

Precision medicine for patients with breast cancer

Fabrice ANDRE

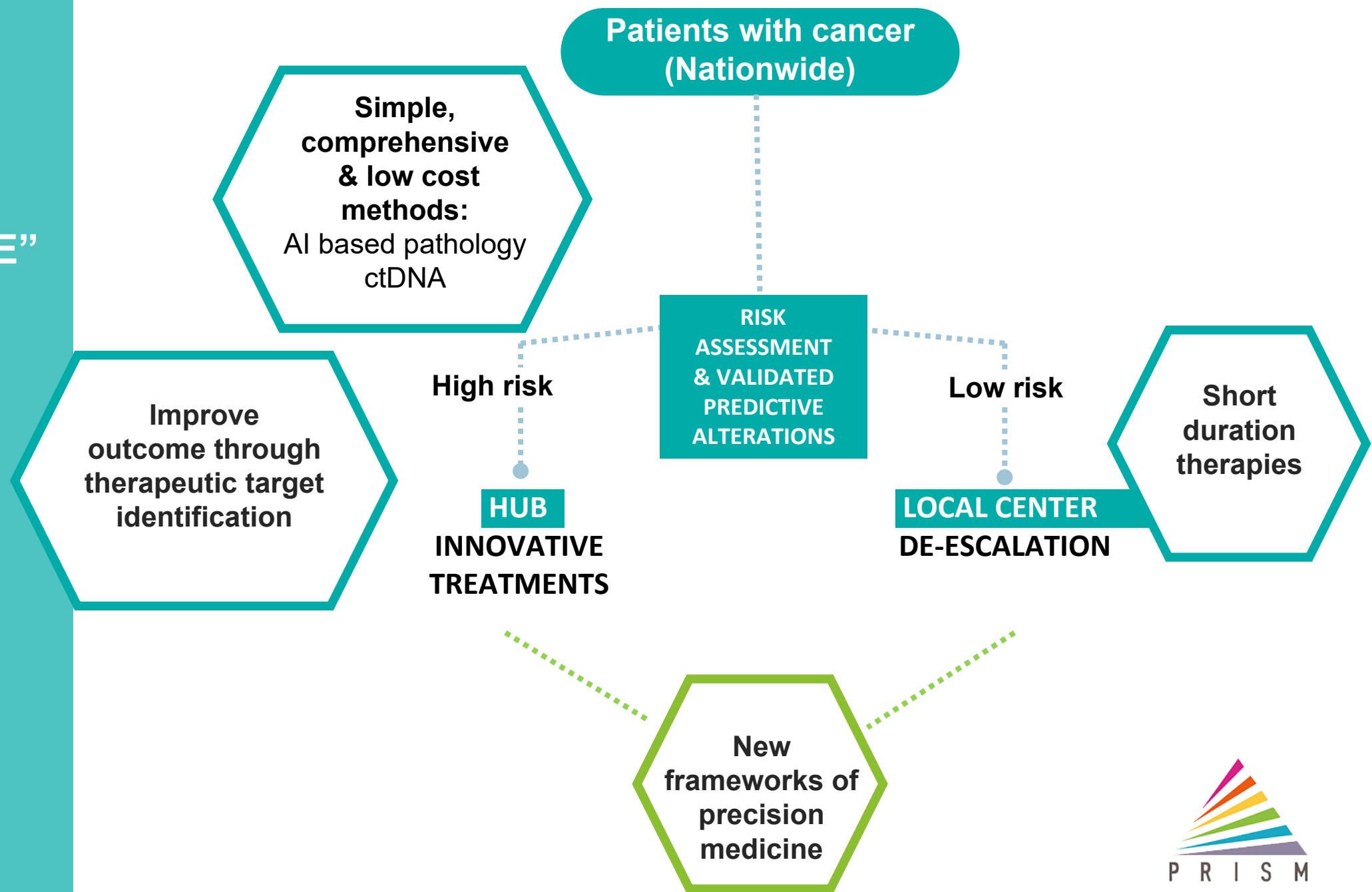
COI

- Pr Fabrice ANDRE:
 - Research funding to the institution and advisory boards / speaker (compensated to the hospital) from AstraZeneca, Lilly, Novartis, Pfizer, Daiichi-Sankyo, Relay Tx and Roche.
 - Advisory board compensate to FA: Lilly, Galapagos
- !!!! : FA is inventor of the patent on pathology assisted by AI mentioned in one slide, FR is founder of Resilience, FRESH is a public private partnership that includes GR

