The Biomedical Evidence Graph

ITCR Update for Face-to-Face

Santa Cruz, CA ***June 1, 2017***

Josh Stuart (UCSC), Kyle Ellrott (OHSU)

BMEG Aims

- **Aim 1** - Develop **automated cancer evidence discovery pipelines**. Formatted for graph analysis.
- **Aim 2** - Determine **genotype-phenotype recognizers**. ID top methods with public challenges.
- **Aim 3** - **Evidence graph** and **network analysis** (e.g. connectivity, co-occurrence, phenotype ID)
- **Aim 4** - Online **use case apps** (e.g. recommenders, infer targets)

Challenges of Interdisciplinary Omics Analyses

- Complex pipelines
  - And many method choices at every step
  - Methods are computationally expensive
  - Every method different requirements

- Diverse sources of data needed
  - Scattered
  - Too large to move around

- Too complex to understand
  - Need interpretation
  - Need intuitive overviews
  - Need integration for “big picture”

Challenges of Interdisciplinary Omics Analyses

- Complex pipelines
  - And many method choices at every step
  - Methods are computationally expensive
  - Every method different requirements

- Diverse sources of data needed
  - Scattered
  - Too large to move around

- Too complex to understand
  - Need interpretation
  - Need intuitive overviews
  - Need integration for “big picture”

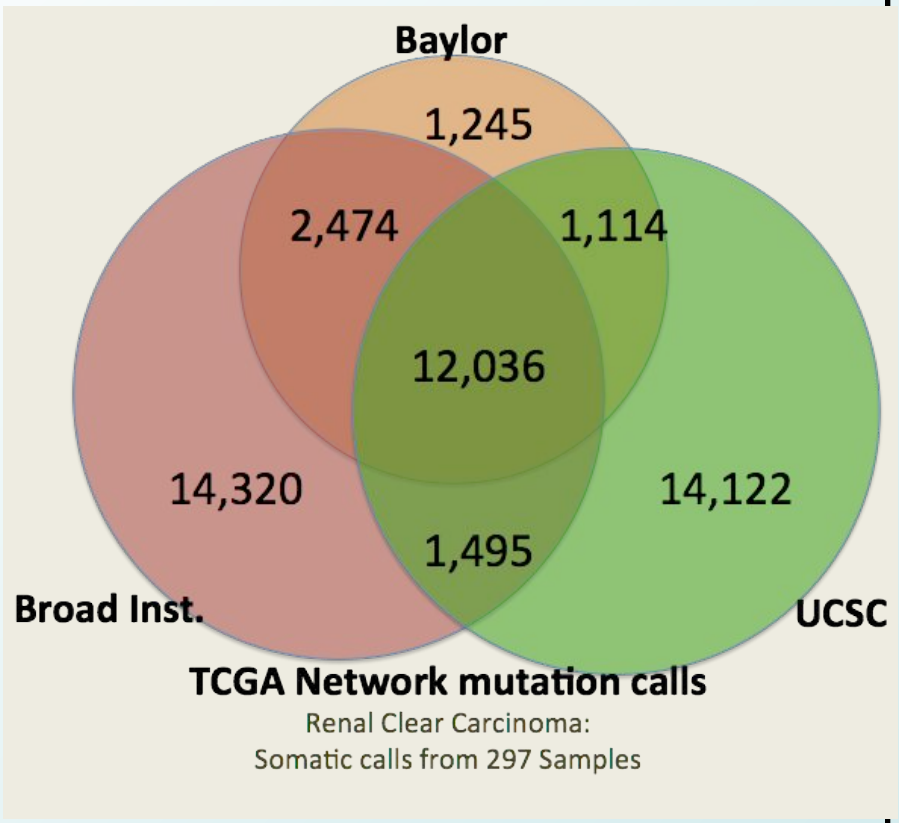
Biomedical Evidence Graph (BMEG) Aims

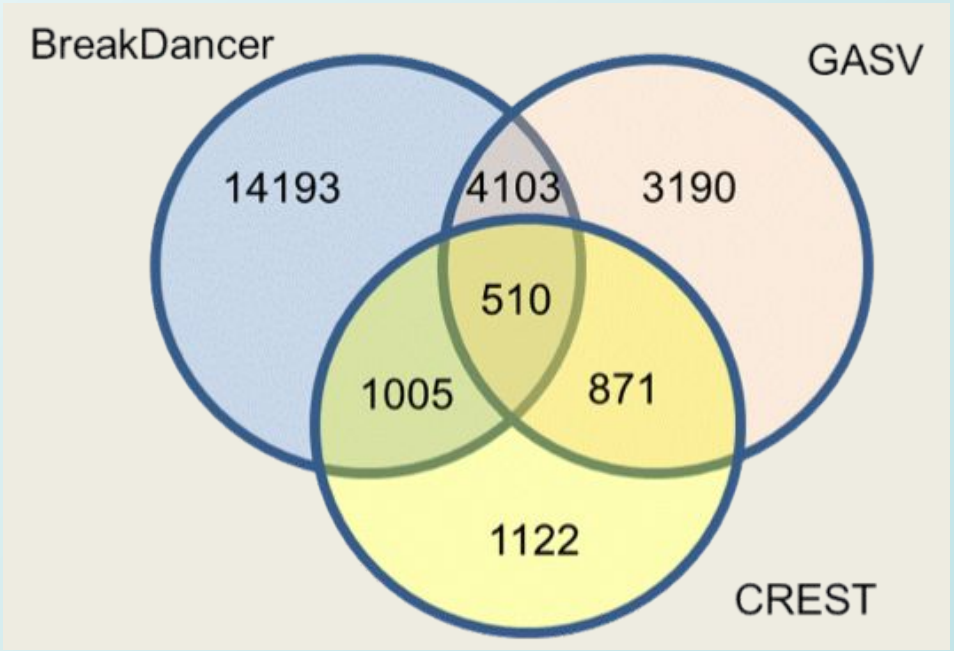
- Complex pipelines
  - And many method choices at every step
  - Methods are computationally expensive
  - Every method different requirements

- Diverse sources of data needed
  - Scattered
  - Too large to move around

- Organize crowdsourced challenges to identify top methods
  - DREAM projects, living benchmarks
- Cloud ready methods for evidence gathering
  - Alignments and somatic variant detectors

Mutation Callers Give Different Answers





Singer Ma (UCSC)

What is the best method?

Have a Bake-Off.

DREAM CHALLENGES

Best Cookies

What is the best method?

Have a Bake-Off.

DREAM CHALLENGES

Best Cookies

and

Best Cooking Components

Somatic Mutation Evidence

1) Identifying Best Methods

- ~400 registrants
- ~3000 entries on 14 genomes
- Completed 2014
- https://synapse.org/DREAM_SMC
- New insights gleaned (*Nat Methods* 2015).

Somatic Mutation Evidence
2) Method Documentation
3) Run on Large Scale Data
TCGA Unified Mutations (MC3)

- Need unified, comprehensive mutation calls for all TCGA samples for PanCanAtlas
- AWG calls vary from group to group
- Different calling techniques
- Different filtering methods
- Stopped work when papers published (incomplete data)
- Inconsistencies from tumor type to tumor type.

MC3 Process With A Uniform Pipeline

10K TCGA Exomes

GATK Preprocessing
(DREAM winner)

BROAD INSTITUTE

UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute

Coherent BAM collection

Cancer Genomics Hub

Consistent Mutation Calling
across all TCGA exomes

BROAD INSTITUTE

Baylor College of Medicine

UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute

Washington University in St. Louis

MD Anderson Cancer Network™

MAF Creation

PanCanAtlas

Methods

(all eval w/ DREAM & dockerized)

Broad - Mutect

Baylor - **MuSE (1.0 RC)**

WashU

VarScan 2.3.9

Somatic Sniper 1.0.5

Pindel 0.2.5b8

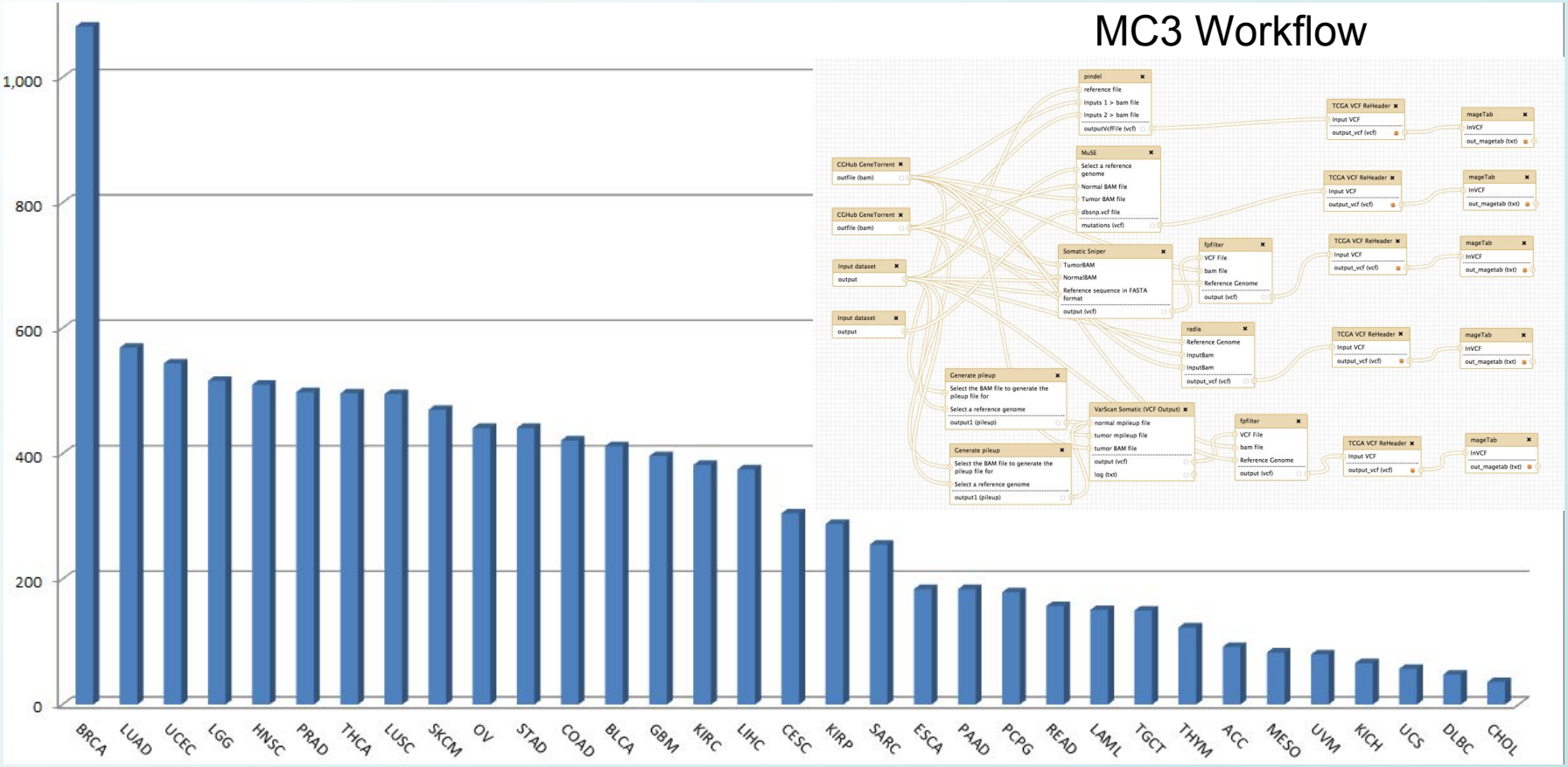
UCSC - **Radia 1.1.5**

MC3 Doubled Sample Coverage

TYPE	TCGA AWGs	MC3
Tumor Samples	5480	10176
Variant Calls	1,396,139	3,397,307
Methods	Varied by group	Consistent 7

Loaded into BMEG DB

MC3 Results, Posted in Summer, 2016

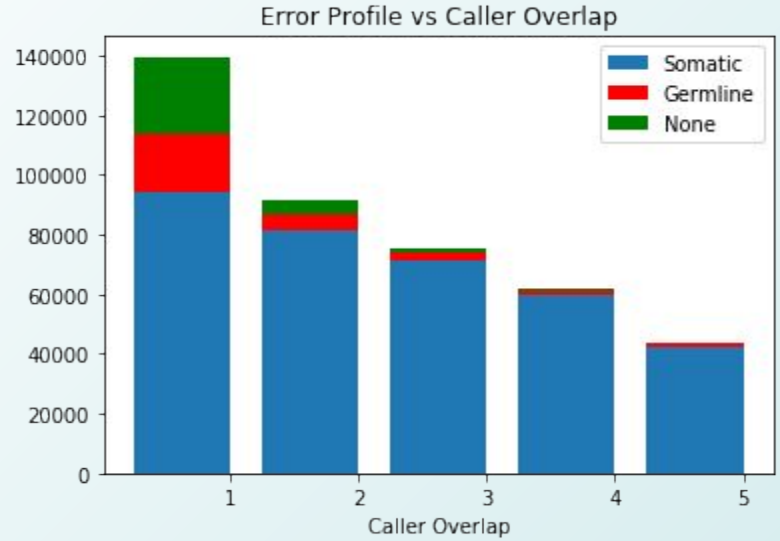


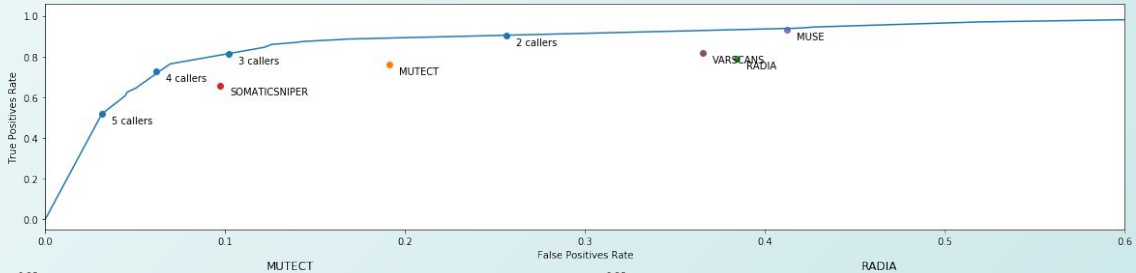
Donors: 10,485

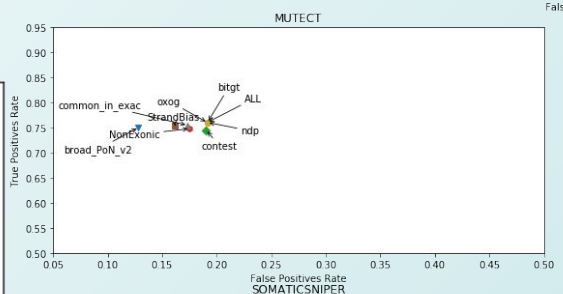
Open Access MAF file released

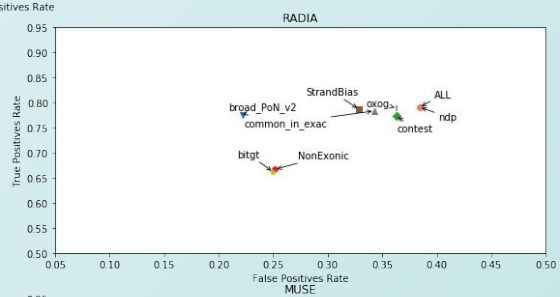
https://www.synapse.org/#!Synapse:syn5917256

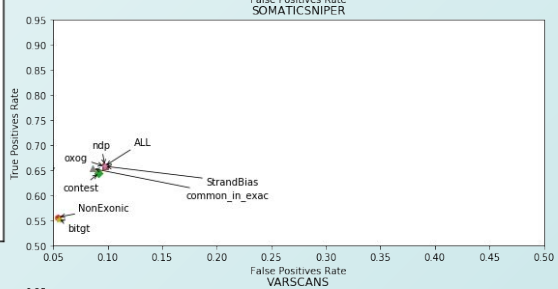
MC3 Analysis

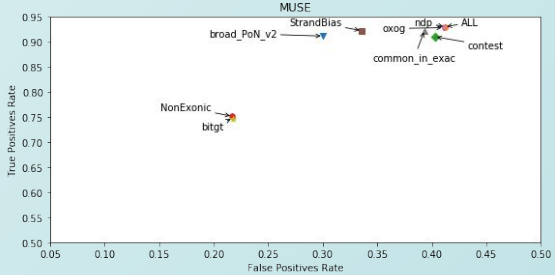


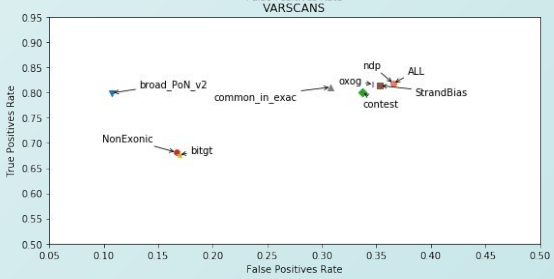












Automating Somatic Mutation calling for Ten Thousand Tumor Exomes. Submitted.

DREAM: From Competition to Science

1) DREAM Challenge Completion

2) Method Documentation

3) Mass Deployment

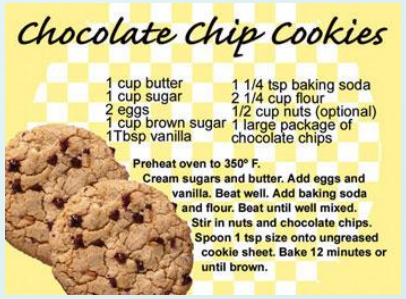
4) Use for real Science

DREAM: From Competition to Science

Getting Stuck Here. Why?

1) DREAM Challenge Completion

2) Method Documentation



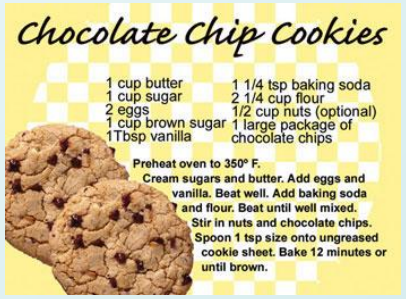
for real
ce

DREAM: From Competition to Science

Getting Stuck Here. Why?

1) DREAM Challenge Completion

2) Method Documentation



for real
ce

Rethink challenge incentives

- score code only when re-runnable.

'Next Gen' DREAM Challenges Will Produce *Re-runnable Code*

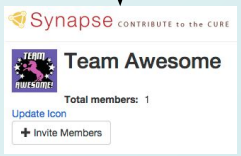
https://synapse.org/SMCHet

https://synapse.org/SMC_RNA

SMC-HET and SMC-RNA

DREAM Participants

1 - Register at Synapse
https://www.synapse.org/SMC_RNA



2 - Go to cloud pilots to view training data and make containerized workflows

Institute for Systems Biology

3 - Submit completed workflow back to Synapse

Synapse

CWL

Global Alliance for Genomics & Health

4 - DREAM organizers apply workflows to held out dataset

DREAM CHALLENGES

SMC-HET and SMC-RNA

NATIONAL CANCER INSTITUTE

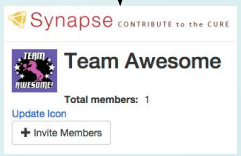
CWL

Global Alliance for Genomics & Health

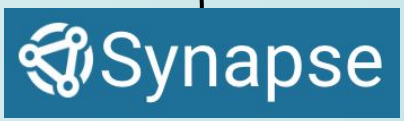
Method only
Scored and Ranked
If ***WE CAN RUN IT***

DREAM Participants

1 - Register at Synapse
https://www.synapse.org/SMC_RNA



2 - Go to cloud pilots to view training data and make containerized workflows



3 - Submit completed workflow back to Synapse

4 - DREAM organizers apply workflows to held out dataset

DREAM CHALLENGES

DREAM Somatic Mutation RNA Challenge (SMC-RNA)

- Expression is a read-out of cellular pathways
- Examples of fusions as key oncogenic mechanism (BCR-ABL, TMPRSS2-ERG)
- Alternative splicing implicated in many tumor types
- Provide treatment clues

- Sub-challenge 1: Identify Isoforms
- Sub-challenge 2: Identify fusions

ICGC-TCGA DREAM Somatic Mutation Calling Challenge – RNA

DREAM CHALLENGES powered by Sage Bionetworks · IBM · Prostate Cancer Canada · OICR · ICGC · UCSC · OHSU · Sage · NSERC CRSNG · GenomeCanada · The Cancer Genome Atlas · Understanding genomics to improve cancer care · National Cancer Institute

SMC RNA Round 3 Isoform Quantification

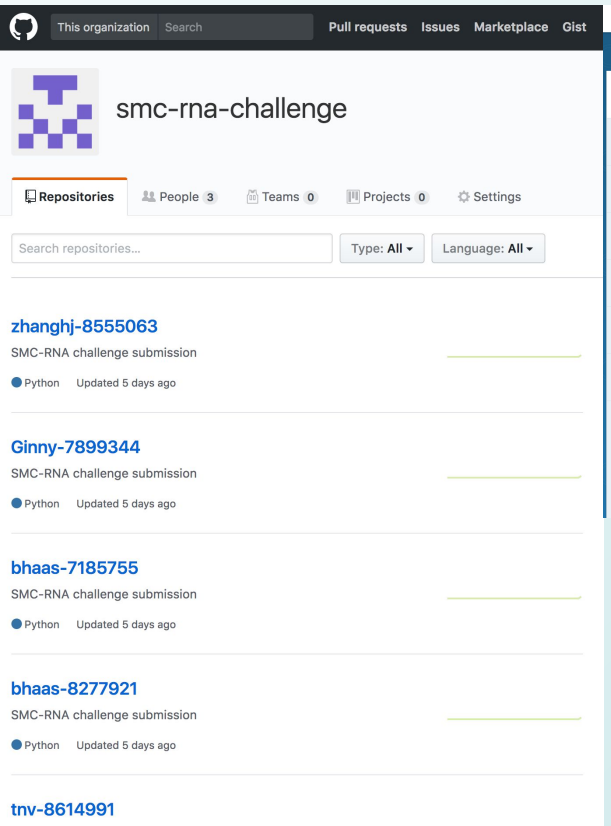
Entry ID	Workflow	sim46	sim47	sim48	sim49	sim50
7150823	isoform_1471603661_merged.cwl	0.900685984	0.901220059	0.8983185	0.900216196	0.899260689
7150898	isoform_1471603893_merged.cwl	0.900685984	0.901220059	0.8983185	0.900216196	0.899260689
7185755	smclsoform_1471960823_merged.cwl	0.937827748	0.938388059	0.935550804	0.938250032	0.936523443
7363252	smclsoform_Hera_workflow_1476415974_merged.cwl	0.847368555	0.857134368	0.84790518	0.860188186	0.860869401
7367548	smclsoform_Hera_workflow_1476549574_merged.cwl	0.860726563	0.854973128	0.845887071	0.859998273	0.857392585
8023084	winterfell_isoform_r2_rspd_b1	0.926925616	0.930314124	0.925143894	0.927371855	0.928692024
8057844	k27	0.901556743	0.901081506	0.898600064	0.900330374	0.898702192
8064391	smclsoform_Hera_workflow_1485238785_merged.cwl	0.902614171	0.920109533	0.919696658	0.918259168	0.922281783
8066038	smclsoform_Hera_workflow_1485267086_merged.cwl	0.902627384	0.92010953	0.919716034	0.918270795	0.913222666
8277921	Isoform - rsem w/ bowtie2	0.929763347	0.933696508	0.927963461	0.930224398	0.931750869
8277922	Isoform - rsem w/ bowtie2	0.929763347	0.933696508	0.927963461	0.930224398	0.931750869
8294423	kilo27	0.901720503	0.902152152	0.89875754	0.90068149	0.898642423
8473425	Salmon	0.898876397	0.897720817	0.896396752	0.897728471	0.89539482

