

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 20 janvier 2020 - Salle Rubis, B2M | |
|--|--|
| 09:00-10:30 | Technologies et données omiques en cancérologie. Daniel GAUTHERET |
| 10:40-12:30 | Structuration et intégration de données omiques, le projet ODIN. Gérôme JULES-CLEMENT, ingénieur bioinformaticien |
| 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 21 janvier 2020 - Salle Rubis, 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 |
| 13:30-15:20 | Problématique de la détection de variants somatiques par séquençage d'exome. D. GAUTHERET |
| 15:30-17:00 | L'analyse des altérations de nombre de copies par microarrays et NGS. Bastien JOB, Ingénieur Bioinformaticien, Gustave Roussy |
| | |
| Mercredi 22 janvier 2020 - Salle Rubis, B2M | |
| 09:00-12:30 | TP Galaxy (fin). Analyse exome. Visualisation de résultats avec IGV. D. GAUTHERET |

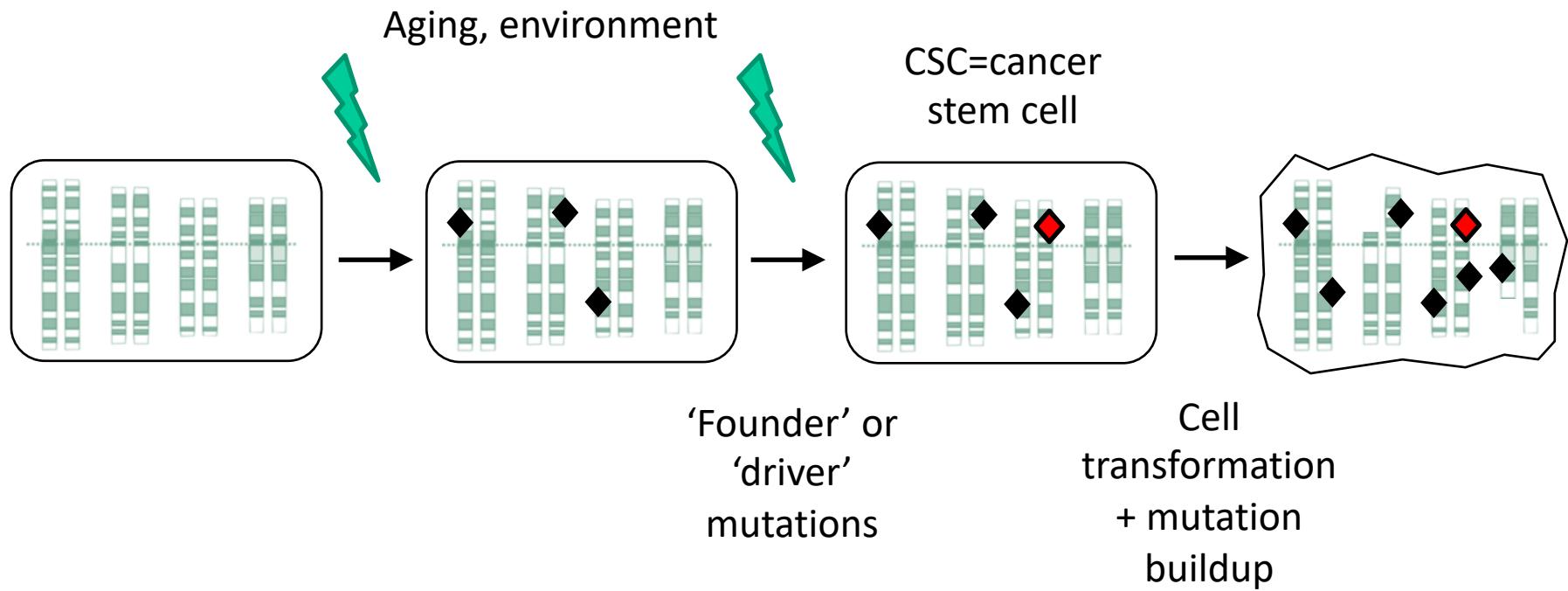
UE12: Big data et modèles prédictifs

| Mercredi 22 janvier 2020 - Salle Rubis, B2M | |
|--|--|
| 13:30-17:00 | Premiers pas avec le langage R. D. GAUTHERET |
| | |
| Jeudi 23 janvier 2020 - Salle Rubis, 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: Analyse de données moléculaires, Enzo BATTISTELLA, UMR 130, (Gustave Roussy) |
| 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 24 janvier 2020 - Salle Rubis, 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: Analyse de données de compte rendus médicaux. Ugo BENASSAYAG (Gustave Roussy) |
| 13:30-17:00 | TP: Construire son premier réseau de neurones. Loic VERLINGUE (Gustave Roussy) et Yoann PRADAT (Centrale-Supelec). |

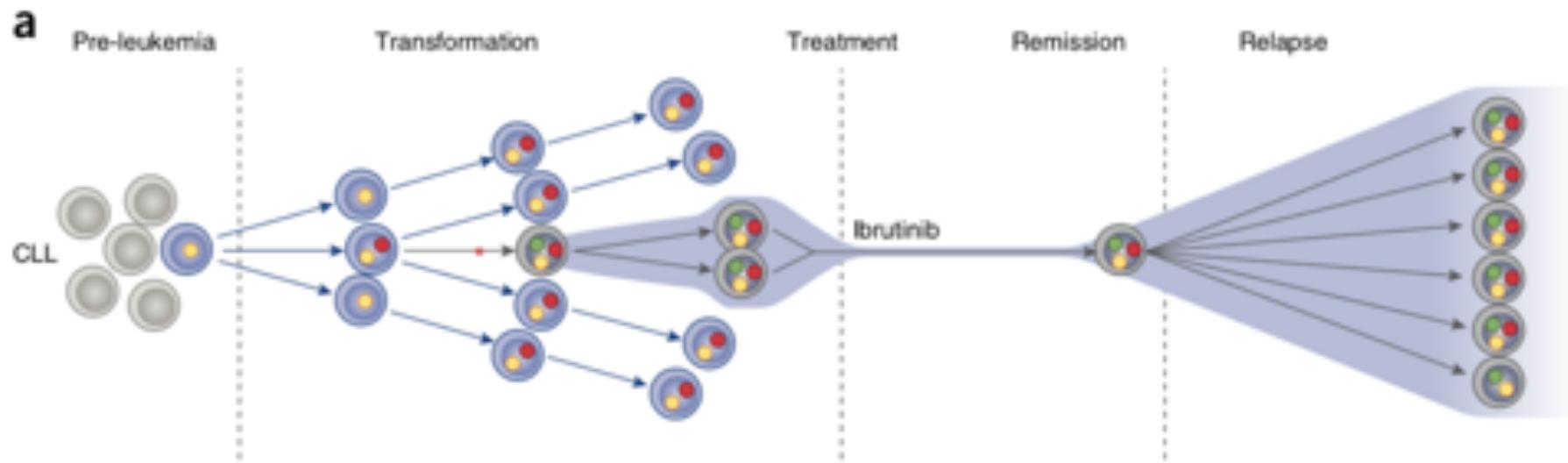
Evaluation:
UE 11: Rapport d'Etonnement
UE 12: Vos protocoles de TP

Introduction

- Le cancer: une maladie du génome

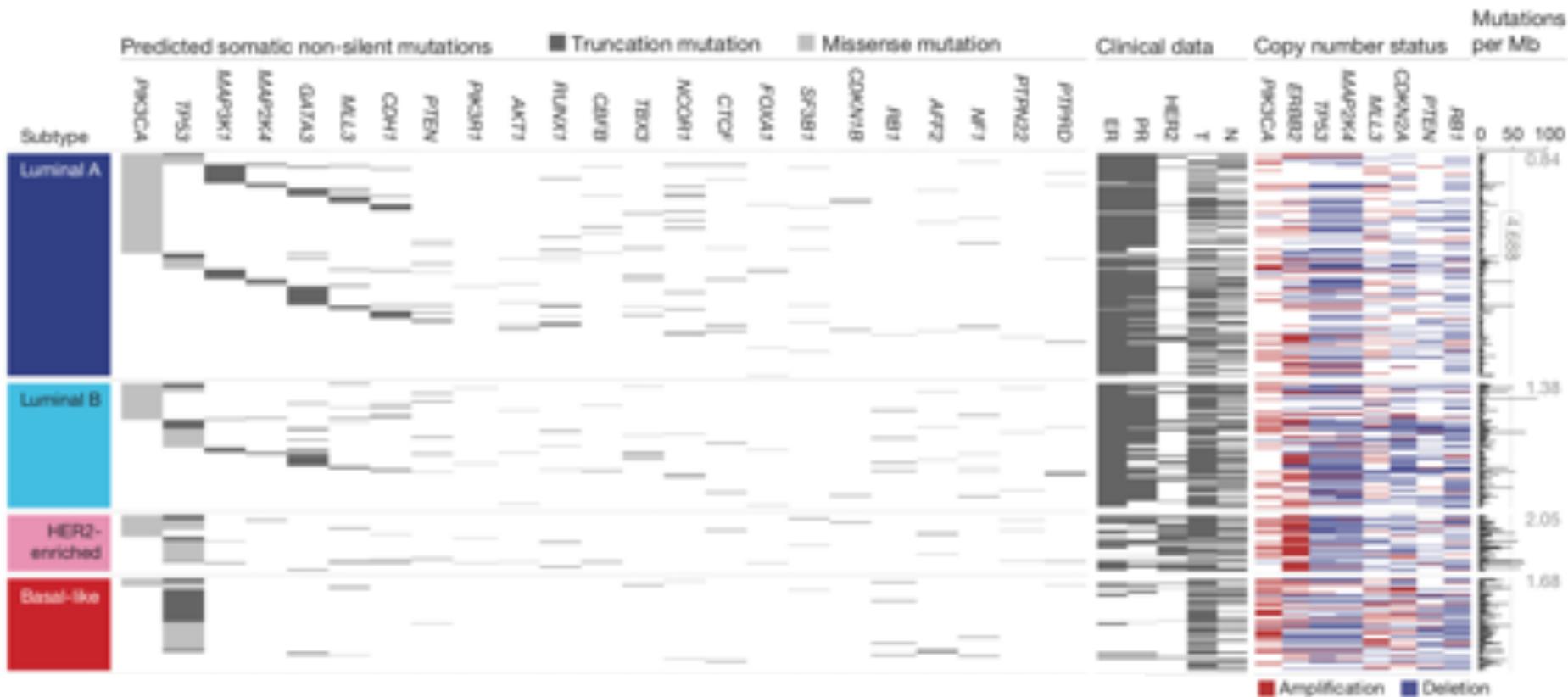


L'évolution clonale du cancer



Ferrando & Lopez-Otin, Nature Med. 2017

Big data génomique: études sur cohortes



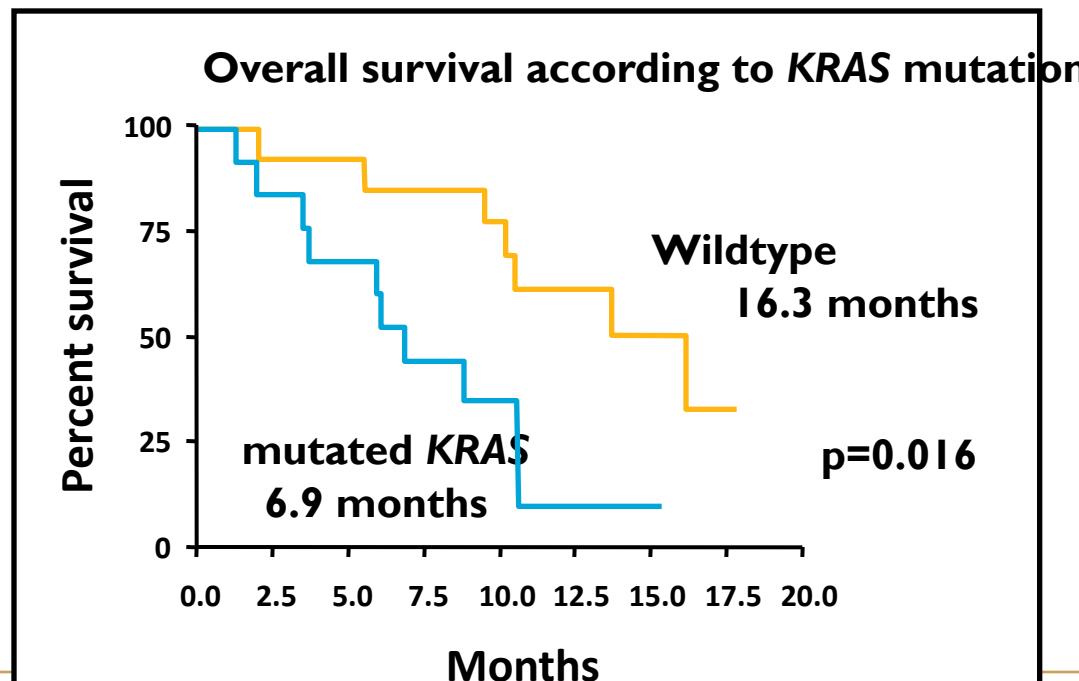
Mutations observées chez 825 patients de cancer du sein
TCGA consortium, Nature, 2012

