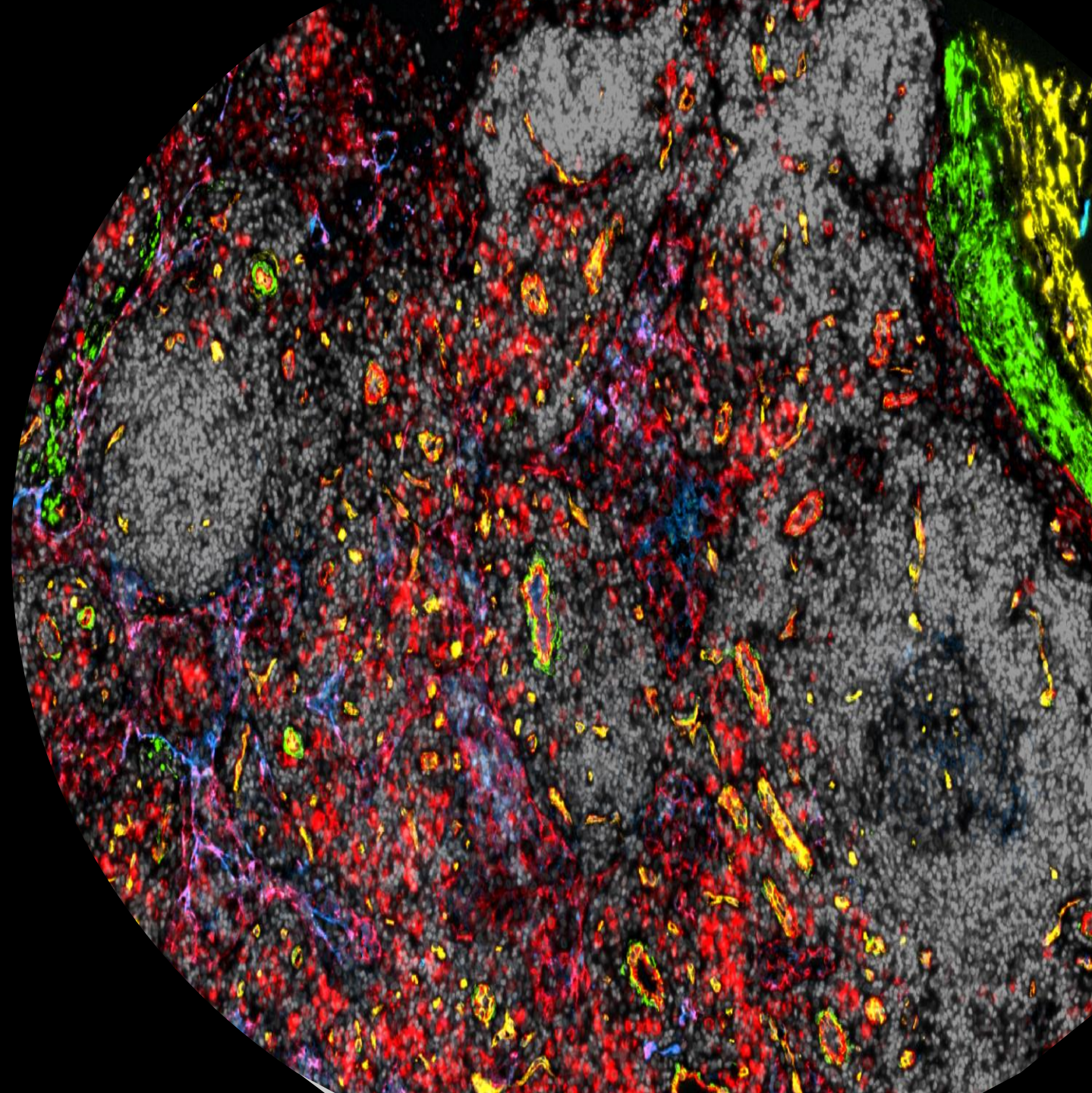


Cancer Biology I

Part-II

Week 9



AGENDA

Nov 3rd: Cancer genomics- mutations

Nov 10th: Cancer genomics-copy number alterations, heterogeneity, tumor evolution

Nov 17th: Cancer Epigenetics- chromatin 3D structure, cell plasticity

Nov 24th: – Major signaling pathways leading to cancer

Dec 1st: Cancer Therapies – chemo and targeted therapies

Dec 8th: Introduction to immunotherapies –

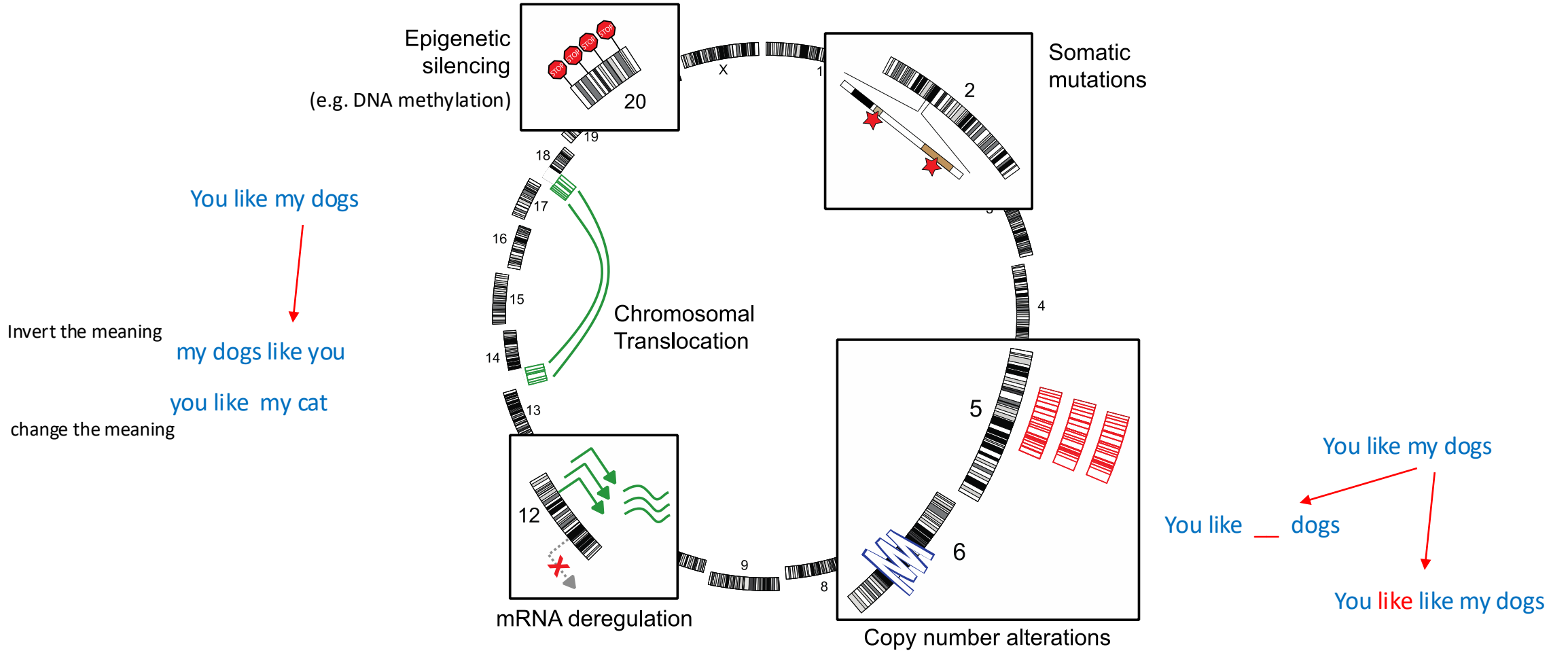
Dec 15th: discussion of unclear points and career development discussion towards a PhD

Dec 17th: Exam 2-4 PM (room to be decided)

Is it cancer only driven by
somatic mutations?

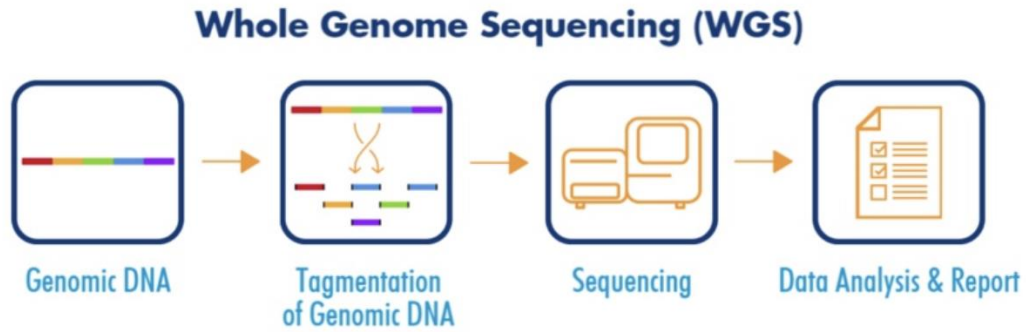
What are they?

Cancer Genomic Alterations

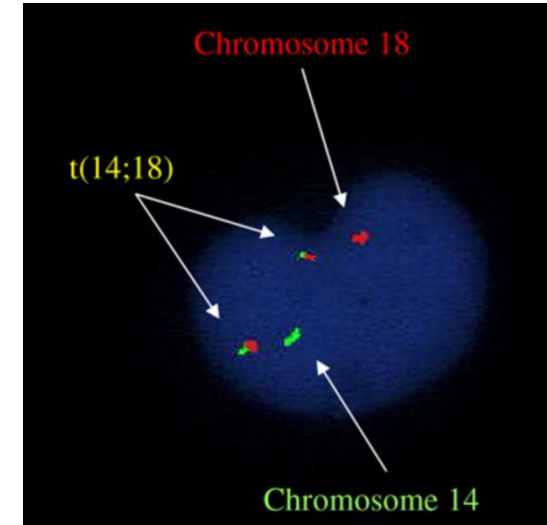


How can we detect copy number alterations?

Copy Number Alterations:



vs

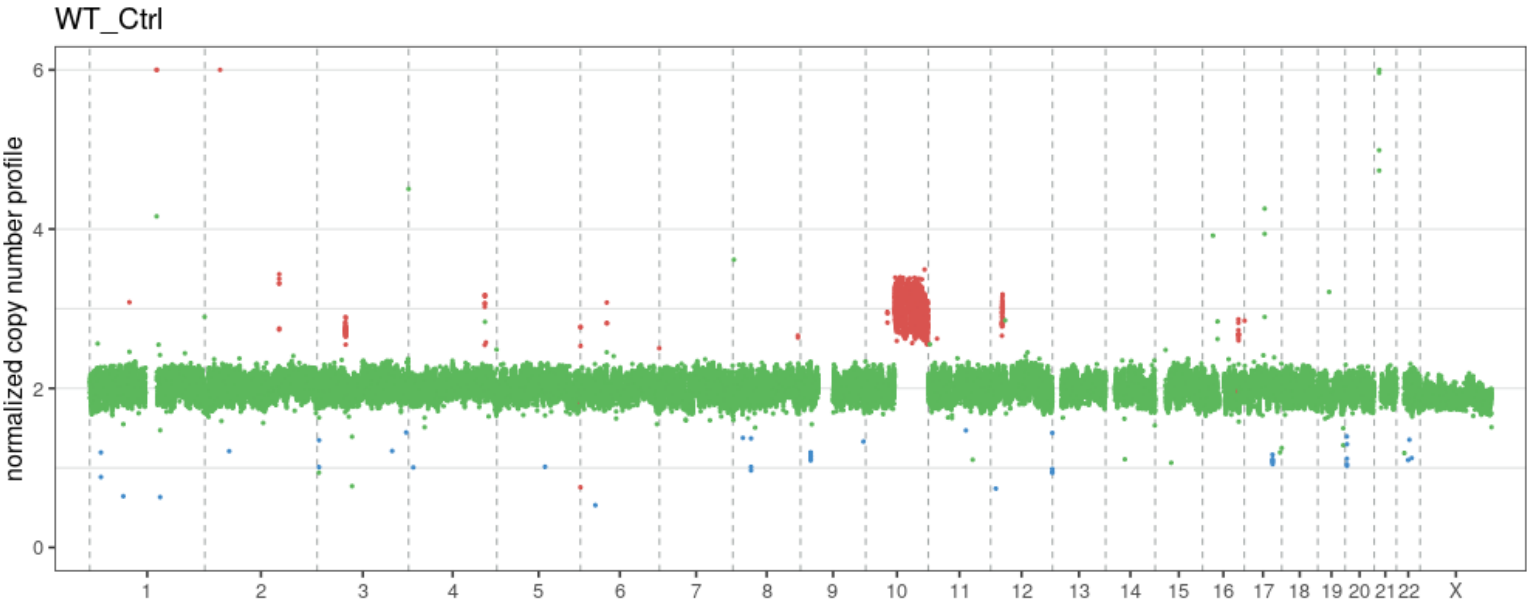


whole genome sequencing
or SNP array

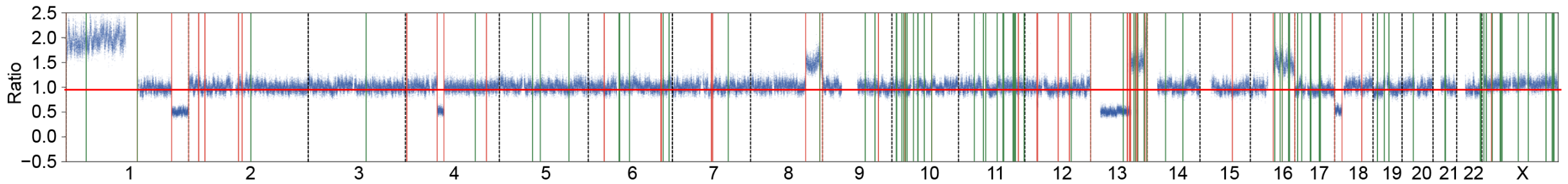
FISH
Fluorescent *in-situ* hybridization

What is the major difference between these two approaches?