SMC-RNA Round 3 Fusion Detection

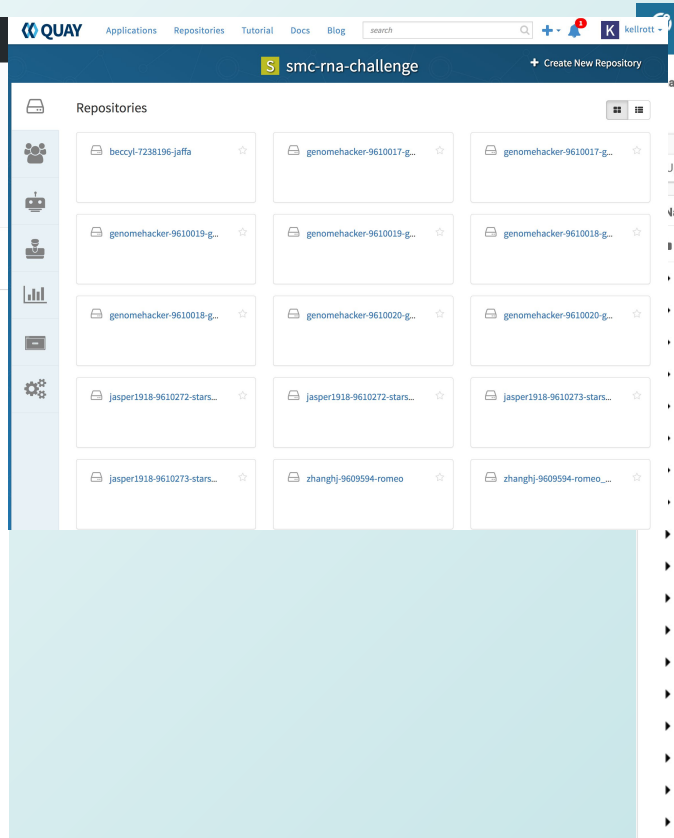
Entry ID	Workflow	sim46	sim47	sim48	sim49	sim50
7185743	smcFusion_1471957621_merged.cwl	0.918919	0.888889	0.967033	0.903226	0.949495
7238196	CWL_jaffa_worklow_1473812025_merged.cwl	NA	0.666667	0.633333	0.685714	0.75
7252855	mps3_workflow_1474050212_merged_1474055180_merged.cwl	NA	NA	NA	0.275862	NA
7269246	FusionRnadt_workflow_1474369510_merged.cwl	0.30137	0.139535	0.191304	0.117647	0.243478
7378934	comb_workflow_v2_1476704303_merged.cwl	0.42515	0.175439	0.401826	0.12844	0.356364
7488045	smcFusion_Hera_workflow_1478021629_merged.cwl	0.265306	0.424242	0.280702	0.1	0.262295
7997358	CWLworkflow_round2_1483936483_merged.cwl	0.878378	0.809524	0.906977	0.896552	0.783505
8114525	STAR_SEQR0_1485986782_merged.cwl	0.900662	0.837209	0.955556	0.933333	0.94
8226744	smcFusion_Hera_workflow_1486535300_merged.cwl	0.333333	0.4375	0.285714	0.222222	0.294118
8281648	Winterfell Fusion Feb-2017	0.918919	0.863636	0.967033	0.866667	0.938776
8396803	Sierra	0.690141	0.470588	0.637363	0.27907	0.510204
8399080	STARSEQRv050_merged_1489019984_merged.cwl	0.932432	0.956522	0.977778	0.967742	0.970297
8517255	fusioncatcher_1	0.780142	NA	0.847826	0.705882	0.690476

The workflows generated by the SMC-RNA challenge have been released publically

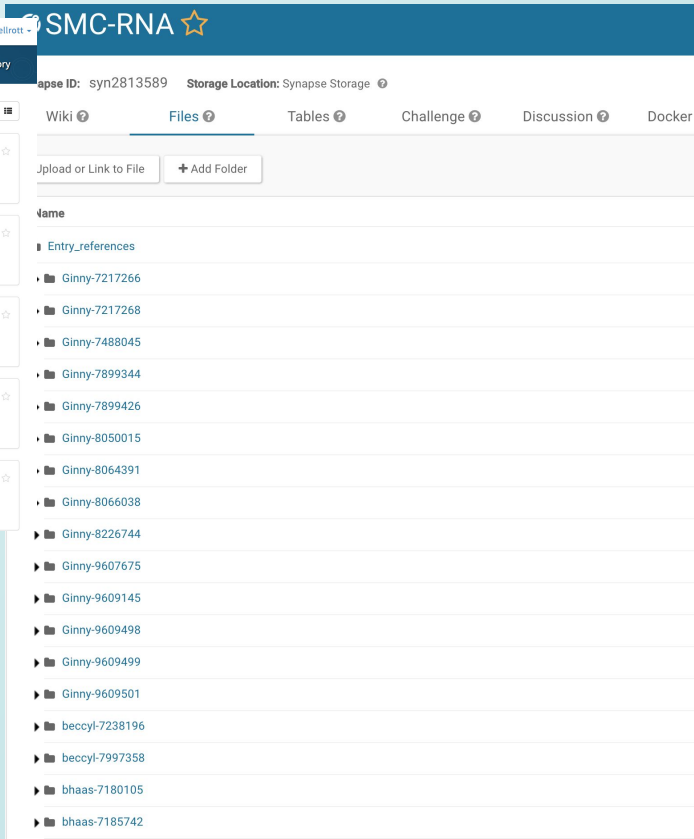
CWL Workflows



Docker Images



Reference Files



Even the Simulator Has Now Been Handed Over to the Community…

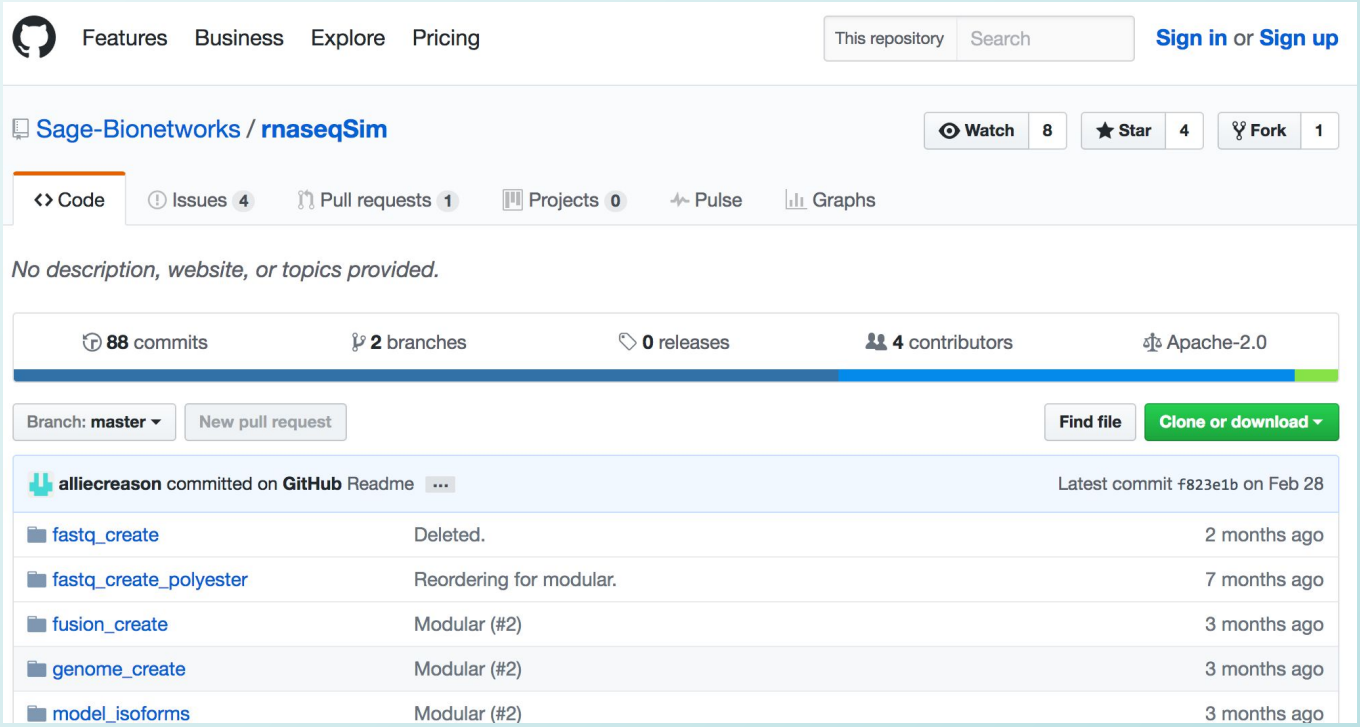
Contestants identified issues with simulator. Admins Debugged

Feature requests posted to forum, ideas for more realism.

Solution: Made simulator available to all to modify.

Community Challenge Phase: Use Community Simulator!

GitHub



Challenges of Interdisciplinary Omics Analyses

- Complex pipelines
  - And many method choices at every step
  - Methods are computationally expensive
  - Every method different requirements

- Diverse sources of data needed
  - Scattered
  - Too large to move around

- Too complex to understand
  - Need interpretation
  - Need intuitive overviews
  - Need integration for “big picture”

Challenges of Interdisciplinary Omics Analyses

- Complex pipelines
  - And many method choices at every step
  - Methods are computationally expensive
  - Every method different requirements

- Diverse sources of data needed
  - Scattered
  - Too large to move around

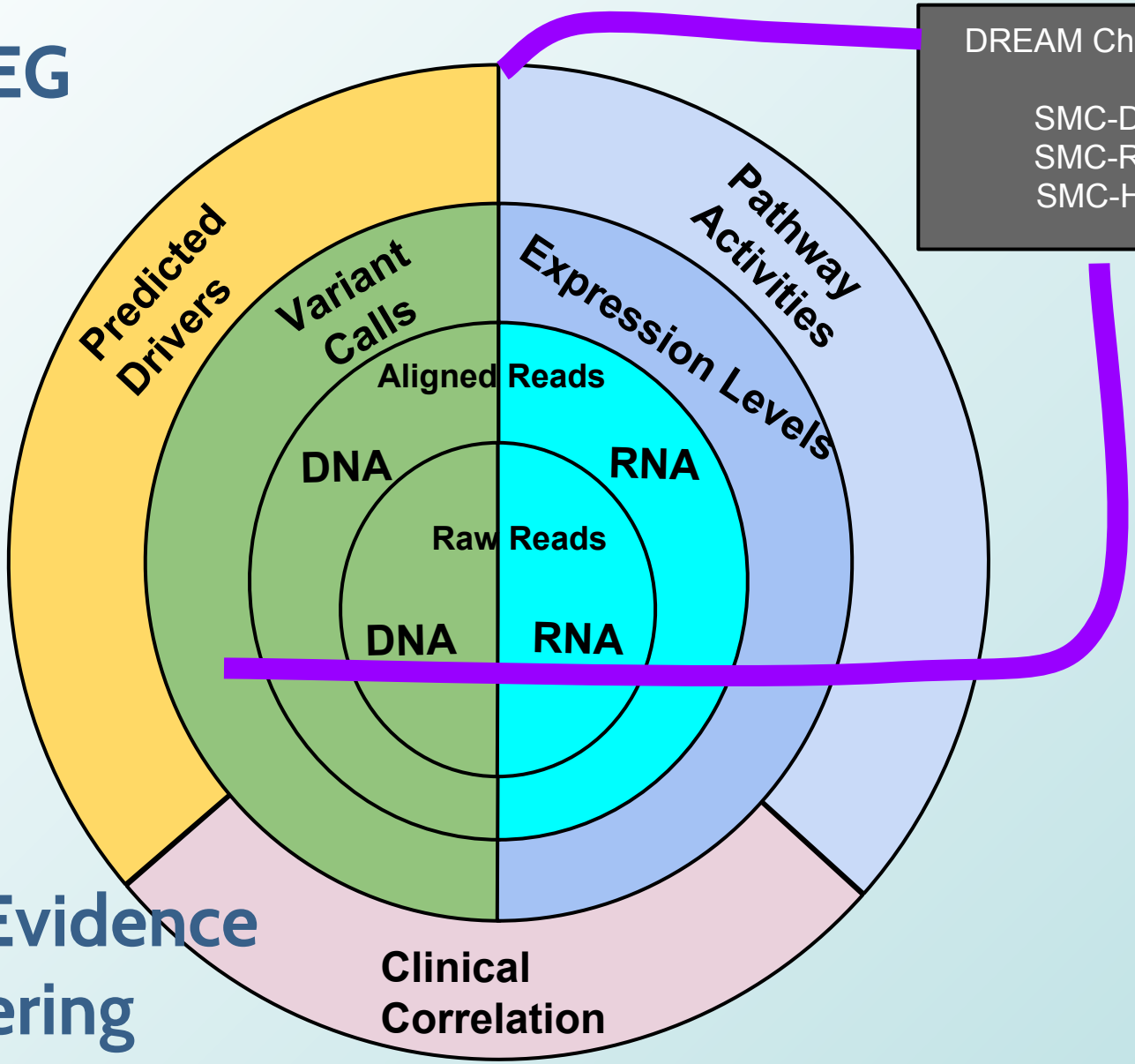
- Too complex to understand
  - Need interpretation
  - Need intuitive overviews
  - Need integration for “big picture”

Biomedical Evidence Graph (BMEG) Aims

- Enable integrative / interconnected analyses
  - Create layers of linked evidence
  - Predictive signatures
  - Correlations to infer subtypes
  - Networks to infer n-of-1 mechanisms

- Too complex to understand
  - Need interpretation
  - Need intuitive overviews
  - Need integration for “big picture”

