Transforming Oncology: ATCC's Cutting-Edge Patient-Derived Models

Fang Tian, PhD
Director, Cell Biology
Biological Content and Product Development
ATCC

Meet the speaker

Fang Tian, PhD

Director, Biological Content, ATCC

Dr. Fang Tian, Director of Biological Content for ATCC, has extensive experience in cell biology and molecular biology. She oversees human, animal cell lines and hybridomas, and product development in the Cell Biology General Collection at ATCC. Dr. Tian was a research fellow in Massachusetts General Hospital, Harvard Medical School. She conducted postdoctoral research at the Hillman Cancer Institute of UPMC.

About ATCC®

- Founded in 1925, ATCC is a non-profit organization with HQ in Manassas, VA, and an R&D and Services center in Gaithersburg, MD
- World's largest, most diverse biological materials and information resource for cell culture – the "gold standard"
- Innovative R&D company featuring gene editing, differentiated stem cells, advanced models

- Partner with government, industry, and academia
- Global supplier of authenticated cell lines and viral and microbial standards
- Sales and distribution in 150 countries, 20 international distributors
- Talented team of 700+ employees, over one-third with advanced degrees

bsi. ISO 9001 Quality Management

bsi. ISO 13485 Medical Devices Quality Management

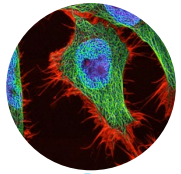
ANAB ACCREDITED ISO/IEC 17025 TESTING LABORATORY

ANAB ACCREDITED ISO 17034 REFERENCE MATERIAL PRODUCER

ATCC® cell biology collection

60+ years of advancement for cancer research

1959
ATCC cell biology established. Its collection of cell lines and hybridomas becomes the most extensive in the world.

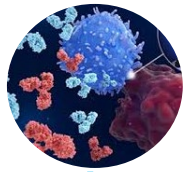


2000
ATCC awarded grant establishing the National Stem Cell Resource.

2012
ATCC tumor cell panels & genetic alteration cell panels released.

2016
ATCC CRISPR gene-edited cell lines for anti-cancer drug development released.

2024
ATCC immuno-checkpoint and CAR-T antigen reporter cell lines released.

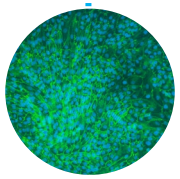


Chemotherapy

Immuno-therapy

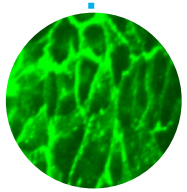
5000+ authenticated cell products, 70+ species, 100+ cell types, 400+ disease types

Targeted therapy

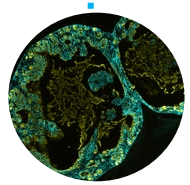


1988
NCI-60 panel announced. Many cell lines distributed through ATCC.

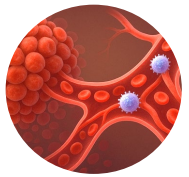
2010
ATCC kicked off major R&D and product development efforts.



2013
ATCC primary cell and hTERT-immortalization program initiated.



2016
HCMI collaboration announced.



2025
First off-the shelf circulating tumor cell line available from ATCC.

ATCC® advanced research cell models

Supporting immuno-oncology and beyond

22
Immuno-oncology reporter lines

27
Live animal imaging lines

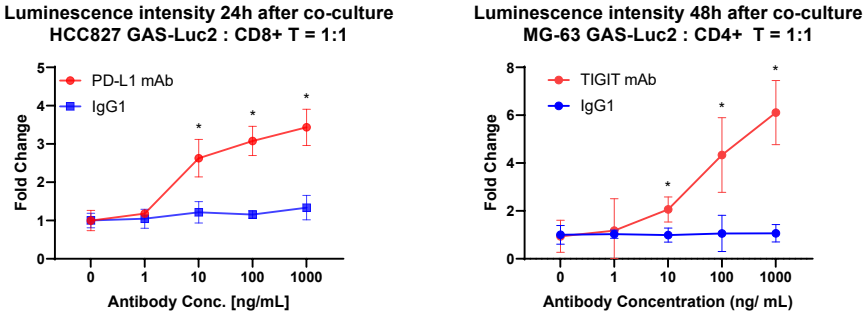
Diverse cell types
- Cancer cell
- T cell
- Myeloid/B cells
- Monocyte/macrophage

Endogenous expression targets
Robust, sensitive, reproducible

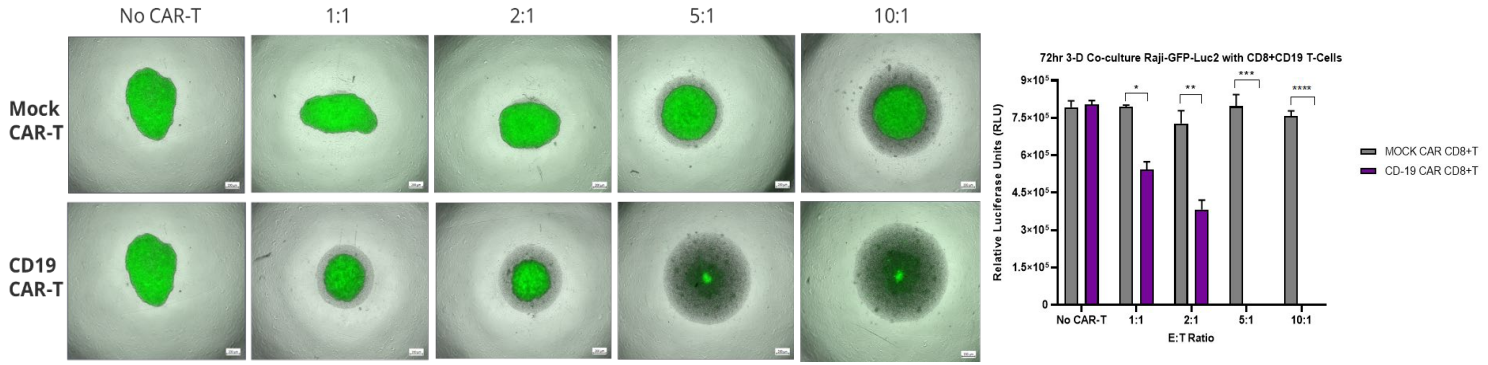
10
Checkpoint targets

4
CAR-T targets hematologic & solid tumor

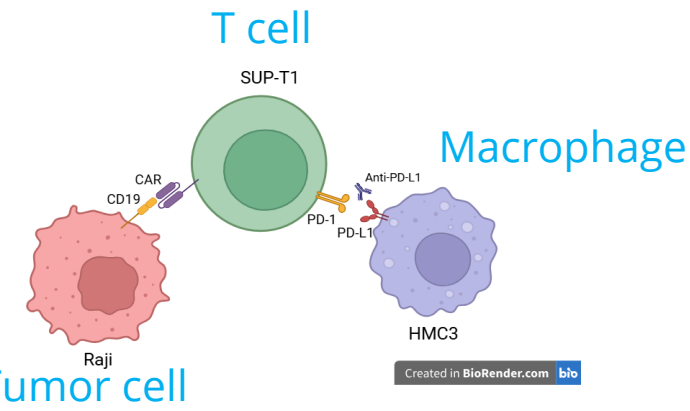
Use ATCC® checkpoint reporter cells to screening checkpoint blockades



Use ATCC® CAR-T antigen dual-reporter cells to evaluate CAR-T in 3-D co-culture (multimodal readout)



Use ATCC® I-O reporter cells to build tumor microenvironment co-culture



An International Community Resource of Organoid Models – the Human Cancer Models Initiative (HCMI)

Jesse Boehm
@boehmjesse

KOCH INSTITUTE for Integrative Cancer Research at MIT

BROAD INSTITUTE

ATCC Session at AACR
04.29.25

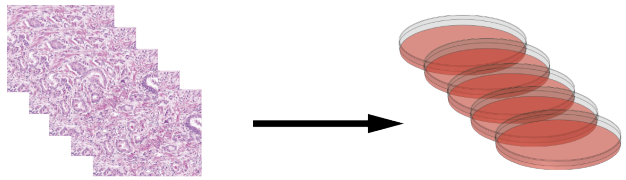
Meet the speaker

Jesse Boehm, PhD

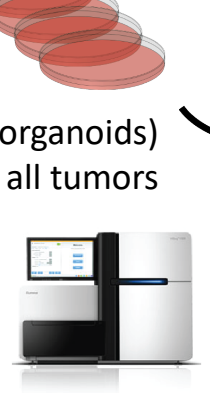
Chief Science officer, Break Through Cancer

Jesse Boehm is the Chief Science Officer of Break Through Cancer and maintains a research lab focused on bringing the power of functional genomics to bear on living samples from cancer patients with particular emphasis on rare and underrepresented tumors. Before joining Break Through Cancer, Jesse spent 14 years in the Broad Institute's Cancer Program, most recently as an Institute Scientist and Scientific Director of the Cancer Dependency Map project. As the Director of the Broad's Cancer Model Development Center (part of the NCI HCMI), he led his laboratory in developing a scalable capacity to convert patient tumors into organoids and other cell models. Prior, he was the recipient of a Broad Institute Merkin Fellowship and the Associate Director of the Broad's Cancer Program. In these leadership roles, he drove the scientific planning and strategic execution of a diverse set of program projects, collaborations, and activities for over a decade. Jesse received his BS in biology from MIT and his PhD from Harvard University, Division of Medical Sciences at Dana-Farber Cancer Institute.

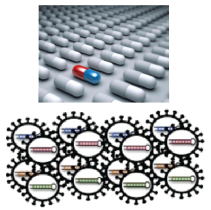
Broadly accessible patient models are the foundation for the Cancer Dependency Map



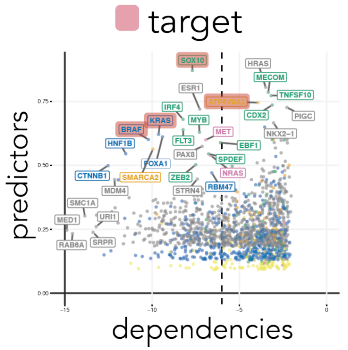
Patient models (cell lines/organoids) representing all tumors



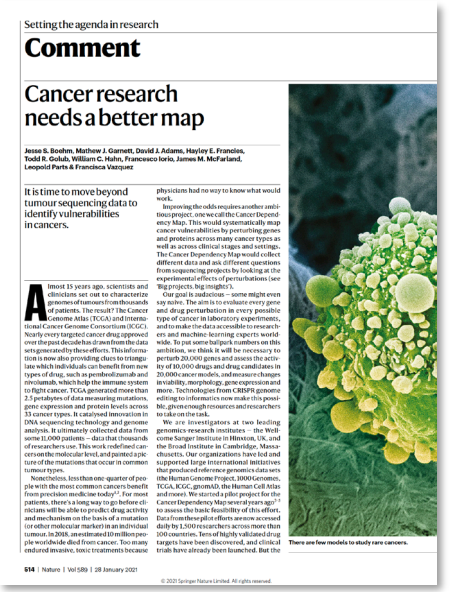
Molecular and genetic information



Genetic dependencies and drug sensitivities



Map of cancer dependencies



Setting the agenda in research

Comment

Cancer research needs a better map

Jesse S. Boehm, Mathew J. Garnett, David J. Adams, Hayley E. Francies, Todd R. Golub, William C. Hahn, Francesco Iorio, James M. McFarland, Leopold Parts & Francisca Vazquez

It is time to move beyond tumour sequencing data to identify vulnerabilities in cancers.

There are few models to study rare cancers.

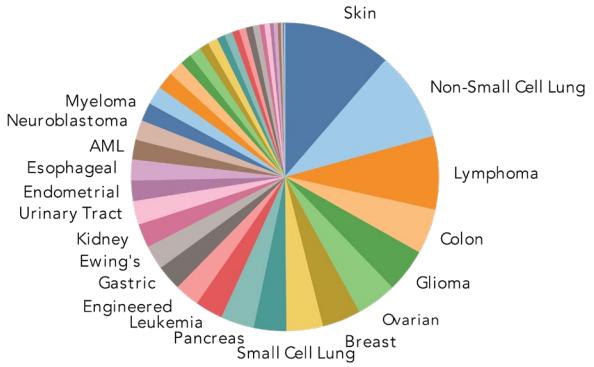
- Discover all **TARGETS** and **DRUG REPURPOSING** hypotheses
- Discover of **PREDICTORS** of patient response

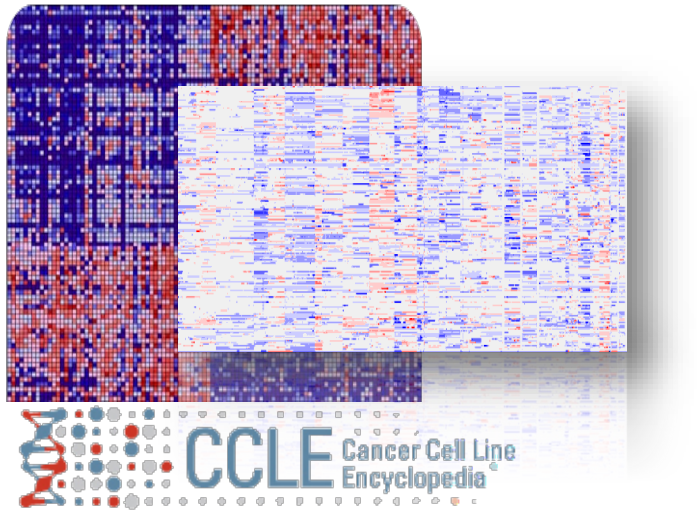
- Create and share foundational data to **EMPOWER THE SCIENTIFIC COMMUNITY**

Our collection of cell models must reflect the full diversity of cancer variation

~1900 existing cancer cell models

deep genomic characterization

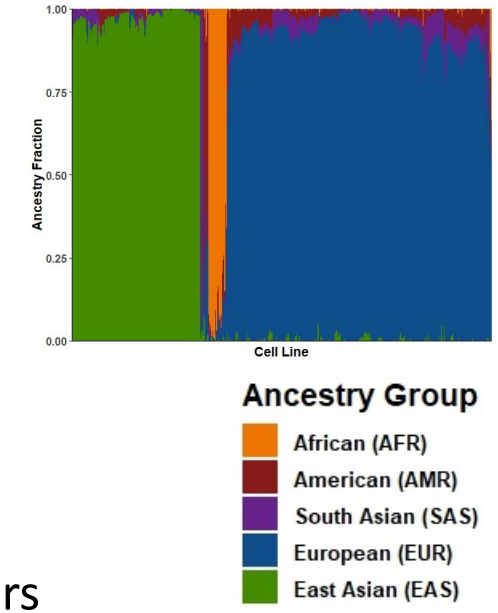




While this seems large, it's probably an order of magnitude too small

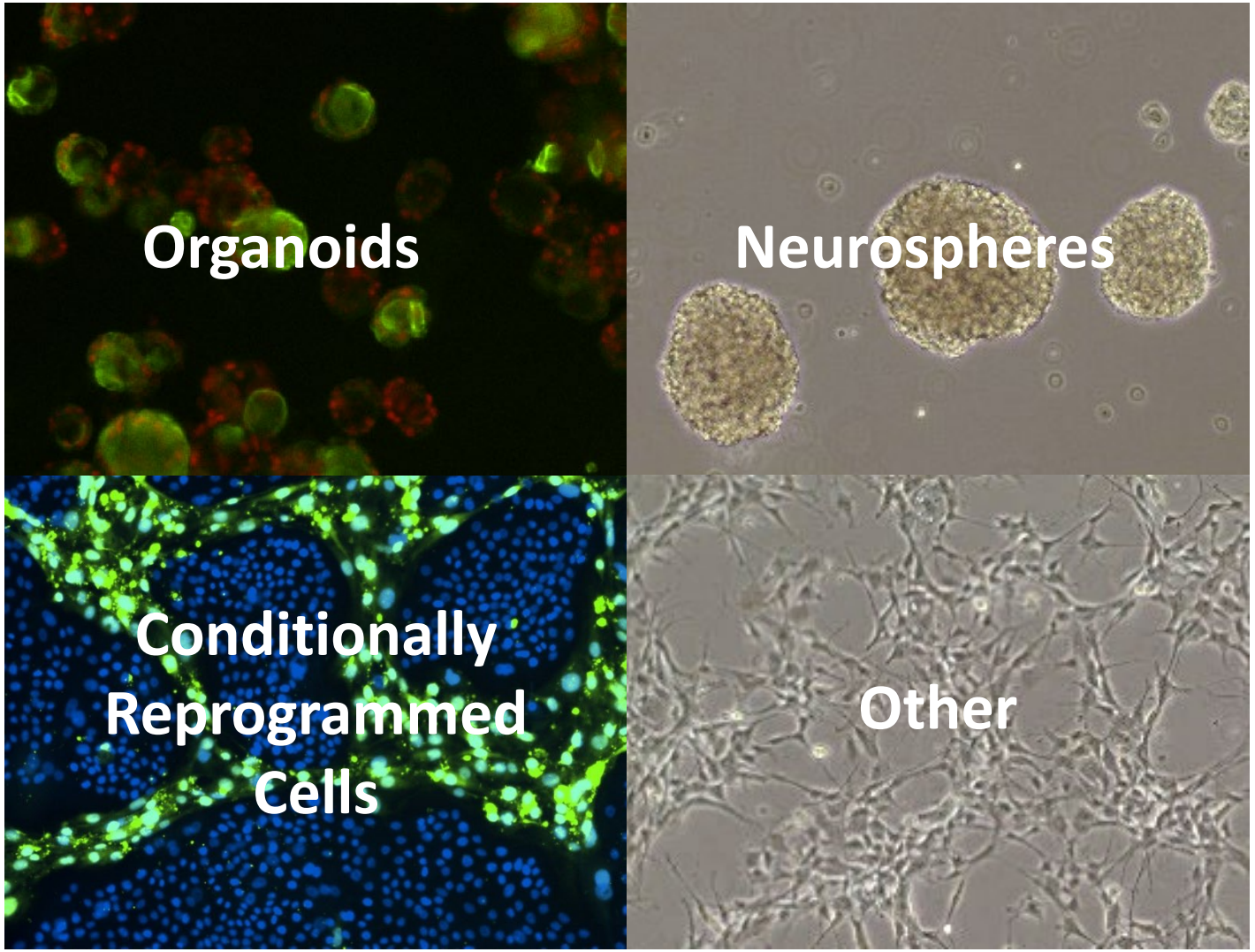
Persistent challenges:

- Many cancers missing (e.g., rare)
- Many genotypes missing
- Many ethnicities missing
- Lacking germline/clinical data



New opportunity: Organoid technologies and patient engagement make model creation possible from 40% of patient tumors (historically ~1%)

Doubling the scale: 1000 next-generation models Human Cancer Models Initiative (HCMI)



Launched in 2016

Molecular characterization

- Somatic and germline sequencing
- 15X tumor WGS
- 150X tumor WES
- 120 million read RNA-seq
- Infinium MethylationEPIC DNA Array

