

Translational impact of multimodal data analysis and integration in oncology

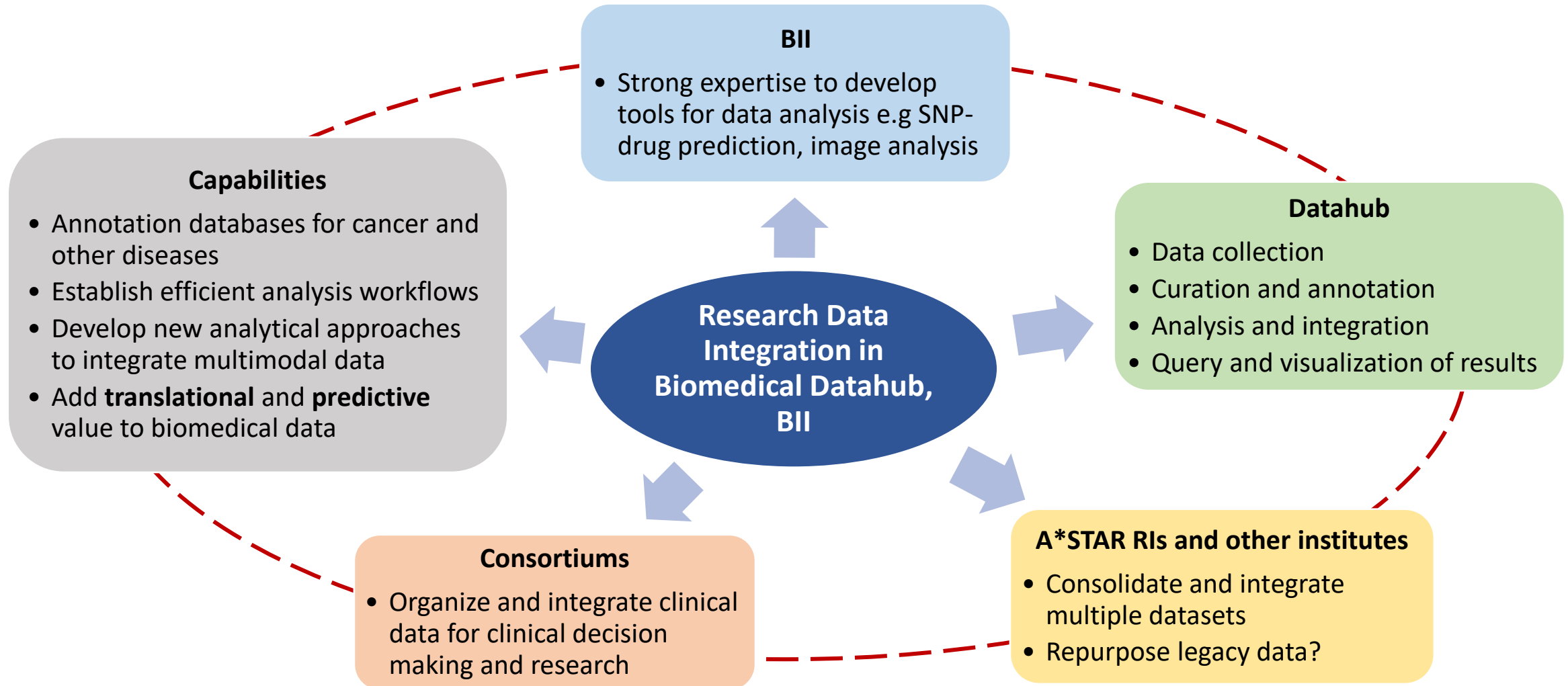
Xing Yi Woo

Senior Principal Investigator and Head of Research Data Integration
(Biomedical Datahub)

Bioinformatics Institute A*STAR

woo_xing_yi@bii.a-star.edu.sg

Our mission: To build an ecosystem that bridges the complexity of computational biology and data science with the needs of researchers and clinicians to drive biological discoveries and predict translational outcomes.



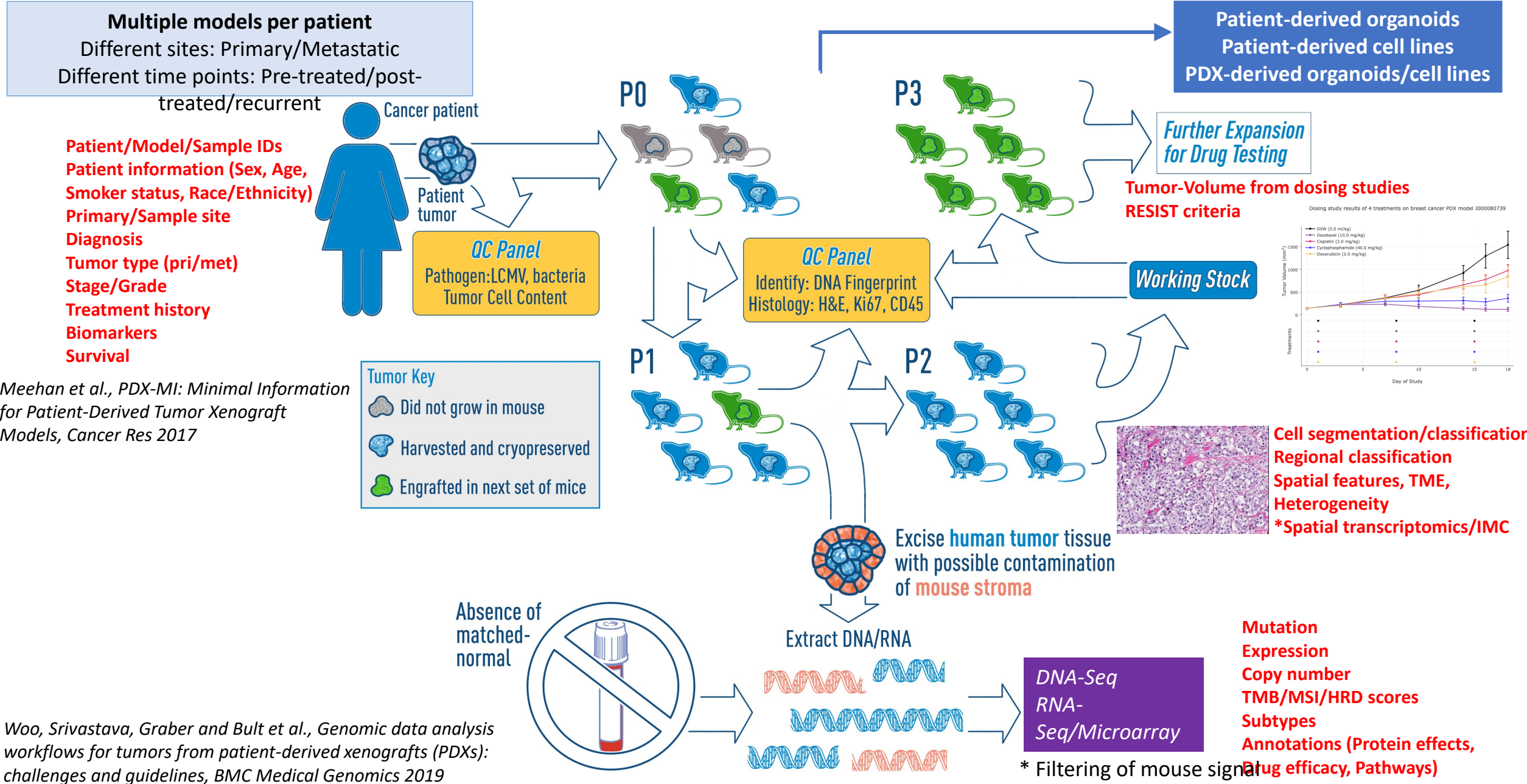
Large-scale collection of cancer genomic and molecular data

