







Breast Journal Club, l'importanza della ricerca in oncologia – Napoli, 7 - 8 Marzo 2025

Liquid biopsy analysis with Al tools

Past is experience, present is experiment, future is expectation

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Conflict of Interest Disclosure Statement Last updated on 07.03.2025

Stock and Other Ownership Interests: None

Honoraria: None

Pfizer, Merck Sharp & Dohme, Menarini Stemline, Abbvie

Expert Testimony: None

Research Funding: None

Patents, Royalties, Other Intellectual Property: None

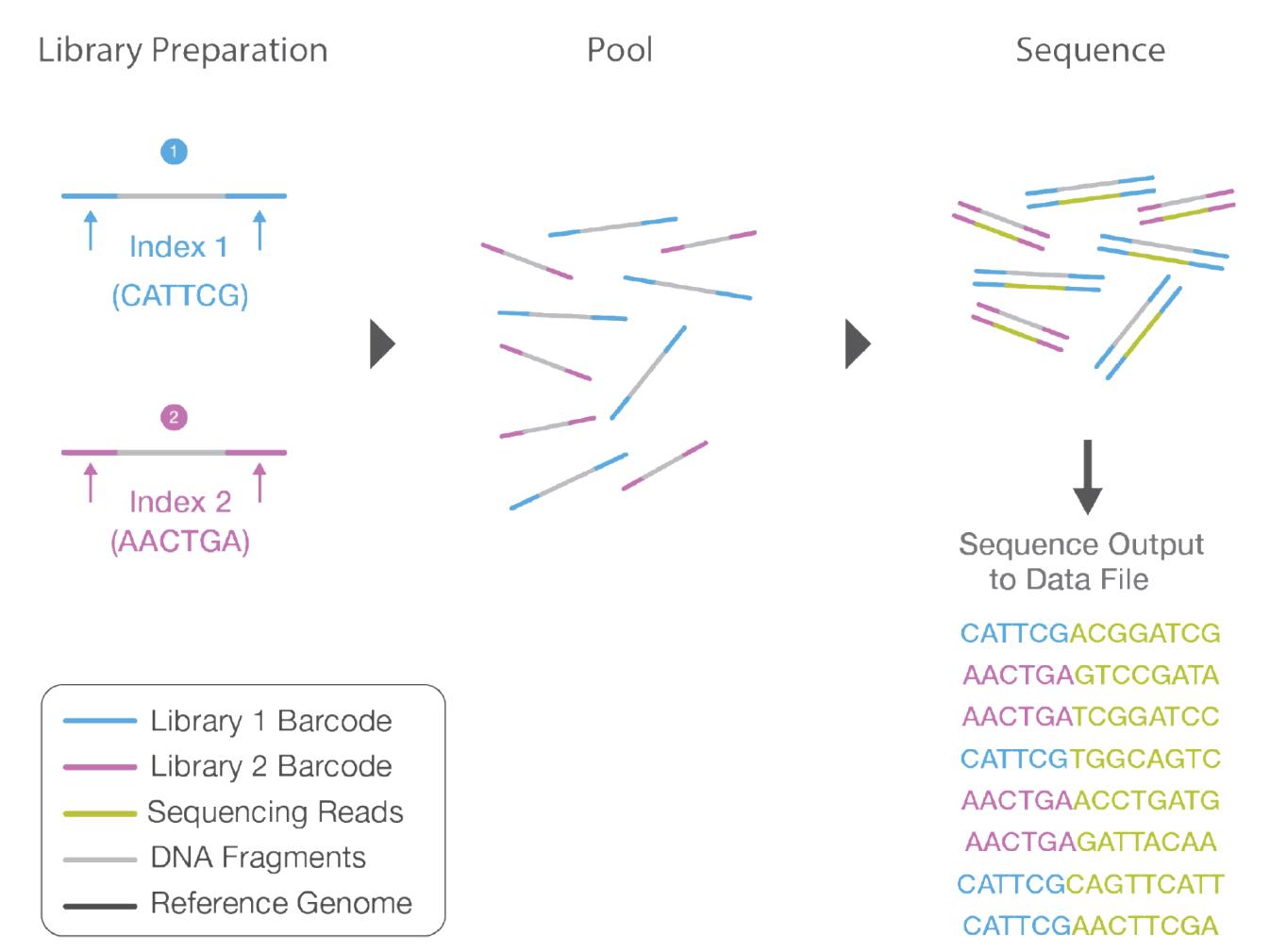
Travel Expenses: Menarini Stemline, Novartis, Gilead

Consulting or Advisory Role: AstraZeneca, Daiichi Sankyo, Eli Lilly, GlaxoSmithKline, Incyte, Novartis,



Al likes to look for patterns in science and life

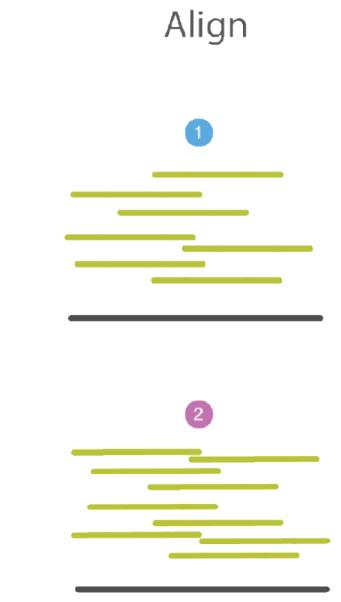
Al likes to look for patterns in science and life The extreme amount of data generated from NGS