Copy Number Alterations: whole genome sequencing or SNP array for each patient

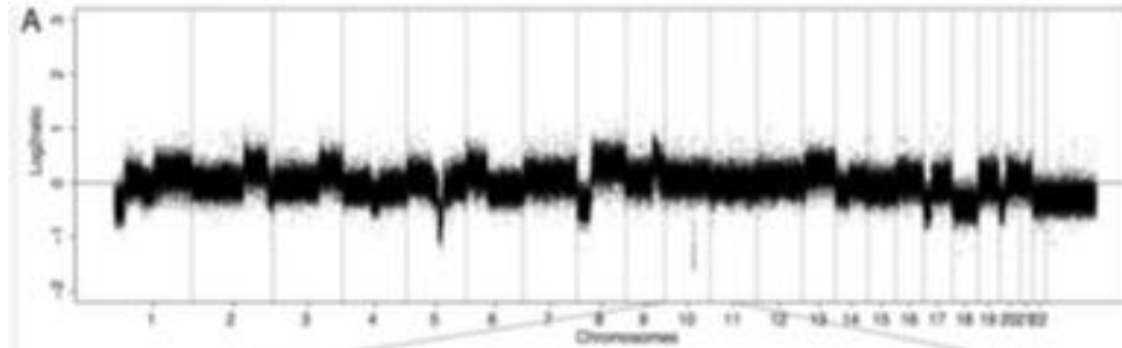


Copy Number Alterations: whole genome sequencing or SNP array for each patient

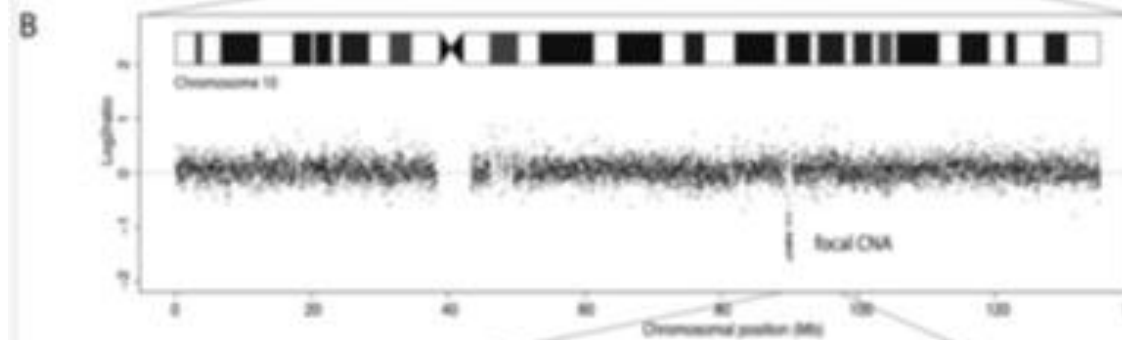


Copy Number Alterations profile for each patient

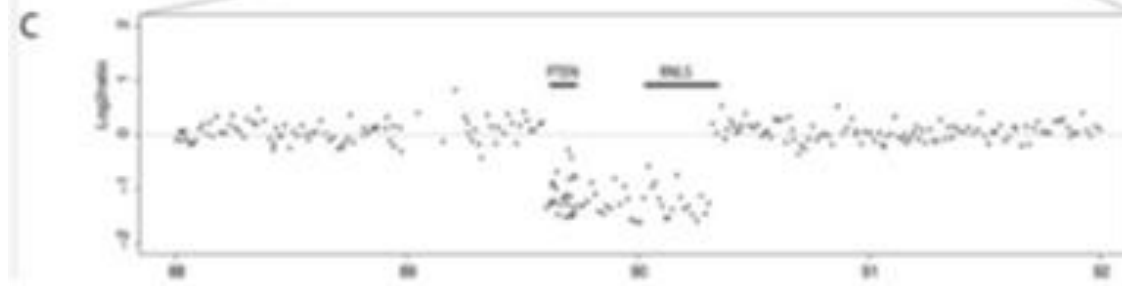
Whole genome



Whole chromosome



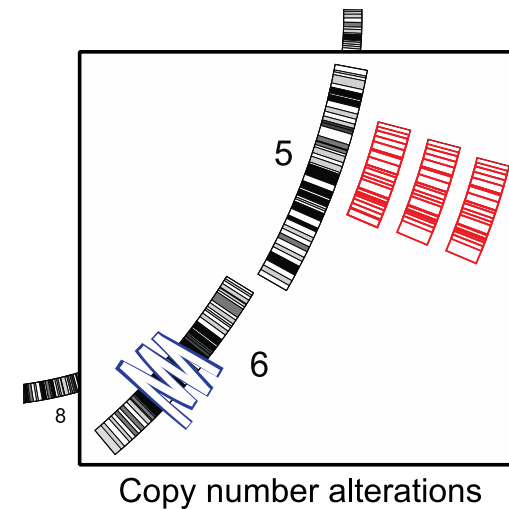
A region
in the chromosome



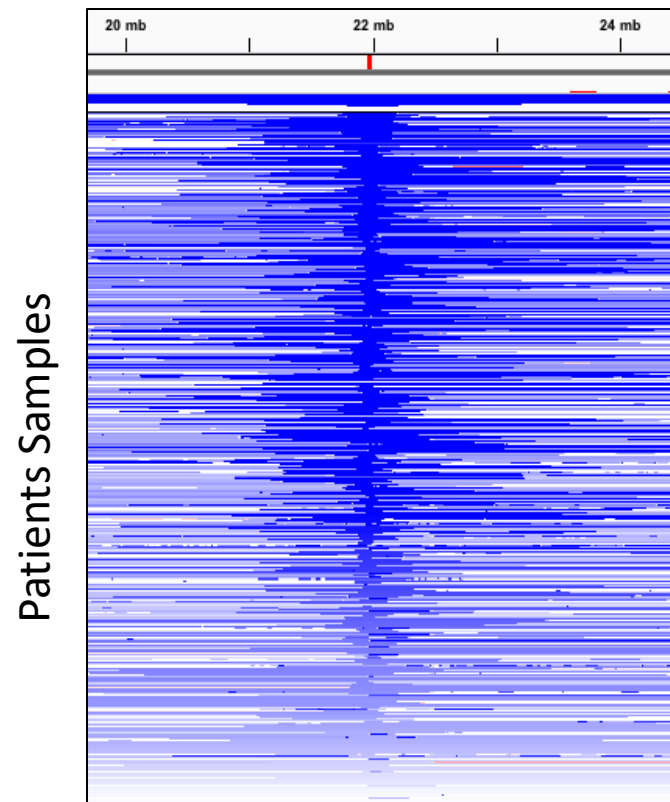
Copy Number Alterations (CNA)

- **Deletion:** Loss of chromosomal regions (Heterozygous or Homozygous)
- **Amplifications:** Acquire one or more copy of chromosomal regions (Duplication or Amplification)

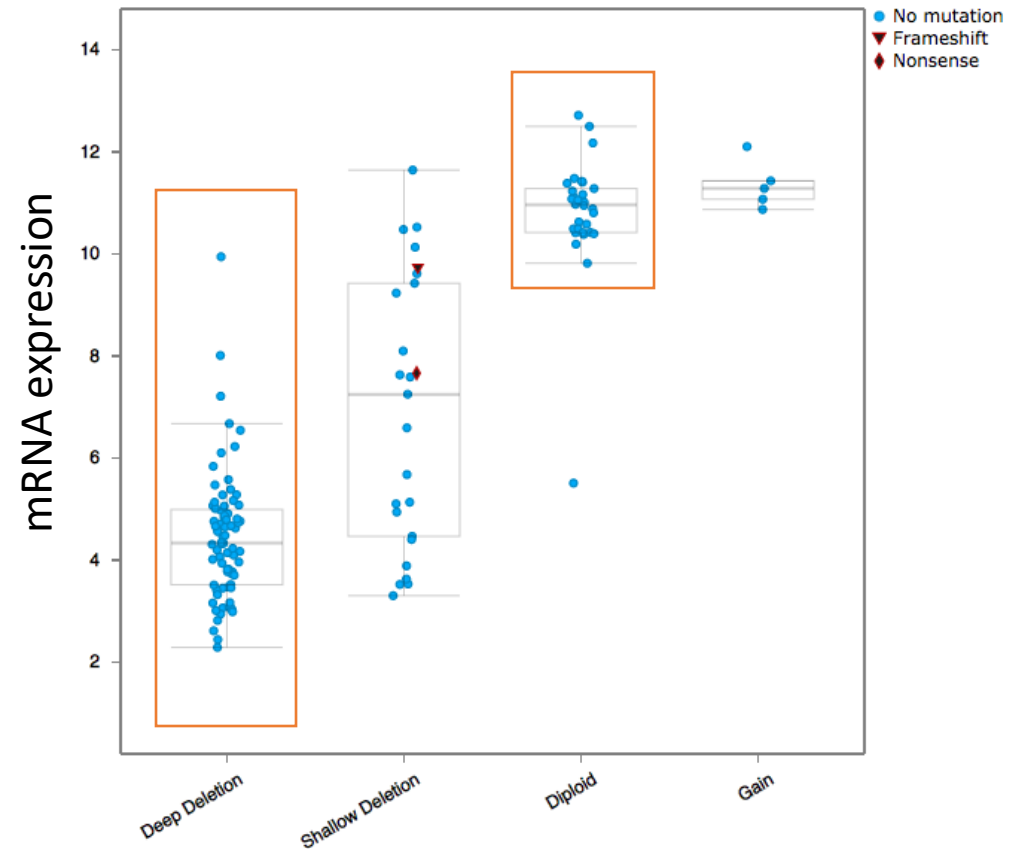
Why do we have heterozygous or homozygous CNA?



Focal Deletions derived from multiple cancer patients

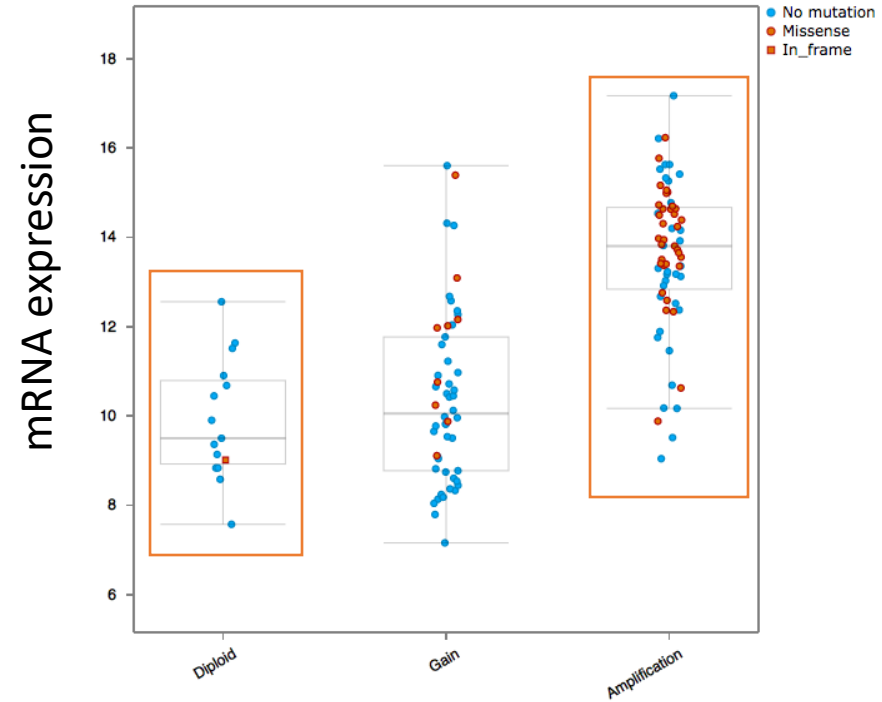
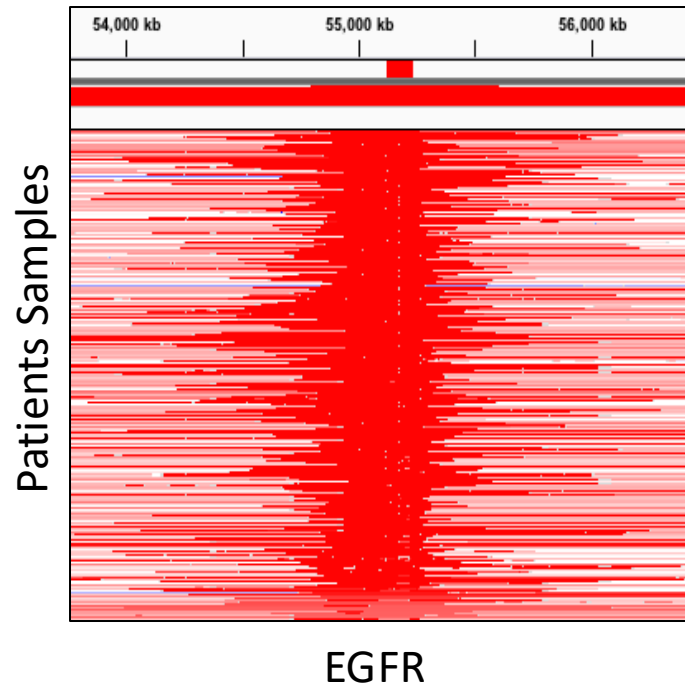


CDKN2A
(ARF/p16)