Cancer data sources

- COSMIC (Catalogue Of Somatic Mutations In Cancer)
- CCLE (Cancer Cell Line Encyclopedia)
- Depmap: Cancer Dependency Map for genetic and pharmacologic dependencies in cell lines
- TCGA (The Cancer Genome Atlas)
- ICGC (International Cancer Genome Consortium)
- PCAWG (Pan-Cancer Analysis of Whole Genomes)
- AACR Project GENIE
- CPTAC (Clinical Proteomic Tumor Analysis Consortium)
- HTAN (Human Tumor Atlas Network)
- TCIA (The Cancer Imaging Archive)
- PDXNet (PDX Development and Trial Centers Research Network)
- ...



Multimodal data of preclinical cancer models – Patient derived xenografts (PDX)



Meehan et al., PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models, Cancer Res 2017

Woo, Srivastava, Graber and Bult et al., Genomic data analysis workflows for tumors from patient-derived xenografts (PDXs): challenges and guidelines, BMC Medical Genomics 2019

Development of multimodal data platforms



(Analysis team)

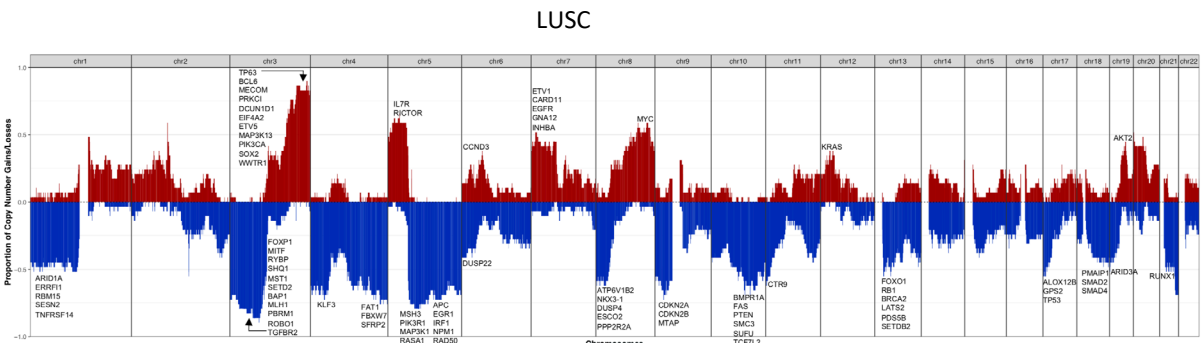
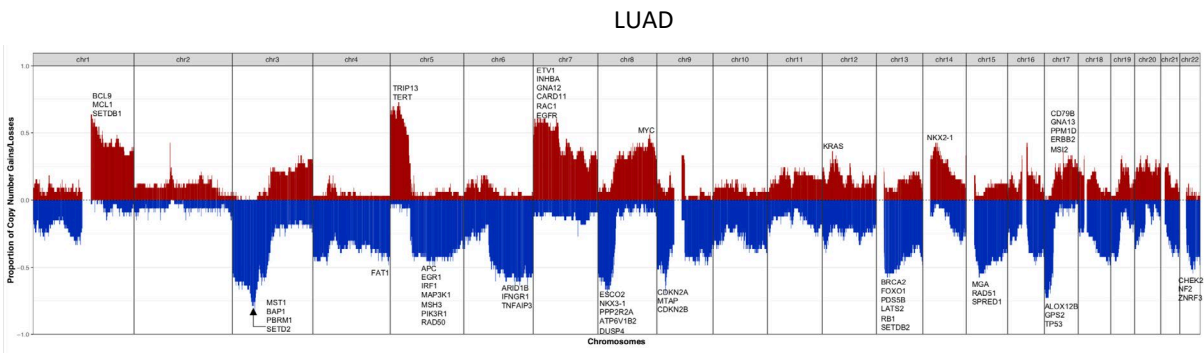
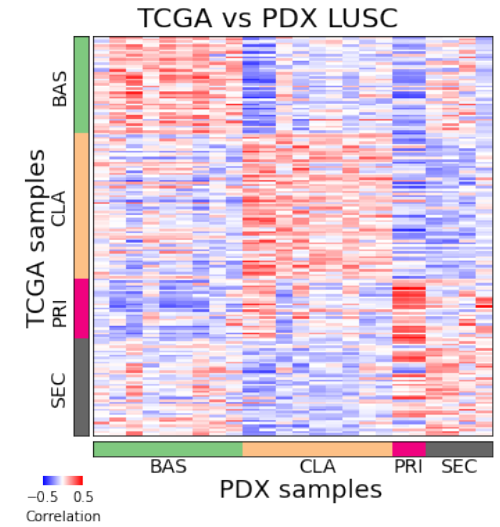
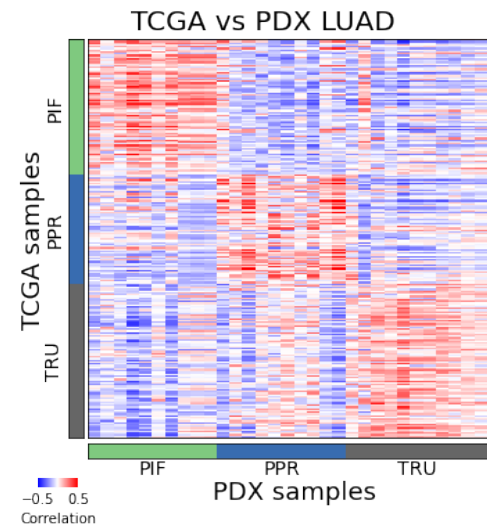
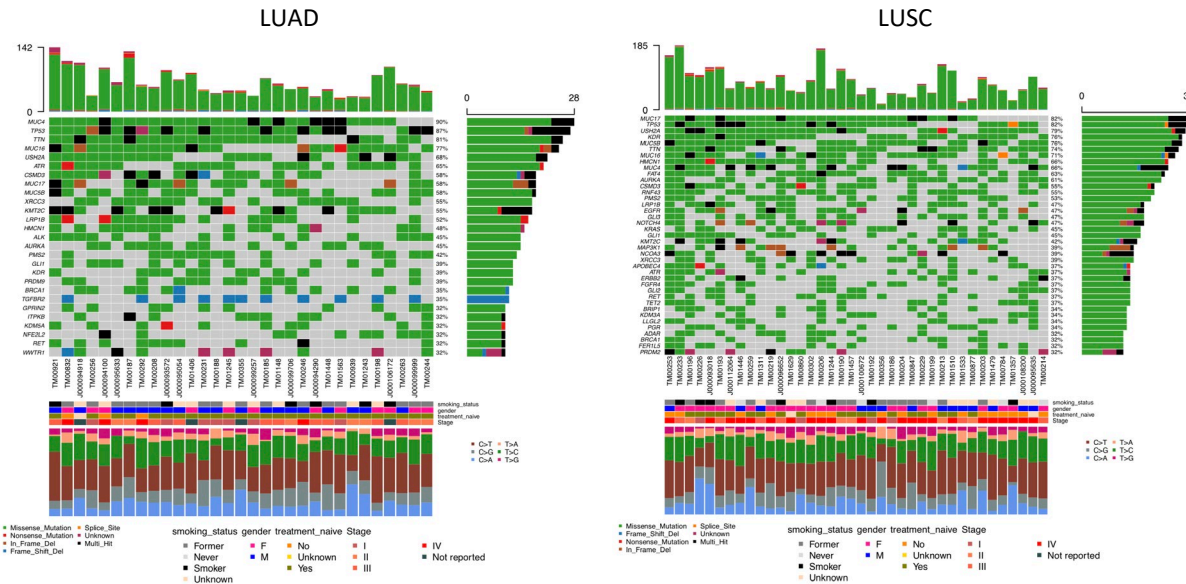
PDXNet (Data coordination center)



