

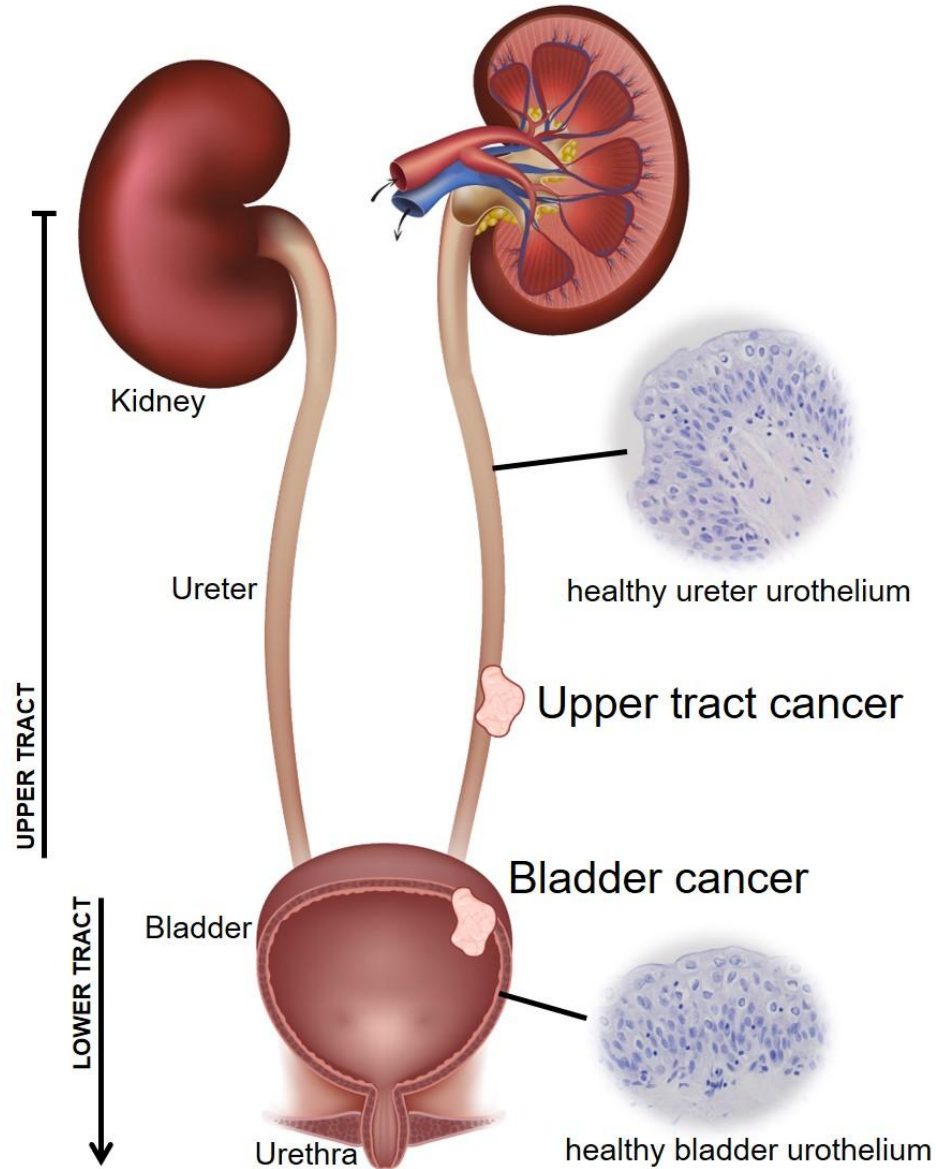
An introduction to bladder cancer

...and patient stratification research in the Mason Lab

Andrew Mason

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asmasonomics.github.io



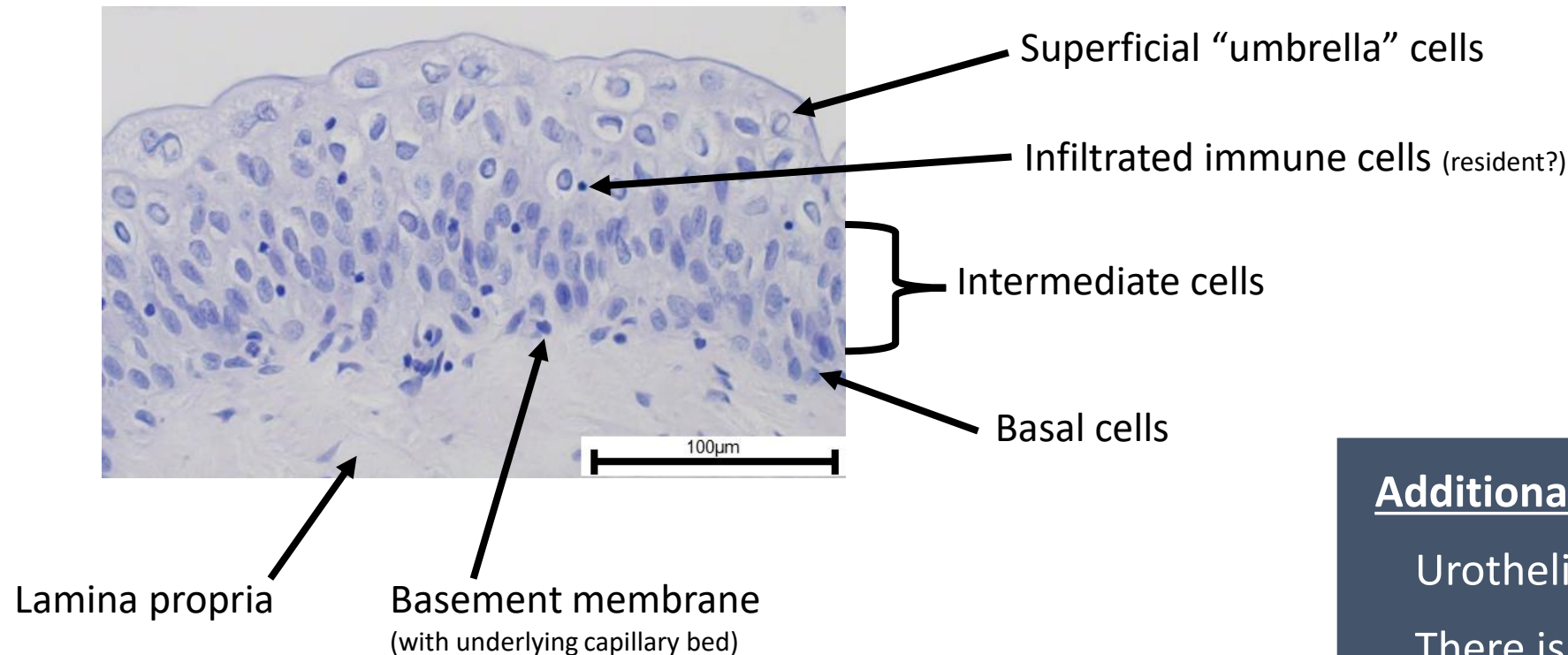
The urinary system falls into 2 distinct zones:

- 1) Upper urinary tract (kidneys and ureters)
- 2) Lower urinary tract (bladder and urethra)

The urinary tract experiences many pressures

- Pathogens
- Urinary toxins
- Fluid pressure changes (incl. size/shape changes)

The urothelium is a specialised, transitional epithelial lining which spans the urinary system, from the kidney renal pelvis to the top of the urethra

