



# **Proteogenomic Characterization of Muscle Invasive Bladder Cancer to Identify Mechanisms of Resistance and Targets for Therapy**

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Baylor College of Medicine

# Disclosures

- Clinical trials
  - Endo, FKD, JBL (SWOG), Roche/Genentech (SWOG), UroGen, Viventia
- Advisory Board/Consultant
  - Anchiano Therapeutics, Ferring, Genentech, QED Therapeutics, UroGen, Vaxiion
- Honoraria
  - Dava Oncology, MSD Korea, Nucleix

# Innovation Award

- Bladder Cancer Research Network (BCRN)
- BCAN
- “Exceptionally novel and creative with great potential to produce breakthroughs in our understanding of the management of bladder cancer”
  - High-risk and high-reward
- Additional funding:
  - CPRIT PDX Pilot project
  - Philanthropy – WES, RNAseq

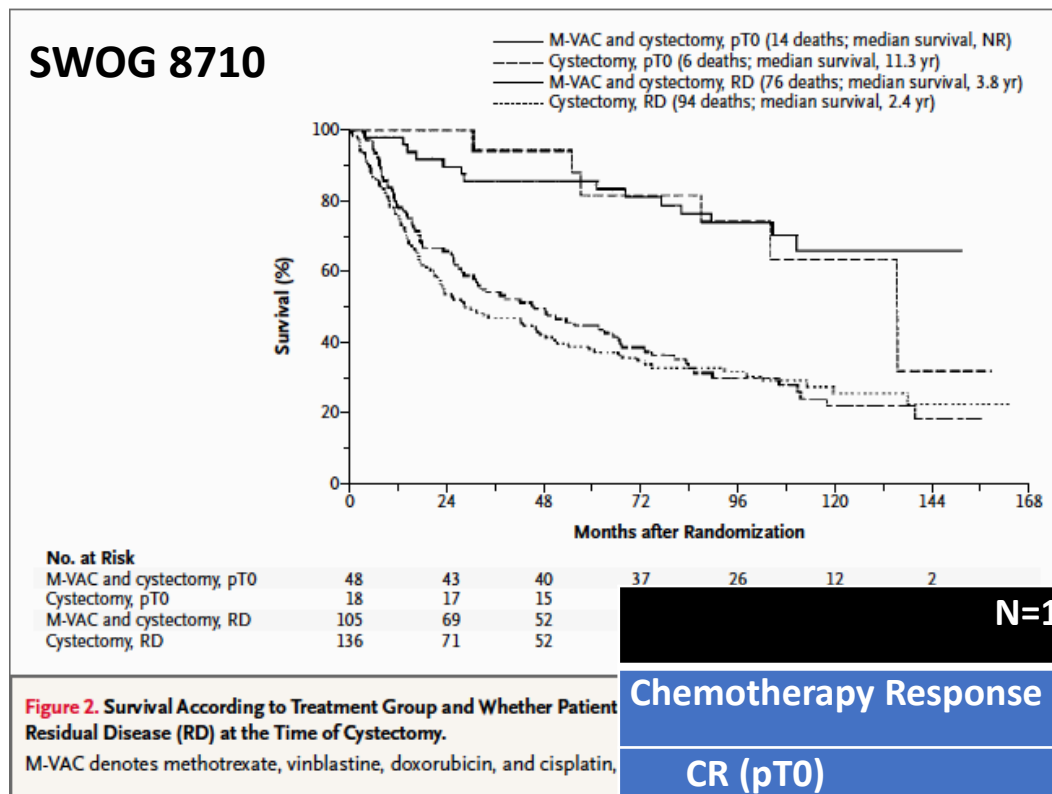
# The Team

- Proteomics Core
  - Anna Malovanaya, Hamssika Chandrasekaran, Sung Jung
- Ellis group
  - Mathew Ellis, Bing Zhang, Beom-Jun Kim (KiP)
  - David Wheeler (WES and RNAseq)
- Genome Center
  - Marie-Claude Gingras
- Mouse PDX
  - Keith Chan, Lacey Dobrolecki, Michael Lewis (PI Core)
- CAM PDX
  - Hugo Vilanueva, Mariana Vilanueva, Ravi Pathak, Andrew Sikora (PI Core)
- Pathology/HTAP
  - Mike Ittman, Patricia Castro
- Urology
  - Karoline Kremers (project mgr), Weiguo Jian, Amanda Watters
- Collaborators (Biospecimens)
  - Lars Dyrskjot (Aarhus, Denmark)
  - Kurshid Guru (Roswell Park)
  - John Taylor (Kansas U)
  - Joshua Meeks (Northwestern)
- Mouse PDX
  - Chong-Xian Pan (UC Davis)

# Rationale – MIBC Integrated Therapy

- MIBC
  - L1 evidence for cisplatin-based NAC
  - No evidence of non-cisplatin-based NAC
- RR in cisplatin-based NAC
  - 50% path response
  - 40% pT0
  - Not a validated endpoint
  - OS absolute margin of benefit < 10%
- Unmet need
  - If 50% eligible and 50% of eligible respond then 75% of patients have no effective integrated treatment options supported by L1 evidence.
  - *Our treatments fail these patients (DZQ)*

Patients with residual muscle invasive cancer following NAC have poor outcomes and there is no standard of care for these patients



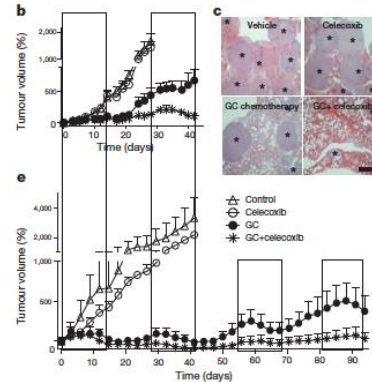
## SWOG 1314 - COXEN

|                               | N=167 | GC (N=82) | ddMVAC (N=85) |
|-------------------------------|-------|-----------|---------------|
| <b>Chemotherapy Response</b>  |       |           |               |
| <b>CR (pT0)</b>               |       | 28 (35%)  | 27 (32%)      |
| <b>PR (downstaged to ≤T1)</b> |       | 12 (15%)  | 20 (24%)      |
| <b>CR + PR</b>                |       | 40 (50%)  | 47 (56%)      |
| <b>Non-responders</b>         |       | 42 (50%)  | 38 (44%)      |

Grossman, et al NEJM 349:859, 2003

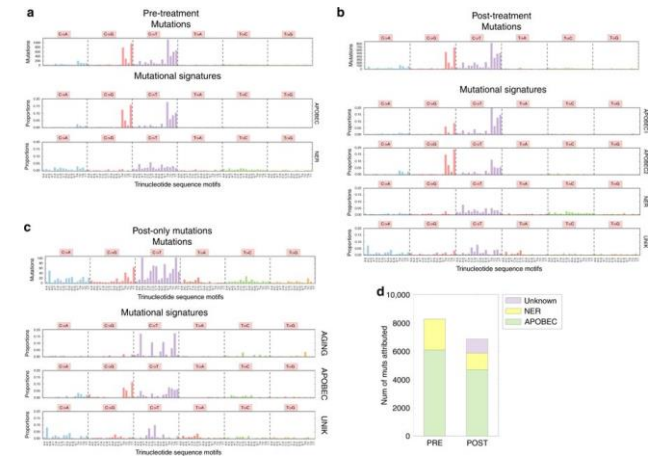
# Resistance pathways

- Wound repair



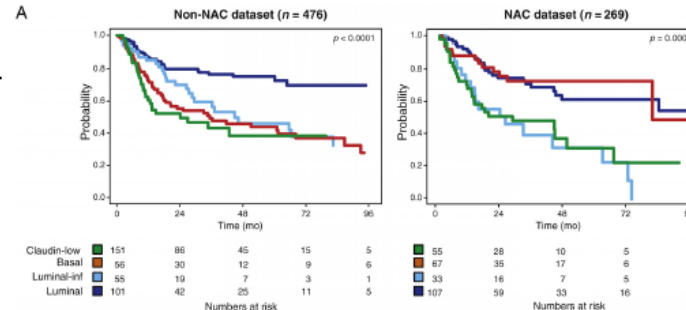
Kurtova, et al Nature  
517:209, 2015

- Cisplatin resistance signature



- Expression subtype

Seiler, et al Eur  
Urol 72:544,  
2017



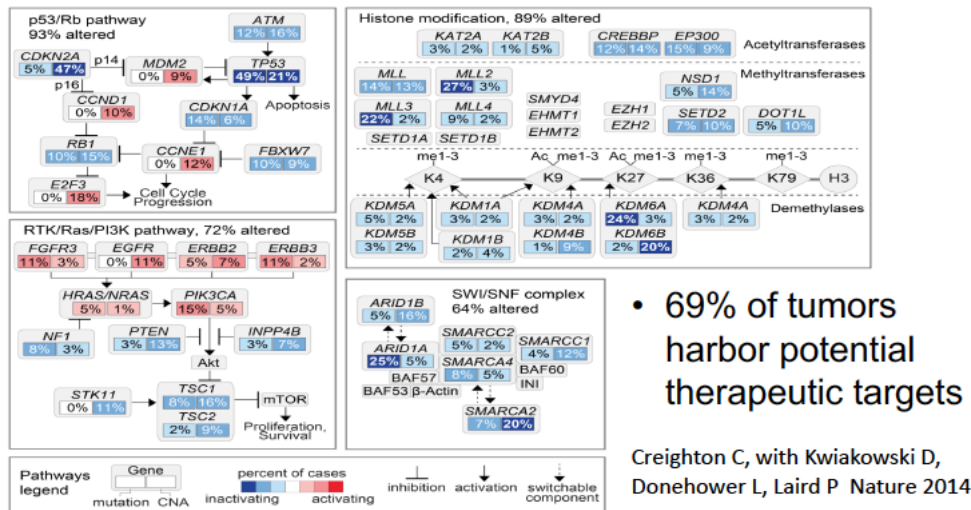
Liu, et al Nature Comm 8:2193, 2017



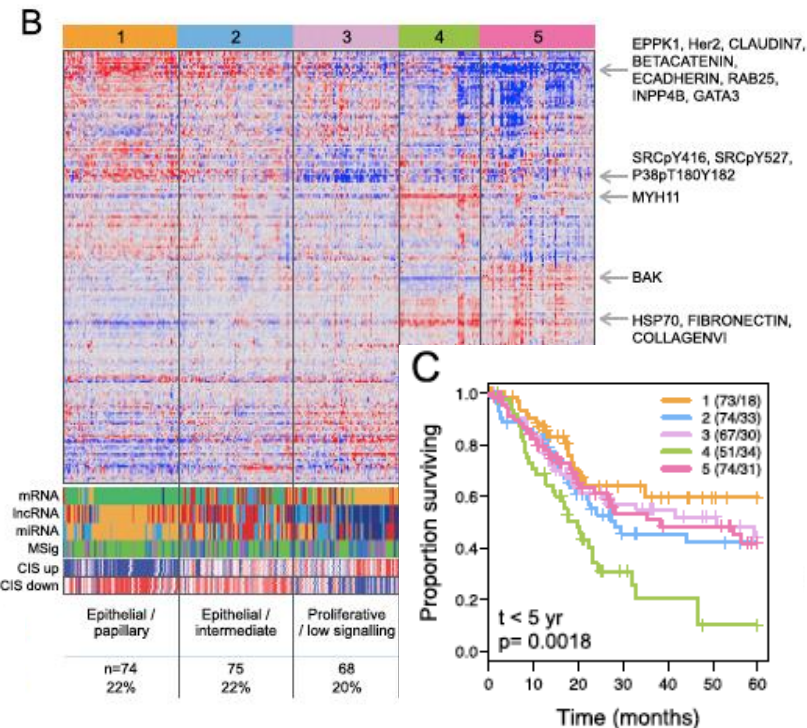
# Alternative Integrated Treatment Options

- Immunotherapy
- Chemotherapy/Immunotx
- Targeted therapy/TKI

## Altered Pathways in Bladder Cancer: Mutation/CNA



## TCGA: RPPA 208 antibodies



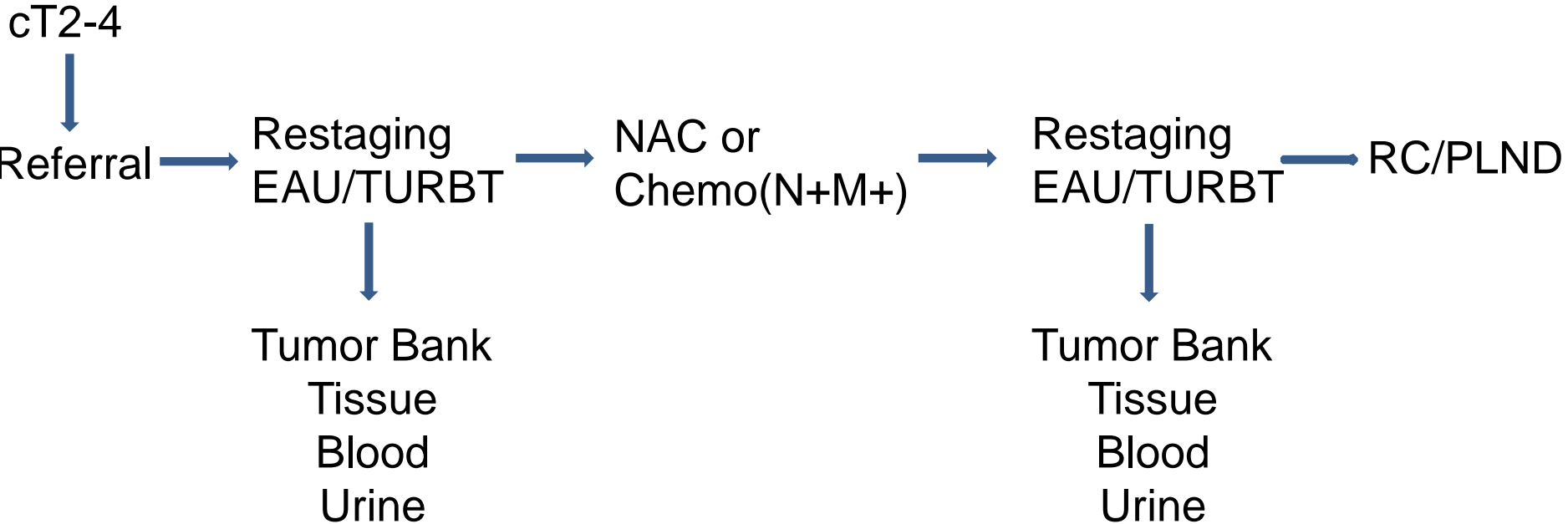


# Hypothesis

- Integrated analysis of proteomics and genomics of primary muscle invasive bladder cancer (MIBC) and their patient-derived xenografts (PDX) will define mechanisms responsible for chemotherapy resistance and identify candidate driver genes leading to the identification of specific targeted therapies for those resistant to the current standard of care.

