

Bienvenue aux UE **Cancer et Génomique**

UE11: Big data moléculaire et son traitement
UE12: Big data et modèles prédictifs

Planning de la semaine

UE11: Big data moléculaire et son traitement

Lundi 18 janvier 2021 - Salle XX, B2M	
09:00-10:30	Technologies et données omiques en cancérologie. Daniel GAUTHERET
10:45-12:15	L'analyse des altérations de nombre de copies par microarrays et NGS. Bastien JOB, Ingénieur Bioinformaticien, Gustave Roussy
13:30-17:00	TP Galaxy I: Cas d'étude RNA-seq (contrôles qualité, alignements des séquences sur le génome de référence et quantification de l'expression des gènes). Gaëlle LELANDAIS

Mardi 19 janvier 2021 - Salle XX, B2M	
09:00-12:30	TP Galaxy II : Cas d'étude RNA-seq (création d'un workflow, matrice d'expression des gènes et analyse différentielle) Gaëlle LELANDAIS
13:30-15:00	Problématique et applications de la détection de variants somatiques par séquençage d'exome. D. GAUTHERET
15:15-16:45	Principes et application de l'analyse d'expression en single-cell. Bastien JOB, Ingénieur Bioinformaticien, Gustave Roussy

Mercredi 20 janvier 2021 - Salle XX, B2M	
09:00-12:30	TP Galaxy: Analyse exome. Visualisation de résultats avec IGV. D. GAUTHERET

UE12: Big data et modèles prédictifs

Mercredi 20 janvier 2021 - Salle XX, B2M	
13:30-17:00	Premiers pas avec le langage R. Cours Video de G. Lelandais. Exercices corrigés par D. GAUTHERET

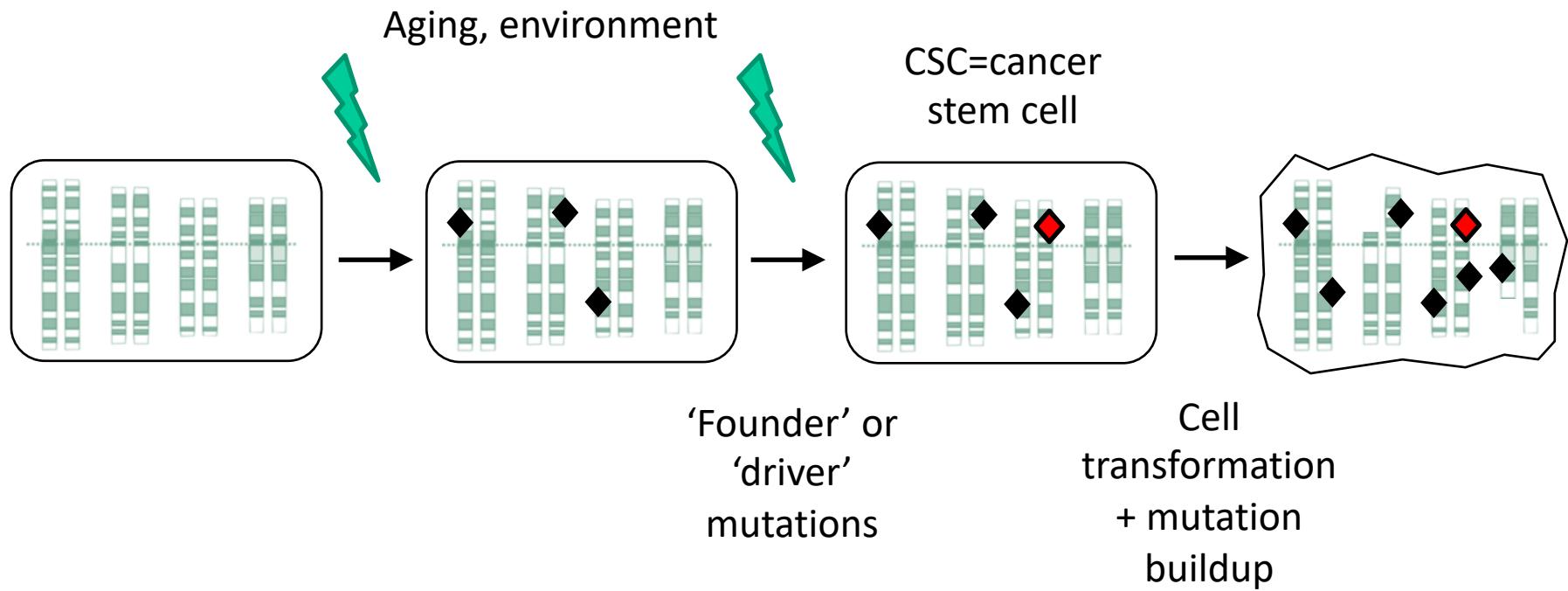
Jeudi 21 janvier 2021 - Salle XX, B2M	
9:00-10:00	Pourquoi utiliser les méthodes d'apprentissage automatique en oncologie personnalisée? Loic VERLINGUE (Gustave Roussy)
10:00-11:00	Méthodes d'apprentissage automatique. Yoann PRADAT (Centrale-Supelec)
11:30-12:30	Exemple d'un projet en machine learning:
13:30-17:00	TP: Machine learning avec des données d'expression issues de TCGA. Loic VERLINGUE (Gustave Roussy) et Yoann PRADAT (Centrale-Supelec).

Vendredi 22 janvier 2021 - Salle XX, B2M	
9:00-11:00	Introduction au Deep Learning: applications en oncologie. Loic VERLINGUE (Gustave Roussy)
10:00-11:00	Introduction aux méthodes de Deep Learning. Yoann PRADAT (Centrale-Supelec)
11:30-12:30	Exemple d'un projet en Deep Learning
13:30-17:00	TP: Construire son premier réseau de neurones. Loic VERLINGUE (Gustave Roussy) et Yoann PRADAT (Centrale-Supelec).

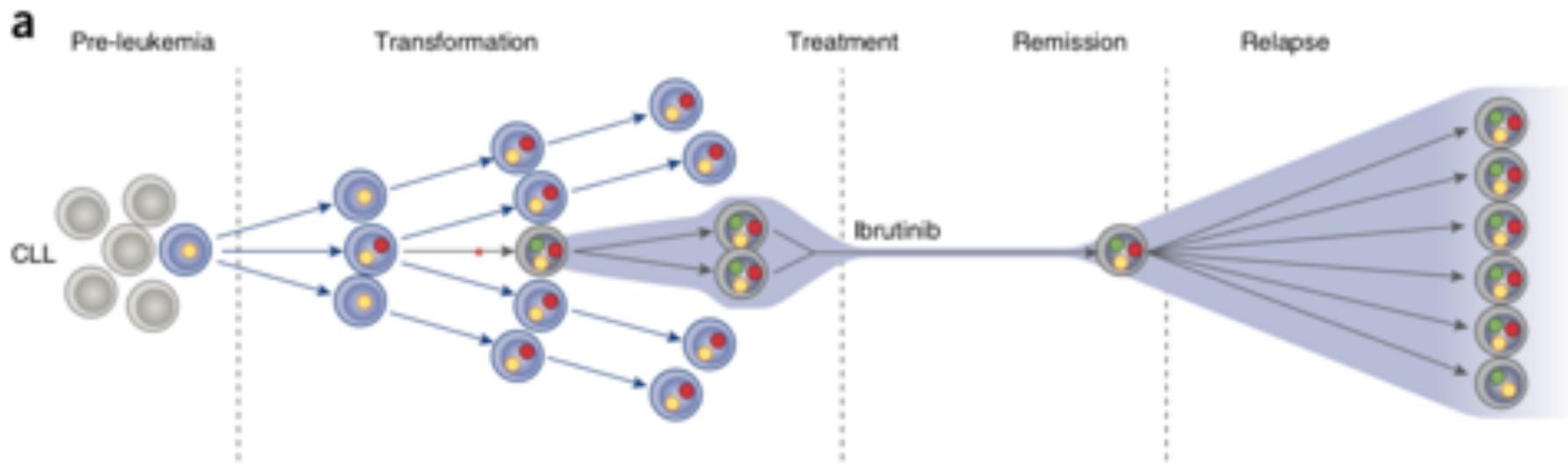
Evaluation:
UE 11: Rapport d'Etonnement
UE 12: Vos protocoles de TP

Introduction

- Le cancer: une maladie du génome



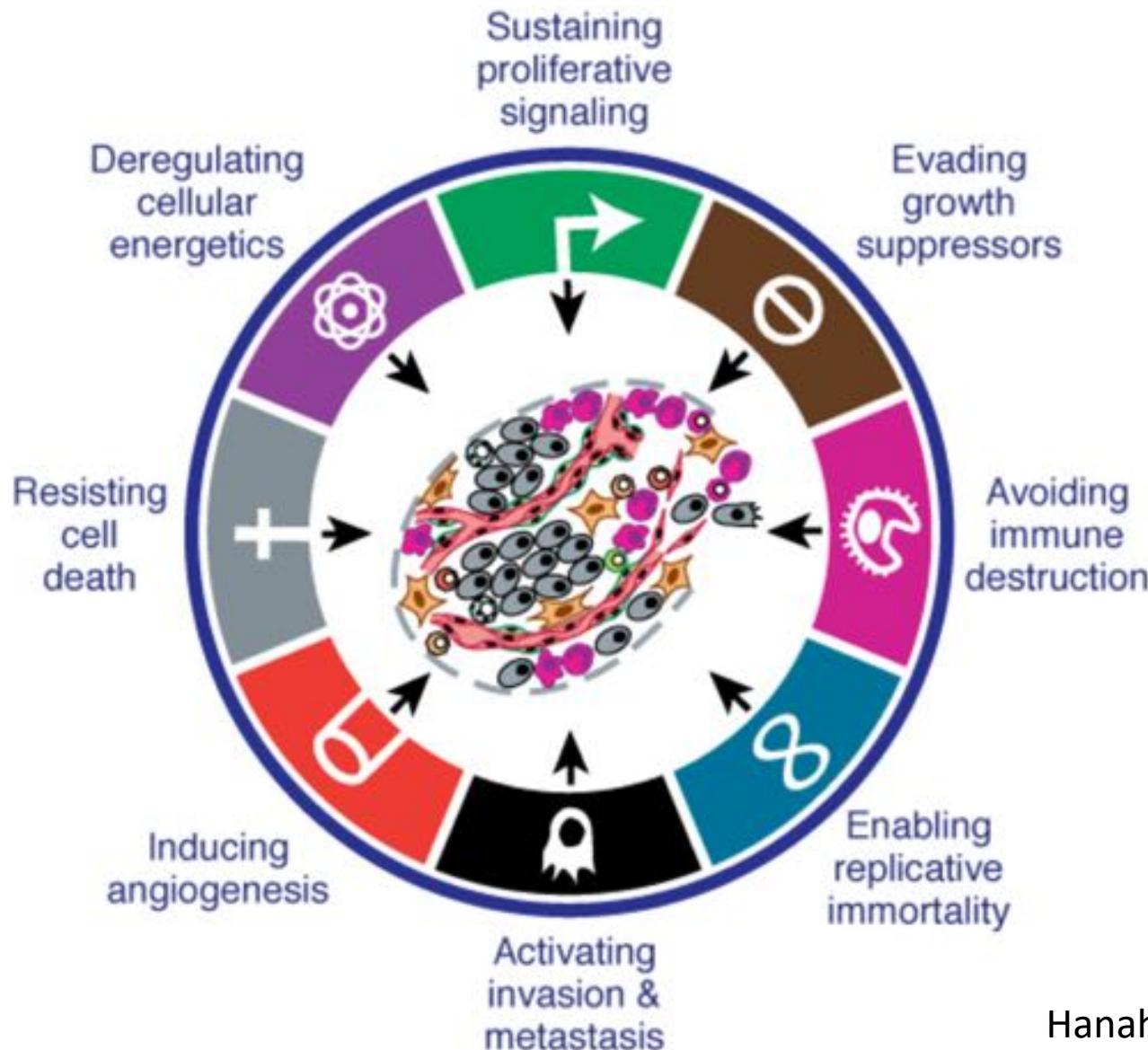
Clonal evolution of cancer



Ferrando & Lopez-Otin, Nature Med. 2017

What is different in a cancer cell?

Hallmarks of cancer



Hanahan & Weinberg, 2015

Chemotherapy with nonspecific cancer drugs

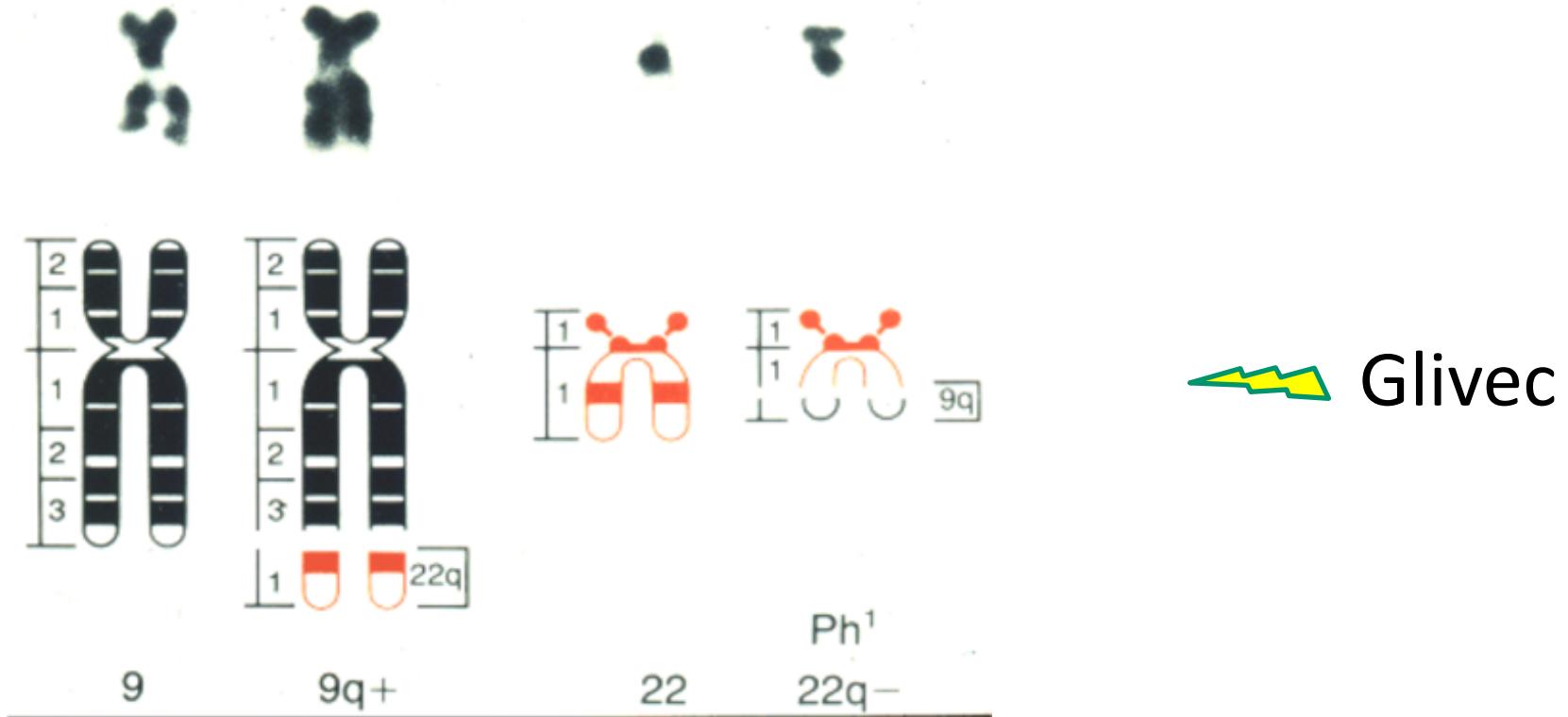


- Taxanes
- Alkylating agents
- Hormones

Precision medicine

Le « chromosome de Philadelphie »

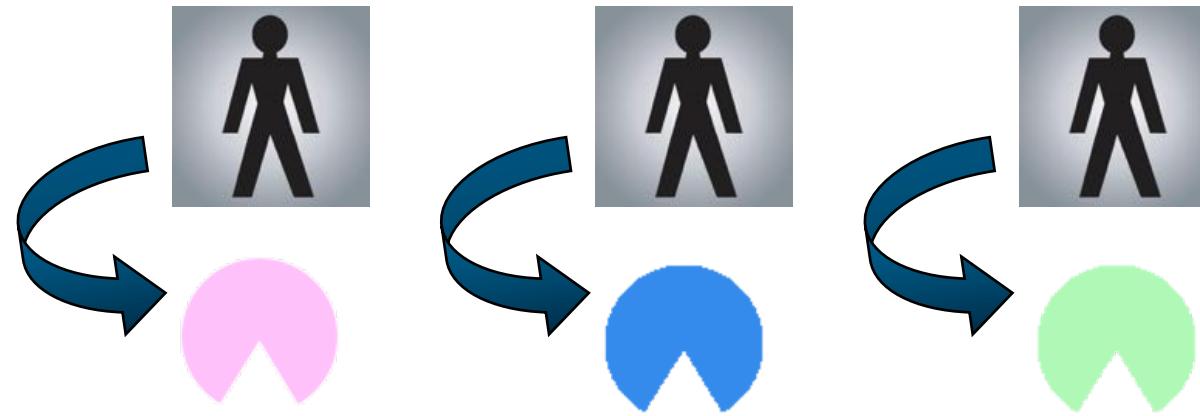
Translocation entre le chromosome 9 et le chromosome 22



Conséquence de la translocation: un oncogène sur chromosome 9 fusionne avec un gène du chromosome 22 : la protéine de fusion BCR-ABL possède une activité tyrosine kinase qui active le cycle cellulaire de manière constitutive et provoque une leucémie myéloïde chronique (LMC).

