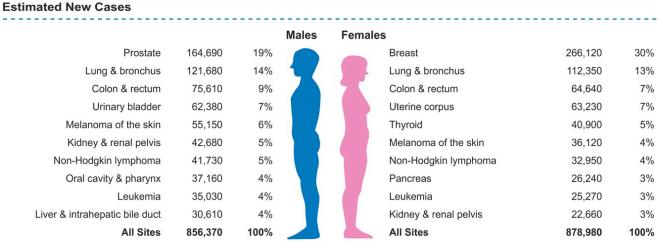


Proteogenomic Characterization of Endometrial Cancer

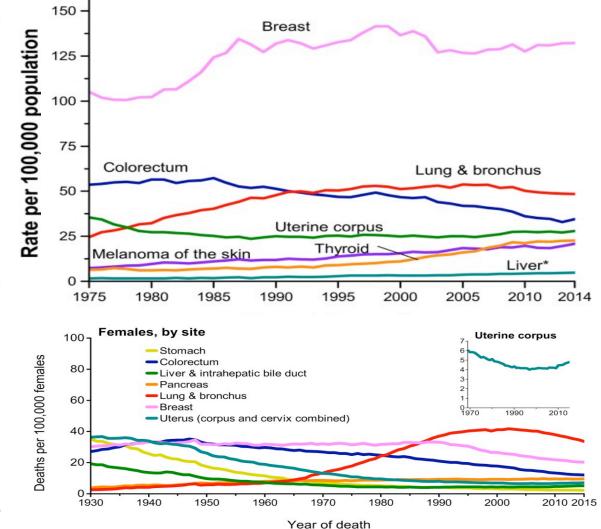
Emily Kawaler
CPTAC Endometrial Cancer Working Group
CPTAC Imaging Special Interest Group Webinar
January 14, 2020

Endometrial Cancer



Estimated Deaths

			Males	Females			
Lung & bronchus	83,550	26%			Lung & bronchus	70,500	25%
Prostate	29,430	9%			Breast	40,920	14%
Colon & rectum	27,390	8%		X	Colon & rectum	23,240	8%
Pancreas	23,020	7%			Pancreas	21,310	7%
Liver & intrahepatic bile duct	20,540	6%			Ovary	14,070	5%
Leukemia	14,270	4%			Uterine corpus	11,350	4%
Esophagus	12,850	4%			Leukemia	10,100	4%
Urinary bladder	12,520	4%			Liver & intrahepatic bile duct	9,660	3%
Non-Hodgkin lymphoma	11,510	4%			Non-Hodgkin lymphoma	8,400	3%
Kidney & renal pelvis	10,010	3%			Brain & other nervous system	7,340	3%
All Sites	323,630	100%			All Sites	286,010	100%



Cancer Statistics, 2018

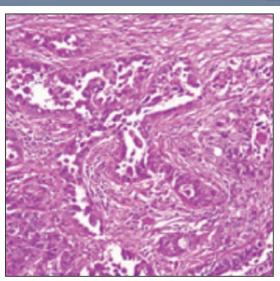
Histologic Subtypes





ENDOMETRIOID

- ~85% of cases
- Usually discovered at a lower grade, lower stage
- Best prognosis



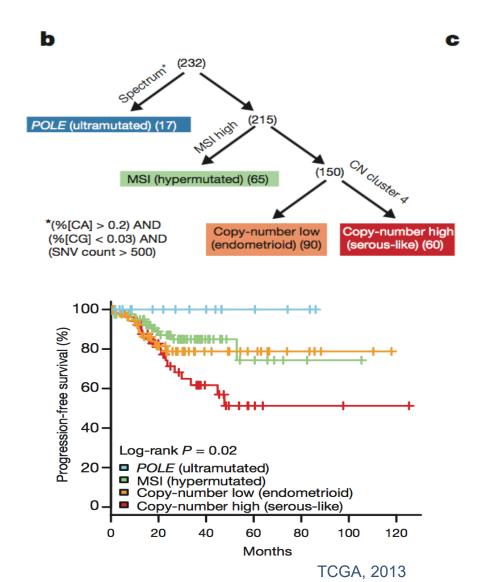
SEROUS

- ~15% of cases, ~40% of deaths
- Usually discovered at a later stage
- More aggressive, poor survival rate

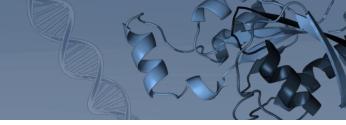
Murali et al, Classification of endometrial carcinoma: more than two types, *Lancet Oncol.* 15 (2014) e268–78.

TCGA Molecular Subtyping

- POLE: mutations in exonuclease domain of POLE, ultramutated
- MSI: hypermutated, most have MLH1 promoter methylation, heavy meth throughout, low SCNA
- Copy Number Low: most MSS endometrioid cancers
- Copy Number High: Mostly serous, some high-grade endometrioid



Data Overview



CPTAC Endometrial Carcinoma Cohort

- 83 endometrioid tumors
- 12 serous tumors
- 49 normal uterine samples
 - 18 normal endometrium
 - 25 mixed endometriummyometrium
 - 6 myometrium