Clinical data

- Standardized case report forms
- Patient demographics
- Disease diagnosis, treatment, and outcome information

Human Cancer Models Initiative (HCMI)

NIH NATIONAL CANCER INSTITUTE

CANCER RESEARCH UK

CSH Cold Spring Harbor Laboratory

wellcome sanger institute

hub Hubrecht Organoid Technology

BROAD INSTITUTE

Hubrecht Institute
Developmental Biology and Stem Cell Research

Cornell University

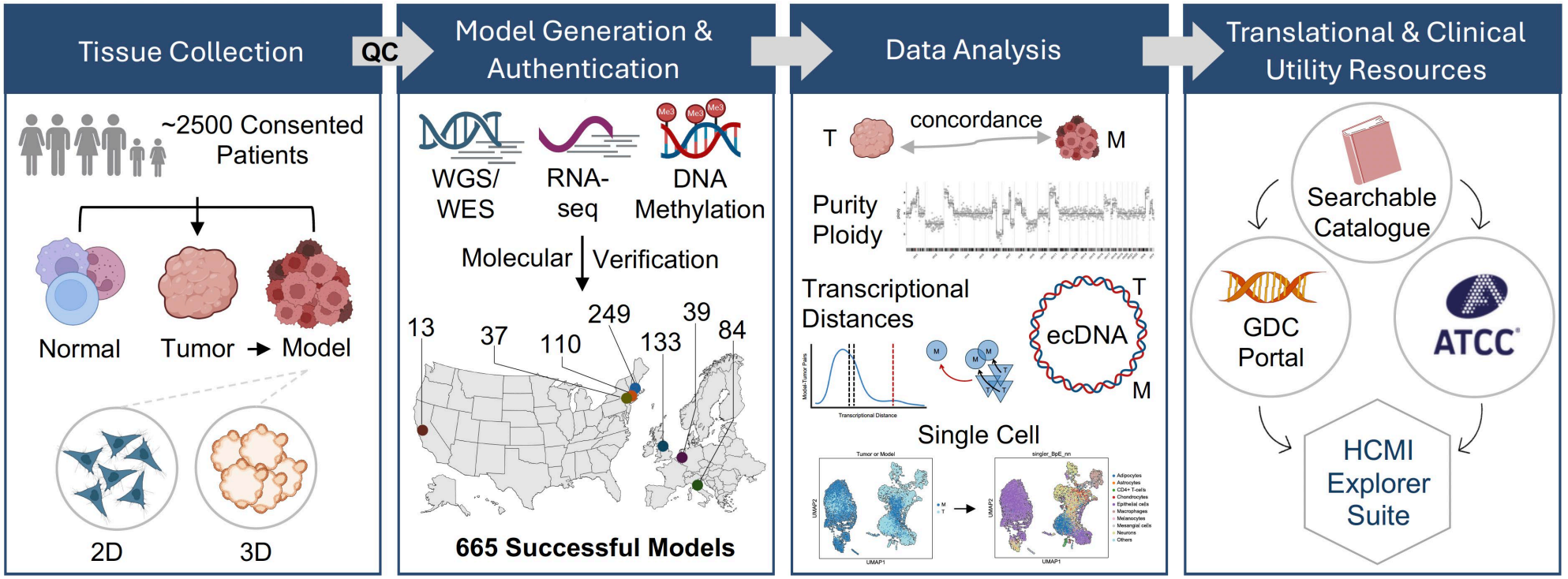
UNIVERSITÀ di VERONA

Stanford University

HCMI Supporting centers

- Nationwide Children's Hospital
- University of North Carolina
- Information Management Systems
- Frederick National Laboratory for Cancer Research, Leidos Biomedical Research, Inc.

HCMI: A compendium of novel patient-derived models as a public resource

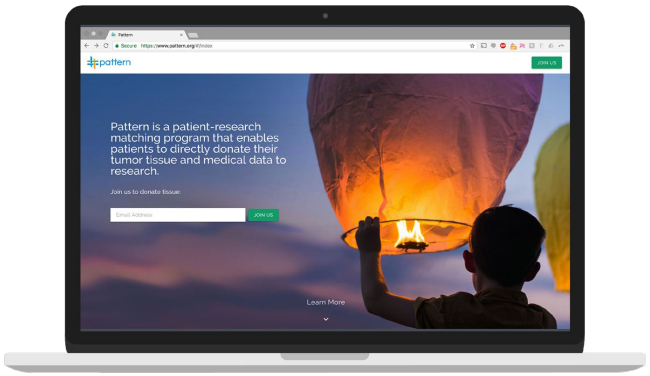


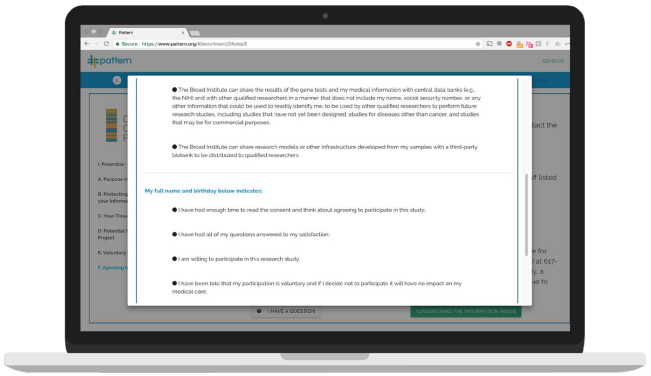
Elharouni et al, submitted

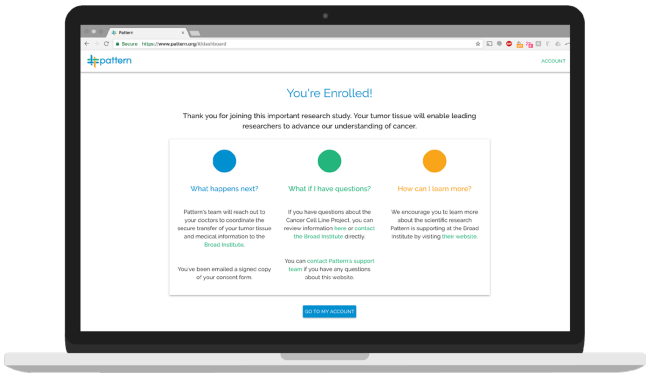

pattern.org
The Rare Cancer Research Foundation launched Pattern.org **to enable** cancer patients to **direct** their tumor tissue and medical data to high impact research at leading labs.

Pattern matches patients to a research study in need of their **fresh** tissue, powering studies that otherwise might not happen.

1 . . . . . 2 3







Patients **learn** about research studies for their cancer

Patients are **matched** to a study in need of their tissue and **consent online**

Pattern's team **coordinates** the **transfer** of tissue and data

pattern.org

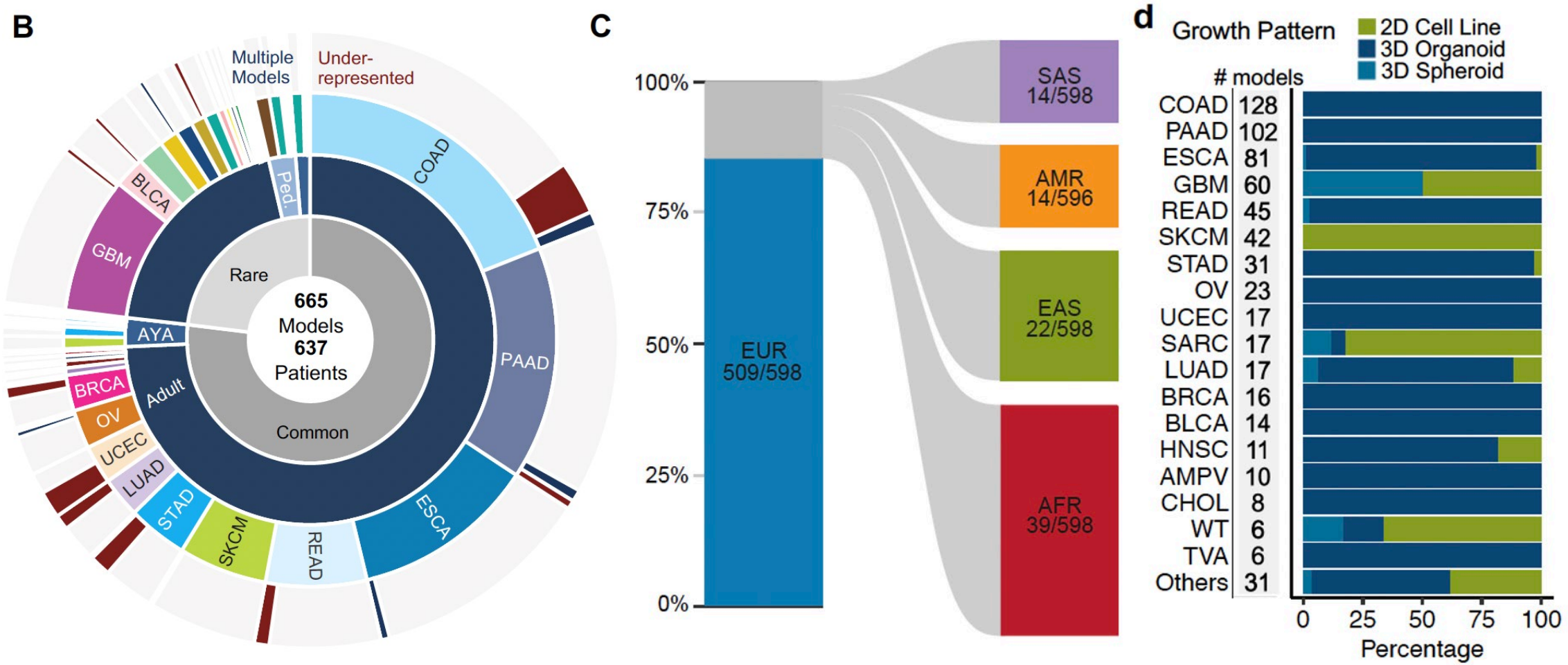
A nationwide movement for rare cancer fresh tissue donation: 435 patients, 215 institutions

- **353** samples successfully obtained from **121** institutions
- **42** States and Canadian provinces
- **20.1%** from non-Caucasian minority populations

pattern.org

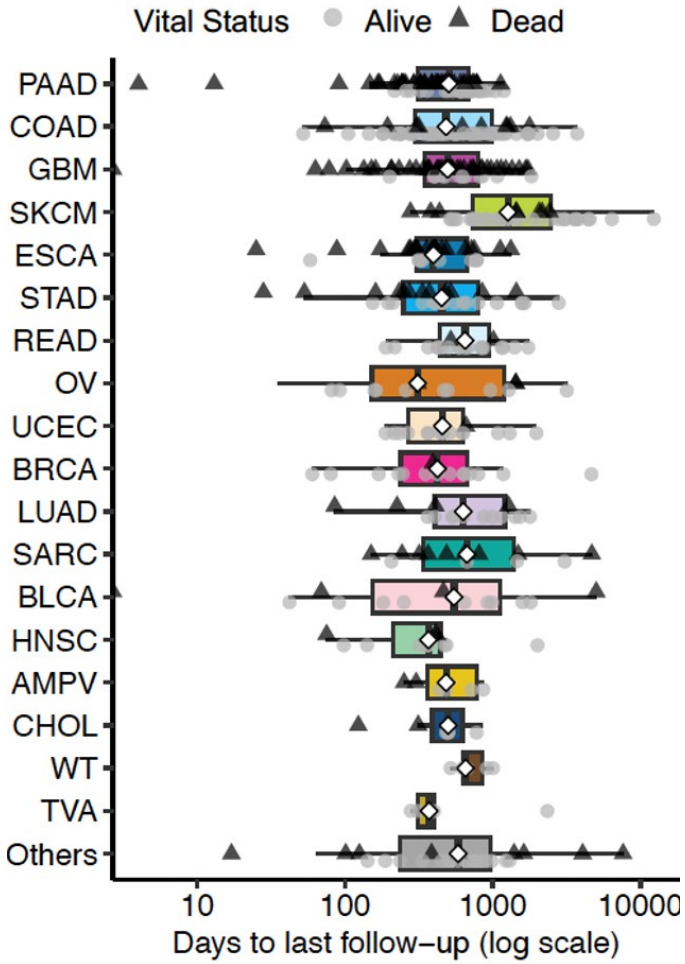
Barbara Van Hare

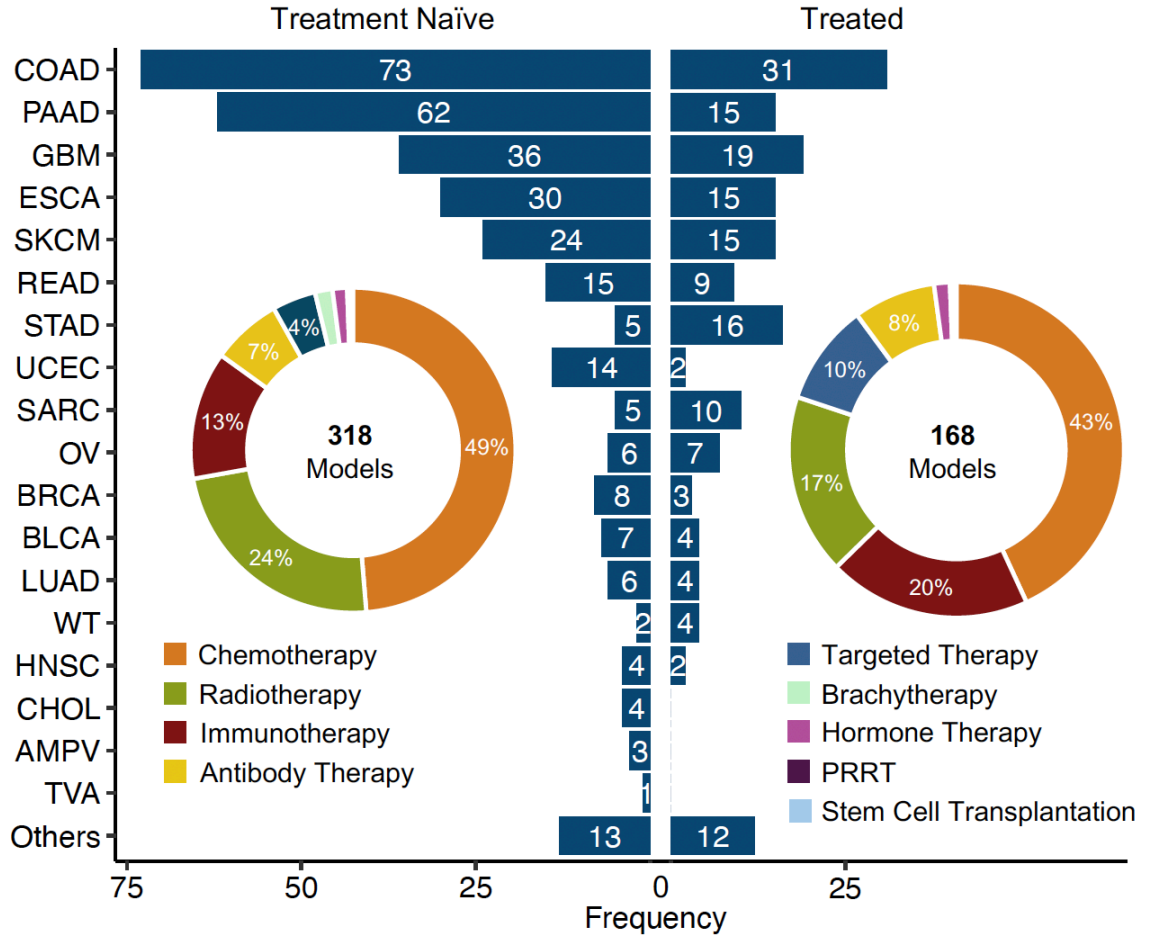
HCMI models (665) provide an opportunity to compare patient drug responses with *ex vivo* responses



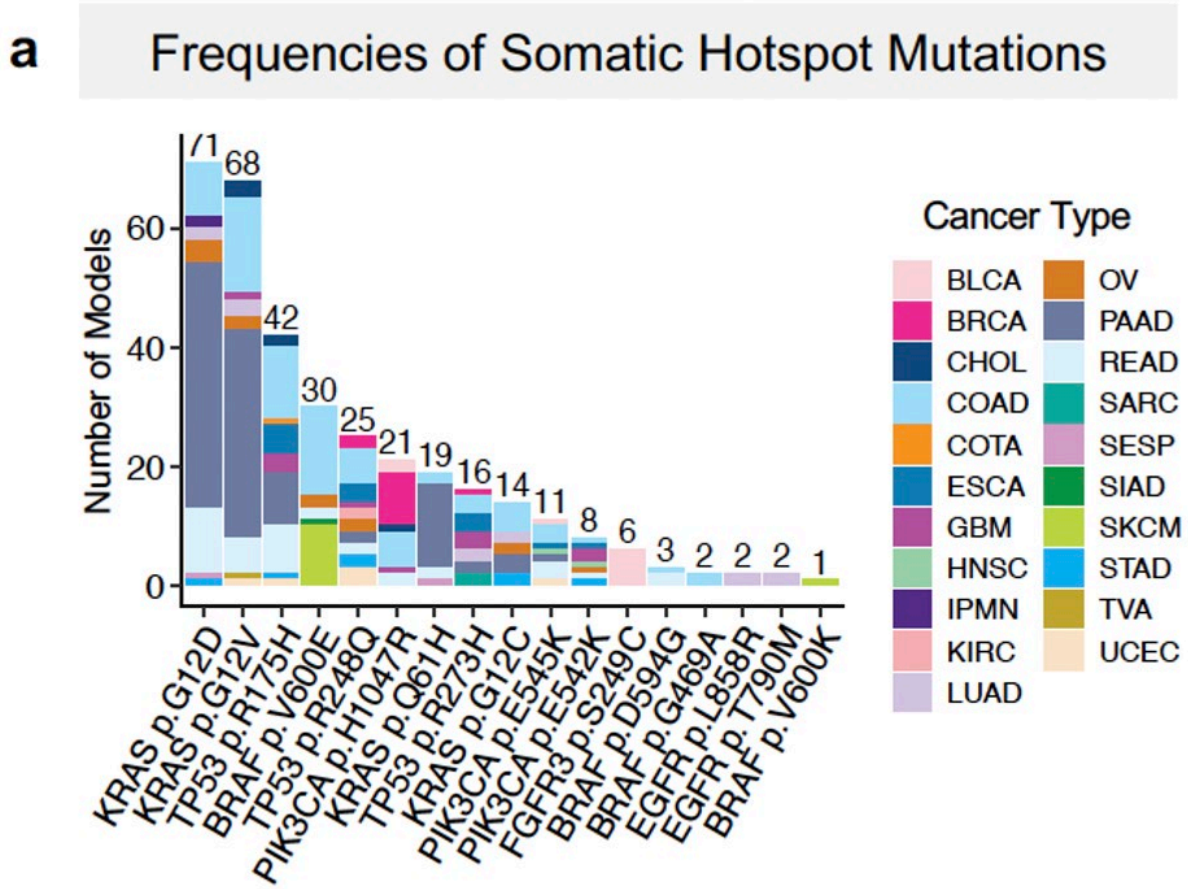
Elharouni et al, submitted

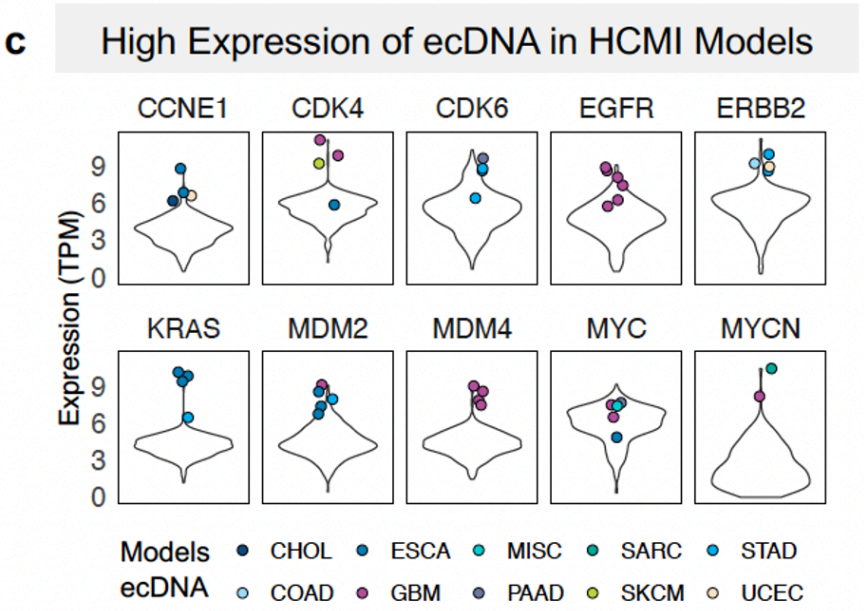
HCMI models (665) provide an opportunity to compare patient drug responses with *ex vivo* responses

