

Personalized medicine: hype or hope

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CSIC



Disclosure slide

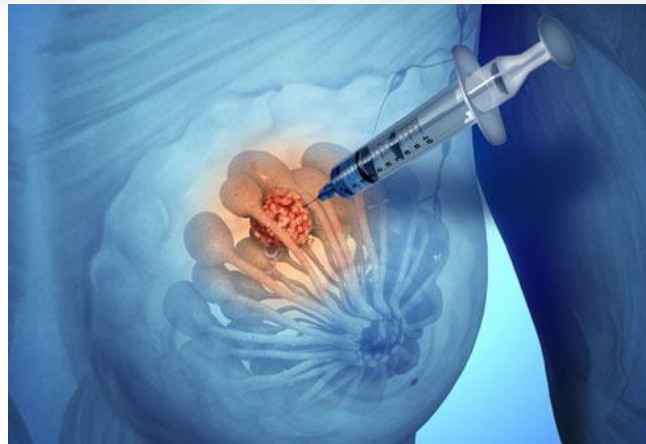
No Conflicts of Interest to declare

Personalised therapies in cancer

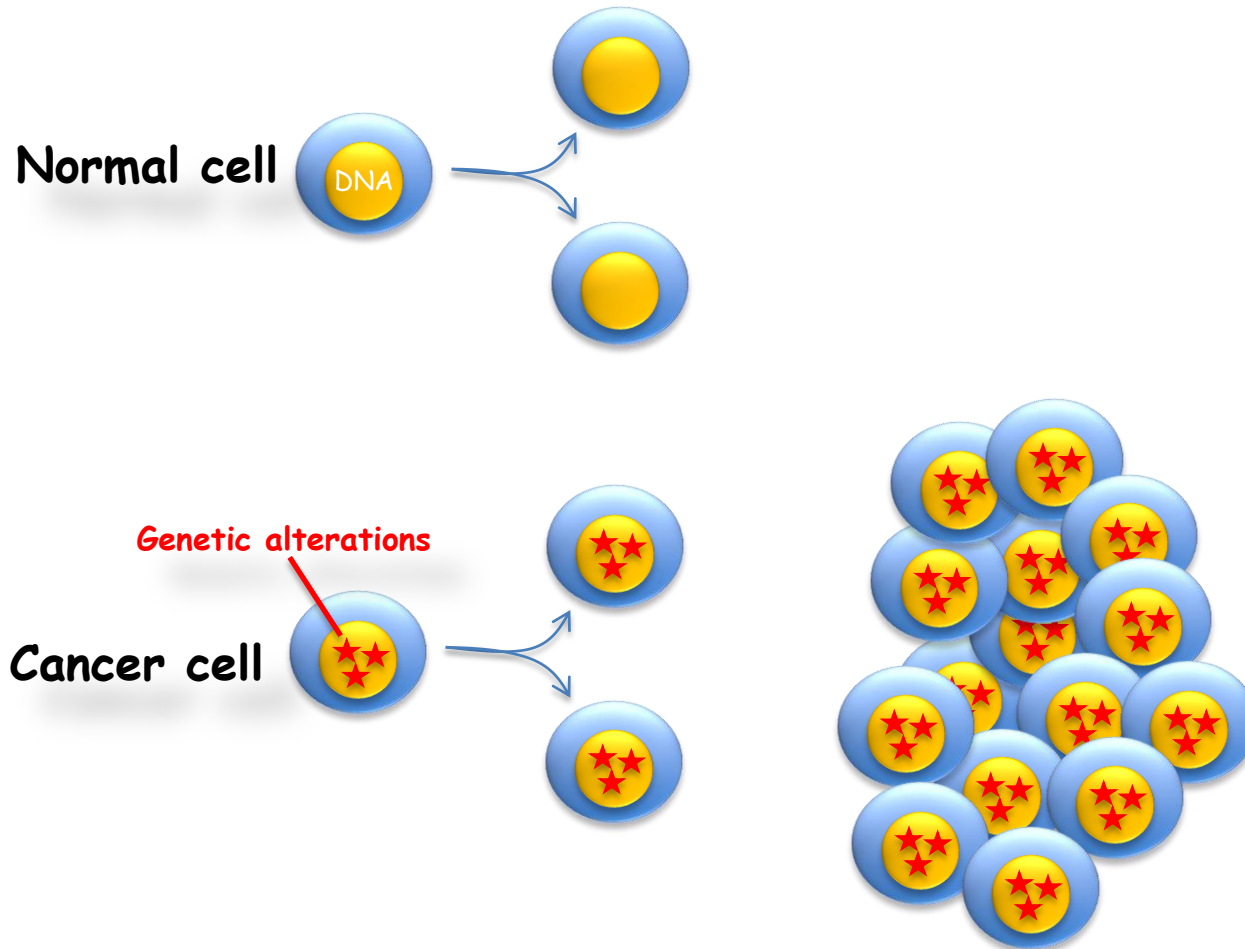
To find out the correct therapy for **each** patient...