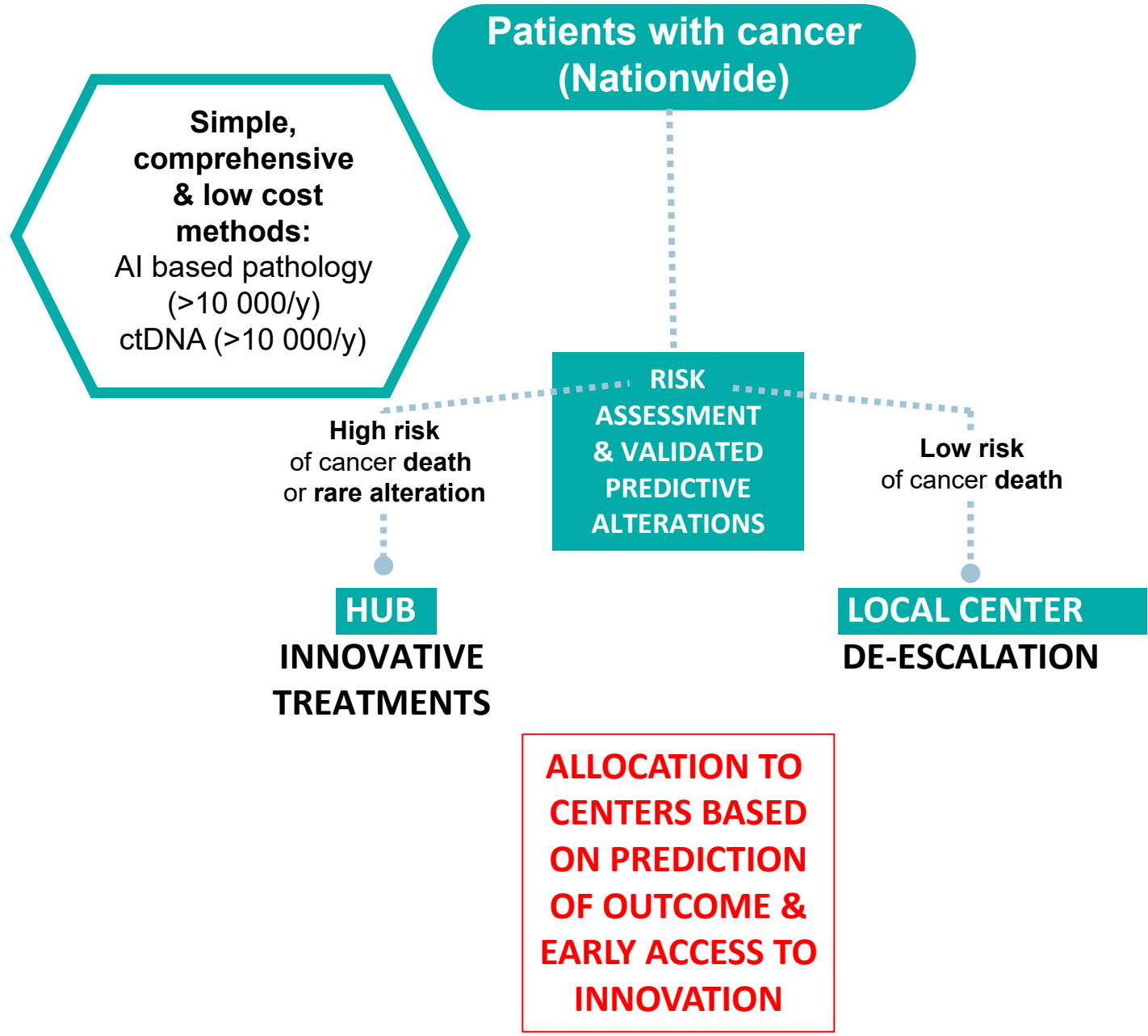
How could precision medicine reduce HC disparities ?