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



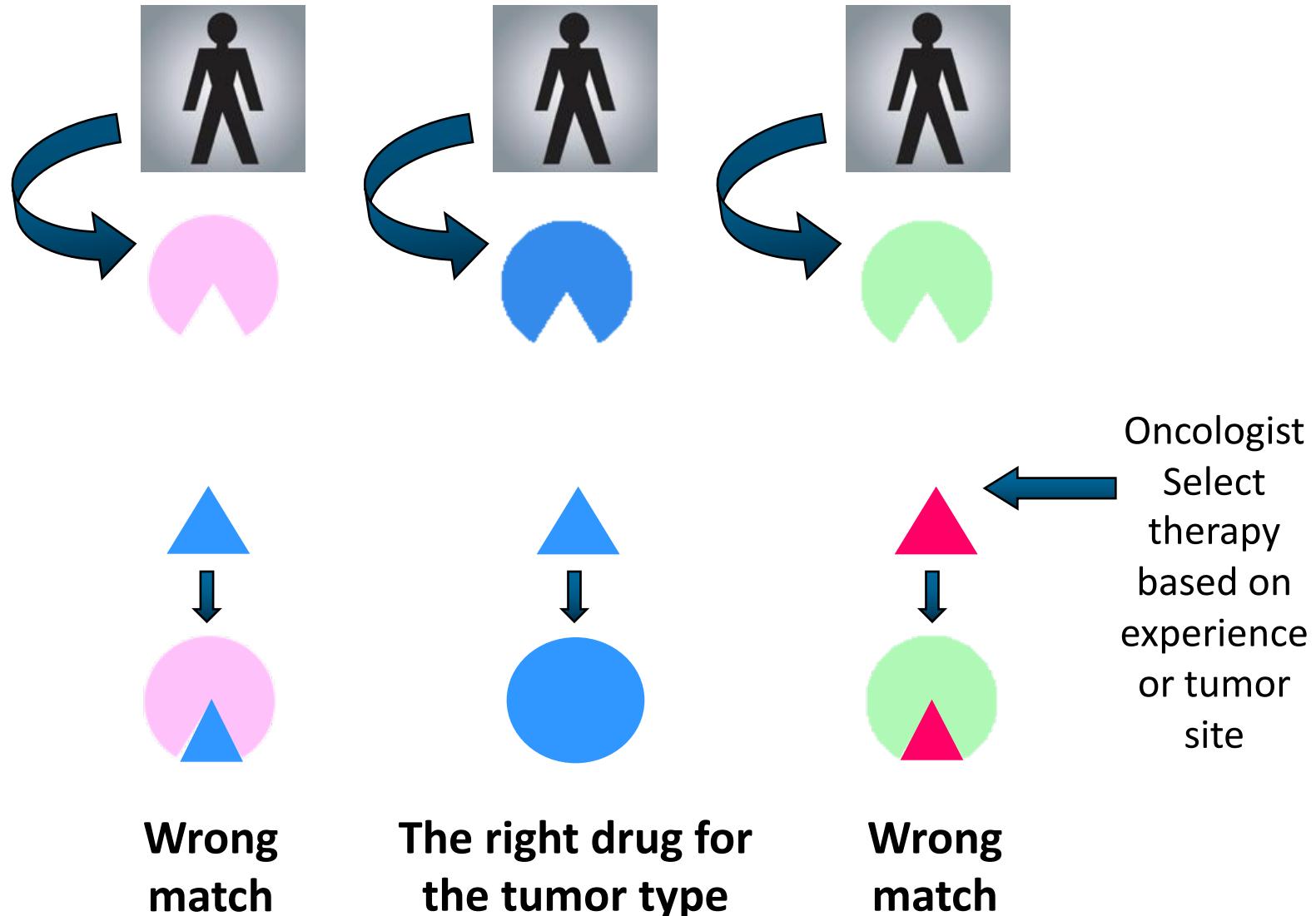
p=0.0003

Selecting the right therapy

**Cancer
Patient**

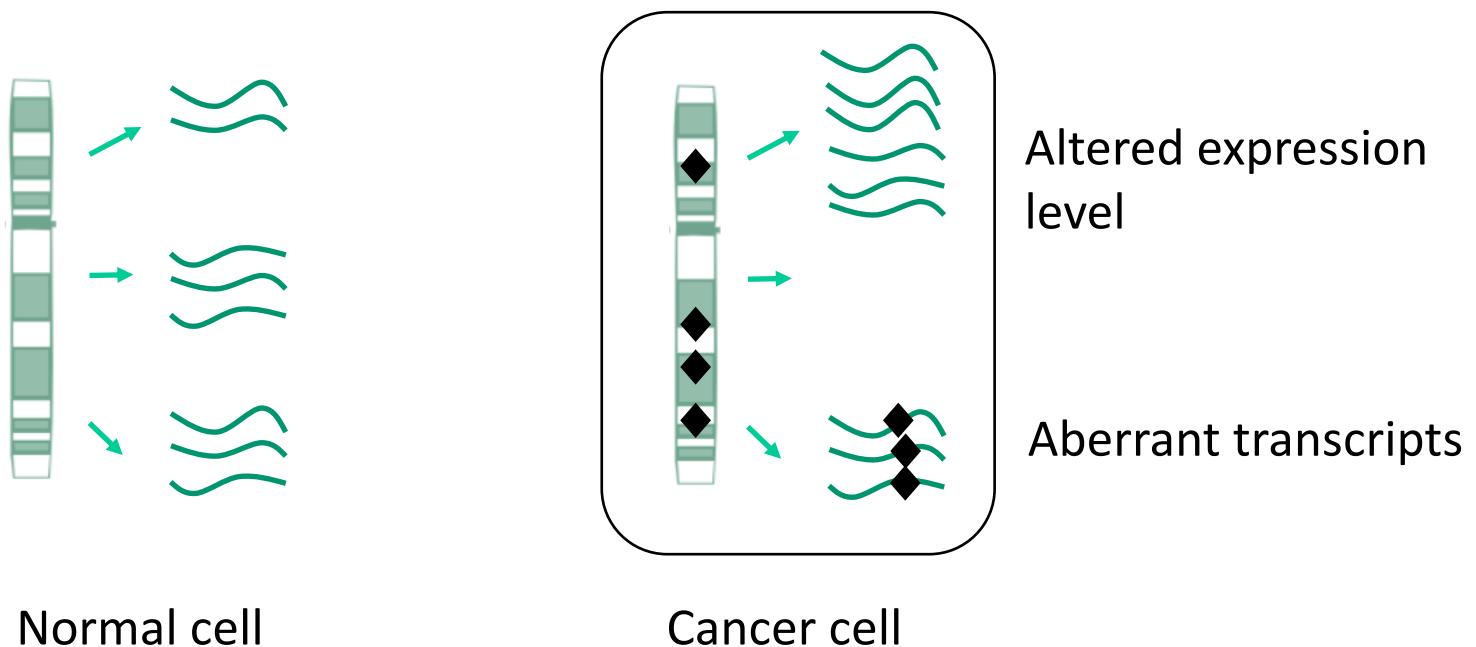
**Tumor
type**

Therapy

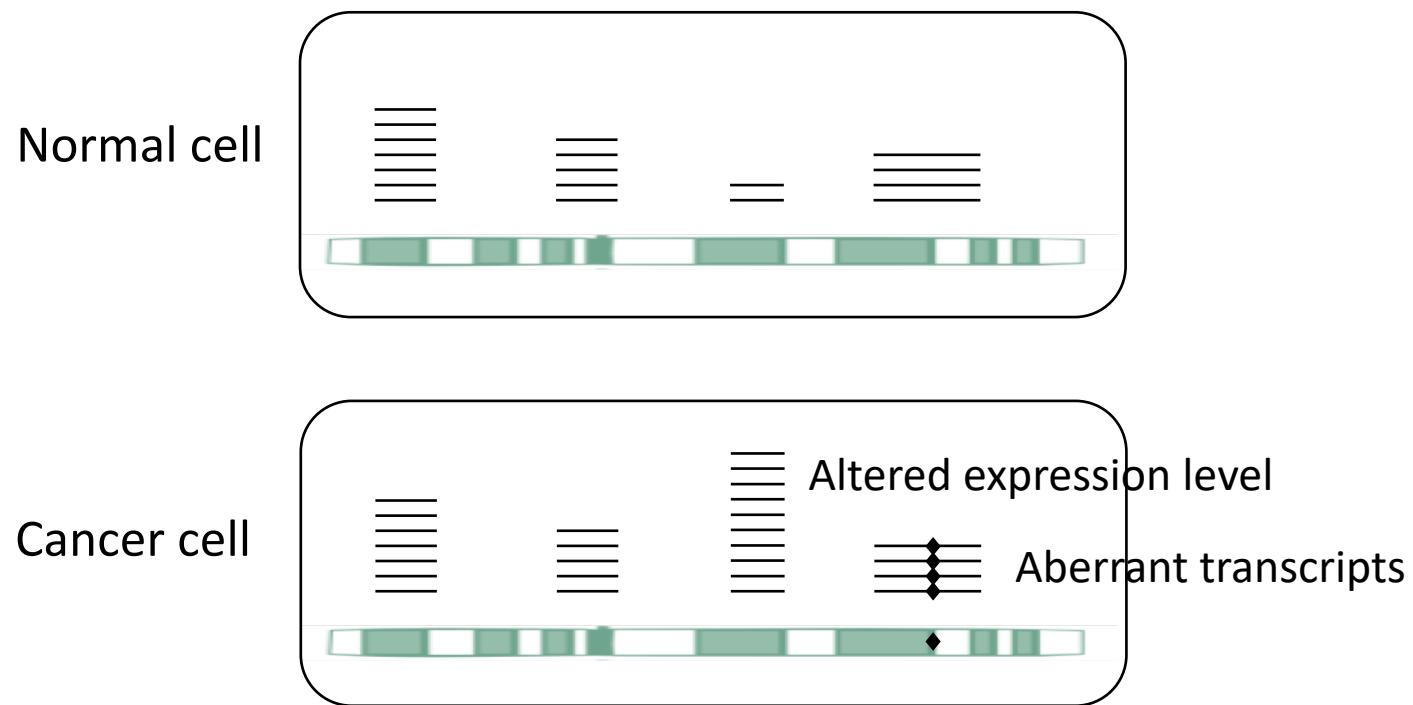


Définir les types de tumeur par la génomique

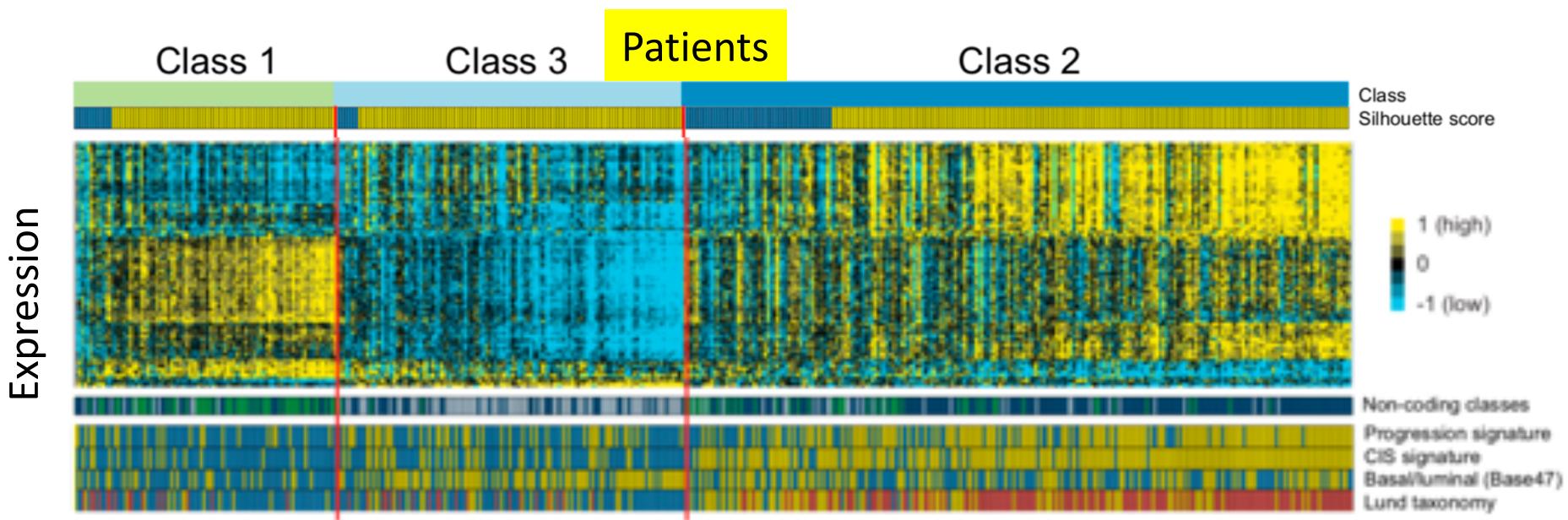
L'ARN: le premier phénotype



L'ARN: le premier phénotype

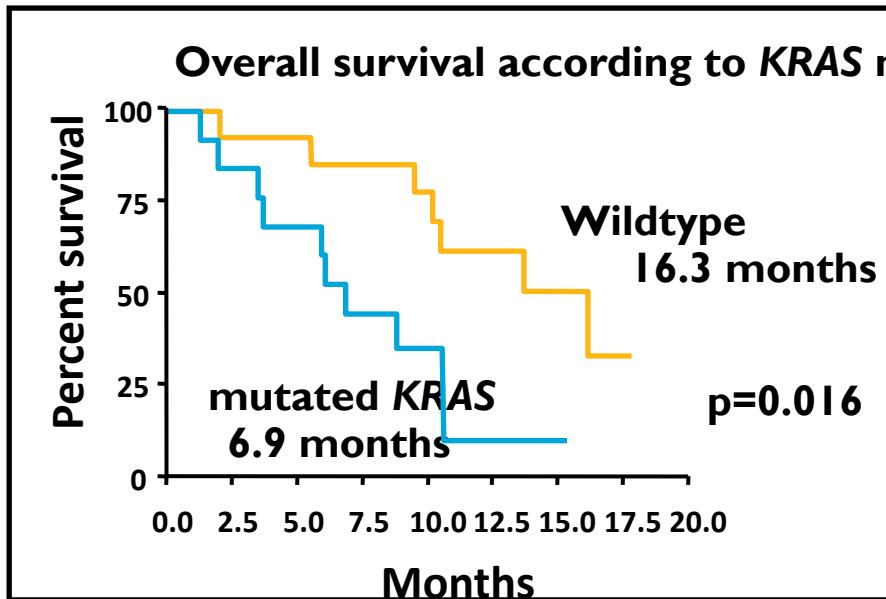


Big data transcriptomique: études de cohorte

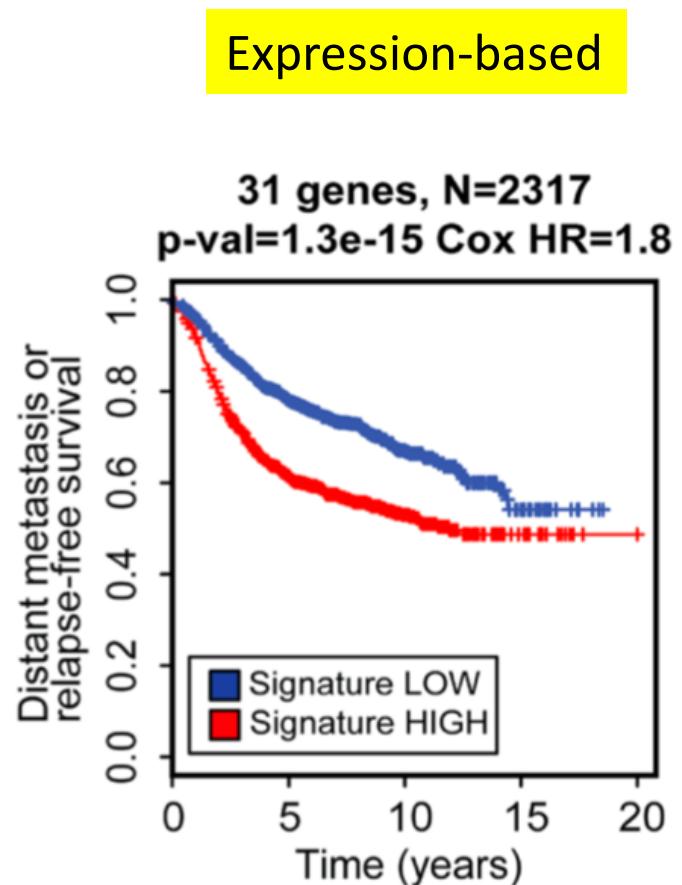


A 117-gene signature for urothelial carcinoma
Hedegaard et al., Cancer Cell, 2016

Signatures prédictives



DNA-based