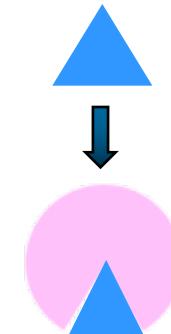
Selecting the right therapy = lower toxicity

Patient

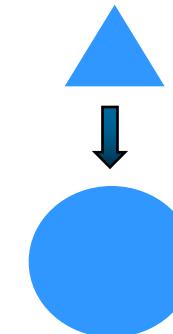


*Tumor-
specific
Alteration*

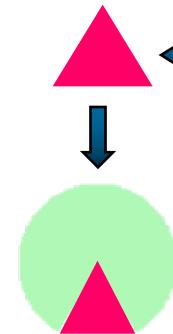
Therapy



**Wrong
match**



**The right drug for
the tumor type**

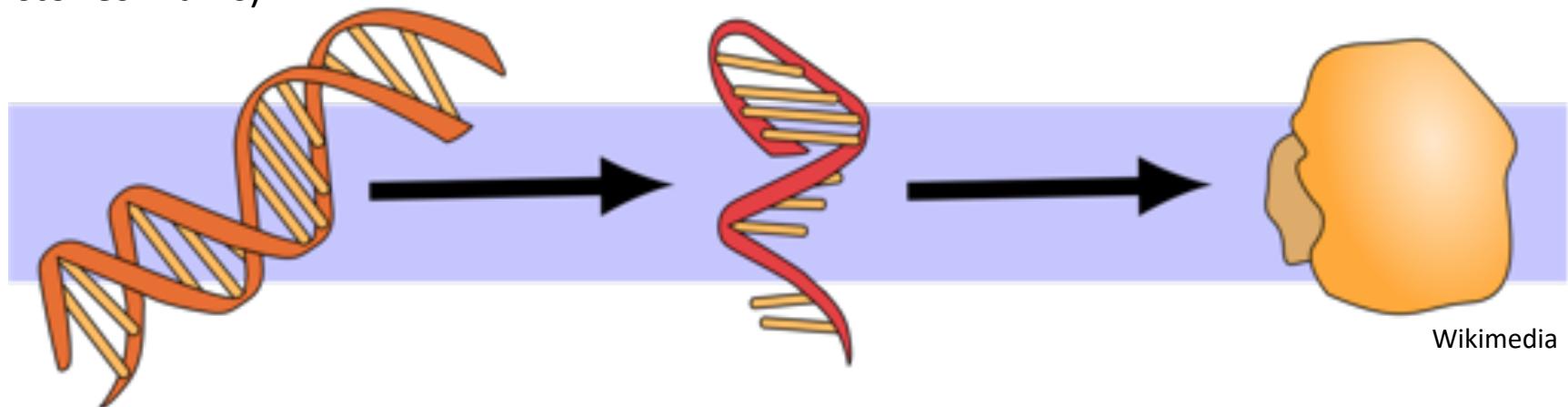


**Wrong
match**

Oncologist
Selects
therapy
based on
experience
or tumor
site

Types of tumor-specific alterations

- Epigenetic changes (methylation, histones marks)



DNA

- Mutations, deletions
- Copy number variations, translocations,
- Transposon insertions

RNA

- Change in expression
- Change in processing (splicing)
- Base modifications
- Activation of noncoding genes

Protein

- Change in quantity
- AA modifications

Cancer driver genes

- Genes whose alterations can be oncogenic
- ~500 known drivers in our 20,000 protein-coding genes
 - Tumor suppressors  Impairing mutations
 - Oncogenes  Activating mutations

Actionable genes

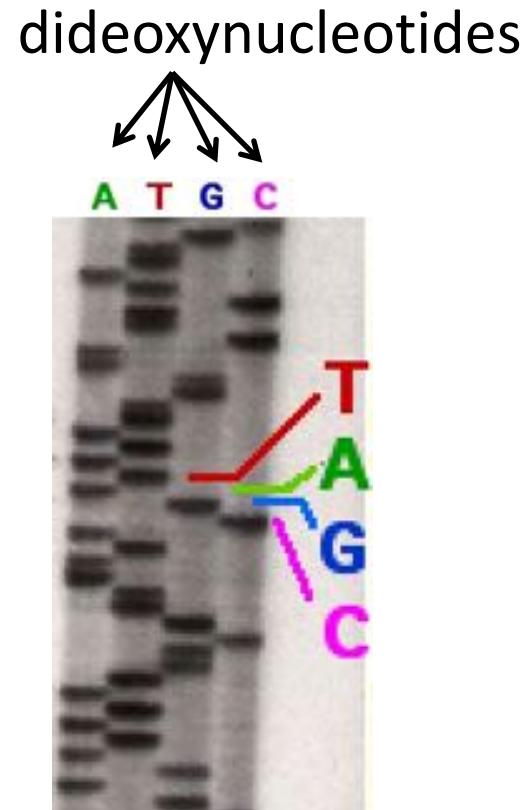
- Genes that can be targeted by a known drug
- Ex:
 - BRCA2: PARP inhibitors
 - ERBB2: anti-HER2 antibody
 - KRAS: RAS inhibitor
- < 50 genes

RNA and DNA sequencing:

The main omics technologies in oncology

Sanger sequencing(1977)

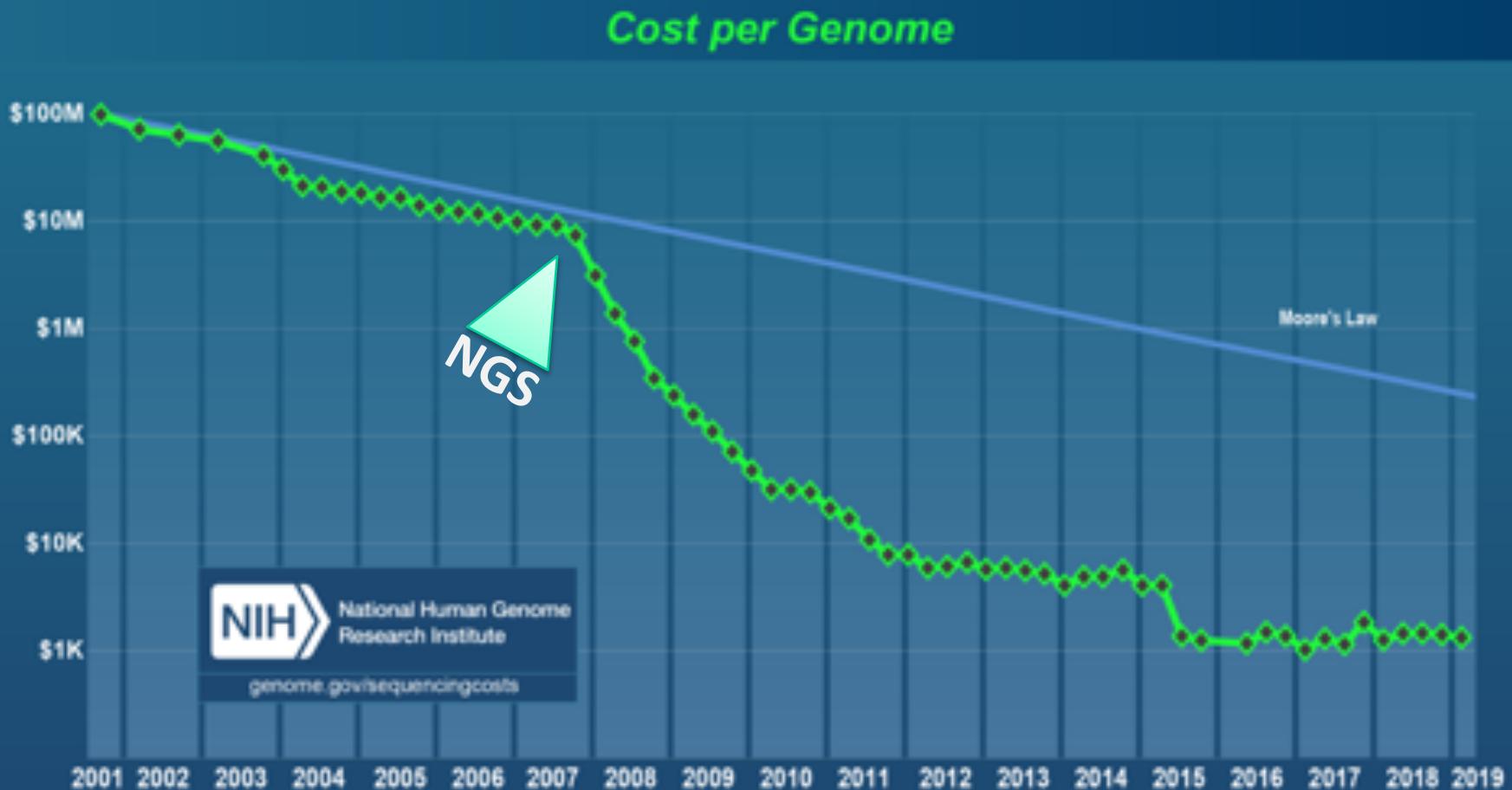
- Chain termination sequencing or "sequencing by synthesis"
 - dideoxynucleotides are used to block synthesis at a specific base.
- Improved in 1987 with fluorescent markers (1 unique reaction), capillaries and automatisation.



Acrylamid gel

Wikipedia

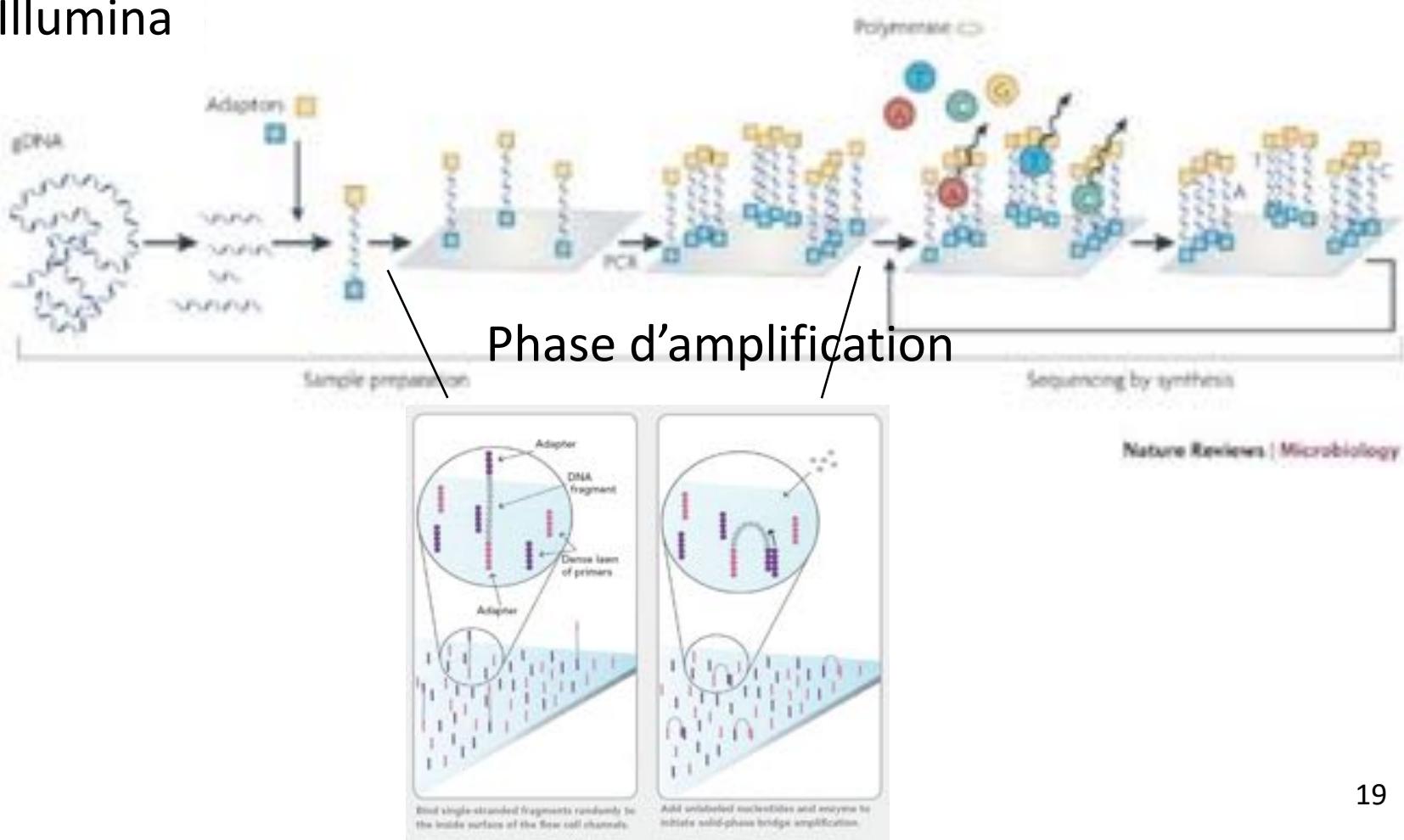
The NGS revolution



NGS :
Next Generation Sequencing
(2005-)

The most common NGS is « sequencing by synthesis » too!

Illumina



Next Generation Sequencing

					
Nanopore Minlon	Lifetech Ion torrent PGM	Illumina MySeq	Lifetech Ion proton	Illumina Hi-Seq 2000	Illumina NovaSeq
50Mb	400 Mb	4 Gb	20 Gb	300 Gb	3Tb

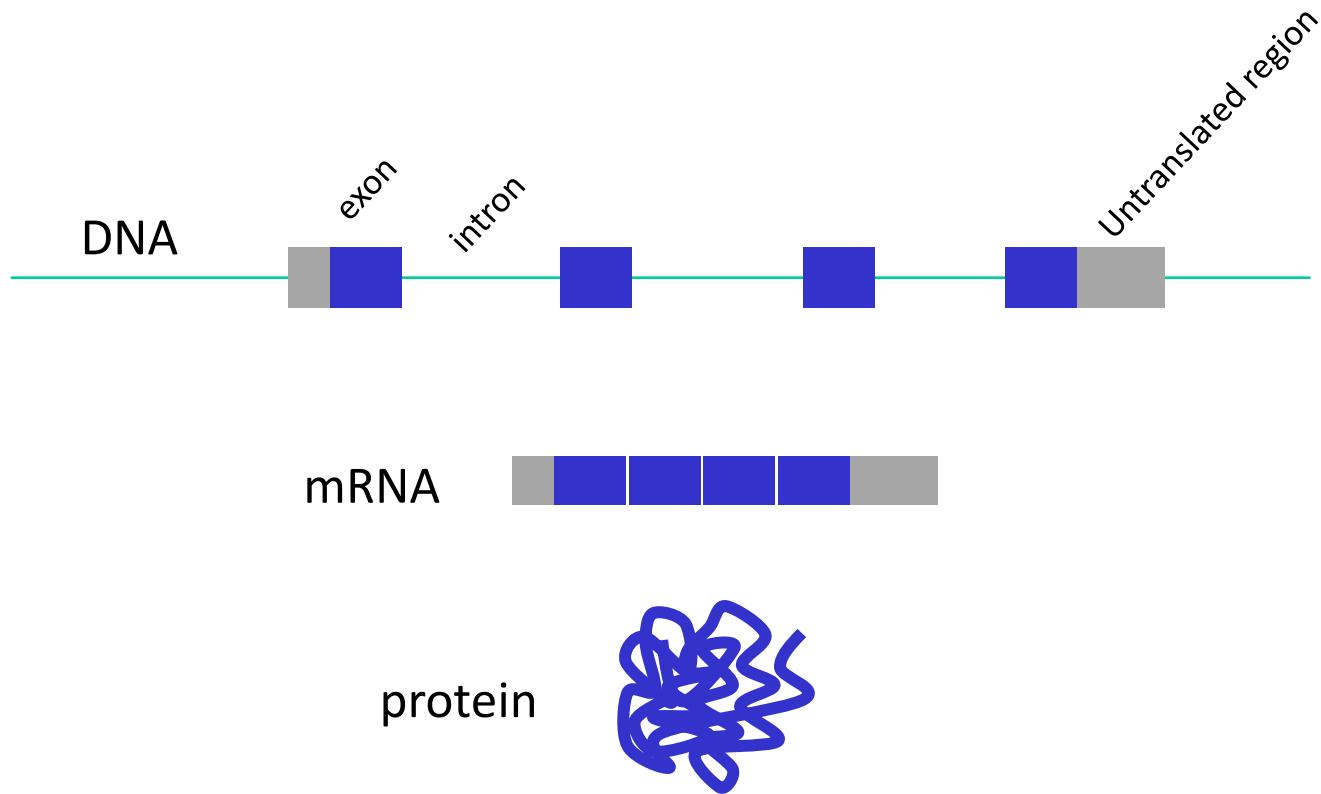
Les grandes applications des NGS

- DNA-seq (variants génomiques, de novo)
- RNA-seq (transcriptome)
- ChiP-Seq (sites de liaisons à l'ADN)
- Autres applications
 - Hi-C, clip-seq, net-seq, ribosome profiling etc.

