

Toxicant Analysis via High-content Screening of Cellular Circuits

11/18/2010

Computational Toxicology Communities of Practice

John K. Westwick, Ph.D.

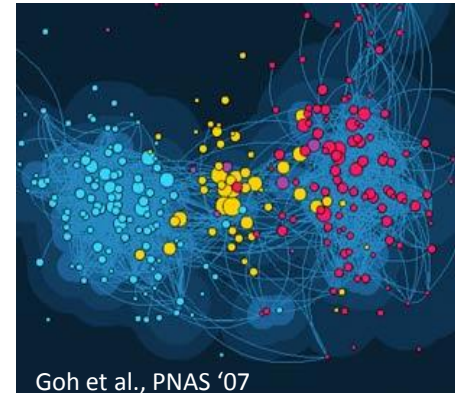
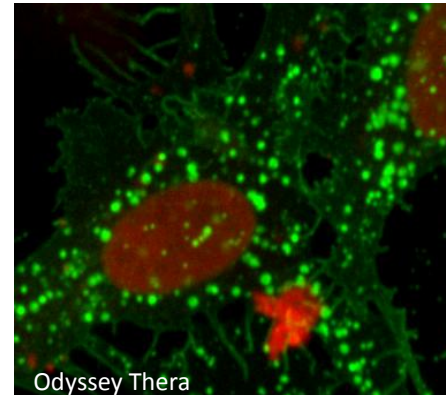
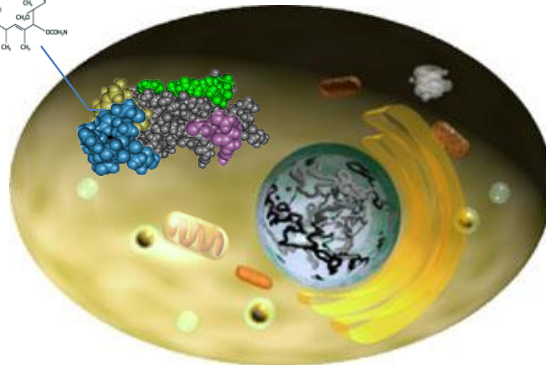
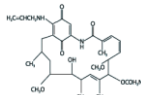
Challenges

Complex Adaptive Systems



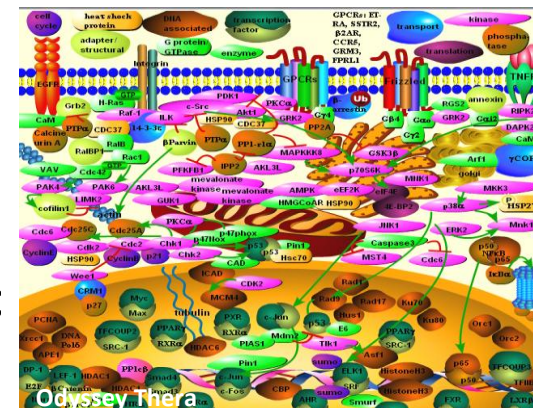
Visible Human Explorer (NLM)

Complex molecular and cellular networks drive cell signaling and toxicity

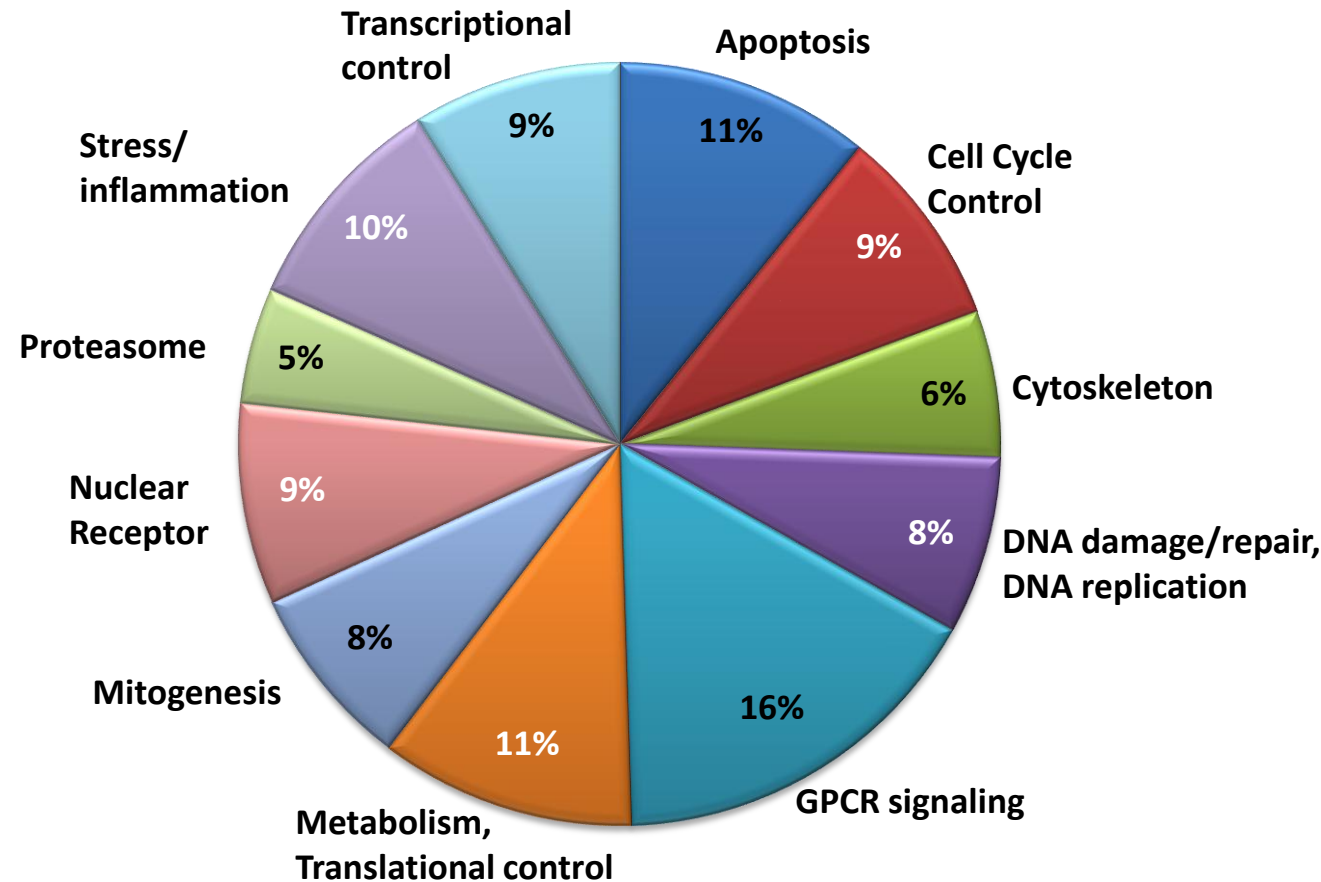


Large and growing number of agents requiring analysis

Need for **assay diversity**, **biological context** and **throughput** in analytical strategies



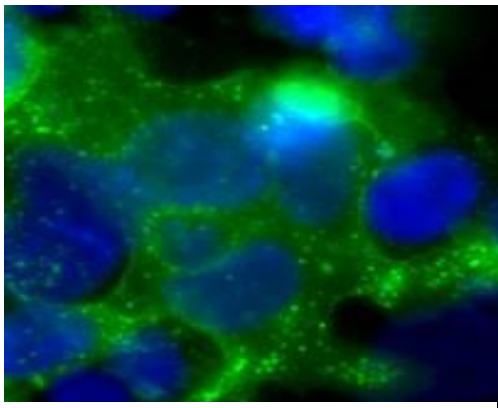
Assay Diversity (performed in living human cells)



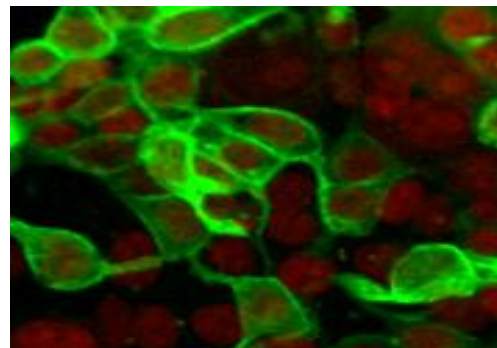
- Odyssey has created and validated the world's largest high-content assay collection
- Capability covers all target classes, including 'un-drugable' targets
- Panel size and breadth enables systems-based profiling
- Major ongoing development program around key target classes and cell types