Demultiplex

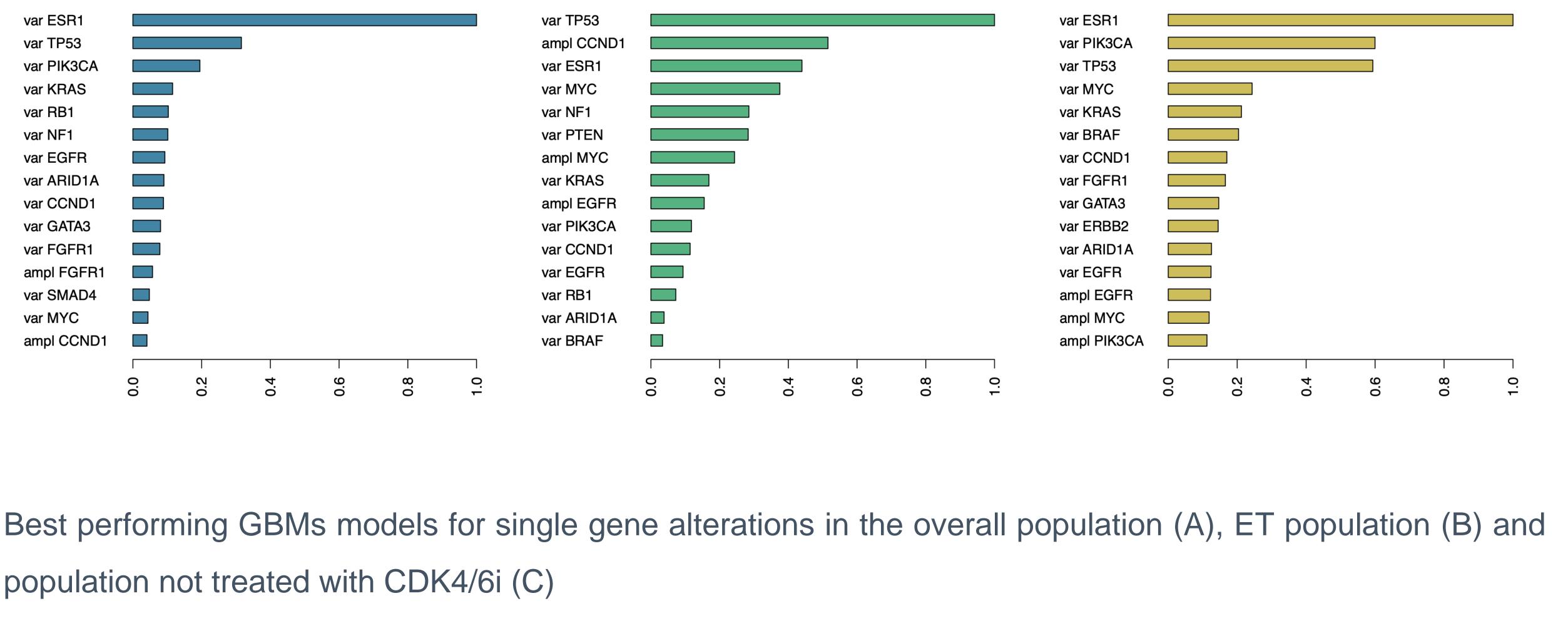
CATTCGACGGATCG CATTCGTGGCAGTC CATTCGCAGTTCATT CATTCGAACTTCGA

AACTGAGTCCGATA AACTGATCGGATCC AACTGAACCTGATG AACTGAGATTACAA



Al likes to look for patterns in science and life

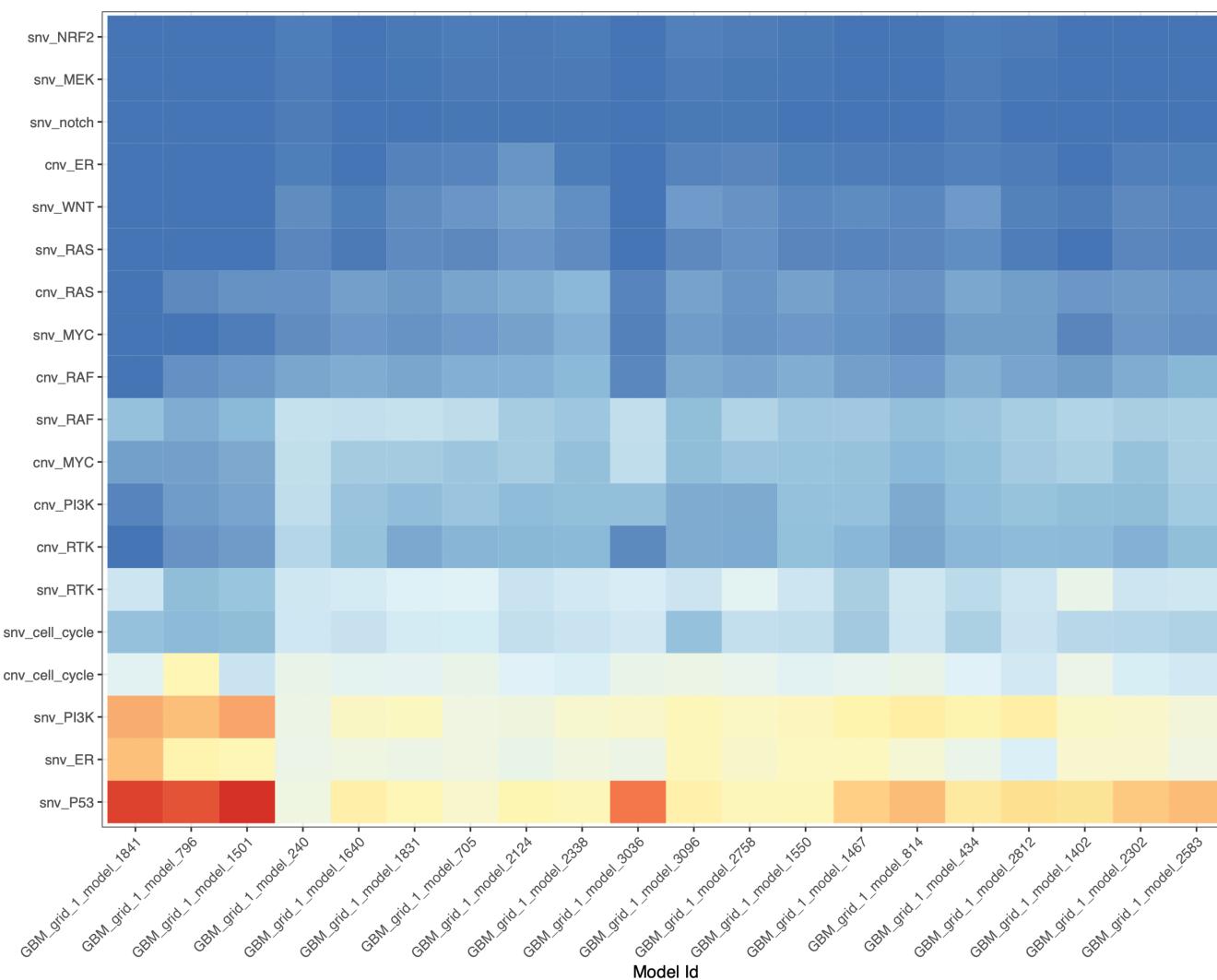
Model training for single gene alterations



population not treated with CDK4/6i (C)

Gerratana L, Reduzzi C, Davis AA, et al. *J Clin Oncol*, 2022; doi:10.1200/JCO.2022.40.16_suppl.3055

Al likes to look for patterns in science and life Top performing GBM models in the endocrine treated population



Feature

0.2

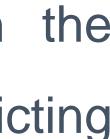
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Top performing GBM models in the endocrine treated population predicting previous exposure to CDK4/6i

The highest RI was observed for P53 SNVs, PI3K SNVs, ER SNVs, Cell Cycle CNVs and RTK SNVs

Gerratana L, Reduzzi C, Davis AA, et al. J Clin Oncol, 2022; doi:10.1200/JCO.2022.40.16_suppl.3055





Al likes to look for patterns in science and life Top performing GBM models in the endocrine treated population

OAGULATION APOPTOSIS RESPONSE Y537S_Veh-WT_Veh D538G_Veh-WT_Veh Y537S_Palbo-WT_Palbo D538G_Palbo-WT_Palbo Y537S_Palbo_and_E2-WT_Palbo_and_E2 D538G_Palbo_and_E2-WT_Palbo_and_E2 Y537S_Palbo_and_Fulv-WT_Palbo_and_Fulv D538G_Palbo_and_Fulv-WT_Palbo_and_Fulv



EPIT

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COMPLEMEN

ANDROGEN

APIC.