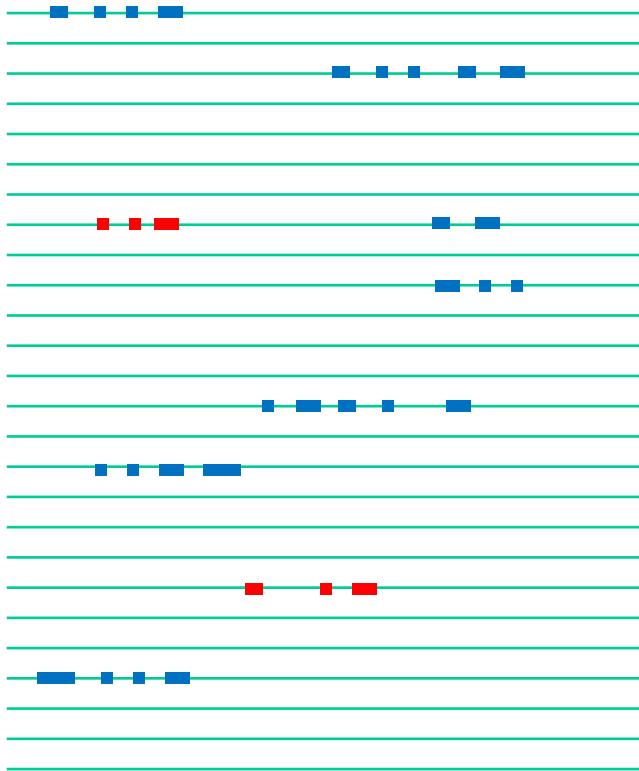
DNA-seq: Recherche de variants génomiques

- En cancérologie, 2 grandes applications
 - Génétique constitutionnelle (recherche de prédisposition)
 - Génétique somatique (diagnostic, médecine de précision)

Reminder: human gene structure

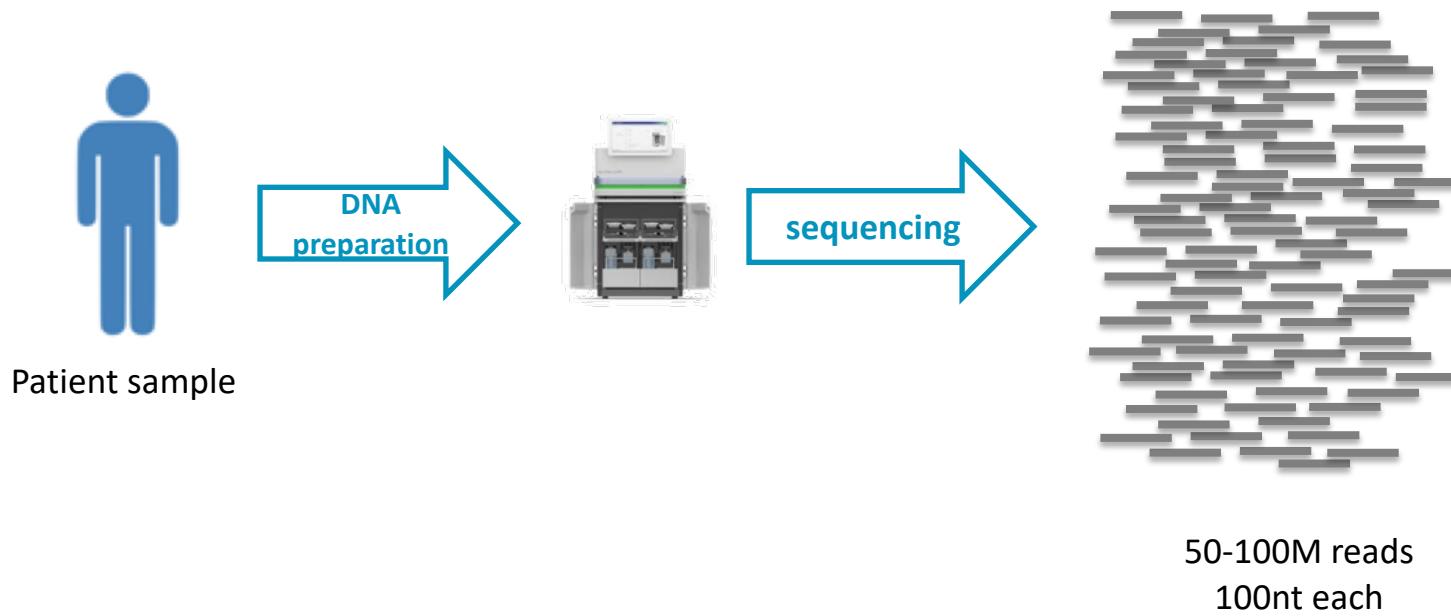


DNA sequencing types

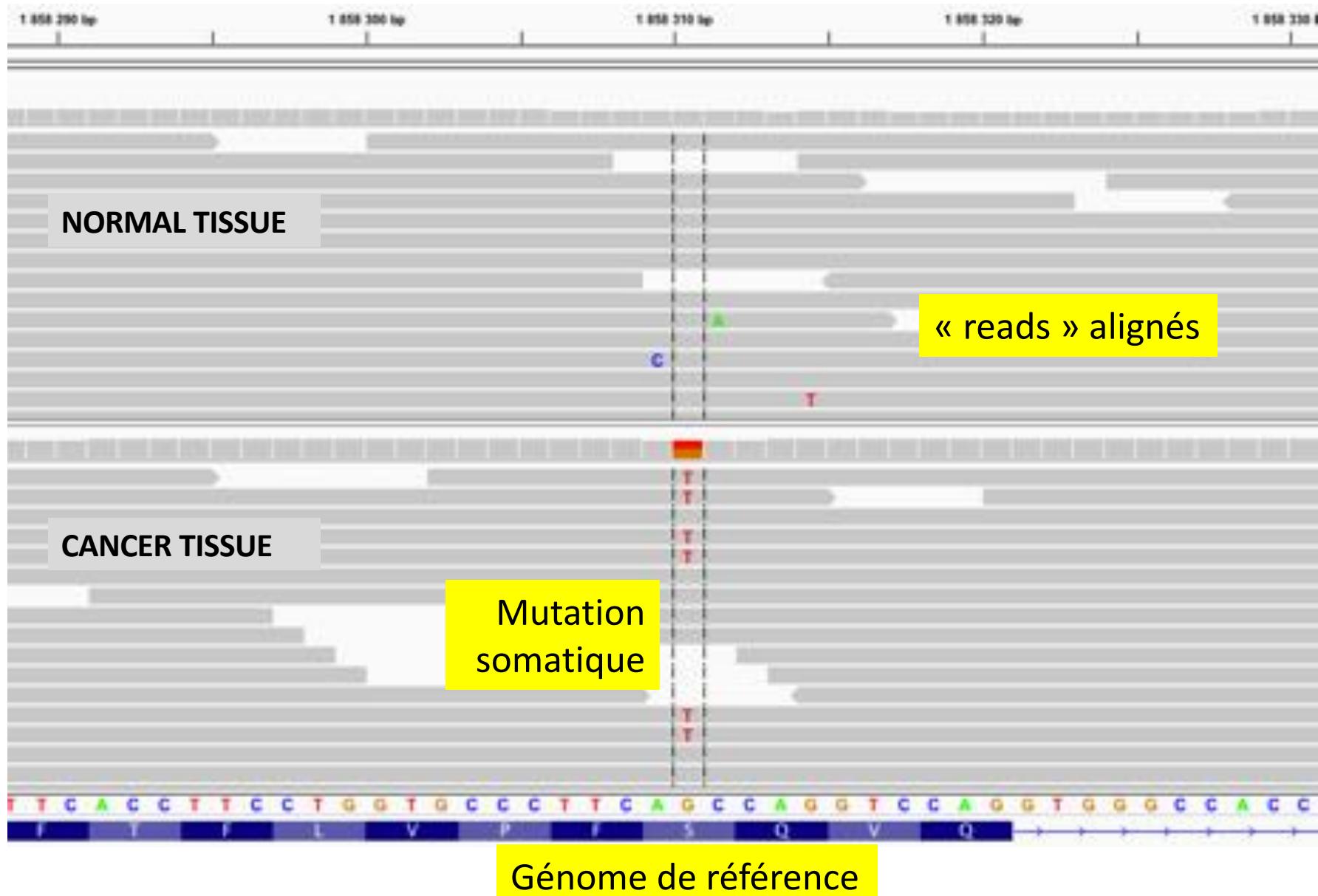


- WGS= Whole genome
- WES: whole exome
- Panel: selected genes

Protocole



Événements recherchés



Événements recherchés par DNA-seq

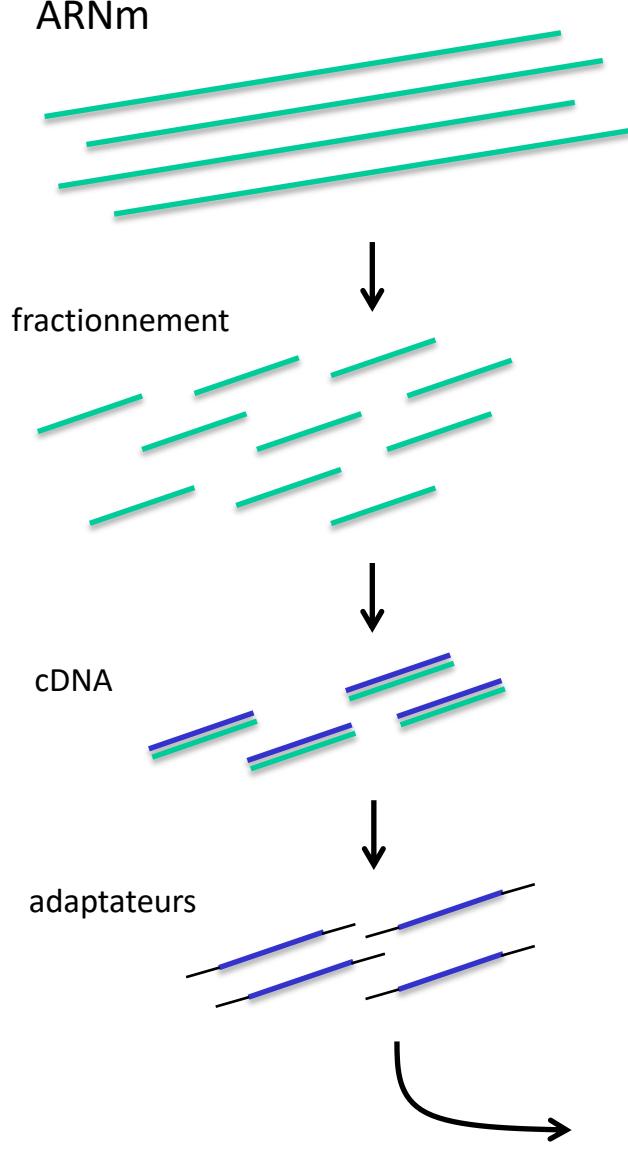
- Variations ponctuelles=SNV
- Réarrangements
- Changement de nombres de copies =CNV
- Amplification de microsatellites
- Profils mutationnels

Cf cours/TP exome
(B Job, D. Gautheret)

RNA-seq

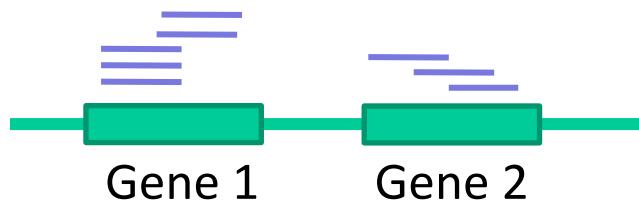
- Pour l'étude du transcriptome
 - Mesure de l'expression de tous les gènes, simultanément

