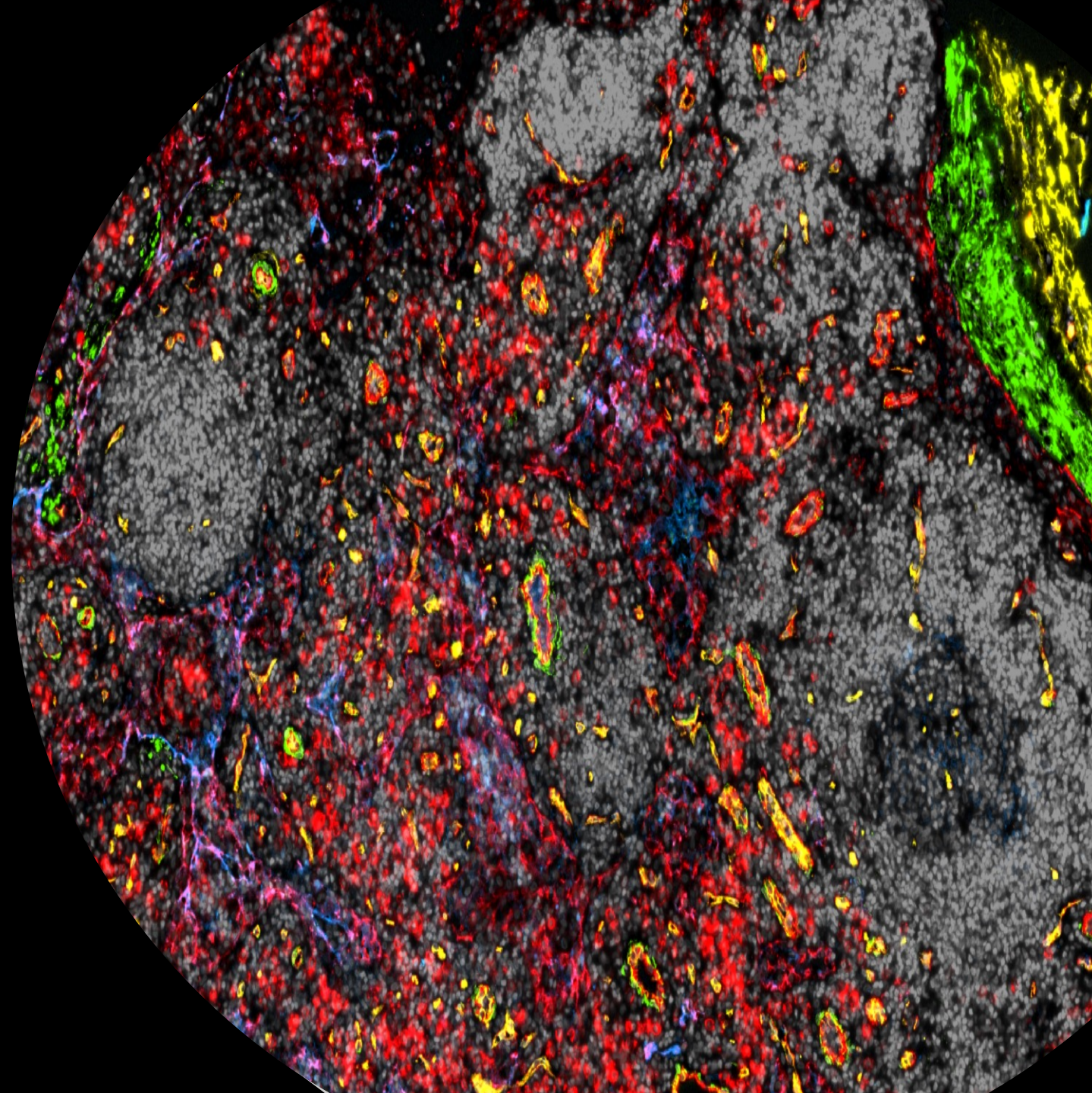


Cancer Biology I

Part-II

Week 9



AGENDA

Nov 5th: Cancer genomics- mutations

Nov 11th: Cancer genomics-copy number alteration, heterogeneity, evolution (recording)

Nov 18th: Cancer Epigenetics- chromatin 3D structure, cell plasticity

Nov 25th: – Major signaling pathways leading to cancer

Dec 2th: Cancer Therapies – chemo and targeted therapies

Dec 9th: Introduction to immunotherapies –

Dec 16th: Exam

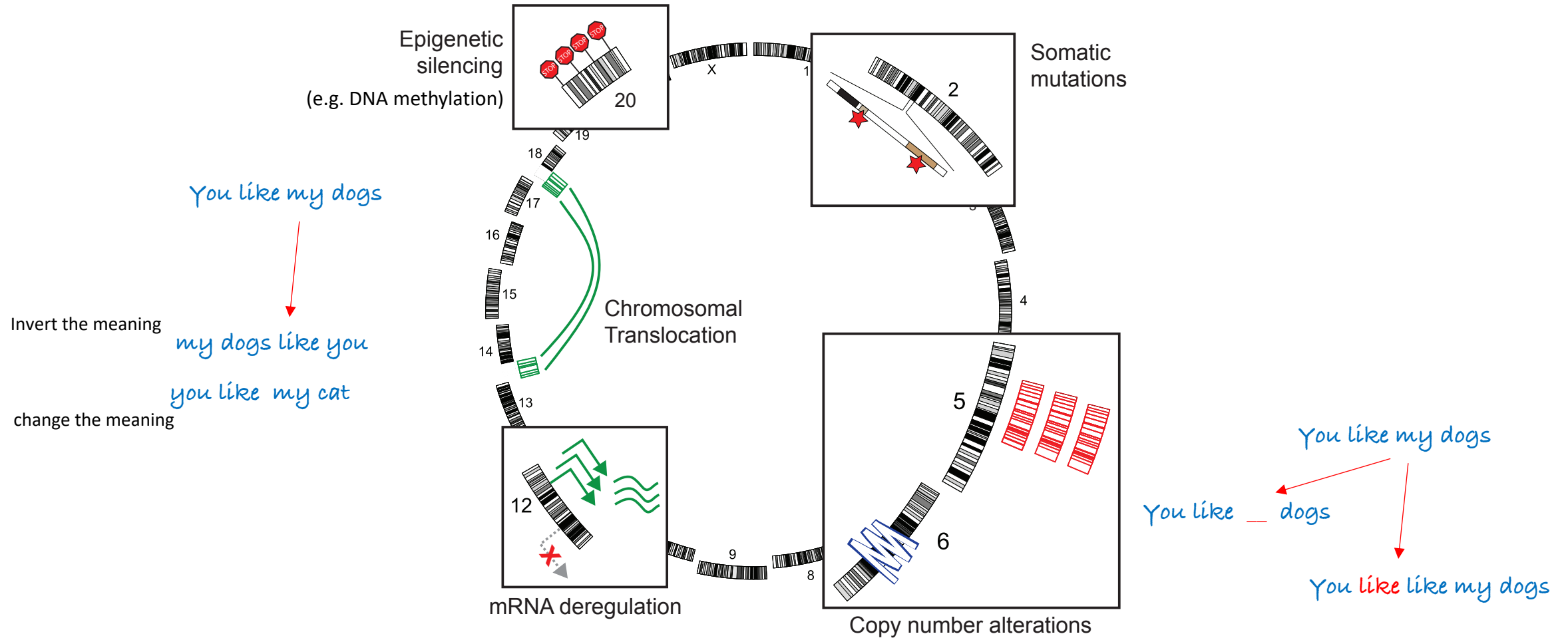
(if it conflicts with another exam it is possible to do the exam on Dec 18th)

Dec 18th: discussion of exam questions and career development discussion towards a PhD or not...

Is it cancer only driven by
somatic mutations?

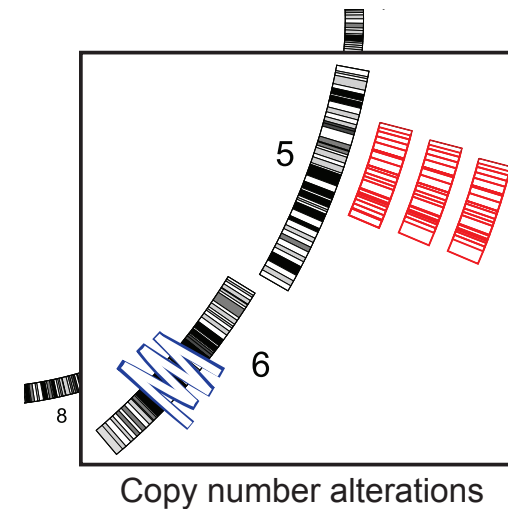
What are they?

Cancer Genomic Alterations

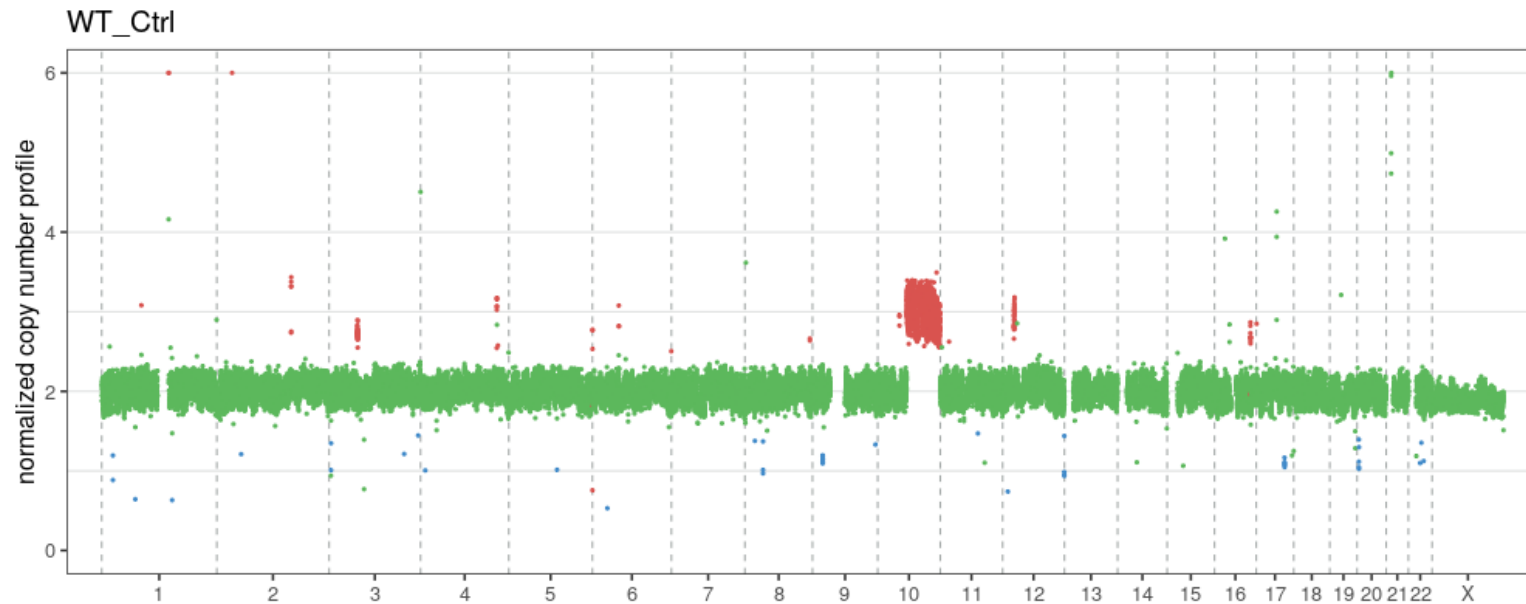


Copy Number Alterations

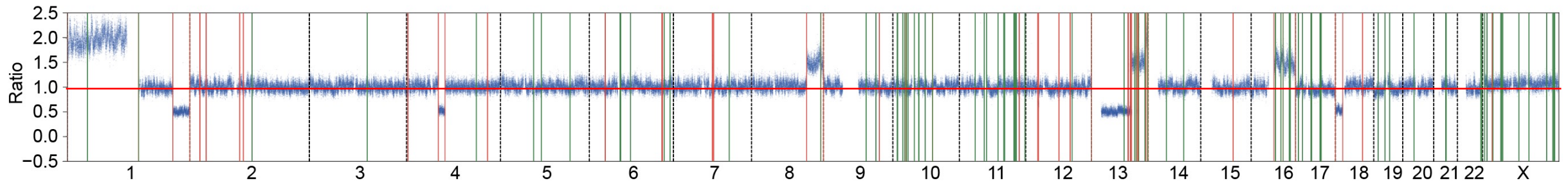
- *Deletion*: Loss of chromosomal regions
(Heterozygous or Homozygous)
- *Amplifications*: Acquire one or more copy of chromosomal regions
(Duplication or Amplification)



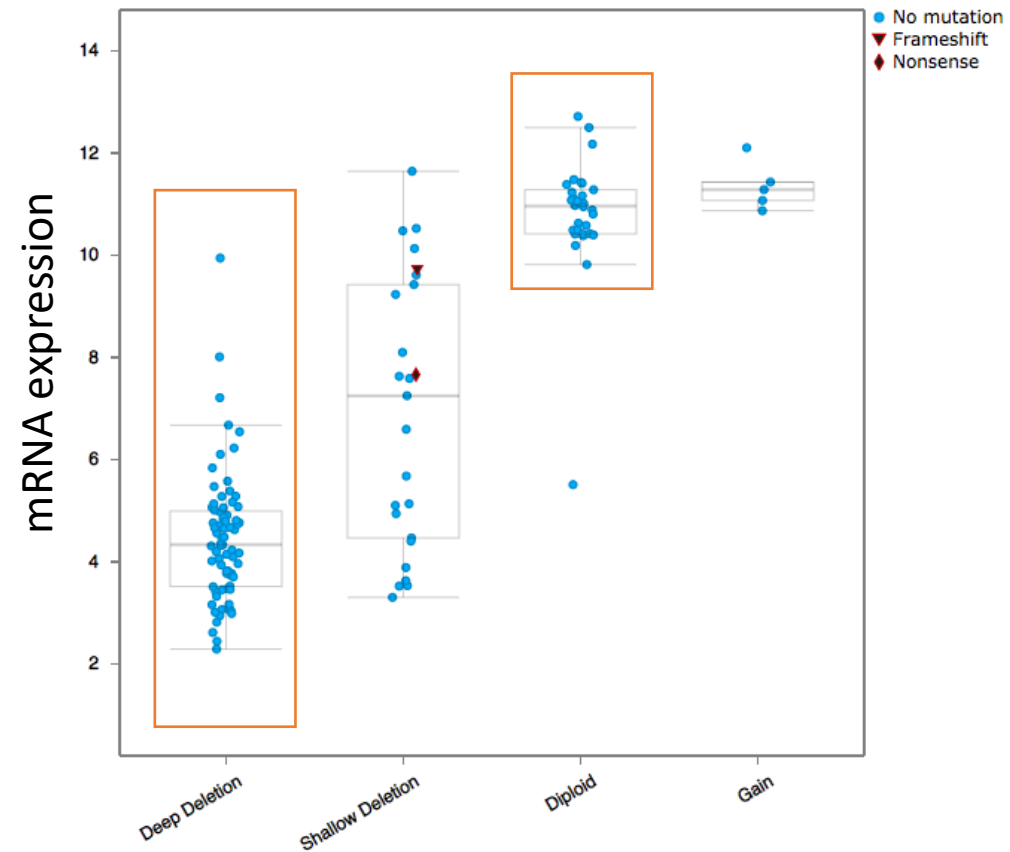
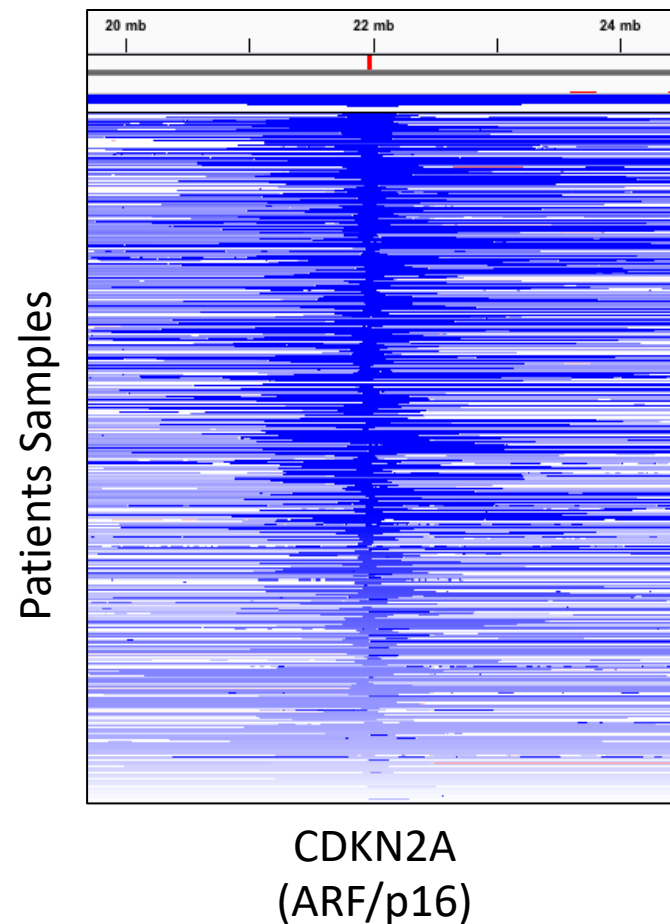
Copy Number Alterations: whole genome sequencing or SNP array