Biological context addressed with PCA, HCS and other technologies

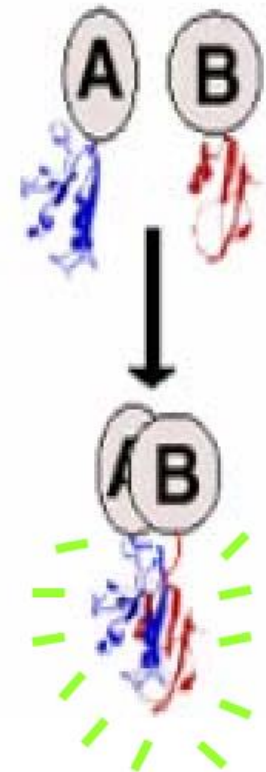
- Protein-fragment Complementation Assay (PCA) technology
 - A reporter protein is rationally dissected into two fragments which are fused to two proteins that are known to interact within a signaling complex
 - Fusion proteins are expressed in living human cells
 - Assembly of the reporter protein from its fragments can only happen if the test proteins exist in a complex
 - Test agent activity is measured via changes in signal intensity and location (e.g. fluorescence)



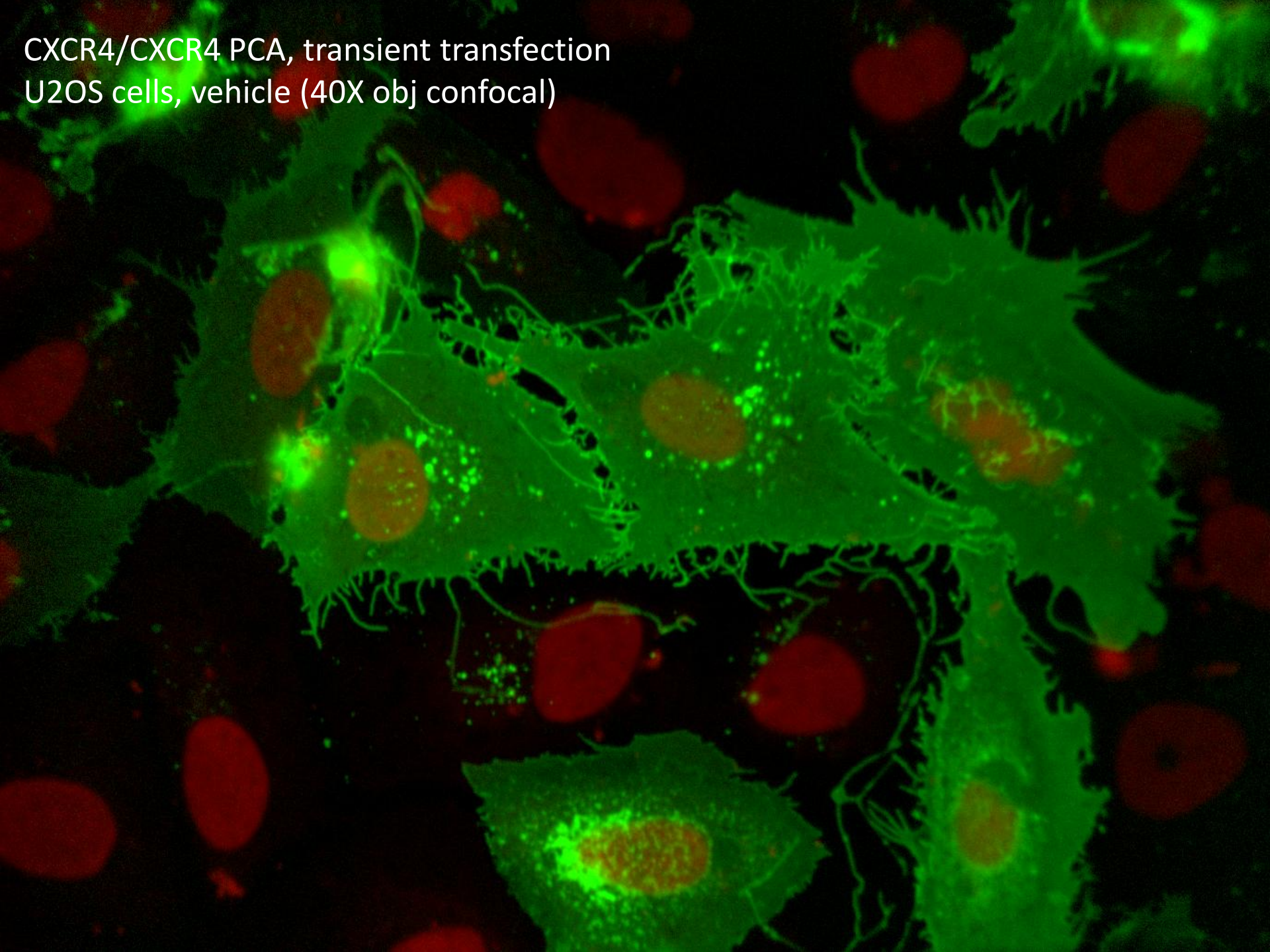
Frizzled4/GRK



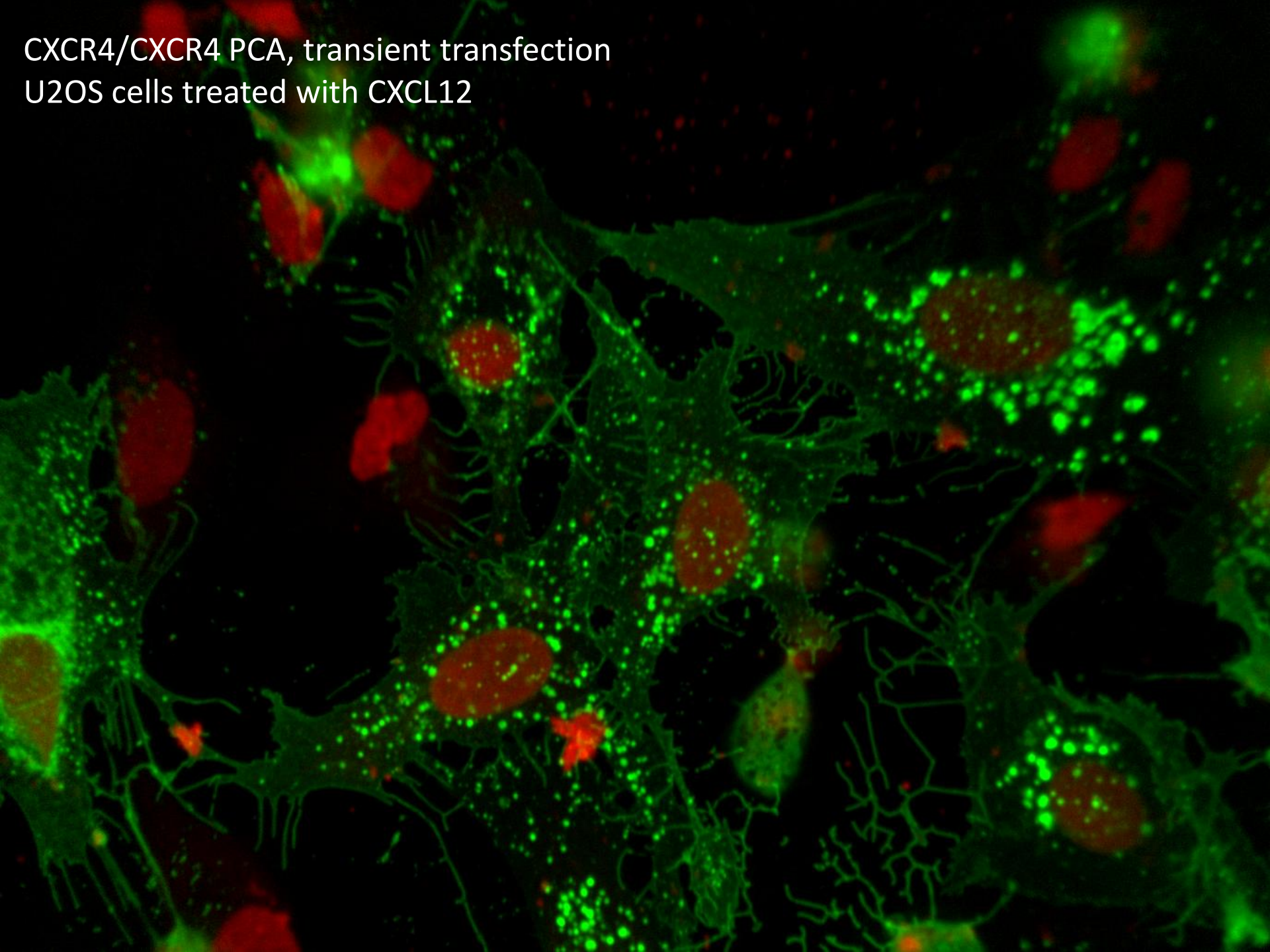
A_{2A}/D_{2L} GPCR heterodimer



CXCR4/CXCR4 PCA, transient transfection
U2OS cells, vehicle (40X obj confocal)



