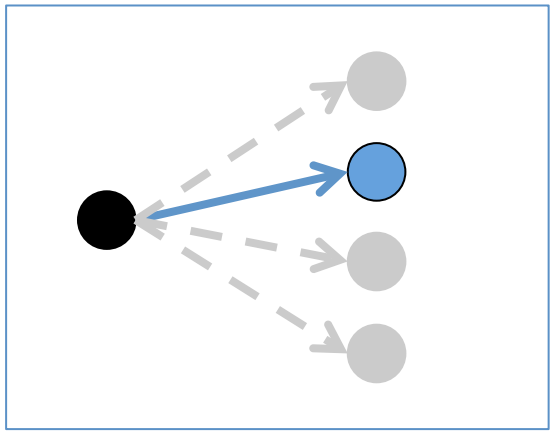
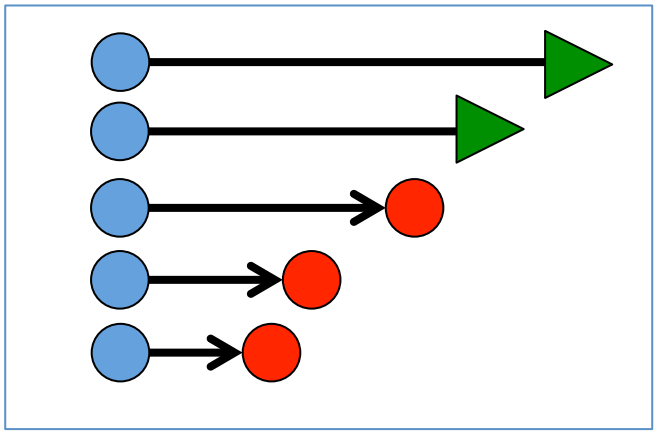
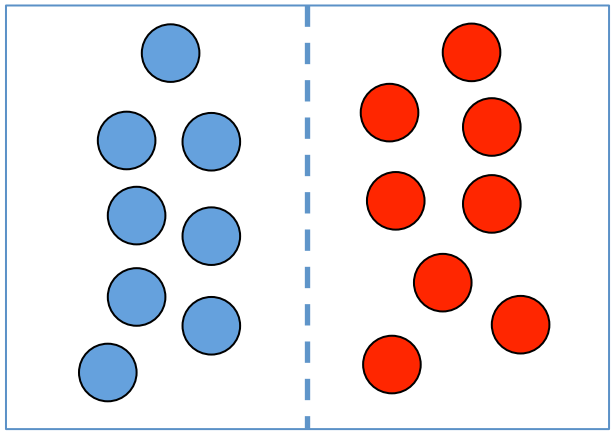
Clinical computational oncology for precision cancer medicine







Eliezer (Eli) Van Allen, MD
Assistant Professor
Harvard Medical School
Dana-Farber Cancer Institute
Broad Institute of MIT and Harvard

September 7, 2016

vanallenlab.dana-farber.org

@VanAllenLab

DANA-FARBER CANCER INSTITUTE

BROAD INSTITUTE

Disclosures

- Consulting/ Advisory
  - Third Rock Ventures
- Equity holder in Microsoft
  - Five shares for my bar-mitzvah in 1993
  - Thanks to the Gros family!

Disclosures

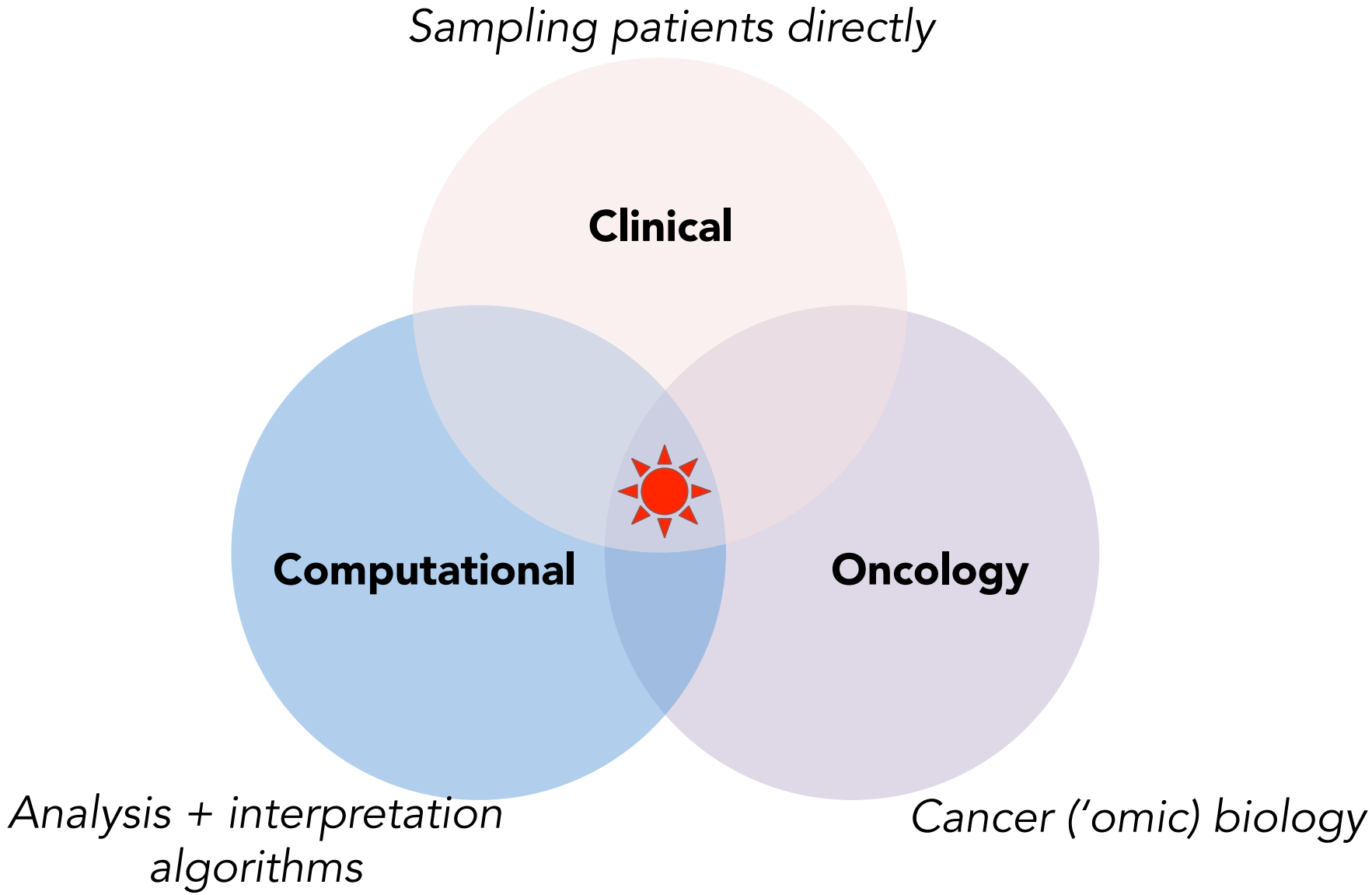
STANFORD UNIVERSITY
SYMBOLIC SYSTEMS PROGRAM

'03

Google™

Camp Kesem

For children of patients who have/ had cancer → …


Sampling patients directly
Clinical
Computational
Oncology
Analysis + interpretation algorithms
Cancer ('omic) biology

Precision medicine

The use of:

genomic technology

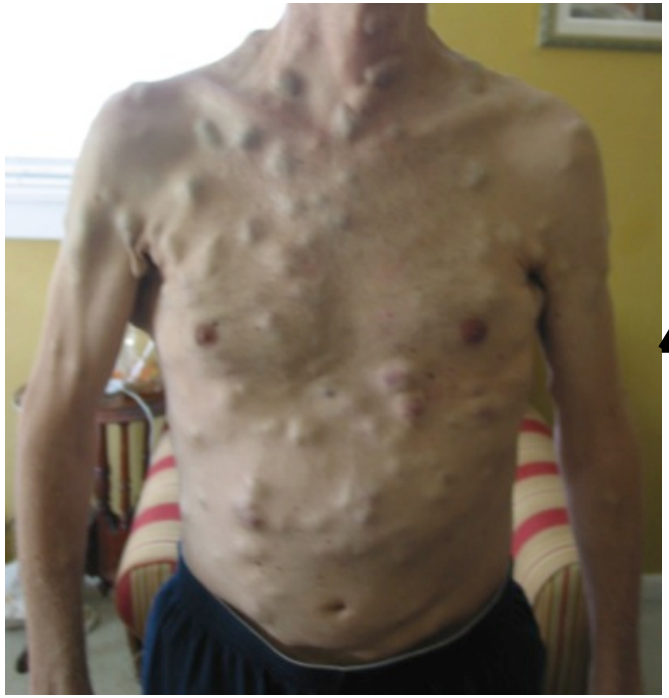
and

large-scale data

to guide:

