



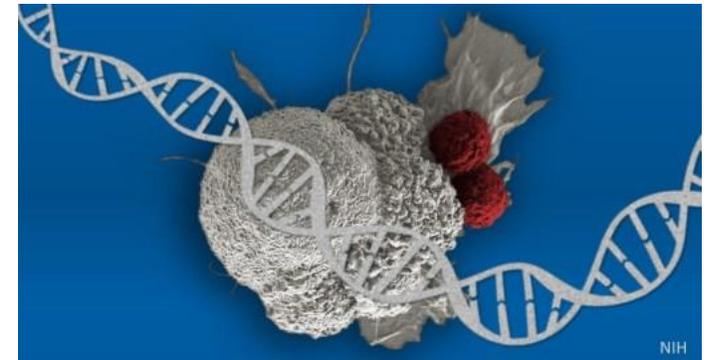
# Cancer Genetics: Cracking Cancer's Code

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NIH Directors Blog



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- I have no actual or potential conflict of interest in relation to this program/presentation.
- I am a co-founder, consultant, and co-owner of NeoClone Biotechnologies, Inc., Discovery Genomics, Inc., (recently acquired by Immusoft, Inc.), B-MoGen Biotechnologies, Inc. (recently acquired by Biotechne, Inc.), and Luminary Therapeutics, Inc. This presentation is not directly related to the business of these companies and I obtain no funds for my laboratory research from these companies.
- Some of my laboratory's work is funded by Genentech, Inc. That work will not be discussed today.
- I hold equity in and serve as the Chief Scientific Officer of Surrogen, a subsidiary of Recombinetics, a genome-editing company. That work will not be discussed today.



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# Learning Objectives

- All cancer has a genetic cause – but that doesn't (usually) mean the genes you're born with cause cancer, instead cancer is primarily caused by mutations occurring in rare cells in your body.



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- Cancer cells typically have many, many gene mutations and about 6 or more of these “drive” the abnormal behavior of the cancer cells, while the rest are merely “passengers”.
- It is thought that the genes mutated in a cancer can produce abnormal proteins allowing the immune system to kill off the cancer cells. This is how “immunotherapies” like Keytruda can work for some cases of cancer.
- The specific genes that are mutated in a tumor or leukemia may determine the prognosis of the patient and dictate the best therapy for the physician to choose.



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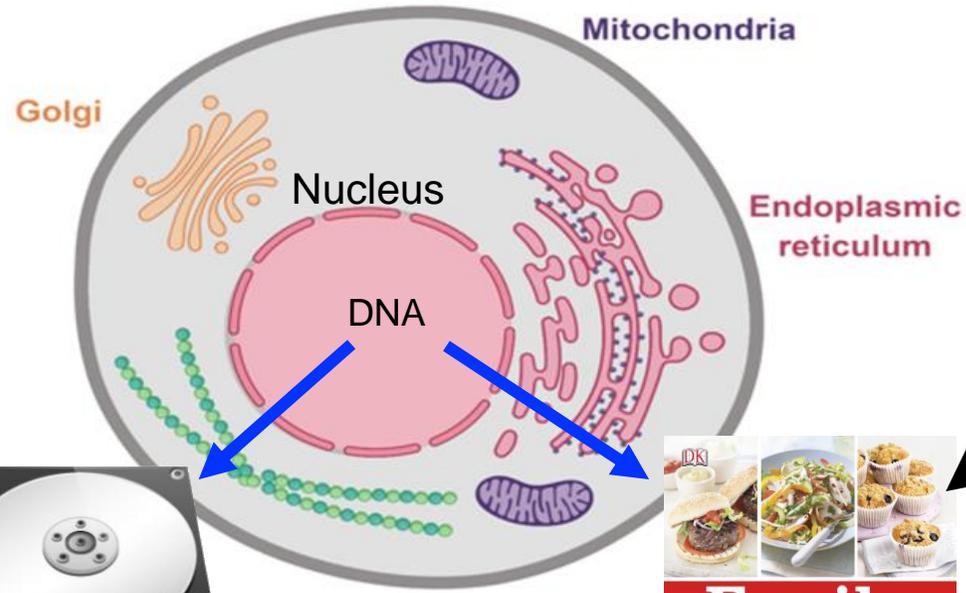
# All Cancer is “Genetic” Because:

- ALL cancer cells have altered genomes compared to a normal cell
- Those DNA alterations are called mutations



# GENOME

# GENOME



## Files



## Hard Drive



## Family Cookbook

More than 700 Recipes  
 Healthy, Quick Meals • Fussy Eaters  
 Smart shopping • Cooking with Kids  
 Easy Entertaining  
 Kids' Party Food • One Meal for All  
 CAROLINE BREHERTON

## Cookbook

## Recipes



## Genes



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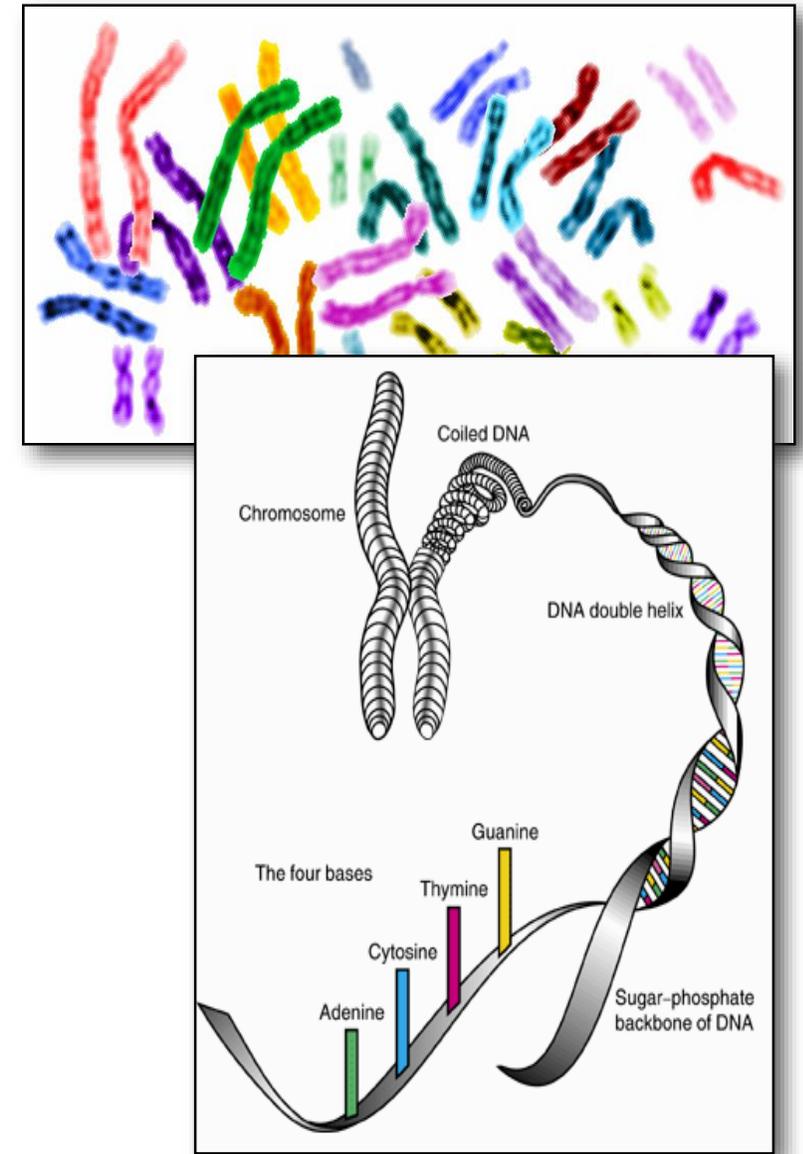
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# Cancers Are Genetic Diseases that Result from Alterations in DNA Sequence &/or Expression

- Cancers result from the **corruption** or **misuse** of DNA.
  - **Corruption** results from changes in DNA that can be small (single nucleotide changes/mutations) or large (chromosomal abnormalities).
  - **Misuse** results from changes in when and what genetic information is accessed (**epigenetics**).
- Cancers are often genetically **unstable**.
  - DNA copying/repair machinery is compromised leading to **greater accumulations** of DNA mistakes during cell division.

# Consider How Much Information is Stored in Every Human Cell

- All the DNA in one cell, if stretched out, would be over 2 meters long!
- The human genome would take 6,000,000 pages of 500 words each just to print out



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GTTCAACACCTAGAAAAAAAAGAATCCCTATTGGTACTACCAATGGTAA

A page a second for 23 days!



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GAAAAAACCGAGAAAGATTTATCTGCTAGAAGATTTGTGCGACGATGATCCTTATGATTTG  
GTTCAACACCTAGAAAAAAGAAATCCCTATTGGTACTACCAATGGTAA

That's a lot of information to copy!



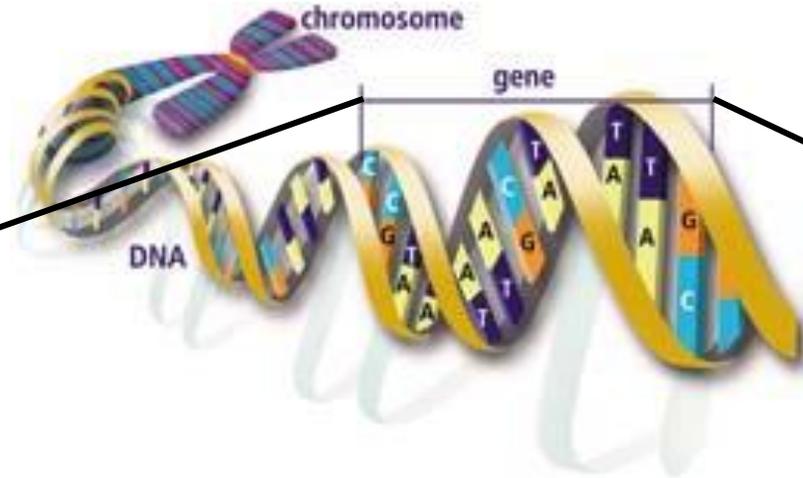
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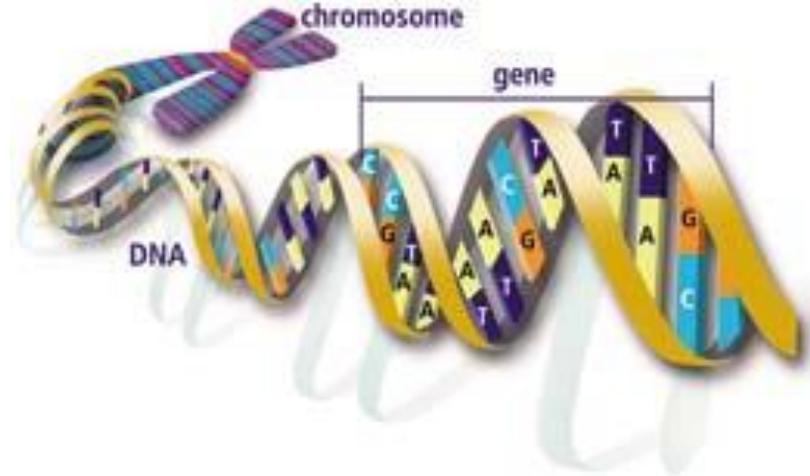


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# Each DNA Strand is Copied During Replication

