



Analyzing Tumor Atlas Datasets from the NCI HTAN Network with the Galaxy Computational Platform

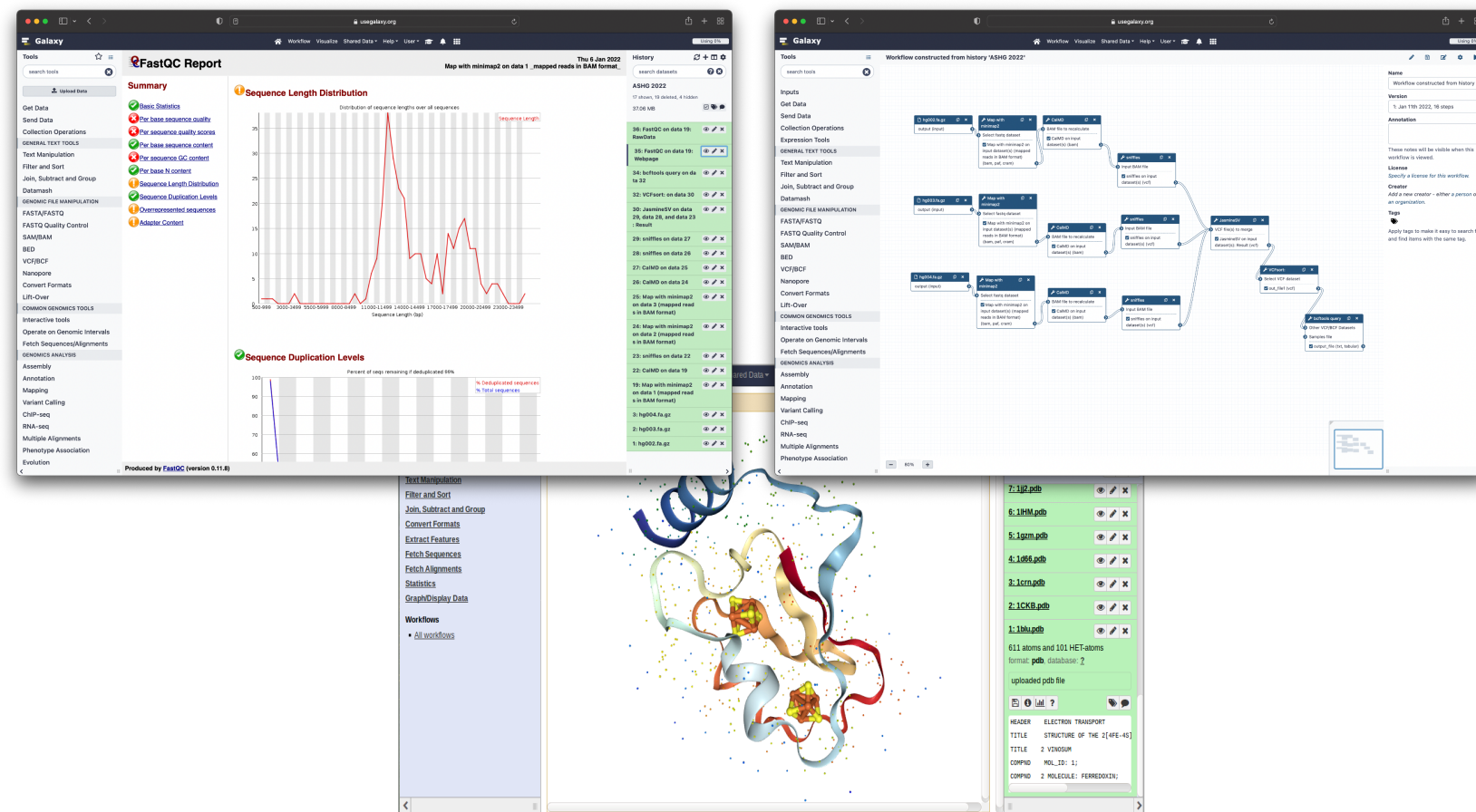
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Enis Afgan², Michael Schatz², and [Jeremy Goecks](#)¹