Whole genome and exome sequencing

Somatic mutation

Copy number variation

POLE status

MSI status



RNA sequencing

Gene expression

circRNA expression

Splice variant

miRNA expression

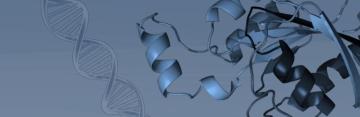


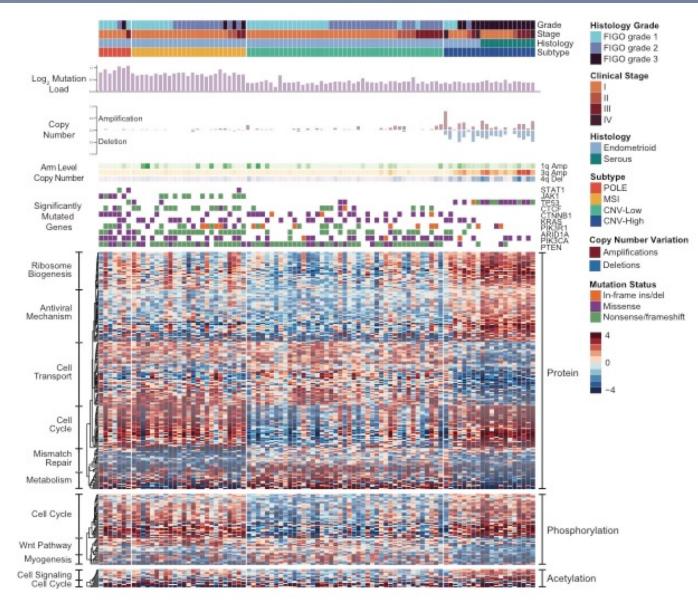
MS protein analysis

Protein

Protein phosphorylation

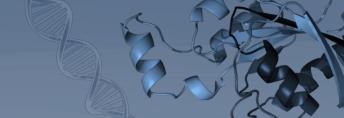
Protein acetylation



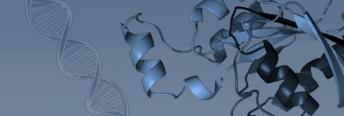


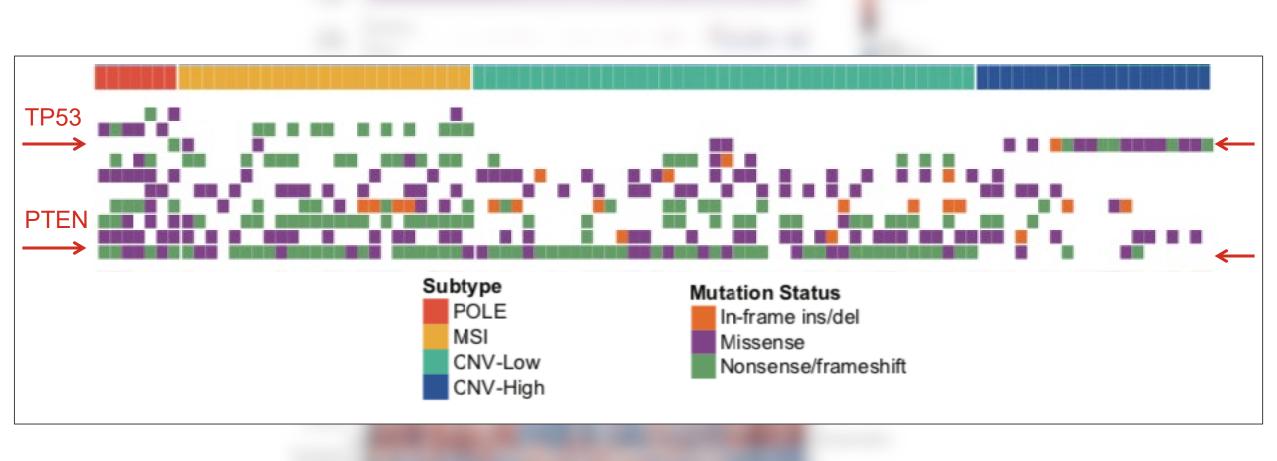


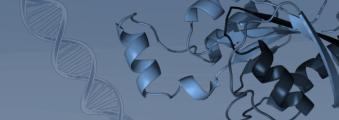


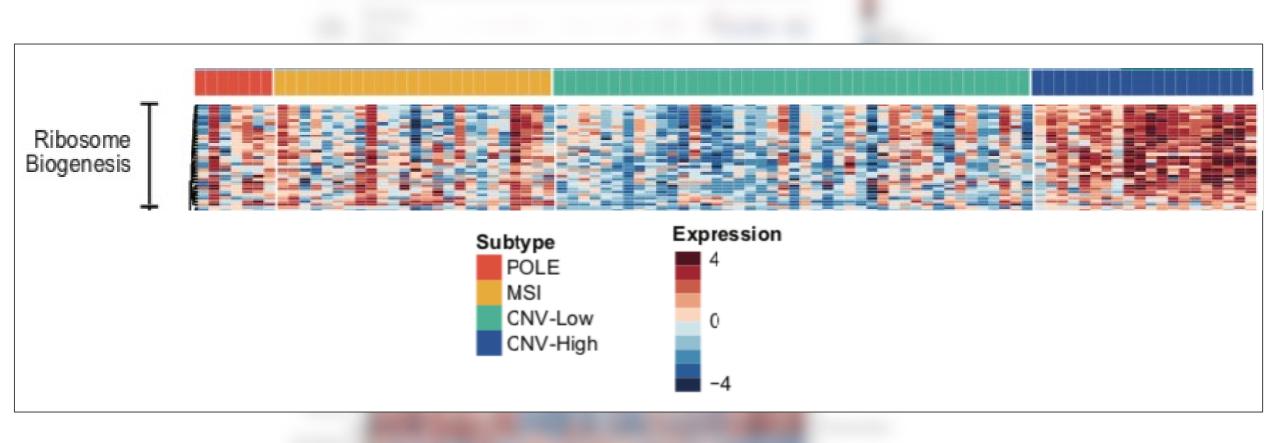




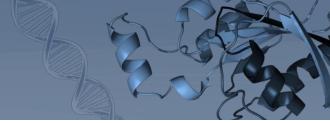