BMEG



Layered Evidence Gathering & Generation

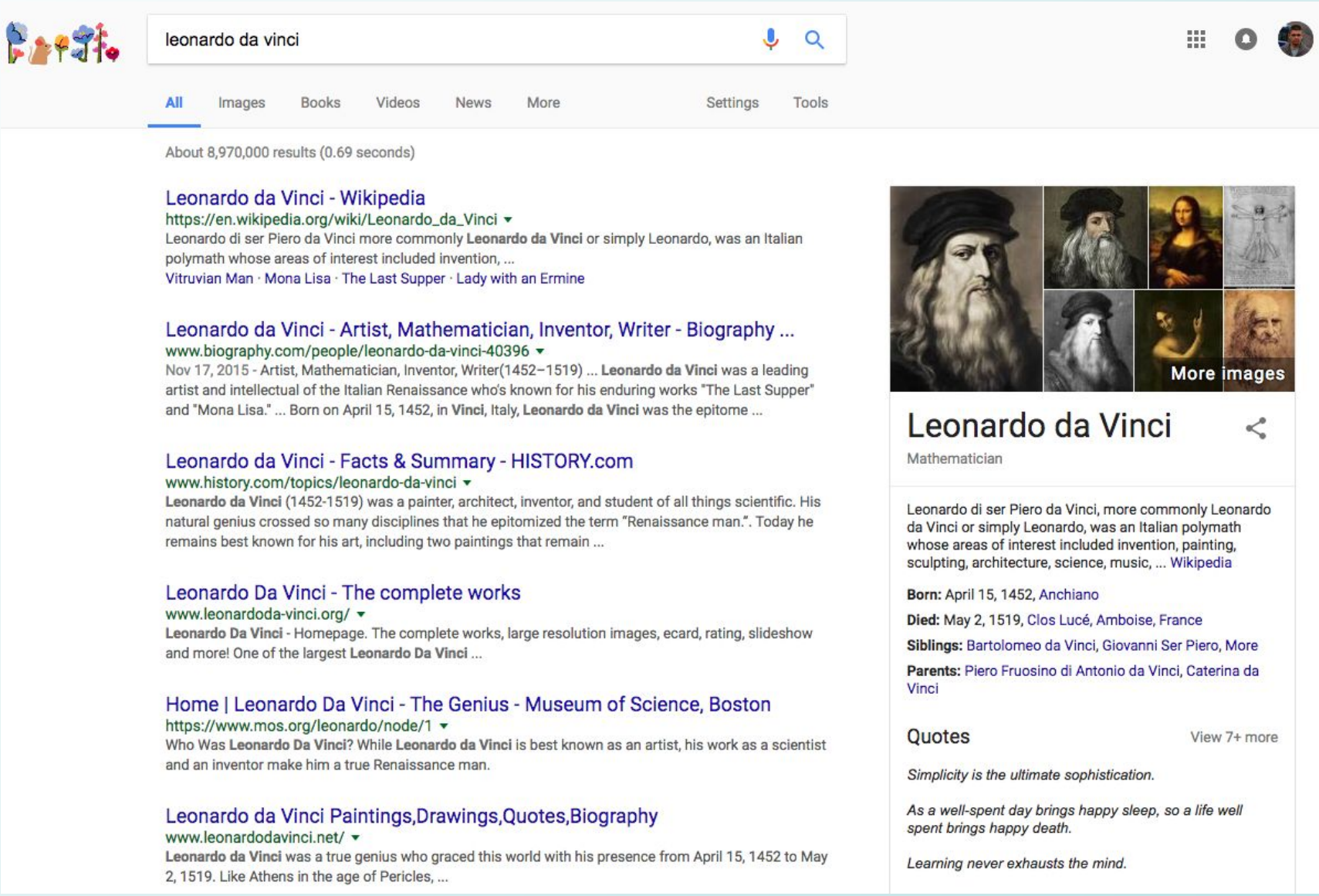
UNIVERSITY OF CALIFORNIA SANTA CRUZ

KNIGHT CANCER Institute OHSU

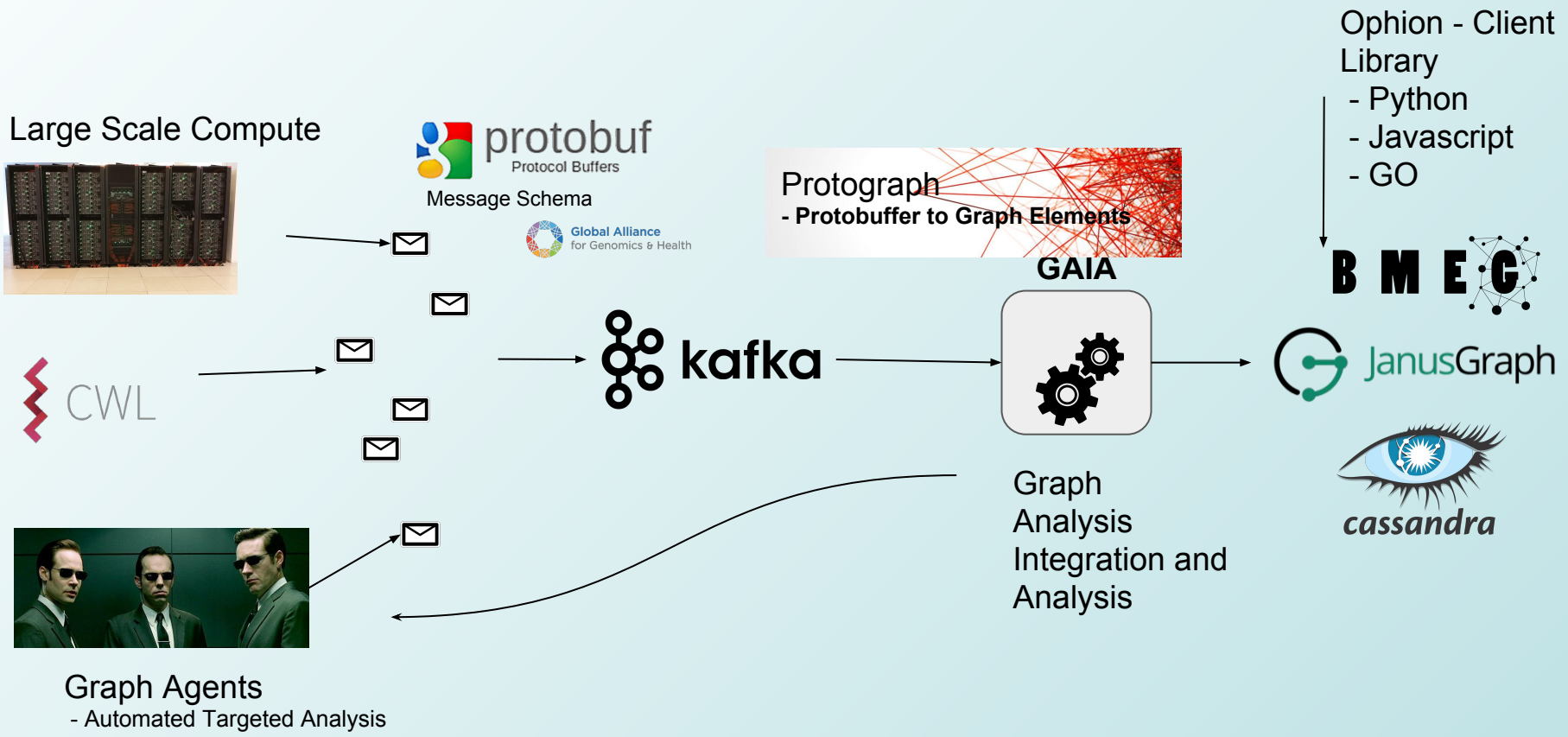
There is lots of data out there

The Google Knowledge Graph

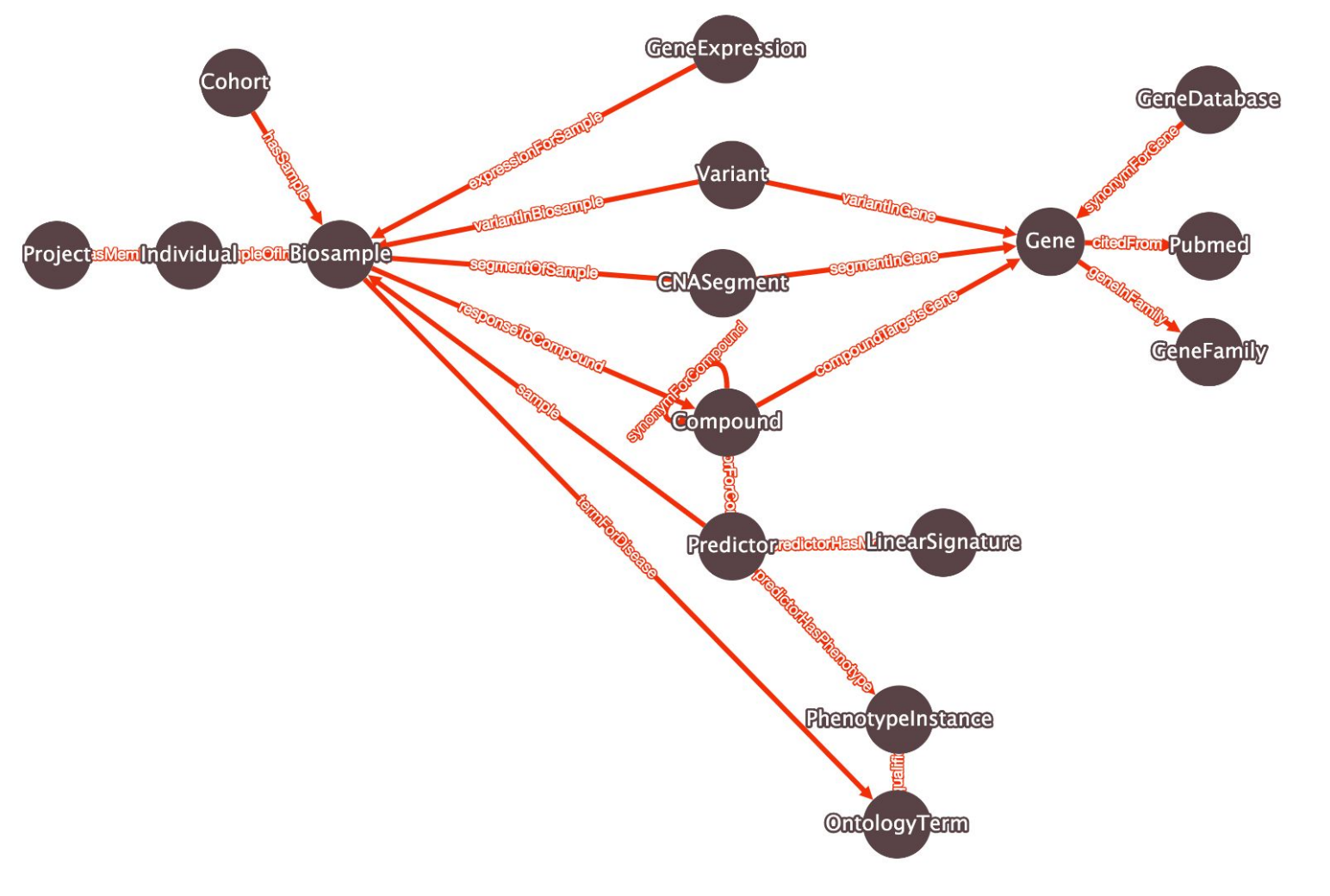
The Google Knowledge Graph



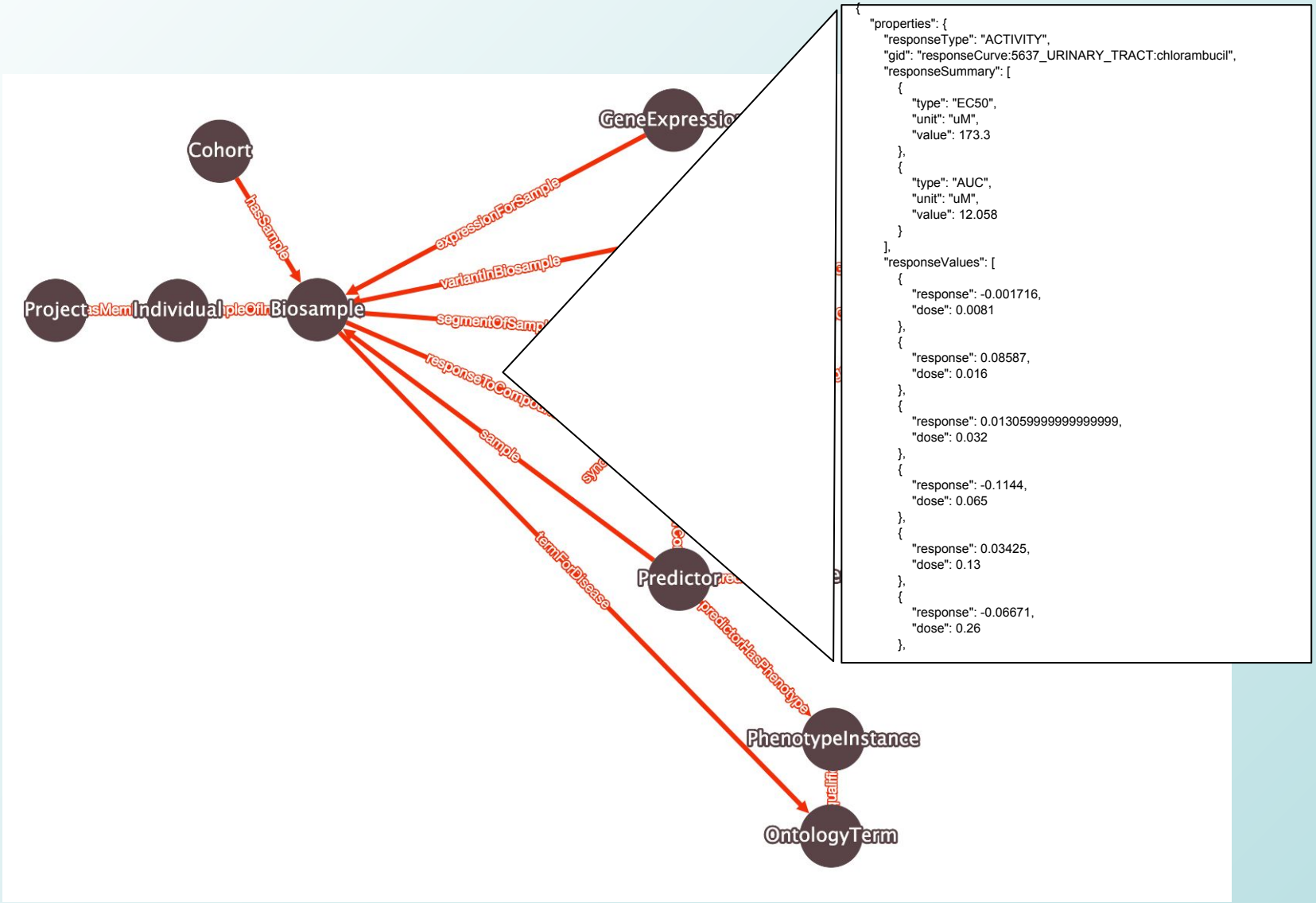
Scalable Graph Database Framework



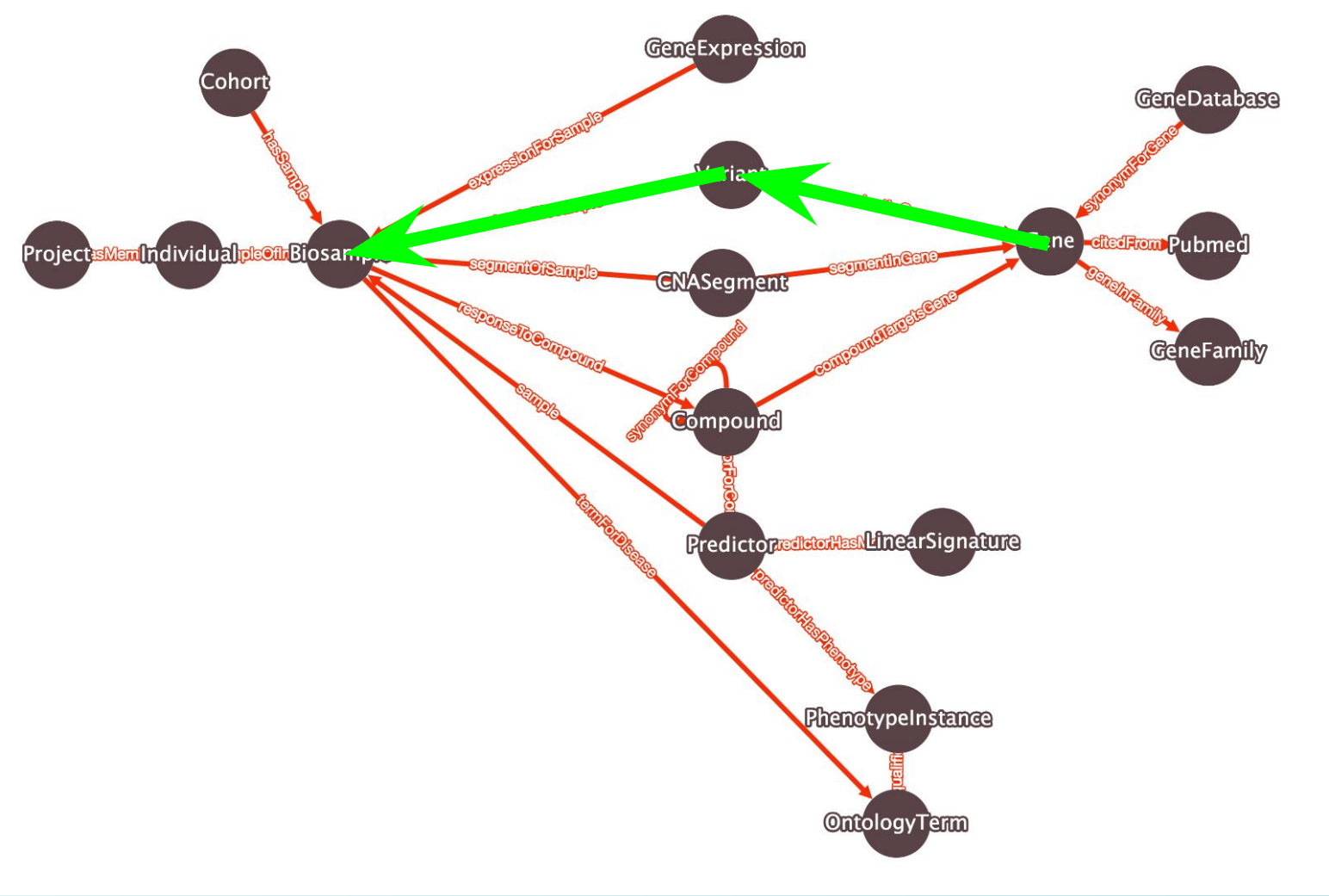
BMEG: Public Graph of Evidence



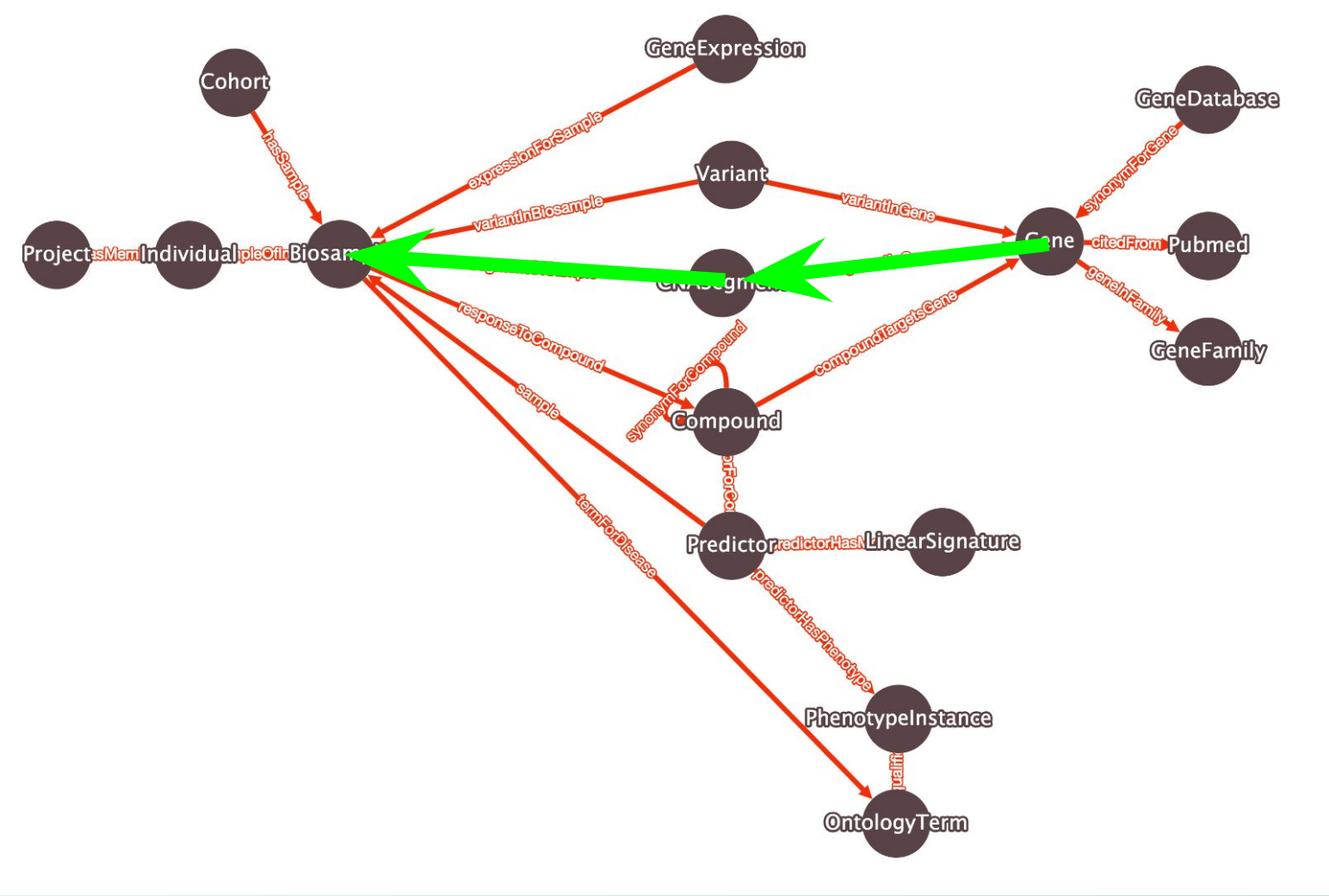
BMEG: A dense property graph



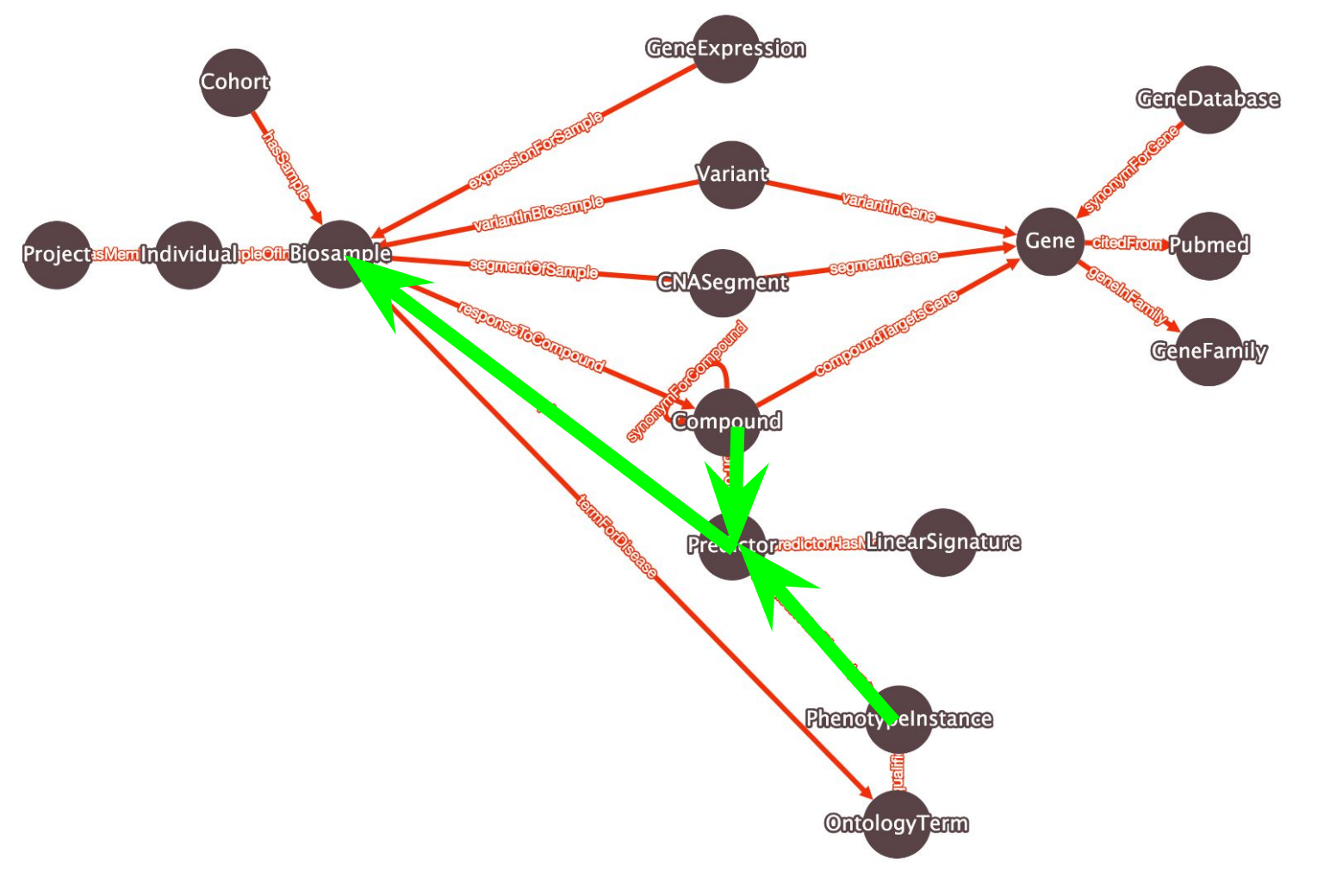
Find Samples by Variant



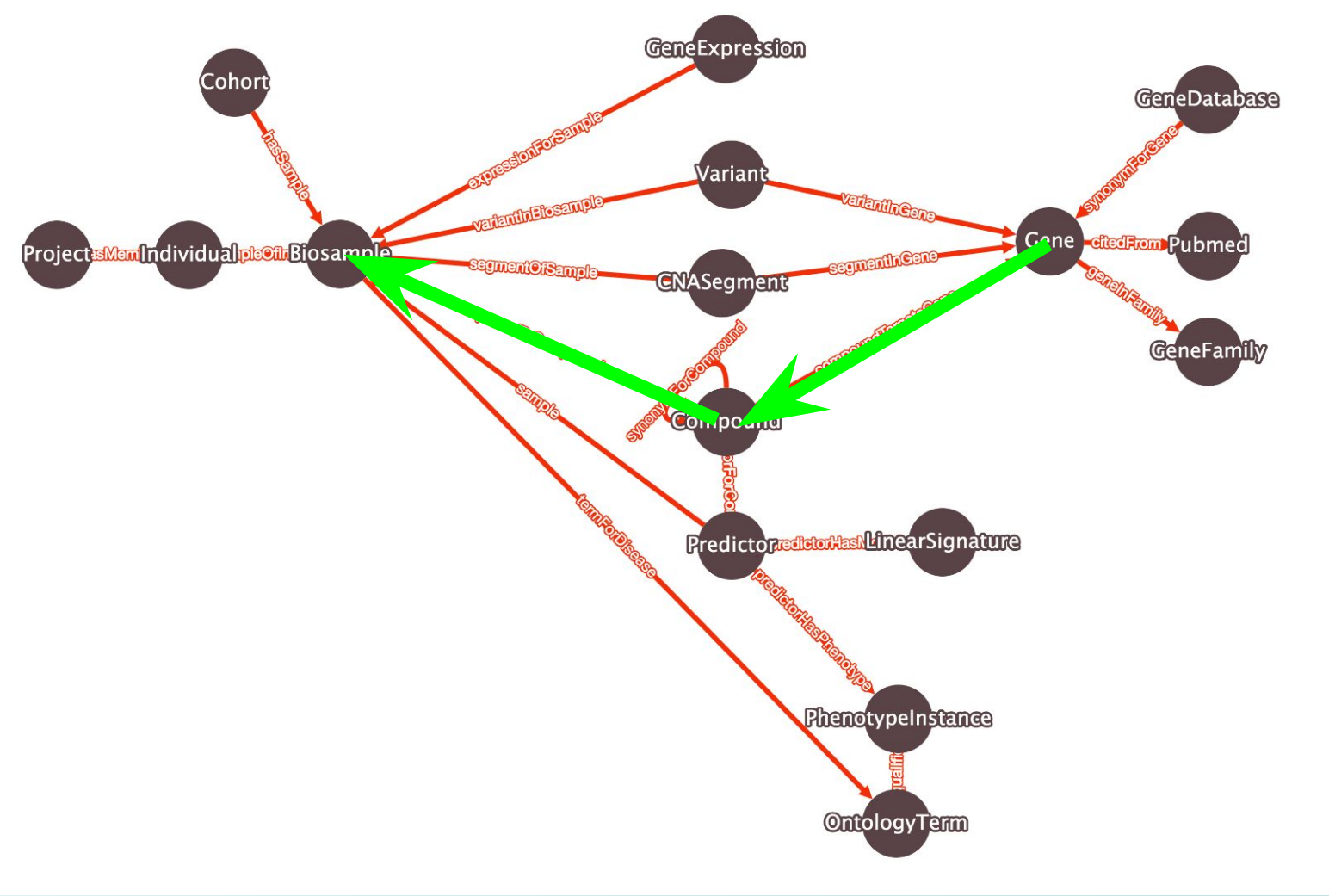
Find Samples by CNA Event



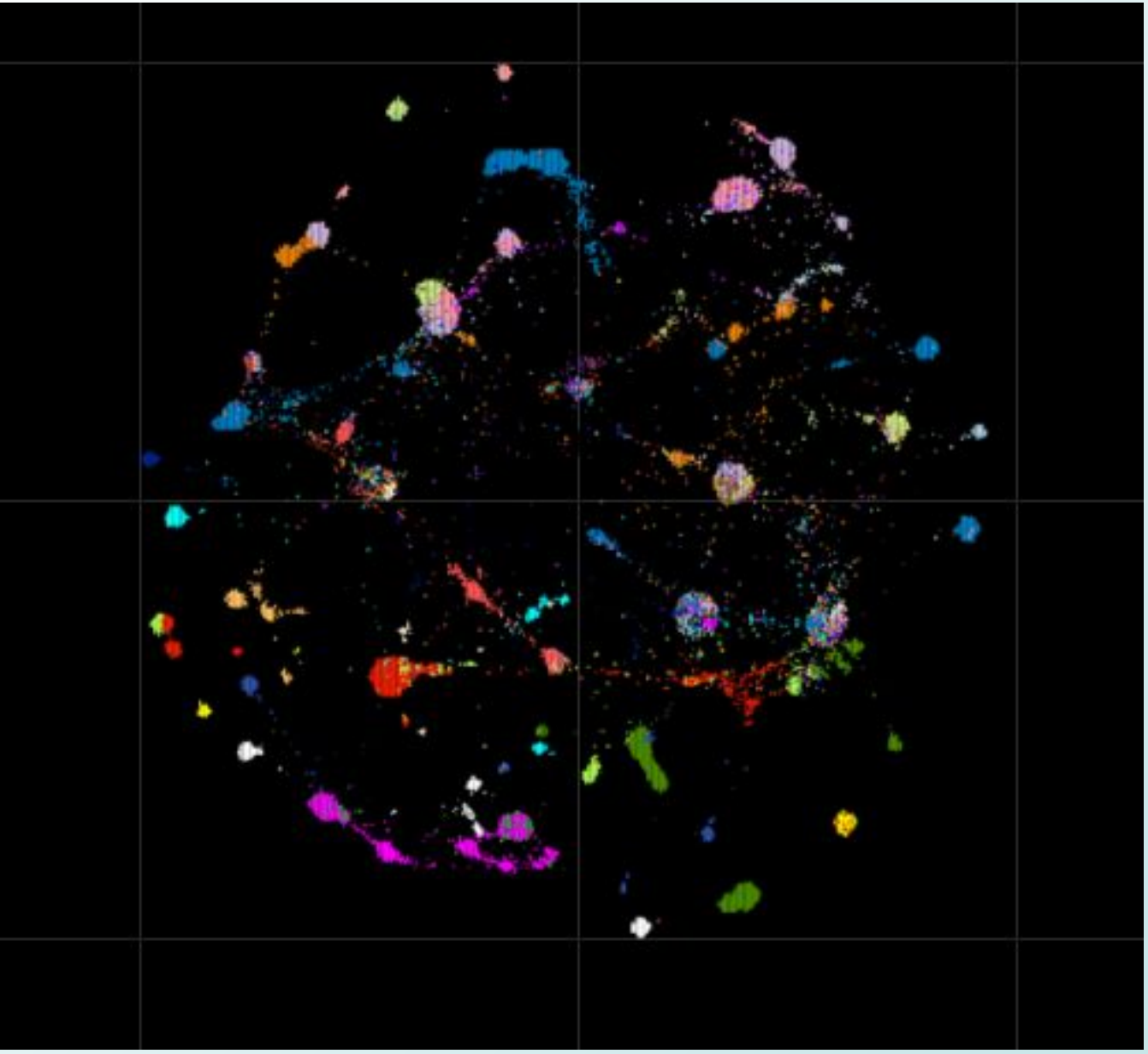
Find Samples predicted to be sensitive to a compound



