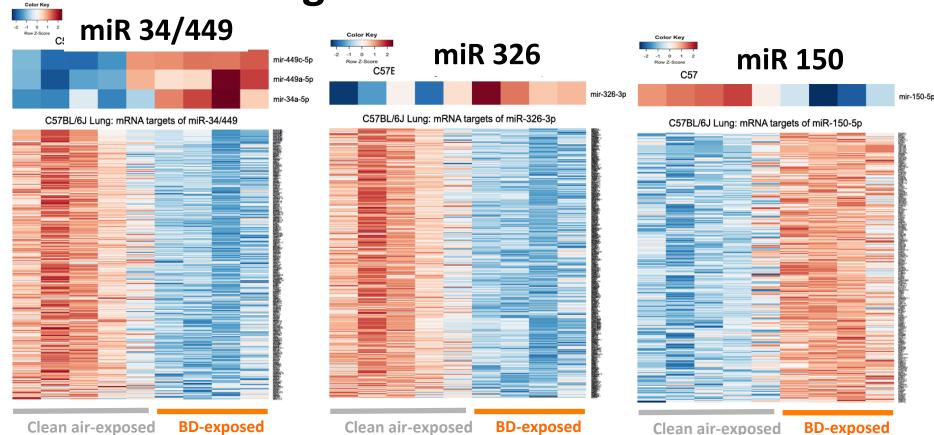
BD exposure-induced changes in lung miRNAs







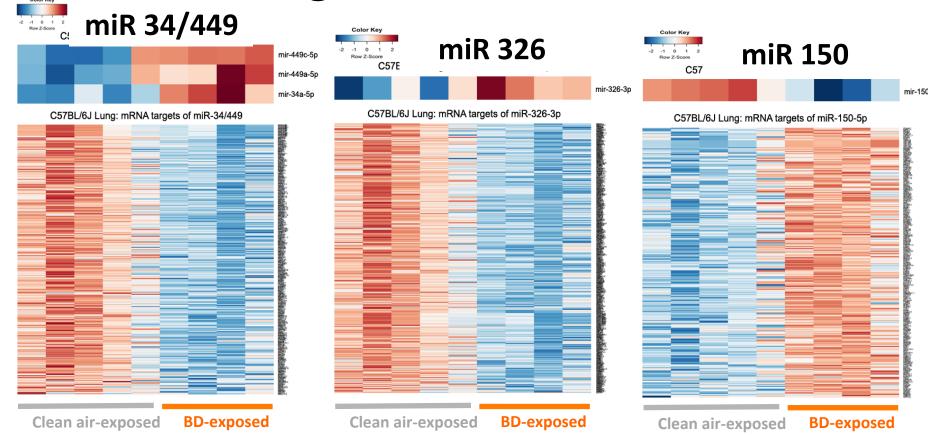
Gene targets of miRNAs – C57BL6







Gene targets of miRNAs – C57BL6



Hemostasis Notch-HLH Transcription

Hemostasis Immune system Regulation of Signaling Glucuronidation (Phase II Metabolism) Membrane Transport





Assay for
Transposase
Accessible
Chromitin

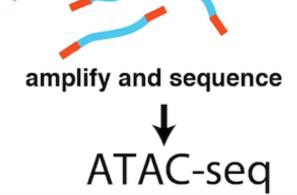
Regulatory element element

nucleosome

Add Tn5 transposase

Crawford Lab

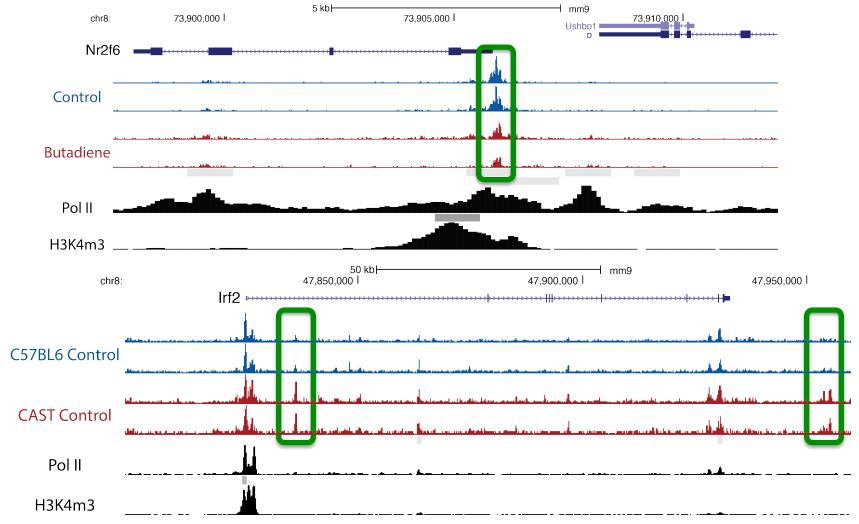
Buenrostro, et al. Nat Methods







Treatment and strain-specific chromatin







Chromatin Alterations on Exposure to BD

Identify "peaks" (F-seq)