(More efficacy, Less toxicity, minimize relapses)

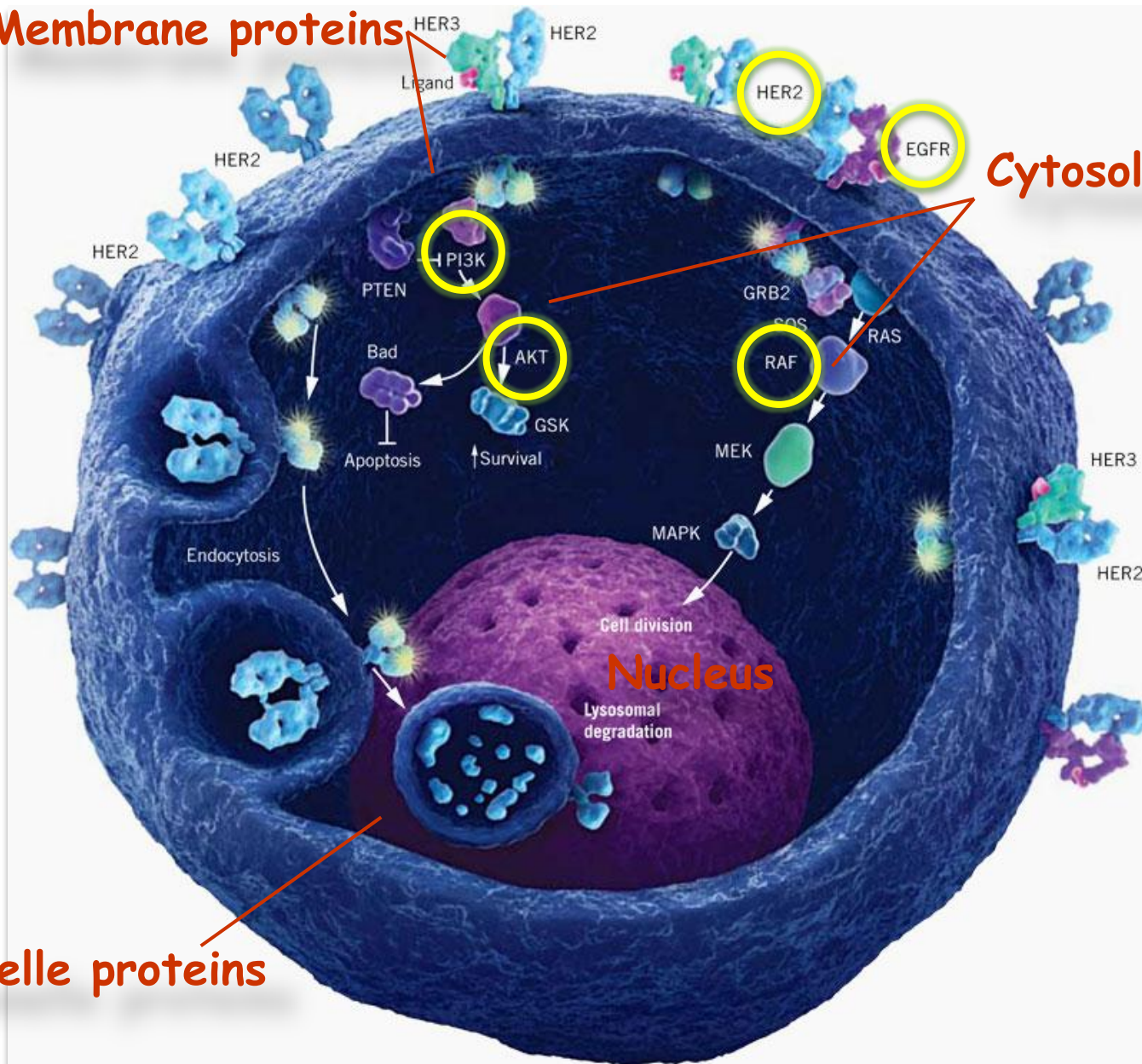
...which requires knowing better the tumors to design effective treatments



Cancer is caused by uncontrolled accumulation of cells, provoked by **genetic alterations**