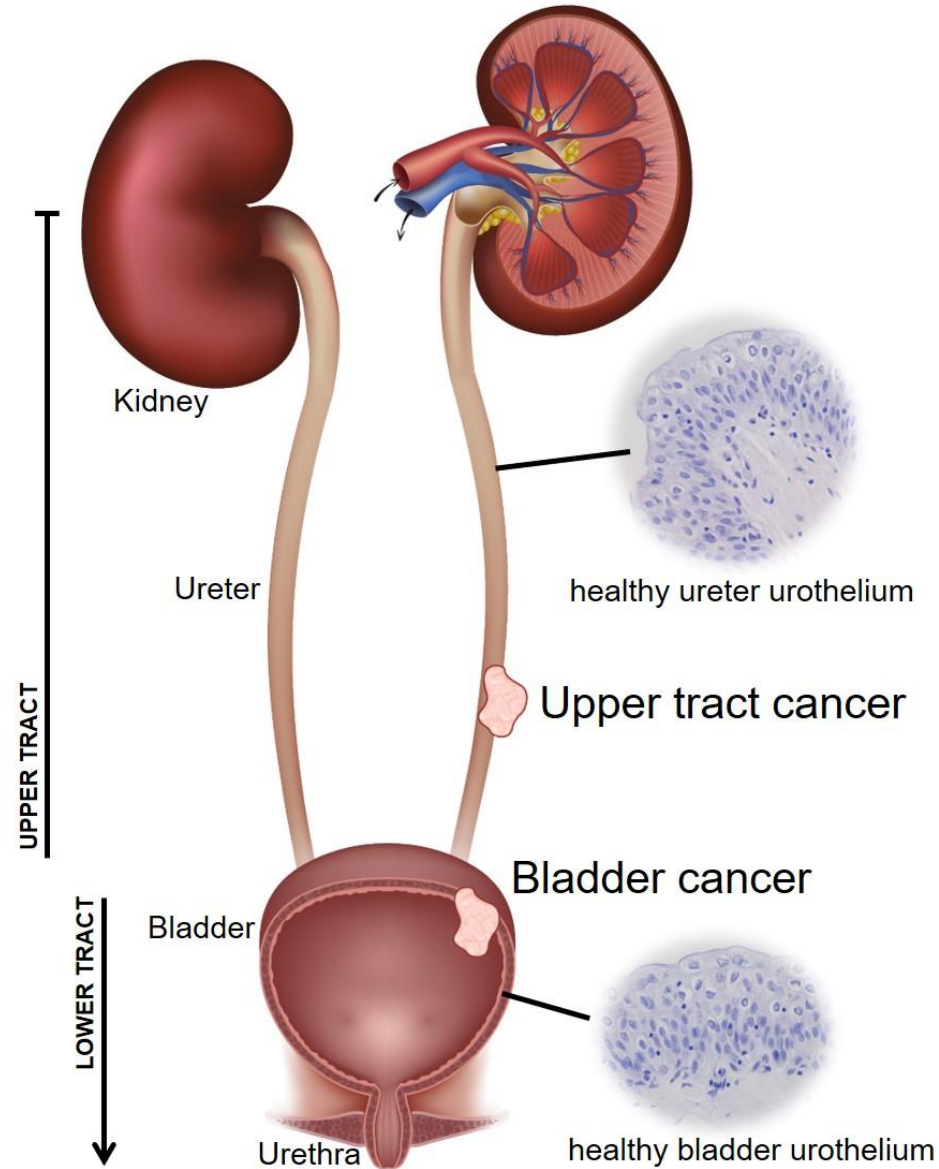


Additional relevant info

Urothelium is quiescent

There is no evidence for a urothelial stem cell

Superficial cells are not “more differentiated” than basal cells



In the global north, >95% of cancers between the renal pelvis and bladder neck are urothelial carcinoma (aka transitional cell carcinoma; TCC)

>92% are urothelial carcinoma of the bladder (UCB)

c.8% are upper tract urothelial carcinoma (UTUC)

UTUC (c.2/100,000)

60% present at T2+

Luminal (immune-poor) tumours

1/3 patients go on to develop UCB

Treatment based on UCB research

UCB (c.20/100,000)

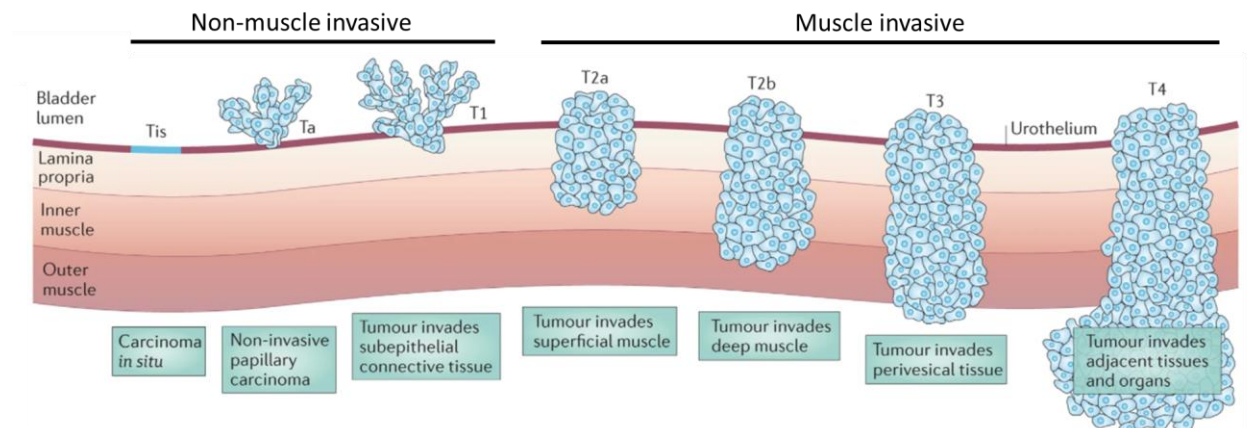
80% present <T2 (non-invasive)

Highly recurrent

Very expensive aftercare

MIBC 5-year survival <50%

MIBC is molecularly diverse



What causes urothelial carcinoma?

Urothelial carcinoma has **high mutational burden** and, consequently, **diverse driver genes**



**CANCER
RESEARCH
UK**

Caused by smoking



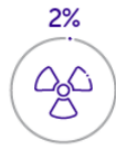
45%
Bladder cancer cases
caused by smoking,
UK, 2015

Caused by occupation

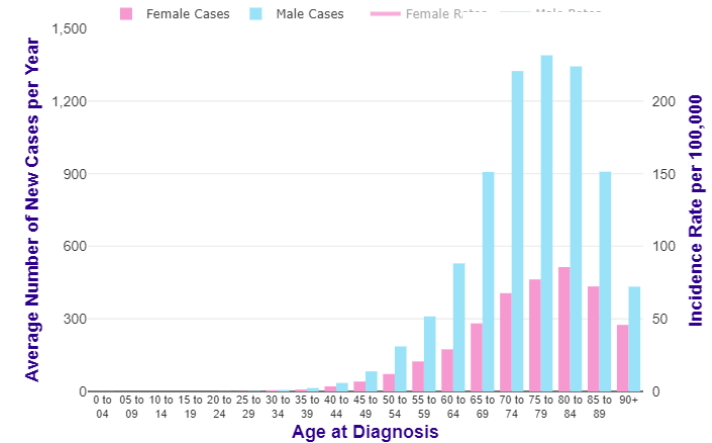


6%
Bladder cancer cases
linked to occupational
exposures, UK

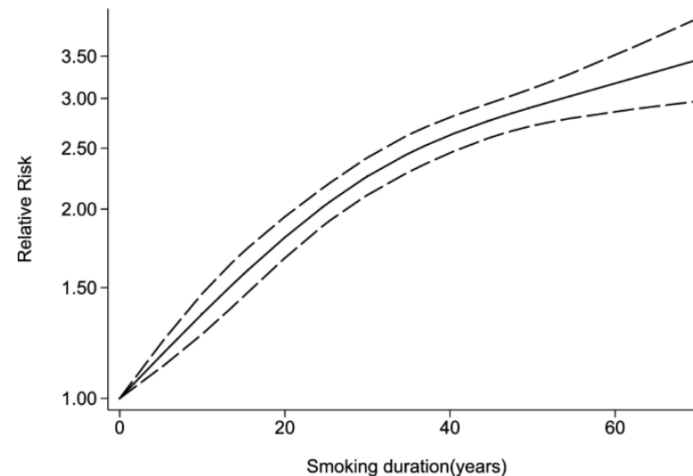
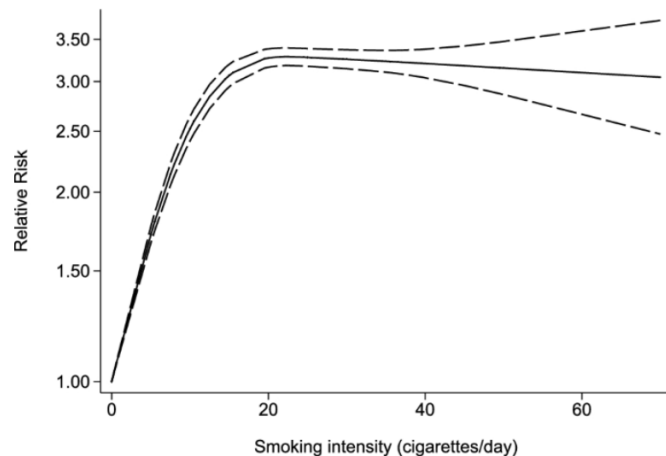
Caused by radiation



2%
Bladder cancer cases
linked to ionising
radiation exposure,
UK

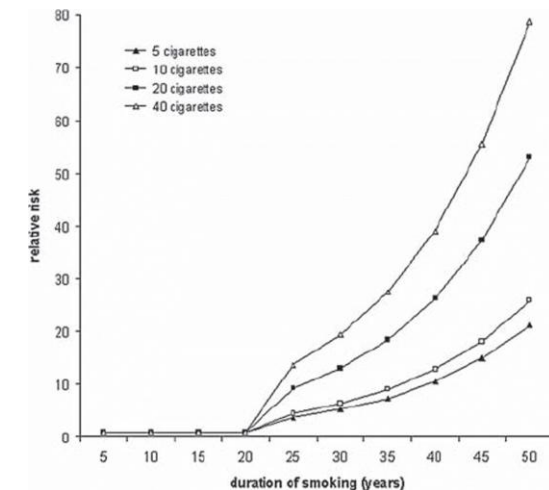


Older age is the main risk factor for cancer. This largely reflects cell DNA damage accumulating over time. Damage can result from biological processes or from exposure to risk factors.



