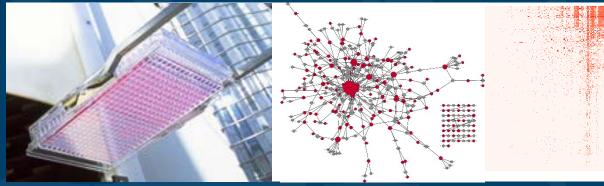


## Strategies for Integrating Transcriptional Profiling into High-Throughput Toxicity Testing



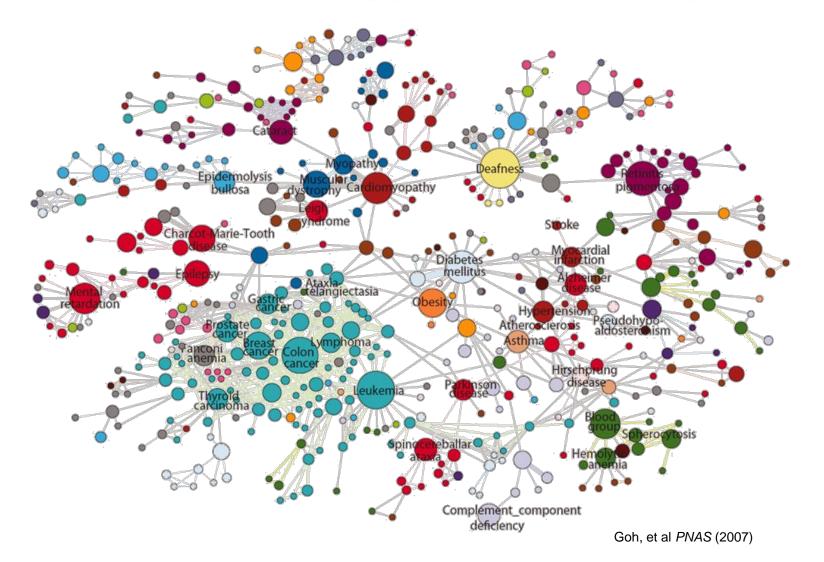
Society of Toxicology Annual Meeting March 25, 2015

Rusty Thomas Director National Center for Computational Toxicology

The views in this presentation are those of the author and do not necessarily reflect policies of the EPA. Mention of trade names, products, or services does not convey EPA approval, endorsement, or recommendation.

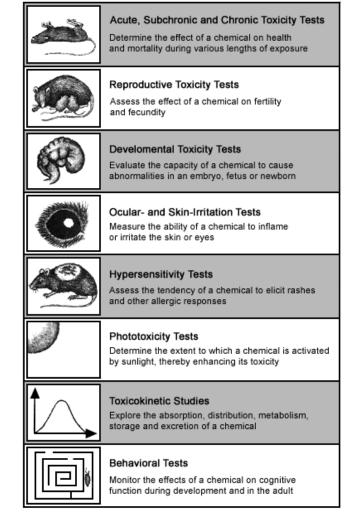


# The Biological Scope for Toxicology is Necessarily Broad





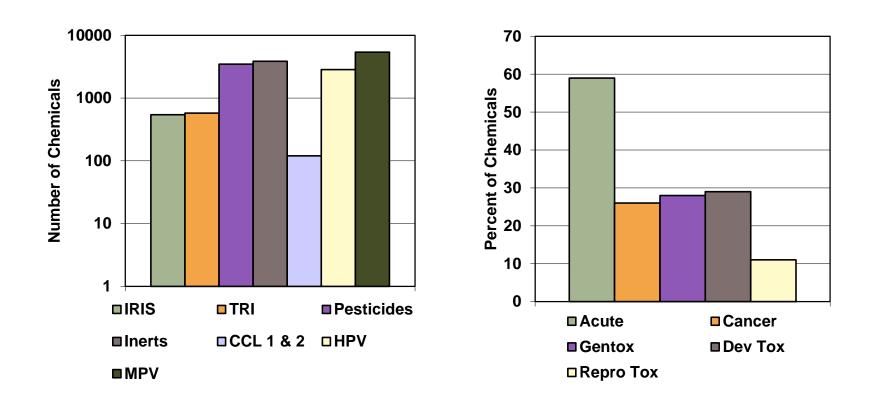
#### **Traditional Studies Attempt to Cover Range of Potential Adverse Responses**