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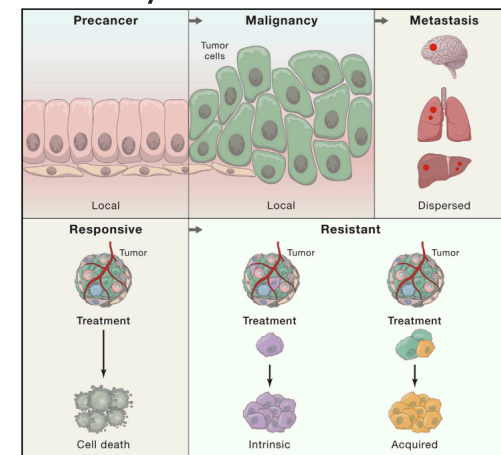
Galaxy

HTAN

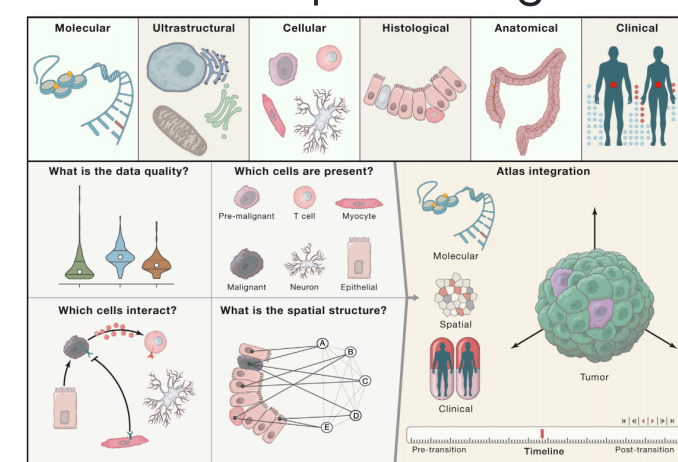
HUMAN TUMOR ATLAS NETWORK



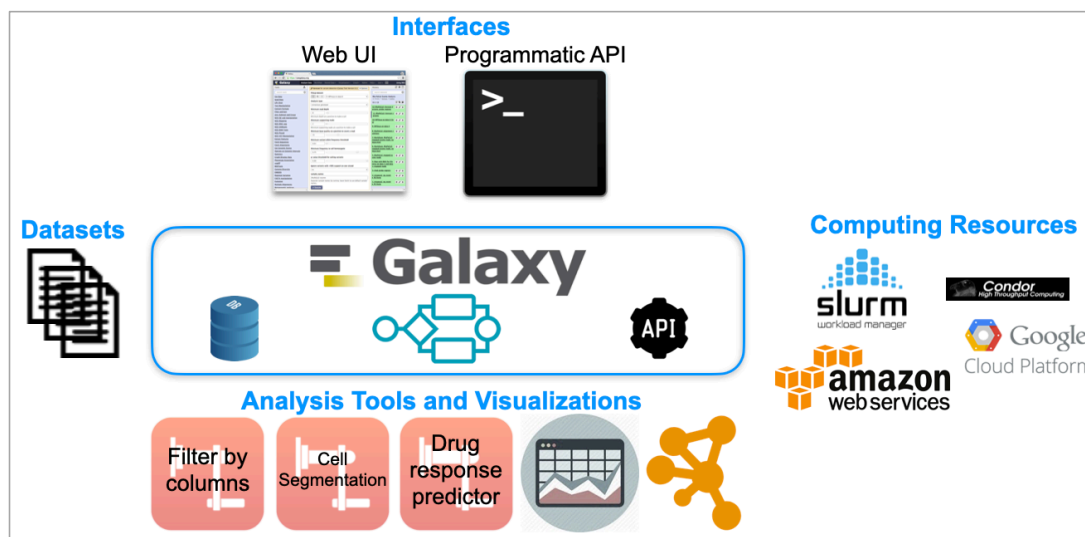
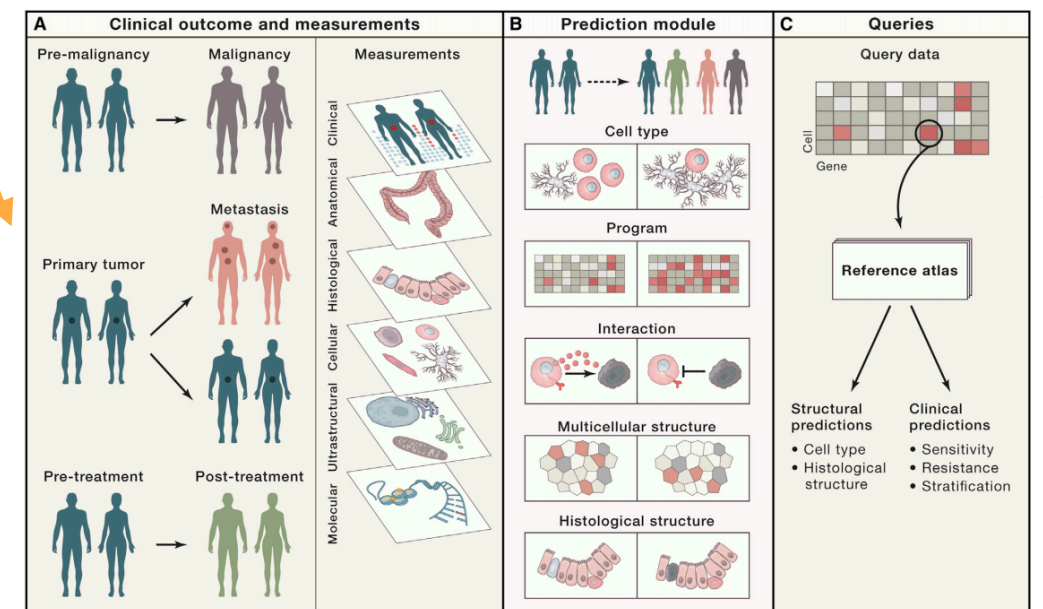
Key Transitions