1) individualized patient care
2) new discoveries

Precision cancer medicine: A paradigm shift

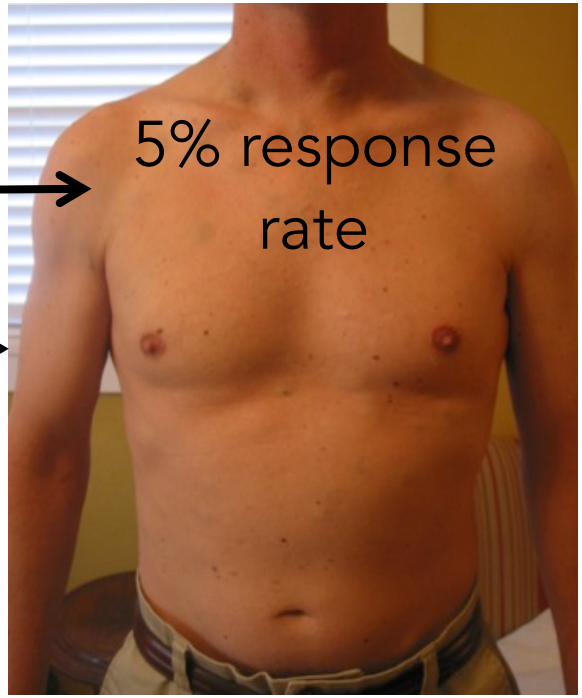


Past
Dacarbazine

5% response rate

Present

BRAF^{V600E}
Vemurafenib



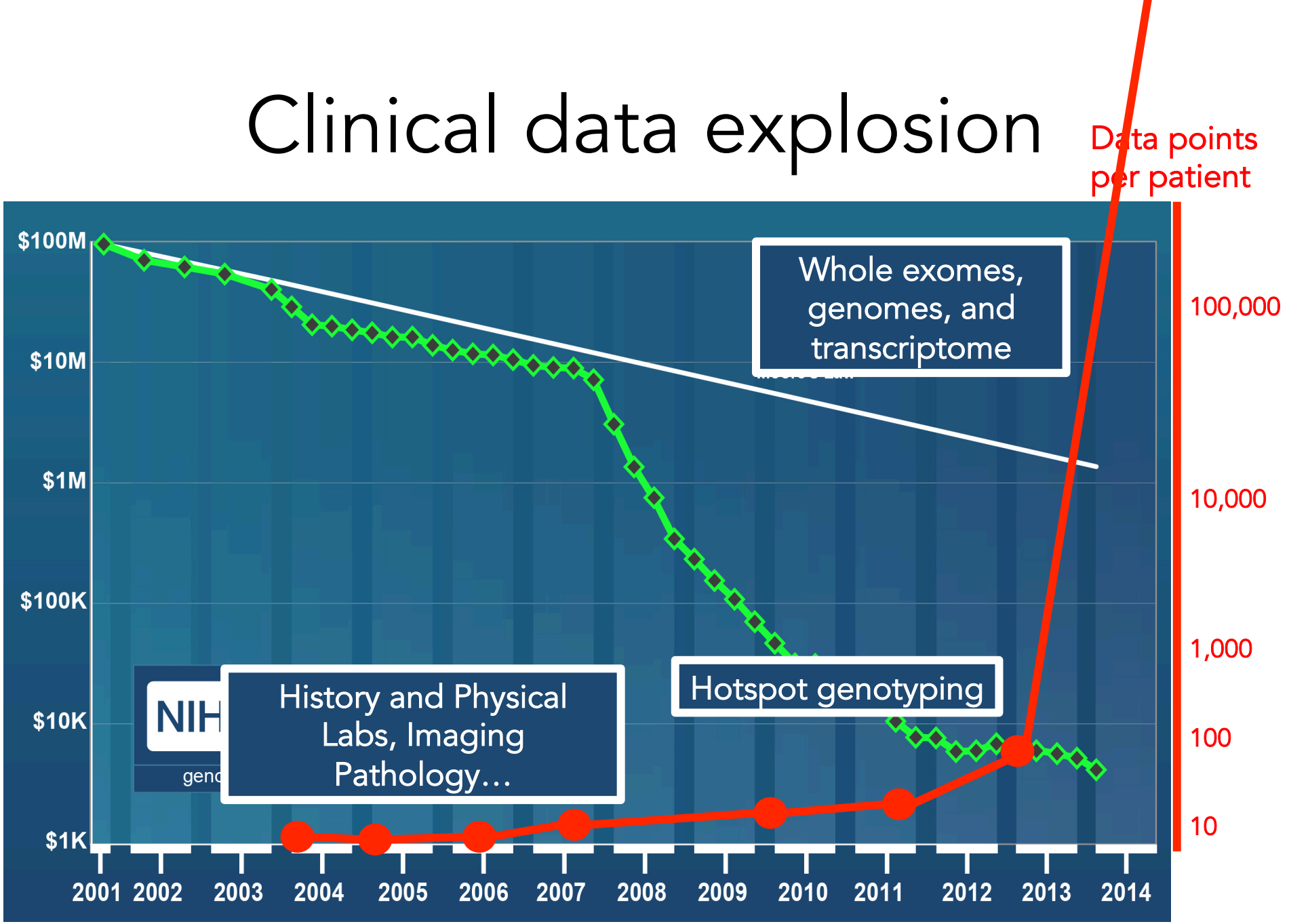
Wagle, Emery, et. al JCO 2011

Precision cancer medicine: A paradigm shift

EGFR	→	erlotinib
BCR-ABL	→	imatinib
ALK	→	crizotinib
HER2	→	trastuzumab
BRAF	→	vemurafenib
MEK1/2	→	trametinib
…		…

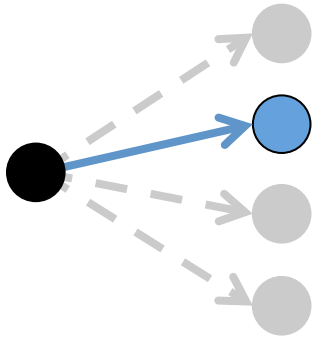
If one gene is good…

Clinical data explosion

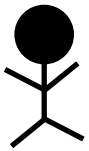


Source: NHGRI

Question #1



Can large-scale genomics guide individualized patient care in oncology?



= one patient

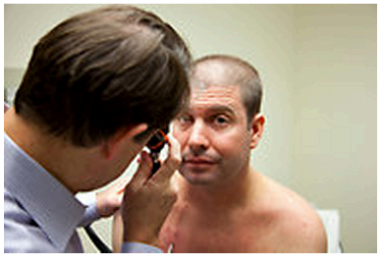
Clinical interpretation (ca. 2012)

In Treatment for Leukemia, Glimpses of the Future

Second Chance: Lukas Wartman, a leukemia doctor and researcher, developed the disease himself. As he faced death, his colleagues sequenced his cancer genome. The result was a totally unexpected treatment.

New York Times; July 7, 2012

Clinical interpretation (ca. 2012)



Dilip Vishwanat for The New York Times

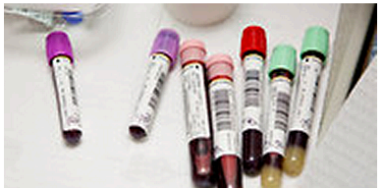
Dr. Lukas Wartman, a leukemia patient in remission, being examined by his doctor, John DiPersio, in January in St. Louis.

Enlarge This Image

Sid Hastings for The New York Times

"I was definitely scared. It was so unreal," said Dr. Wartman on first suspecting that he had leukemia, the very disease he had devoted his medical career to studying.

Enlarge This Image



NOW PLAYING

Why not throw everything we have at seeing if we can find a rogue gene spurring Dr. Wartman's cancer, adult acute lymphoblastic leukemia, he asked? "It's now or never," he recalled telling them. "We will only get one shot."

Dr. Ley's team tried a type of analysis that they had never done before. They fully sequenced the genes of both his cancer cells and healthy cells for comparison, and at the same time analyzed his RNA, a close chemical cousin to DNA, for clues to what his genes were doing.

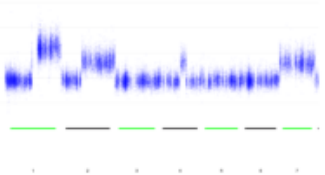
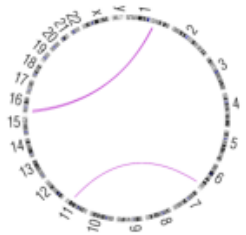
The researchers on the project put other work aside for weeks, running one of the university's 26 sequencing machines and supercomputer around the clock. And they found a culprit — a normal gene that was in overdrive, churning out huge amounts of a protein that appeared to be spurring the cancer's growth.

Even better, there was a promising new drug that might shut down the malfunctioning gene — a drug that had been tested and approved only for advanced kidney cancer. Dr. Wartman became the first person ever to take it for leukemia.

And now, against all odds, his cancer is in remission and has been since last fall.

New York Times; July 7, 2012

The deranged cancer genome

		Per patient
Mutations	…ACC… …TAG…	*10s– 1000s*
Insertion/ deletions	…TCG… …AACCC…	*1s– 1000s*
Copy number alterations		*10s– 1000s*
Rearrangements		*1s– 1000s*

Manual interpretation → not scalable

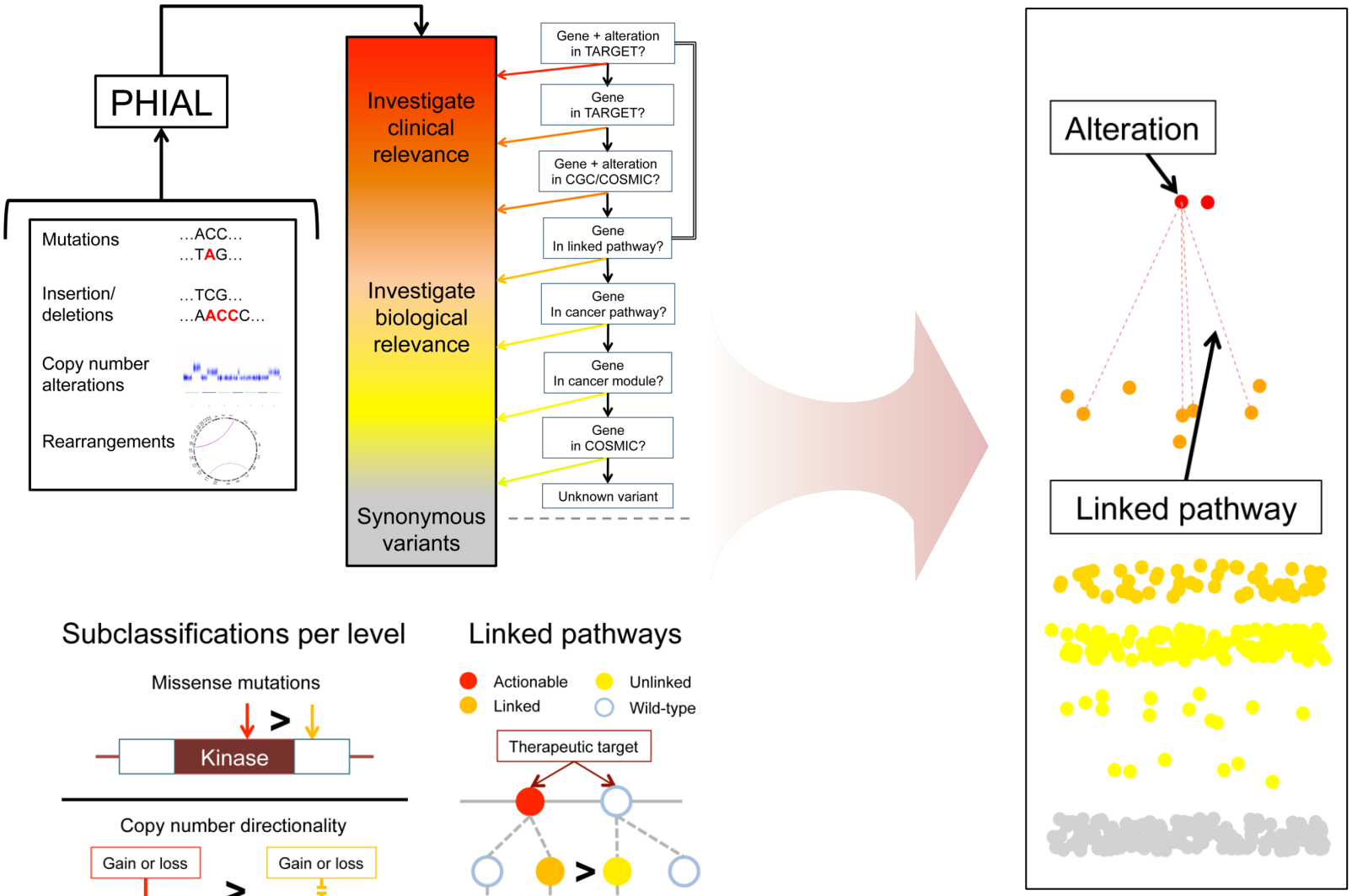
PHIAL

Precision Heuristics for Interpreting the Alteration Landscape

"May it be a light to you in dark places, when all other lights go out."[1]

[1]Galadriel, *in* Tolkien, *The Fellowship of the Ring*

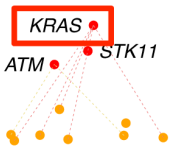
PHIAL



Van Allen, Wagle, et al. *Nature Medicine* 2014

Impact on clinical decision-making

a



Lung Adenocarcinoma

KRAS A146V

- Rare activating alteration
- Not detected with deployed profiling technologies

Cancer Cell

Article

A Synthetic Lethal Interaction between K-Ras Oncogenes and Cdk4 Unveils a Therapeutic Strategy for Non-small Cell Lung Carcinoma

