

High-throughput Transcriptomics for Accelerated Toxicity Screening

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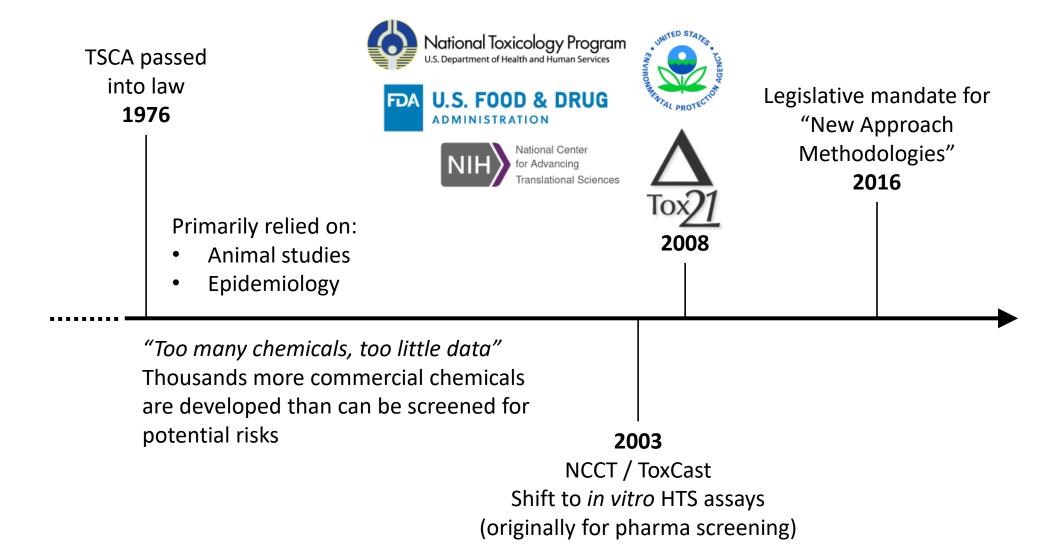




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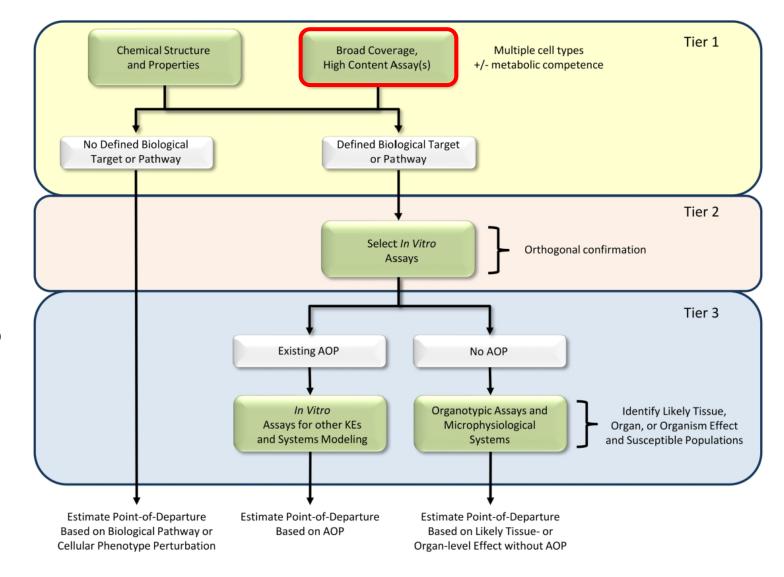
History of Chemical Risk Assessment





Tiered Testing Strategy

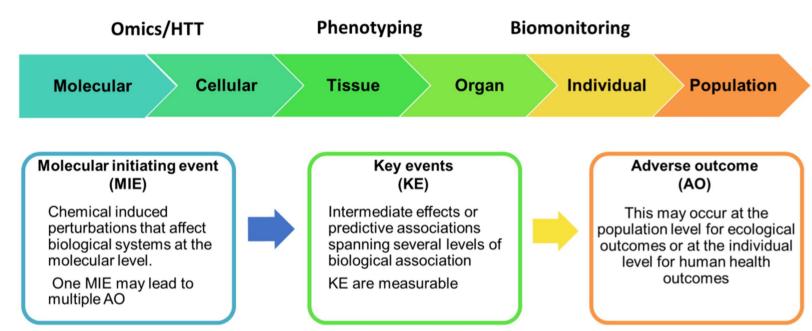
- Use transcriptomics to:
 - Screen for bioactive chemicals
 - Predict benchmark dose
 - Infer mode of action
 - Predict adverse outcomes
- Adverse Outcome Pathways (AOPs) link cell & molecular perturbations to organism-level effect