ESTROGEN

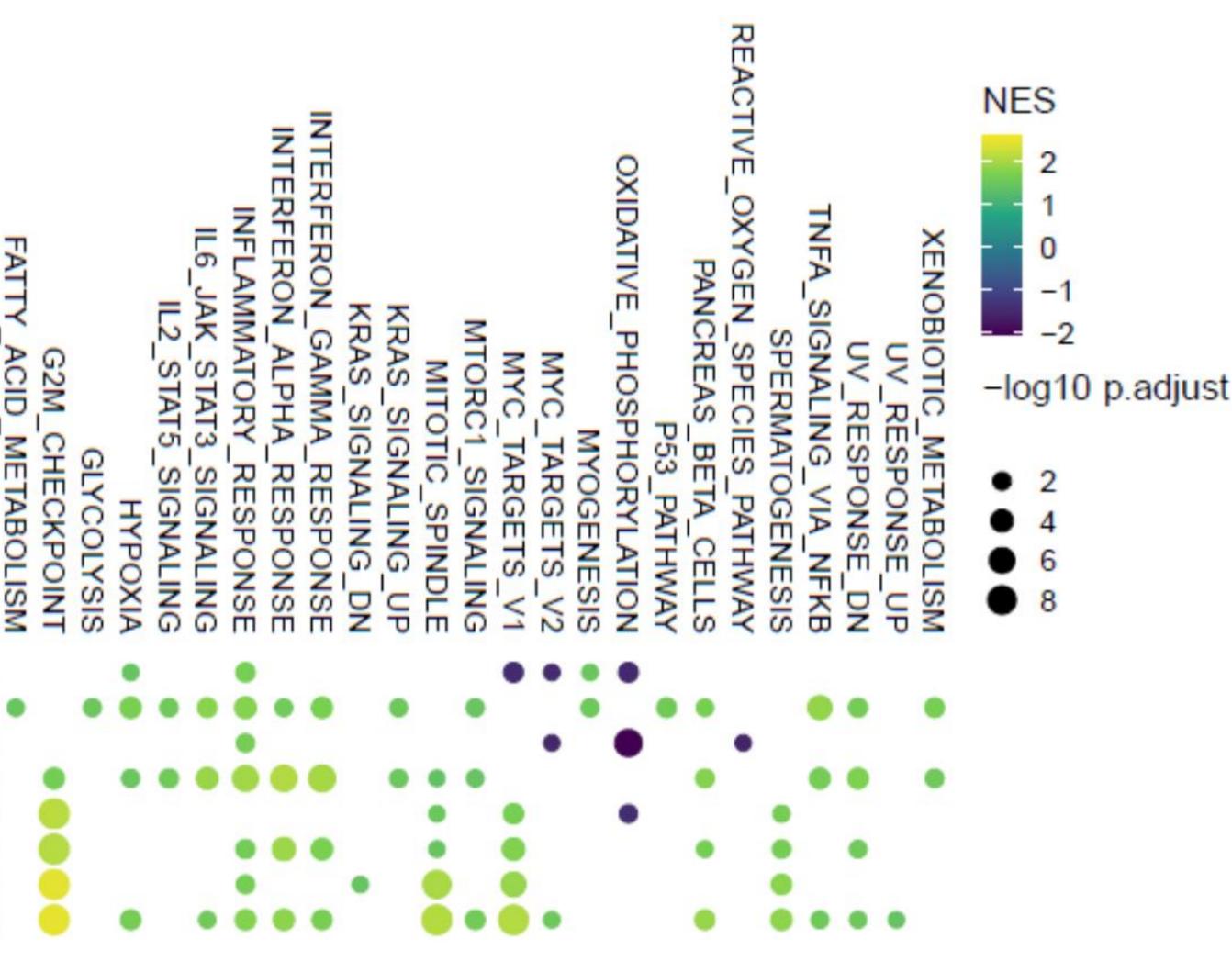
ONSE

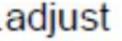
EARL

FRANSITION

S

TROGE

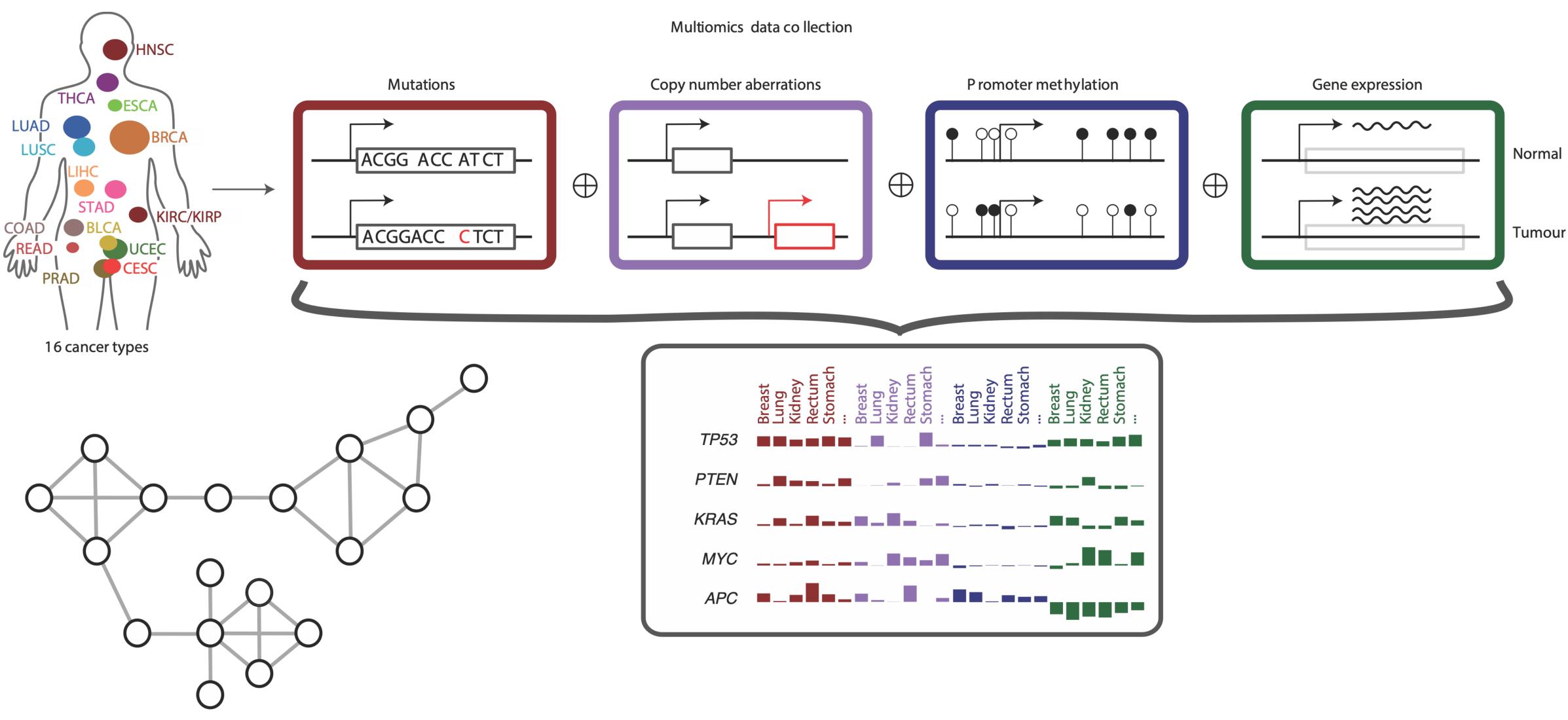




A step further: neural networks

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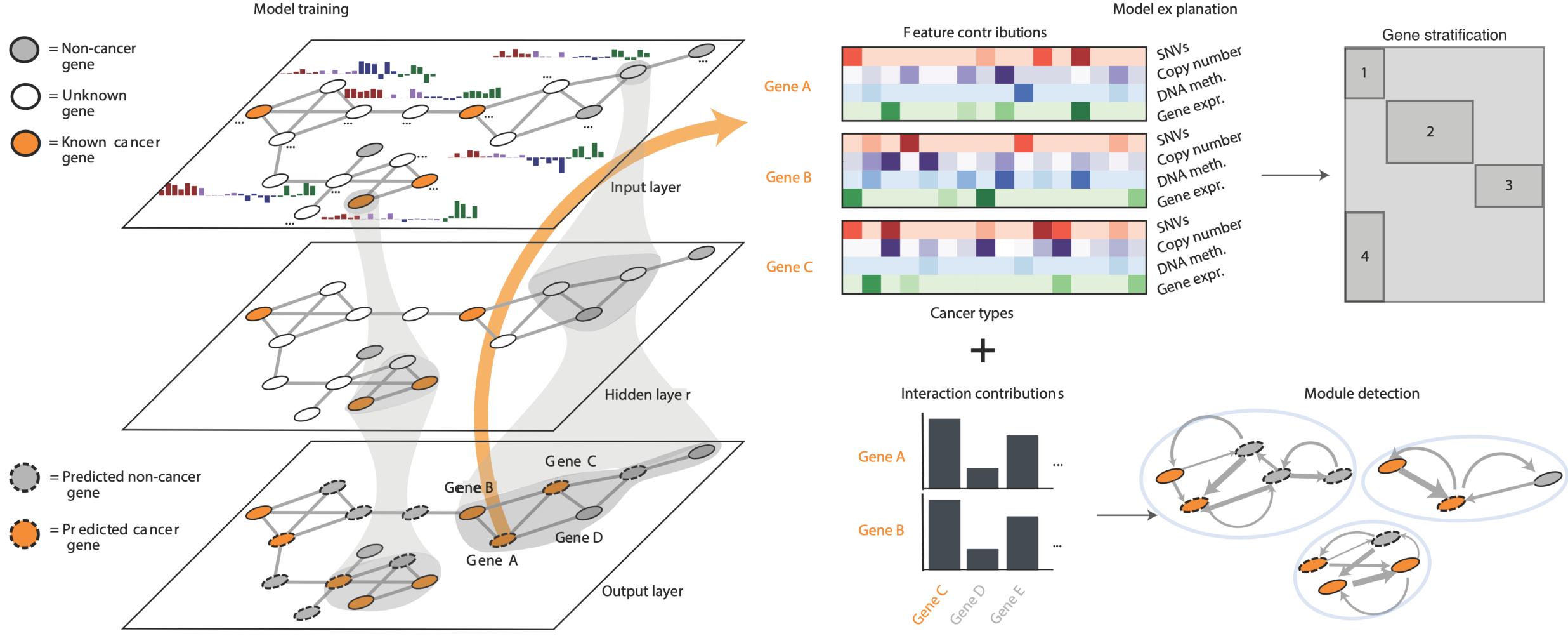
Integrate multiple omics to discover new cancer genes



Protein-protein interactions

A step further: neural networks

Integrate multiple omics to discover new cancer genes

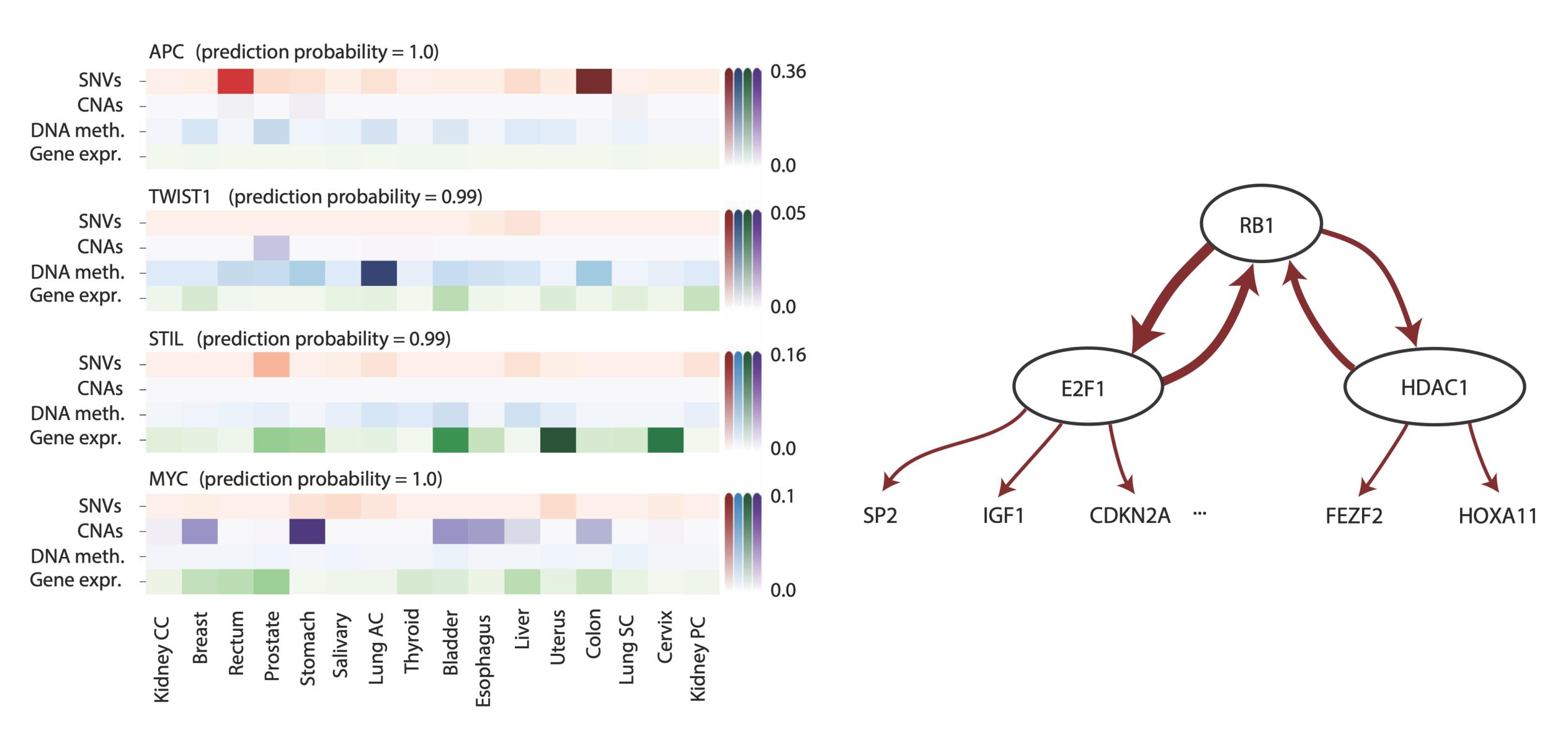


Schulte-Sasse R, Budach S, Hnisz D, Marsico A. Nat Mach Intell, 2021; doi:10.1038/s42256-021-00325-y