Deep Profiling

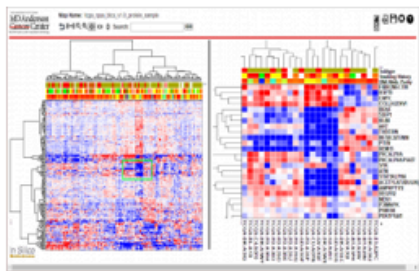


Systems Biology Understanding and Clinical Predictors

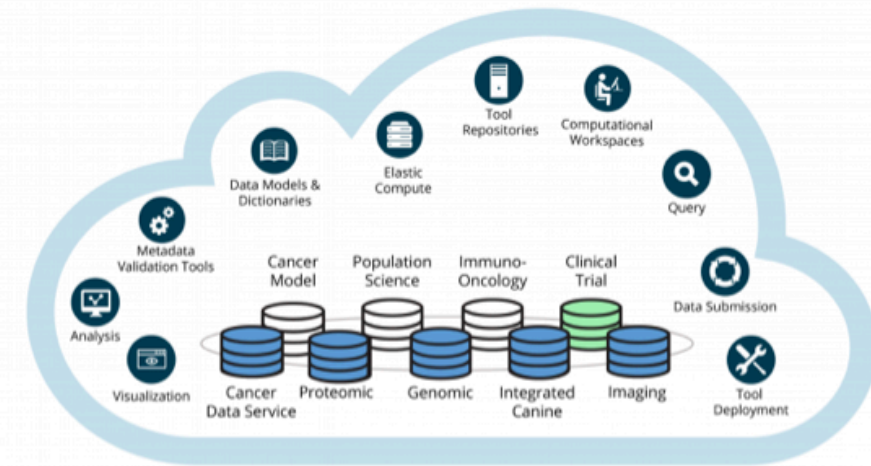


Galaxy ITCR U24

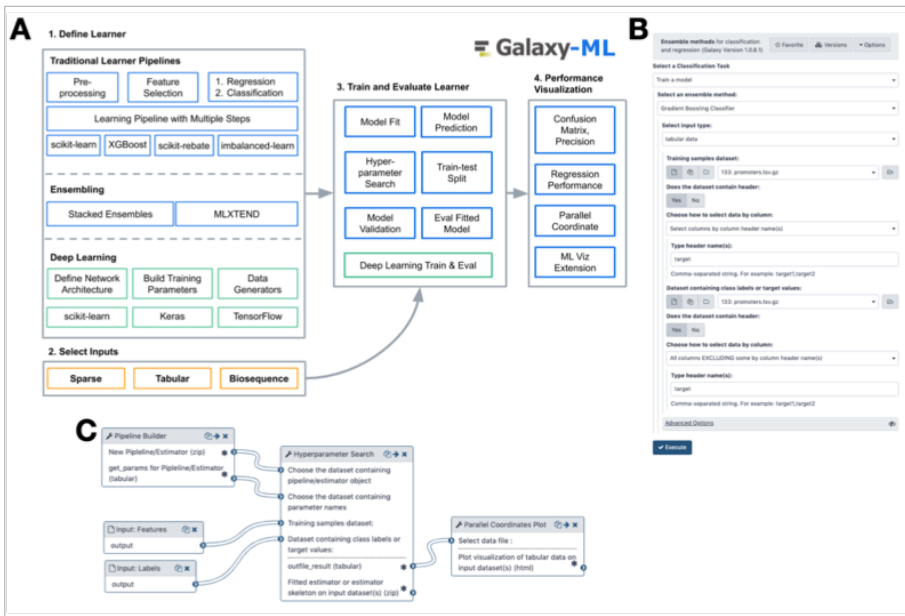
- ▶ Integrate cancer tools—including many ITCR tools—into the Galaxy ecosystem
- ▶ Federated and data-local computing in Galaxy for large datasets
- ▶ Precision oncology applications via multimodal analyses and machine learning
- ▶ <https://cancer.usegalaxy.org/>



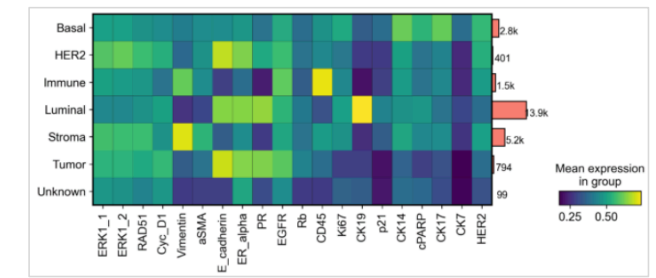
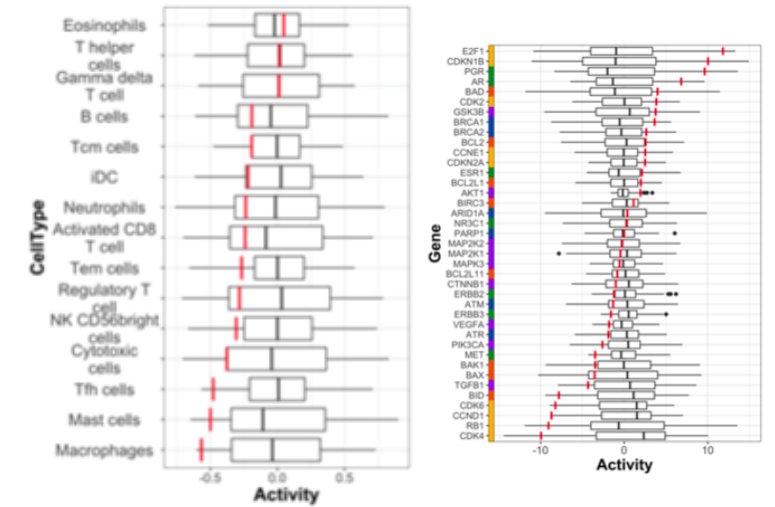
NCI Cancer Research Data Commons (CRDC)