CXCR4/CXCR4 PCA, transient transfection
U2OS cells treated with CXCL12



Cellular assays proposed for ToxCast (examples)

- GPCR, developmental paths
 - Frizzled PCA (Wnt pathway), mGluR3 PCA, Smo (smoothened) PCA

- Nuclear receptors and other transcription and translation regulators
 - HDAC PCA, CAR PCA, ERR γ PCA, HCA of active ER units, myc/max

- Functional Analyses of Stress and Toxicity
 - Human ESC-derived motorneurons (Wst-8); ESC-derived hu hepatocytes (multiTox)

- Kinases, phosphatases, GTPases, GEFs, metabolic, nucleases/proteases, structural, proteasome
 - TGF β R1 PCA, p38 α /Mnk1, Vav/Cdc42

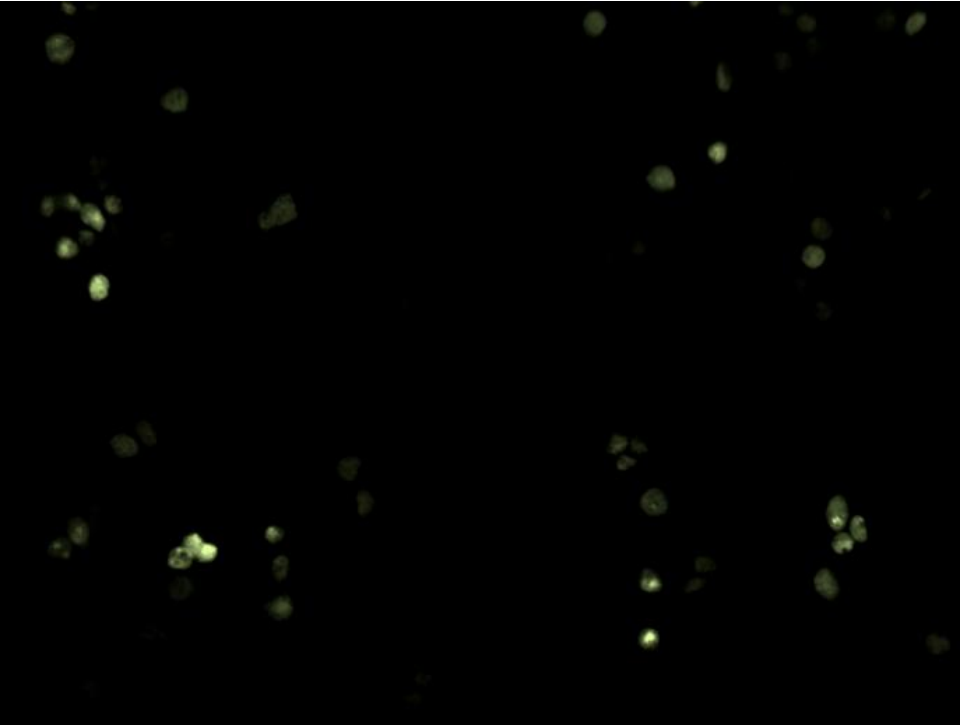
- Protein level and post-translational modification
 - GRP78 IF

- Apoptosis, Damage, transport, hypoxia, immunomodulation, 2nd messenger signaling
 - p53/Pin1, Rad51 PCA, ARF/ γ COP, BAD/BclxL, Hif1 α PCA

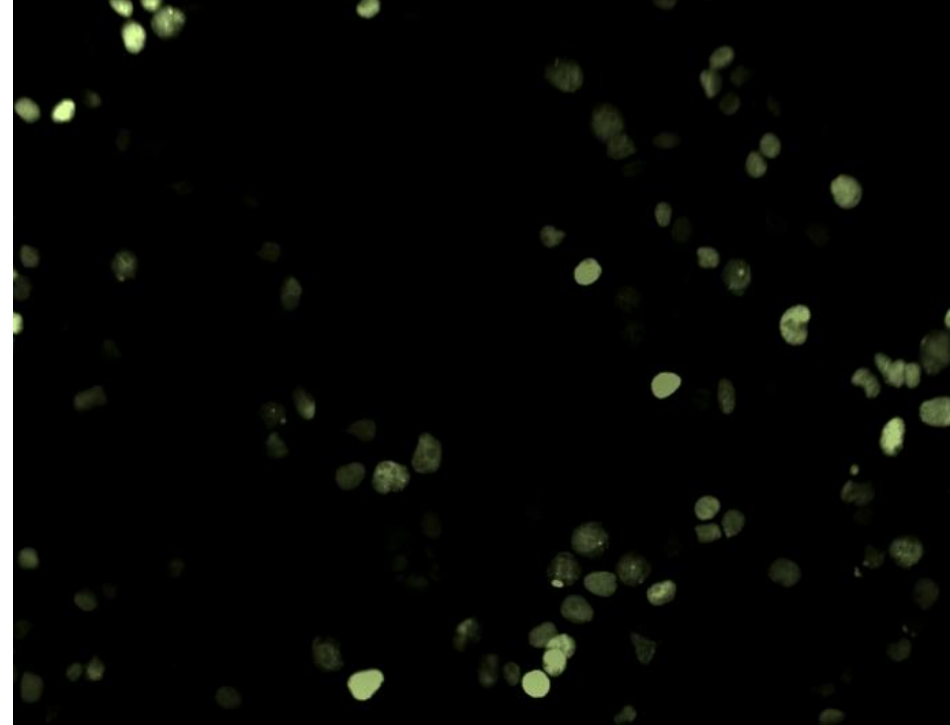
- PCAs + metabolic activation
 - Androgen receptor PCA (+ compound metabolism)

NB: >90% of the assays involve high content screening and automated image analysis

Development Program: LXR α Homodimer PCA (transient probe transfection)



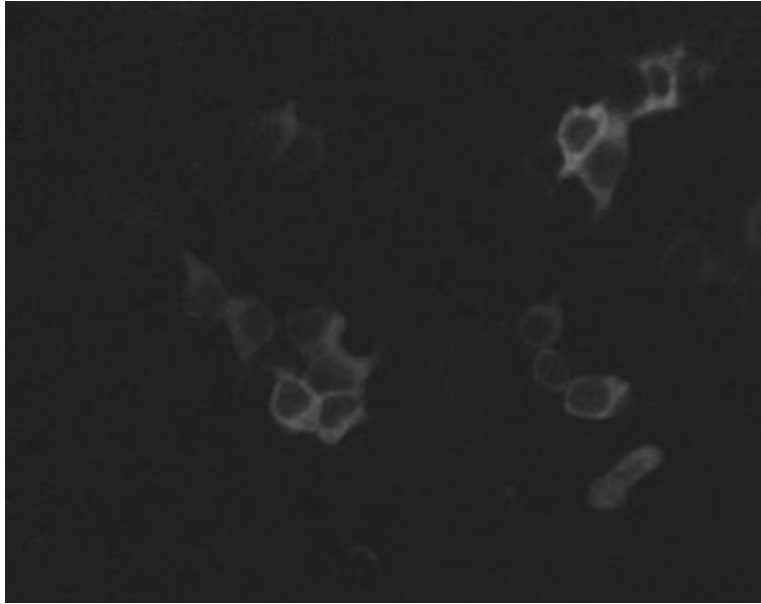
Vehicle-treated cells show weak nuclear staining