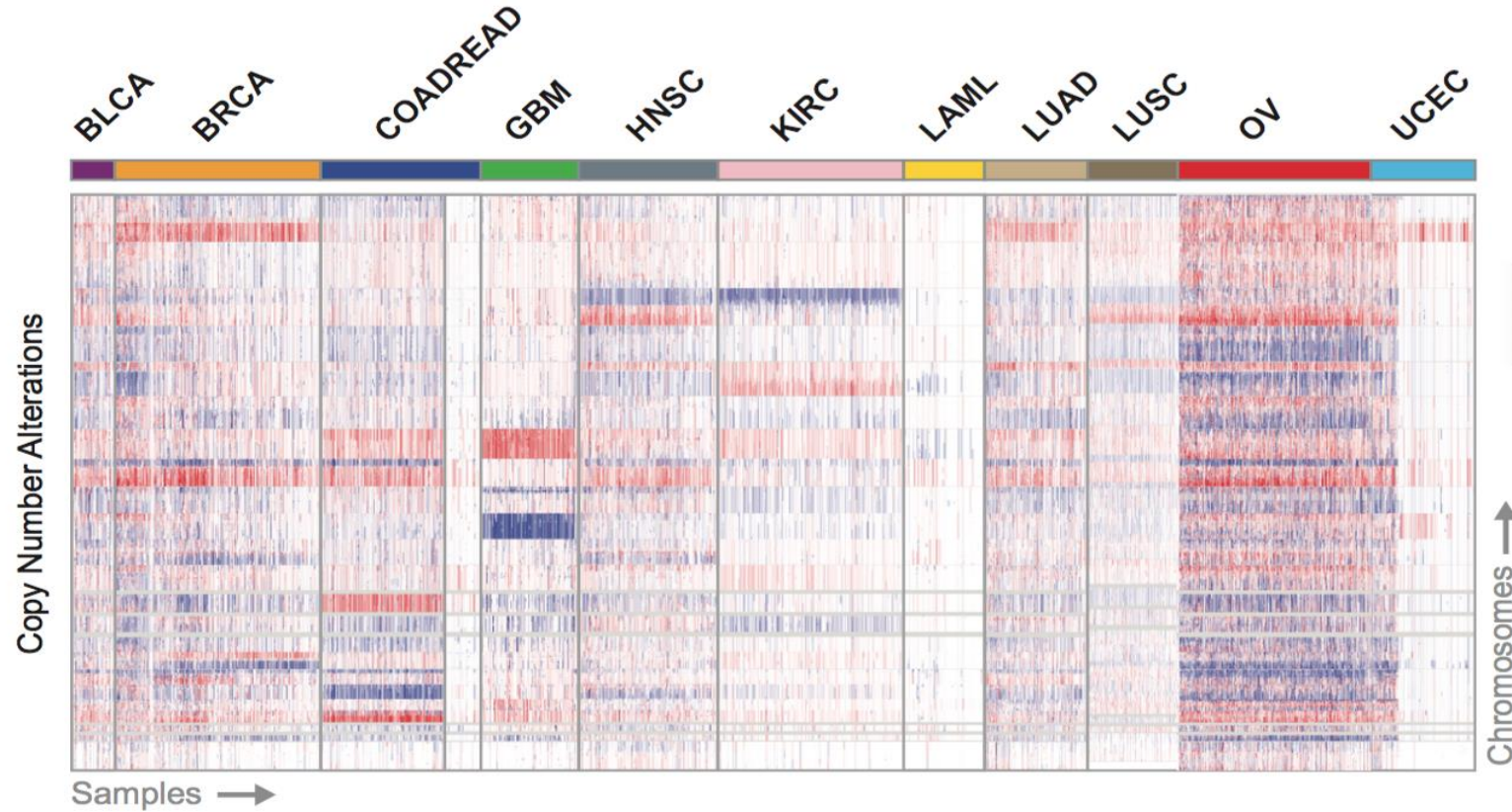
inactivating a **tumor suppressor**

Focal Amplifications

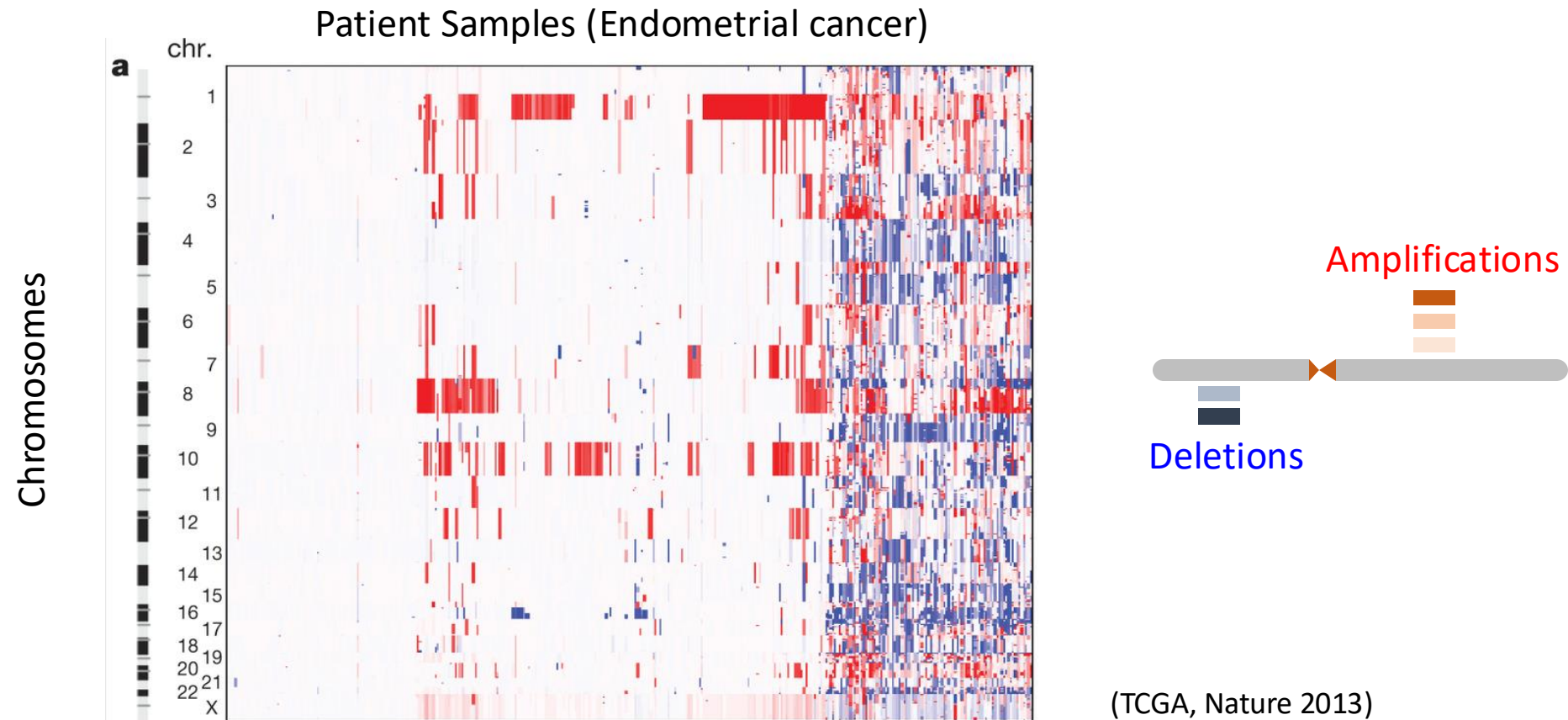


(activating an **oncogene**)

Copy Number Alterations inter-tumor heterogeneity



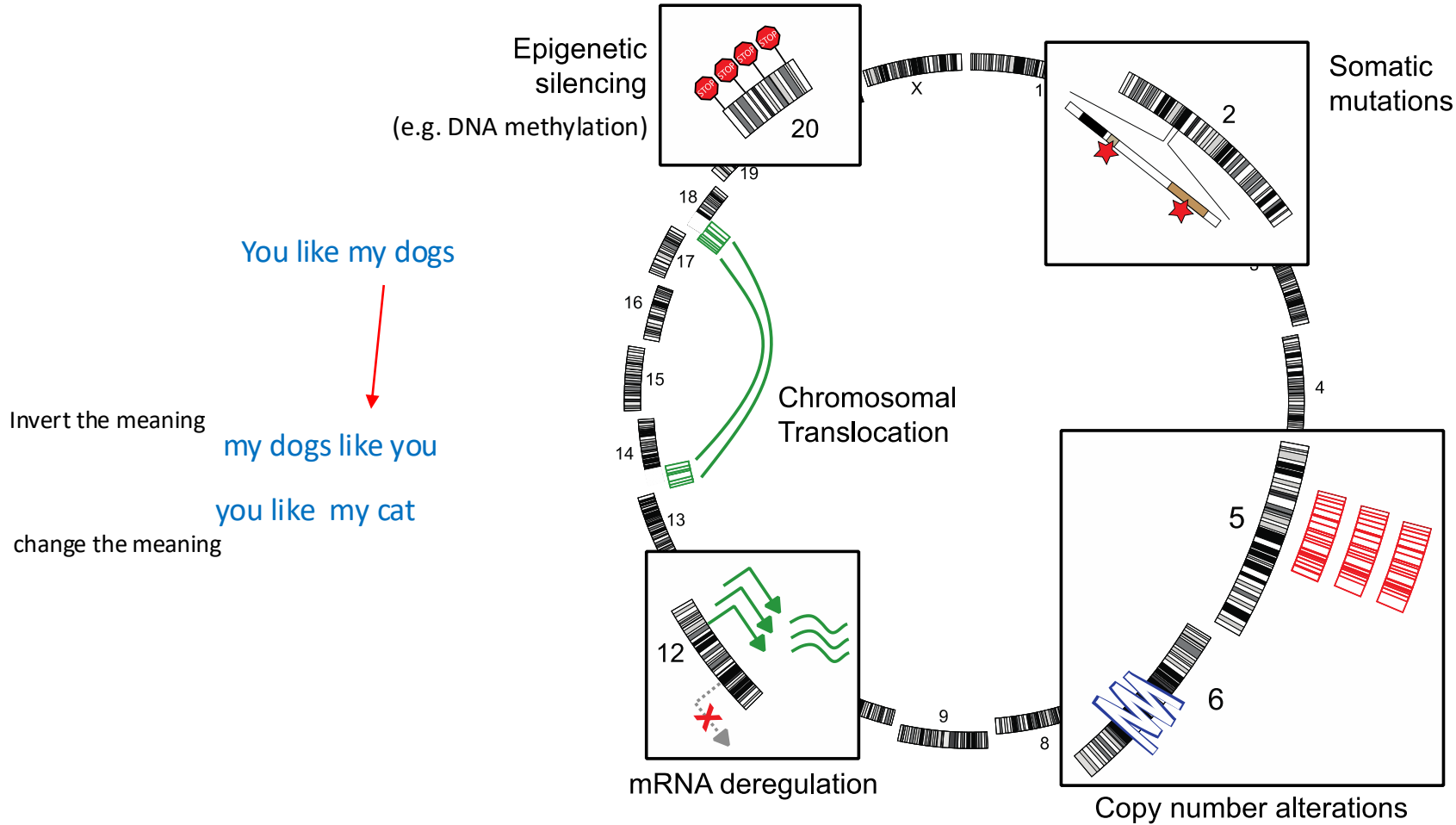
Copy Number Alterations inter patient heterogeneity



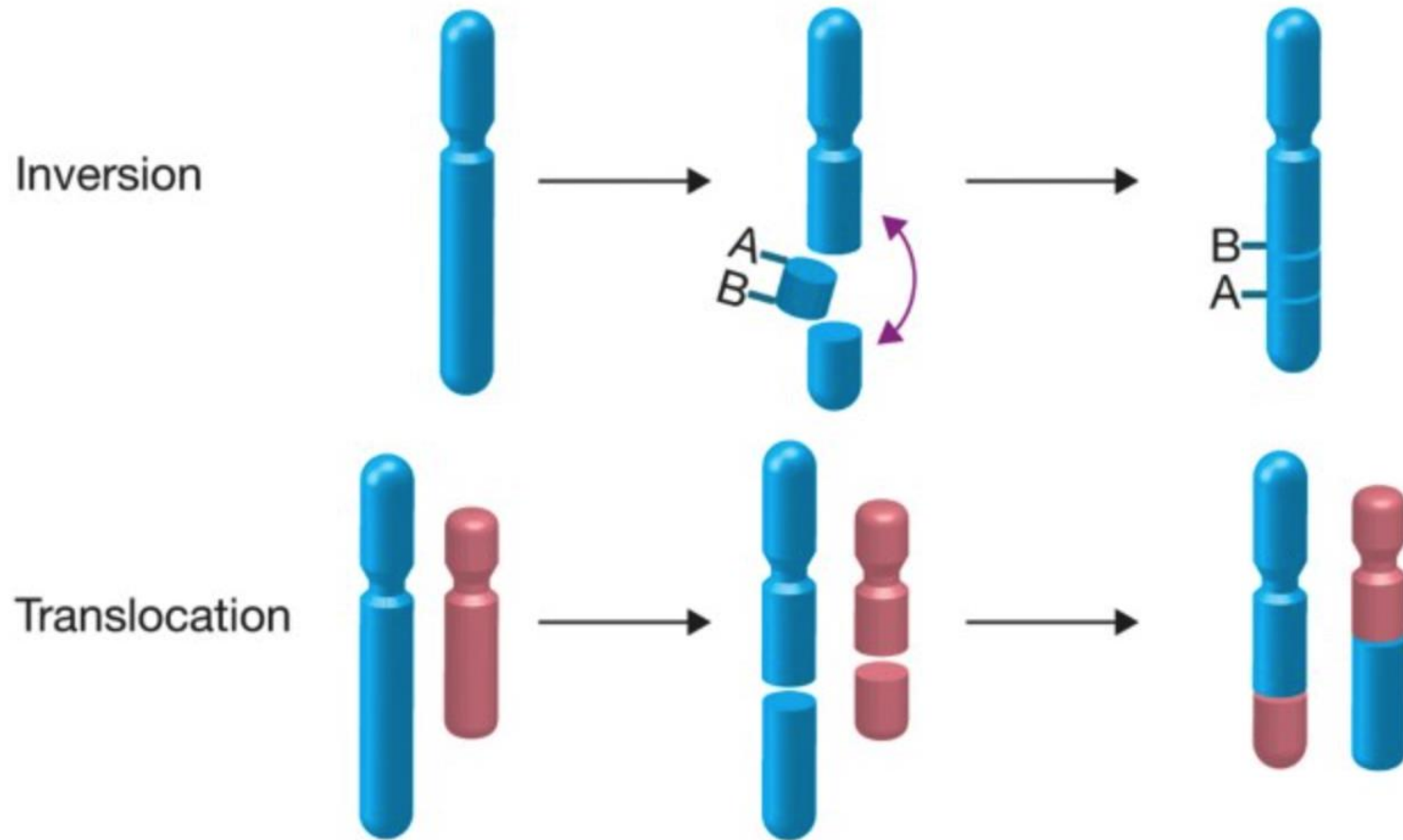
- Tumor subtypes defined by copy number alterations

What are they?

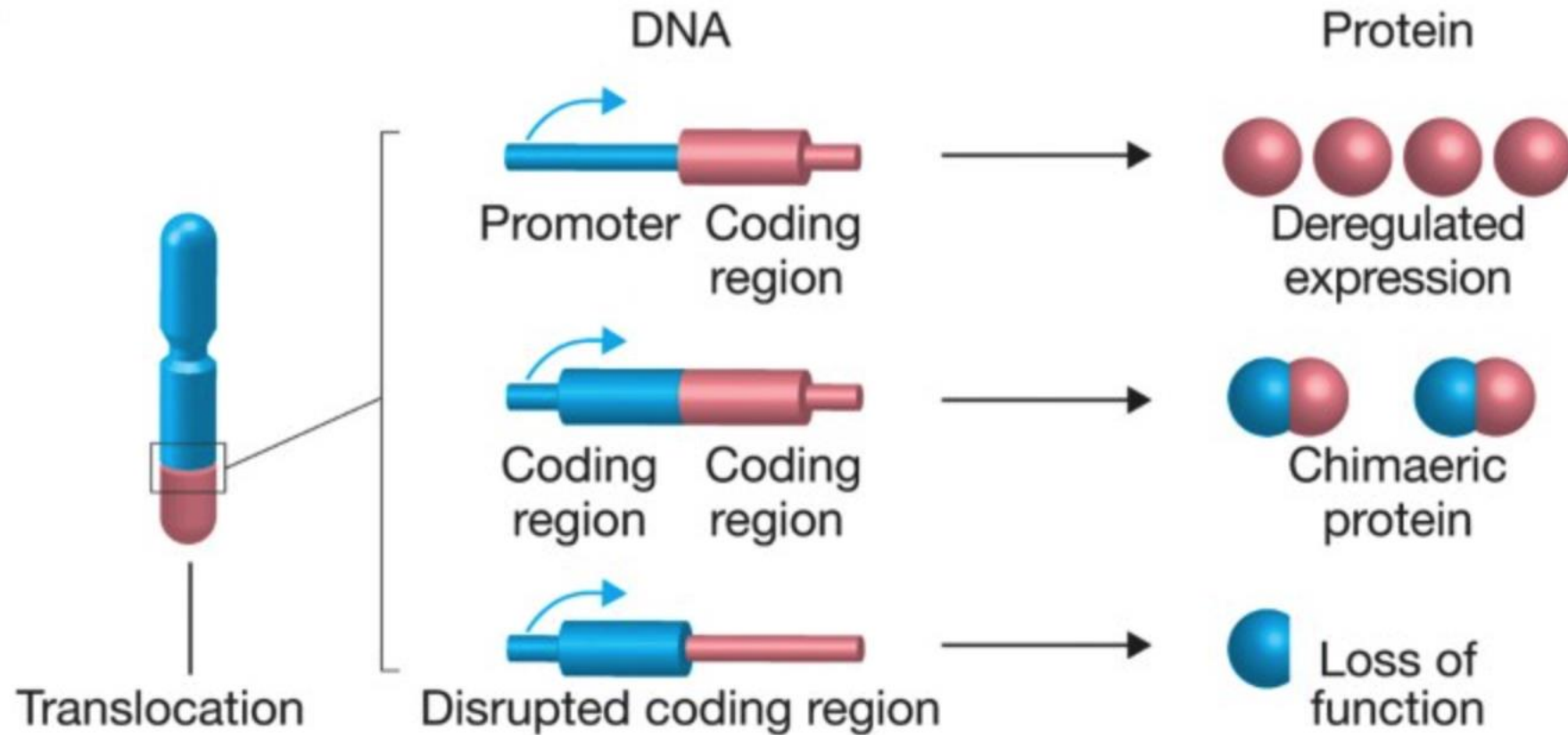
Cancer Genomic Alterations



Chromosomal Structural Variants

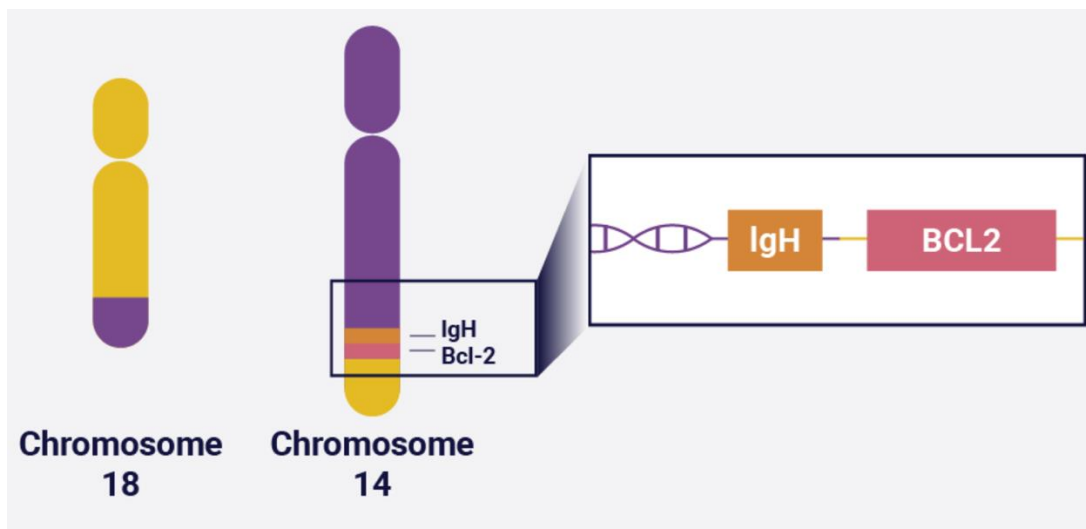


Chromosomal Structural Variants

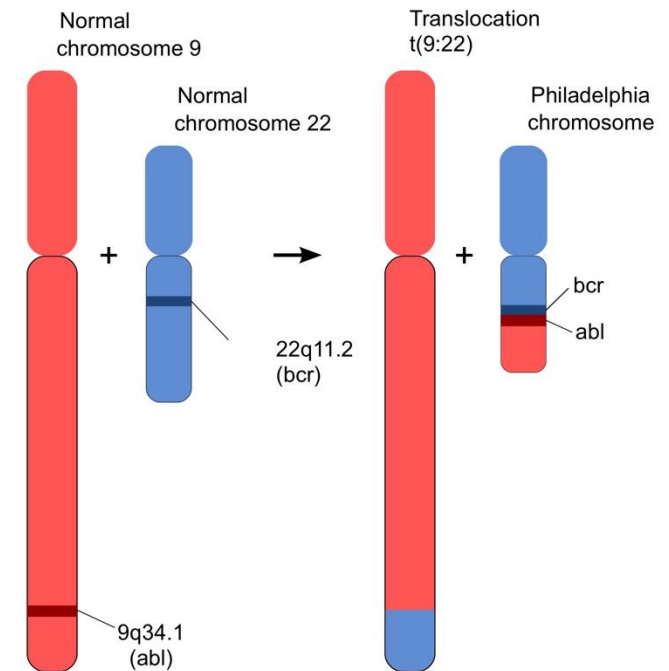


Chromosomal Structural Variants

t(14,18) translocation puts BCL2 under the IgH promoter:
BCL2 gets upregulated in lymphoma