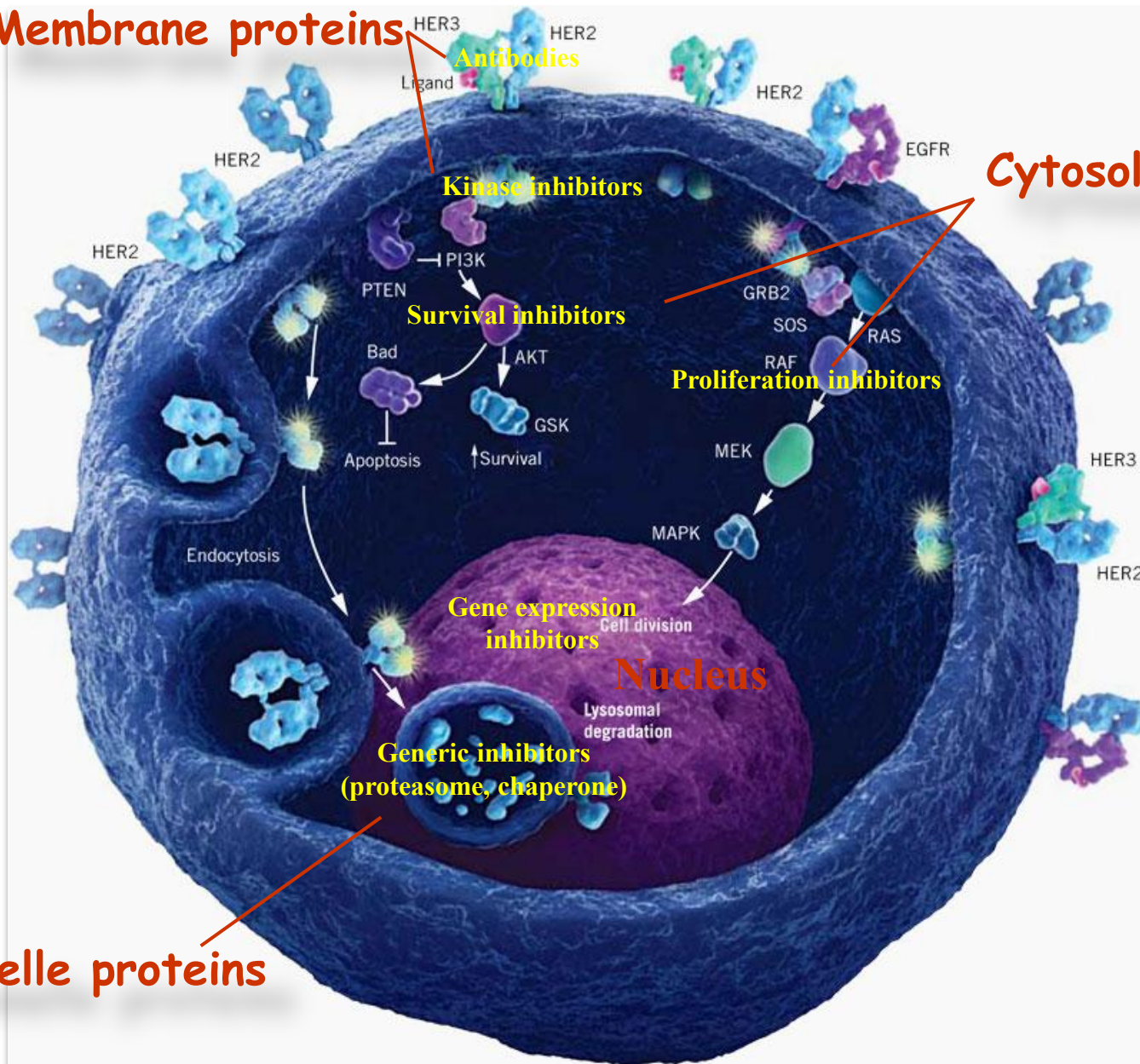
Membrane proteins



Cytosolic proteins

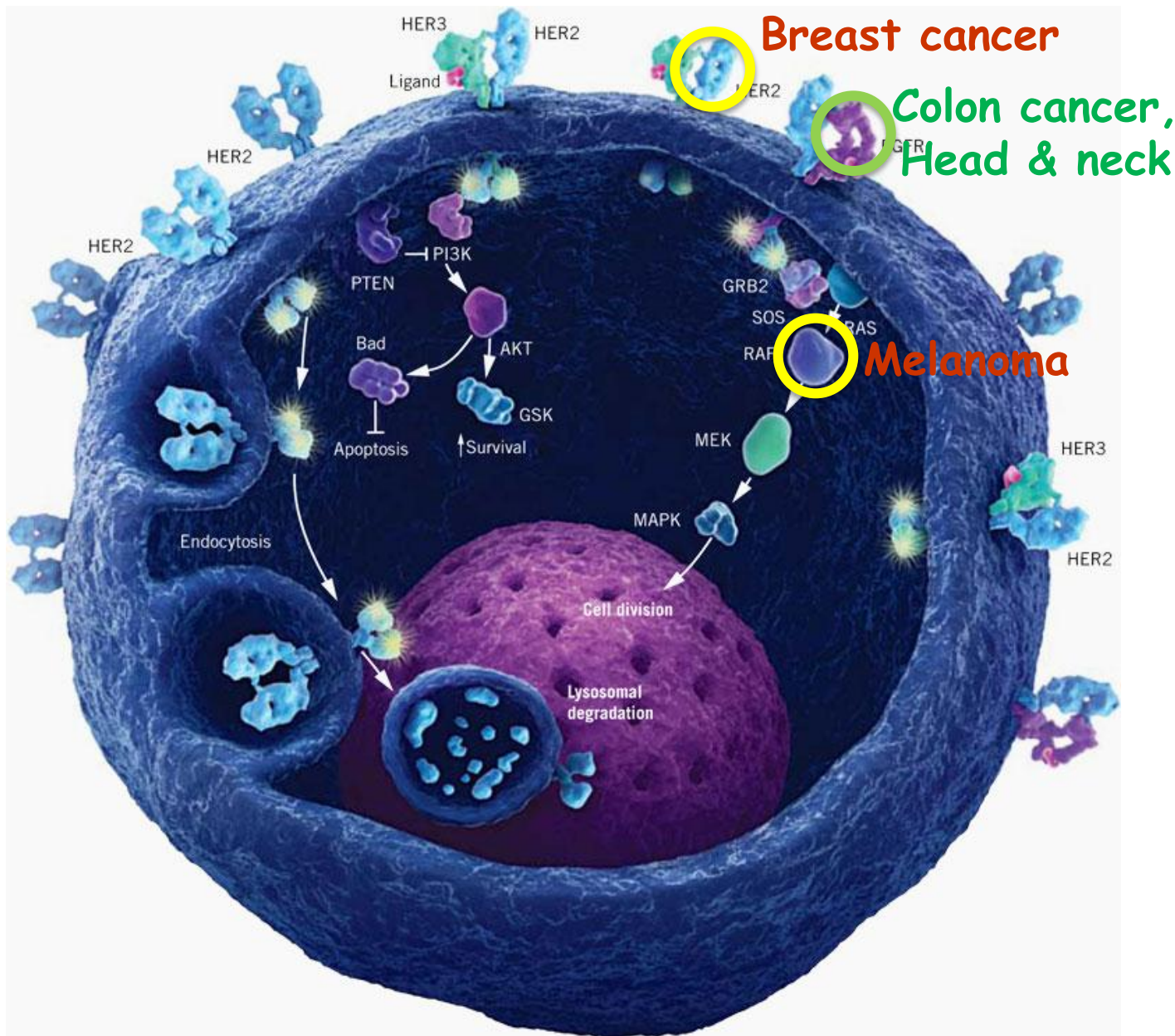
Organelle proteins

Membrane proteins



Cytosolic proteins

Organelle proteins

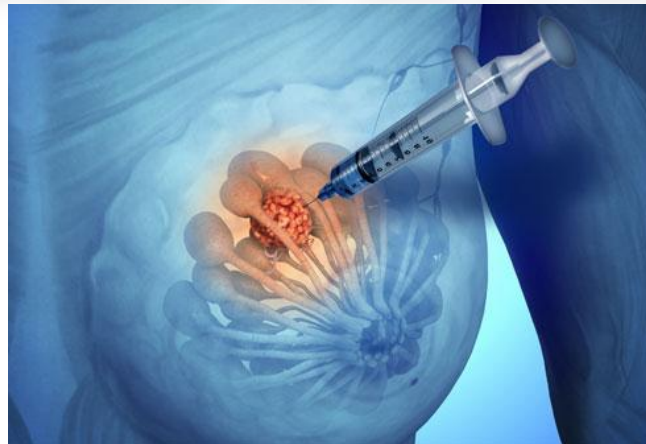


Personalised therapies in cancer

To find out the correct therapy for **each** patient...

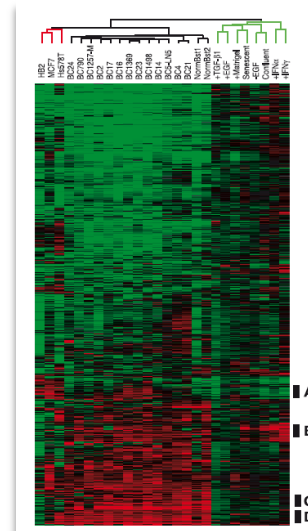
(More efficacy, Less toxicity, minimize relapses)

...which requires knowing better the tumors to design effective treatments