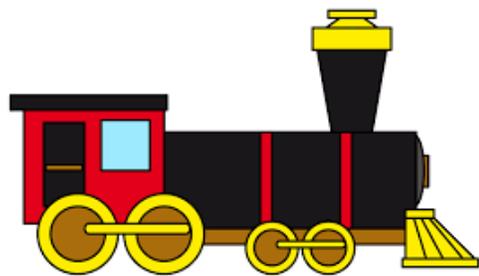


# Each DNA Strand is Copied During Replication



GGAAATTGAAACCCAGAACT  
CCTTAACTTTGGGTCTTGATTGAT

# Radiation Can Break DNA



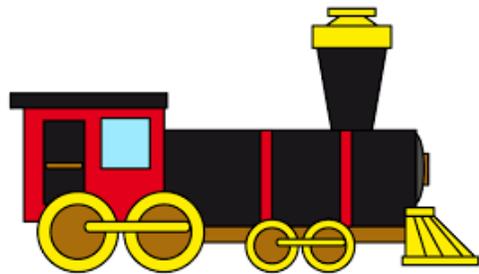
T G A A A C C C

C C T T A A C T T T G G G



G A T T G A T

# Errors in DNA Repair Cause Mutations



AG A A A C C C A G **T** A C T A A

C C T T A A C T T T G G G

G A T T G A T

# Carcinogens Can Alter DNA

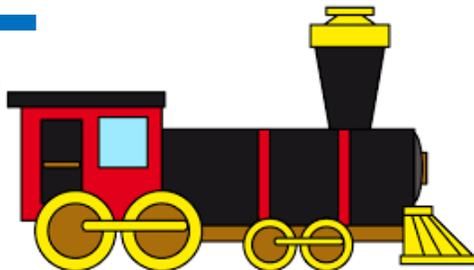
ADDUCT



# Carcinogens Can Alter DNA

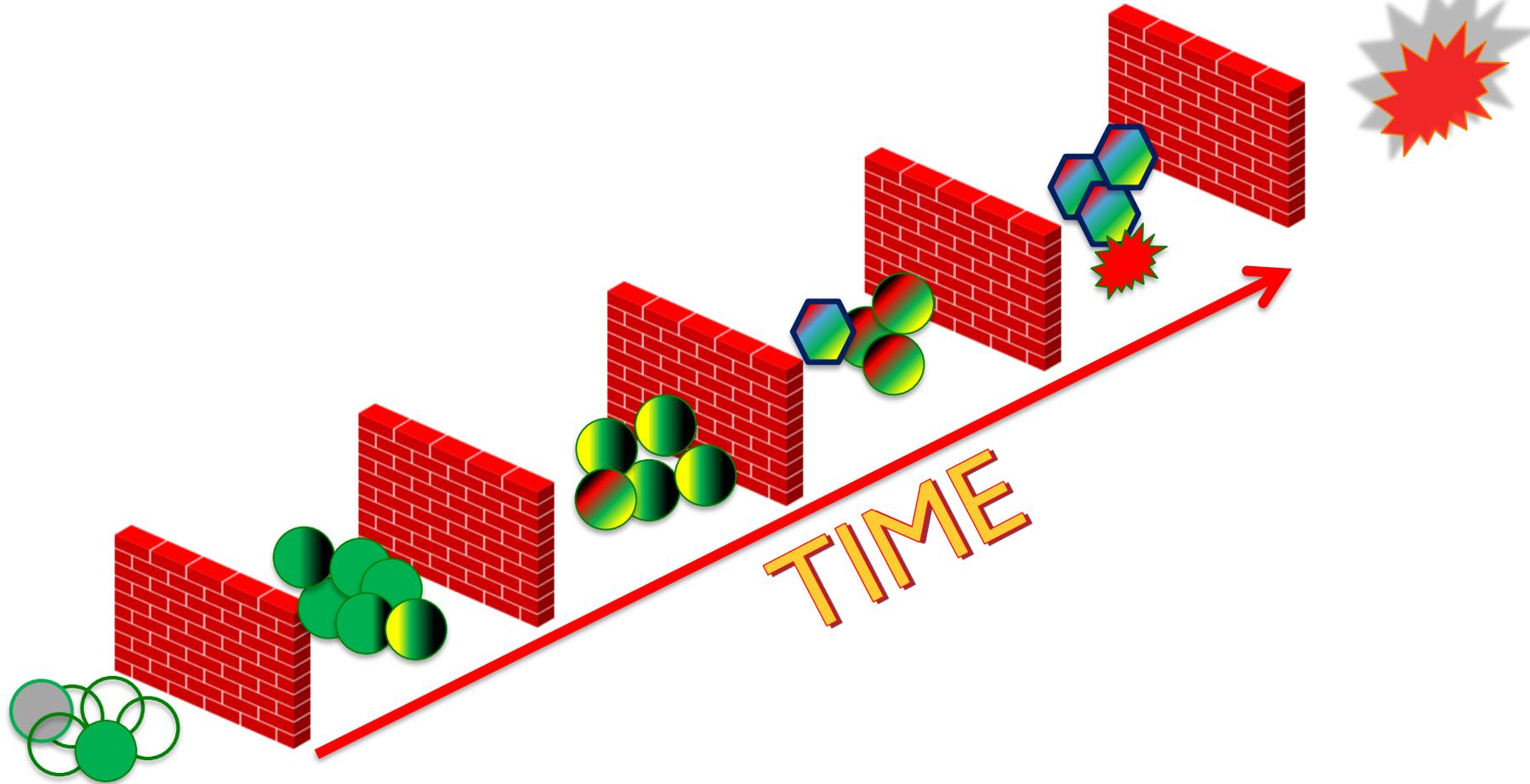
**ADDUCT**  
*(add a duck)*

GG AATT

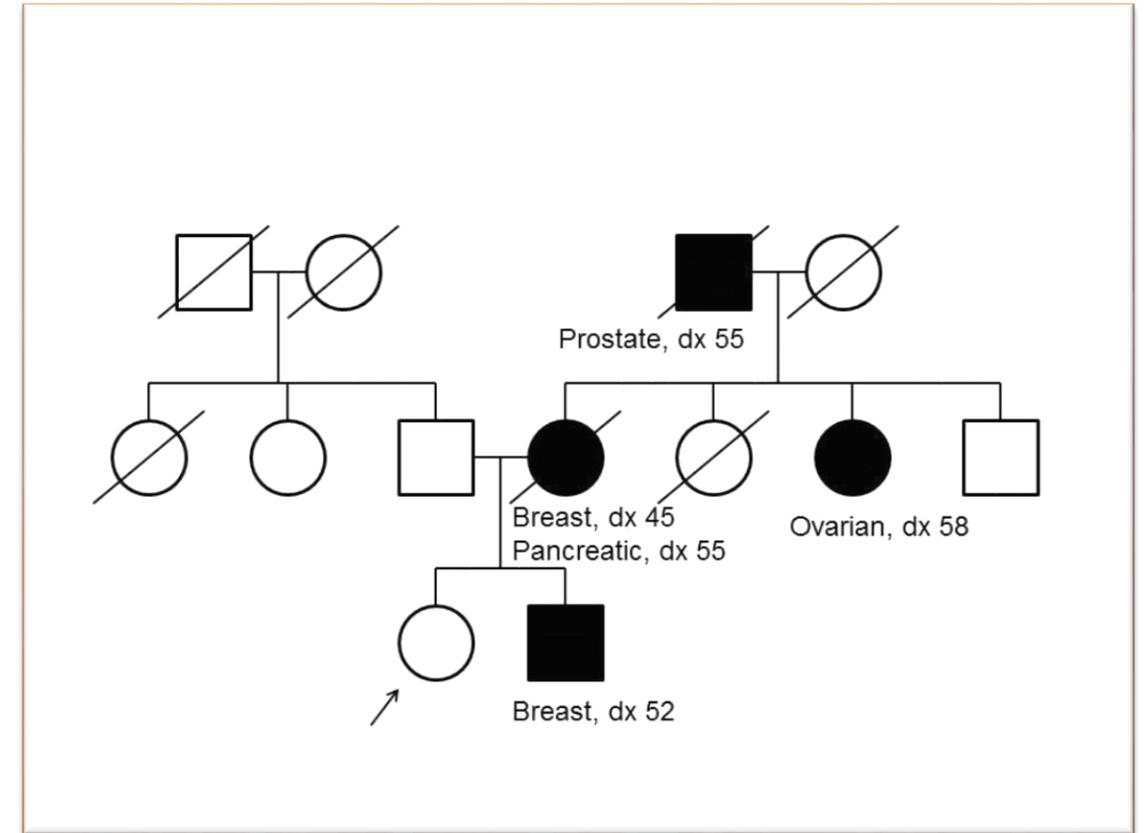


AACGTTGCCTAACTCTT GATTGAT

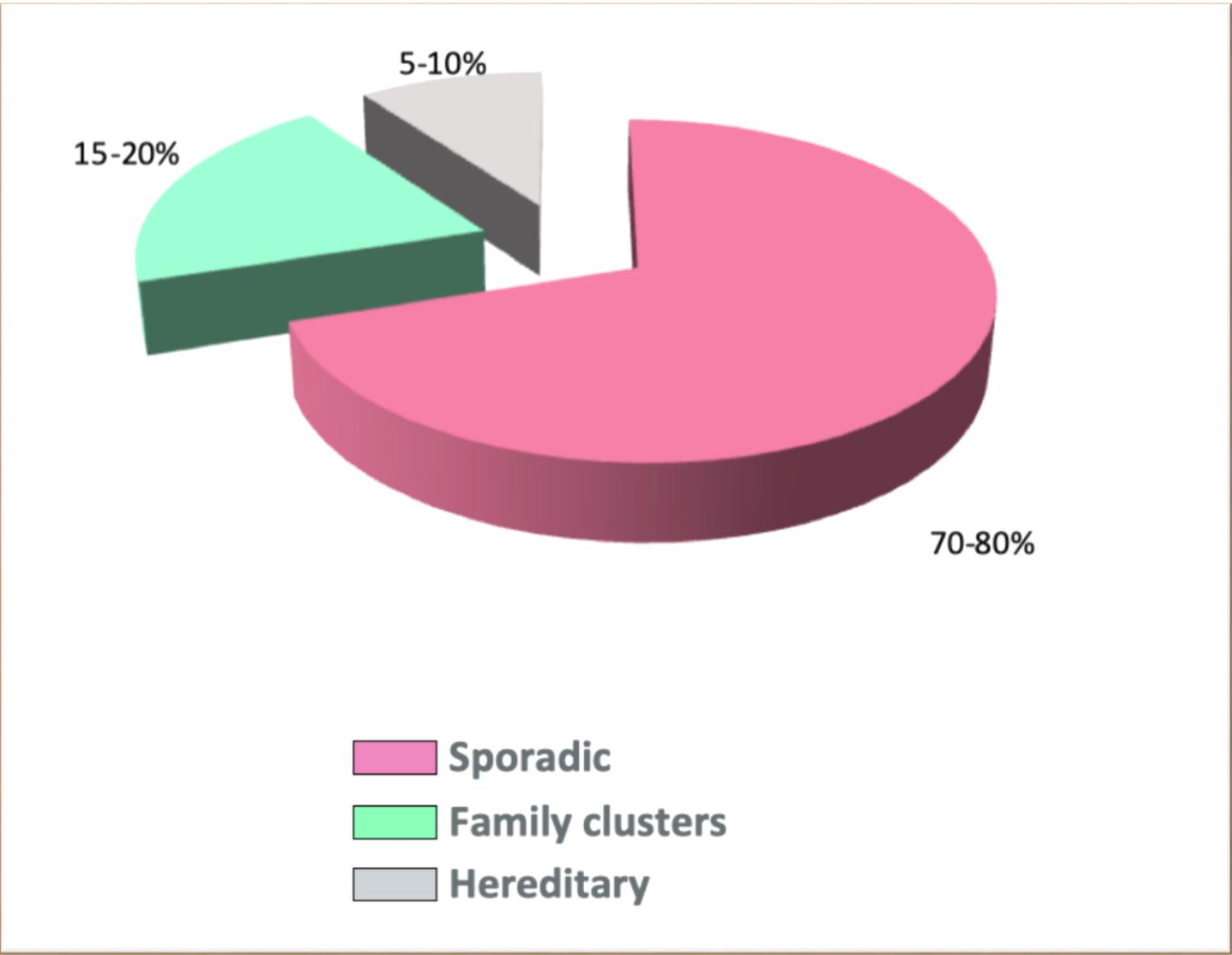
# Mutations Allow Cells to Overcome Barriers to Cancer



# If Cancer is Caused by DNA Damage During our Lifetimes, Then Why Does Cancer “Run in the Family” Sometimes?

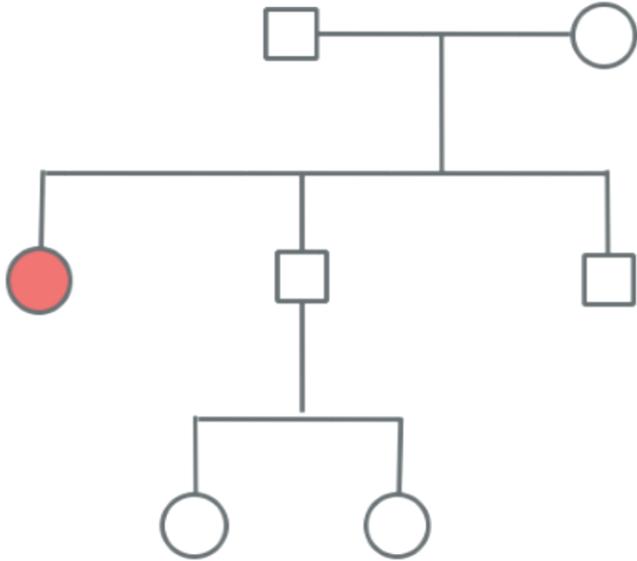


# How Much of Cancer is Hereditary?



## Sporadic

70-80% of cancer  
in families



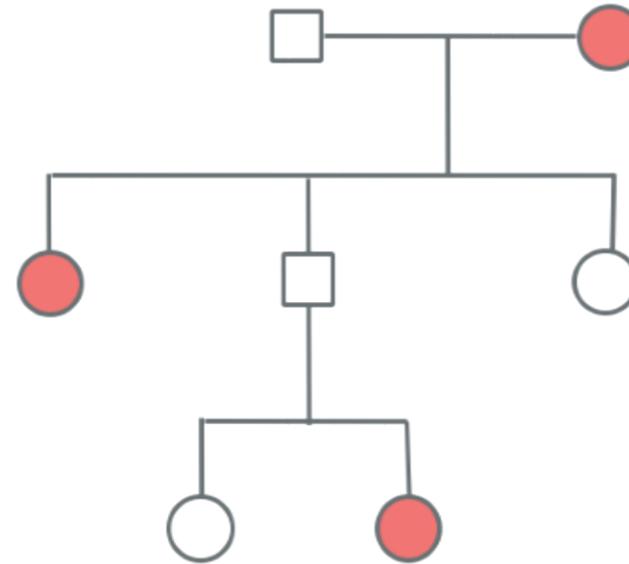
Acquired mutations in the tumor

Single or Unilateral Tumor

Later age of onsets

## Familial

15-20% of cancer  
in families



Germline Mutation??

Single or Unilateral Tumors

Early/late age of onset

# “Red Flags” for Hereditary Breast and Ovarian Cancer?

- ❖ Breast cancer before age 50
- ❖ Ovarian cancer at any age
- ❖ Male breast cancer at any age
- ❖ Multiple primary cancers
- ❖ Ashkenazi Jewish ancestry
- ❖ Relatives of a mutation carrier

# Cancer Risk Spectrum

## HIGH

- ❖ Multiple generations affected (AD inheritance)
- ❖ Early onset
- ❖ Multiple primary tumors

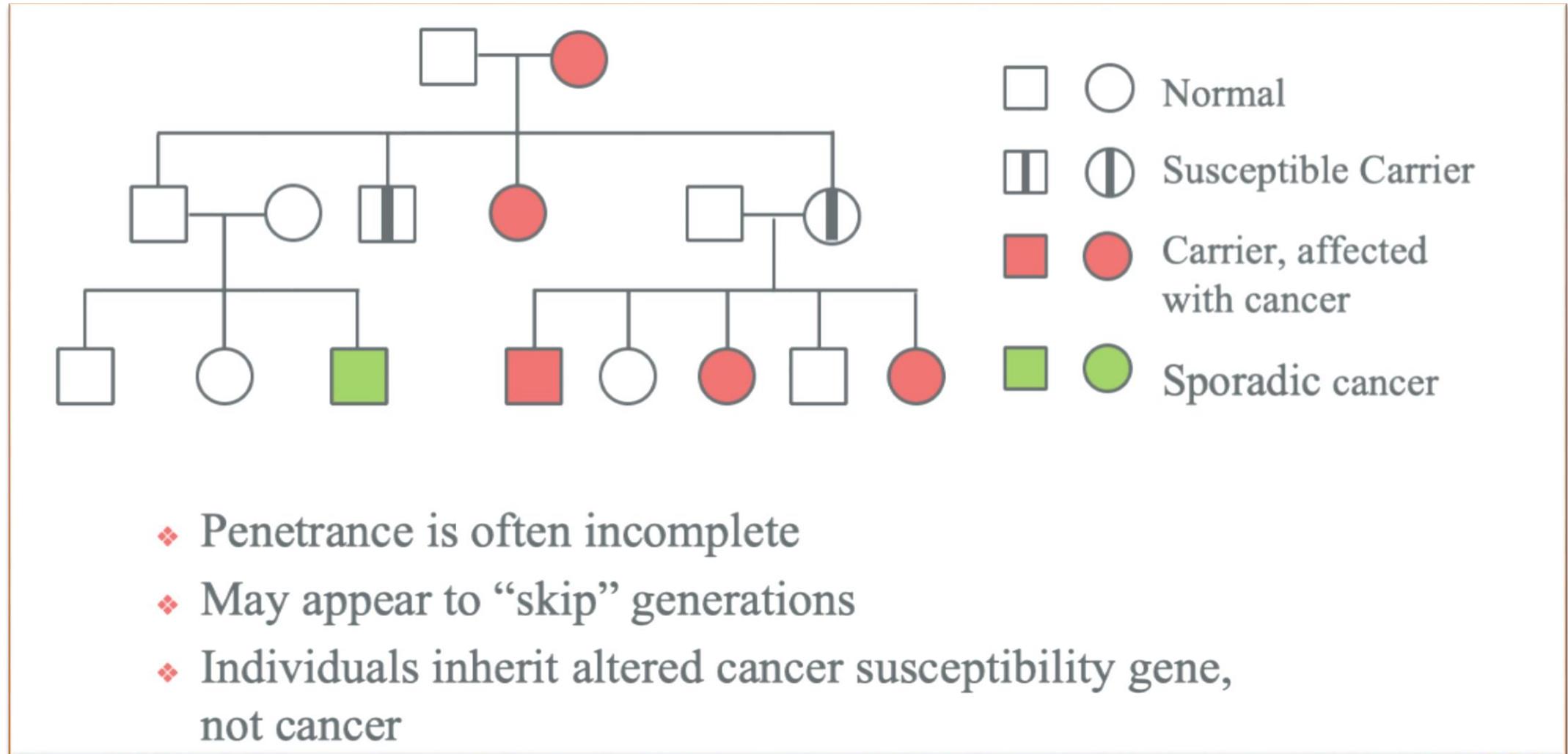
## MODERATE

- ❖ Several family members affected
- ❖ No single gene pattern
- ❖ Variable onset

## LOW

- ❖ No family history
- ❖ Late onset

# Hereditary Cancer is Usually Inherited as Dominant Trait



# What if You're Concerned your Family is Affected?

- Cancer management clinic contact information thru M Health: <https://www.mhealth.org/care/services/cancer-risk-management-program>
- There are hereditary cancer clinics in all the major health systems
- There are online telehealth genetic counseling options like GeneMatters or Genome Medical that consumers can use as a resource.

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# Large Study of Twins Suggests Lifestyle Choices have a Strong Role in Determining Cancer Risk

FOR MOST PEOPLE!



## ENVIRONMENTAL AND HERITABLE FACTORS IN THE CAUSATION OF CANCER

### Analyses of Cohorts of Twins from Sweden, Denmark, and Finland

PAUL LICHTENSTEIN, PH.D., NIELS V. HOLM, M.D., PH.D., PIA K. VERKASALO, M.D., PH.D., ANASTASIA ILIADOU, M.Sc., JAAKKO KAPRIO, M.D., PH.D., MARKKU KOSKENVUO, M.D., PH.D., EERO PUUKKALA, PH.D., AXEL SKYTTHE, M.Sc., AND KARI HEMMINKI, M.D., PH.D.