Copy Number Alterations: whole genome sequencing or SNP array

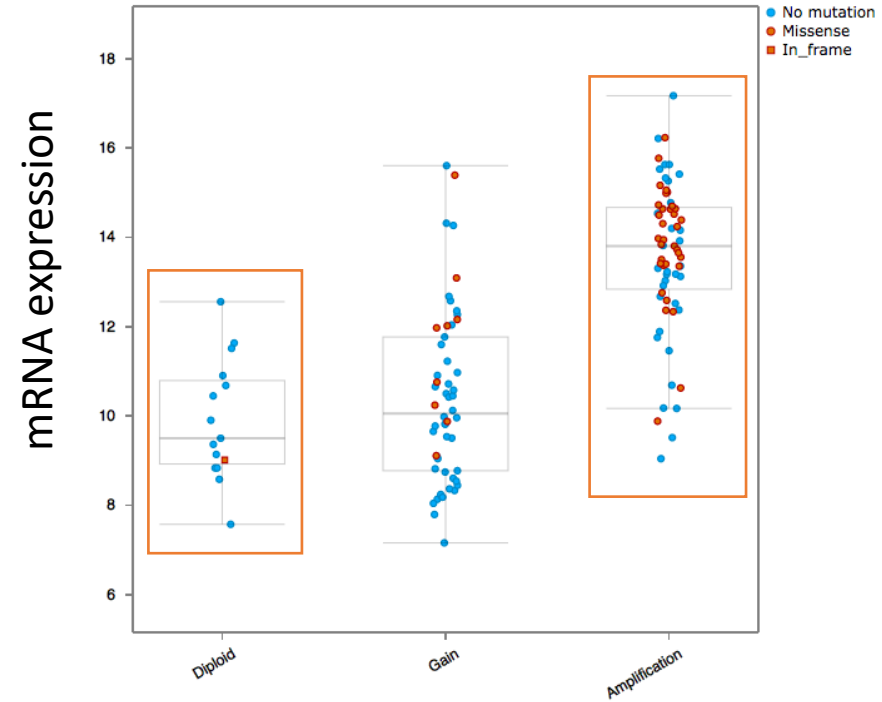
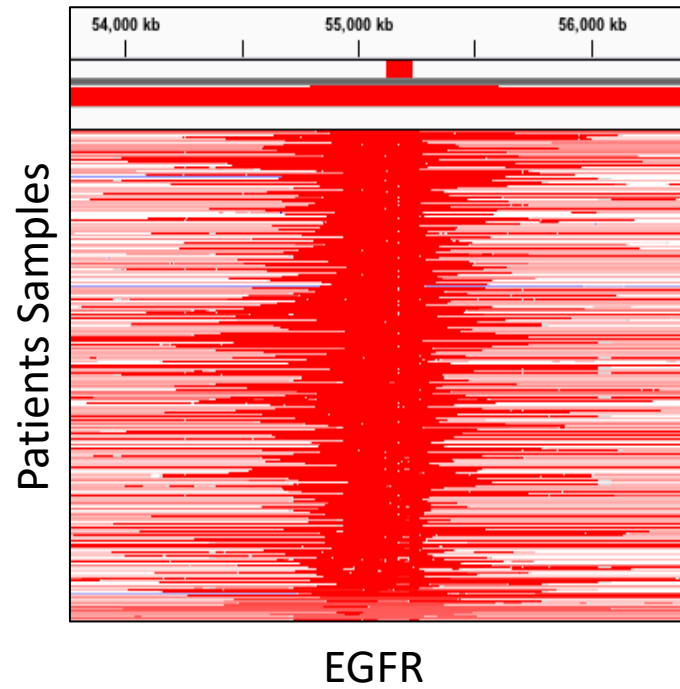


Focal Deletions derived from multiple cancer patients (inactivating a **tumor suppressor**)

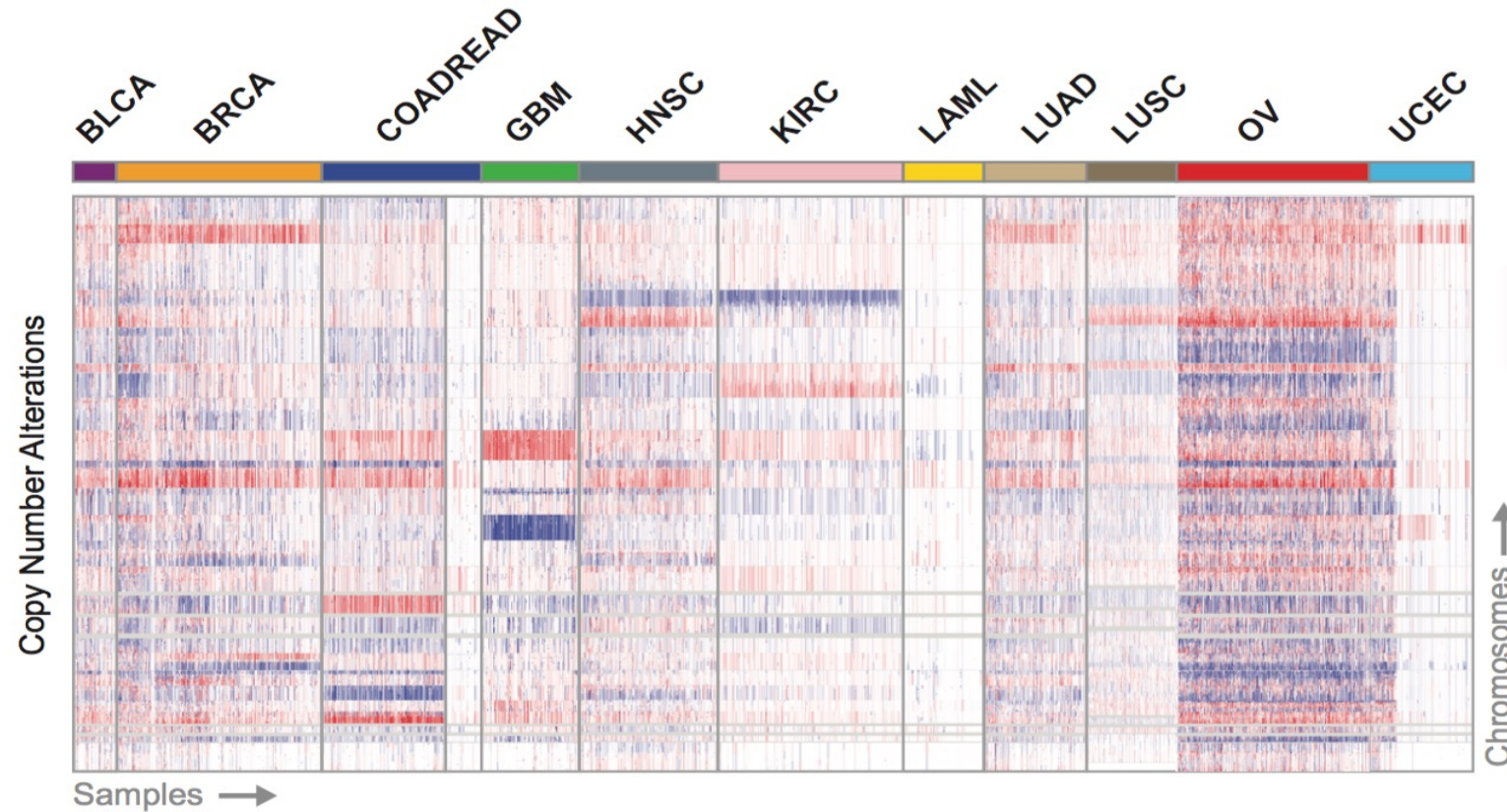


Focal Amplifications

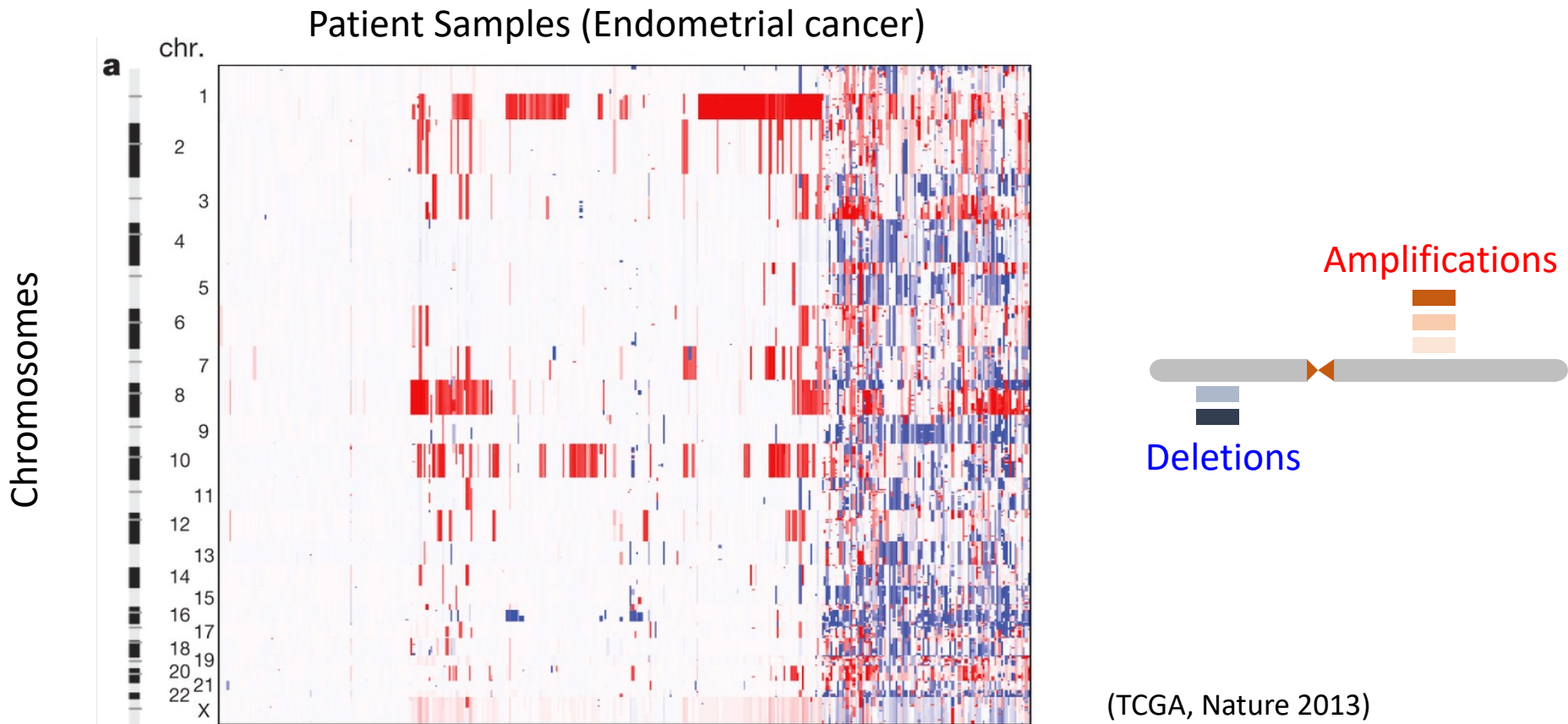
(activating an *oncogene*)



Copy Number Alterations inter-tumor heterogeneity



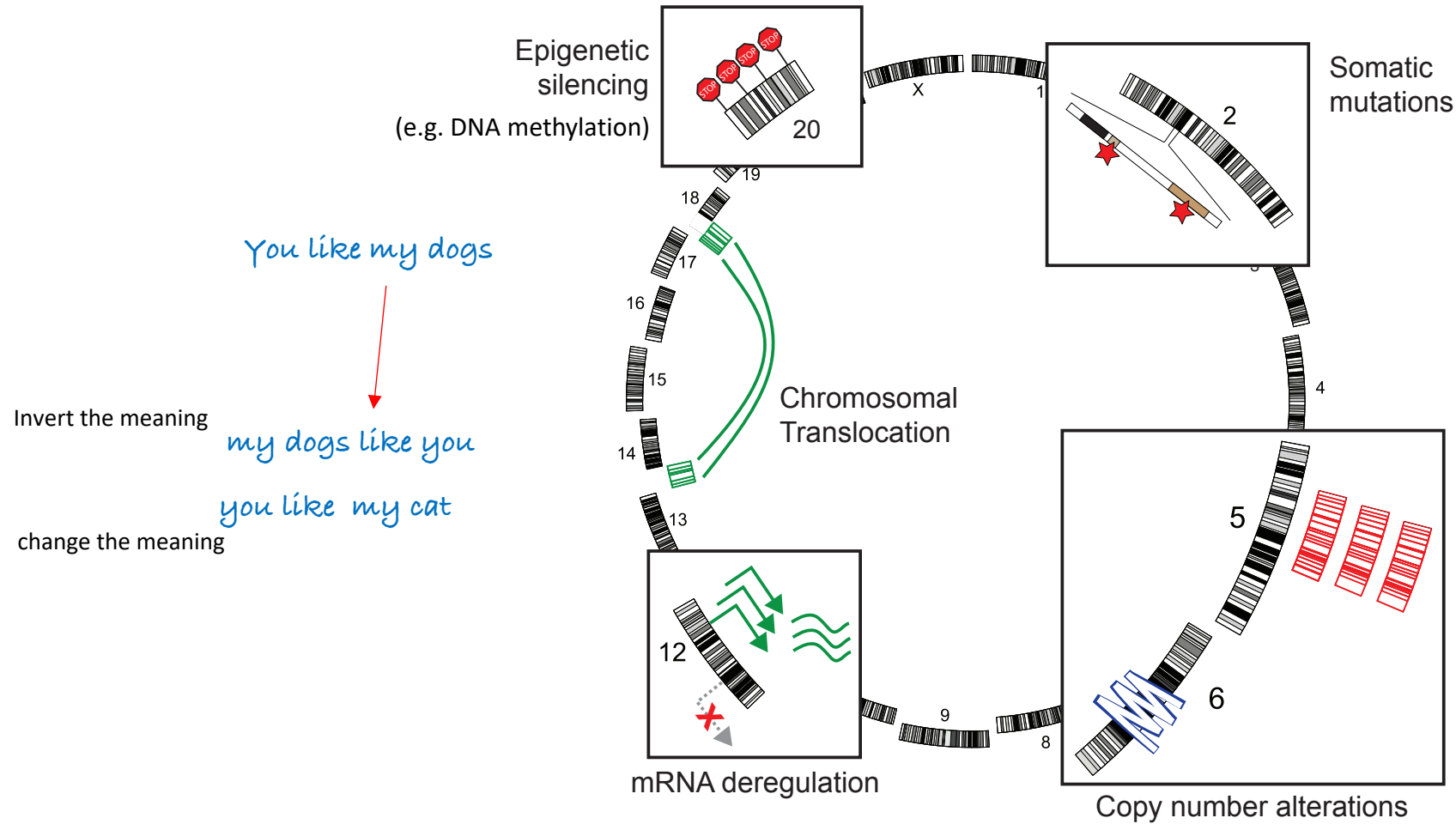
Copy Number Alterations inter patient heterogeneity



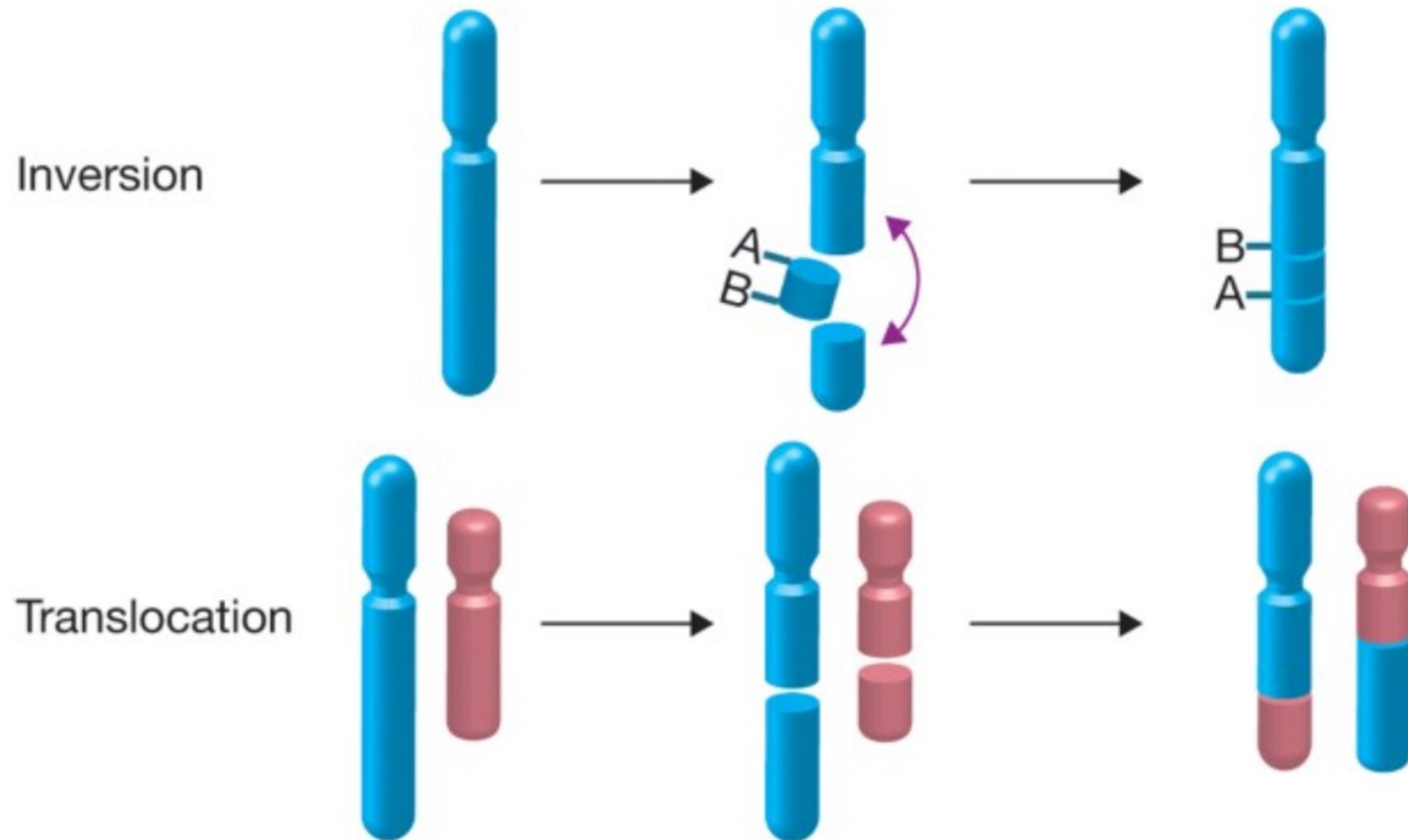
- Tumor subtypes defined by copy number alterations

What are they?