RNA-Seq

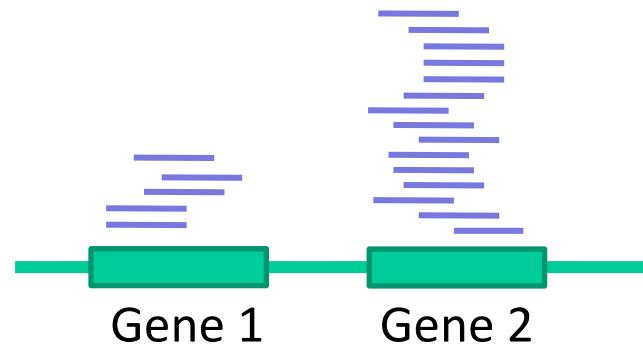


Séquençage

Mesure d'expression par RNA-seq

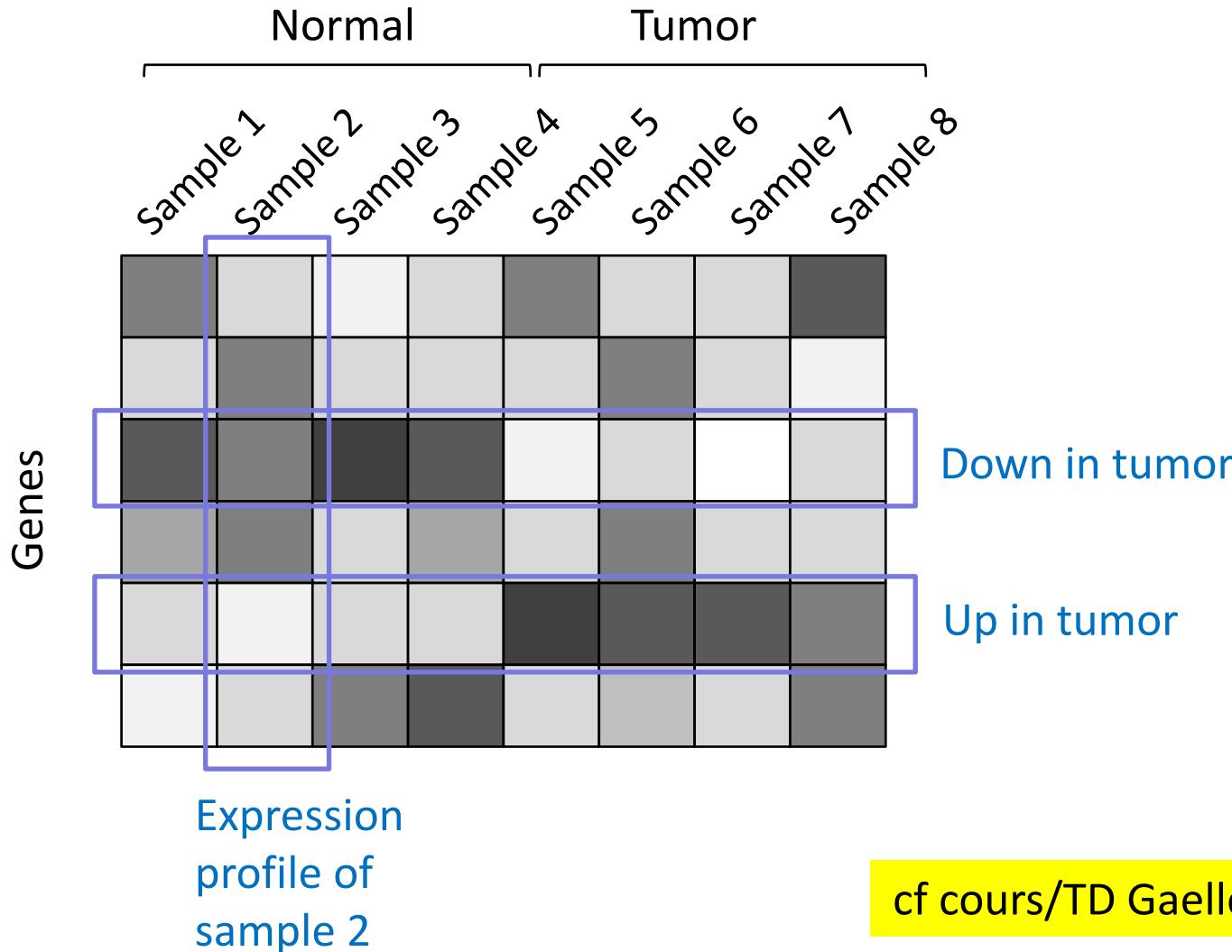


Sample 1



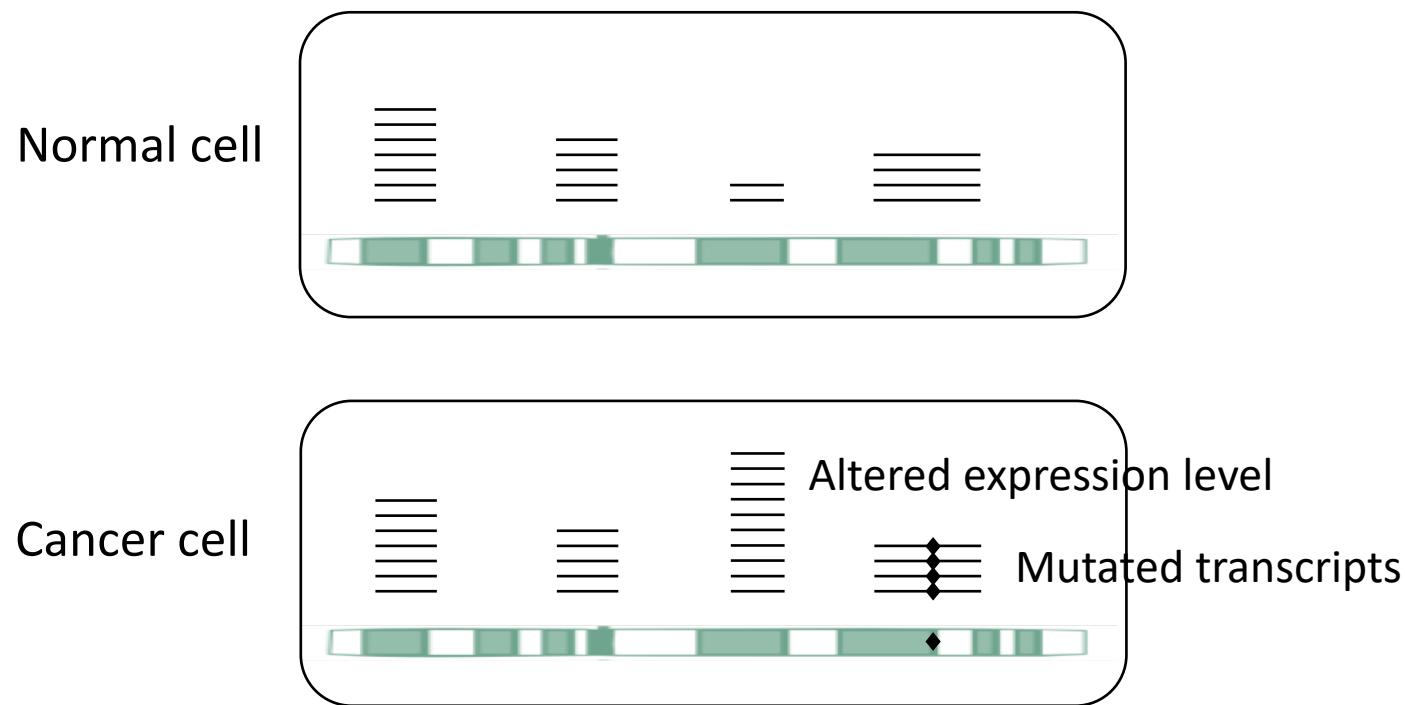
Sample 2

Differential expression analysis & expression profiling



cf cours/TD Gaelle Lelandais

L'ARN permet aussi de détecter certaines mutations

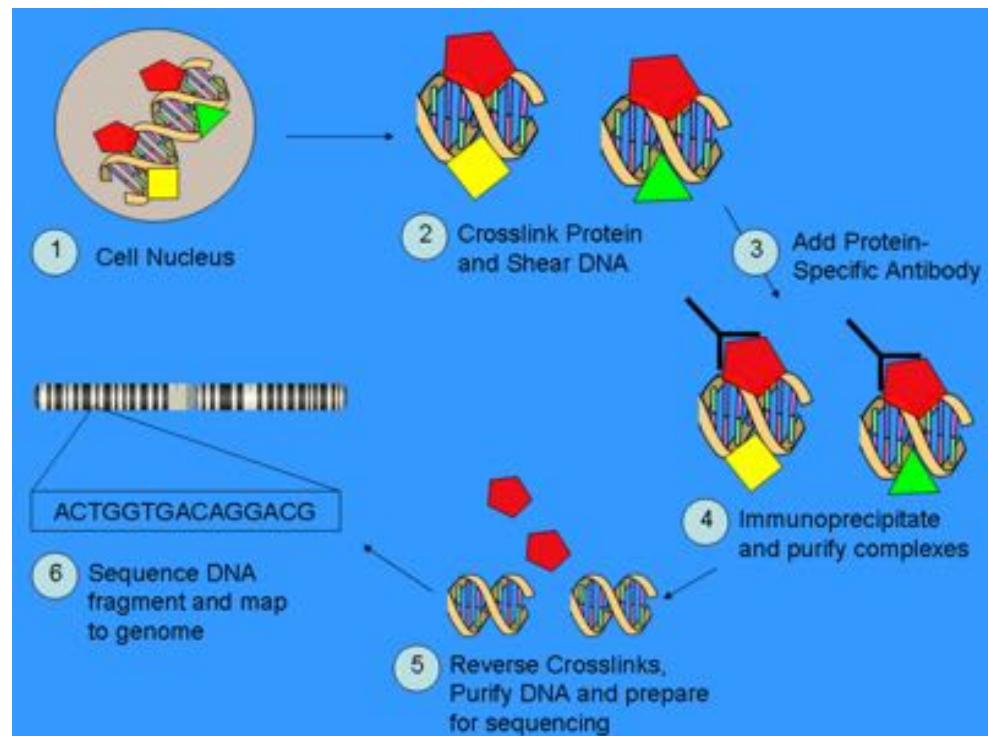


ChIP-Seq

- Chromatin ImmunoPrecipitation & Sequencing

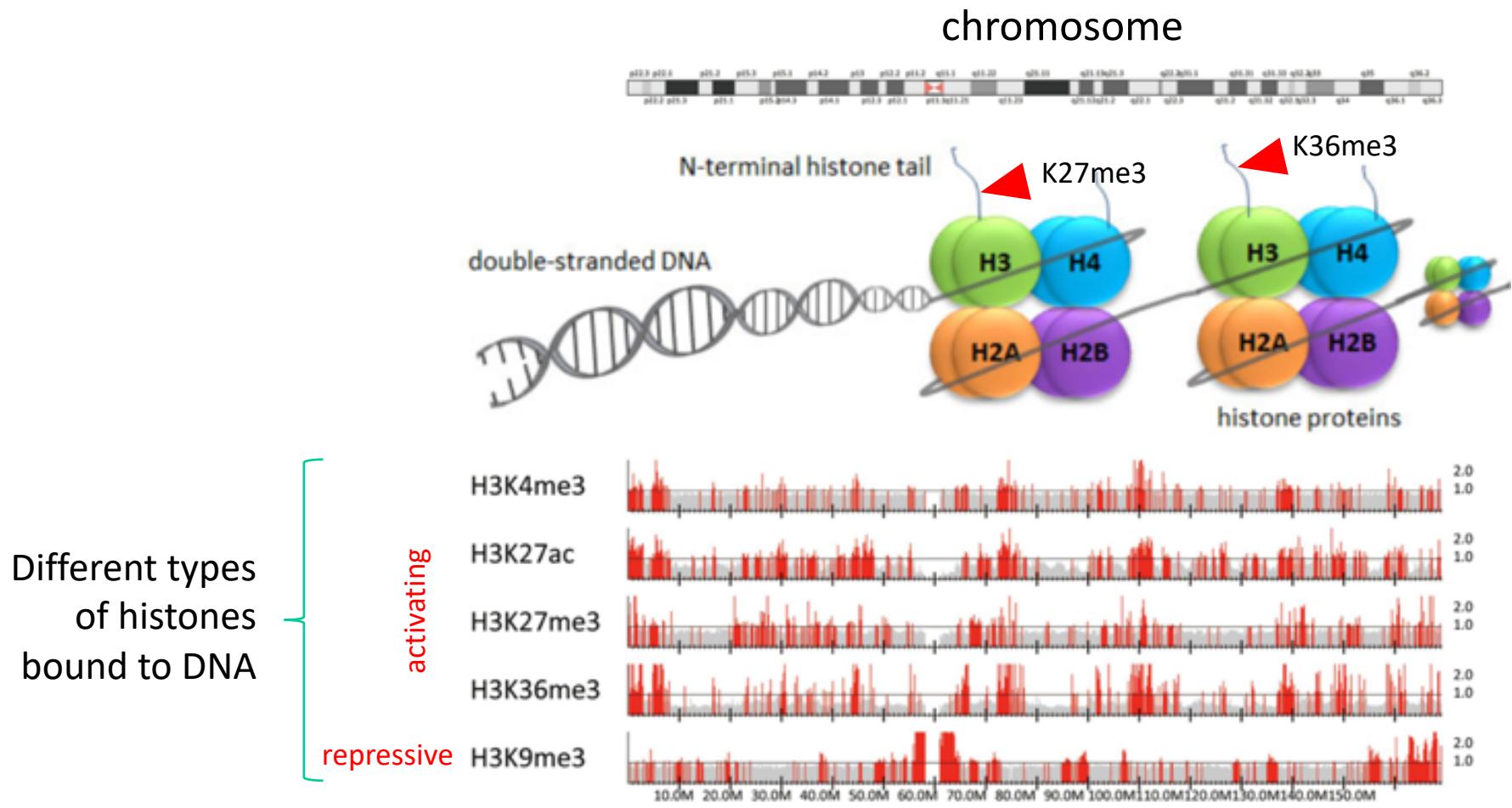
ChIP-Seq

- Permet d'identifier les sites de liaison de protéines (histones, facteurs de transcription, represseurs, enhancers, etc.) sur l'ADN génomique

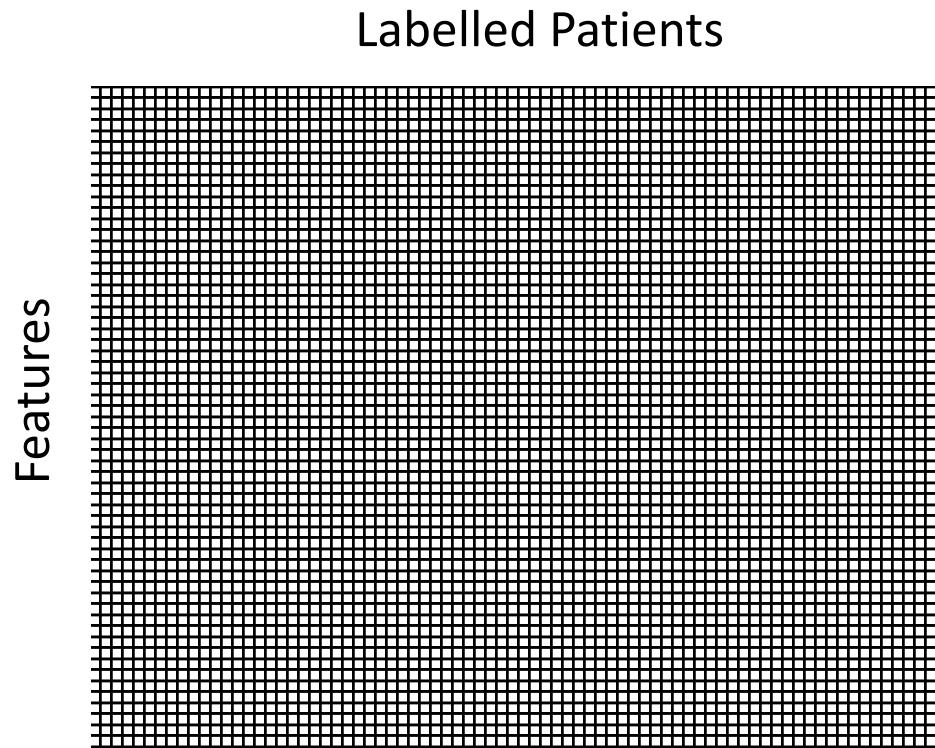


Wikipedia

ChIP-seq in oncology



Big data in oncology



Vers une utilisation systématique du séquençage en médecine



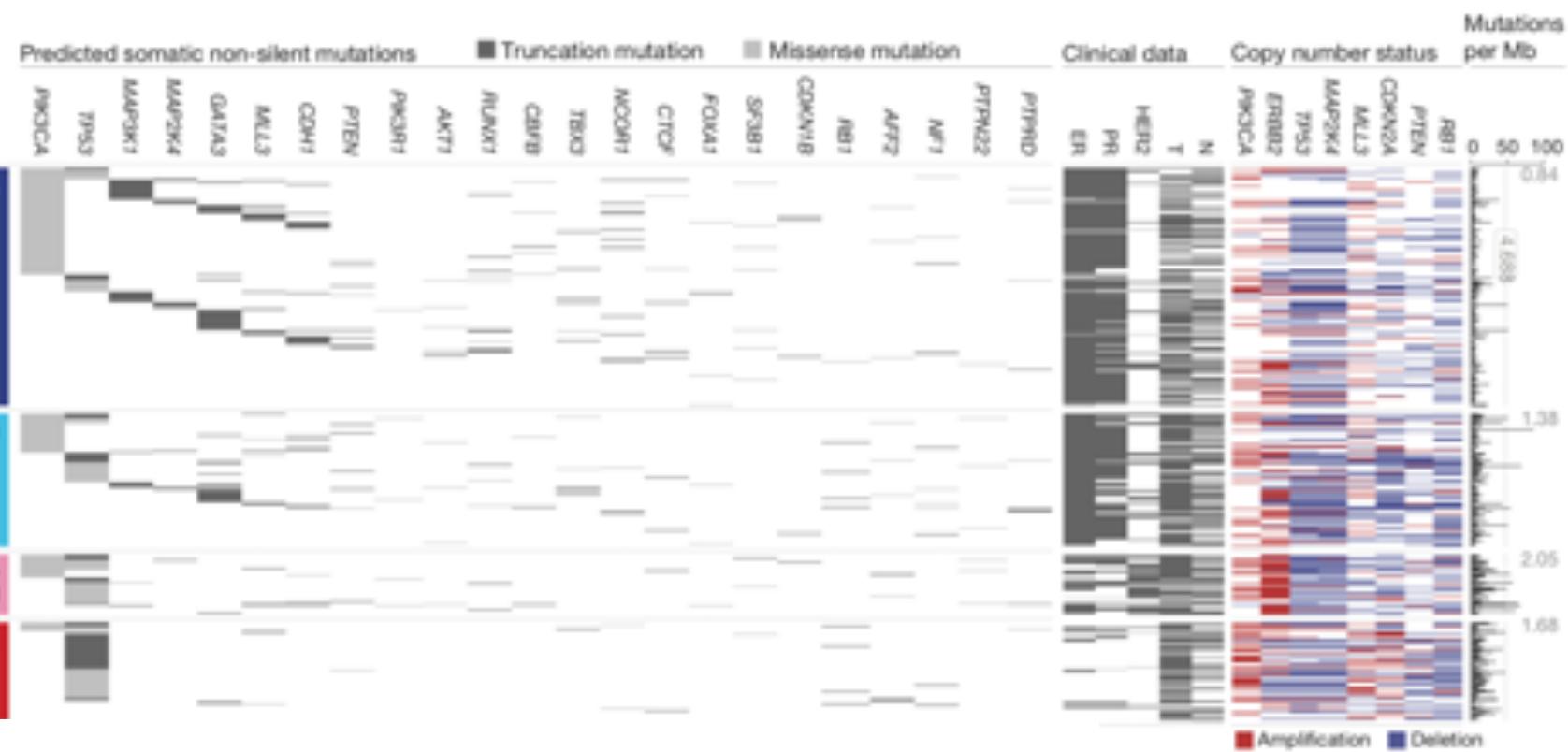
Cohorte "population générale"

A screenshot of the 'Médecine France génomique 2025' website. The main title is 'Médecine France génomique 2025' in large bold letters. Below it, a blue bar indicates 'mise à jour : 19.07.17'. There are three buttons below the bar: 'A+' (highlighted), 'A-', and a printer icon. To the right are social media icons for email, Twitter, and Facebook. A dark grey box at the bottom contains the following text:

Le plan « Médecine France génomique 2025 », se concrétise. En effet, le ministère chargé de la santé a lancé en décembre 2016 un appel à projets national amorçant le financement des 2 premières plateformes génomiques à visée diagnostique et de suivi thérapeutique, sur les 12 attendues dans les 5 ans. Ces équipements d'excellence illustrent le soutien constant des pouvoirs publics vis-à-vis de l'innovation médicale, en l'occurrence du séquençage à très haut débit du génome humain qui fonde la médecine génomique, dite aussi « personnalisée ».