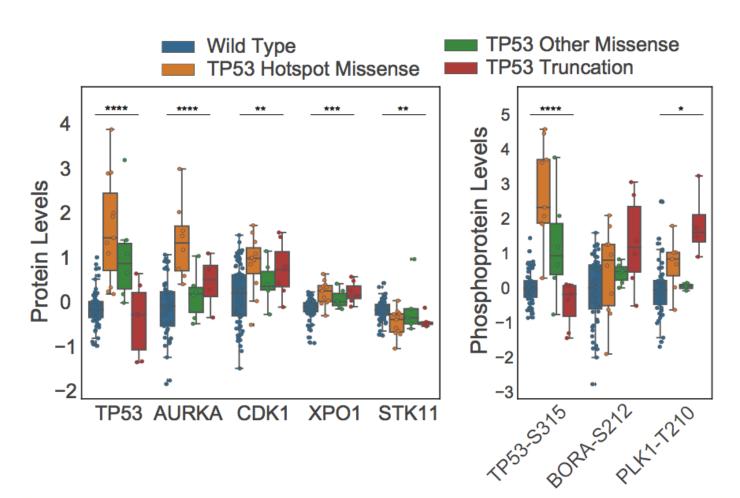


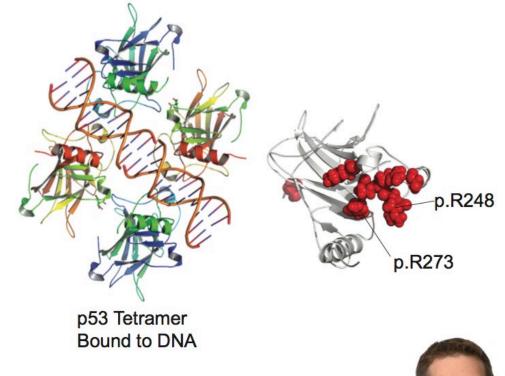




Effects of TP53 Mutations

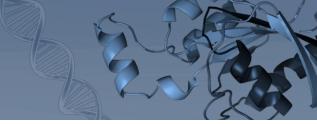


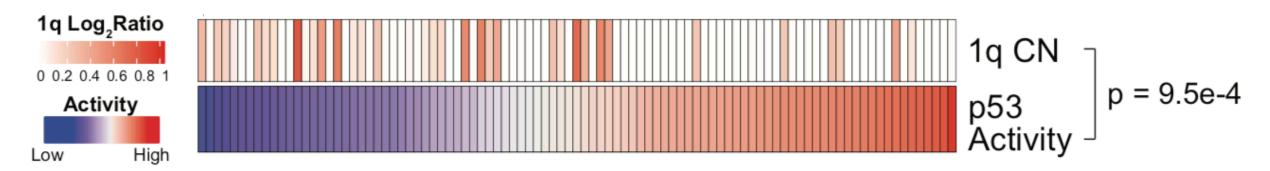


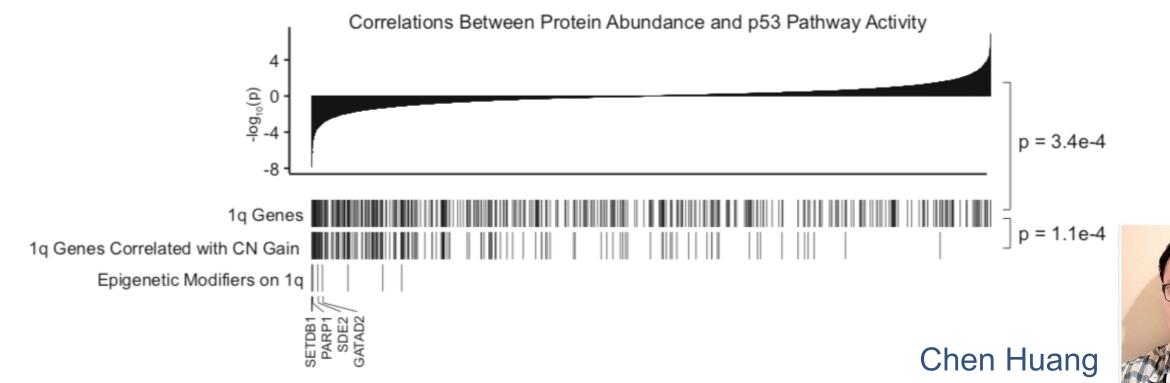


Samuel Payne

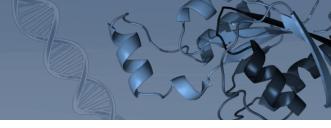
p53 Activity and Chromosome 1q Gain

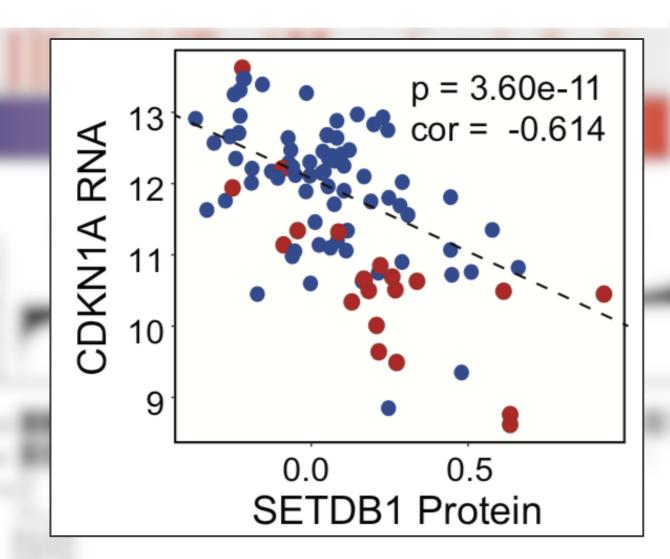




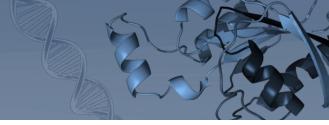


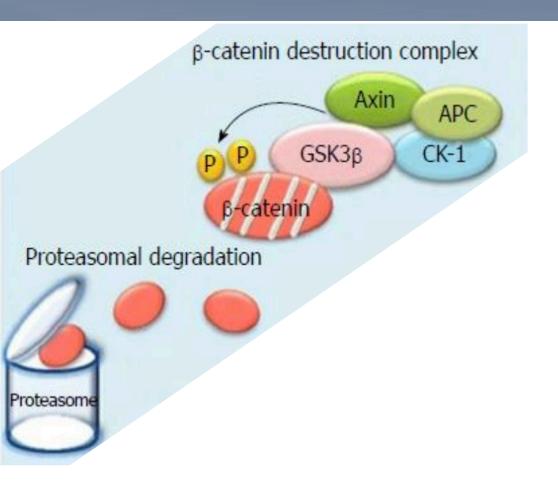
p53 Activity and Chromosome 1q Gain

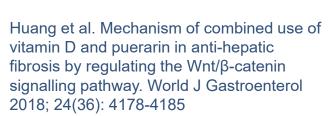


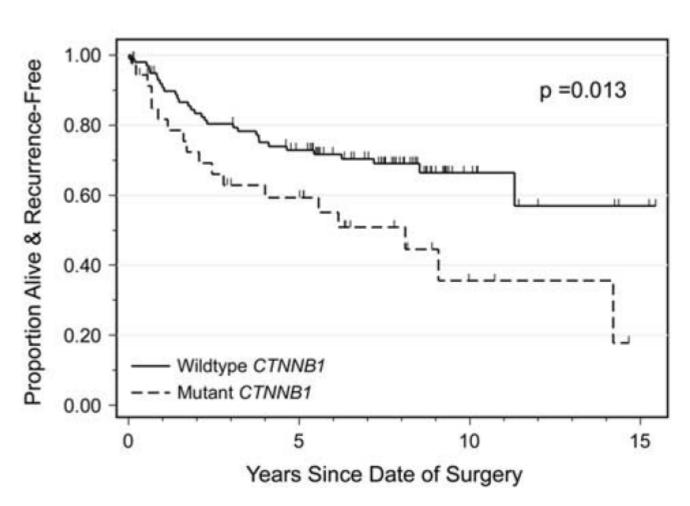