(Data coordination center)

- Coordination of PDX generation, genomic technologies, pathology, bioinformatics and customer service teams
- Data curation, organization and QC
- Analysis workflows and benchmarking/validation
- Database of metadata and genomic/spatial data
- Annotation of mutations
- Public portal
- Further research – integration of data of different modalities

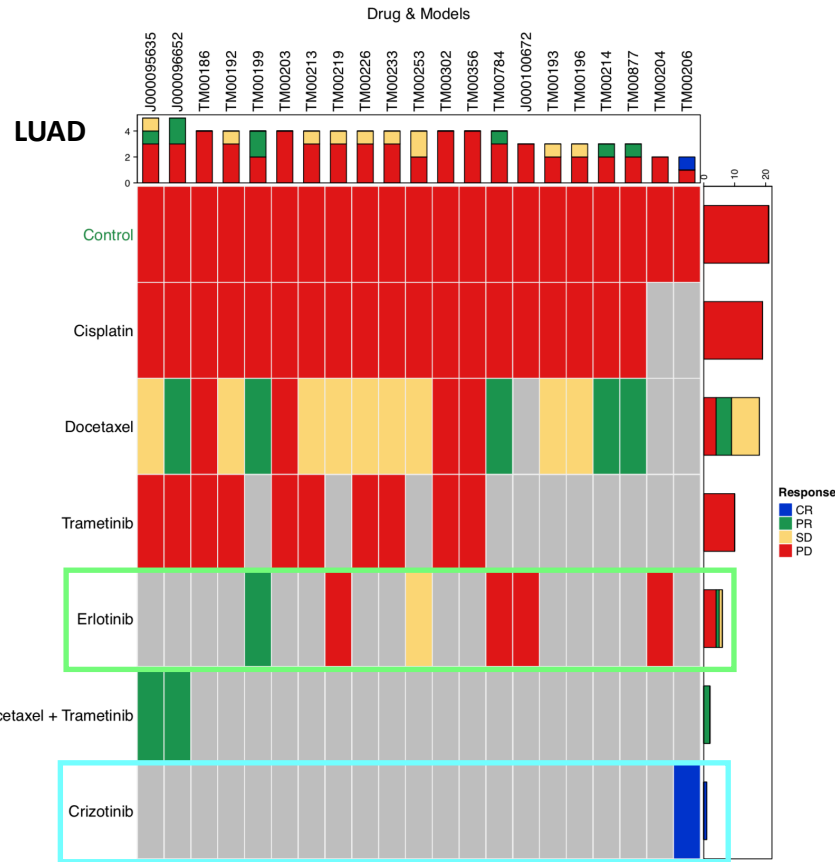
Genomic characterization JAX PDX resource – Non-small cell lung cancer



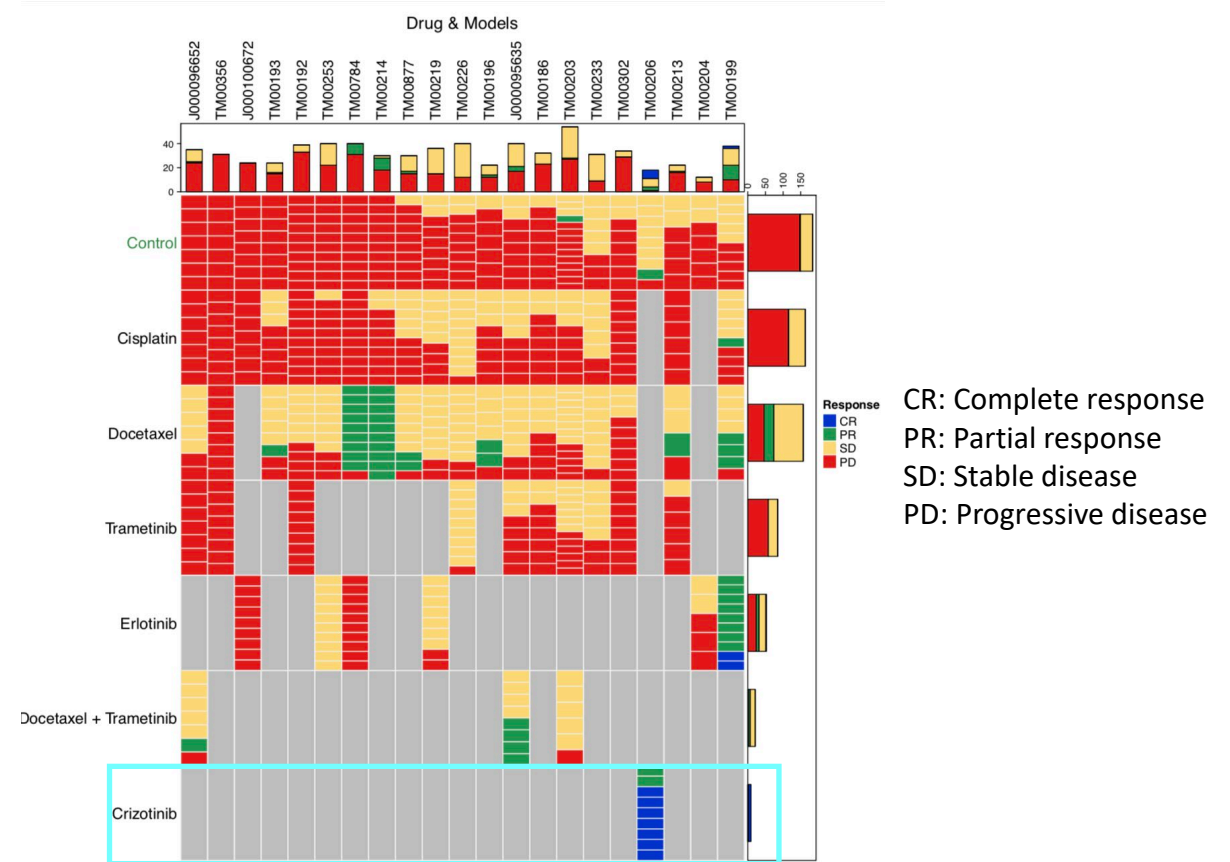
Majority of patient markers are found in PDXs