Find Samples with a particular IC50 for a compound that targets a particular gene



PanCan-33 TumorMap

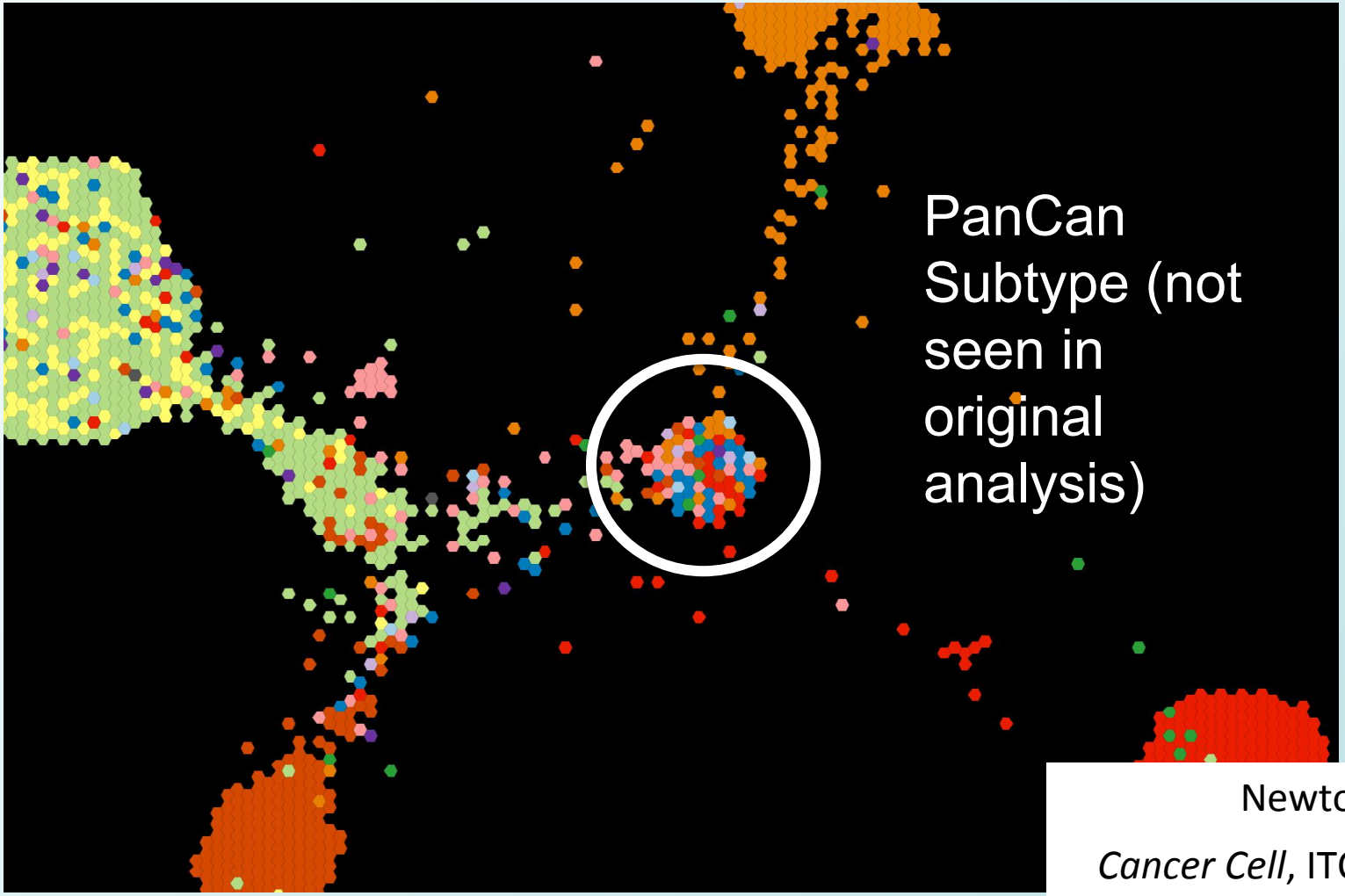


Colors show Tissue of origin.

Newton, UCSC

Cancer Cell, ITCR issue, *in review*

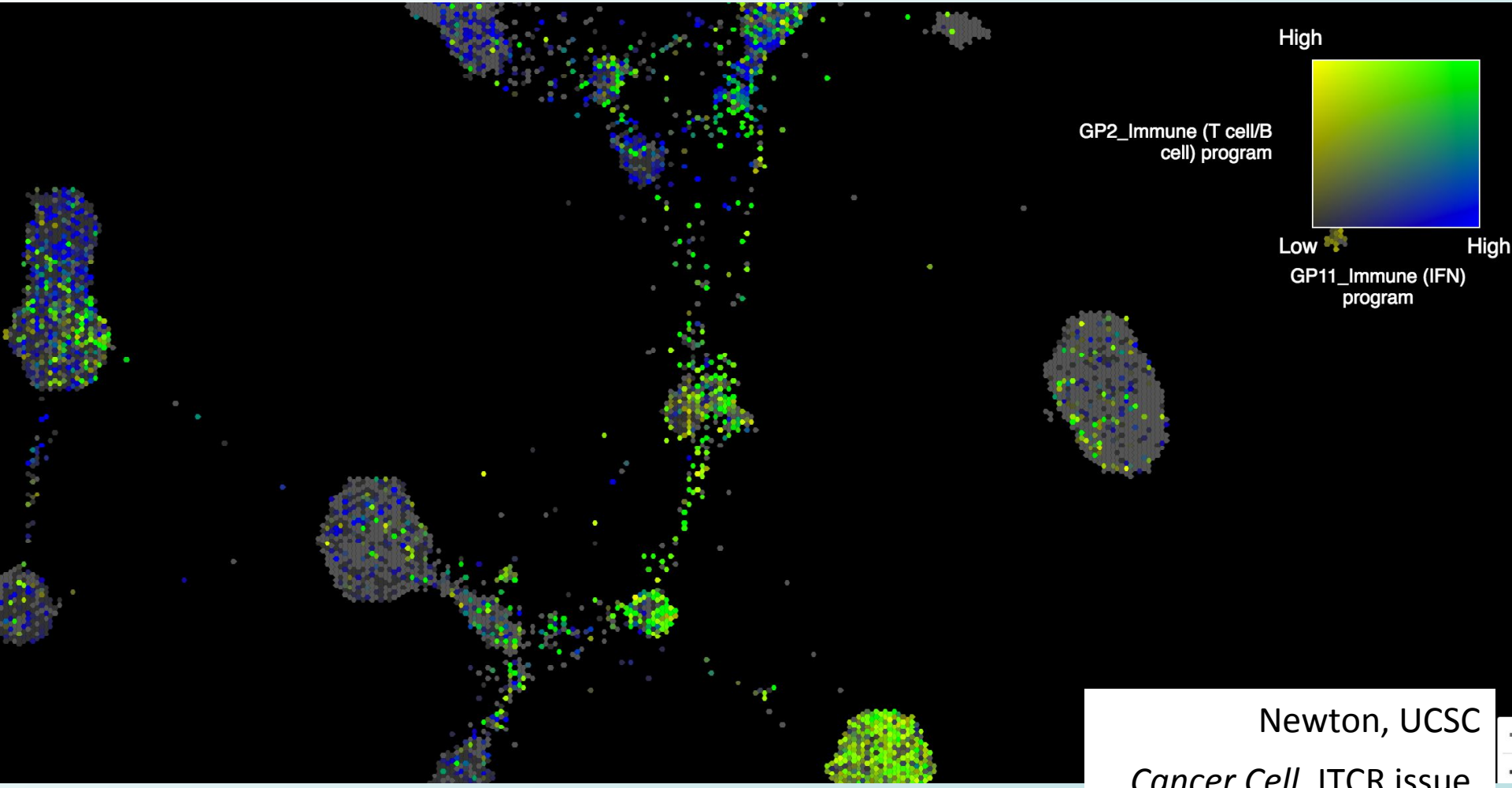
Integrated map reveals pancan subtypes



Newton, UCSC

Cancer Cell, ITCR issue, *in review*

Enriched for t/B and IFN immune (D. Wolf's) programs

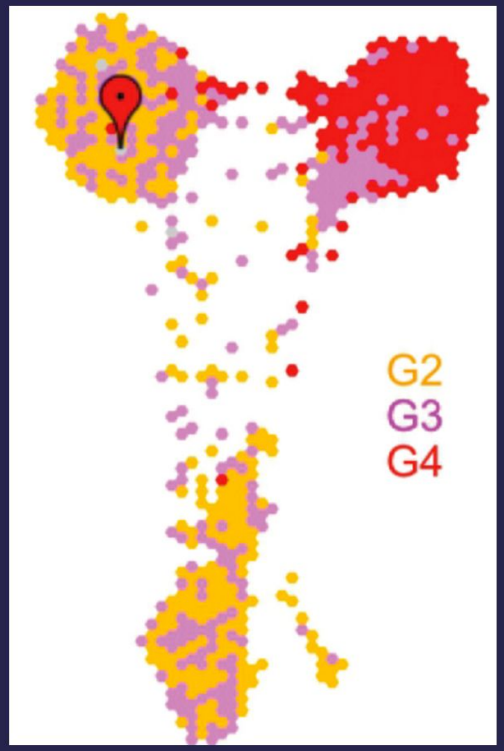


Newton, UCSC

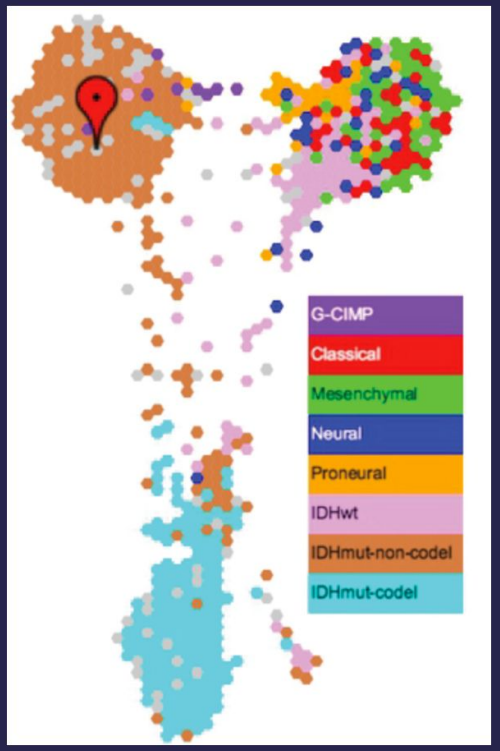
Cancer Cell, ITCR issue, *in review*

Treehouse
CHILDHOOD CANCER INITIATIVE

Bird's eye view



Zoom in on the glioma region
(tumors now colored by grade)

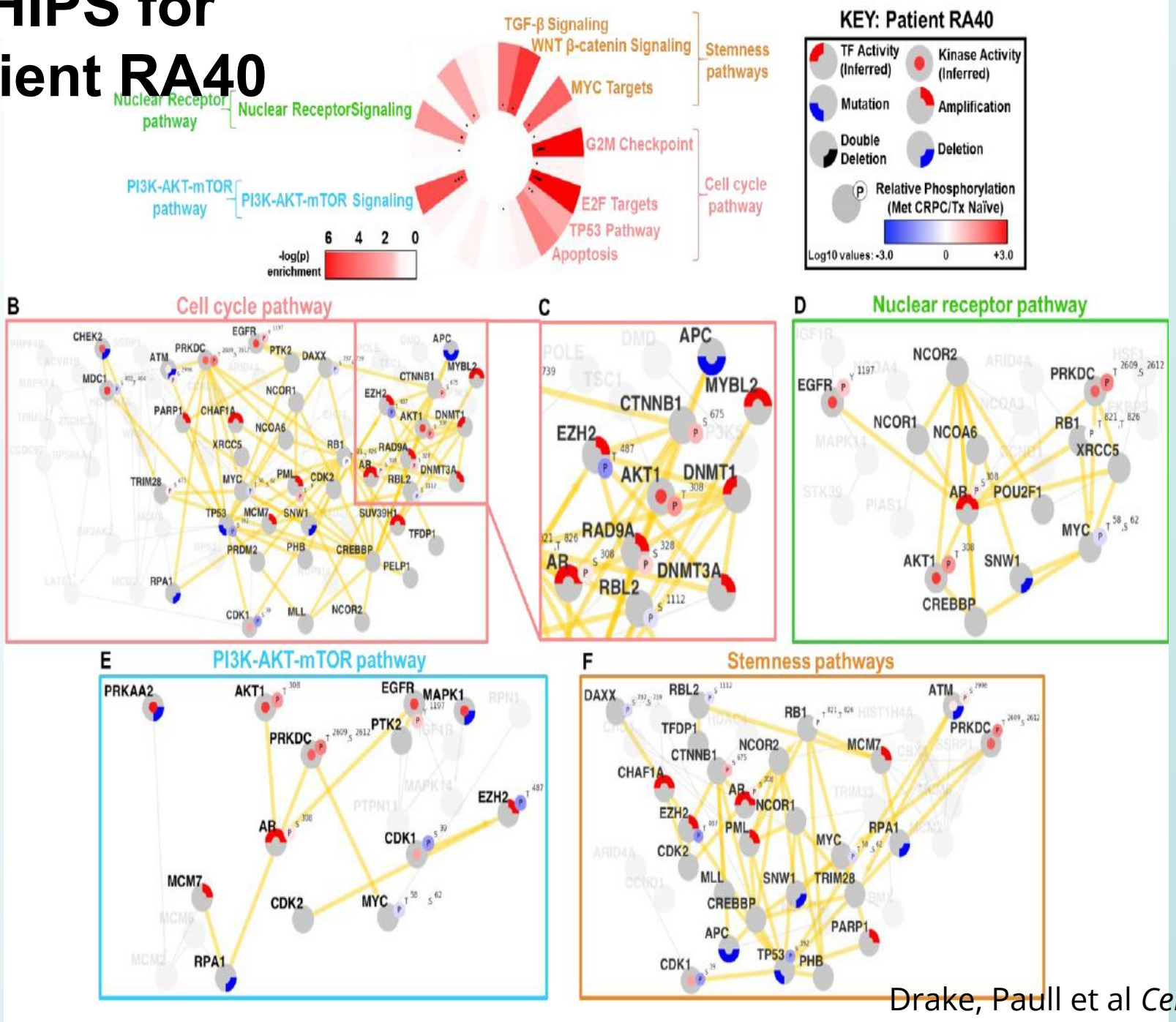


Zoom in on the glioma region
(tumors now colored by gliona subtype)