Cancer Genomic Alterations

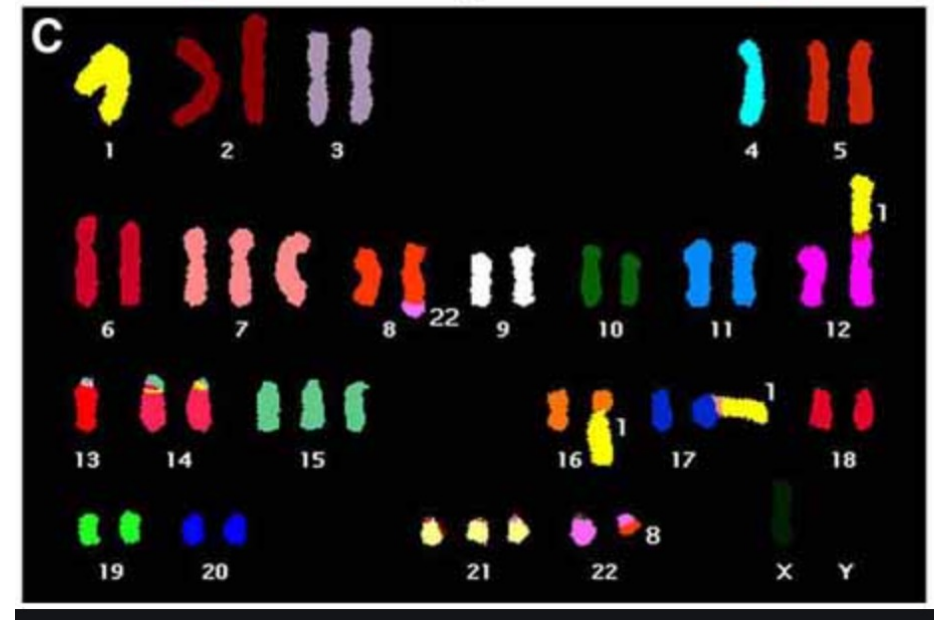
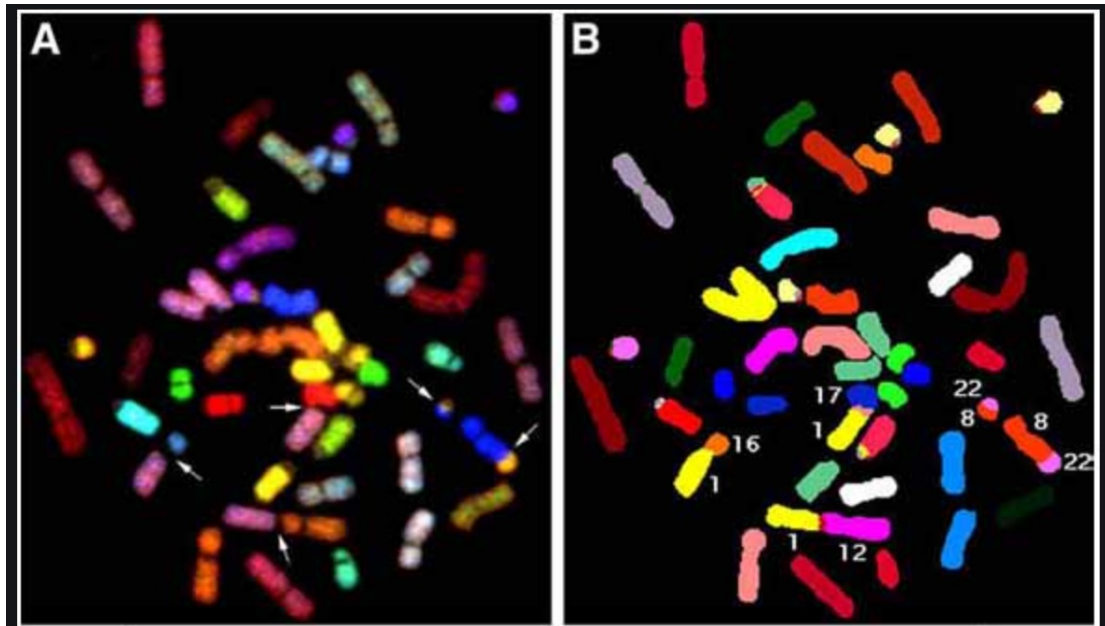


Chromosomal Structural Variants



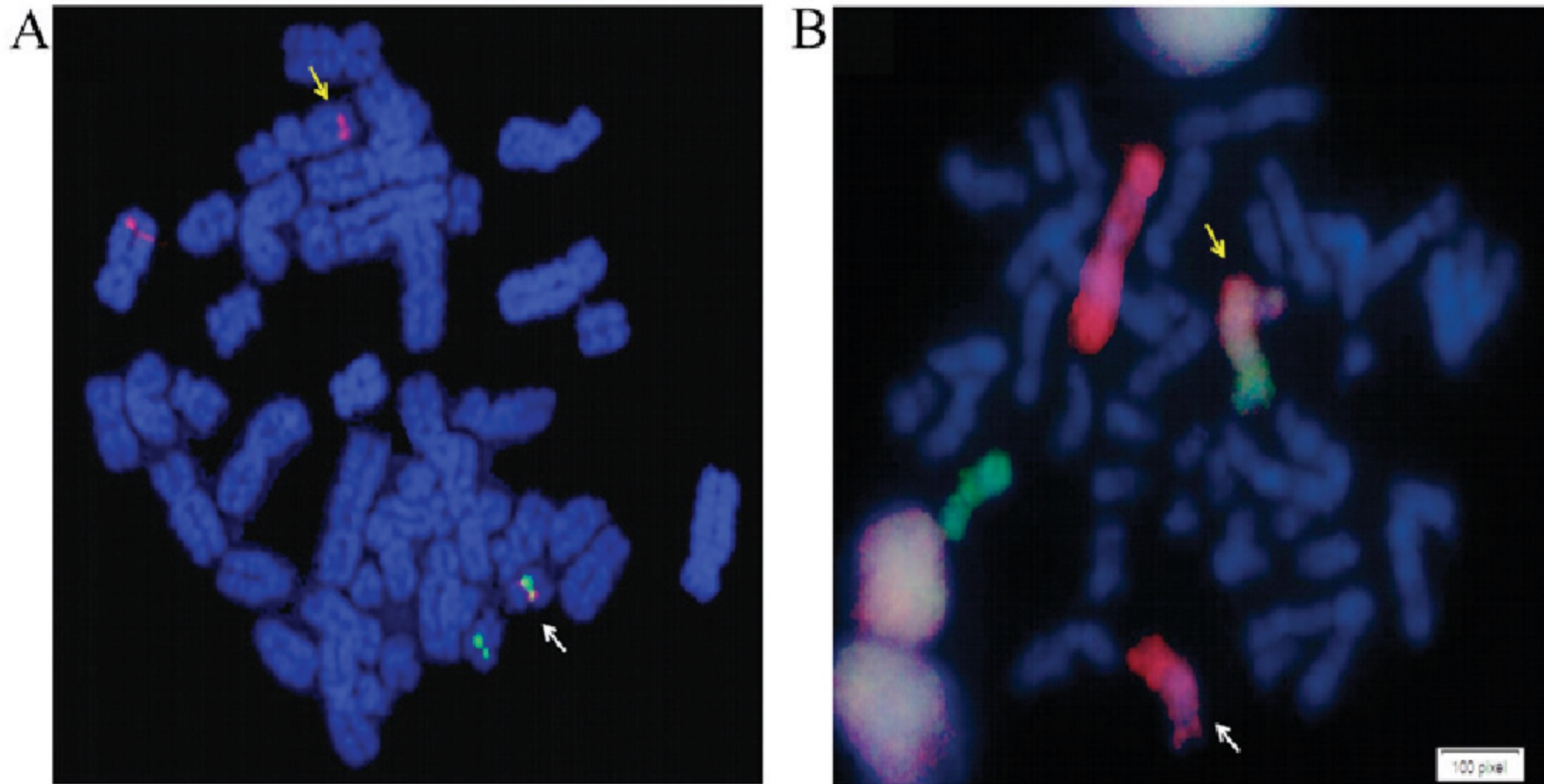
Chromosomal Structural Variants

Translocations became apparent from “chromosome painting” (long before NGS techniques)

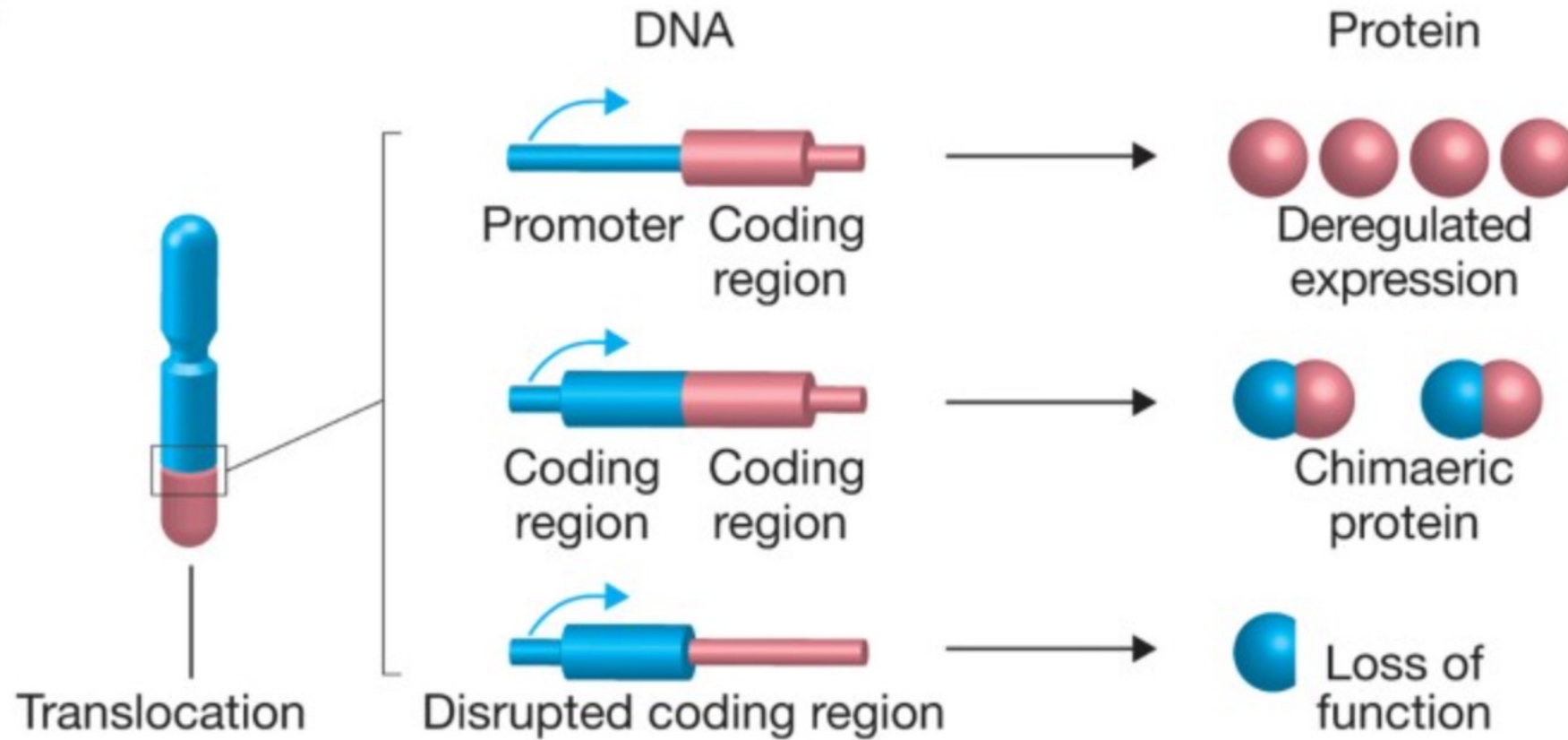


Chromosomal Structural Variants

Translocations became apparent from “chromosome painting” (long before NGS techniques)

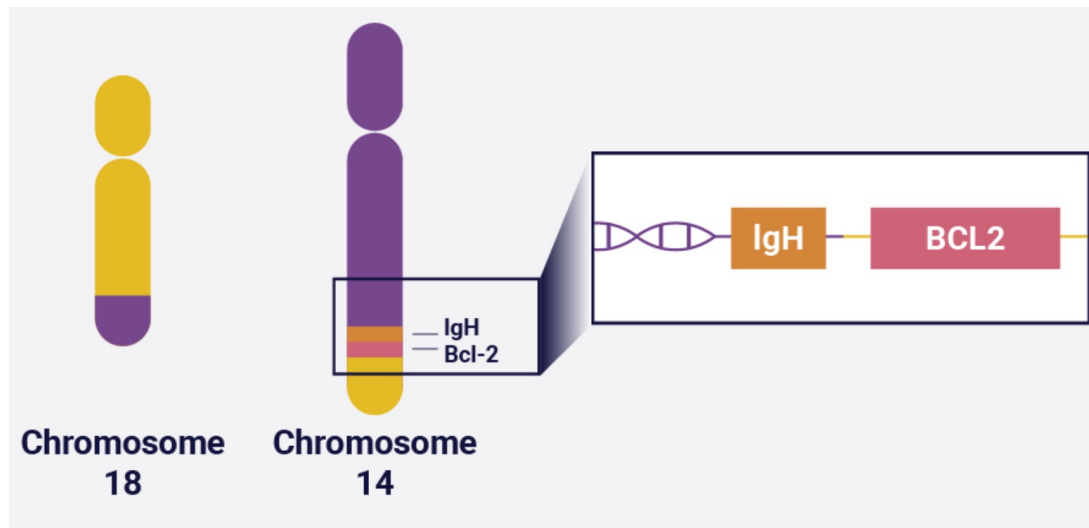


Chromosomal Structural Variants

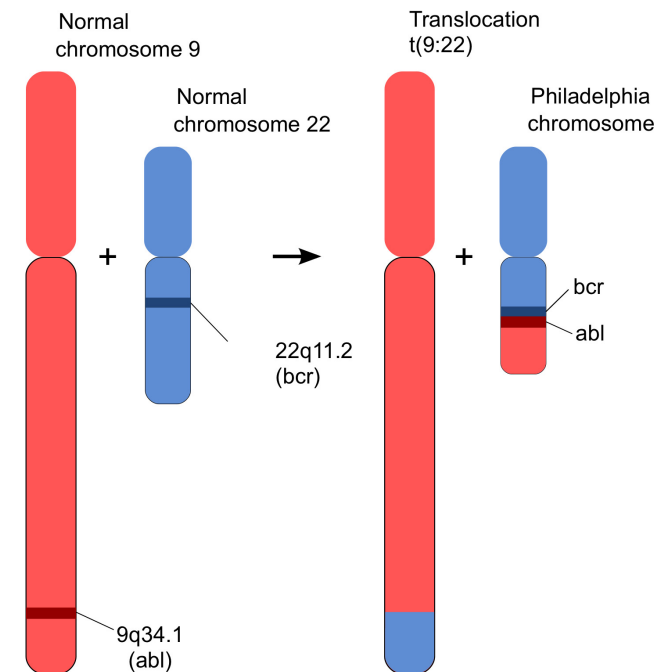


Chromosomal Structural Variants

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



Patterns of genomic alterations

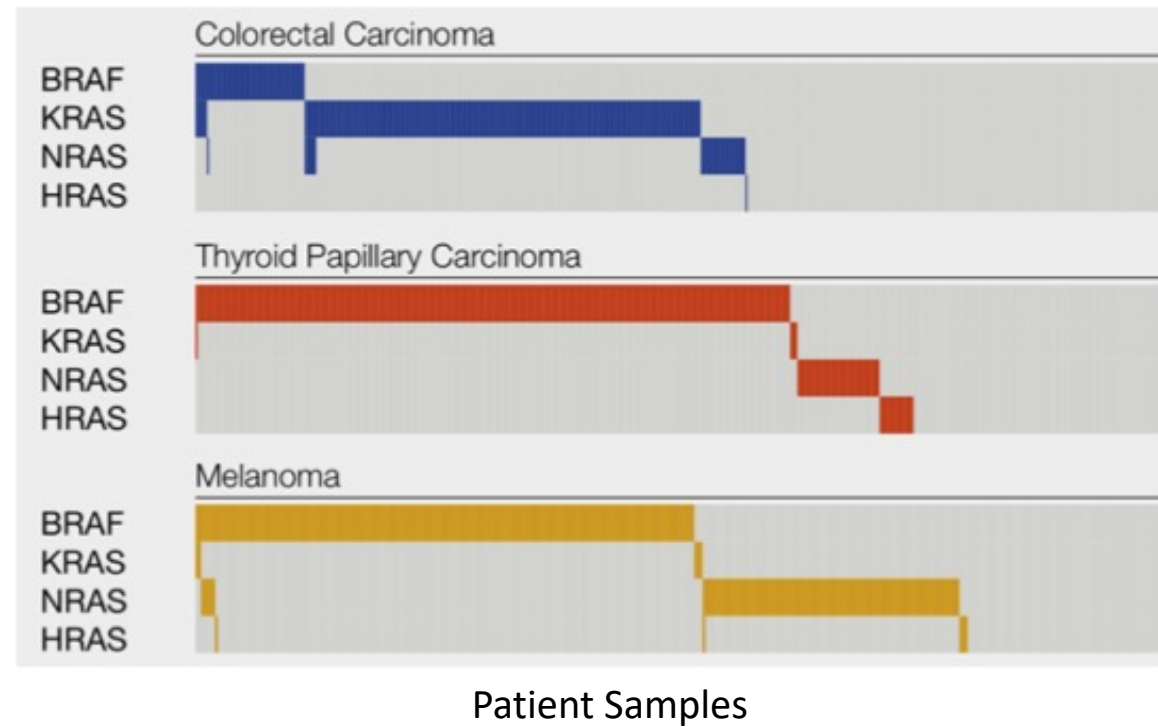
Considering both mutations and copy number changes:

MUTUALLY EXCLUSIVE: rarely occur together

CONCURRENT ALTERATIONS: frequently occur together

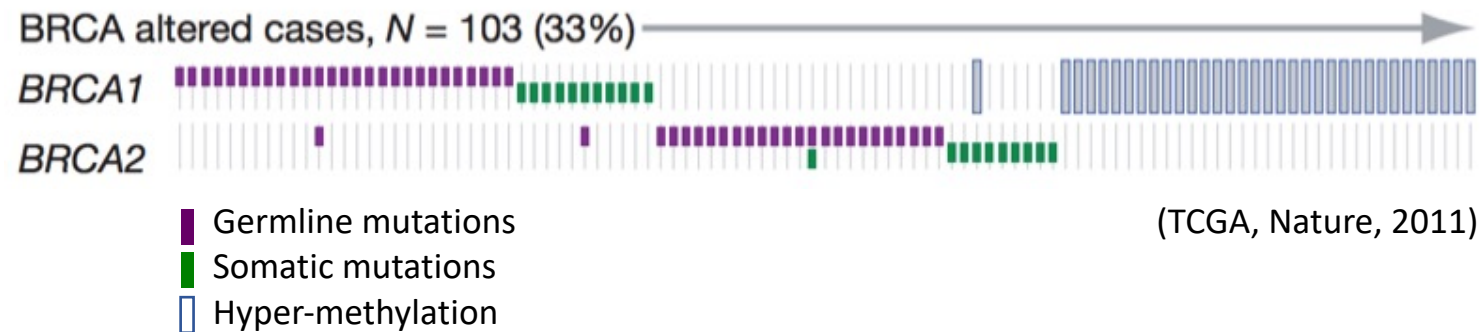
Mutual Exclusivity

- Observations of mutually exclusive alterations



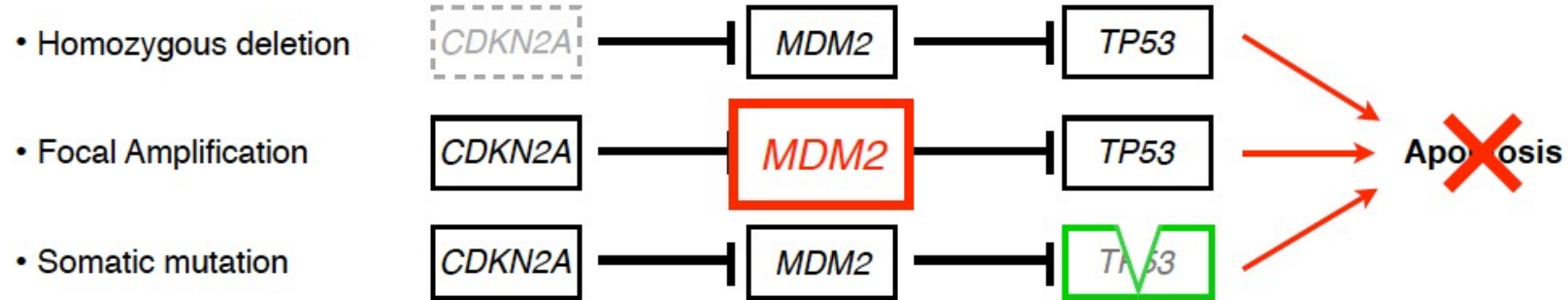
Mutual Exclusivity

- Observations of mutually exclusive alterations



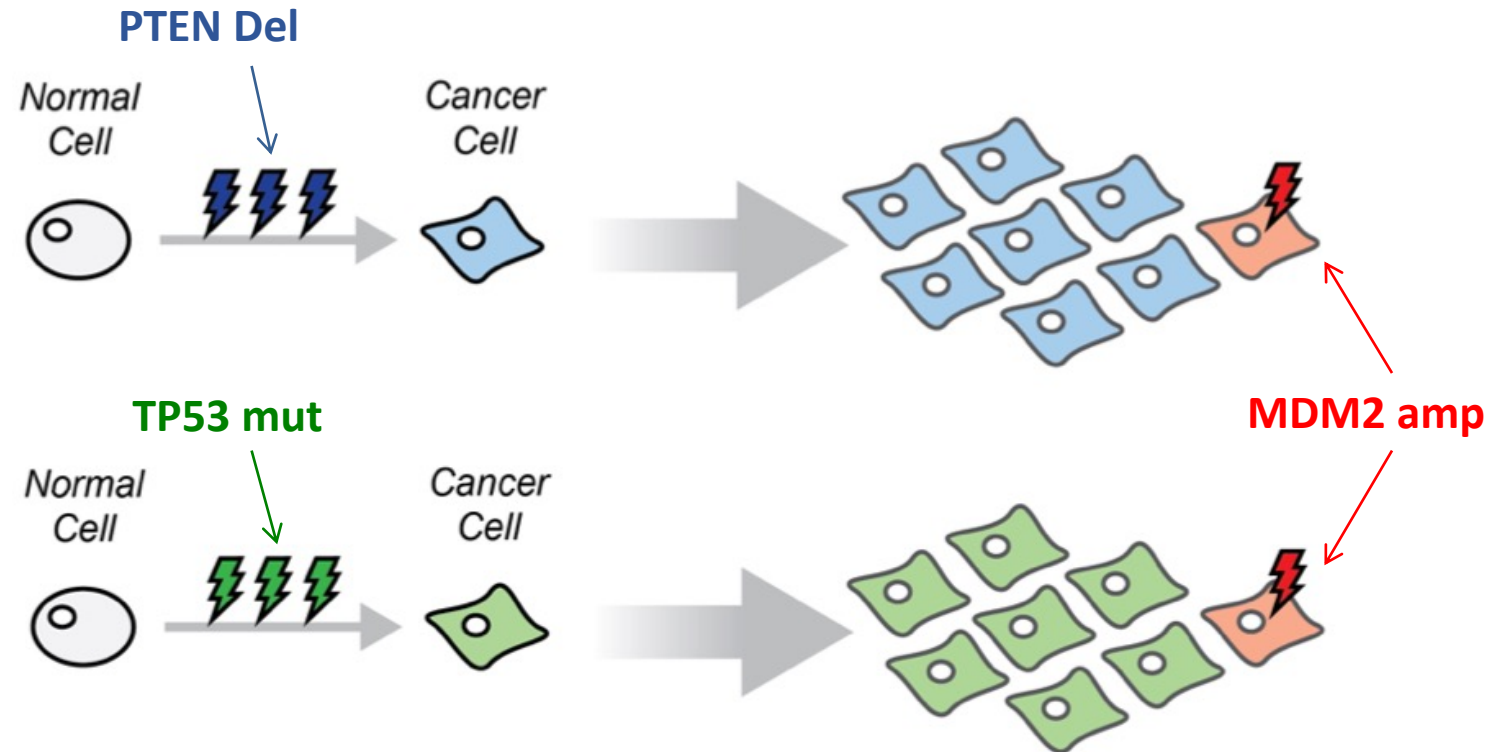
Why Mutual Exclusivity?

1) Selective Advantage



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

Mutual Exclusivity reflects Selection

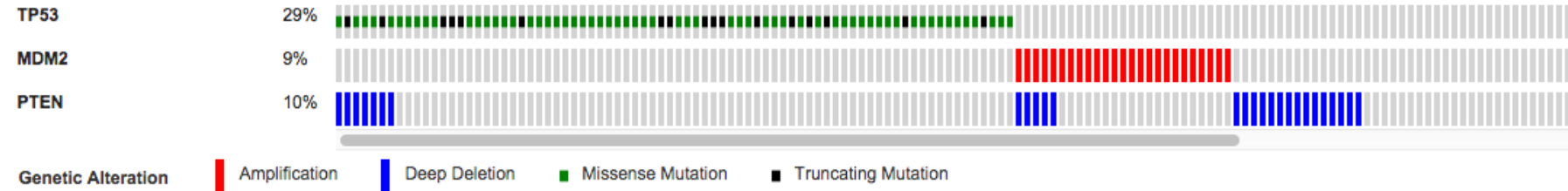


Is MDM2 amplification giving the same advantage in the 2 cases?

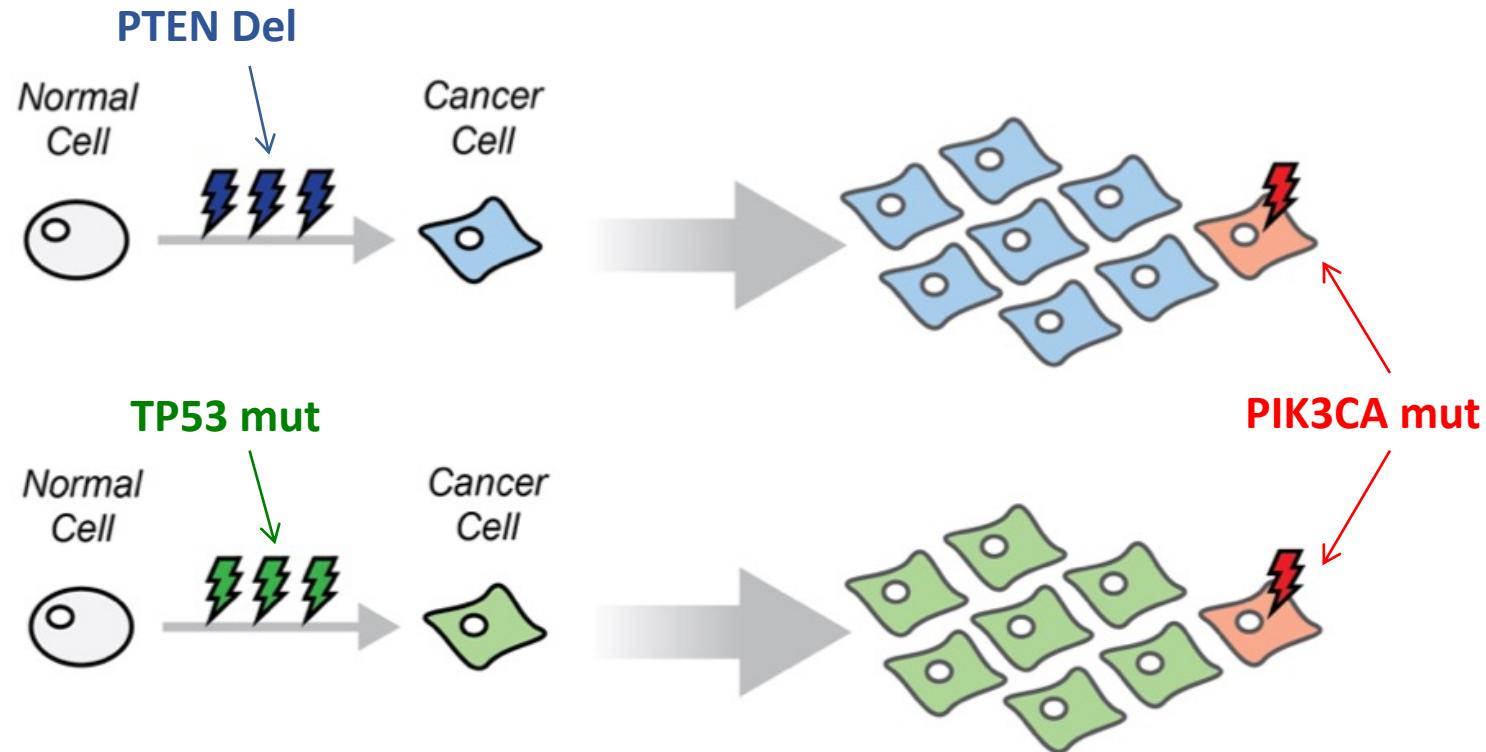
Mutual Exclusivity reflects Selection

TCGA Glioblastoma Dataset

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



Mutual Exclusivity reflects Selection

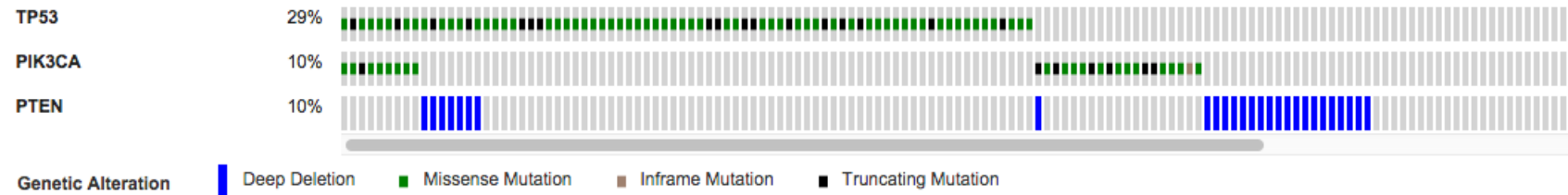


Is PIK3CA mutation giving the same advantage in the 2 cases?

Mutual Exclusivity reflects Selection

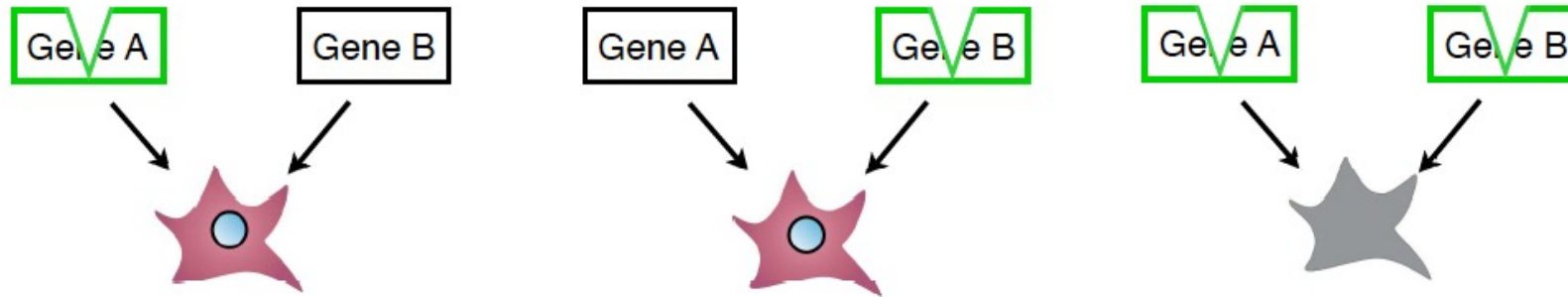
TCGA Glioblastoma Dataset (source cBioPortal)

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



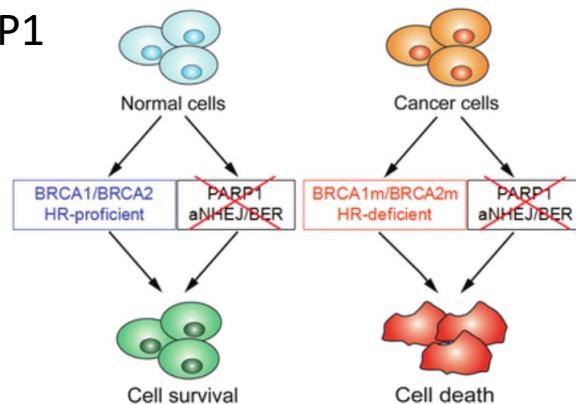
Why mutual exclusivity?

2) Synthetic Lethality



A second hit actually confers a disadvantage!

e.g. BRCA1/2 and PARP1

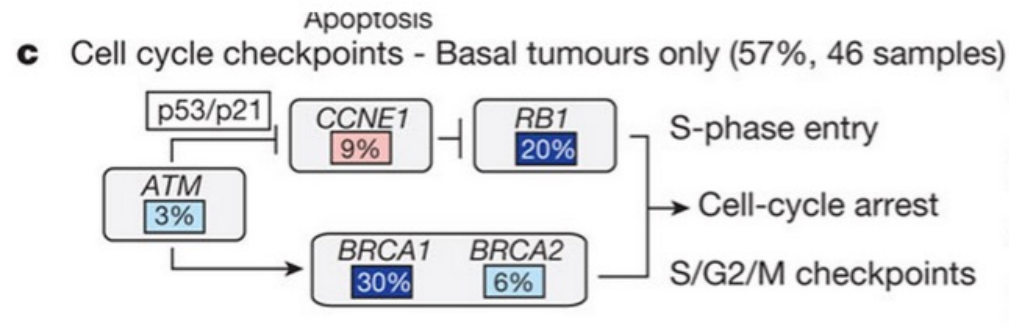


Synthetic Lethal interactions

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)

ADODTOSIS

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

Dariusz 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)

What are the challenges?

- **Prioritize the multitude of genetic aberrations**

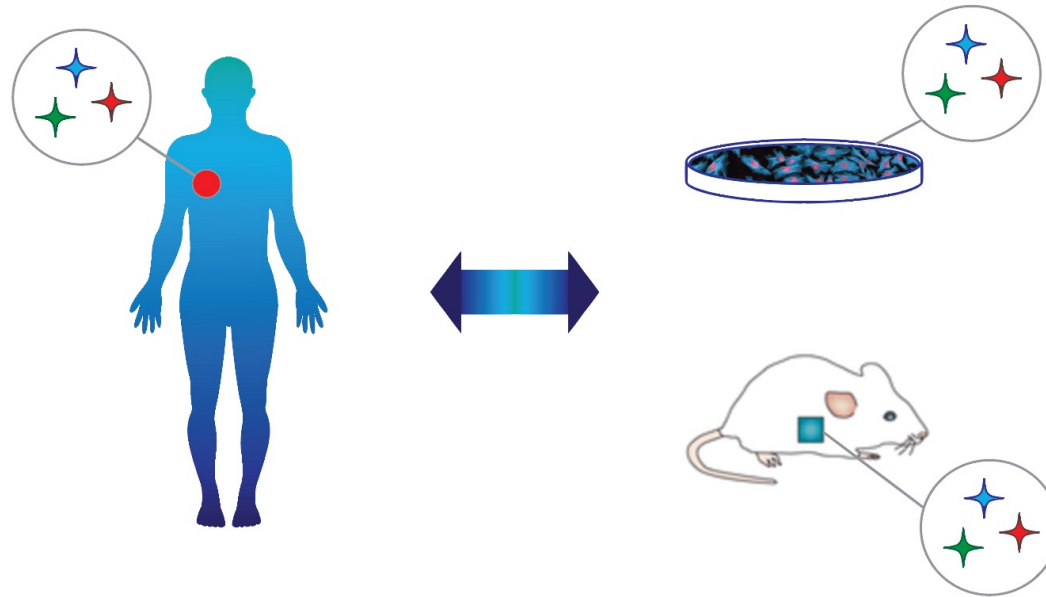
Several studies classified genomic alteration based on **statistical analyses**

- **Functional Annotations of Genomic Alterations**

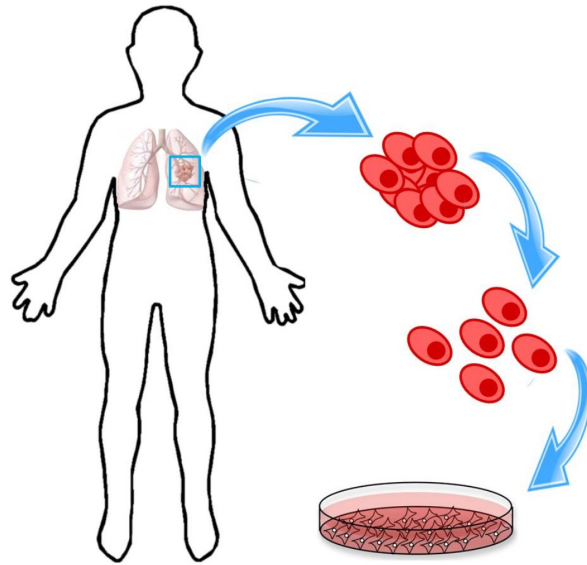
Define the biological impact of genetic alteration in the tumor development

How to study this complexity?