Cohortes cancer

Patients



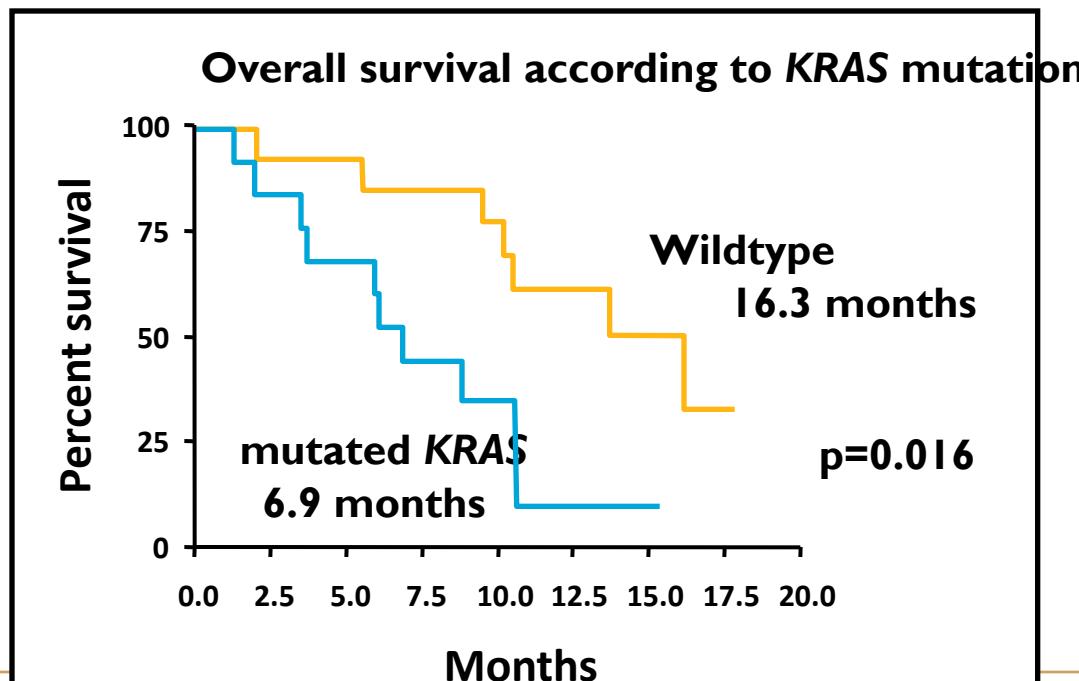
Mutations observées chez 825 patientes de cancer du sein
TCGA consortium, Nature, 2012

KRAS Mutation and Anti-EGFR therapy in advanced colorectal cancer

Christophe Massard

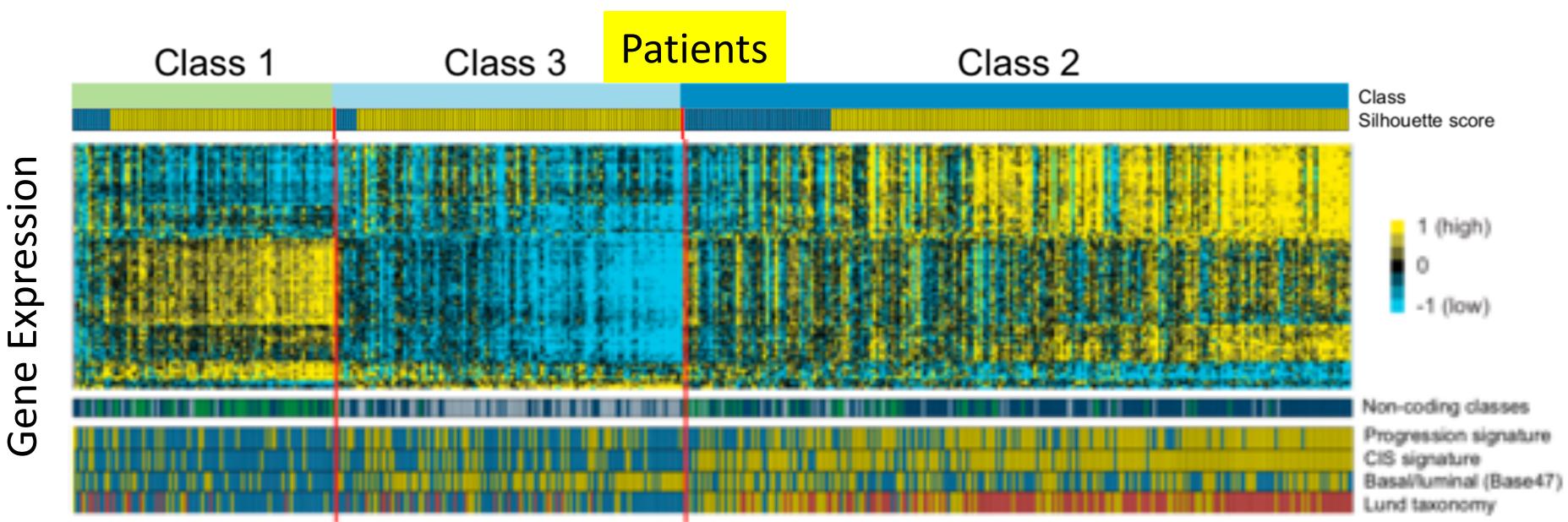
KRAS Status	Responders*	Non responders*	Total
KRAS mutation (%)	0 (0)	13 (100)	13
Wildtype (%)	11 (65)	6 (35)	17

p=0.0003



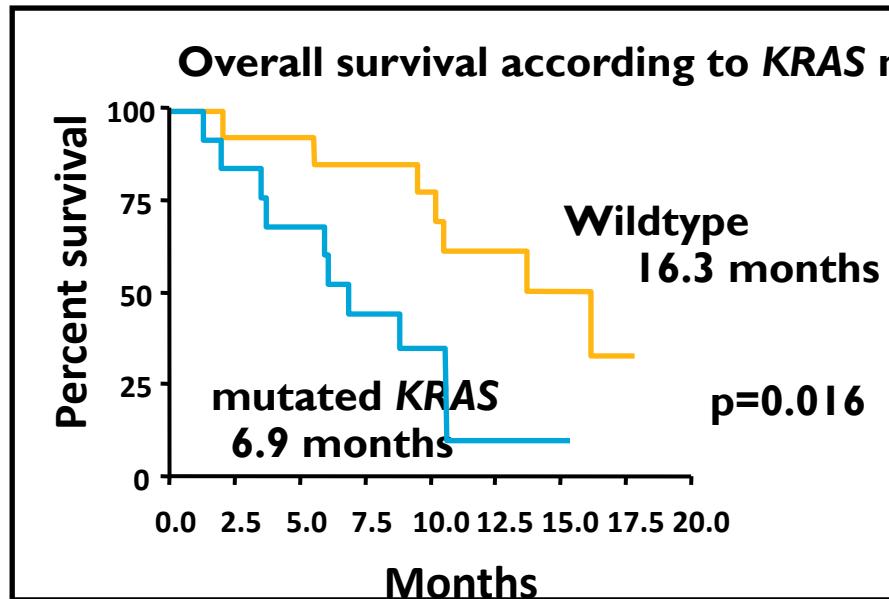
p=0.0003

Transcription profiles for tumor subtyping

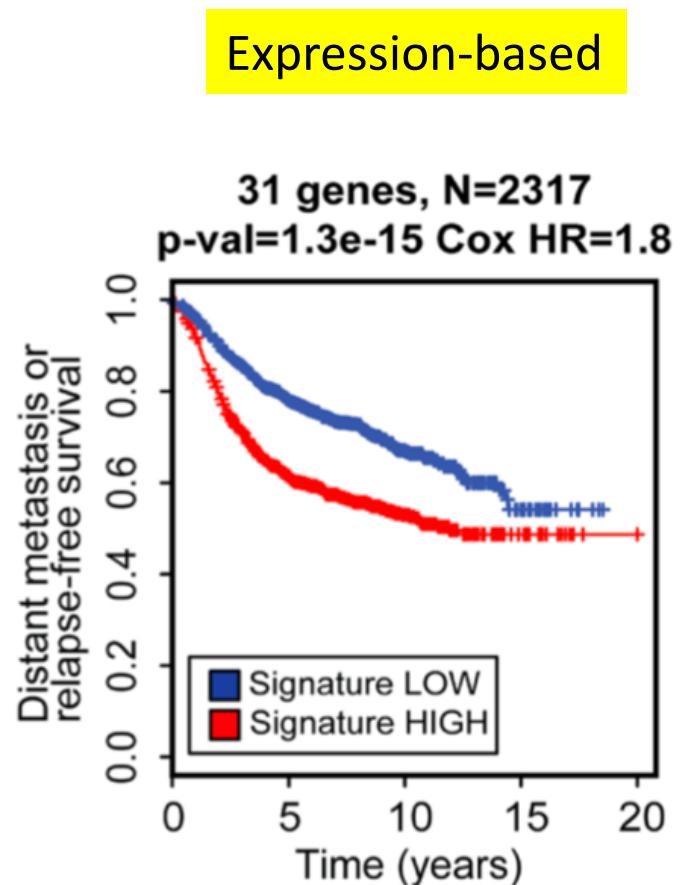


A 117-gene signature for urothelial carcinoma
Hedegaard et al., Cancer Cell, 2016

Modèles prédictifs de survie



DNA-based



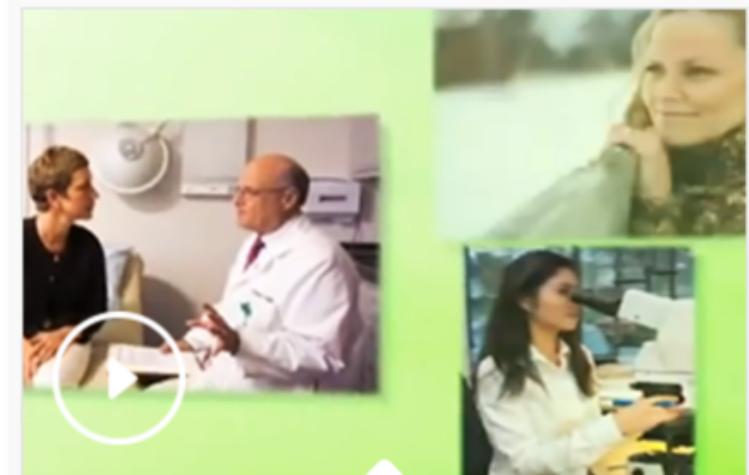
Transcriptional signatures: current applications

Diagnostic

- Tumor vs normal
- Tumor subtyping

Precision medicine

- Response to treatment
- Relapse prediction



Genomic Health et le test Oncotype DX

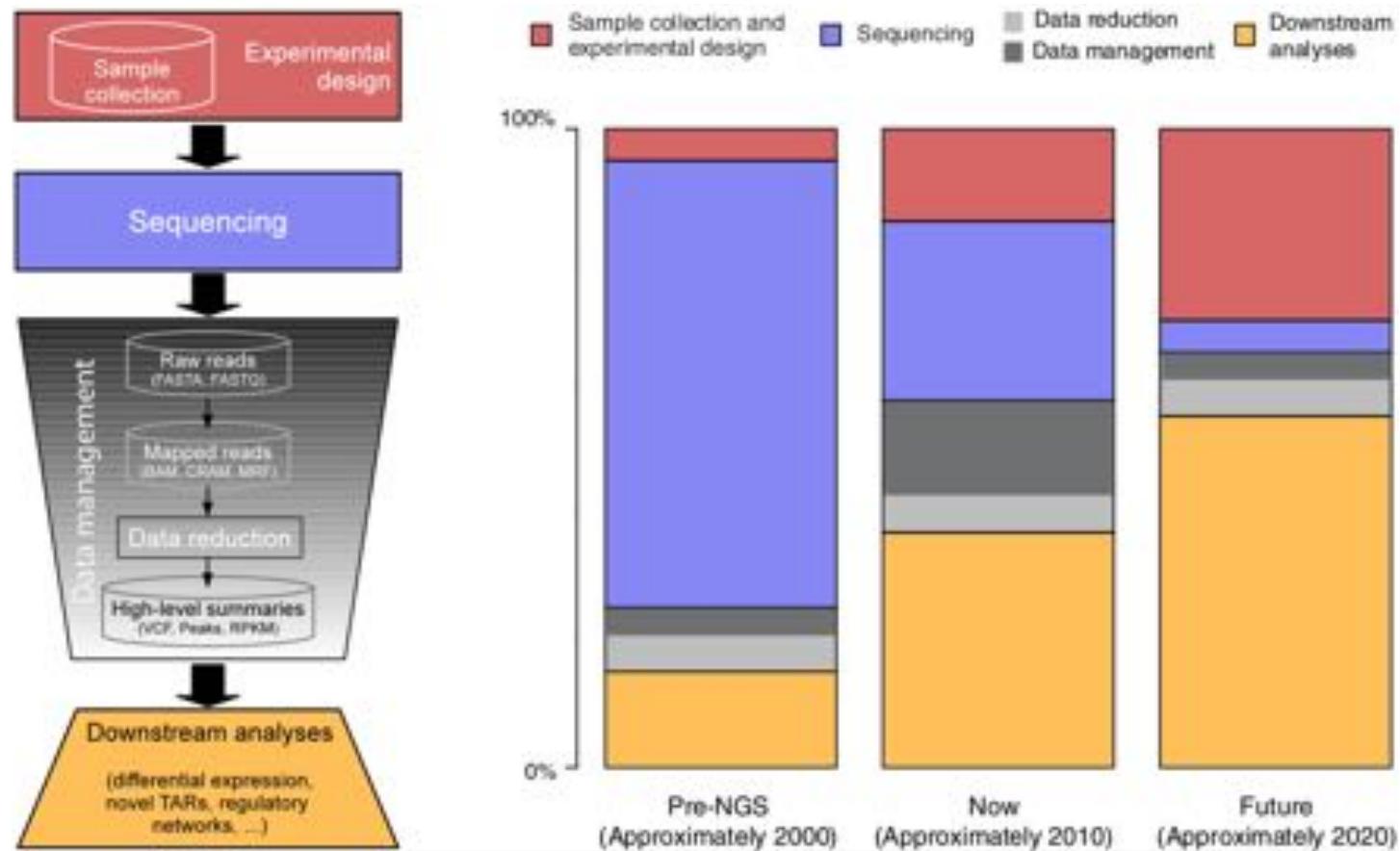
Traitement du Cancer: Comment les tests Oncotype DX permettent de personnaliser les décisions thérapeutiques.