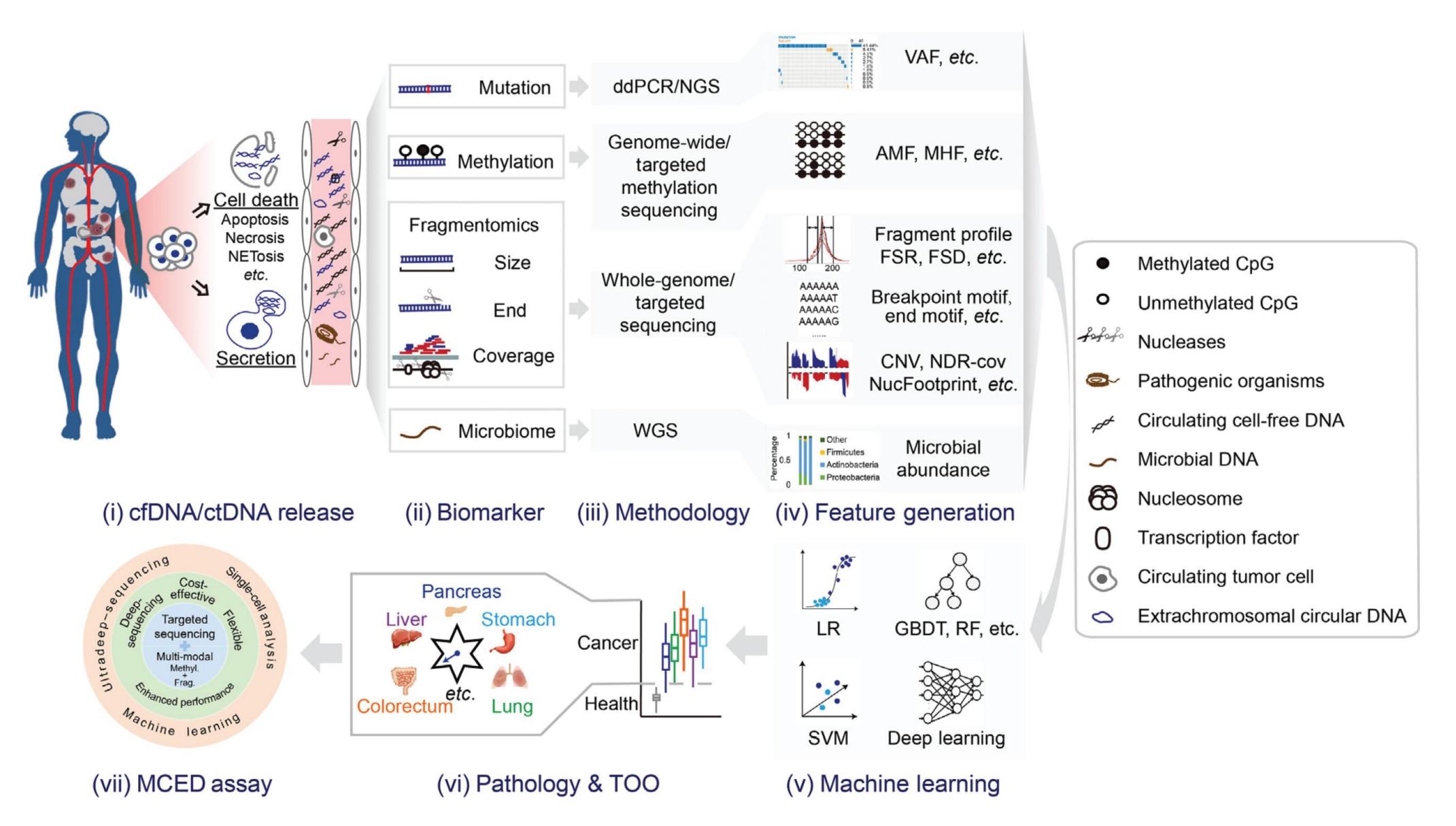
Integrate multiple omics to discover new cancer genes The ground-proof



Schulte-Sasse R, Budach S, Hnisz D, Marsico A. Nat Mach Intell, 2021; doi:10.1038/s42256-021-00325-y

Fragmentomics: following the trail of crumbs

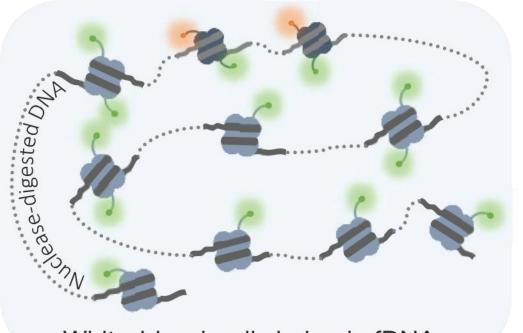
Fragmentomics: following the trail of crumbs What's in our liquid-biopsy toolchain?



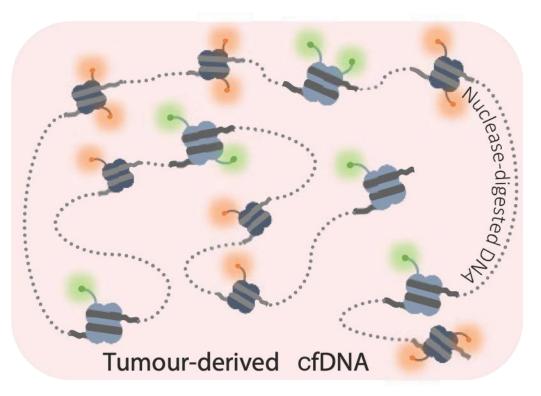


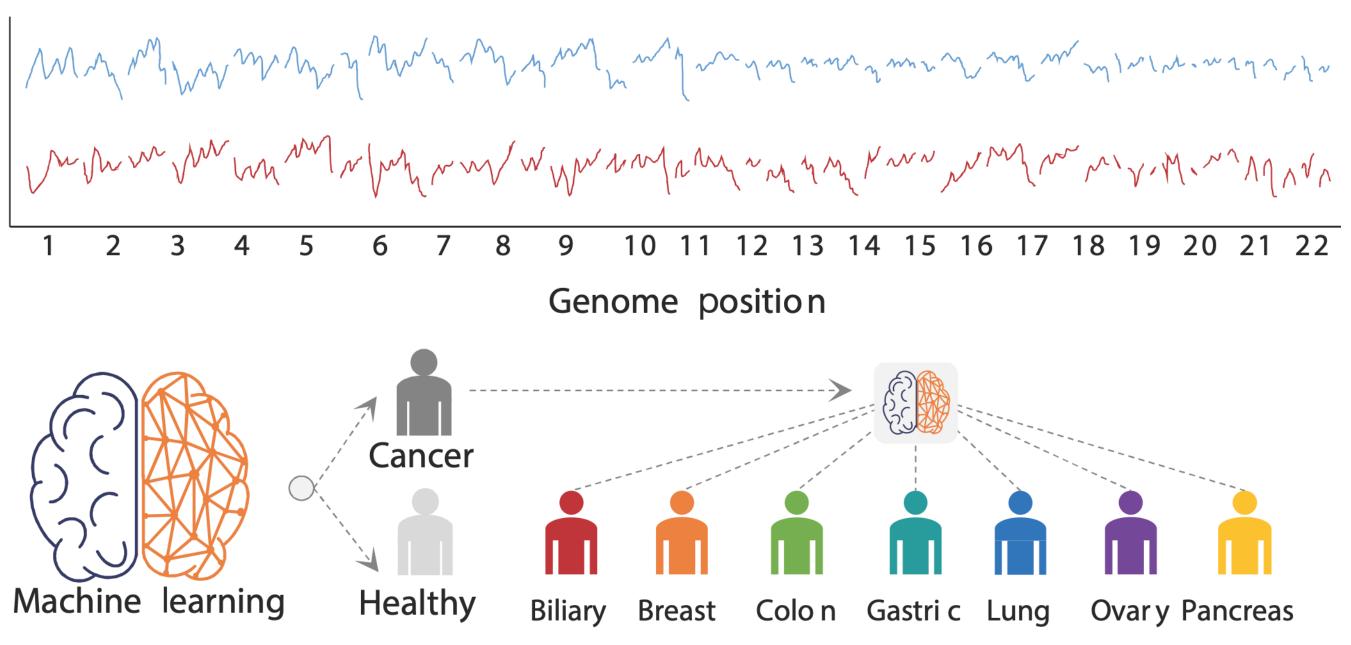
Genome-wide cfDNA fragmentation DELFI: DNA evaluation of fragments for early interception

Noninvasive cancer screening (DELFI)



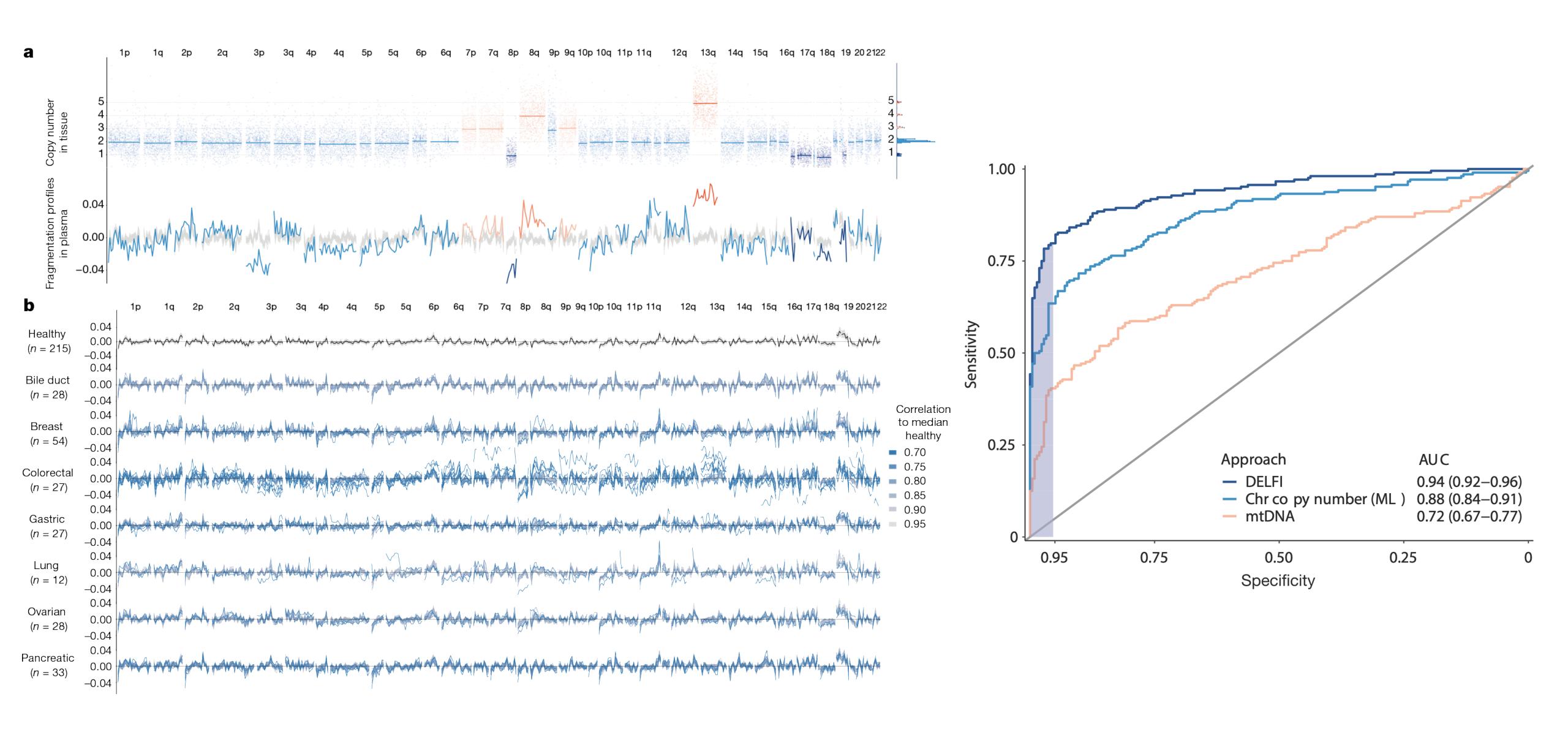
White-blood-cell-derived cfDNA





Cristiano S, Leal A, Phallen J, et al. Nature, 2019; doi:10.1038/s41586-019-1272-6

