

The Cancer Proteome Atlas

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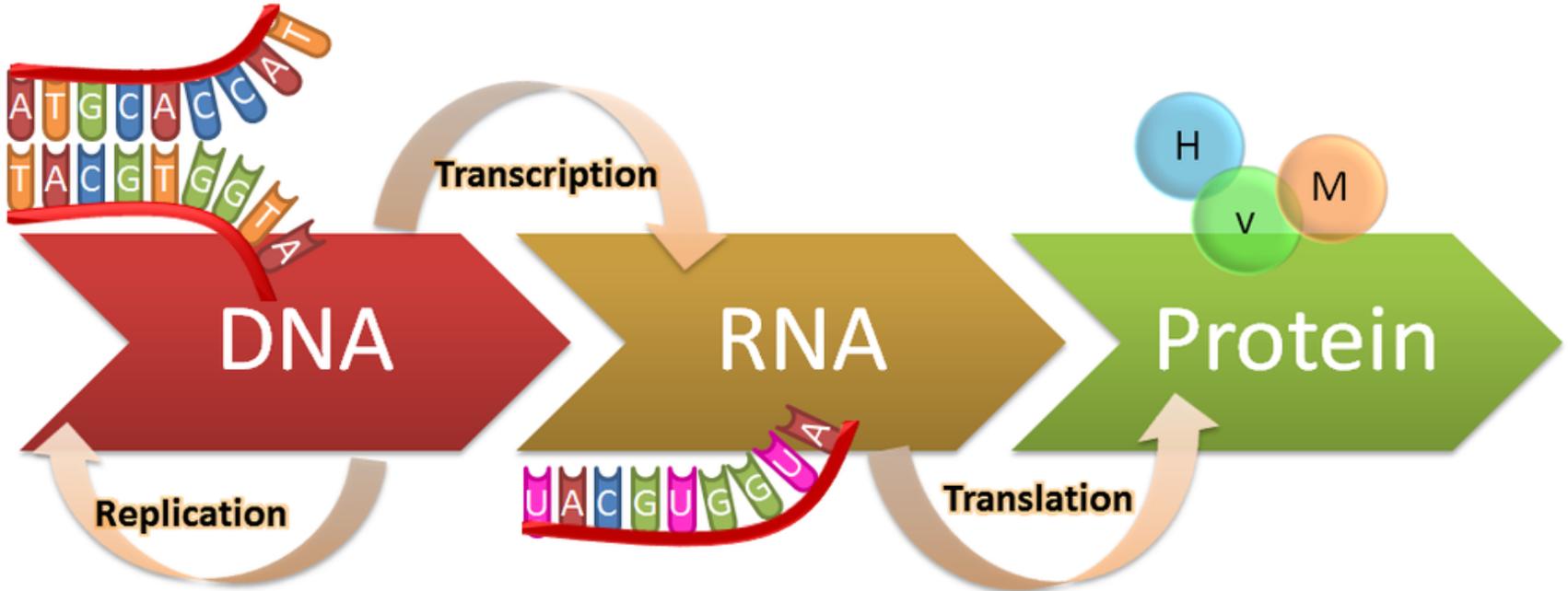
**MDAnderson
Cancer Center**

Making Cancer History®

Grant no.; U24CA209851-01

Co-PI: Gordon Mills

Functional Proteomics

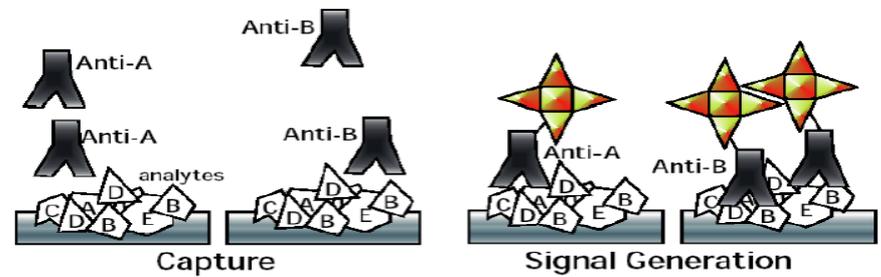
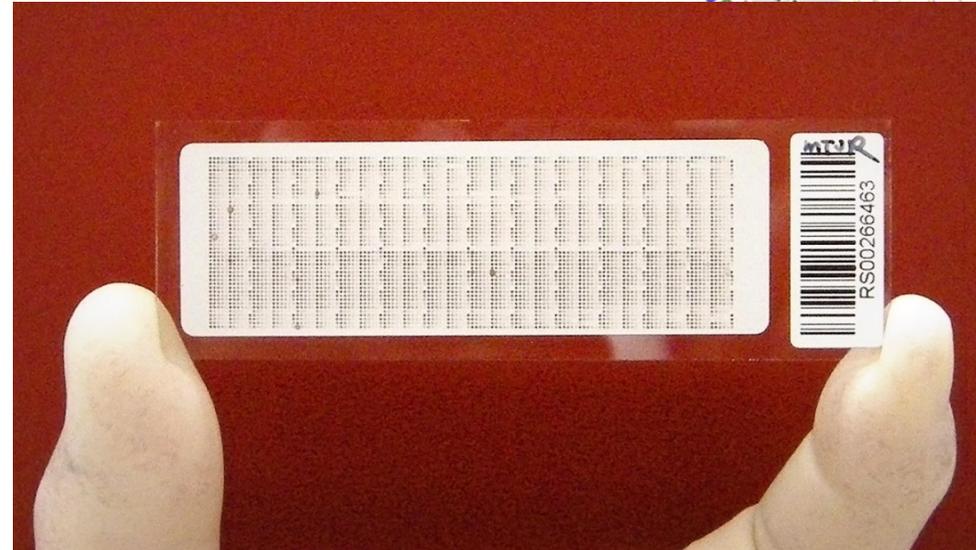


It is PROTEINS, rather than DNA or RNA, that are the basic functional units in various biological processes and the targets of cancer therapy.