Disease-model matching



Multiple cell lines isolated from different tumors



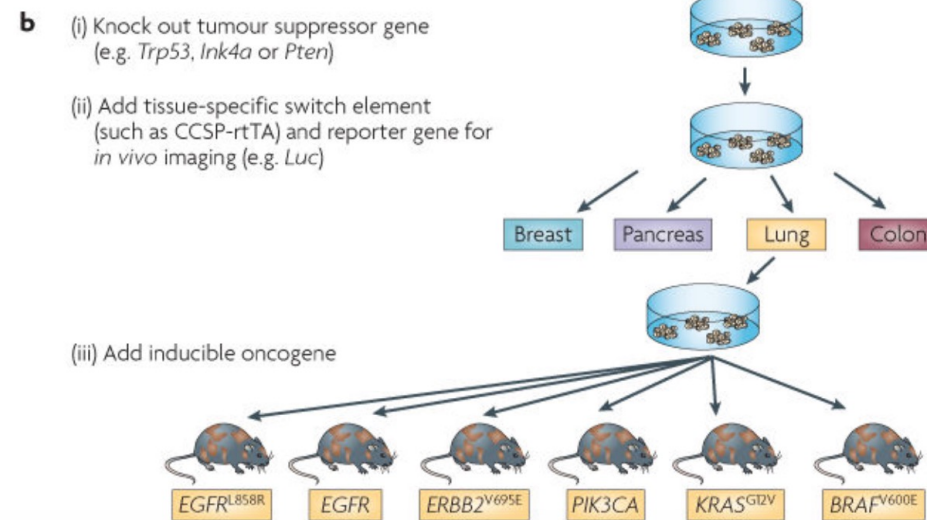
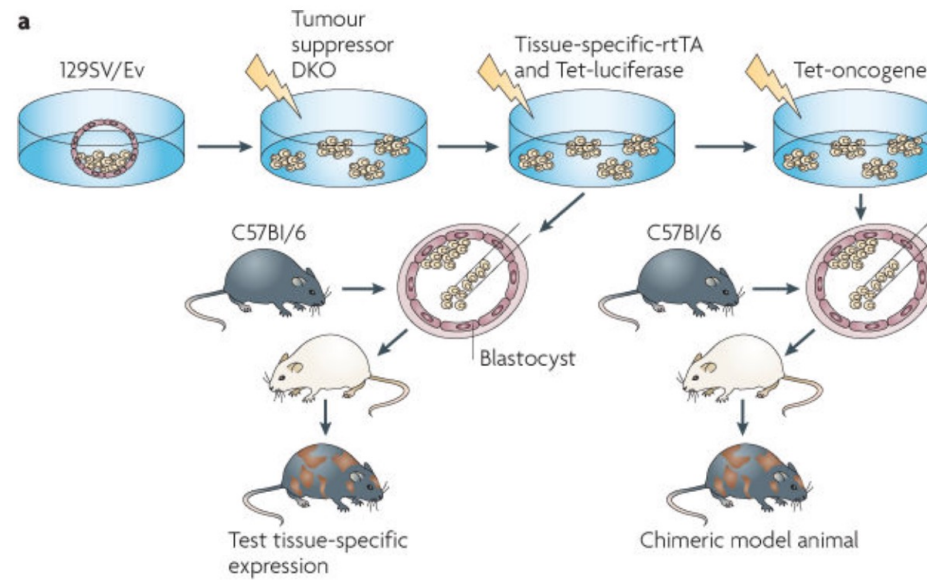
Cancer cells grow
for forever



Cancer cell line encyclopedia

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

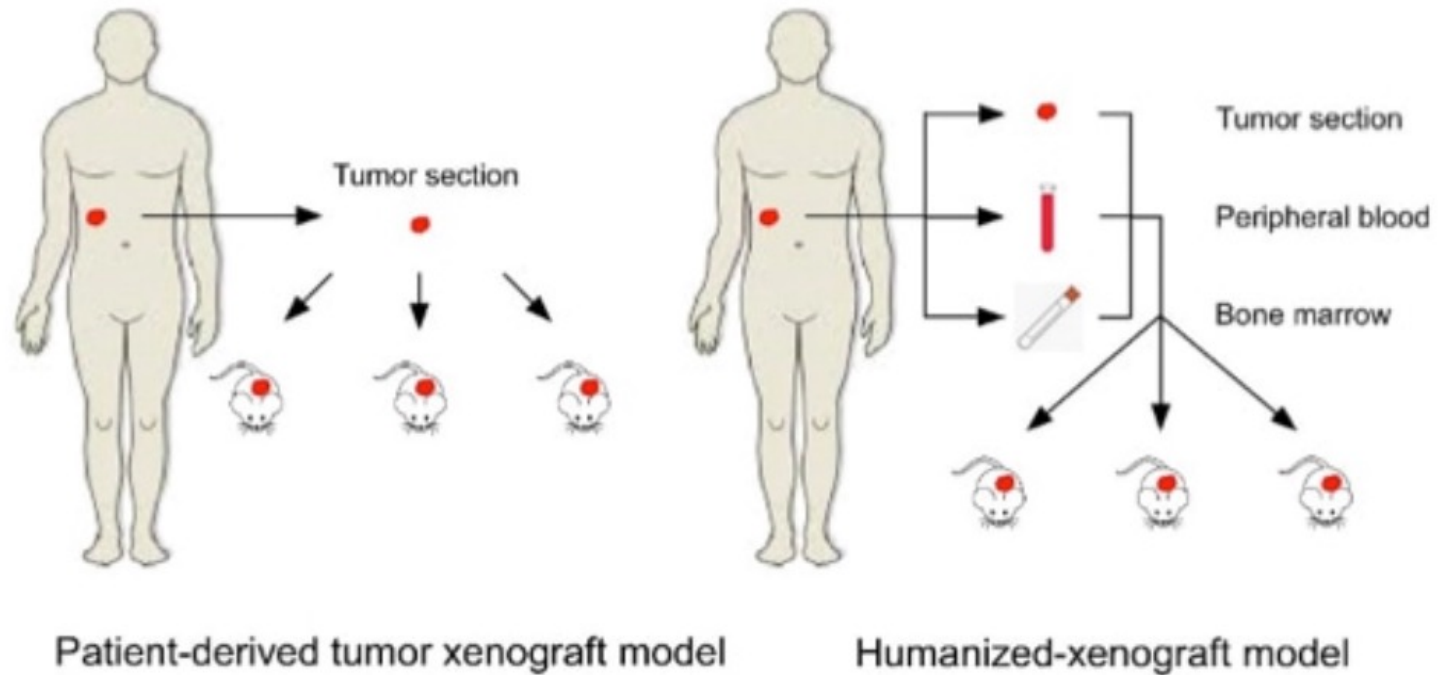
Transgenic animal models



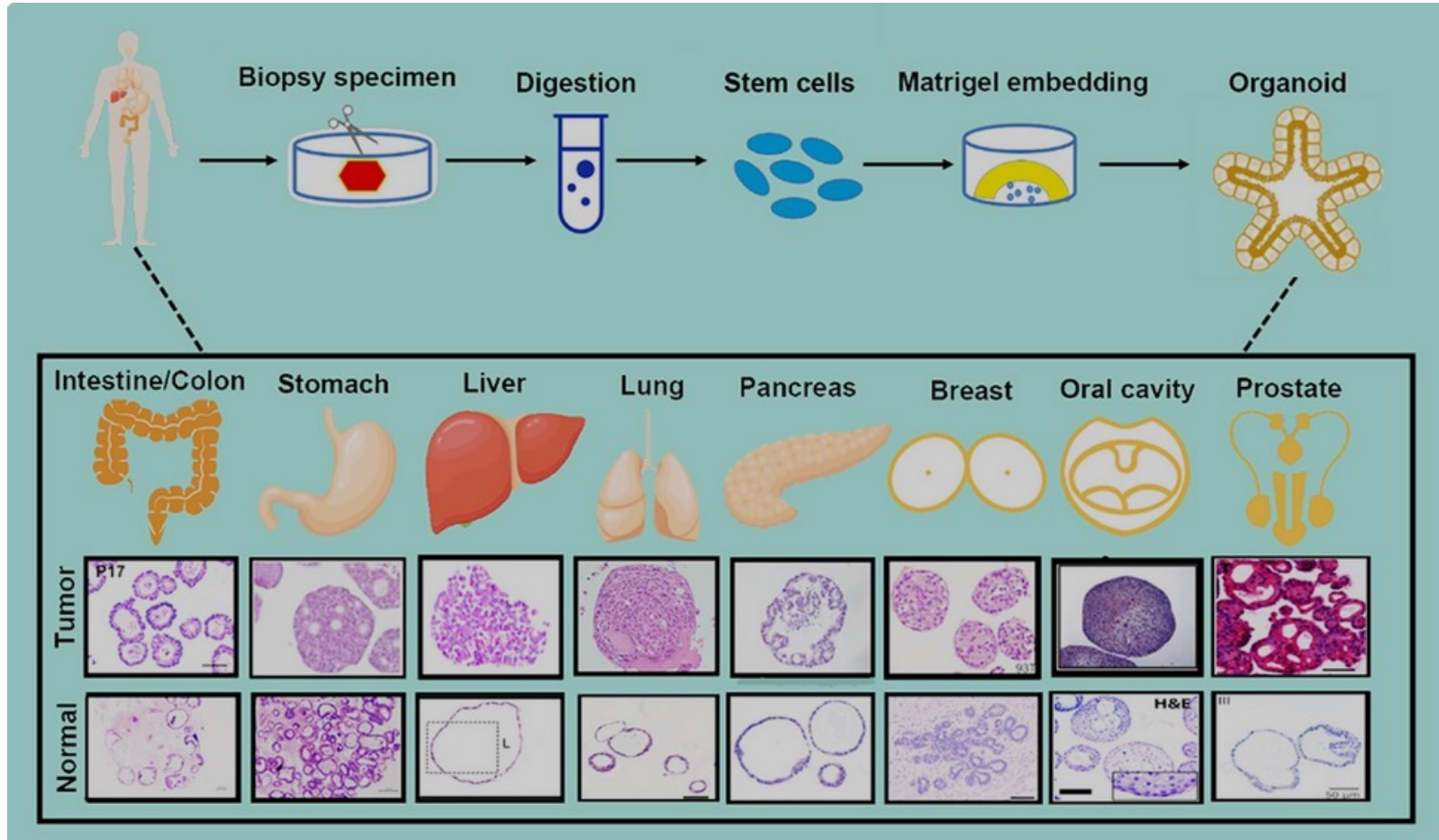
The Human Relevance



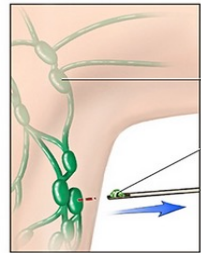
Patient derived xenograft and Humanized-xenograft model



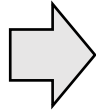
Organoids



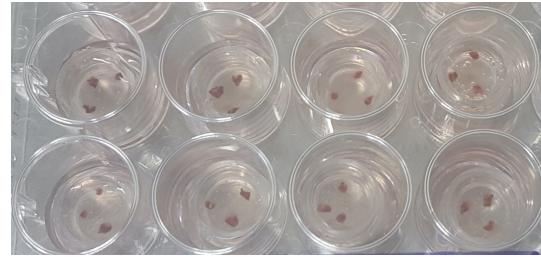
Fragments of tumors



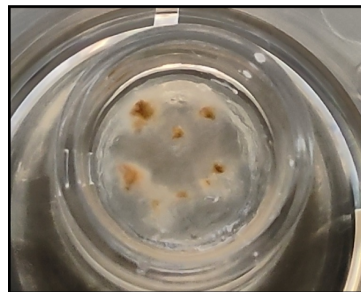
Tumor biopsies
from the surgery room



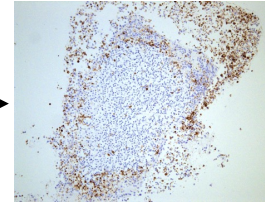
untreated drug A drug B drug C



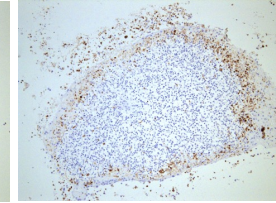
Treatment for
1-2 weeks



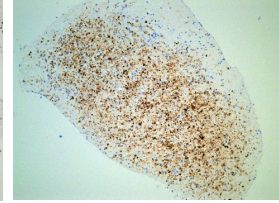
Patient #1
before treatment



Patient #1
drug A
No response

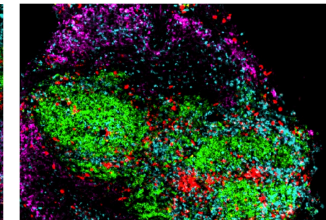
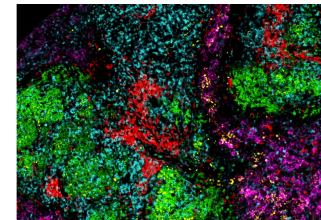


Patient #1
drug B
Good response



Determine the most effective therapeutic option
for each cancer patient

Compare response with clinical outcome



Analyses of tumor structures with
advanced imaging and molecular technologies

Patient avatars

A

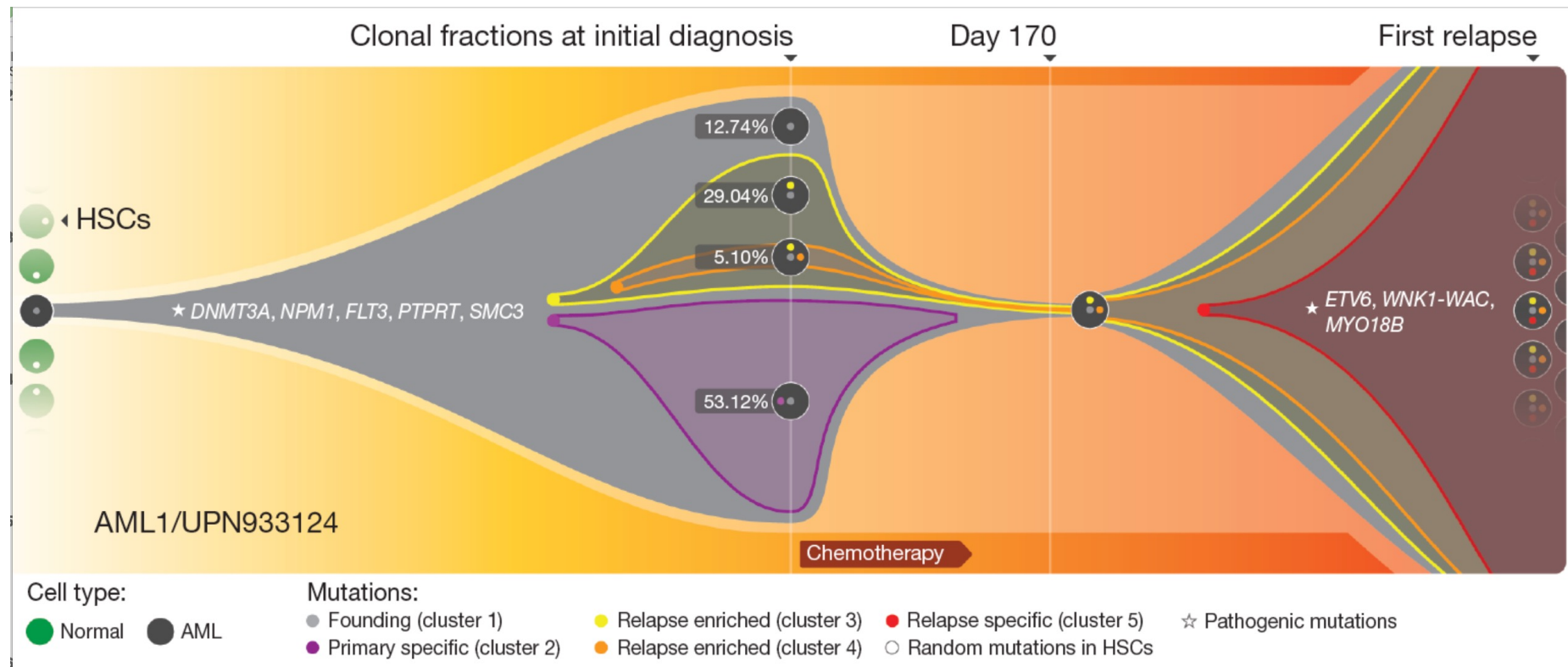
							
	Genomic Sequencing	Metabolomics/ Proteomics	Patient-Derived Cell Lines	Patient-Derived Xenografts	Patient-Derived Tissue Explants	Patient-Derived Organoids	Patient-Derived 3D Micro-Models
Predictive Power	+++	++	+	+++	++	+++	+++
Predictable Therapies	T	T	C/R	T/C/IO*/R	T/C/IO/R	T/C/R	T/C/IO/R
Speed	+++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

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

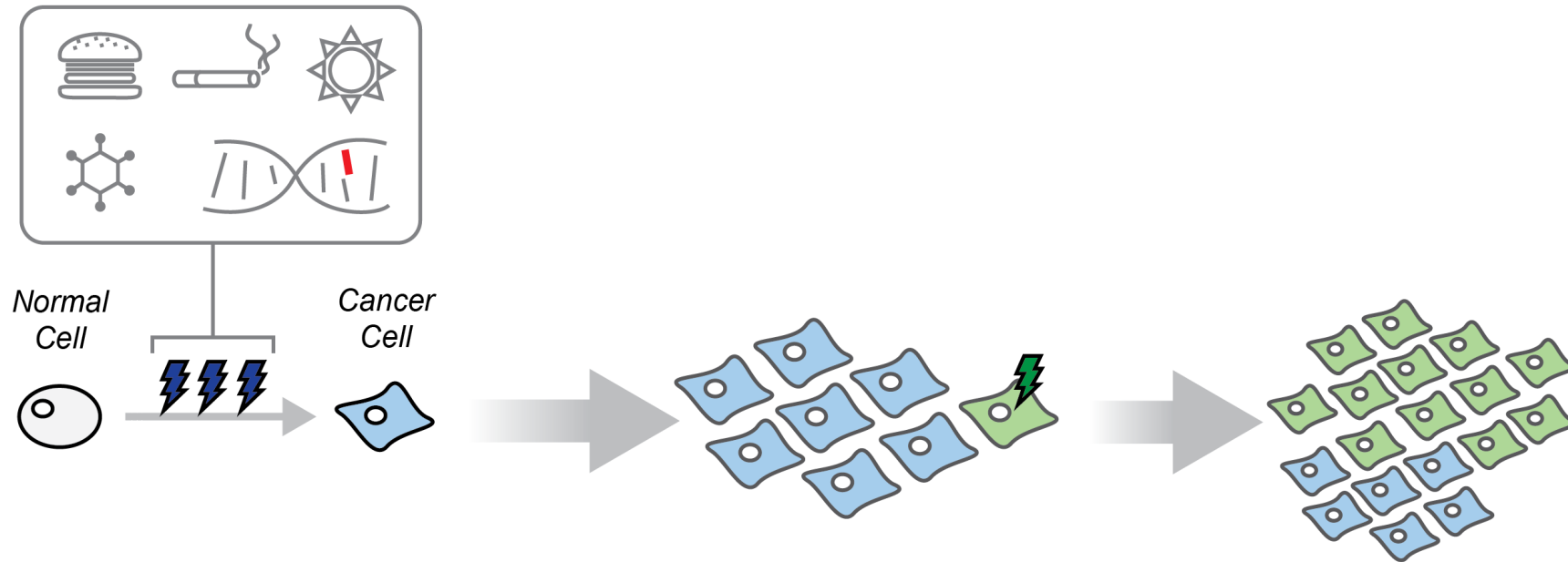
*PDX models include mouse stromal cells in the TME and require immune reconstitution with humanized mouse models to adequately recapitulate IO therapies.