# Biobanking

## Clinical and banking workflow

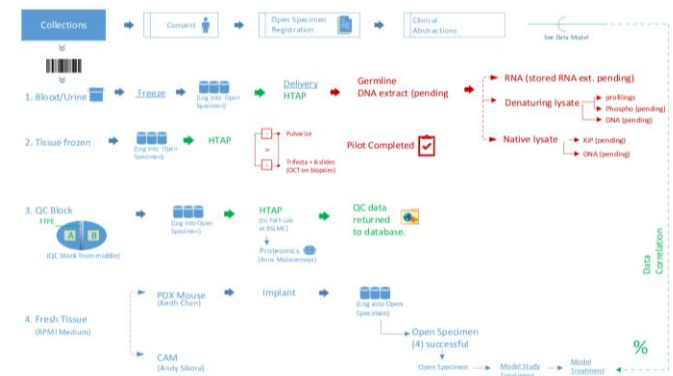


OpenSpecimen

Quick search for specimens, containers, and others...

Administration Biobanking Search Seth Lerner

| Collection Protocol                        | Dashboard        | Reports | Report Scheduler |
|--|------------------|---------|------------------|
| Bladder Collection                         |                  |         |                  |
| Participant                                |                  |         |                  |
| Select Participant                         |                  |         |                  |
| + Register Participant                     | View Participant |         |                  |
| <b>Participant Details</b>                 |                  |         |                  |
| Registered Participants                    | 414              |         |                  |
| Consented Participants                     | 329              |         |                  |
| Male Participants                          | 284              |         |                  |
| Female participants                        | 78               |         |                  |
| <b>SCG Details</b>                         |                  |         |                  |
| Total Completed Specimen Collection Groups | 535              |         |                  |
| Pending Specimen Collection Groups         | 340              |         |                  |
| <b>Specimen Details</b>                    |                  |         |                  |
| Pending Specimens as of today              | 0                |         |                  |
| Available Specimens                        | 2794             |         |                  |
| Fluid Specimens                            | 1758             |         |                  |
| Tissue Specimens                           | 1125             |         |                  |
| Cell Specimens                             | 0                |         |                  |



# Cohort Annotation

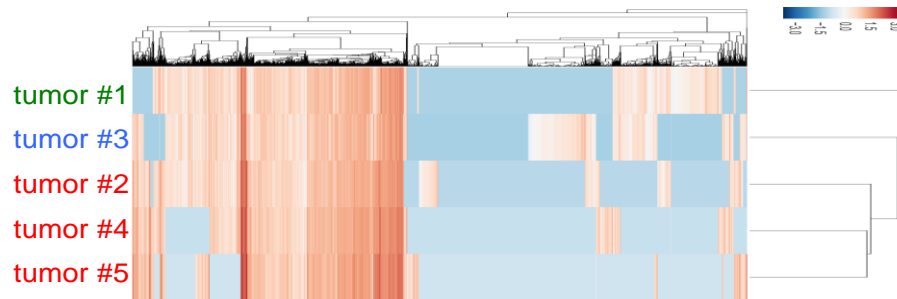
- Target n = 80
- Pre-NAC or pre-Chemotherapy N+/M+
- Fresh tissue from TURBT
  - Prior BCG allowed
  - No prior systemic therapy
- QC GU pathologist
- Minimum >50% tumor cellularity
- Urothelial, NOS
- Variants: Small cell, plasmacytoid, SCCa

## Tissue Source Sites

- BCM
- Aarhus (Lars Dyrskjot)
- Buffalo (Khurshid Guru)
- University of Kansas (John Taylor)
- Northwestern (Josh Meeks)

# Preliminary Data

(A) Proteomics Expression Clusters of 5 Bladder Cancer Samples.



Anna Malovannaya  
Hamssika Chandrasekaran  
Sung Jung

(B) DNA and cell cycle biology overexpressed in Tumor #3.

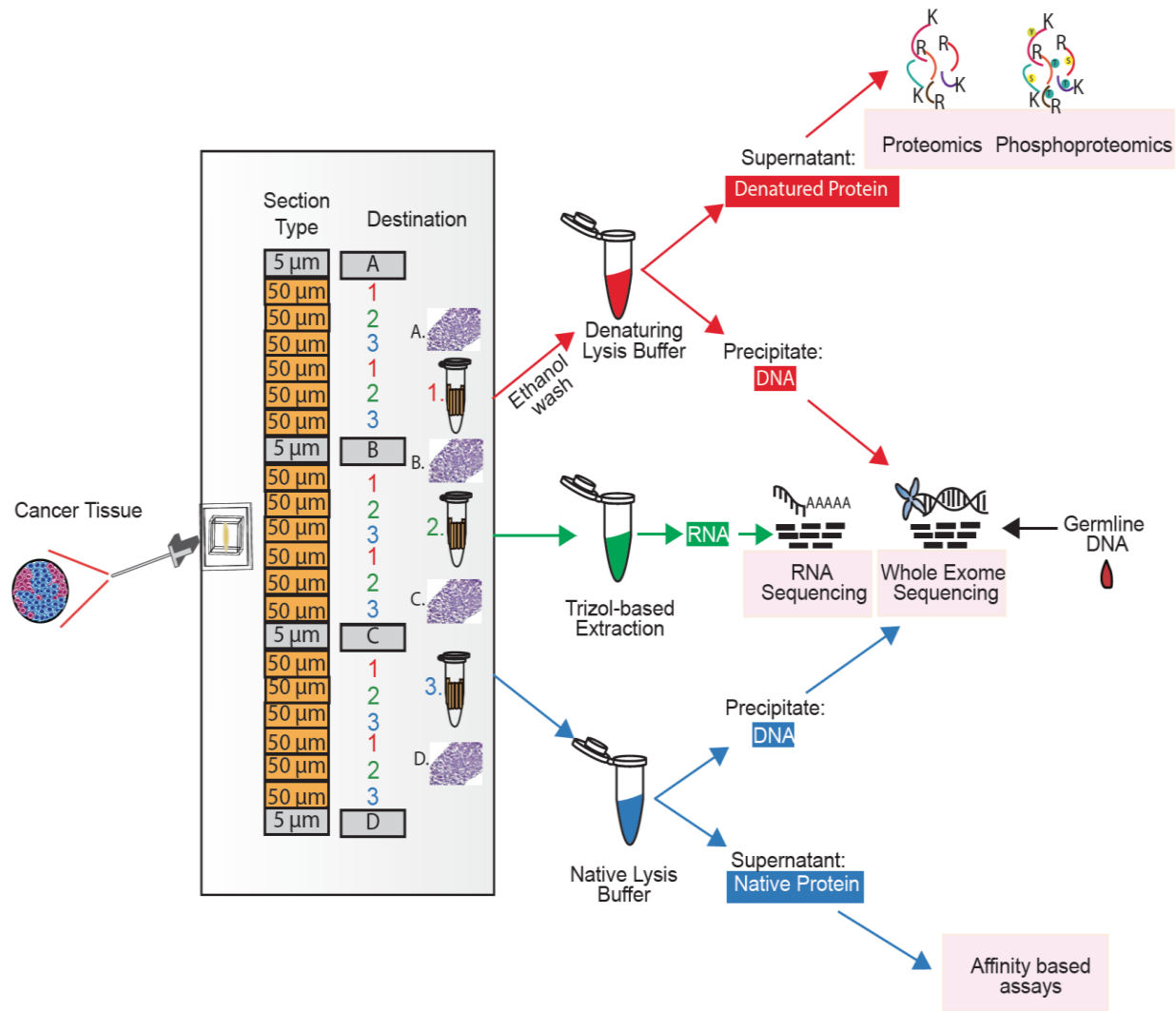
| Symbol | tumor #1 |        |      |       |      |       | tumor #2 |        |      |       |      |       | tumor #3 |        |      |       |      |       | tumor #4 |        |       |       |      |       | tumor #5 |        |       |       |      |       |
|--------|----------|--------|------|-------|------|-------|----------|--------|------|-------|------|-------|----------|--------|------|-------|------|-------|----------|--------|-------|-------|------|-------|----------|--------|-------|-------|------|-------|
|        | PSMs     |        | AUC7 |       |      |       | PSMs     |        | AUC7 |       |      |       | PSMs     |        | AUC7 |       |      |       | PSMs     |        | AUC7  |       |      |       | PSMs     |        | AUC7  |       |      |       |
|        | SRA      | Pepits | abs  | ratio | abs  | ratio | SRA      | Pepits | abs  | ratio | abs  | ratio | SRA      | Pepits | abs  | ratio | abs  | ratio | SRA      | Pepits | abs   | ratio | abs  | ratio | SRA      | Pepits | abs   | ratio | abs  | ratio |
| HMG2   |          |        |      |       |      |       |          |        |      |       |      |       | 5        | 22     | 1000 | 1035  | 1000 |       |          |        |       |       |      |       |          |        |       |       |      |       |
| SMC2   | ●        | 1      | 1    |       |      |       |          |        |      | 0.001 | 1    |       | 44       | 69     | 69   | 430   | 1000 |       |          |        | 0.001 | 1     |      |       |          |        |       | 0.001 | 1    |       |
| SMC4   |          |        |      |       |      |       |          |        |      |       | 1    |       | 46       | 72     | 1000 | 341   | 1000 |       |          |        | 1     |       |      |       |          |        | 1     |       | 1    |       |
| TYMS   |          |        |      |       |      |       |          |        |      |       | 1    |       | 12       | 27     | 1000 | 335   | 1000 |       |          |        | 1     |       |      |       |          |        | 1     |       | 1    |       |
| MDC1   | ●        | 4      | 4    |       |      |       |          |        |      | 0.001 | 1    |       | 37       | 56     | 14   | 216   | 1000 |       |          |        | 0.001 | 1     |      |       |          |        | 0.001 | 1     |      |       |
| NCAPD2 |          |        |      |       |      |       |          |        |      |       | 1    |       | 37       | 55     | 1000 | 212   | 1000 |       |          |        | 1     |       |      |       |          |        | 1     |       | 1    |       |
| CCNB1  |          |        |      |       |      |       |          |        |      |       | 1    |       | 7        | 8      | 1000 | 24.8  | 1000 |       |          |        | 1     |       |      |       |          |        | 1     |       | 1    |       |
| RFC4   | ●        | 4      | 5    |       | 2.3  |       | ●        | 1      | 1    | 0.2   | 0.15 | 0.07  | 14       | 22     | 4.4  | 195   | 67.4 |       | ●        | 2      | 2     | 0.4   | 0.43 | 0.19  | ●        | 2      | 4     | 0.8   | 0.21 | 0.09  |
| MSH6   | ●        | 8      | 8    |       | 12.6 |       | ●        | 1      | 1    | 0.13  |      | 0.001 | 24       | 39     | 4.9  | 252   | 20   |       | ●        | 1      | 1     | 0.13  |      | 0.001 | ●        | 2      | 2     | 0.25  | 0.95 | 0.08  |

(C) Druggable kinases overexpressed in Tumor #3.