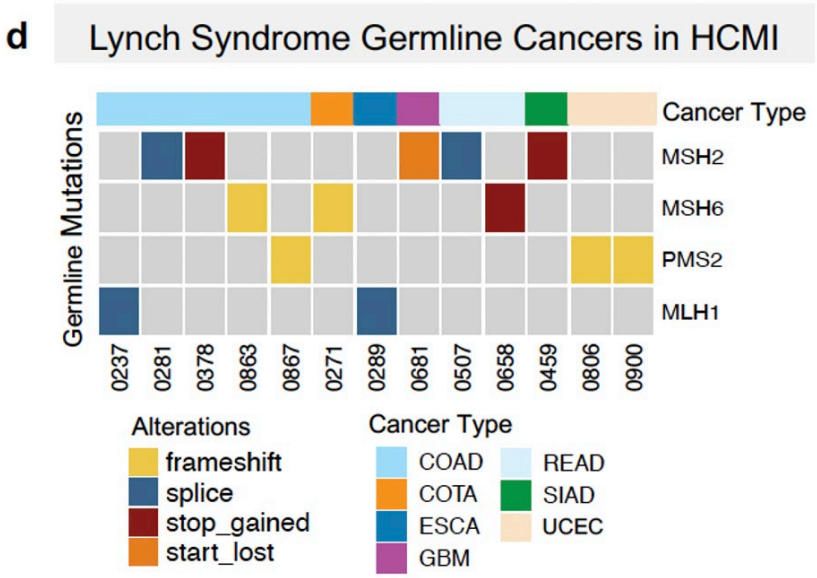




Mutational features of HCMI models enable translational applications





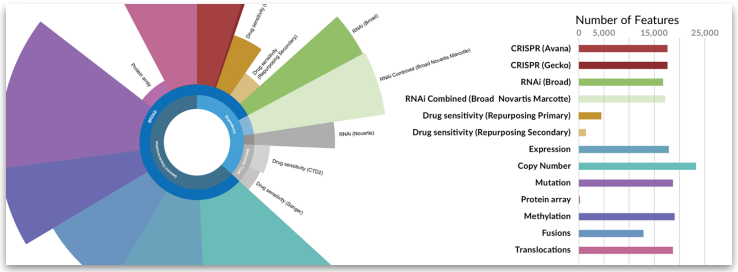


Dina Elharouni

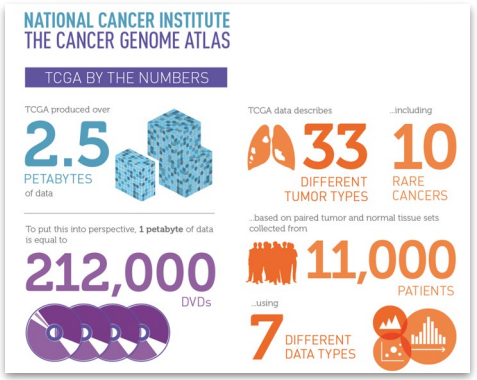
What do new HCMI models transcriptionally represent?

Models

CCLE Cancer Cell Line Encyclopedia

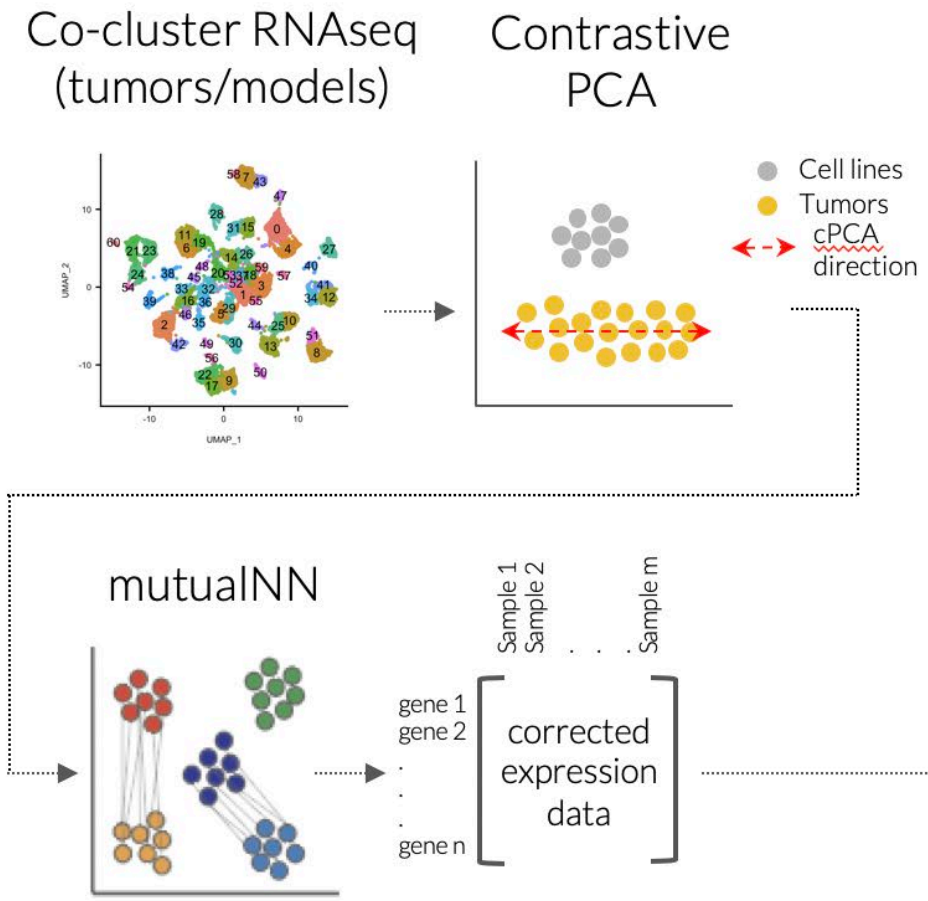


TCGA

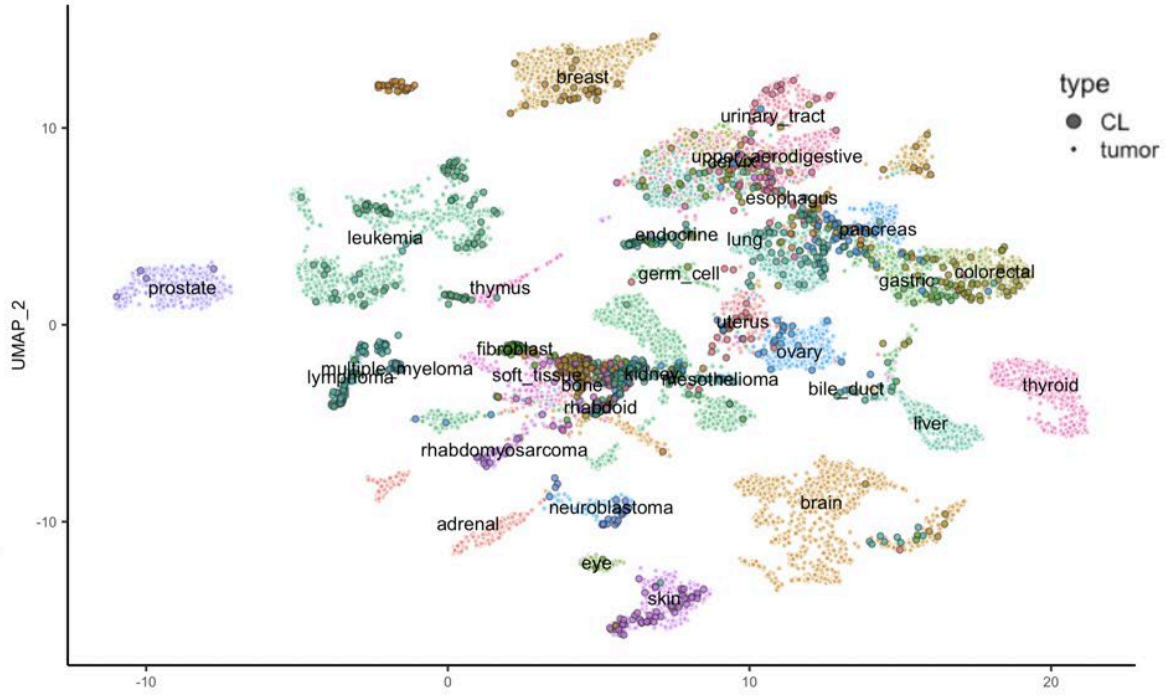


Tumors

Celligner: use transcription to assess cell state fidelity (tumor vs. models)

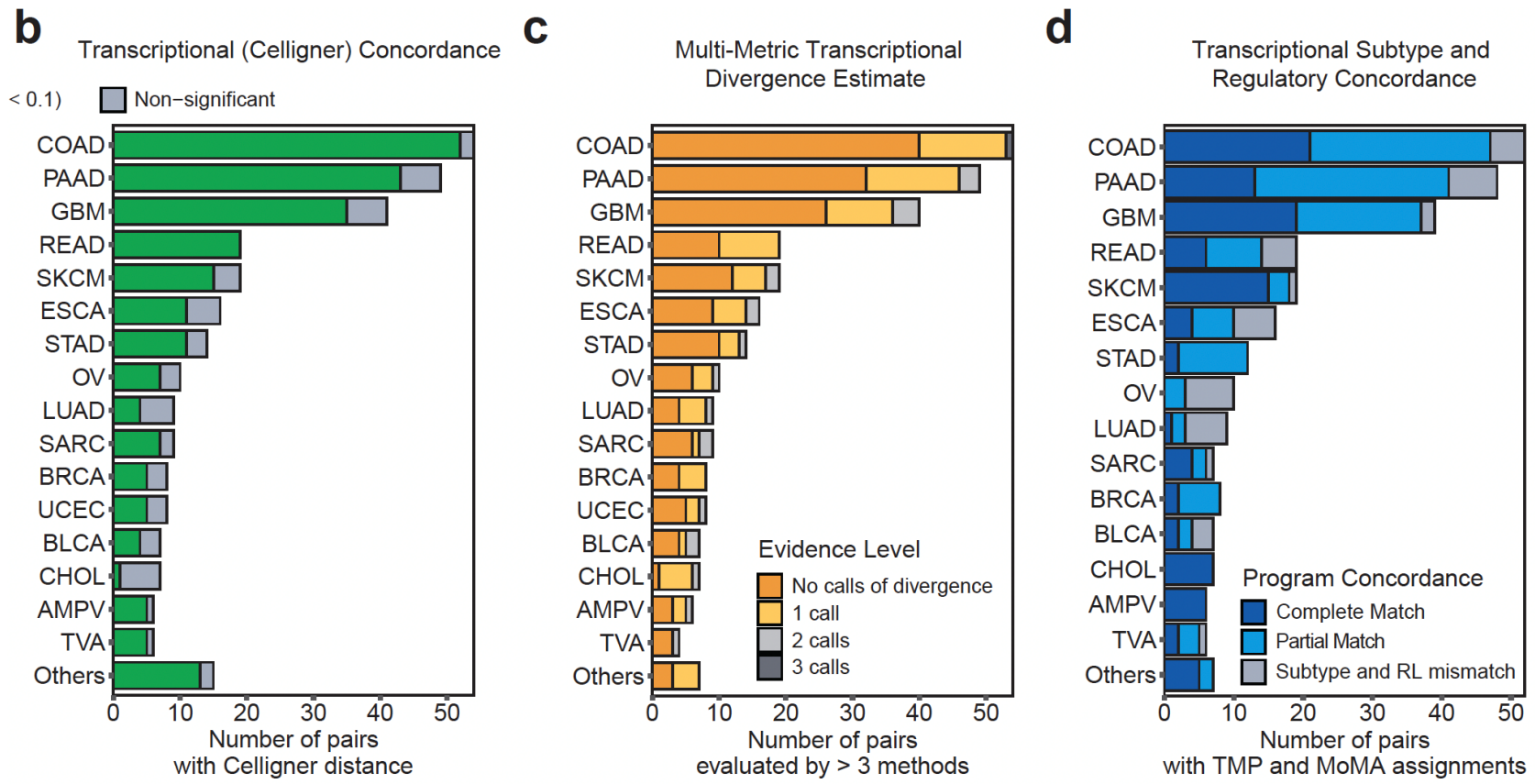


global alignment (/misalignment)
of historical cell lines and tumors



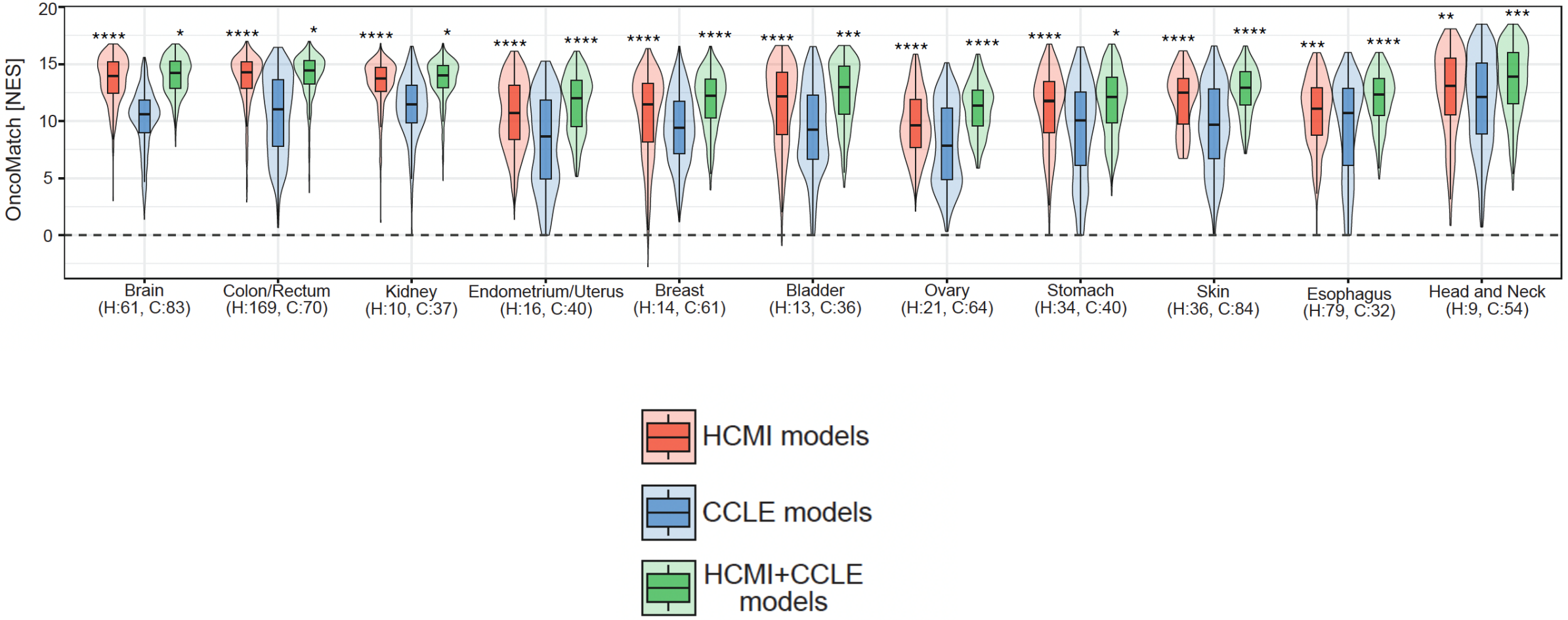
Warren et al, Nat Comm 2021

92% of HCMI models are closely matched to their parent tumor in transcriptional space