#### ABSTRACT

**Background** The contribution of hereditary factors to the causation of sporadic cancer is unclear. Studies of twins make it possible to estimate the overall contribution of inherited genes to the development of malignant diseases.

**Methods** We combined data on 44,788 pairs of twins listed in the Swedish, Danish, and Finnish twin registries in order to assess the risks of cancer at 28 anatomical sites for the twins of persons with cancer. Statistical modeling was used to estimate the relative importance of heritable and environmental factors in causing cancer at 11 of those sites.

**Results** At least one cancer occurred in 10,803 persons among 9512 pairs of twins. An increased risk was found among the twins of affected persons for stomach, colorectal, lung, breast, and prostate cancer. Statistically significant effects of heritable factors were observed for prostate cancer (42 percent of the risk may be explained by heritable factors; 95 percent confidence interval, 29 to 50 percent), colorectal cancer (35 percent; 95 percent confidence interval, 10 to 48 percent), and breast cancer (27 percent; 95 percent confidence interval, 4 to 41 percent).

**Conclusions** Inherited genetic factors make a minor contribution to susceptibility to most types of neoplasms. This finding indicates that the environment has the principal role in causing sporadic cancer. The relatively large effect of heritability in cancer at a few sites (such as prostate and colorectal cancer) suggests major gaps in our knowledge of the genetics of cancer. (N Engl J Med 2000;343:78-85.)

©2000 Massachusetts Medical Society.

**E**XCEPT for certain types of familial cancer, such as adenomatous polyposis coli, the contribution of hereditary factors to the development of cancer is thought to be relatively minor.<sup>1,2</sup> This premise, however, applies mainly to dominant genes, which have been assessed in family studies that cover two or more generations. By contrast, the contributions of recessive traits and combinations of genes to the causation of sporadic cancer are difficult to determine from family studies.<sup>4</sup> Consequently, the risks associated with single-gene mutations with low penetrance, recessive genes, and oncogenic mechanisms that involve multiple genes are poorly understood.

Family studies of breast, prostate, ovarian, and uterine cancer can estimate risks for siblings and parent-offspring pairs<sup>5-12</sup> but cannot distinguish between genetic and nongenetic (environmental or infectious) causes of familial aggregations of cancer. By contrast, comparisons of the concordance of cancer between monozygotic and dizygotic pairs of twins provide information on whether the familial pattern is due to hereditary or environmental influences.<sup>13</sup>

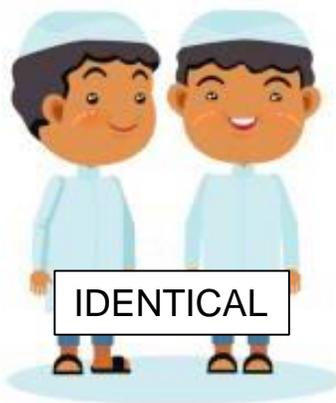
If studies of groups of twins show that concordance for cancer is higher among monozygotic twins (who share all genes) than among dizygotic twins (who, on average, share 50 percent of their segregating genes), genetic effects are likely to be important.

From the Departments of Medical Epidemiology, Karolinska Institute, Stockholm, Sweden (P.L., A.I.); the Institute of Public Health (Epidemiology) and the Danish Twin Registry, University of Southern Denmark, Odense (N.V.H., A.S.); the Department of Public Health, University of Helsinki, Helsinki, Finland (P.K.V., J.K., M.K.); the Department of Public Health and General Practice, University of Oulu, Oulu, Finland (J.K.); the Departments of Public Health, University of Turku, Turku, Finland (M.K.); the Finnish Cancer Registry, Helsinki, Finland (E.P.); and the Department of Biosciences à Novum, Karolinska Institute, Stockholm, Sweden (K.H.). Address reprint requests to Dr. Lichtenstein at the Departments of Medical Epidemiology, Karolinska Institute, Box 281, SE-171 77 Stockholm, Sweden, or at paul.lichtenstein@mep.ki.se.

# Determined Concordance Rate for Cancer in Identical Twins Versus Fraternal Twins



How often did both get cancer?  
How often did just one of the two get cancer?



How often did both get cancer?  
How often did just one of the two get cancer?

- Allows estimate of heritability
- If fraternal twins are concordant as often as identical twins, then it suggests shared environmental effects important in cancer risk
- If identical twins are concordant more often than fraternal twins, then it suggests shared heritable effects important in cancer risk

# For Most Cancers, for Most People, Environment has Principal Role in Determining Cancer Risk

*Conclusions* Inherited genetic factors make a minor contribution to susceptibility to most types of neoplasms. This finding indicates that the environment has the principal role in causing sporadic cancer. The relatively large effect of heritability in cancer at a few sites (such as prostate and colorectal cancer) suggests major gaps in our knowledge of the genetics of cancer. (N Engl J Med 2000;343:78-85.)

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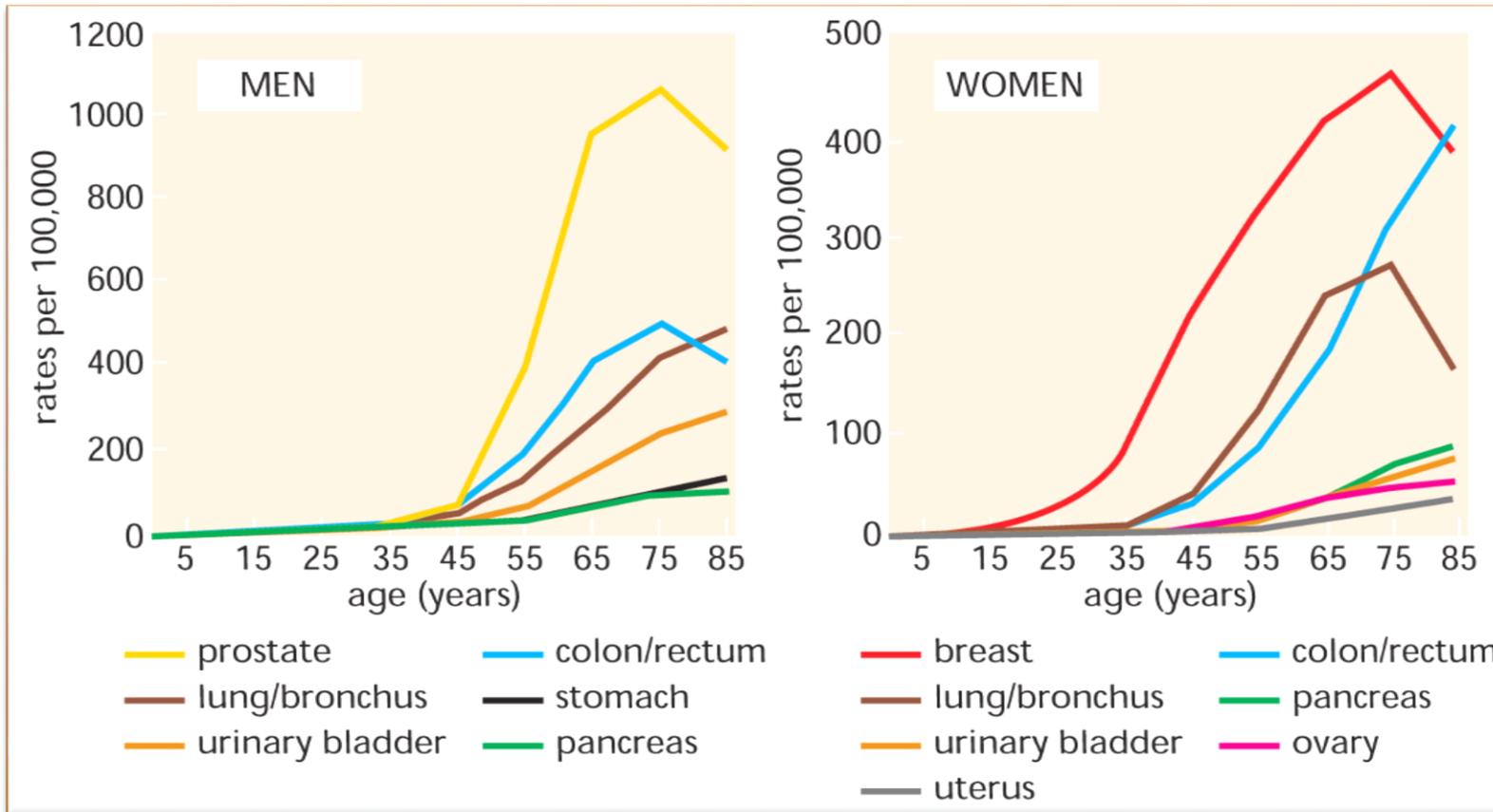
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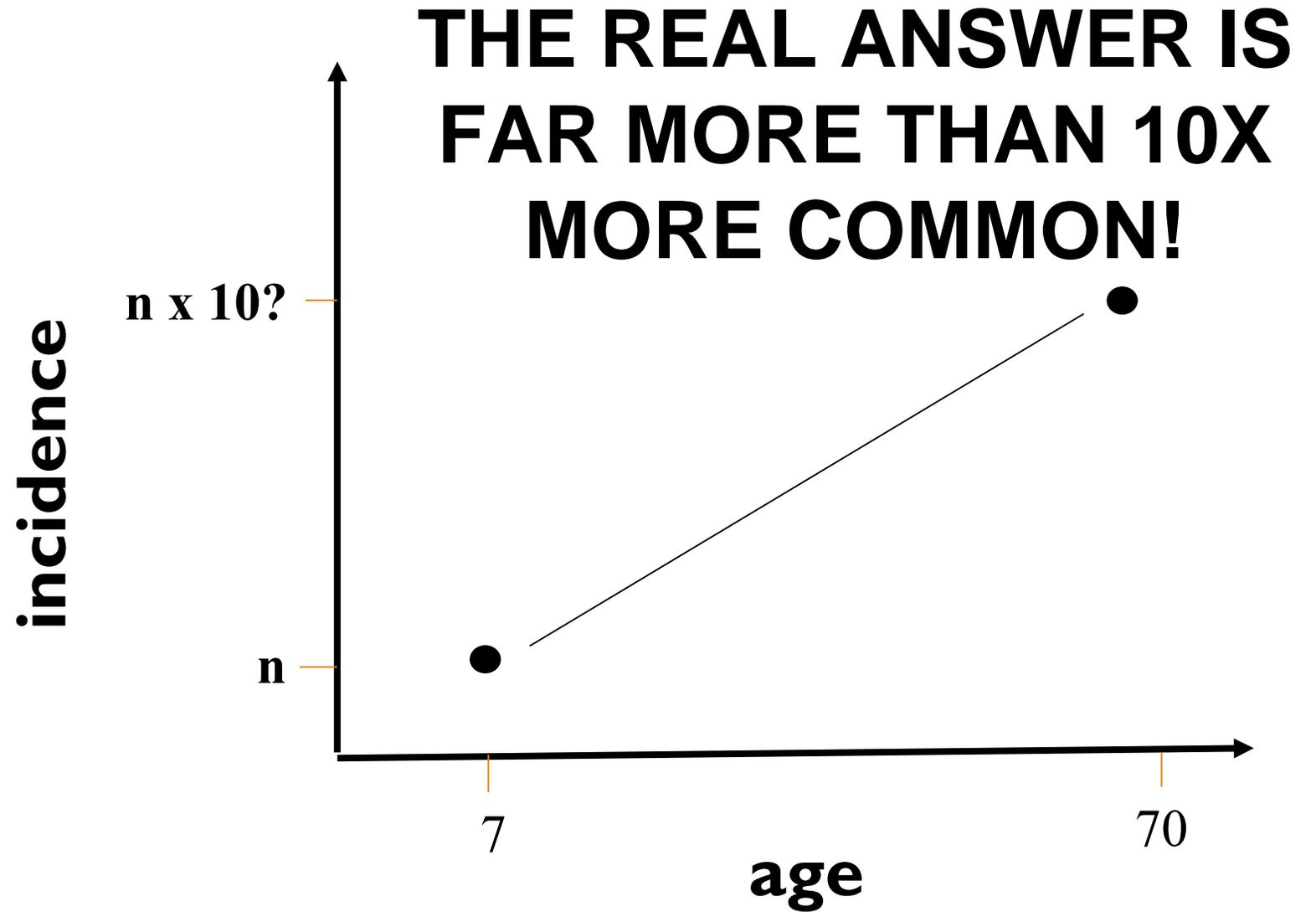
# Epidemiologic Studies Have Shown that **Age** is a Surprisingly **Large Factor in the Incidence of Cancer**



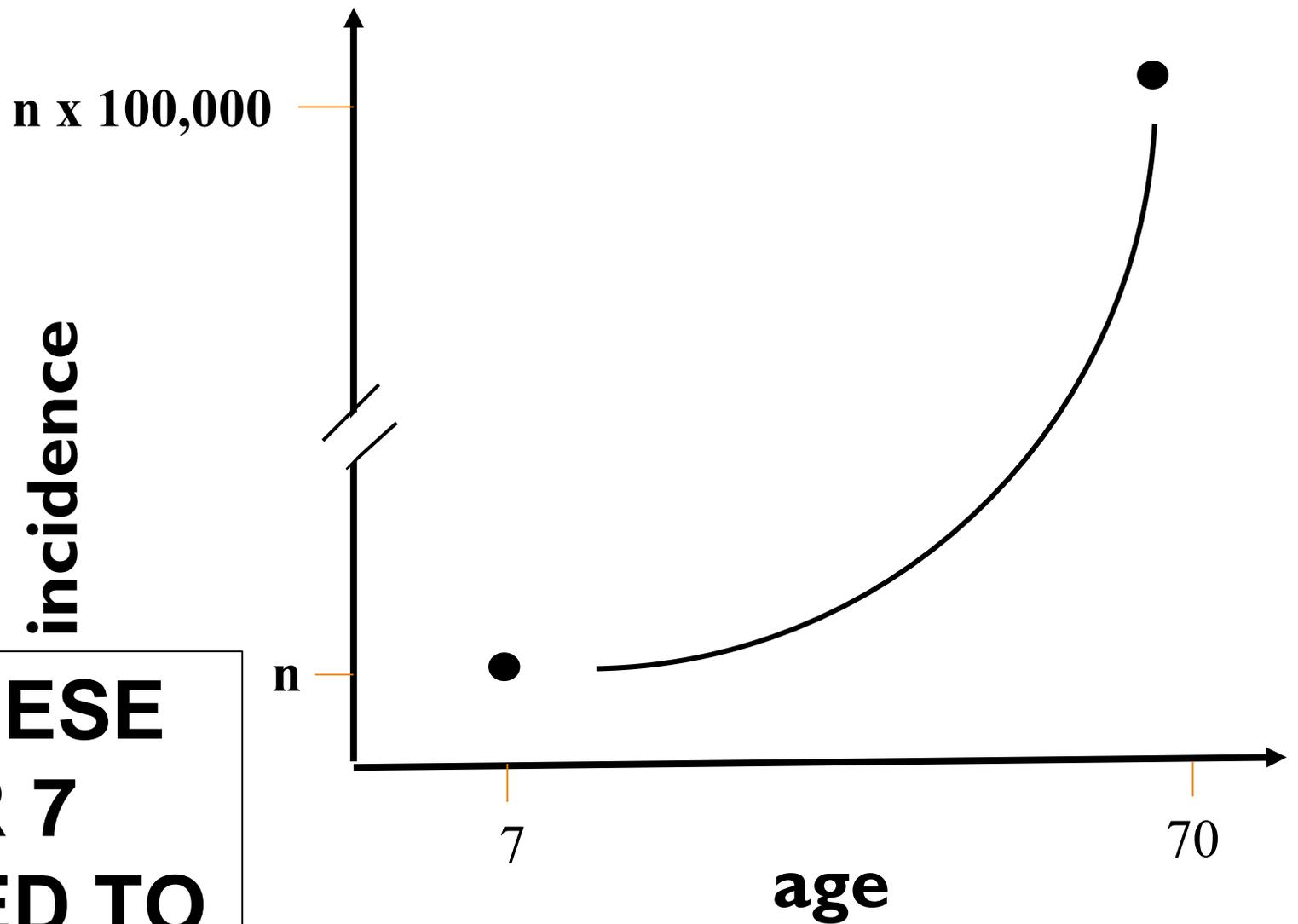
- **Late age of onset indicates that the development of most cancers requires an extended period of time**

Figure 11.1 *The Biology of Cancer* (© Garland Science 2007)

How Much More Likely is Cancer in Aged Versus Young People?