Zhao *et al* (2022) meta-analysis in bladder cancer
PMID:35332429

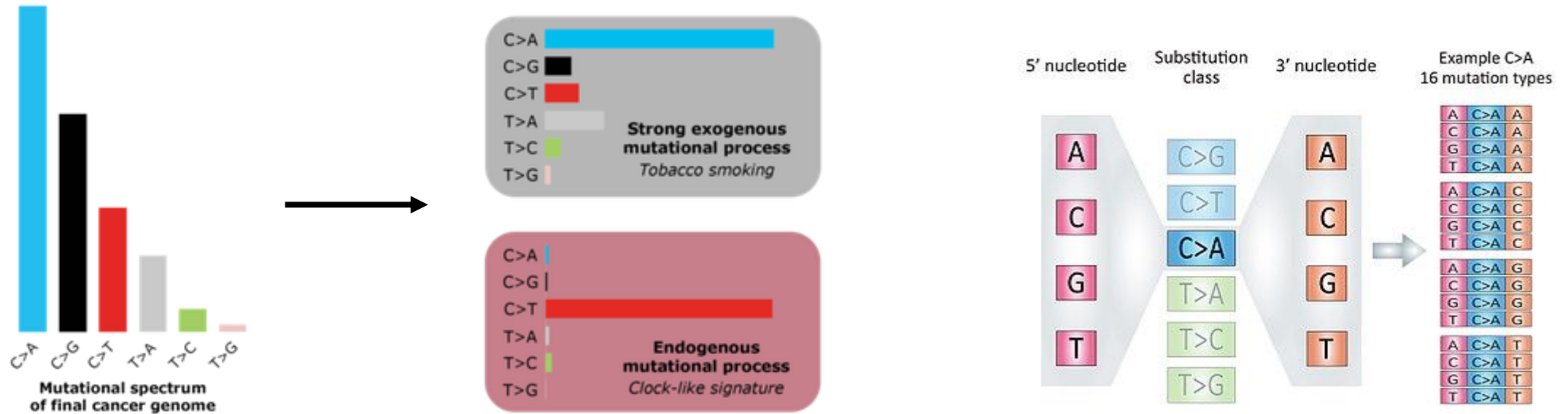
Smoking relationship different in lung cancer



Didkowska *et al* (2011; PMID:20553096) from
data in Simonata *et al* (2001; PMID:11275995)

Urothelial carcinoma has **high mutational burden** and, consequently, **diverse driver genes**

High mutational burden allows us to construct mutational signatures very confidently

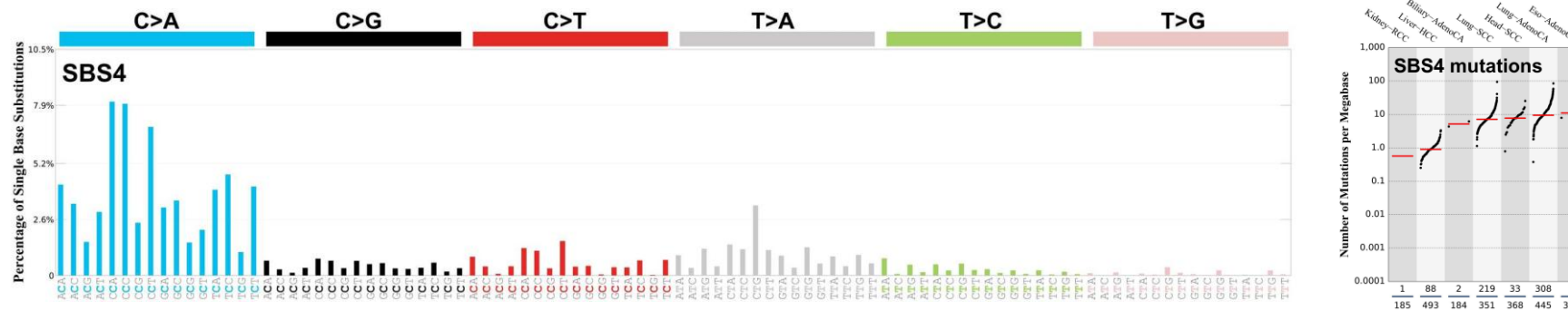


Specific base change, plus surrounding chemistry creates very specific signatures of mutational processes

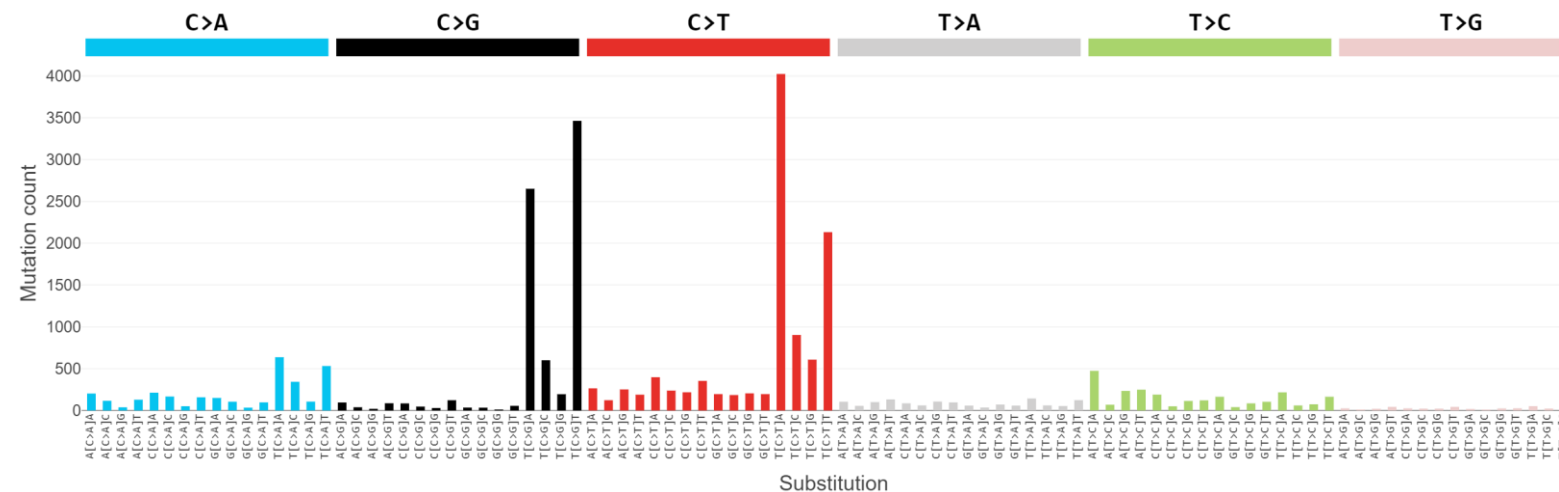
Urothelial carcinoma has **high mutational burden** and, consequently, **diverse driver genes**

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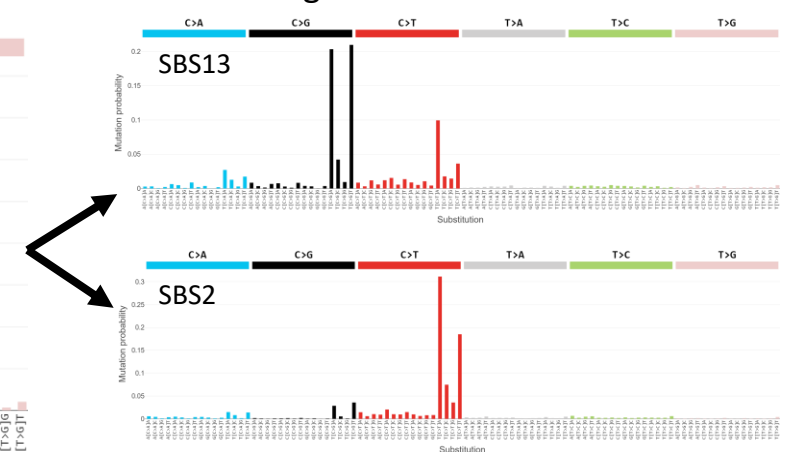
Smoking signature characteristic in lung cancer



Typical bladder cancer mutational signature



APOBEC mutagenesis



Urothelial carcinoma has **high mutational burden** and, consequently, **diverse driver genes**

High mutational burden allows us to construct mutational signatures very confidently

Mutational signatures (and epidemiological data) now support a **viral cause of urothelial carcinoma**

Induction of APOBEC3-mediated genomic damage in urothelium implicates BK polyomavirus (BKPyV) as a hit-and-run driver for bladder cancer

[Simon C. Baker](#) , [Andrew S. Mason](#), [Raphael G. Slip](#), [Katie T. Skinner](#), [Andrew Macdonald](#), [Omar Masood](#), [Reuben S. Harris](#), [Tim R. Fenton](#), [Manikandan Periyasamy](#), [Simak Ali](#) & [Jennifer Southgate](#)

[Oncogene](#) **41**, 2139–2151 (2022) | [Cite this article](#)



Smoking may dampen the immune system and/or specific toxins may damage urothelium and facilitate viral infection