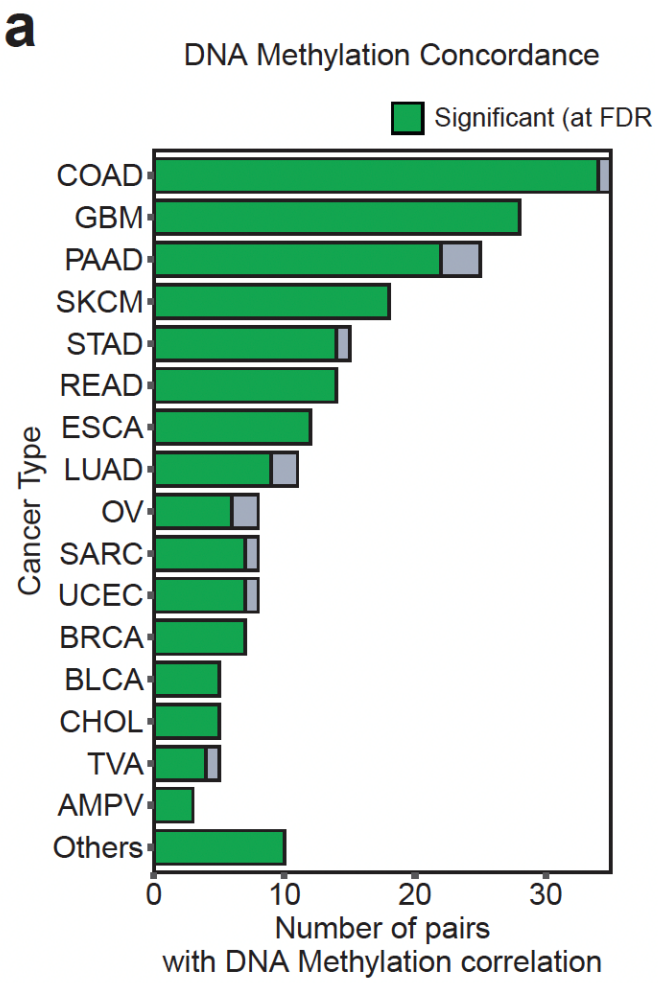


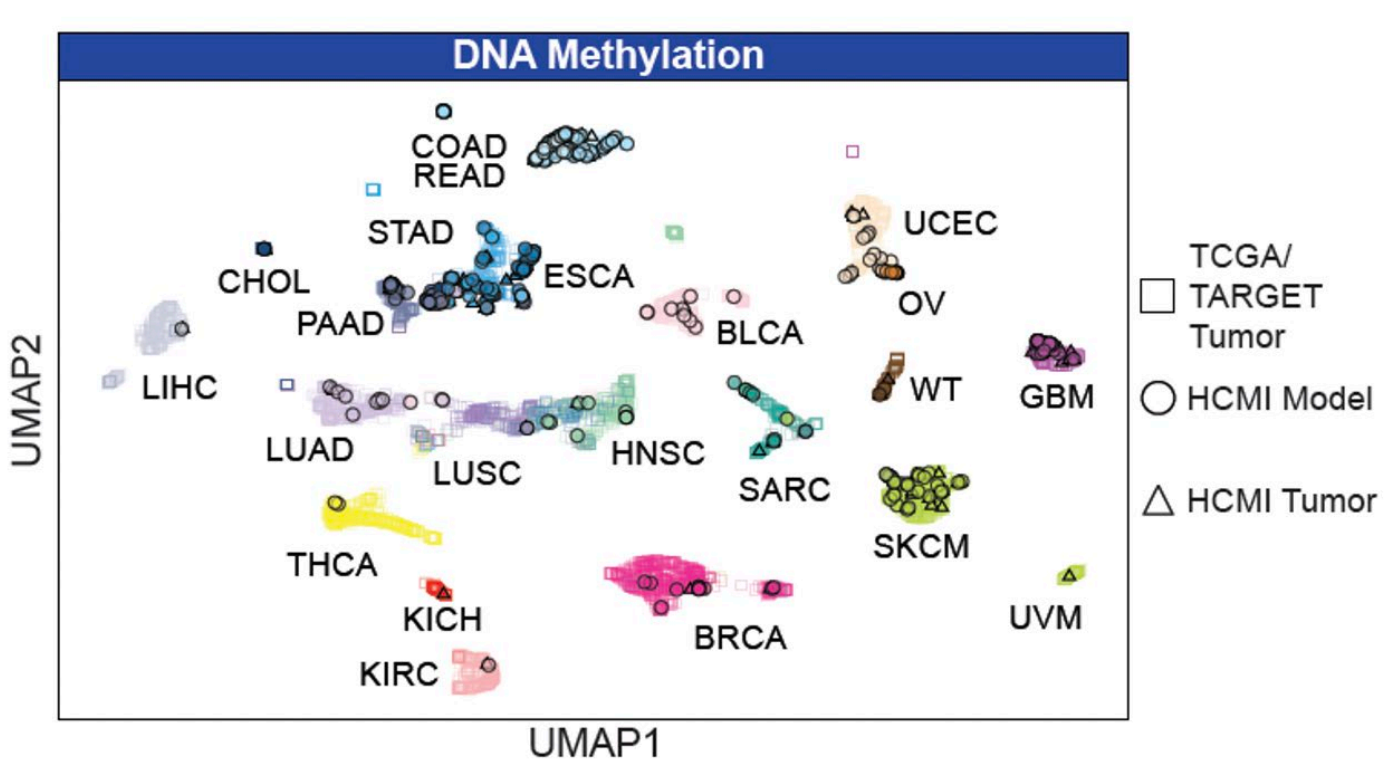
Mushriq Al-Jazrawe, Merve Dede, Heeju Noh

In many cases, HCMI models are closer transcriptional matches to TCGA samples than CCLE models



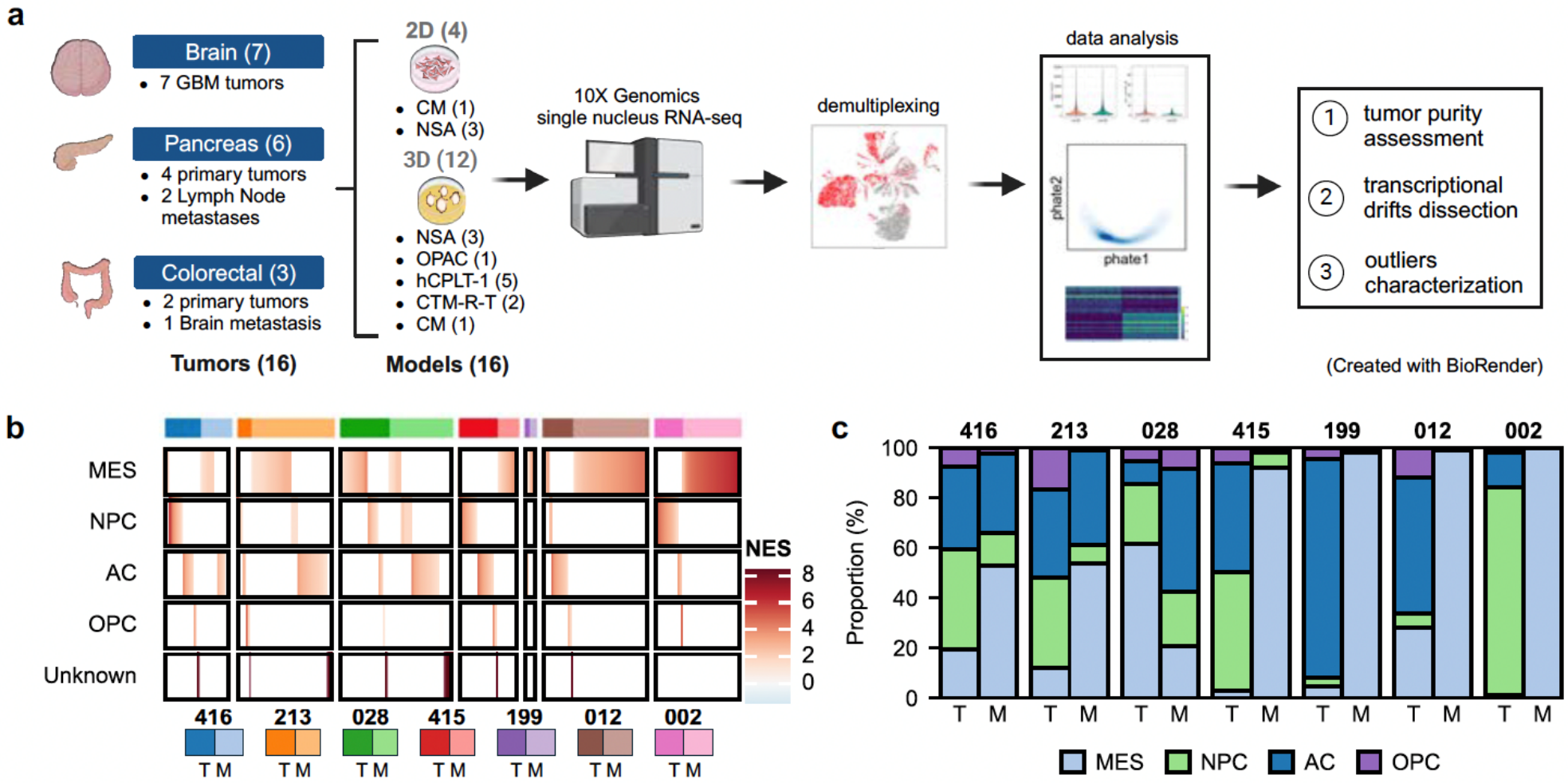
DNA methylation analyses reveal 95% concordance with parent tumors and representation of TCGA



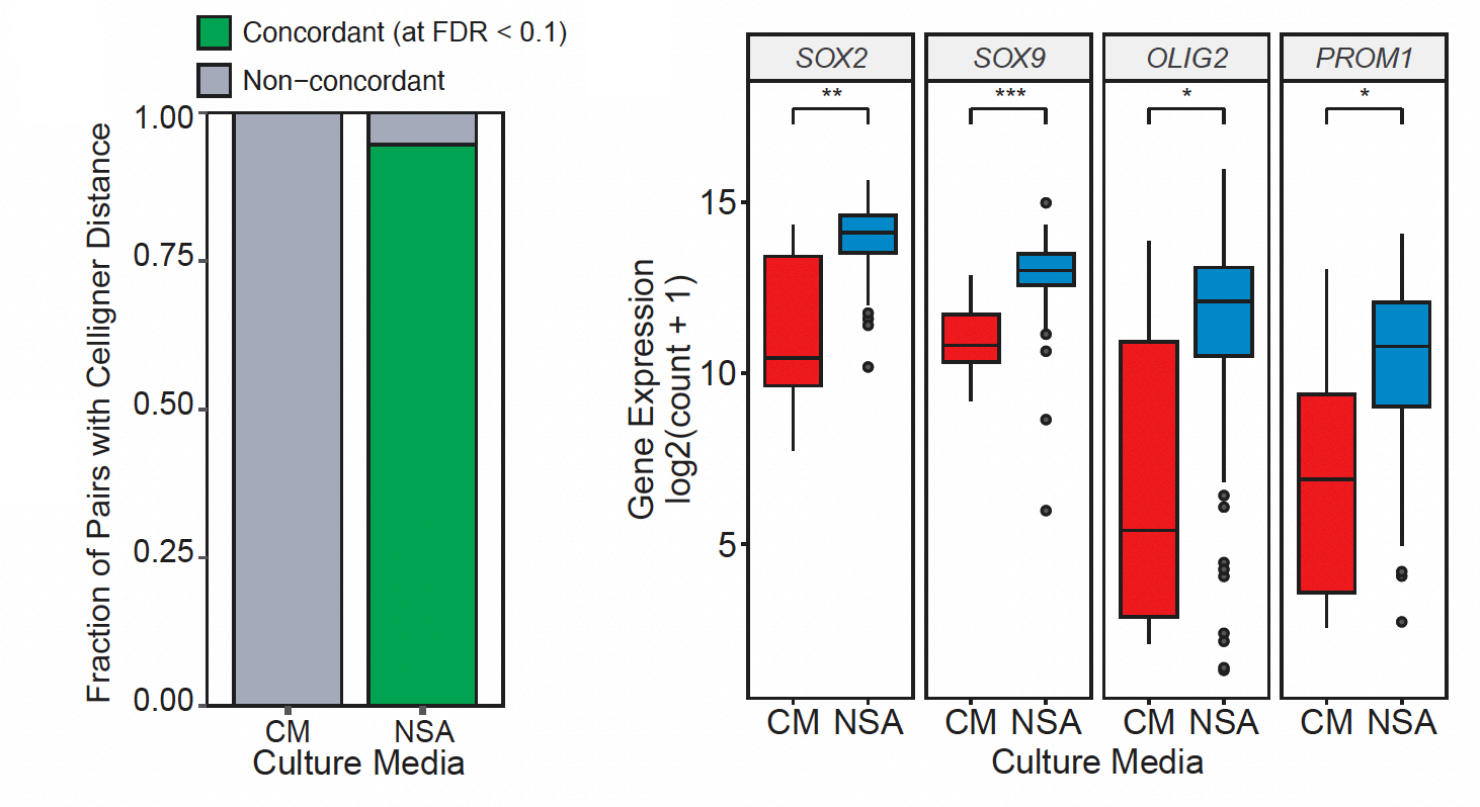


Toshi Hinoue, Peter Laird

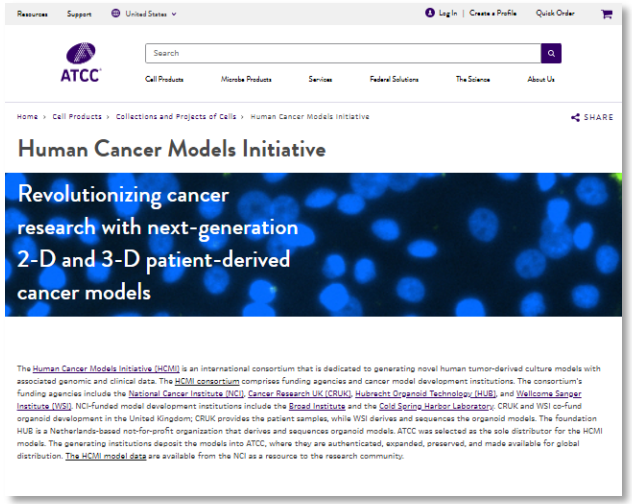
Media formulations may explain some cases of dissimilarity between tumors and derived model pairs (GBM example)



Media formulations may explain some cases of dissimilarity between tumors and derived model pairs (GBM example)

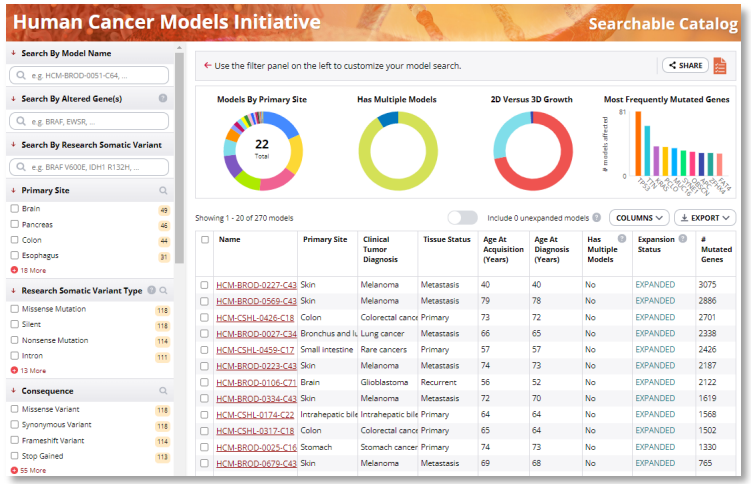


Resources to learn more about the HCMI



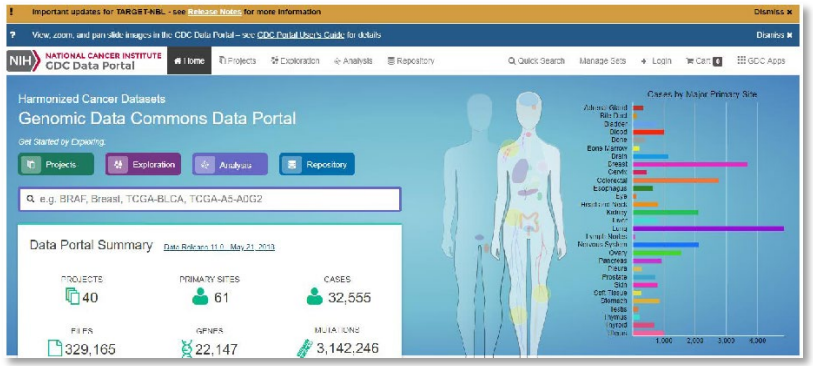
HCMI Landing page

atcc.org/hcmi



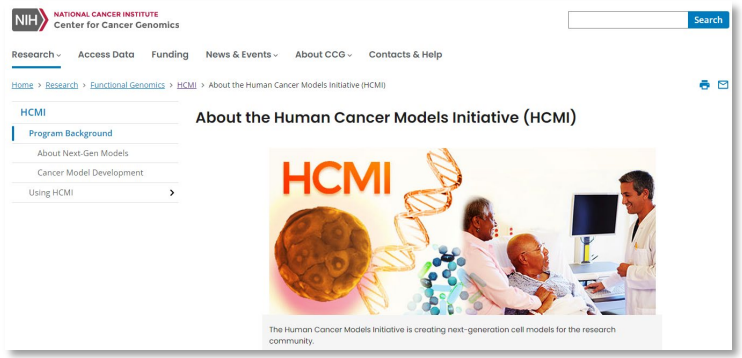
HCMI Searchable Catalog

hcmi-searchable-catalog.nci.nih.gov



NCI Genomic Data Commons

portal.gdc.cancer.gov/



Center for Cancer Genomics

www.cancer.gov/ccg/

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ATCC 100 YEARS Carolina Lucchesi

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- University of North Carolina
- Information Management Systems
- Frederick National Laboratory for Cancer Research, Leidos Biomedical Research, Inc.

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Timothy R. Chu
William F. Hooper
Xavi Loinaz
Paula Keskula
Jordan A. Lee
Peyton C. Kuhlers
Bahar Tercan
Sylvia F. Boj
Alessandro Vasciaveo
Lorenzo Tomassoni
James M. Crawford
Shawna Walsh
Claire Sinai
Sonam Bhatia
Priya Sridevi
Hardik Patel
Maria Antonietta Cerone

Comprehensive genomic validation of tumor model pairs for HCMI

Andrew McPherson

HCMI AWG

Memorial Sloan Kettering Cancer Center

Meet the speaker

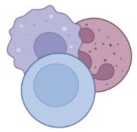
Andrew McPherson, PhD

Assistant Attending, Computational Oncologist, Memorial Sloan Kettering Cancer Center

Andrew McPherson is an Assistant Attending Computational Oncologist in the Department of Epidemiology and Biostatistics and a faculty member of Computational Oncology. Andrew's research focuses on computational methods for analysis of single cell genomic data. During his doctoral research, Dr. McPherson developed methods for cancer genome sequence analysis, including detection and characterization of genome rearrangements, and inference of clonal phylogenies. Dr. McPhersons post-doctoral research at University of British Columbia focused on the development of computational methods and infrastructure for a novel single cell whole genome sequencing (scWGS) platform, Direct Library Preparation. During his time at MSKCC, Dr. McPherson has led efforts to establish a production implementation of scWGS via DLP within MSKCC, and support use of the platform through collaborations with investigators throughout the institute.