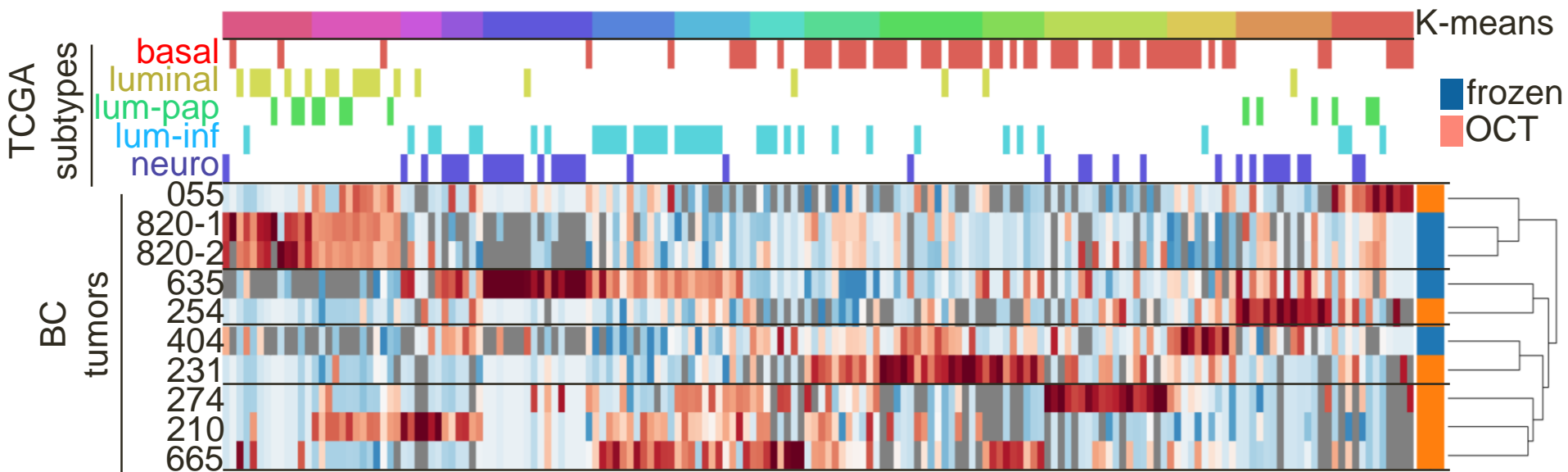
| Symbol | tumor #1 |        |       |      |       |      | tumor #2 |        |     |       |       |       | tumor #3 |        |       |      |       |      | tumor #4 |        |     |       |      |       | tumor #5 |        |       |       |       |       |       |
|--------|----------|--------|-------|------|-------|------|----------|--------|-----|-------|-------|-------|----------|--------|-------|------|-------|------|----------|--------|-----|-------|------|-------|----------|--------|-------|-------|-------|-------|-------|
|        | SRA      | Pepits |       | PSMs |       | AUC7 | SRA      | Pepits |     | PSMs  |       | AUC7  | SRA      | Pepits |       | PSMs |       | AUC7 | SRA      | Pepits |     | PSMs  |      | AUC7  | SRA      | Pepits |       | PSMs  |       | AUC7  |       |
|        |          | abs    | ratio | abs  | ratio | abs  |          | ratio  | abs | ratio | abs   | ratio |          | abs    | ratio | abs  | ratio | abs  |          | ratio  | abs | ratio | abs  | ratio |          | abs    | ratio | abs   | ratio | abs   | ratio |
|        |          |        |       |      |       |      |          |        |     |       |       |       |          |        |       |      |       |      |          |        |     |       |      |       |          |        |       |       |       |       |       |
| BTK    | ●        | 1      |       | 1    |       |      |          |        |     |       | 0.001 | 1     |          | 3      | 4     | 4    | 3.5   | 1000 |          |        |     | 0.001 | 1    |       | 2        | 2      | 2     | 1     |       |       |       |
| ATR    |          |        |       |      |       |      |          |        |     |       | 1     |       | 2        | 2      | 1000  | 1.3  | 1000  |      |          |        | 1   |       | 1    | ●     | 1        | 1      | 1000  | 1     |       |       |       |
| AURKA  |          |        |       |      |       |      |          |        |     |       | 1     |       | 1        | 1      | 1000  | 1.2  | 1000  |      |          |        | 1   |       | 1    |       |          |        | 1     |       | 1     |       |       |
| CSF1R  |          |        |       |      |       |      |          |        |     |       | 1     |       | 1        | 1      | 1000  | 0.65 | 1000  |      |          |        | 1   |       | 1    |       |          |        | 1     |       | 1     |       |       |
| CDK6   | ●        | 3      | 3     |      | 2.3   |      | ●        | 3      | 4   | 1.3   | 16.2  | 7     | 7        | 7      | 2.3   | 54.2 | 23.6  |      | ●        | 1      | 1   | 0.33  |      | 0.001 | ●        | 1      | 3     | 1     |       | 0.001 |       |
| ABL1   | ●        | 2      | 2     |      | 0.06  |      | ●        | 1      | 1   | 0.5   |       | 0.001 | 4        | 4      | 2     | 1.4  | 23.3  |      | ●        | 1      | 1   | 0.5   | 0.56 | 9.3   |          |        |       | 0.001 |       | 0.001 |       |
| CDK4   | ●        | 5      | 6     |      | 2.8   |      | ●        | 3      | 4   | 0.67  | 16    | 5.7   | 7        | 11     | 1.8   | 47.1 | 16.8  |      | ●        | 1      | 1   | 0.17  |      | 0.001 | ●        | 3      | 5     | 0.83  | 8.9   | 3.2   |       |
| EGFR   | ●        | 7      | 8     |      | 20.8  |      | ●        | 13     | 16  | 2     | 29.6  | 1.4   | 15       | 23     | 2.9   | 88.5 | 4.3   |      | ●        | 5      | 6   | 0.75  | 3.1  | 0.15  | 4        | 4      | 0.5   | 3.9   | 0.19  |       |       |
| MAP2K1 | ●        | 10     | 20    |      | 63    |      | ●        | 10     | 12  | 0.6   | 51.2  | 0.81  | 13       | 22     | 1.1   | 149  | 2.4   |      | ●        | 5      | 8   | 0.4   | 30.7 | 0.49  | 6        | 12     | 0.6   | 23.2  | 0.37  |       |       |
| LYN    | ●        | 5      | 7     |      | 48.6  |      | ●        | 9      | 11  | 1.6   | 29.3  | 0.6   | 14       | 18     | 2.6   | 97.1 | 2     |      | ●        | 5      | 5   | 0.71  | 7    | 0.14  | 5        | 8      | 1.1   | 17.9  | 0.37  |       |       |

No photos  
No social media

# Biopsy Trifecta Extraction (BioTExt)



## Compared to TCGA subtype signatures



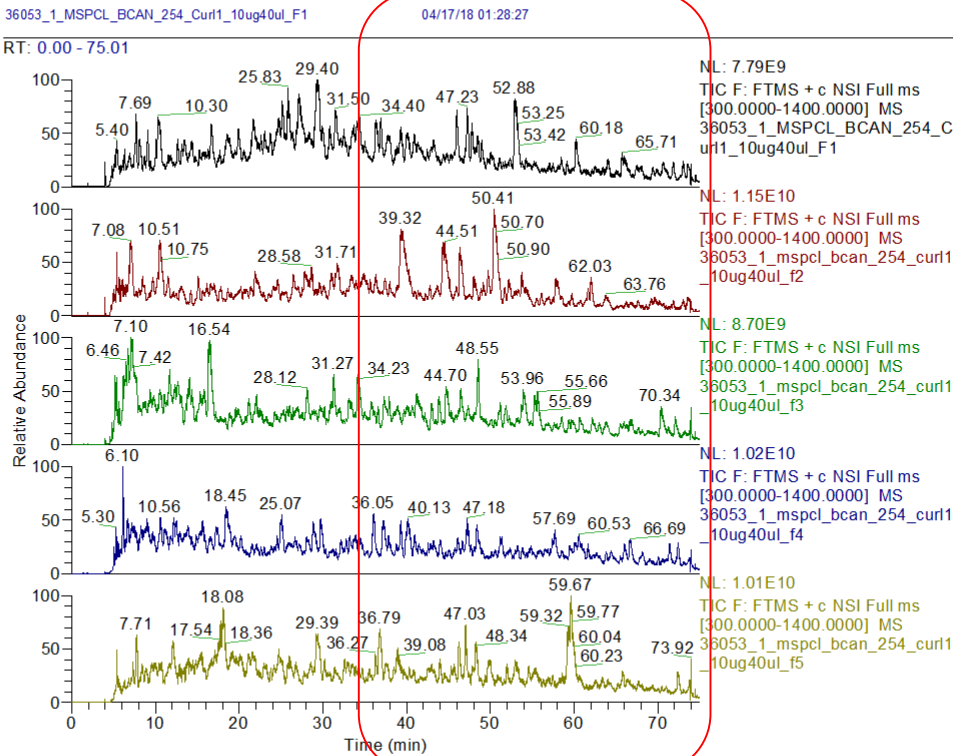
- by total profiles also largely along these lines
- finer heterogeneity evident in proteomics data

- about 50% of samples give much lower recovery numbers – why?



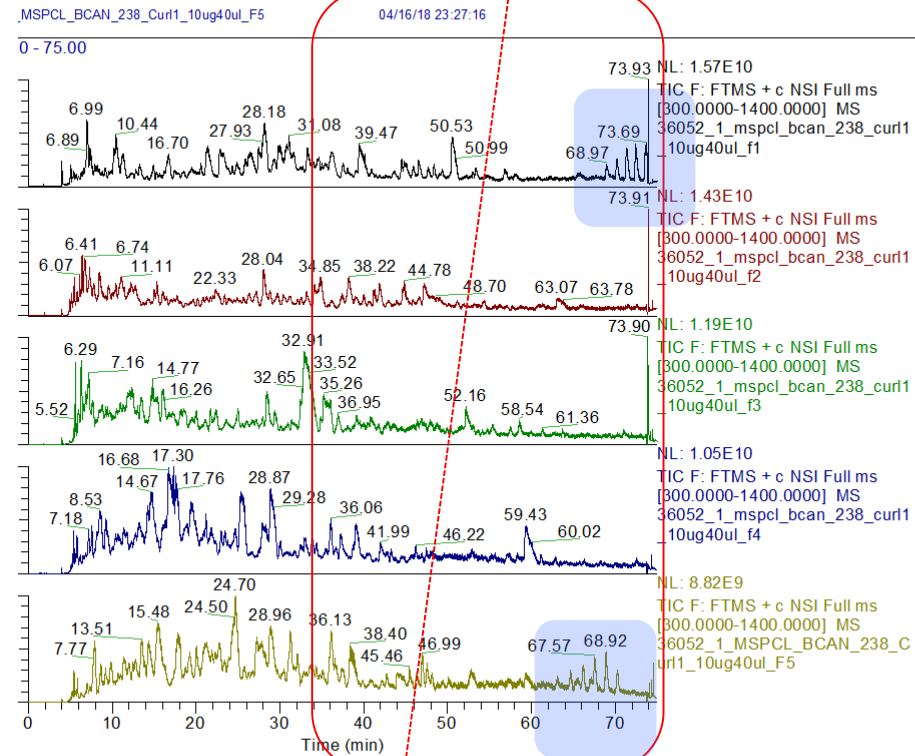
good data

Tumor #254



bad data

Tumor #238



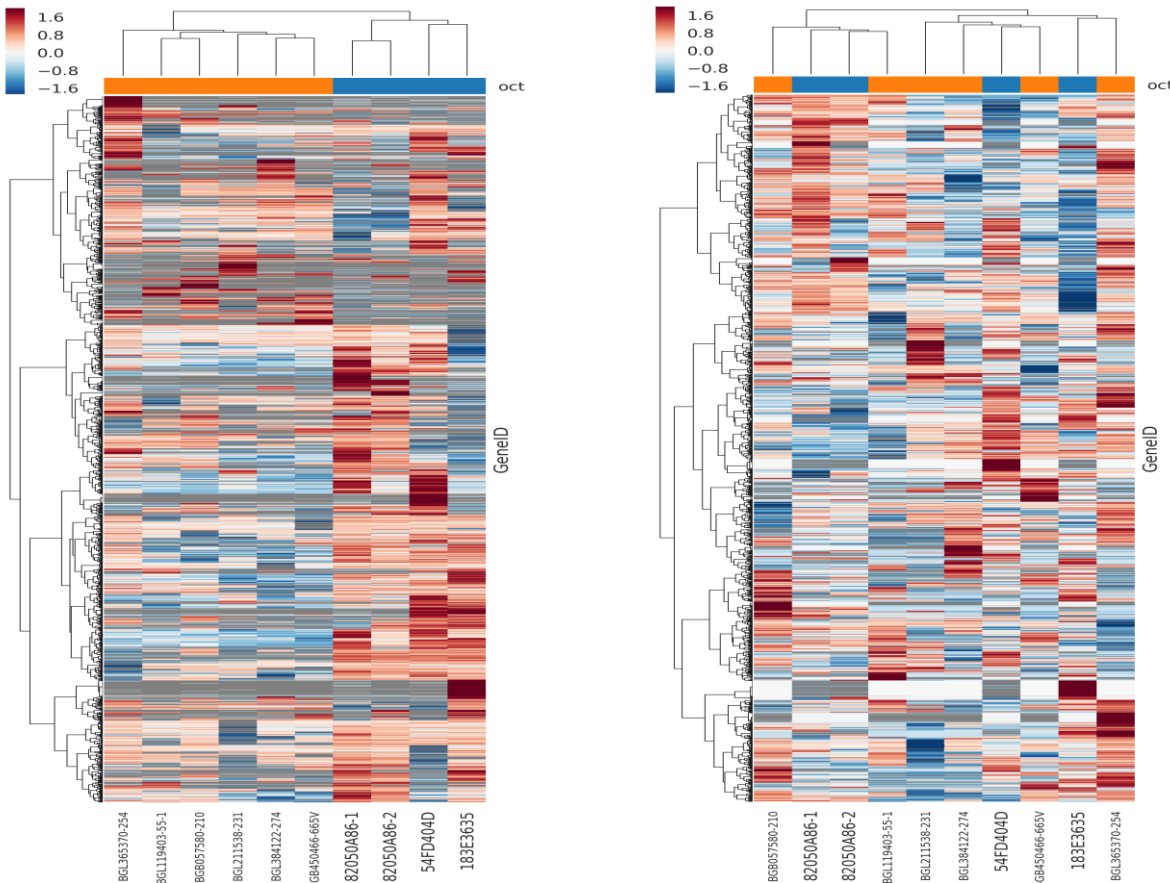
missing a whole class of peptides  
not fully cleared of OCT