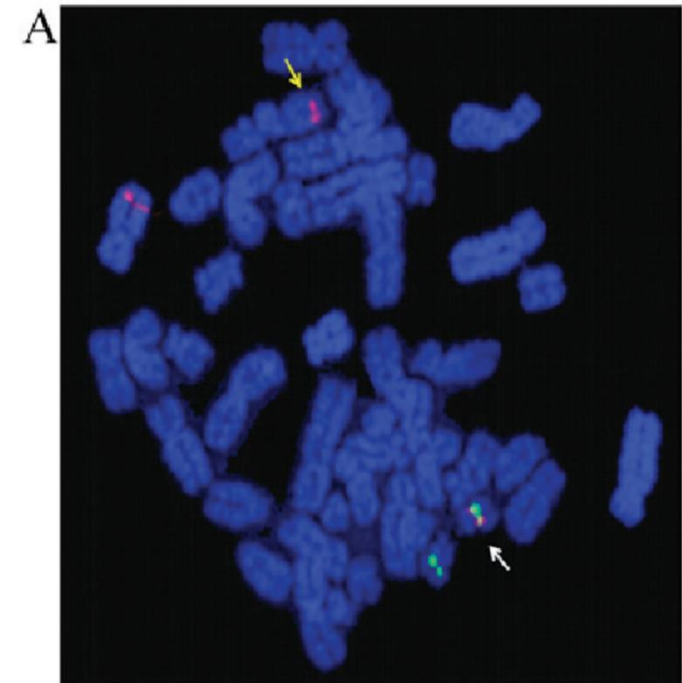
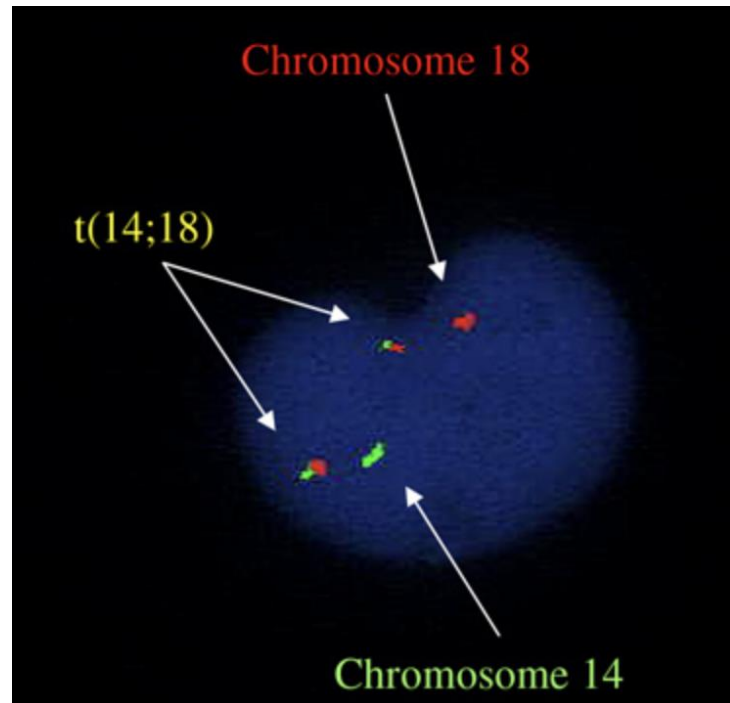
BCR-ABL fusion protein: fusion
generate a new protein with
hyper-active kinase activity



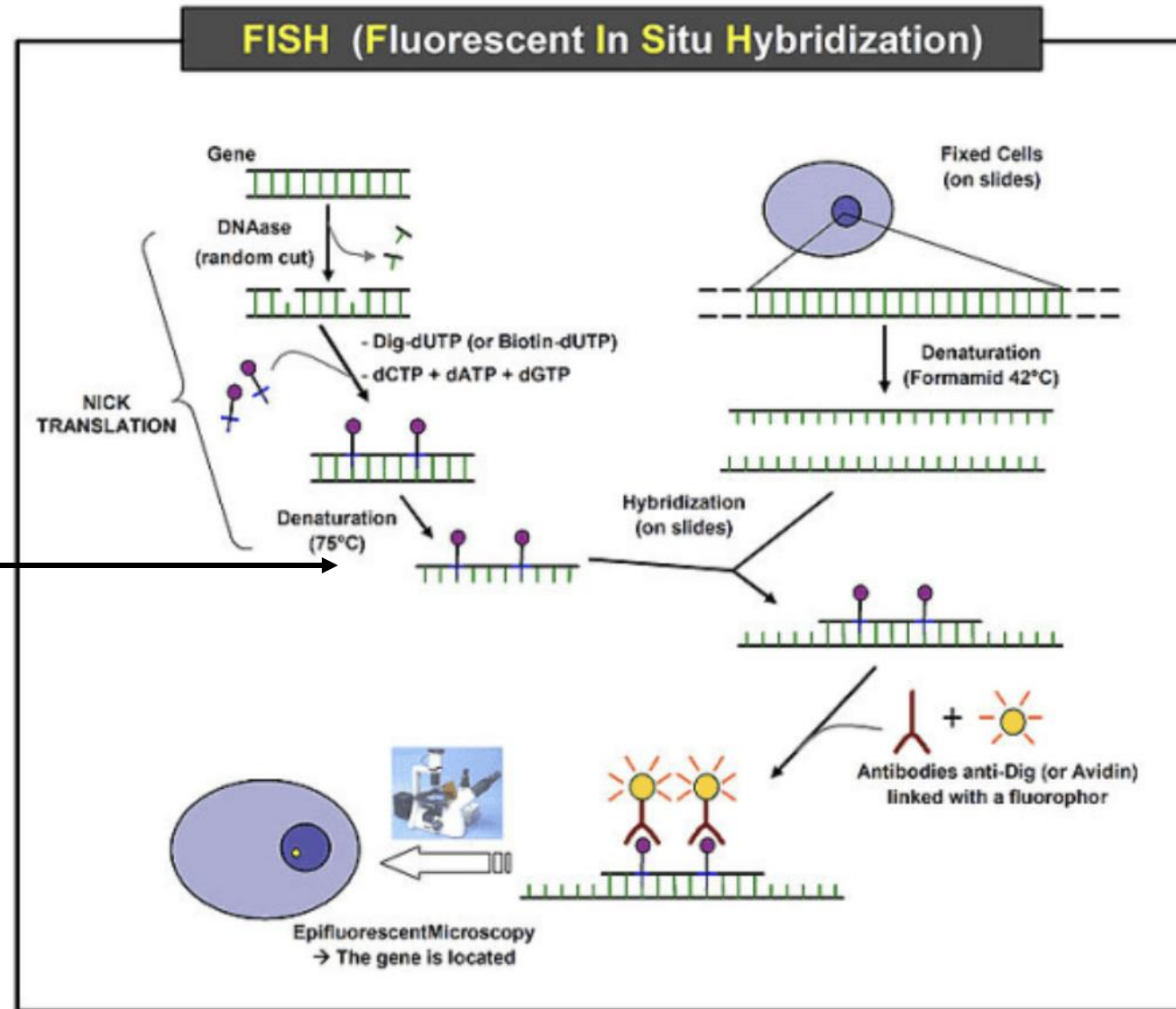
Can we use whole genome sequencing to
Identify chromosomal translocation?

Chromosomal Structural Variants: individual genomic loci

Translocations became apparent from FISH (long before NGS techniques)



Fluorescent in situ hybridization for a single genomic locus

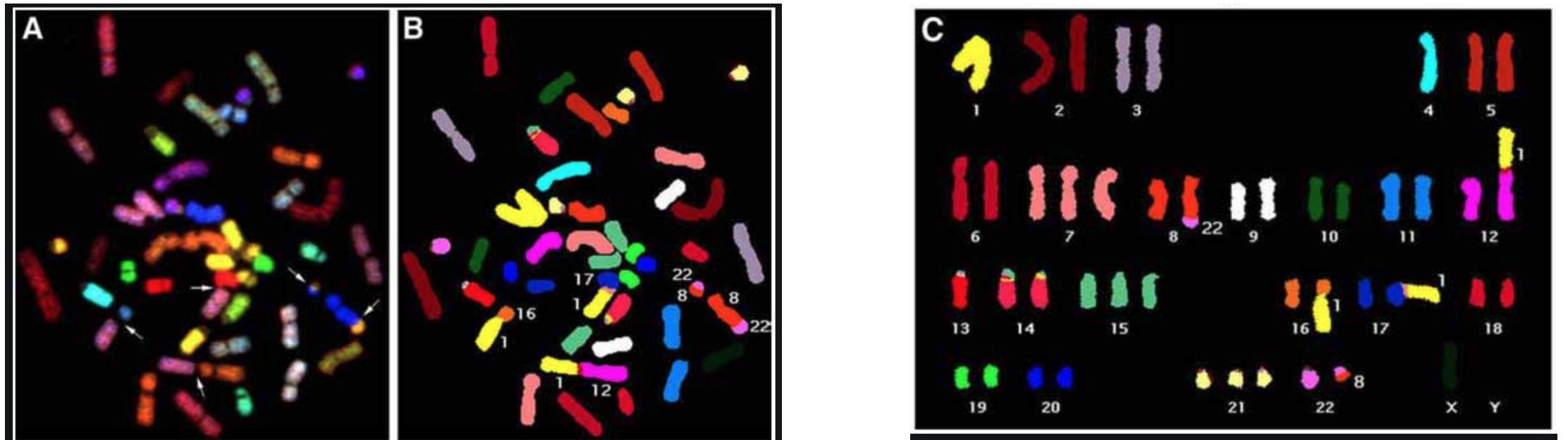


Synthesis of a fluorescent label oligonucleotide probe

Synthesis of a fluorescent label oligonucleotide probe

Chromosomal Structural Variants: Chromosome painting

Translocations became apparent from “chromosome painting”



Patterns of genomic alterations

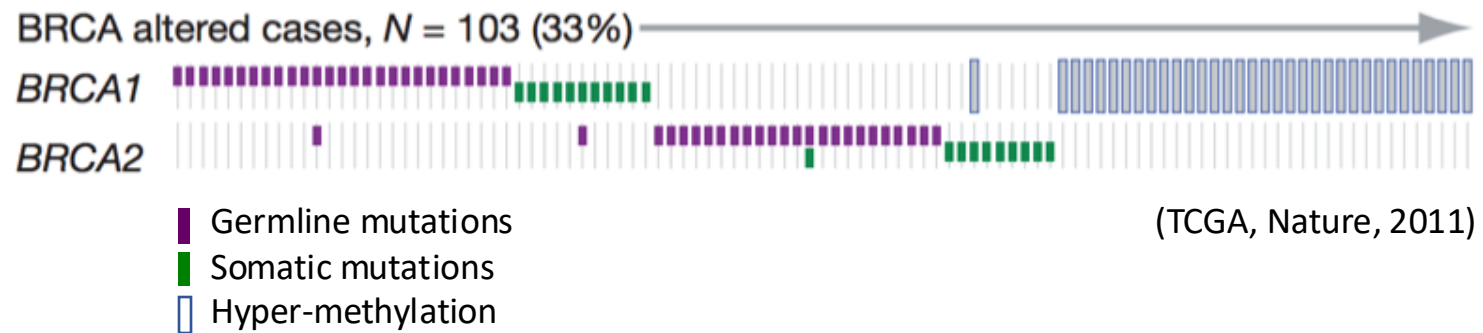
Considering both mutations and copy number changes:

MUTUALLY EXCLUSIVE: rarely occur together

CONCURRENT ALTERATIONS: frequently occur together

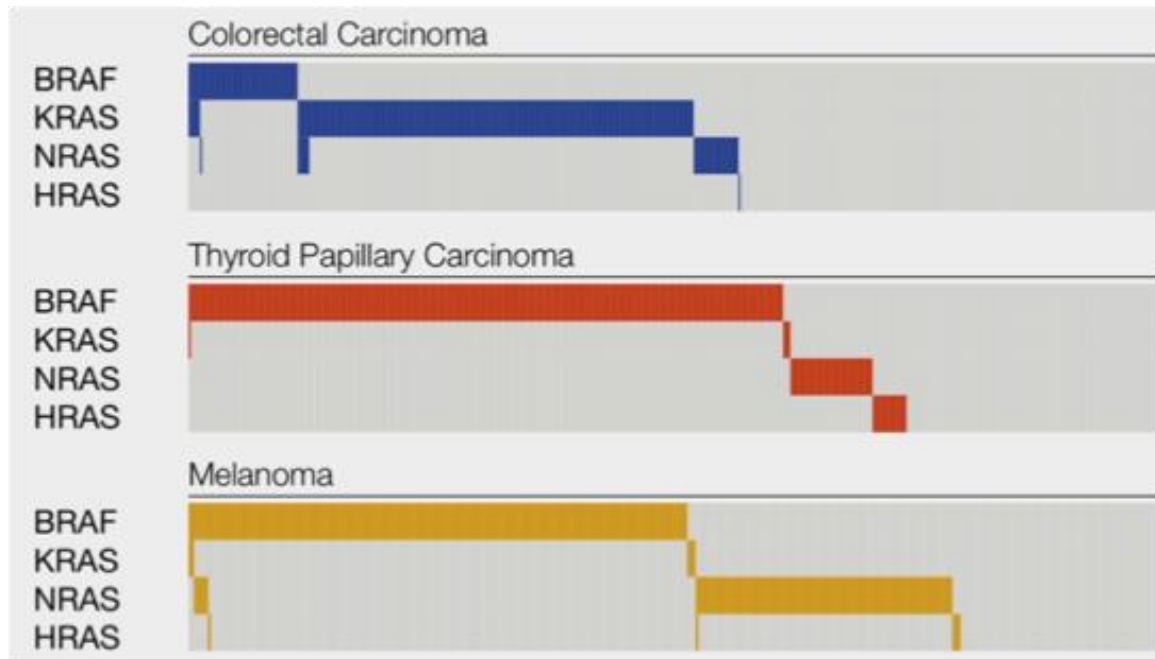
Mutual Exclusivity

- Observations of mutually exclusive alterations



Mutual Exclusivity

- Observations of mutually exclusive alterations

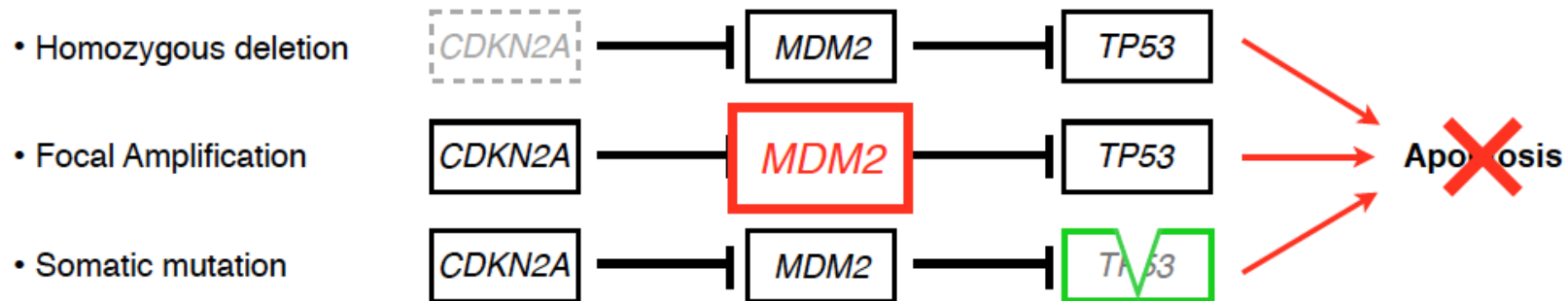


Patient Samples

Why Mutual Exclusivity?