Cancer intra-tumor heterogeneity and its evolution

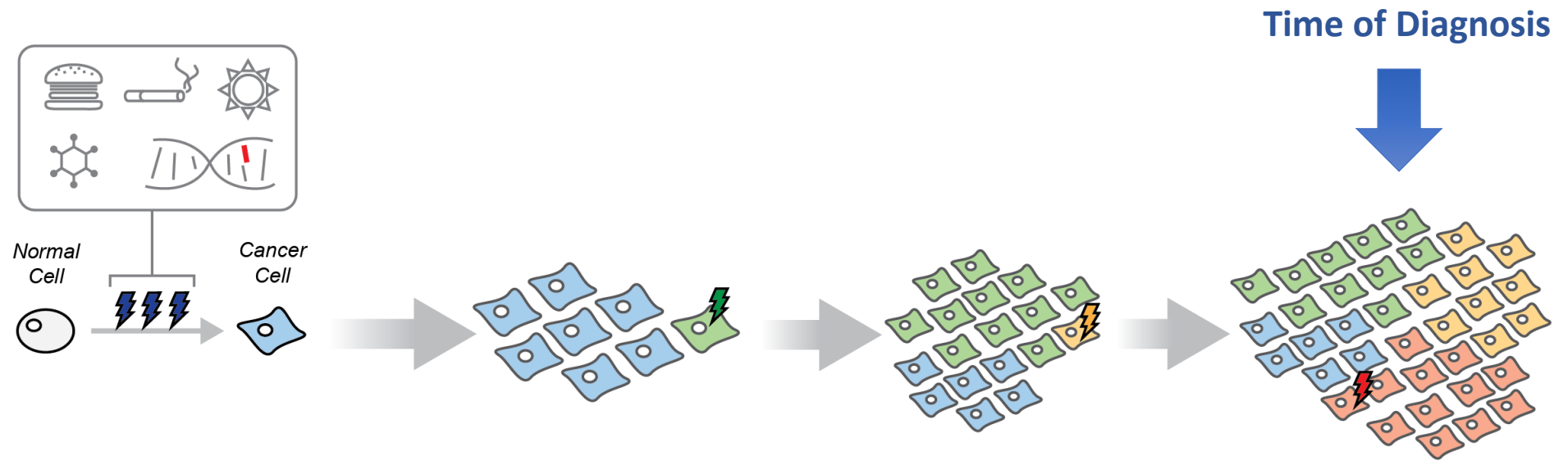
Cancer is a disease that evolves



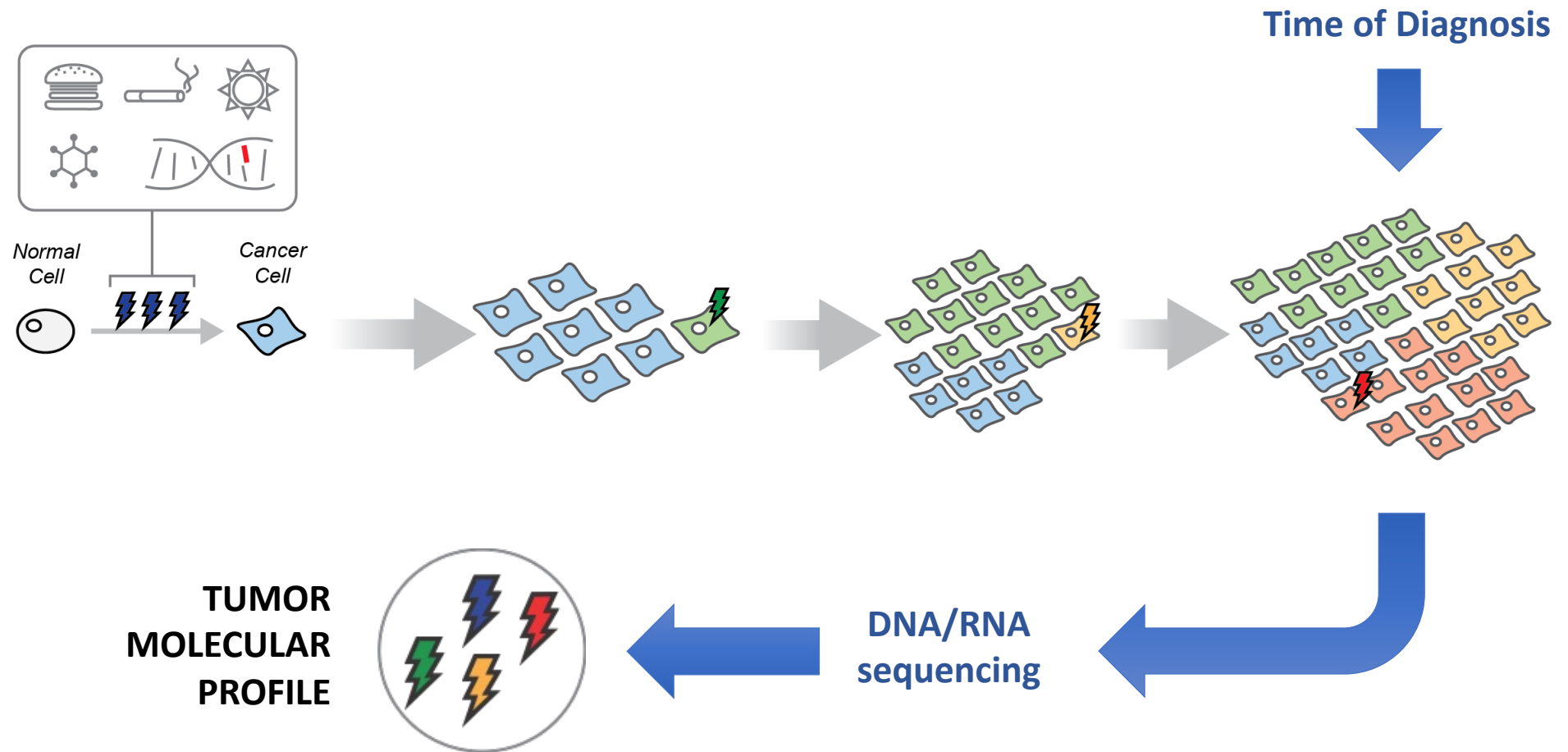
A simplified model of cancer evolution



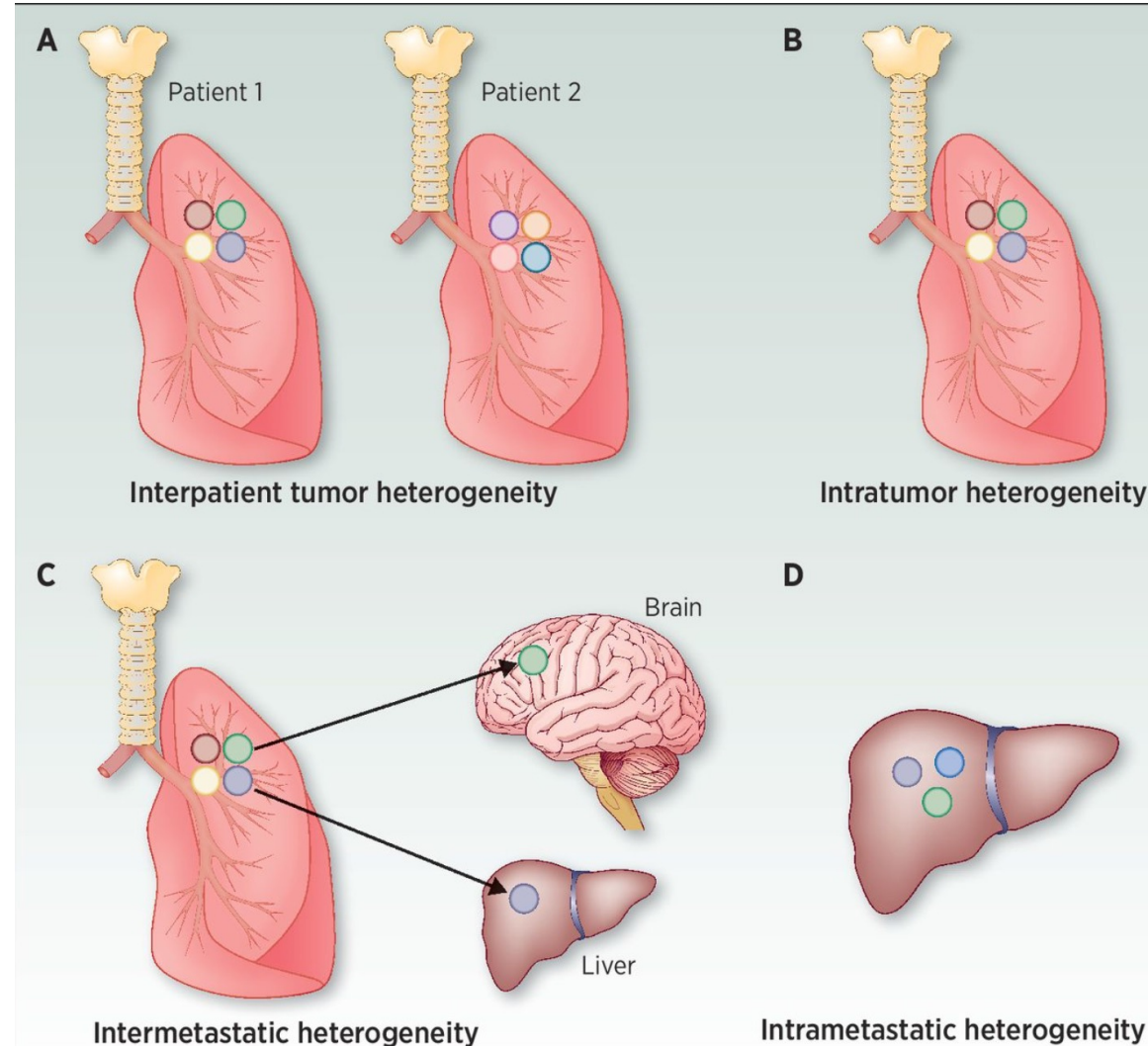
A simplified model of cancer evolution



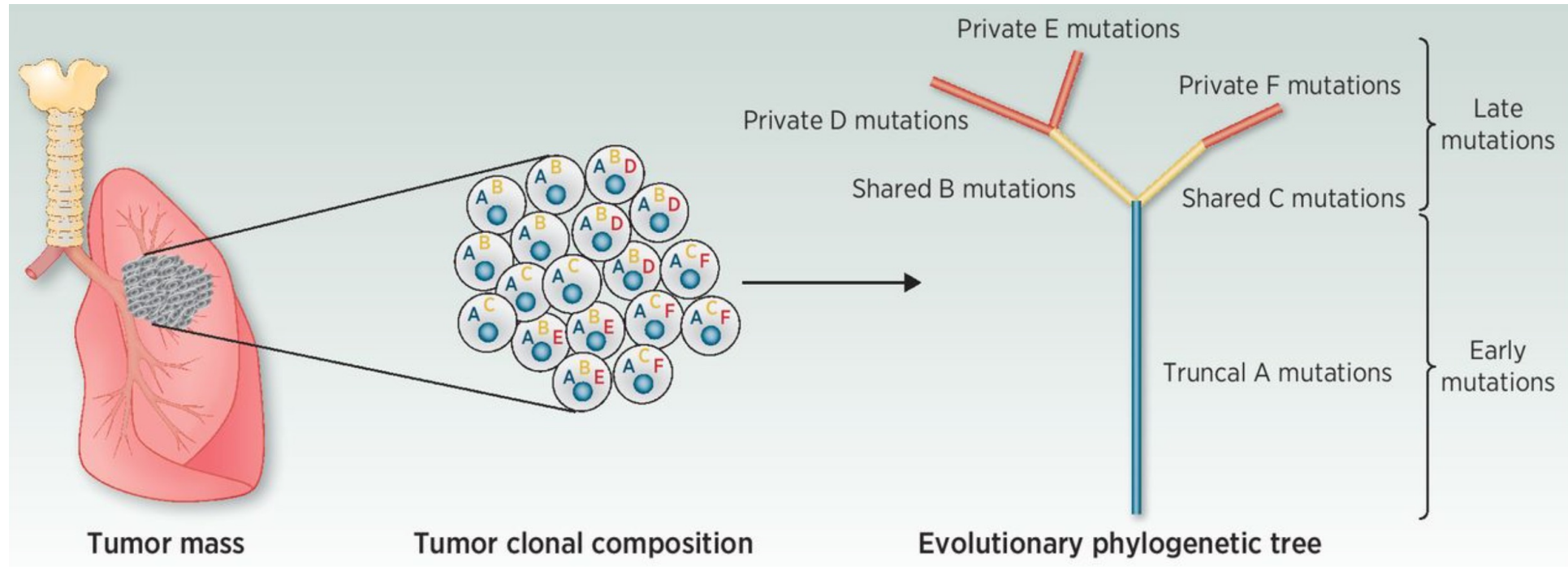
A simplified model of cancer evolution



Intra-tumor heterogeneity and metastasis



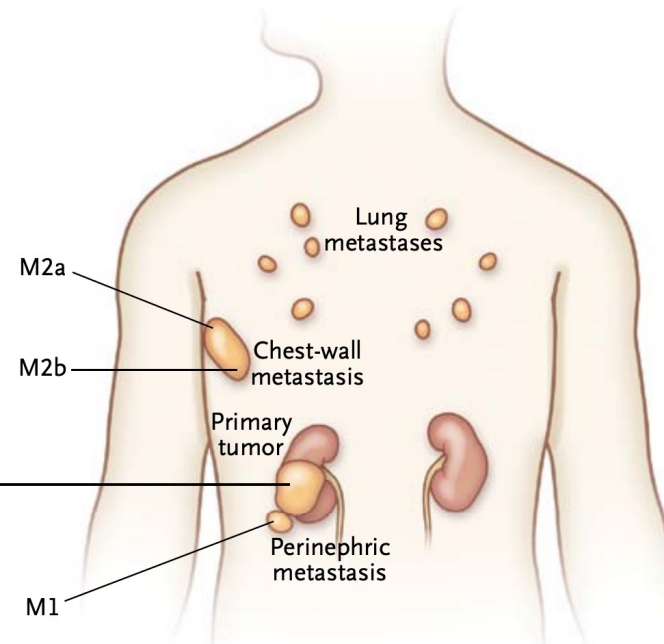
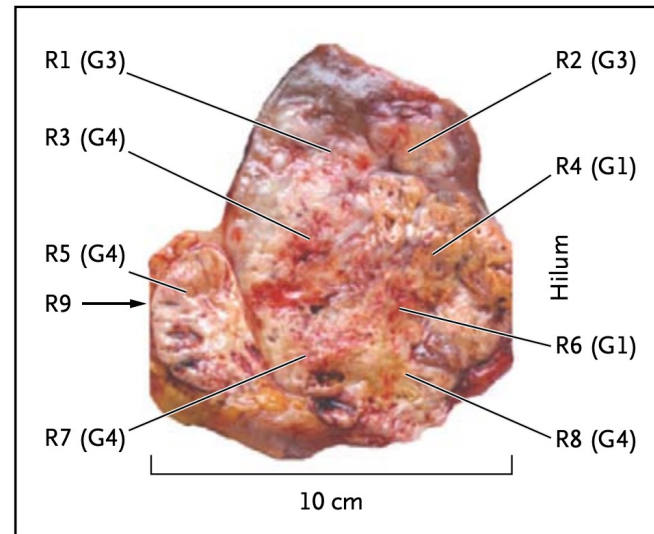
Intra-tumor heterogeneity



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

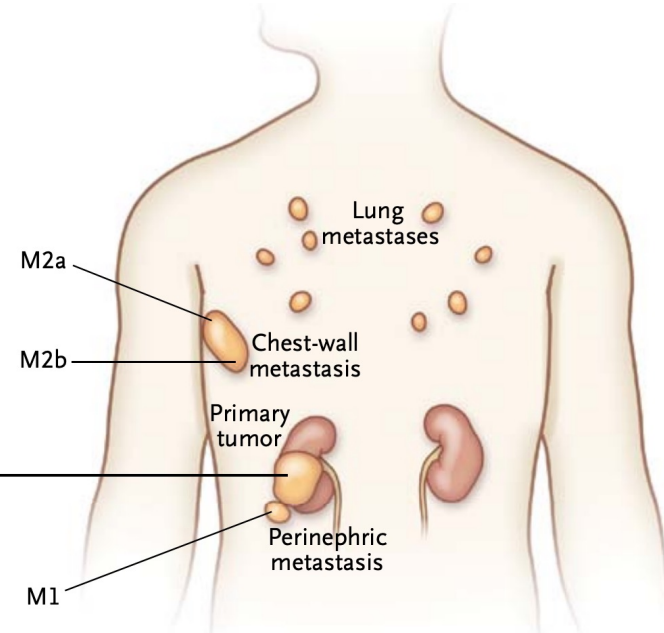
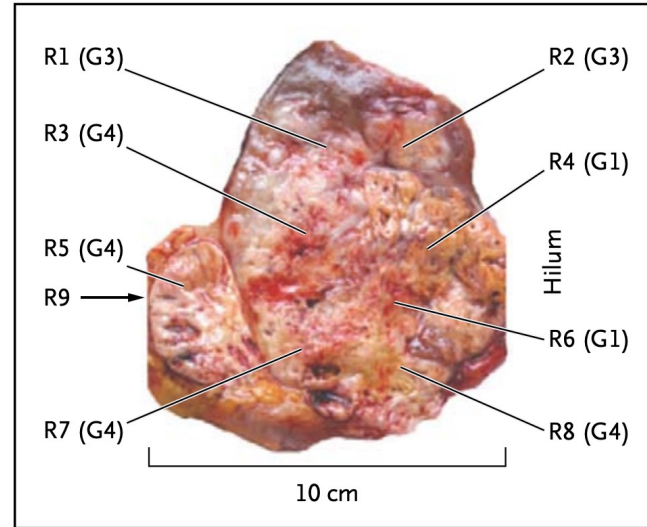
Multi-regional sampling

