



Microsoft Research

Faculty
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2014 15TH ANNUAL



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Dana-Farber Cancer Institute
Harvard Medical School
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Precision cancer medicine
in the era of genomics



Disclosures

~~None~~

Equity holder in Microsoft

Five shares for my bar-mitzvah in 1993

Thanks to the Gros family!



Definitions

Clinical computational biology:
the development and application of computational algorithms to analyze and interpret 'omic data from patient samples

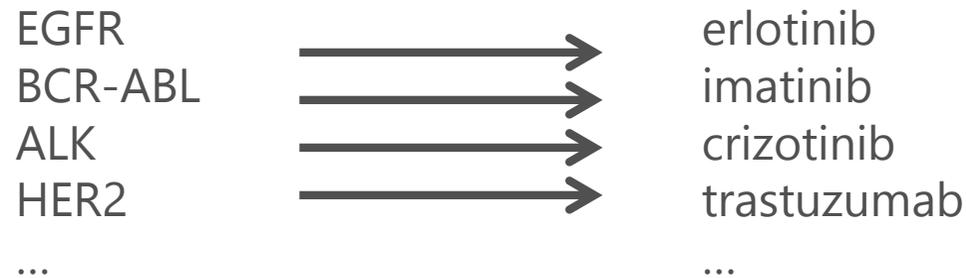
Precision cancer medicine:
The use of "pan-omic" technology to inform patient care and translational studies

Precision oncology: A paradigm shift

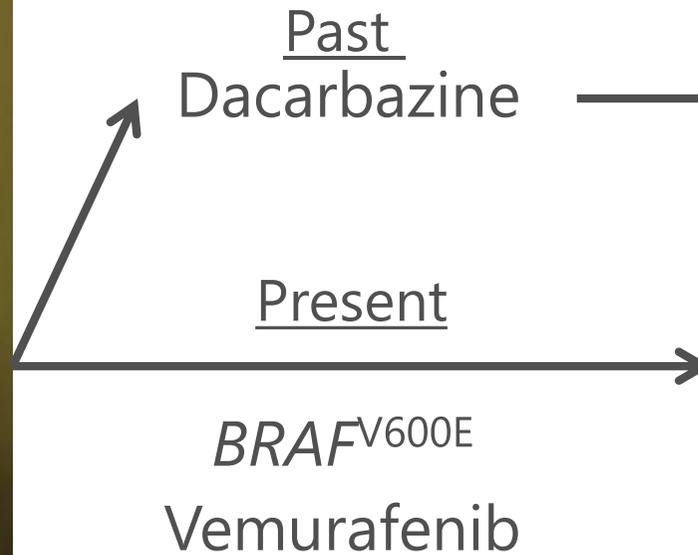
Past → Present



Present → Future



Precision oncology: A paradigm shift



5% response rate

Wagle, Emery, et. al JCO 2011

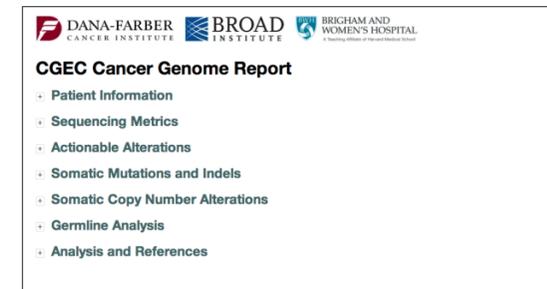
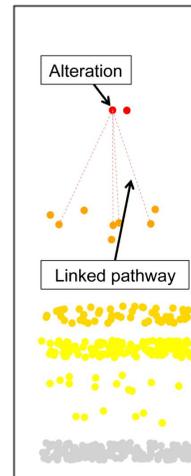
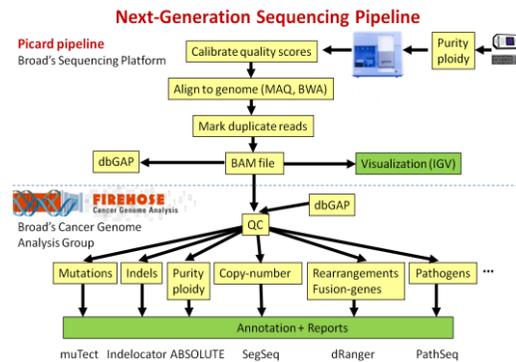
Big question: Can prospective knowledge of *all* alterations in a tumor genome impact patient care?