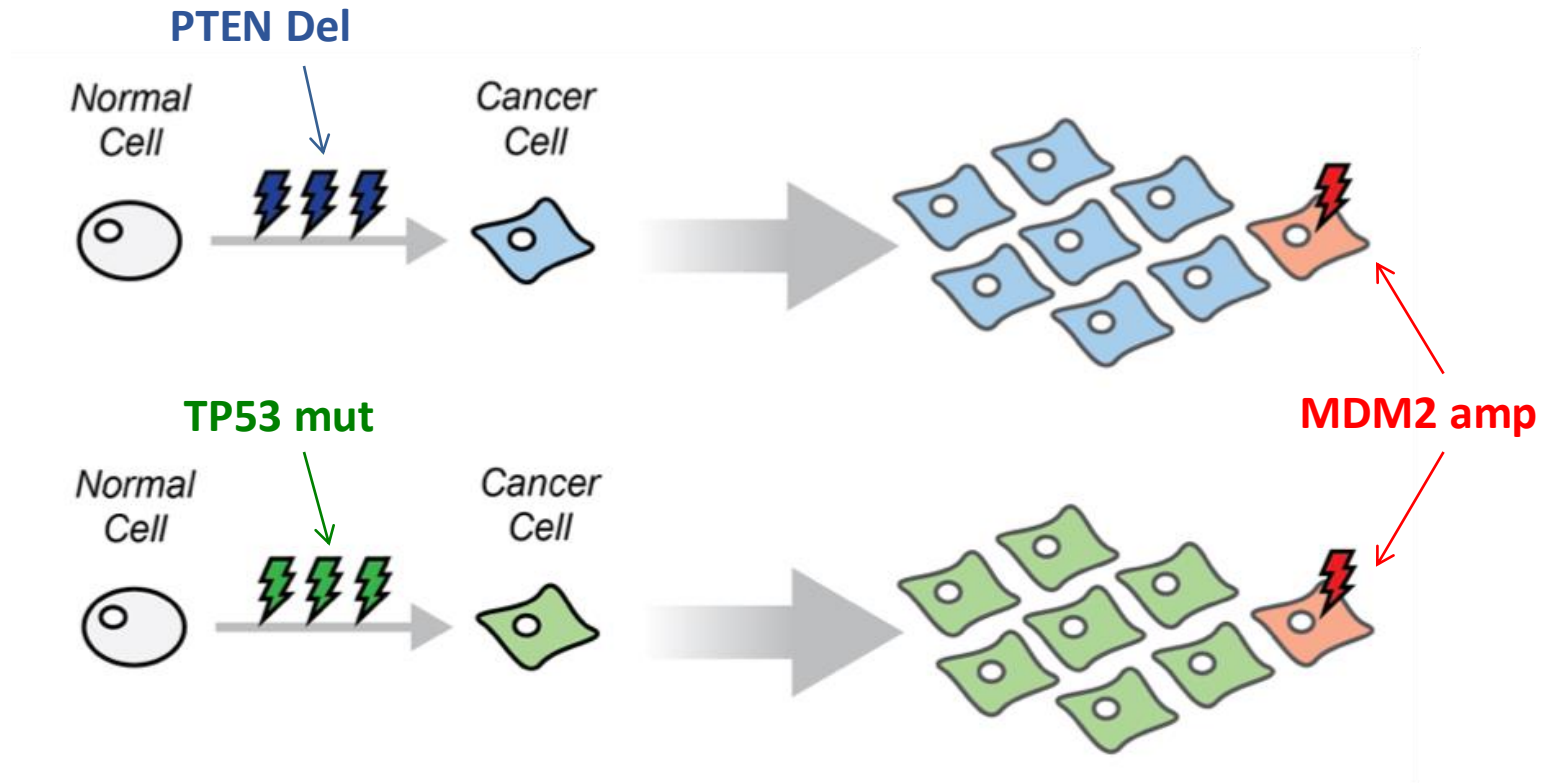
Why Mutual Exclusivity?

1) Selective Advantage



A second hit in the same pathway doesn't offer a further selective advantage

Mutual Exclusivity reflects Selection

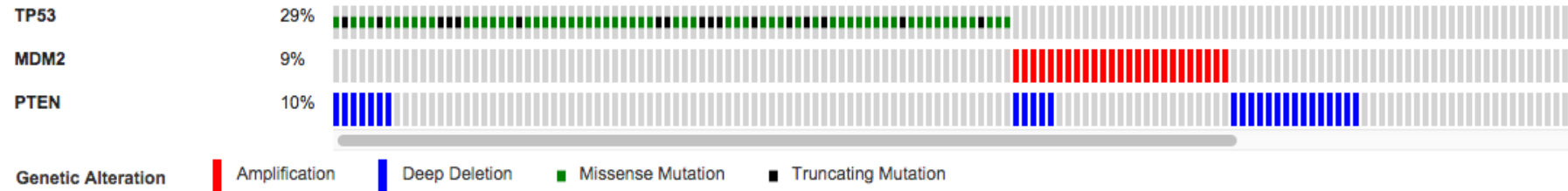


Is MDM2 amplification giving the same advantage in the 2 cases?

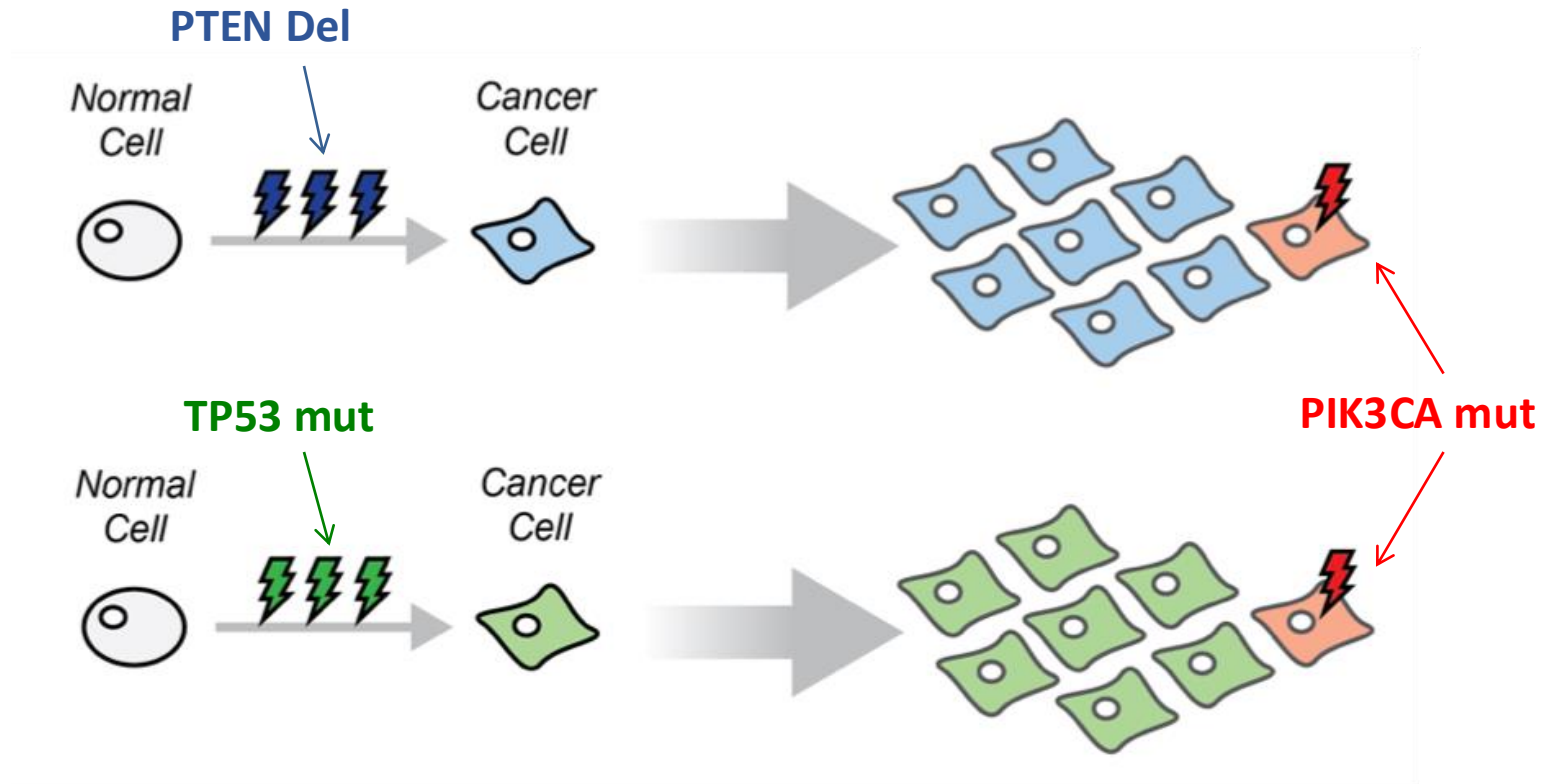
Mutual Exclusivity reflects Selection

TCGA Glioblastoma Dataset

Altered in 118 (43%) of 273 cases/patients



Mutual Exclusivity reflects Selection

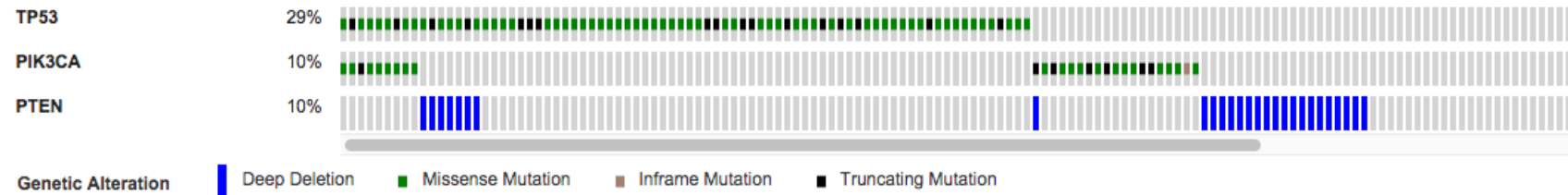


Is PIK3CA mutation giving the same advantage in the 2 cases?

Mutual Exclusivity reflects Selection

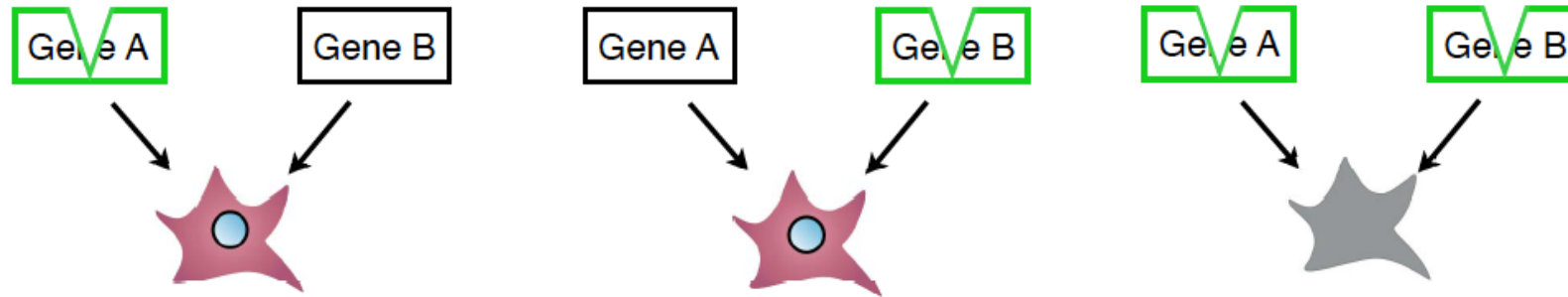
TCGA Glioblastoma Dataset (source cBioPortal)

Altered in 116 (42%) of 273 cases/patients



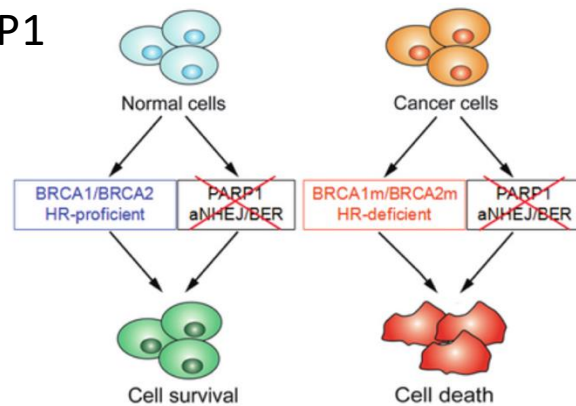
Why mutual exclusivity?

2) Synthetic Lethality



A second hit actually confers a disadvantage!

e.g. BRCA1/2 and PARP1

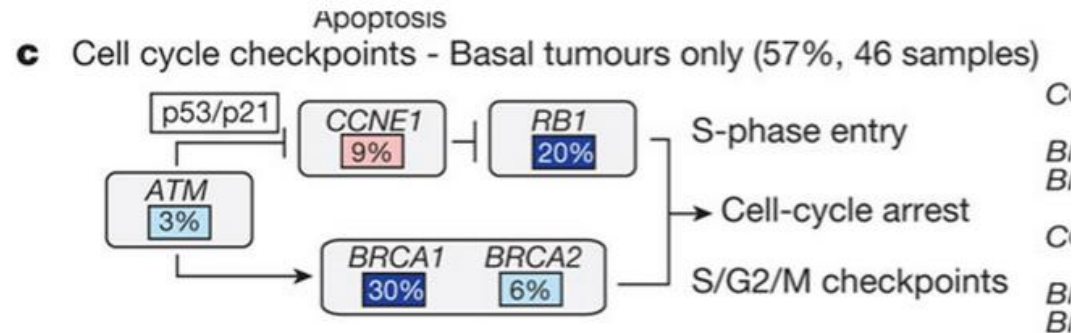


Synthetic Lethal interactions

Mutual exclusivity between alterations in DNA repair genes BRCA1/2 and cell cycle regulators CCNE1 and RB1 in **ovarian cancer** and **Basal breast cancer**



(Ciriello et al. Genome Res. 2012)



(TCGA, Nature 2012)

Synthetic Lethal interactions

Mutual exclusivity between alterations in DNA repair genes BRCA1/2 and cell cycle regulators CCNE1 and RB1 in **ovarian cancer** and **Basal breast cancer**



(Ciriello et al. Genome Res. 2012)

Apoptosis

c Synthetic lethality between *CCNE1* amplification and loss of *BRCA1*

Darius Etemadmoghadam^{a,b,c}, Barbara A. Weir^{d,e}, George Au-Yeung^{a,f}, Kathryn Alsop^{a,f}, Gillian Mitchell^{a,b}, Joshy George^{a,f}, Australian Ovarian Cancer Study Group^{a,g,h,i,1}, Sally Davis^{a,c}, Alan D. D'Andrea^d, Kaylene Simpson^{b,c,j}, William C. Hahn^{d,e}, and David D. L. Bowtell^{a,b,c,f,2}

(PNAS, 2013)

(TCGA, Nature 2012)

Why is it important to find pairs of genomic alterations that are synthetic lethal?