Functional Proteomics

REVERSE PHASE PROTEIN ARRAYS

- Inexpensive, high-throughput method utilizing automation for increased quality and reliability
- Sample preparation requirements are similar to that of Western blots
- Sensitive to detect signals at Femtomogram level. Complete assay requires only 40 micrograms of cellular protein in 40 microliters of each sample for 302 antibodies
- Robust quantification due to serial dilution of samples
- Up to 1056 samples per slide with 1000 controls
- Dot blot: Less sensitive to degradation
- Require high quality validated antibodies and robotics



Complexity of Data Analysis of Reverse Phase Protein Array



Frozen Tumor Samples

Culture cells in regular condition

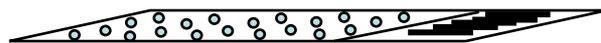
Protein extraction

Lysed cells and Extract protein

Adjust protein concentration
And denature protein by SDS

Serial dilution
(2-fold for 5 dilutions)
>1000 control samples for Quality Control,
Spatial Correction and Merging data across
slides

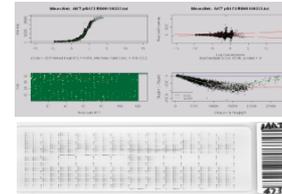
Array on nitrocellulose coated slides



Probe with validated antibodies
Signal detection by
DAB colorimetric reaction

Spot density determination by **Array Pro**
(Automatic spot finding and background subtraction)

Protein concentration determination
By **Super Curve Fitting**



Spatial
Correction
Quality Control
Curve Fitting

Normalization for protein loading
Merging data across slides

Excel file of protein expression
and modification
(relative concentration)

MD Anderson RPPA Platform



- *Characterized >100,000 samples for users worldwide*
- *Characterized >10,000 patient samples through The Cancer Genome Atlas (TCGA)*
- *One of two NCI Genome Characterization Centers*
- *Will characterize the samples from important ongoing NCI initiatives from the Exceptional Responders Initiative and the ALCHEMIST precision medicine trials.*

The Cancer Proteome Atlas

THE UNIVERSITY OF TEXAS
MD Anderson
Cancer Center

Making Cancer History*

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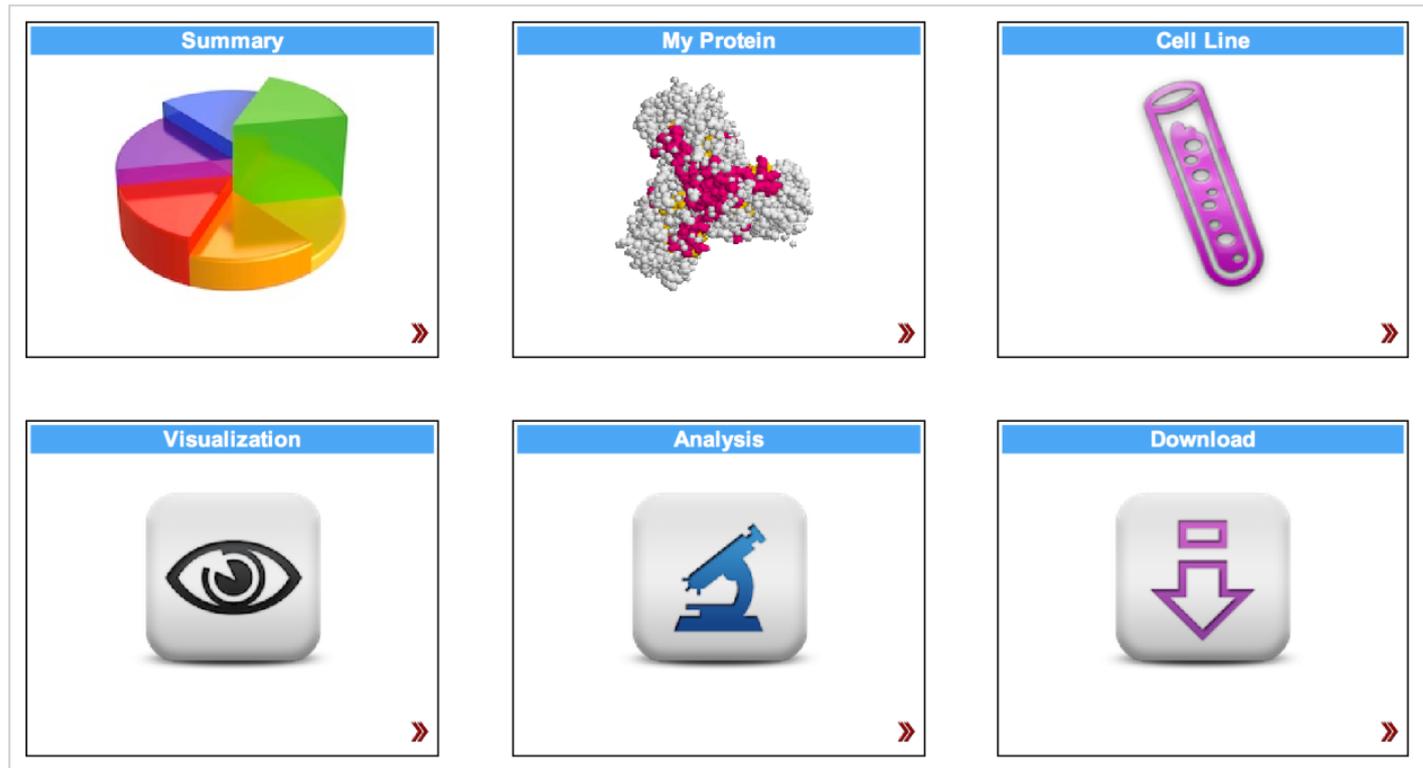
Credits