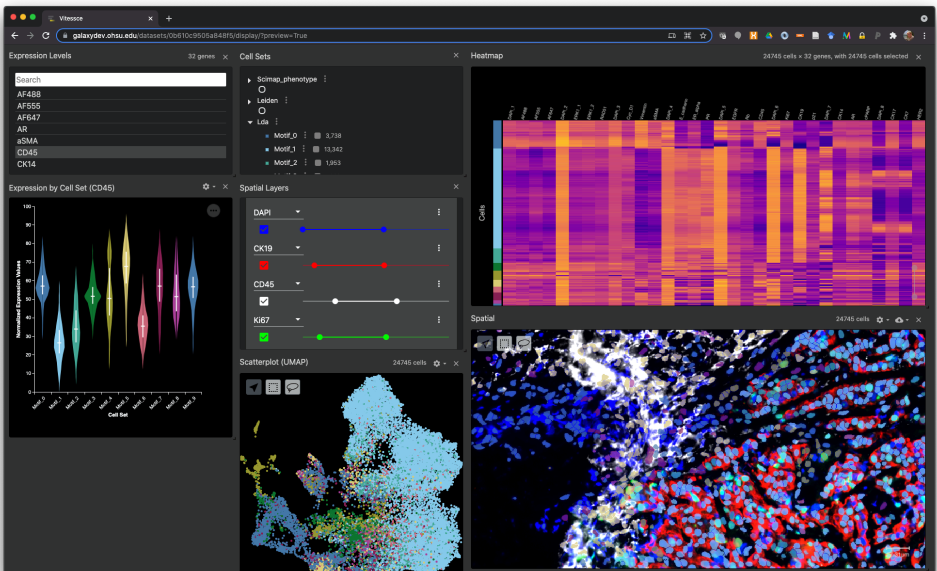
Machine Learning



Research Tumor Board Reports



Multiplex Tissue Imaging Analysis



IO.BIO visualizations

This collage highlights several IO.BIO web tools and their capabilities:

- bam.iobio & vcf.iobio:** A web-based, real-time, sequence alignment file inspector. Cited in *NATURE METHODS* | VOL.11 NO.12 | DECEMBER 2014 | 1189.
- taxonomer.com:** Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling.
- genepanel.iobio:** BMC Medical Genomics. Genepanel.iobio: an easy-to-use web tool for generating disease- and phenotype-associated gene lists.