Cell PRESS

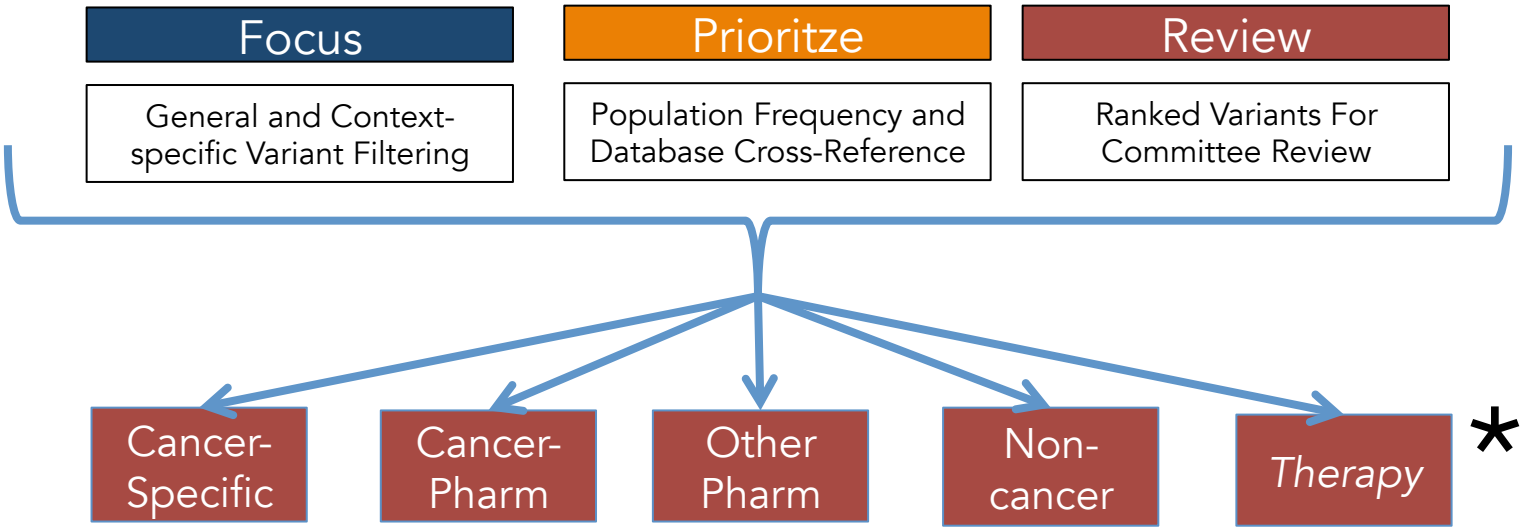
So 2014…

David Barbie
Leena Ghandi

Inherited genomics and interpretation

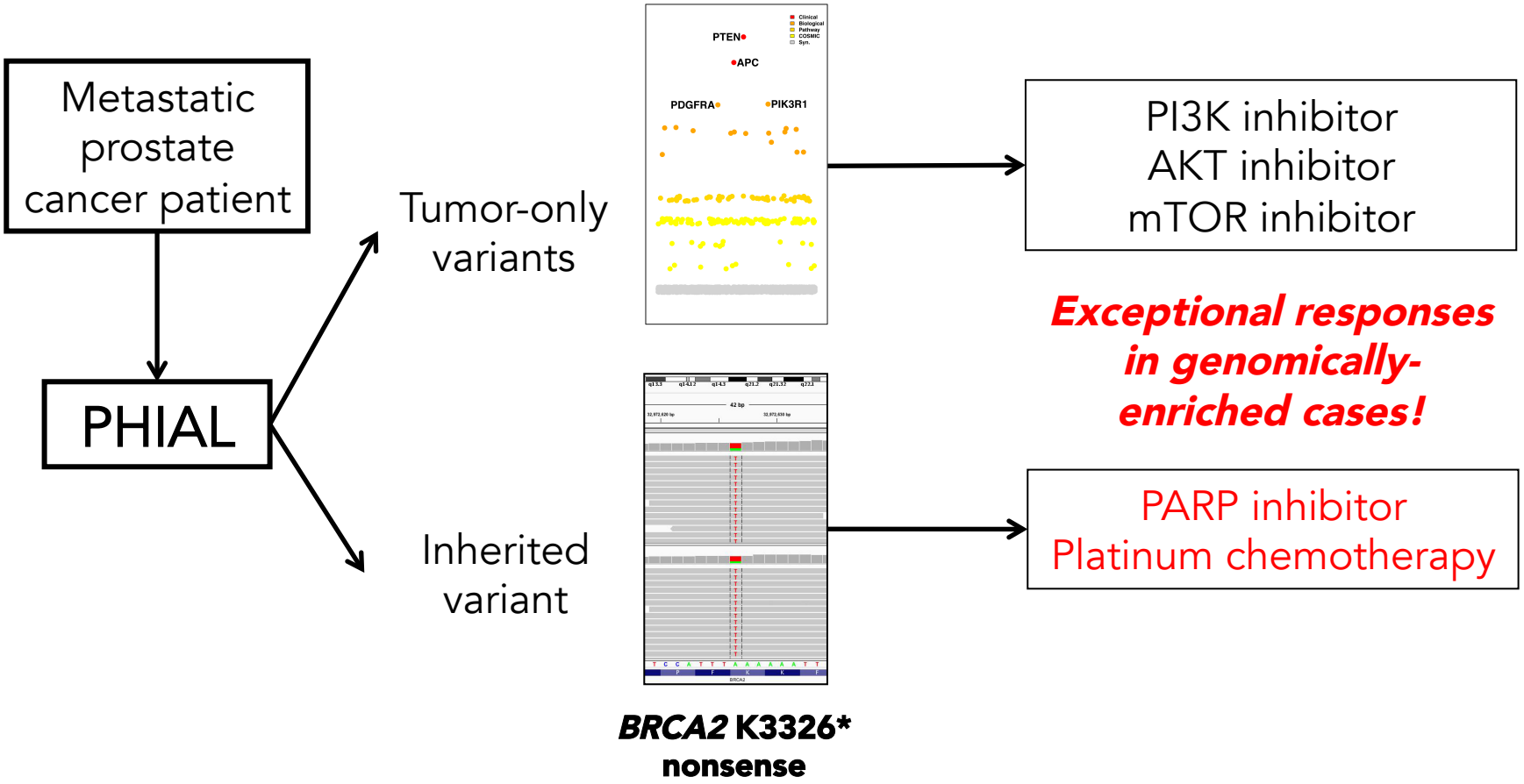
Tumor genome **-** Inherited genome **=** *Tumor-only mutations*

20,000-50,000 inherited variants per patient



Van Allen et al AACR 2013

Role for inherited genomics in treatment decision-making

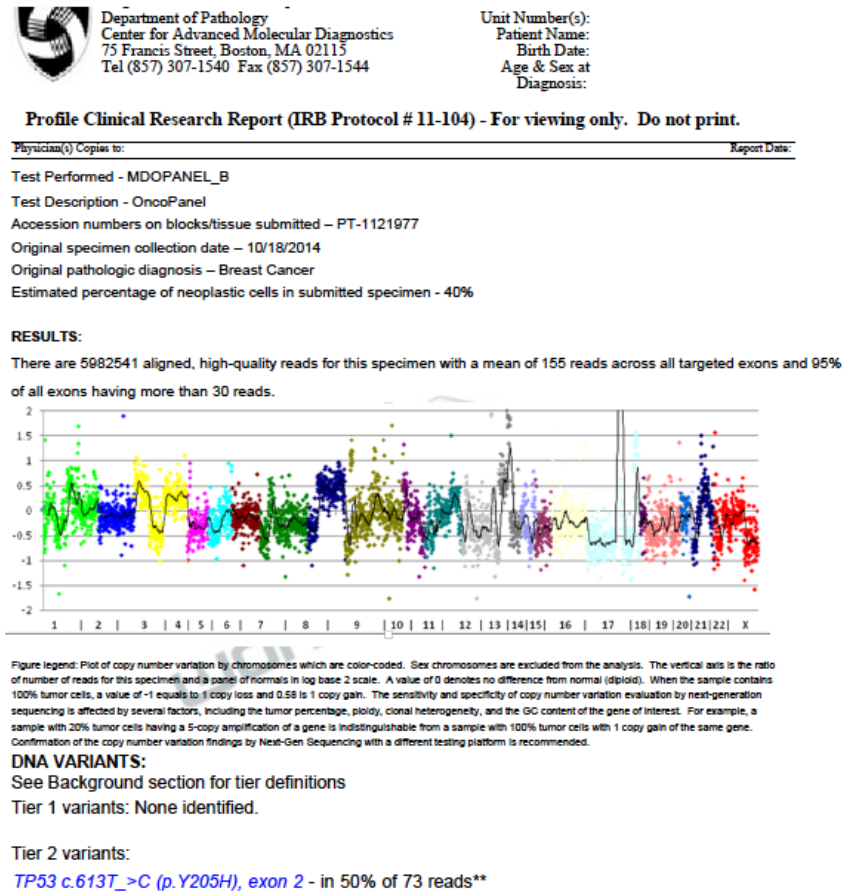


Van Allen, et al *Prostate Cancer Prostatic Dis.* 2014
Robinson, Van Allen, et al *Cell* 2015
Pritchard, et al *NEJM* 2016

Remember the consumer

Usability testing genomic reports

- "What do all those colors mean?"
- "Look at this actionable Tier 4 mutation!"
- "Which copy number events are important?"
- …



Department of Pathology
Center for Advanced Molecular Diagnostics
75 Francis Street, Boston, MA 02115
Tel (857) 307-1540 Fax (857) 307-1544

Unit Number(s):
Patient Name:
Birth Date:
Age & Sex at Diagnosis:

Profile Clinical Research Report (IRB Protocol # 11-104) - For viewing only. Do not print.

Physician(s) Copies to: Report Date:

Test Performed - MDOPANEL_B
Test Description - OncoPanel
Accession numbers on blocks/tissue submitted – PT-1121977
Original specimen collection date – 10/18/2014
Original pathologic diagnosis – Breast Cancer
Estimated percentage of neoplastic cells in submitted specimen - 40%

RESULTS:

There are 5982541 aligned, high-quality reads for this specimen with a mean of 155 reads across all targeted exons and 95% of all exons having more than 30 reads.

Figure legend: Plot of copy number variation by chromosomes which are color-coded. Sex chromosomes are excluded from the analysis. The vertical axis is the ratio of number of reads for this specimen and a panel of normals in log base 2 scale. A value of 0 denotes no difference from normal (diploid). When the sample contains 100% tumor cells, a value of -1 equals to 1 copy loss and 0.58 is 1 copy gain. The sensitivity and specificity of copy number variation evaluation by next-generation sequencing is affected by several factors, including the tumor percentage, ploidy, clonal heterogeneity, and the GC content of the gene of interest. For example, a sample with 20% tumor cells having a 5-copy amplification of a gene is indistinguishable from a sample with 100% tumor cells with 1 copy gain of the same gene. Confirmation of the copy number variation findings by Next-Gen Sequencing with a different testing platform is recommended.

DNA VARIANTS:

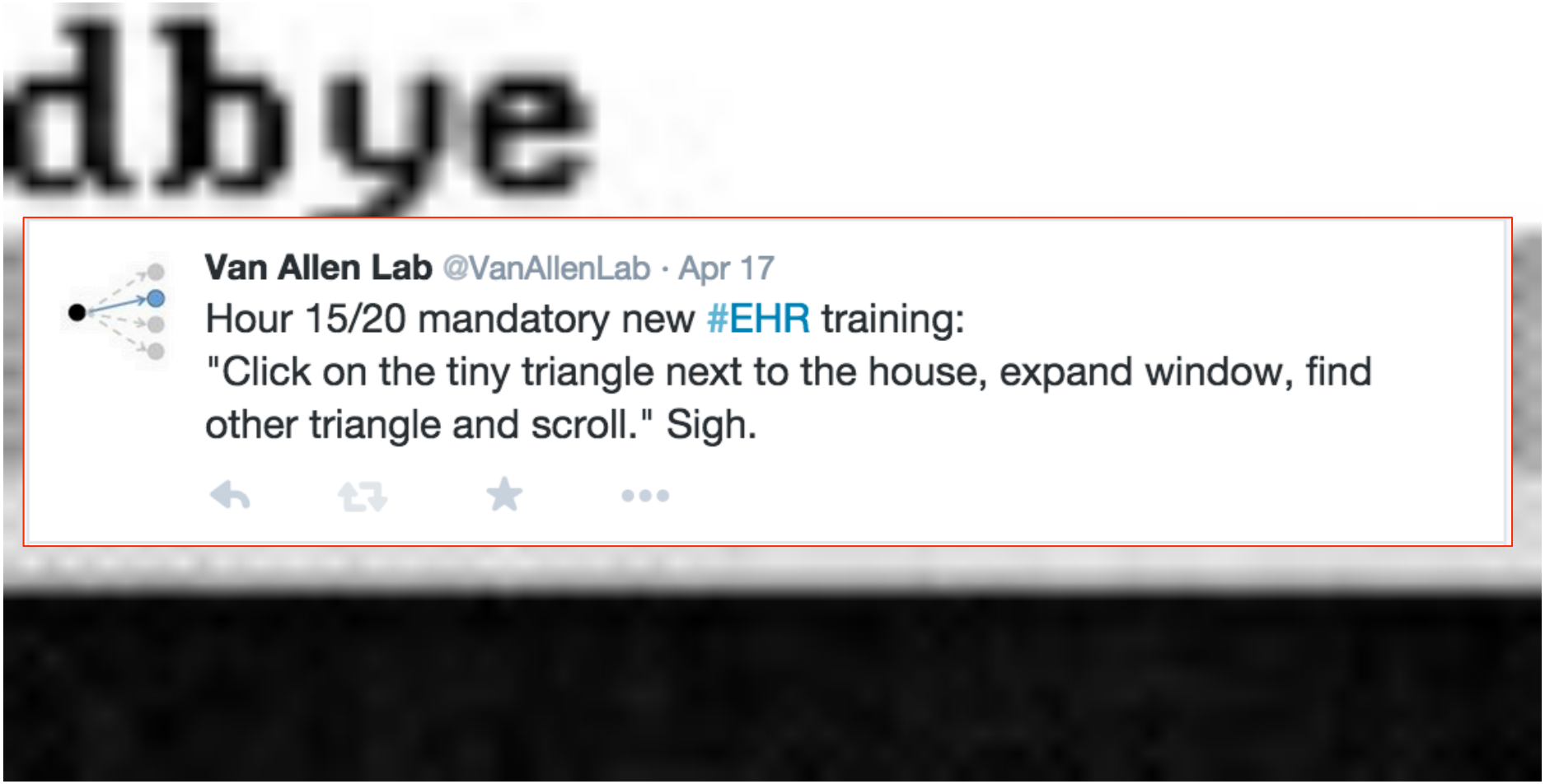
See Background section for tier definitions

Tier 1 variants: None identified.