# Proteomic Profiling

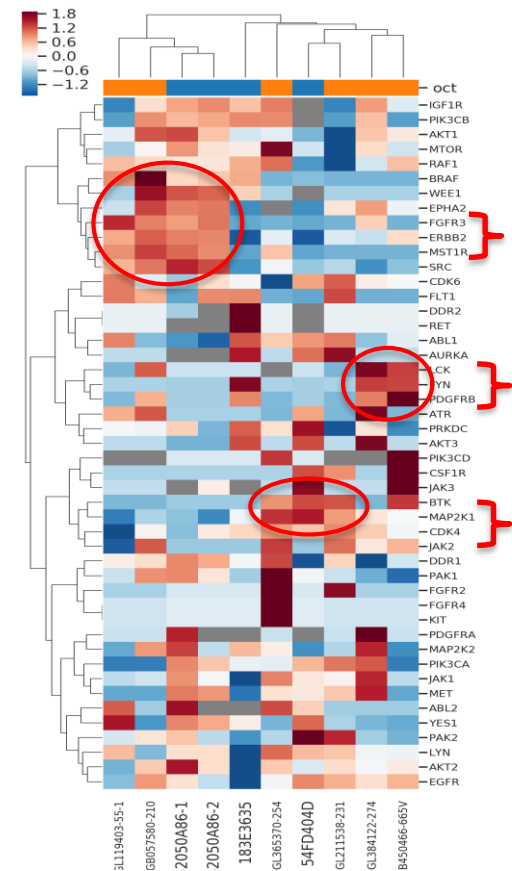
## OCT batch effect

Left: OCT lower observed protein abundances vs frozen tumor

Right: After Bioinformatic correction



## Druggable kinases



# Multiplexed inhibitor bead Kinome Pull-down (KiP) profiling

## Kinome Pull-down (KiP) with 9 kinase inhibitor-conjugated beads

abemaciclib\*: *CDK4, CDK6*

afatinib\*: *EGFR, ERBB2*

axitinib\*: *VEGFR, PDGFR, KIT*

AZD4547: *FGFR, VEGFR*

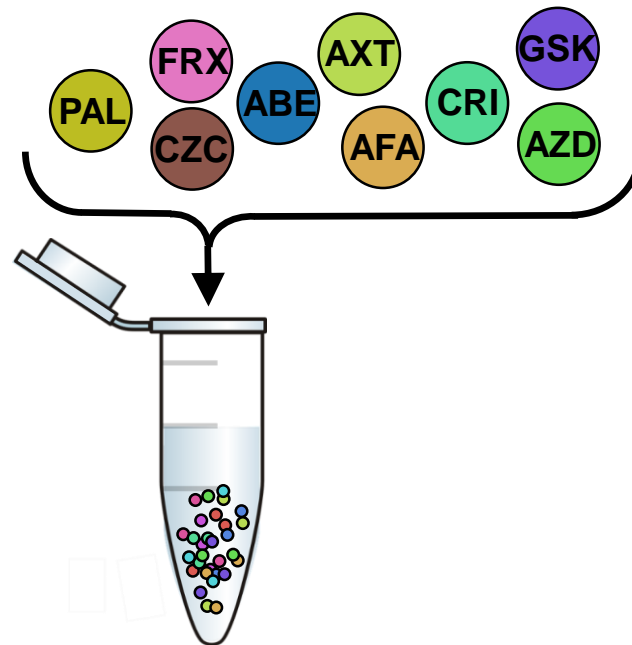
Crizotinib: *ALK, MET, AXL*

CZC-8004: *pan tyrosine kinase*

FRAX597\*: *PAKs*

GSK690693: *AKTs*

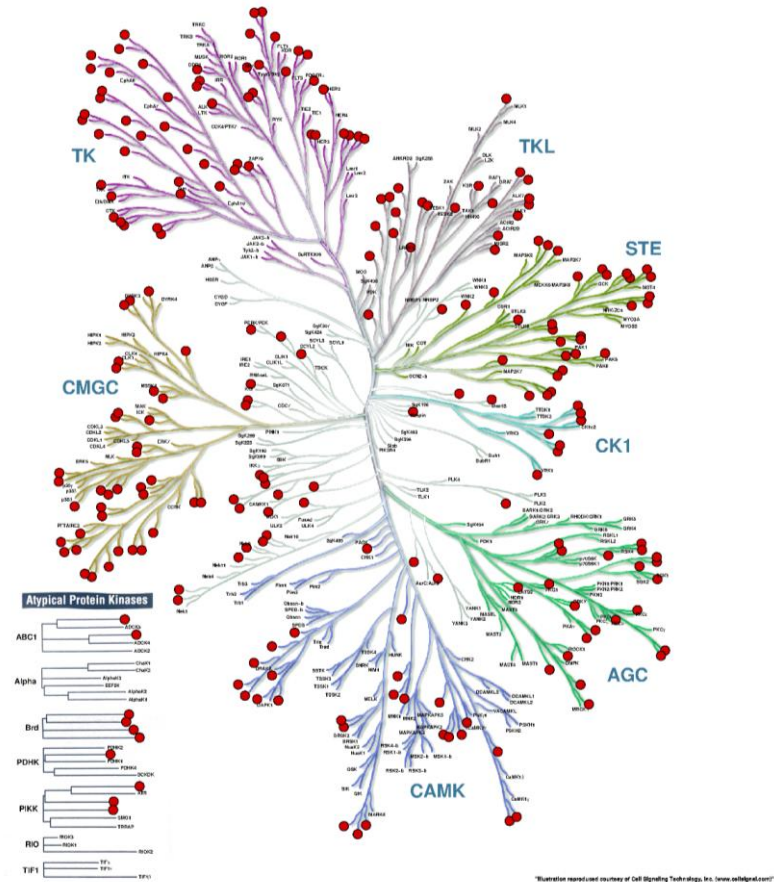
Palbociclib: *CDK4, CDK6*



The mixture of 9 kinase inhibitor beads is designed to isolate and enrich the kinases with most activity

# KiP Breast Cancer

Ellis, Kim unpublished  
No photo/social media



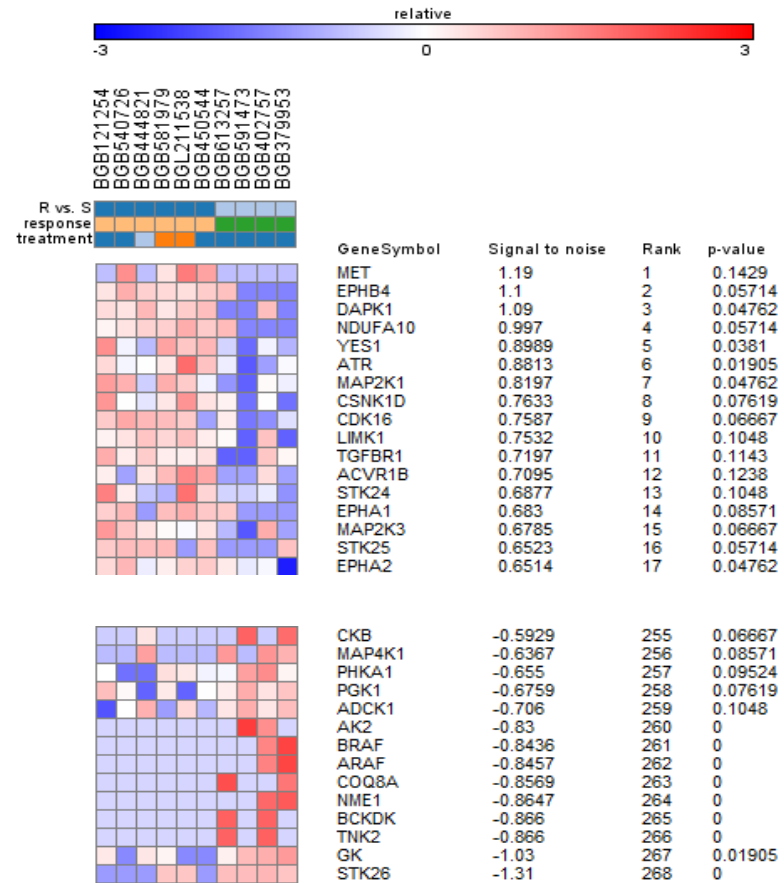
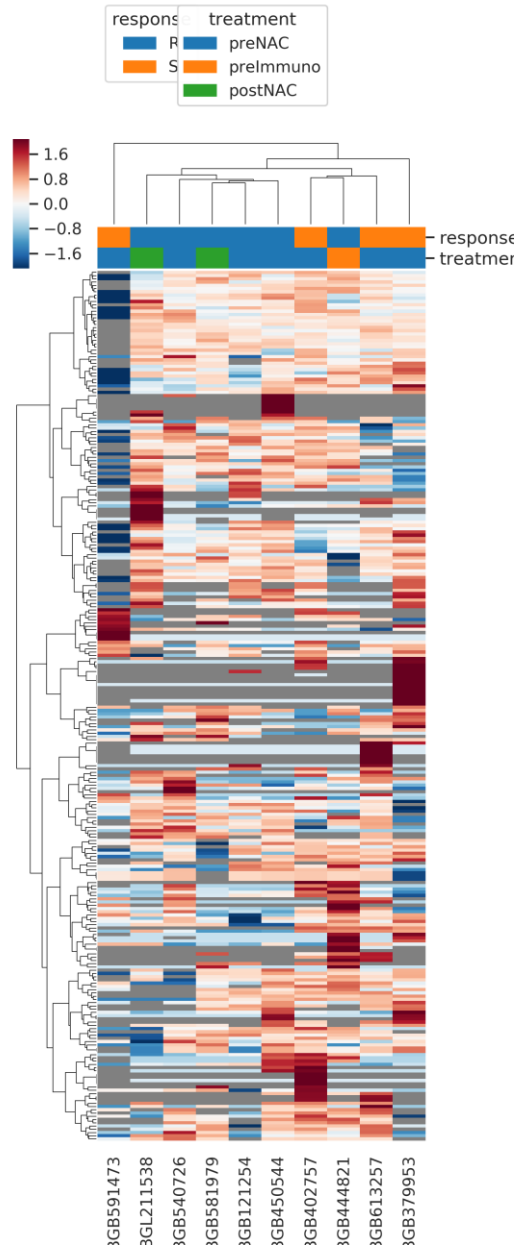
**Table 2.** Duplicate PDX (WHIM series) analysis comparing macroscale with microscale input showing high reproducibility and only modest reduction in kinase identification with 25 fold reduction in sample input.

**Figure 2** Broad kinase coverage with a

| WHIM number                           | Macro-scale (500ug)       | Micro-scale (20ug)     |
|---------------------------------------|---------------------------|------------------------|
| Numbers of experiments                | 47 duplicates from 24 PDX | 44 duplicates 22 PDX   |
| # total kinases (human & mouse)       | 723                       | 524                    |
| # human kinases                       | 388                       | 285                    |
| # human kinase quantified             | 382                       | 284                    |
| Average duplicate correlation (range) | 0.983 (1.000 to 0.901)    | 0.975 (0.999 to 0.927) |

# KiP profiling

Beom-Jun Kim  
Ellis lab (BCM)



- Pre NAC clusters together with similar kinase expression profile

- Kinase enrichment stratified by chemosensitivity
- DAPK1, YES1, ATR, MAP2K1, and EPHA2 higher in Res
- Sens higher in BRAF, ARAF

# PDX - Principles

- Faithfully represent parental human tumor
- Maintain genomic and biologic fidelity and heterogeneity in passage
- Serially passaged x 3: P0 (initial engraftment), P1,P2
- Take rates may vary by subtype
  - Enhanced with Matrigel
- Gender and ethnicity may affect treatment response
- Does the PDX respond to treatment similar to tumor of origin in the patient?
  - Not affected by immunodeficiency of the host (PDX)



[illegible]

# BCM PDX Portal: Collection Summary Page

## PDX PORTAL

Patient-Derived Xenograft and Advanced in Vivo Models (PDX-AIM) Core

Log In

Home Collections Contact Us Portal Team

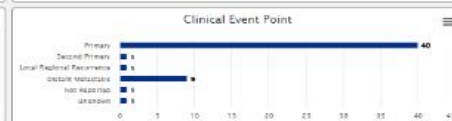
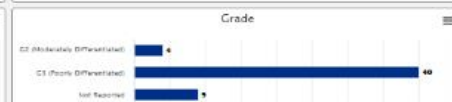
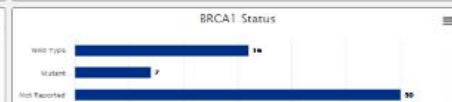
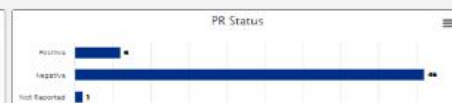
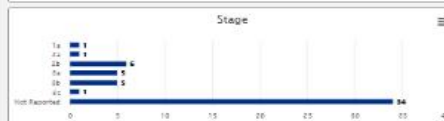
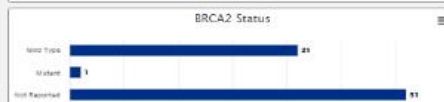
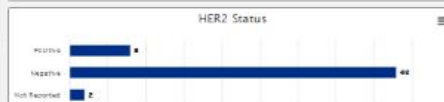
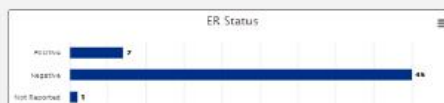
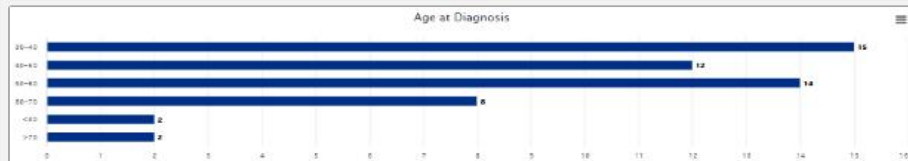
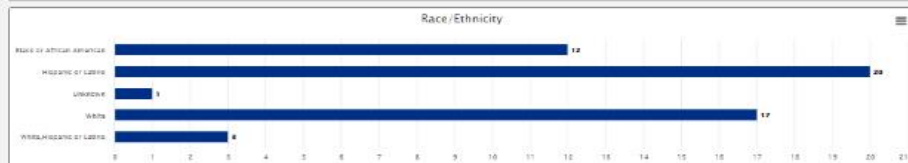
Breast Collection

Clinical View Gene View CSV View

Filter Data:

BCM 100 HCC 100 PDX (25) Patients (46)

Collection Summaries:

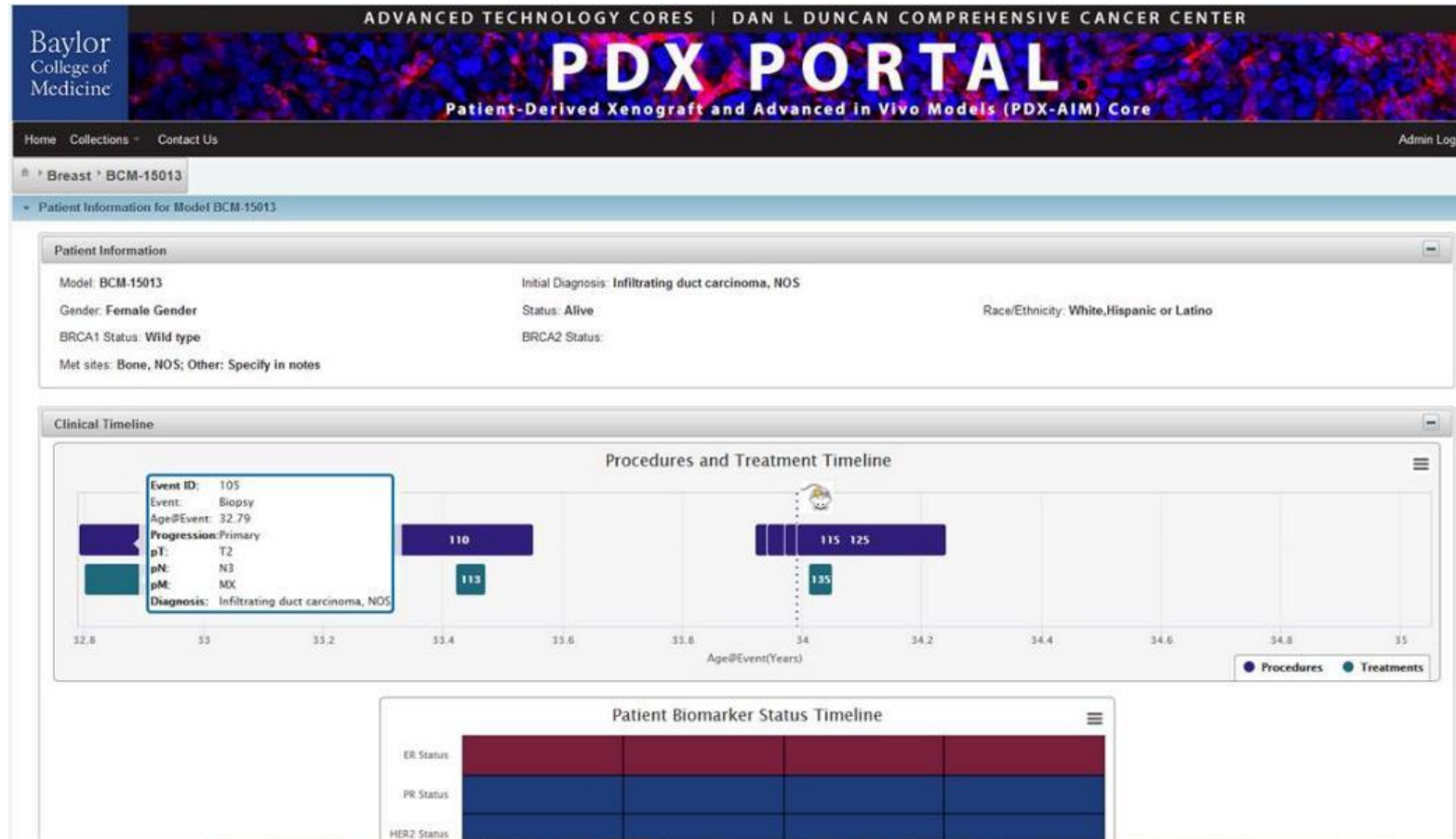


Heidi Dowst  
Apollo McOwiti  
Kerri Zheng  
Ram Srinivasan  
John Landua

Lacey Dobrolecki  
Alaina Lewis  
Christina Sallas  
Ana Hernandez-Herra  
Alphi Kuriakose

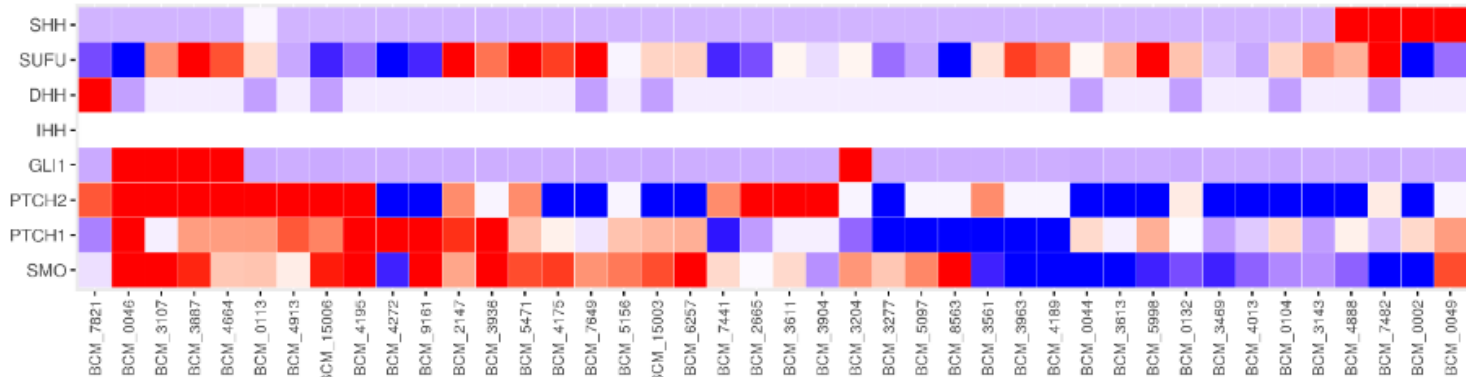
Chen Huang  
Bing Zhang

# BCM PDX Portal: Patient Clinical Information View

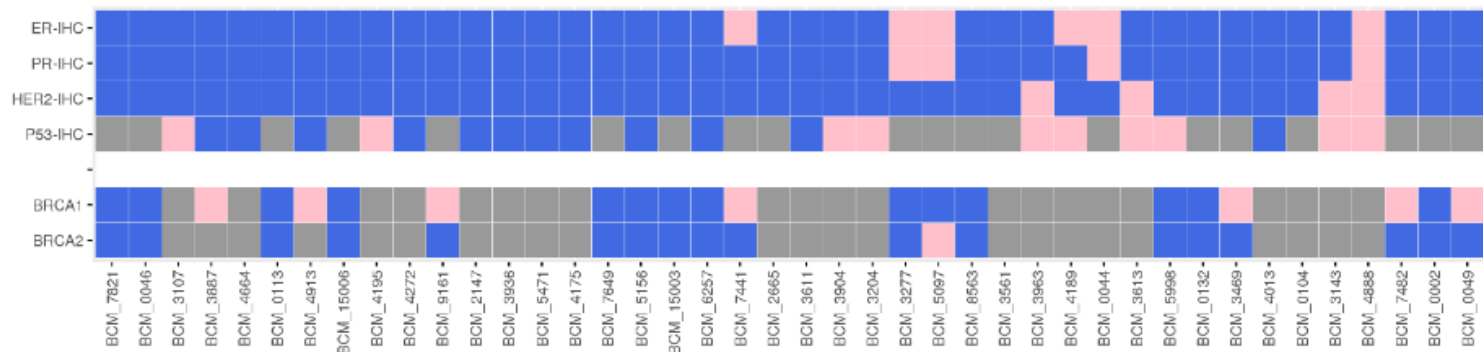


# BCM PDX Portal: Gene Expression View

Heatmap :  
(All samples) [N:42]



-1.0 -0.5 0.0 0.5 1.0



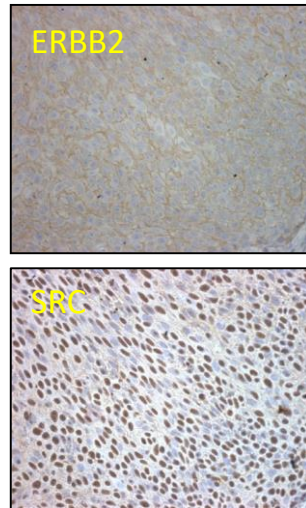
Positive/Mutant Negative/WT No Data

# Screening for effective targeted therapies

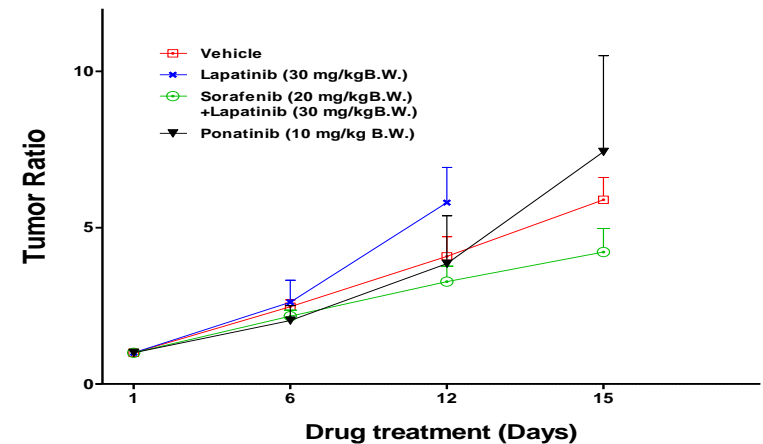
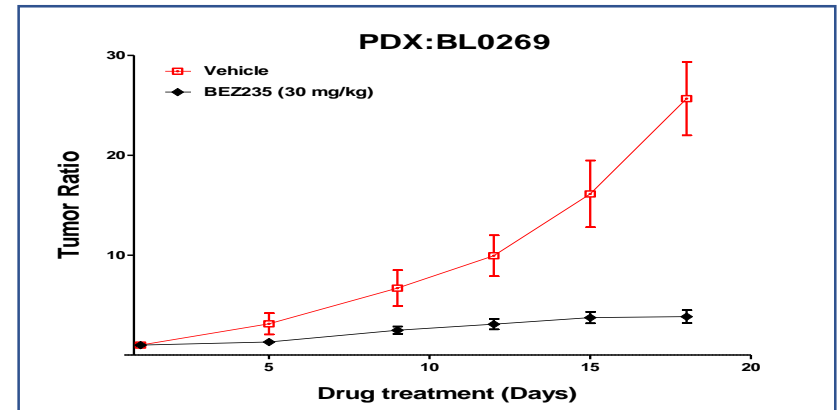
| PDXs          |         | BL0269               |
|---------------|---------|----------------------|
| <b>ERBB2</b>  | Protein | +++                  |
|               | mRNA    | 51.2582              |
| <b>ERBB3</b>  | Protein | weak                 |
|               | mRNA    | 46.4868              |
| <b>FGFR3</b>  | Protein | Dirty ++ (30% cells) |
|               | mRNA    | 158.192              |
| <b>SRC</b>    | Protein | ++++                 |
|               | mRNA    | 22.964               |
| <b>EphB4</b>  | Mouse   | N/A                  |
| Human         |         | POSITIVE             |
| <b>PIK3CA</b> |         | H1047R               |

PDX BL0269 has overexpression of ERBB2 and SRC, and PIK3CA mutation. Only PIK3CA inhibitor BEZ was effective.

(In the table, the numbers are RNA seq results; the “+” is the IHC staining results)

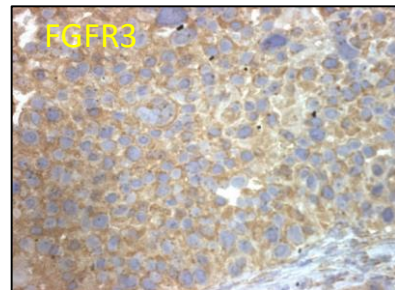
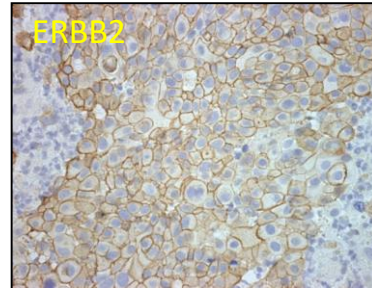


BEZ235: PIK3CA inhibitor  
Lapatinib: EGFR and ERBB2 inhibitor  
Sorafenib: Raf inhibitor  
Ponatinib: Src inhibitor

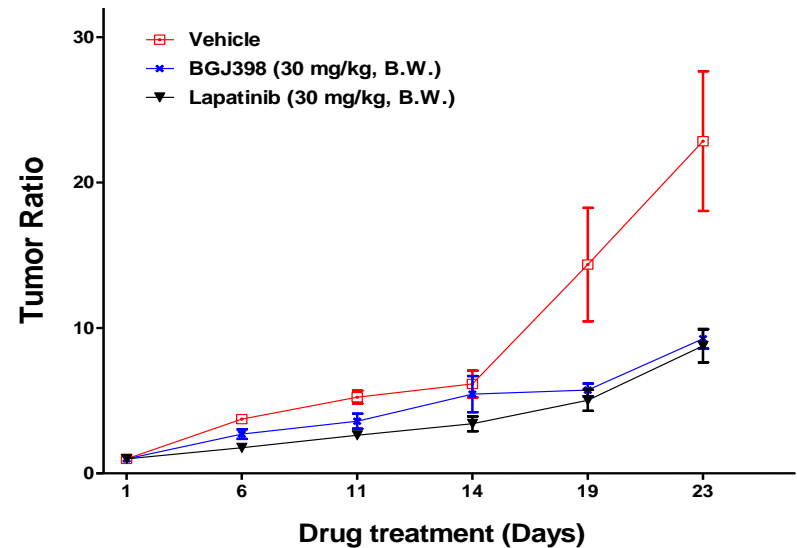


# Repurposing FDA-approved drugs

| PDXs   |         | BL0440   |
|--------|---------|----------|
| ERBB2  | Protein | +++      |
|        | mRNA    | 158.051  |
| ERBB3  | Protein | ++       |
|        | mRNA    | 46.0066  |
| FGFR3  | Protein | +++      |
|        | mRNA    | 80.387   |
| SRC    | Protein | 5%+      |
|        | mRNA    | 70.0928  |
| EphB4  | Mouse   | NEGATIVE |
|        | Human   | NEGATIVE |
| PIK3CA |         |          |



PDX BL0440 has overexpression of ERBB2, ERBB3 and FGFR3. Both lapatinib and FGFR3 inhibitor BGJ398 were effective.