Goldberg and Frazier (1989)



#### Current System for Chemical Safety Testing Has Not Kept Pace





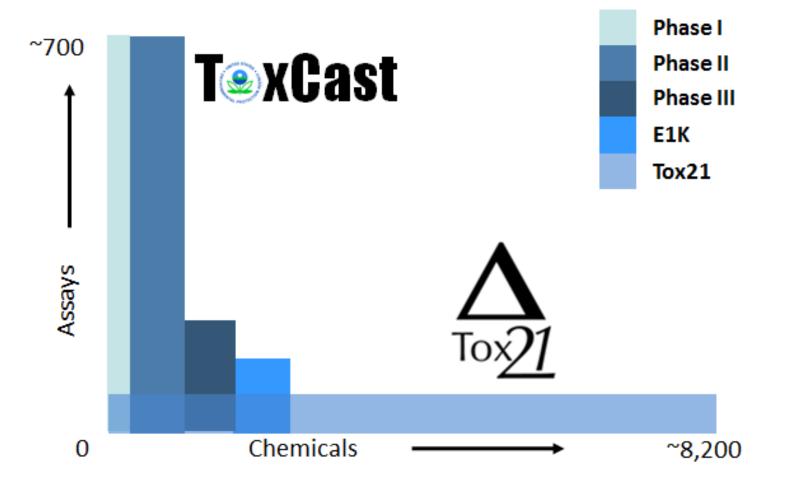
# Significant Economic and Animal Costs Associated with Testing

	Number of	
Toxicity Study	Animals	Approx. Cost
Skin sensitization ( <i>in vivo</i> )	20	\$7,000.00
Acute toxicity by oral route	20	\$2,500.00
Repeated dose toxicty (one species, male and female (28 d), most		
appropriate route) (OECD407)	40	\$100,000.00
In vivo somatic cell genotoxicity study	80	\$35,000.00
Sub-chronic repeated dose toxicity, most appropriate route (90 d) (OECD		
408)	80	\$220,000.00
Pre-natal developmental toxicity, one species, most appropriate route		
(OECD 414)	80	\$150,000.00
Chronic tox/Carcinogenicity study combined (> 12 month)	280	\$1,500,000.00
Two generation reproductive toxicity, one species, male, female (OECD		
416)	360*	\$500,000.00
Developmental neurotoxicity (OECD 426)	80*	\$750,000.00