Clinical interpretation needs

Clinical Sequencing Pipeline Development

Clinical Genomics Data Interpretation

Data Representation for Clinicians



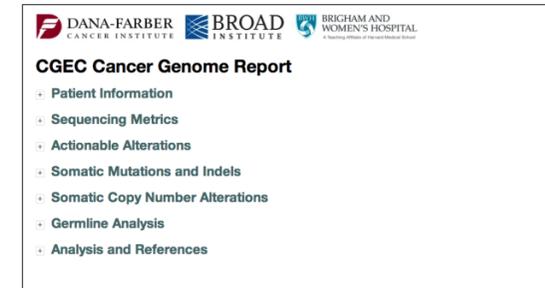
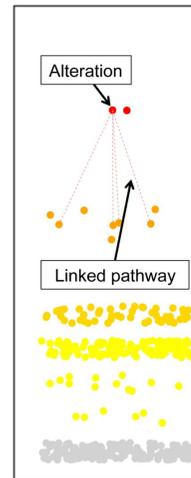
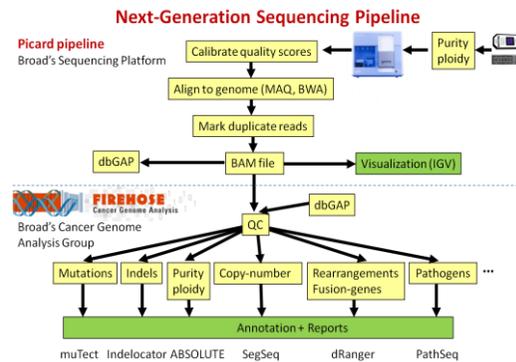
Van Allen, et al ASCO oral abstract (2012)