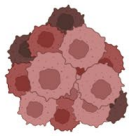
Genomic profiling of normal / tumor / model trios

399 Models and Parental Tumors



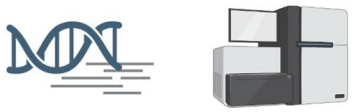
Normal

Tumor

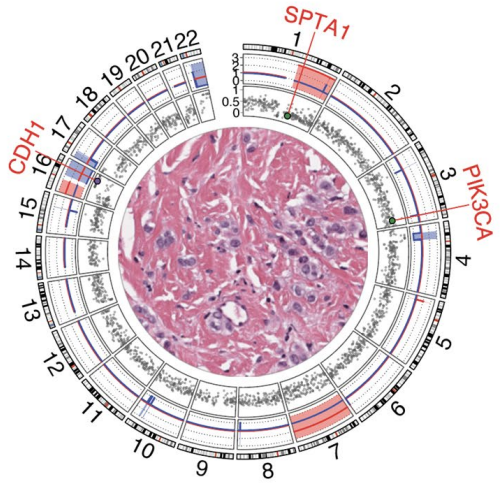


Model

Whole Genome Sequencing

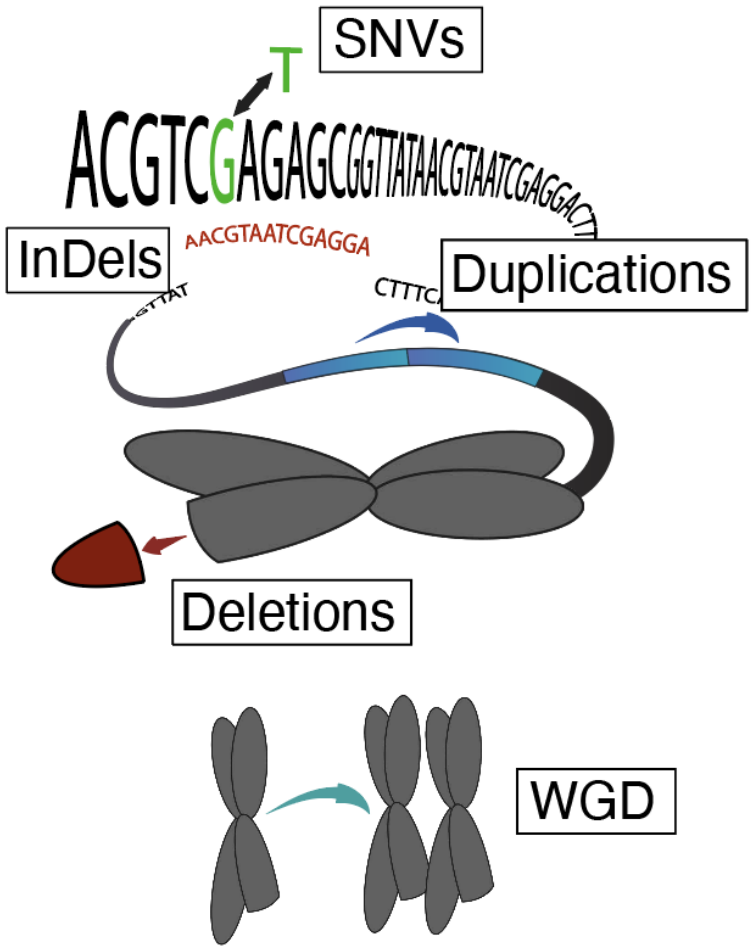


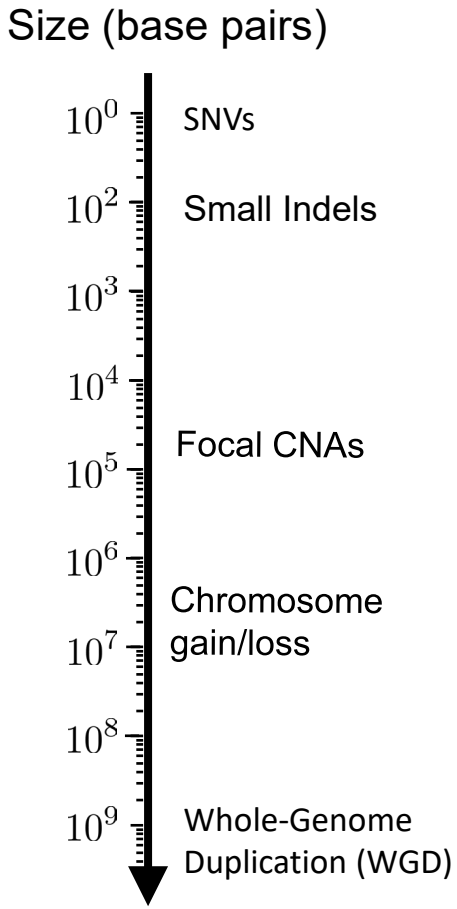
Comprehensive Genomic Profiling

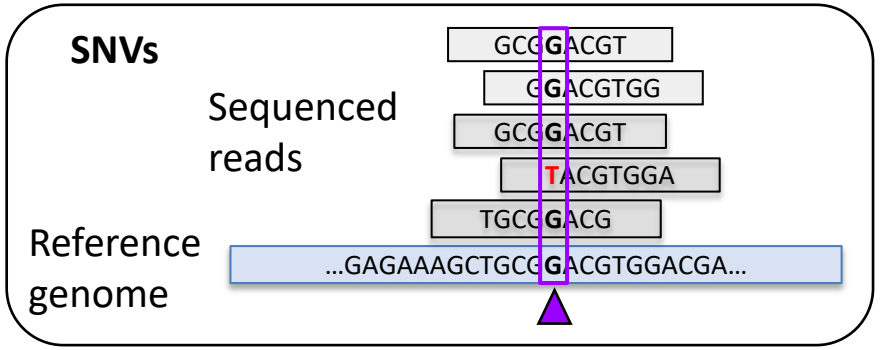


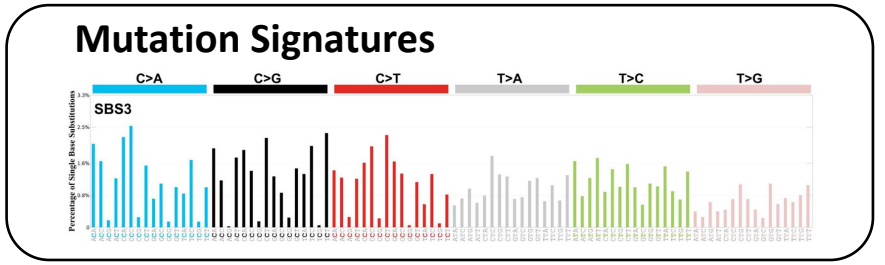
- **Validate** model origin
- Discern **somatic** vs **germline** genomic changes in models
- Investigate tumor / model **divergence**
- Catalog **driver mutations** for each model

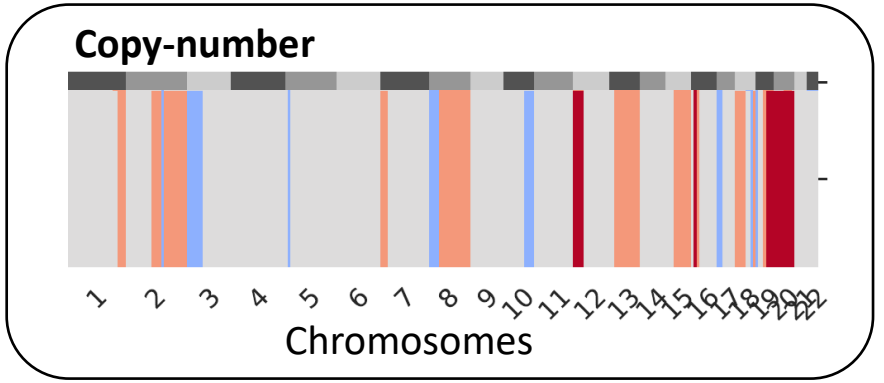
Whole-genome sequencing–based genomic validation