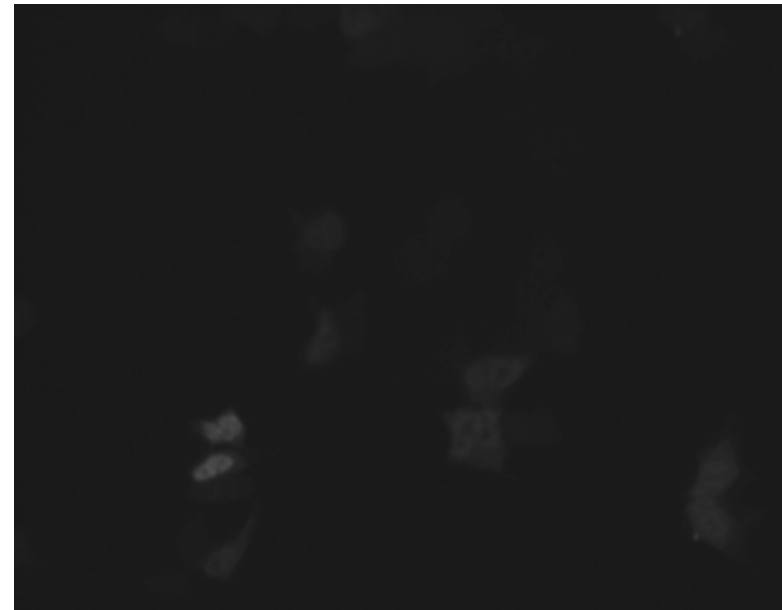
Agonist-stimulated cells show strong nuclear staining
(T0901317)

- Dose-responsive induction seen with known agonist (TO compound)
- Status: results with transient led to decision to develop stable line (in progress)

Development Program: Androgen Receptor/SRC-1 PCA (transient probe transfection)



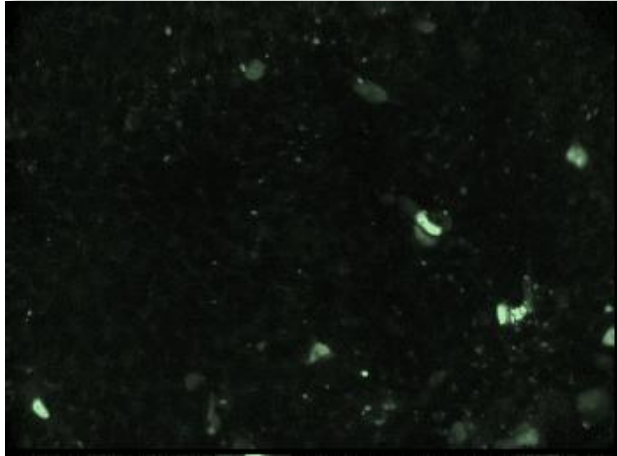
Vehicle-treated cells show diffuse cytoplasmic staining



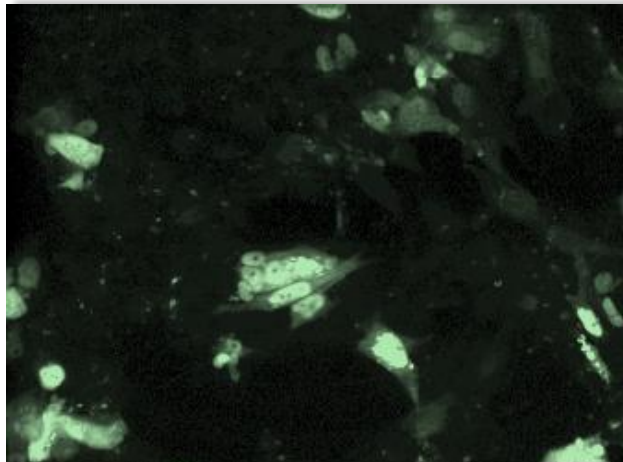
Ligand-stimulated cells (4-HT) demonstrate nuclear staining and cytoplasmic speckling

status: selecting stable cell lines

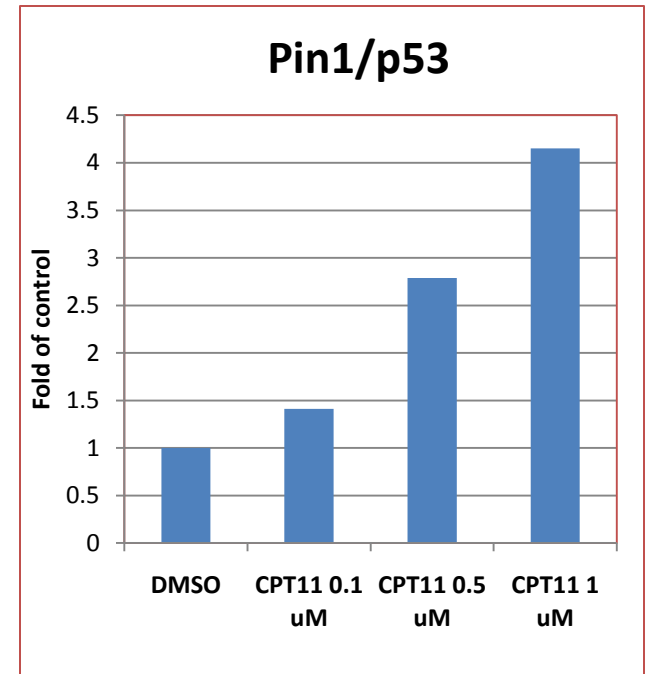
Development Program: Dose responsive PCA in human stem cells



Pin1/p53 transient transfection
(vehicle)