Clinical interpretation needs

Clinical Sequencing Pipeline Development

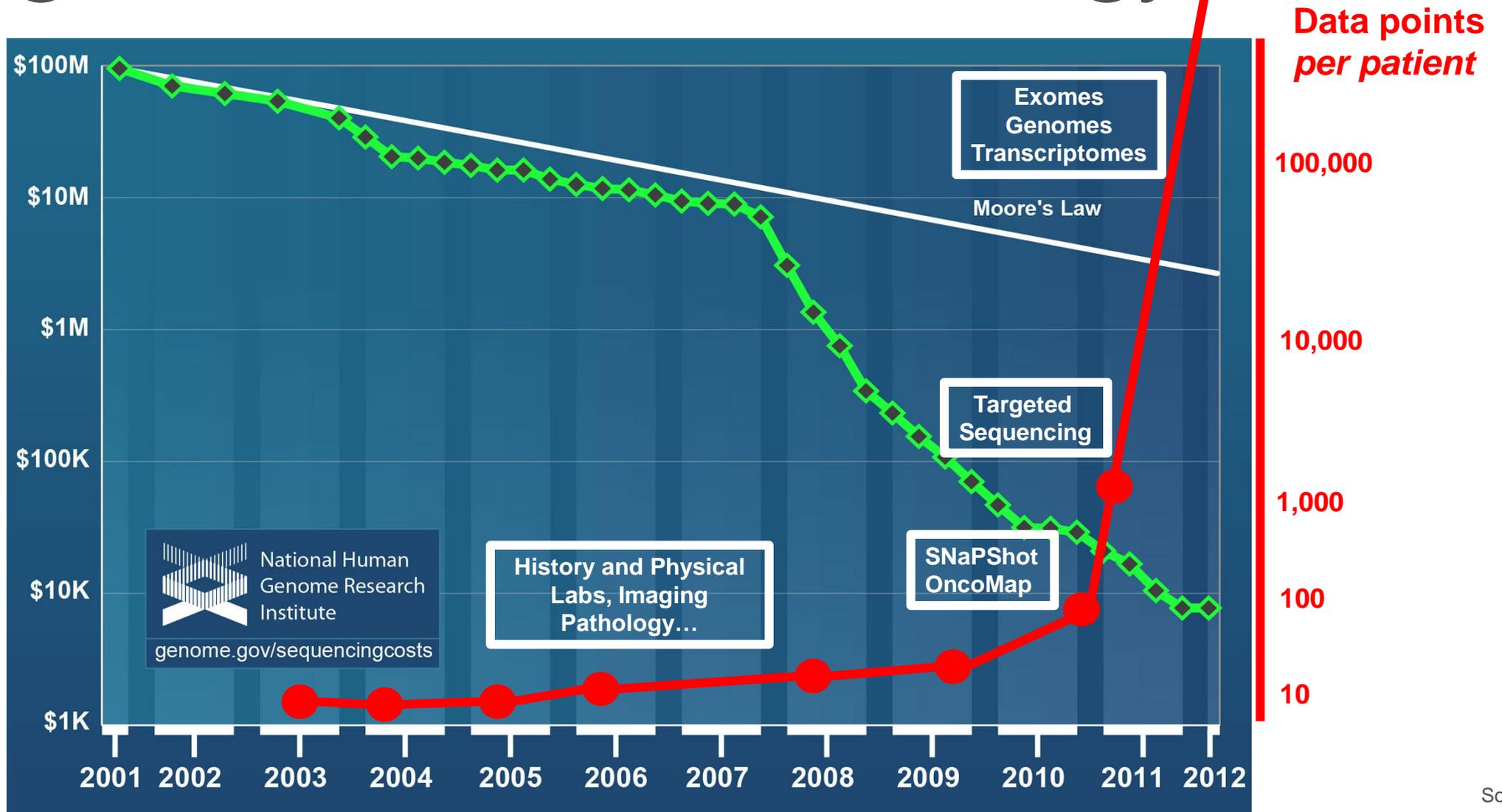
Clinical Genomics Data Interpretation

Data Representation for Clinicians



Van Allen, et al ASCO oral abstract (2012)

"Big (genomic) data" in oncology



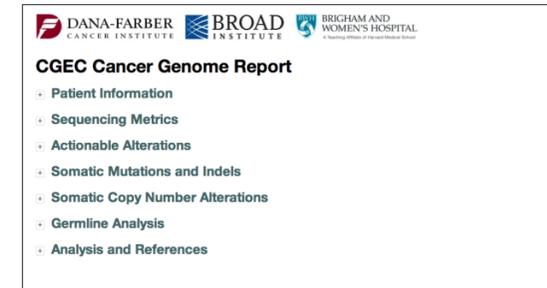
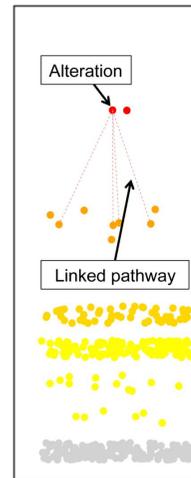
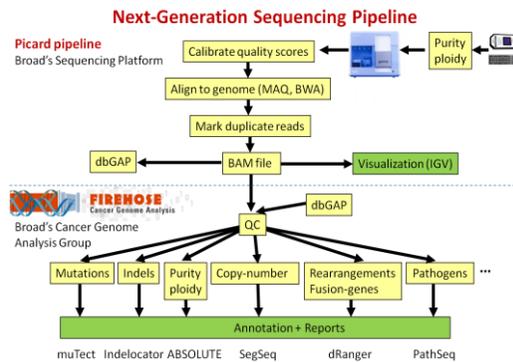
Source: NHGRI