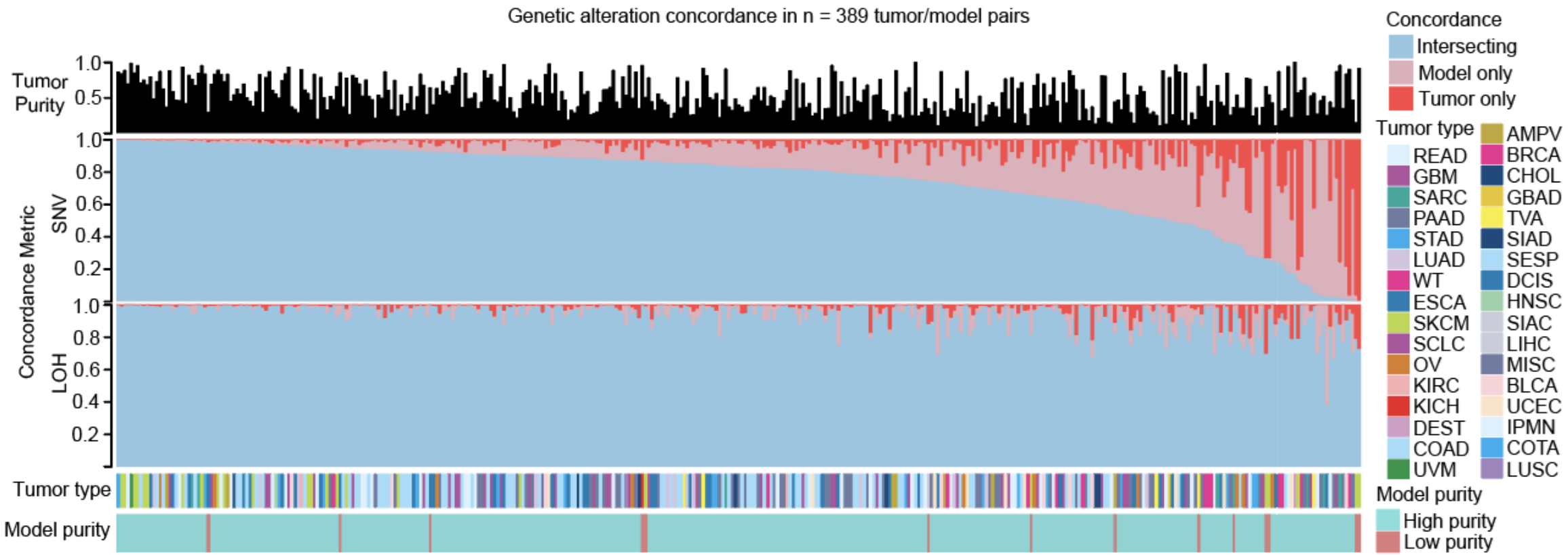




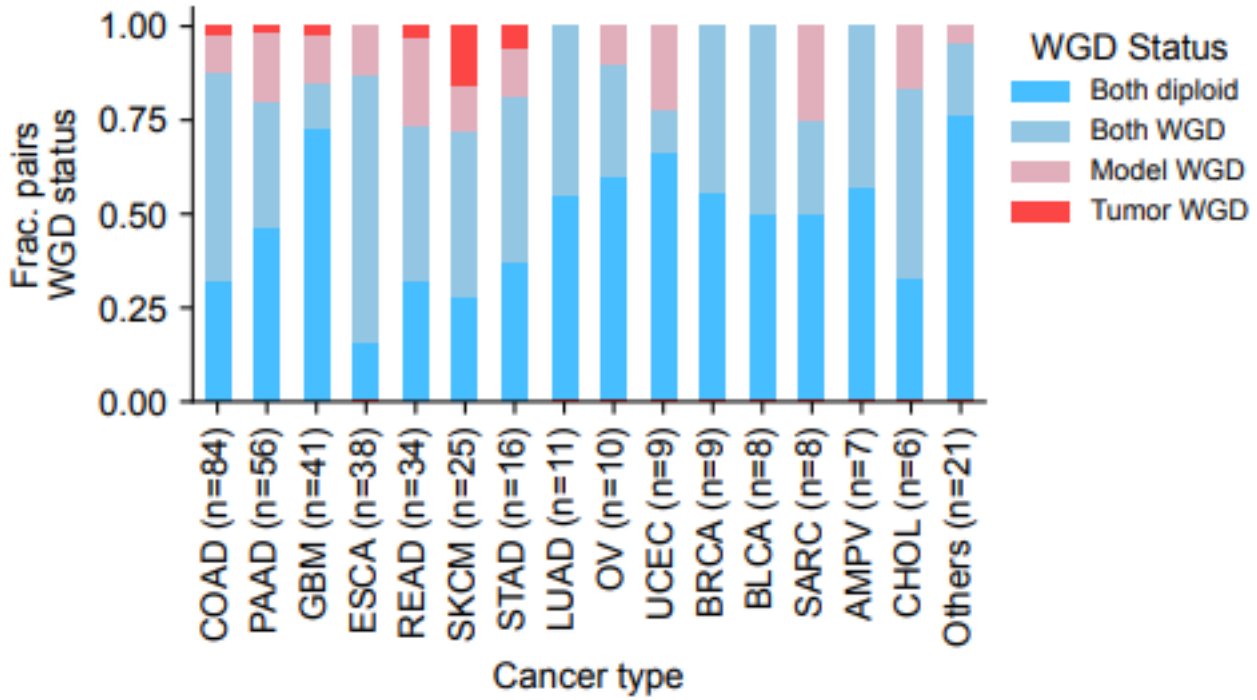


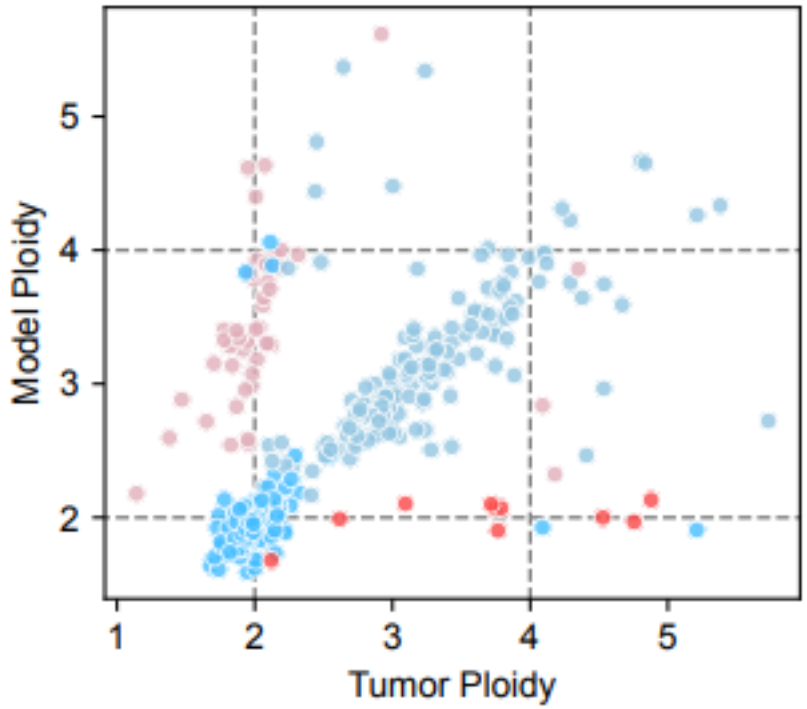


Concordance of SNVs and loss of heterozygousity across 389 tumor / model pairs

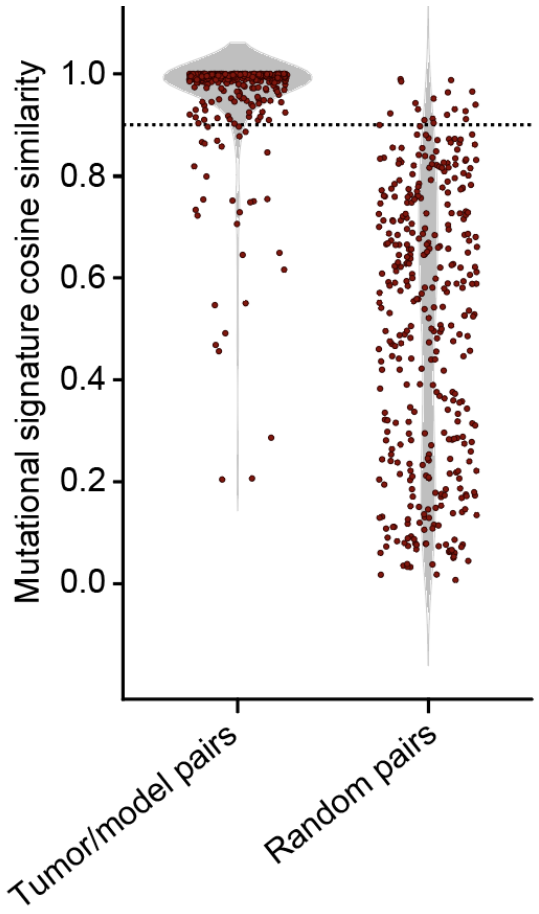


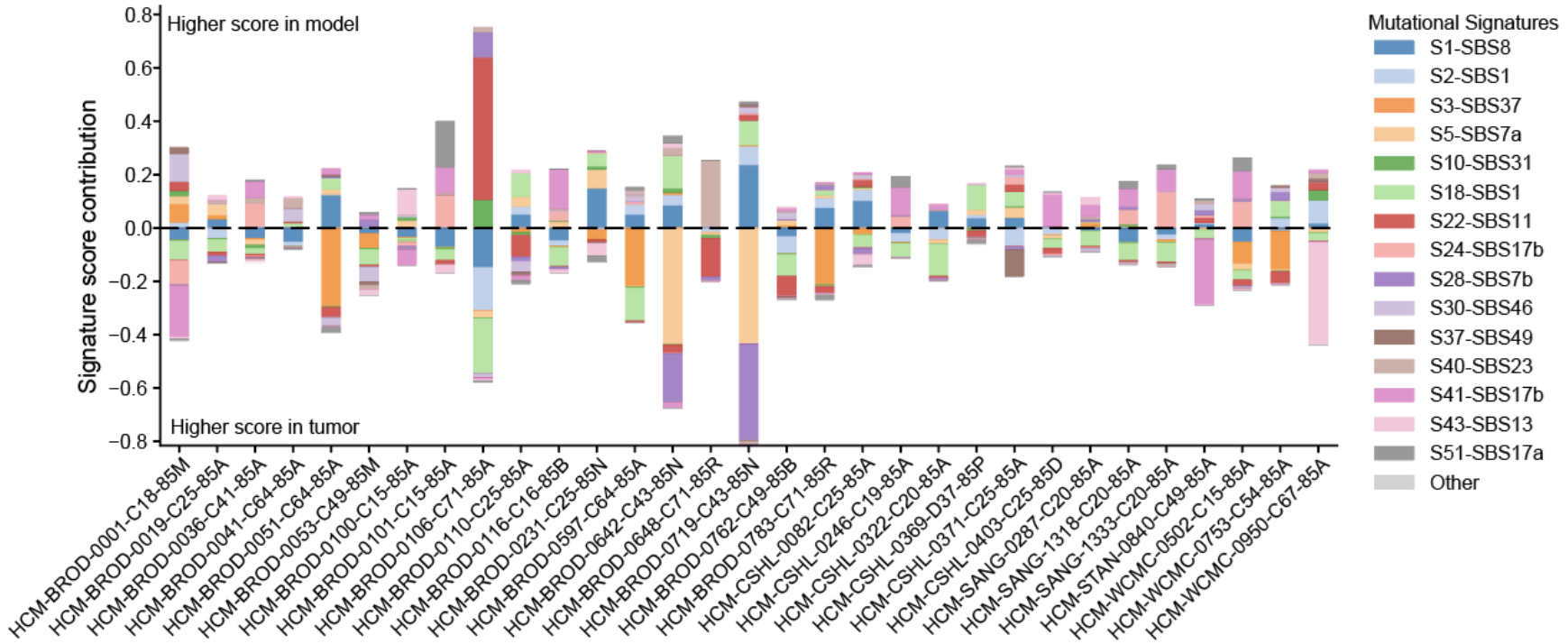
High concordance of WGD status



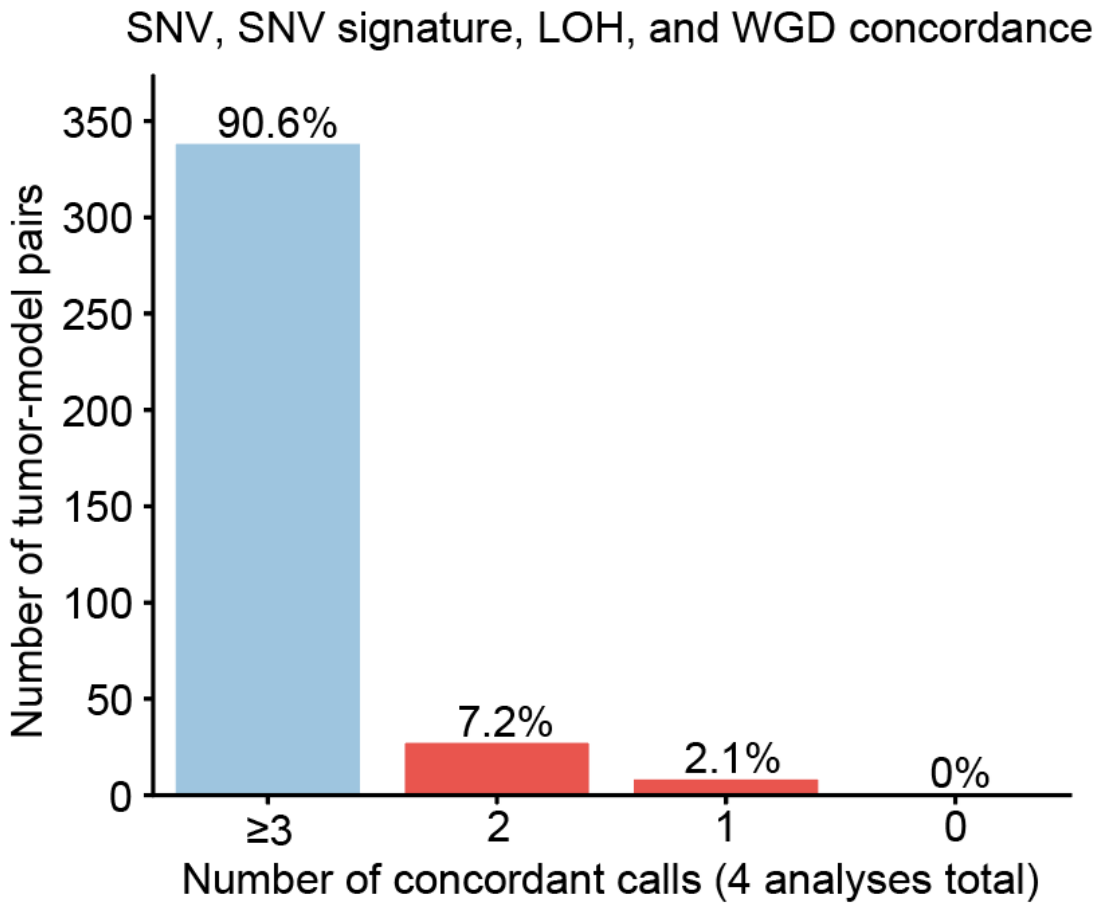


Models recapitulate mutation signatures of tumors

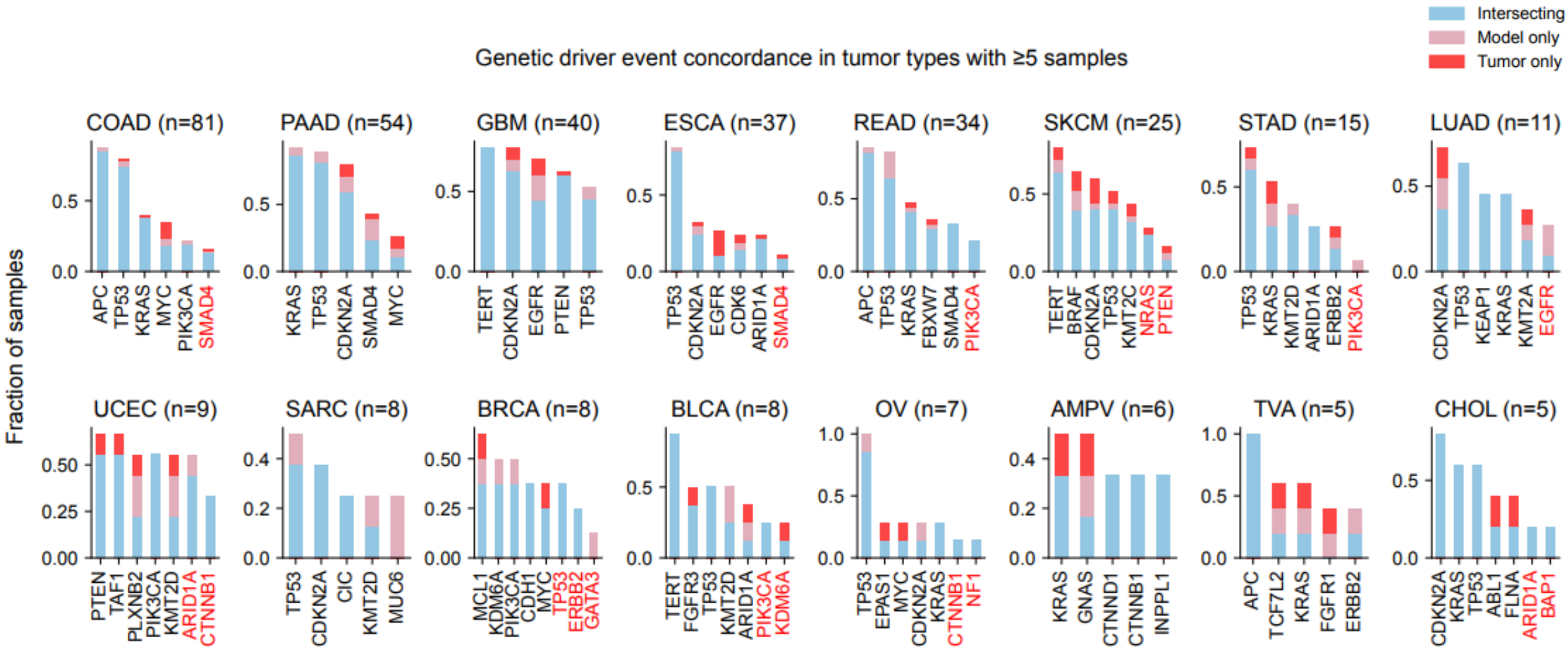




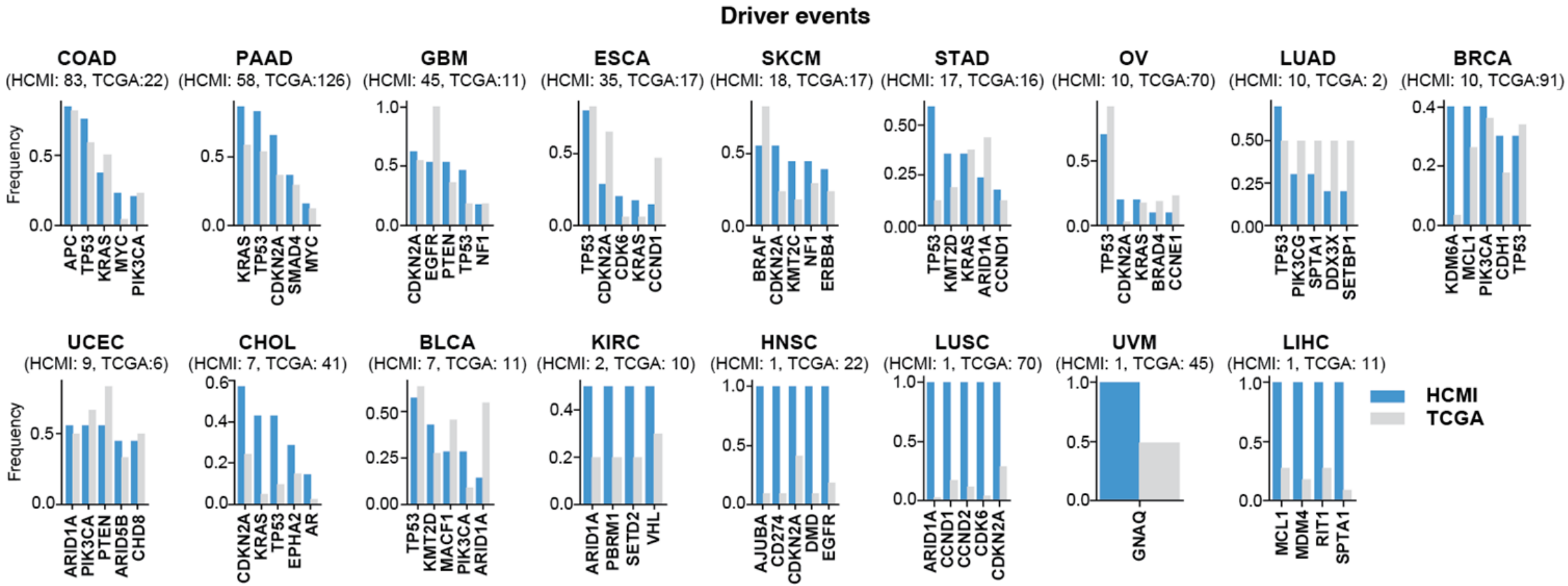
High overall concordance of genomic features



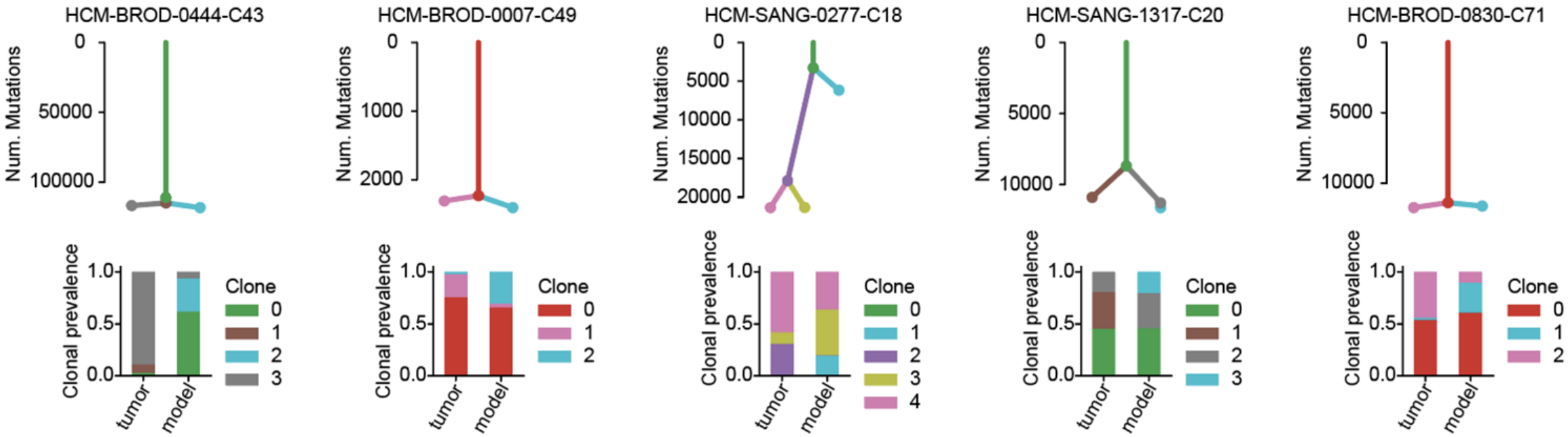
Tumor model concordance of genetic drivers



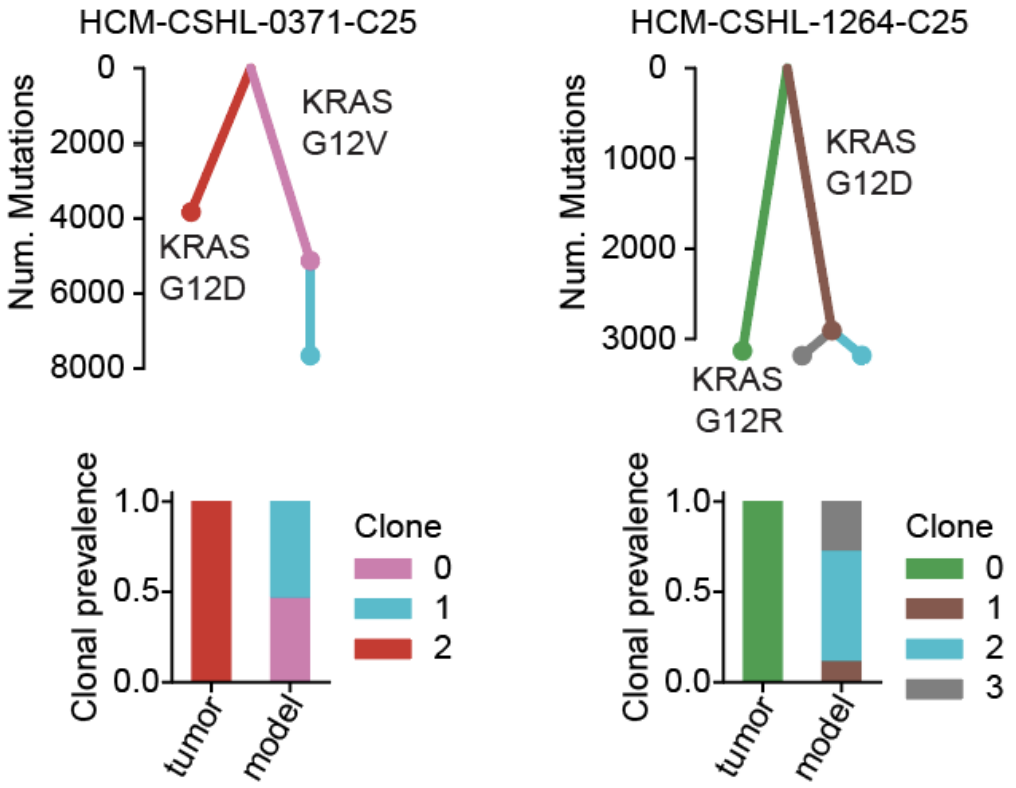
Consistency with TCGA drivers by cancer type



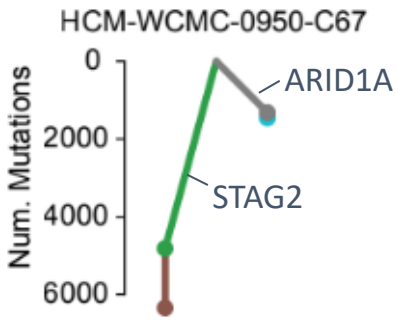
Phylogenetic analysis of tumor/model clones show generally low divergence

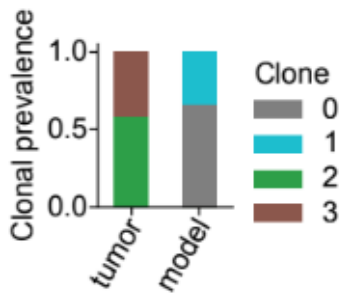


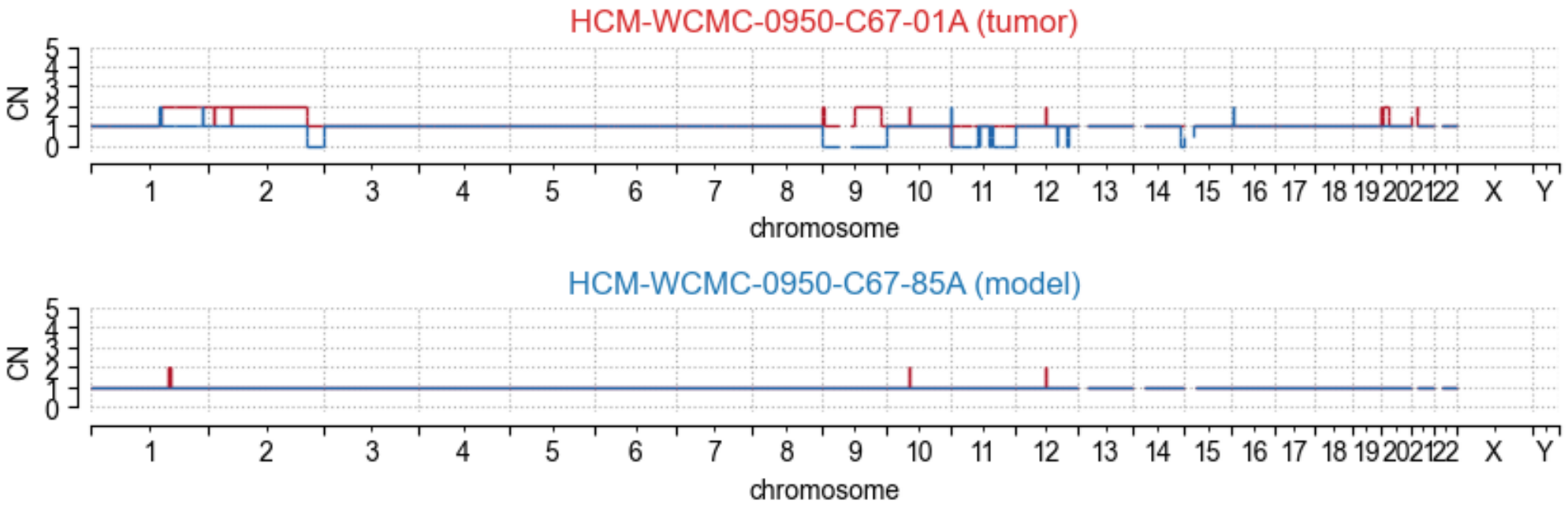
Divergence in two pancreatic adenocarcinoma driven by selection of distinct KRAS clones during model development



Selection of an independent tumor in a bladder cancer model







Conclusions

- Distribution of genetic drivers similar between HCMI and TCGA
- High genomic concordance between tumors and models
- Examples of highly divergent models reflect outgrowth of independent tumors or divergent subclones
- Importantly, most divergent models are still faithful representatives of their tumor type

Enhancing Oncology Research with ATCC's Advanced Models

Carolina Lucchesi, PhD
Principal Scientist, BioNexus, ATCC

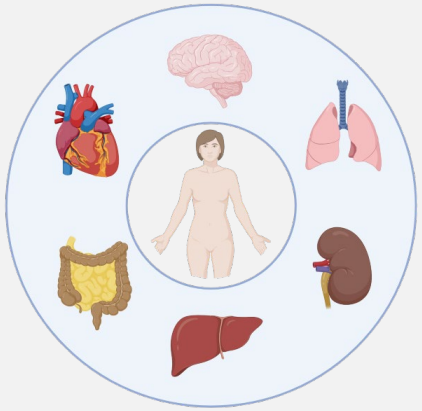
Meet the speaker

Carolina Lucchesi, PhD

Principal Scientist, BioNexus, ATCC

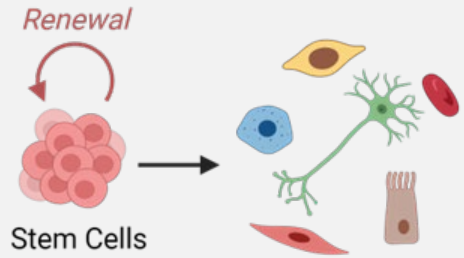
Carolina Lucchesi is BioNexus Foundation Principal Scientist leading the Microphysiological Systems program at ATCC. Dr. Lucchesi received her PhD in Cellular and Molecular Biology from the University of Campinas in Brazil and has over 20 years of experience in Tissue Engineering and Organ-on-Chip technology. In her current role, Dr. Lucchesi leads the MPS program bringing new capabilities in the use of advanced 3D models and developing existing and new content to be applied in state-of-art technologies.