UNIVERSITY OF CALIFORNIA
SANTA CRUZ | Genomics Institute

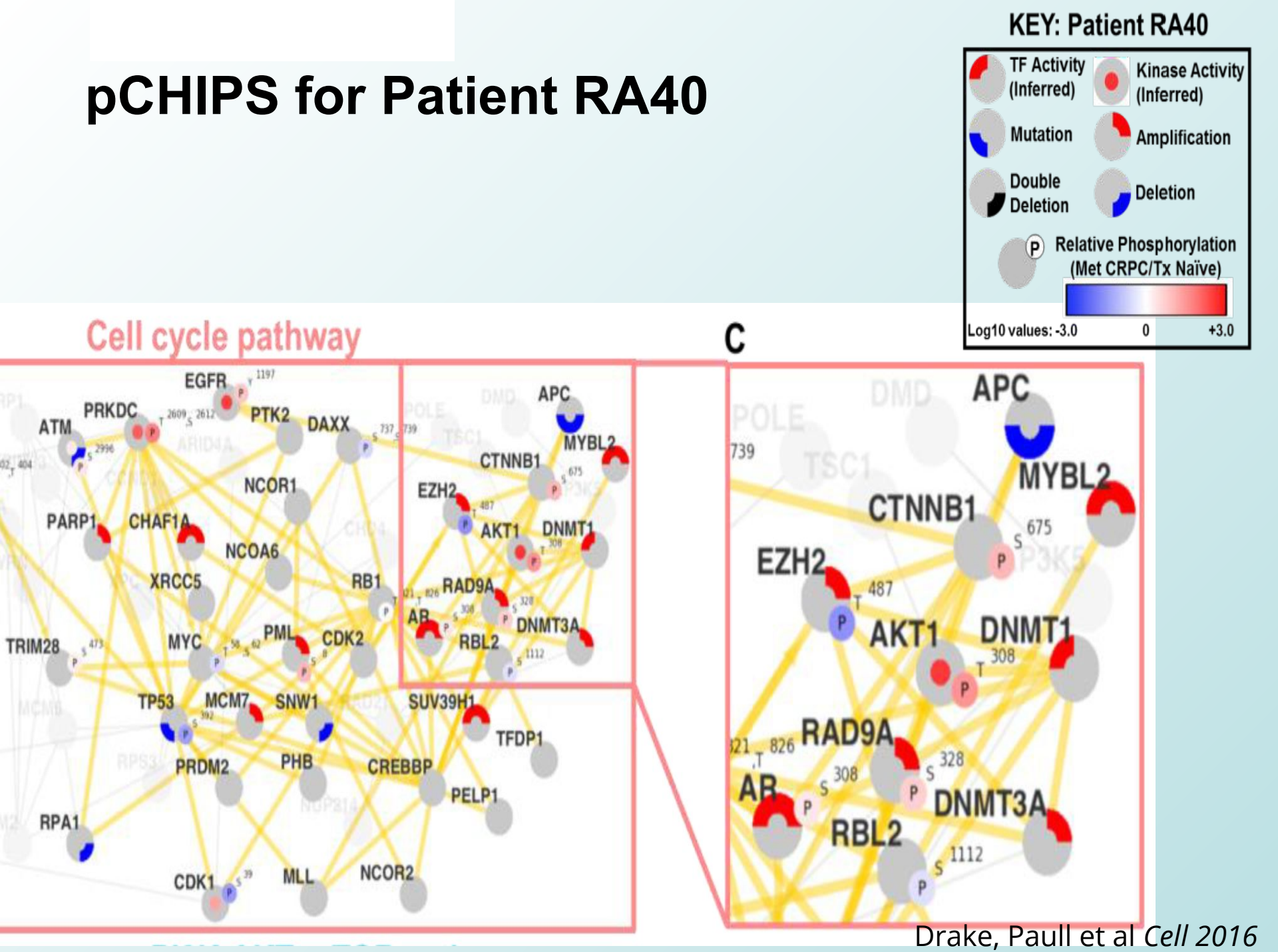
https://treehousegenomics.soe.ucsc.edu/

pCHIPS for Patient RA40



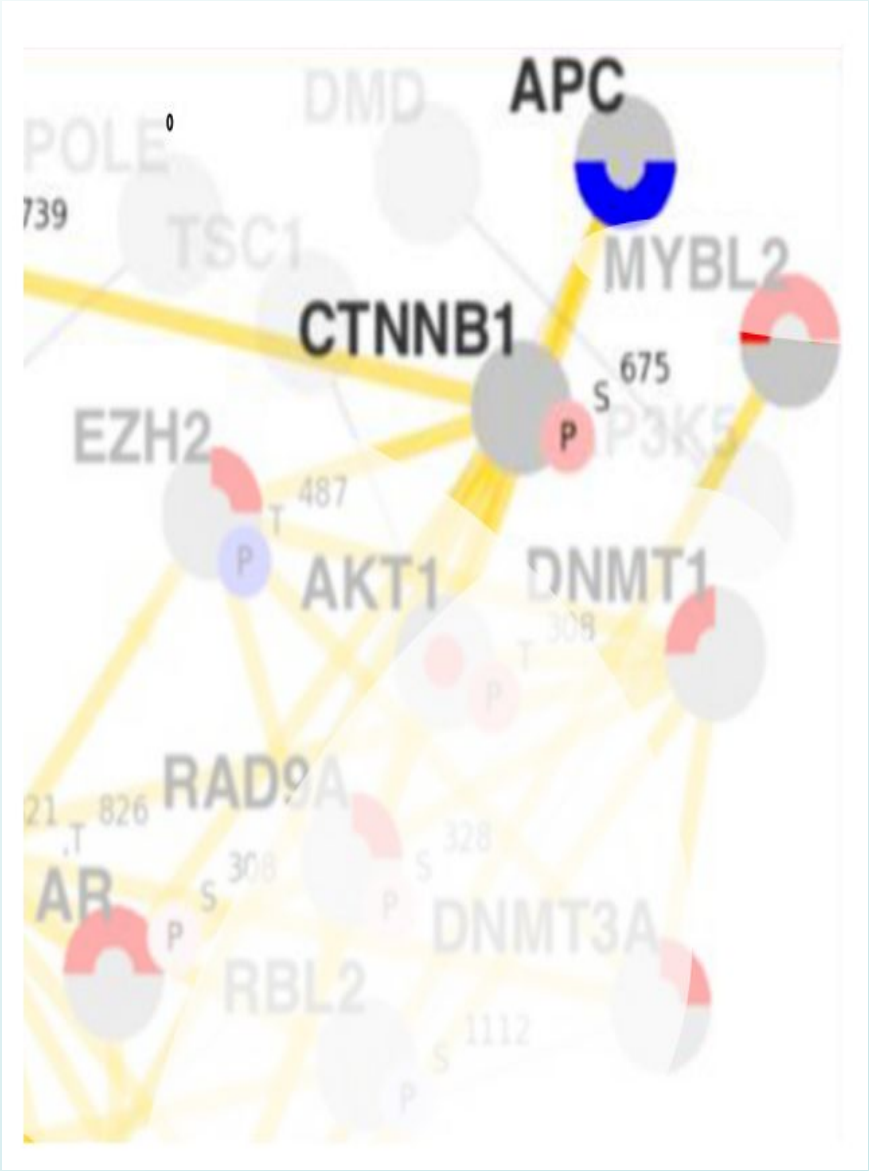
Drake, Paull et al *Cell 2016*

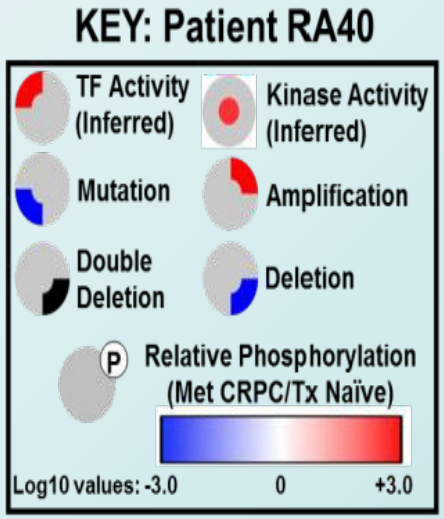
pCHIPS for Patient RA40



Drake, Paull et al *Cell 2016*

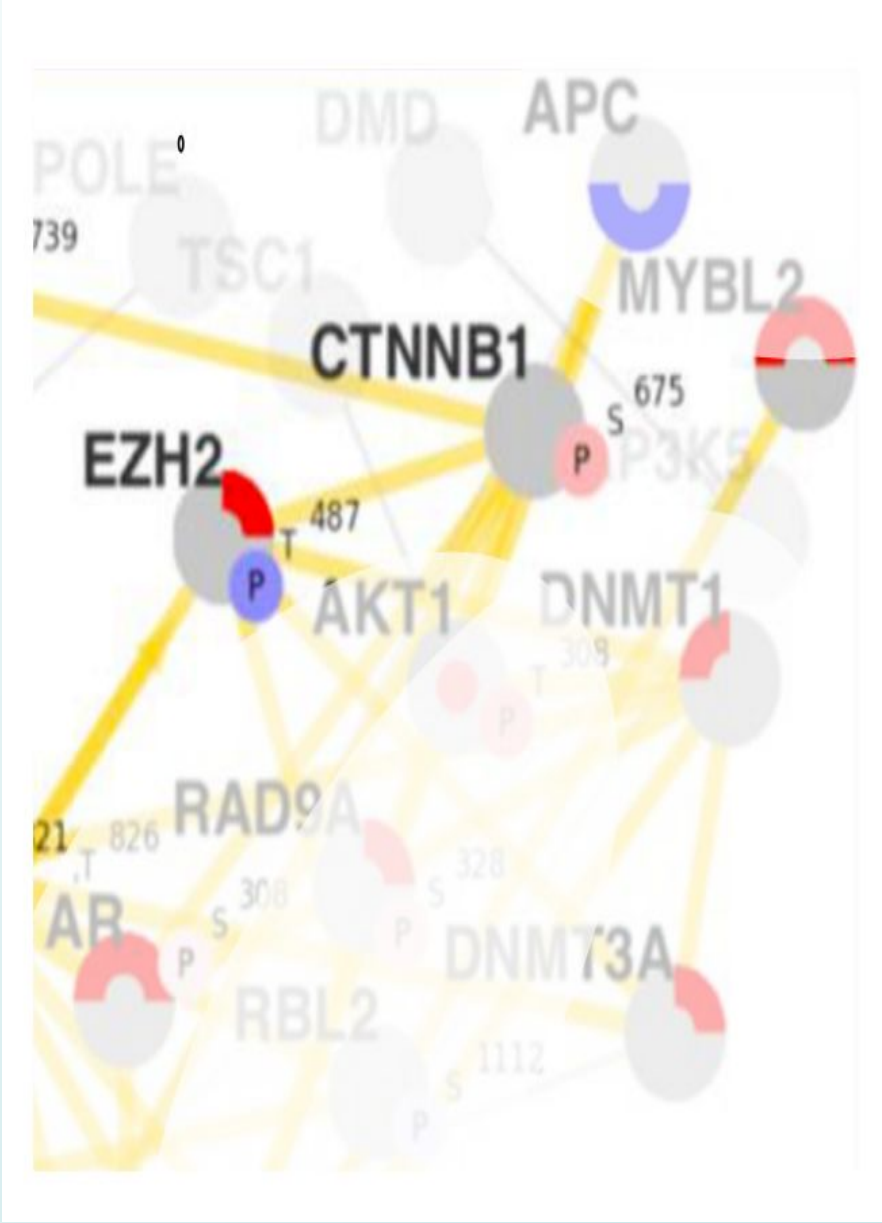
pCHIPS for Patient RA40

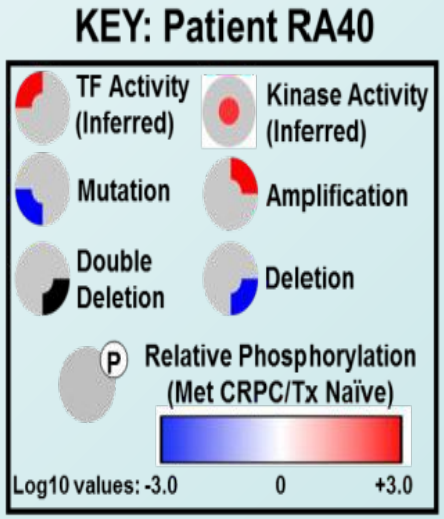




Drake, Paull et al *Cell 2016*

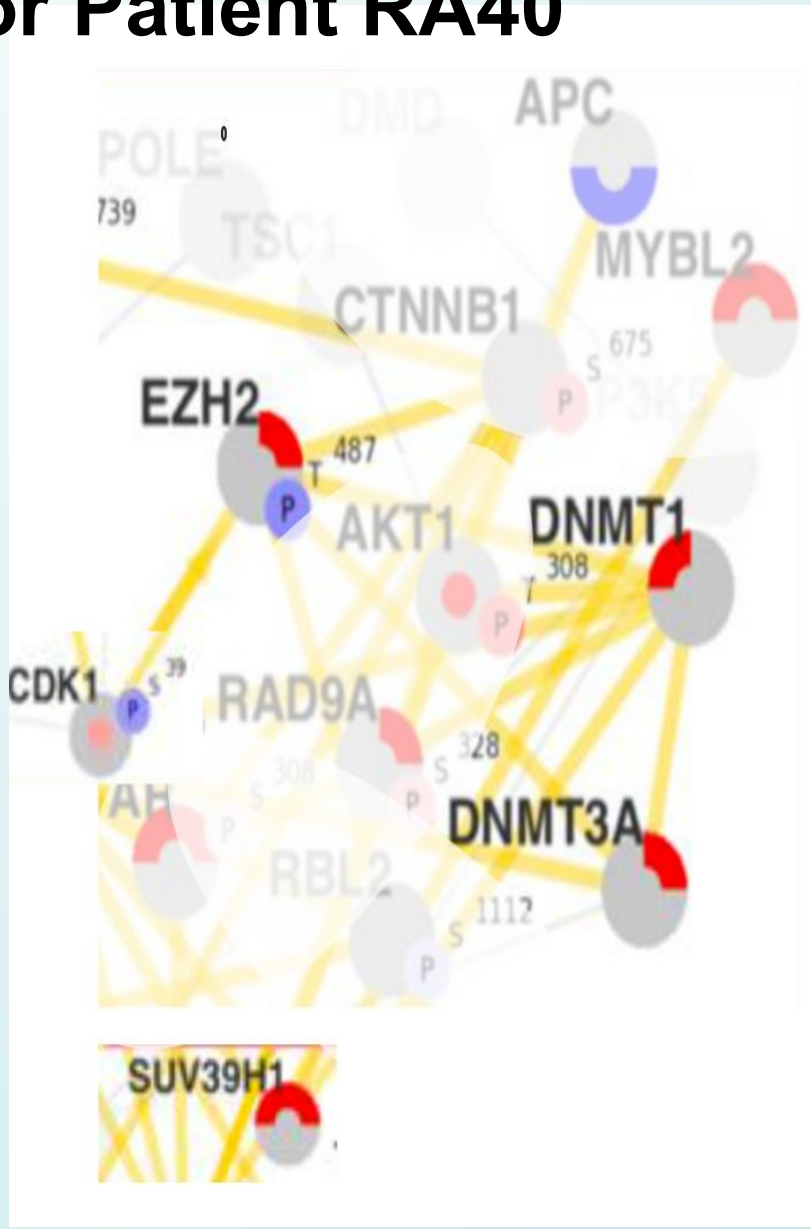
pCHIPS for Patient RA40

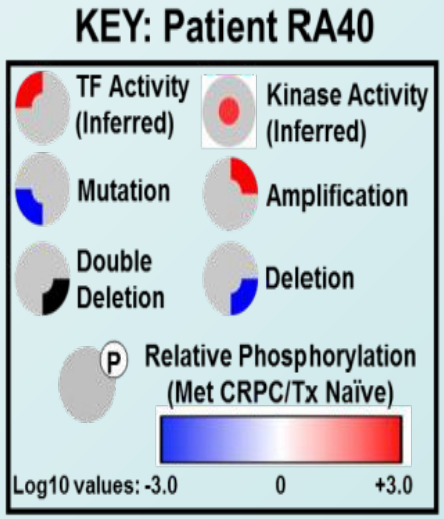




Drake, Paull et al *Cell 2016*

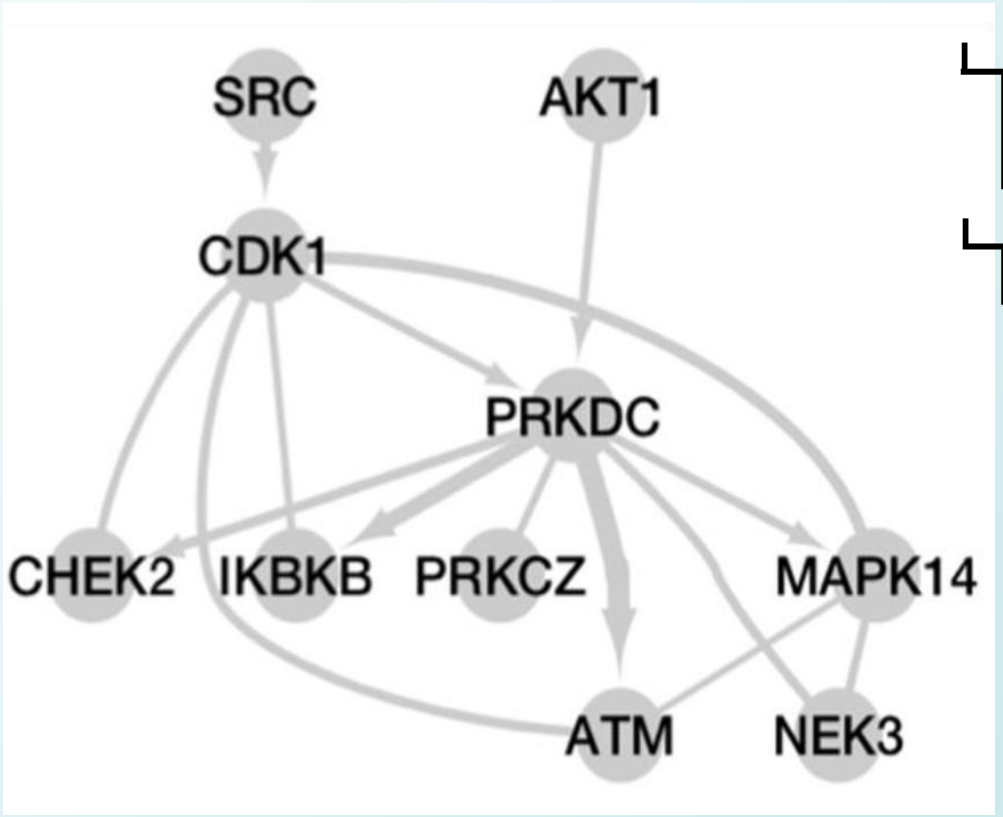
pCHIPS for Patient RA40

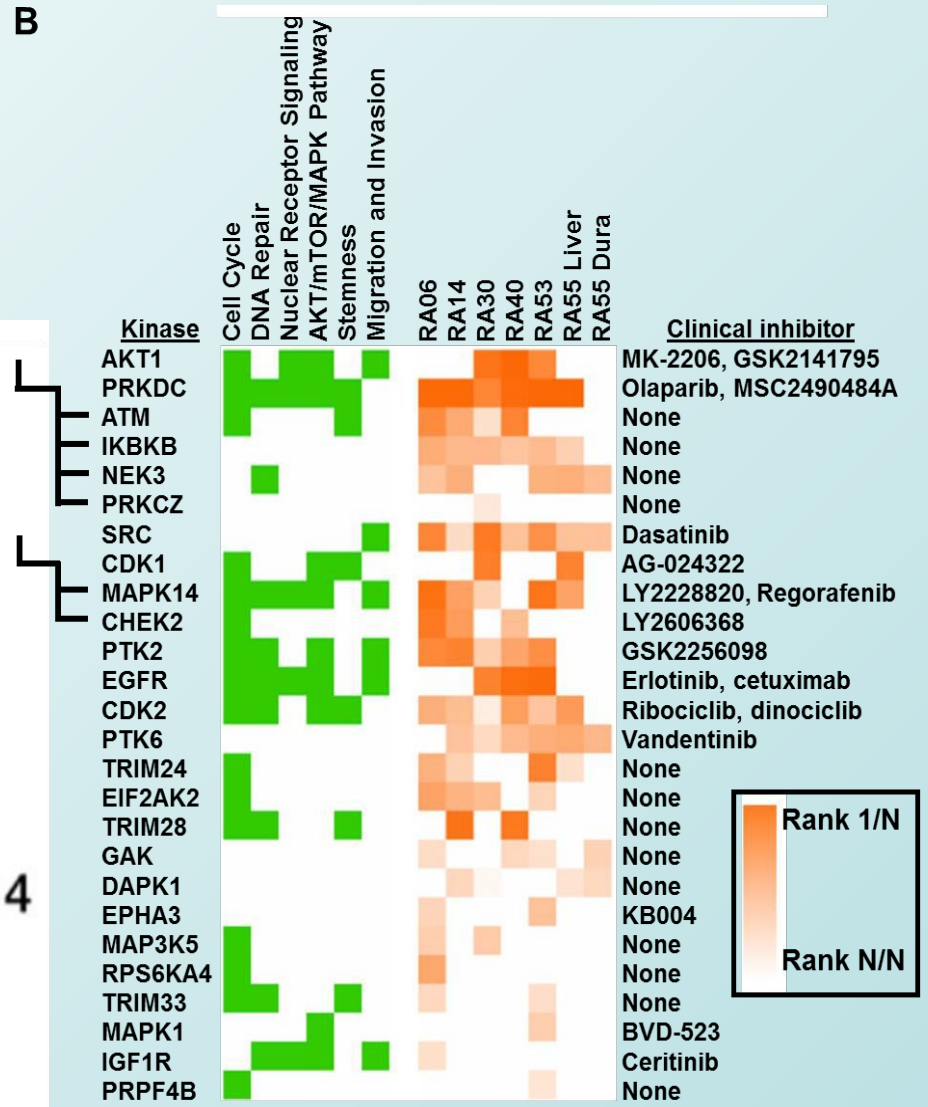




Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

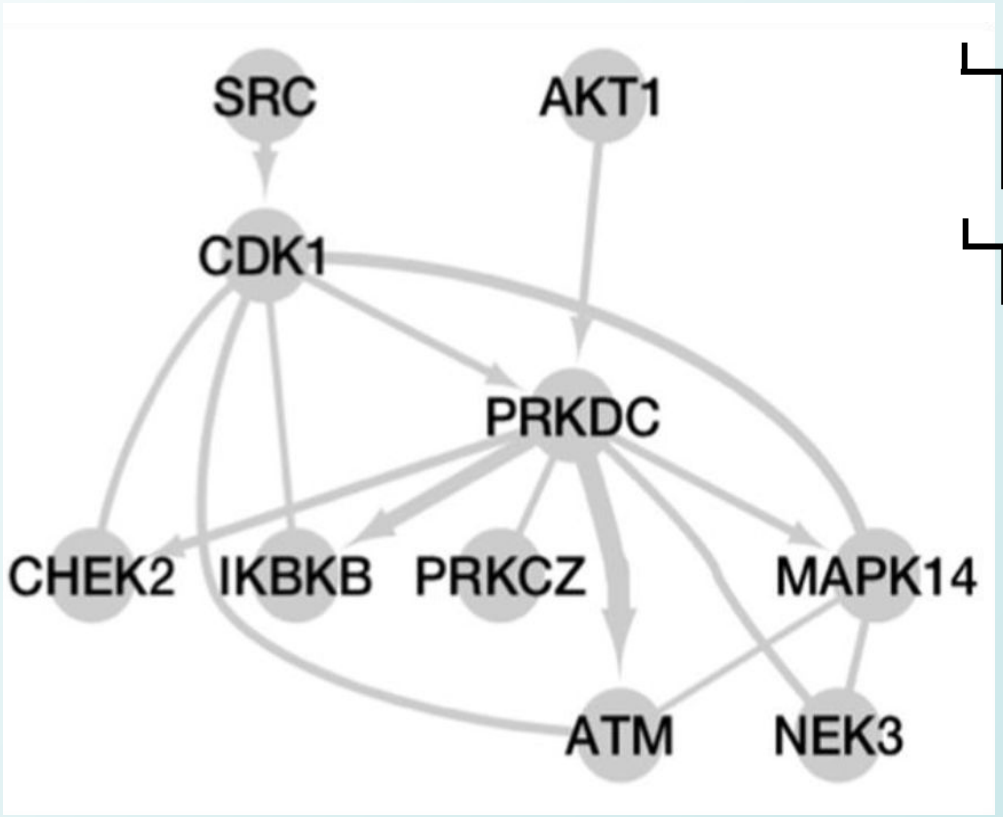


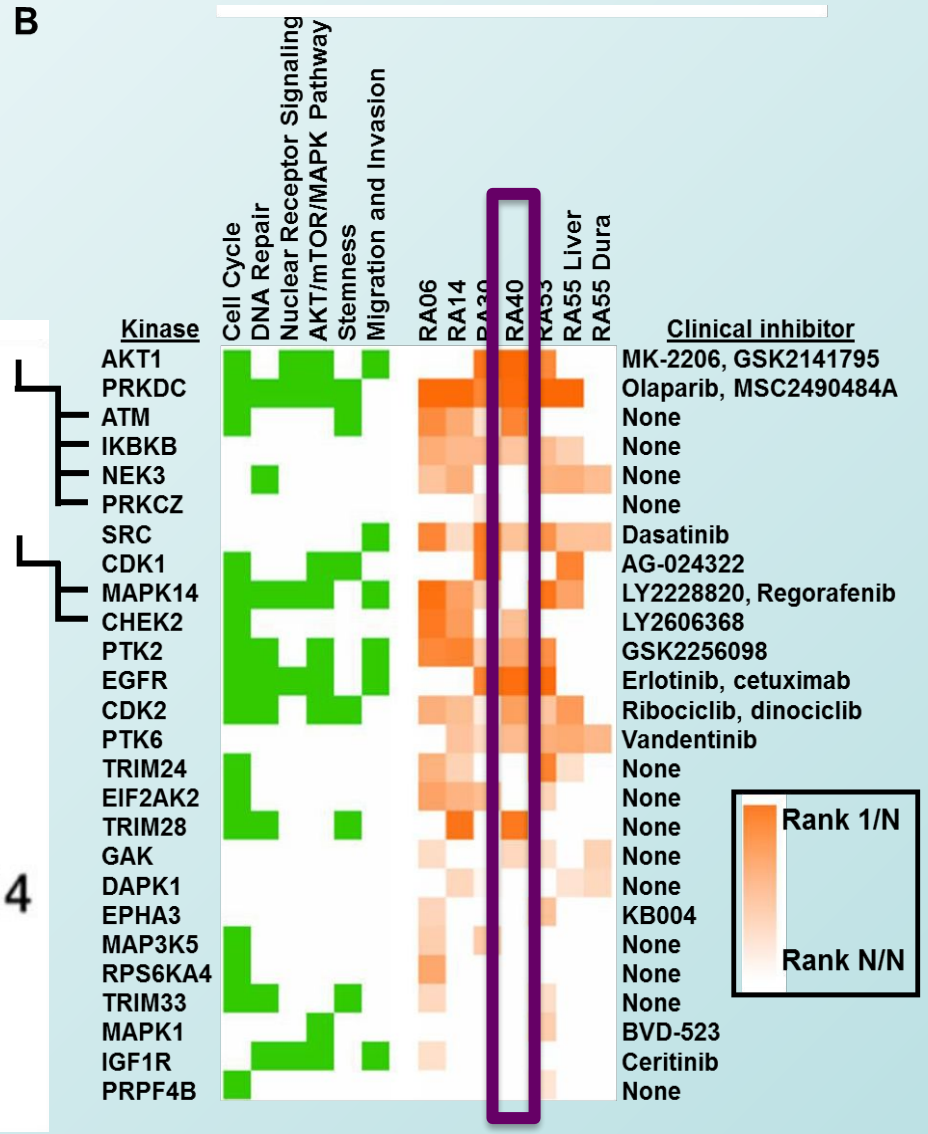


Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

Patient 40

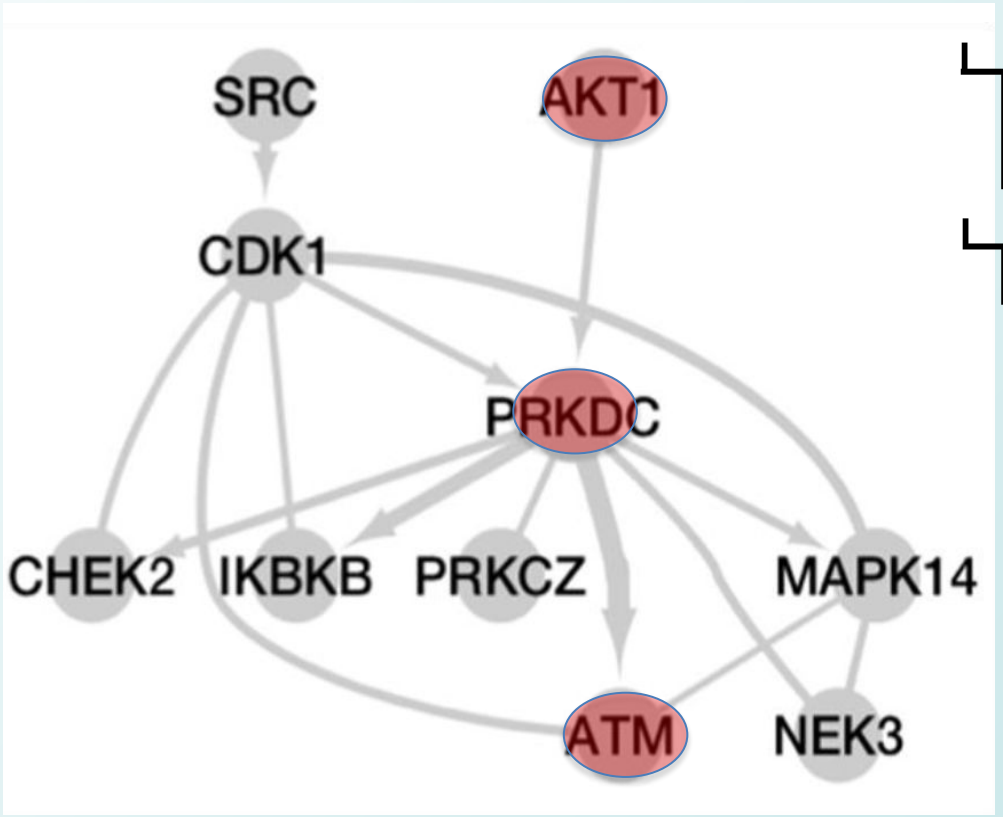


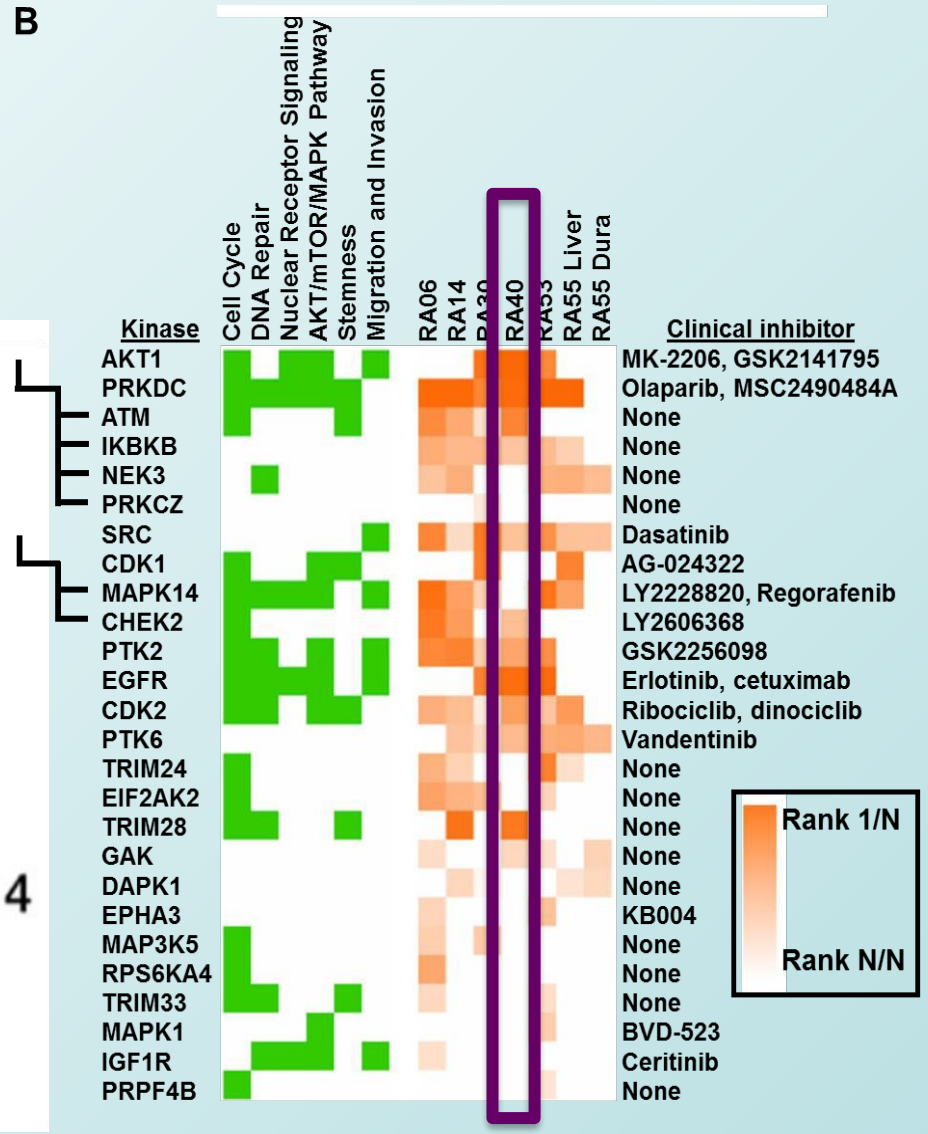


Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

Patient 40

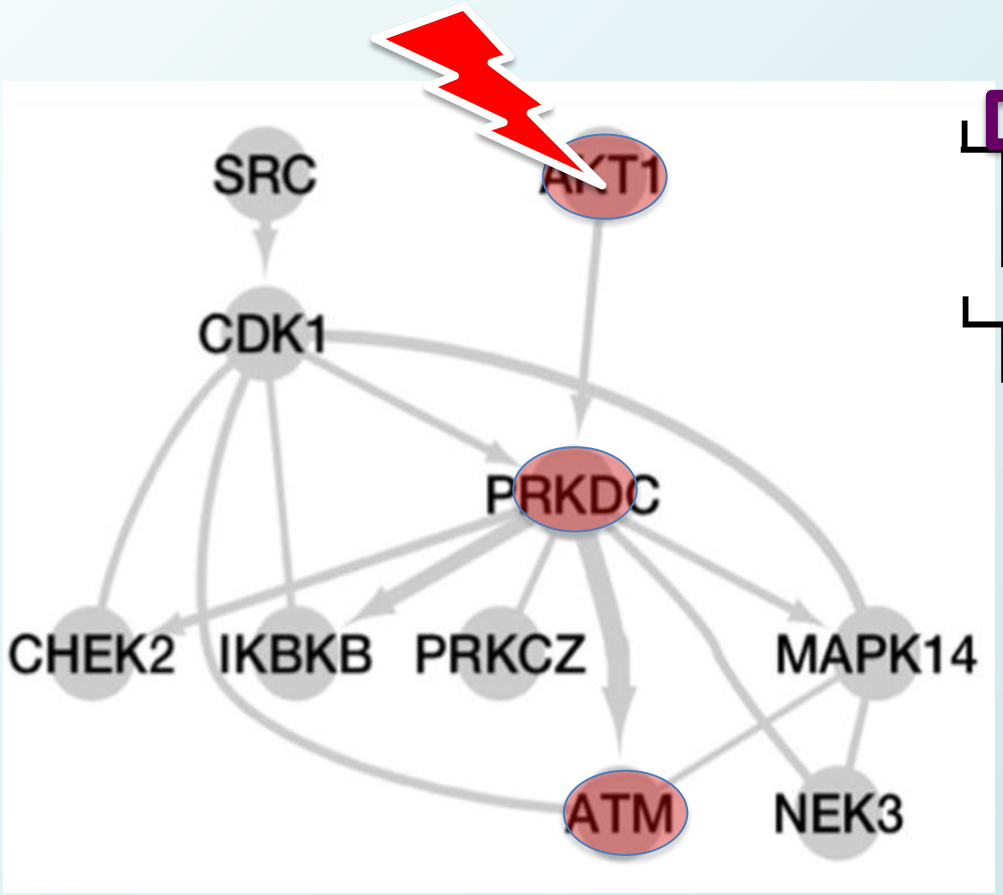


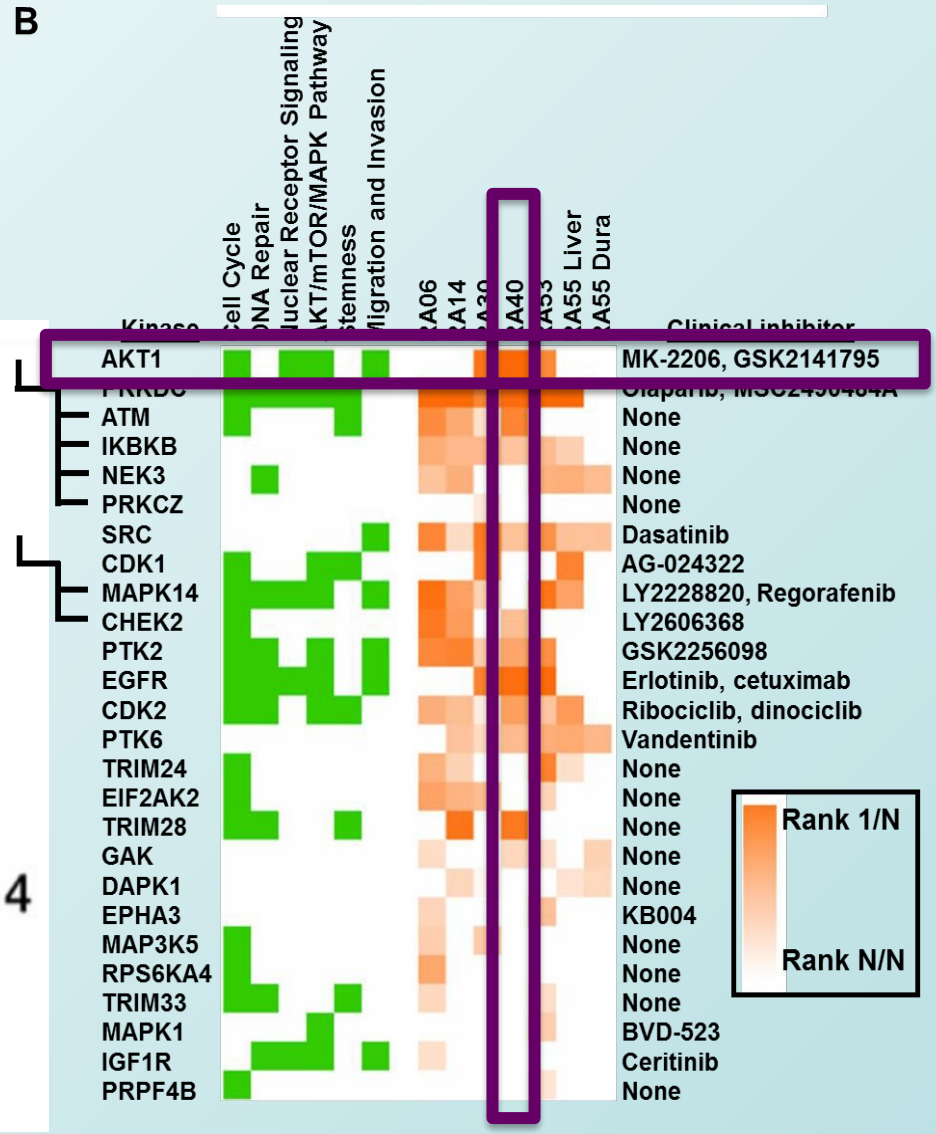


Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

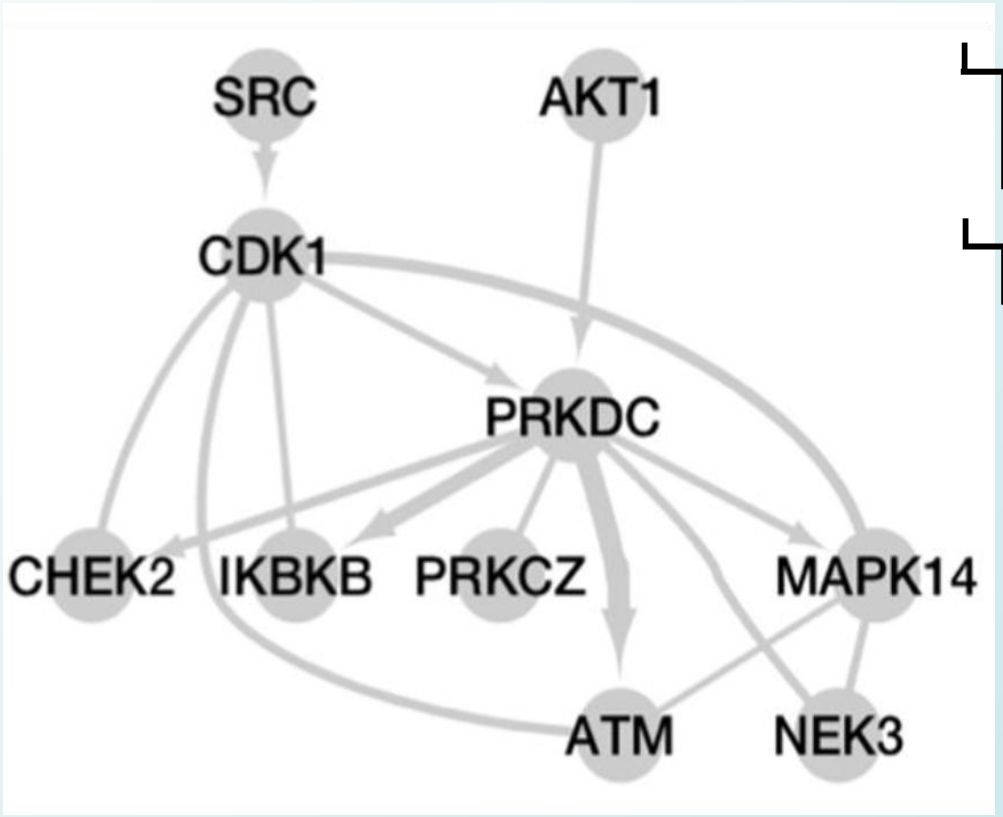
Patient 40

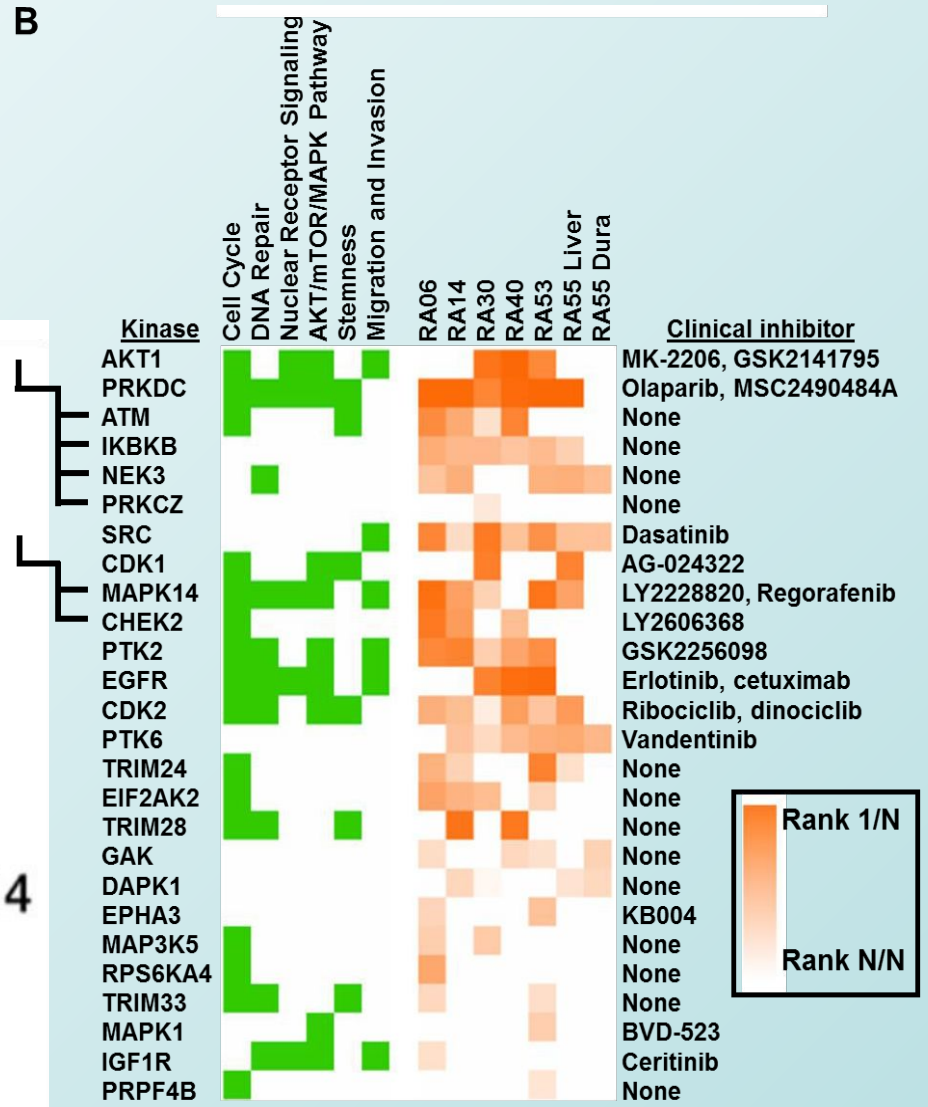




Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

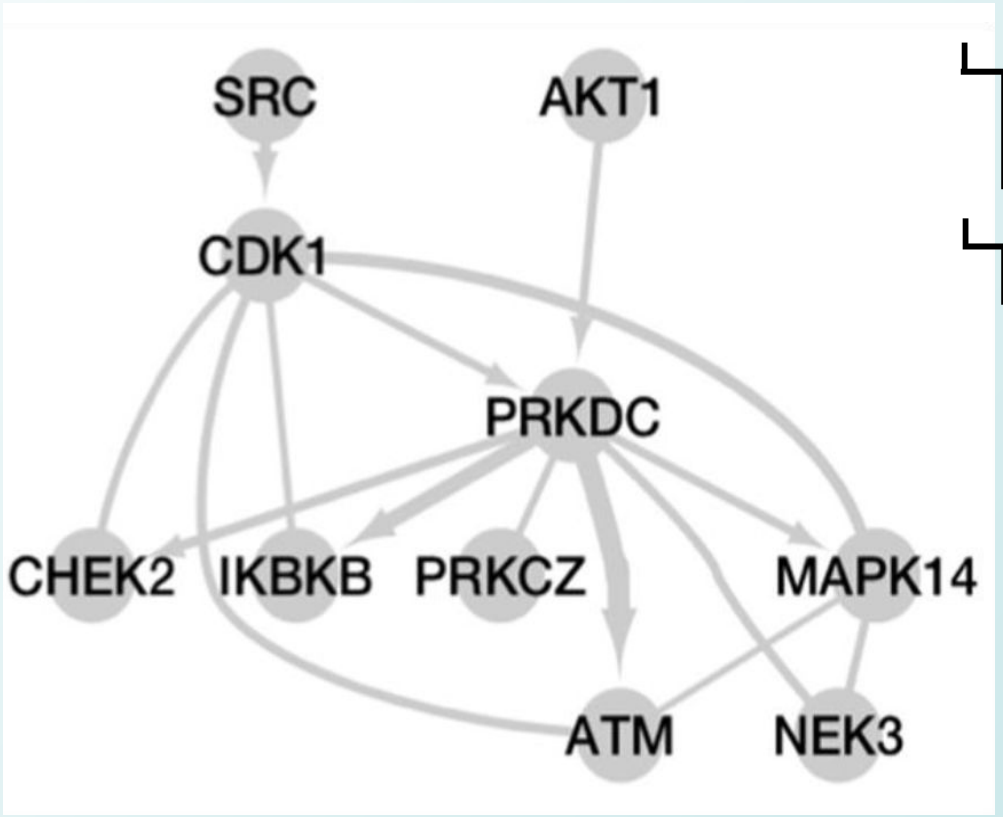


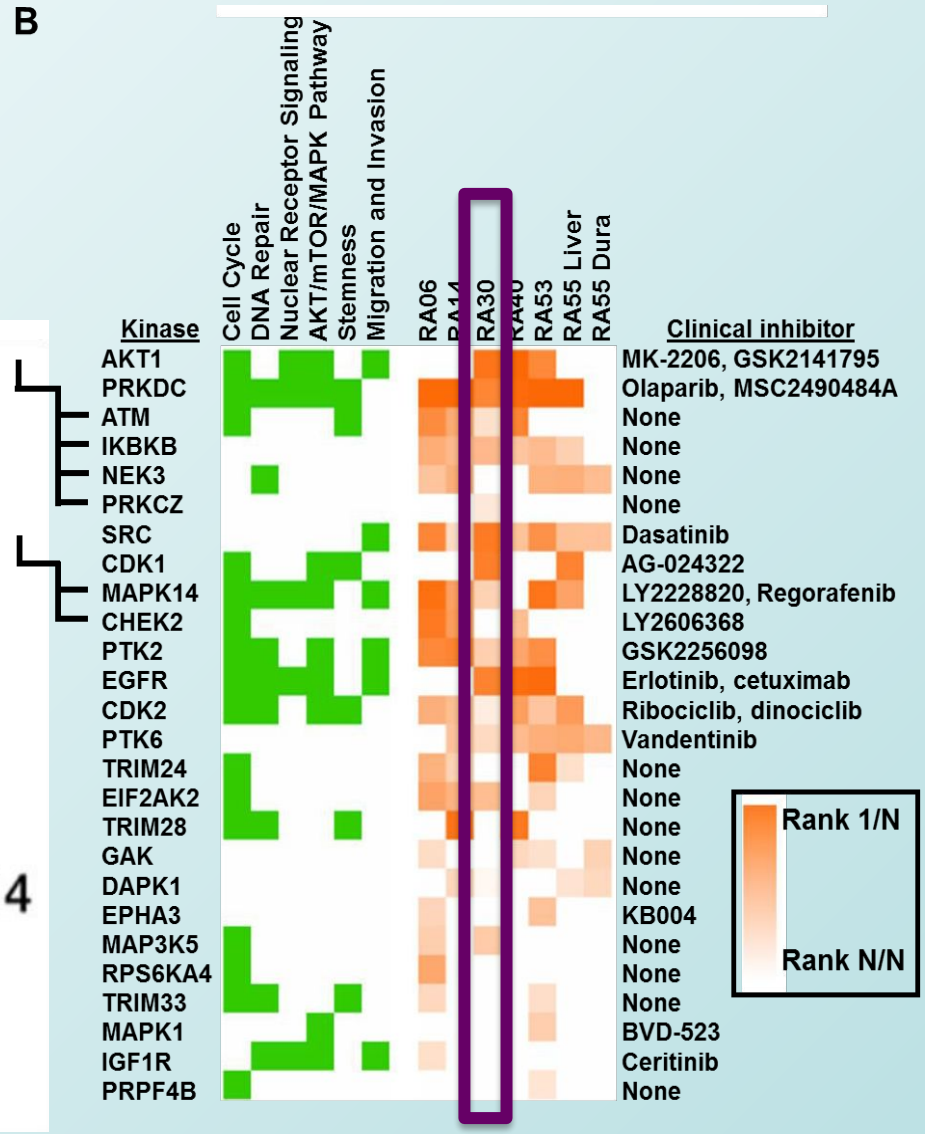


Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

Patient 30

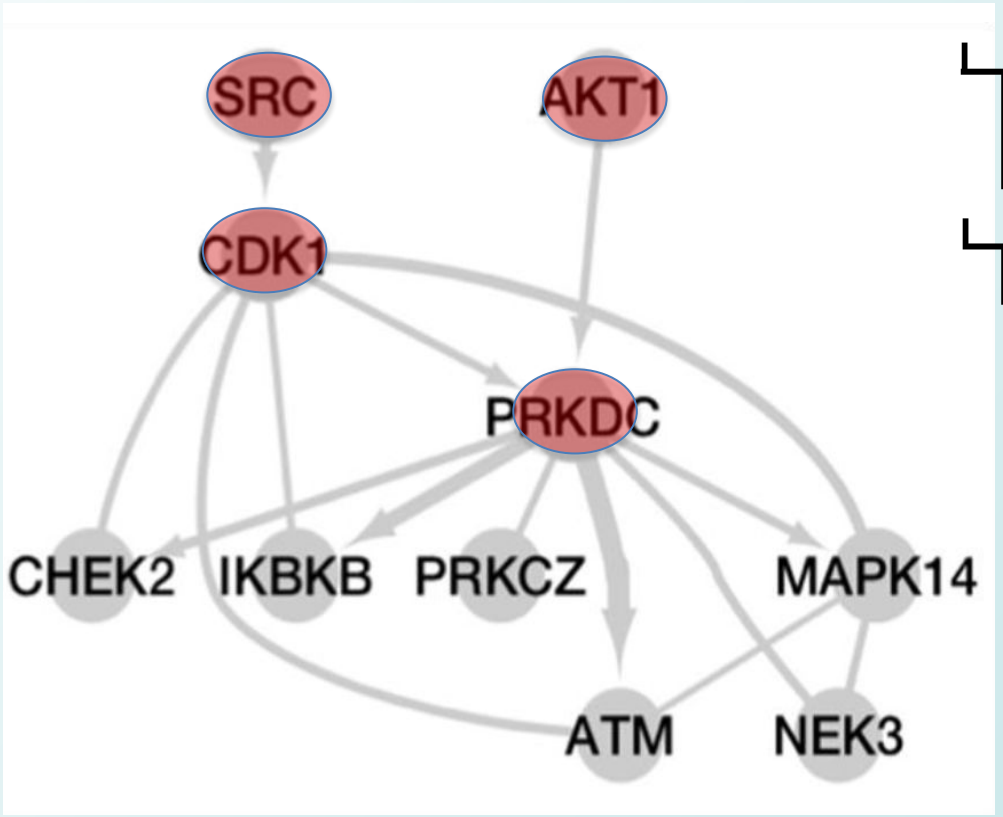


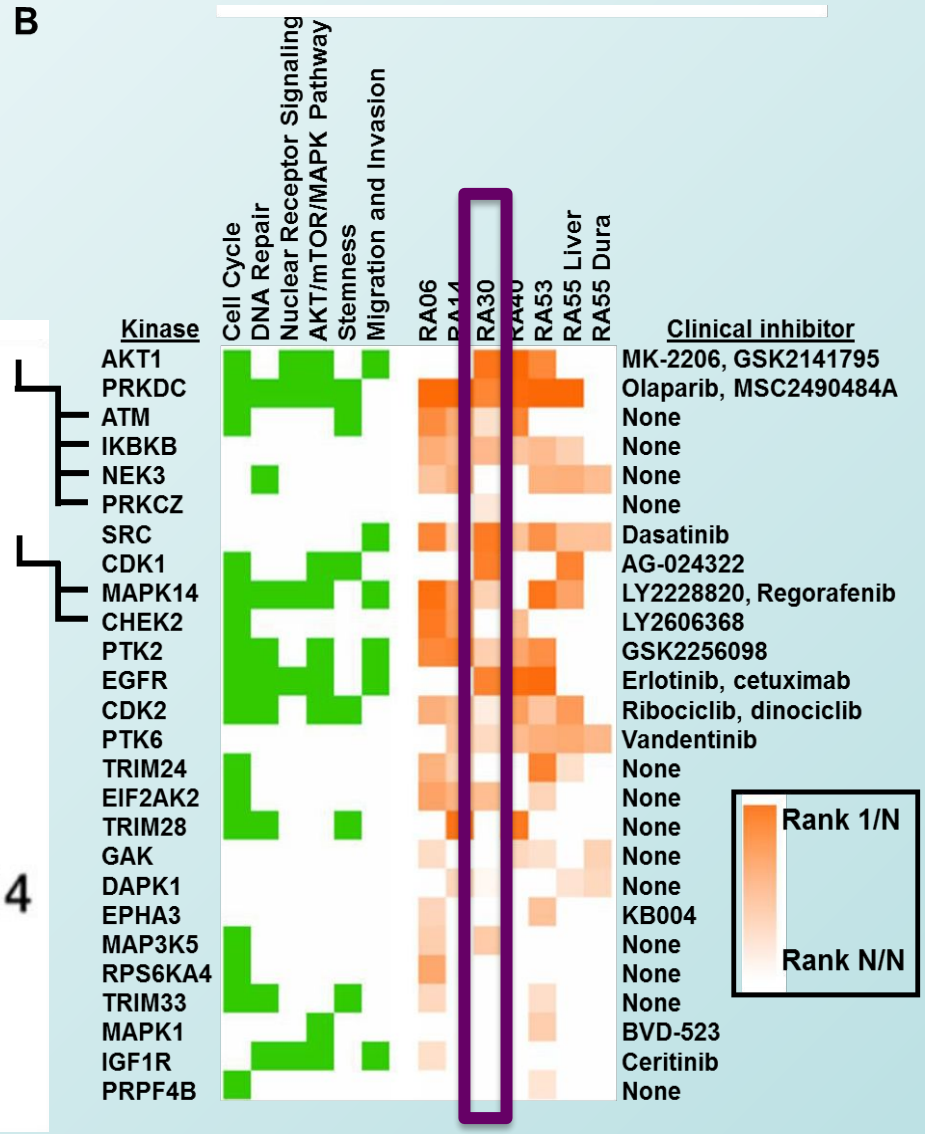


Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

Patient 30

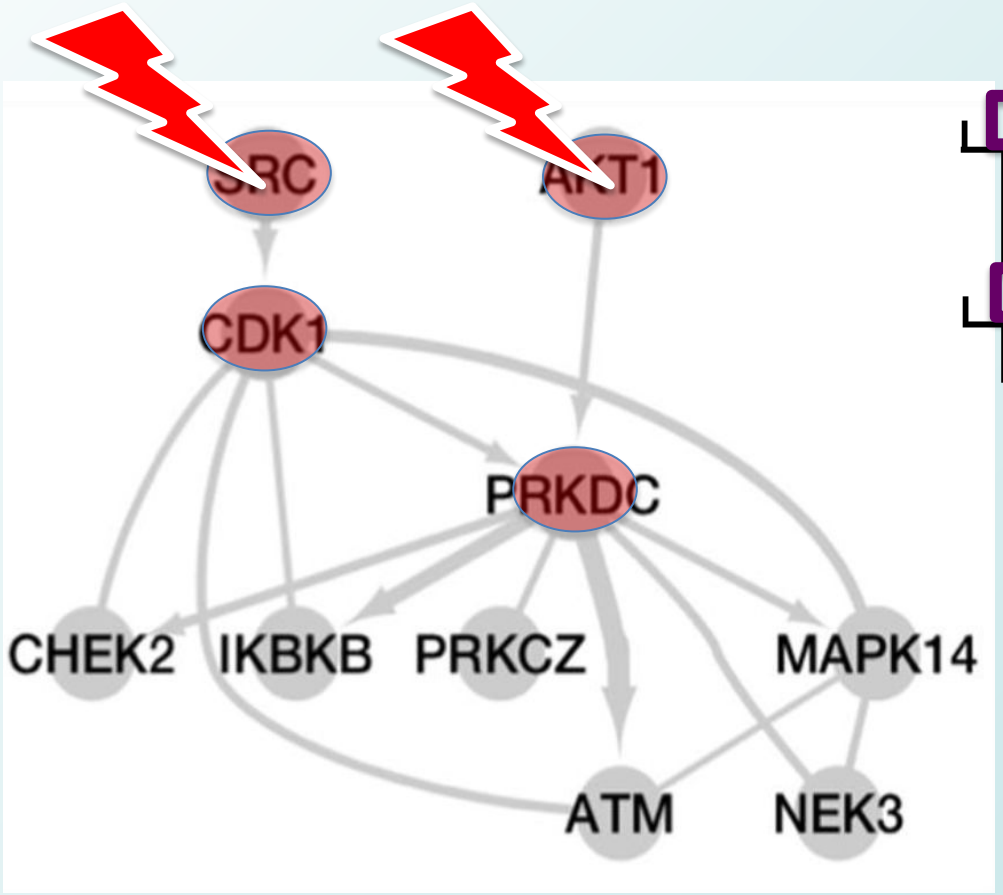


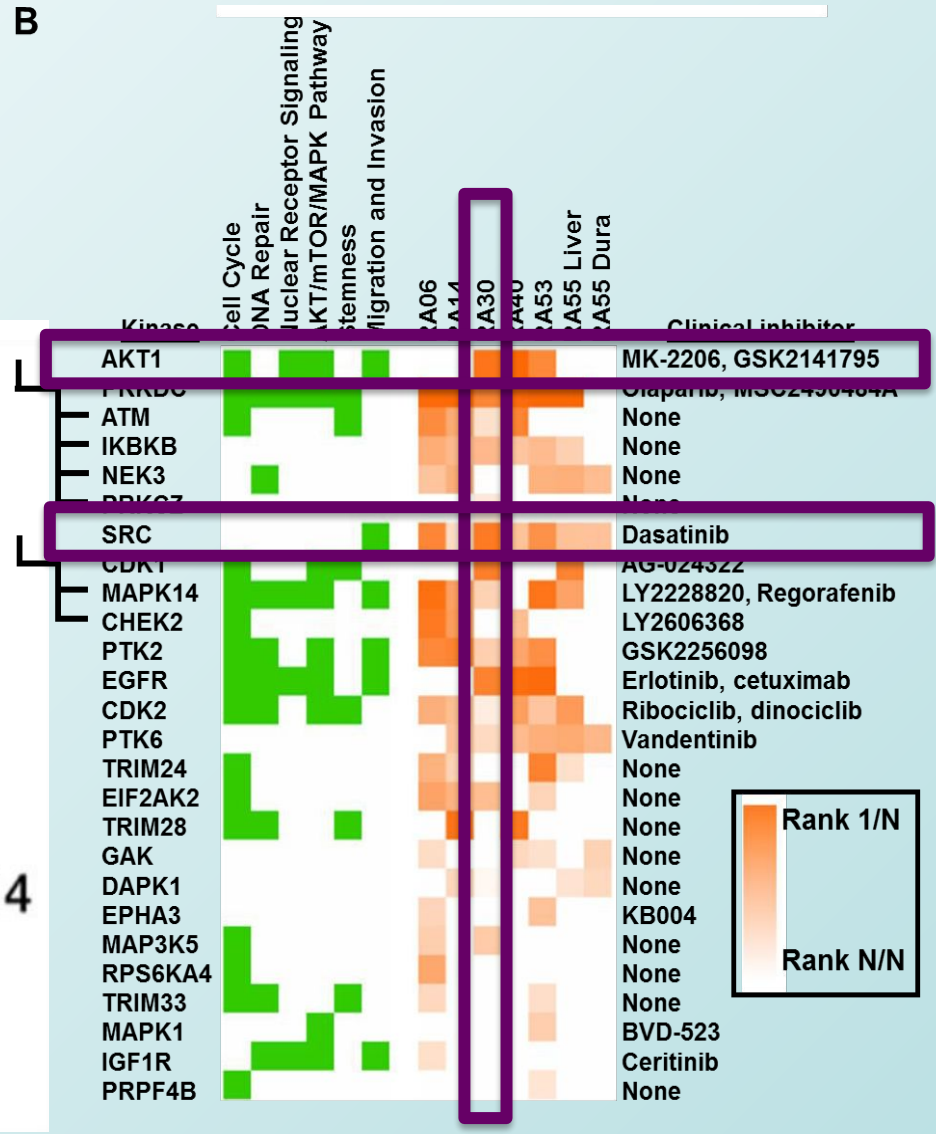


Drake, Paull et al *Cell 2016*

pCHIPs: Network-based selection of targets and target combinations for individual patients

Patient 30





Drake, Paull et al *Cell 2016*

BMEG Portal of Patient-Specific Hallmarks (pCHIPS)

BMEG Progress Summary

- New DREAM brain-sourcing challenges produce re-runnable, cloud-ready code
  - Compare methods, reusable, rerunnable code

- Established calls for PanCan consortia.
  - Data & code adopted to GDC

- Graph of knowledge to capture high-level information

- Introspective inference methods
  - Granger causality-based gene network inference
  - ID patient-specific altered pathway diagrams (pCHIPS)