Laboratories working on cancer genomics EPFL/UNIL

Sebastian Martin Waszak



EPFL

Group of Giovanni Ciriello

UNIL



Computational Biology & Cancer Genomics group

We have open positions for postdoc candidates and phd students. Please check our website <http://ciriello.org/>

Research in our group focuses on computational and system biology approaches to study functional interrelationships between molecular alterations selected in cancer. **Computational biology** studies focus on the design and development of systematic approaches to nominate candidate functional alterations from molecular profiles of human tumors, how these events are

What are the challenges?

- **Prioritize the multitude of genetic aberrations**

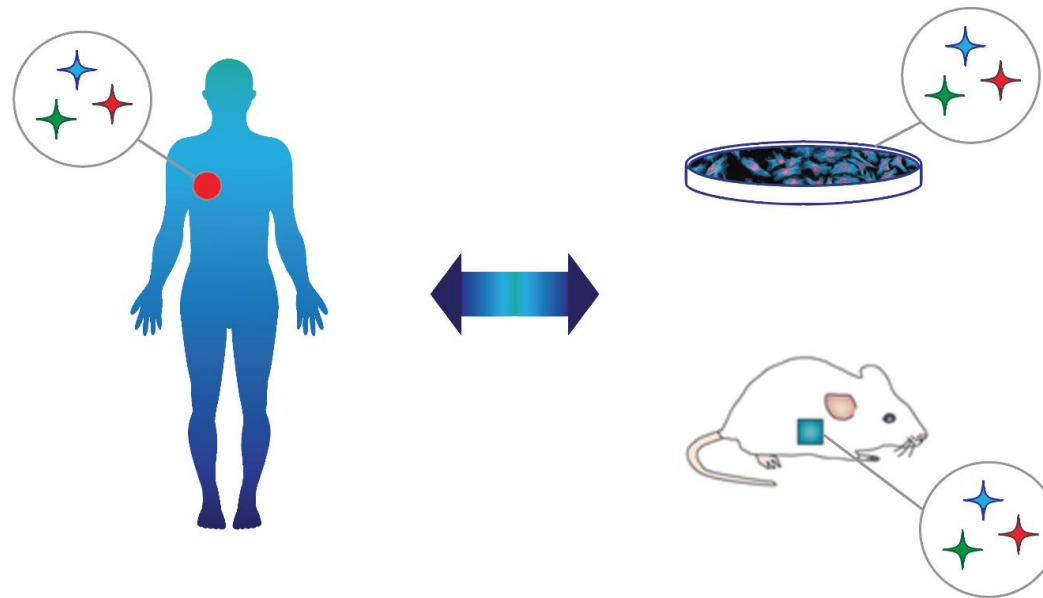
Several studies classified genomic alteration based on **statistical analyses**

- **Functional Annotations of Genomic Alterations**

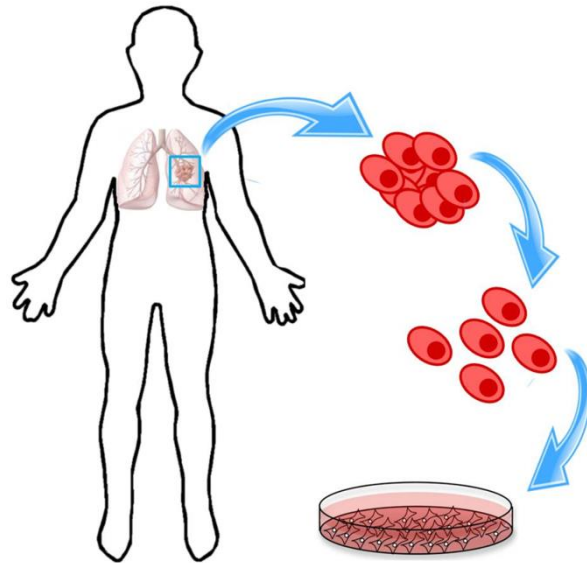
Define the biological impact of genetic alteration in the tumor development

How to study this complexity?

Disease-model matching



Multiple cell lines isolated from different tumors



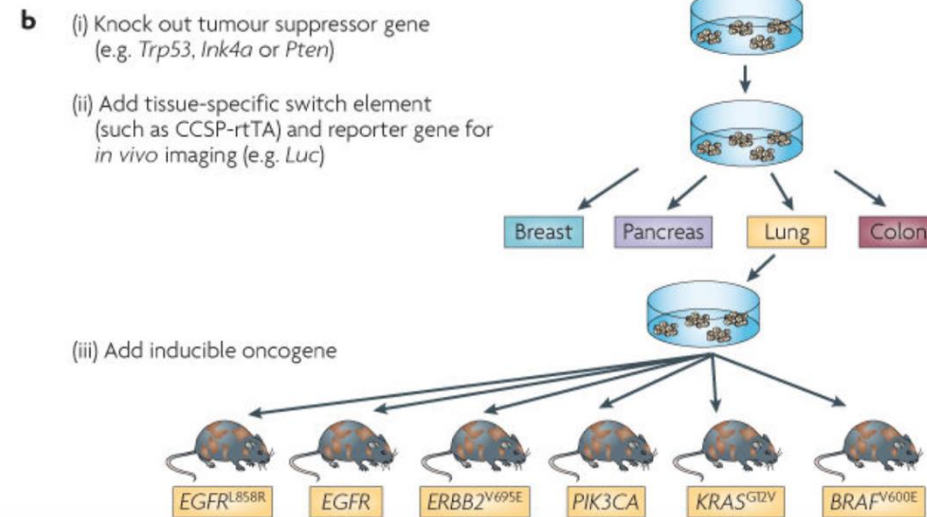
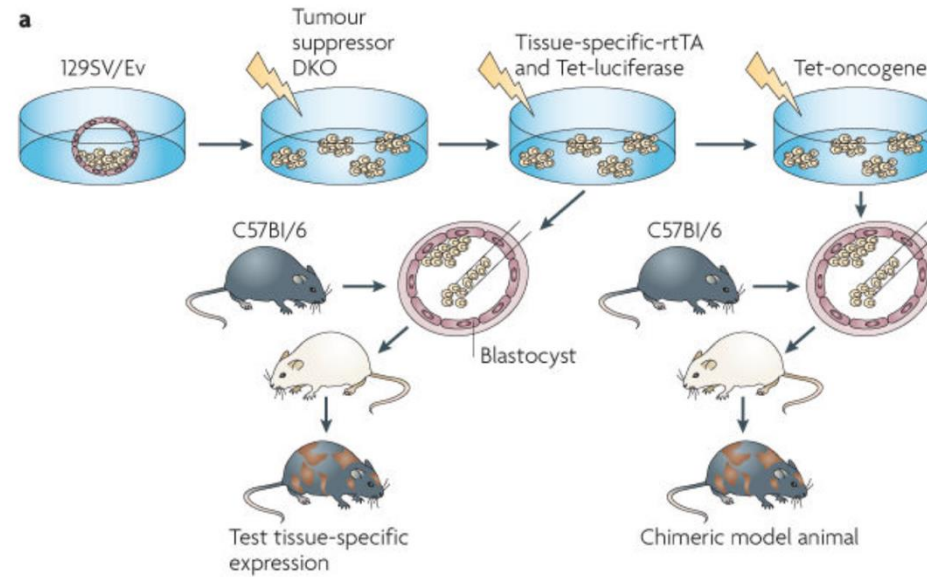
Cancer cells grow
for forever



Cancer cell line encyclopedia

<https://portals.broadinstitute.org/ccle>

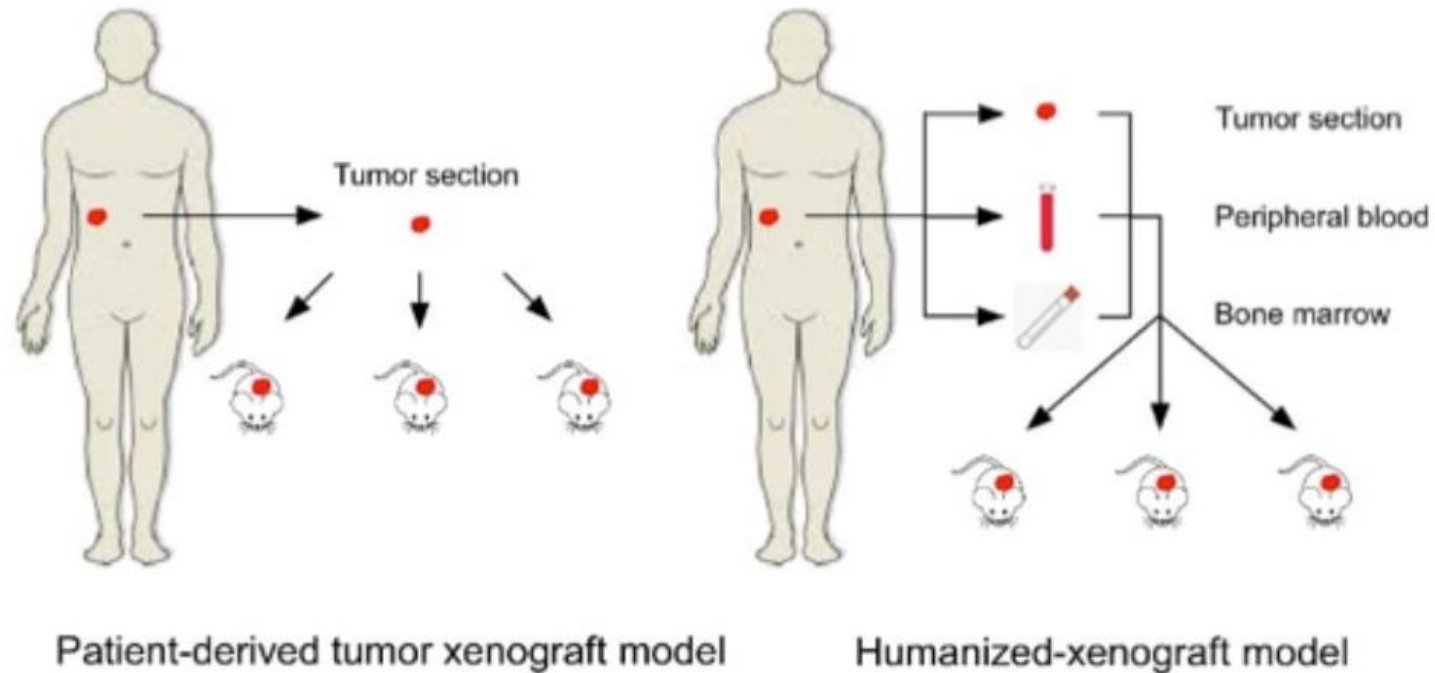
Transgenic animal models



The Human Relevance

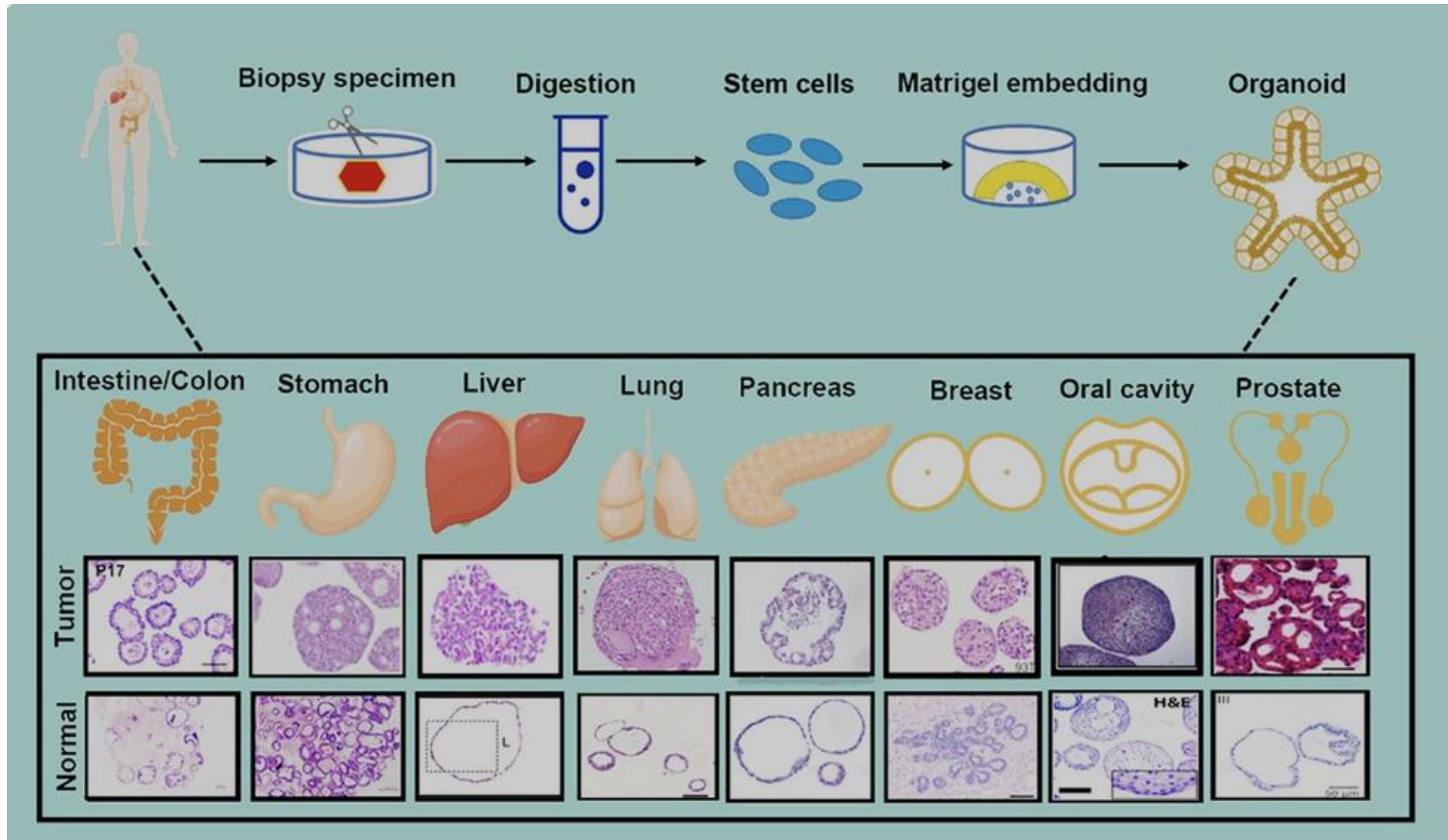


Patient derived xenograft and Humanized-xenograft model



What is the difference between these two models?