Microphysiological systems program at ATCC®



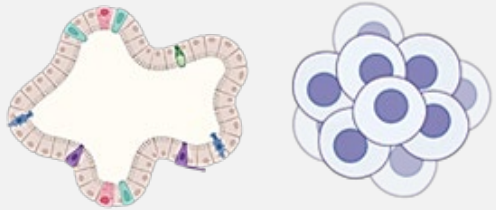
Primary Cells

- Product development
- Isolation
- Preservation
- Manufacture
- Characterization



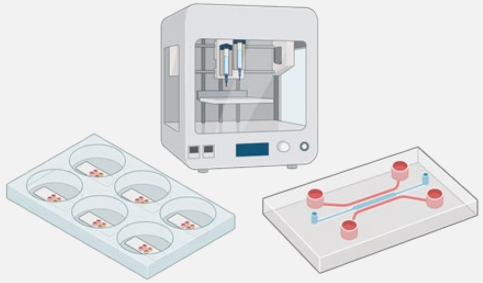
Stem Cells

- Product development
- Characterization
- Differentiation
- Functional assays



3-D Models

- Product development
- Manufacture
- Model replenishment
- Characterization



Technology

- Model development
- Characterization
- Functional assays
- Standards protocol
- Application data
- Collaboration

Created with BioRender.com

Supporting the HCMI since 2016

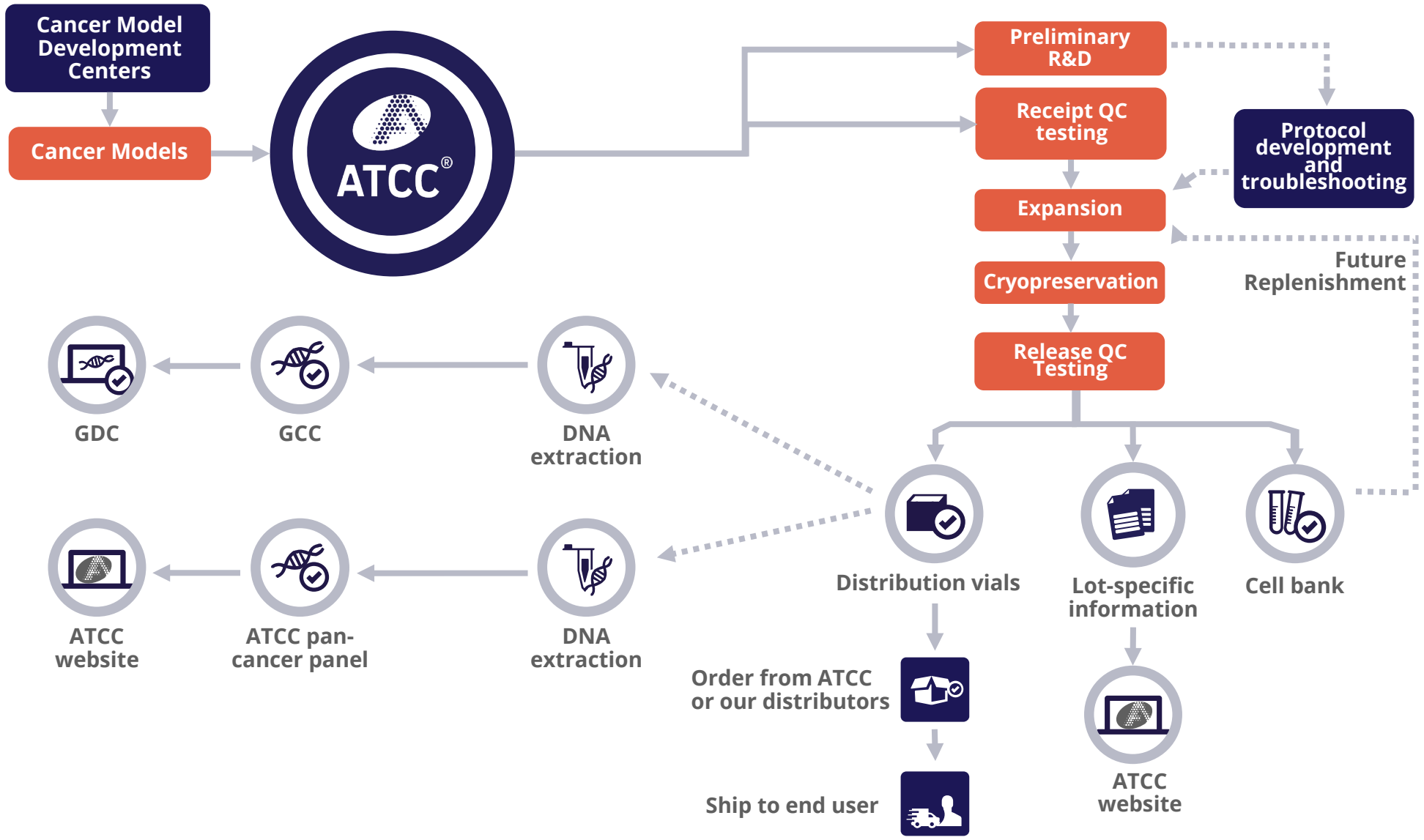
Authentication and quality control testing

Manufacturing and cell bank generation

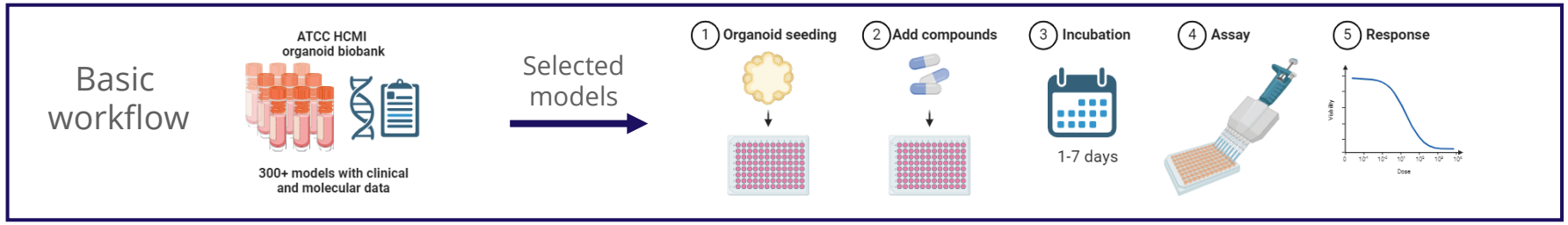
HCMI model information resource

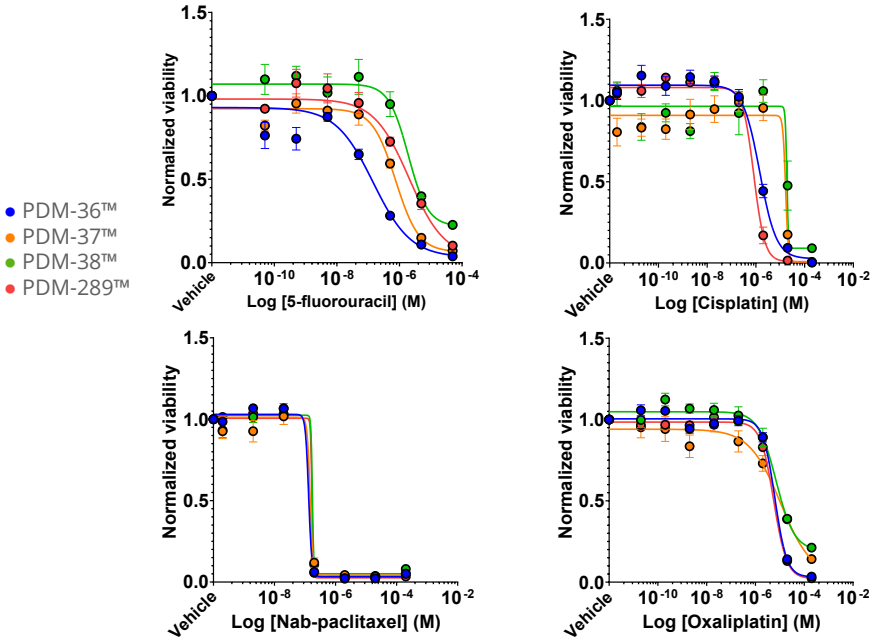
Distribution of models through the ATCC catalog

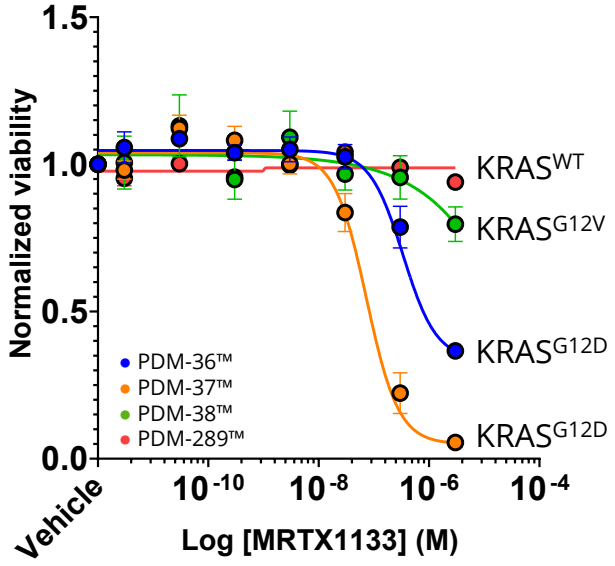
Manufacturing and cell bank generation

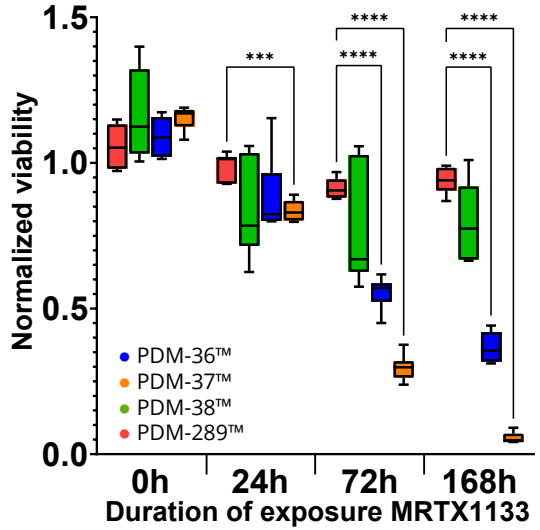


Targeting KRAS in pancreatic cancer organoids (PCOs)







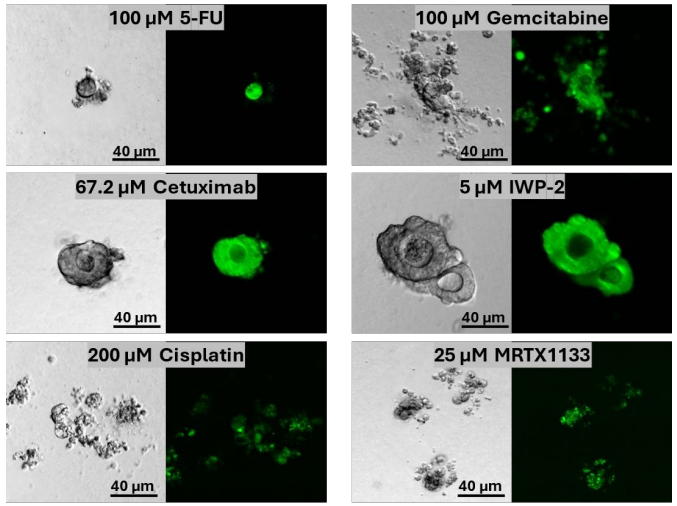


- Single agent chemotherapies (5-FU, Cisplatin, Oxaliplatin, and Nab-Paclitaxel) exhibited a clear concentration-response with significant toxicity across all models.
- MRTX1133, a small molecule inhibitor of $KRAS^{G12D}$, exhibited increased toxicity in PCOs harboring KRAS mutations with a greater effect in G12D vs. G12V.

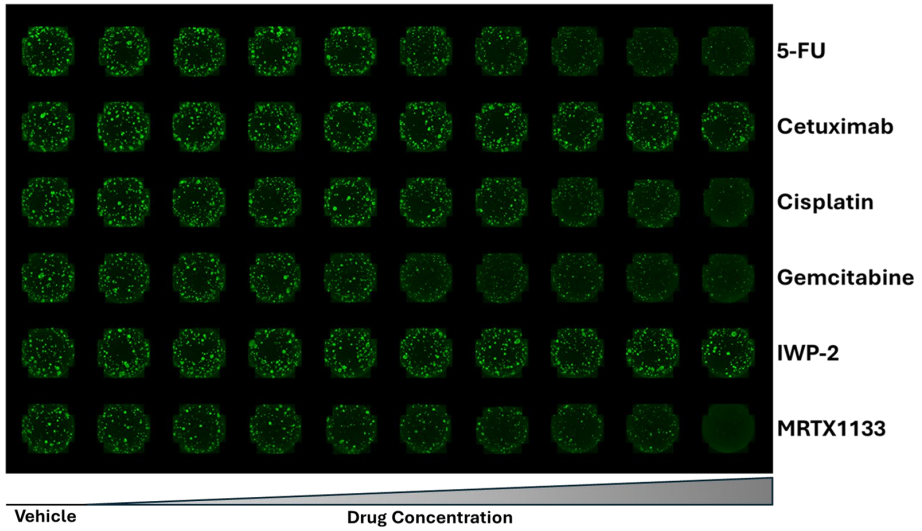
Assessing MRTX1133 as a selective KRAS-G12D inhibitor

ATCC®

ATCC® PDM-43™

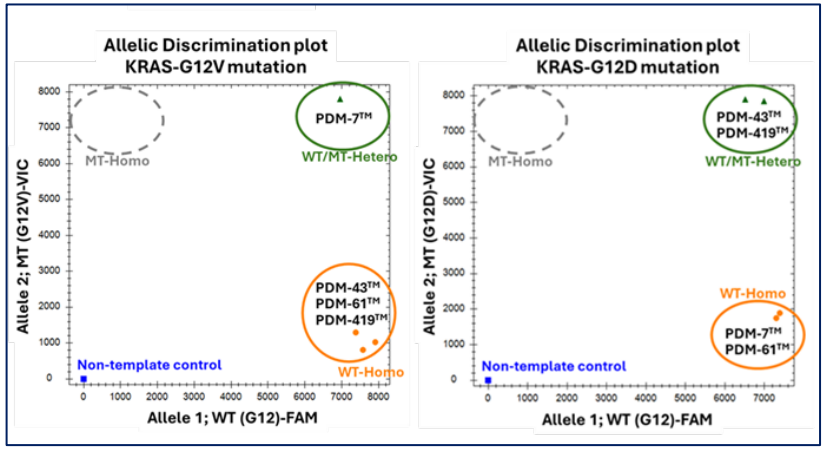


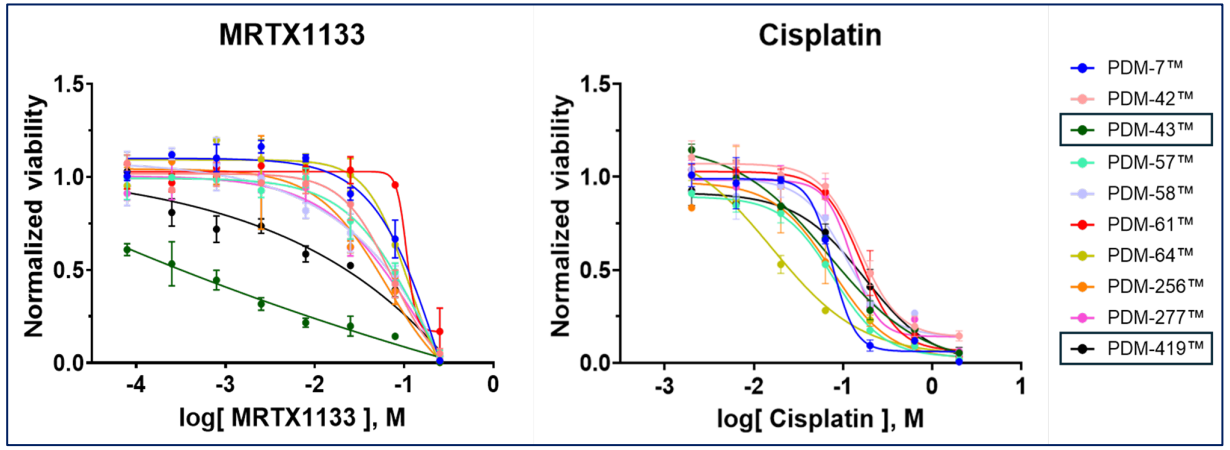
ATCC® PDM-43™



Matthew Graziano

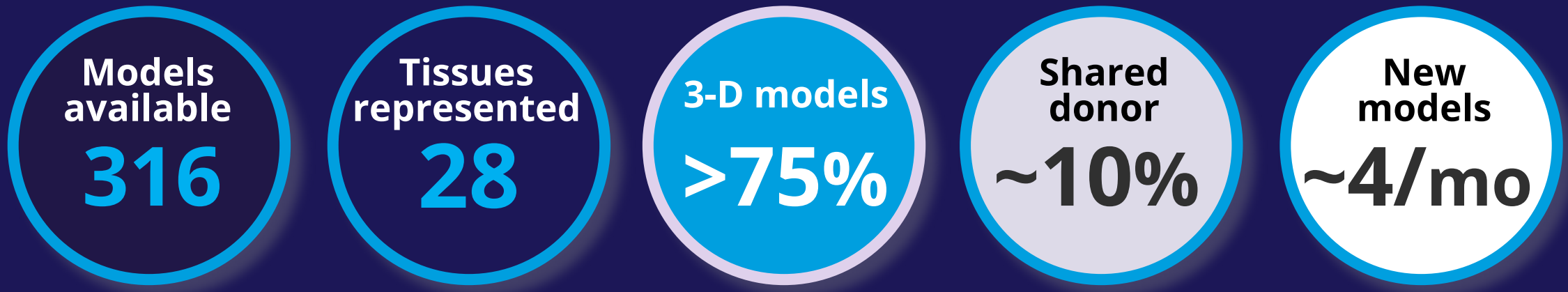
Poster presentation
Tuesday, April 29
2:00-5:00 PM
Poster Board:17





- The allelic discrimination plots confirm KRAS-G12D and KRAS-G12V mutation in selected CCOs.
- KRAS-G12D mutated CCOs (ATCC® PDM-43™ and ATCC® PDM-419™) are more sensitive to MRTX1133.