Therapeutic response in PDX models

Li et al. DRAP: a toolbox for drug response analysis and visualization tailored for preclinical drug testing on patient-derived xenograft models. *J Transl Med* 2019



Model	Treatment naïve?	EGFR act mut	Response	Resistance mut
TM00199	Erlotinib	EGFR L858R	PR	
TM00204	Erlotinib	EGFR exon 19 del	PD	EGFR T790M
TM00219	Erlotinib	EGFR exon 19 del	PD	EGFR T790M
TM00253	Erlotinib	EGFR L858R	SD	EGFR V834L
TM00784	Erlotinib	EGFR L858R	PD	MET amp
J000100672	Yes		PD	EGFR exon 20 ins



Model	Treatment naïve?	ALK act mut	Response	Resistance mut
TM00206	Crizotinib	EML4-ALK fusion	CR (2PR, 7 CR)	ALK L1196M (Alt AF 22%) KIT amp (low) [PO – mouse A]
				ALK, EML4 amp (low) [PO – mouse B]

Dosing studies in PDXs recapitulate treatment response in patients and explain cause of resistance with markers found in PDX 7

PDXNet



PDMR NCI Patient-Derived Models Repository
An NCI Precision Oncology InitiativesSM Resource



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**MD Anderson
Cancer Center**

Making Cancer History[®]



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<https://doi.org/10.1038/s41588-020-00750-6>

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Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts

Xing Yi Woo^{1,6,65}, Jessica Giordano^{2,3,64}, Anuj Srivastava¹, Zi-Ming Zhao¹, Michael W. Lloyd⁴, Roebi de Bruijn⁵, Yun-Suhk Suh⁶, Rajesh Patidar⁷, Li Chen⁷, Sandra Scherer⁸, Matthew H. Bailey^{8,9}, Chieh-Hsiang Yang⁸, Emilio Cortes-Sanchez⁸, Yuanxin Xi¹⁰, Jing Wang¹⁰, Jayamanna Wickramasinghe¹¹, Andrew V. Kossenkov¹¹, Vito W. Rebecca¹¹, Hua Sun¹², R. Jay Mashl¹², Sherri R. Davies¹², Ryan Jeon¹³, Christian Frech¹³, Jelena Randjelovic¹³, Jacqueline Rosains¹³, Francesco Galimi^{2,3}, Andrea Bertotti^{2,3}, Adam Lafferty¹⁴, Alice C. O'Farrell¹⁴, Elodie Modave^{15,16}, Diether Lambrechts^{15,16}, Petra ter Brugge⁵, Violeta Serra¹⁷, Elisabetta Marangoni¹⁸, Rania El Botty¹⁸, Hyunsoo Kim¹, Jong-Il Kim¹⁹, Han-Kwang Yang⁶, Charles Lee^{19,20}, Dennis A. Dean II¹³, Brandi Davis-Dusenbery¹³, Yvonne A. Evrard⁷, James H. Doroshov²¹, Alana L. Welm⁸, Bryan E. Welm^{8,22}, Michael T. Lewis²³, Bingliang Fang²⁴, Jack A. Roth²⁴, Funda Meric-Bernstam²⁵, Meenhard Herlyn¹¹, Michael A. Davies²⁶, Li Ding¹², Shunqiang Li¹², Ramaswamy Govindan¹², Claudio Isella^{2,3,65}, Jeffrey A. Moscow^{27,65}, Livio Trusolino^{2,3,65}, Annette T. Byrne^{14,65}, Jos Jonkers^{5,65}, Carol J. Bult^{4,65}, Enzo Medico^{2,3,65}, Jeffrey H. Chuang^{1,65}, PDXNET Consortium* and EurOPDX Consortium*

CANCER RESEARCH | TUMOR BIOLOGY AND IMMUNOLOGY

Systematic Establishment of Robustness and Standards in Patient-Derived Xenograft Experiments and Analysis

Yvonne A. Evrard¹, Anuj Srivastava², Jelena Randjelovic³, The NCI PDXNet Consortium, James H. Doroshov⁴, Dennis A. Dean II³, Jeffrey S. Morris⁵, and Jeffrey H. Chuang^{2,6}



bioRxiv

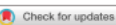
PDXNet Portal: Patient-Derived Xenograft model, data, workflow, and tool discovery (in revision)

Soner Koc¹, Michael W. Lloyd, Jeffrey Grover, Sara Seepo, Sai Lakshmi Subramanian, Manisha Ray, Christian Frech, John DiGiovanna, Phillip Webster, Steven Neuhauser, Anuj Srivastava, Xing Yi Woo, Brian J. Sanderson, Brian White, Paul Lott, PDXNet Consortium, Yvonne A. Evrard, Tiffany A. Wallace, Jeffrey A. Moscow, James H. Doroshov, Nicholas Mitsiades, Salma Kaochar, Chong-xian Pan, Moon S. Chen Jr., Luis Carvajal-Carmona, Alana L. Welm, Bryan E. Welm, Michael T. Lewis, Ramaswamy Govindan, Li Ding, Shunqiang Li, Meenhard Herlyn, Mike Davies, Jack Roth, Funda Meric-Bernstam, Peter N. Robinson, Carol J. Bult, Brandi Davis-Dusenbery, Dennis A. Dean II, Jeffrey H. Chuang, for the PDXNet Consortium Members

ARTICLES

<https://doi.org/10.1038/s43018-022-00337-6>

nature
cancer



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A human breast cancer-derived xenograft and organoid platform for drug discovery and precision oncology

Katrin P. Guillen^{1,2,13}, Maihi Fujita^{1,2,13}, Andrew J. Butterfield^{1,2,13}, Sandra D. Scherer^{1,2}, Matthew H. Bailey^{2,3}, Zhengtao Chu^{1,2}, Yoko S. DeRose^{1,2}, Ling Zhao^{1,2}, Emilio Cortes-Sanchez^{1,2}, Chieh-Hsiang Yang^{1,2}, Jennifer Toner^{1,2}, Guoying Wang^{1,2}, Yi Qiao³, Xiaomeng Huang³, Jeffery A. Greenland^{1,2}, Jeffery M. Vahrenkamp^{1,2}, David H. Lum², Rachel E. Factor^{2,4}, Edward W. Nelson^{2,5}, Cindy B. Matsen^{2,5}, Jane M. Poretta^{2,5}, Regina Rosenthal^{2,5}, Anna C. Beck^{2,6}, Sandra S. Buys^{2,6}, Christos Vaklavas^{2,6}, John H. Ward^{2,6}, Randy L. Jensen^{1,2,7}, Kevin B. Jones^{1,2,8}, Zheqi Li⁹, Steffi Oesterreich⁹, Lacey E. Dobrolecki¹⁰, Satya S. Pathi^{1,2}, Xing Yi Woo¹¹, Kristofer C. Berrett^{1,2}, Mark E. Wadsworth^{1,2}, Jeffrey H. Chuang^{11,12}, Michael T. Lewis¹⁰, Gabor T. Marth^{2,3}, Jason Gertz^{1,2}, Katherine E. Varley^{1,2}, Bryan E. Welm^{2,5} and Alana L. Welm^{1,2}



ARTICLE

<https://doi.org/10.1038/s41467-021-25177-3>

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Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment



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Session PO.BCS01.03 - Database Resources and Web Applications

1202 / 14 - A repository of PDX histology images for exploring spatial heterogeneity and cancer dynamics

Add to My Itinerary

April 11, 2022, 9:00 AM - 12:30 PM

Section 28 (manuscript in preparation)

Presenter/Authors

Brian S. White*, Xingyi Woo*, Soner Koc*, Todd Sheridan, Steven B. Neuhauser, Akshat M. Savaliya, Lacey E. Dobrolecki, John D. Landua, Matthew H. Bailey, Maihi Fujita, Kurt W. Evans, Bingliang Fang, Junya Fujimoto, Maria Gabriela Raso, Shidan Wang, Guanghua Xiao, Yang Xie, Sherri R. Davies, Ryan C. Fields, R Jay Mashl, Jacqueline L. Mudd, Yeqing Chen, Min Xiao, Xiaowei Xu, Melinda G. Hollingshead, Shahanawaz Jiwanji, PDXNet Consortium, Yvonne A. Evrard, Tiffany A. Wallace, Jeffrey A. Moscow, James H. Doroshov, Nicholas Mitsiades, Salma Kaochar, Chong-xian Pan, Moon S. Chen Jr., Luis G. Carvajal-Carmona, Alana L. Welm, Bryan E. Welm, Michael T. Lewis, Ramaswamy Govindan, Li Ding, Shunqiang Li, Meenhard Herlyn, Michael A. Davies, Jack A. Roth, Funda Meric-Bernstam, Carol J. Bult, Brandi Davis-Dusenbery, Dennis A. Dean II, Jeffrey H. Chuang. The Jackson Laboratory for Genomic Medicine,

PDXNET Portal and workflows

NCI Cancer Genomics Cloud

PDXNet Portal
Powered by Seven Bridges

The PDXNet Portal provides a way for researchers to learn about the PDX models, sequencing data (DNA and RNA), and PDX Minimum Information metadata tools generated by the network for public use.

The National Cancer Institute (NCI) launched the PDX (patient-derived xenografts) Development and Trial Centers Research Network (PDXNet) in September 2017 to accelerate translational research that uses PDX models and sequencing data. The PDXNet includes six PDX Development and Trial Centers (PDTCs) and the PDX Data Commons and Coordinating Center (PDCCC). The two PDTCs added in 2018 focus exclusively on developing PDXs from minority patients. PDXNet also works closely with the NCI Patient-Derived Model Repository (PDMR) to ensure data are collected and provided in a standardized format.

Collectively, the PDTCs and the PDCCC work together to test and advance multi-agent cancer treatments from PDX studies to human clinical trials. PDXNet is an inclusive consortium welcoming collaborations. Please [contact us](#) to discuss how we can work together to advance new cancer treatments.

[PDXNet Models](#) [PDTC Data](#) [PDMR Data](#)

Data Summary

CONTRIBUTORS: 6 MODELS: 273 SEQ. FILES: 12,314 IMAGES: 868 CANCER TYPES: 33

PDXNet Models | Sequencing Files | Ancestry | Images | Portal Update Timeline

PDX Models by Contributor

Contributor	Model Count
BCM	~10
HCI	~10
MDACC	~10
UC Davis	~10
WISTAR	~10
WUSTL	~10

Public apps

Search: pdx Category: Toolkit: Reset search

- PDX RNA Expression Estimation Workflow**
This RSEM workflow (RSEM 1.2.31) for quantifying gene expression uses the STAR aligner and is optimized to work with F...
- PDX RNA Expression Estimation Workflow - Single End**
This RSEM workflow (RSEM 1.2.31) for quantifying gene expression uses the STAR aligner and is optimized to work with F...
- PDX WES CNV (Xenome) Tumor-Normal Workflow**
JAX PDX - version matched
This Whole Exome Sequencing (WES) Tumor-Normal workflow identifies copy number variants from a human exome experiment ...
- PDX WES Tumor-Normal (Xenome) with Variant Calling, CNV estimation, TMB, MSI, and HRD scores**
This Whole Exome Sequencing (WES) tumor-normal workflow first uses the [Broad Institute's] (https://software.broadinst...
- PDX WES Tumor-Only (Xenome) with Variant Calling, MSI, and TMB scores**
This Whole Exome Sequencing (WES) tumor-normal workflow first uses the [Broad Institute's] (https://software.broadinst...
- RNA Expression Estimation Workflow for Patient Tumor**
This RSEM workflow (RSEM 1.2.31) for quantifying gene expression uses the STAR aligner and is optimized to work with F...
- RNA Expression Estimation Workflow - Patient Tumor - Single End**
This RSEM workflow (RSEM 1.2.31) for quantifying gene expression uses the STAR aligner and is optimized to work with F...
- WES Tumor-Normal with Variant Calling, CNV estimation, TMB, MSI, and HRD scores**
This Whole Exome Sequencing (WES) tumor-normal workflow first uses the [Broad Institute's] (https://software.broadinst...
- WES Tumor-Only with Variant Calling, MSI, and TMB scores**
This Whole Exome Sequencing (WES) tumor-only workflow first uses the [Broad Institute's] (https://software.broadinsti...