\*Offspring not counted

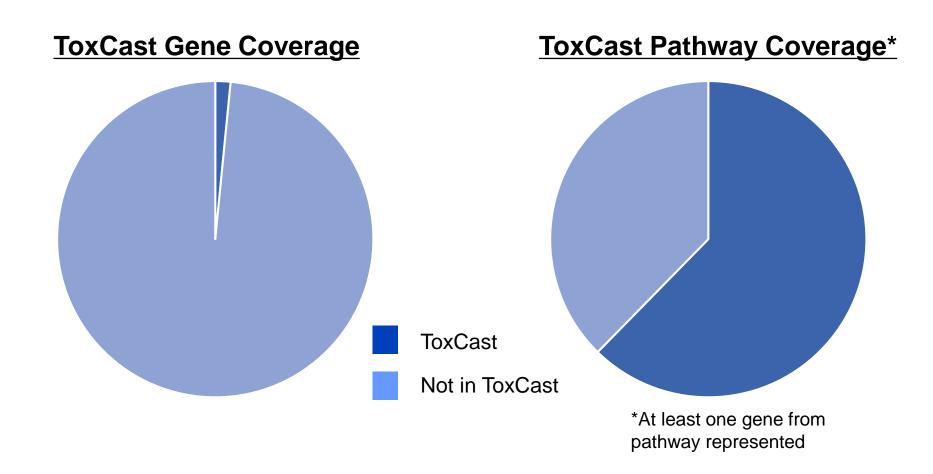


## Multiple Federal Efforts Have Begun to Address the Data Gap



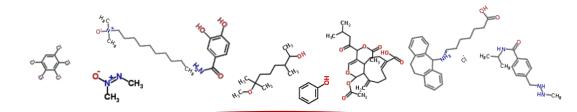


## **Current Coverage of Biological Space is Less Than Optimal**





# Incorporating a Broad Biological Screening Platform



Broad Primary Screen for Bioactivity/MOA

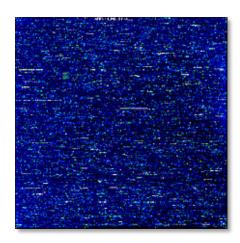
Secondary Confirmation Screen

> Tertiary Screen to Discriminate Perturbation from Adverse Effect



## **Requirements and Potential Platforms for HT Transcriptomics**

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#### <u>Requirements</u>

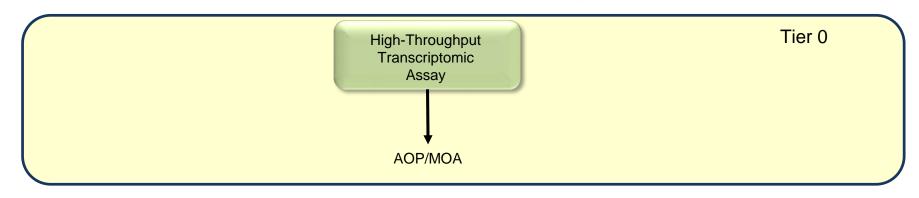
- Measure or infer transcriptional changes across the whole genome (or very close to it)
- Compatible with 96- and 384-well plate formats (maybe 1536?) and laboratory automation
- Work directly with cell lysates (no separate RNA purification)
- Compatible with multiple cell types and culture conditions
- Low levels of technical variance and robust correlation with orthogonal measures of gene expression changes
- Low cost (\$20 \$40 per sample or less)

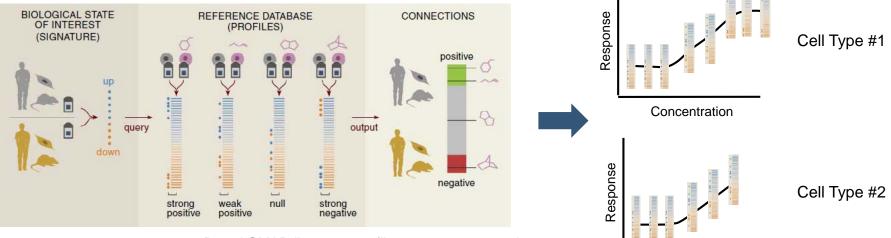
#### Potential Platforms

- Low coverage whole transcriptome RNA-seq (3 5 million mapped reads)
- Targeted RNA-seq (e.g., TempO-seq, TruSeq, SureSelect)
- Microarrays (e.g., Genechip HT)
- Bead-based (e.g., L1000)



# How Would a HT Transcriptomic Platform be Deployed?





Lamb et al. Science (2006)

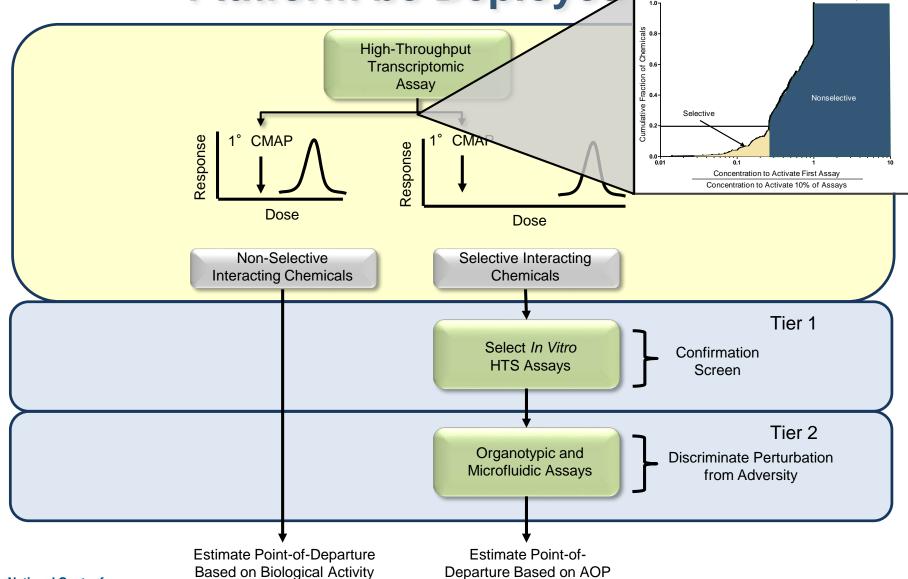
Broad CMAPdb: 7,000 profiles; 1,309 compounds NIH LINCs CMAPdb: 9,000 shRNAs, 3,000 over expression ORFs, and 4,000 compounds in 20 cell types/lines (cell lines and primary cells)