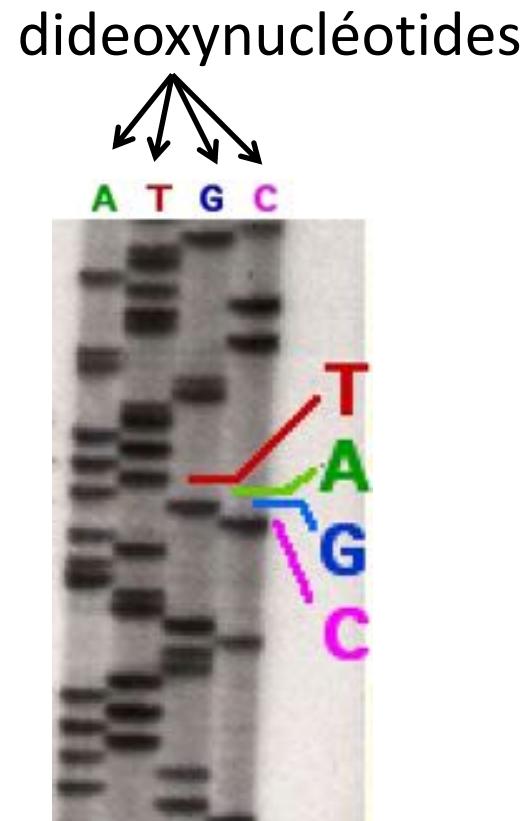
Les principales technologies omiques en cancérologie

Daniel Gautheret

2019

Le séquençage de Sanger (1977)

- Séquençage par terminaison de chaîne
 - Utilisation de dideoxynucléotides pour interrompre la synthèse à un certain type de base.
 - 4 réactions + marquage radioactif
- Amélioré en 1987 par l'introduction de marqueurs fluorescents (1 seule réaction) et l'automatisation.



Wikipedia

The Human Genome Project

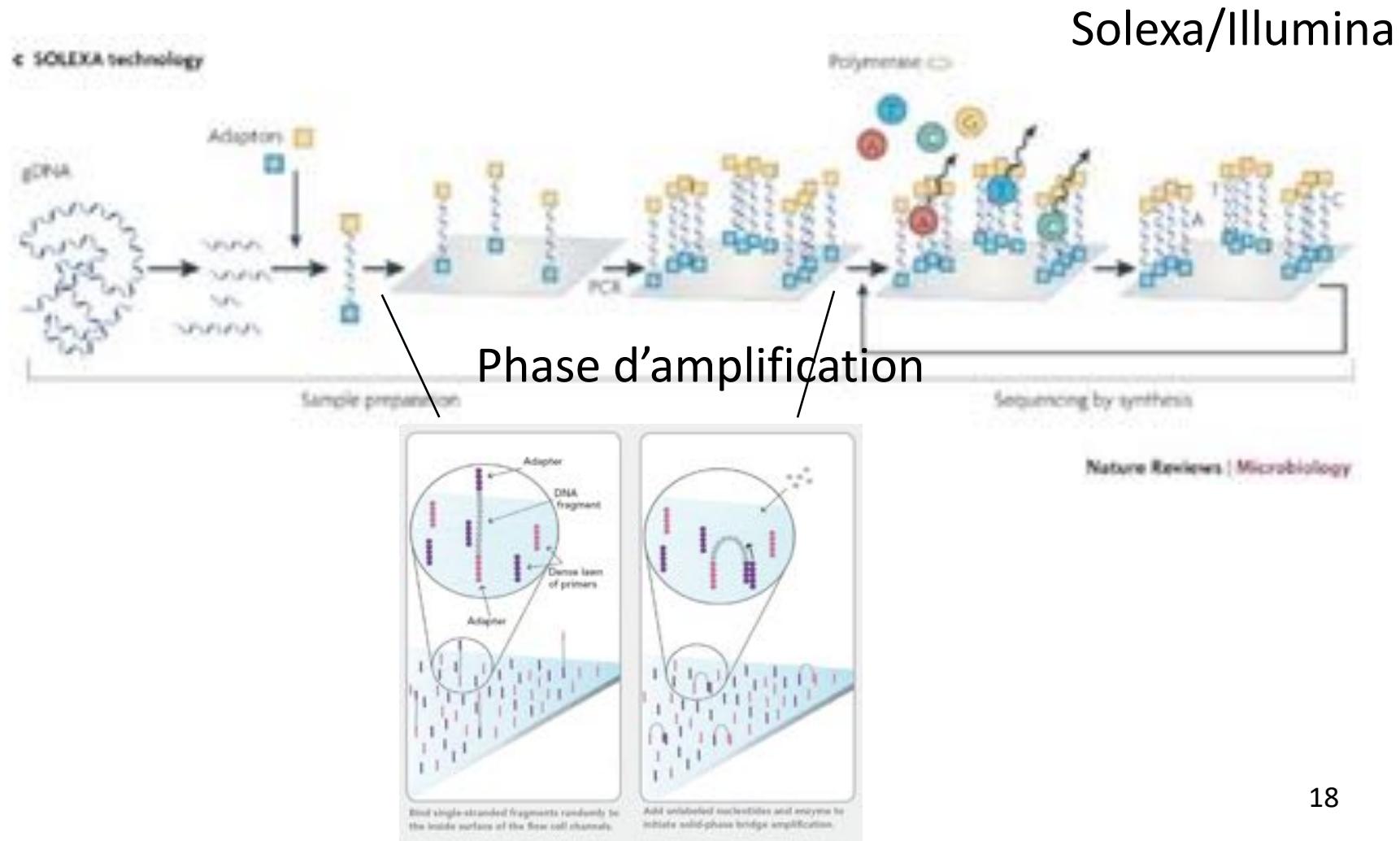
« I expect that within a few years, our technology will be able to sequence one megabase/technician-year. At that rate 100 technicians could sequence the genome in 30 years. »