Overview of AOP Framework

- Use transcriptomics to:
 - Screen for bioactive chemicals
 - Predict benchmark dose
 - Infer mode of action
 - Predict adverse outcomes
- Adverse Outcome Pathways (AOPs) link cell & molecular perturbations to organism-level effect

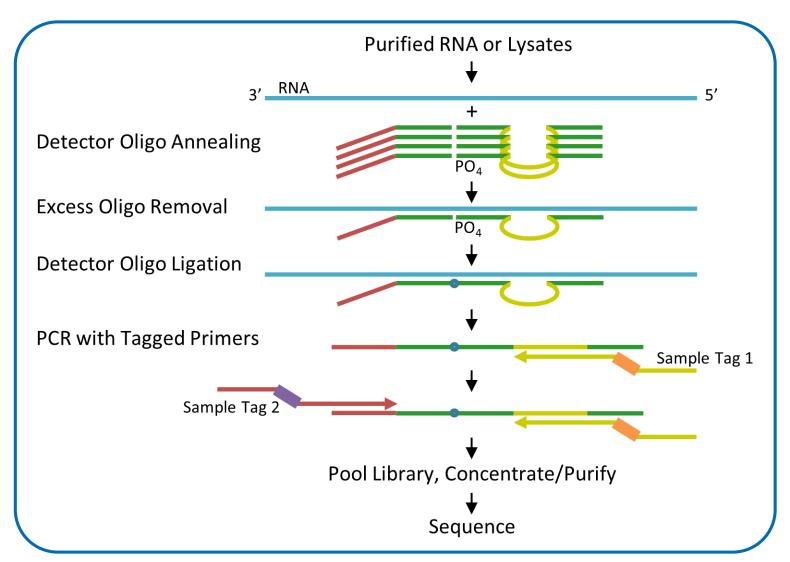


Hamm, et al. Toxicol in Vitro 2017



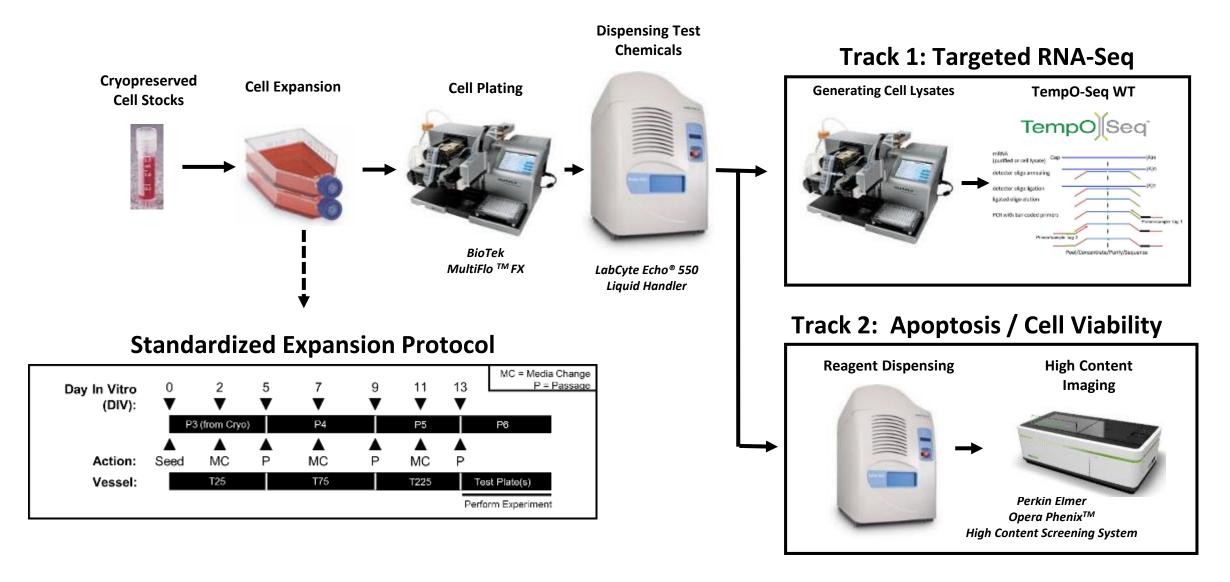
TempO-seq Enables High-throughput Transcriptomics