Organoids



Laboratories working on organoids EPFL

Wouter Richard Karthaus

wouter.karthaus@epfl.ch

+41 21 693 81 49

[vCard](#)

PhD program committee member, Doctoral Program Molecular life sciences ▼

+41 21 693 81 49

[EPFL](#) › [VPA](#) › [VPA-AVP-DLE](#) › [AVP-DLE-EDOC](#) › [EDMS-GE](#)

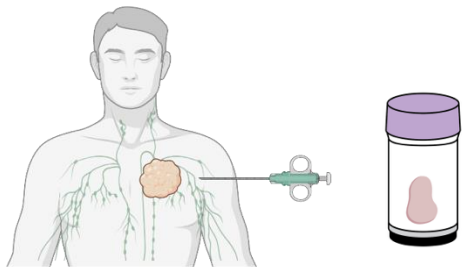
<https://go.epfl.ch/phd-edms>



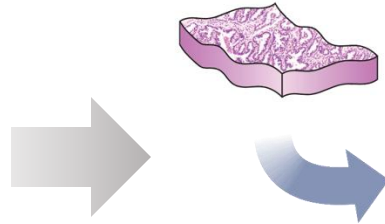
Fragments of tumors: tissue explants

Hospitals (CHUV)

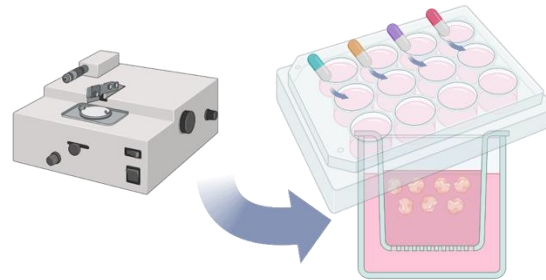
Laboratory



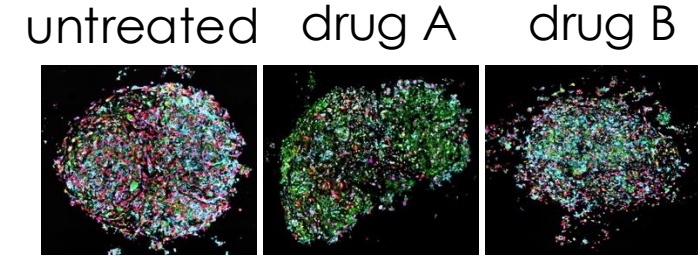
1. Obtain a fresh tumor tissue



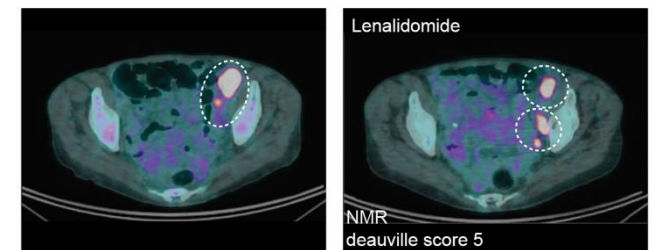
2. Reduce it in small fragments



3. Test different therapies



4. Assess response to therapies using image-based analyses



5. Matches with clinical response

Laboratories working on tissue explants in EPFL

Albert Santamaria Martinez

[Edit profile](#)



albert.santamariamartinez@epfl.ch

[+41 21 693 36 26](tel:+41216933626)

Scientist, Prof. Oricchio Group ▲

EPFL SV ISREC UPORICCHIO

SV 2824 (Bâtiment SV)

Station 19

1015 Lausanne

Web site: <https://oricchiolab.epfl.ch>

[+41 21 693 36 26](tel:+41216933626)








Office: [SV 2824](#)

[EPFL](#) > [SV](#) > [ISREC](#) > [UPORICCHIO](#)

Oricchio lab: for new model development and Albert for clinical development

Patient avatars

A

	 Genomic Sequencing	 Metabolomics/ Proteomics	 Patient-Derived Cell Lines	 Patient-Derived Xenografts	 Patient-Derived Tissue Explants	 Patient-Derived Organoids	 Patient-Derived 3D Micro-Models
Predictive Power	+++	++	+	+++	++	+++	+++
Predictable Therapies	T	T	C/R	T/C/IO*/R	T/C/IO/R	T/C/R	T/C/IO/R
Speed	+++	+++	+	-	+++	++	+++
Establishment Success from Biopsy	+++	++	-	+	-	+	++
Throughput	+++	+++	+	-	-	+	+++
TME	-	-	-	++*	+++	-	++
Reproducibility	+++	+++	++	+++	-	++	+++
Cost	+	+	+	+++	++	++	+

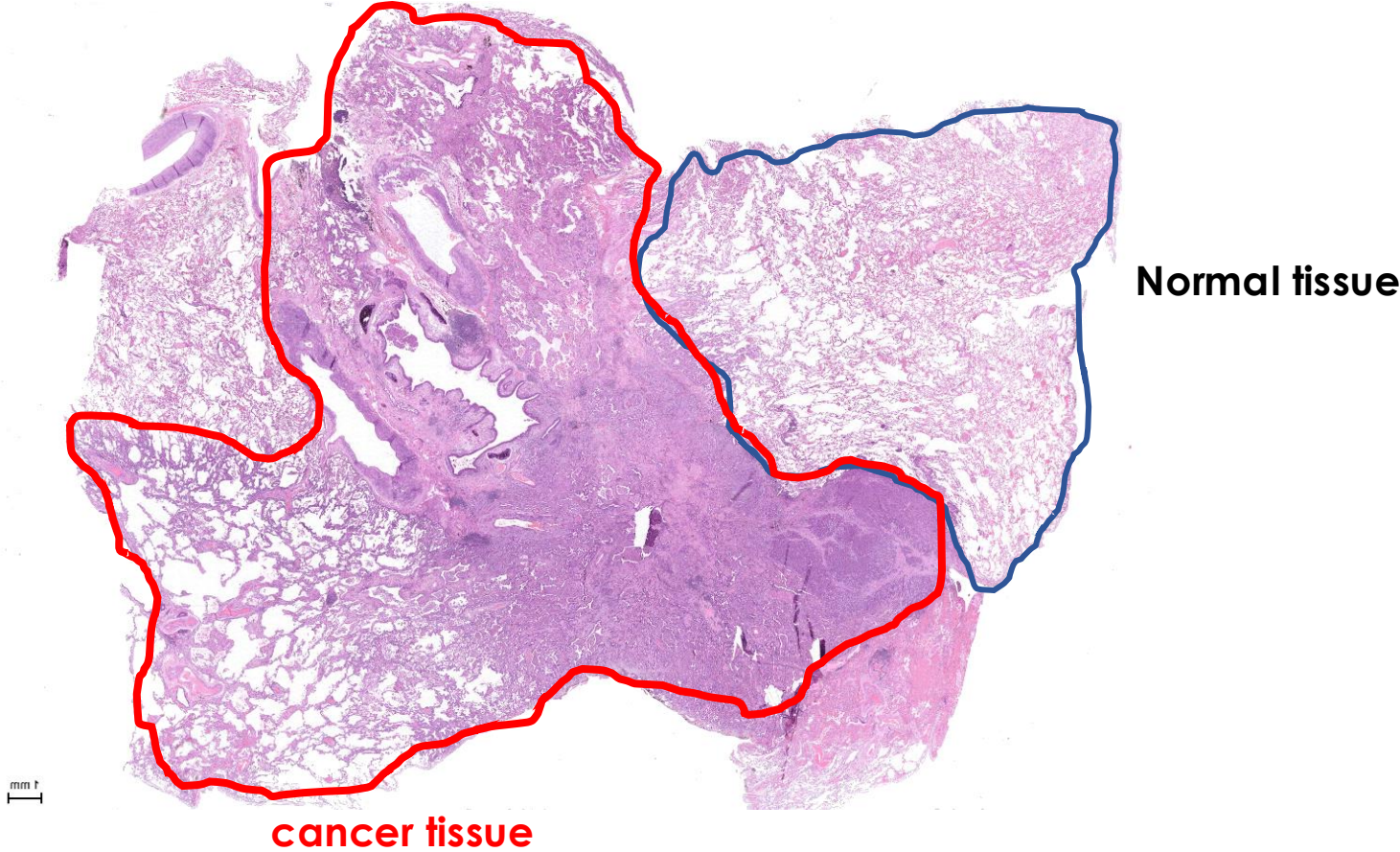
T = Targeted Therapies, C = Chemotherapies, R = Radiation, IO = Immuno-oncology Therapies, TME = Tumor Microenvironment

*PDX models include mouse stromal cells in the TME and require immune reconstitution with humanized mouse models to adequately recapitulate IO therapies.

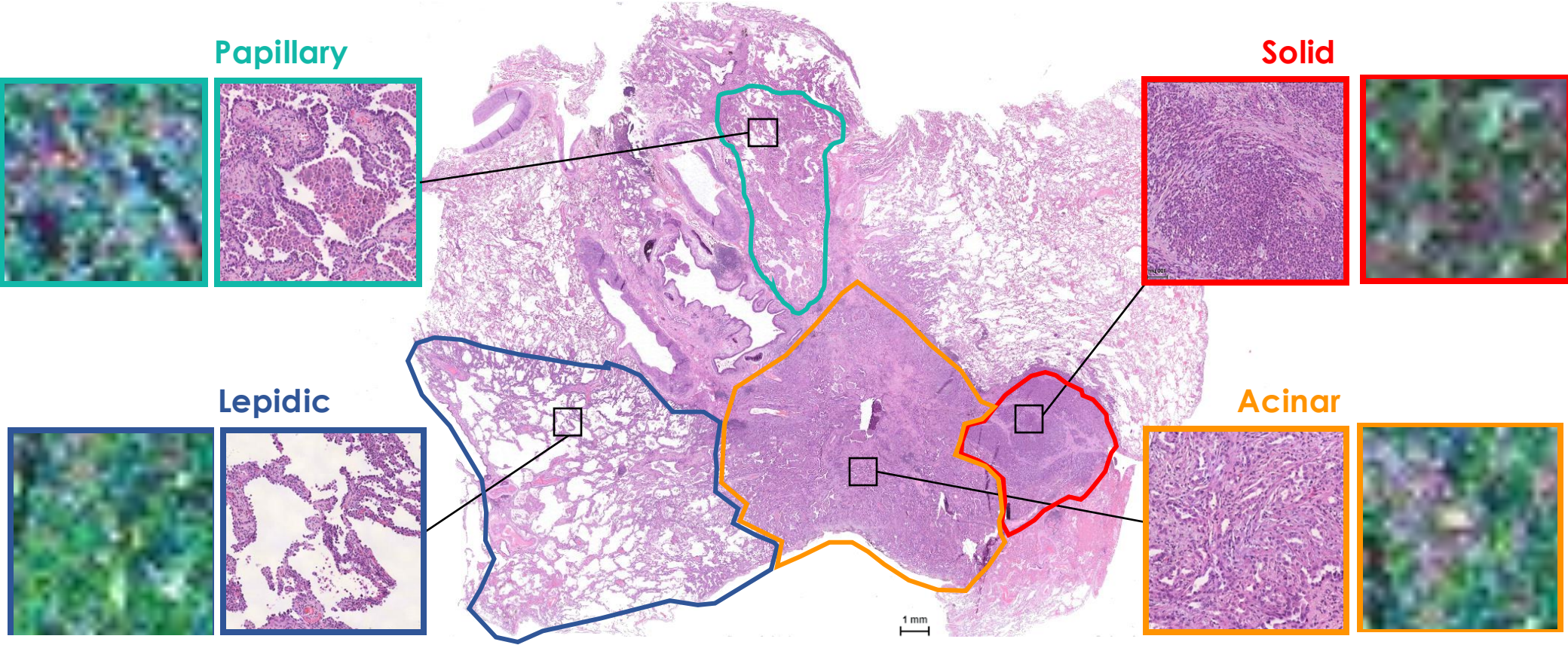
Cancer intra-tumor heterogeneity and its evolution