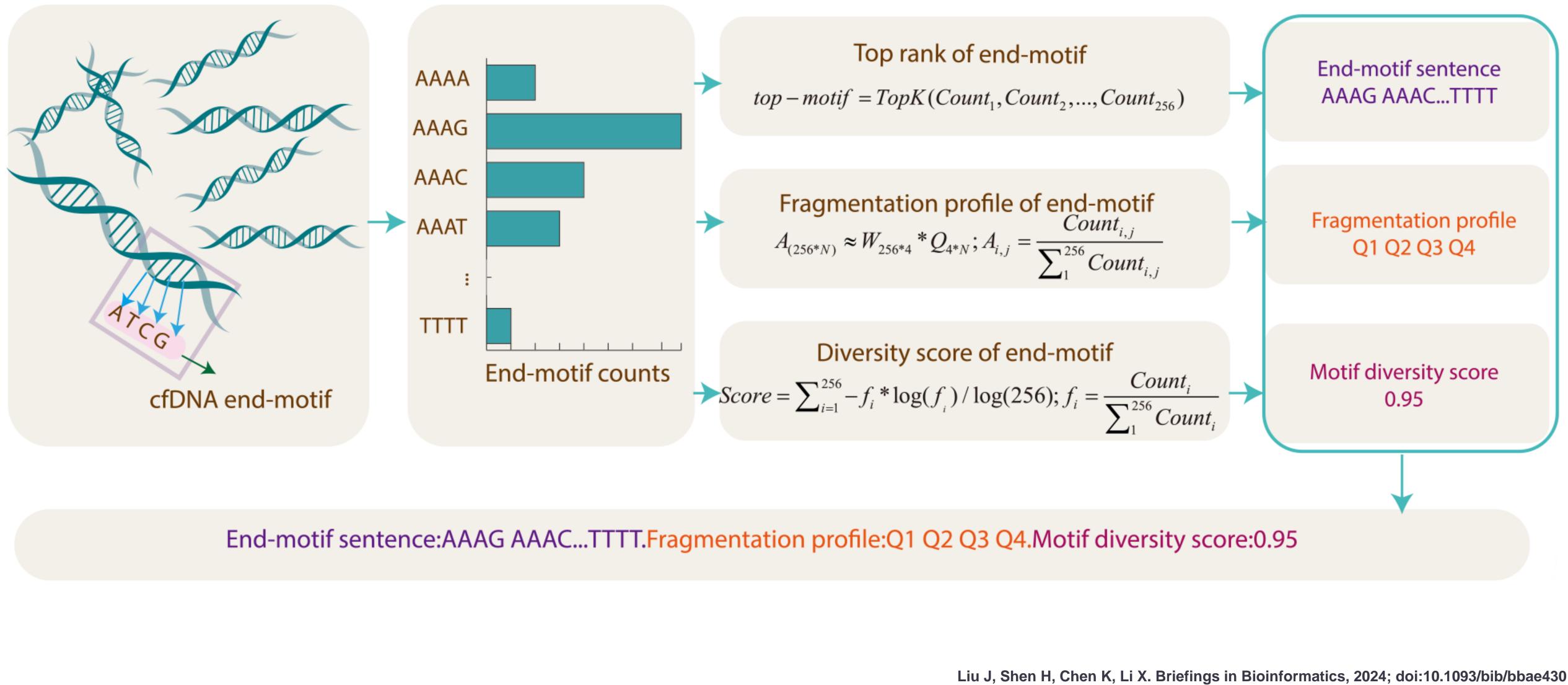
Genome-wide cfDNA fragmentation cfDNA fragmentation profiles in healthy individuals and patients with cancer



The next level: DNA is the language of life, after all

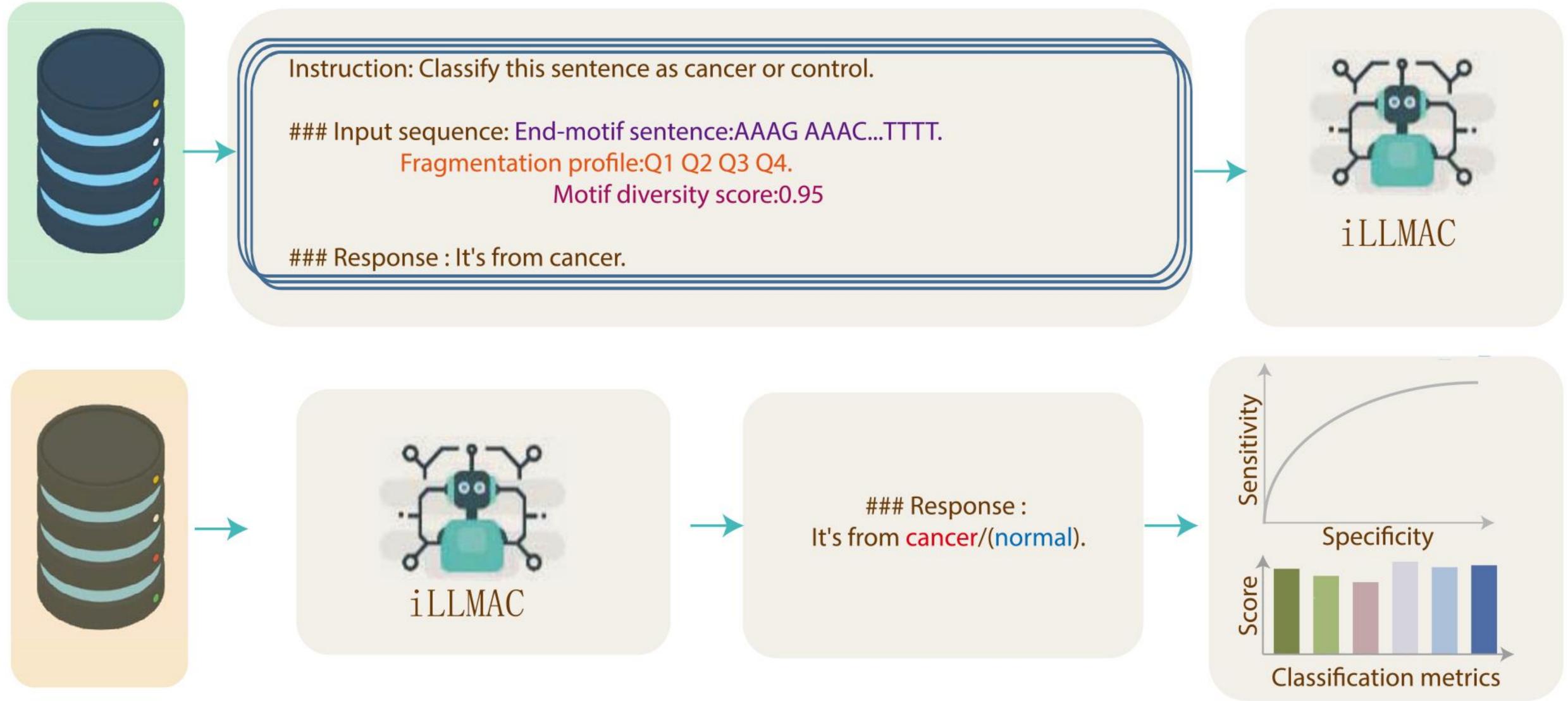


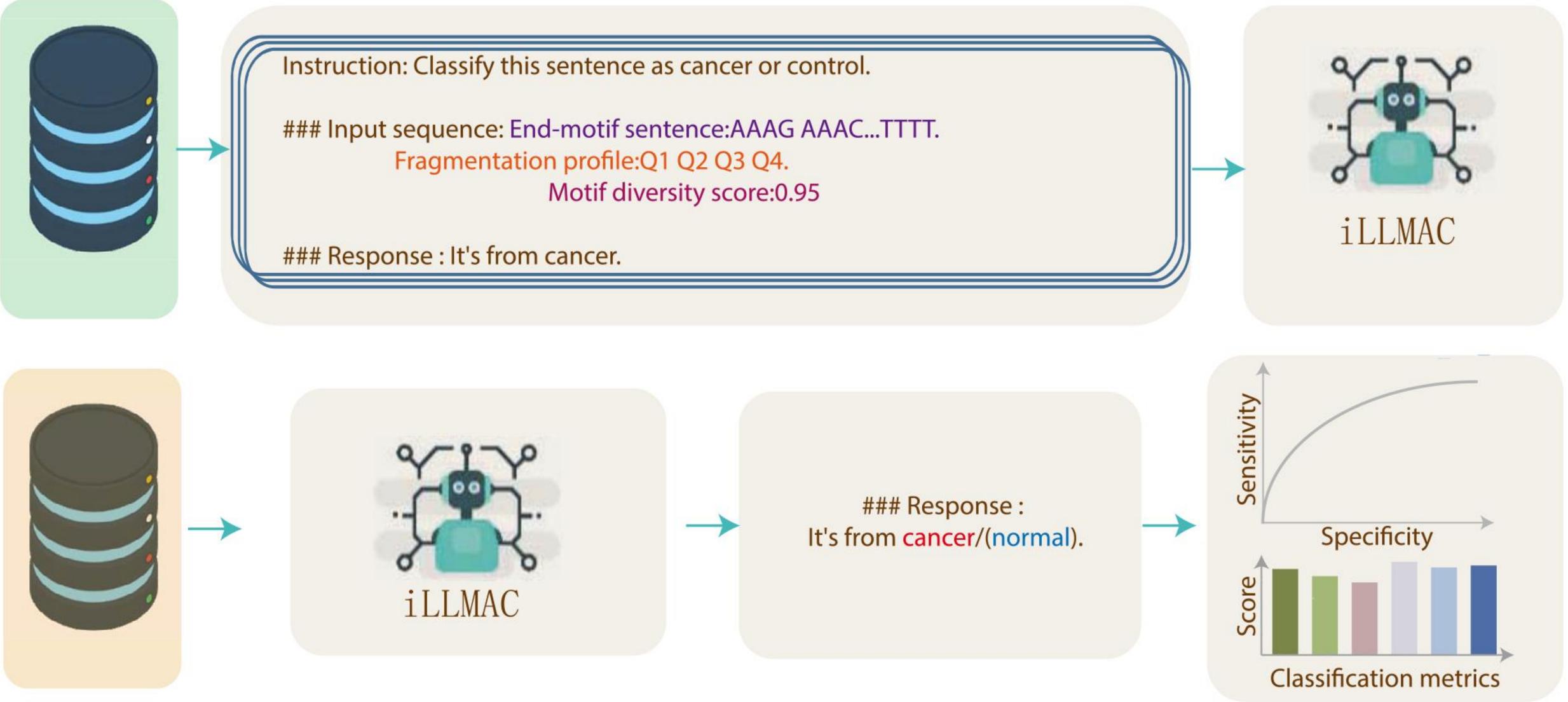
The next level: DNA is the language of life, after all Large language models and end-motif profiles for cancer detection