To know better the genetic and proteic characteristics of cancer cells...

...to act on them more efficiently



Genomic and
proteomic
analyses



How many genetic alterations exist?

Are all important?

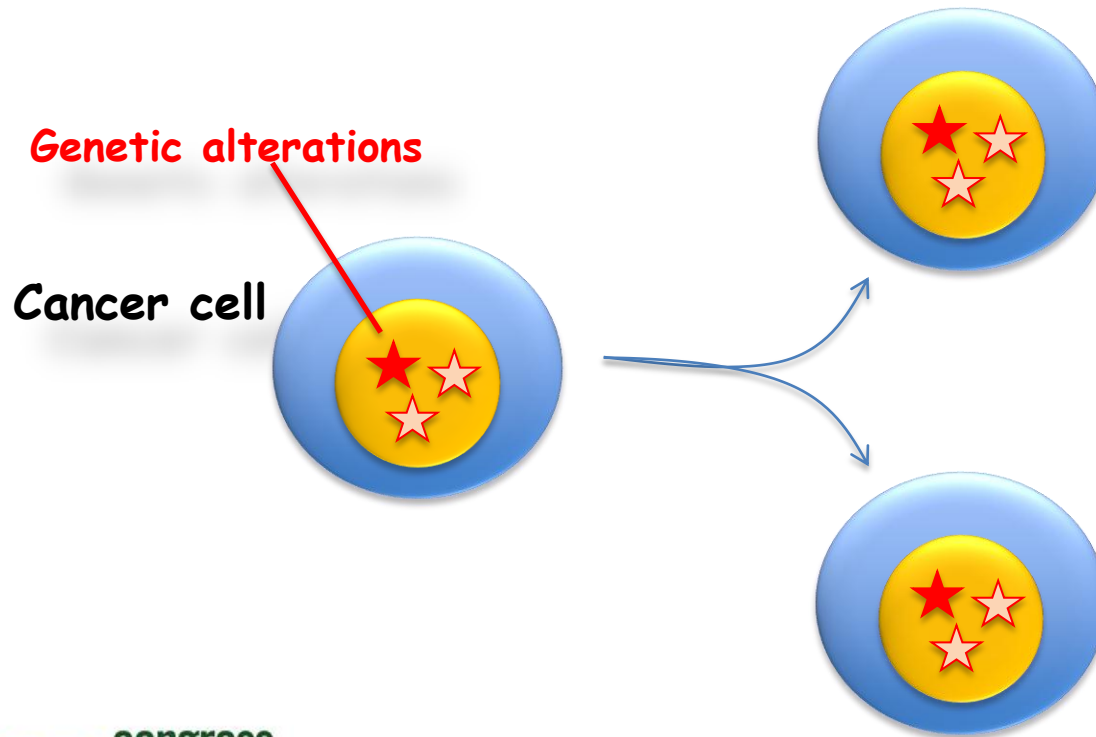
How can we design effective treatments on the bases of these alterations?

Etiopathogenic alterations:

- 1.- A single alteration
- 2.- Multiple alterations

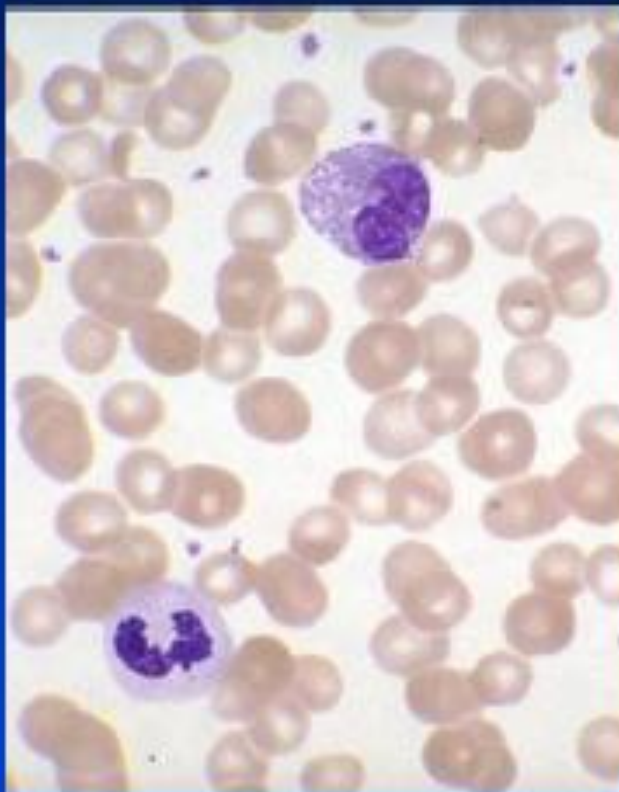
Etiopathogenic alterations:

1.- A single alteration

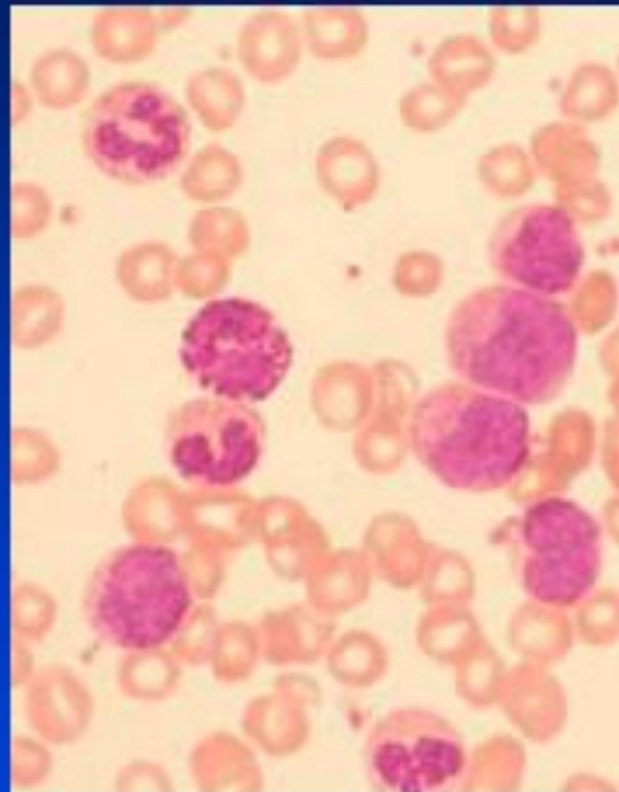


CML: Peripheral Blood Smear

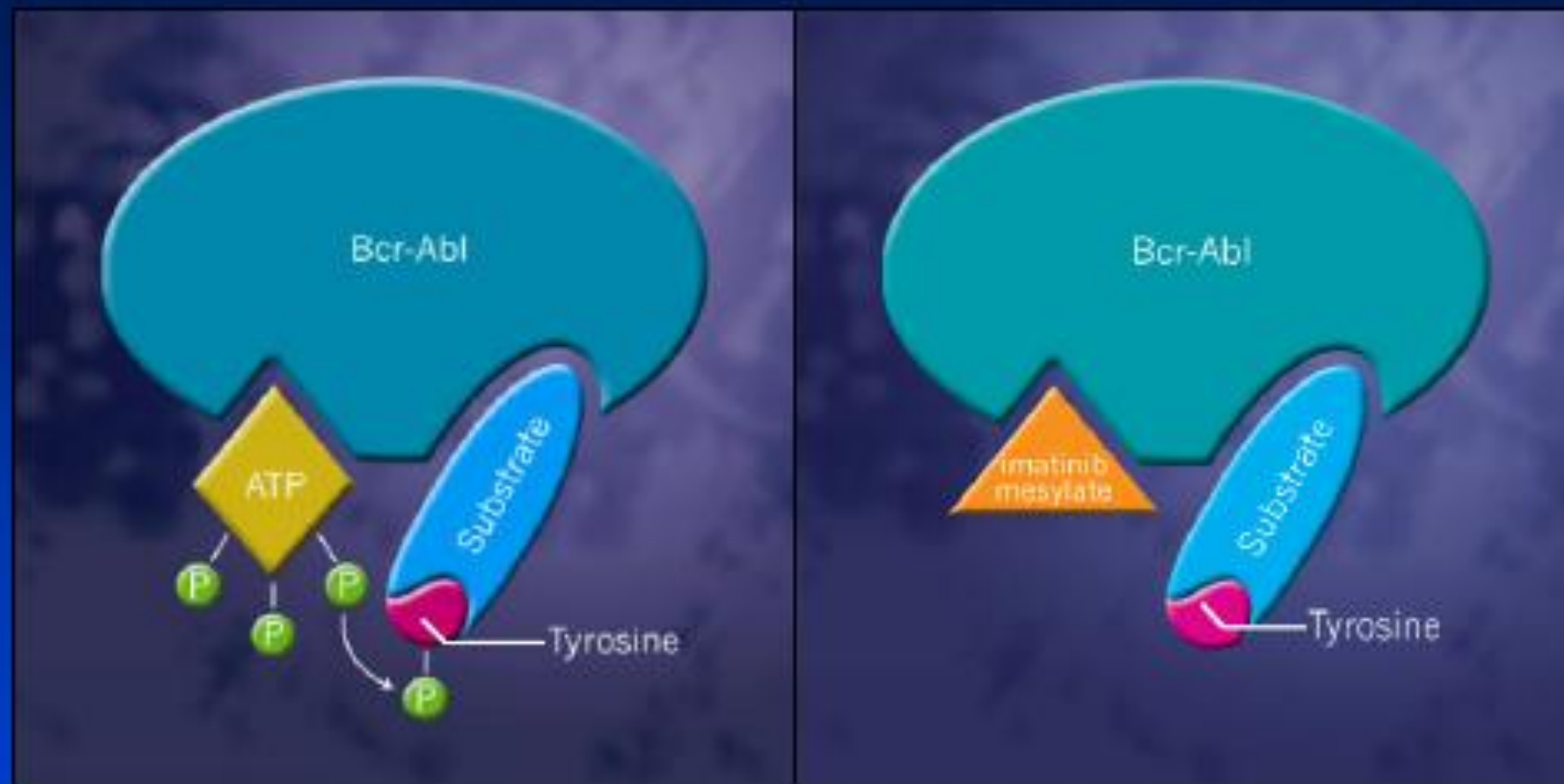
Normal



Chronic phase CML



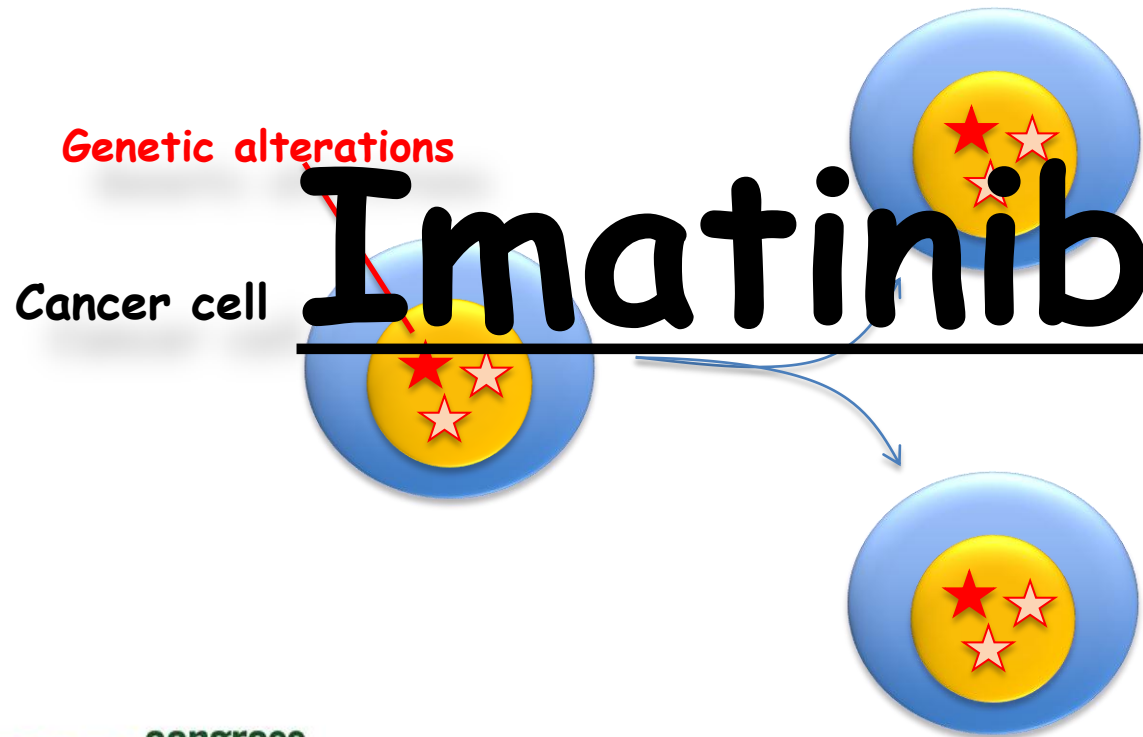
Imatinib Targets the Cause of CML



- Imatinib—a specific inhibitor of a small family of tyrosine kinases, including Bcr-Abl

Etiopathogenic alterations:

1.- A single alteration



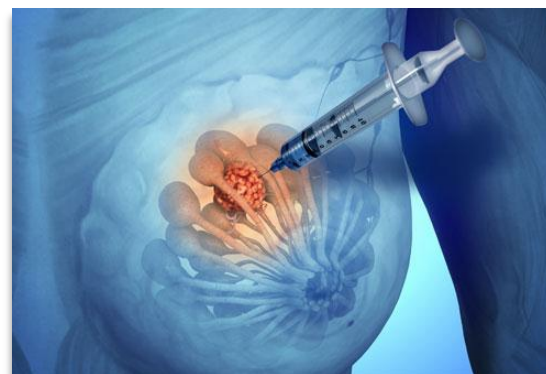
Science 16 November 2007:

The Genomic Landscapes of Human Breast and Colorectal Cancers

Laura D. Wood,¹ D. Williams Parsons,¹ Siân Jones,¹ Jimmy Lin,¹ Tobias Sjöblom,¹ Rebecca J. Leary,¹ Dong Shen,¹ Simina M. Boca,^{1,2} Thomas Barber,¹ Janine Ptak,¹ Natalie Silliman,¹ Steve Szabo,¹ Zoltan Dezso,³ Vadim Ustyansky,³ Tatiana Nikolskaya,^{3,4} Yuri Nikolsky,³ Rachel Karchin,⁵ Paul A. Wilson,⁵ Joshua S. Kaminker,⁶ Zemin Zhang,⁶ Randal Croshaw,⁷ Joseph Willis,⁸ Dawn Dawson,⁸ Michail Shipitsin,⁹ James K. V. Willson,¹⁰ Saraswati Sukumar,¹¹ Kornelia Polyak,⁹ Ben Ho Park,¹¹ Charit L. Pethiyagoda,¹² P. V. Krishna Pant,¹² Dennis G. Ballinger,¹² Andrew B. Sparks,¹² James Hartigan,¹³ Douglas R. Smith,¹³ Erick Suh,¹³ Nickolas Papadopoulos,¹ Phillip Buckhaults,⁷ Sanford D. Markowitz,¹⁴ Giovanni Parmigiani,¹ Kenneth W. Kinzler,¹ Victor E. Velculescu,¹ Bert Vogelstein¹