- clin.iobio:** A tool for clinical genomics analysis, showing conservation, phylogenetic trees, and quality metrics.
- gene.iobio:** A tool for gene analysis, showing quality metrics and inheritance patterns.
- scientific reports:** OPEN Gene.iobio: an interactive web tool for versatile, clinically-driven variant interrogation and prioritization.

<https://iobio.io>

Omic and Multidimensional Spatial (OMS) Atlas

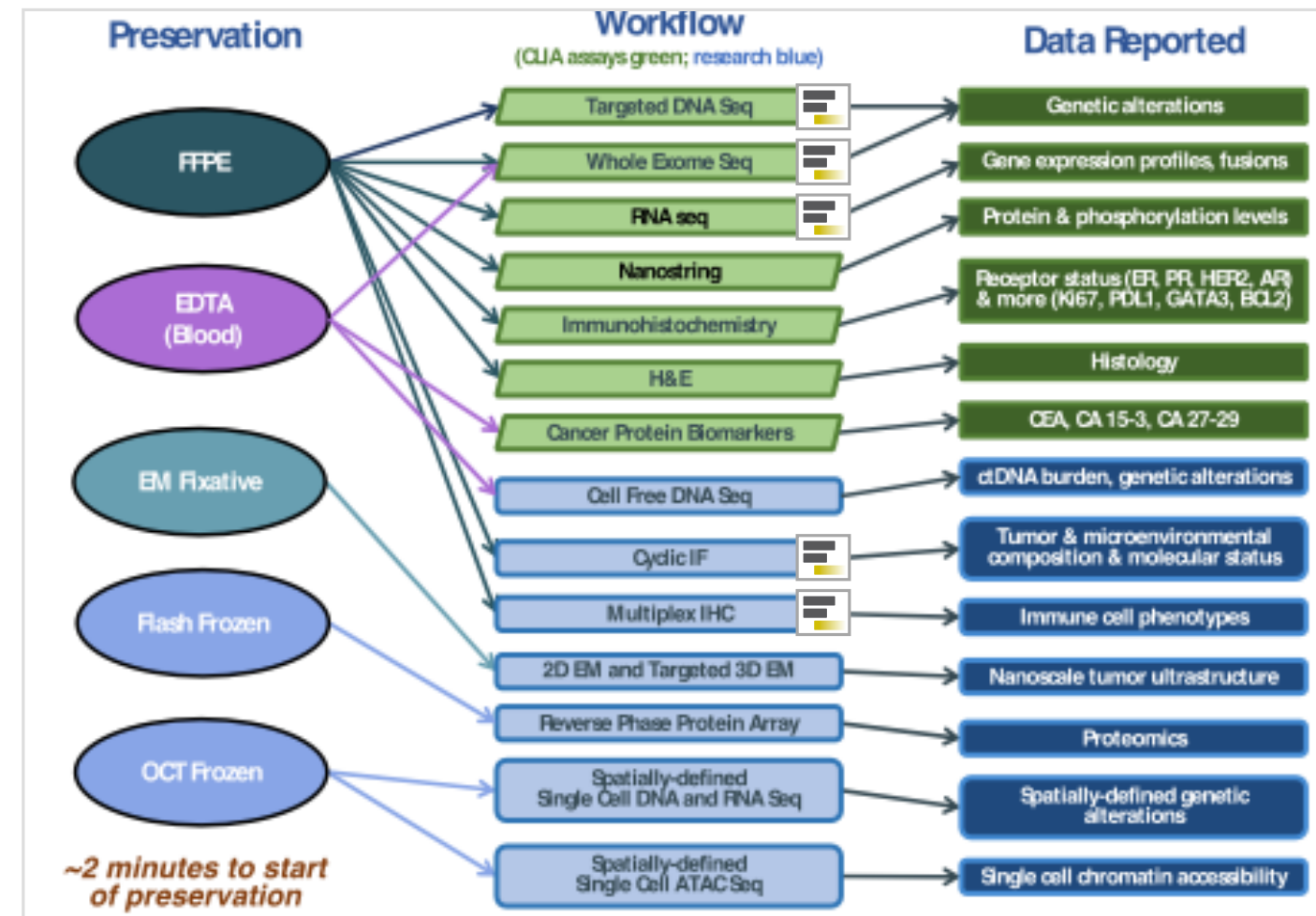
A cohort of matched biopsies from metastatic breast cancers