Cell Type #3

Concentration

. . .

## How Would a HT Transcriptomic Platform be Deployed?



National Center for Computational Toxicology

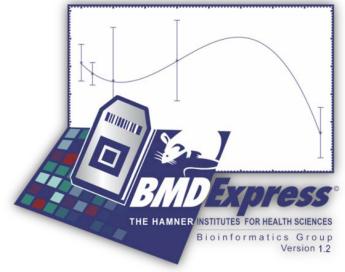
Environmental Protection

Agency



## Approaches for Estimating a Transcriptomic Point of Departure

#### **BMDExpress**



http://sourceforge.net/projects/bmdexpress/

Yang et al., BMC Genomics, 2007 Thomas et al., Toxicol Sci., 2007

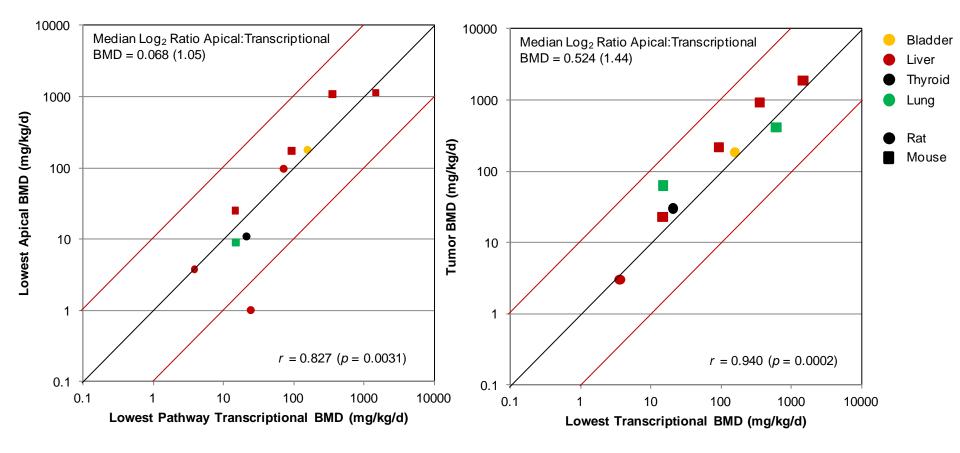
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Settings Help				
2202	102002	AV204	1005a	1050
C:\Users\Ivan\Desktop\DR	Pack\DR_Pack\data\toy.data.cs\	,	Select file	Results
2 - 1				Show input data
Microarray Platform	rat2302.db	-		
Testine				
Testing				11.
Method	Express	•	Ŋ	
Global statistic	D	•		THE UNIVERSITY
Local statistic	Score	•		of NORTH CAROLINA
Pathway Database	GO.BP	•		Gillings School
Correction method	Benjamini & Hochberg FDR	<b>•</b>		of Global Public Health
	$\sim \sim \sim \sim$			Department of
Confidence an	lysis			Biostatistics
P-value threshold for	nclusion: 0.1			
Number of data re-sa	ples: 100			
Pathway FDR thresh	d: 0.05			Run