Tier 2 variants:

TP53 c.613T_>C (p.Y205H), exon 2 - in 50% of 73 reads**

State of the art in clinical informatics



Standard or web-based/interactive reporting

Department of Pathology
Center for Advanced Molecular Diagnostics
75 Francis Street, Boston, MA 02115
Tel (857) 307-1540 Fax (857) 307-1544

Unit Number(s):
Patient Name:
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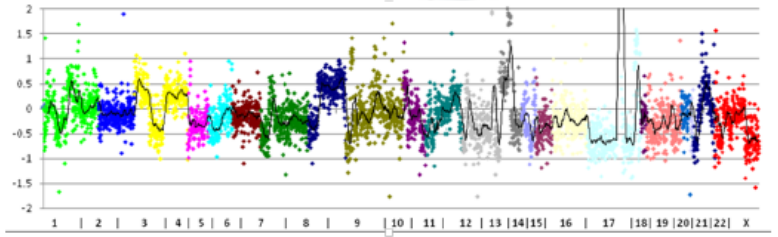

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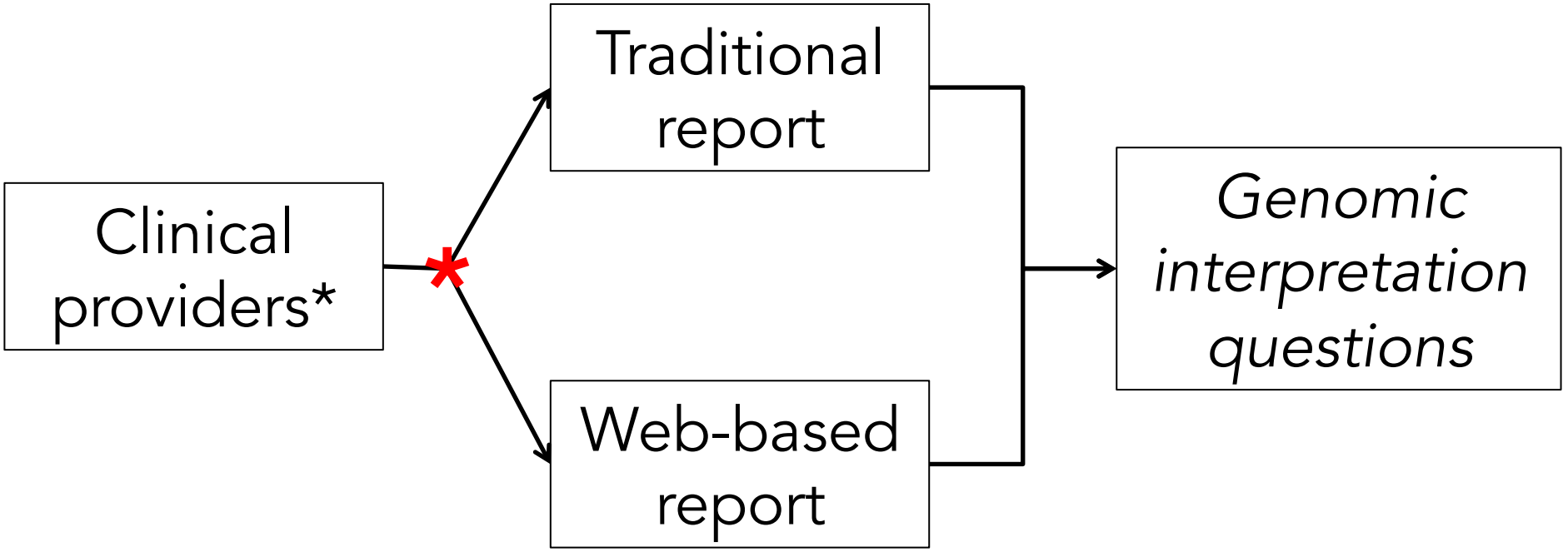
Or

Web-based report (revealed in survey)

Stacy Gray, Jordan Bryan

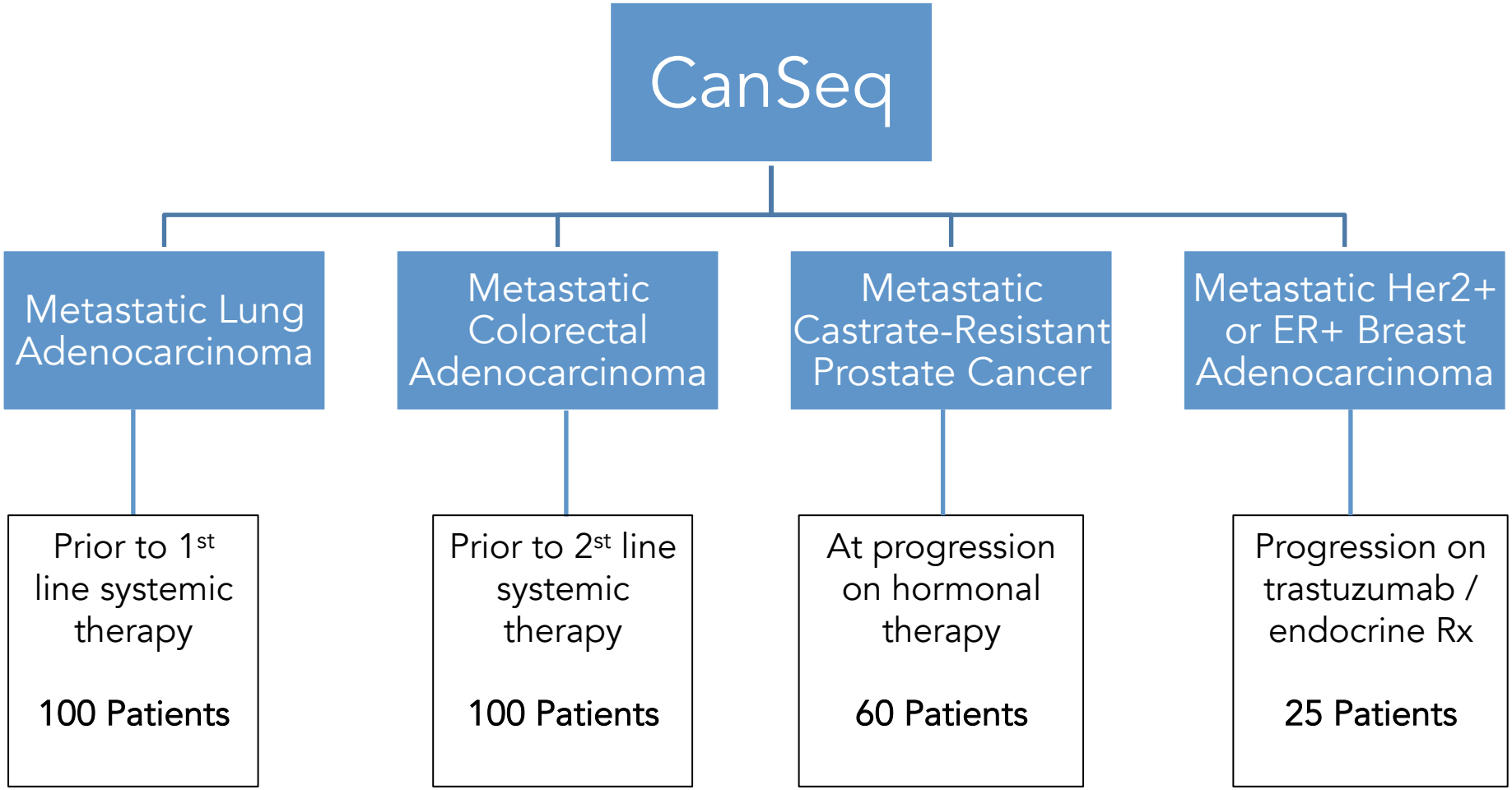
OncoSkins survey study



Protocol is live
~100 respondents thus far
Stay tuned…

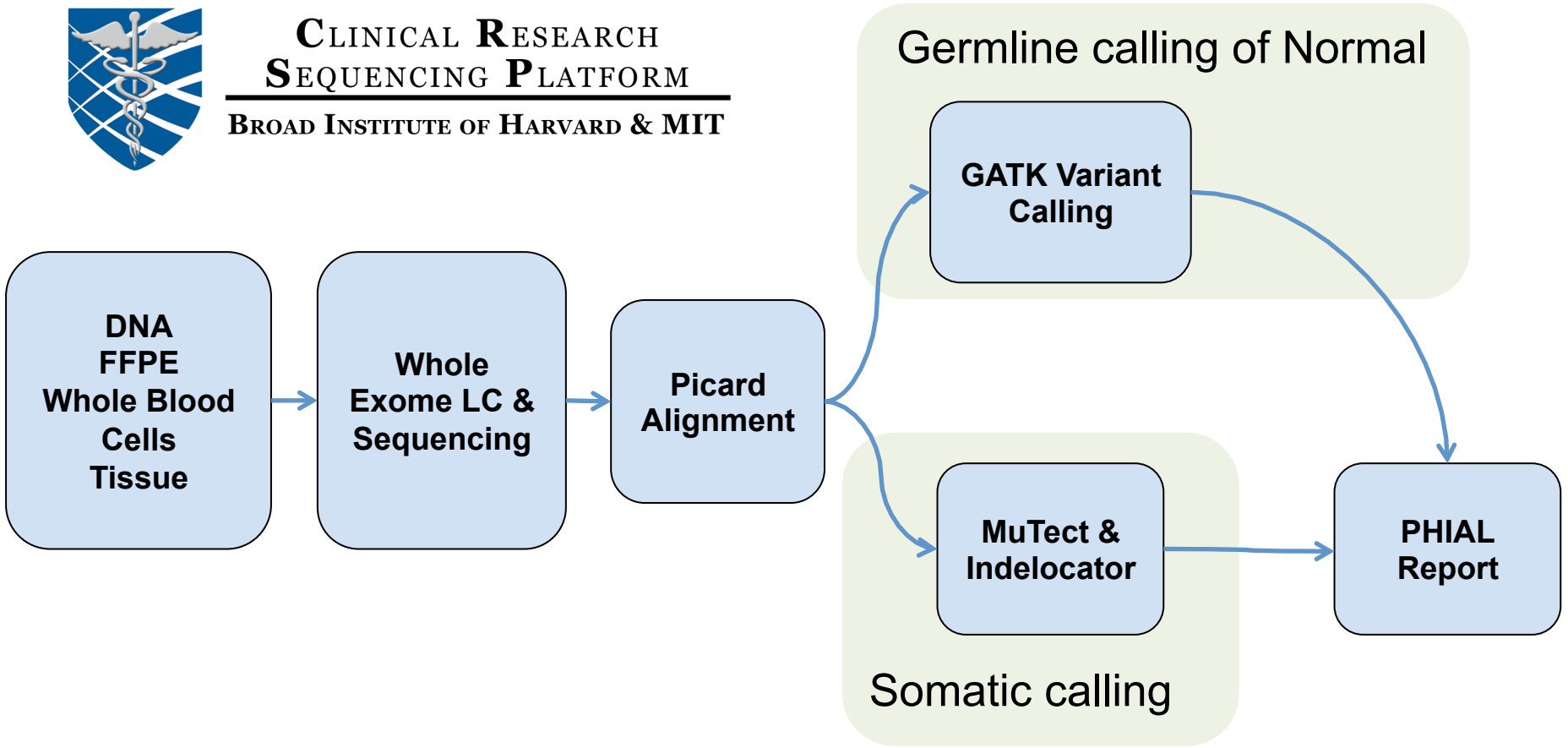
*Medical, radiation, surgical, and pediatric oncology