How Much More Likely is Cancer in Aged Versus Young People?



**STUDIES LIKE THESE SUGGEST 6 OR 7 "STEPS" REQUIRED TO GET CLINICALLY EVIDENT CANCER**

# Histopathology Provides Evidence of Multi-Step Tumor Formation

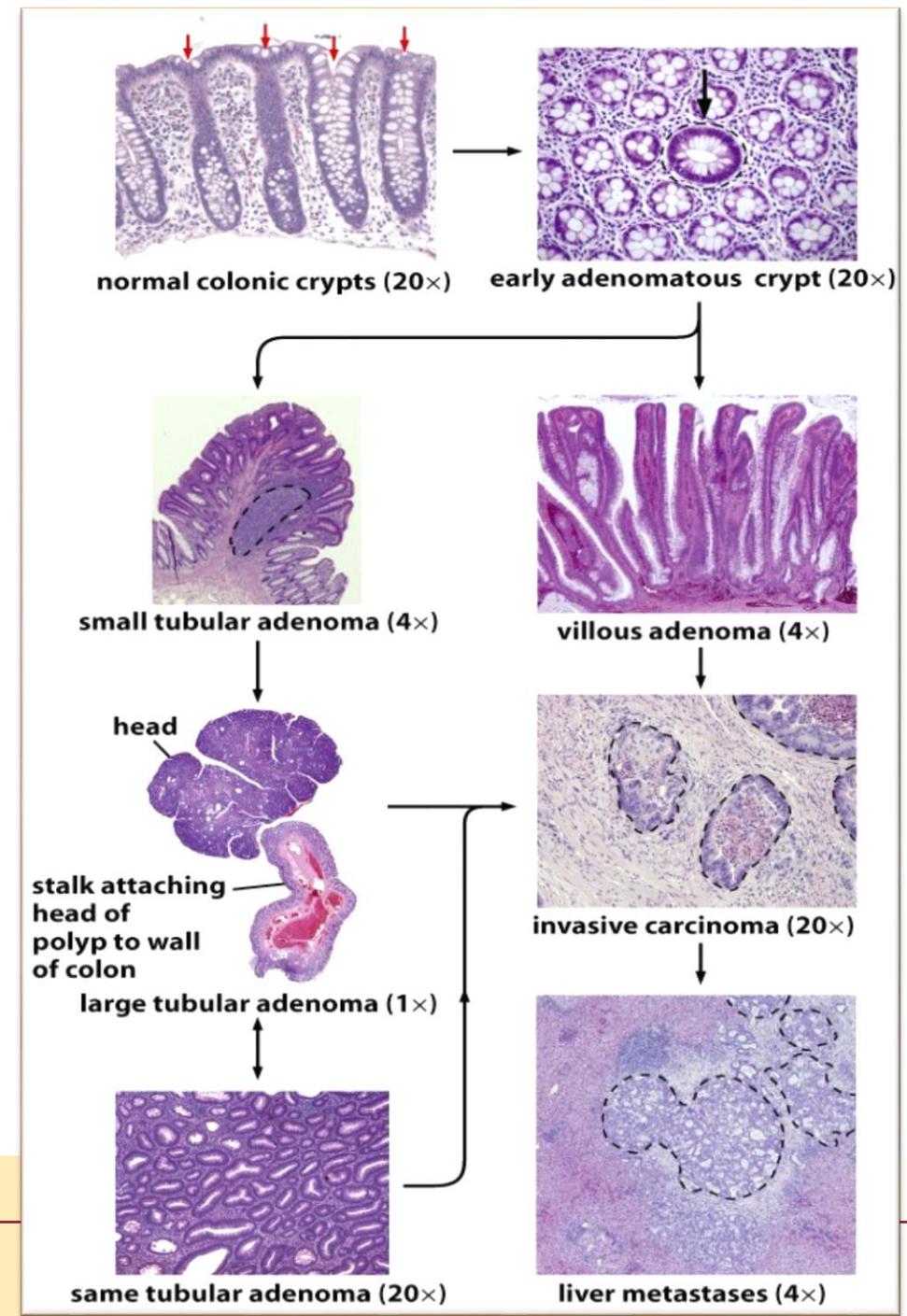


Figure 11.6 *The Biology of Cancer* (© Garland Science 2007)

# Genetic Alterations Cause These Multiple Steps

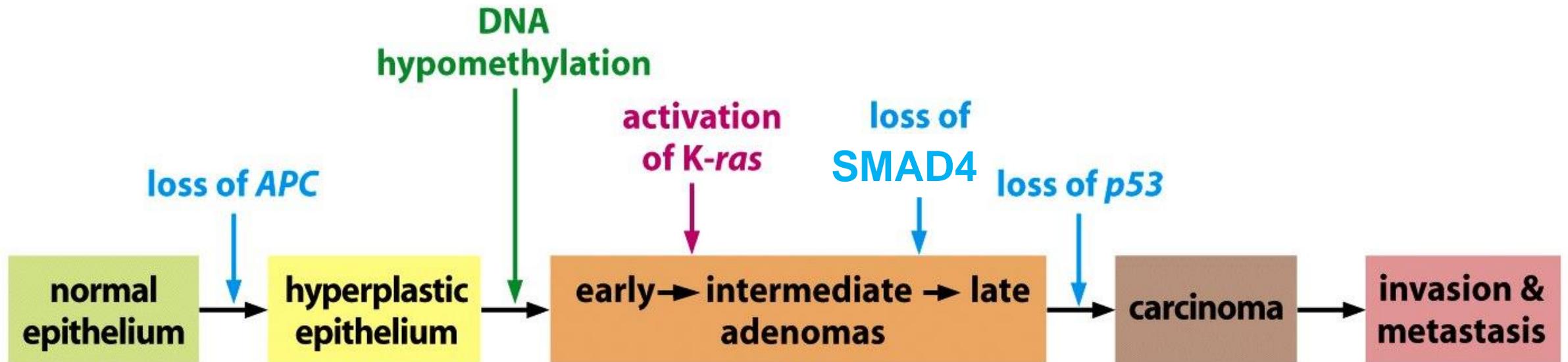
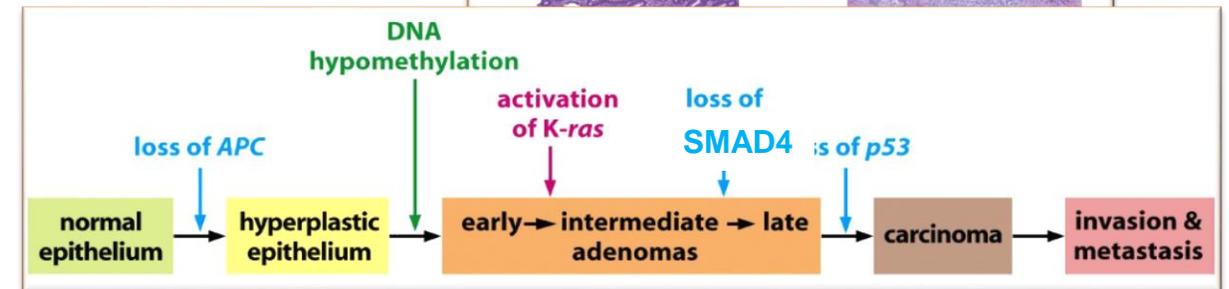
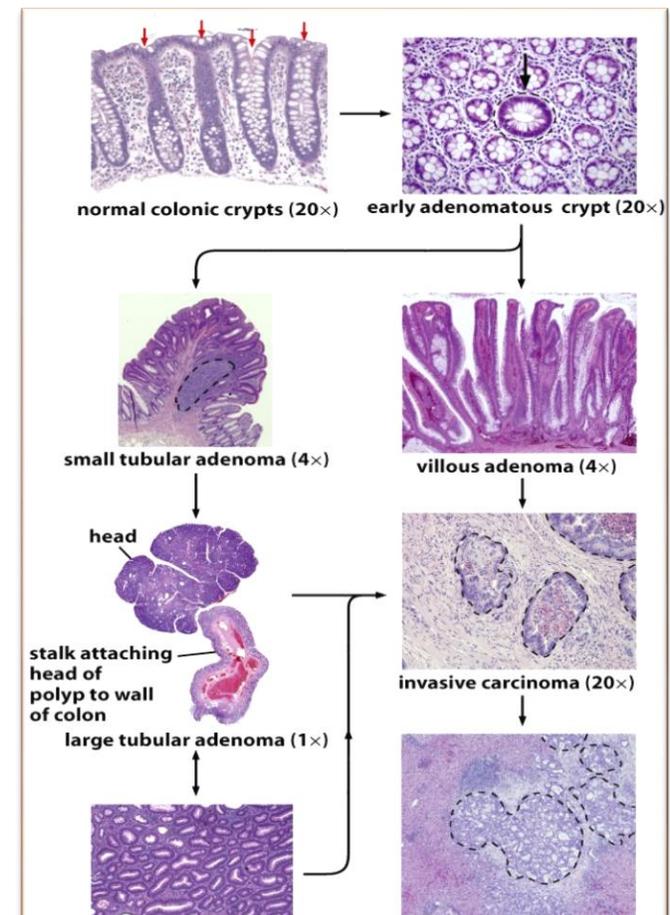


Figure 11.9 *The Biology of Cancer* (© Garland Science 2007)

# Why is this Important to Know?

- We can detect cancer at early stages!
- We can intervene in the process!
  - Remove it
  - Prevent progression
- Knowing the specific mutations that are present informs therapy



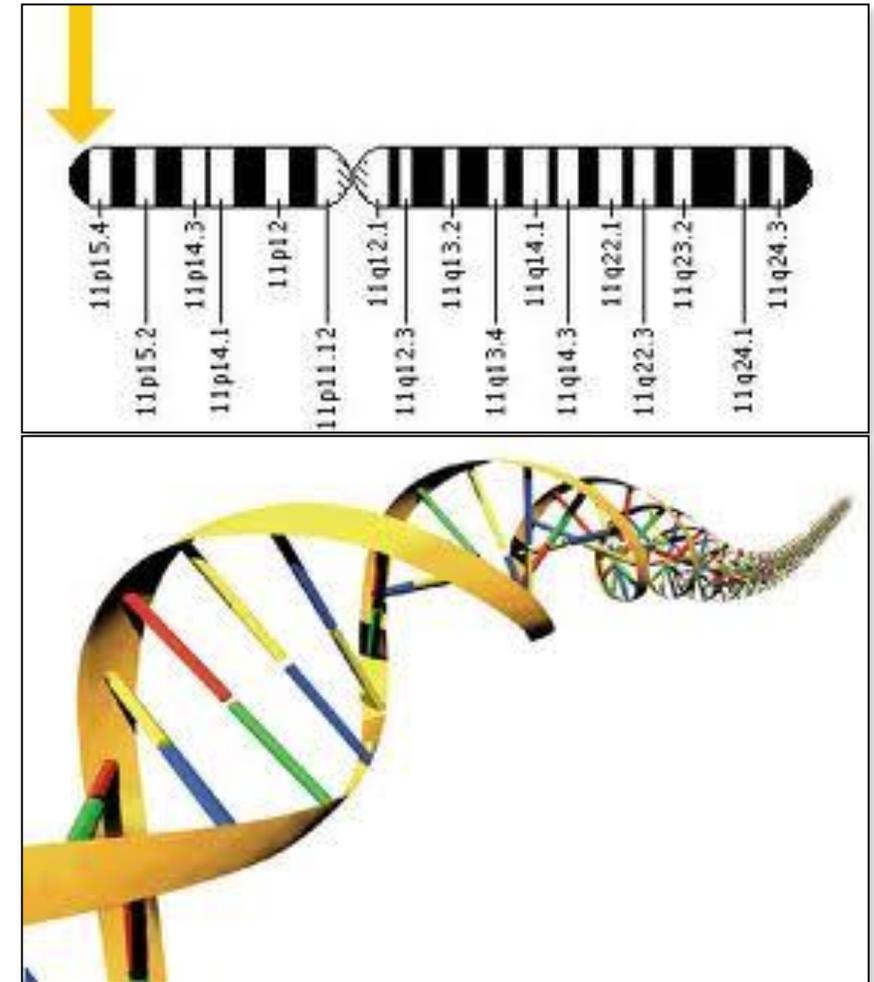
# Remember All Mutations Are Not Created Equal

- Many mutations discovered in cancer cells are **neutral passengers** that merely accompany **functionally important drivers** that have been subject to selective pressure.
- These mixtures of passenger and driver mutations together comprise the mutated gene sets of the tumors in question.



# Basic Research Has Revealed Many of These Cancer Drivers

- In 1970's we didn't know that cancer was caused by mutated genes
- The first cancer gene discovered in 1982 – *HRAS*
- The first hereditary cancer gene identified in 1986 – *RBI*
- Now hundreds of cancer genes known
- The first cancer genome sequenced completely in 2008



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**KEYTRUDA will not work for everyone. Results may vary.**