A Biopsy Sites

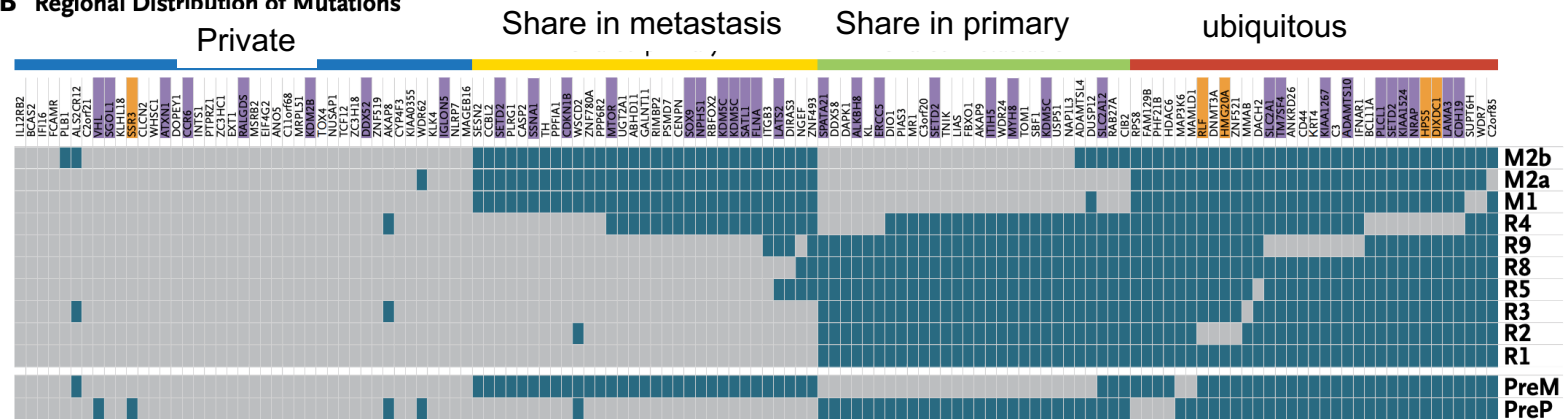


Multi-regional sampling

A Biopsy Sites

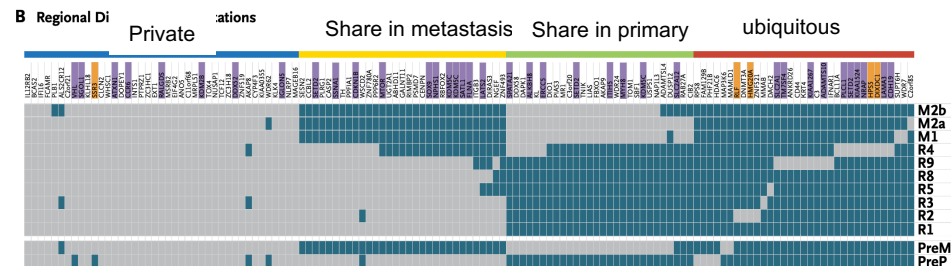
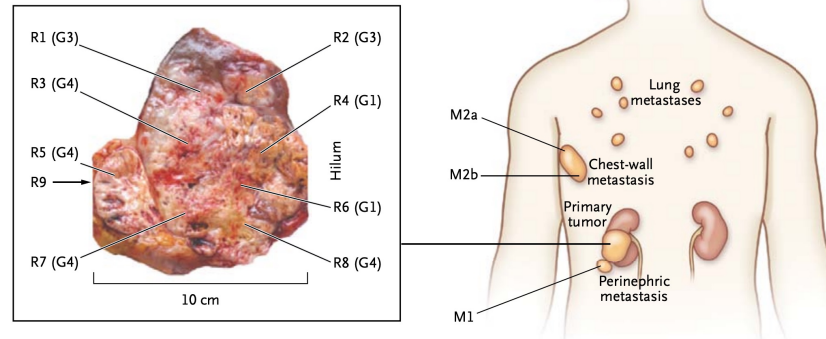


B Regional Distribution of Mutations



Multi-regional sampling

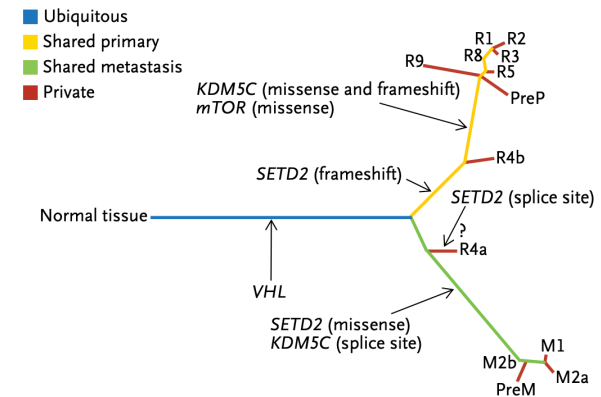
A Biopsy Sites



Tumor phylogenetic trees

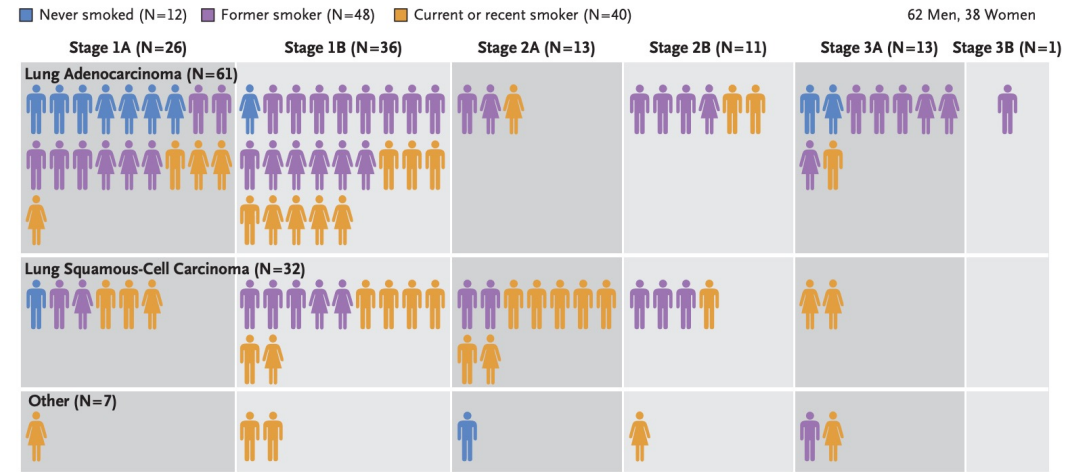
Ubiquitous / Shared / Private mutations allows to reconstruct the evolutionary history of the tumor

C Phylogenetic Relationships of Tumor Regions

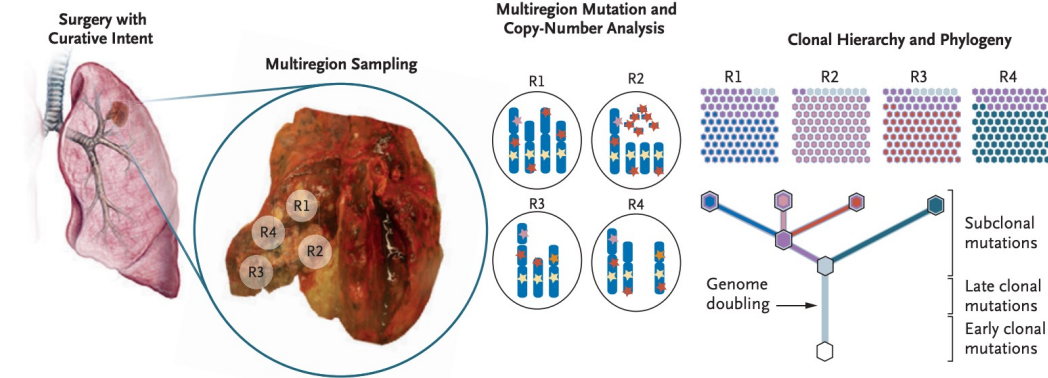


Tracking tumor evolution

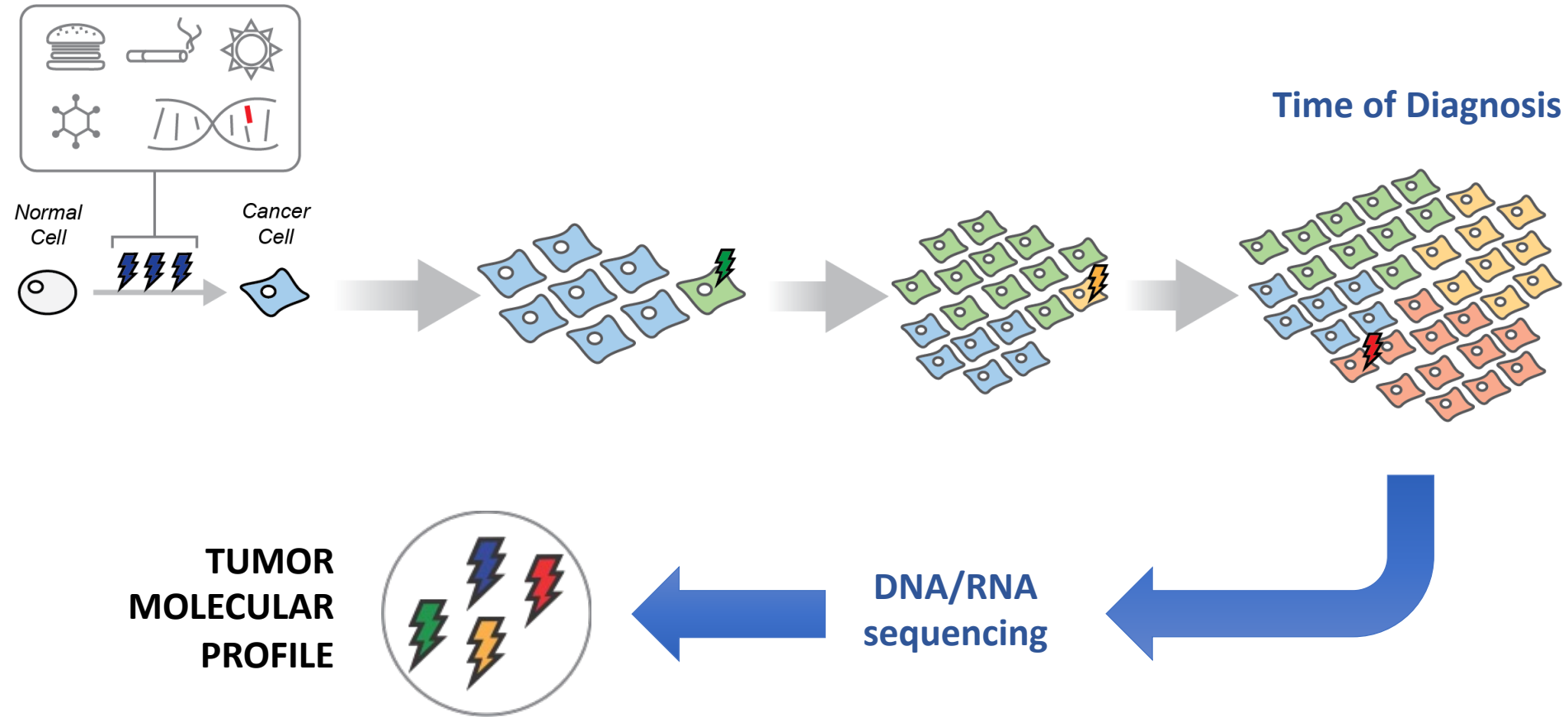
A TRACERx 100 Cohort



B Multiregion Intratumor Heterogeneity Analysis



(Jamal-Hanjani et al. NEJM 2017)

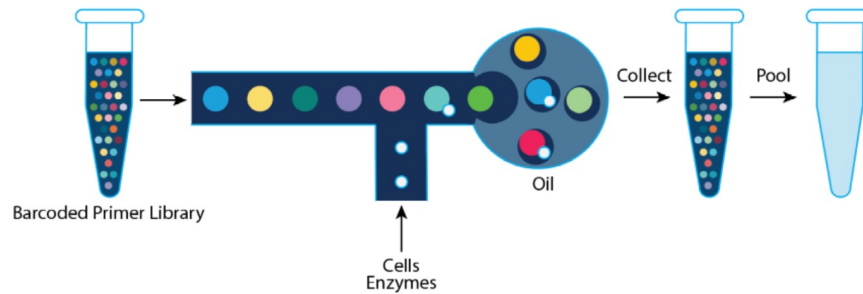


How can we analyze
intra tumor heterogeneity?

What is the problem of bulk analyses?

Single-cell molecular profiles

scRNA: Cell barcoding allows to determine which transcript come from which cells



Bulk RNAseq



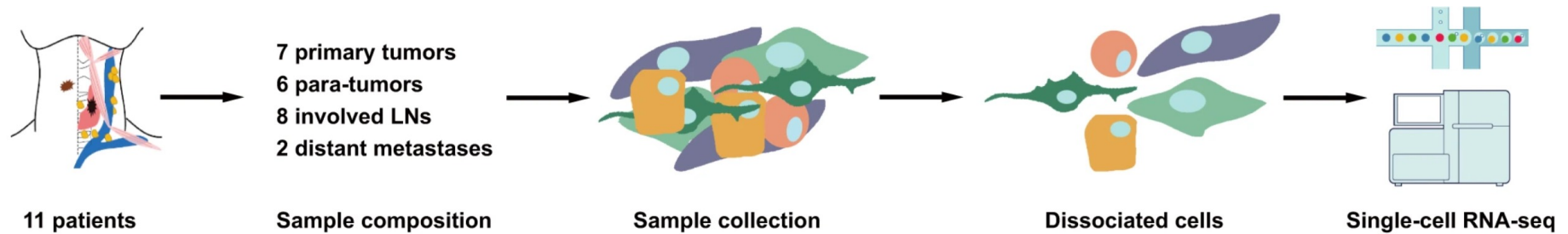
Single cell RNAseq



Single-cell molecular profiles

Single cell omics has revolutionized our ability to study **intra-tumor heterogeneity**

- Diversity among different cancer cells within the same tumor
- Diversity of non-tumor cells (e.g., immune cells) surrounding the tumor (tumor microenvironment)

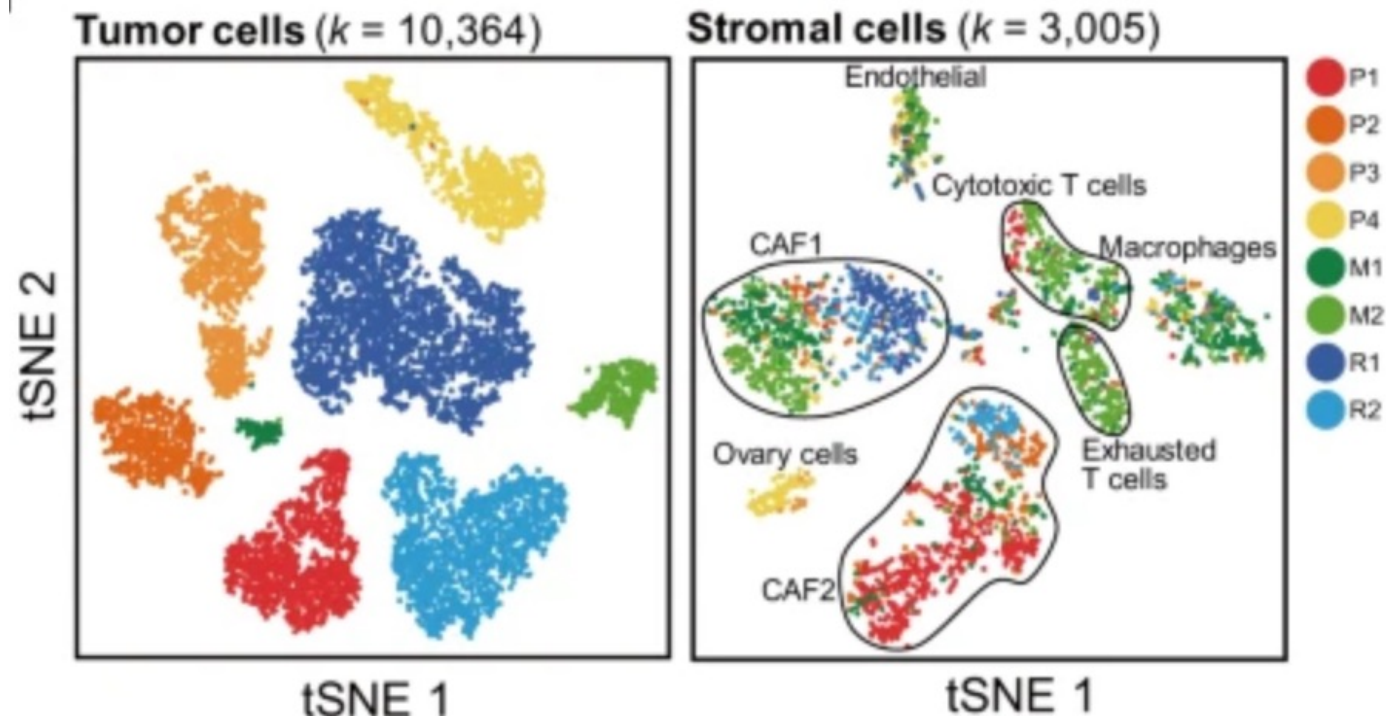


Single-cell molecular profiles

Single cell omics has revolutionized our ability to study [intra-tumor heterogeneity](#)