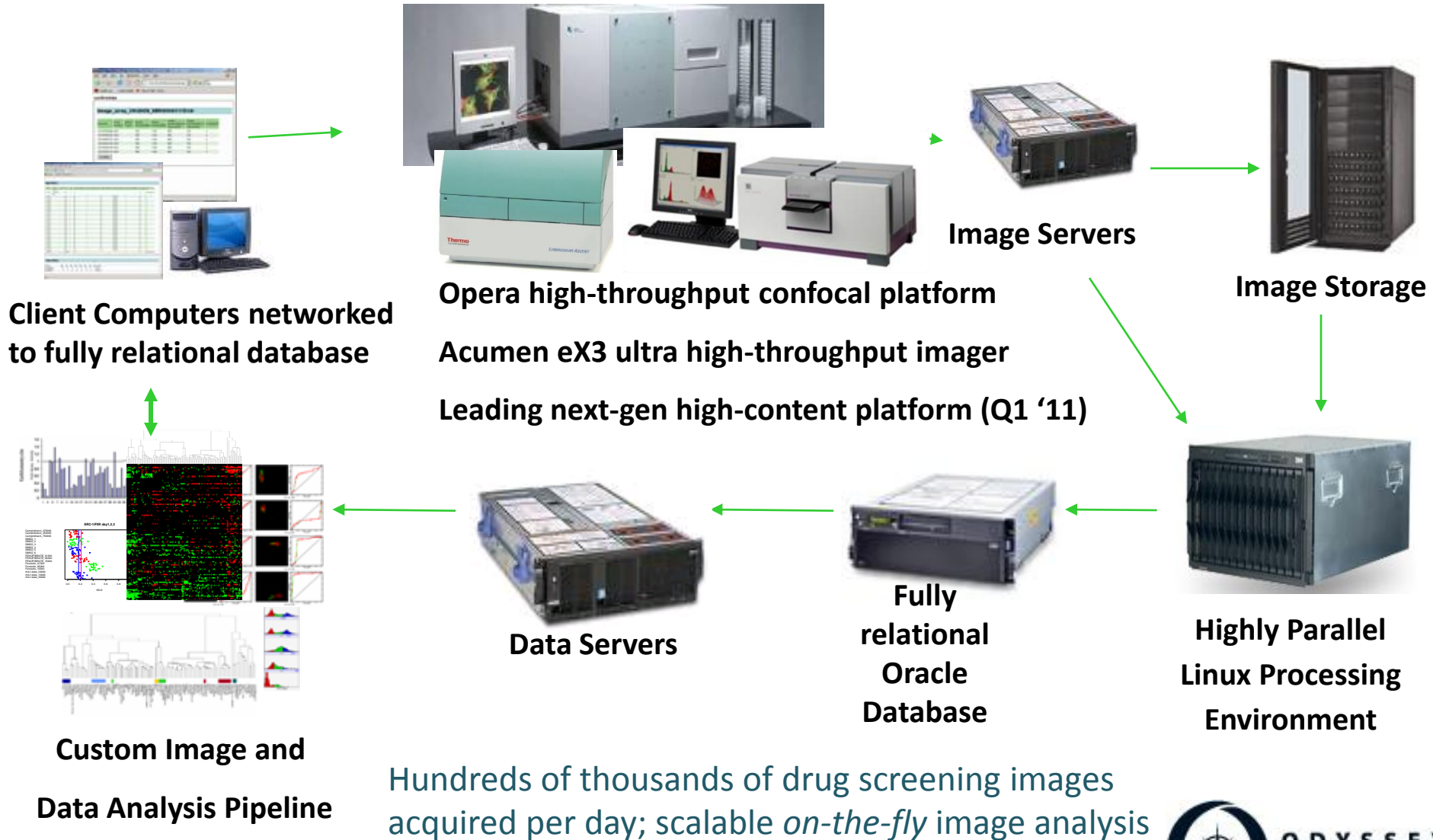


Pin1/p53
topoisomerase inhibitor



Dose-response from high-throughput, high-content screening

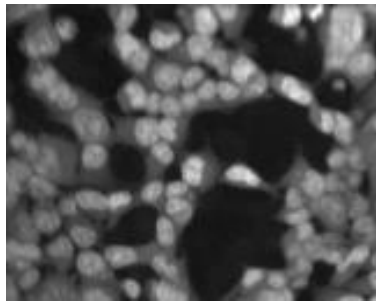
Throughput Requirements Addressed by Integrated Technology Platform and LIMS



Automated image analysis quantifies pixels from defined sub-cellular compartments @ 2 or 3 wavelengths

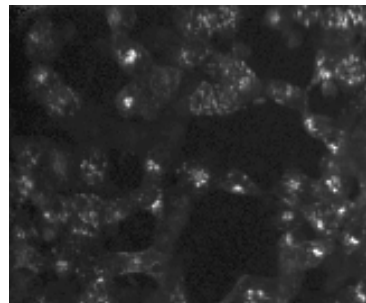
Raw images

635nm



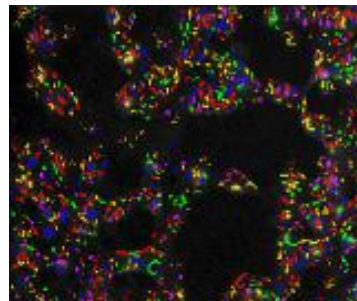
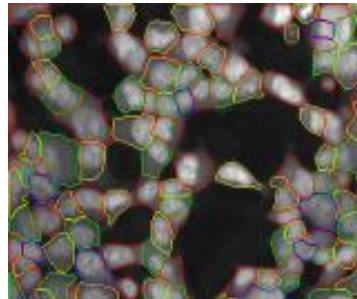
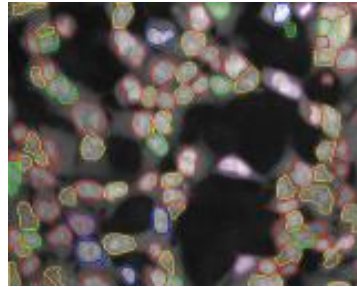
Stains: define nuclear and cytoplasm boundaries

488nm

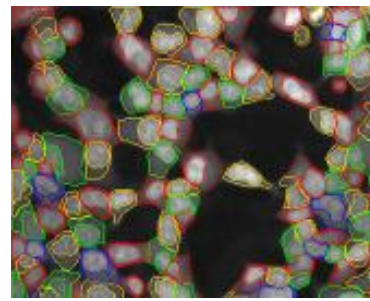
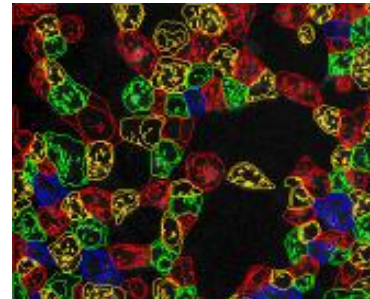
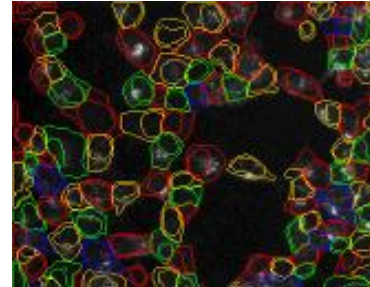


Assay signal(s): localization intensity granularity

Masks

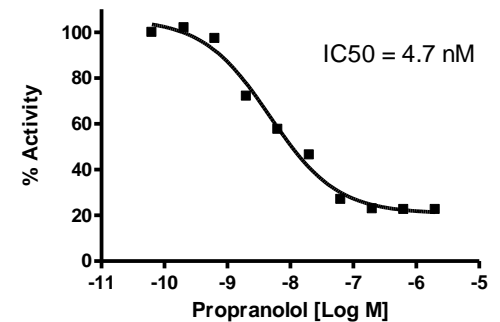
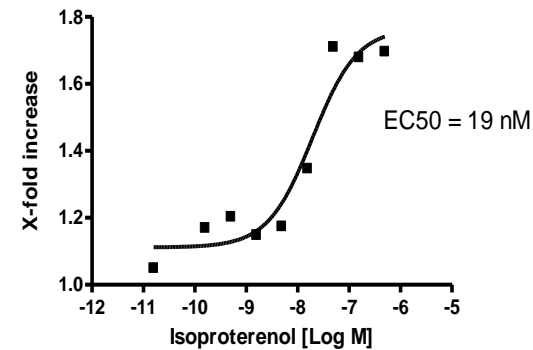


Composite masks

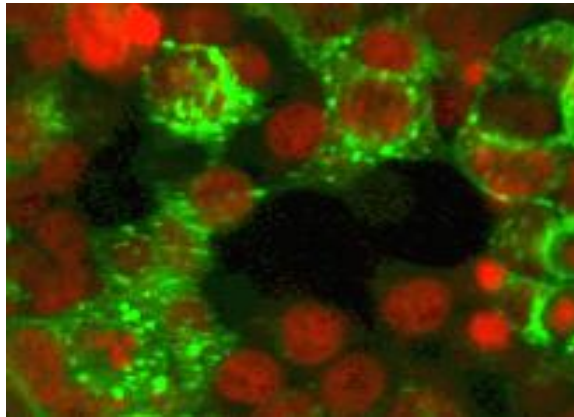


Example:

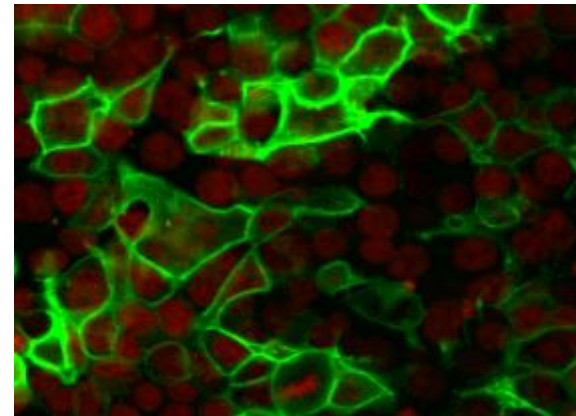
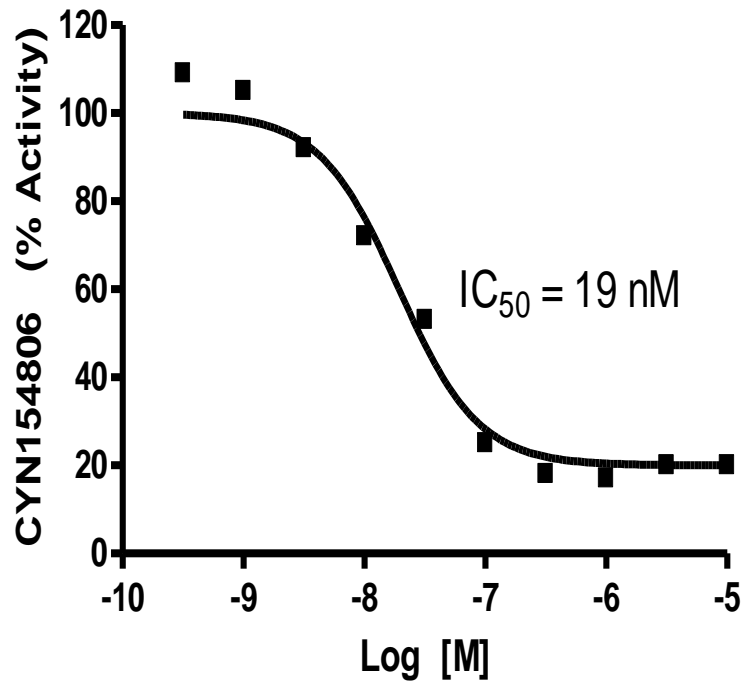
GPCR (b2AR)/arrestin complex internalization