Les données NGS

Volume des données NGS

- Un exome humain (N+T) avec fichiers de mapping et analyse: 70 Go
 - (~5 fois le volume des séquences brutes)
- Données génomiques produites annuellement dans un hôpital universitaire: >500 To
- La banque TCGA complete: 1 Po

Costs of sequencing vs analysis



Les outils

« Pipelines » & « workflows »

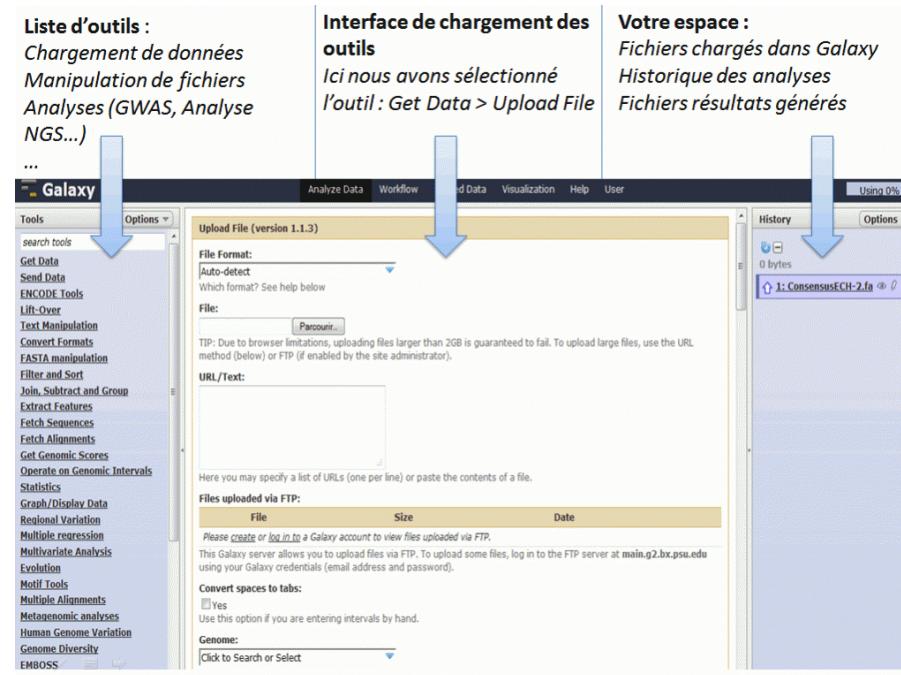
« Bricks » from
Unix open
source programs

Combined into
pipelines
(typically a few
hours to days to
run)

Example: an RNA-seq pipeline



Galaxy: user-friendly interface to NGS pipelines



Credit: Biorigami

- Interest: avoiding Unix command line + traçability
- But: running NGS workflow on real human data often requires a computer cluster (will not run on a single-node Galaxy server)

Les bases de données en génomique du cancer

Cancer Genomics Databases

- TCGA: the Cancer Genome Atlas
- COSMIC
- cBioPortal
- CCLE: Cancer Cell Lines Encyclopedia
- GDSC: Genomics of Drug Sensitivity in Cancer
- dbGaP: database of Genotypes and Phenotypes
- GEO: Gene Expression Omnibus
- ArrayExpress

The Cancer Genome Atlas



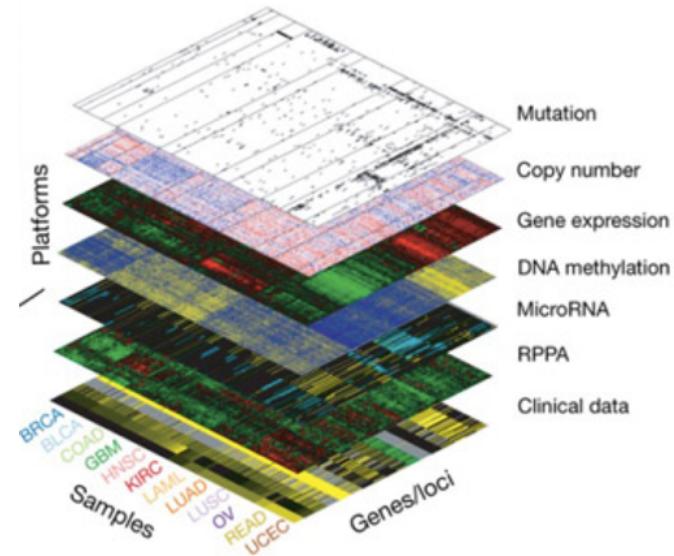
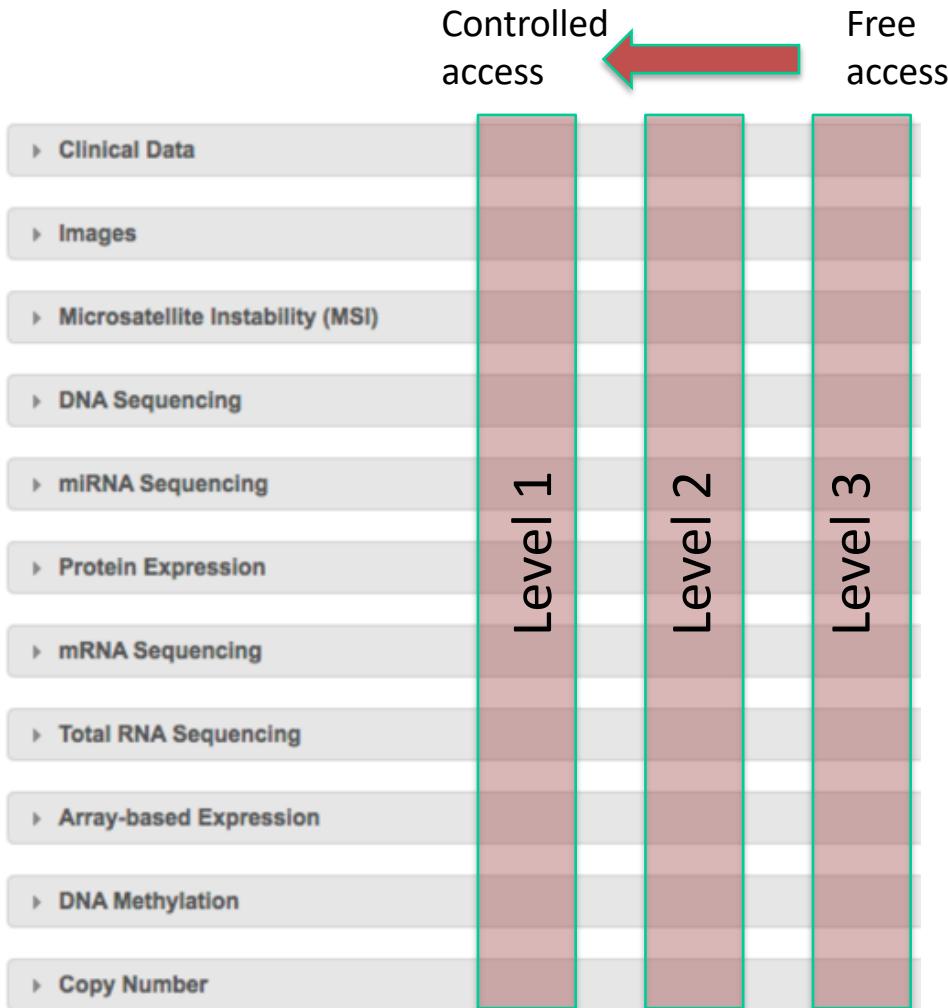
*Understanding genomics
to improve cancer care*

NCI, NHGRI, USA

TCGA

- launched in 2006
- 33 tumor types
- 11,000 patients
- whole-genome sequencing (WGS) for 1,000 tumors

TCGA data types and levels



Example of access levels

	Level 1	Level 2	Level 3
RNA-seq	mRNA sequence for each participant's tumor sample		The calculated expression signal of a particular composite exon of a gene, per sample
DNA-seq	Whole exome sequence for both tumor and normal sample for each participant	Somatic mutation calls for each participant	

Main data types

- DNA sequencing
 - Whole exome or whole genome DNA sequence
 - Platform: Illumina HiSeq
- mRNA sequencing / miRNA sequencing
 - PolyA+ RNA / small RNA expression from RNA-seq
 - Platform: Illumina HiSeq or similar
- Array-based expression
 - mRNA expression levels (1 or 2 colors)
 - Illumina or Agilent DNA microarrays

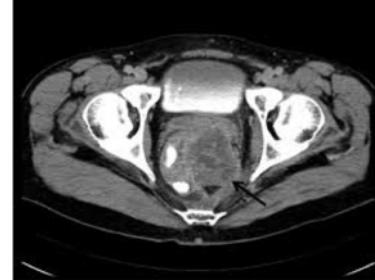
Main data types

- DNA Methylation
 - covalent modification of cytosine bases at the C-5 position, generally within a CpG sequence context
 - platforms: Illumina Methyl arrays
- Protein expression
 - protein expression & concentration
 - Platform: custom antibody array (5ABx1000 samples/slide)
- Copy number
 - Loss and gain of DNA fragments
 - Platform: Agilent CGH array

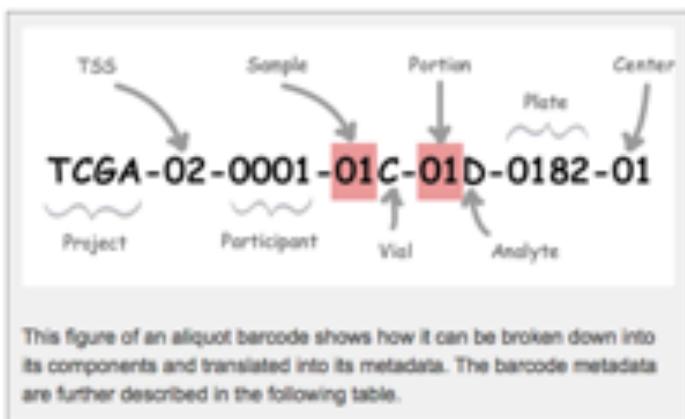


Main data types

- Microsatellite instability
 - MSI-Mono-Dinucleotide Assay: panel of 4 mononucleotide and 3 dinucleotide repeat loci
- Image
 - Images of tissue samples
 - CT (computed tomography), DX (digital radiography), CR (computed radiography)
- Clinical data
 - Available clinical information for each participant (demographic, treatment, survival, etc)
 - Biospecimen data: how specimen was processed



1 sample = 1 TCGA barcode



Label	Identifier for	Value	Value description	Possible values
Project	Project name	TCGA	TCGA project	TCGA
TSS	Tissue source site	02	GBM (brain tumor) sample from MD Anderson	See Code Tables Report
Participant	Study participant	0001	The first participant from MD Anderson for GBM study	Any alpha-numeric value
Sample	Sample type	01	A solid tumor	Tumor types range from 01 - 09, normal types from 10 - 19 and control samples from 20 - 29. See Code Tables Report for a complete list of sample codes
Vial	Order of sample in a sequence of samples	C	The third vial	A to Z
Portion	Order of portion in a sequence of 100 - 120 mg sample portions	01	The first portion of the sample	01-99
Analyte	Molecular type of analyte for analysis	D	The analyte is a DNA sample	See Code Tables Report
Plate	Order of plate in a sequence of 96-well plates	0182	The 182nd plate	4-digit alphanumeric value
Center	Sequencing or characterization center that will receive the aliquot for analysis	01	The Broad Institute GCC	See Code Tables Report

TCGA Clinical Data (patient or sample XML file)

Clinical – emacs – 179x47

```
<?xml version="1.0" encoding="UTF-8"?>
<tcga_bcr>
  <admin>
    <bcr xsd_ver="1.17">Nationwide Children's Hospital</bcr>
    <batch_number xsd_ver="1.17">88_48_0</batch_number>
    <disease_code xsd_ver="2.3">BRCA</disease_code>
    <day_of_doc_upload xsd_ver="1.17">27</day_of_doc_upload>
    <month_of_doc_upload xsd_ver="1.17">2</month_of_doc_upload>
    <year_of_doc_upload xsd_ver="1.17">2014</year_of_doc_upload>
    <patient_withdrawn>
      <withdrawn>false</withdrawn>
    </patient_withdrawn>
  </admin>
  <patient>
    <shared:tumor_tissue_site>Breast</shared:tumor_tissue_site>
    <shared:gender>FEMALE</shared:gender>
    <shared:vital_status>Alive</shared:vital_status>
    <shared:race>WHITE</shared:race>
    <shared:bcr_patient_barcode>TCGA-BH-A8B2</shared:bcr_patient_barcode>
    ...
    <shared:history_of_neoadjuvant_treatment>No</shared:history_of_neoadjuvant_treatment>
    <shared:informed_consent_verified>YES</shared:informed_consent_verified>
    ...
    <shared:age_at_initial_pathologic_diagnosis>43</shared:age_at_initial_pathologic_diagnosis>
    ...
    <shared:histological_type>Infiltrating Ductal Carcinoma</shared:histological_type>
    <brca_shared:breast_carcinoma_progesterone_receptor_status>Positive</brca_shared:breast_carcinoma_progesterone_receptor_status>
    ...
    <brca_shared:breast_carcinoma_estrogen_receptor_status>Positive</brca_shared:breast_carcinoma_estrogen_receptor_status>
    <brca_shared:lab_proc_her2_neu_immunohistochemistry_receptor_status>Negative</brca_shared:lab_proc_her2_neu_immunohistochemistry_receptor_status>
    ...
    <brca_nre:new_tumor_events>
      <nre:new_tumor_event_after_initial_treatment>
    </brca_nre:new_tumor_events>
  </patient>
</tcga_bcr>
```

200/300 lines per file

Extract of patient xml clinical file

TCGA access via the GDC portal (Genomics Data Commons)



TCGA data access via the GDC Data portal

NATIONAL CANCER INSTITUTE
GDC Data Portal

Home Projects Data Analysis Quick Search Login Cart GDC Apps

Cases Files < Hide Filters Add a Case/Biospecimen Filter

Start searching by selecting a facet or try the Advanced Search

Advanced

Case Submitter ID Prefix Primary Site Cancer Program Project

Search for Case Id Search for Submitter Id

Search for Primary Site

Kidney Brain Nervous System Breast Lung

TCGA TARGET

TARGET-NBL TCGA-BRCA TARGET-AML TARGET-WT TCGA-GBM

Summary Cases (14,551) Files (274,724)

Add all files to the Cart Download Manifest

FILES 274,724 CASES 14,551 FILE SIZE 470.57 TB

File Counts by Project 39 Projects

File Counts by Access Level 2 Access Levels

File Counts by Data Format 7 Data Formats

File Counts by Primary Site

File Counts by Data Type

File Counts by Experimental Str...

The screenshot displays the GDC Data Portal's main dashboard. On the left, there are several filter panels: 'Case' (with a search bar), 'Case Submitter ID Prefix' (with a search bar), 'Primary Site' (listing Kidney, Brain, Nervous System, Breast, Lung with counts 1,081, 1,130, 1,147, 1,266, 1,046 and '24 More...'), 'Cancer Program' (listing TCGA, TARGET with counts 11,215, 3,336), and 'Project' (listing TARGET-NBL, TCGA-BRCA, TARGET-AML, TARGET-WT, TCGA-GBM with counts 3,147, 1,046, 988, 882, 817 and '34 More...'). The top navigation bar includes links for Home, Projects, Data (which is selected and highlighted in dark grey), Analysis, Quick Search, Login, Cart, and GDC Apps. The main content area features a search bar with an 'Advanced' button, summary statistics (274,724 files, 14,551 cases, 470.57 TB file size), and nine data distribution charts using pie charts and donut charts. These charts cover File Counts by Project (39 projects), File Counts by Access Level (2 levels), File Counts by Data Format (7 formats), File Counts by Primary Site, File Counts by Data Type, and File Counts by Experimental Str... (partially visible).

TCGA is over PCAWG is ongoing

- PCAWG¹: a collaboration TCGA-ICGC² to analyze whole genome data from 2,800 pairs of tumor and normal samples and integrate the results with clinical and other molecular data available on those same cases.