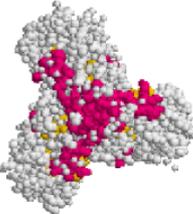
Forum

Contact

The Cancer Proteome Atlas

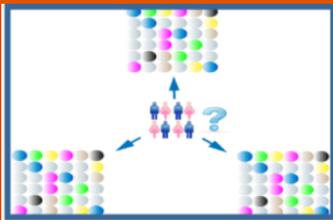
Enable Scientific Discovery through Functional Proteomics



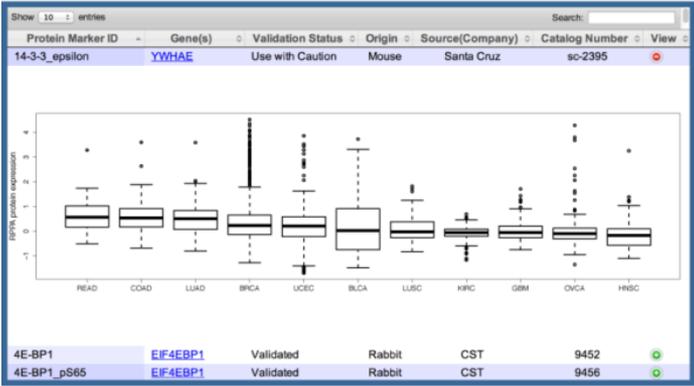
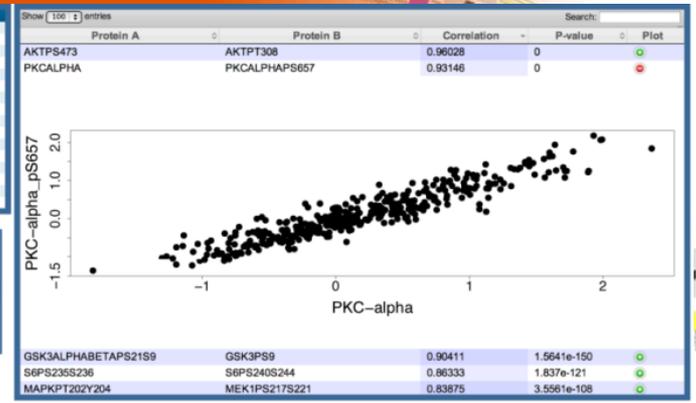
Summary  »	My Protein  »	Cell Line  »
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The Cancer Proteome Atlas (TCPA) is a joint project of the Departments of [Systems Biology](#) and [Bioinformatics & Computational Biology](#) at [The University of Texas MD Anderson Cancer Center](#).

This website is for educational and research purposes only.



Data Set	Source	#Samples	#Protein
BLCA	TGSA	527	191
BRCA	TGSA	137	191
COAD	TGSA	334	191
GBM	TGSA	218	191
HNSC	TGSA	272	191
KIRC	TGSA	454	191
LIAD	TGSA	237	191
LUSC	TGSA	188	191
OVCA	TGSA	472	191
PRAD	TGSA	138	191
LEUC	TGSA	404	191
Cell Line Set 20	MDACC	289	209
Cell Line Set 35	MDACC	197	191
Cell Line Set 40	MDACC	89	191
Cell Line Set 51	MDACC	244	191
Proteome	MDACC	244	191



Cell Line



Summary



My Protein



Analysis

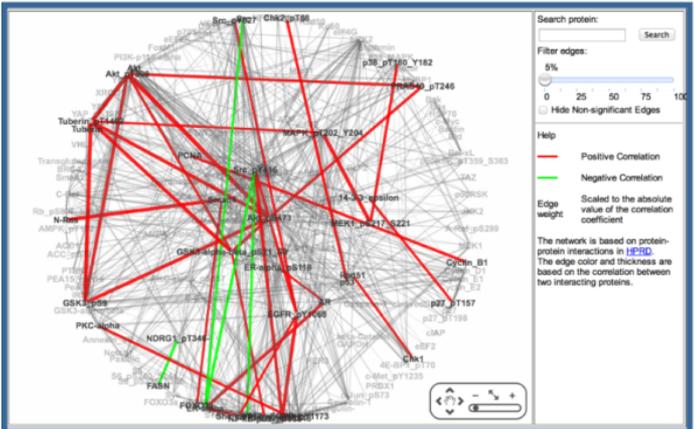
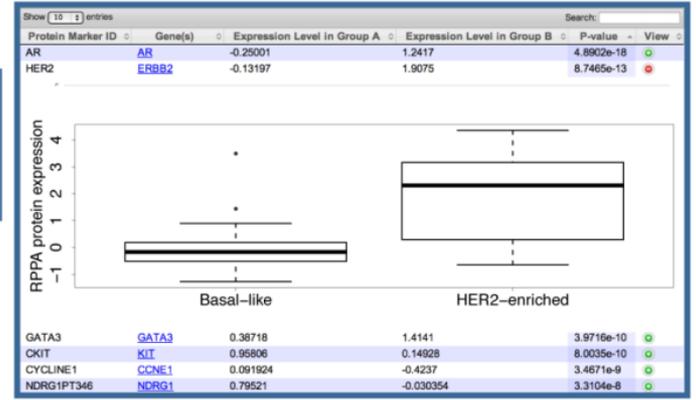