HCMI models in the ATCC® catalog



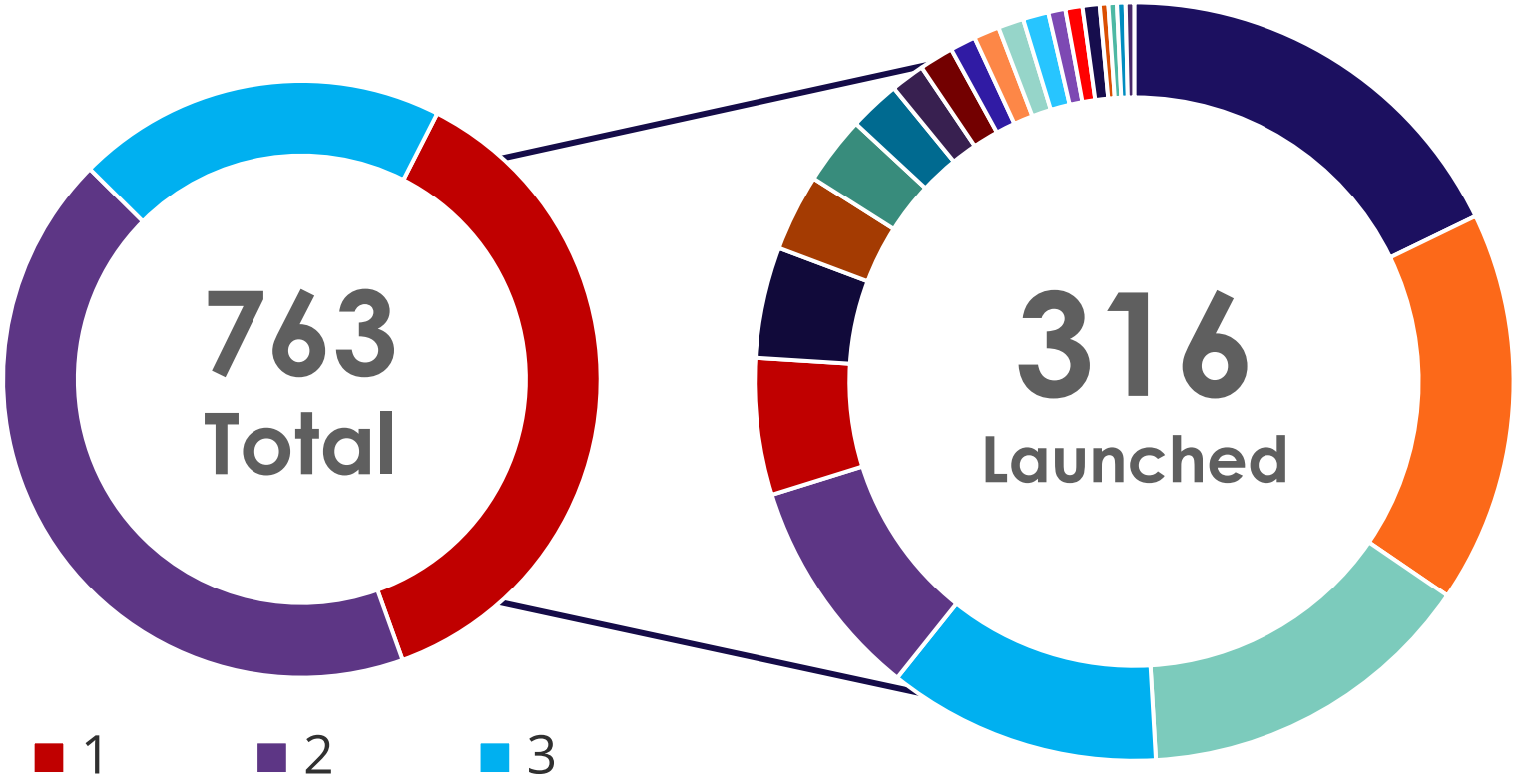
Recent releases

First head and neck cancer model
First desmoid tumor cell line

In the production pipeline

Additional lung, breast, endometrial, ovarian, kidney and first bladder models

HCMI portfolio model diversity



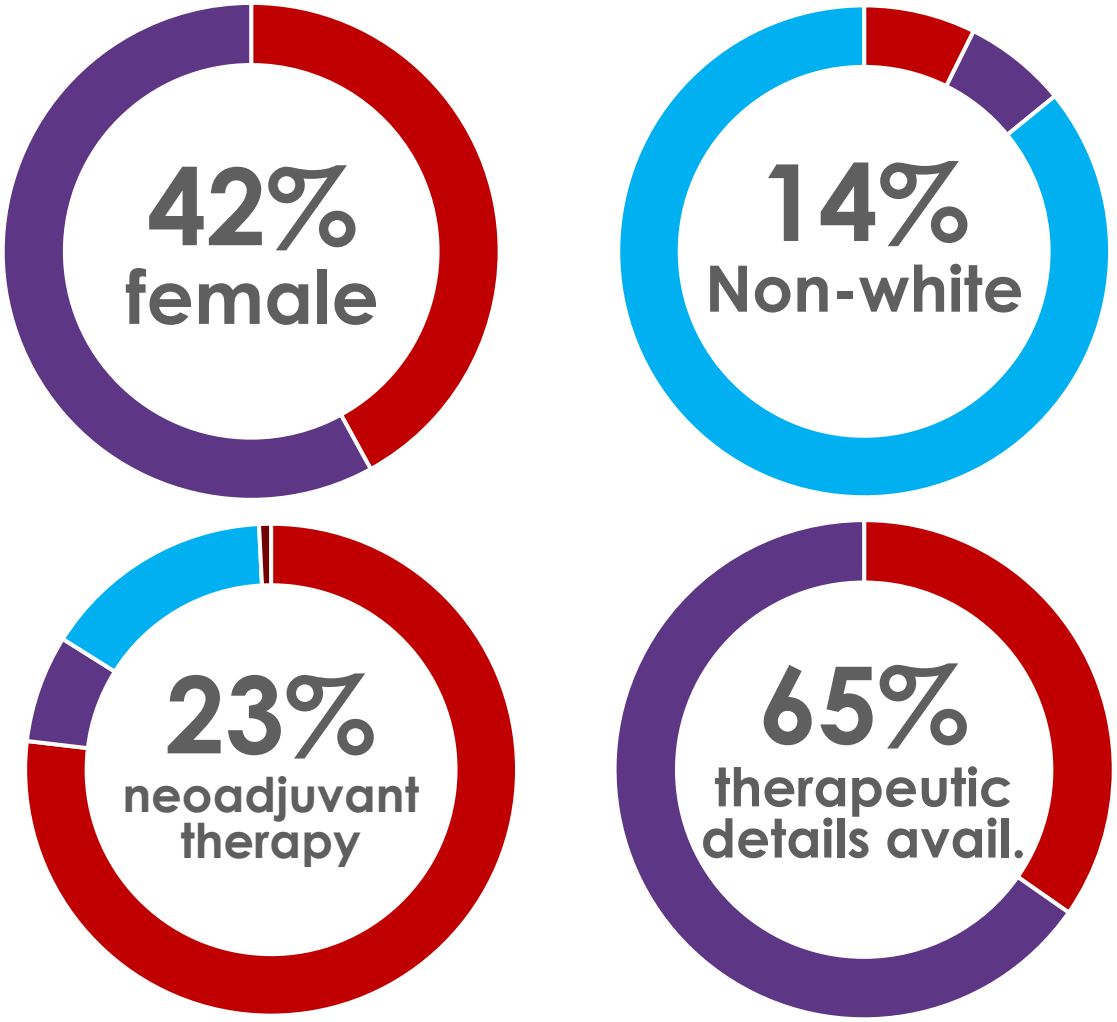
TOP 10 (90% of total)

Colon	55
Pancreas	52
Brain	50
Esophagus	36
Skin	29
Rectum	21
Stomach	18
Lung	7
Breast	7
Connective tissue	5

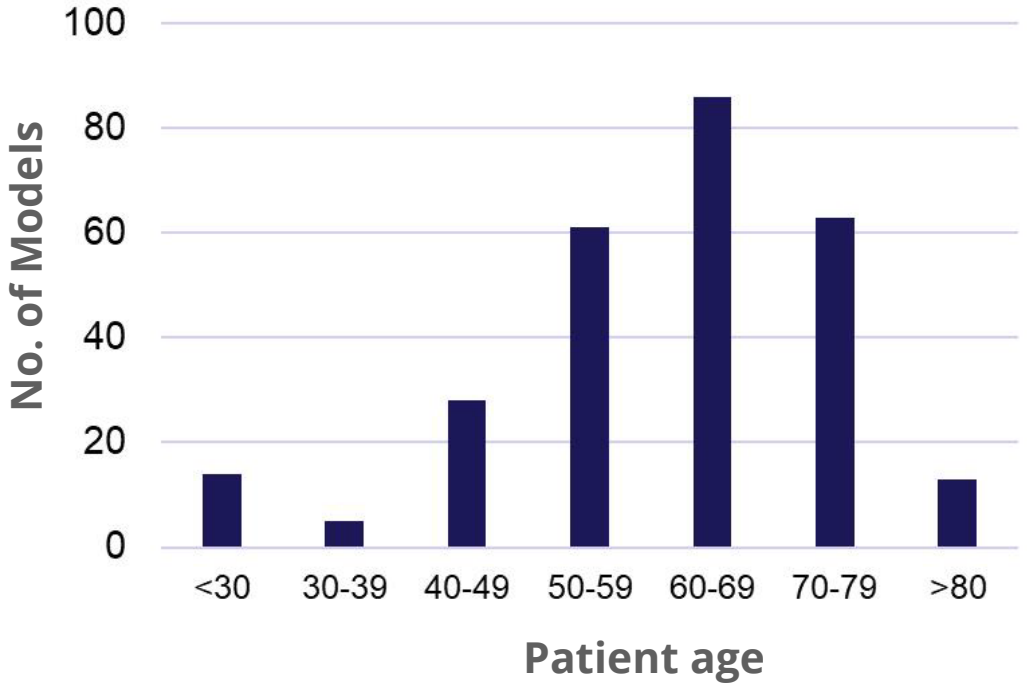
Collection includes models derived from rare adult and pediatric cancers such as rhabdomyosarcoma, leiomyosarcoma, Ewing sarcoma, and Wilms tumor.

Explore the HCMI portfolio

HCMI portfolio clinical and demographic characteristics



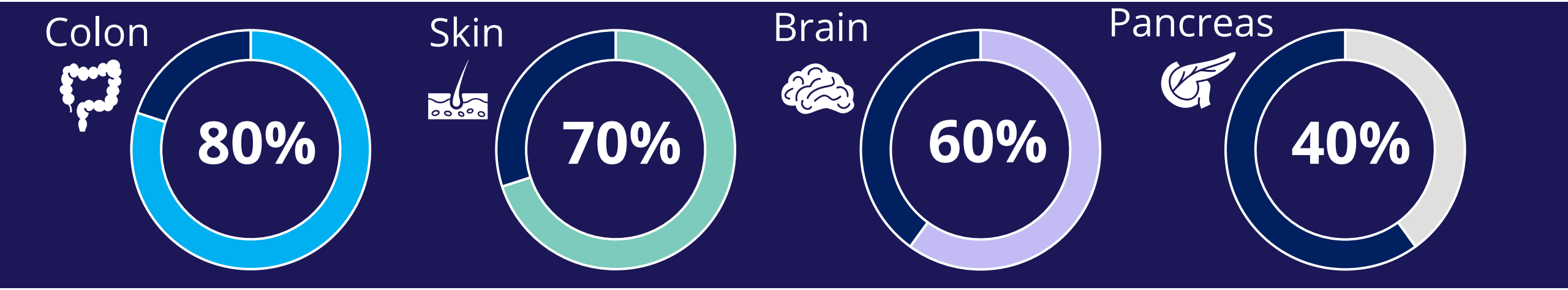
Age distribution



Additionally, 15 pediatric models recently acquired by ATCC®

HCMI data aligns with patient genotypes

Top 10 frequently mutated genes vs. The Cancer Genome Atlas



Top 10 genes captured in the HCMI models

APC	LRP1B
TP53	ZFHX4
KRAS	CSMD3
MUC16	ROBO2
FAT4	ALK

TP53, BRAF, NRAS, NF1	
MUC16	GRIN2A
LRP1B	MECOM
CSMD3	FAT4
FAT3	DCC
FAM135B	COL1A1

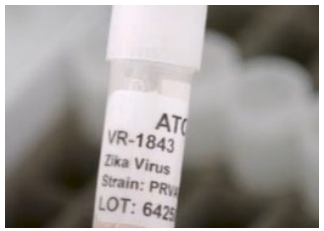
PTEN	PIK3CA
TP53	CSMD3
EGFR	BCOR
CNTNAP2	NF1
PIK3CR1	FAT1

KRAS	MUC4
TP53	MUC16
SMAD4	KMT2D
CDKN2A	FAT3
ACVR2A	RHOH

Canonical mutation	Matching mutation

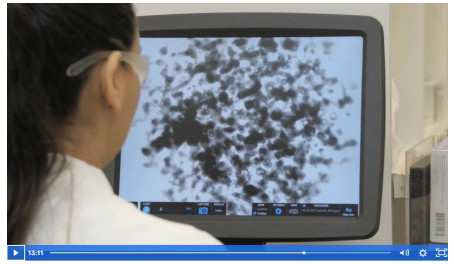
HCMI model information resource

Validated companion reagents



- Seven HCMI model formulation-specific reagent kits
- Extracellular matrix
- Growth factor secreting cell lines

Video protocols, other educational resources



Also, application notes, webinars, poster presentations, and troubleshooting tips.

Help us prioritize future HCMI model releases

Hundreds of models have not yet entered the ATCC® HCMI manufacturing pipeline

Browse and search unreleased HCMI models at ATCC®

- Use the “Submit your Input” button on the HCMI Landing page

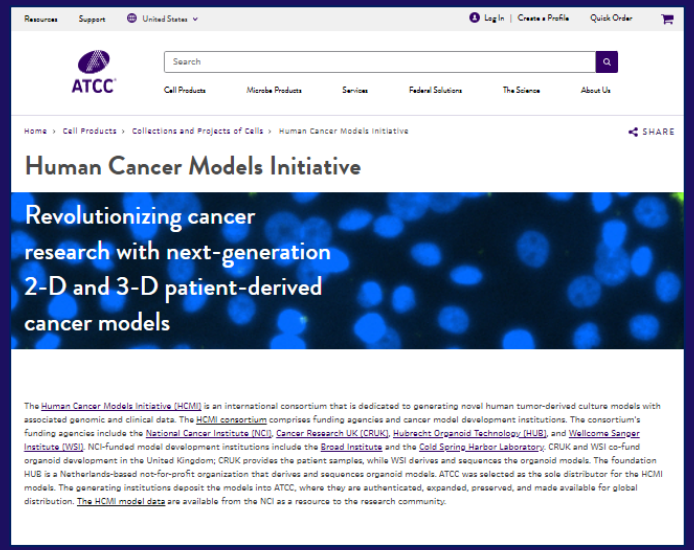
  Direct link: www.atcc.org/hcmi-input

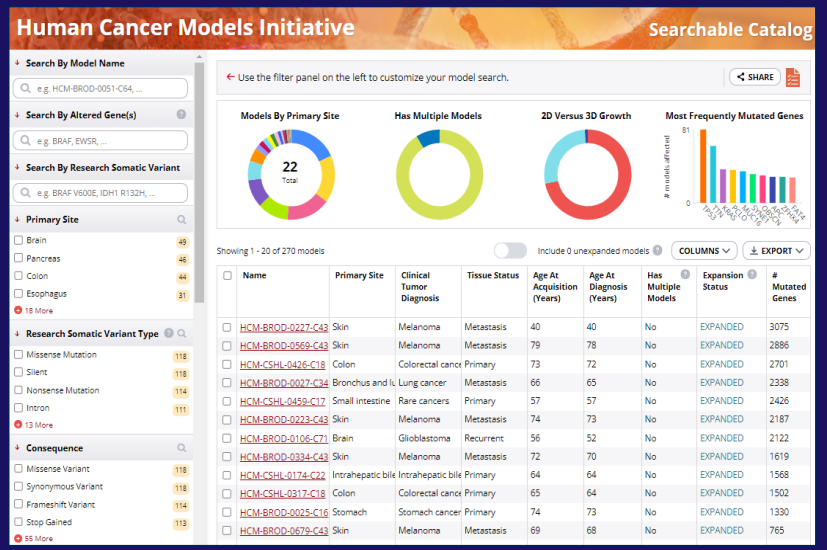
- *Coming soon*: Look for “Expansion Status” on the HCMI Searchable Catalog

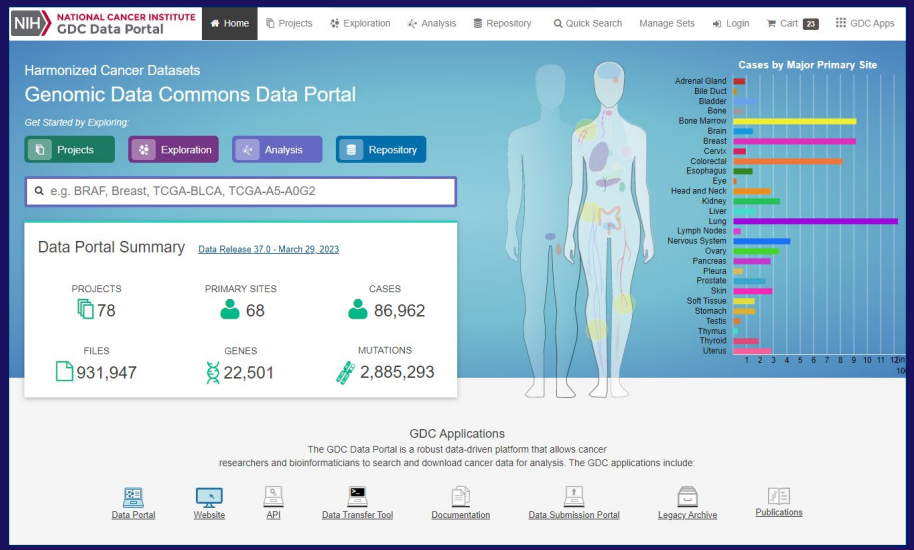
Email us which HCMI models are most relevant for your research

✉ hcmi@atcc.org

Resources to learn more about ATCC® and the HCMI







Find HCMI models

Browse the HCMI Searchable Catalog

Explore the NCI Genomic Data Commons

ATCC®

CREDIBLE LEADS TO INCREDIBLE

Thank You