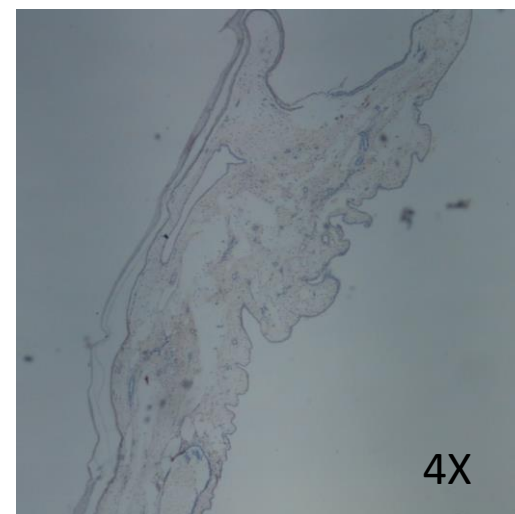
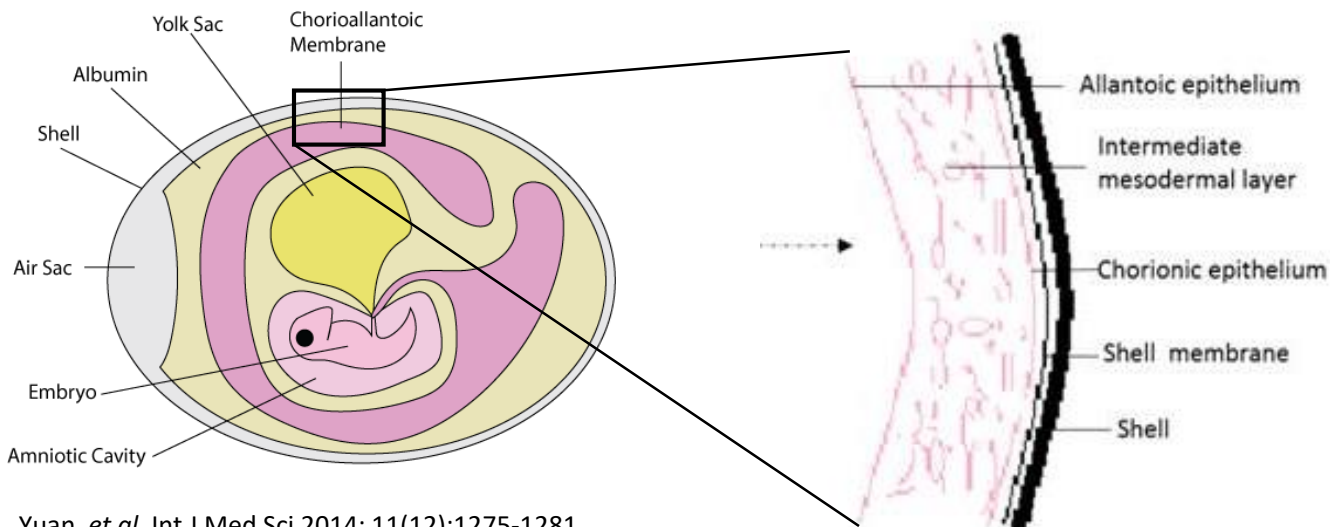
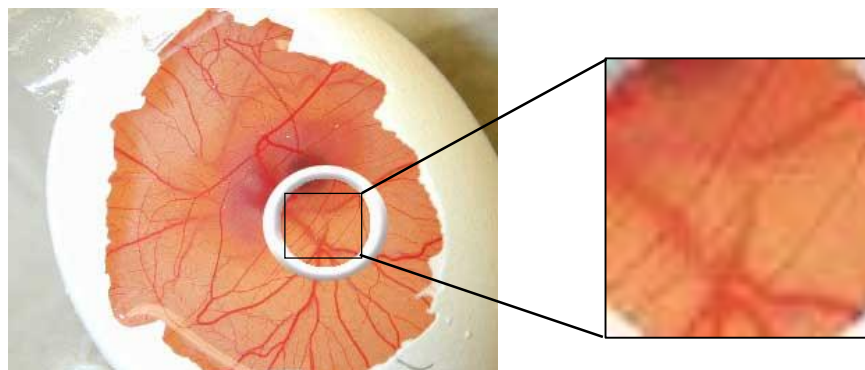
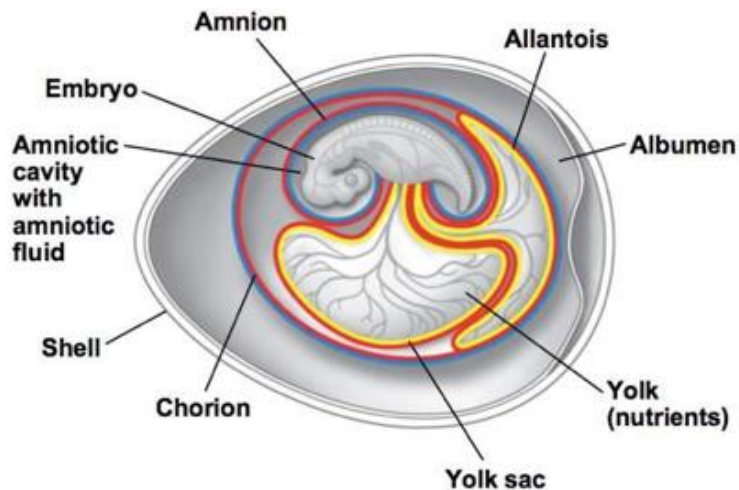


BGJ398: FGFR inhibitor

Lapatinib: EGFR and ERBB2 dual inhibitor.

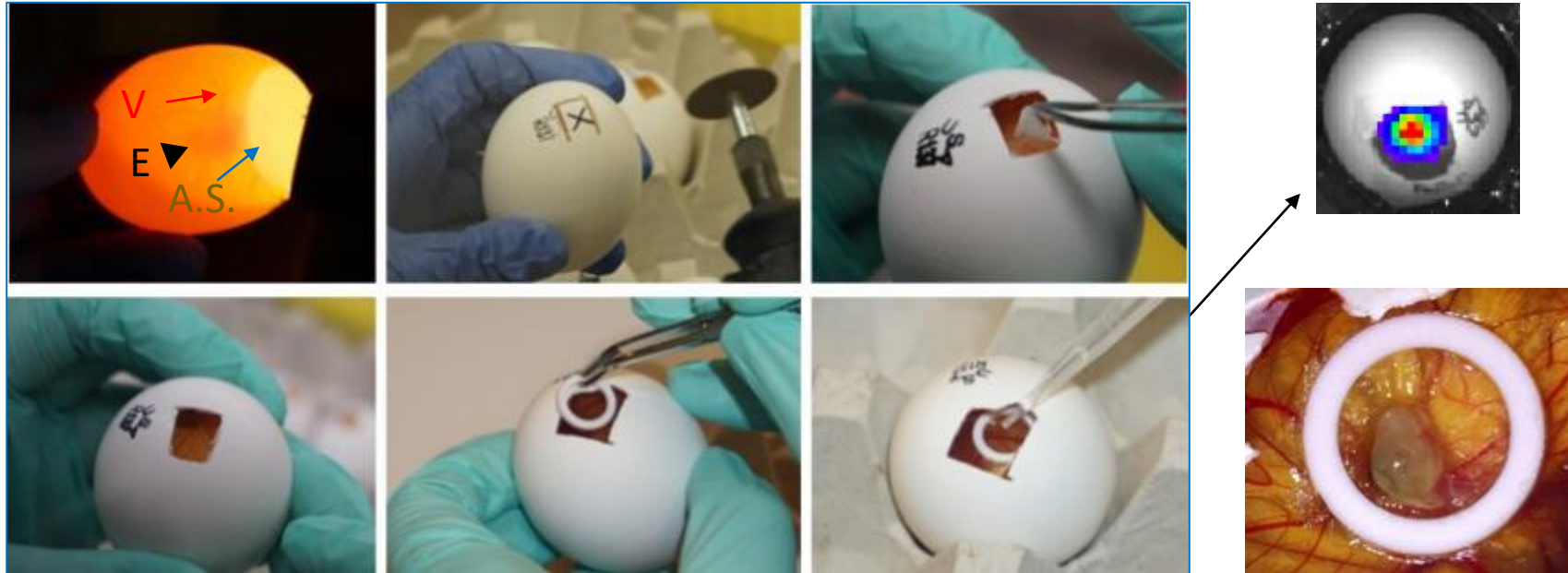


# The Chorioallantoic Membrane (CAM)



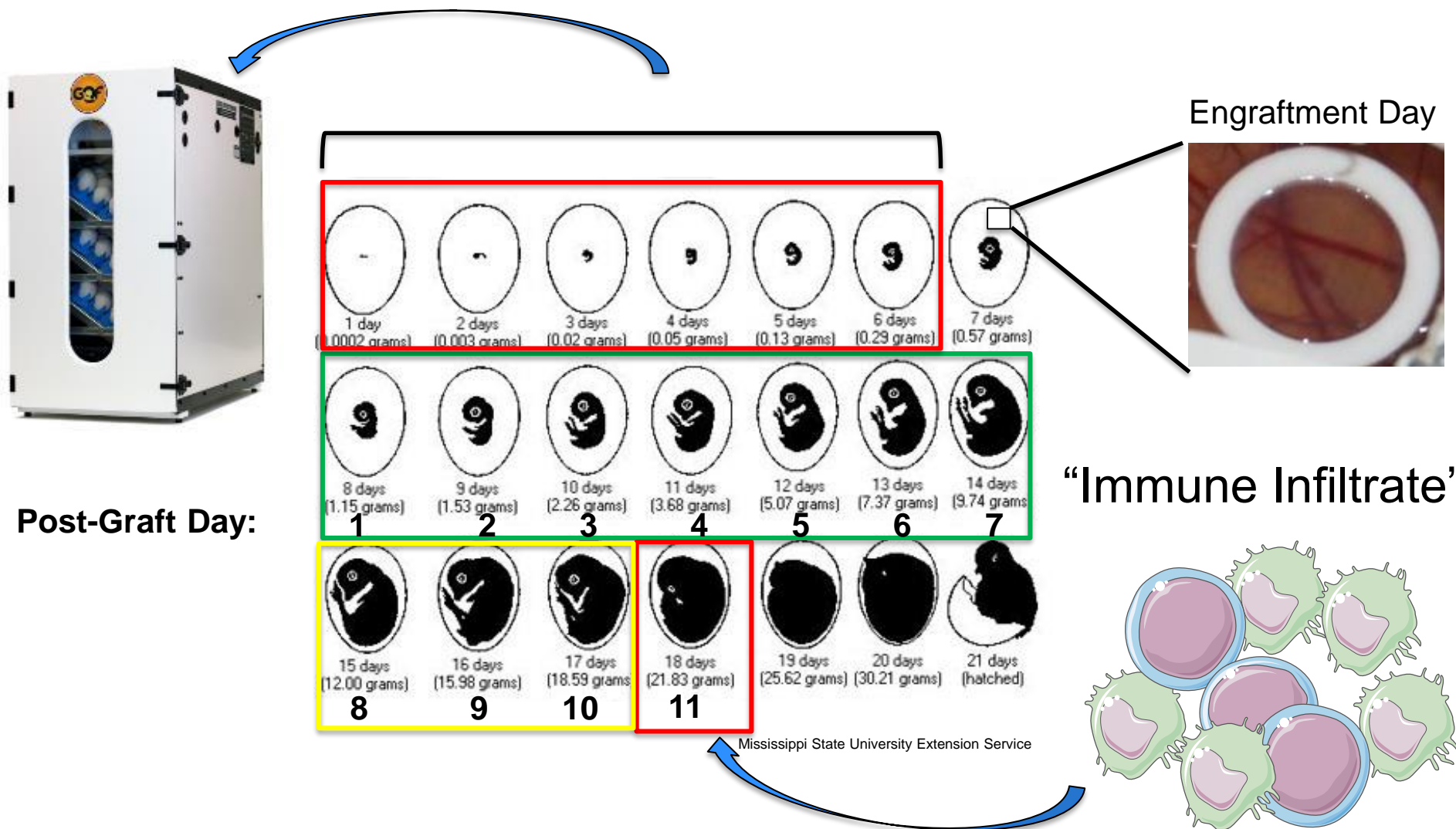
Yuan, *et al*, Int J Med Sci 2014; 11(12):1275-1281

# Preparing the Chorioallantoic Membrane (CAM) for Growth of Cell Lines and PDX



Li, M., Pathak, R. R., Lopez-Rivera, E., Friedman, S. L., Aguirre-Ghiso, J. A., Sikora, A. G. **The In Ovo Chick Chorioallantoic Membrane (CAM) Assay as an Efficient Xenograft Model of Hepatocellular Carcinoma.** *Journal of Visualized Experiment* (104), e52411, doi:10.3791/52411 (2015).

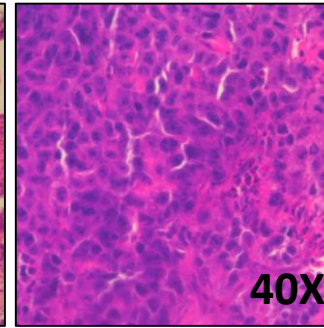
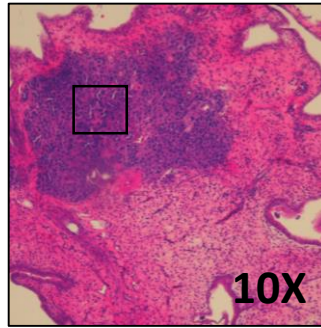
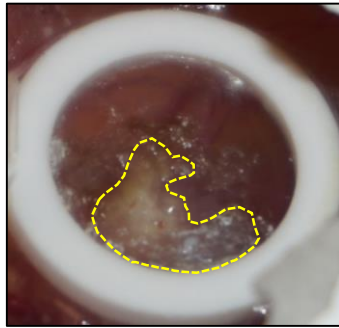
# CAM - The “Window of Opportunity”



- Angiogenesis
- Tumor xenograft models
  - Glioblastoma, pancreatic cancer, melanoma, and osteosarcoma, HCC
- Both in ovo and ex ovo techniques
- Relatively high incidence of embryonic death after manipulation of the egg
  - Chick embryo mortality rates ranging from 25 – 50%
- BCM bladder CAM inventory
  - 101 tumors (51 viably frozen for future engraftment)
  - 31/50 (62%) attempts engrafted

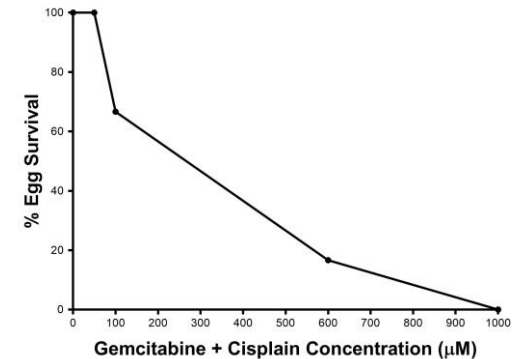
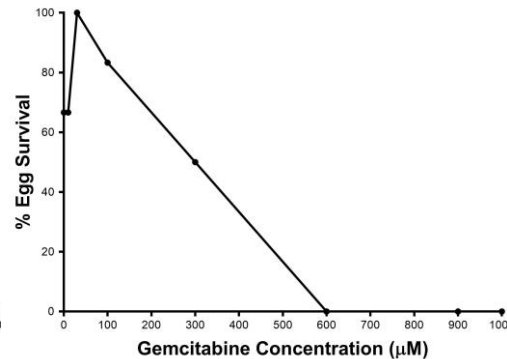
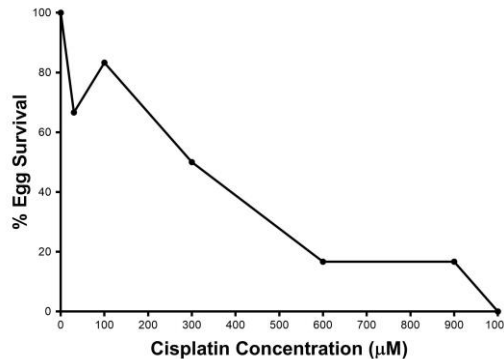