Visualization



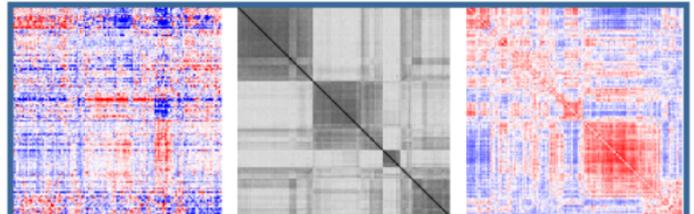
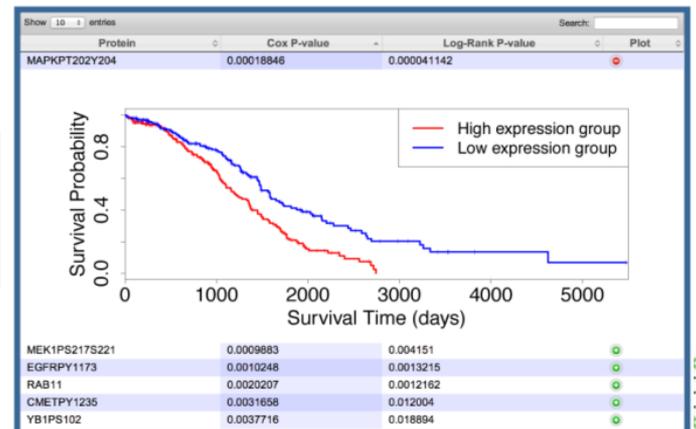
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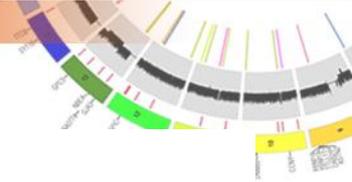


Downloads

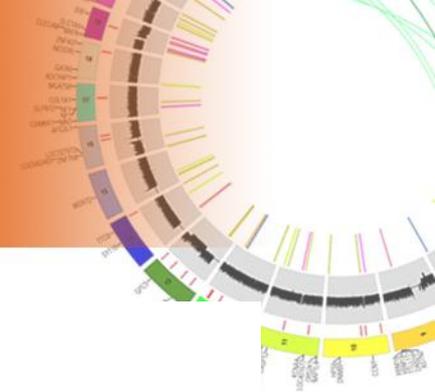
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 - 📁 TCGA
 - 📁 BLCA
 - 📁 Level 3
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 - 📁 COAD
 - 📁 GBM
 - 📁 HNSC
 - 📁 KIRC
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 - 📁 OVCA
 - 📁 PANCAN11
 - 📁 READ
 - 📁 UCEC
 - 📁 MDAAC