Effects of CTNNB1 Hotspot Mutations



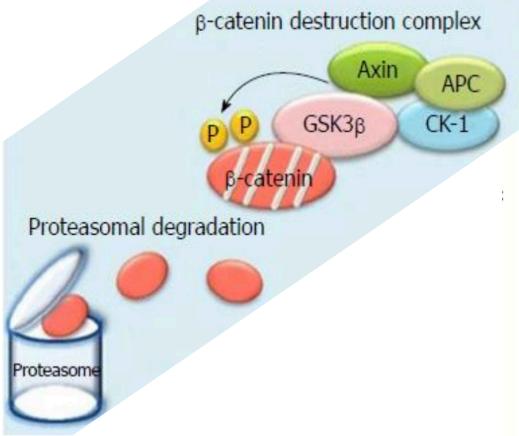




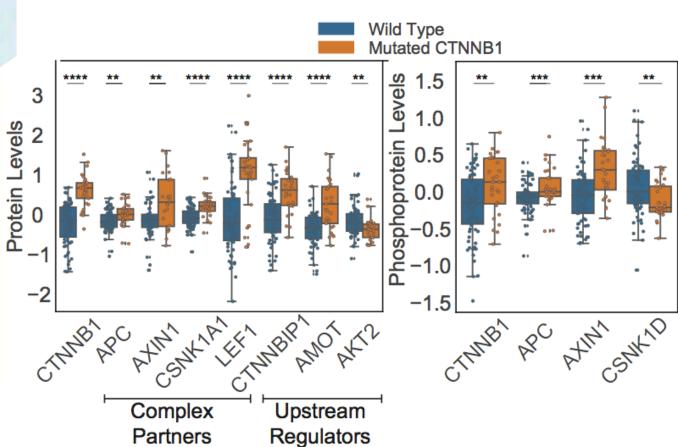


Kurnit et al. CTNNB1 (beta-catenin) mutation identifies low grade, early stage endometrial cancer patients at increased risk of recurrence. Mod Pathol 2017 Jul;30(7):1032-1041.

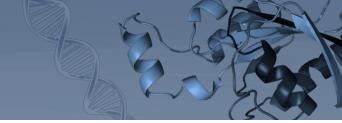
CTNNB1 Mutations and the Destruction Complex

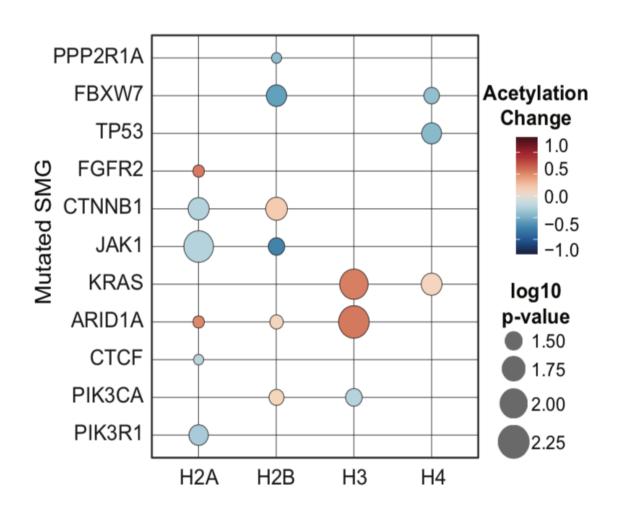


Huang et al. Mechanism of combined use of vitamin D and puerarin in anti-hepatic fibrosis by regulating the Wnt/β-catenin signalling pathway. World J Gastroenterol 2018; 24(36): 4178-4185