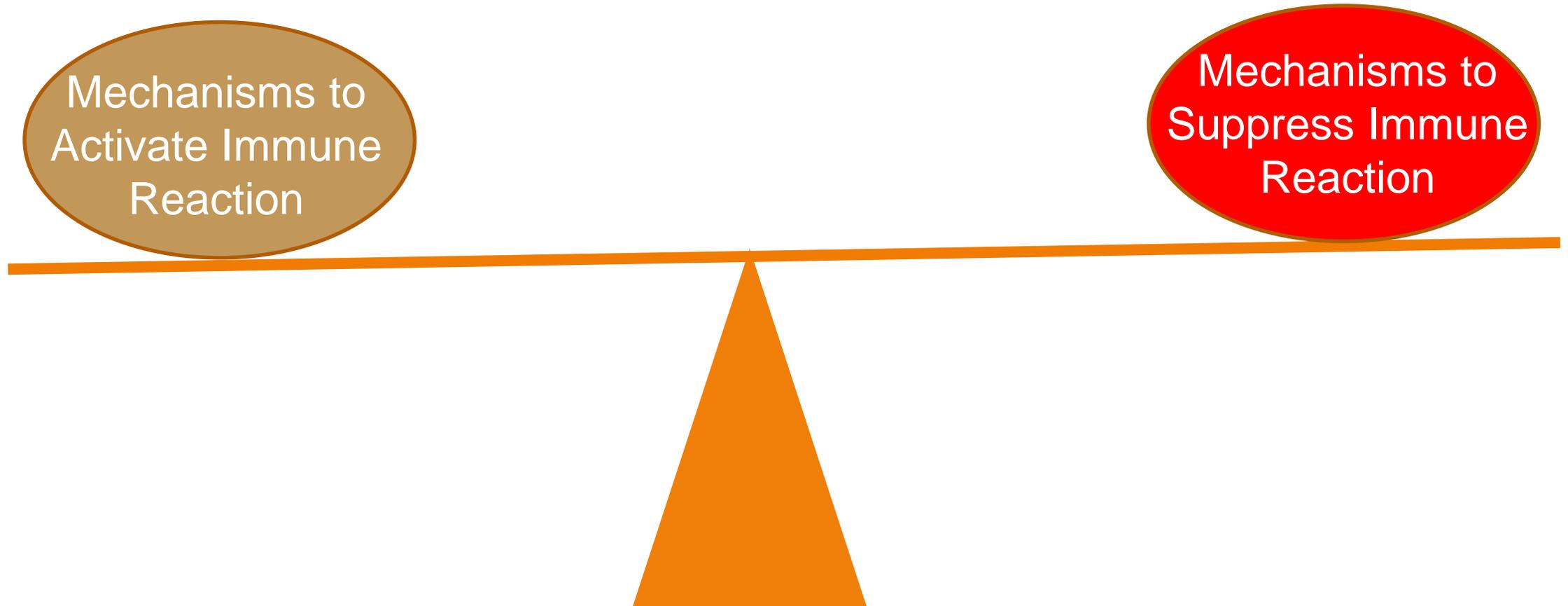


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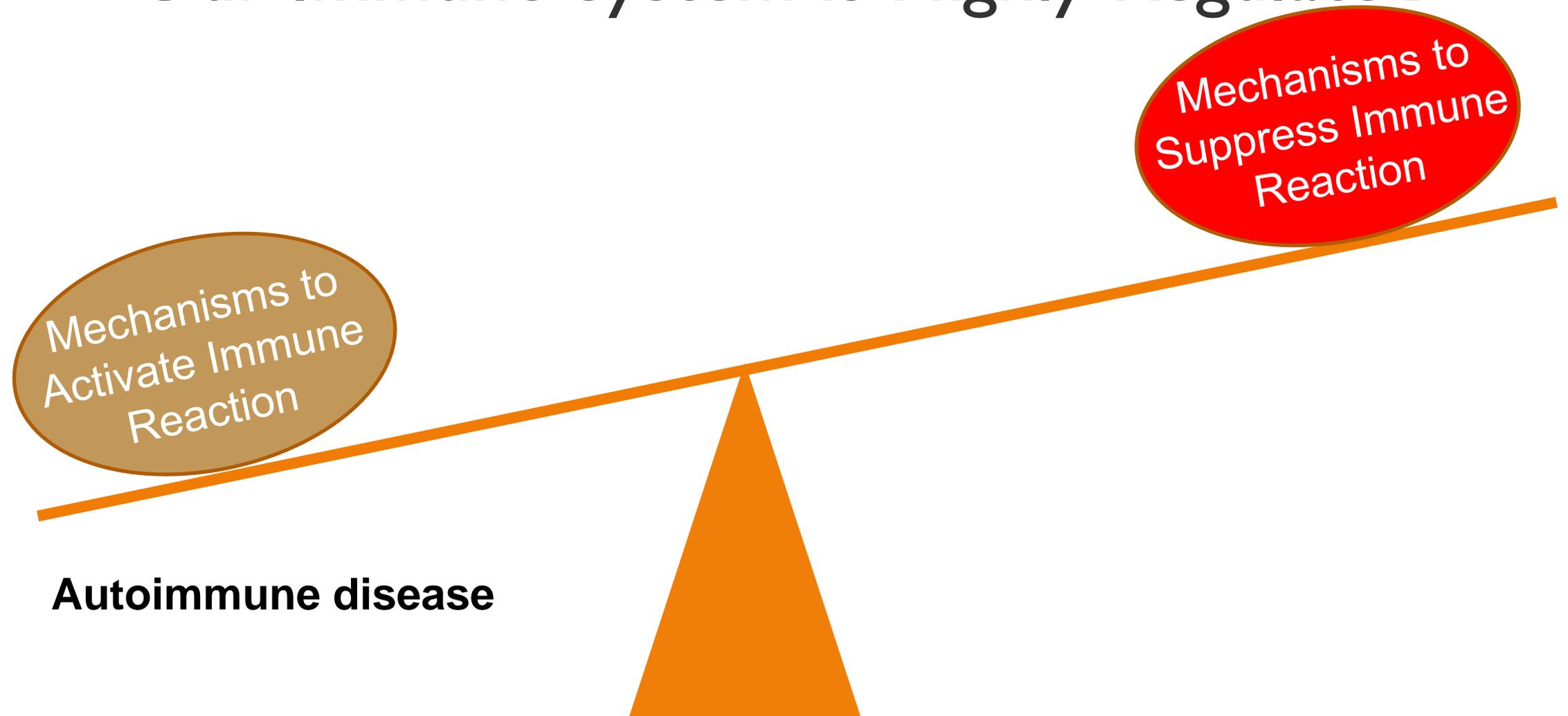
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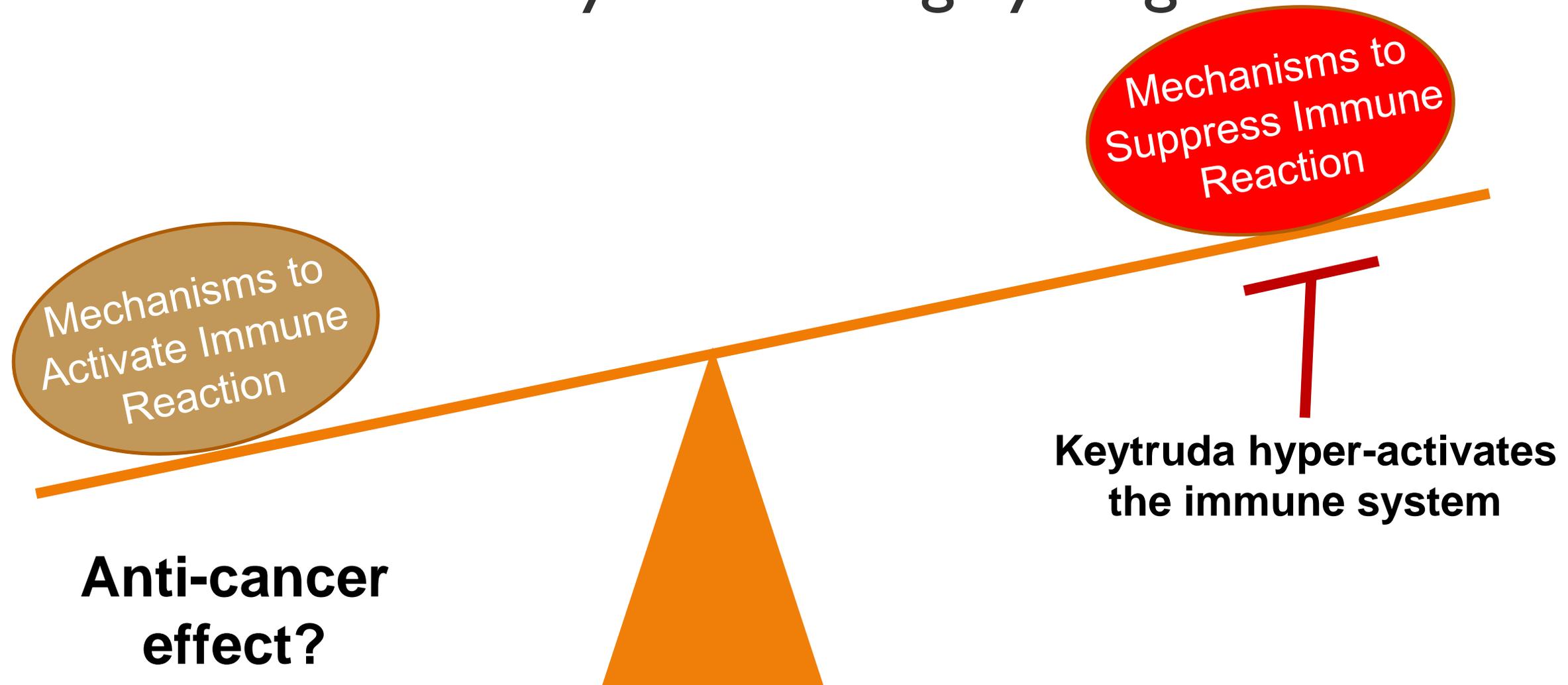
# Our Immune System is Highly Regulated



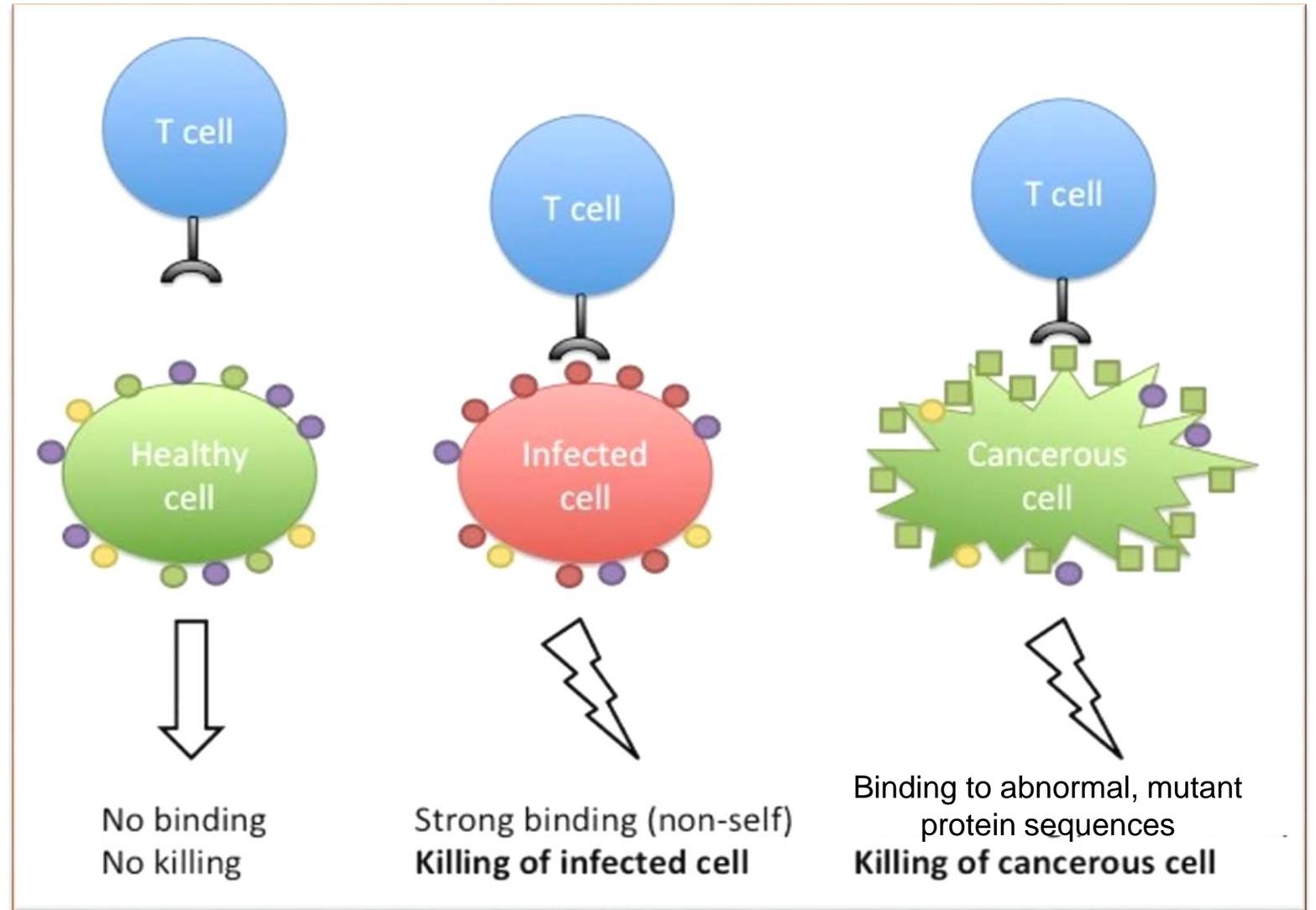
# Our Immune System is Highly Regulated



# Our Immune System is Highly Regulated



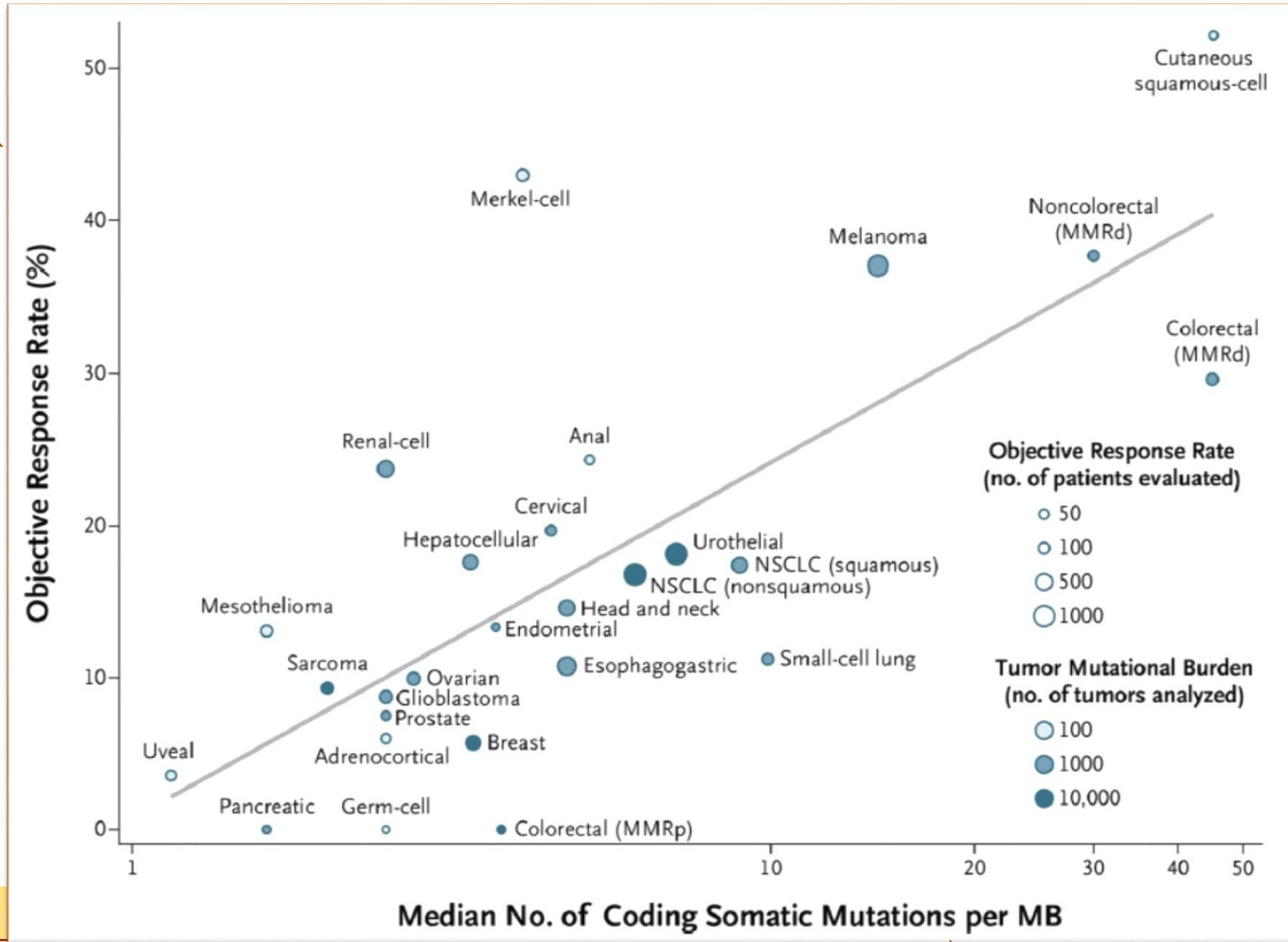
# If Tumors Express Many Non-normal Proteins, Due to Mutations, They May Respond to this Kind of Immunotherapy