- Diversity among different cancer cells within the same tumor
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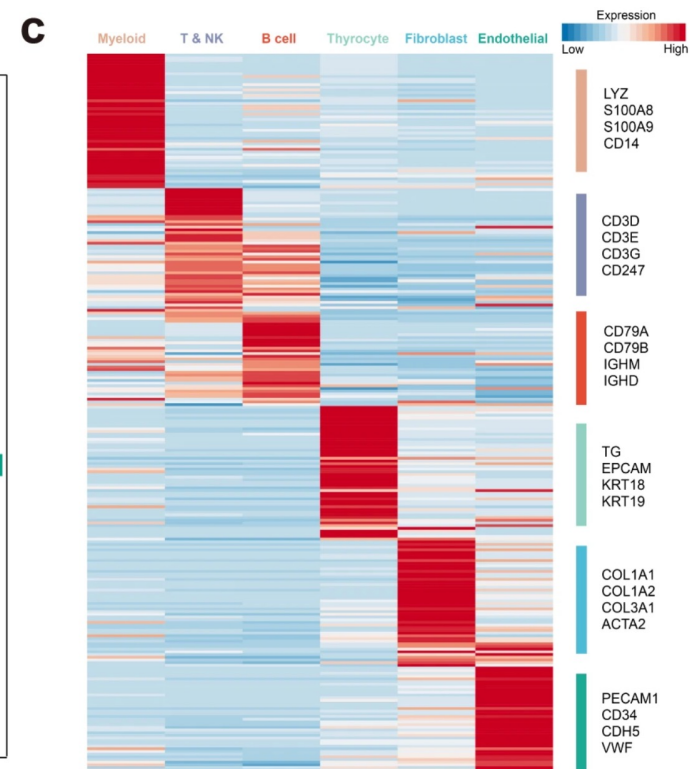
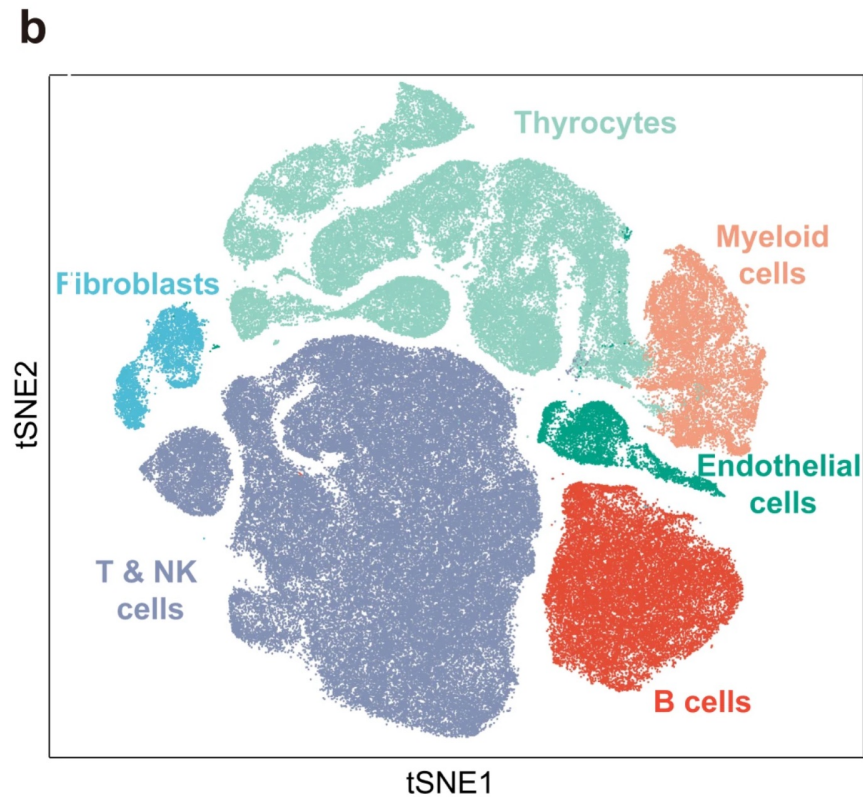
Ovarian cancer



Single-cell molecular profiles

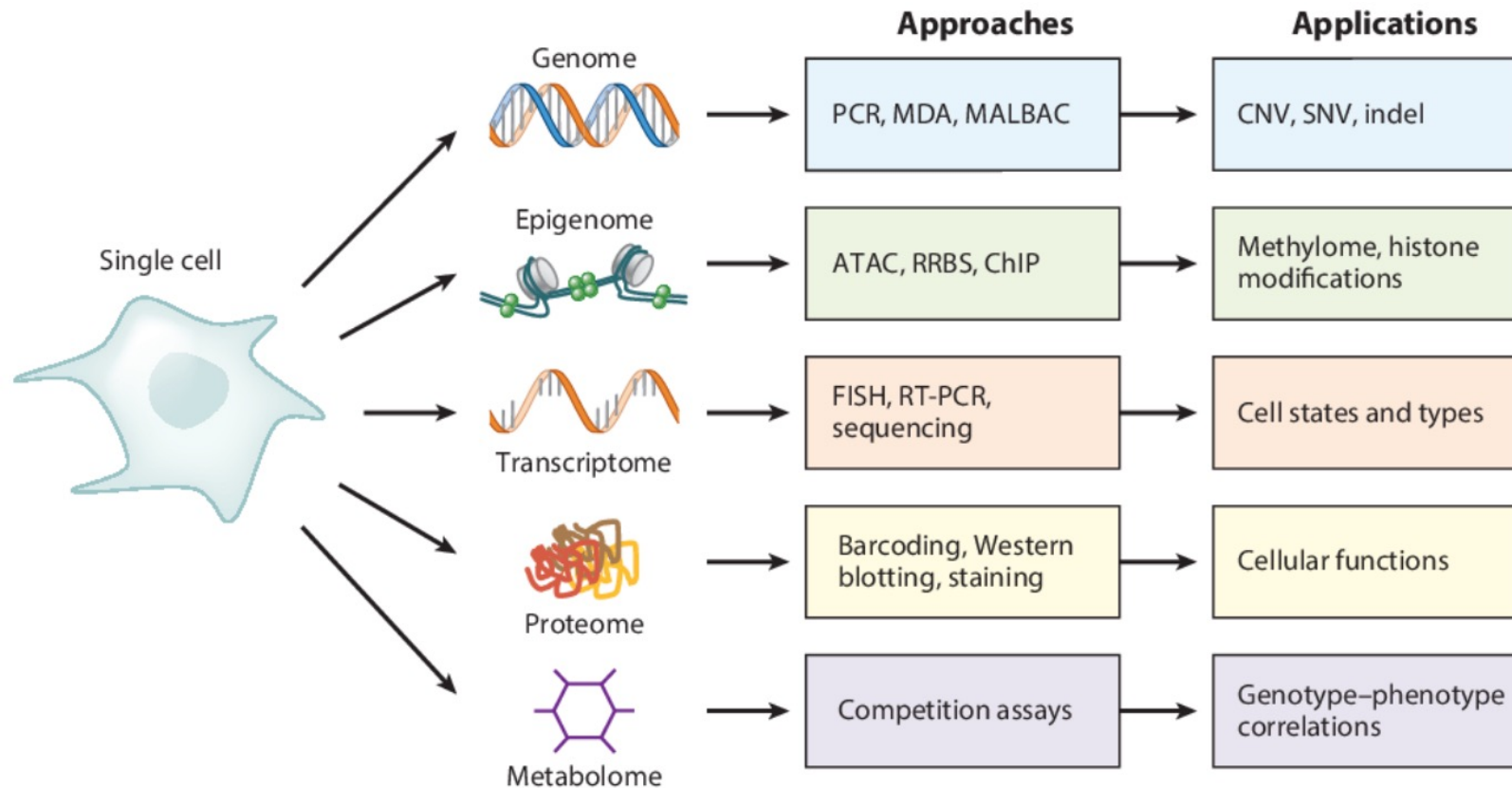
Single cell omics has revolutionized our ability to study **intra-tumor heterogeneity**

- Diversity among difference cancer cells within the same tumor
- Diversity of non-tumor cells (e.g., immune cells) surrounding the tumor (tumor microenvironment)



Single-cell molecular profiles

Single cell omics: Nowadays (almost) all genomic data can be generated at the single cell level

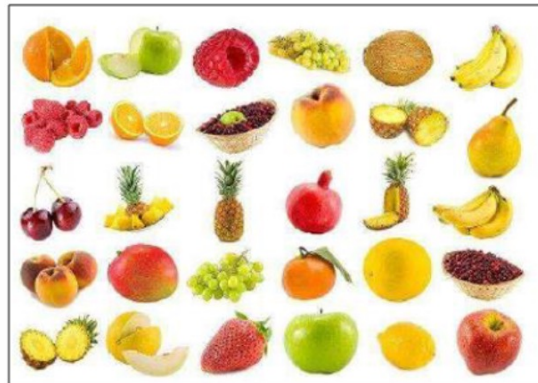


Spatial omics

Bulk RNAseq



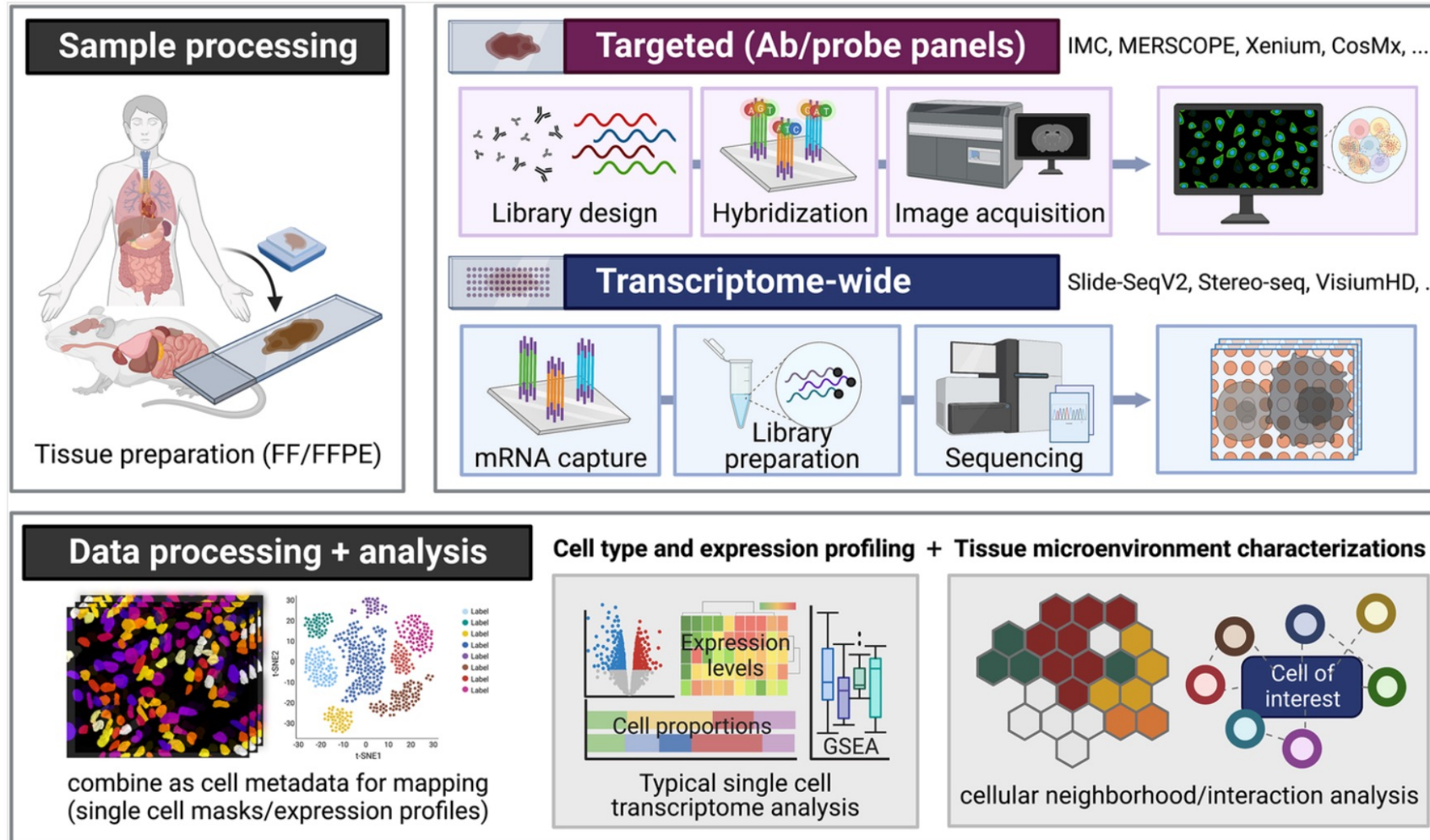
Single cell RNAseq



***Spatial
Transcriptomics***

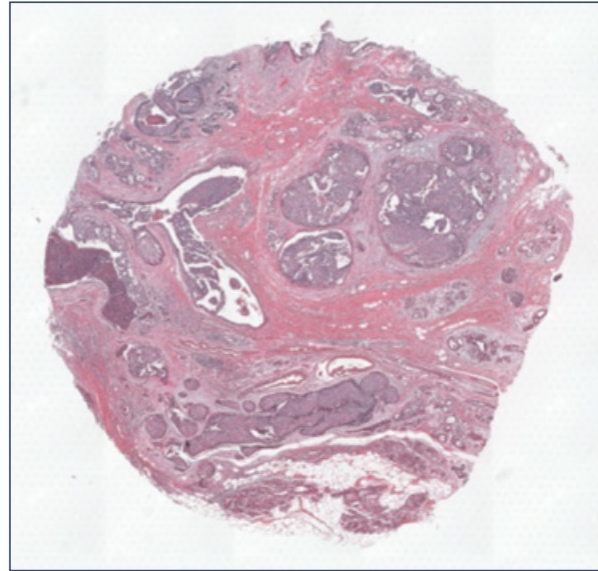


Spatial transcriptomics



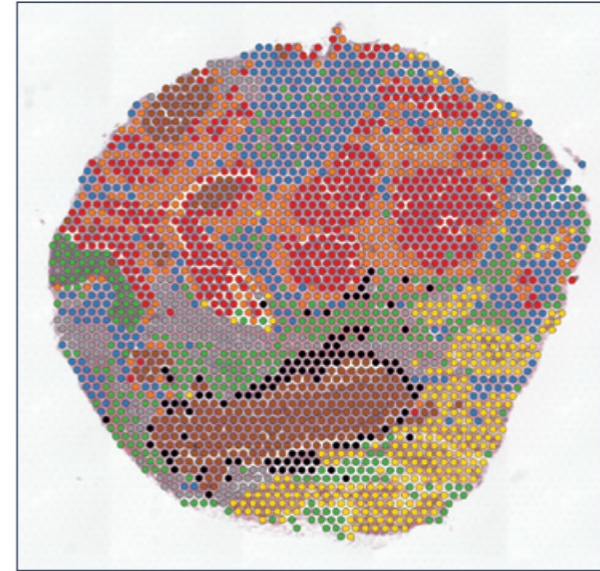
Spatial transcriptomics

A. H&E



Tumor tissue

C. Spot clusters



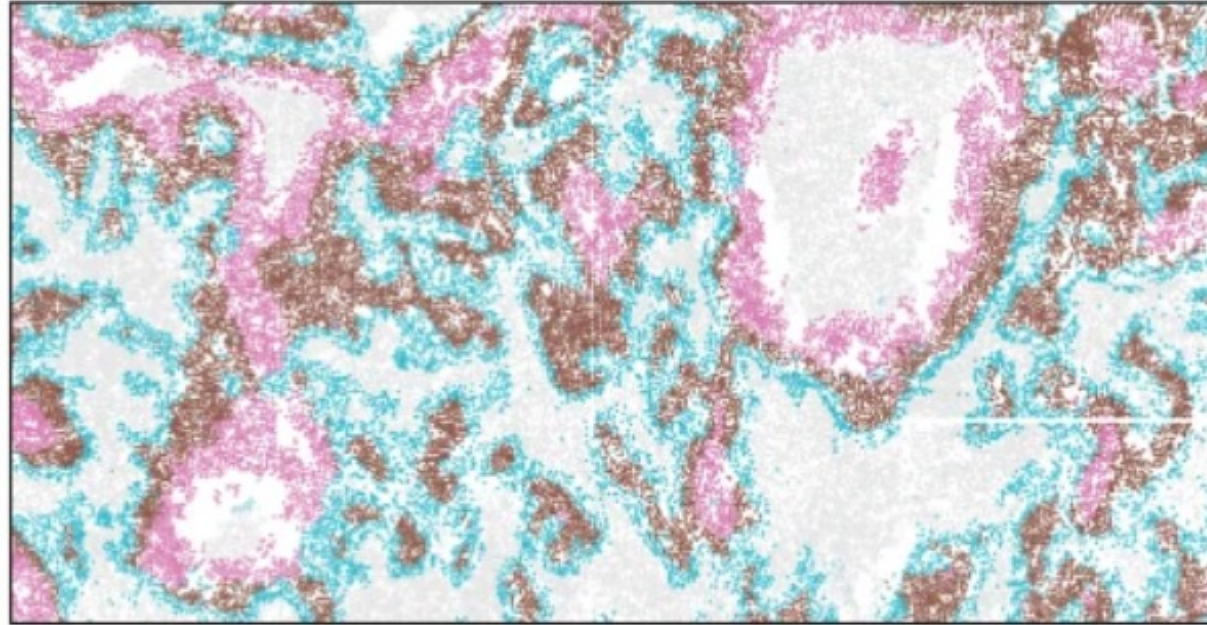
Cluster

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8

*spatial clusters based
on gene expression*

Spatial transcriptomics

Lung adenocarcinoma- tumor cells



Varrone et al. 2023

3 categories of tumor cells

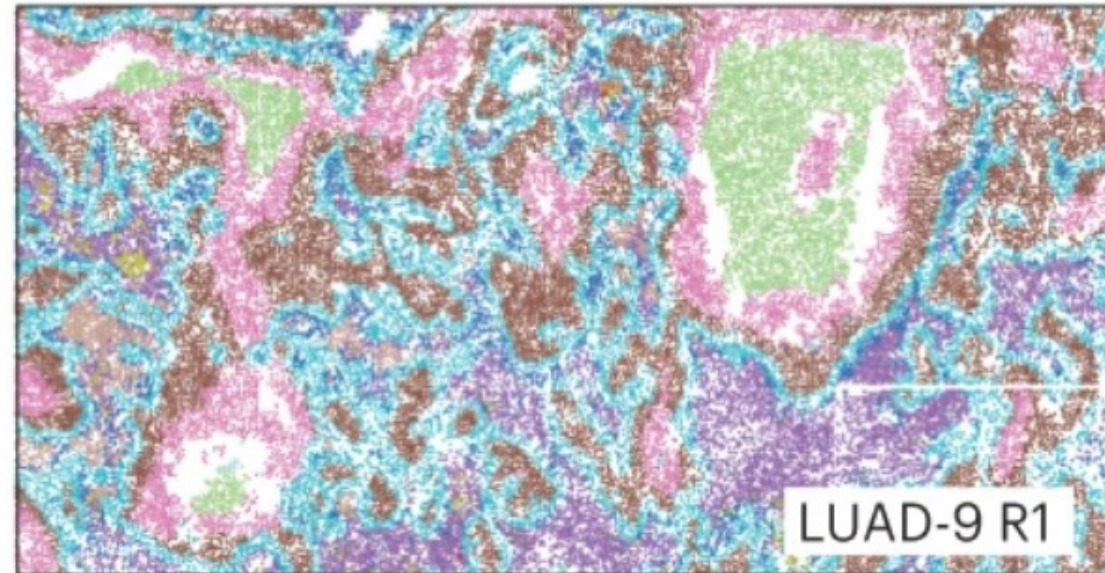
pink

Brown

clear-blue

Tumor cells spatially distribute have a distinct expression profile

Spatial transcriptomics



■ C11 (neutrophils) ■ C17 (fibroblasts) Varrone et al. 2023

*The gene expression of the tumor cells might be influenced by their proximity
With the tumor microenvironment and vice versa*

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