Walter Gilbert 1980

- Project started in 1991 and completed in 2001.
- ...using Sanger sequencing

NGS :
Next Generation Sequencing
(2005-)

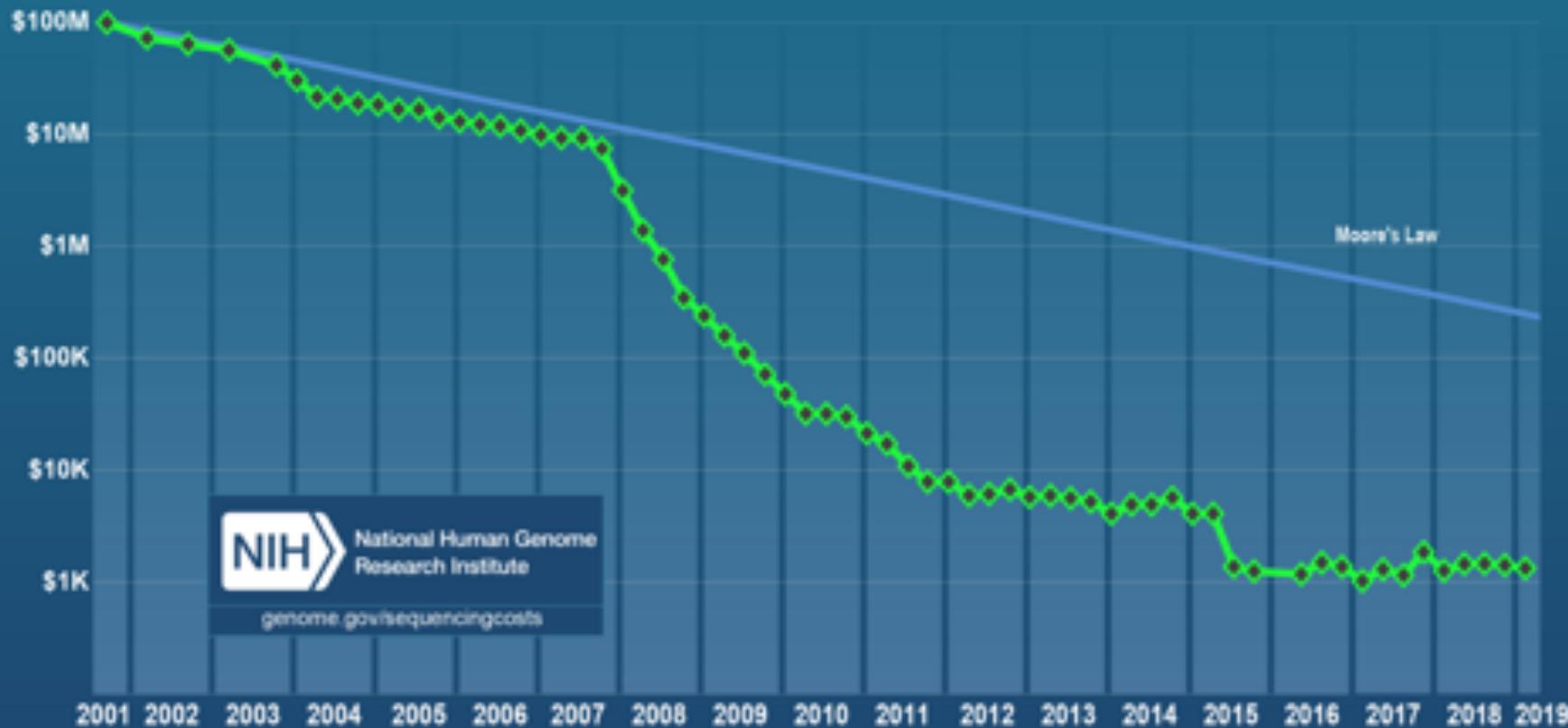
The most common NGS is « sequencing by synthesis » too!



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 |

Cost per Genome



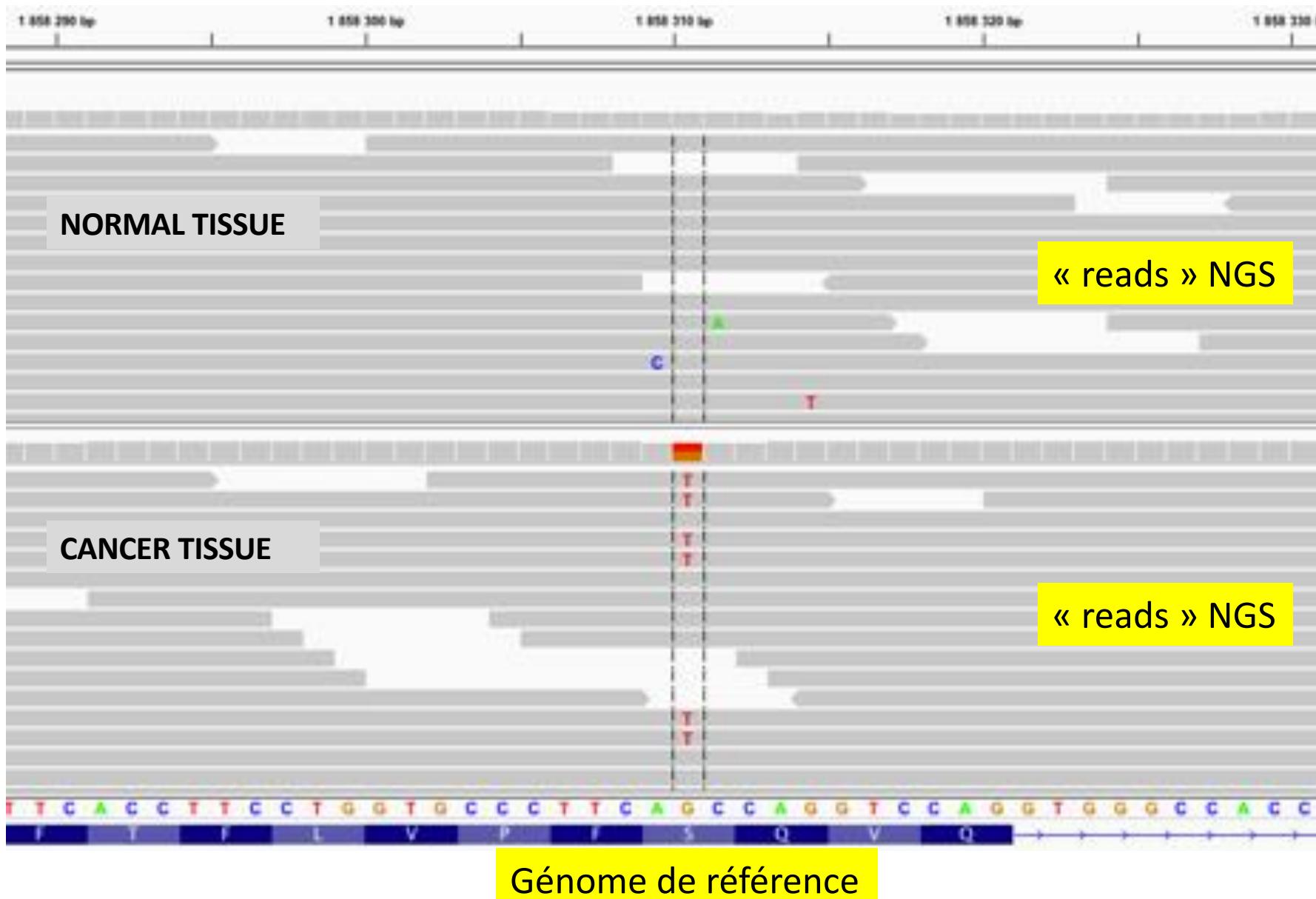
Les grandes applications des NGS

- 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)

Evénements identifiés par DNA-seq



Evénements identifiés par DNA-seq

- Mutations ponctuelles
- Réarrangements
- CNV
- Amplification de microsatellites
- Profils mutationnels

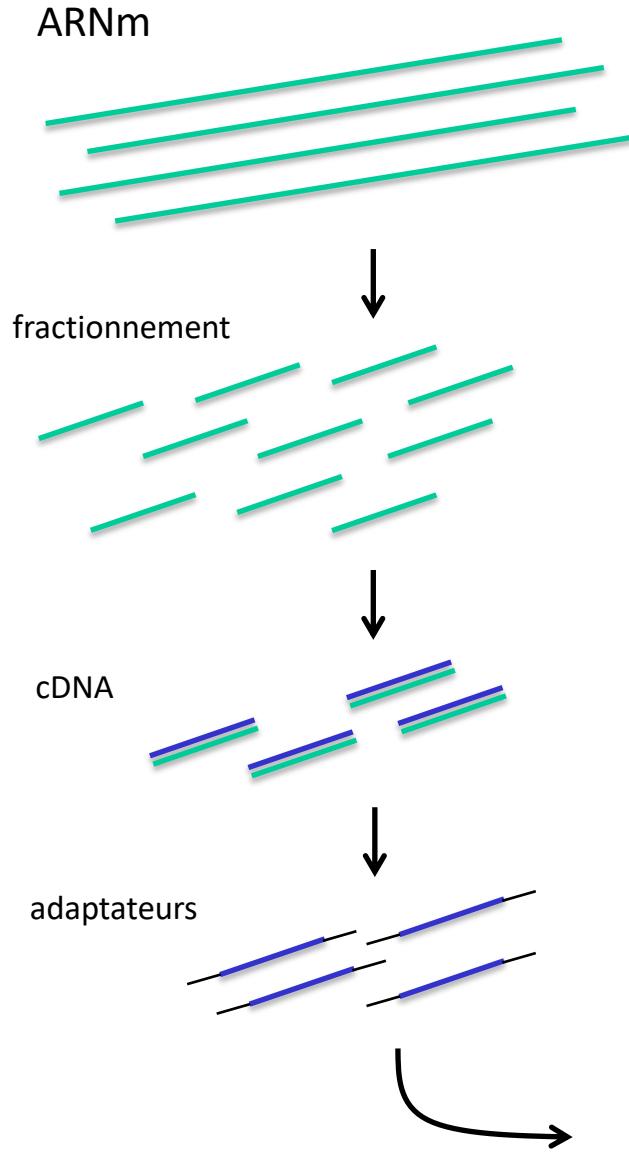
Cf cours/TP exome
(B Job, D. Gautheret)

RNA-seq

- Transcriptome par NGS = « deep sequencing »

Cf cours/TP RNA-seq
(T Dayris, G Lelandais)