Cancer is an heterogenous disease

Lung cancer patient

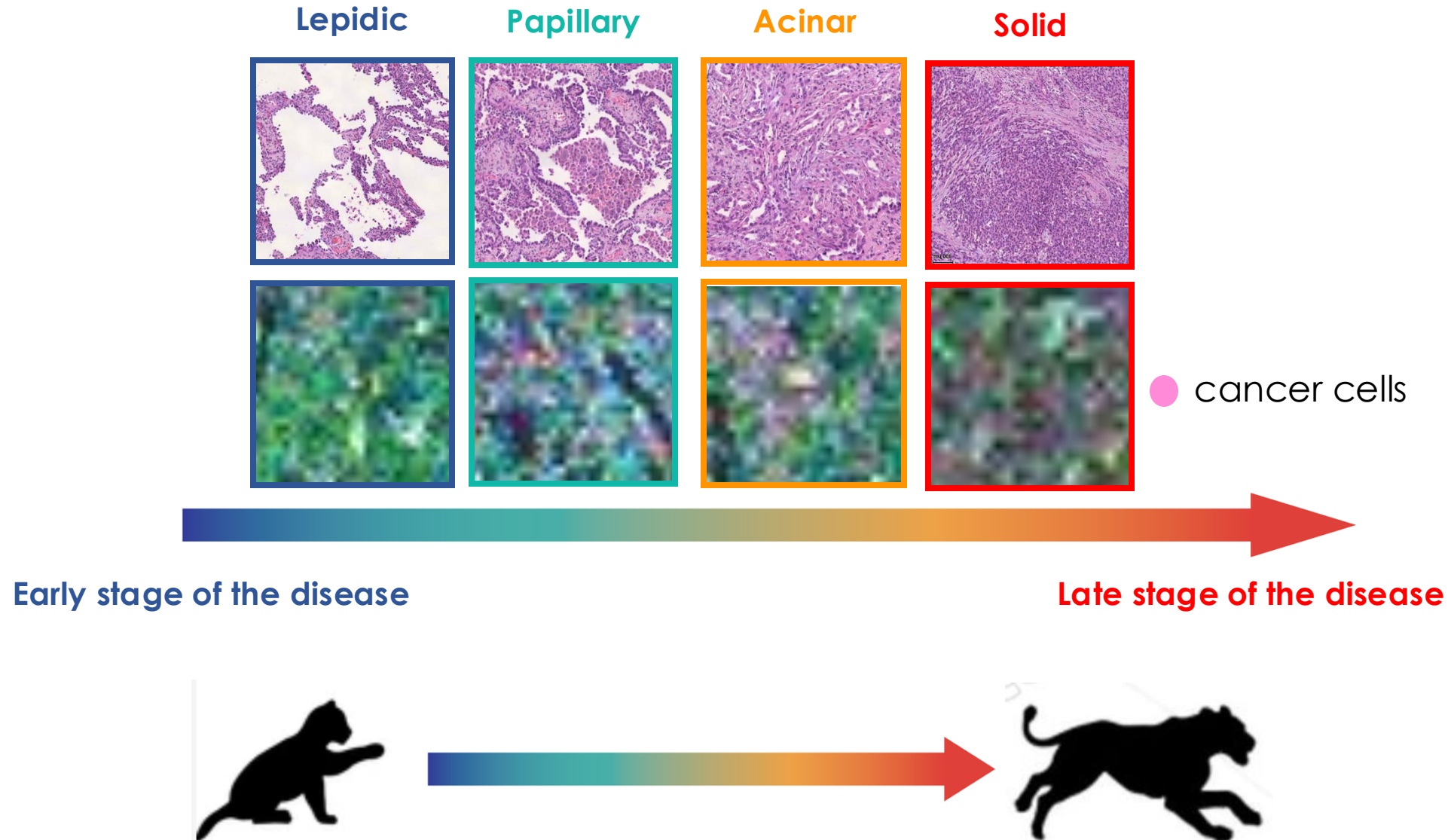


Cancer is an heterogenous disease

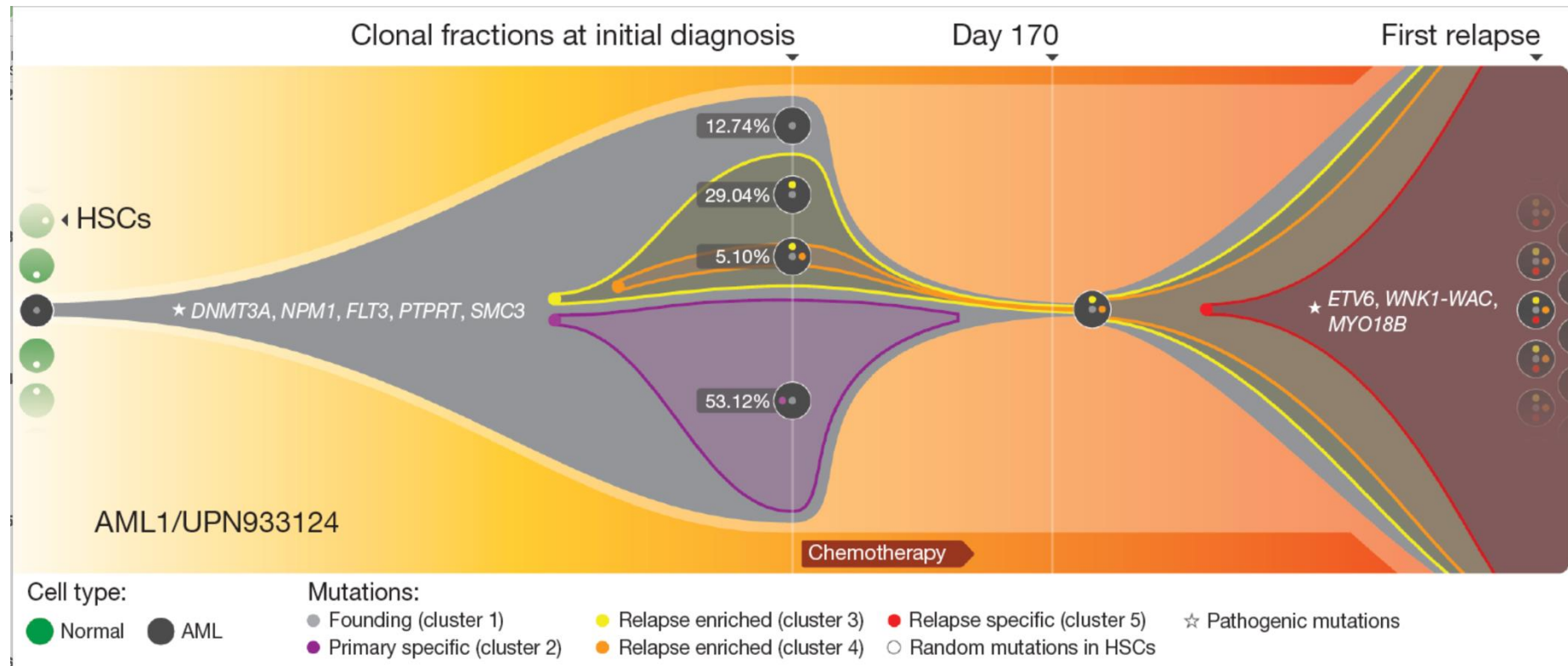


● cancer cells

Cancer is an heterogenous disease **that evolves over time**

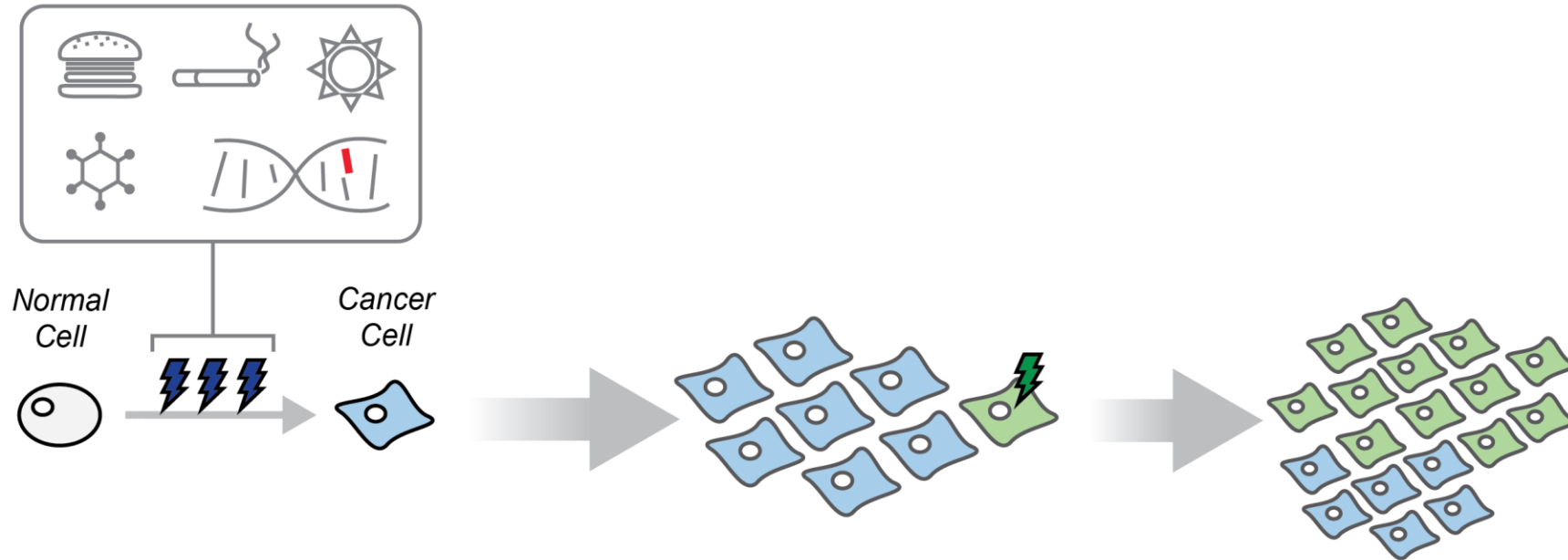


Cancer is a disease that evolves following the principle of species evolution

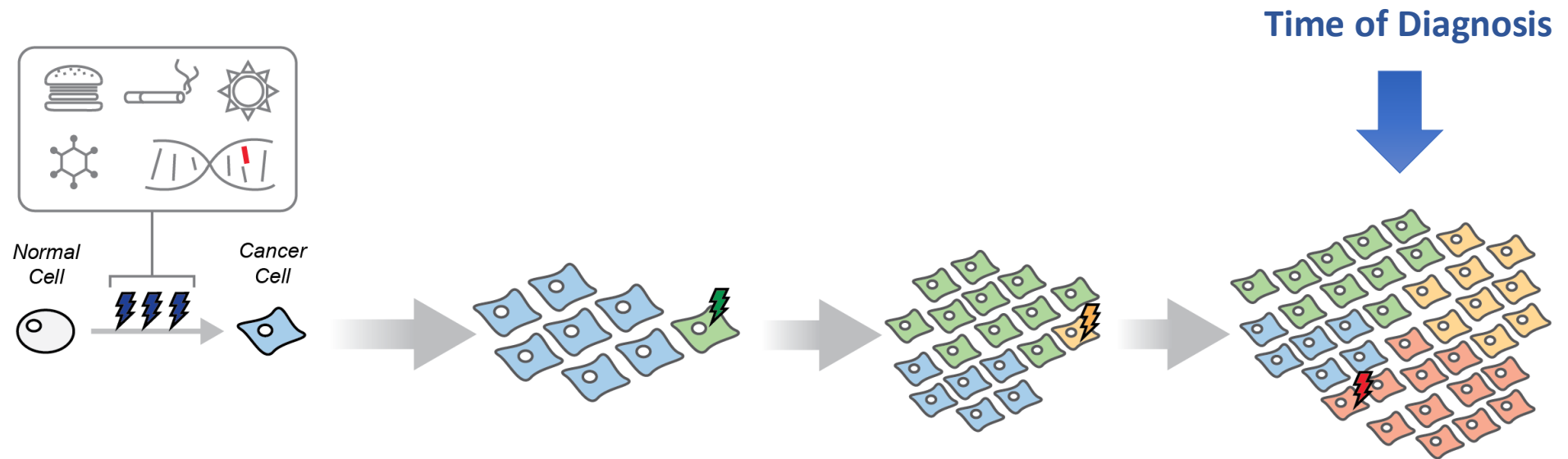


What happens during the time of chemotherapy treatment to tumor evolution?

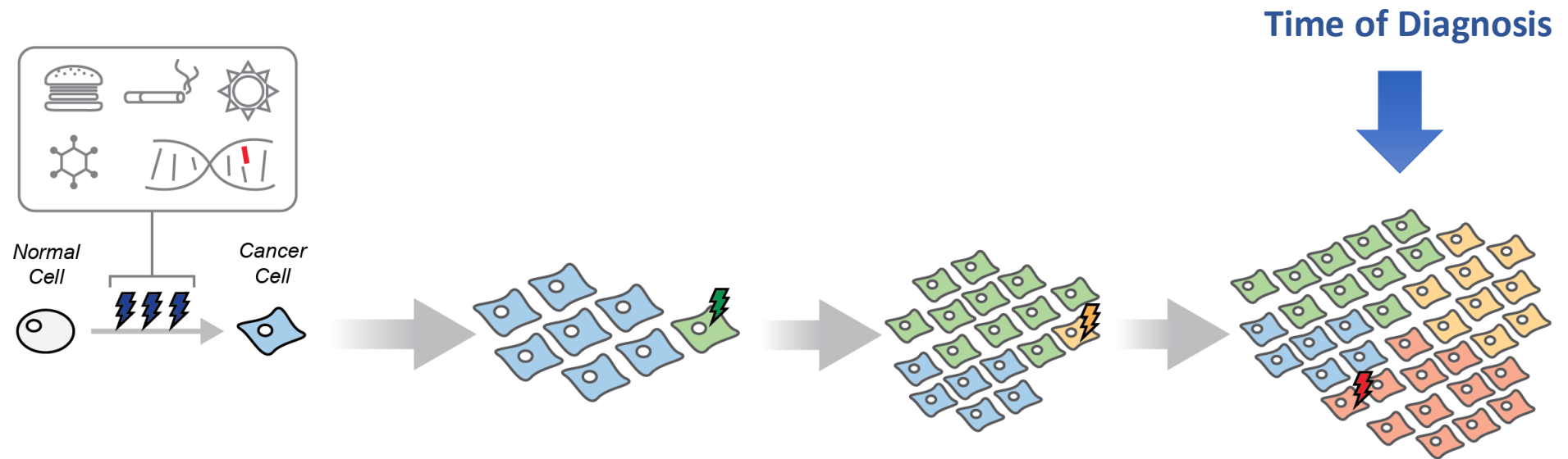
A simplified model of cancer evolution



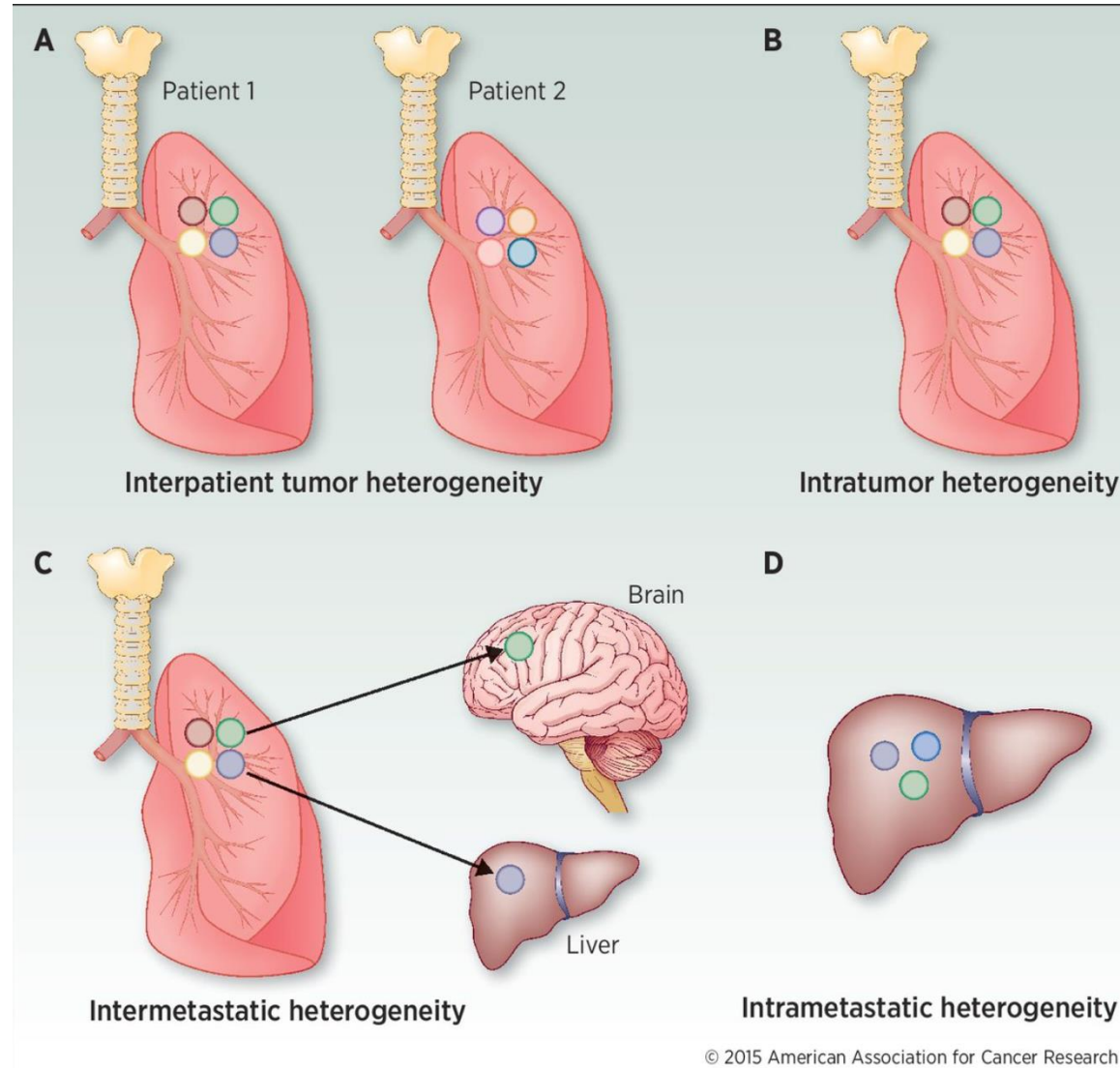
A simplified model of cancer evolution



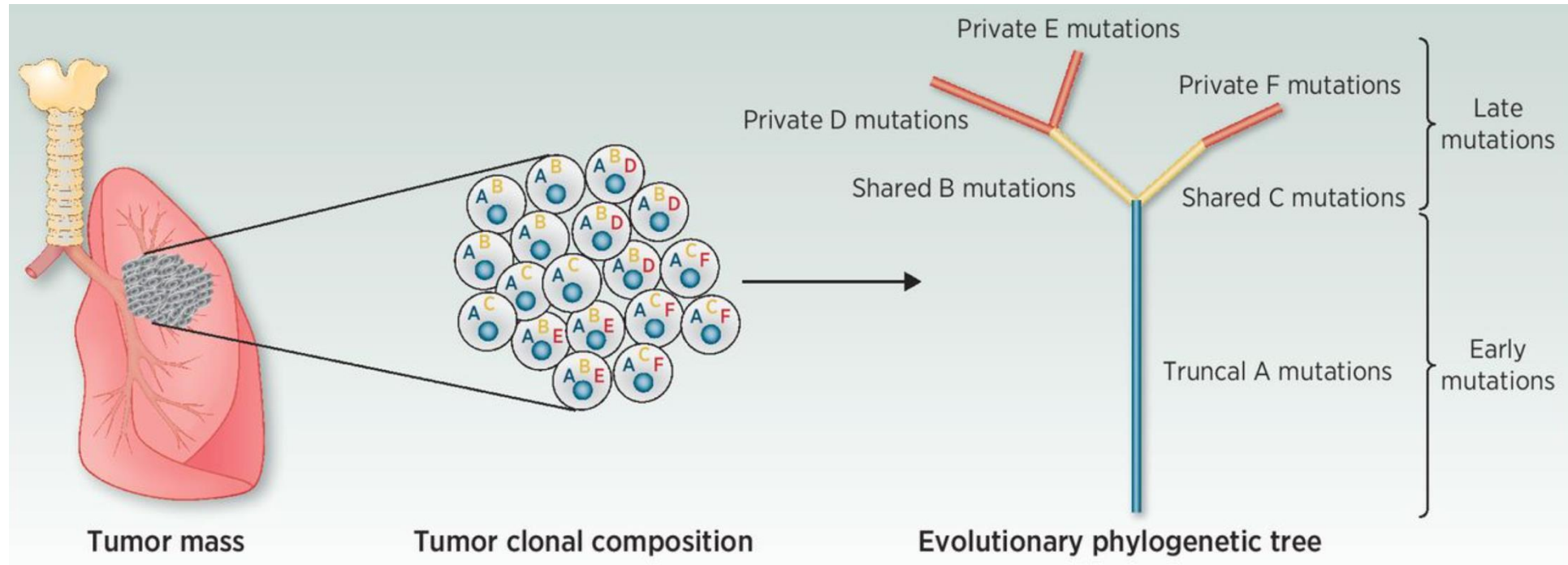
A simplified model of cancer evolution



Intra-tumor heterogeneity and metastasis



Intra-tumor heterogeneity



Phylogenetic tree analyses: study of cancer evolution driven by accumulation of genetic mutations

Paper for Wednesday

<https://www.nejm.org/doi/pdf/10.1056/NEJMoa1616288>

Pdf will be in the moodle with a list of questions to guide the discussion