Expanding whole exome clinical sequencing

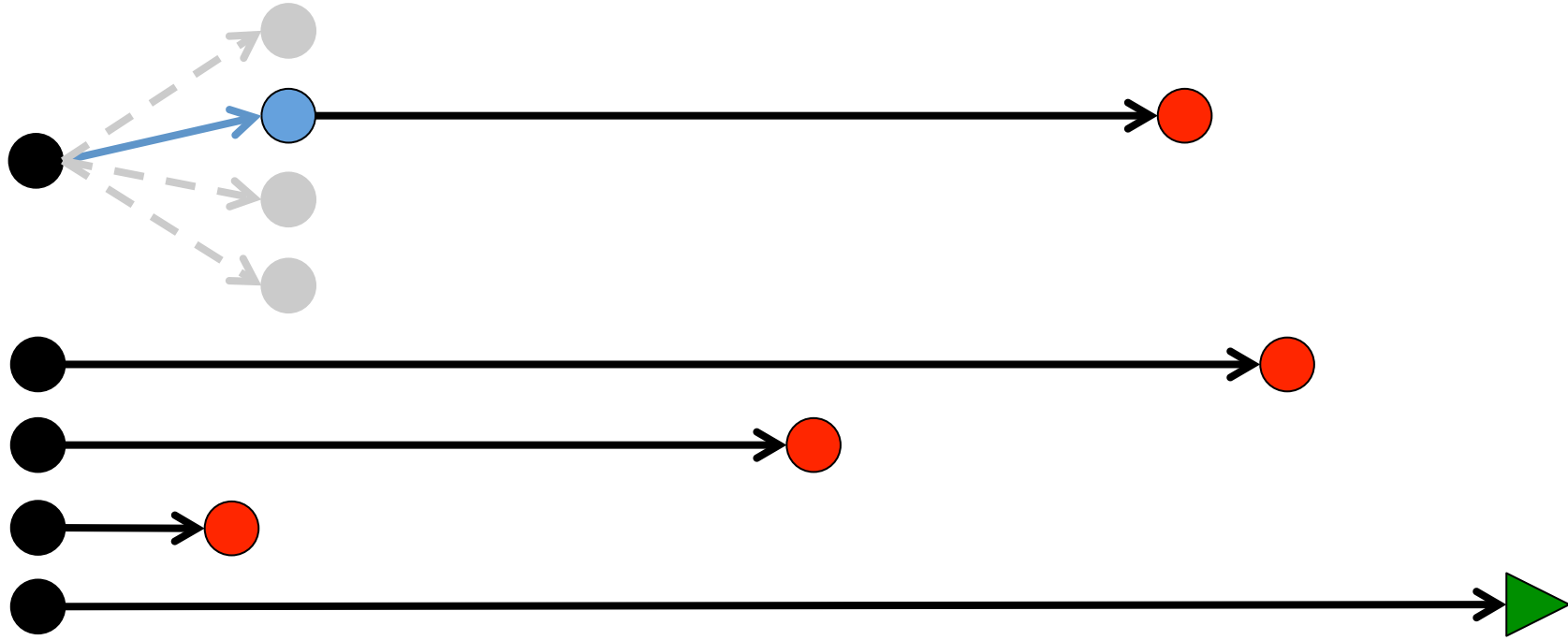


Levi Garraway, Nikhil Wagle, Stacy Gray, Judy Garber, Pasi Janne, Nelly Oliver, Philip Kantoff, Mary-Ellen Taplin, *many others*

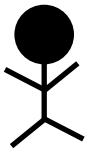
PHIAL in a CLIA lab!



Question #2

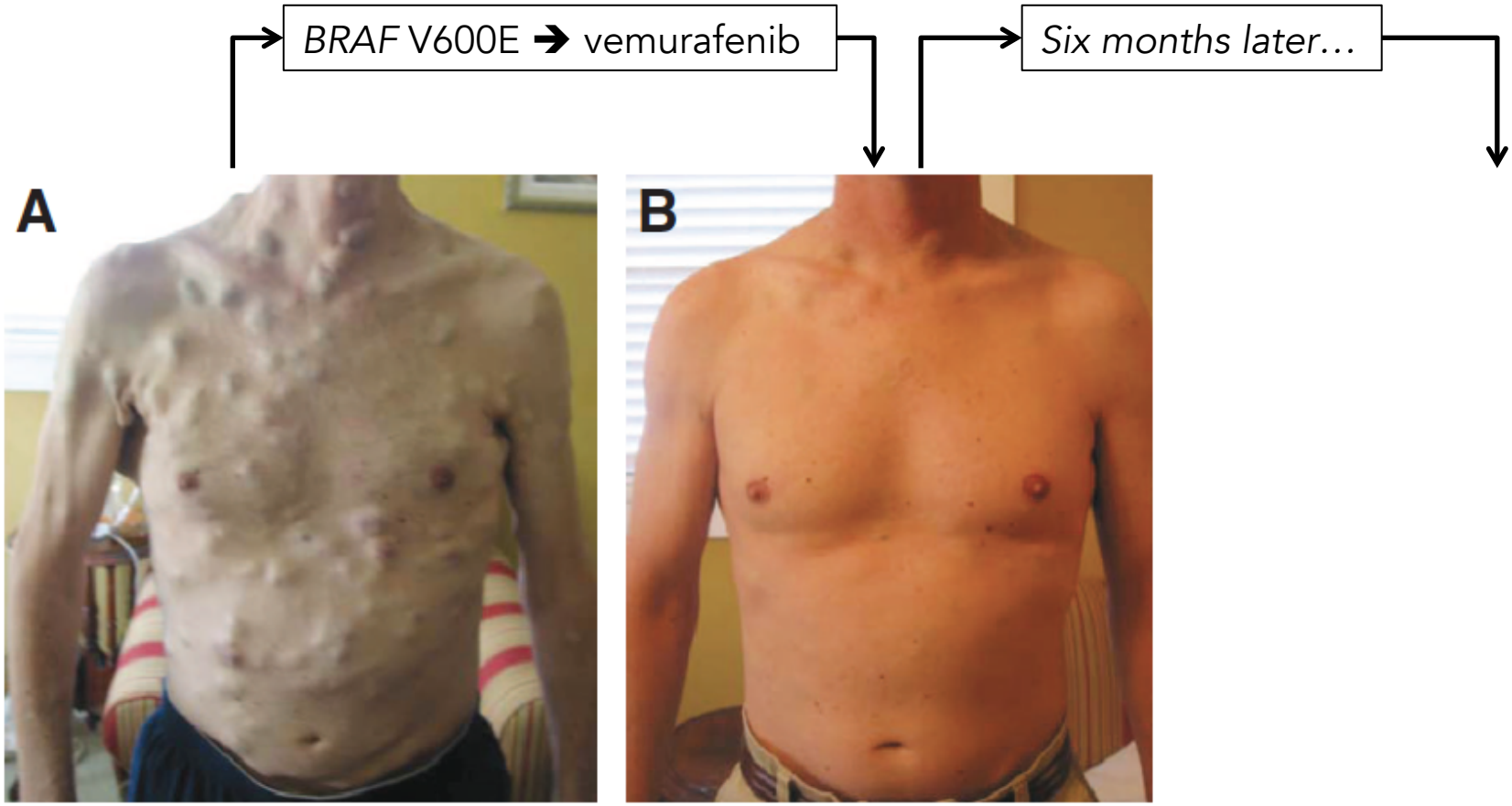


Can genomics explain clinical resistance to cancer therapies?