- Use purified RNA or cell lysates
- Probe set for whole human transcriptome target ~21,000 human genes
- Captures majority of signal with much lower sequencing depth (~6M reads)
- Attenuation of highly expressed genes reduces depth further (~3M reads)
- Barcoding and pooling allows hundreds of samples per flowcell
- Data pre-processing is much faster



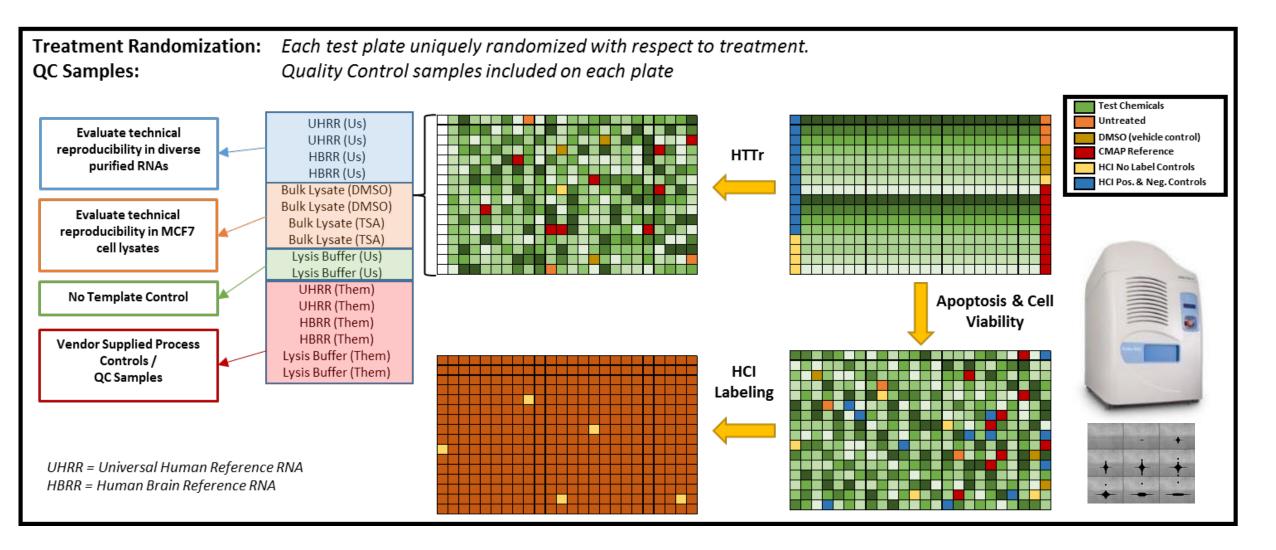


Screening Protocol





Screening Protocol





First Screen: MCF-7 Cells

Study 1: Pilot Screen 6,804 Samples

Study 2: Large Scale Screen ~54,432 Samples (>50TB)

Parameter	Multiplier	Notes	Multiplier	Notes
Cell Type(s)	1	MCF-7	1	MCF-7
Culture Condition	2	DMEM + 10% HI-FBS PRF-DMEM + 10% CS-HI-FBS	1	DMEM + 10% HI-FBS ^a
Chemicals	44	Mechanistic Diversity w/ Redundancy	2,112	ToxCast ph1, ph2, e1k / ph3
Time Points:	3	6, 12, 24 hours	1	6 hours
Assay Formats:	2	TempO-Seq HCI Cell Viability & Apoptosis	2	TempO-Seq HCI Cell Viability & Apoptosis
Concentrations:	8	3.5 log ₁₀ units; semi log ₁₀ spacing	8	3.5 log ₁₀ units; semi log ₁₀ spacing
Biological Replicates:	3		3	