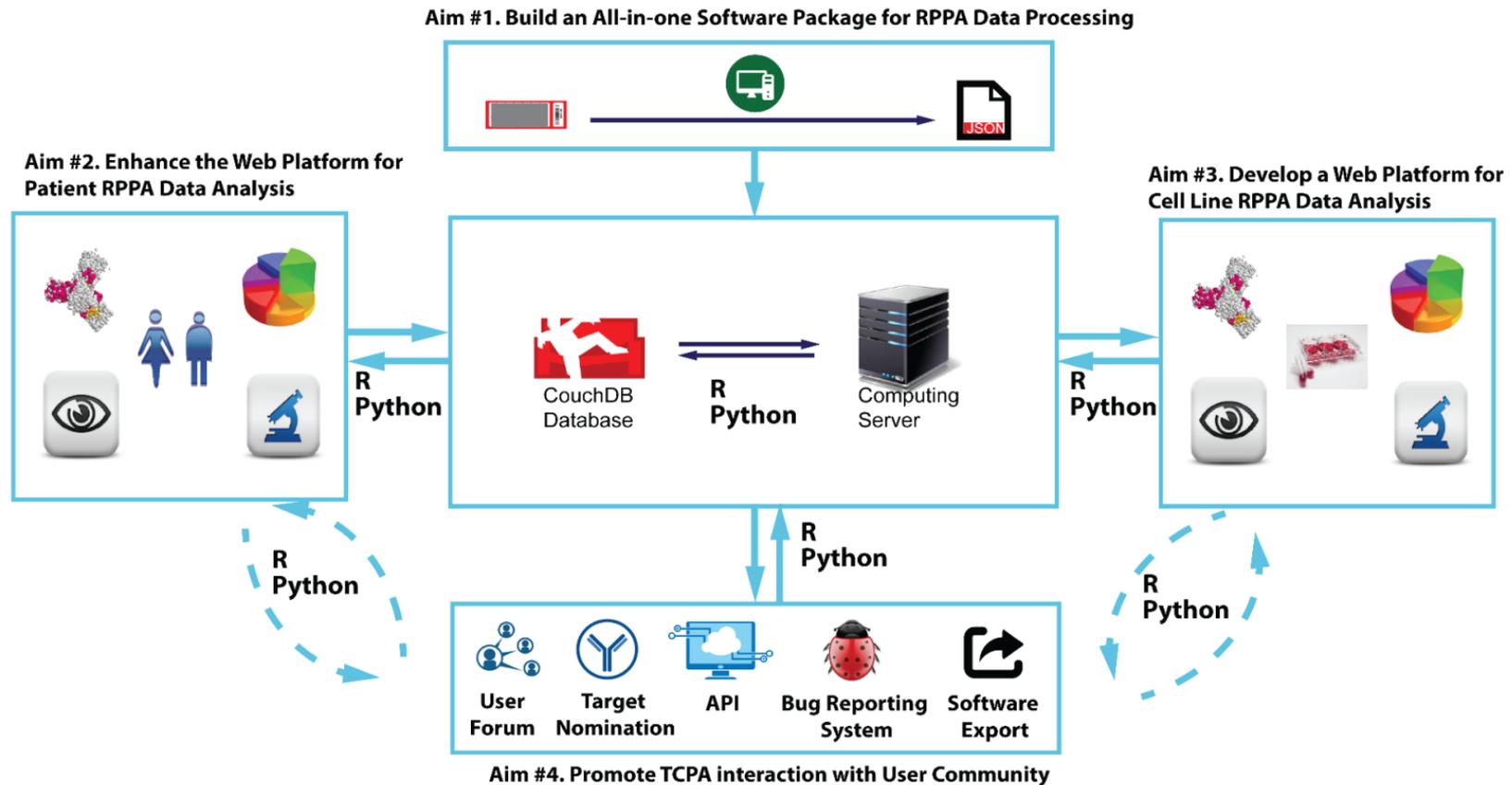
>8000 users from >90 countries



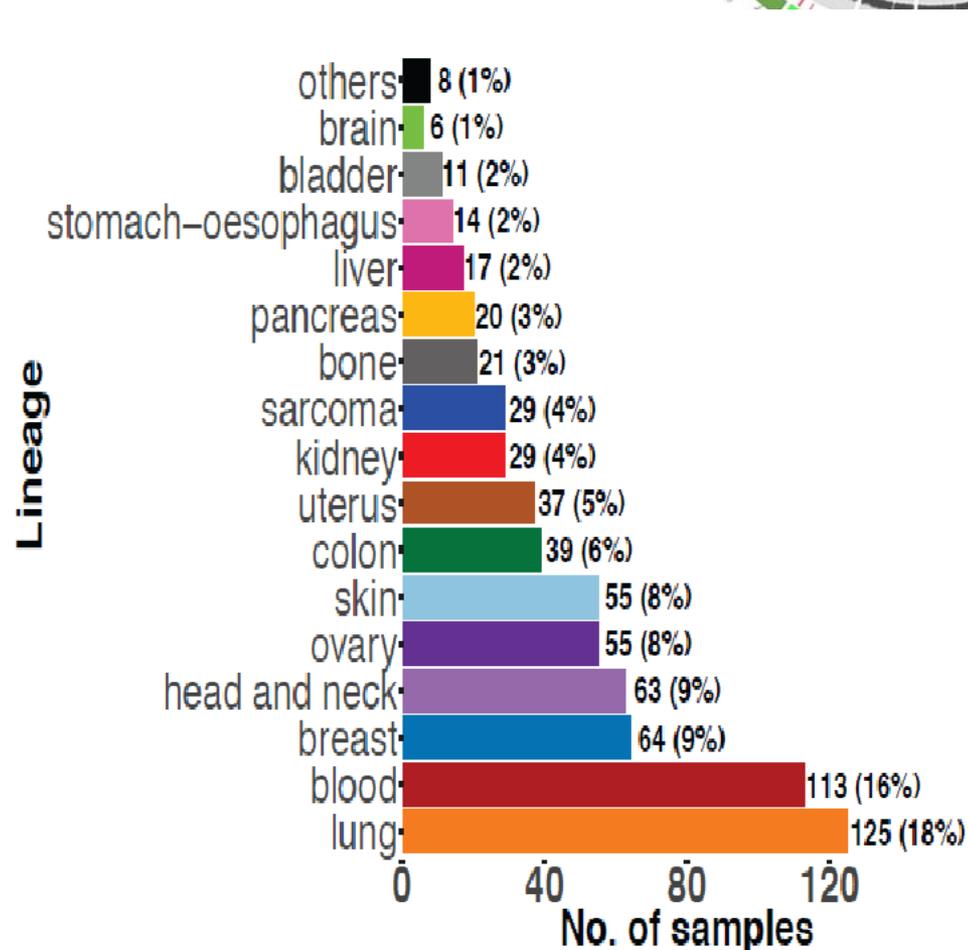
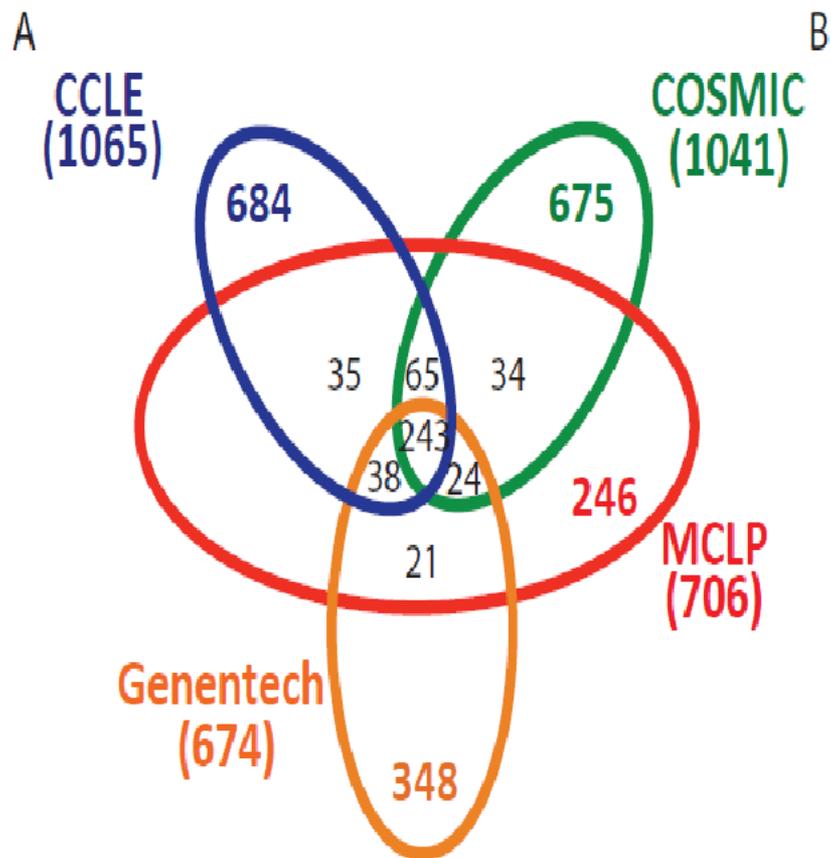
Overview of the U24 Project