The Conversation , May 26, 2015

# The More Mutations Present the Better the Chance to Respond to Immunotherapies like Keytruda

Chance the therapy worked



Aurora et al., Adv. Ther., 2019

Number of abnormal proteins

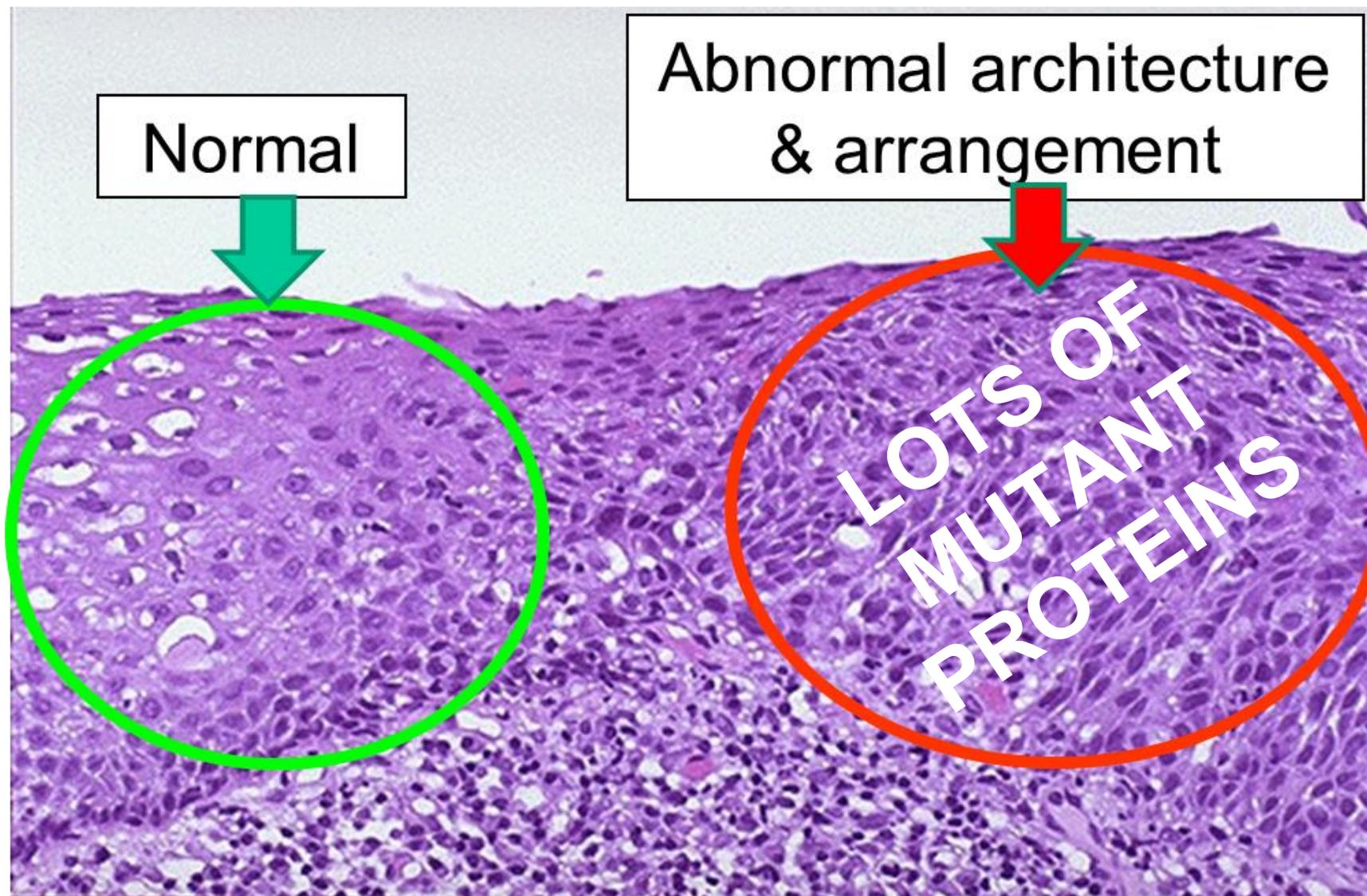


Image source: <http://library.med.utah.edu/WebPath/FEMHTML/FEM008.html>

# Learning Objectives

- All cancer has a genetic cause – but that doesn't (usually) mean the genes you're born with cause cancer, instead cancer is primarily caused by mutations occurring in rare cells in your body.
- For most people, their cancer risk is more determined by lifestyle choices than who their parents are. But some families do pass along high risk cancer-causing gene mutations from parent to child.
- Cancer cells typically have many, many gene mutations and about 6 or more of these “drive” the abnormal behavior of the cancer cells, while the rest are merely “passengers”.
- It is thought that the genes mutated in a cancer can produce abnormal proteins allowing the immune system to kill off the cancer cells. This is how “immunotherapies” like Keytruda can work for some cases of cancer.
- The specific genes that are mutated in a tumor or leukemia may determine the prognosis of the patient and dictate the best therapy for the physician to choose.

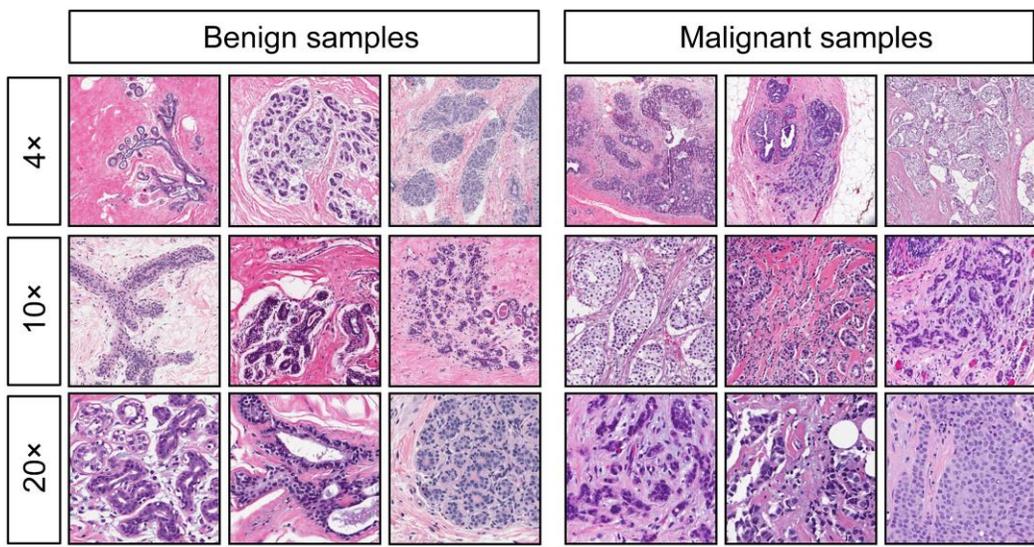


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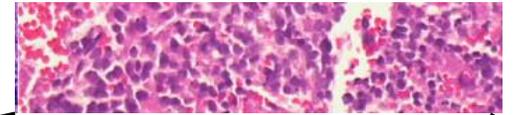


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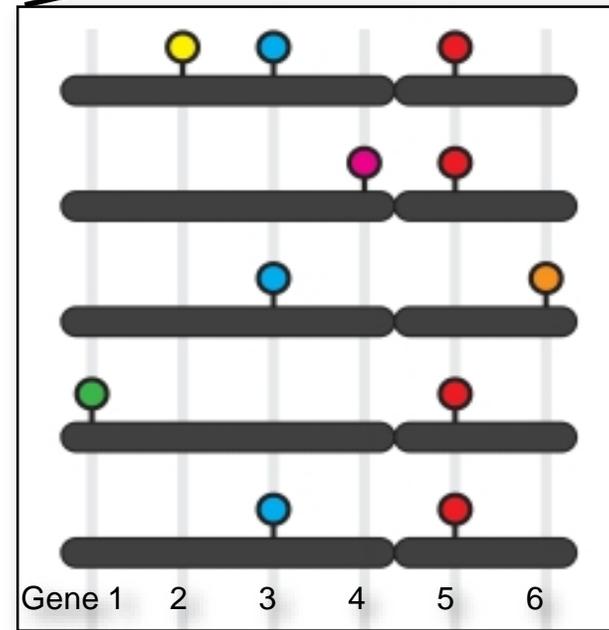


# A picture is worth a thousand words...true

# But...you can't judge a book by it's cover either



Case 1



Case 2

Case 3

Case 4

Case 5



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# Altered Genes = Altered Proteins

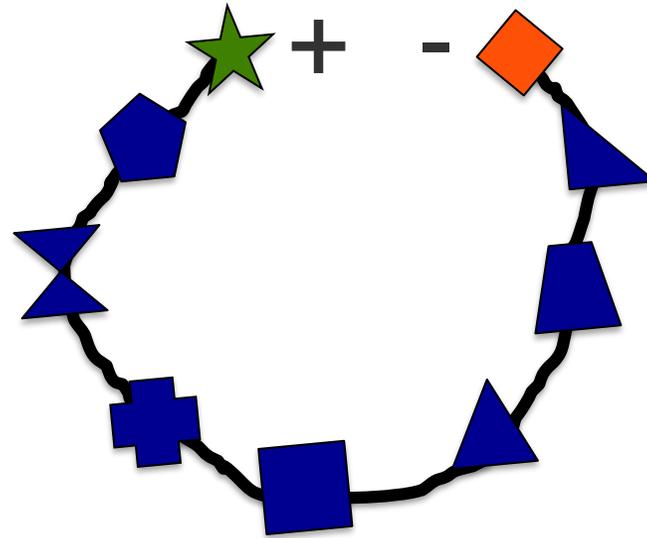
- Despite cancers being genetic diseases, aberrant and dysregulated genes **indirectly** cause pathology.
  - *That is, genes underlie the pathology but are not themselves the causative agents.*
- Altered gene products –**altered proteins** - are the direct causes of pathology.



# Form = Function

...AAA GGG ACT GCC TGG CAT TGC GTT **GAC**...

...Lys Gly Thr Ala Trp His Cys Val **Asp**...



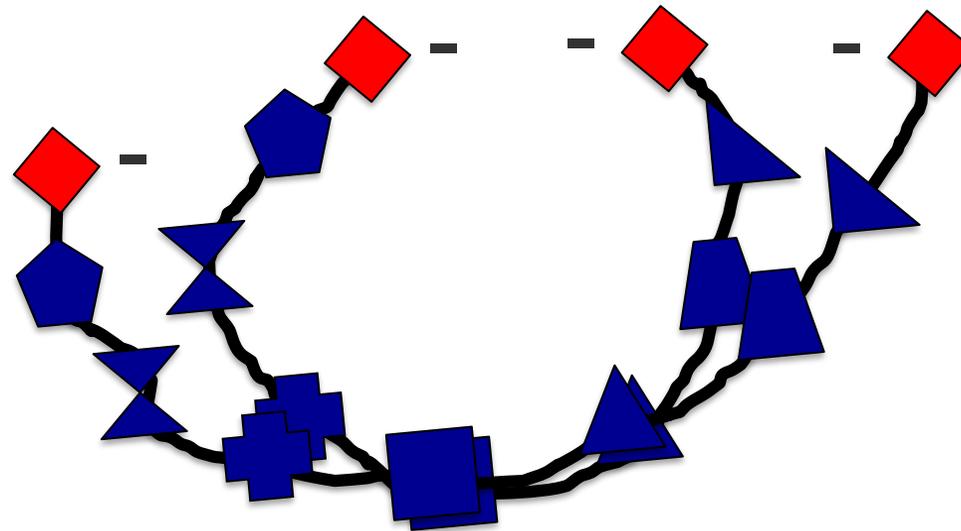
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# Mutations Disrupt Form/Function

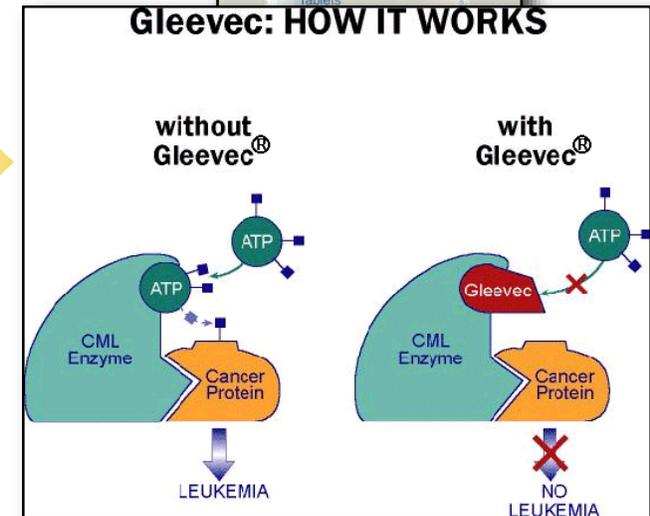
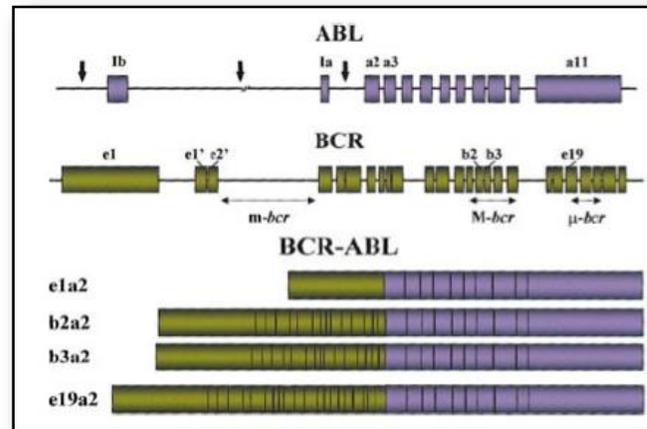
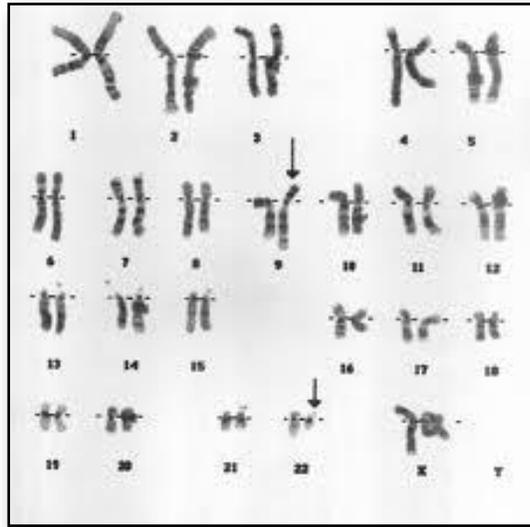
...**GAA** GGG ACT GCC TGG CAT TGC GTT **GAC**...

...**Asp** Gly Thr Ala Trp His Cys Val **Asp**...