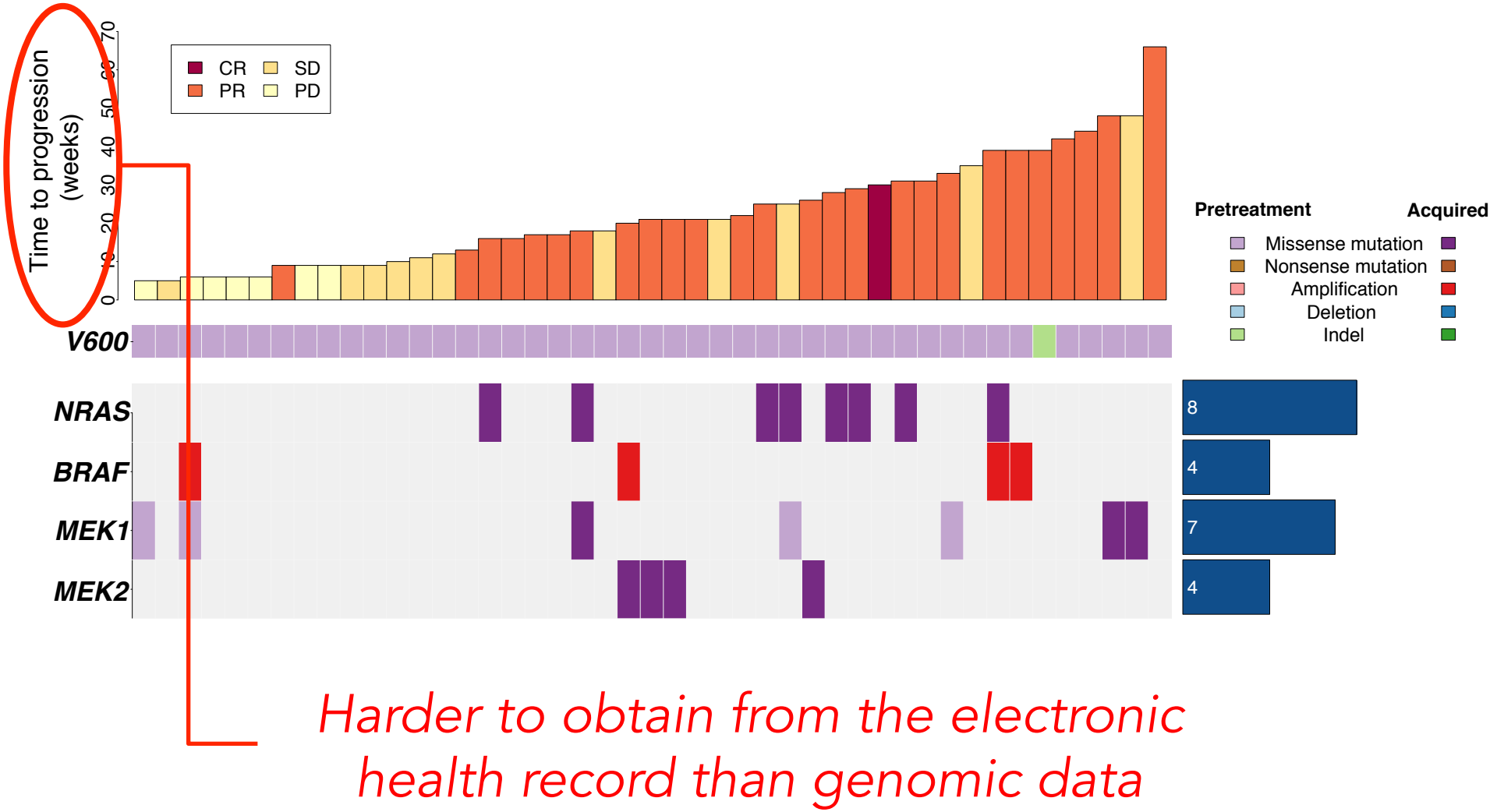
= one patient

Targeted therapies and resistance



Wagle et al *JCO* 2011

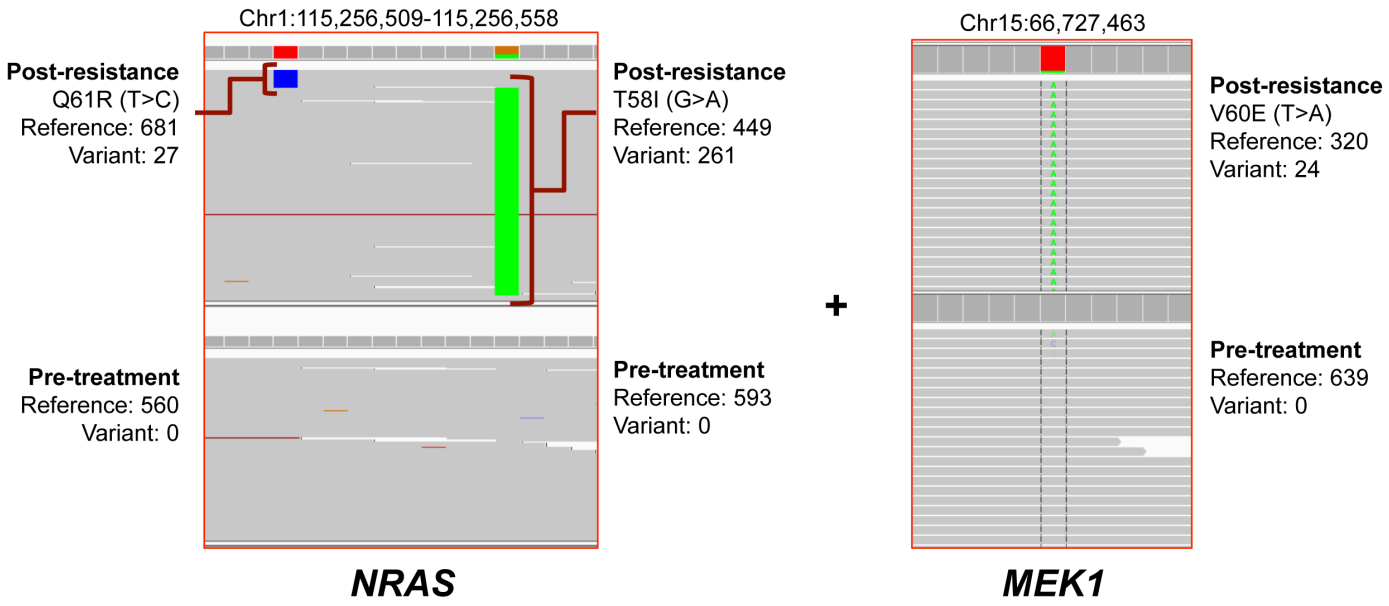
Linking clinical data to genomics



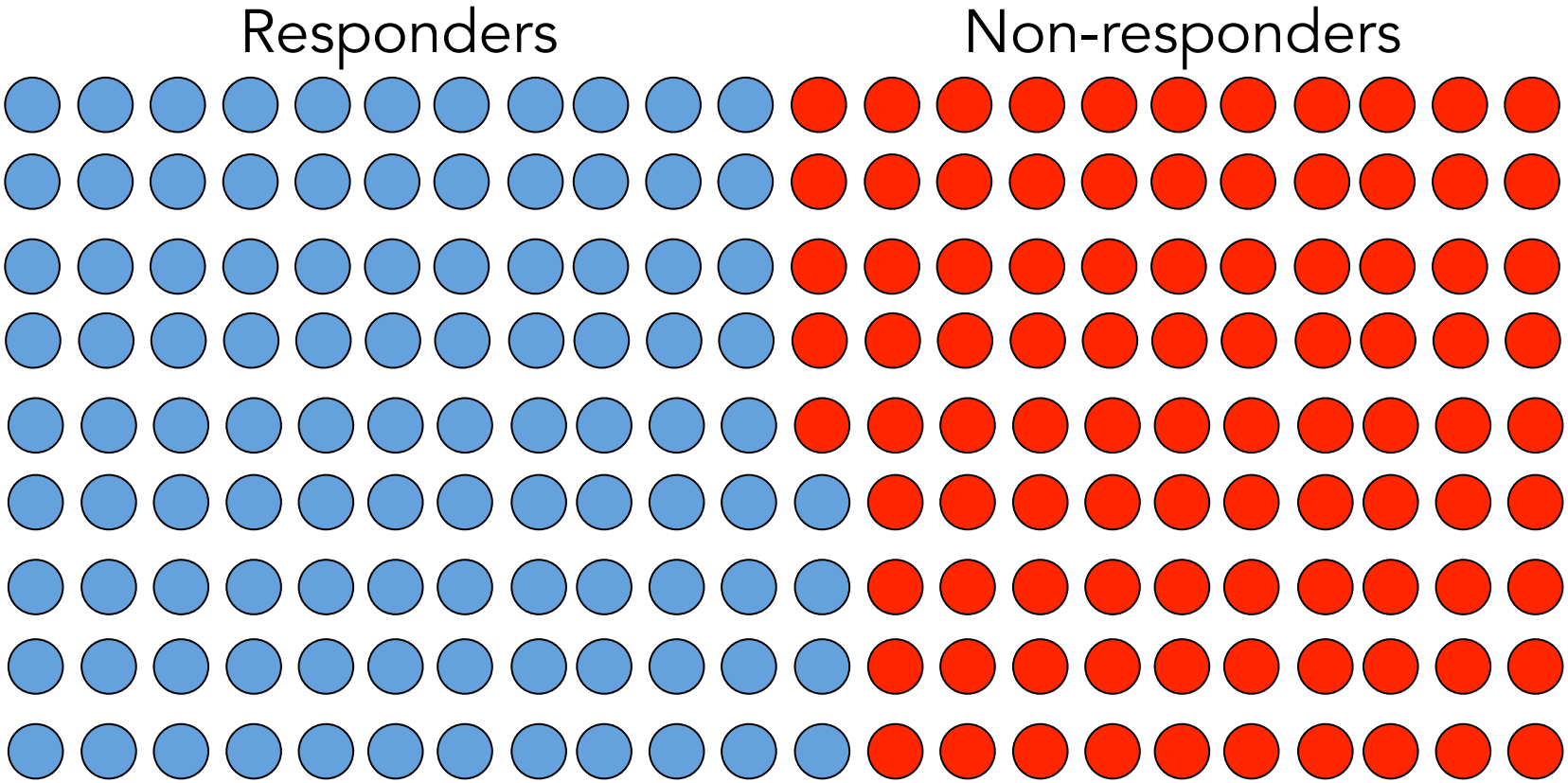
Harder to obtain from the electronic health record than genomic data

Resistance heterogeneity

A

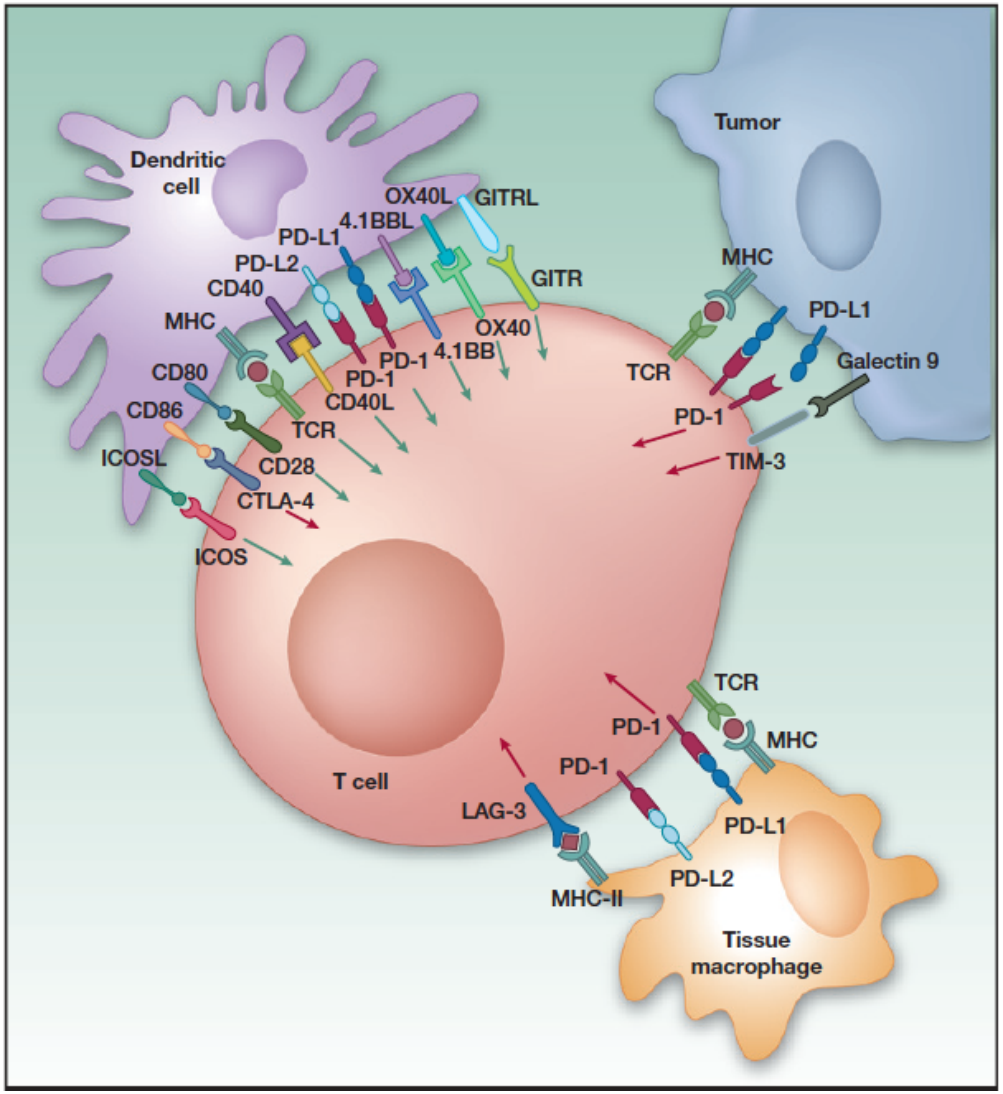


Question #3



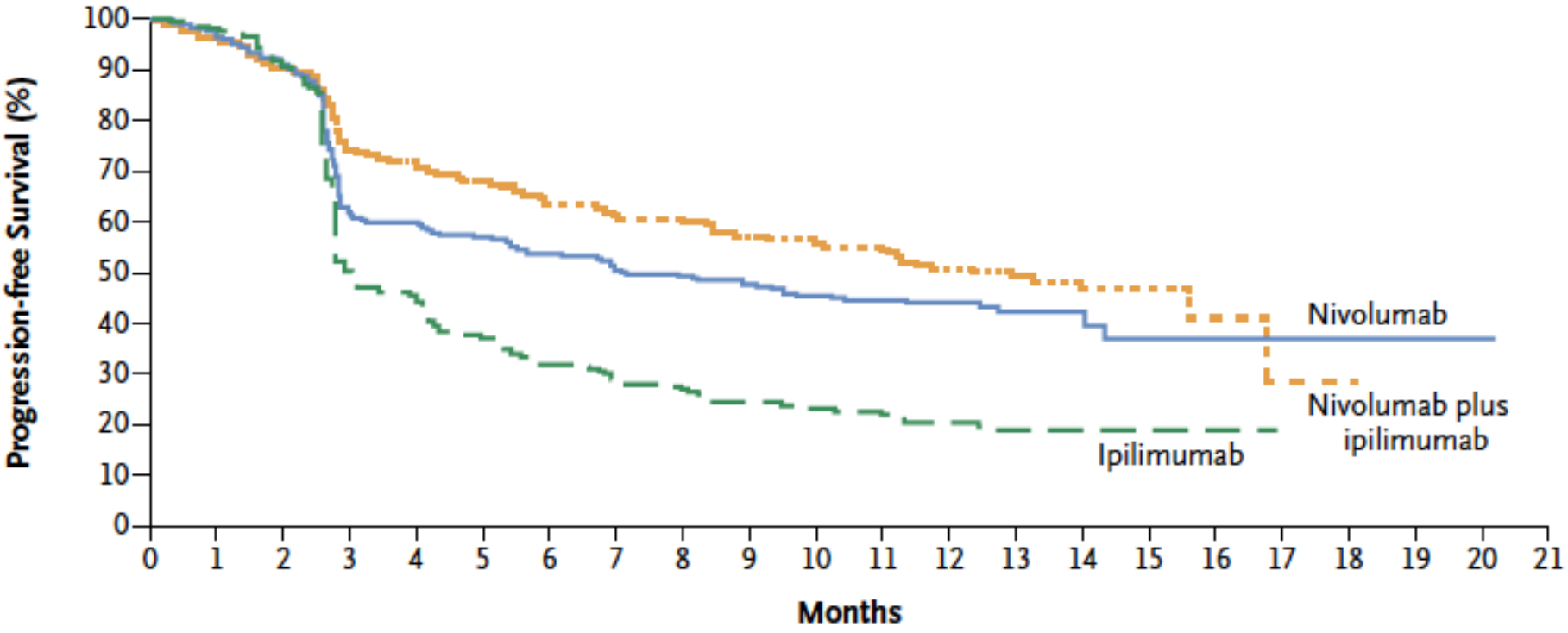
Can computational oncology enable discovery of genomic mechanisms of response to cancer therapies?