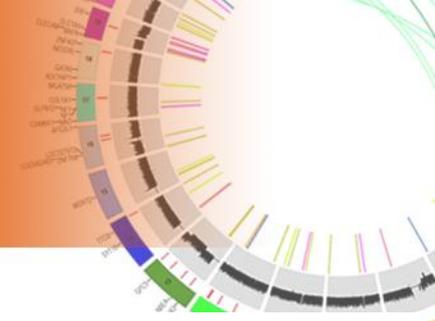
The Cancer Proteome Atlas



RPPA profiling of large-scale cell lines

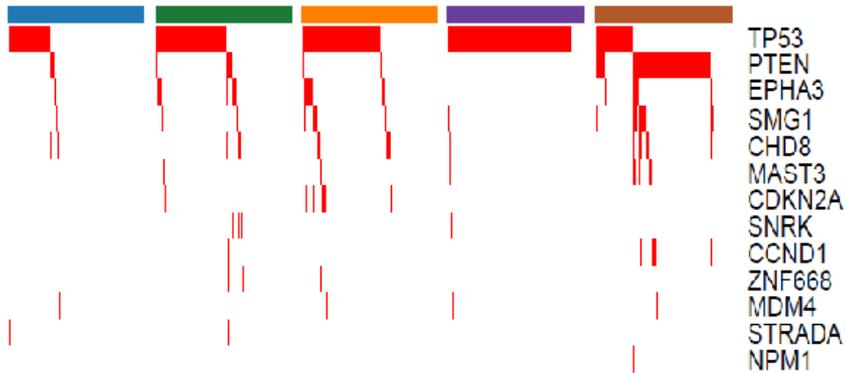


Similarity of cell lines and patient samples

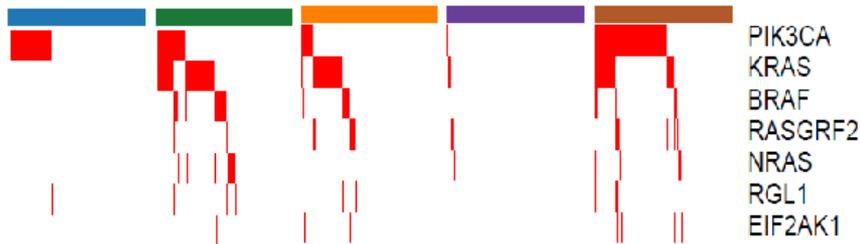


Patient Cohorts

p53 signaling



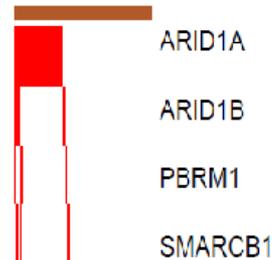
PI3K signaling



Notch signaling

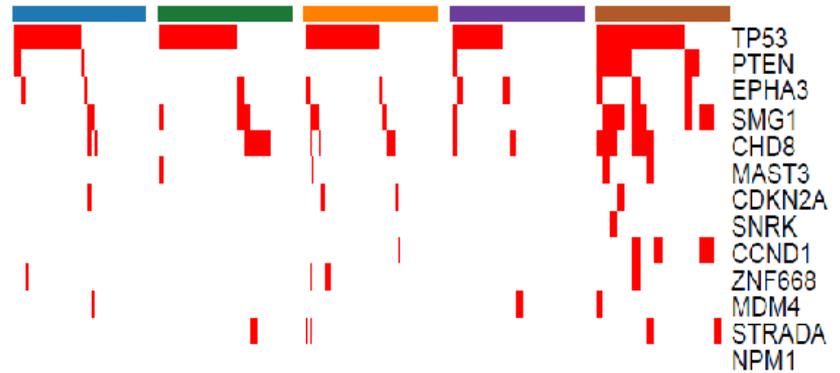


SWI/SNF complex