Additional relevant info

Mice do not get the relevant virus

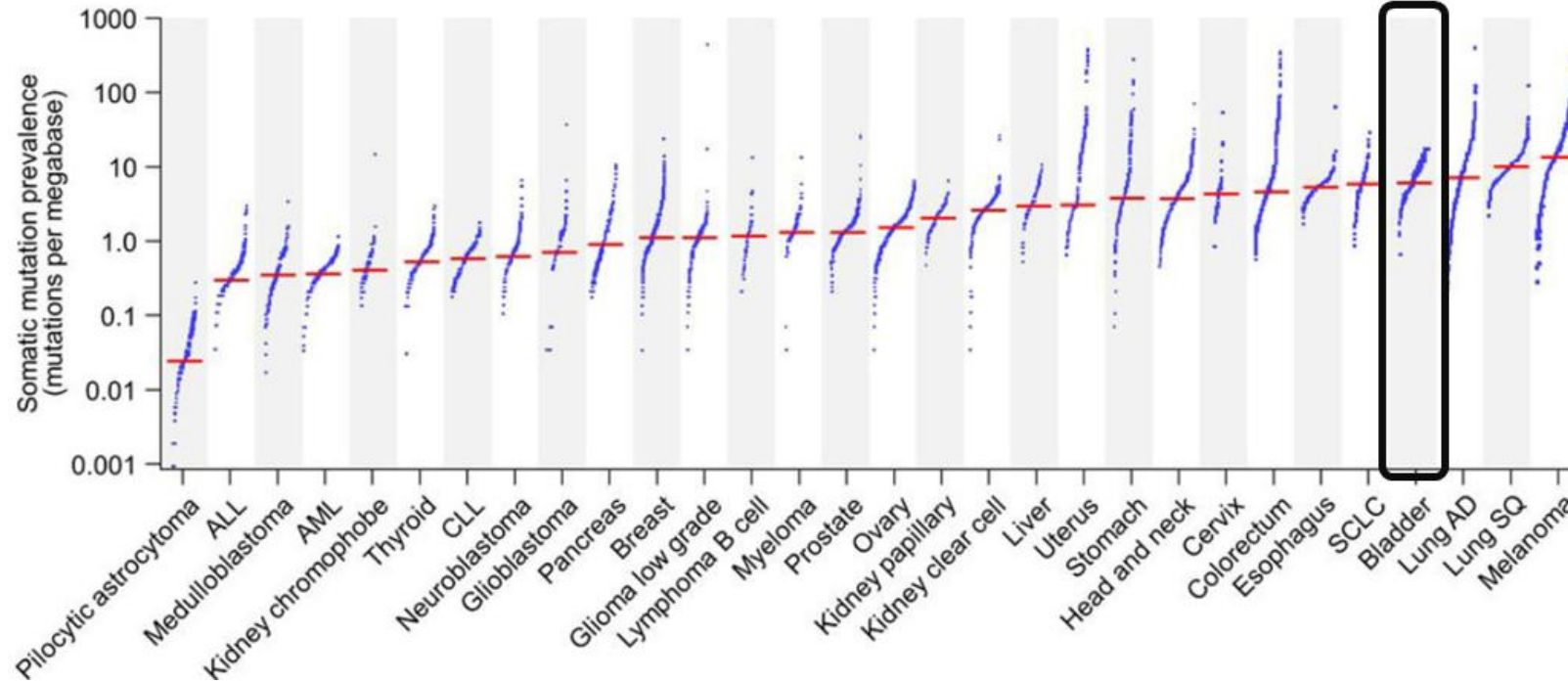
Mice do not have the relevant
APOBEC3 enzymes

Mice UC models are chemically-induced

Rodent urothelium is different

Rodents are effectively incontinent

Very high mutational burden (TMB) and diverse driver genes

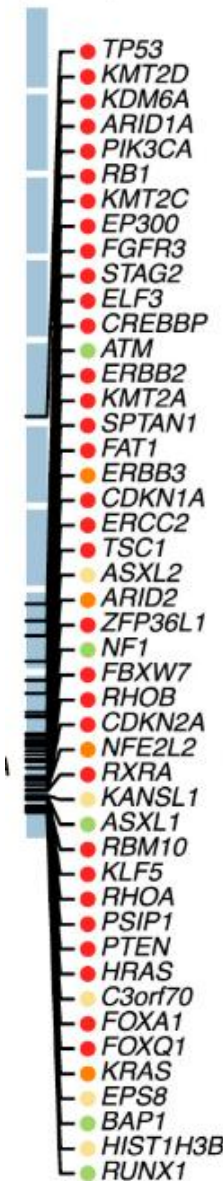


Unclear which are tumour drivers, and which are unimportant passengers

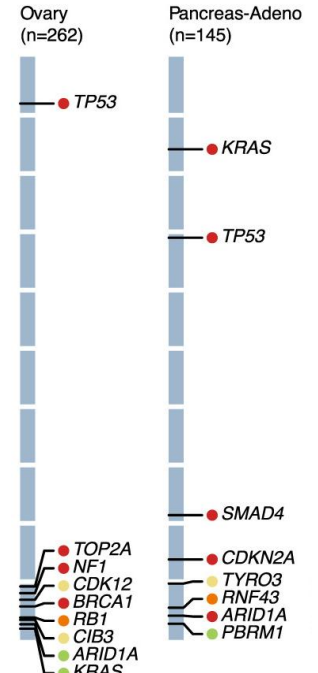
Diverse pathways to try to find druggable targets

Issues with pathway redundancy and pathway interactions

Bladder
(n=390)



For comparison

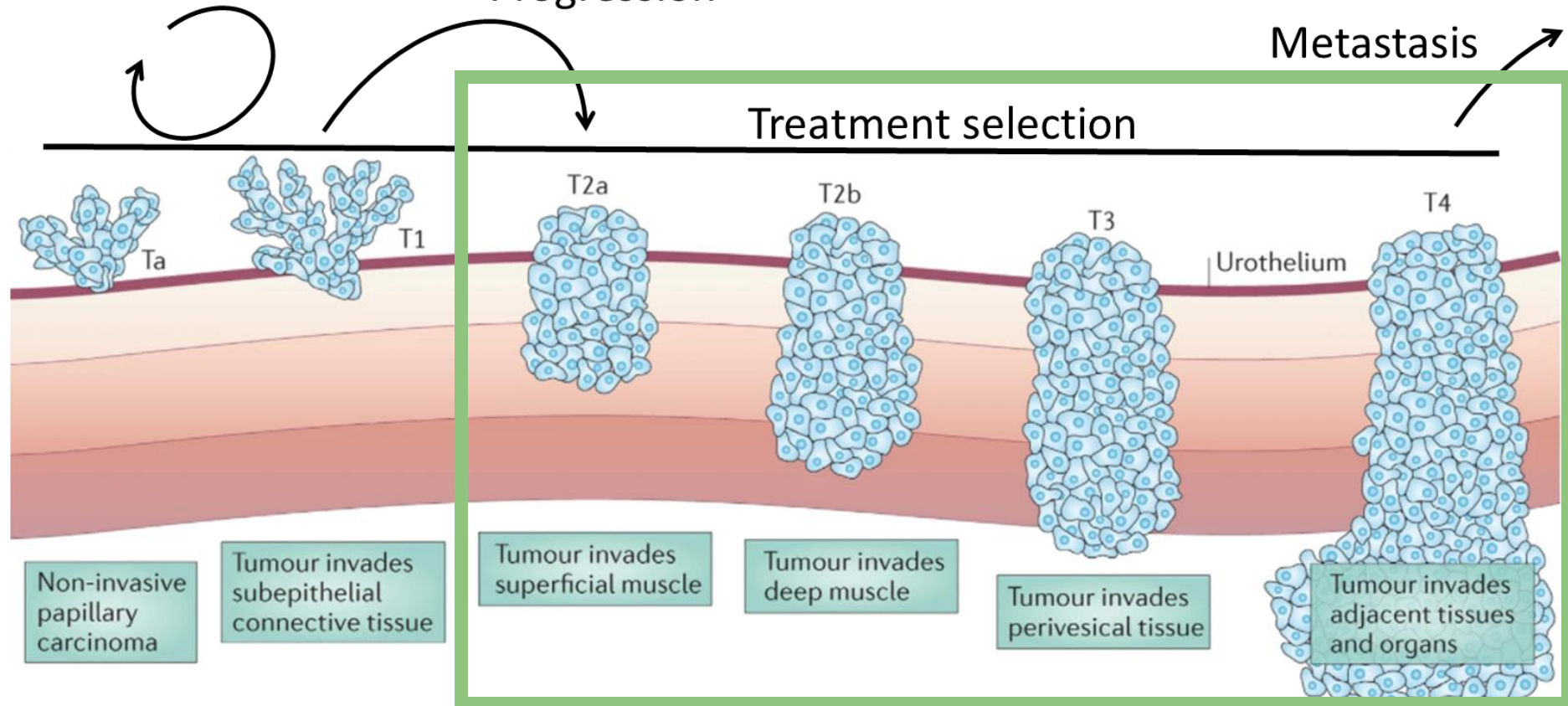


Can we use data to personalise patient experience and treatment?