RNA-Seq

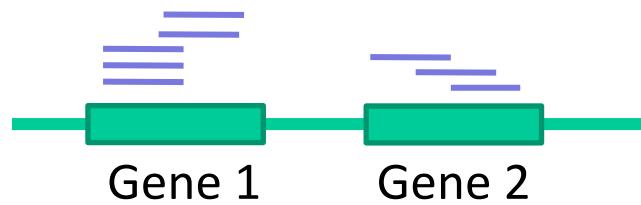


Cf cours DG Lundi pm
TD mardi am

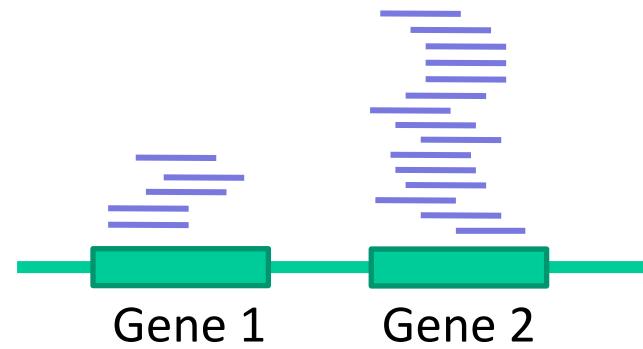


Séquençage

Mesures d'expression par RNA-seq



Sample 1



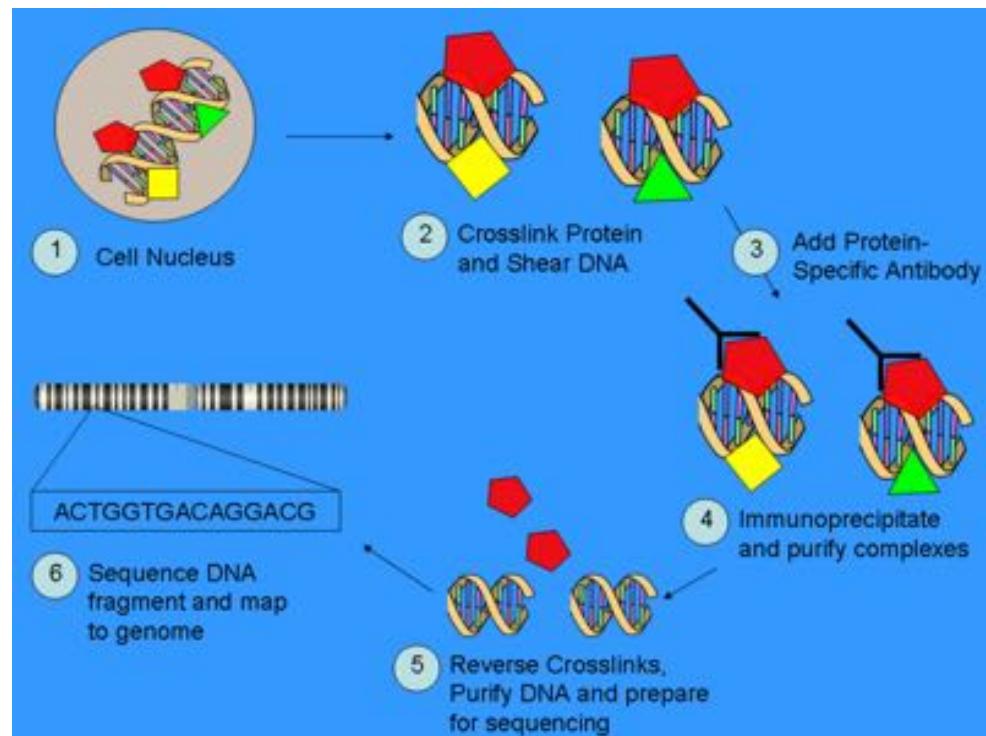
Sample 2

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

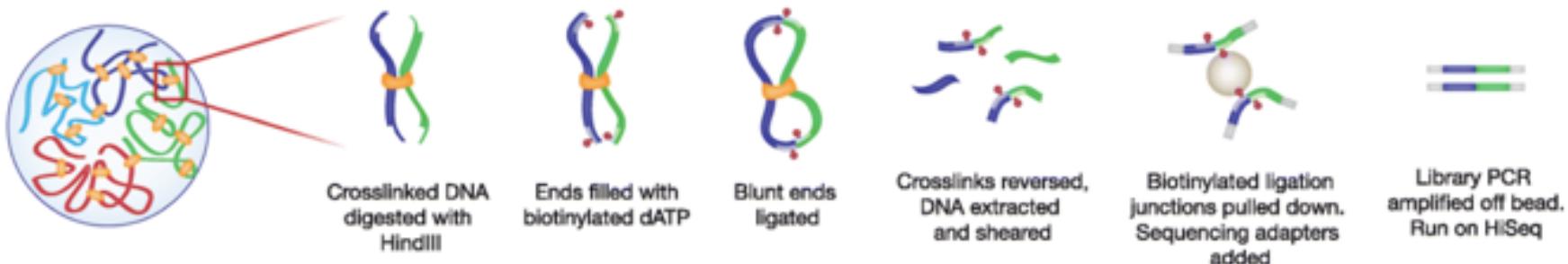


Wikipedia

Hi-C

- Chromosome conformation capture

Hi-C



Vers une utilisation systématique du séquençage en médecine



Médecine France génomique 2025

mise à jour : 19.07.17

A+

A-



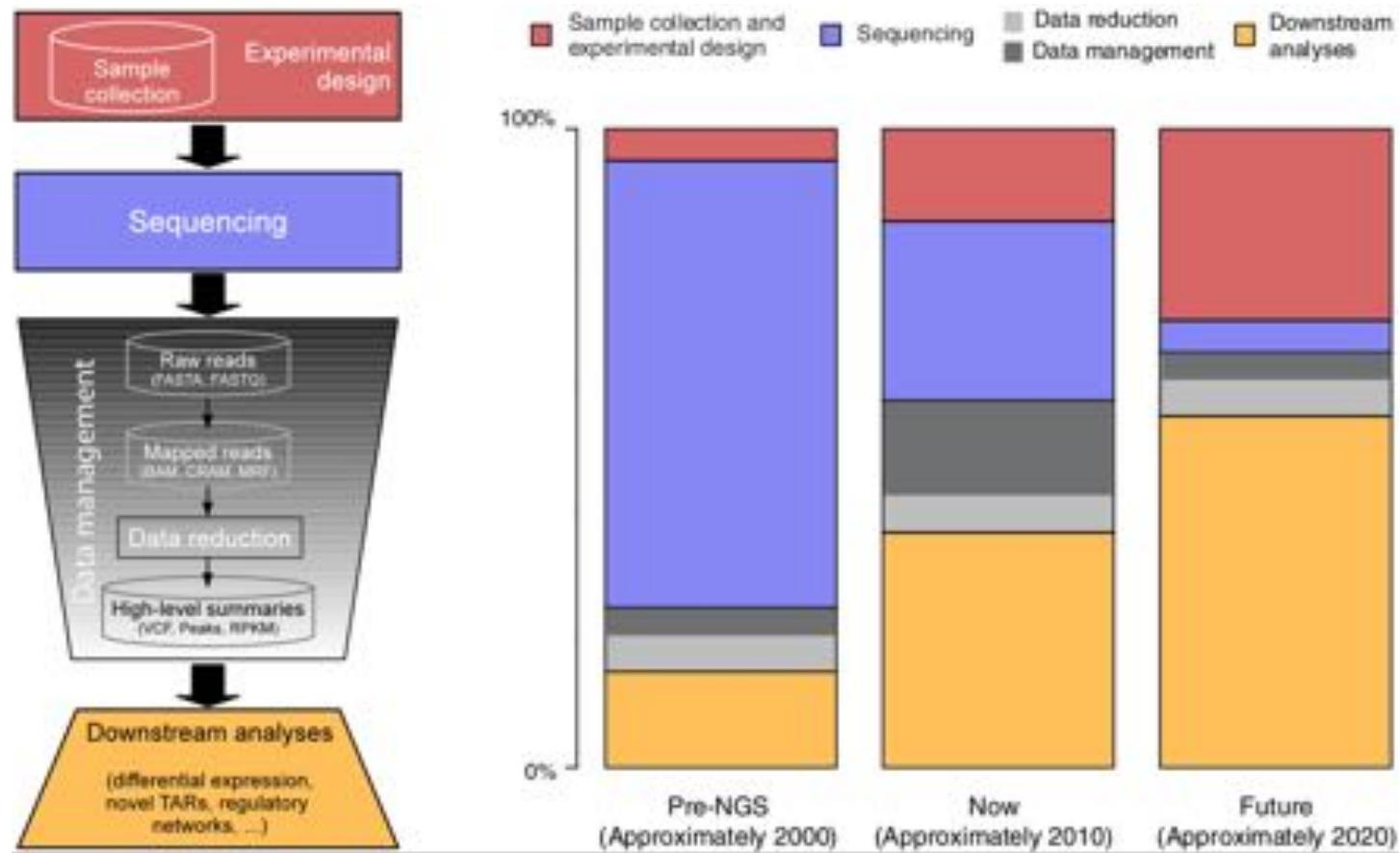
Le plan « Médecine France génomique 2025 », se concrétise. En effet, le ministère chargé de la santé a lancé en décembre 2016 un appel à projets national amorçant le financement des 2 premières plateformes génomiques à visée diagnostique et de suivi thérapeutique, sur les 12 attendues dans les 5 ans. 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 ».

Les données NGS

Volume des données NGS

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

Costs of sequencing vs analysis



Les outils

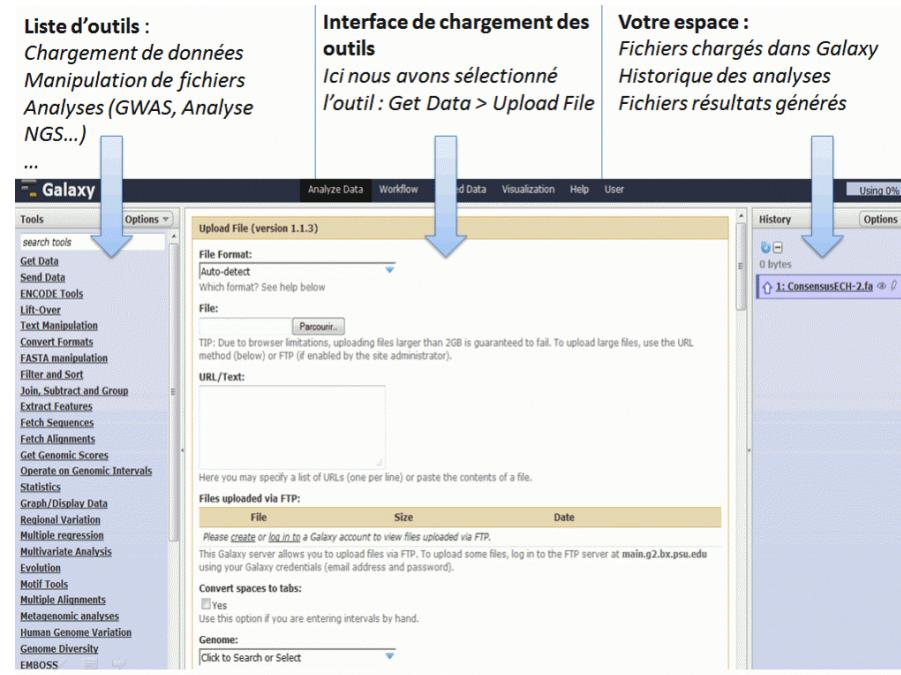
« Pipelines » & « workflows »