- Same patients on **CDK4/6i therapies**

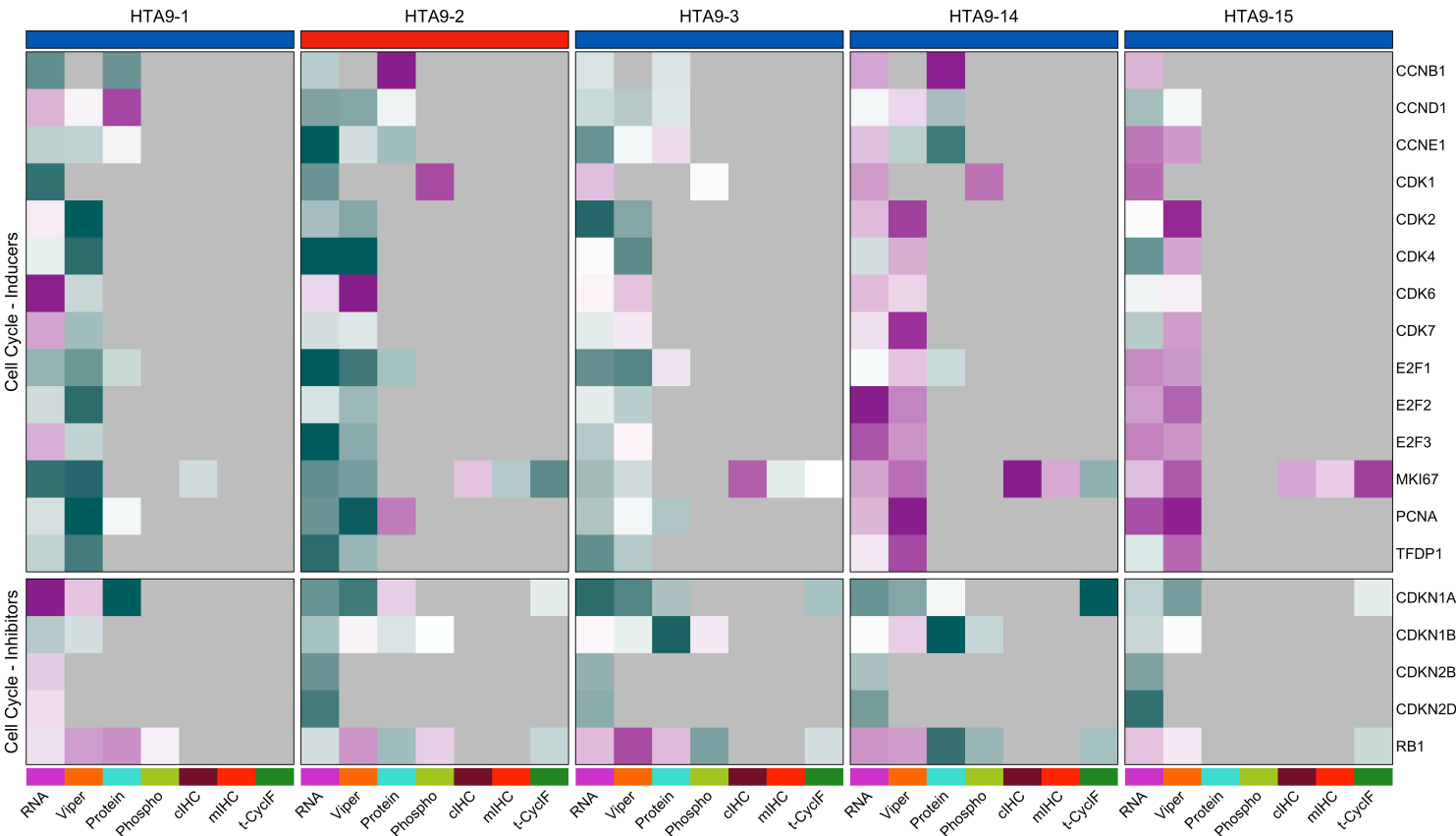
A large suite of omics and imaging assays is applied to each biopsy