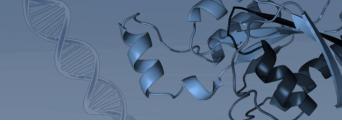
Acetylation and CTNNB1 Mutations

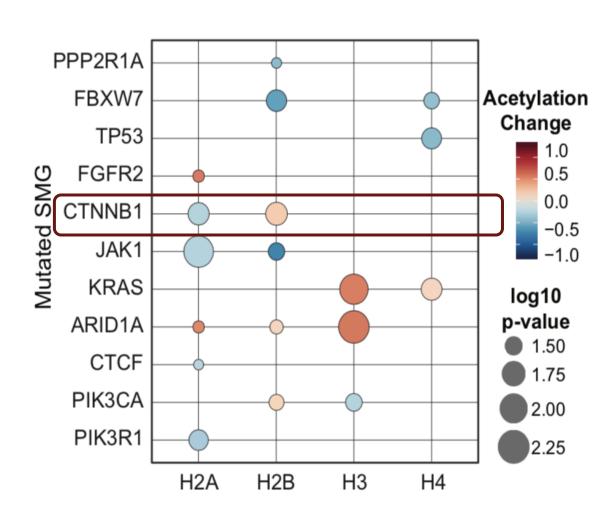


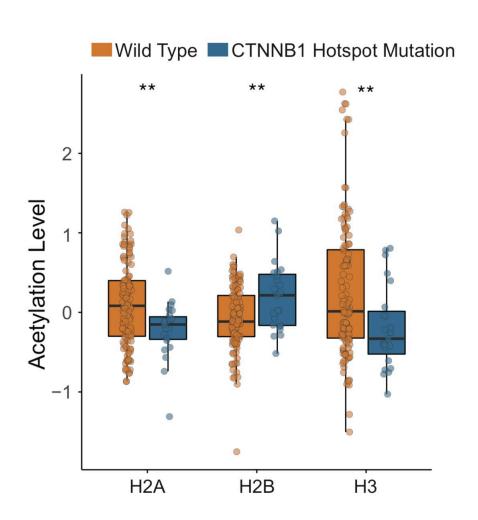




Acetylation and CTNNB1 Mutations

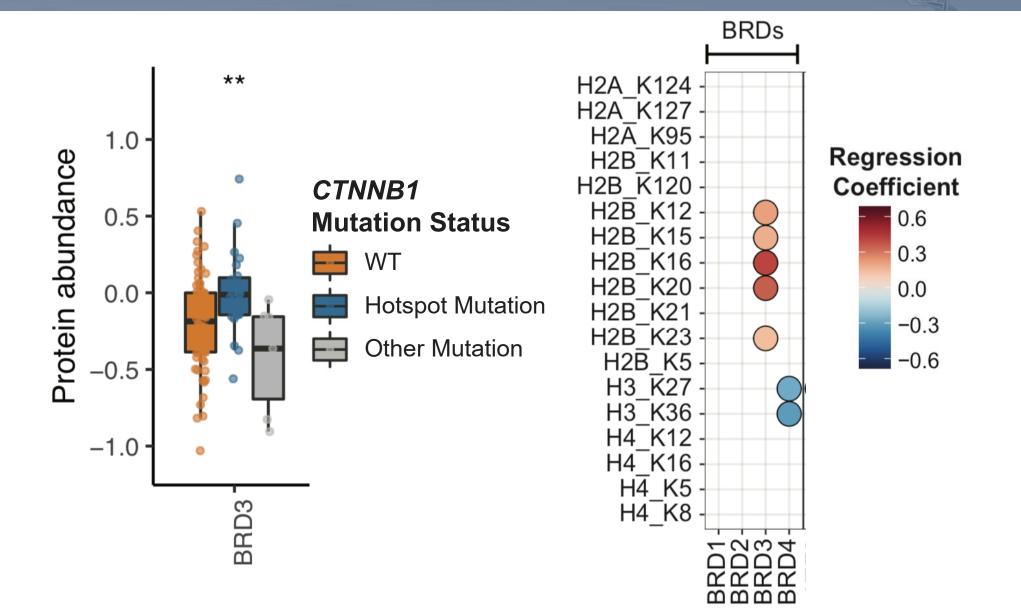




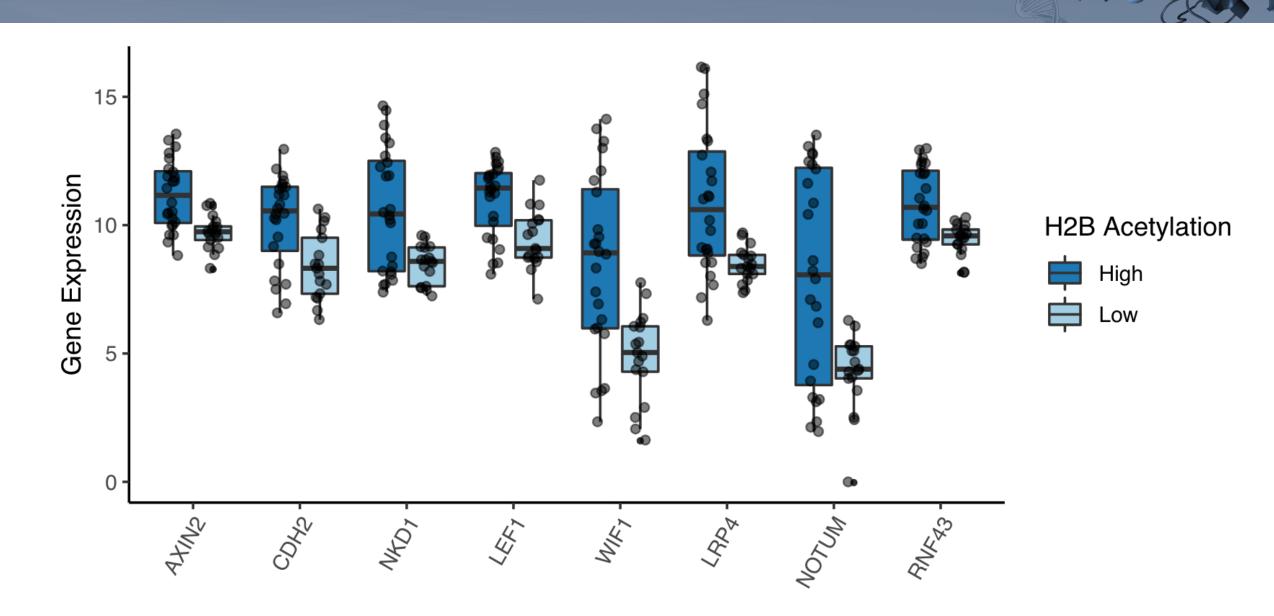


Alla Karpova

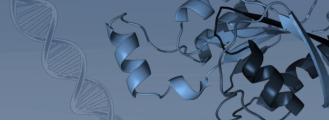
CTNNB1 Mutations and Histone H2B Acetylation