The next level: DNA is the language of life, after all

Instruction tuning LLM and inference for cancer detection

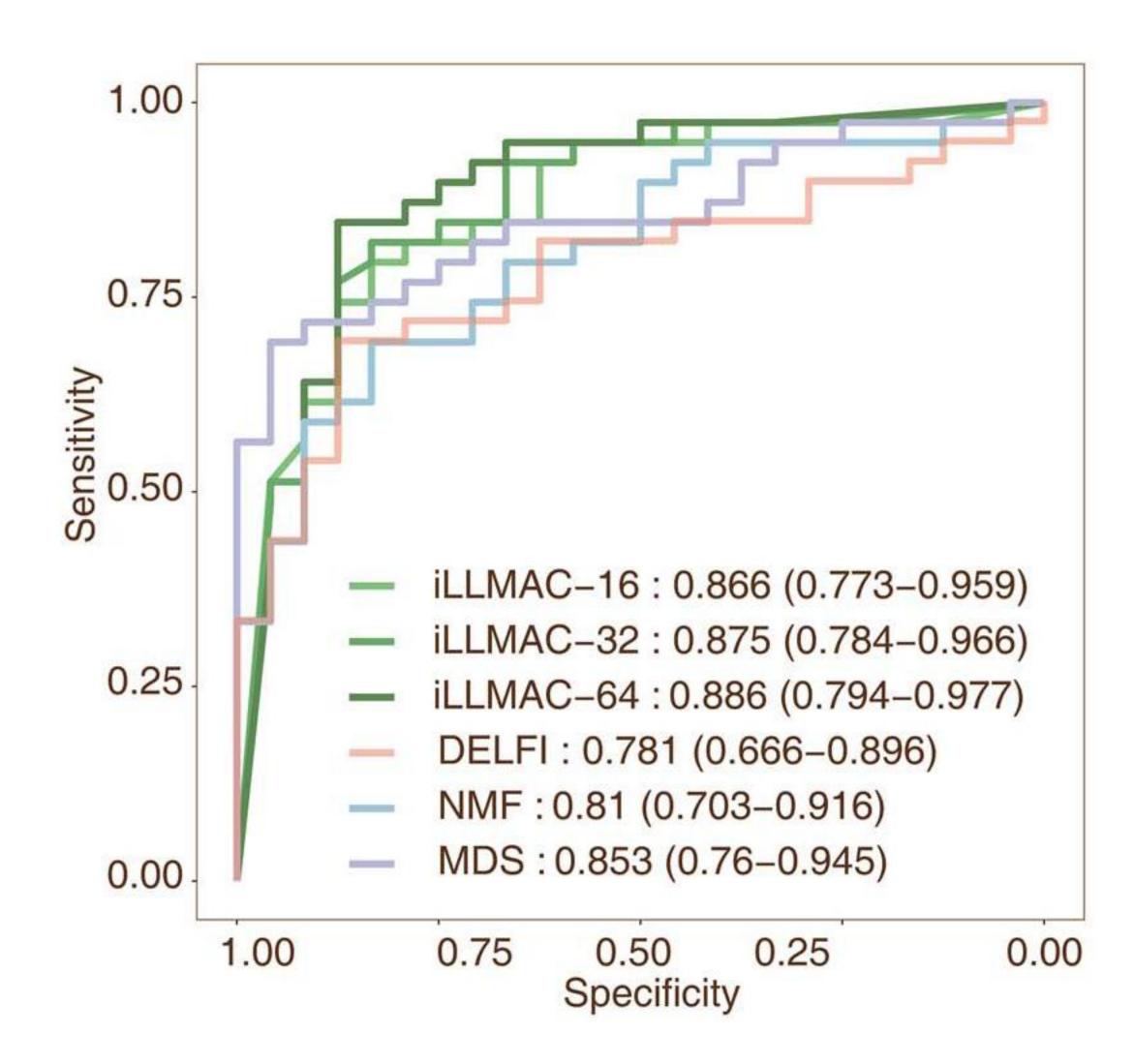


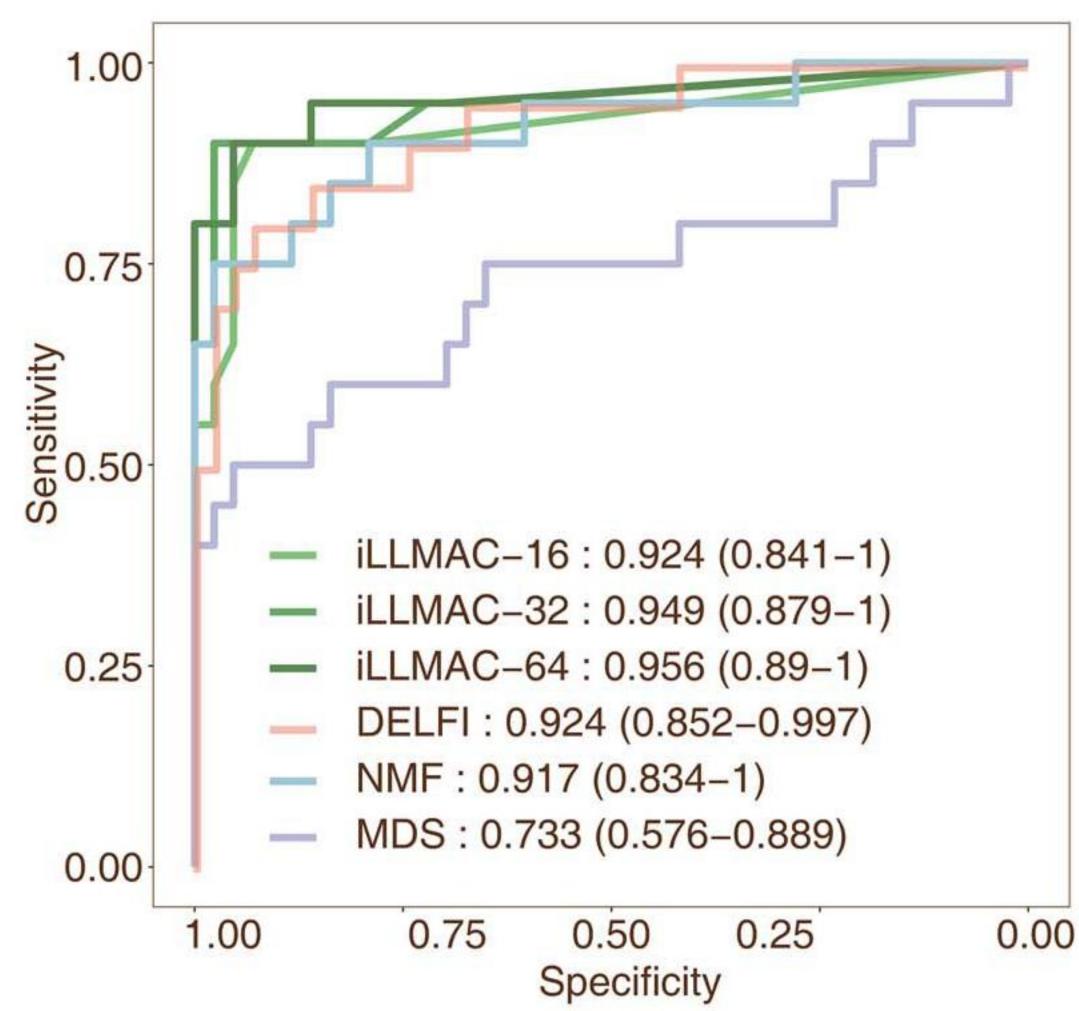


Liu J, Shen H, Chen K, Li X. Briefings in Bioinformatics, 2024; doi:10.1093/bib/bbae430

The next level: DNA is the language of life, after all

Different number of end-motifs and benchmarked baseline methods in the diagnosis of cancer





Liu J, Shen H, Chen K, Li X. Briefings in Bioinformatics, 2024; doi:10.1093/bib/bbae430

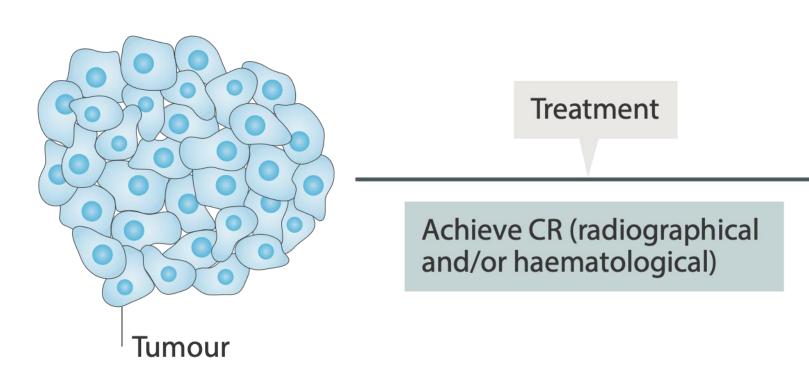


Is it just about research and a future far away?