The rise of immunotherapies



Ott et al *Clin Cancer Res* 2013

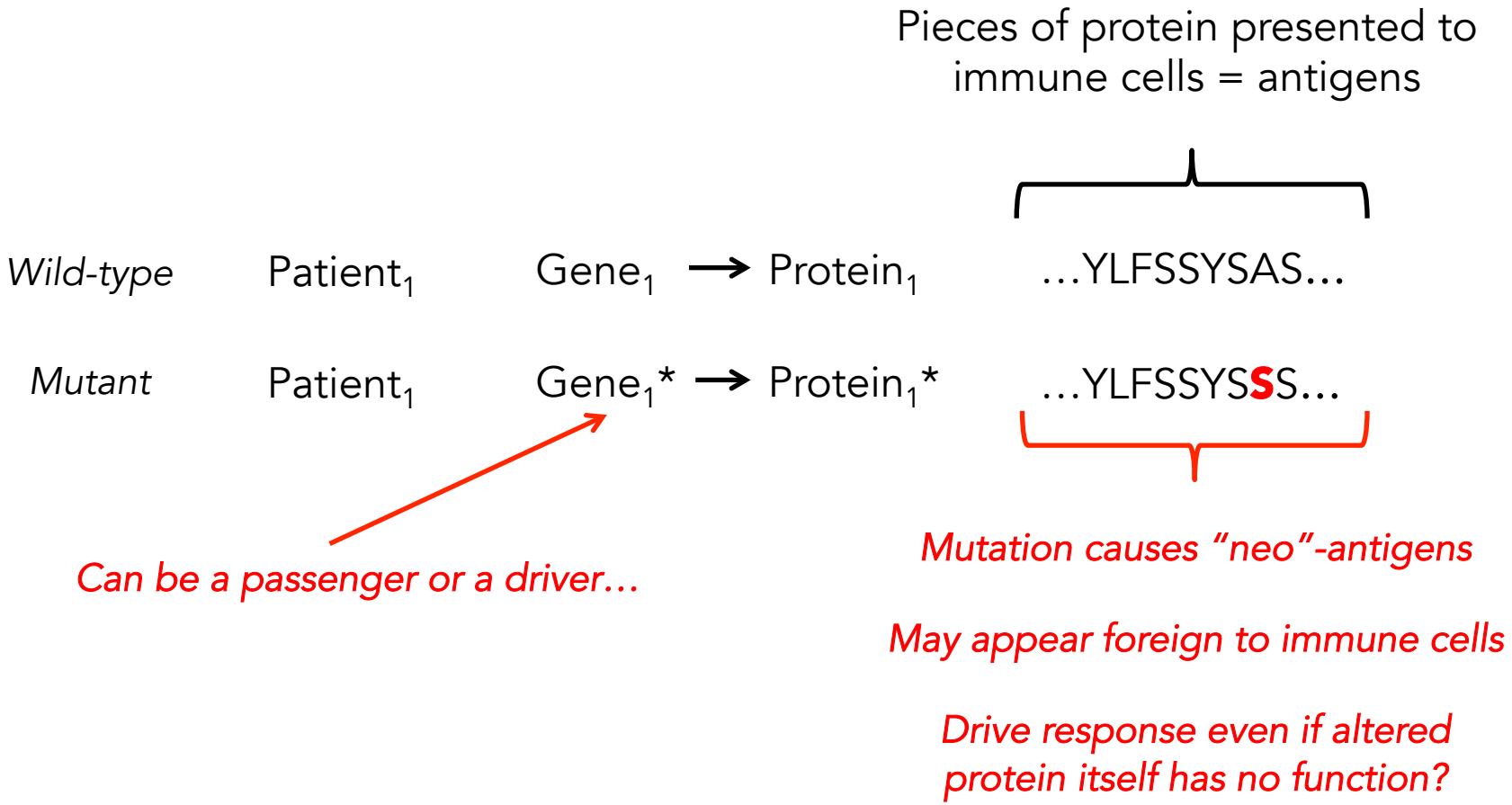
Combining immunotherapies



Do genomic features drive selective response?

Larkin et al *NEJM* 2015

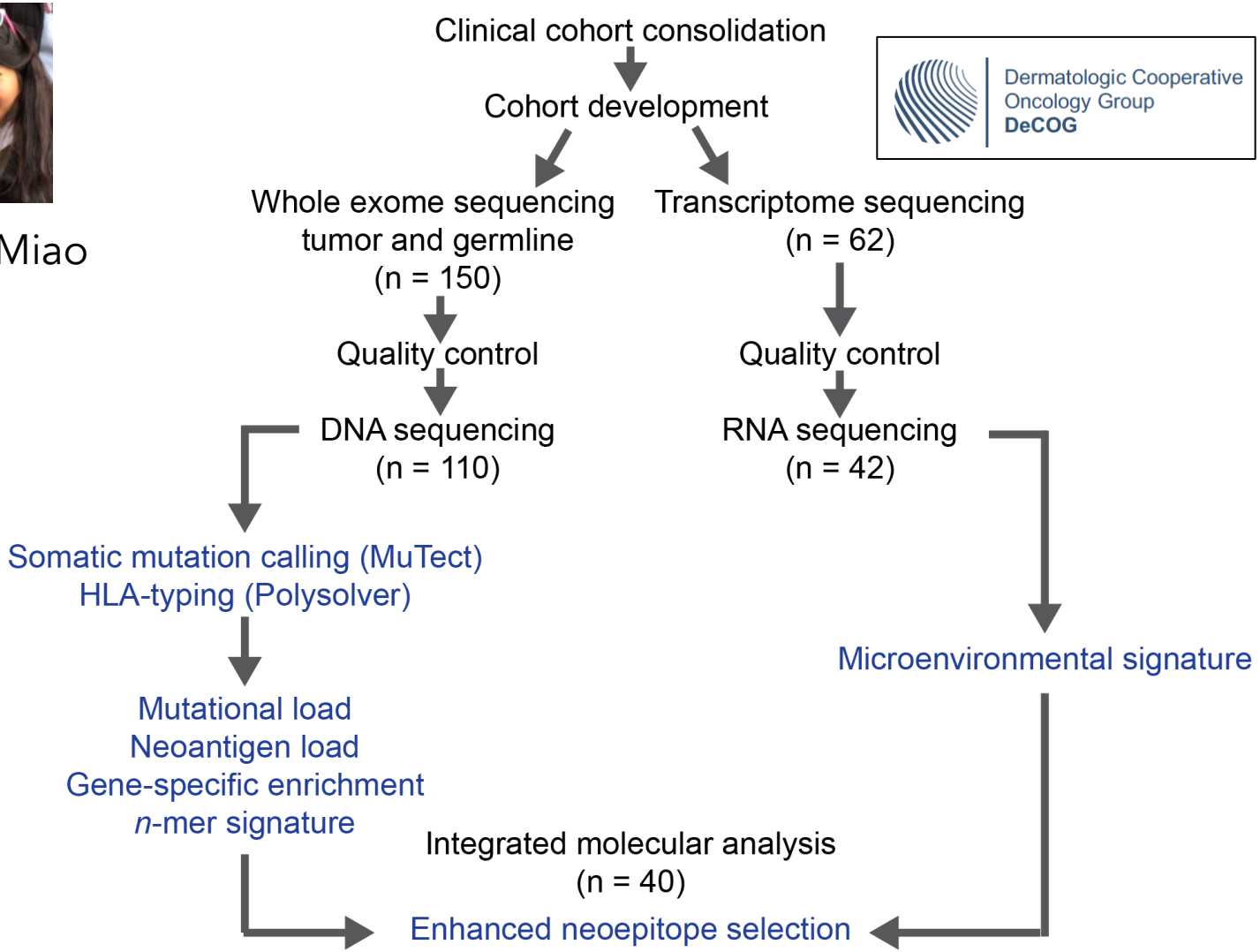
Mutations and "neo"-antigens



Sachet Shukla
Catherine Wu

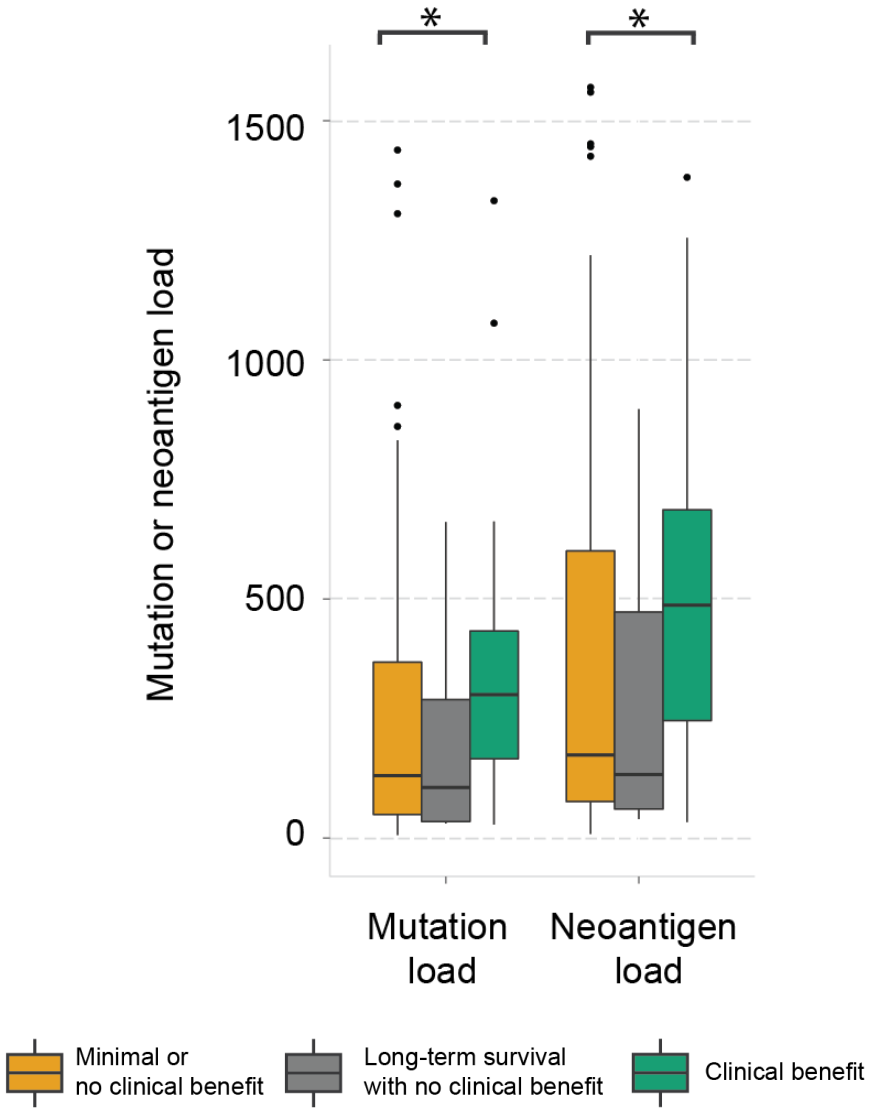
Searching for melanoma neoantigens

Diana Miao



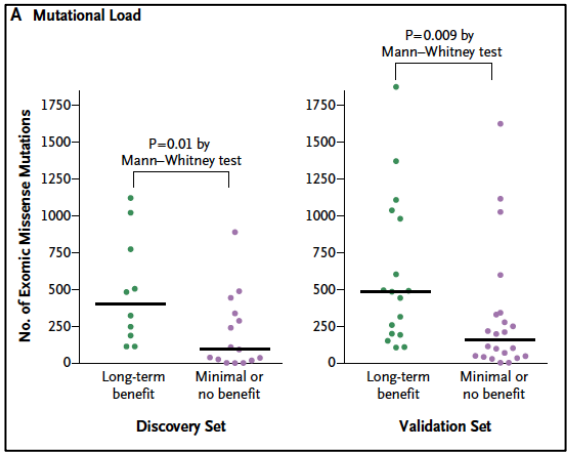
Van Allen, Miao, Schilling et al, *Science* 2015