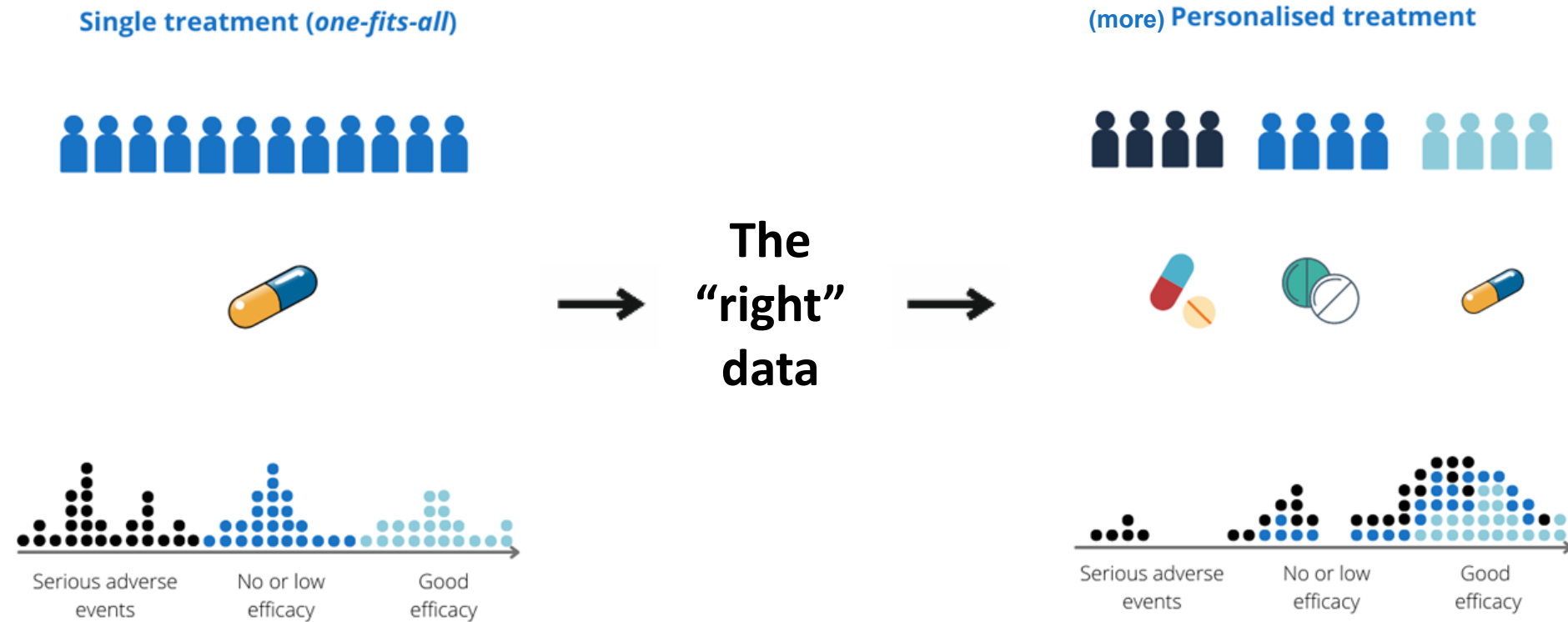
Mode of recurrence

Progression

Metastasis

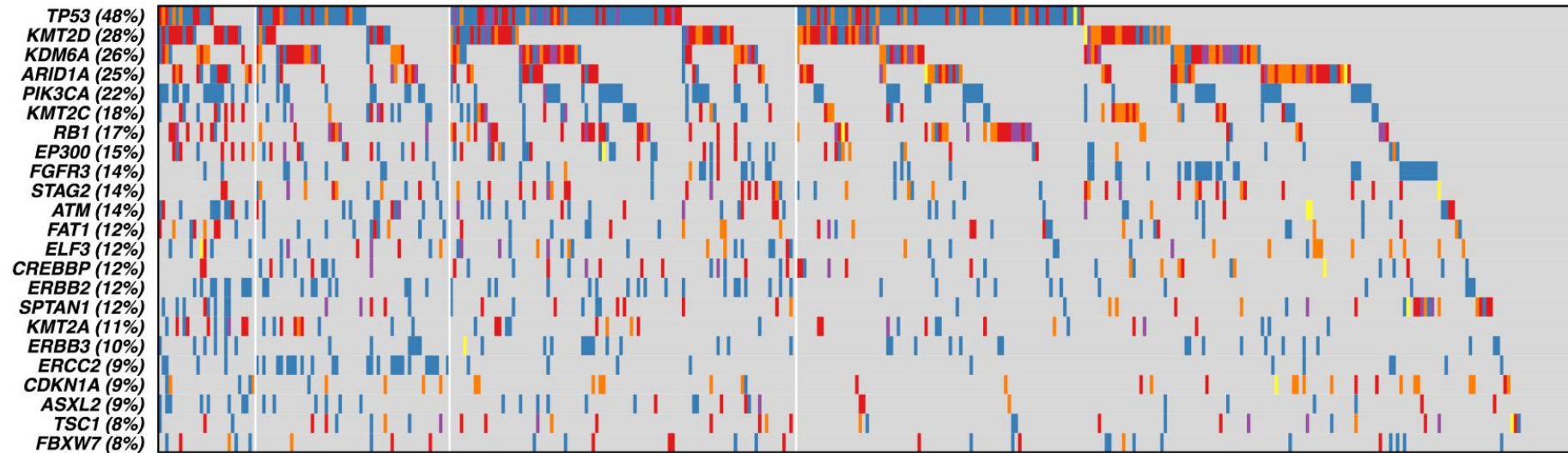


The problem is stratification



Unsupervised clustering → finding order without knowing the answer

Mutations are appealing as they are easy and cost-effective to profile, and often give clear binary answers



Overlaps between different mutation types

Difficult to predict the impact of each mutation

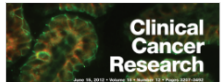
Very limited data on mutation interactions

High number of mutations found in only one or two patients

As with many cancers, BLCA research focused on gene expression profiles in the 2010s

Standard approach → retain “most variable” genes, dimension reduction, most parsimonious number of groups

Volume 18, Issue 12
15 June 2012



IMAGING, DIAGNOSIS, PROGNOSIS | JUNE 14 2012

A Molecular Taxonomy for Urothelial Carcinoma FREE

Gottfrid Sjö Dahl¹, Martin Lauss², Kristina Lövgren³, Gunilla Chebil⁴, Sigurdur Gudjonsson⁵, Srinivas Veerla⁶, Oliver Patschan⁷, Mattias Aine⁸,
Mårten Fernö⁹, Markus Ringnér¹⁰, Wiking Månsson¹¹, Fredrik Liedberg¹², David Lindgren¹³, Mattias Höglund¹⁴ ✉



ARTICLE · Volume 171, Issue 3, P540-556.E25, October 19, 2017 · [Open Archive](#)

[Download Full Issue](#)

Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer

A. Gordon Robertson^{1,25} · Jaegil Kim^{2,25} · Hikmat Al-Ahmadie³ · ... · John N. Weinstein^{8,22} ✉ · David J. Kwiatkowski^{9,23} ✉ ·
Seth P. Lerner^{9,24,26} ✉ ... [Show more](#)

Cancer Cell



Volume 25, Issue 2, 10 February 2014, Pages 152-165

Article

Identification of Distinct Basal and Luminal Subtypes of Muscle-Invasive Bladder Cancer with Different Sensitivities to Frontline Chemotherapy

Woonyoung Choi¹, Sima Porten¹, Seungchan Kim⁶, Daniel Willis¹, Elizabeth R. Plimack⁷,
Jean Hoffman-Censits⁸, Beat Roth¹, Tiewei Cheng^{1,5}, Mai Tran^{1,5}, I-Ling Lee¹,
Jonathan Melquist¹, Jolanta Bondaruk³, Tadeusz Majewski³, Shizhen Zhang³, Shanna Pretzsch¹,
Keith Baggerly⁴, Arlene Siefker-Radtke², Bogdan Czerniak³, Colin P.N. Dinney¹,
David J. McConkey^{1,5} ✉

Intrinsic subtypes of high-grade bladder cancer reflect the hallmarks of breast cancer biology

Jeffrey S. Damarrauer, Katherine A. Hoadley, David D. Chism, ✉, and William Y. Kim ✉ [Authors Info & Affiliations](#)

Edited* by William G. Kaelin, Jr., Harvard Medical School, Boston, MA, and approved January 15, 2014 (received for review October 2, 2013)

February 11, 2014 | 111 (8) 3110-3115 | <https://doi.org/10.1073/pnas.1318376111>

Prognostic Power of a Tumor Differentiation Gene Signature for Bladder Urothelial Carcinomas FREE

Qianxing Mo ✉, Fotis Nikolos, Fengju Chen, Zoe Tramel, Yu-Cheng Lee,
Kazukuni Hayashi, Jing Xiao, Jianjun Shen, Keith Syson Chan ✉

JNCI: Journal of the National Cancer Institute, Volume 110, Issue 5, May 2018, Pages 448–459, <https://doi.org/10.1093/jnci/djx243>

Published: 12 January 2018 [Article history](#) ▼

Journal of Pathology
J Pathol 2017; 242: 113–125
Published online 28 March 2017 in Wiley Online Library
(wileyonlinelibrary.com) DOI: 10.1002/jpath.4886

ORIGINAL PAPER

Molecular classification of urothelial carcinoma: global mRNA classification versus tumour-cell phenotype classification

Gottfrid Sjö Dahl¹, Pontus Eriksson², Fredrik Liedberg³ and Mattias Höglund^{2*} ✉

Tumour gene expression
profiling (e.g. RNAseq)



Normalised expression
values (e.g. TPMs)



Remove low expression
genes and expressed in
few samples



Order and select genes
based on variance (e.g.
top 3000, top 5000)



Apply hierarchical- or
centroid-based UML



Clinical associations and
biomarker discovery

Tumour sequencing includes
TME and adjacent tissue –
combination of surgical sampling
“error” and actual biology