Is it just about research and a future far away?

Targeting what you cannot see: Minimal residual disease and treatment intensity

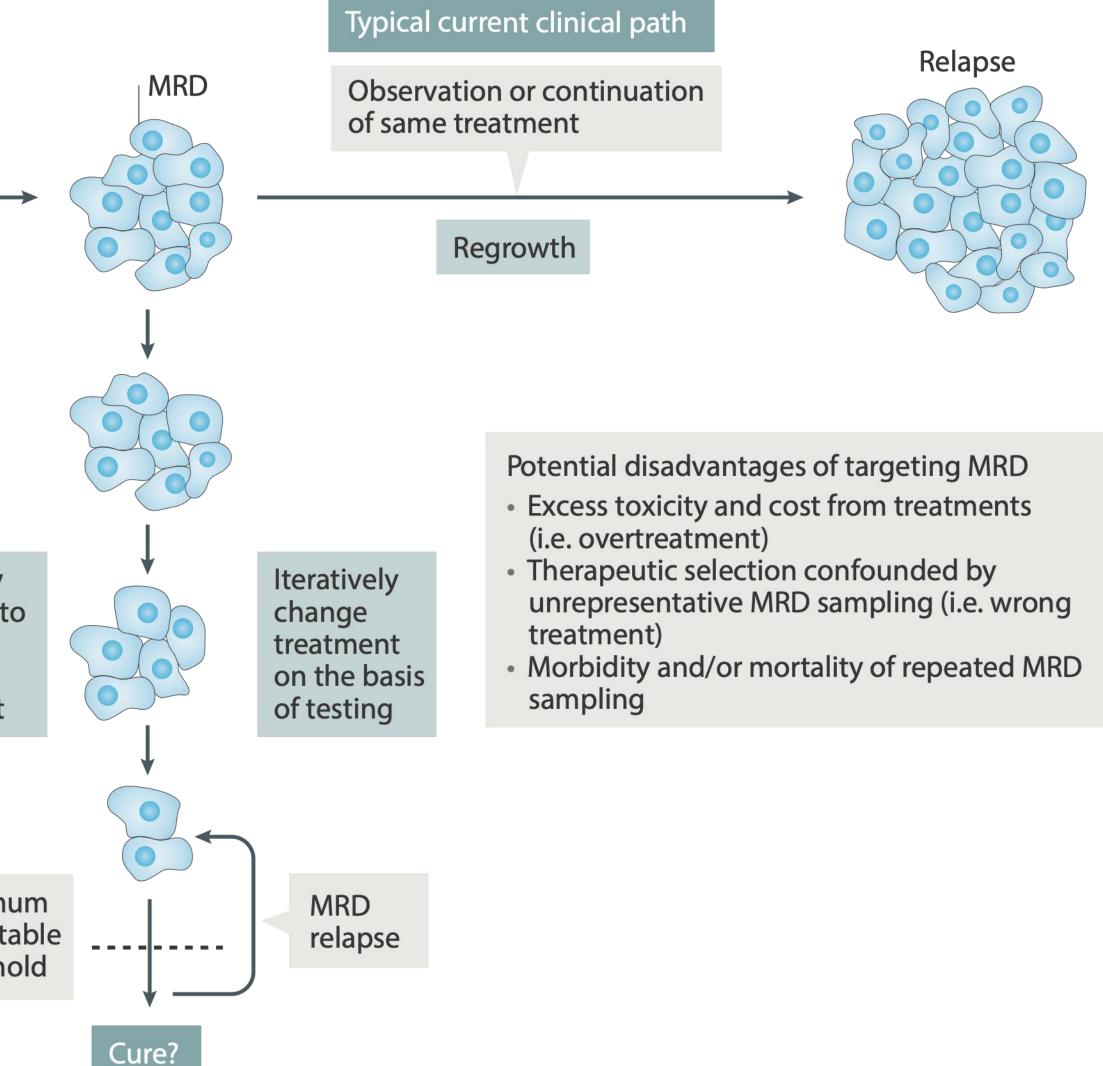


Potential advantages of targeting MRD

- Less clonal complexity
- Loss of chemoprotective microenvironment
- Improved patient performance status
- Enrichment of cancer stem cells tested for functional responses
- Fewer cells to cure

Iteratively test MRD to identify effective treatment

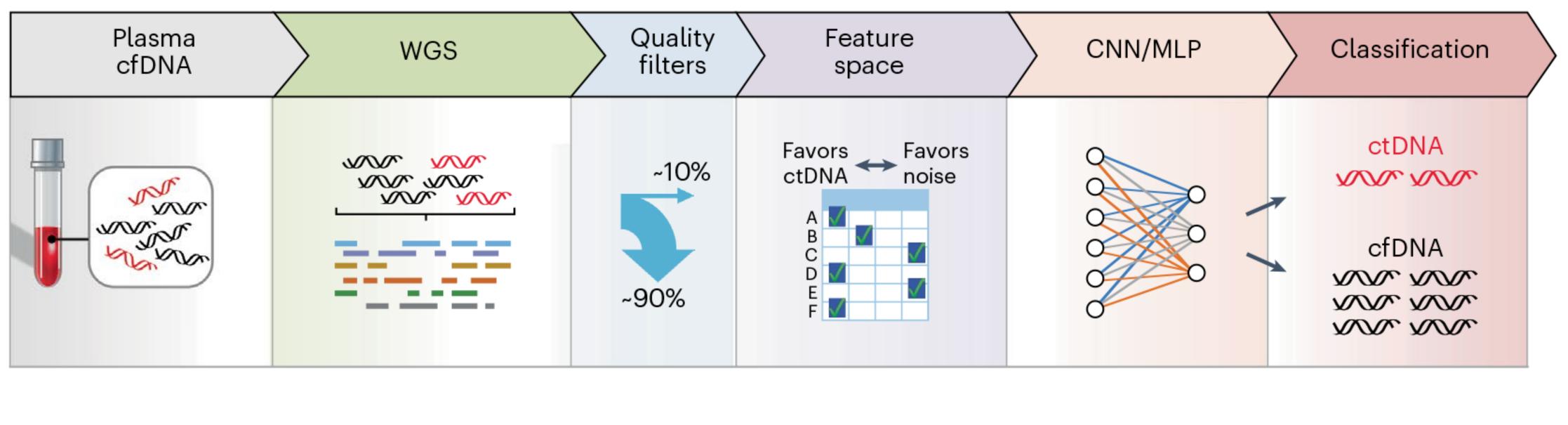
> Minimum detectable threshold

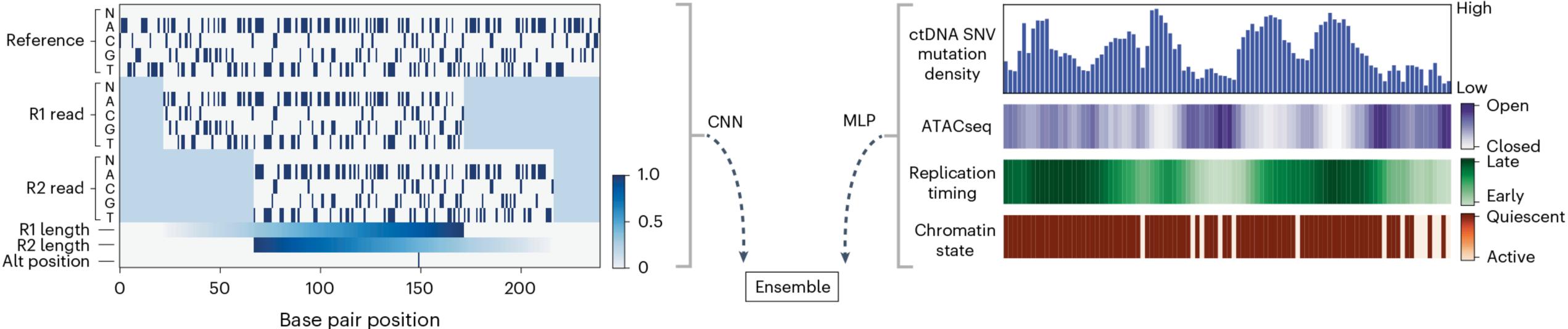




Is it just about research and a future far away?