http://comptox.unc.edu/DRPathway.php

#### **DR** Pathway

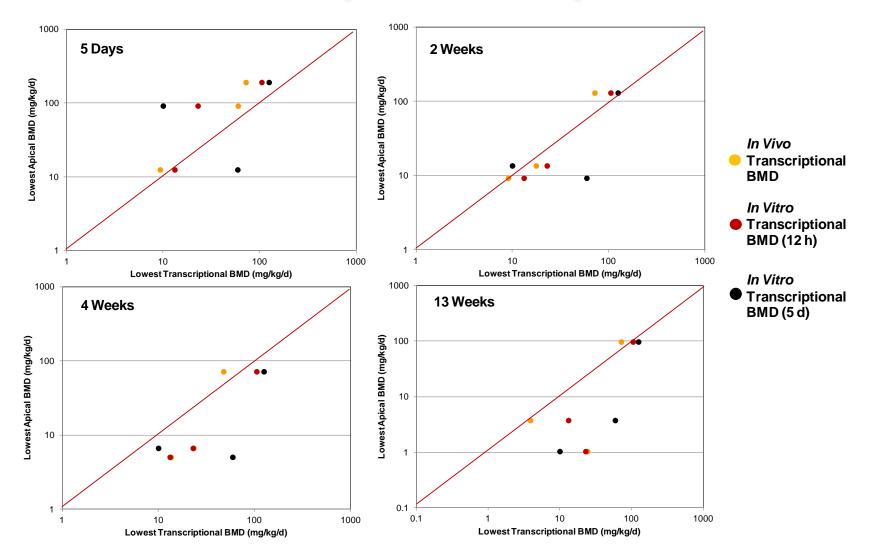


## **Correlation of** *In Vivo* **Apical and Transcriptional Points of Departure**



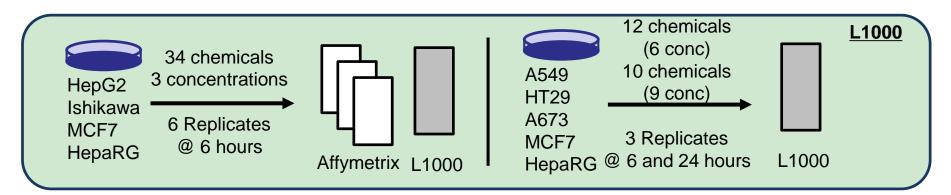


# What About *In Vitro* Transcriptional Responses?





# Beginning the Search for a Platform

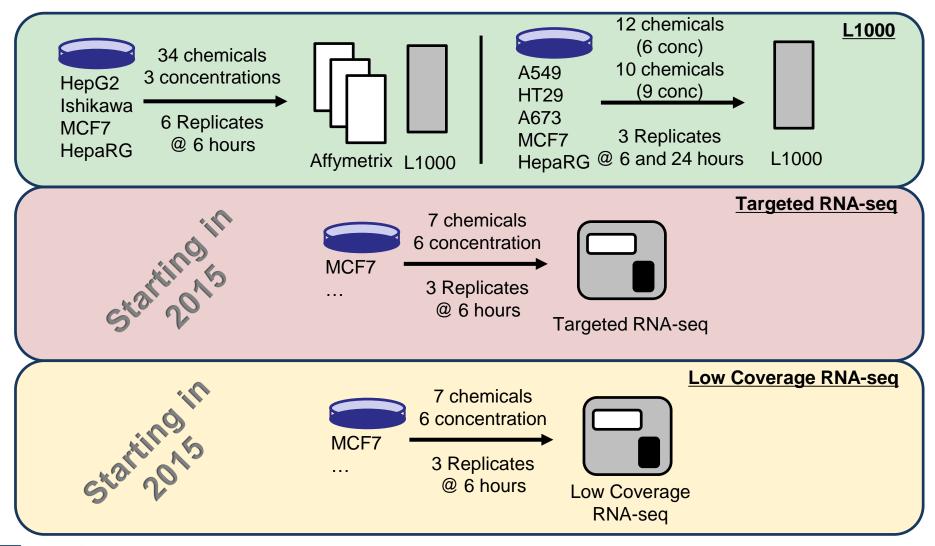


Collaboration with Proctor & Gamble (G. Daston and J. Naciff) and Hamner Institutes (B. Wetmore and M. Black)

Visit Posters: M. Martin *et al.,* Poster #434; Wednesday afternoon M. Black *et al.,* Poster #316; Thursday morning