Identify significant changes (DESeq)



Tile 300bp windows across peaks

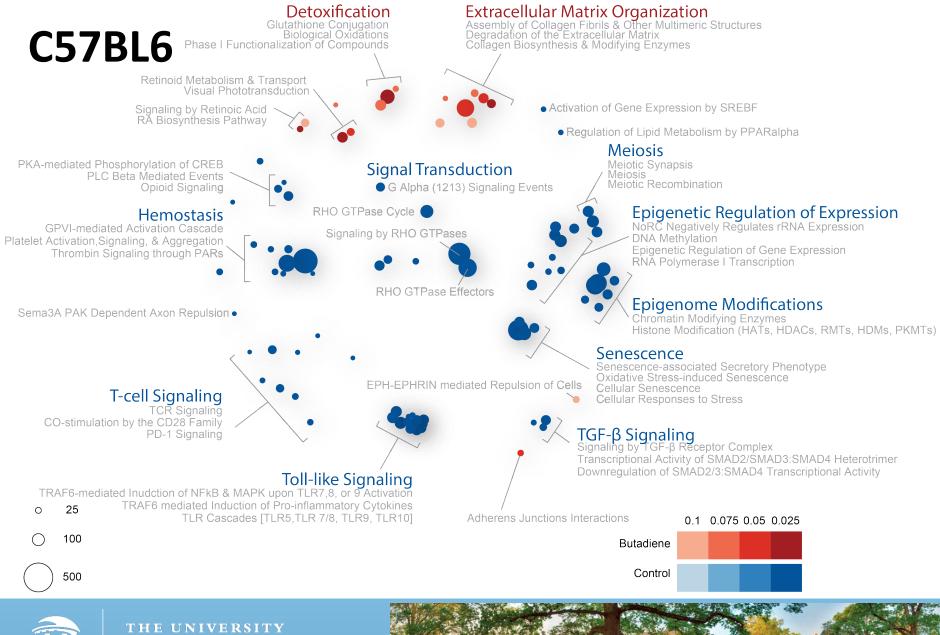


Merge nearby windows

	<u>Windows</u>	<u>Significant</u>	<u>Mapped</u>	
	<u>Tested</u>	<u>Windows</u>	<u>Genes</u>	
<u>C57BL6</u>	325,103	2,610	3,274	
CAST	326,645	0	0	



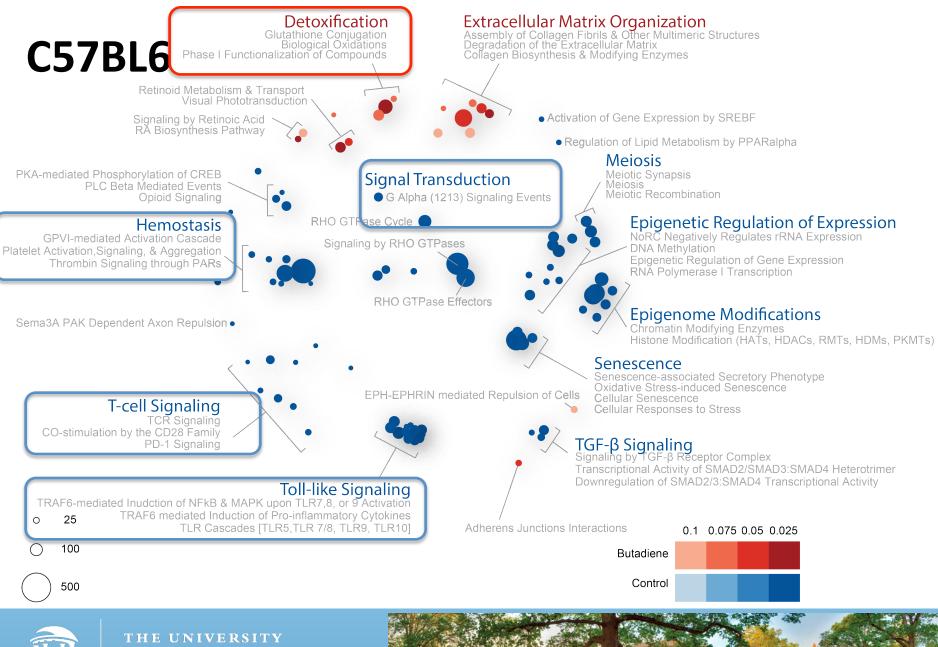






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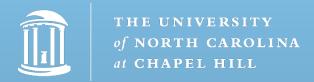




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at CHAPEL HILL



What drives differences between C57BL6 and CAST in response to butadiene exposure?