Clinical interpretation needs

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Van Allen, et al ASCO oral abstract (2012)

PHIAL

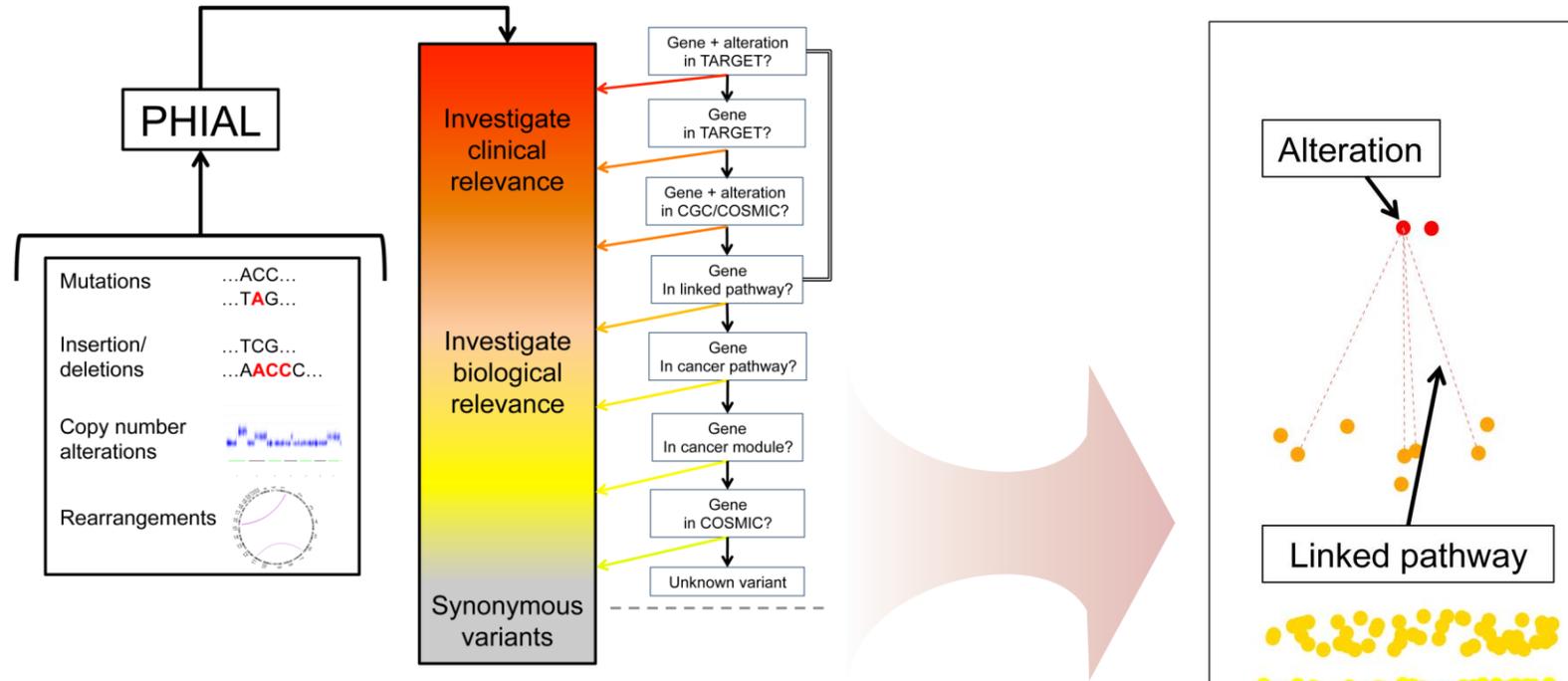
Precision **H**euristics for Interpreting the **A**lteration **L**andscape