Quantitation of complex biology



vehicle

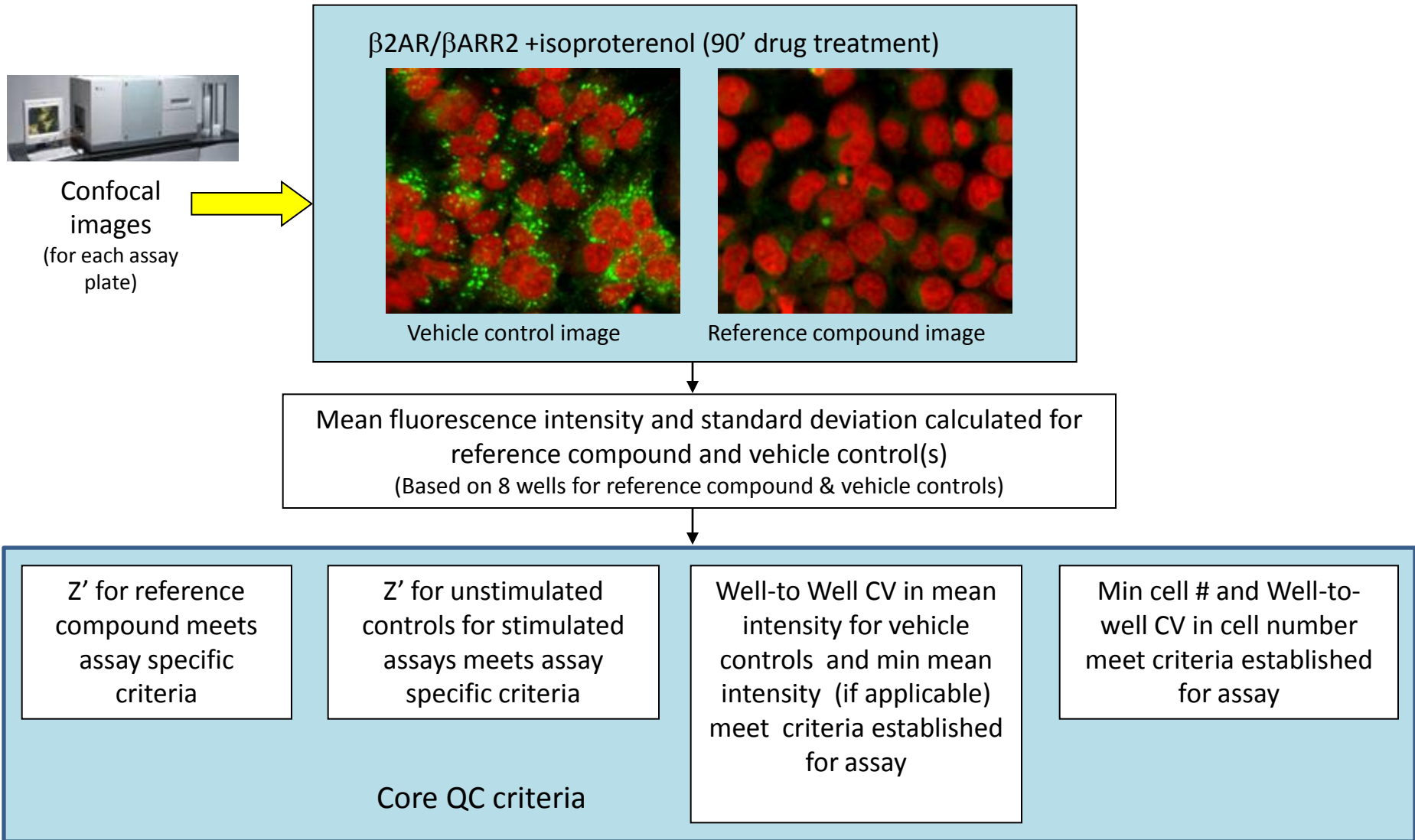


CYN 154806 (10 μM)

Image-based QC

- nucSize filter
 - Cell type / assay dependent
 - Both upper and lower size limits are defined per cell type
- Nuclear stain intensity filter
 - Stain, cell type and assay dependent
 - Upper and lower intensity limits are defined
 - Cells that don't meet criteria are filtered out
- Cell count filter
 - Max and min values defined for each cell type
 - Images that don't meet criteria are filtered out

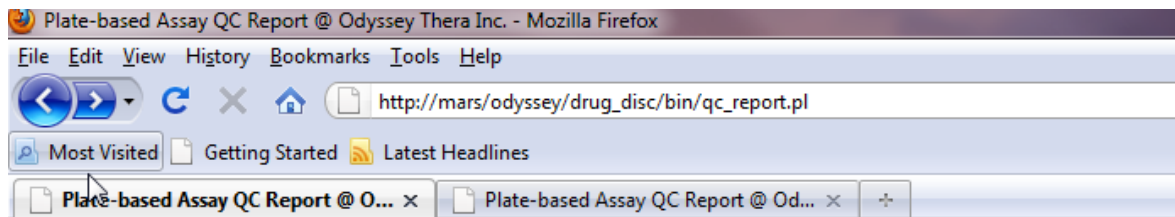
Plate-Based Assay QC for High Content Data



If an assay plate meets criteria, the plate PASSES

If an assay plate fails one or more criteria, the plate is FAILED and repeated

QC Team reviews quantitative results via custom web interfaces




Get QC Report - Select Screens (Use CTRL/SHIFT-Click for Multiple Selections)



Get QC Report - More Query Selections (Use CTRL/SHIFT-Click for Multiple Selections)

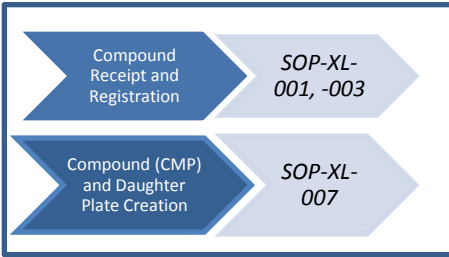
Assays		YFP Descriptor2														
Assay ID	Assay Name Assay Type	Barcode Exp Name As	Descriptor	Z-Stim	Z-Sig	Sig/Ctrl MeanRatio	ScanMean	ScanCV	#Scan Flagged	WellMean	WellCV	#Well Flagged	PlateMean	PlateCV	#Plate Flagged	#Scan Passed
415	Akt1/Pdk1 PCA	ASC0056620 KUD008600	MCRatio	-10.25	0.70	0.83	1.109	1.5		1.109	0.7		1.115	0.7		76
91	Artifact detection I (Fluorescence) OTHER	ASC0056621 KUD008600	MCRatio	-7.40	0.52	0.84	1.104	2		1.103	1.5		1.115	0.7		73
688	Artifact detection II (empty reporter) OTHER	ASC0056622 KUD008600	MCRatio	-11.75	0.58	0.84	1.109	1.7		1.109	0.7		1.115	0.7		76
414	beta2AR/b-arrestin2 PCA	ASC0056623 KUD008600	MCRatio	-30.50	0.61	0.85	1.107	1.5		1.107	0.9		1.115	0.7		74
607	beta2AR/b-arrestin2~Isoproterenol~250~nM PCA	ASC0056624 KUD008600	MCRatio	-8.00	0.45	0.85	1.113	1.8		1.113	0.8		1.115	0.7		75
966	Cdc2/Cdc25C PCA	ASC0056626 KUD008600	MCRatio	-10.14	0.58	0.85	1.117	2.1		1.117	0.8		1.115	0.7		74
426	Chk1/Cdc25C PCA	ASC0056627 KUD008600	MCRatio	-27.50	0.65	0.82	1.123	2		1.124	1.2		1.115	0.7		75
991	Chk1/Cdc25C~CPT~500~nM PCA	ASC0056628 KUD008600	MCRatio	-9.50	0.60	0.82	1.124	2		1.125	1.2		1.115	0.7		73
982	Cleaved PARP_U2OS_IF IF	ASC0056629 KUD008600	MCRatio	-7.40	0.78	0.83	1.113	1.5		1.113	0.5		1.115	0.7		75
860	CXCR4/bARR2 PCA	ASC0056630 KUD008600	MCRatio	-7.50	0.66	0.83	1.127	1.7		1.127	0.5		1.115	0.7		75
823	CXCR4/bARR2~CXCL12~100~ng/ml PCA	ASC0056631 KUD008600	MCRatio	-10.50	0.64	0.84	1.123	1.8		1.123	1.1		1.115	0.7		75
699	GRP78 (pan)_HeLa_IF IF	ASC0056632 KUD008600	MCRatio	-7.50	0.72	0.84	1.091	2		1.091	0.8		1.090	0.7		73
417	Limk2/Cofilin1 PCA	ASC0056633 KUD008600	MCRatio		0.63	0.85	1.096	1.9		1.096	1.1		1.090	0.7		73
419	Mdm2/p53 PCA	ASC0056634 KUD008600	MCRatio	-11.86	0.53	0.85	1.087	2.7		1.088	1.7		1.090	0.7		67
960	Mdm2/p53 PCA	ASC0056635 KUD008600	MCRatio	-41.00	0.80	0.86	1.085	1.8		1.085	0.6		1.090	0.7		66
			MCRatio	-22.00	0.65	0.87	1.084	2.3		1.084	1.0		1.090	0.7		75
			MCRatio	-3.15	0.60	0.87	1.074	1.9		1.074	0.8		1.090	0.7		71
			MCRatio	-25.00	0.69	0.83	1.103	1.8		1.104	1.1		1.090	0.7		75
			MCRatio	-5.86	0.65	0.84	1.1	1.8		1.1	0.9					