¹. PCAWG: Pan-Cancer Analysis of Whole Genomes

². ICGC: International Cancer Genome Consortium



Sanger Institute, UK

COSMIC Curation

- Manual curation
 - >25000 articles analyzed
- Automated curation
 - 1.4M samples (incl. 31k WGS) (TCGA & ICGC)
 - Annotation pipeline (Variant effect predictor)

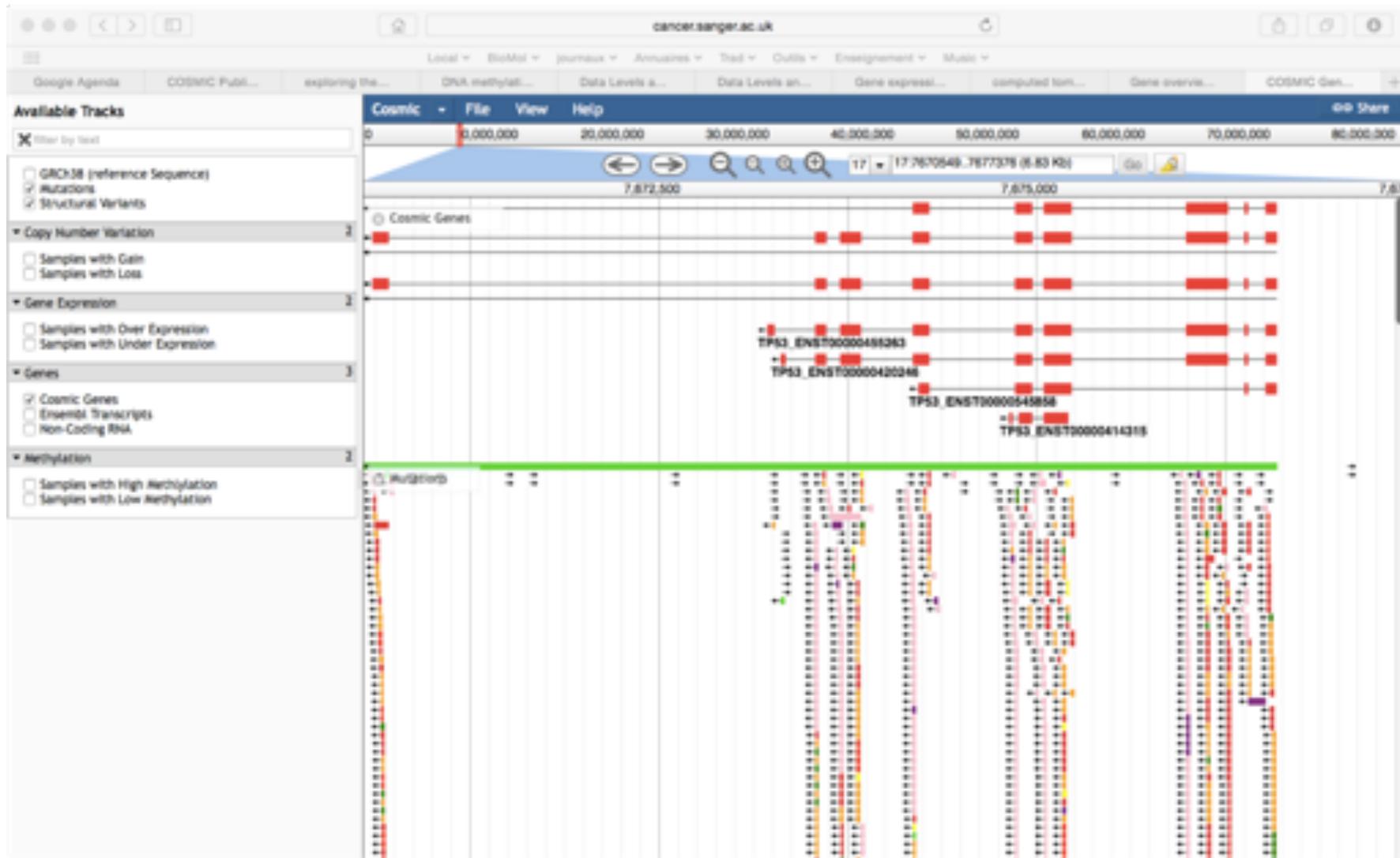
« Most [mutations] have no effect on the development of disease. We are adapting our curation processes to reduce this noise and highlight high-value information. »

« Samples with over 20 000 point mutations, none of which have been validated are excluded from curation as their noise vastly outweighs their signal. »



- Expert-curated database of cancer somatic mutations & other events
- 2019 (V90):
 - 29M coding point mutations
 - 13M non-coding variants
 - 19k gene fusions
 - 1.2 M CNV
 - 9M gene expression variants
 - 576 cancer genes (tier 1)

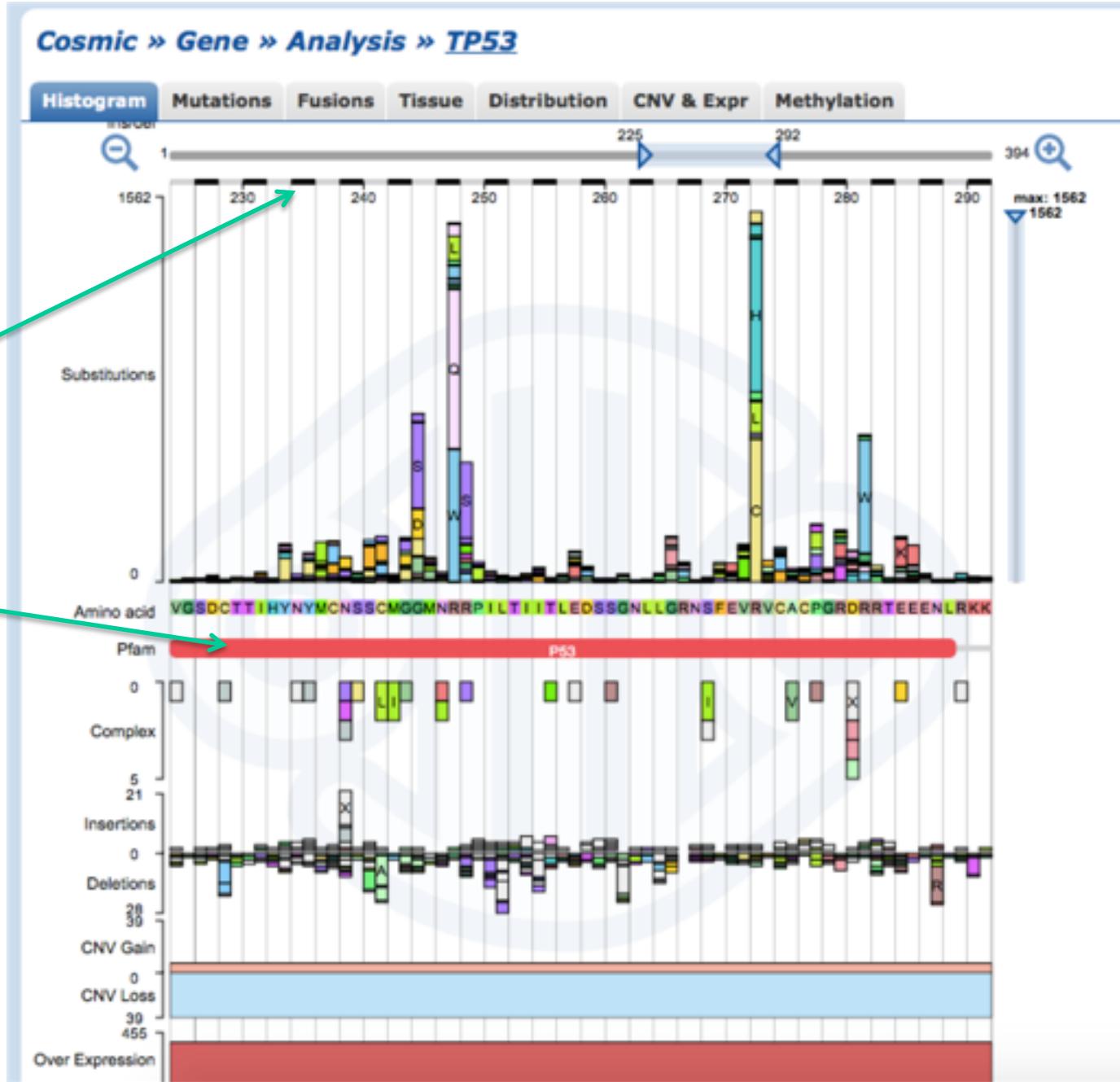
COSMIC genome browser



Histogram view

Protein coordinates

Protein domain



Tissue-distribution of mutations

Cosmic » Gene » Analysis » TP53 View in GRCh37 Archive

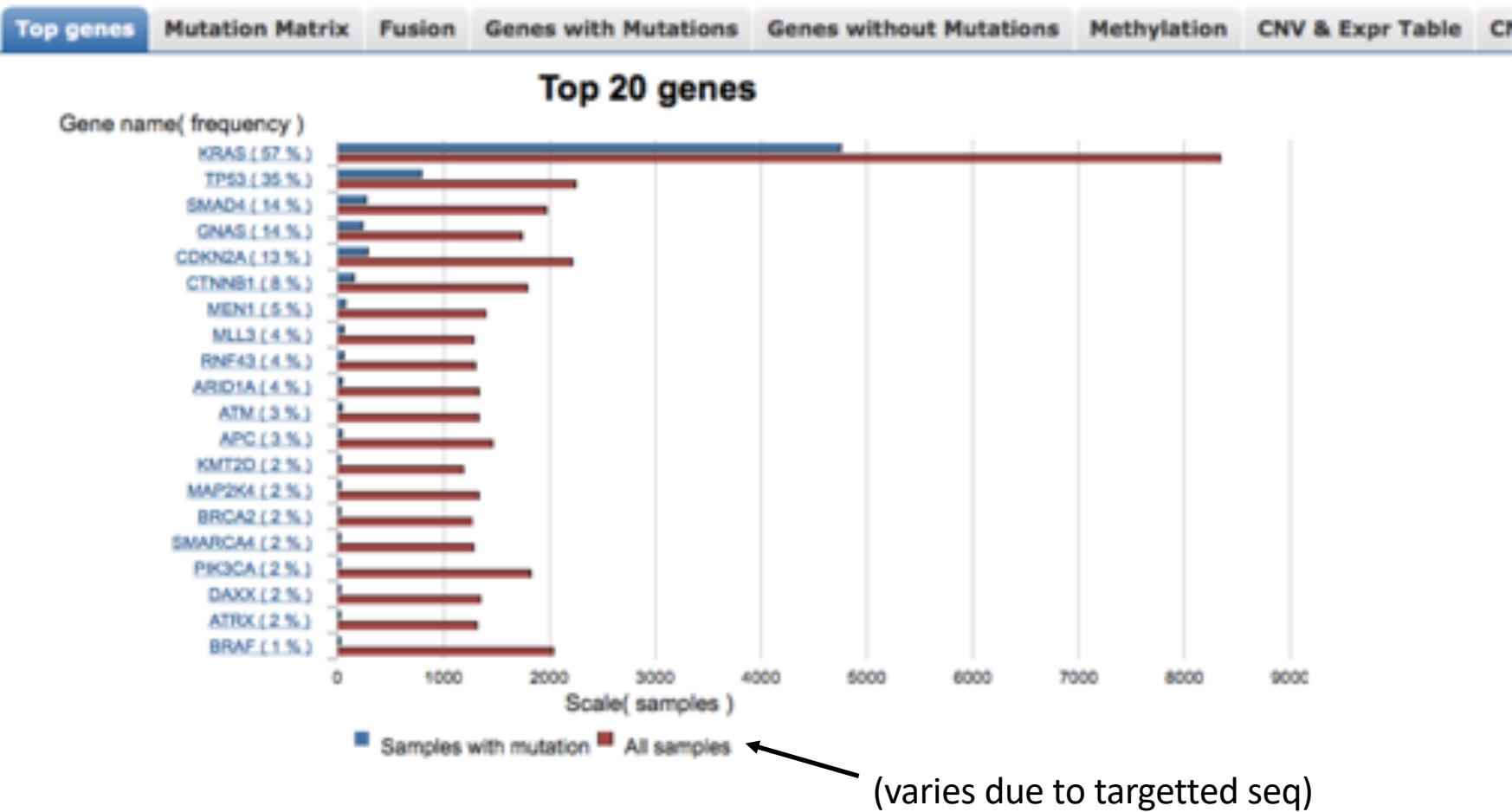
Histogram Mutations Fusions Tissue Distribution CNV & Expr Methylation

Show All 0 entries Search: ?

Tissue	Point Mutations		Copy Number Variation		Gene Expression		Methylation	
	% Mutated	Tested	Variant %	Tested	% Regulated	Tested	% Diff. Methylated	Tested
Adrenal gland	—	508	—	—	—	79	—	—
Autonomic ganglia	—	586	—	—	—	—	—	—
Biliary tract	—	872	—	—	—	—	—	—
Bone	—	955	—	83	—	—	—	—
Breast	—	11869	—	966	—	1032	—	707
Central nervous system	—	6949	—	787	—	615	—	—
Cervix	—	1439	—	—	—	241	—	—
Endometrium	—	1464	—	405	—	564	—	—
Eye	—	206	—	—	—	—	—	—
Fallopian tube	—	5	—	—	—	—	—	—
Gastrointestinal tract (site indeterminate)	—	1	—	—	—	—	—	—
Genital tract	—	94	—	—	—	—	—	—
Haematopoietic and lymphoid	—	12075	—	277	—	216	—	—
Kidney	—	2149	—	411	—	585	—	305
Large intestine	—	13101	—	585	—	587	—	—
Liver	—	4177	—	452	—	235	—	—
Lung	—	7681	—	986	—	894	—	294
Meninges	—	228	—	—	—	—	—	—
NS	—	343	—	261	—	—	—	—
Oesophagus	—	4213	—	95	—	125	—	—
Ovary	—	4095	—	708	—	266	—	—

Cancer browser

[Cosmic](#) » [Cancer Browser](#) » [Pancreas](#)





Memorial Sloan-Kettering
Cancer Center, USA

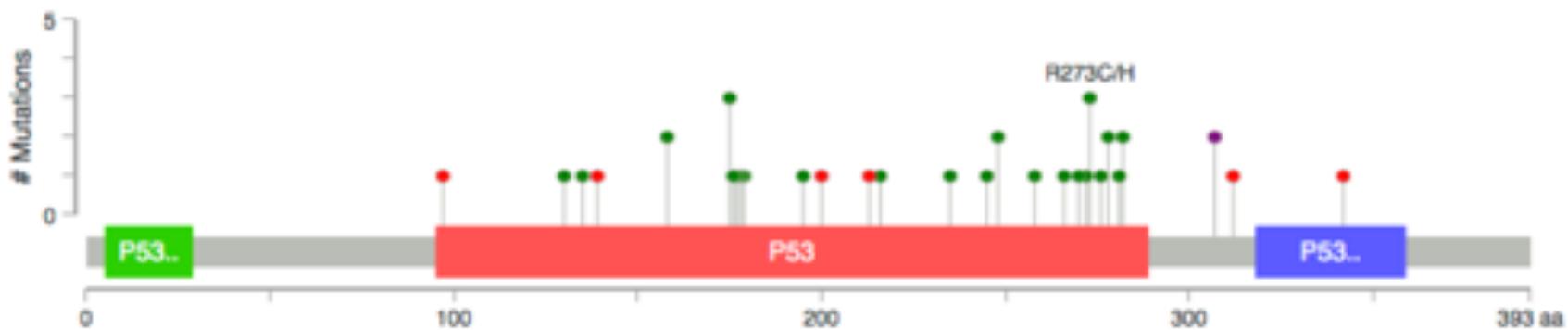


- Integration of Data from 89 cancer genomics studies.
- Focus on analysis tools
 - Mutual exclusivity
 - Gene networks

Mapped mutations on proteins

TP53: [Somatic Mutation Rate: 34.1%]