Omic and imaging data is connected to clinical attributes to:

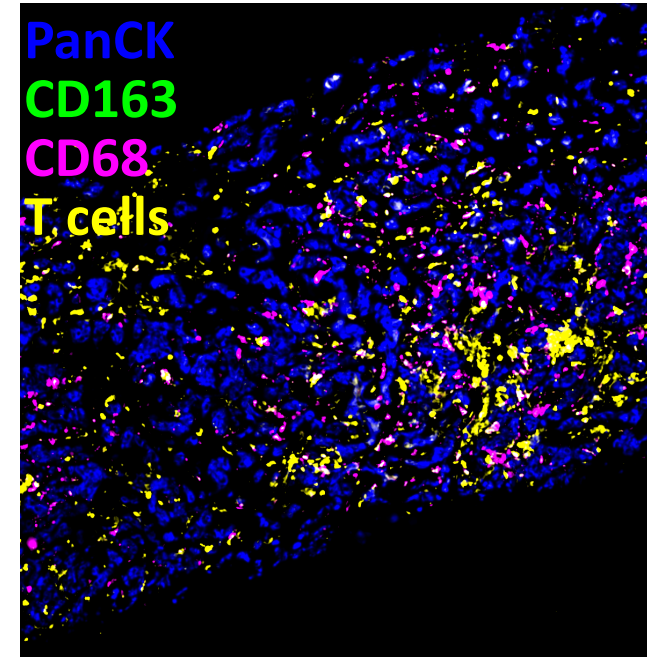
- Characterize how tumor is adapting to therapy
- Identify potential mechanisms of resistance to therapy
- Develop actionable guidance for addressing therapeutic resistance