BMEG Year 5 Research Plan

- Implementing several use-cases
  - E.g. **tumor recommender**
  - Link TCGA tumors to predicted **drug sensitivities** (CCLE)
  - Connect **non- to coding variants** (from ICGC PCAWG)
  - Load high-level **imaging data**

- Distributed and **Automated Introspective Machine-Learning**

- Load **top DREAM results on SMC-Het & SMC-RNA**

- Ongoing Collaborative Projects
  - GDAN analyses - PanCanAtlas, Driver Discovery, ALCHEMIST, Exceptional Responders, LUSC survival
  - DREAM - Plan for **next RNA-Seq deconvolution challenge**

BMEG Team

UCSC Group

Chris Wong

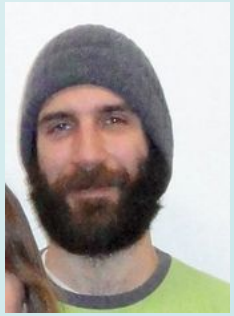
David Haan

Pablo Cordero

Teresa Swatloski

James Durbin

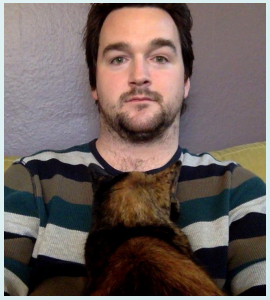
Vlado Uzunangelov



OHSU Group

Kyle Ellrott

Ryan Spangler



Allison Creason

Alexander Buchanan

Malisa Smith

Jeena Lee

Acknowledgments

David Haussler

UCSC Genome Browser Staff

- David Haussler
- Mark Diekins
- Melissa Cline
- Jorge Garcia
- Erich Weiler

Ted Goldstein

UCSF / Buck Institute for Aging

- Chris Benz, Buck
- Christina Yau, Buck
- Denise Wolf, UCSF
- Laura van't Veer, UCSF
- Eric Collisson, UCSF

Chris Benz,

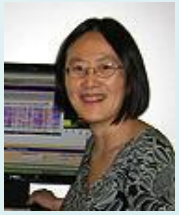
UCSF Medbook Team

- Ted Goldstein

UCSC Cancer Genomics

- Jing Zhu
- Sofie Salama
- Teresa Swatlowski
- Brian Craft

Jing Zhu



Olena Morozova

UCSC Tree House Project

- Olena Morozova
- Melissa Cline

Collaborators

- Katie Hoadley, UNC
- Rehan Akbani, MDACC
- Justin Guin ney, Sage
- Larsson Omberg, Sage

PCF

ORACLE

STAND UP TO CANCER

THE CANCER GENOME ATLAS

TREEHOUSE FOLKS

Olena Morozova, UC Santa Cruz
Atul Butte, CIAPM
Marco Marra, BC Cancer Agency
David Haussler, UC Santa Cruz
Ted Goldstein, UC Santa Cruz
Sofie Salama, UC Santa Cruz
Linda Rosewood, UC Santa Cruz
Ann Pace, UC Santa Cruz
Melissa Cline, UC Santa Cruz
Jing Zhu, UC Santa Cruz
Yulia Newton, UC Santa Cruz

Olena Morozova

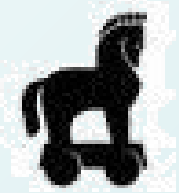
Yulia Newton

<u>Clinical Collaborators</u>
S. Rod Rassekh, BC Children's Hospital
Rebecca Deyell, BC Children's Hospital
Stephen Yip, BC Cancer Agency
Leonard Sender, Children's Hospital of Ora
Sabine Mueller, UC San Francisco
Adam Resnick, Children's Hospital of Philad
Alejandro Sweet-Cordero, Stanford

TCGA Pan-Can AWG

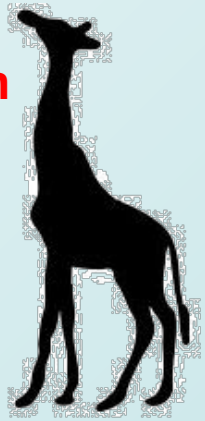
UCSF/Buck Inst
Chris Benz
Eric Collisson
Christina Yau
Denise Wolf

UNC
Katherine Hoadley
Chuck Perou



USC