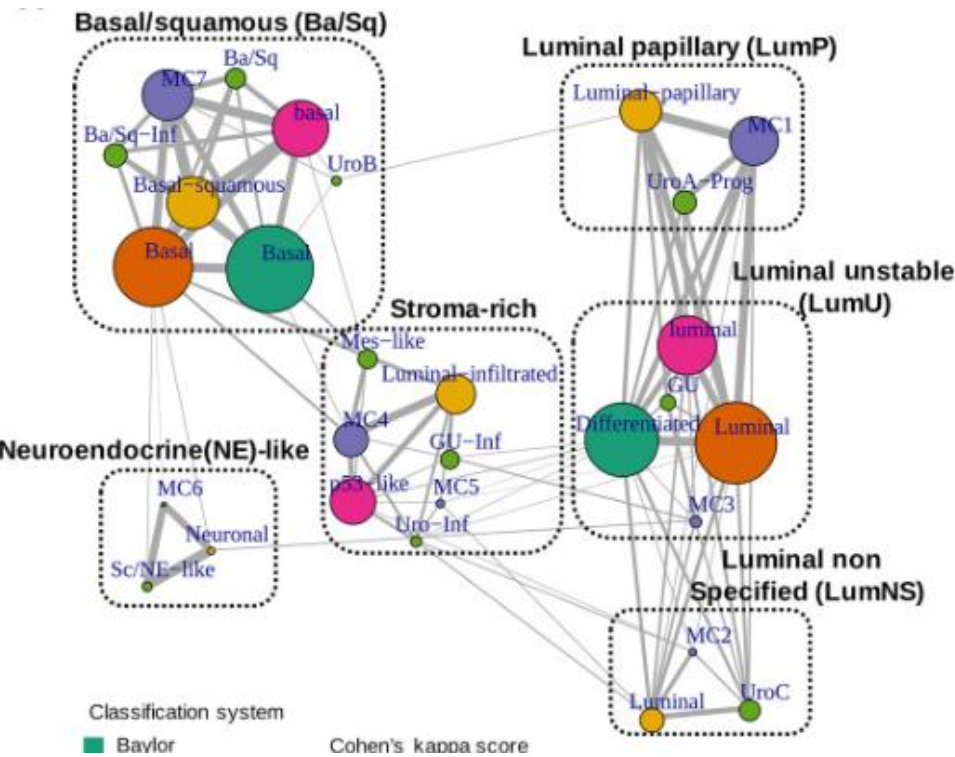
Can derive groups based
on “contamination”





Platinum Priority – Bladder Cancer – Editor's Choice
Editorial by Kenneth B. Yatai, Mark J. Dunning and Dennis Wang on pp. 434–435 of this issue

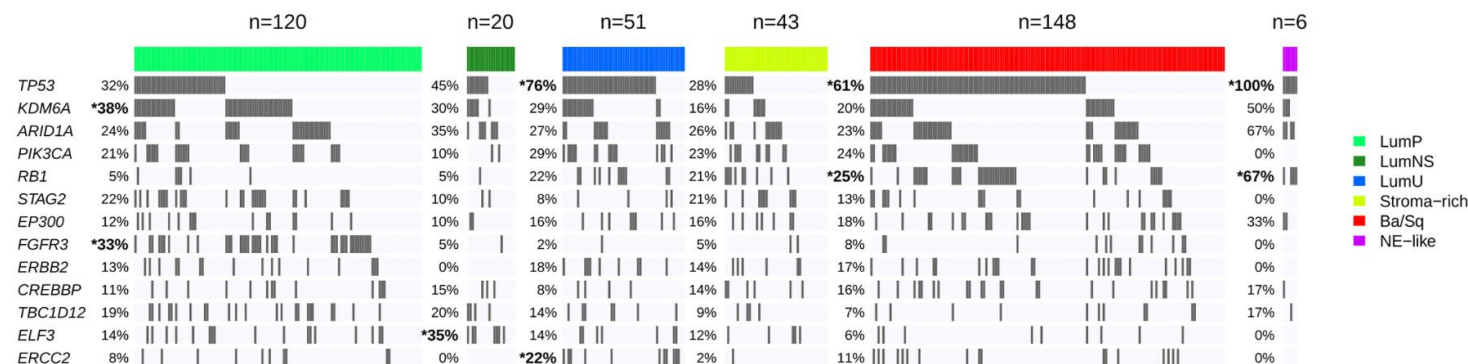
A Consensus Molecular Classification of Muscle-invasive Bladder Cancer ^{EU} ^{ACME} ☆



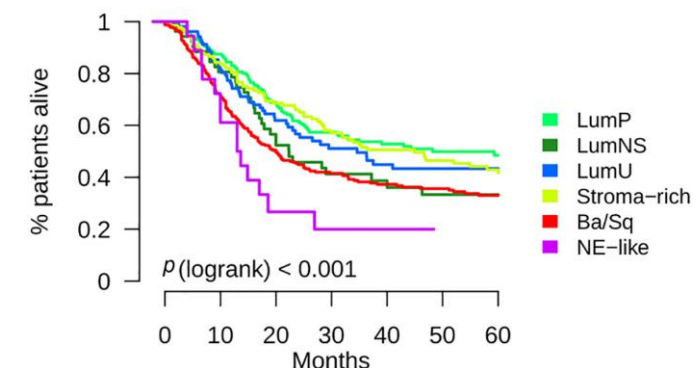
| % of MIBC | 24% | 8% | 15% | 15% | 35% | 3% |
|---------------------------------|----------------------------|-------------------------------|--|--|--------------------------------|--------------------------------------|
| Class Name | Luminal Papillary (LumP) | Luminal Non-Specified (LumNS) | Luminal Unstable (LumU) | Stroma-rich | Basal/Squamous (Ba/Sq) | Neuroendocrine-like (NE-like) |
| | | | | | | |
| Differentiation | Urothelial / Luminal | | | | Basal | Neuroendocrine |
| Oncogenic mechanisms | FGFR3 + PPARG + CDKN2A- | PPARG + | PPARG + E2F3 +, ERBB2 + Genomic instability Cell cycle + | | EGFR + | TP53 -, RB1 -, Cell cycle + |
| Mutations | FGFR3 (40%), KDM6A (38%) | ELF3 (35%) | TP53 (76%), ERCC2 (22%) TMB +, APOBEC + | | TP53 (61%), RB1 (25%) | TP53 (94%) RB1 (39%)* |
| Stromal infiltrate | | Fibroblasts | | Smooth muscle Fibroblasts Myofibroblasts | Fibroblasts Myofibroblasts | |
| Immune infiltrate | | | | B cells | CD8 T cells NK cells | |
| Histology | Papillary morphology (59%) | Micropapillary variant (36%) | | | Squamous differentiation (42%) | Neuroendocrine differentiation (72%) |
| Clinical | T2 stage + | Older patients + (80+) | | | Women + T3/T4 stage + | |
| Median overall survival (years) | 4 | 1.8 | 2.9 | 3.8 | 1.2 | 1 |

* 94% of these tumors present either RB1 mutation or deletion

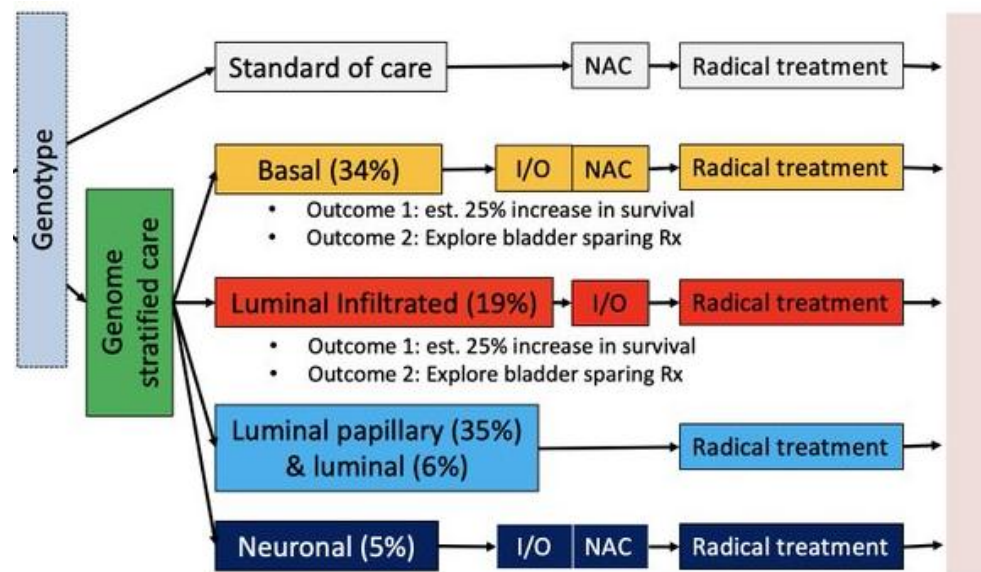
“Clinically relevant” mutations were still very divided