Massive sequencing of:

- 11 colon cancer tumors
- 11 breast cancer tumors
- *2 cDNAs from normal tissues*



Colorectal Cancers

Co74 123

Co92 90

Co108 82

Mx22 69

Mx27 86

Mx30 57

Mx32 76

Mx38 77

Mx41 99

Mx42 81

Mx43 102

Breast Cancers

B1C 41

B2C 176

B3C 83

B4C 76

B5C 95

B6C 79

B7C 221

B8C 95

B9C 85

B10C 130

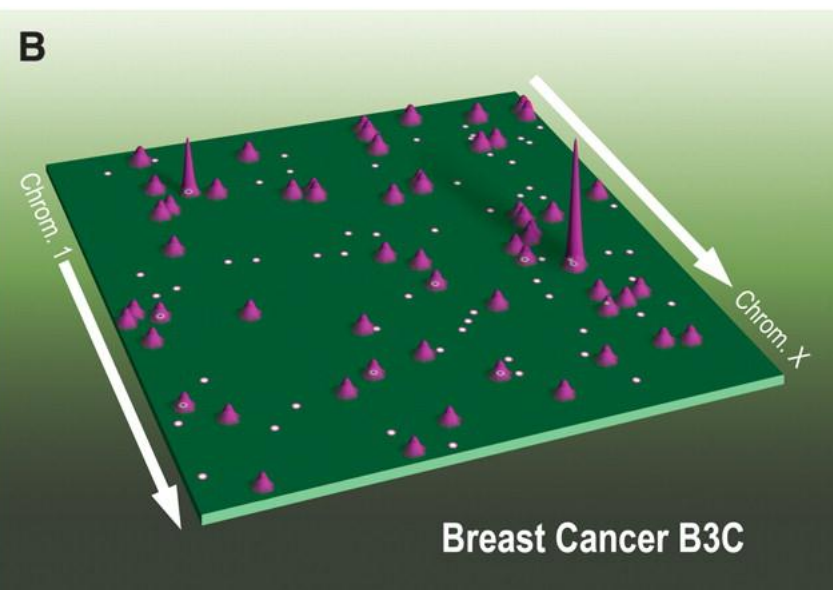
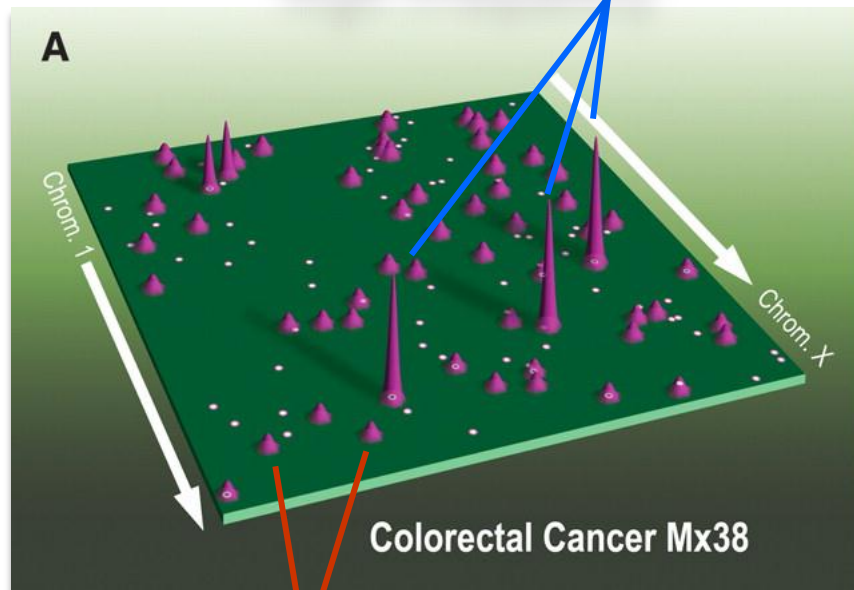
B11C 162

Massive sequencing of:

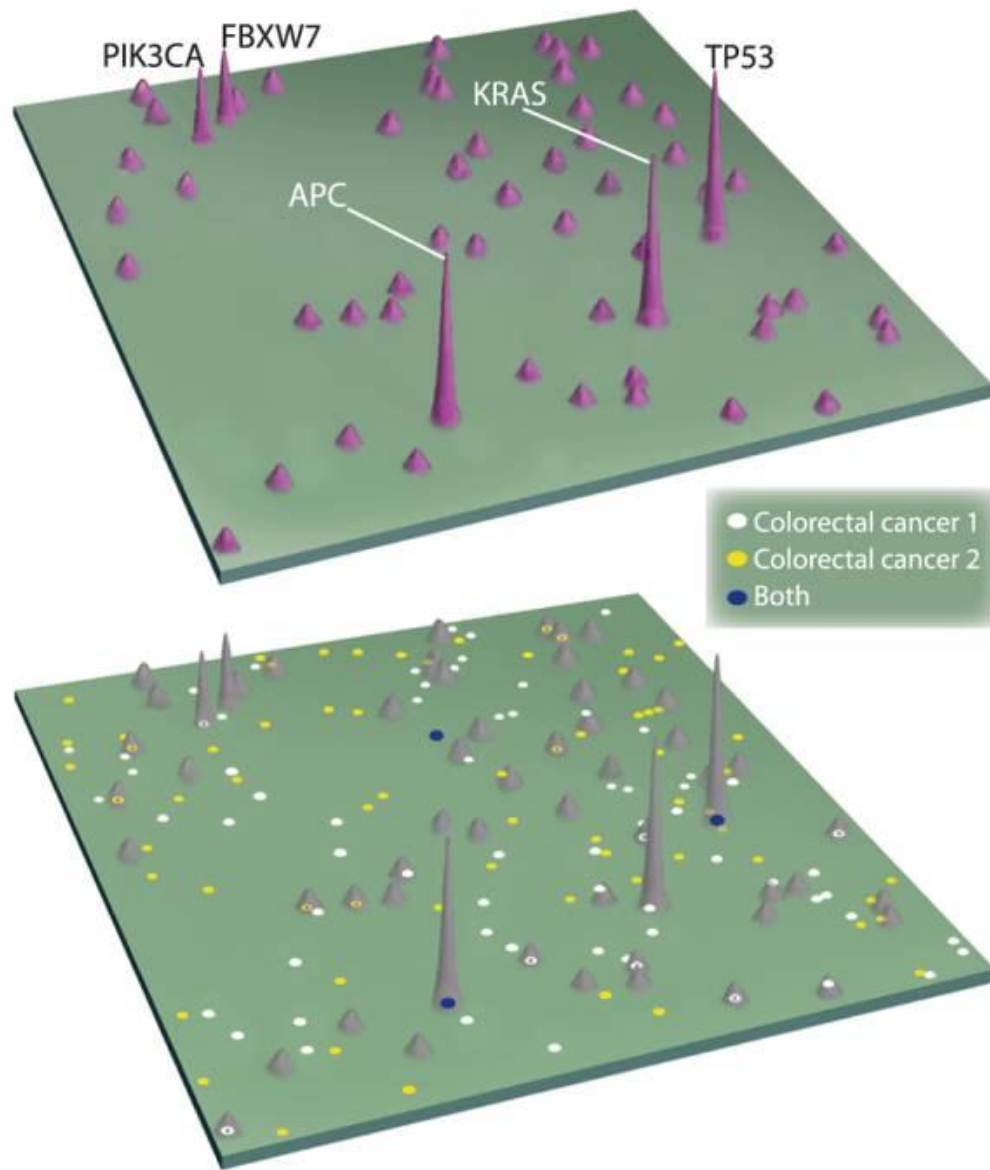
- 11 colon cancer tumors: 76 mutations/tumor
- 11 breast cancer tumors: 84 mutations/tumor

.....but only some (15?) of these genes appear to drive cancer (CAN/driver genes).

CAN genes mutated at high frequency



CAN genes mutated at low frequency



Multiple genetic alterations

How many genetic alterations exist?

≈80 mutations/tumor

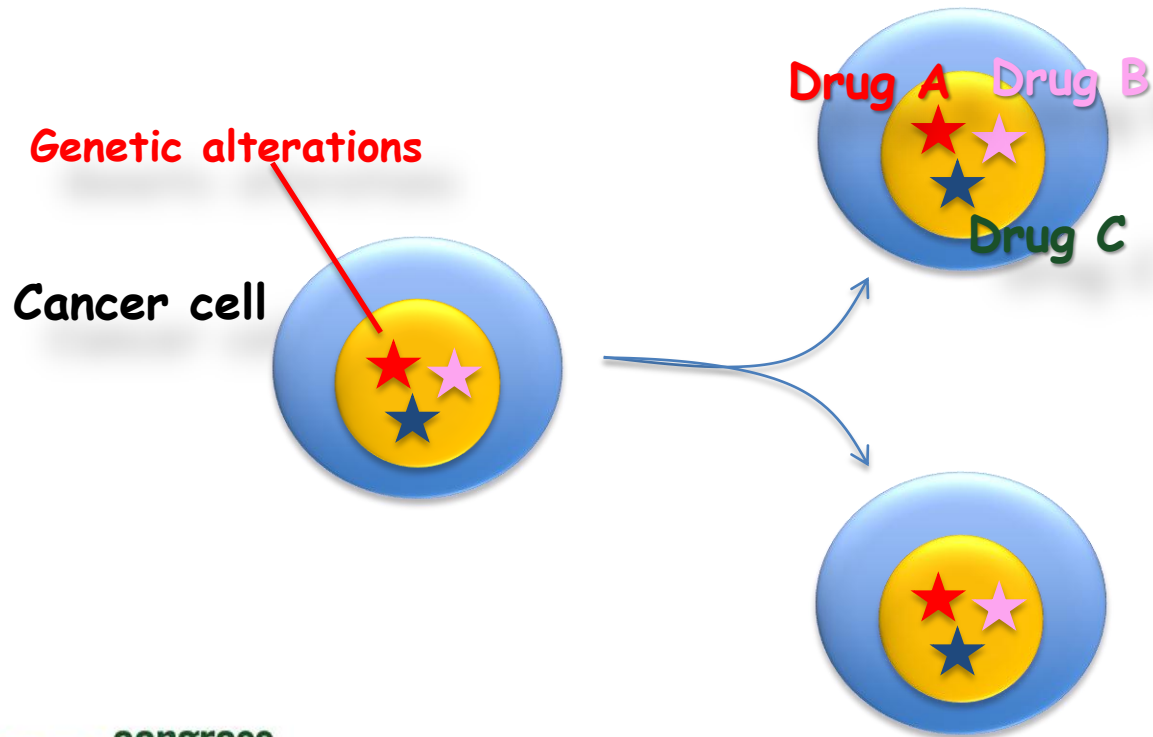
Are all important?

≈ 15 "driver" tumor mutations

How can we design effective treatments on the bases of these alterations?

Etiopathogenic alterations:

2.- Multiple alterations



Etiopathogenic alterations:

1.- A single alteration

2.- Multiple alterations

Drug combinations against different targets are efficient!!!



Cancer Research Center, Salamanca (Spain)

A comprehensive cancer center