Gene expression and chromatin landscape differ at basal state

mRNA expression:

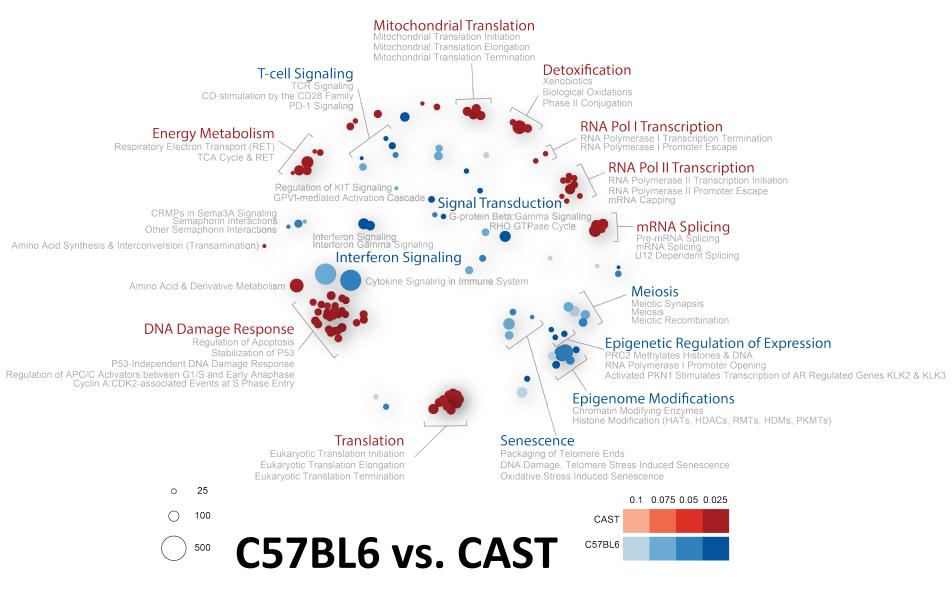
	Total Genes	<u>Differential</u>
C57BL6 vs CAST	20868	10250
C57BL6 exposure	20868	4116

Chromatin Accessibility:

	<u>Windows</u> <u>Tested</u>	<u>Significant</u> <u>Windows</u>	<u>Mapped</u> <u>Genes</u>
C57BL6 vs CAST	304,385	19,220	11,184
C57BL6 exposure	325,103	2,610	3,274











Summary

Hemostasis**
Signal Transduction
T-cell Signaling
Interferon Signaling

DNA Damage Energy Metabolism **Detoxification**** Mitochondrial Translation

C57BL6 Control ←

→ C57BL6 Butadiene

CAST Control ←

CAST Butadiene





Summary

Hemostasis** **Signal Transduction T-cell Signaling** Interferon Signaling

DNA Damage Energy Metabolism **Detoxification**** Mitochondrial Translation

C57BL6 Control ←

→ C57BL6 Butadiene

CAST Butadiene

Energy Metabolism Hemostasis Phase I Metabolism

Detoxification





Summary

Hemostasis**
Signal Transduction
T-cell Signaling
Interferon Signaling

DNA Damage Energy Metabolism **Detoxification**** Mitochondrial Translation

C57BL6 Control ←

Immune System (T-cell, Interferon Signaling)
Signal Transduction
Epigenetic Regulation of Expression
Epigenome Modifications

DNA Damage Energy Metabolism Detoxification Mitochondrial Translation

Energy Metabolism Hemostasis Phase I Metabolism → CAST Butadiene

→ C57BL6 Butadiene

Detoxification





Epigenetic data in toxicology studies enables

- Understanding better how expression phenotypes arise in cells and tissues
- Understanding how basal epigenetic state contributes to altered susceptibility
- Investigations into how genetic variation contributes to phenotype through effects on epigenome



Acknowledgements

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Karl Eklund

Jennifer Israel

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Jeremy Wang

Matt Weiser

<u>Ivan Rusyn (Texas A&M)</u>

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Greg Crawford (Duke)

Alexias Salas