The sound of noise: the deeper you go the higher it gets

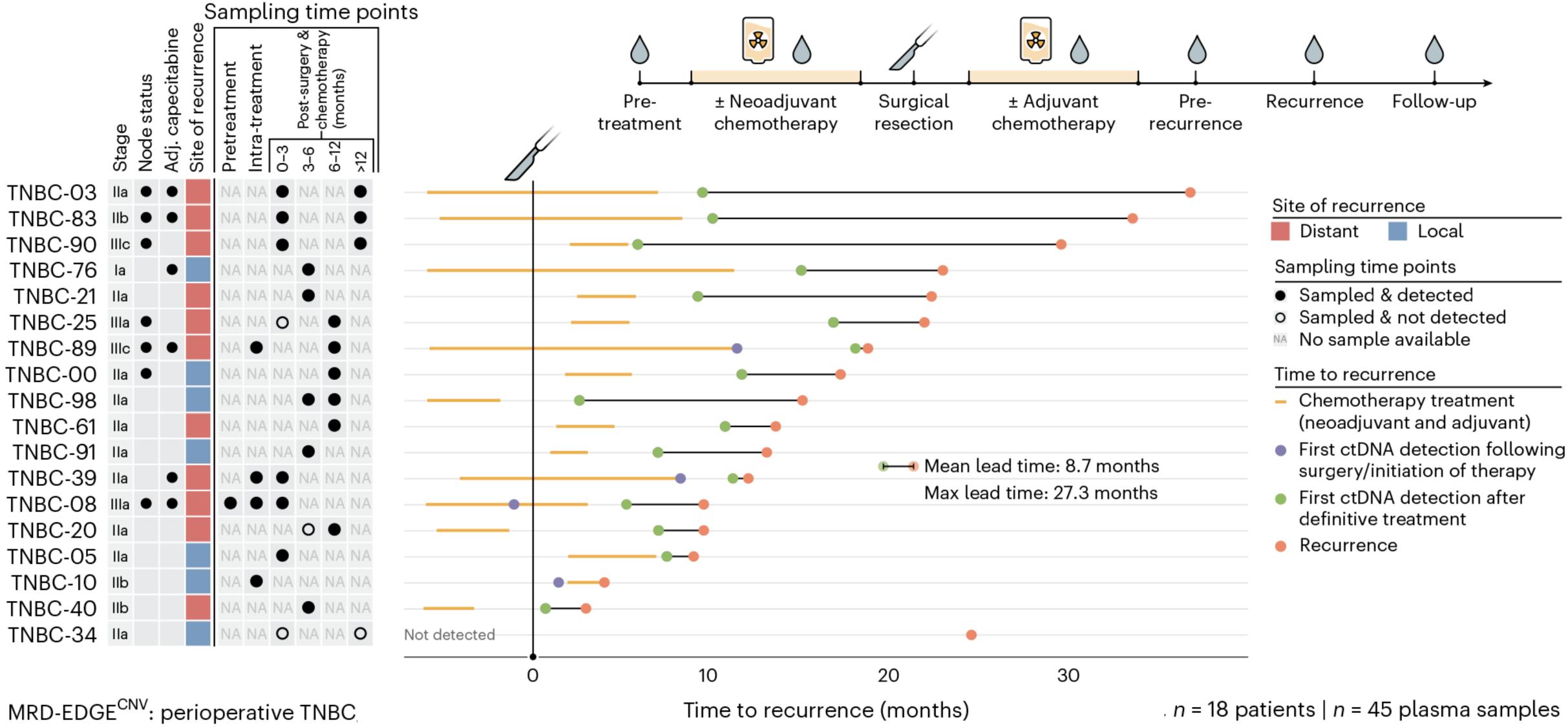




Widman AJ, Shah M, Frydendahl A, et al. Nat Med, 2024; doi:10.1038/s41591-024-03040-4

The power of a classifier of classifiers

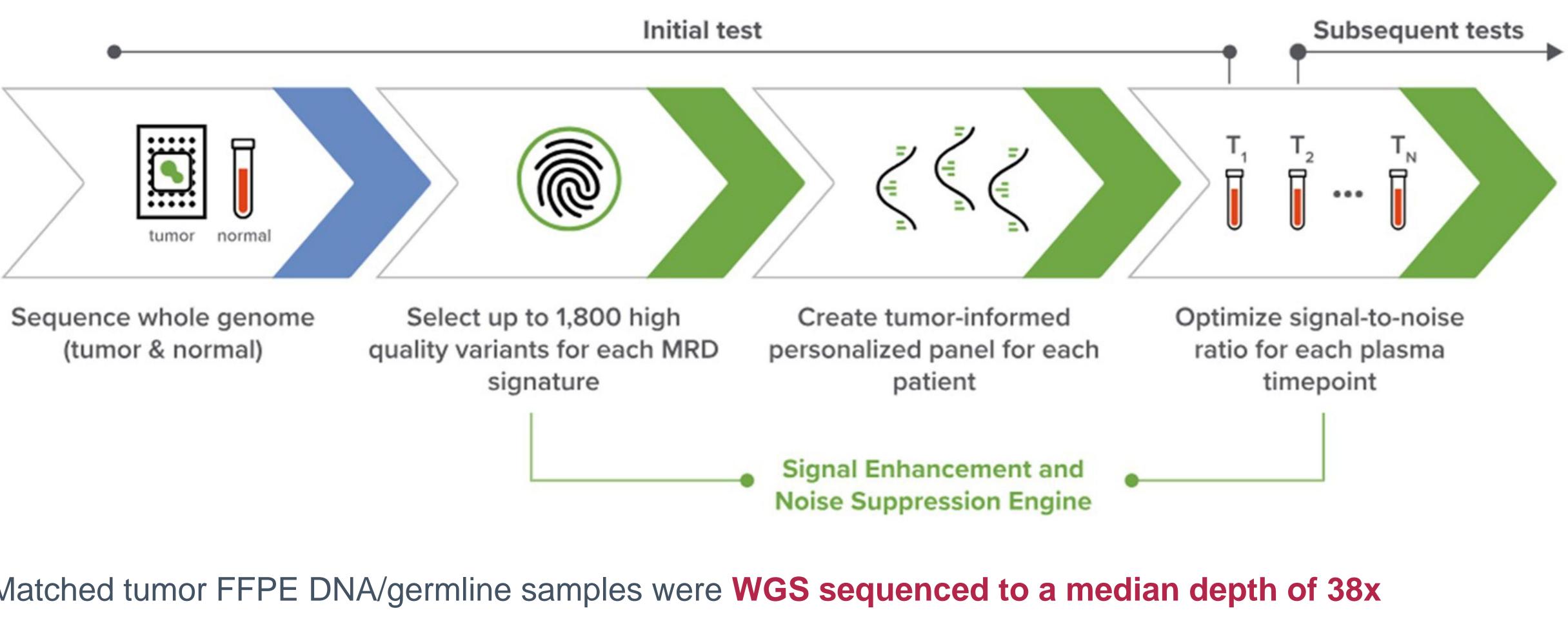
A multi-cancer early detection model based on liquid biopsy of multi-omics biomarkers



Widman AJ, Shah M, Frydendahl A, et al. Nat Med, 2024; doi:10.1038/s41591-024-03040-4

Al denoising in an assay near you

Increase sensitivity to enhance detection



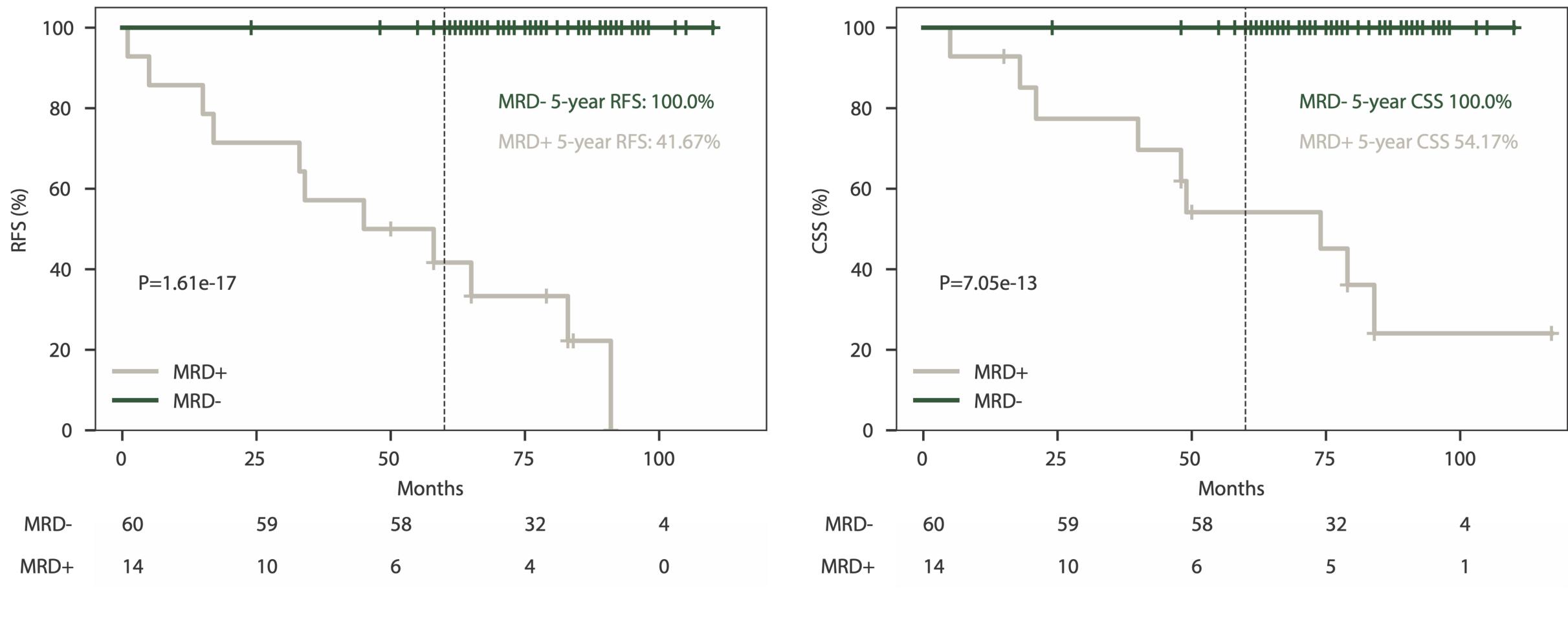
Matched tumor FFPE DNA/germline samples were WGS sequenced to a median depth of 38x cfDNA was extracted from a median volume of 3.3 ml of plasma (range 1-4.8 ml) and panels designed contained a median of 1421 variants/panel (range 706-1,934/panel)

Garcia-Murillas I, Abbott CW, Cutts RJ, et al. Annals of Oncology, 2025; doi:10.1016/j.annonc.2025.01.021



Al denoising in an assay near you

The added value: longitudinal monitoring



Median Lead Time 15 months (range 4-41 months) over clinical relapse

Garcia-Murillas I, Abbott CW, Cutts RJ, et al. Annals of Oncology, 2025; doi:10.1016/j.annonc.2025.01.021

Wrapping up

Use your experience in your experiments to achieve your expectations



Artificial intelligence has a great potential in Medical Oncology



Machine learning as a support for interpreting multi-parameter datasets



And we are just scraping the surface

Al's capability to detect patterns can be of pivotal importance to assist Big data Filtering and enhancing tool will be the cornerstone of highly complex diagnostic technologies

High throughput technologies generate a high quantity of data that are not readily interpretable Latent patterns can be used to generate new hypothesis and assist clinical trial design

ctDNA is not just about mutations, epigenetics and fragmentomics are complementary biomarkers New downstream analyses for CTCs (e.g. RNAseq, WGS) will unlock a even higher amount of data















Doy angles

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