Peter Laird
Hui Shen

MDACC
John Weinstein
Rehan Akbani
Lauren Byers
Han Liang
Roel Verhaak
Gordon Mills



WashU
Li Ding
Cyriac Kandoth
Beifang Liu
Mike McLellan

UCSC
Vlado Uzunangelov
Sam Ng
Evan O. Paull
Kyle Ellrott
David Haussler
Jing Zhu

Broad
Andrew Cherniak
Matt Meyerson
Gaddy Getz
Rameen Beroukhim
Scott Carter
Travis Zack
Mike Lawrence
Angela Brooks

MSKCC
Chris Sander
Giovanni Ciriello
Anders Jacobsen

NCI / NHGRI
Zhong Chen
Carter Van Waes

Baylor
Mark Hamilton
David Wheeler

Brown
Ben Raphael
Max Leiserson

UPF Barcelona
Nuria Lopez-Bigas
David Tamborero
Abel
Gonzalez-Perez

Sage Bionetworks
Adam Margolin
Larsson Ohmberg

UBC
Gordon Robertson
Andy Chu

ISB
Ilya Shmulevich
Sheila Reynolds

Harvard
Raju Kucherlapati

Univ Toronto
Gary Bader
Juri Reimand

BMEG Overview Video → [Play Youtube Video]

Additional

Future Challenges

- Deconvolve tumors
  - Subclones, evolution, migration
  - ID all cells in tumor environment (new DREAM deconvolution challenge)
  - Leverage single cell data

- Translate omics to patients
  - Reproducible / reliable *patients-like-me*
  - Recommenders to identify relevant evidence for submitted tumor specimens
    - E.g. implicated drugs, activated pathways
  - End-to-end sequence to prediction (DNA & RNA)

- Contribute to early detection
  - Precursor mutations that lead to later stage mutations.

Quest for the best: not just a dream but a DREAM challenge

ICGC-TCGA (SMC) Challenge Series for Cancer

SMC-DNA

- Identify the best methods mutation calling methods (wrapping up)

SMC-RNA

- Identify the best methods for fusion gene finding from RNA-seq data
- (launching Jan, 2015)

SMC-HET

- ID best methods for deconvolving subclonal heterogeneity from VAFs.
- Estimate sub-clone proportions
- Predict lineage tree
- (launching Jan 2015)

Collaboration: OICR, TCGA, UCSC, SAGE

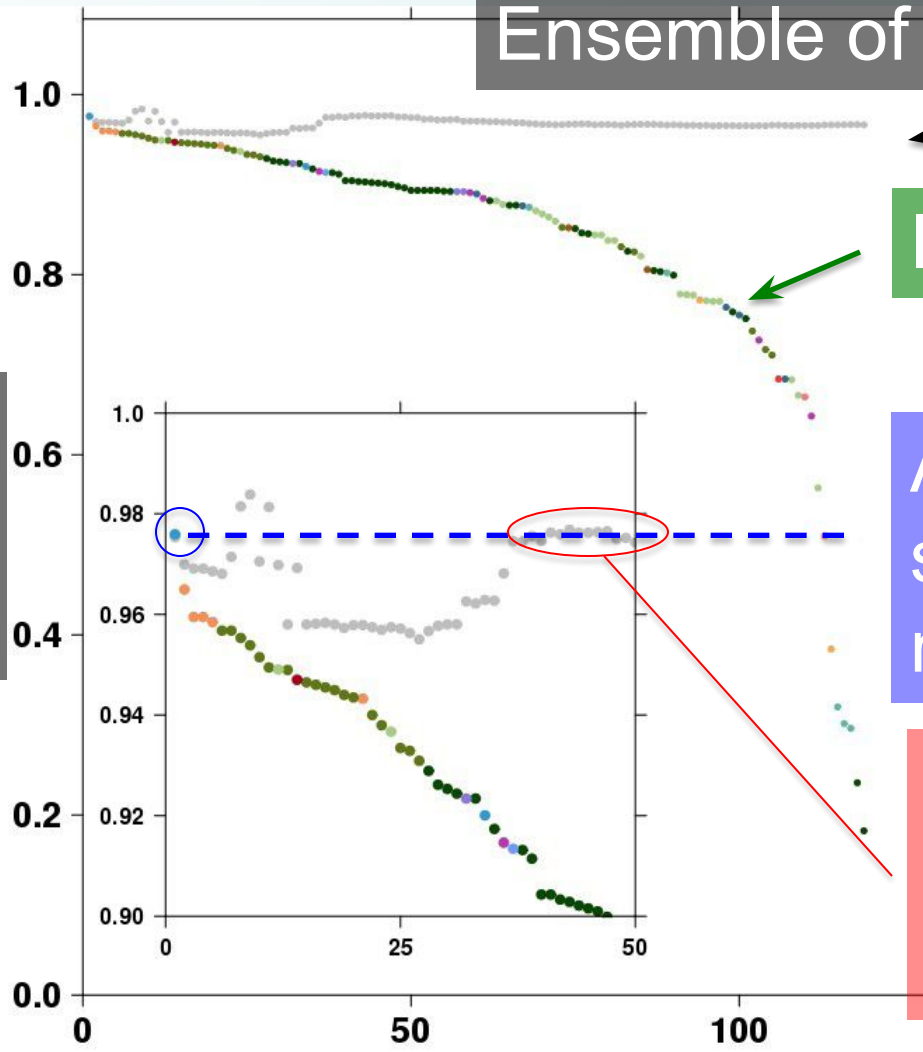
Results of DREAM-SMC

- Participation At Closing Time:
  - **345** contestants
  - 948 entries on 4 *in silico* genomes

- On-going post-challenge submissions (*living benchmark*)

- Key insights into simulating cancer genomes (BamSurgeon)

Wisdom of the Crowds for DREAM-SMC



Ewing et al. *Nat Meth* 2014

Distinguish True Variation from Artifact

needlestack

A needle in a human genome ~~haystack~~

- A human genome has **23** chromosomes.
- **6 billion** individual DNA basepairs per genome.
- A **single basepair** error can be a disease mutation.