PDX-8035

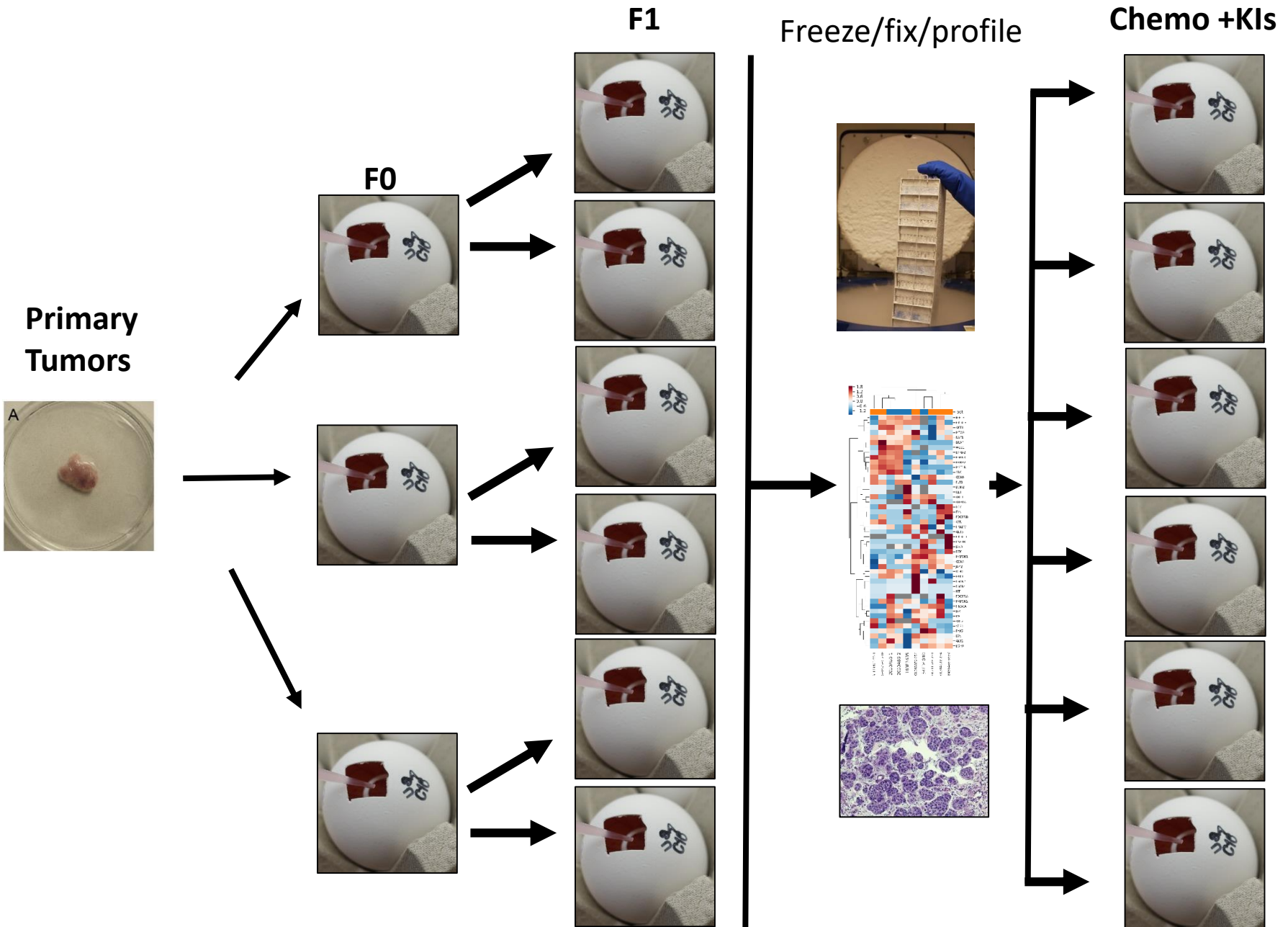


**Patient-derived xenograft on chorioallantoic membrane.** Bladder tumor grown on CAM after seven days of culture. Hematoxylin and eosin stained section of CAM-engrafted bladder cancer histology at 10X and 40X.

“Kill” curves

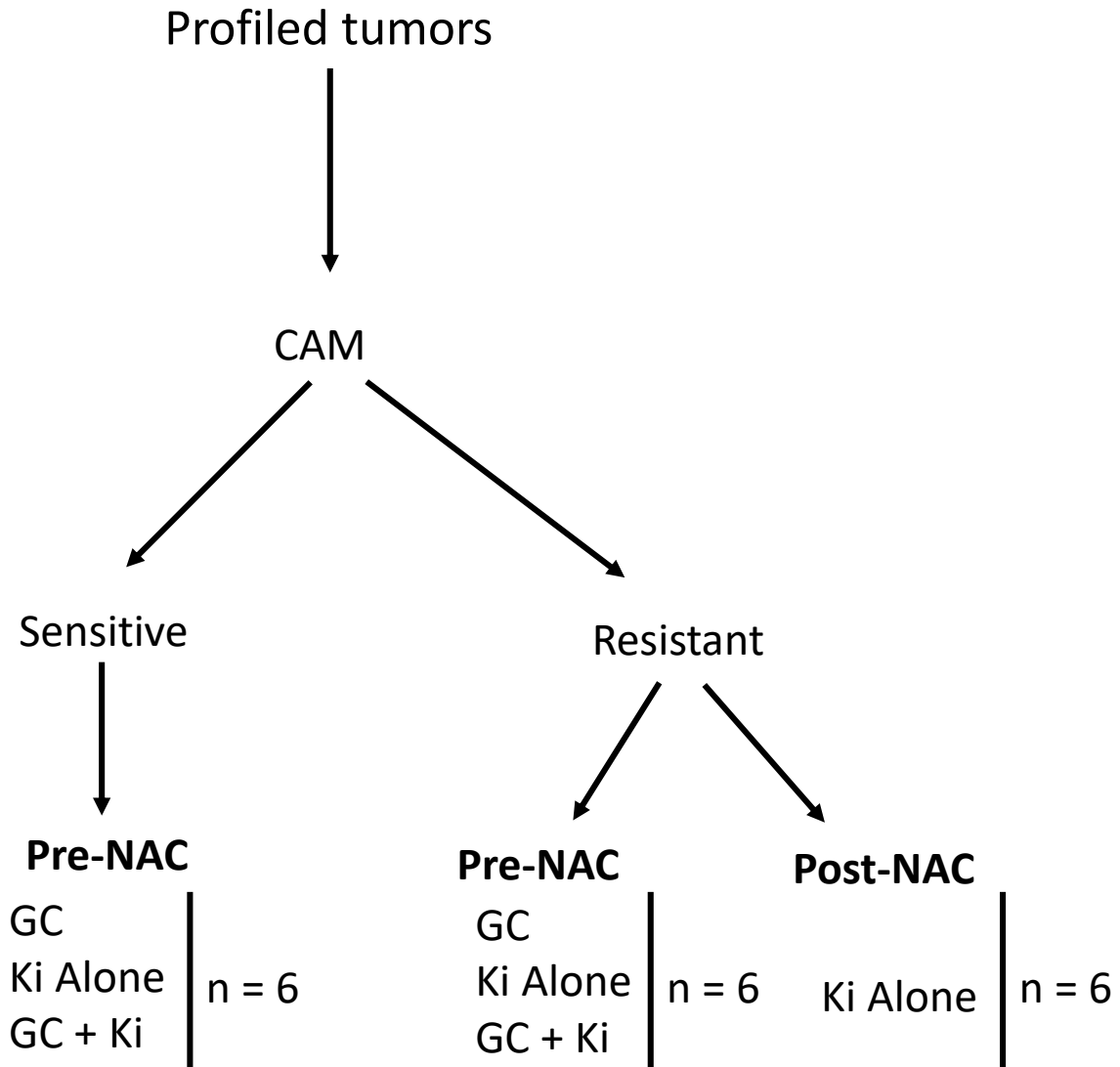


# Bladder Cancer PDX Treatment Plan





# CAM PDX Workflow



**AZD4547** (FGFR)

18 nM - 30 uM

**Abemaciclib**

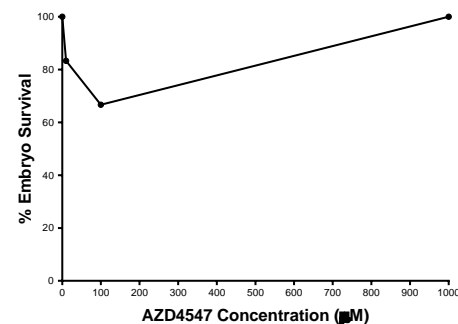
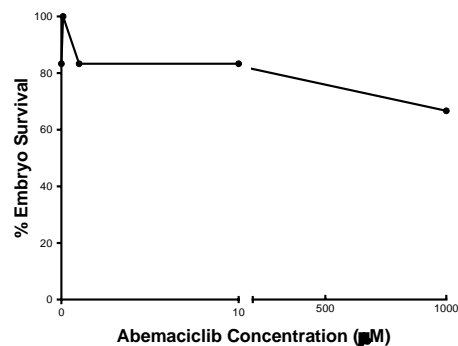
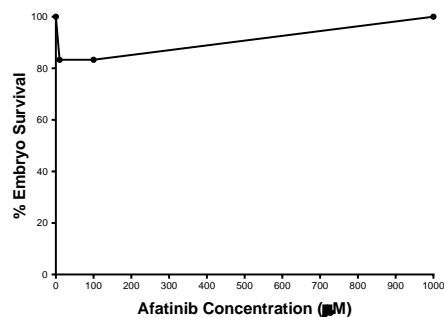
(CDK4/6 )

0.12 - 2.7 uM

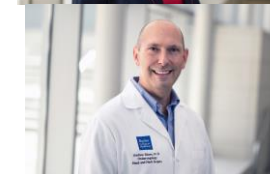
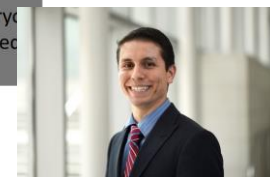
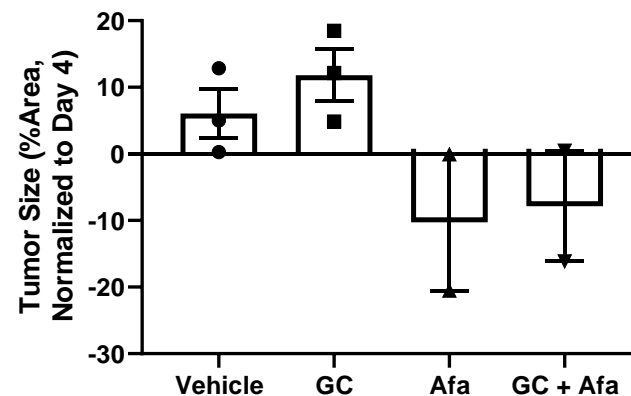
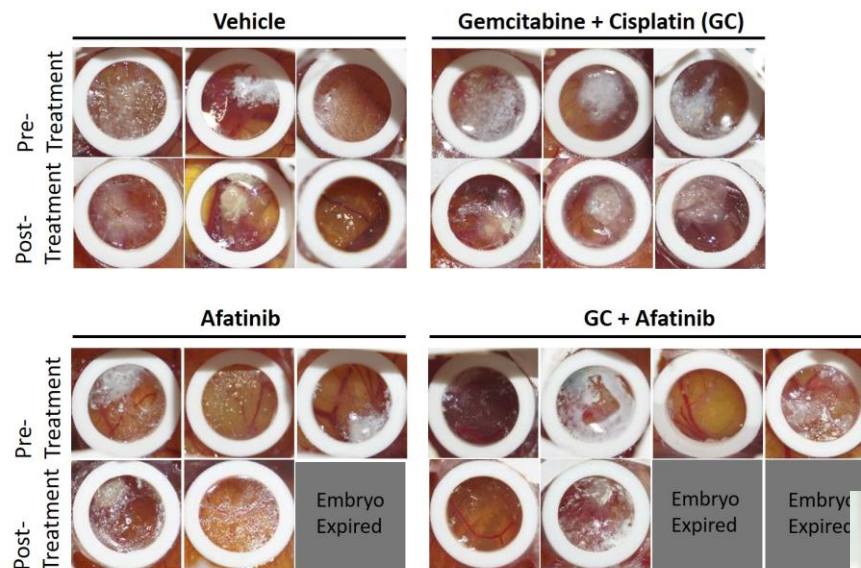
**Afatinib** (EGFR)