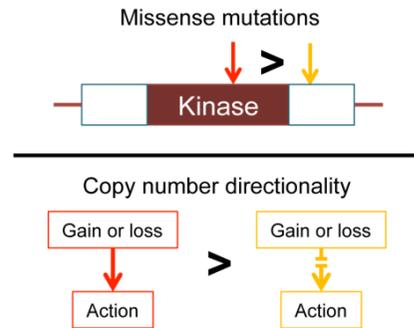
“May it be a light to you in dark places, when all other lights go out.”¹

¹Galadriel, in Tolkien, The Fellowship of the Ring

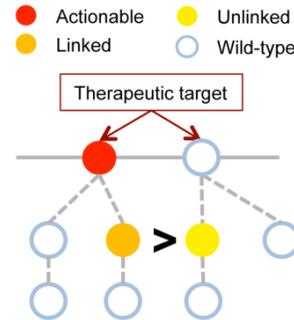
PHIAL



Subclassifications per level

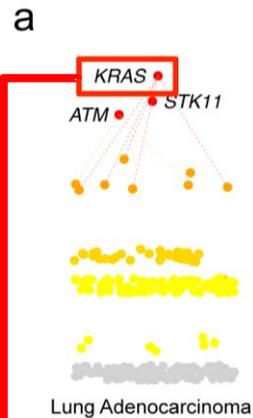


Linked pathways



Van Allen, Wagle et al. Nature Medicine 2014

Impact on clinical decision-making



KRAS A146V

- Rare activating alteration
- Not detected with deployed profiling technologies (at that time)

Cancer Cell Article

Cell
PRESS

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

Marta Puyol,^{1,6,7} Alberto Martín,^{1,6,8} Pierre Dubus,⁴ Francisca Mulero,² Pilar Pizcueta,³ Gulfaraz Khan,⁵ Carmen Guerra,¹ David Santamaria,¹ and Mariano Barbacid^{1,*}

¹Molecular Oncology Programme

²Biotechnology Programme

³Experimental Therapeutics Programme

Centro Nacional de Investigaciones Oncológicas (CNIO), E-28029 Madrid, Spain

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⁵Department of Microbiology and Immunology, Faculty of Medicine and Health Sciences, United Arab Emirates University, United Arab Emirates