- Broad implementation of devices: simple, low cost, comprehensive (ctDNA and AI)
- Reduce requirement of complex infrastructures or expertise (ctDNA and AI)
- Allocate patients in the optimal center based on DATA (« screen for risk »)
- Address shortage of workforce by re-allocating resources to patients who need them (short treatment durations)
- Reduce impact of low education on outcome (adherence, perception)
- Substitute the MD where it does not exist anyway... (digital monitoring)
- Reduce disparities between cancer types

CLINICAL RESEARCH: "SCREEN AND CHARACTERIZE" APPROACH



**CLINICAL
RESEARCH:
“SCREEN AND
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APPROACH**



Can pathology assisted by AI reduce healthcare disparities ?

Applications:

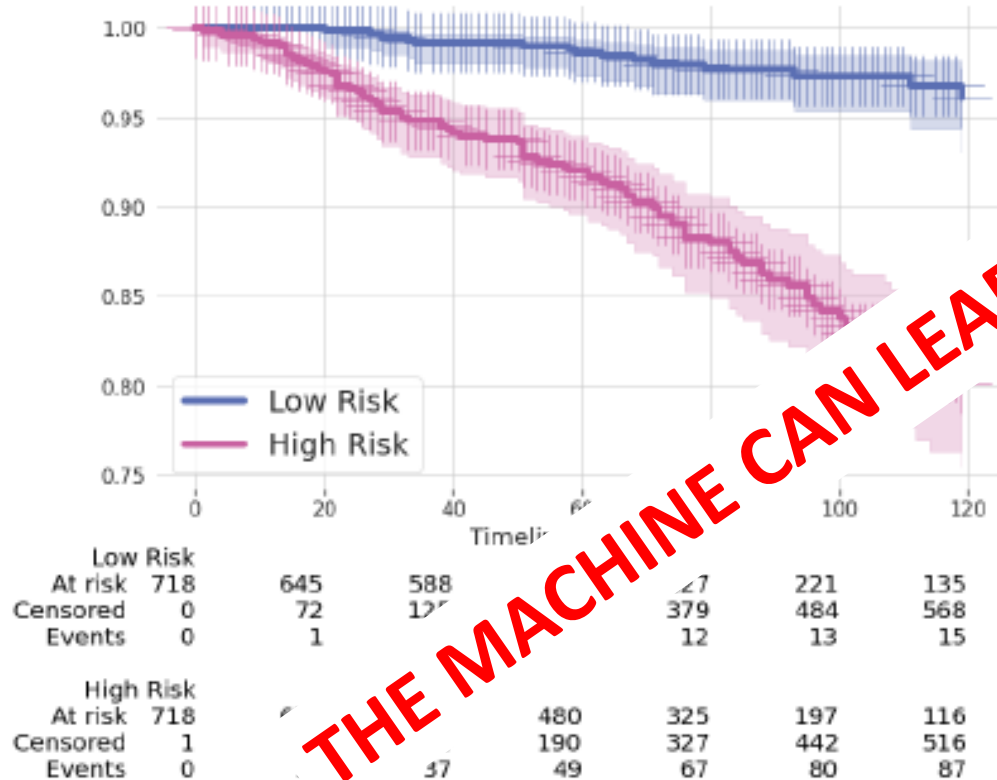
New low-cost predictors (RlapsRisk BC)

Detect molecular targets (MSI, BRCA, ERBB2...)