« Bricks » from Unix open source programs

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



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



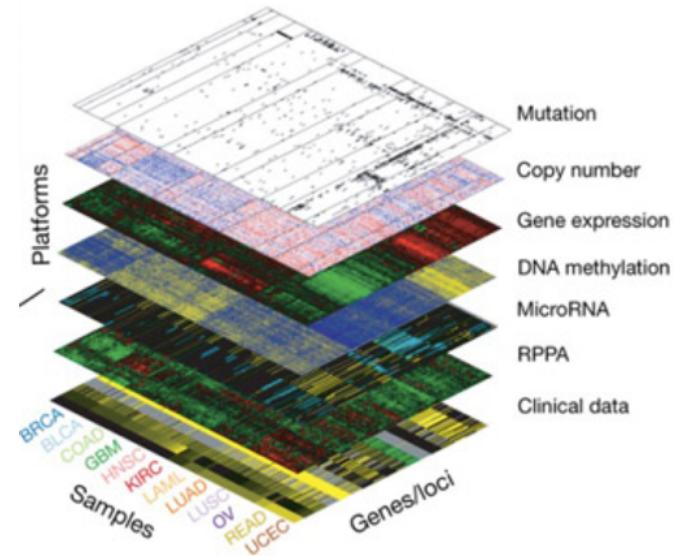
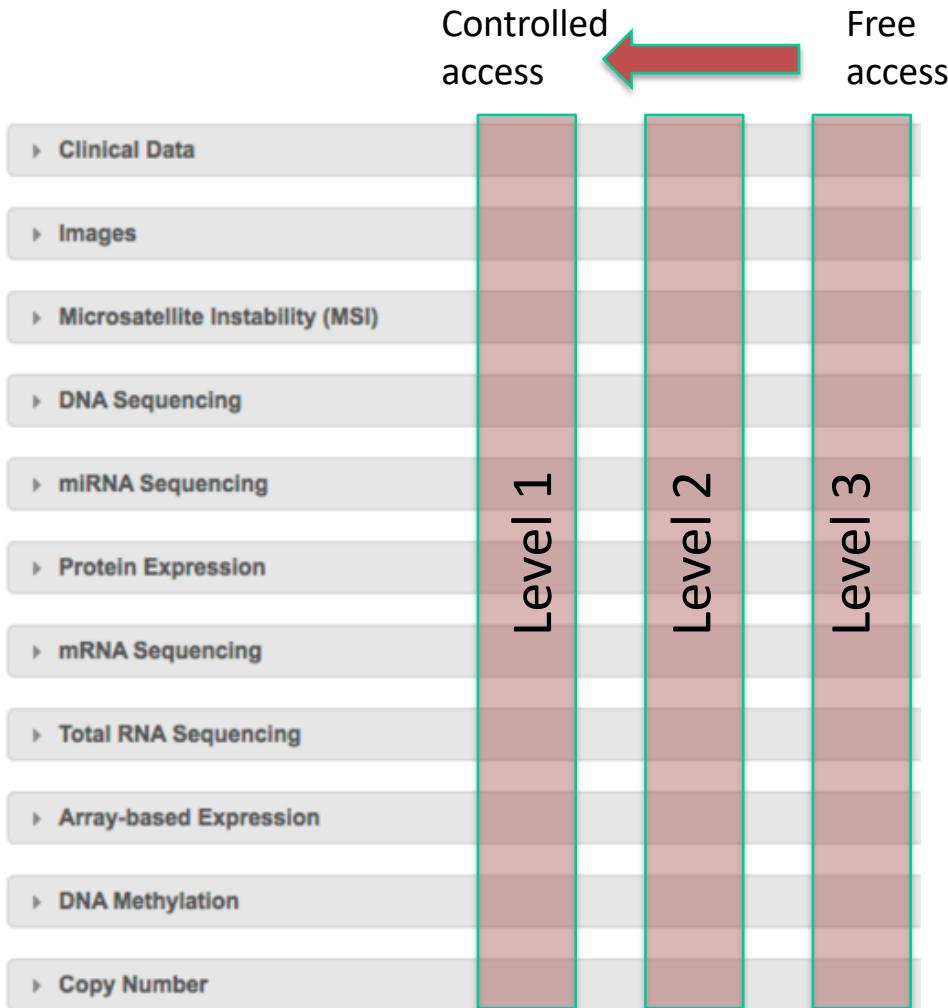
*Understanding genomics
to improve cancer care*

NCI, NHGRI, USA

TCGA

- launched by the National Cancer Institute (NCI) and the National Human Genome Research Institute (NHGRI) 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

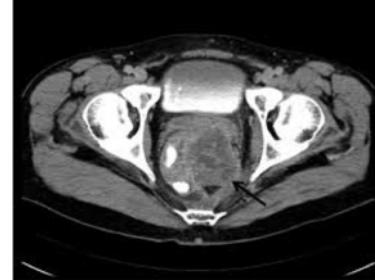
Main data types

- 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

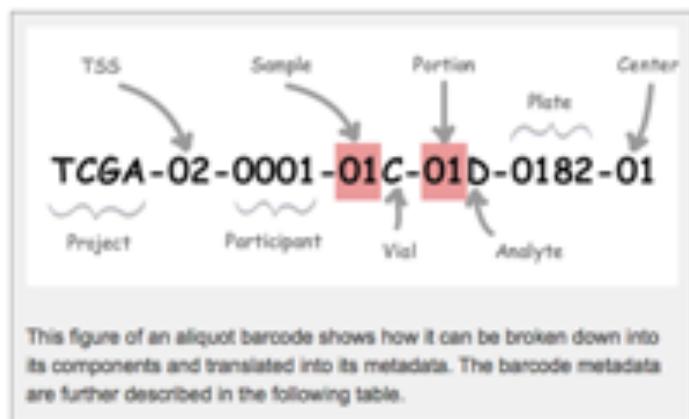


Main data types

- 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)