⁶These authors contributed equally to this work

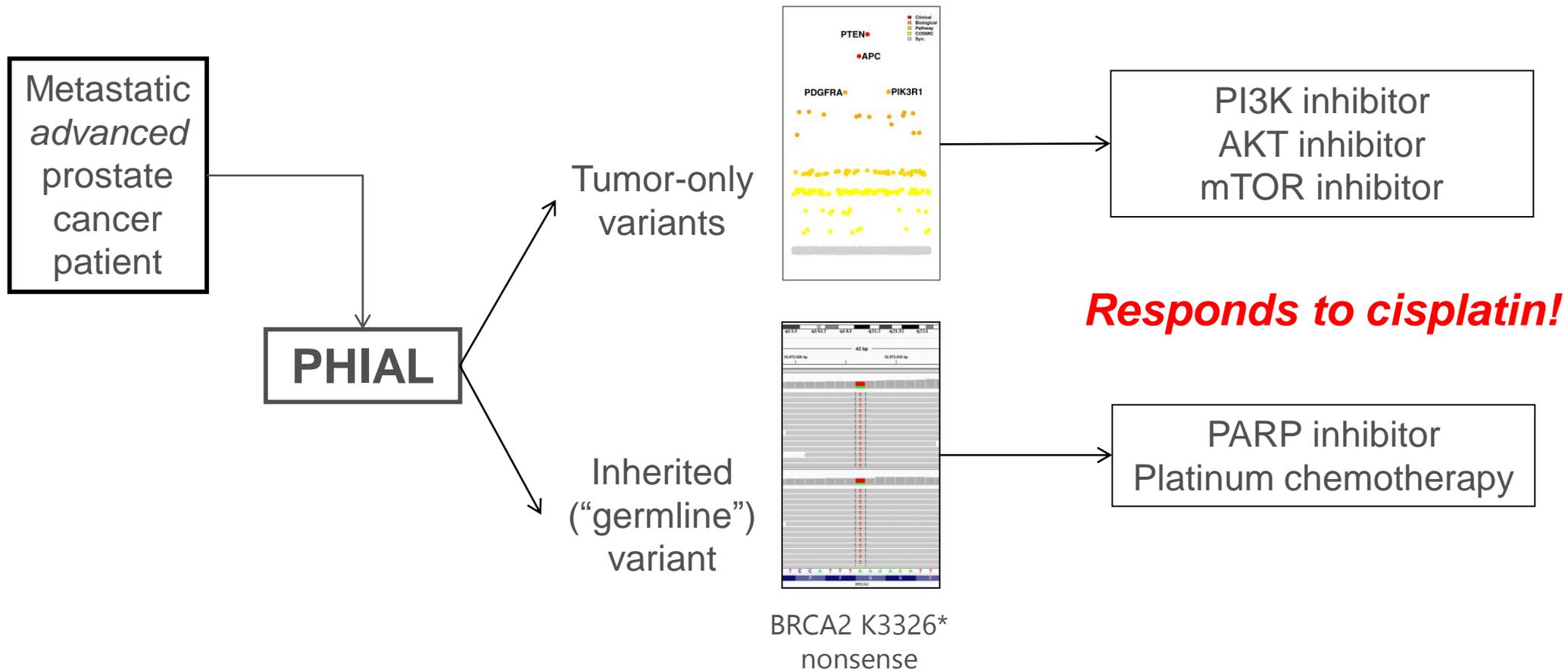
⁷Present address: Koch Institute for Integrative Cancer Research at MIT, 77 Massachusetts Avenue, E17-227, Cambridge, MA 02139, USA

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DOI 10.1016/j.ccr.2010.05.025