BMEG's DREAM-SMC Paved the Way for MC3

Method Name	Team	Sensitivity	Precision	Balanced Accuracy
MuTect - L10	Broad SMC	0.9672	0.9836	0.9754
Dream_Set1_MuSE_Setting8	Wang-Wheeler-HGSC	0.9208	0.9778	0.9493
Strelka_aln-0.5.7_recSNV_filters_default	SMC_Admins	0.8325	0.953	0.8928
somaticsniper_bwa_2	SMC_Admins	0.9341	0.8317	0.8829
radia	UCSC	0.884	0.8815	0.8828
varscan-default-params	SMC_Admins	0.9859	0.1206	0.5532

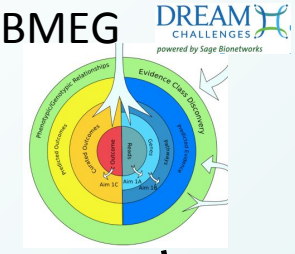
Preprocessing of winning method (GATK cleaning) adopted for all MC3 methods

All MC3 callers (and more) evaluated in challenge

Methods containerized after challenge completion

Overview of **BMEG** Pipelines

BMEG

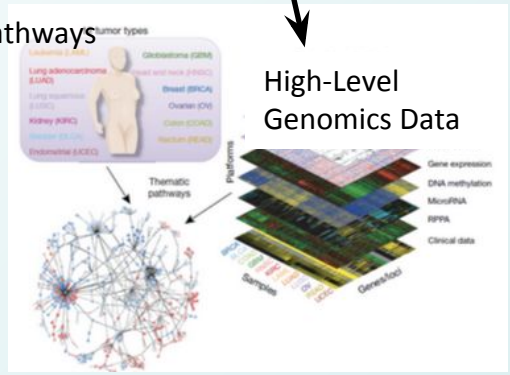


Data Sources

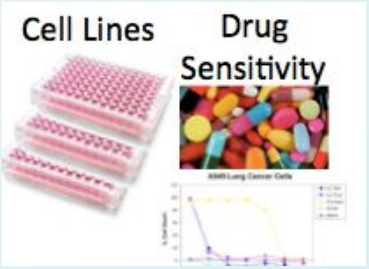
TCGA/ICGC/
SU2C / CKCC

Top Methods

Pathways

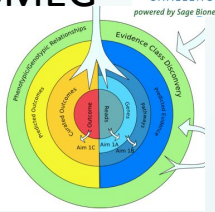


High-Level Genomics Data



Overview of **BMEG** Pipelines

BMEG



DREAM CHALLENGES
powered by Sage Bionetworks

Data Sources

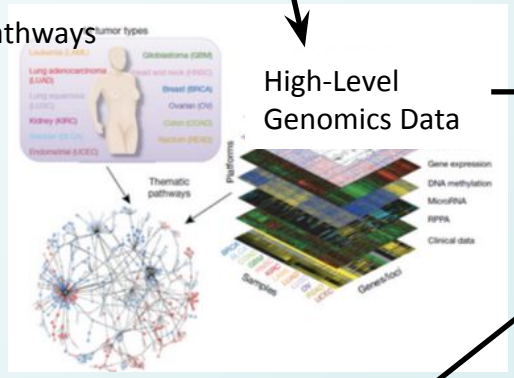
TCGA/ICGC/
SU2C / CKCC

Top Methods

DREAM CHALLENGES
powered by Sage Bionetworks

Outcomes / Phenotype Inferences

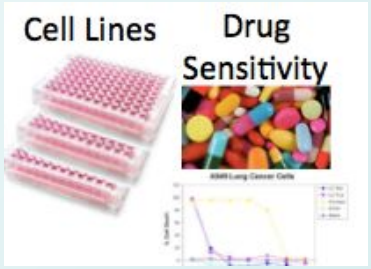
Pathways



High-Level Genomics Data

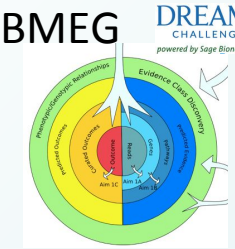
Aggressive

Gene Essentiality



Overview of **BMEG** Pipelines

BMEG



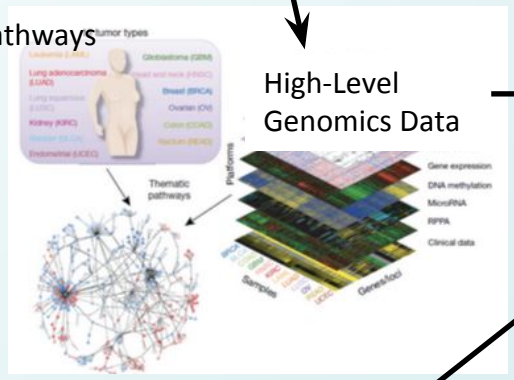
DREAM CHALLENGES powered by Sage Bionetworks

Data Sources

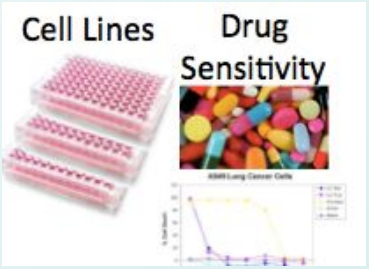
TCGA/ICGC/
SU2C / CKCC

Top Methods

Pathways



High-Level Genomics Data



Cell Lines

Drug Sensitivity

DREAM CHALLENGES powered by Sage Bionetworks

Outcomes / Phenotype Inferences

Aggressive

Gene Essentiality

Predictive Signature DB

Subtypes

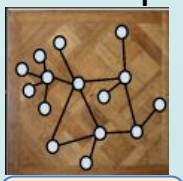
Cells-Of-Origin

Development (stemness)

Drug Sensitivity

Gene Essentiality

BME Graph

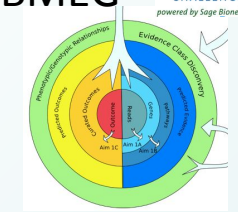


GA4GH

GA4GH API (G2P)

Overview of **BMEG** Pipelines

BMEG



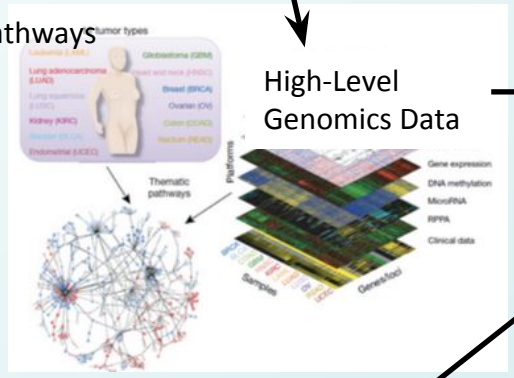
DREAM CHALLENGES powered by Sage Bionetworks

Data Sources

TCGA/ICGC/
SU2C / CKCC

Top Methods

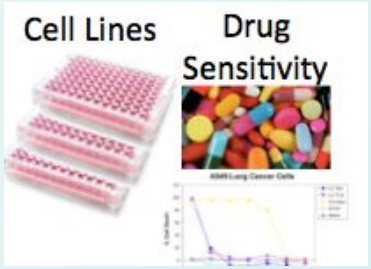
Pathways



High-Level Genomics Data

Cell Lines

Drug Sensitivity



DREAM CHALLENGES powered by Sage Bionetworks

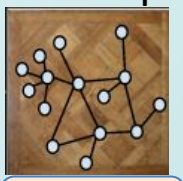
Outcomes / Phenotype Inferences

- Aggressive
- Gene Essentiality

Predictive Signature DB

- Subtypes
- Cells-Of-Origin
- Development (stemness)
- Drug Sensitivity
- Gene Essentiality

BME Graph

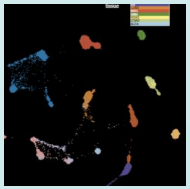


GA4GH

GA4GH API (G2P)

BMEG **Apps**

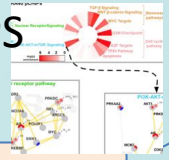
TumorMap



SamplePsychic

Observation Deck

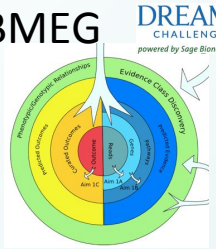
pCHIPS



GA4GH

Overview of **BMEG** Pipelines

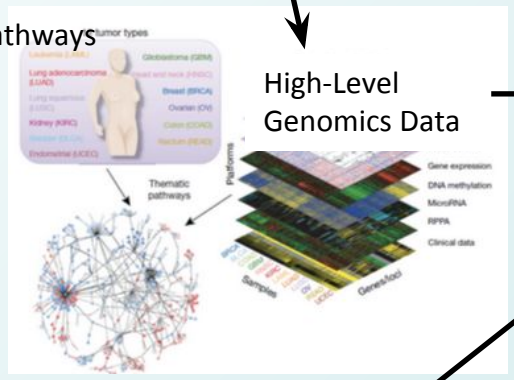
BMEG



Data Sources

Top Methods

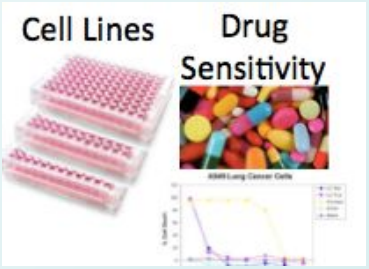
Pathways



High-Level Genomics Data

Cell Lines

Drug Sensitivity



Interfacing Projects

DREAM CHALLENGES powered by Sage Bionetworks

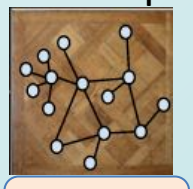
Outcomes / Phenotype Inferences

- Aggressive
- Gene Essentiality

Predictive Signature DB

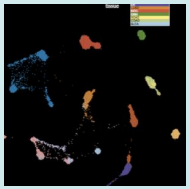
- Subtypes
- Cells-Of-Origin
- Development (stemness)
- Drug Sensitivity
- Gene Essentiality

BME Graph



GA4GH API (G2P)

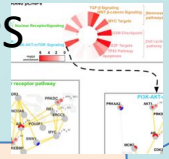
GA4GH-Compliant Apps TumorMap



SamplePsychic

Observation Deck

pCHIPS



GA4GH

GA4GH

TCGA

Treehouse (CKCC)

BeatAML (OHSU)

SU2C

ISPYII (UCSF)

Overview of **BMEG** Pipelines

BMEG

DREAM CHALLENGES powered by Sage Bionetworks

Data Sources

Top Methods

DREAM CHALLENGES powered by Sage Bionetworks

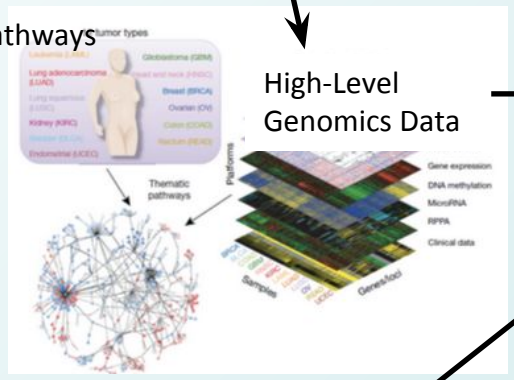
Outcomes / Phenotype Inferences

Aggressive

Gene Essentiality

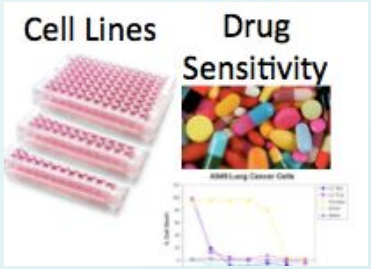
Pathways

High-Level Genomics Data



Cell Lines

Drug Sensitivity



Interfacing Projects

Predictive Signature DB

Subtypes

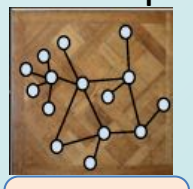
Cells-Of-Origin

Development (stemness)

Drug Sensitivity

Gene Essentiality

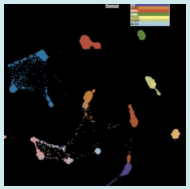
BME Graph



GA4GH API (G2P)

GA4GH-Compliant Apps

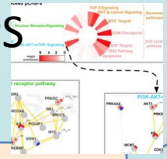
TumorMap



SamplePsychic

Observation Deck

pCHIPS



GA4GH

GA4GH

TCGA

Treehouse (CKCC)

BeatAML (OHSU)

SU2C

ISPYII (UCSF)

Overview of **BMEG** Pipelines

BMEG

DREAM CHALLENGES powered by Sage Bionetworks

Data Sources

Top Methods

Pathways

High-Level Genomics Data

Cell Lines

Drug Sensitivity

Interfacing Projects

DREAM CHALLENGES powered by Sage Bionetworks

Outcomes / Phenotype Inferences

Aggressive

Gene Essentiality

Predictive Signature DB

Subtypes

Cells-Of-Origin

Development (stemness)

Drug Sensitivity

Gene Essentiality

BME Graph

GA4GH API (G2P)

GA4GH-Compliant Apps

TumorMap

SamplePsychic

Observation Deck

pCHIPS

GA4GH

GA4GH

TCGA

Treehouse (CKCC)

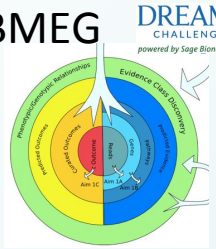
SU2C

ISPYII (UCSF)

BeatAML (OHSU)

Overview of **BMEG** Pipelines

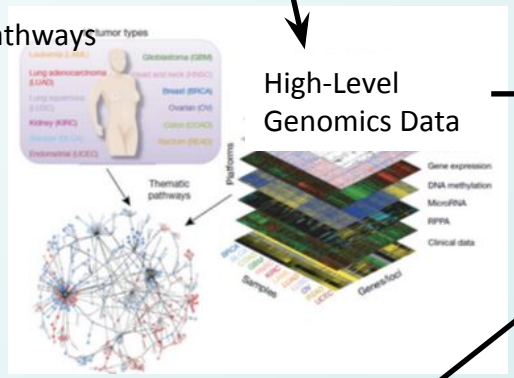
BMEG



Data Sources

Top Methods

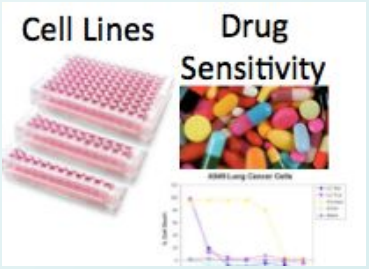
Pathways



High-Level Genomics Data

Cell Lines

Drug Sensitivity



Interfacing Projects

DREAM CHALLENGES powered by Sage Bionetworks

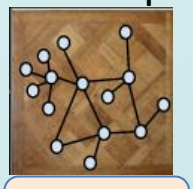
Outcomes / Phenotype Inferences

- Aggressive
- Gene Essentiality

Predictive Signature DB

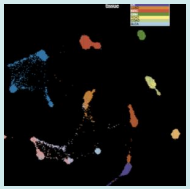
- Subtypes
- Cells-Of-Origin
- Development (stemness)
- Drug Sensitivity
- Gene Essentiality

BME Graph



GA4GH API (G2P)

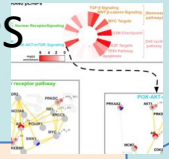
GA4GH-Compliant Apps TumorMap



SamplePsychic

Observation Deck

PCHIPS



GA4GH

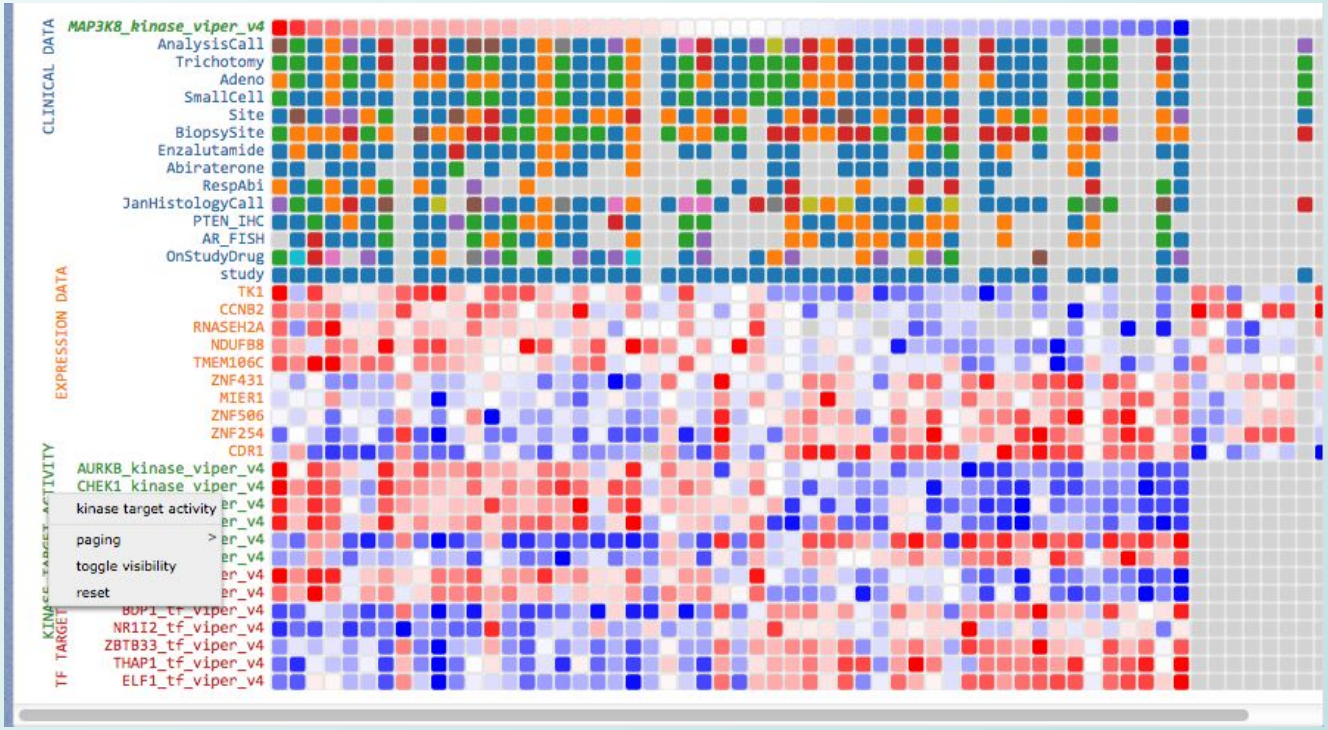
GA4GH

- TCGA
- Treehouse (CKCC)
- SU2C
- ISPYII (UCSF)
- BeatAML (OHSU)

Demo: DNA Damage Genes -> Gemcitibine Sensitivity

Link: [MOV File on Google]

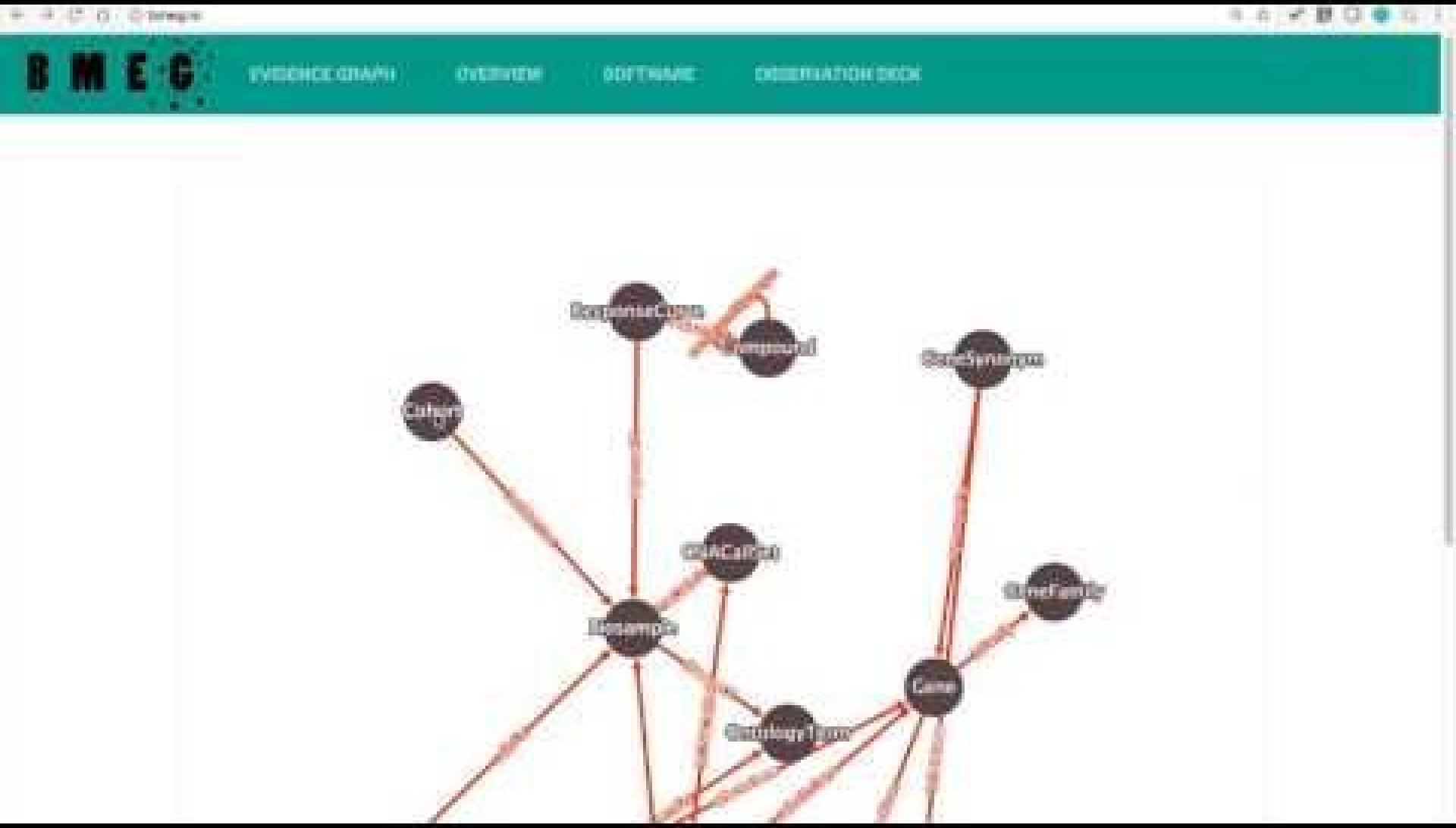
BMEG ObservationDeck



Demo: Query the TumorMap

Link: MOV File on Google

Demo: Query pCHIPS

Link: MOV File on Google

https://www.youtube.com/watch?v=WU3yd5zjnt8