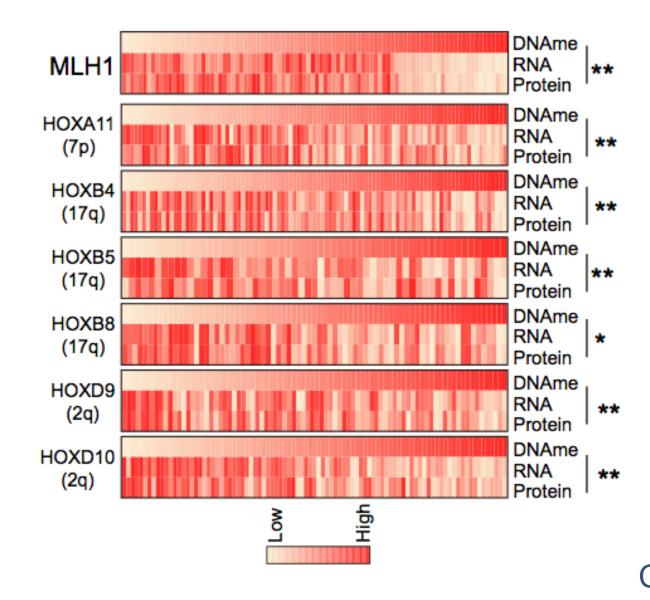


Acetylation, CTNNB1 Mutations, and the Wnt Pathway



DNA Methylation and HOX Proteins

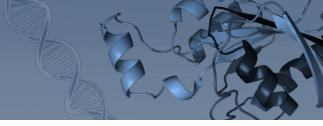


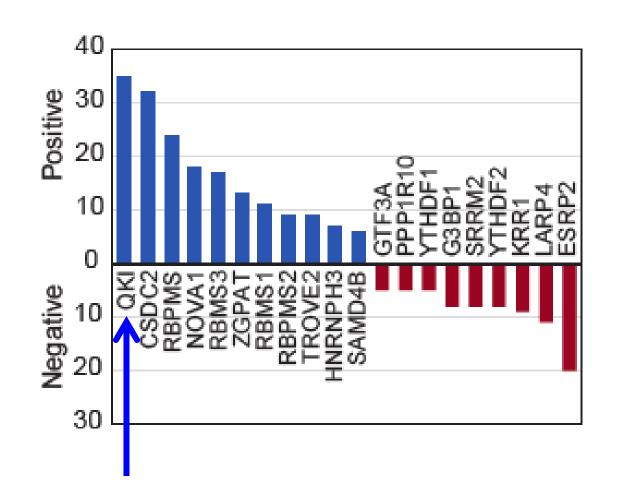


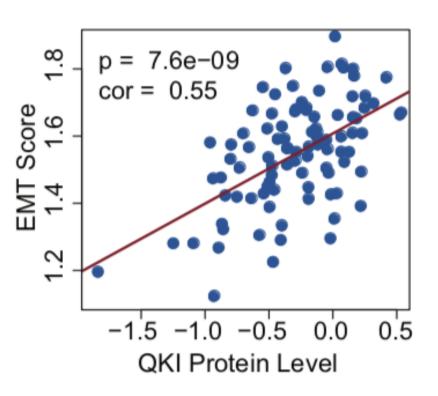


Chen Huang

Circular RNA and the EMT Pathway



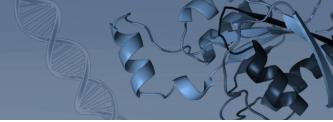


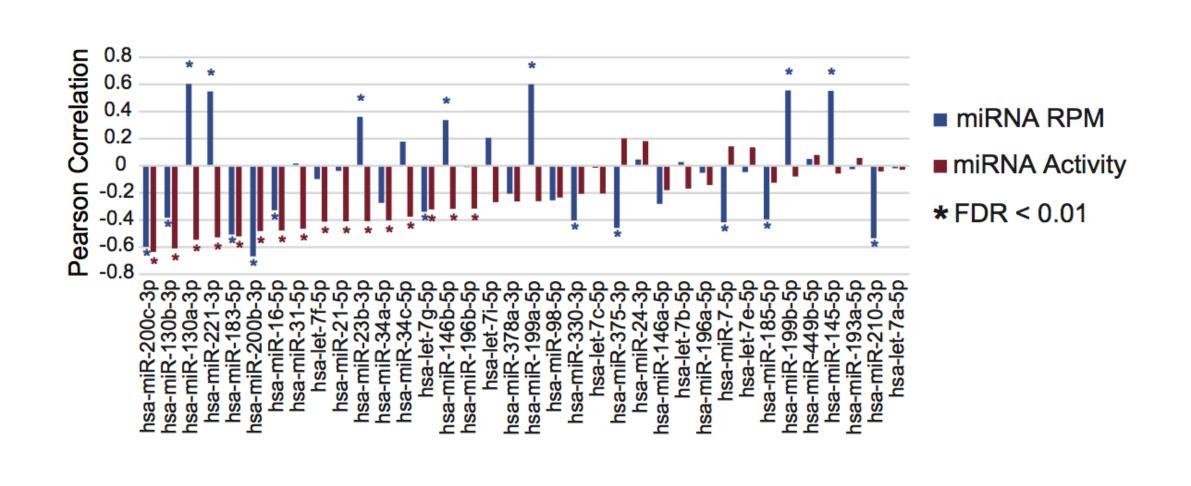




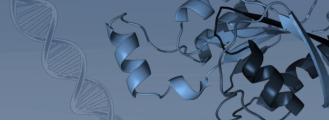
Yongchao Dou

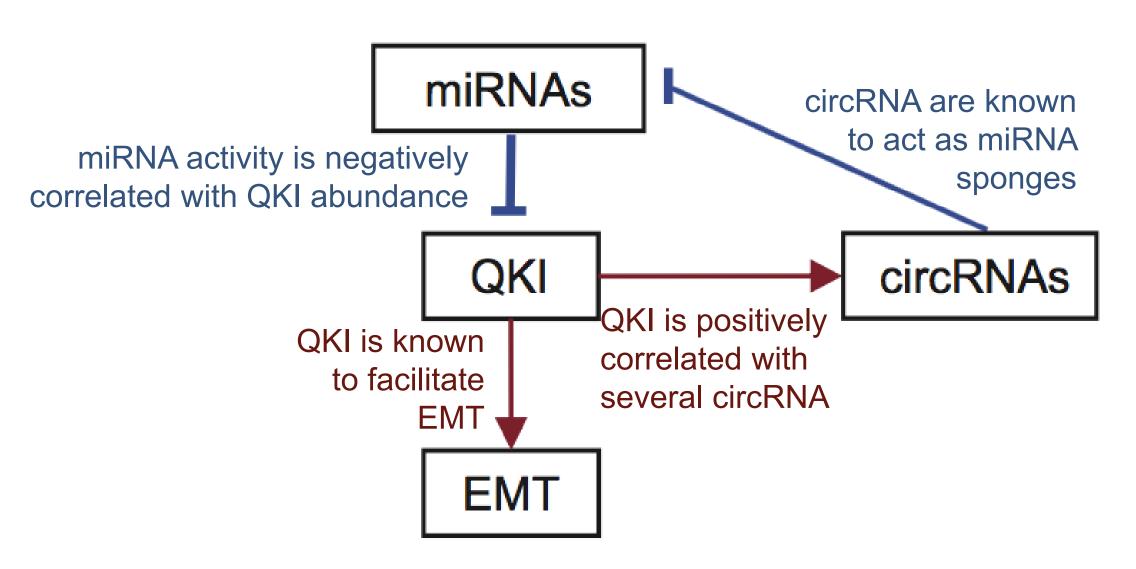
Circular RNA and the EMT Pathway





Circular RNA and the EMT Pathway

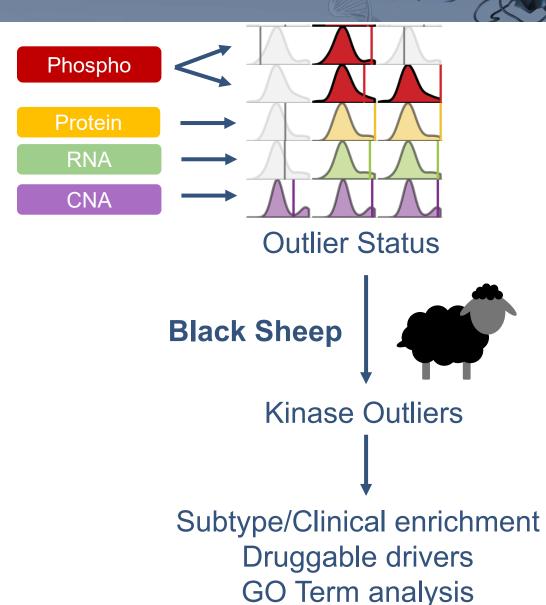




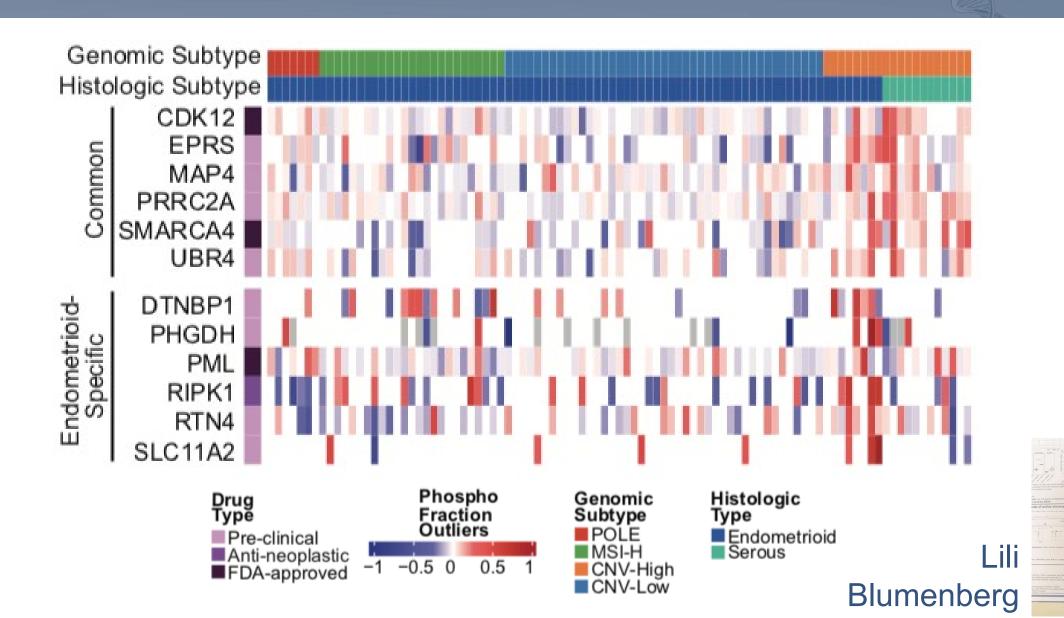
Identifying Aberrant Kinases Using Black Sheep