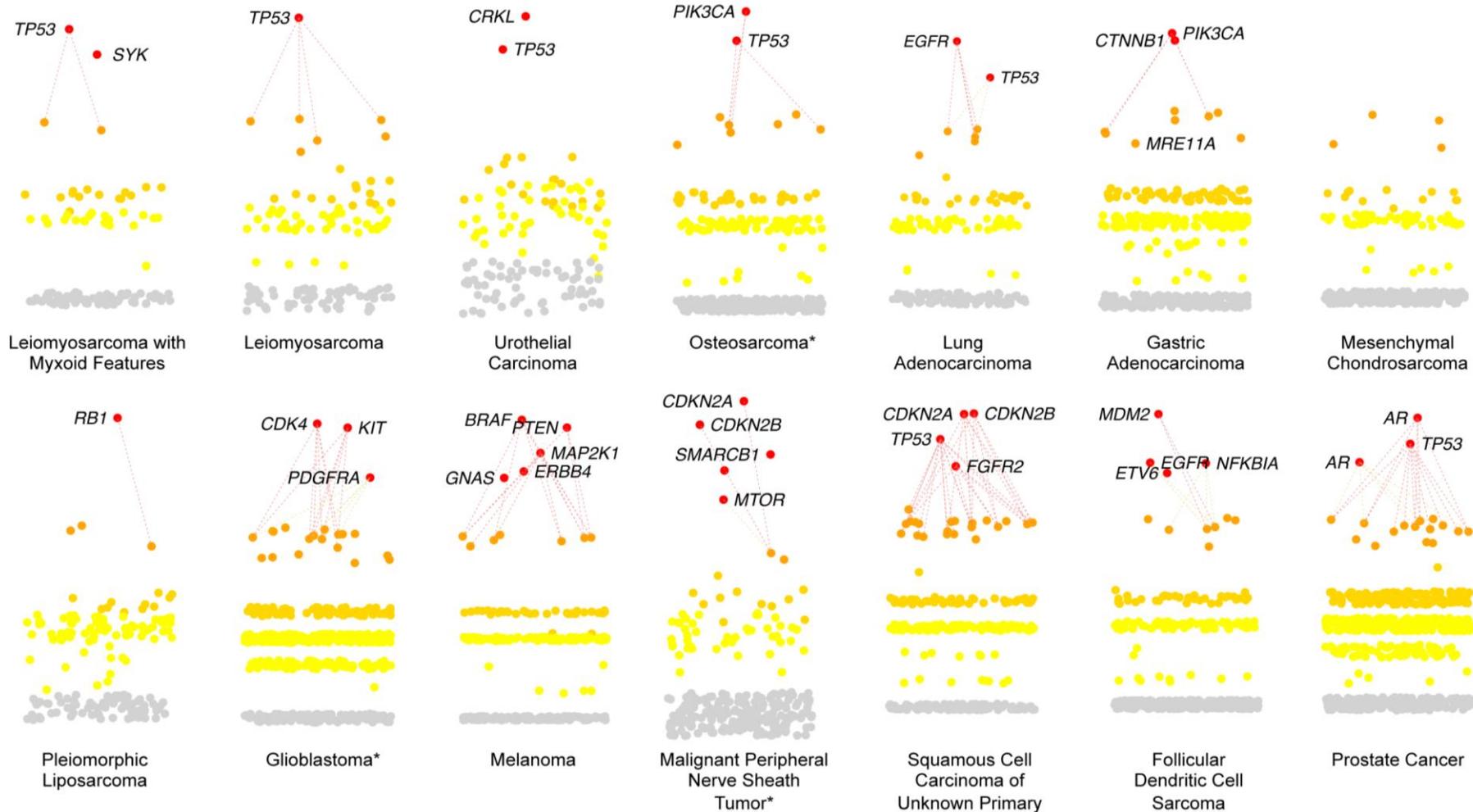
Impact on clinical decision-making



Five potential therapies for a patient who exhausted standard-of-care options!

Van Allen, et al, Prostate Cancer Pros. Dis., 2014

PHIAL applied to diverse cancer types



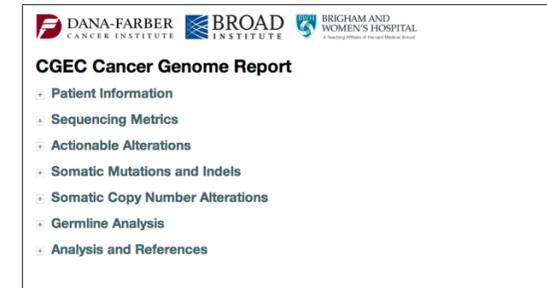
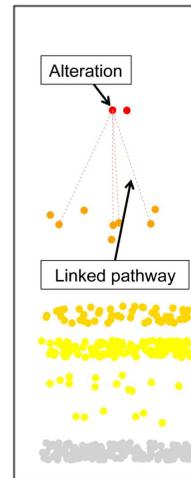
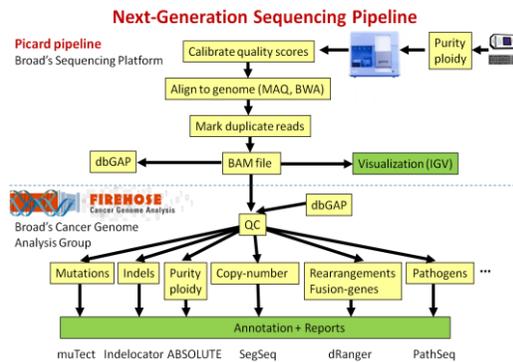
87

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Van Allen, et al ASCO oral abstract (2012)

The challenge of representation

Microsoft phone interview (~2002):

“Describe how you might make a mouse from scratch?”



Eli: “I would start with a white-ish color, shaped around the palm of my hands...”