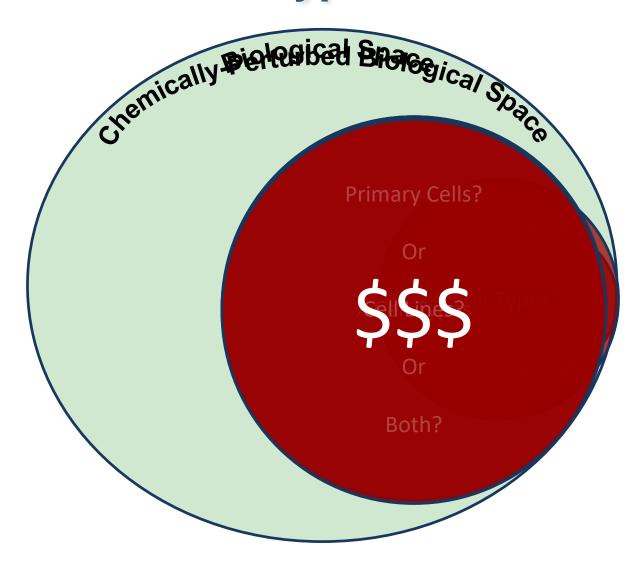


# Beginning the Search for a Platform



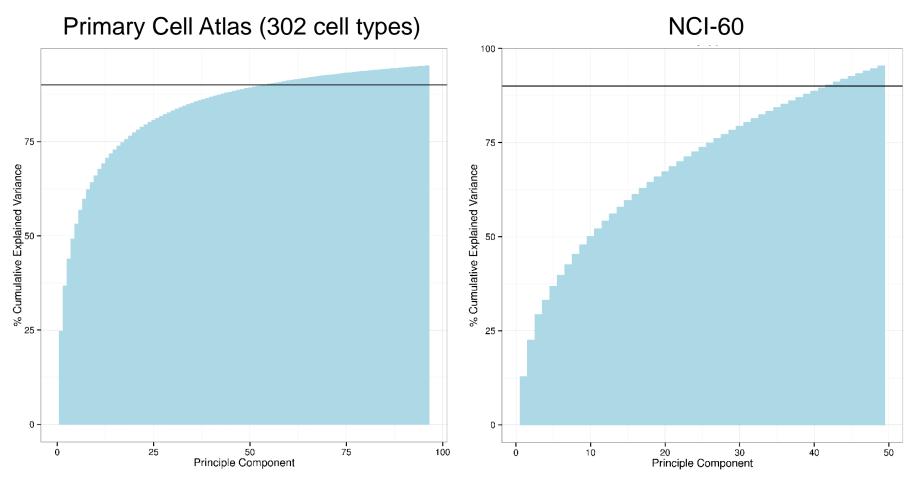


# **Beginning the Search for the Cell Types/Lines**





# **Exploring Cell Line Requirements**

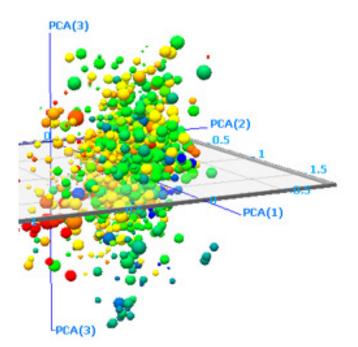


(GSE49910)



# Scientific Rationale for Cell Type/Line Selection





#### **Biologically-Driven?**

Data-Driven?

See poster by N. Sipes et al., Poster #349; Thursday morning





- High-throughput transcriptomics has the potential to fundamentally change the way we evaluate chemicals for safety
  - Greater coverage of biological space
  - Reduced cost
  - Ability to leverage large existing databases of gene expression data
  - Fits logically in a tiered testing approach
  - Allows estimates of points-of-departure for both selective and nonselective chemicals
- Technical evaluations of multiple platforms are underway
- Cell type/line selection challenges remain



# Acknowledgements

Tox21 Colleagues: NTP Crew FDA Collaborators NCATS Collaborators

Hamner Collaborators: Barbara Wetmore Michael Black

P&G Collaborators: George Daston Jorge Naciff