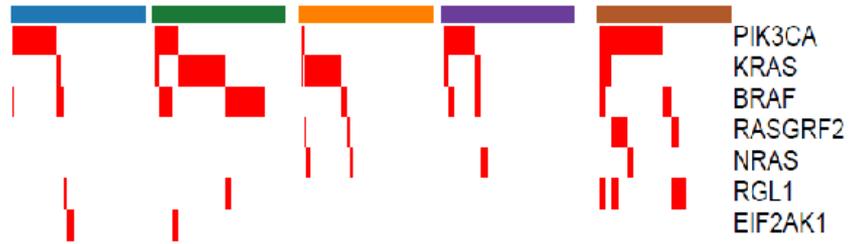


Cell lines

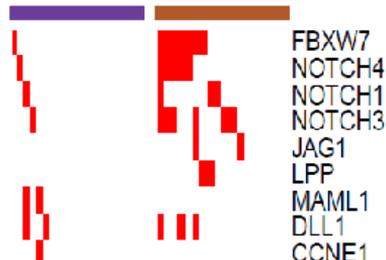
p53 signaling



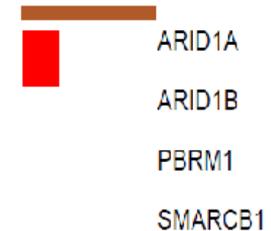
PI3K signaling



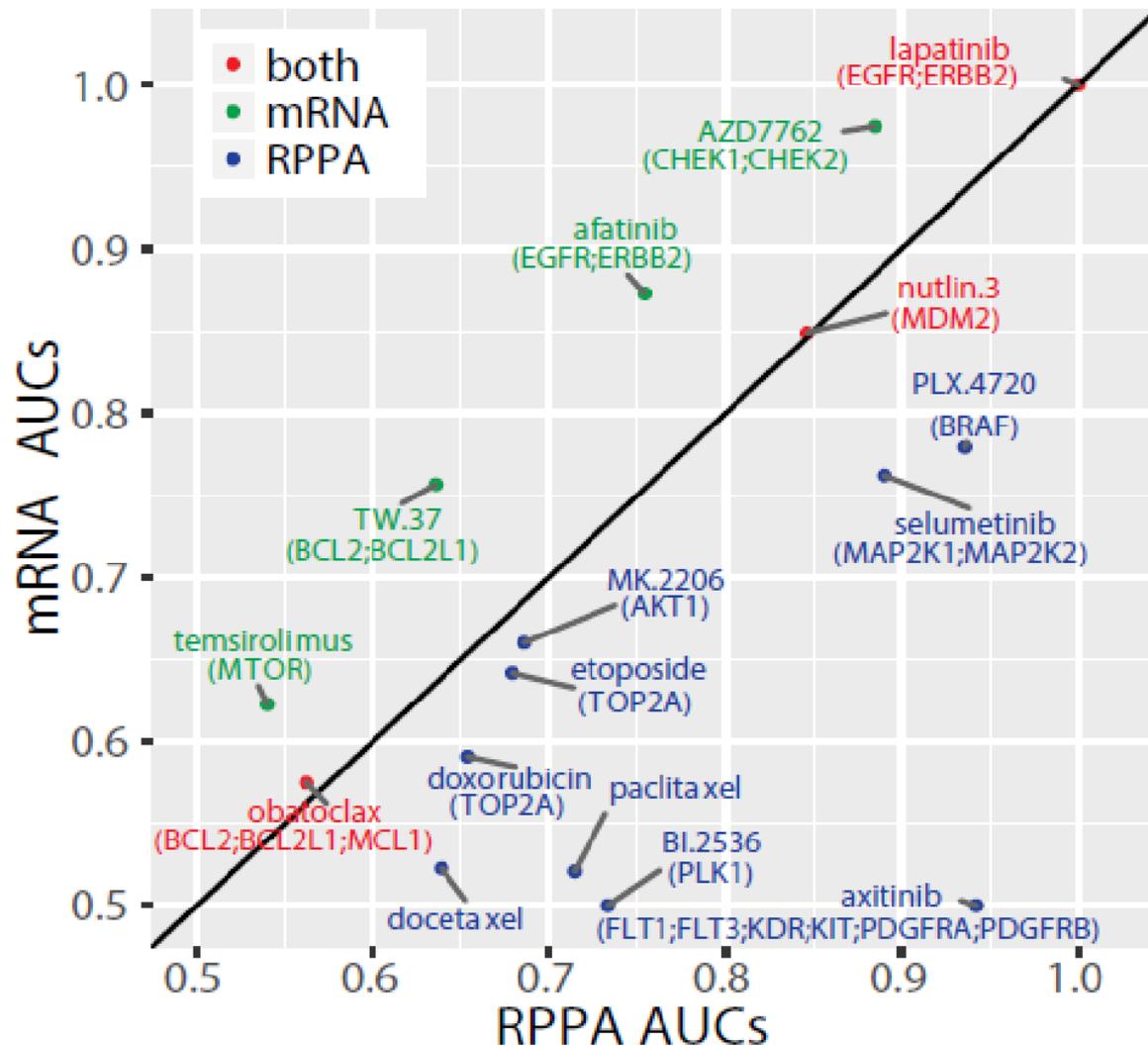
Notch signaling



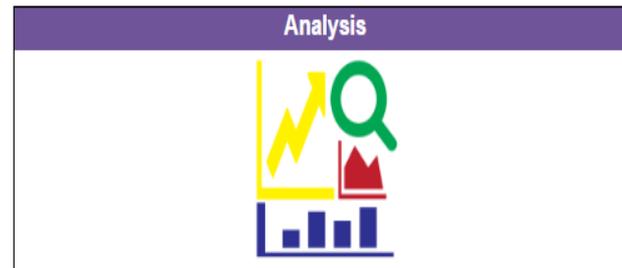
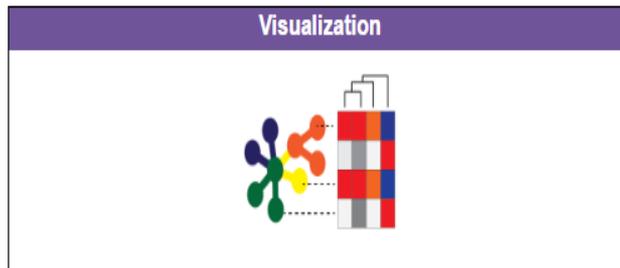
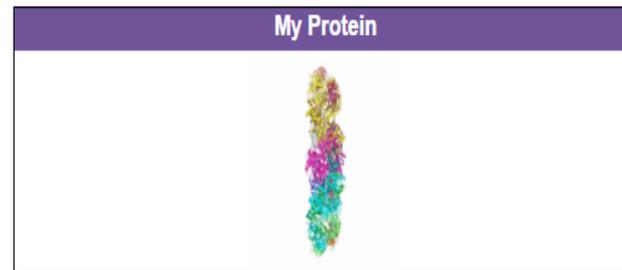
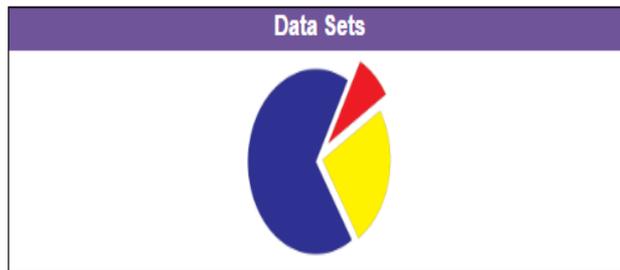
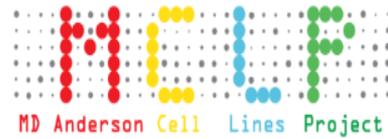
SWI/SNF complex