Did not get call back for second interview

The challenge of representation

True stories from oncology clinic (12/9/2013):

Patient's genomic testing reveals *PIK3CA*^{E545K} mutation

Specific inhibitors of this gene and pathway ("PI3K inhibitors") are in clinical trials

"Why might you suggest PI3K inhibitor?" - Doc

"There is an activating PIK3CA mutation." - Eli

"Oh, is PIK3CA part of the PI3K pathway?" - Doc

The state of clinical informatics

dhya

THE STATE OF CLINICAL INFORMATICS



Digital genomics report

CGEC Cancer Genome Rep: x

<https://www.broadinstitute.org/collaboration/canseq/CANSEQU01-0100027-TP-NB-SM-3057P-SM-30570/CANSEQU01-010...>

UP < > EXPAND ALL COLLAPSE ALL SET FIXED WIDTH PRINT

DANA-FARBER
CANCER INSTITUTE BROAD
INSTITUTE BRIGHAM AND
WOMEN'S HOSPITAL
A Teaching Affiliate of Harvard Medical School

CGEC Cancer Genome Report

- + Clinical Information
- + Sequencing Metrics
- + Actionable Highlights
- + Somatic Analysis
- + Germline Analysis
- + Integrative Analysis
- + References

MADE WITH NOZZLE

Digital genomics report

Somatic Analysis

This section investigates somatic mutations, insertion/deletions, and copy number alterations across

Table and Details

able findings with details, sorted by actionability score

Gene	Alteration	Variant	Coverage	Allelic_fraction	UniProt_Region	
KRAS	p.G12D	Missense Mutation	84	0.44	GTP.	Click here
STK11	p.S69fs	Frame Shift Ins	38	0.63	Protein kinase.	Click here
EZH2	p.S277I	Missense Mutation	228	0.17	Interaction with DNMT1, DNMT3A and DNMT3B.	Click here

Reveals IGV screenshot

Links to MutationAssessor

Links to focused ClinicalTrials.gov results

Curated data

Table 6. Somatic Curation Team results for selected alterations

	4/25/13 9:05	4/25/13 14:17	4/21/13 11:26
Gene	KRAS	STK11	EZH2
Alteration	p.G12D	p.S69fs	p.S277I
Patient ID	CANSEQU01-0100027	CANSEQU01-0100027	CANSEQU01-0100027
Tumor Type	Lung adenocarcinoma	Lung adenocarcinoma	Lung Adenocarcinoma
Primary Curator	Nikhil Wagle	Nikhil Wagle	Marios Giannakis
Sequencing Issues	Good coverage at KRAS and allelic fraction of 44%	Allelic fraction is 63% suggestive of LOH.	

OMIM

Reference table used

Cancer Germline Risk Alleles

Cancer risk alleles are based on a compilation of [Cancer Gene Census germline genes \(build 3-15-2012\)](#) plus additional cancer risk genes determined by the CGEC germline group.

Table 12. SNPs sorted by ESP-6500 total allele frequencies. Only those with 1% or less are shown here.

Gene	Alteration	Variant_Classification	Chromosome	Start_position	Allele_change	Genotype	dbSNP_RS	Allele_Frequencies	Cancer_syndromes
ERCC5	p.K1172T	Missense_Mutation	13	103528207	A->C	Heterozygous		0% 0% 0%	Xeroderma pigmentosum (G)

dbSNP

Big question: Can prospective knowledge of *all* alterations in a tumor genome impact patient care?

With the right computational approaches, we can study this on growing numbers of patients

What are we missing?

A lot.

“Clinical” computational oncology is in its infancy

Much room for improvement

Open/eager for collaboration

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The patients



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Yotam Drier
Nils Gehlenborg
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Sheila Fisher
William Hahn
Matthew Meyerson
Todd Golub
Eric Lander

...

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Starr
Prostate Cancer Foundation
American Cancer Society





Save the planet and return
your name badge before you
leave (on Tuesday)