5.72 nM - 50 uM

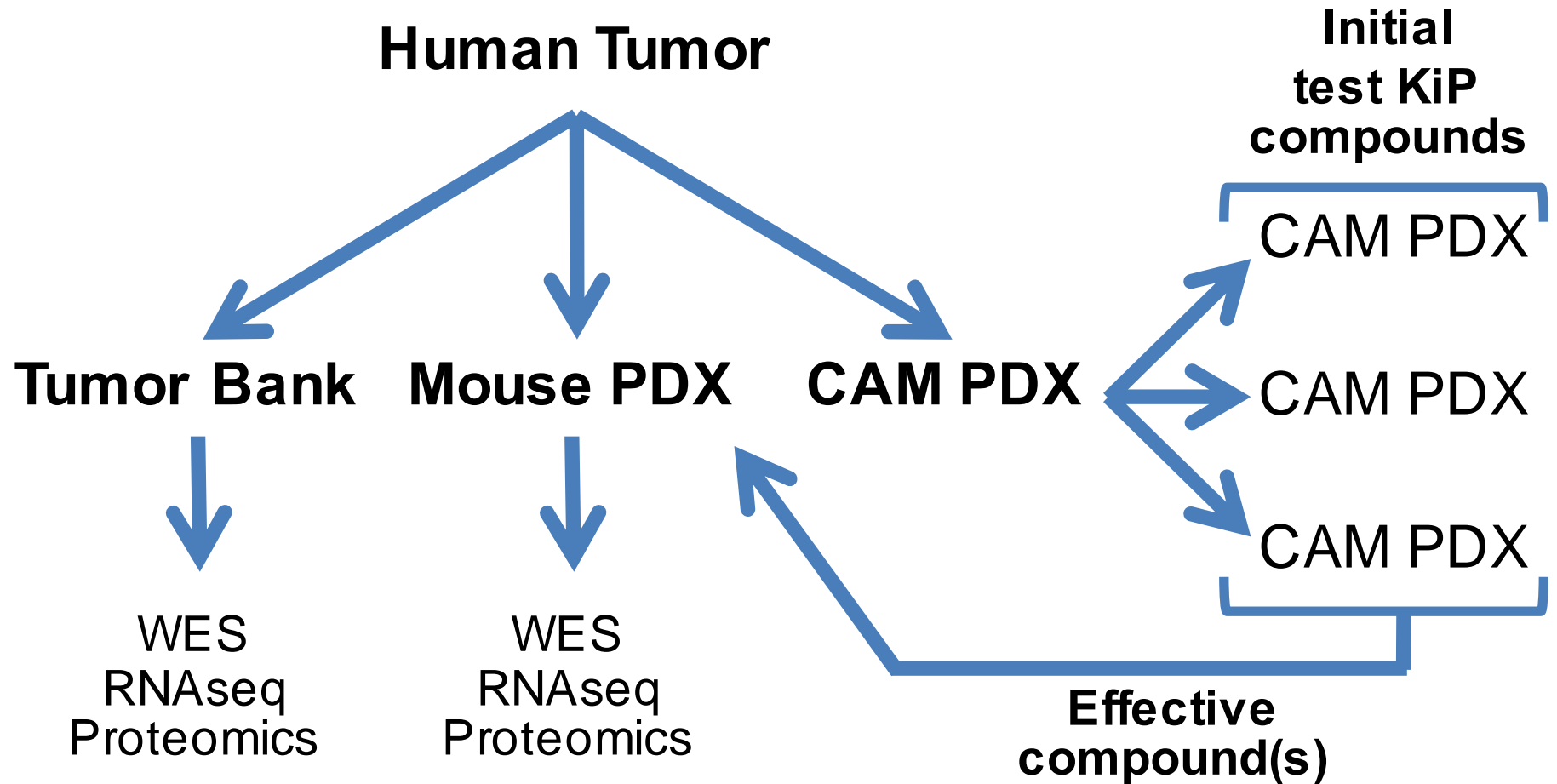
# TKI on CAM Proof of Concept



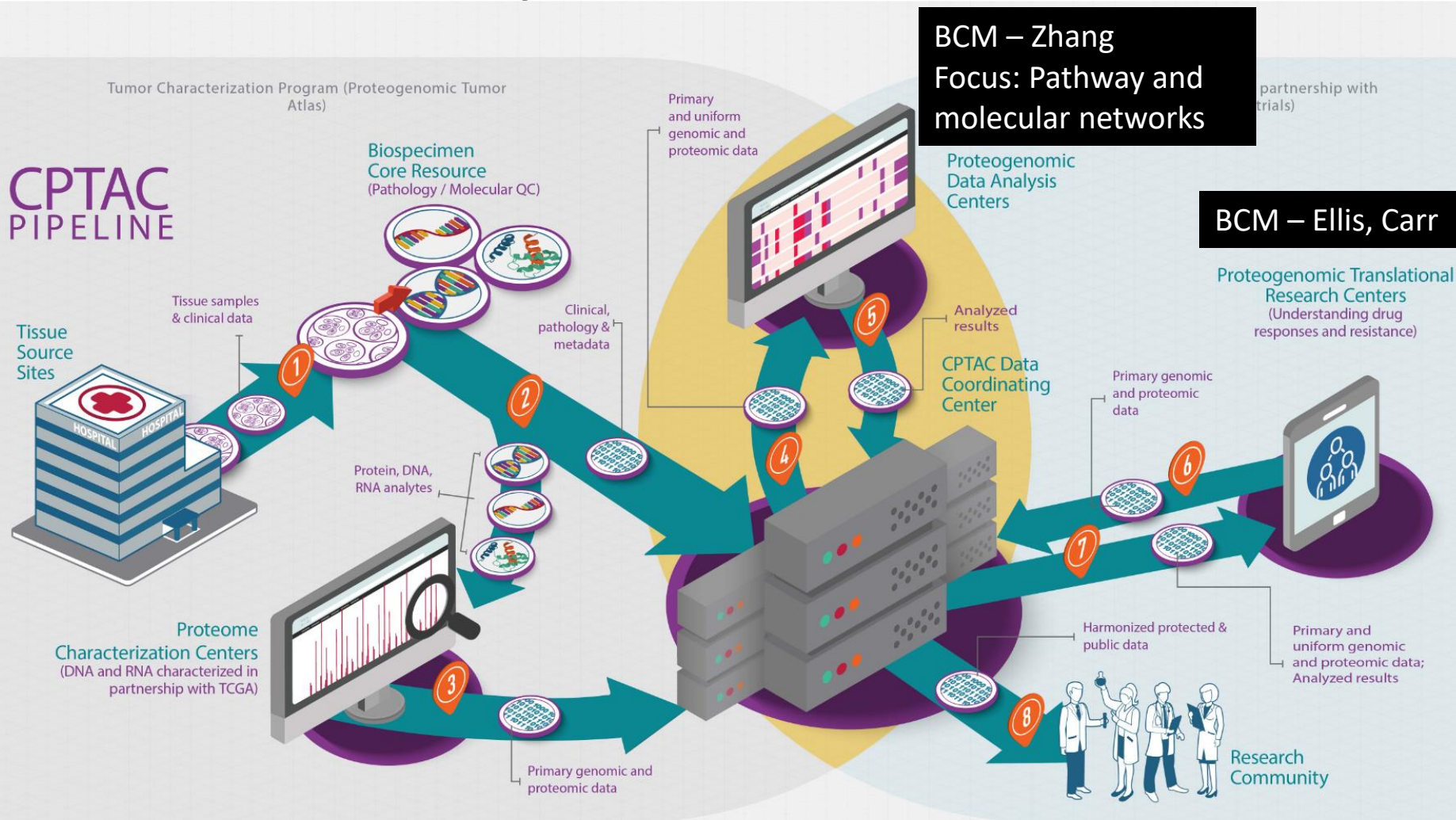
## Pre-NAC Resistant Specimens



# PDX Workflow

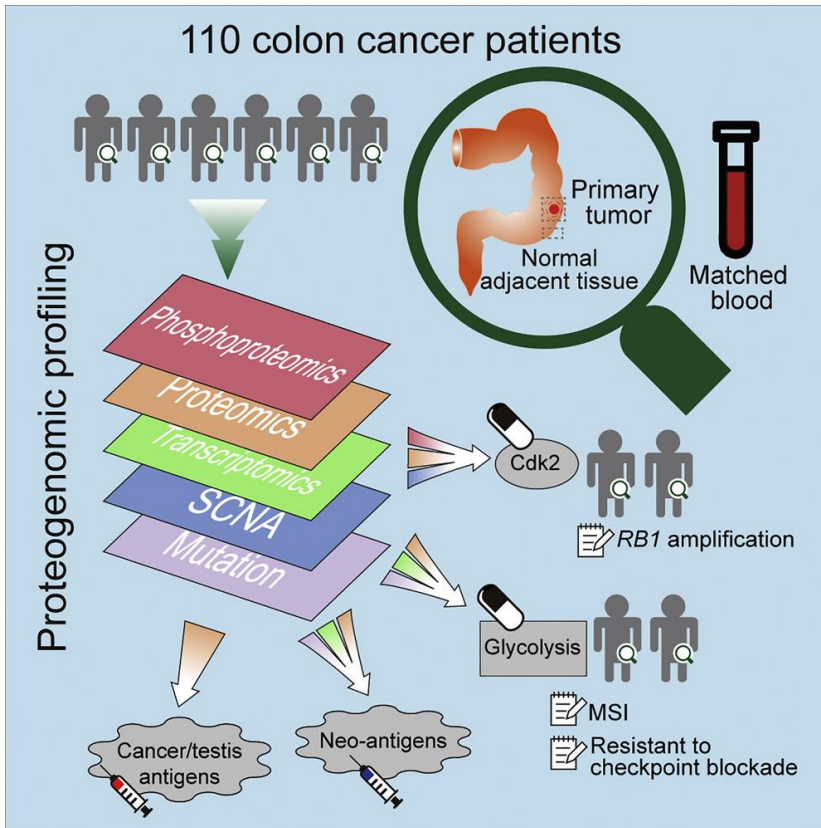


# CPTAC –Clinical Proteomic tumor Analysis Consortium



# CPTAC - Colorectal Cancer

## Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities

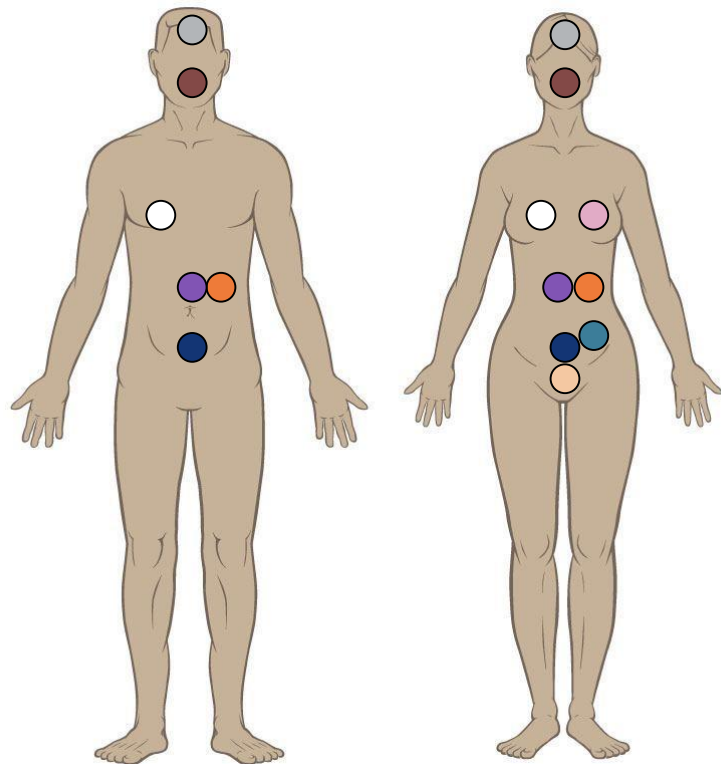
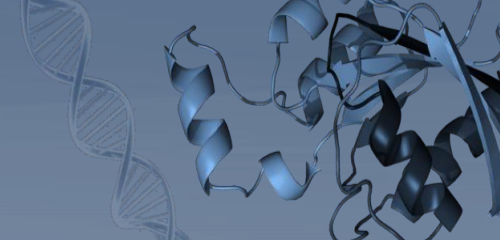


### Highlights

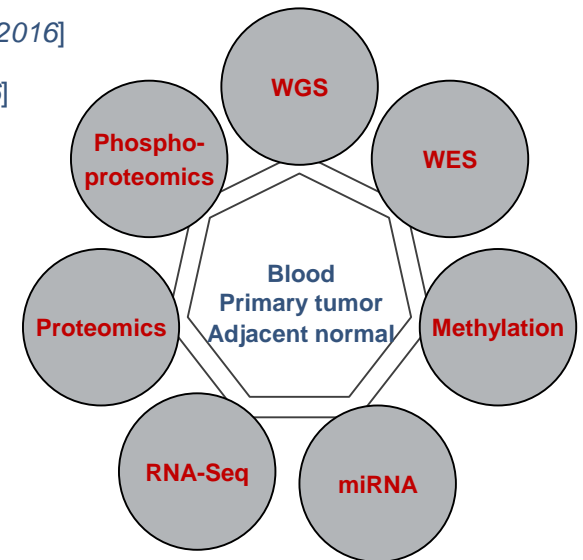
- Systematic identification of colon cancer-associated proteins and phosphosites
- Proteomics-supported neoantigens and cancer/testis antigens in 78% of the tumors
- Rb phosphorylation is an oncogenic driver and a putative target in colon cancer
- Glycolysis inhibition may render MSI tumors more sensitive to checkpoint blockade



# Clinical Proteome Tumor Analysis Consortium (CPTAC)



- Colorectal [Zhang et al., Nature, 2014; Vasaikar et al., Cell, 2019]
- Breast [Mertins et al., Nature, 2016]
- Ovary [Zhang et al., Cell, 2016]
- Kidney
- Uterus
- Lung
- Head and neck
- Pancreas
- Brain
- .....



# CPTAC V04.02 – Bladder

## Inclusion criteria

- New dx, untreated, undergoing primary cytoreductive surgery
- New tumor event in an existing or concurrent patient
- Recurrence, metastasis or second primary

## Exclusion criteria

- No prior cancer within last 12 months except BCE
- No prior systemic therapy for another cancer within last 10 yrs

Blood and urine collection required

### 11.3 Appendix B: Summary of Key Study Criteria

| CPTAC code | Cancer                       | Percent Tumor Nuclei | Percent Total Cellularity | Percent Necrosis | Maximum Tumor Ischemic Time (min) | Normal Tissue                      |
|------------|------------------------------|----------------------|---------------------------|------------------|-----------------------------------|------------------------------------|
| BLCA       | Bladder Urothelial Carcinoma | ≥80%                 | ≥50%                      | ≤20%             | 30 (45 for robotic)               | Normal adjacent tissue as feasible |

# Conclusions

- Proteomic profiling identifies clusters with similar protein kinase expression patterns
- KiP assay offers high throughput mass spec to identify druggable kinases and candidate kinase inhibitors
- Mouse PDX models established with proof of concept testing kinase inhibitors stratified by chemosensitivity.
- CAM PDX offers high throughput testing of chemotherapy and kinase inhibitors
- CPTAC for bladder cancer 2020-21