Methods:

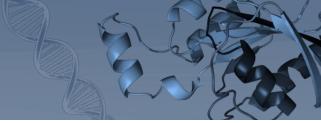
- Create distributions of normalized phosphosite expression across samples
- Flag outliers (>X IQR from median)
- Repeat for CNA, RNA and protein expression if desired
- Why focus on kinases?
 - Play key roles in cancer development and progression
 - Many highly selective and effective therapies directed against kinases

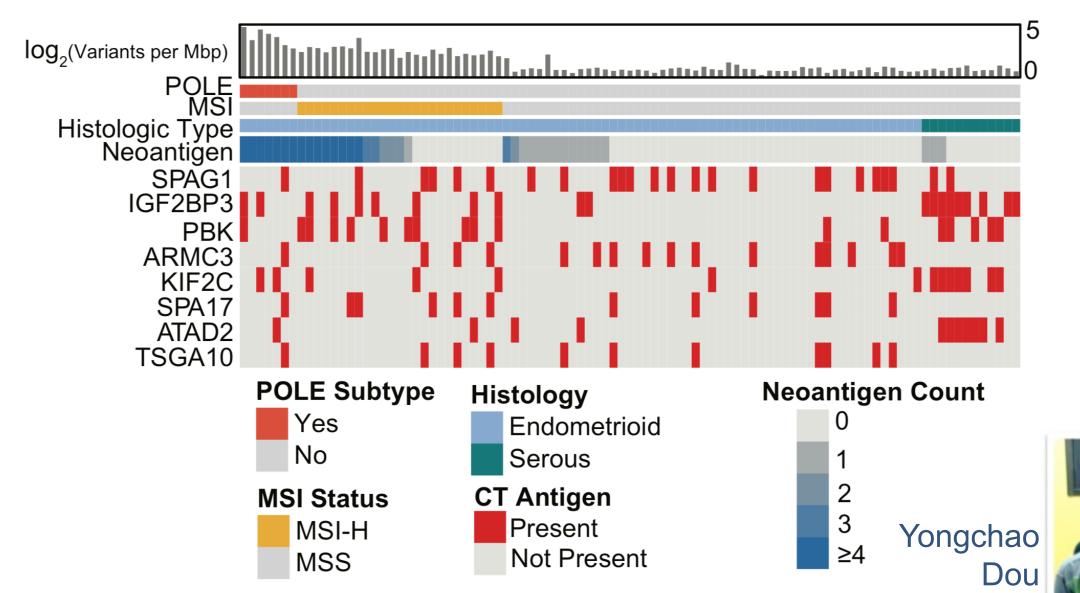


Phosphoproteomic Analysis of CNV-High Patients

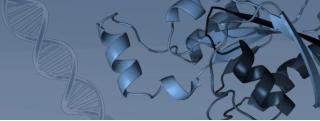


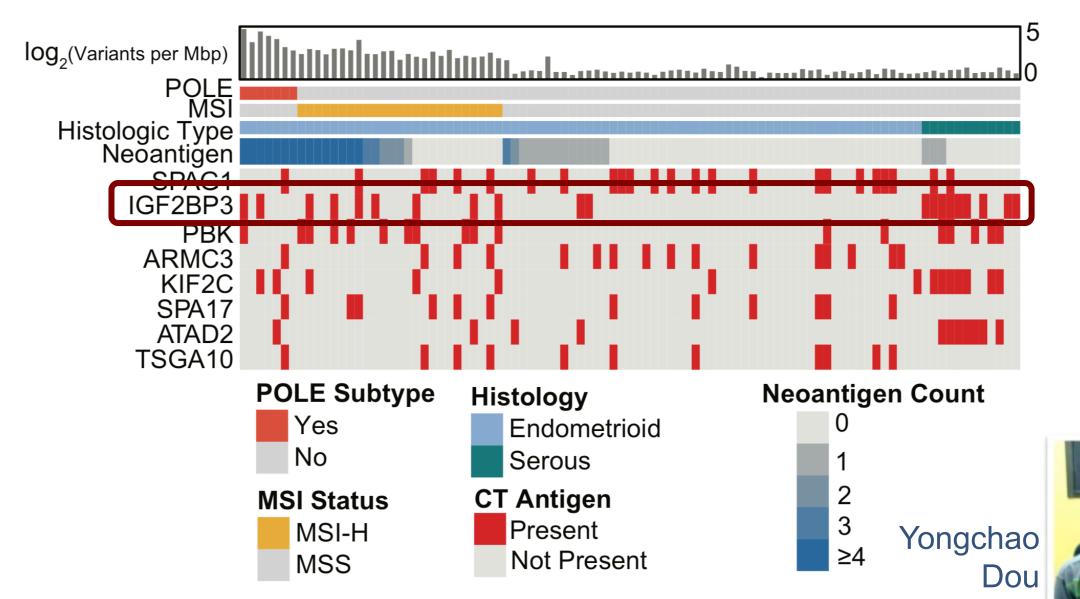
C/T Antigens and Putative Neoantigens



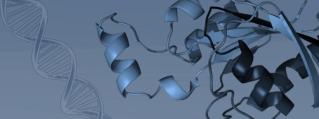


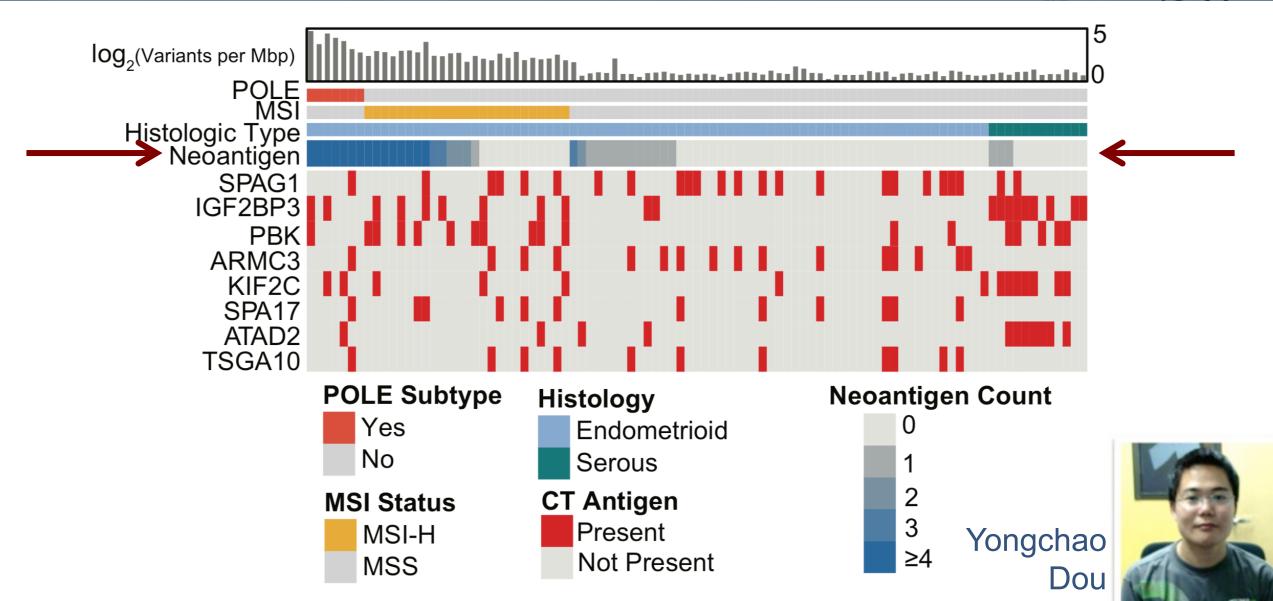
C/T Antigens and Putative Neoantigens



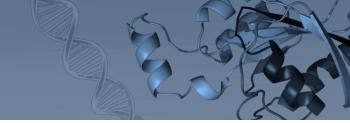


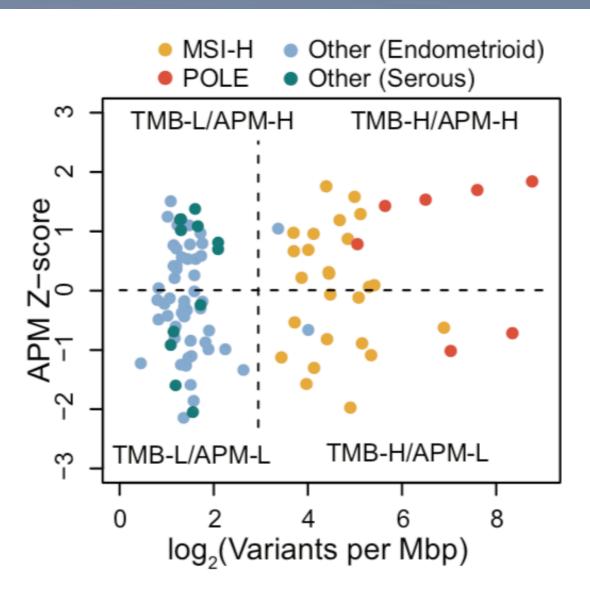
C/T Antigens and Putative Neoantigens



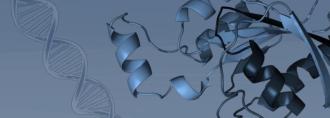


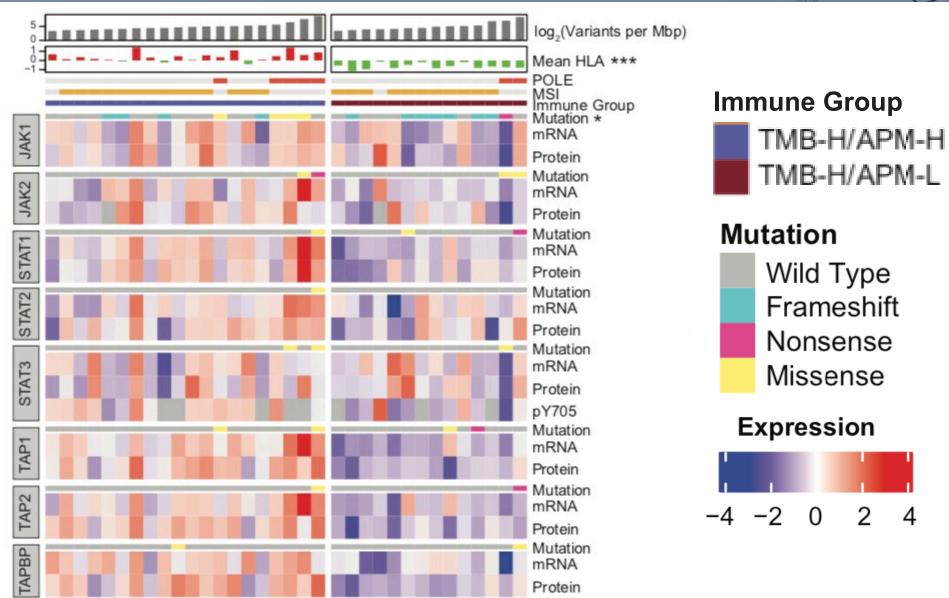
Tumor Immune Subgroups





Markers of Immune Evasion





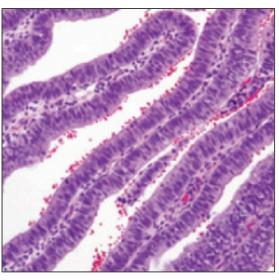
Protein

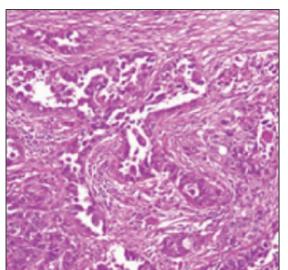
Major Takeaways

- Comprehensive proteogenomic characterization of 95 endometrial carcinomas