Limited differences in patient outcome



There are some propensities for treatment response → opportunities for trials



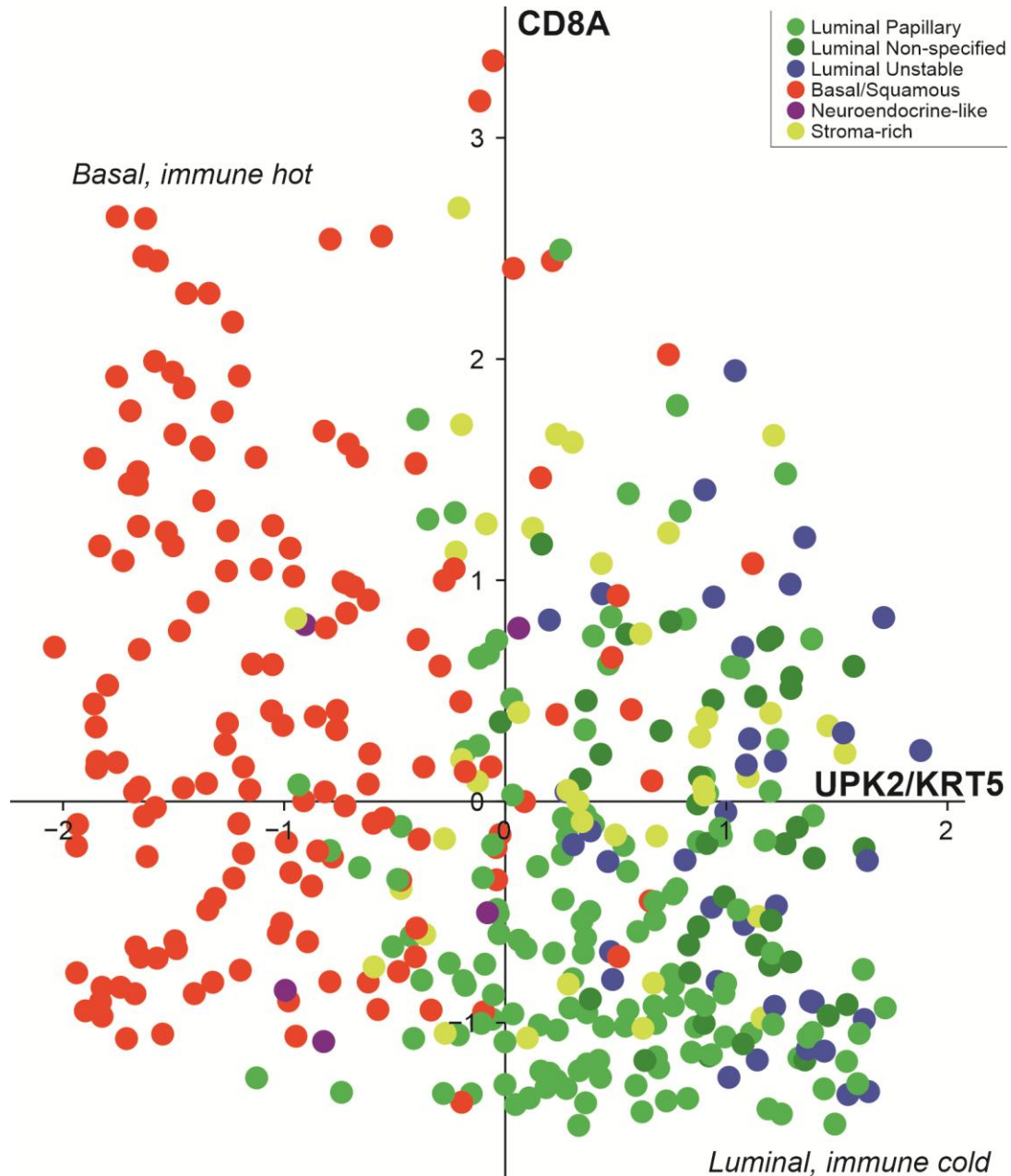
Genotype of Urothelial cancer: Stratified Treatment and Oncological outcomes (GUSTO): Phase II study

Plain English Summary:

Award:
£2,888,145.70

Award ID: NIHR128103

We want to improve the outcomes from Bladder Cancer. We think this can be achieved by using the genetic information within each cancer to tailor treatments to individual patients. However, before testing our approach, we have to understand if this is possible within the NHS and if our choices appear to work.



Despite this work, we can largely represent MIBC molecular subtypes with 3 genes / 2 axes

- basal/luminal differentiation state
- immune activity

New classification systems already proposed

THE PROBLEMS

ML is giving us very limited gains in understanding

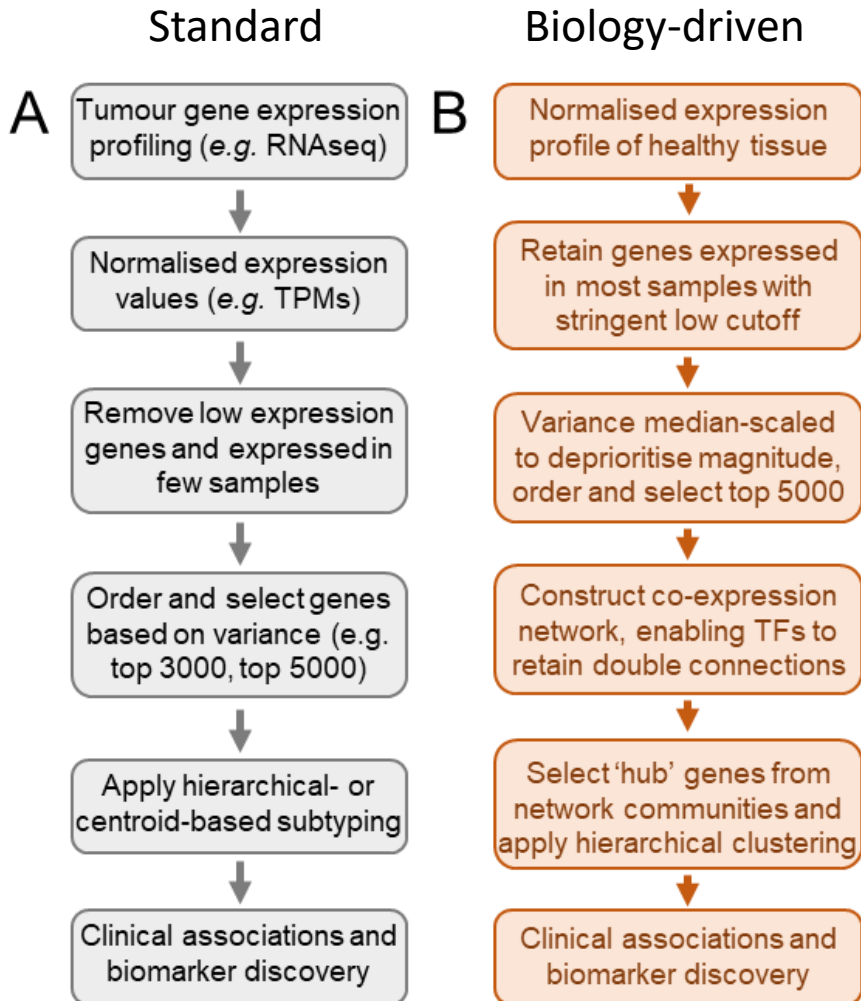
Subgroupings are arbitrary

- Even splits
- Group edge cases swap with new annotations, different filtering strategies *etc.*

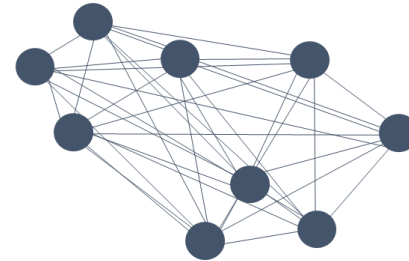
Subgroupings are academic, not clinical

We can't rely on data alone.

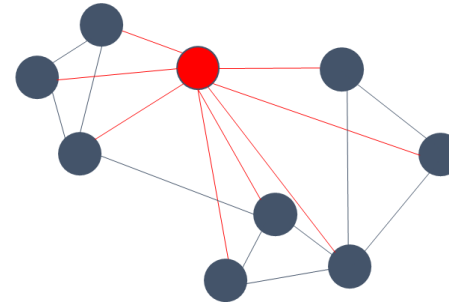
Biological knowledge is essential.



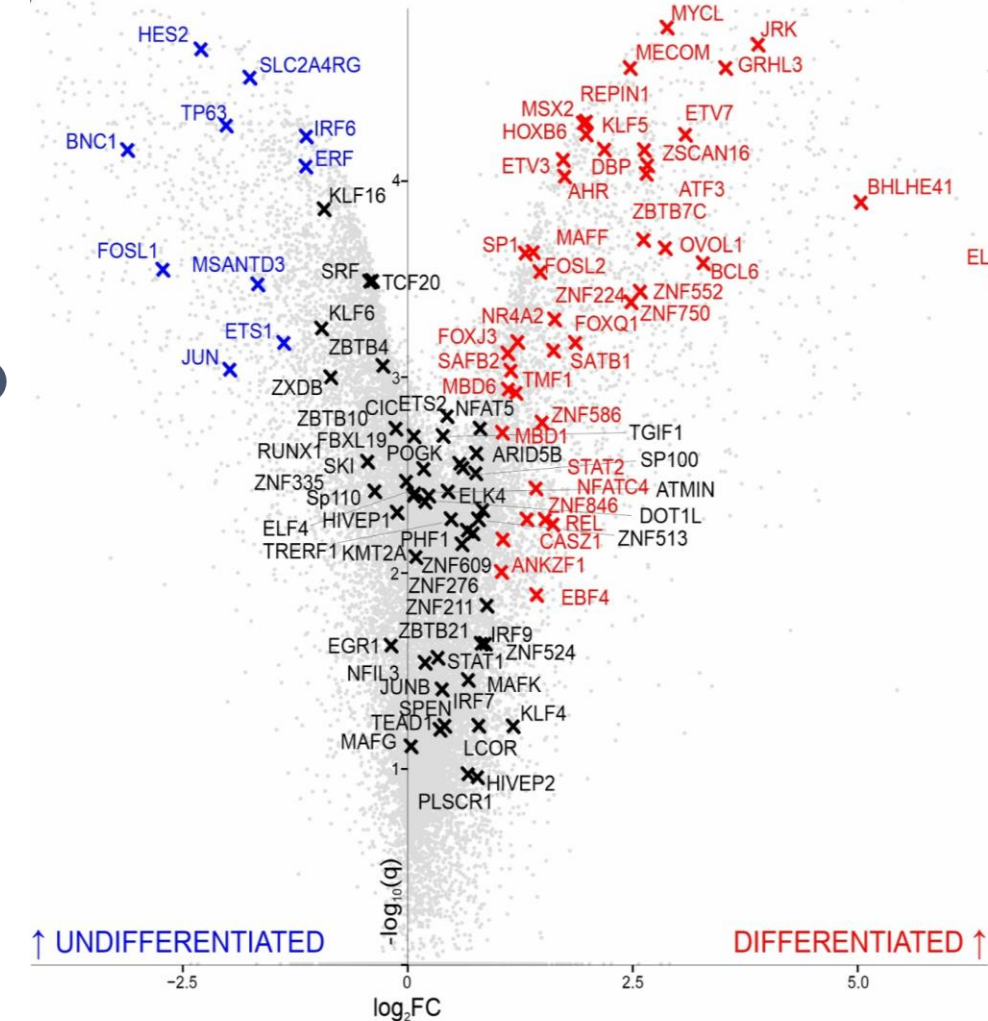
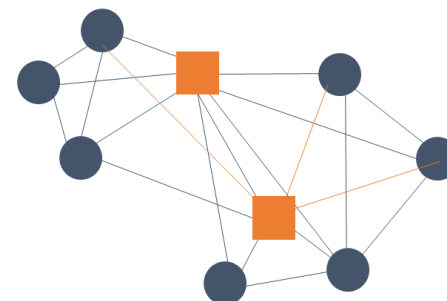
(1) Co-correlation network (Spearman rank)