Showing 9 of 9

> 800 PDX models with multiple samples and data of different modalities

Conservation of copy number profiles during engraftment and passaging of PDXs

10 contributing centers

16 tumor types

509 PDX models

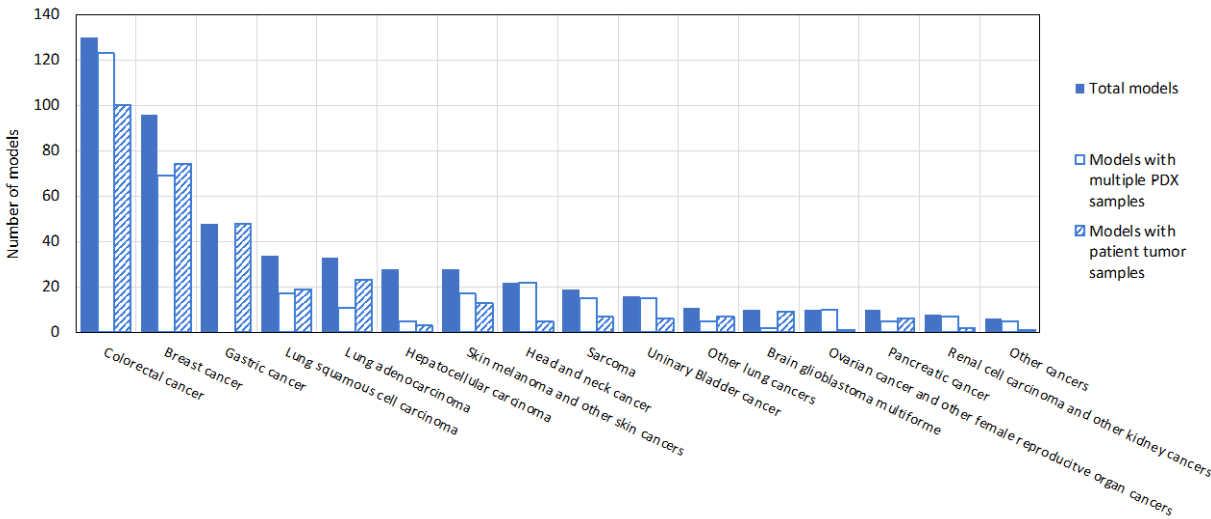
1,451 PT/PDX samples

1,548 tumor datasets

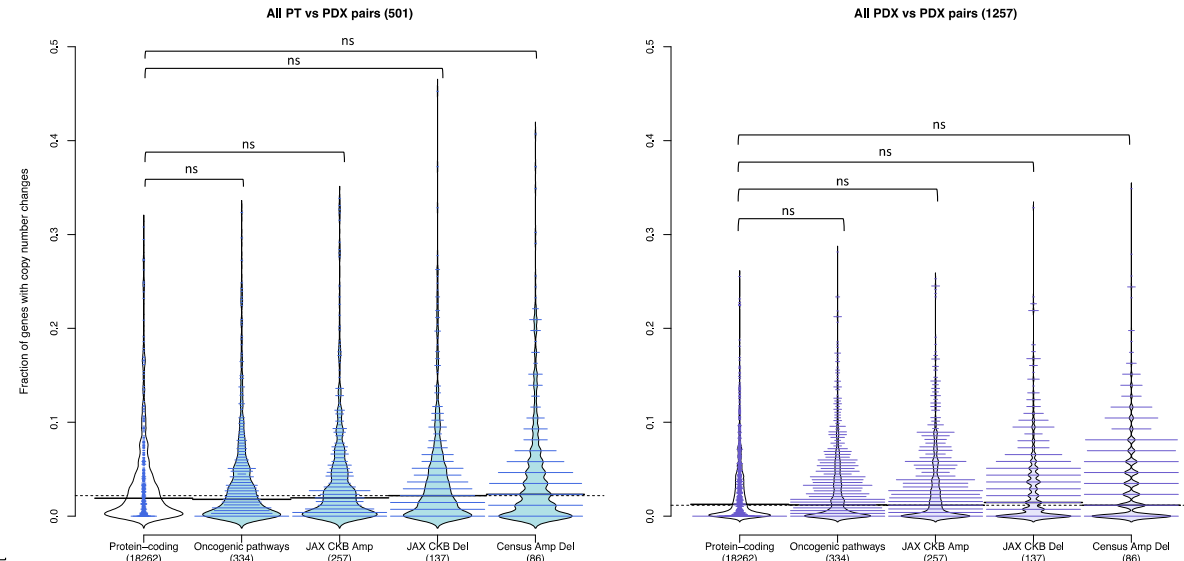
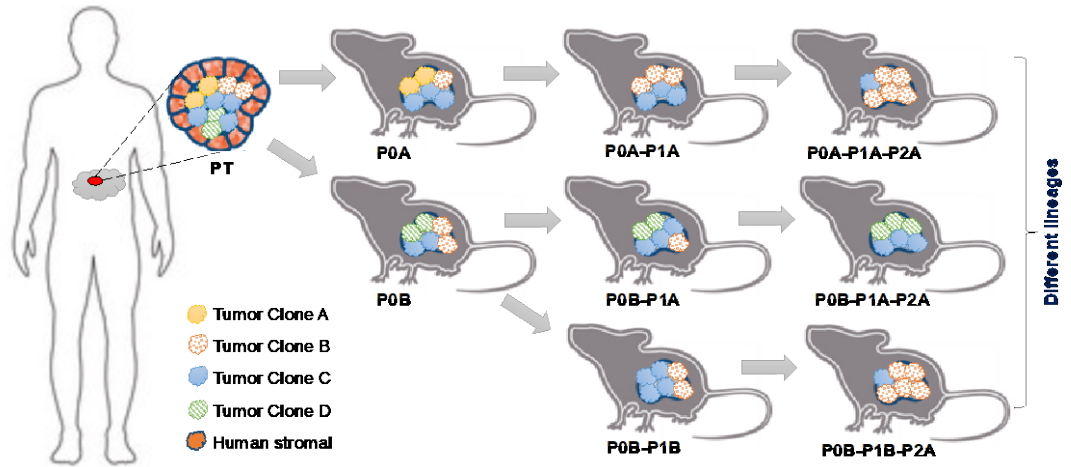
(WES, WGS, SNP array, RNA-Seq & microarray expression)

CNA profiles with gene annotations

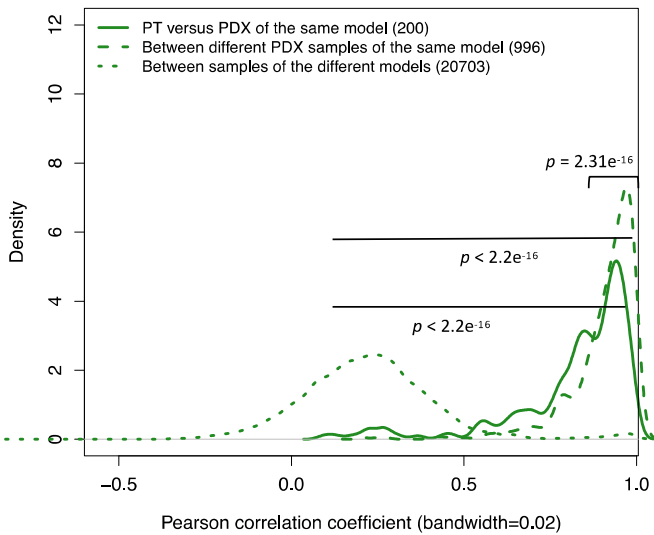
■ SNP ■ WES ■ SNP+WES ■ WGS ■ RNASEQ ■ EXPARR ■ WES+RNASEQ ■ SNP+EXPARR



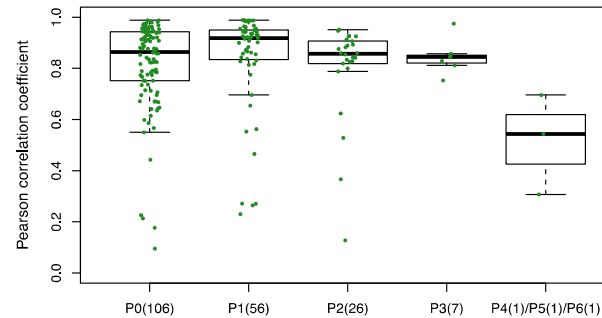
Comparisons of CNAs from PTs with early and late PDX passages



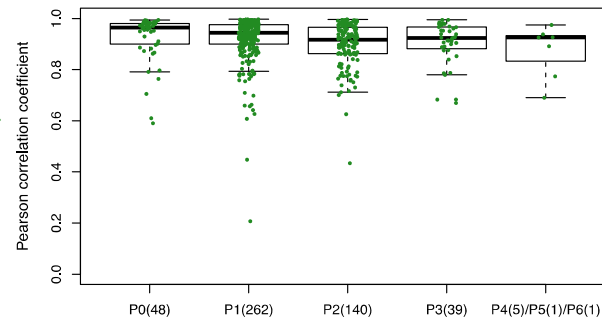
All WES data



Comparison relative to PT (all WES data)