Neoantigen load and clinical benefit

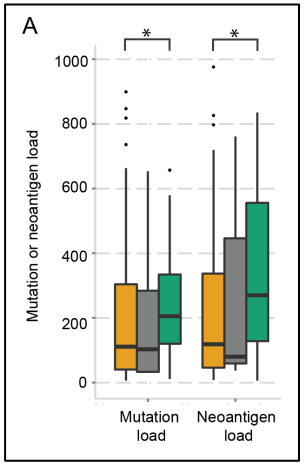


Genomic features and immunotherapy response

Mutational load



CTLA4 Ab
and melanoma



CTLA4 Ab
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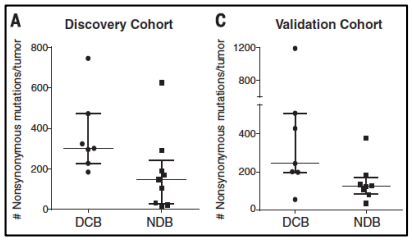
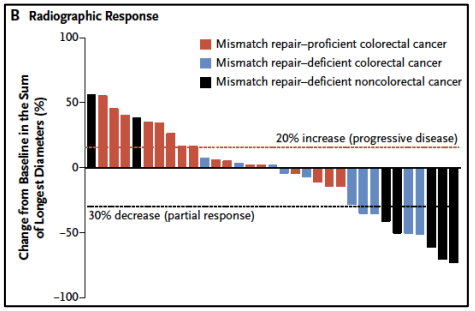


PD-1 Ab
and NSCLC

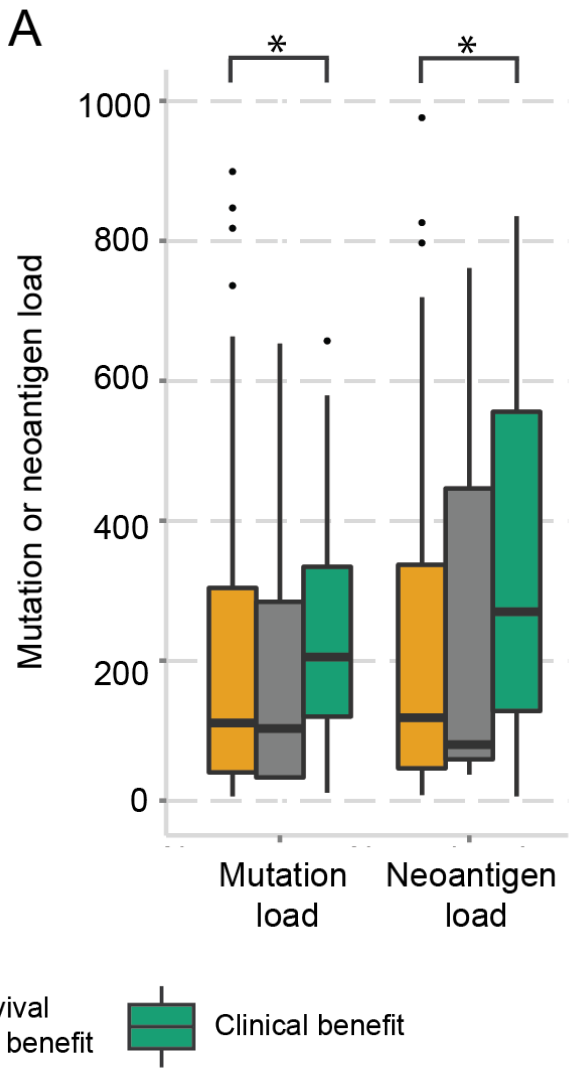


PD-1 Ab and
MSI-high tumors

Snyder et al *NEJM* 2014
Rizvi et al *Science* 2015
Van Allen et al *Science* 2015
Le et al *NEJM* 2015

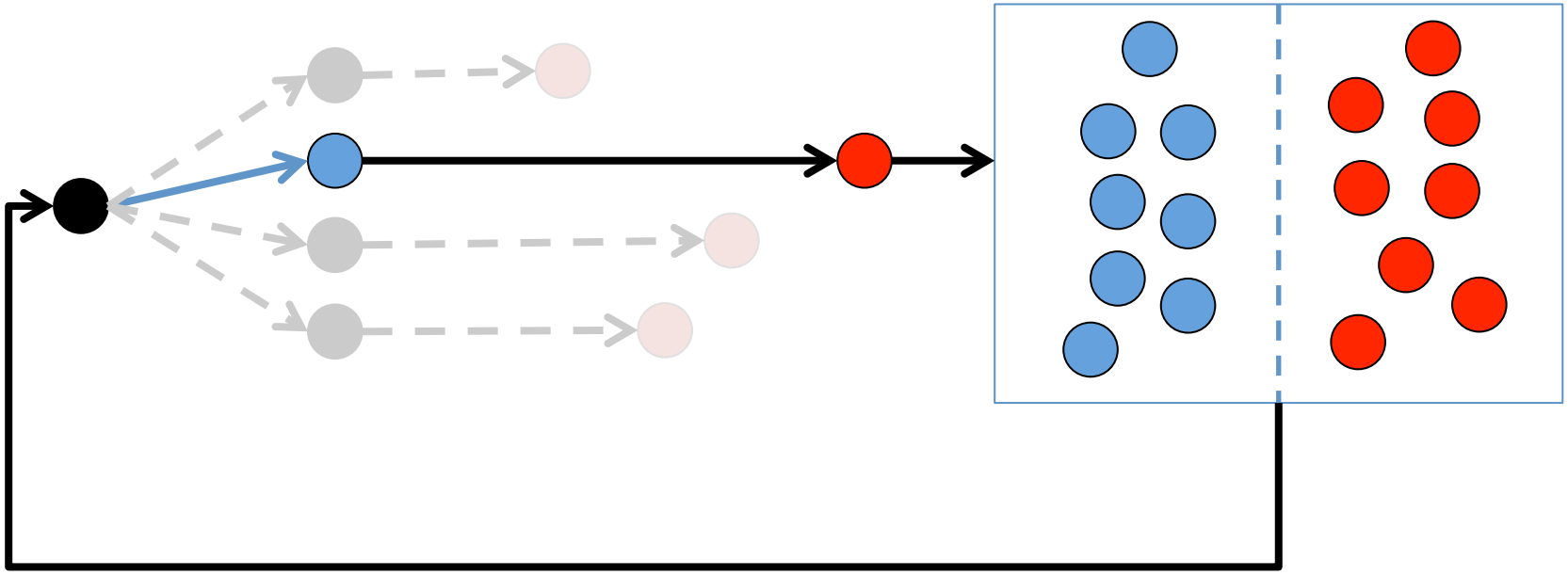
Mutational and neoantigen load

- Mutation/neoantigen load ~ clinical benefit

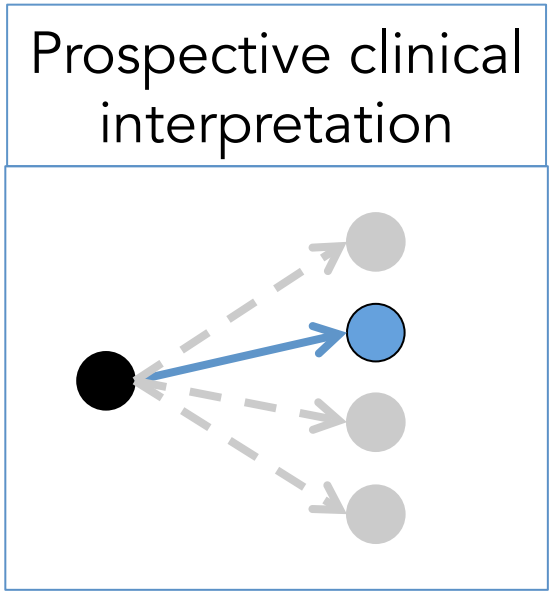


Van Allen, Miao, Schilling et al Science 2015

Clinical computational oncology

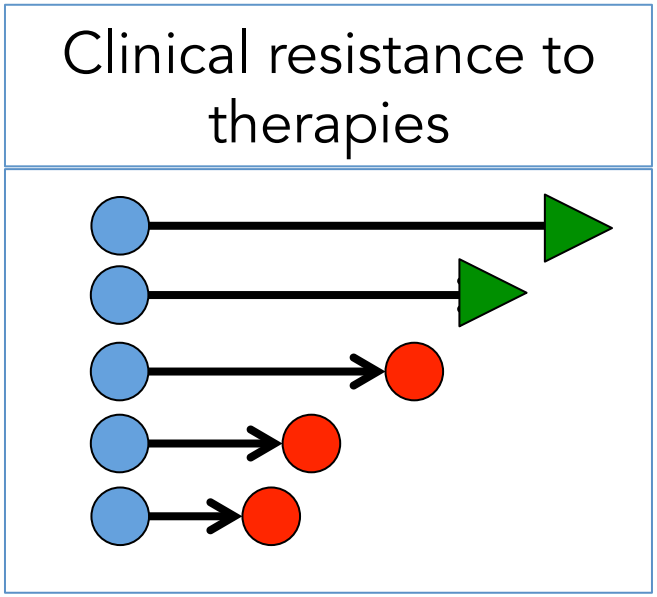


Question #1 (Interpretation): Next Steps



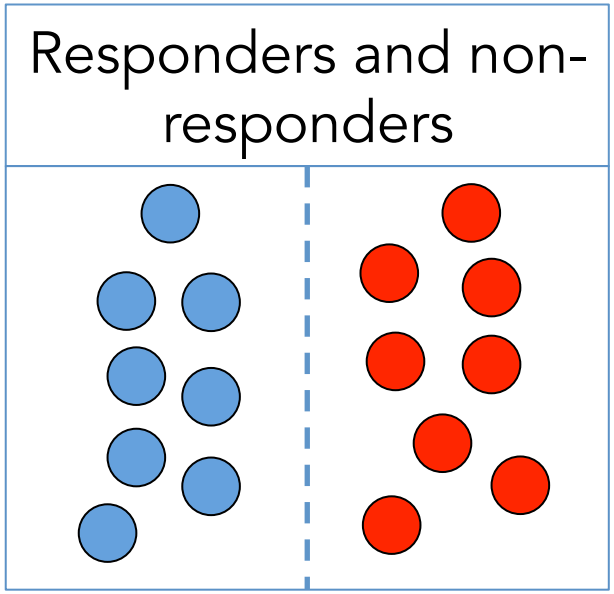
- Improve integrative analyses
- Expanding tumor types
- Expanding clinical scenarios
- …

Question #2 (Resistance): Next steps

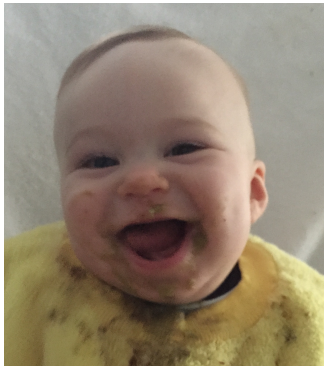


- More biopsies
- More cohorts
- More therapies
- More!

Question #3 (Response): Next steps



- Studying response to all therapy types (targeted, chemo, immuno)
- Integration into trials
- Algorithm enhancement



Let's work together!

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The Patients

Funding

BroadIgnite