(2) Selective edge pruning



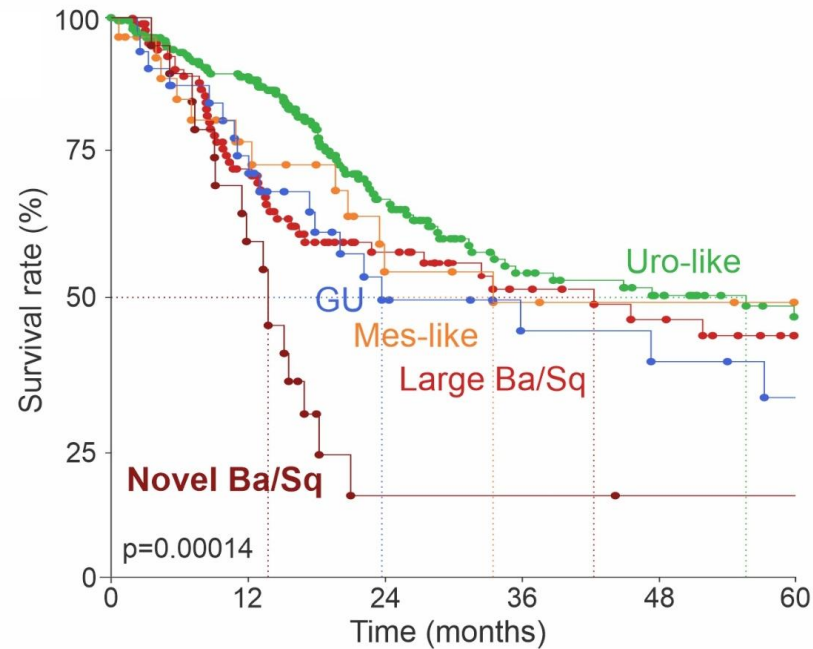
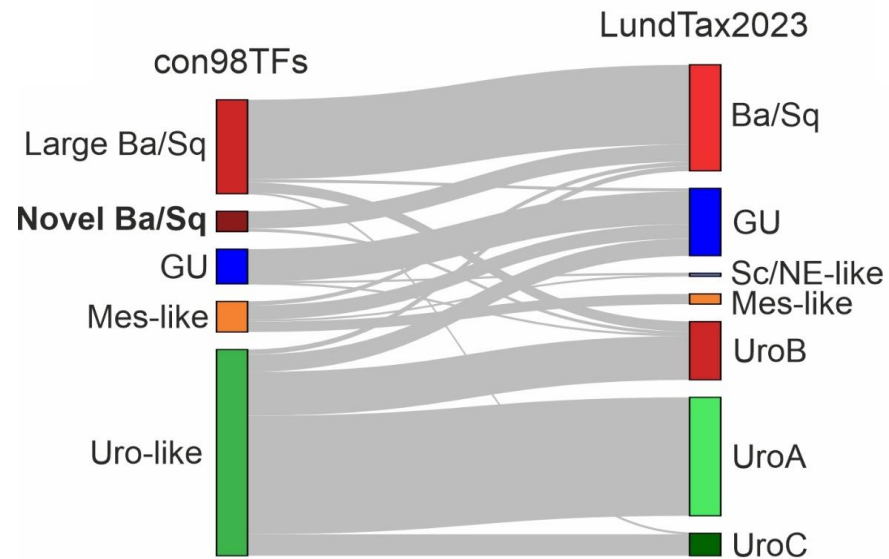
(3) Gene Prioritisation



A case study in this strategy (ii)

This approach allowed us to choose different genes to use as markers to stratify the cancers

This revealed a novel group of basal cancers with particularly bad survival

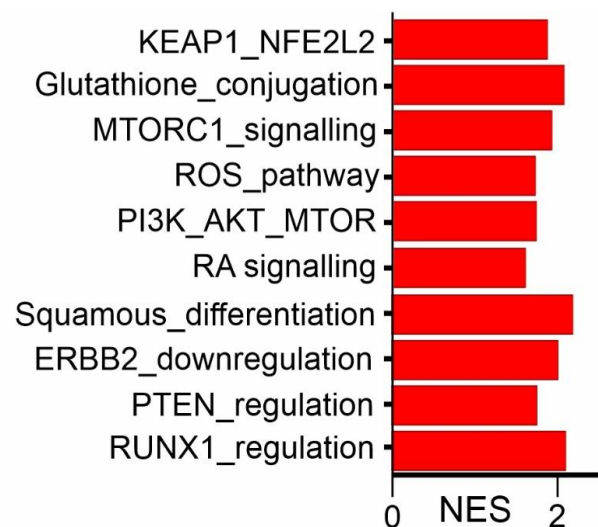


A case study in this strategy (iii)

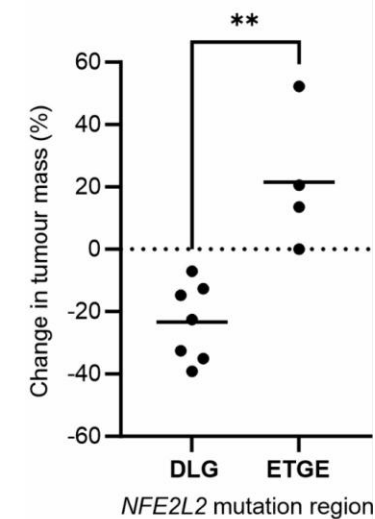
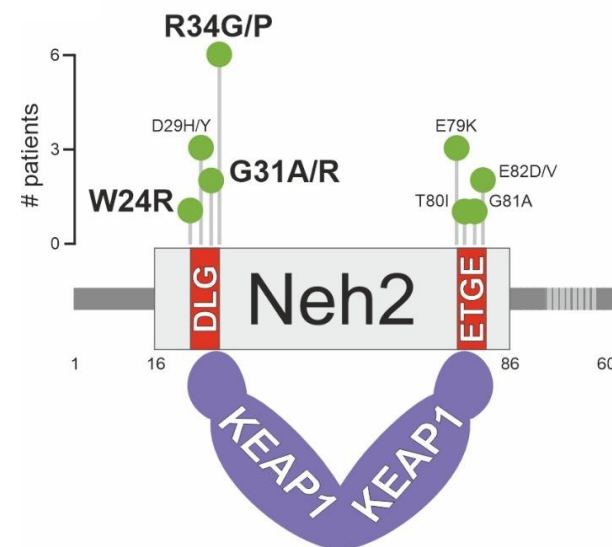
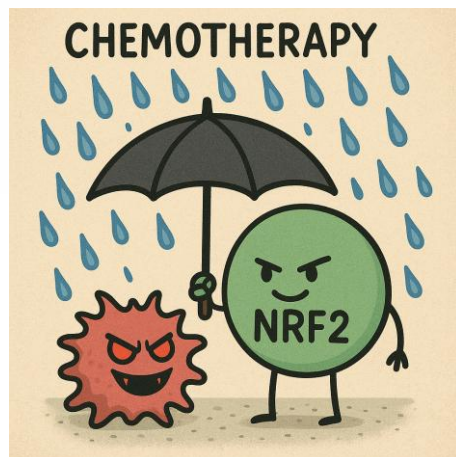
This approach allowed us to choose different genes to use as markers to stratify the cancers

This revealed a novel group of basal cancers with particularly bad survival

Novel group characterised by NRF2 overactivity – this is a druggable target in other cancers



Our work goes beyond a mutation-only classifier



If a single classification strategy is not practical, we need to keep asking biologically and clinically relevant questions to find groups of patients we can treat more effectively.

- END -

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