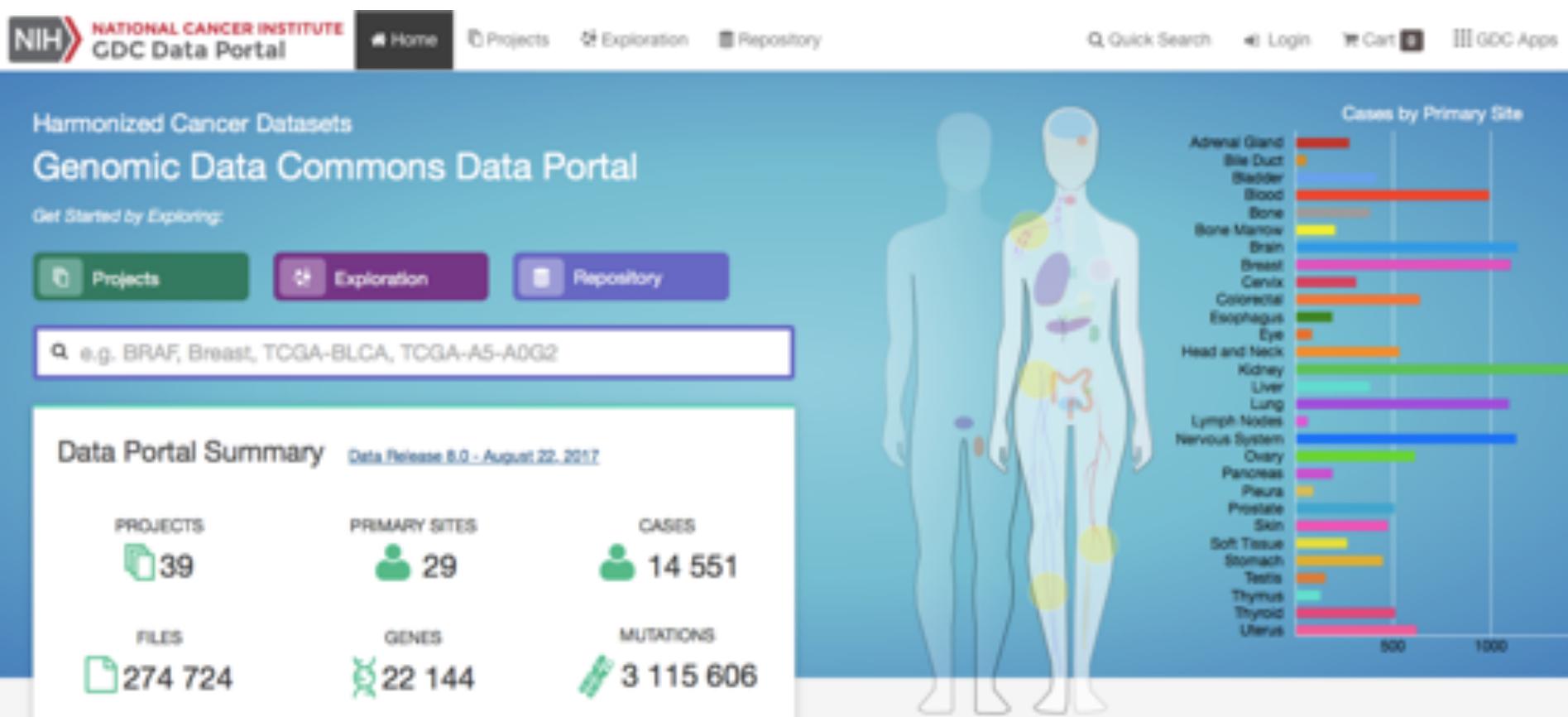


```
<?xml version="1.0" encoding="UTF-8"?>
<tcga_bcr>
  <admin>
    <bcr xsd_ver="1.17">Nationwide Children's Hospital</bcr>
    <batch_number xsd_ver="1.17">88_48_0</batch_number>
    <disease_code xsd_ver="2.3">BRCA</disease_code>
    <day_of_doc_upload xsd_ver="1.17">27</day_of_doc_upload>
    <month_of_doc_upload 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</nre>
    </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 1,147, 1,046, 988, 982, 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 on

- PCAWG¹: a collaboration with 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)

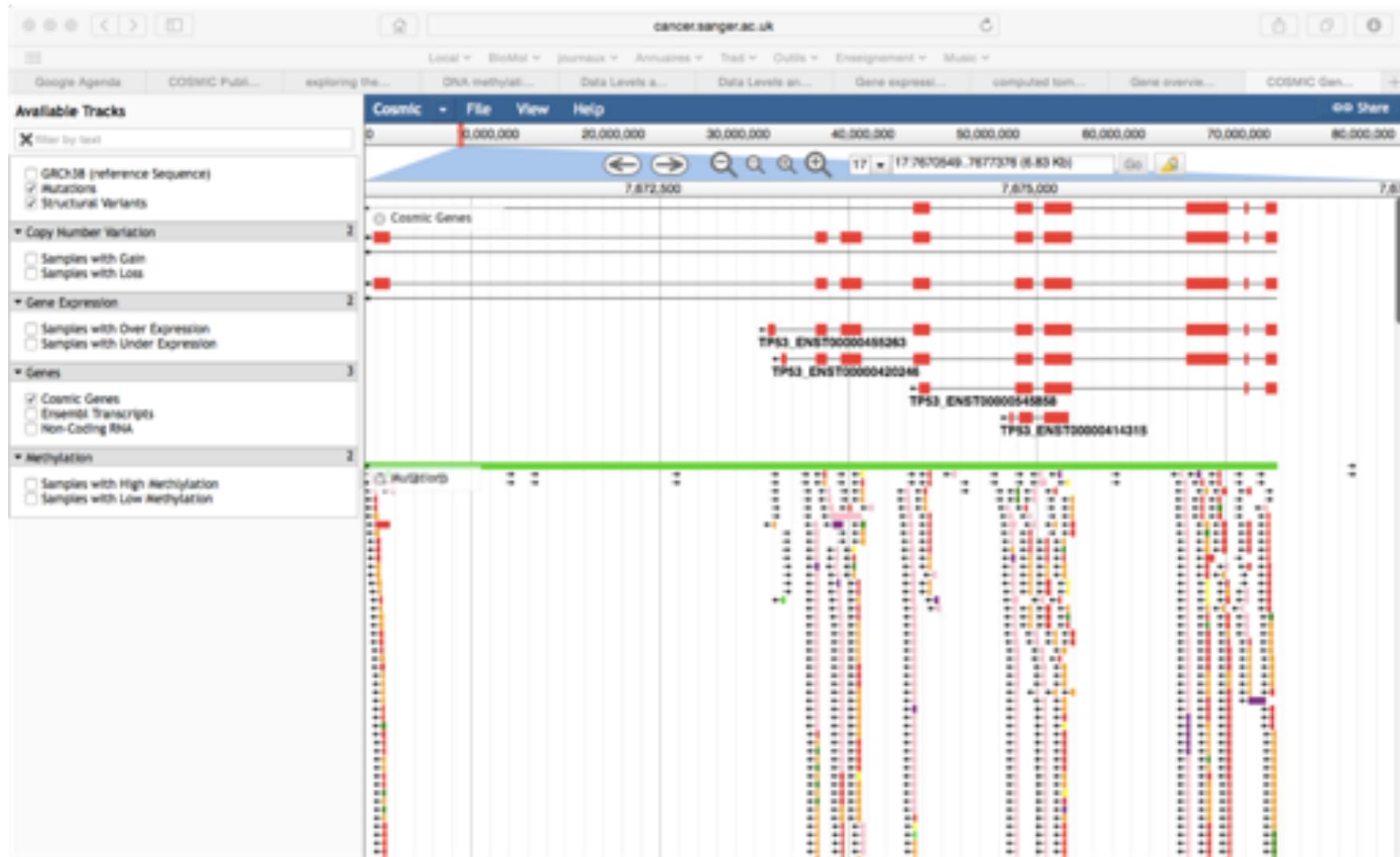
« Most [mutations] have no effect on the development of disease. We are adapting our curation processes to reduce this noise and highlight high-value information. »

« 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)

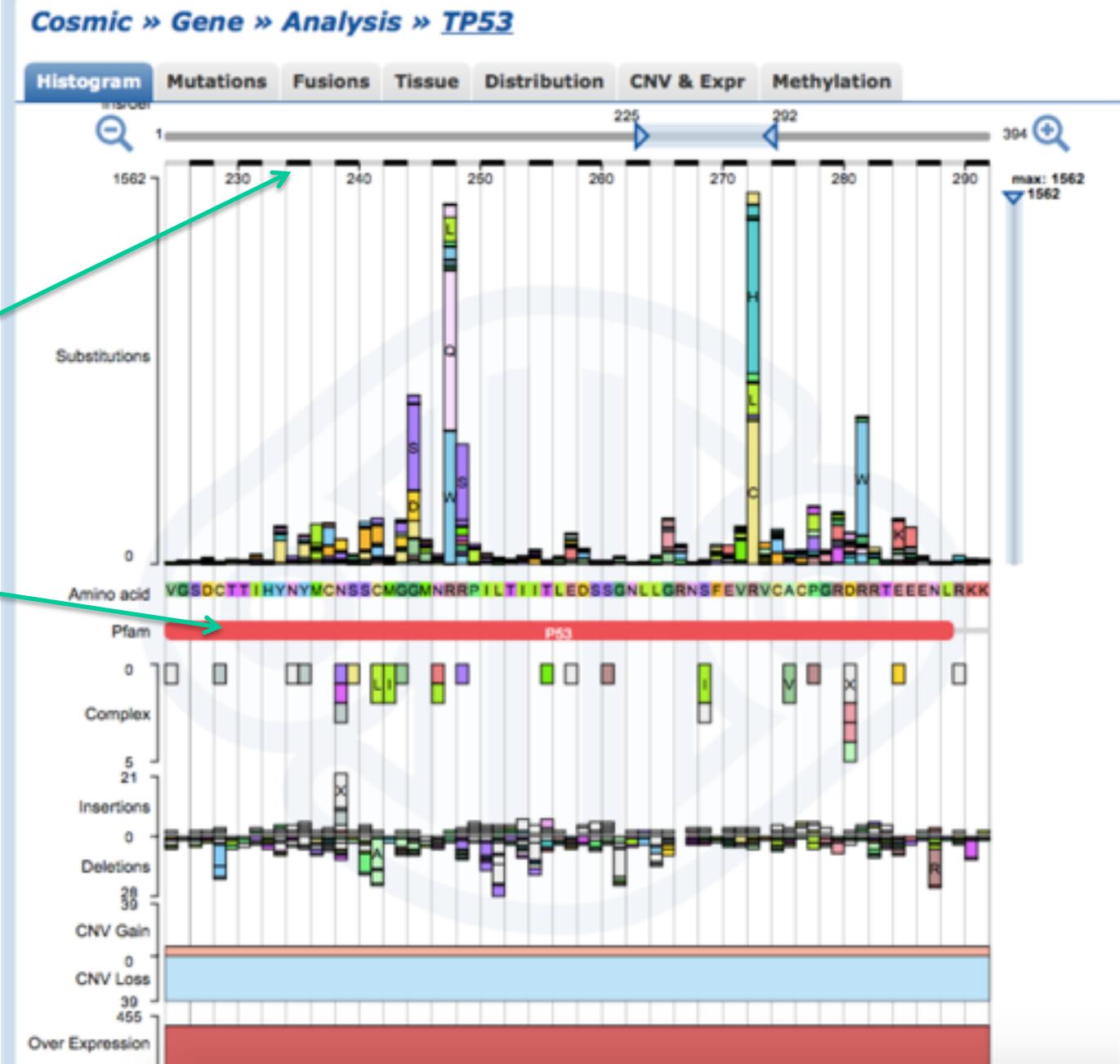
COSMIC genome browser



Histogram view

Protein coordinates

Protein domain



Tissue-distribution of mutations

Cosmic » Gene » Analysis » TP53

View in GRCh37 Archive

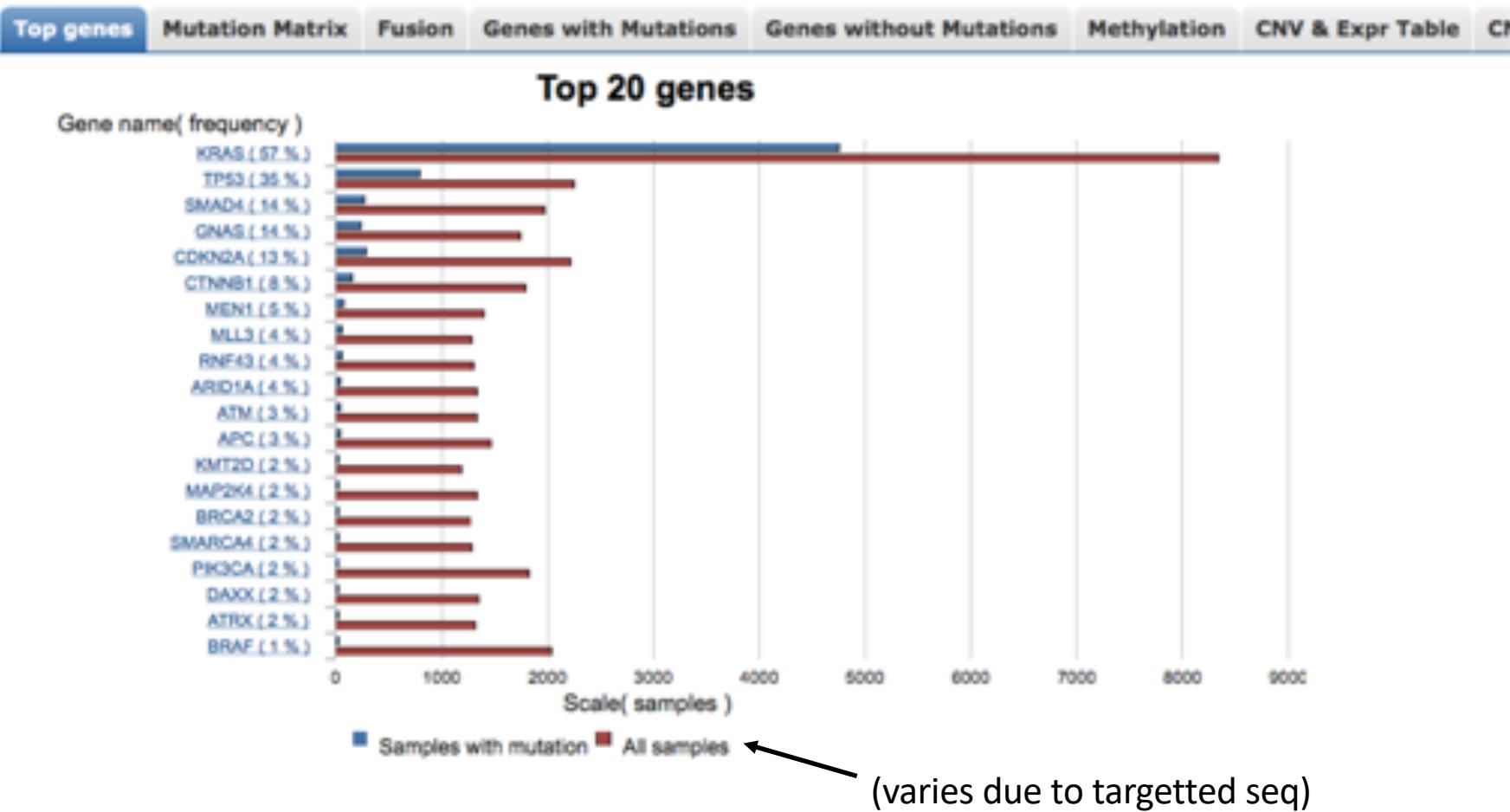
Histogram Mutations Fusions Tissue Distribution CNV & Expr Methylation

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

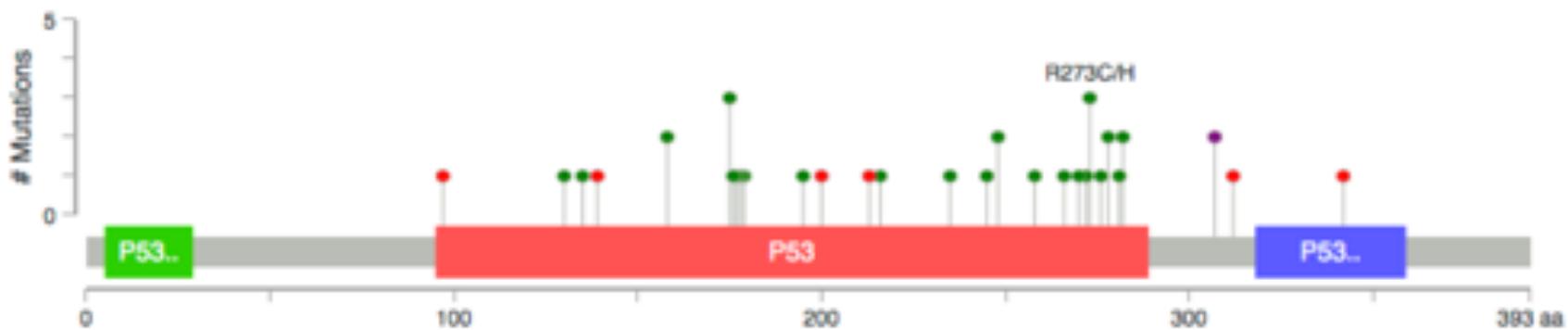


- Integration of Data from 89 cancer genomics studies.
- Focus on analysis tools
 - Mutual exclusivity
 - Gene networks

Mapped mutations on proteins

TP53: [Somatic Mutation Rate: 34.1%]

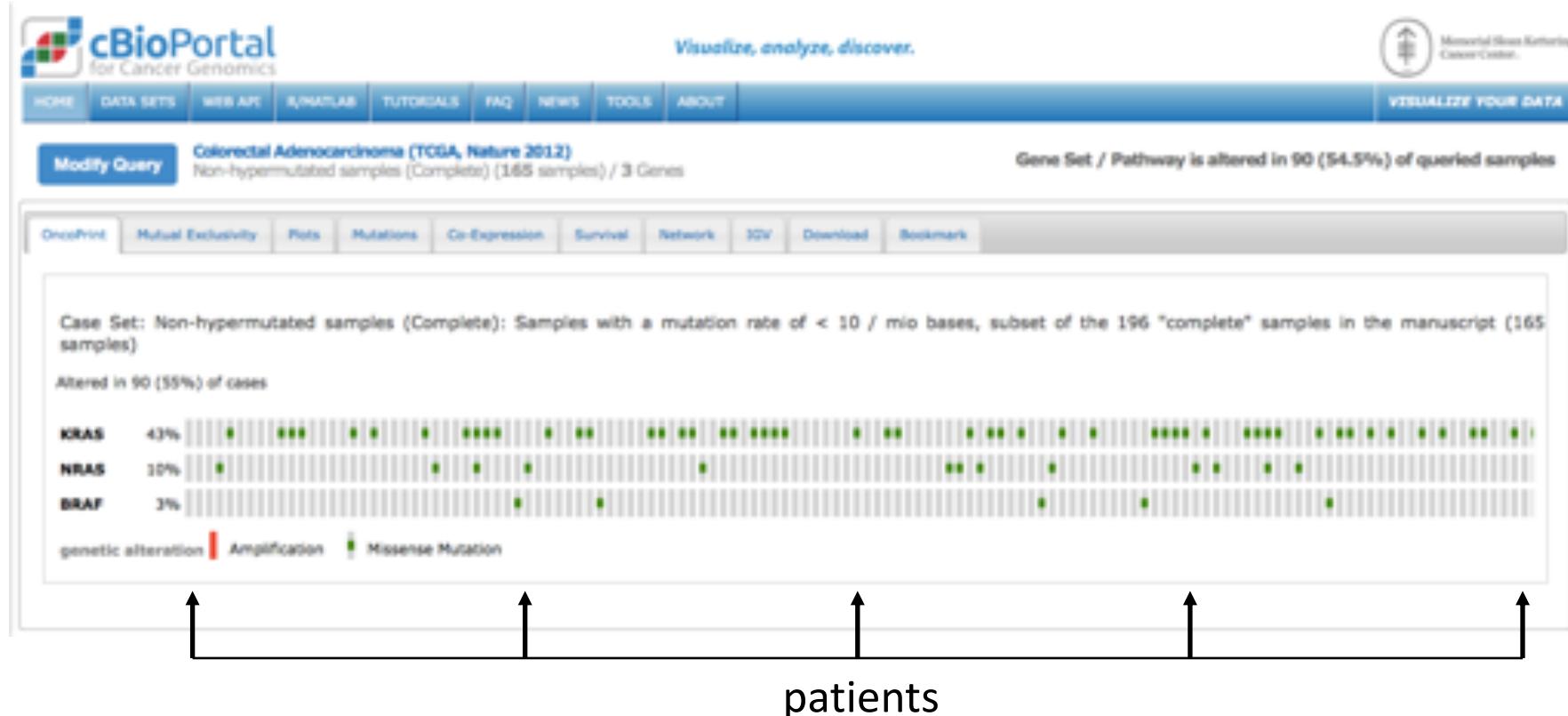
P53_HUMAN PDF SVG Customize Color Codes



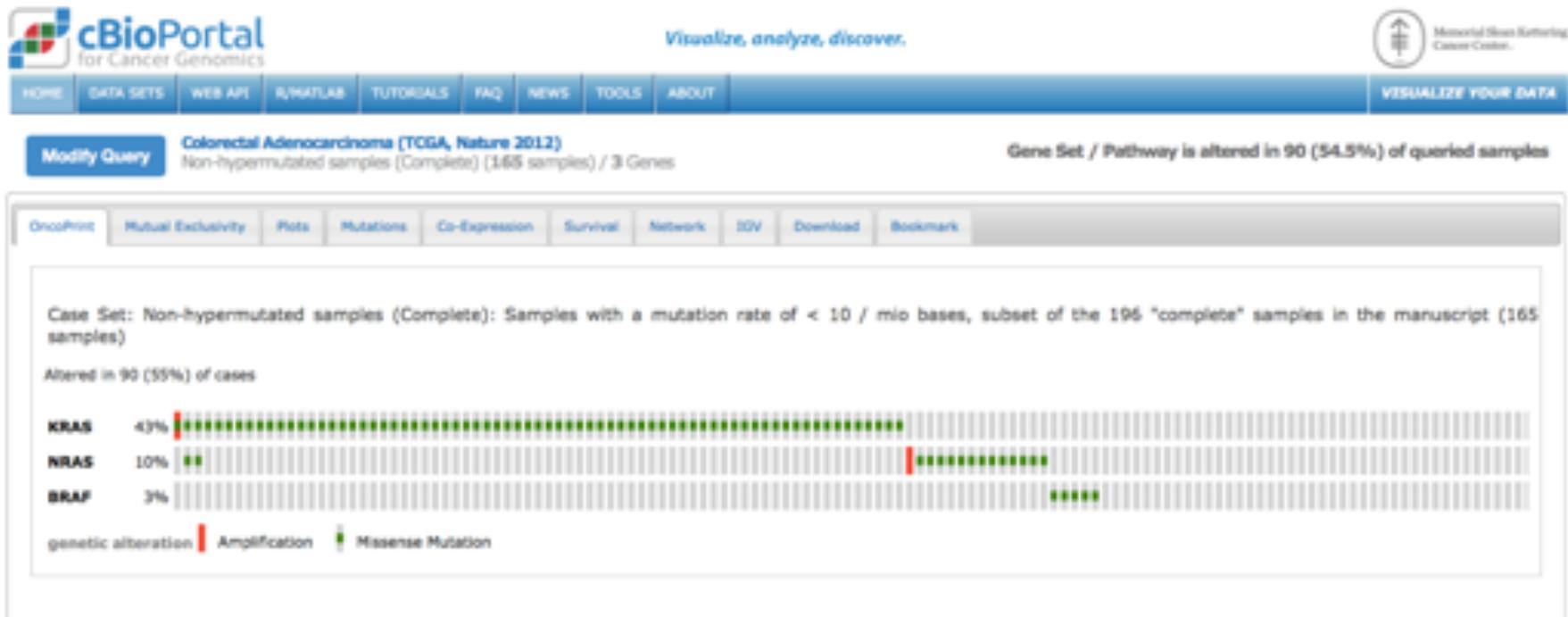
Mutations mapped on TP53 in Glioblastoma dataset (TCGA, Nature 2008)

See also « MutationMapper » tool

« Oncoprint » view

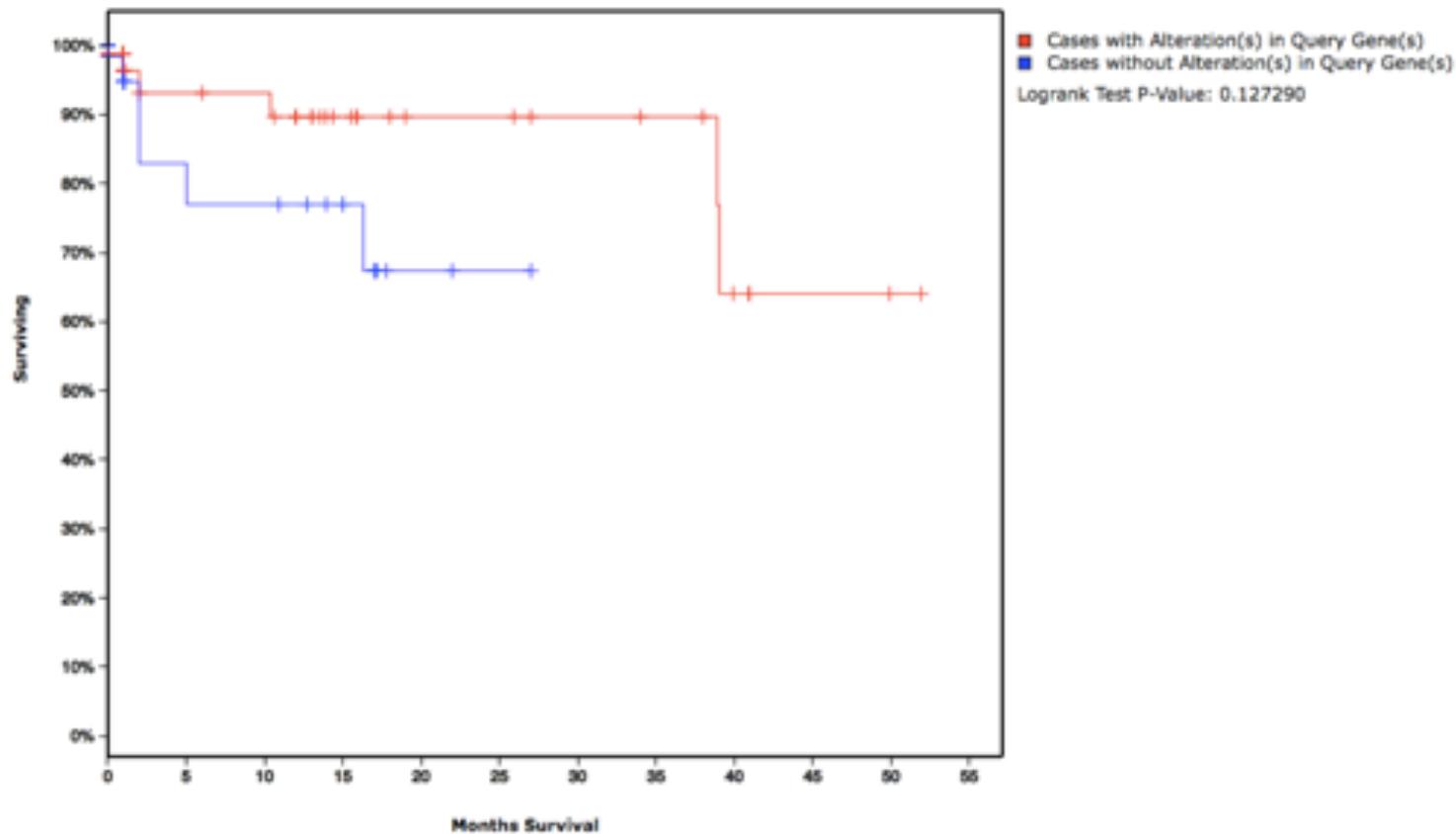