[Make another query](#)

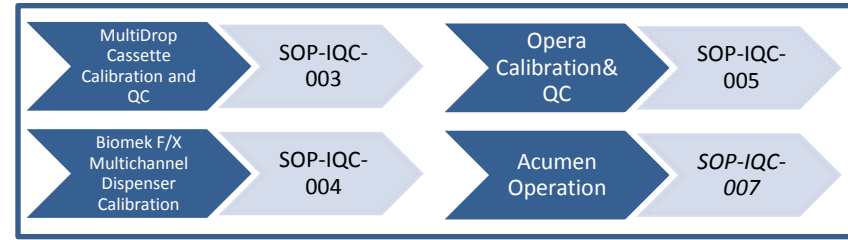


Flow Chart of SOP's Governing Performance of OT Cell-based Assays

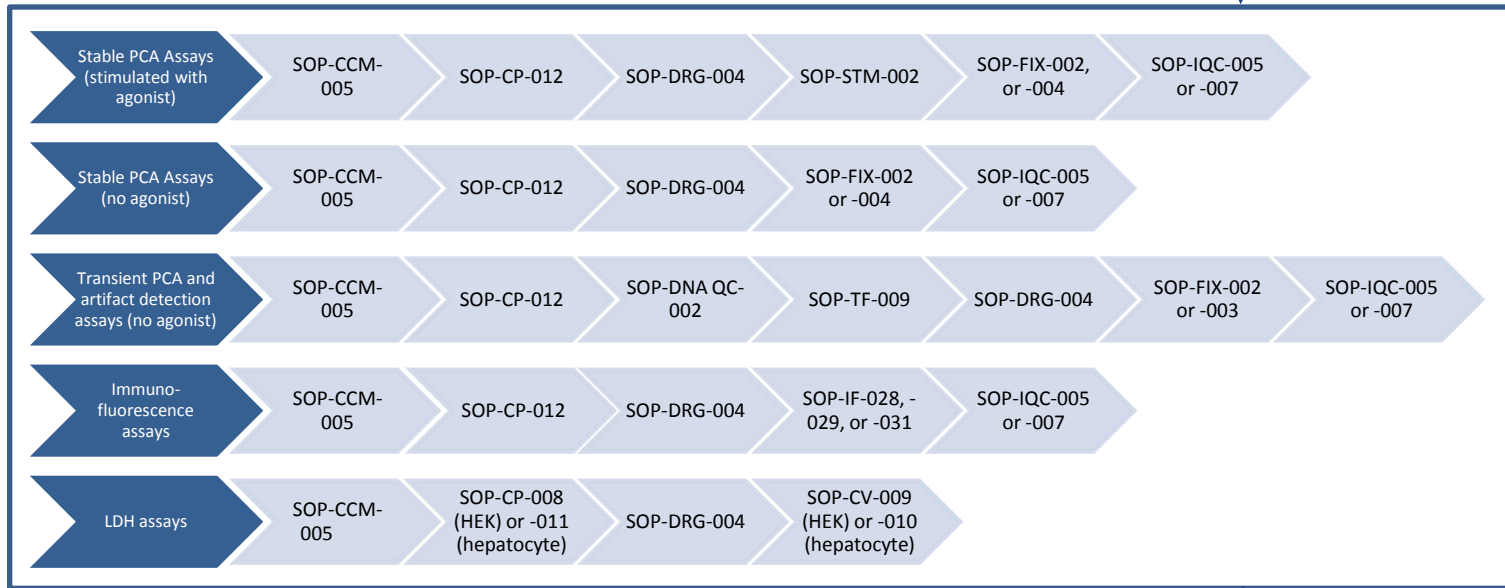
Compounds (Samples)



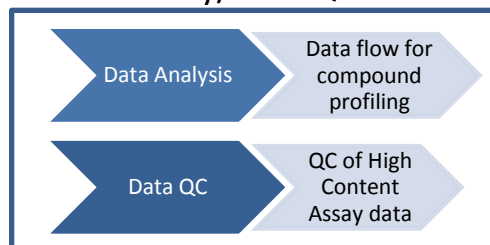
Instrument QC



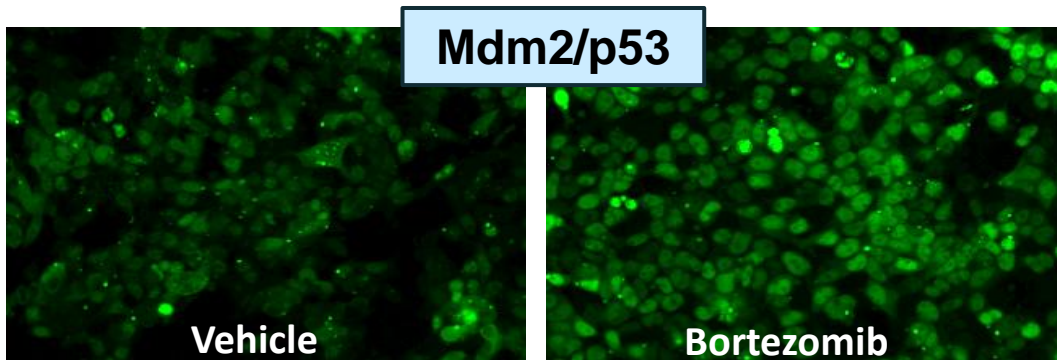
Cell-based Assays



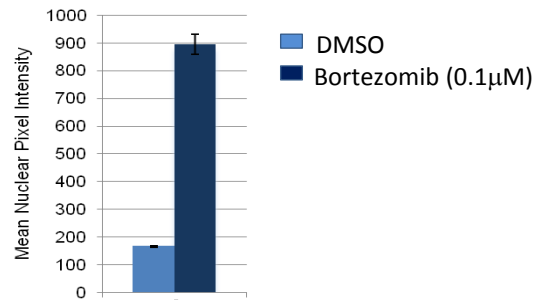
Assay/Data QC



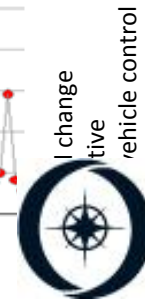
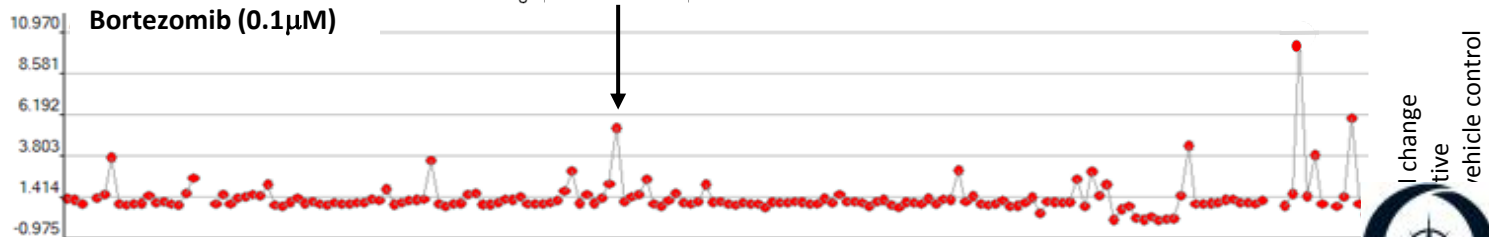
Every compound (and target) generates a unique signature