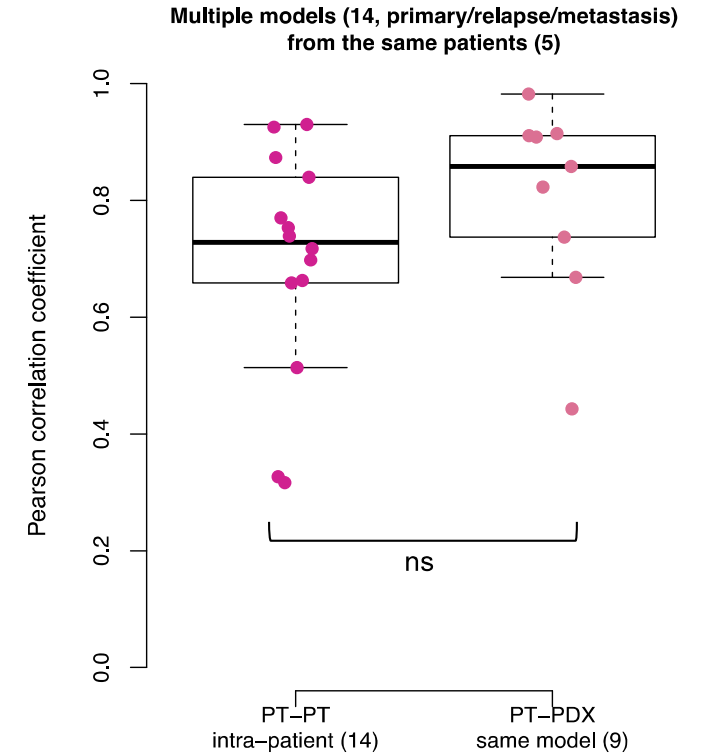
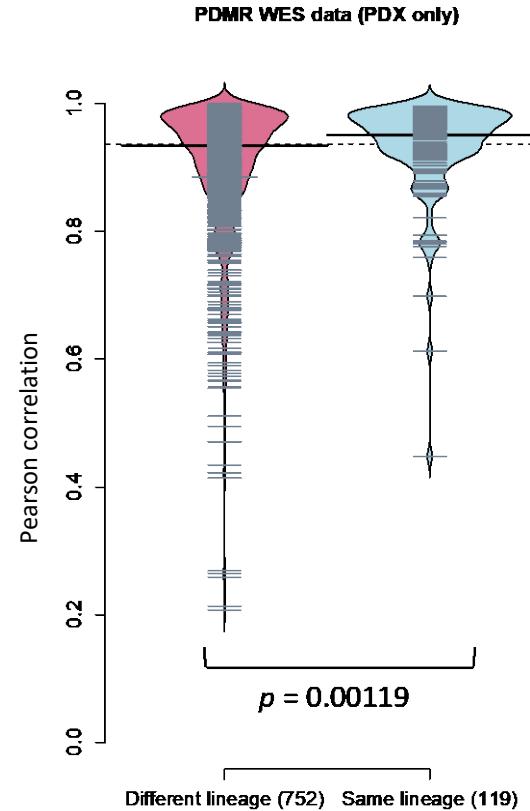
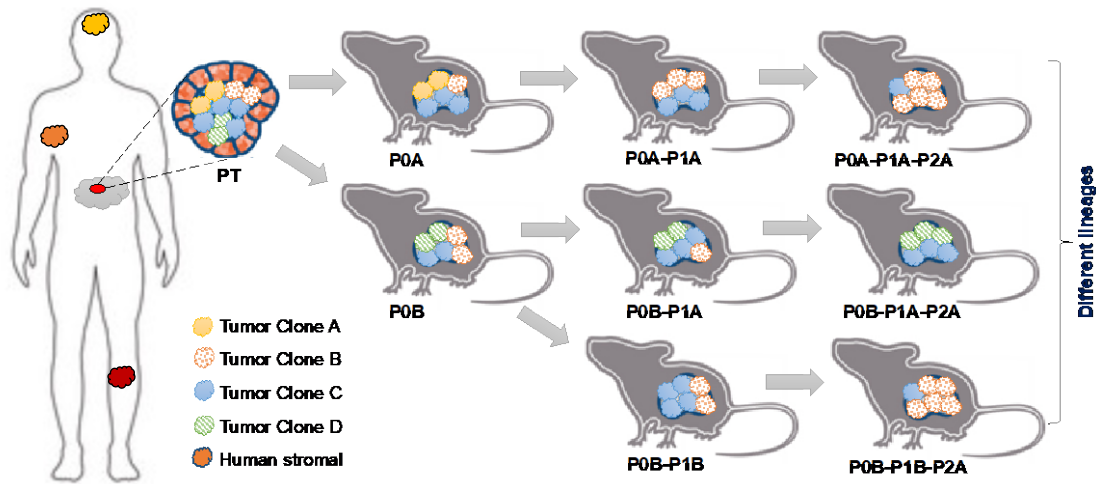


Comparison relative to P0 (all WES data)



- **Pairwise comparison of CNA between PT-PDX and PDX-PDX**
- **No systematic CN changes during engraftment (PT-PDX) and passaging (PDX-PDX)**
- **Genes with CNAs acquired during engraftment and passaging show no preference for cancer or treatment-related functions**
- **No mouse-specific selection to alter the CNA profile different from the evolutionary process of the original patient tumor**

Evolution across PDX lineages and intra-patient samples

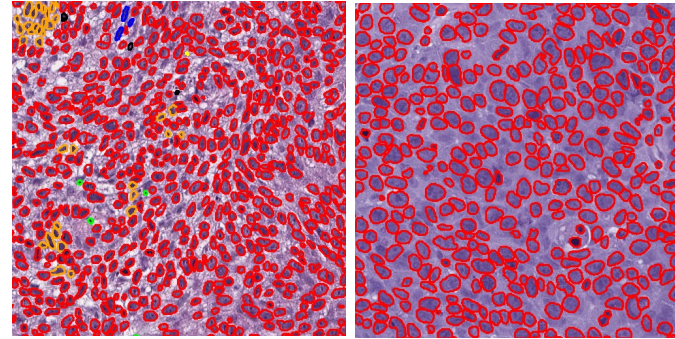


- Random sampling of heterogenous tumor can result in divergence in copy number
- Genetic stability of the PDX system are likely to be less important than the evolution and heterogeneity of solid tumors themselves which can affect successful treatment

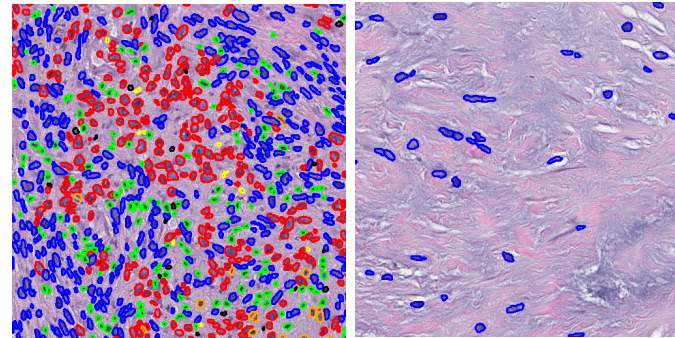
Spatial features of PDX tumors from image analysis

- Cell/regional classification of histopathology images to understand spatial heterogeneity, tumor-microenvironment and tumor-stromal infiltration
- To associate spatial features with genomics and clinical/treatment outcomes