Next Screens: HepaRG (~2k chemicals) + additional cell type

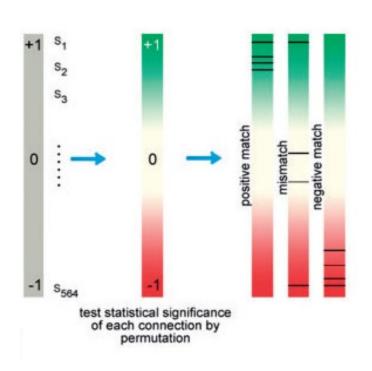


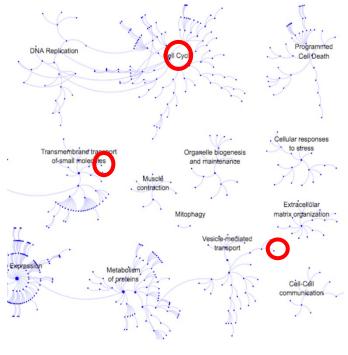
Molecular Target Prediction

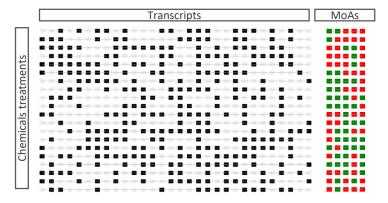
Connectivity mapping analysis using DEGs and CRGs

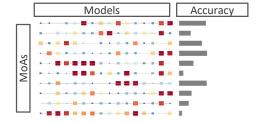
Pathway / Network analysis using DEGs and CRGs

Machine learning to build Target-specific models







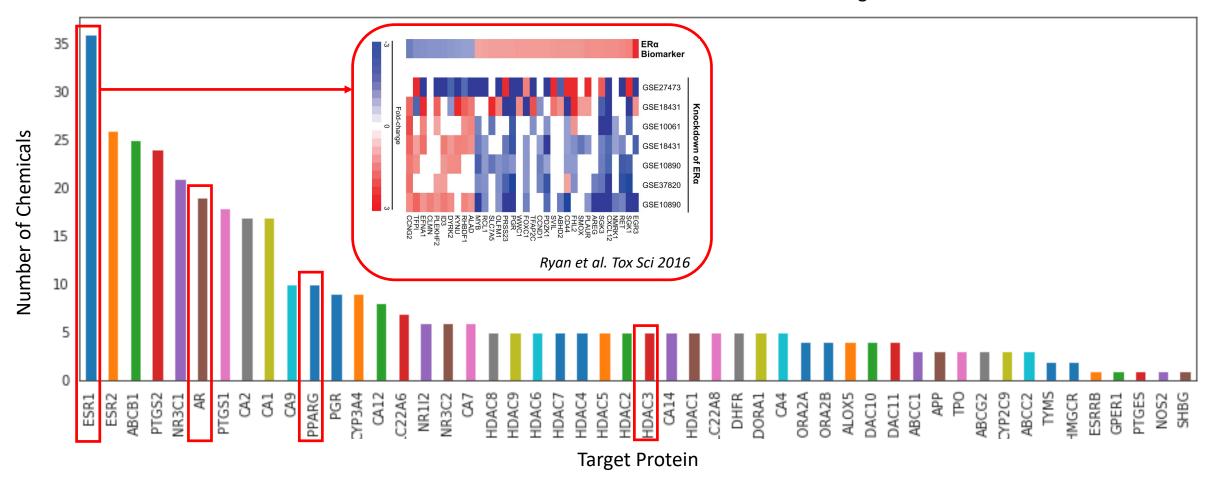


reactome.org



Chemicals with Known Targets

All Chemicals in Phase-I MCF-7 Screen with Annotated Target





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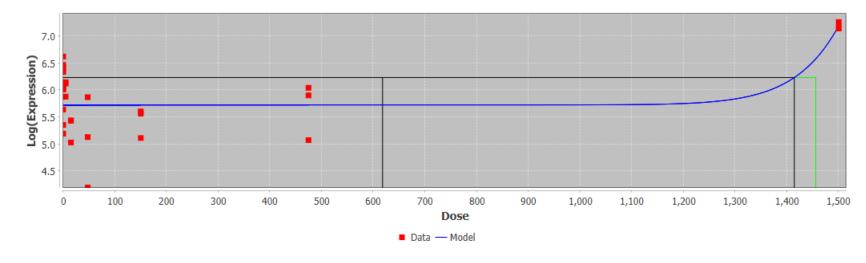




Curve Fitting & POD Estimation

- Goal: Determine concentration at which bioactivity occurs
- Challenge 1: Statistical properties of seq-based assays violate standard assumptions (normality)
- Challenge 2: Summarization of curves/PODs from thousands of genes
- Use concordance with in vivo and HTS results as a guide

BMDExpress – Phillips, et al. Bioinf 2019



ToxCast Pipeline (tcpl) – *Filer, et al. Bioinf 2017*