Quantitative image analysis



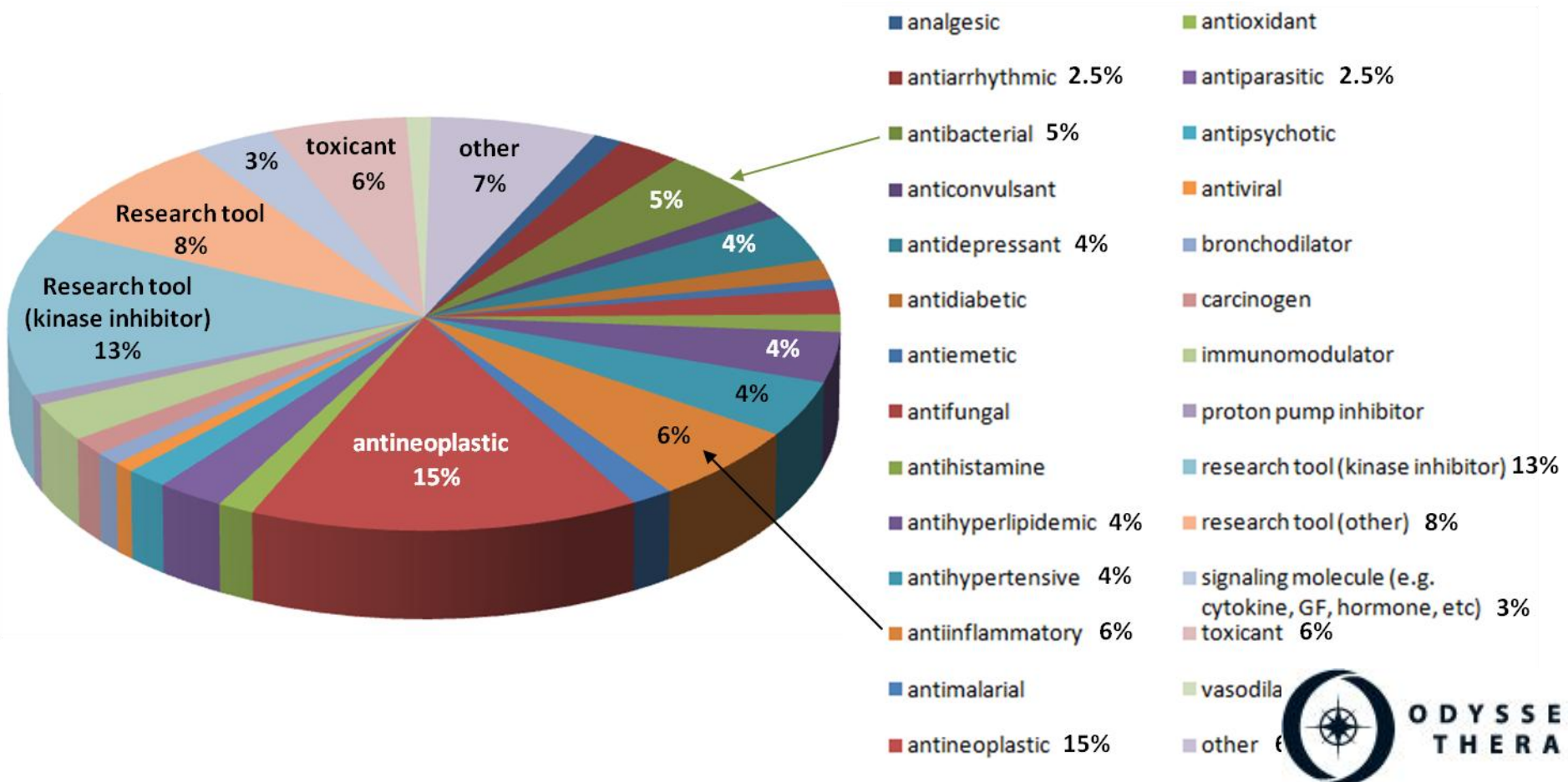
Compound profile:
activity across assay panel



ODYSSEY
THERA

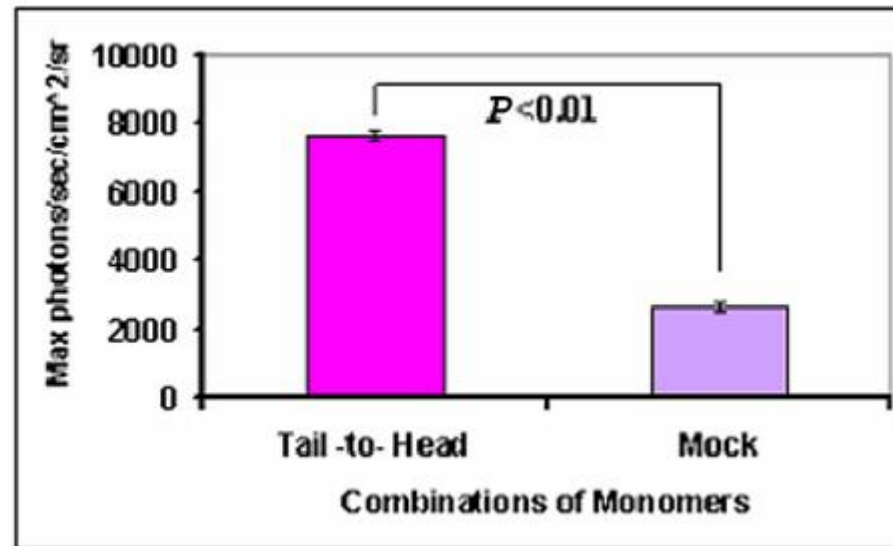
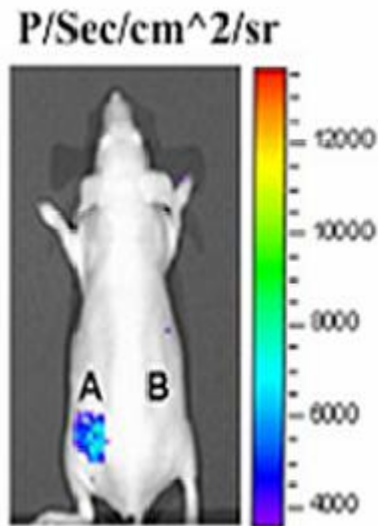
Odyssey internal efforts: Database of drugs, toxicants and targets

- Thousands of drugs, toxicants, targets (si/miRNA) represented in this evolving resource
- New test agents are compared to database -> mechanistic and safety information



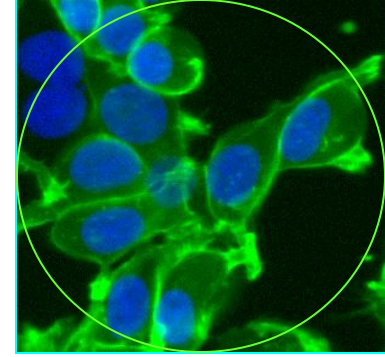
The final frontier (or, full circle?)

Visualizing/confirming toxicant activity *in vivo* with PCA



Massoud *et al.* 2004

Toxicant Analysis via High-content Screening of Molecular Circuits



- We believe that the combination of highly contextual assays + HT/HC analysis + diverse parallel screens will contribute to toxicant identifiers and classifiers
- We've engaged internally in a process similar to that underway with ToxCast computational biologists, namely looking for patterns or "signatures" of activity that represent a particular biological phenotype
- (NB: the majority of our time has been devoted to engineering the capability and not mining the data)
- We look forward to continued partnership with EPA scientists to better define the functional relevance of particular patterns of activity



Thanks

Biology and Screening:

Jane Lamerdin
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Eddie Wehri
Shayla Hart
Veronica Alves
Helen Chan
Tomoe Minami

Bioinformatics:

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Cedric Wiesner
Jie Hu

John Westwick
Jane Lamerdin

EPA

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Jennifer Hill
David Reif

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References

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