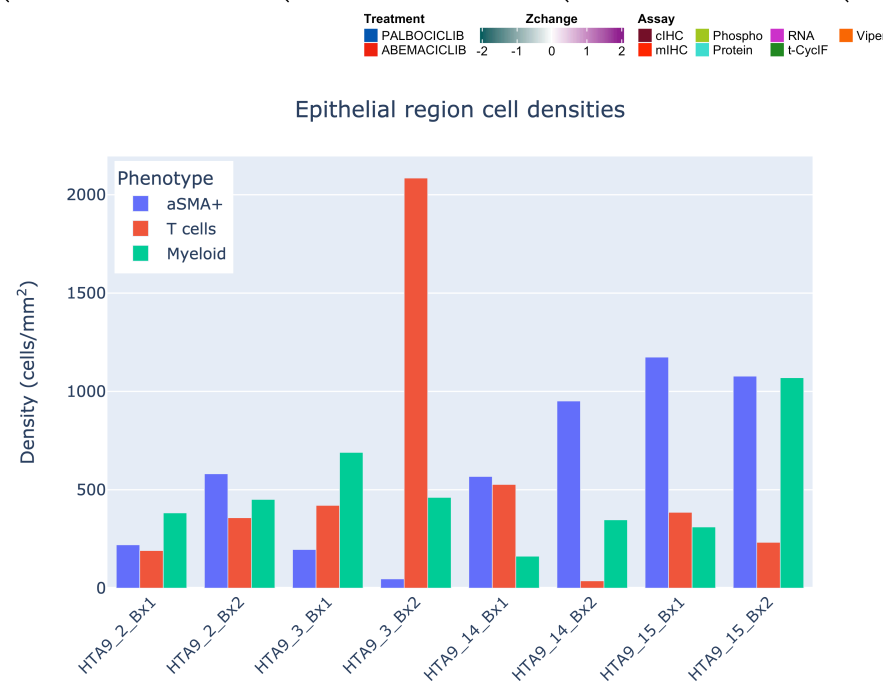
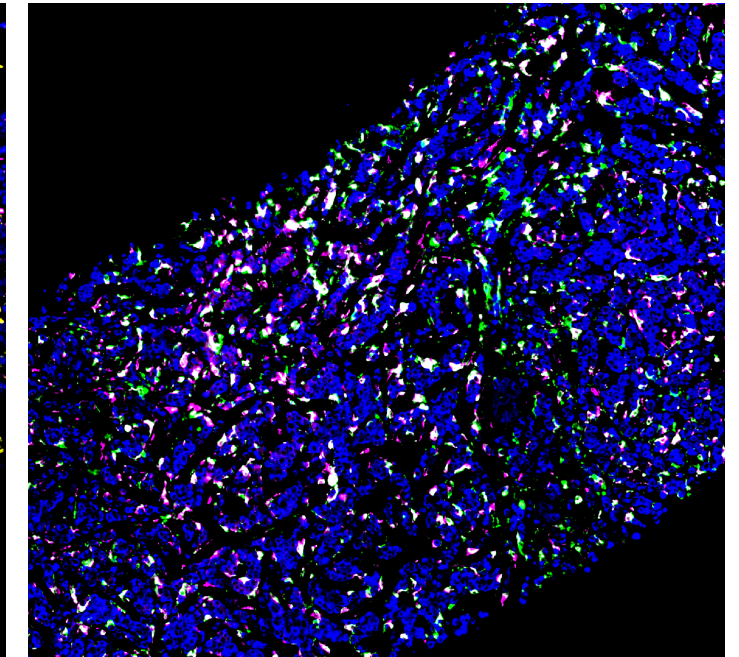
Diverse Patient Changes Observed



HTA9-3 Bx2



HTA9-15 Bx2



Mechanisms	Cases	Observations
Mitogenic signals, Cell Cycle Entry	HTA9-1, HTA9-14, HTA9-15	Increased E2F, CDK2, CDK6, CCNE1
Cell Cycle Checkpoint Bypass	HTA9-14, HTA9-15	Increased Ki67, PCNA, CCNB1, G2M Checkpoint
Immunoreactive	HTA9-1, HTA9-3, HTA9-15	Increased interferon, Jak/Stat, immune density, T cell density
Immunosuppressive	HTA9-3, HTA9-15	Elevated FOXP3 (Treg), CTLA4, PD-L1 Elevated Myeloid density
Immune Cold	HTA9-2, HTA9-14	Low immune infiltrate in both Bxs, Minimal change or reduction in immune cells

Acknowledgements: The Galaxy Community



All things Galaxy:

<https://galaxyproject.org/>

Public Galaxy servers:

<https://galaxyproject.org/use/>

Download and run Galaxy locally:

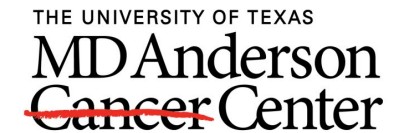
<https://getgalaxy.org>

Galaxy training network:

<https://training.galaxyproject.org/>



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