# Identifying cancer drivers has had profound implications for therapy

## *Chronic myelogenous leukemia*



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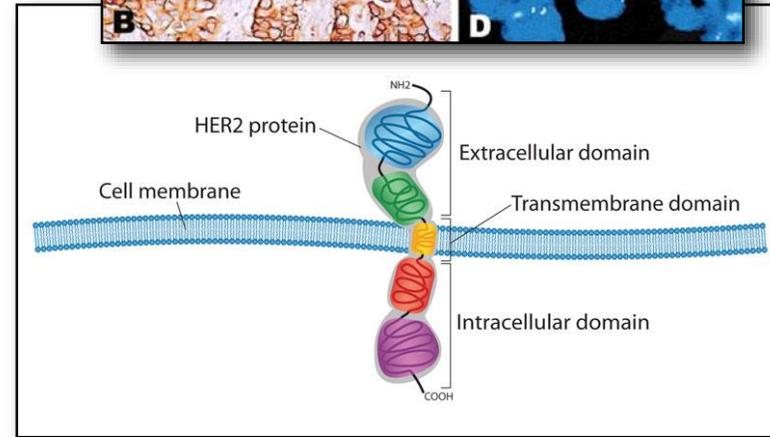
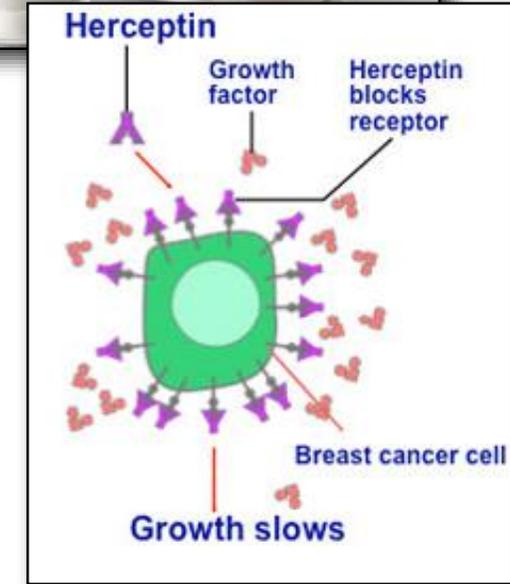
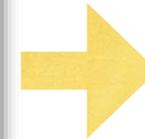
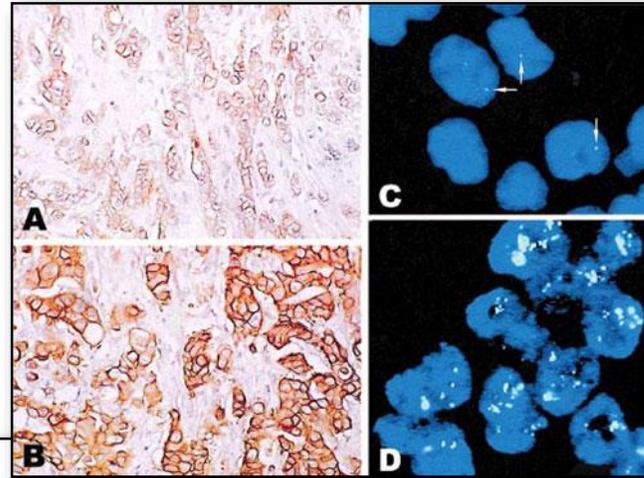
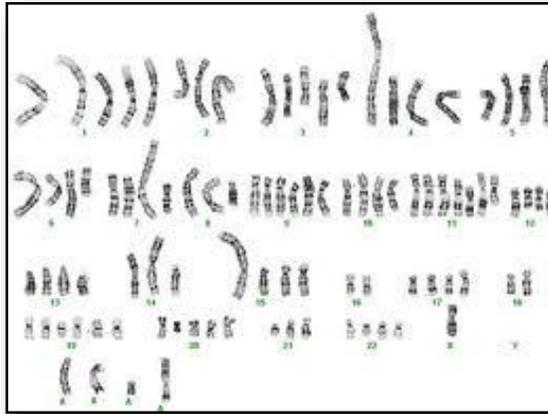
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# Identifying cancer drivers has had profound implications for therapy

## Breast cancer



# Cancer Driver Gene Identification is an FDA Approved Concept for Precision Medicine

## FoundationOne CDx™, the First FDA-Approved Comprehensive Genomic Profiling Assay for All Solid Tumors Incorporating Multiple Companion Diagnostics

-- FoundationOne CDx is the First Next Generation Sequencing Test for All Solid Tumors to Complete the FDA/CMS Parallel Review Process and Launch with National Medicare Coverage --

CAMBRIDGE, Mass.--(BUSINESS WIRE)-- **Foundation Medicine, Inc.** (NASDAQ:FMI) today announced that FoundationOne CDx™, the first U.S. Food and Drug Administration (FDA) approved comprehensive genomic profiling (CGP) assay for all solid tumors incorporating multiple companion diagnostics, is now available in the United States. FoundationOne CDx is a first-of-its-kind test for individuals with advanced cancer that is offered as a nationally covered benefit across all solid tumors for Medicare and Medicare Advantage beneficiaries who meet eligibility requirements.

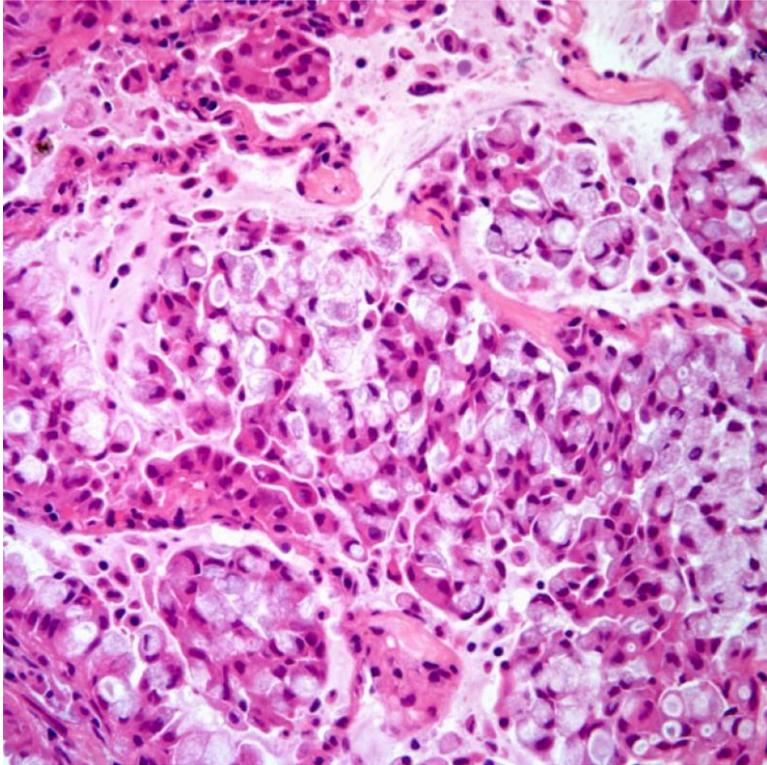
"Now that FoundationOne CDx is widely available in the U.S., oncologists can begin using this valuable test to help guide and simplify personalized treatment decisions for their patients," Vincent Miller, M.D., chief medical officer at Foundation Medicine. "By integrating FoundationOne CDx early into routine clinical care, oncologists can create treatment efficiencies and expand access to biomarker-driven medicines for patients, with the potential to

Validated genomic profiling may establish a path toward improved patient outcomes. Personalized, biomarker-driven therapy with clinical benefit across tumor types and biomarkers,<sup>1</sup> making therapy selection ever more complex. FoundationOne CDx is a single, FDA-approved comprehensive platform for all solid tumors to detect specific genomic alterations and inform treatment decisions, while reducing the time and tissue needed when testing for biomarkers one at a time.

FoundationOne CDx is a single, FDA-approved comprehensive platform for all solid tumors, assesses genomic alterations in 324 genes known to drive cancer growth, providing treatment options. FoundationOne CDx is also FDA-approved as a broad companion diagnostic for patients with melanoma, colorectal cancer, ovarian cancer or breast cancer to identify those patients who may benefit from targeted therapies, 12 of which are approved as first line therapy for their respective indications. FoundationOne CDx also assesses microsatellite instability (MSI) and tumor mutational burden (TMB), that can help inform the use of other therapies and relevant clinical trial information. In all of these ways, FoundationOne CDx is available to inform clinical research and as a CGP platform for biopharma companies seeking to develop companion



# Old Situation for Lung Cancer



**Everyone gets the same therapy**

**Surgery, radiation,  
Chemotherapy  
(anti-folates, platinum drugs, gemcitabine)**



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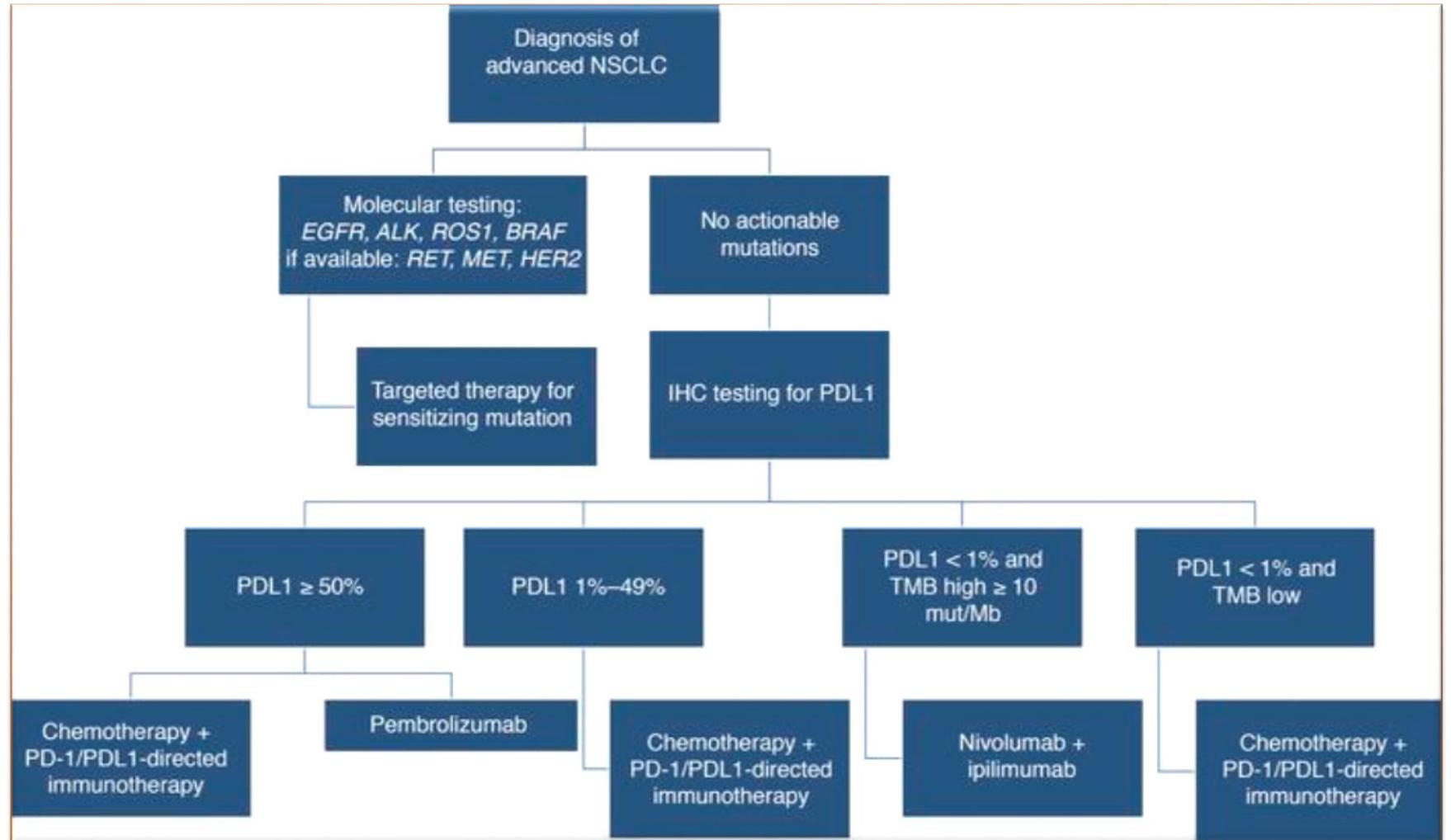


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# Personalized Therapy for Lung Cancer



Pakala and Ramalingam, JCI Insight, 2018



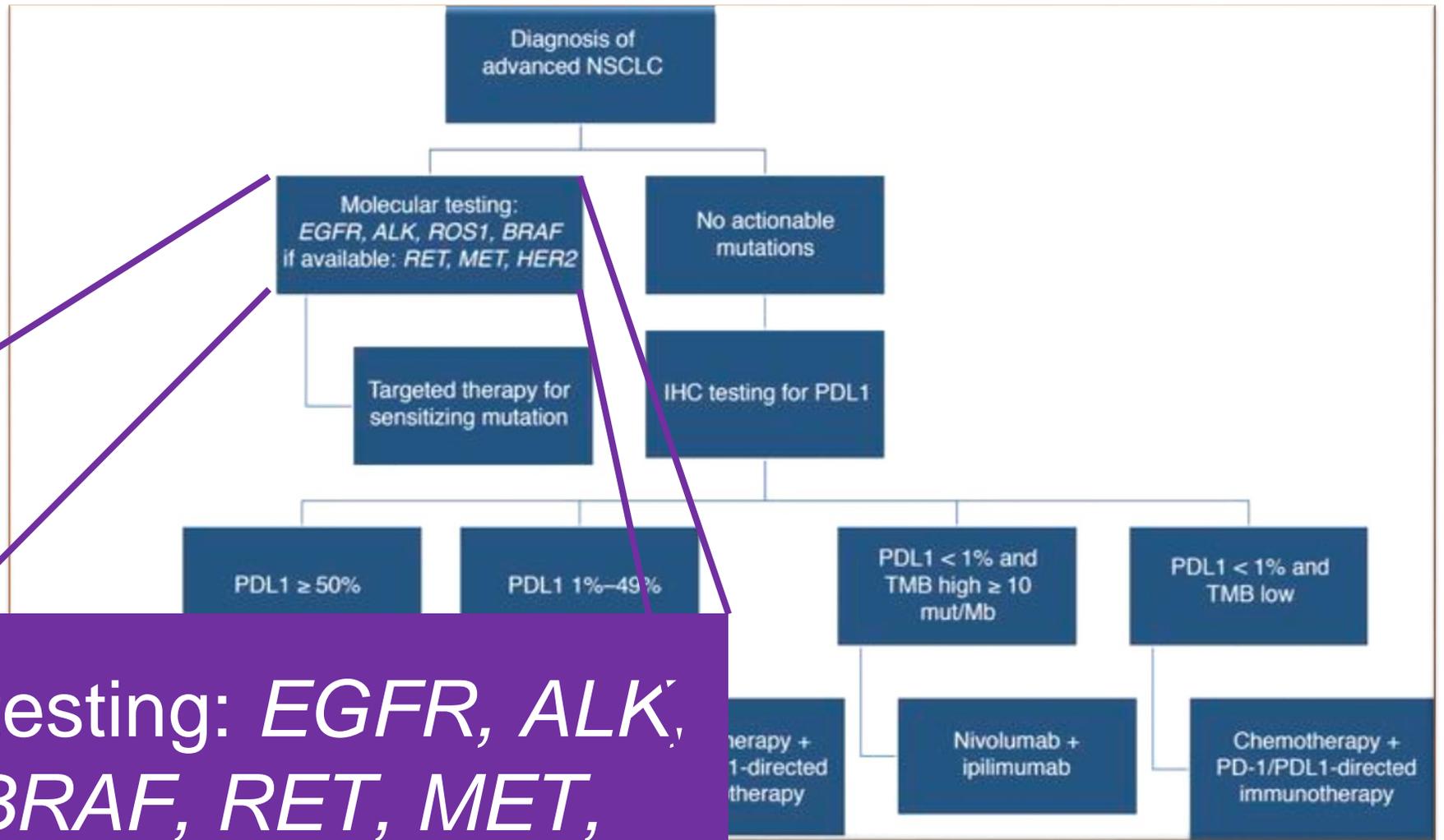
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# Personalized Therapy for Lung Cancer



Molecular testing: *EGFR, ALK, ROS1, BRAF, RET, MET, HER2*



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# Personalized Therapy for Lung Cancer

Molecular testing:

*EGFR*

*ALK*

*ROS1*

*BRAF*

*RET*

*MET*

*HER2*



Specific Drug :