Mutual exclusivity



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 | | |
| 2558-01 | TCGA-06-2559-01 | TCGA-06-2561-01 TCGA-06-2562-01 TCGA-06-2563-01 TCGA-06-2564-01 TCGA-06-2565-01 TCGA-06-2566-01 TCGA-06-2567-01 | | |
| 2570-01 | TCGA-14-0790-01 | TCGA-14-1456-01 TCGA-14-2554-01 TCGA-27-1831-01 TCGA-27-1835-01 TCGA-27-1836-01 TCGA-27-1837-01 TCGA-27-1838-01 | | |
| 2519-01 | TCGA-27-2521-01 | TCGA-27-2523-01 TCGA-27-2524-01 TCGA-27-2526-01 TCGA-27-2527-01 TCGA-27-2528-01 TCGA-28-1747-01 TCGA-28-1753-01 | | |
| 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 | | |
| 0119-01 | TCGA-06-0121-01 | TCGA-06-0122-01 TCGA-06-0124-01 TCGA-06-0125-01 TCGA-06-0126-01 TCGA-06-0128-01 TCGA-06-0129-01 TCGA-06-0130-01 | | |
| 0137-01 | TCGA-06-0139-01 | TCGA-06-0140-01 TCGA-06-0141-01 TCGA-06-0142-01 TCGA-06-0143-01 TCGA-06-0145-01 TCGA-06-0147-01 TCGA-06-0148-01 | | |
| 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 | | |
| 2555-01 | TCGA-14-3477-01 | TCGA-19-1390-01 TCGA-19-1787-01 TCGA-19-2619-01 TCGA-19-2620-01 TCGA-19-2621-01 TCGA-19-2623-01 TCGA-19-2624-01 | | |
| 2629-01 | TCGA-32-2615-01 | TCGA-32-2616-01 TCGA-32-2632-01 TCGA-32-2634-01 TCGA-32-2638-01 TCGA-41-2571-01 TCGA-41-2573-01 TCGA-41-2575-01 | | |
| 0132-01 | TCGA-06-0138-01 | TCGA-06-0150-01 TCGA-06-0151-01 TCGA-06-0154-01 TCGA-06-0156-01 TCGA-06-0157-01 TCGA-06-0158-01 TCGA-06-0159-01 | | |
| 0165-01 | TCGA-06-0166-01 | TCGA-06-0168-01 TCGA-06-0171-01 TCGA-06-0173-01 TCGA-06-0174-01 TCGA-06-0176-01 TCGA-06-0178-01 TCGA-06-0184-01 | | |
| 0187-01 | TCGA-06-0188-01 | TCGA-06-0189-01 TCGA-06-0190-01 TCGA-06-0195-01 TCGA-06-0197-01 TCGA-06-0201-01 TCGA-06-0206-01 TCGA-06-0208-01 | | |
| 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:
 - GJ Clement on data structuration
 - G Lelandais on Gene Expression Analysis via Galaxy