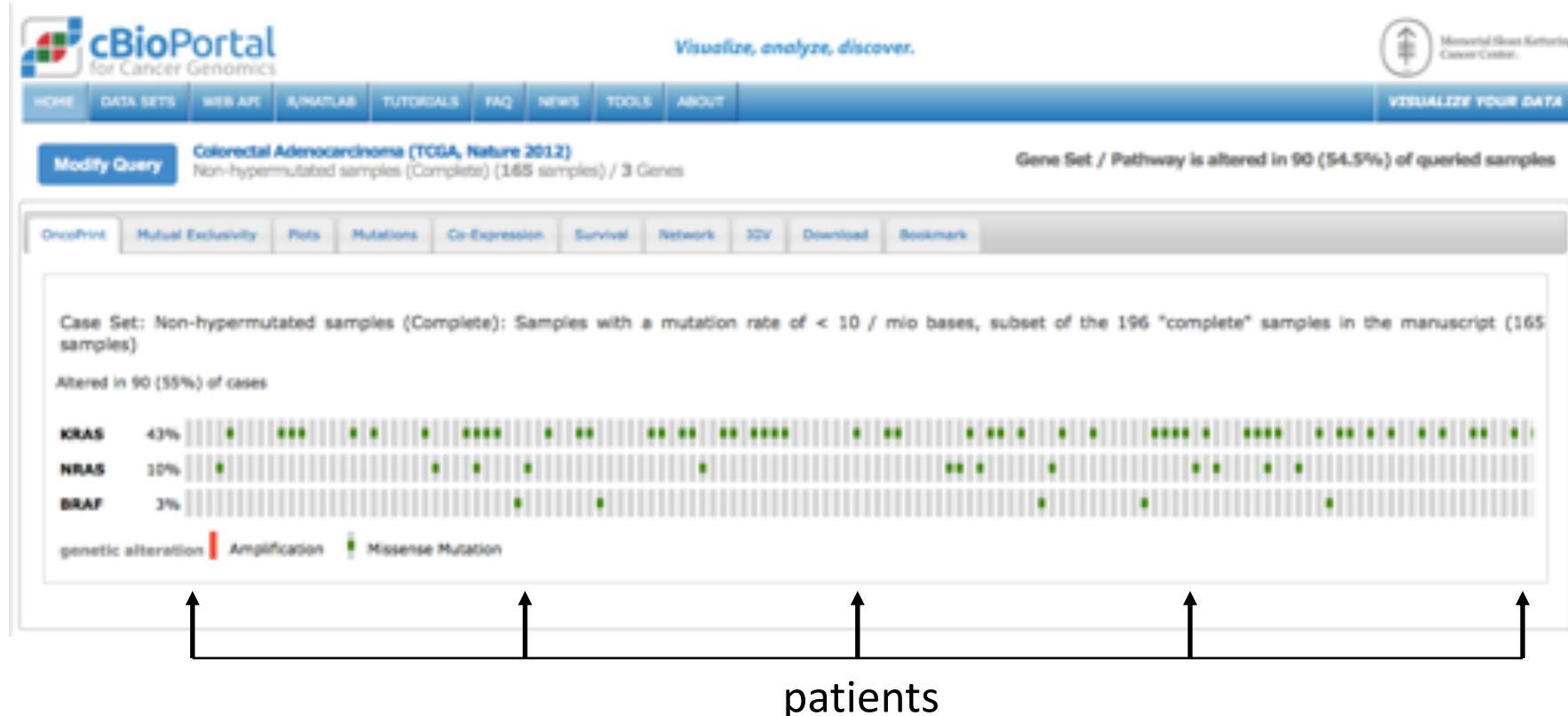
P53_HUMAN PDF SVG Customize Color Codes



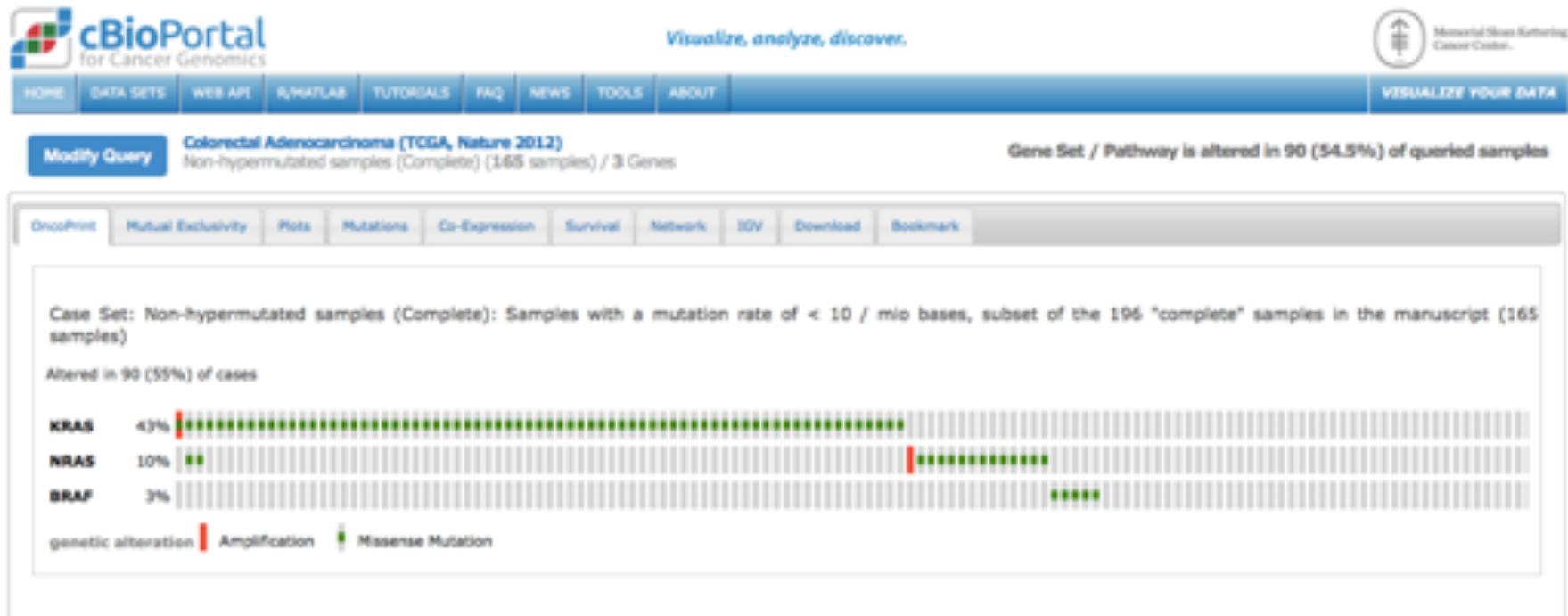
Mutations mapped on TP53 in Glioblastoma dataset (TCGA, Nature 2008)

See also « MutationMapper » tool

« Oncoprint » view

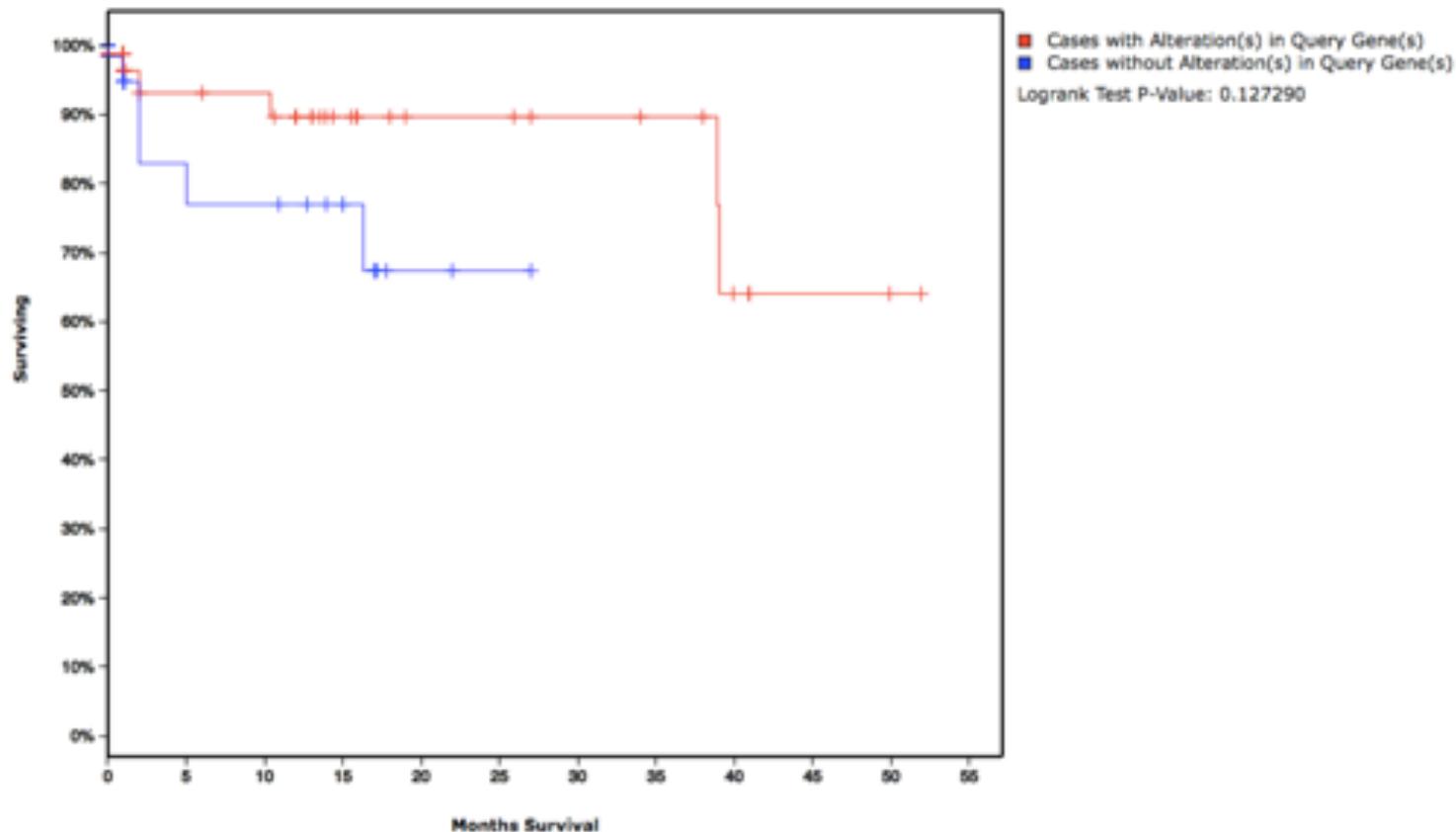


Mutual exclusivity



Kaplan-Meier Curves

Overall Survival Kaplan-Meier Estimate [SVG](#) [PDF](#)



Programmatic Interfaces to cBioPortal

- Webservice (via URL)
- R library
 - CGDS package (CRAN)
- Matlab Library
 - CGDS toolbox @ MatLab Central

http://www.cbioportal.org/webservice.do?cmd=getCaseLists&cancer_study_id=gbm_tcga

Result:

case_list_id	case_list_name	case_list_description	cancer_study_id	case_ids
gbm_tcga_all	All samples	All samples (842 samples)	1863	TCGA-02-0001-01 TCGA-02-0003-01 TCGA-02-0006-01 TCGA-02-0007-01
0010-01	TCGA-02-0011-01	TCGA-02-0014-01 TCGA-02-0021-01 TCGA-02-0024-01 TCGA-02-0027-01 TCGA-02-0028-01 TCGA-02-0033-01 TCGA-02-0034-01		
0038-01	TCGA-02-0043-01	TCGA-02-0046-01 TCGA-02-0047-01 TCGA-02-0052-01 TCGA-02-0054-01 TCGA-02-0055-01 TCGA-02-0057-01 TCGA-02-0058-01		
0875-01	TCGA-06-0876-01	TCGA-06-0877-01 TCGA-06-0878-01 TCGA-06-0879-01 TCGA-06-0881-01 TCGA-06-0882-01 TCGA-12-0678-01 TCGA-12-0818-01		
0820-01	TCGA-12-0821-01	TCGA-12-0822-01 TCGA-12-0826-01 TCGA-12-0827-01 TCGA-12-0828-01 TCGA-12-0829-01 TCGA-14-0787-01 TCGA-14-0789-01		
0817-01	TCGA-14-0867-01	TCGA-14-0871-01 TCGA-16-0846-01 TCGA-16-0848-01 TCGA-16-0849-01 TCGA-16-0850-01 TCGA-16-0861-01 TCGA-06-0850-01		
5408-01	TCGA-06-5410-01	TCGA-06-5411-01 TCGA-06-5412-01 TCGA-06-5413-01 TCGA-06-5856-01 TCGA-06-5858-01 TCGA-06-5859-01 TCGA-06-6389-01		
6391-01	TCGA-14-0781-01	TCGA-15-1444-01 TCGA-19-5947-01 TCGA-19-5950-01 TCGA-19-5951-01 TCGA-19-5952-01 TCGA-19-5954-01 TCGA-19-5955-01		
5958-01	TCGA-19-5959-01	TCGA-19-5960-01 TCGA-26-1442-01 TCGA-28-2501-01 TCGA-28-2510-01 TCGA-28-6450-01 TCGA-32-1979-01 TCGA-32-1980-01		
6191-01	TCGA-76-6192-01	TCGA-76-6193-01 TCGA-76-6282-01 TCGA-76-6285-01 TCGA-81-5910-01 TCGA-87-5896-01 TCGA-06-1806-01 TCGA-06-6388-01		
6694-01	TCGA-06-6695-01	TCGA-06-6697-01 TCGA-06-6698-01 TCGA-06-6699-01 TCGA-06-6700-01 TCGA-06-6701-01 TCGA-14-0746-01 TCGA-14-0862-01		
1395-01	TCGA-14-1458-01	TCGA-19-5953-01 TCGA-26-6173-01 TCGA-26-6174-01 TCGA-28-5211-01 TCGA-41-6646-01 TCGA-74-6573-01 TCGA-74-6575-01		
6578-01	TCGA-74-6581-01	TCGA-74-6584-01 TCGA-76-6280-01 TCGA-76-6283-01 TCGA-76-6286-01 TCGA-76-6656-01 TCGA-76-6657-01 TCGA-76-6660-01		
6662-01	TCGA-76-6663-01	TCGA-76-6664-01 TCGA-81-5911-01 TCGA-06-0155-01 TCGA-06-1084-01 TCGA-06-1086-01 TCGA-06-1087-01 TCGA-12-1088-01		
1090-01	TCGA-12-1091-01	TCGA-12-1092-01 TCGA-12-1093-01 TCGA-12-1094-01 TCGA-12-1095-01 TCGA-12-1096-01 TCGA-12-1097-01 TCGA-12-1098-01		
0736-01	TCGA-14-0783-01	TCGA-14-0786-01 TCGA-14-1034-01 TCGA-14-1396-01 TCGA-14-1401-01 TCGA-14-1402-01 TCGA-14-1451-01 TCGA-14-1452-01		
1454-01	TCGA-14-1459-01	TCGA-15-1446-01 TCGA-15-1447-01 TCGA-15-1449-01 TCGA-16-1045-01 TCGA-16-1047-01 TCGA-16-1055-01 TCGA-16-1056-01		
1062-01	TCGA-16-1063-01	TCGA-19-0955-01 TCGA-19-0960-01 TCGA-19-0962-01 TCGA-19-0963-01 TCGA-19-0964-01 TCGA-19-1392-01 TCGA-26-1438-01		
1443-01	TCGA-19-4065-01	TCGA-02-0064-01 TCGA-02-0069-01 TCGA-02-0071-01 TCGA-02-0074-01 TCGA-02-0075-01 TCGA-02-0080-01 TCGA-02-0083-01		
0086-01	TCGA-02-0089-01	TCGA-02-0099-01 TCGA-02-0102-01 TCGA-02-0107-01 TCGA-02-0113-01 TCGA-02-0114-01 TCGA-02-0115-01 TCGA-02-0116-01		
1801-01	TCGA-06-1802-01	TCGA-06-1805-01 TCGA-12-1598-01 TCGA-12-1599-01 TCGA-12-1600-01 TCGA-12-1602-01 TCGA-14-0812-01 TCGA-14-0865-01		
1037-01	TCGA-14-1455-01	TCGA-14-1458-01 TCGA-14-1794-01 TCGA-14-1795-01 TCGA-14-1821-01 TCGA-14-1823-01 TCGA-14-1825-01 TCGA-14-1827-01		
1460-01	TCGA-19-0957-01	TCGA-19-1385-01 TCGA-19-1386-01 TCGA-19-1387-01 TCGA-19-1388-01 TCGA-19-1389-01 TCGA-19-1786-01 TCGA-19-1788-01		
1791-01	TCGA-26-1799-01	TCGA-27-1830-01 TCGA-27-1832-01 TCGA-27-1833-01 TCGA-27-1834-01 TCGA-28-1746-01 TCGA-28-1749-01 TCGA-28-1750-01		
1752-01	TCGA-28-1755-01	TCGA-28-1757-01 TCGA-28-1760-01 TCGA-02-2466-01 TCGA-02-2470-01 TCGA-02-2483-01 TCGA-02-2485-01 TCGA-02-2486-01		
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2499-01	TCGA-28-2502-01	TCGA-28-2506-01 TCGA-28-2509-01 TCGA-28-2513-01 TCGA-28-2514-01 TCGA-32-1970-01 TCGA-32-1976-01 TCGA-32-1982-01		
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A5U0-01	TCGA-06-A5U1-01	TCGA-06-A680-01 TCGA-06-A681-01 TCGA-19-A601-01 TCGA-19-A634-01 TCGA-19-A635-01 TCGA-OK-A56R-01 TCGA-RR-A6KA-01		
A6KC-01	TCGA-12-1597-01	TCGA-12-3644-01 TCGA-12-3646-01 TCGA-12-3648-01 TCGA-12-3649-01 TCGA-12-3650-01 TCGA-12-3651-01 TCGA-12-3652-01		
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0210-01	TCGA-06-0211-01	TCGA-06-0213-01 TCGA-06-0214-01 TCGA-06-0219-01 TCGA-06-0221-01 TCGA-06-0237-01 TCGA-06-0246-01 TCGA-06-0241-01		

Thank you

- Today:
 - Bastien Job on genome alterations
 - G Lelandais on Gene Expression Analysis via Galaxy