*EGFR*

*ALK*

*ROS1*

*BRAF*

*RET*

*MET*

*HER2*



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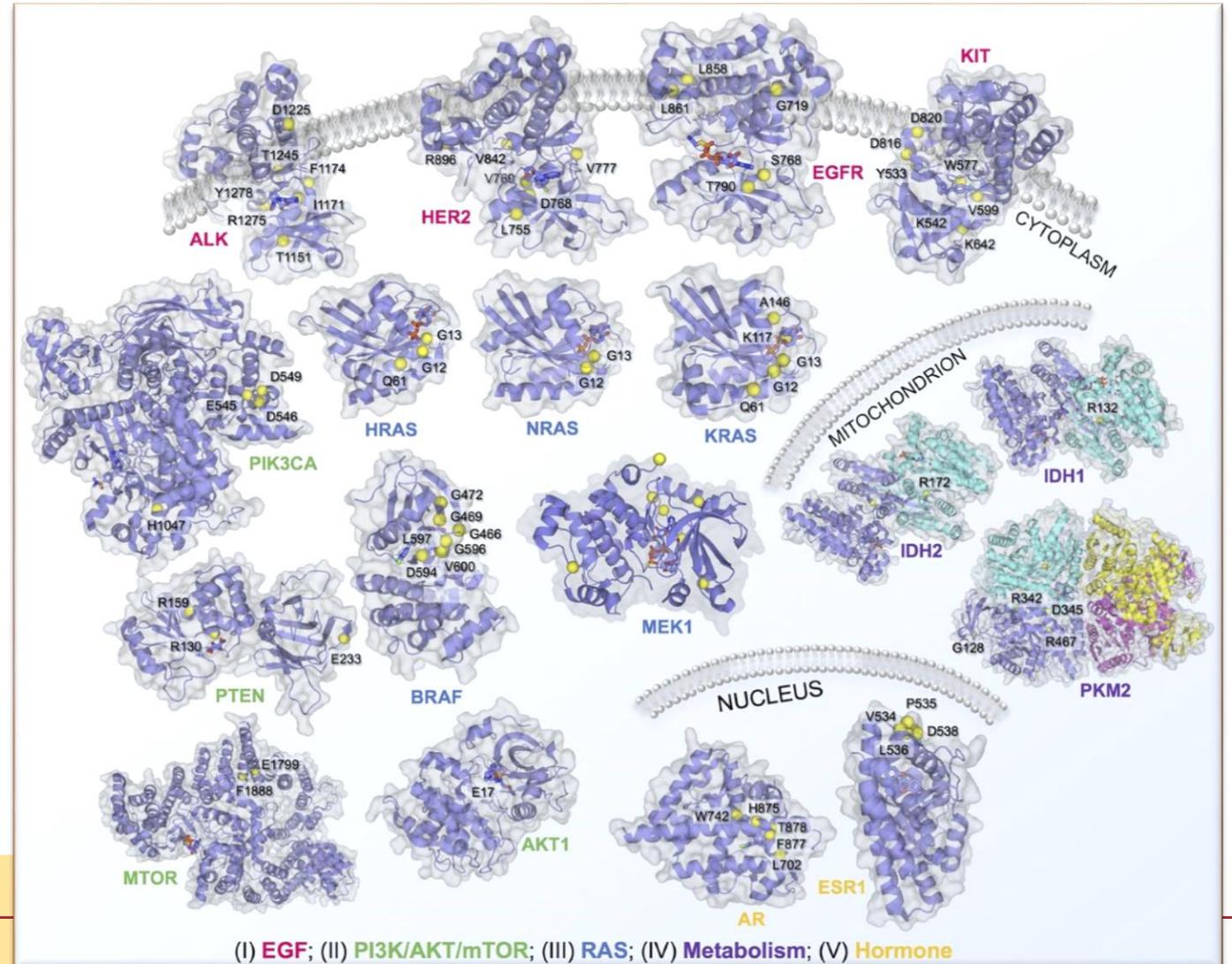
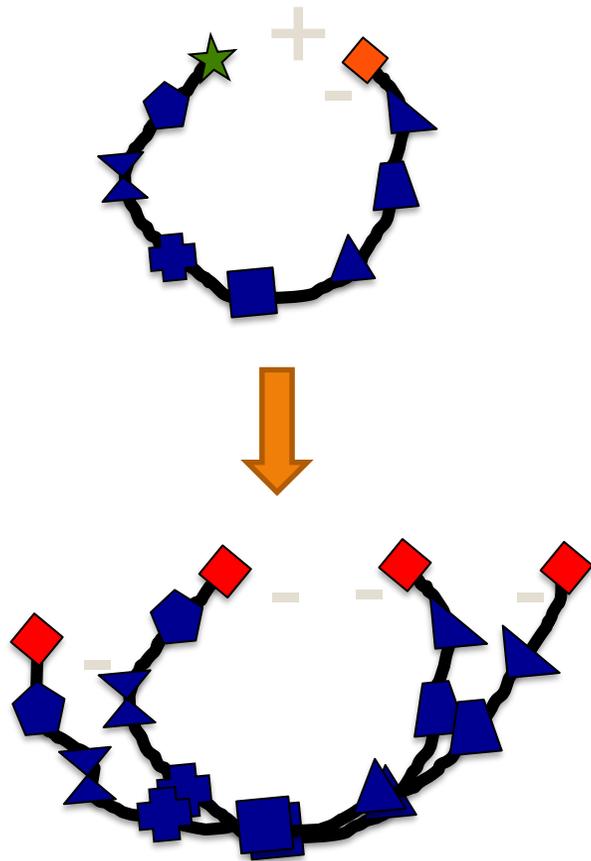


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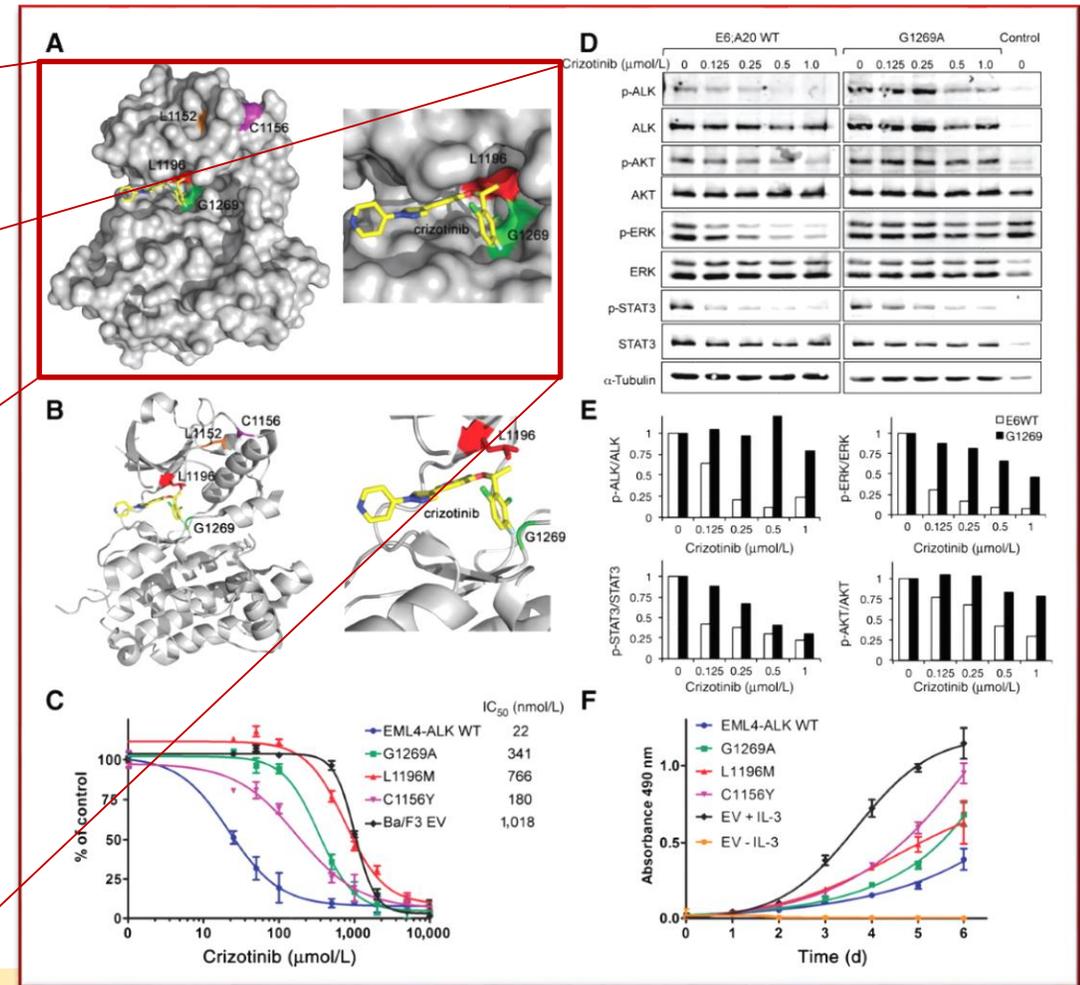
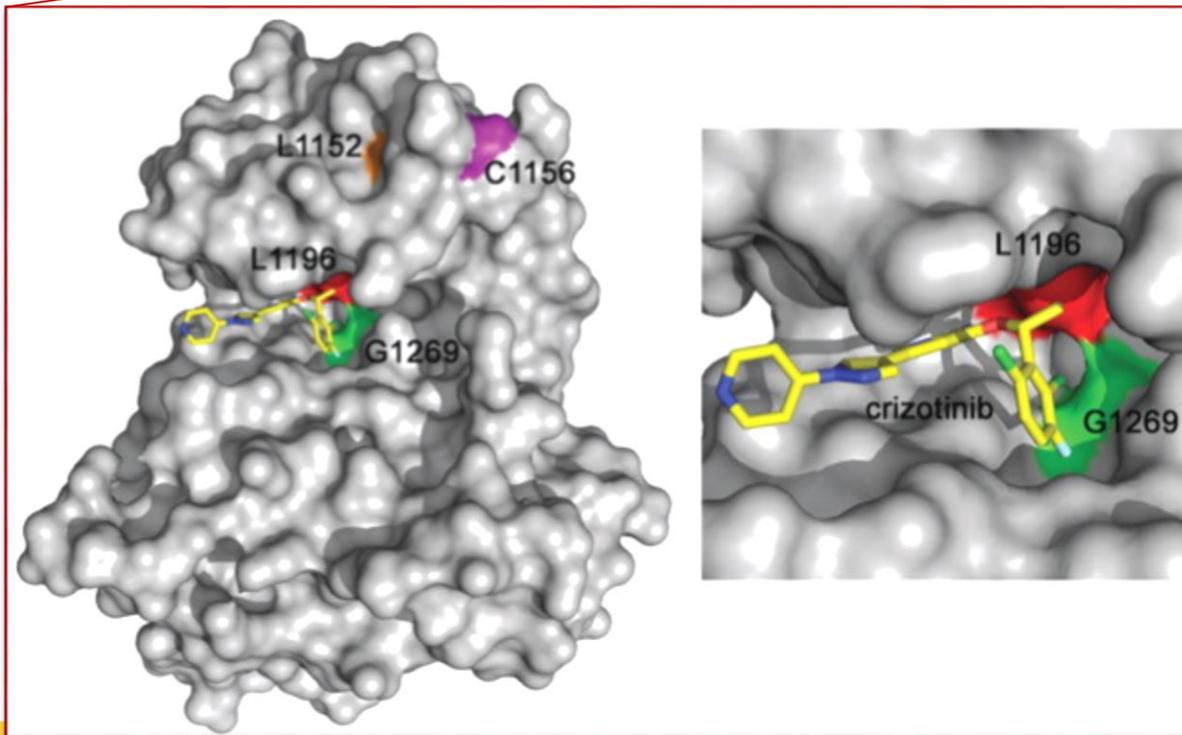
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# Reversing the "Altered Function" of an Oncogene



# Reversing the "Altered Function" of an Oncogene



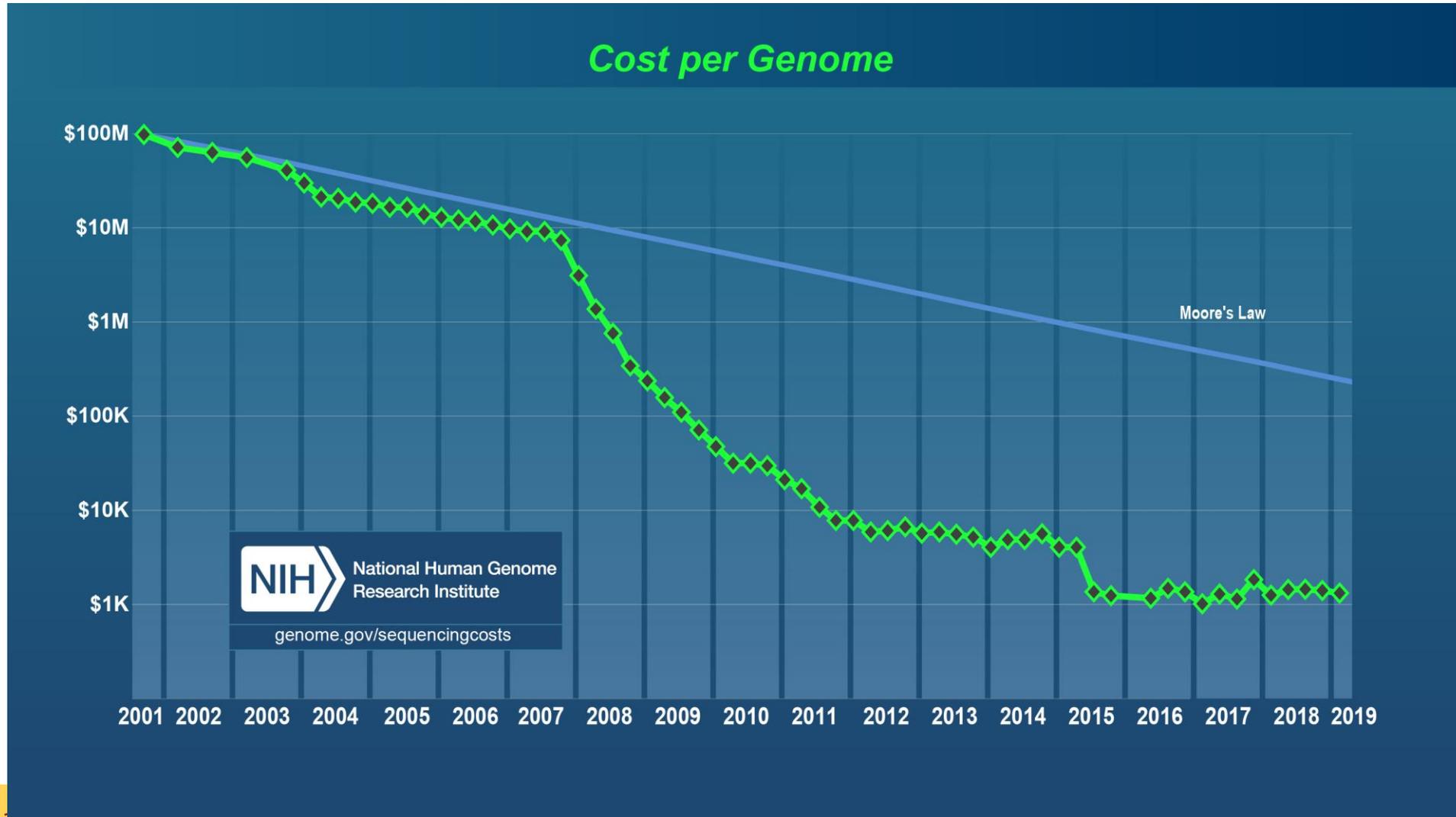
# Reversing the "Altered Function" of an Oncogene

The screenshot shows a webpage from ONS VOICE. The header includes the logo 'ONS VOICE' and navigation links for 'News & Views' and 'Advocacy'. Below the header, there are links for 'HOME' and 'NEWS AND VIEWS'. The main headline is 'FDA Grants Accelerated Approval to Brigatinib for ALK-Positive NSCLC' in orange text, dated 'April 28, 2017'. The article text begins with 'On April 28, 2017, the U.S. Food and Drug Administration (FDA) granted accelerated approval to brigatinib for the treatment of patients with metastatic anaplastic lymphoma kinase (ALK)-positive non-small cell lung cancer (NSCLC) who have progressed on or are intolerant to crizotinib.' To the left of the text are social media share icons for Twitter, Facebook, Pinterest, and LinkedIn. To the right is a graphic with a stethoscope and the text 'FDA UPDATE'. A speaker icon with sound waves is overlaid on the graphic, and a progress bar is visible below it.

- Inhibits activated, mutant ALK
- Used once crizotinib fails



# Cost of DNA Sequencing



# The Future of Cancer Prevention and Care

- We all get sequenced?
- DNA from blood monitored for mutant DNA to detect cancer early
- Our tumors get completely sequenced – every few months during course of disease
- More “matched” therapies
- Immune therapy versus mutant proteins



# Acknowledgements

- The Largaespada lab
  - Bryant Keller
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  - Flavia Popescu
  - Kyle Williams
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  - Minu Bhunia
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  - Alex Larsson
  - Sandi Wagner
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  - Mahathi Patchava

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- Masonic Cancer Center



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Advancing Knowledge, Enhancing Care



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