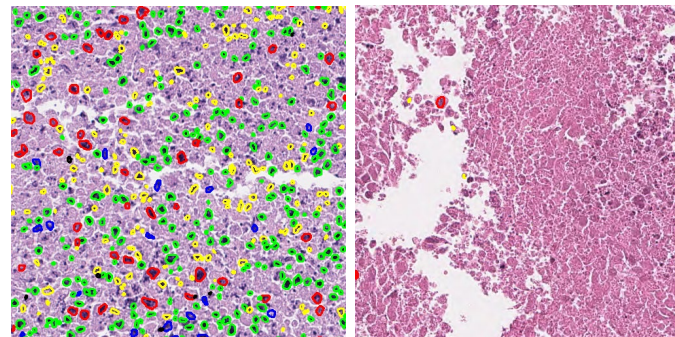
Tumor



Stroma

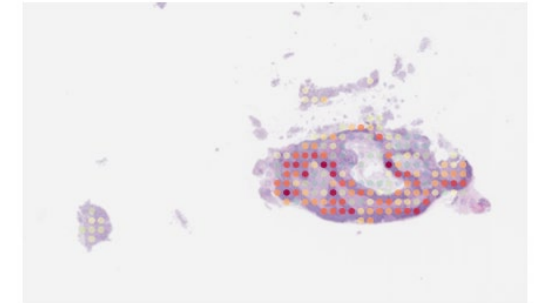


Necrosis

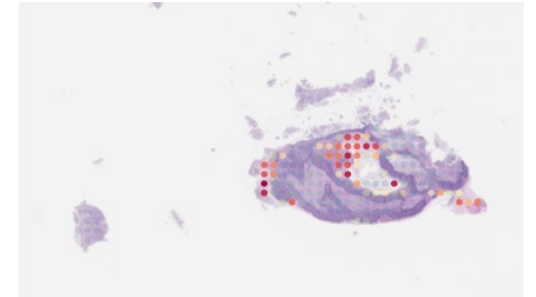


■ Neoplastic ■ Non-Neoplastic Epithelial ■ Inflammatory ■ Connective ■ Dead

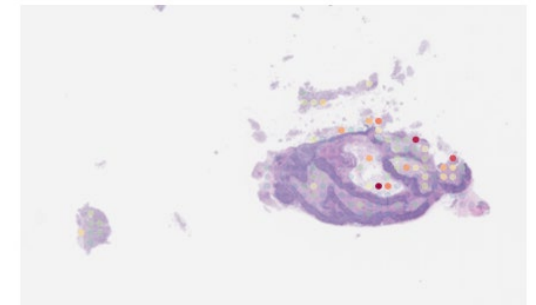
TumorFraction 0.00 0.25 0.50 0.75



StromaFraction 0.0 0.2 0.4 0.6 0.8



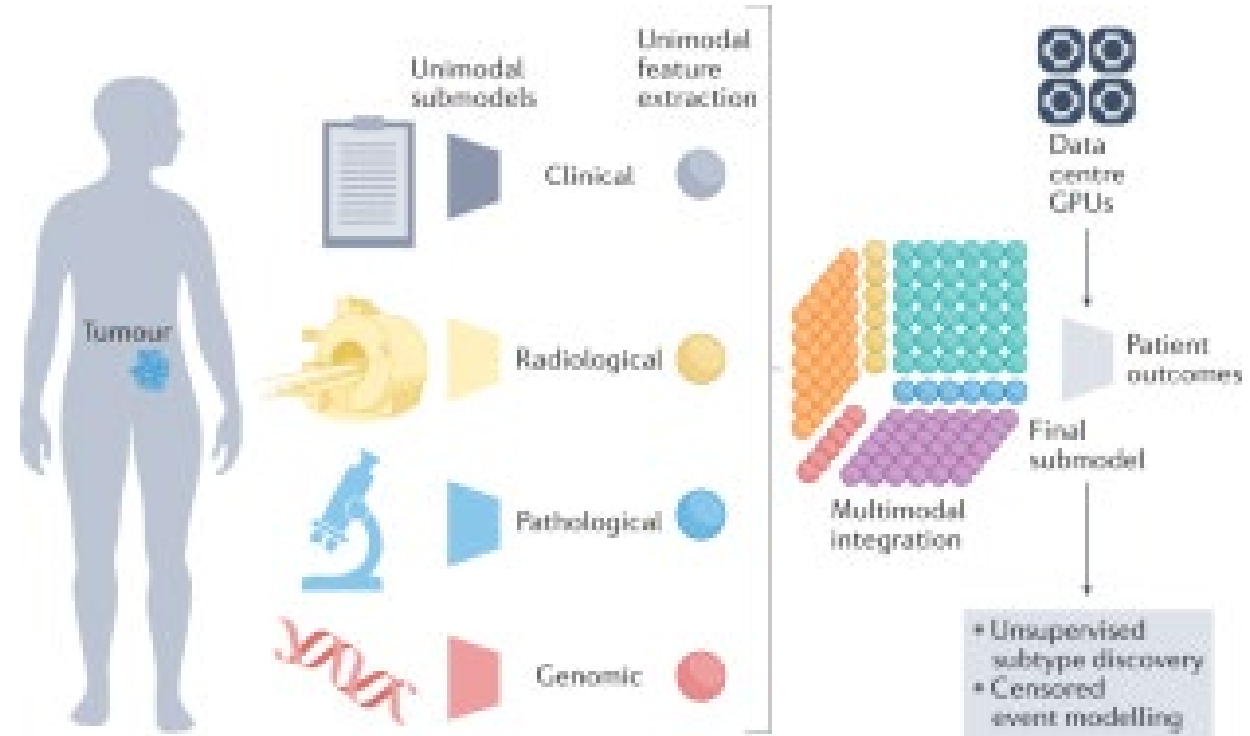
NecroticFraction 0.0 0.1 0.2



Data analysis and integration of multimodal cancer data and its translation outcomes

- PDX models are robust and genomically stable for preclinical studies, where mouse-specific pressures to alter cancer or treatment-related functions is clearly absent
- Integrating omics data of PDX models with curated clinical annotations for efficient mining of PDX models for preclinical trials
- Integrating annotated genomic/molecular profiles with dosing studies of PDX resources to validate and discover biomarkers
- Explore effects of tumor heterogeneity, subclonality and spatial features on clinical/treatment outcomes

Multimodal ML models integrate features across modalities



Boehm et al. Harnessing multimodal data integration to advance precision oncology. Nat Rev Cancer 2022



- **Better prediction of treatment outcomes and patient stratification**
- **Multimodal features can uncover new understanding of cancer biology underlying patient outcomes**

Acknowledgements



Sebastian Maurer-Stroh

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CS

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Brian White

Sergii Domanskyi

Grace Stafford

Carolyn Paisie

Jim Peterson

Stephen Grubb

Al Simons

Mandy Chen

Chuang Lab

Jeffrey Chuang

Ali Foroughi pour

Todd Sheridan

Jill Rubinstein

Yun-Suhk Suh

Ziming Zhao

JAX PDX Resource

Carol Bult

Steven Neuhauser

Emily Jocoy

Margaret Bundy

Susie Airhart

Muneer Hasham

Liu Lab

Edison Liu

Francesca Menghi

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woo_xing_yi@bii.a-star.edu.sg