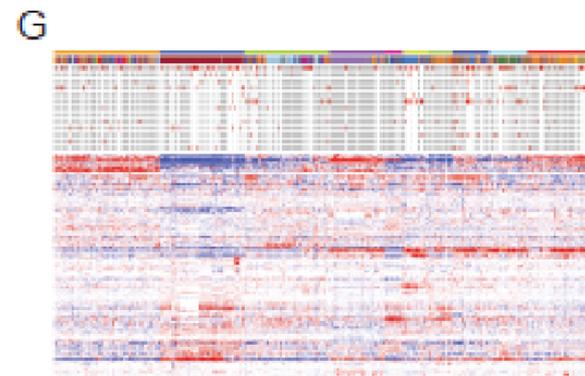
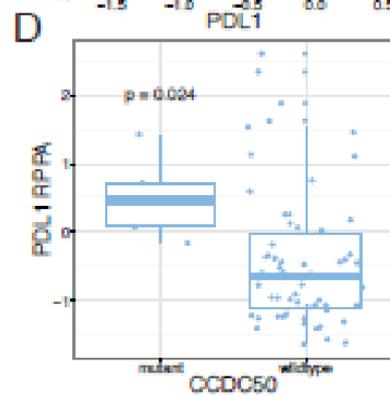
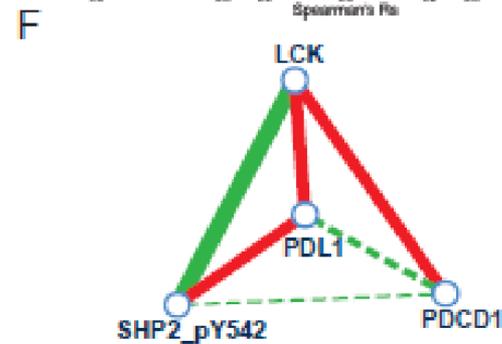
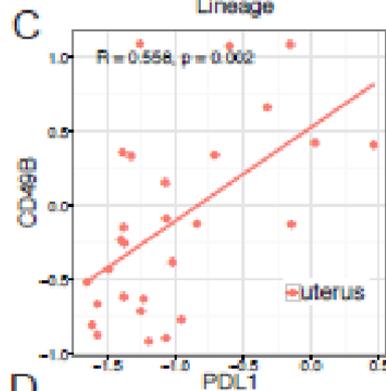
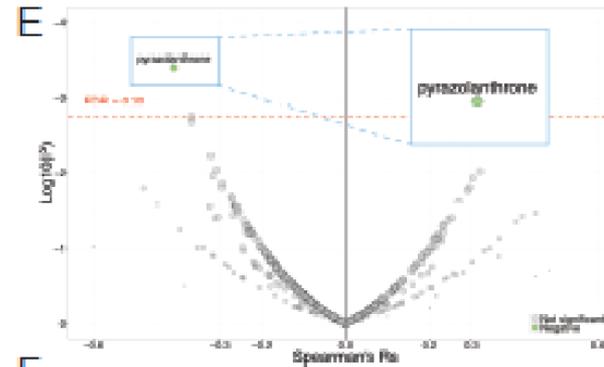
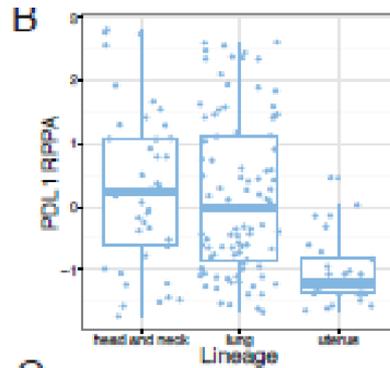
Predictive power for drug sensitivity



MD Anderson Cell Lines Project



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Acknowledgements

MD Anderson

Gordon Mills

John Weinstein

Yiling Lu

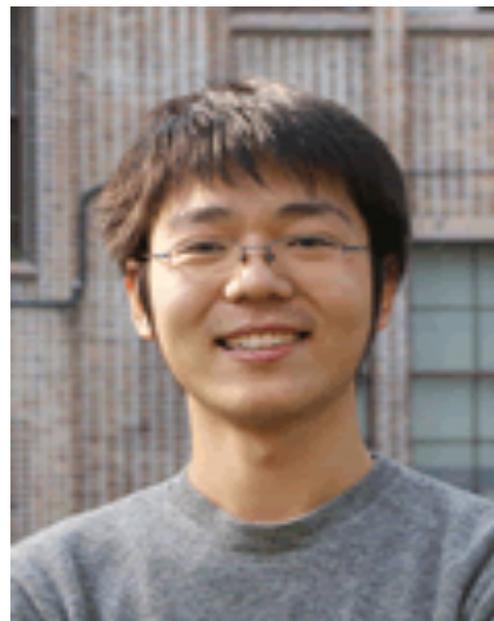
Rehan Akbani

Brad Broom

Jun Li

Wei Zhao

Levi Garraway (Broad)



Jun Li