- Proteomic, phosphoproteomic, and acetylomic coidentification of CTNNB1 complex partners and upstream regulators via mutation association analyses
- Proteomics data identifies putative EMT regulator QKI via circRNA
- Multi-omic analysis pinpoints potential therapeutic targets in clinically significant patient subsets
- Immune groupings identify immunotherapy candidates

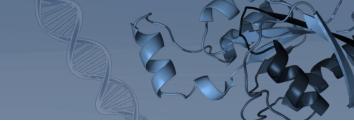
How Can Imaging Help?

- Differentiation between serous and endometrioid
- Differentiation between genomic subtypes
- Annotation of specific features characteristic of certain subgroups





Where Is The Data?



CPTAC-UCEC

\$	Radiology Image Statistics	Pathology Image Statistics
Modalities	CT, MR, PT, CR, DX, SR	Pathology
Number of Patients	60	250
Number of Studies	84	N/A
Number of Series	1,257	N/A
Number of Images	121,109	888
Images Size (GB)	46.9	154

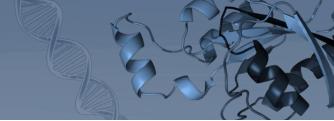
TCGA-UCEC

Image Statistics		
Modalities	CT, CR, MR, PT	
Number of Patients	65	
Number of Studies	226	
Number of Series	912	
Number of Images	75,829	
Images Size (GB)	36.1	

https://www.cancerimagingarchive.net/

Path images for 560 more patients: https://portal.gdc.cancer.gov/projects/TCGA-UCEC

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