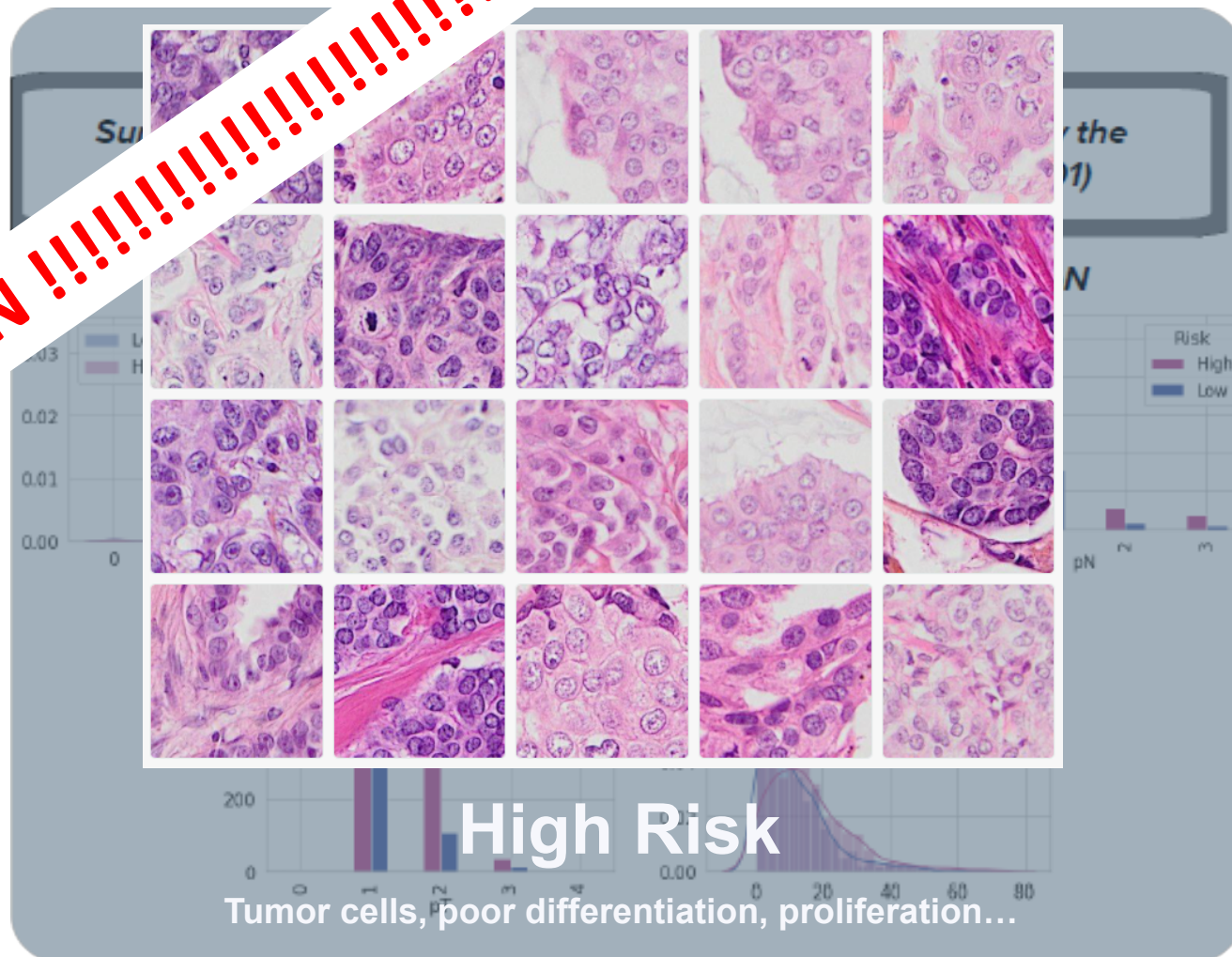
Automatize difficult to read markers (Ki67)

AI model to predict relapse in patients with HR+/Her2- early stage Breast Cancer

Machine was asked to learn which features from HES slides are associated with relapse



THE MACHINE CAN LEARN !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!



PortrAlt a French consortium to accelerate precision medicine with AI-enabled digital pathology solutions, funded by BPI

2 industrial actors



4 Partner Centers / Networks



33M € budget

5 years project

PortrAlt Lab: a collaborative **platform** to **accelerate and optimise** the development of AI diagnostics models

15 CE-marked digital pathology models in 3 indications:

- breast cancer
- lung cancer
- multi-cancers

- 🔍 Outcome Prediction
- 🔄 Biomarker Pre-Screen
- 📄 Pathologist enhancements

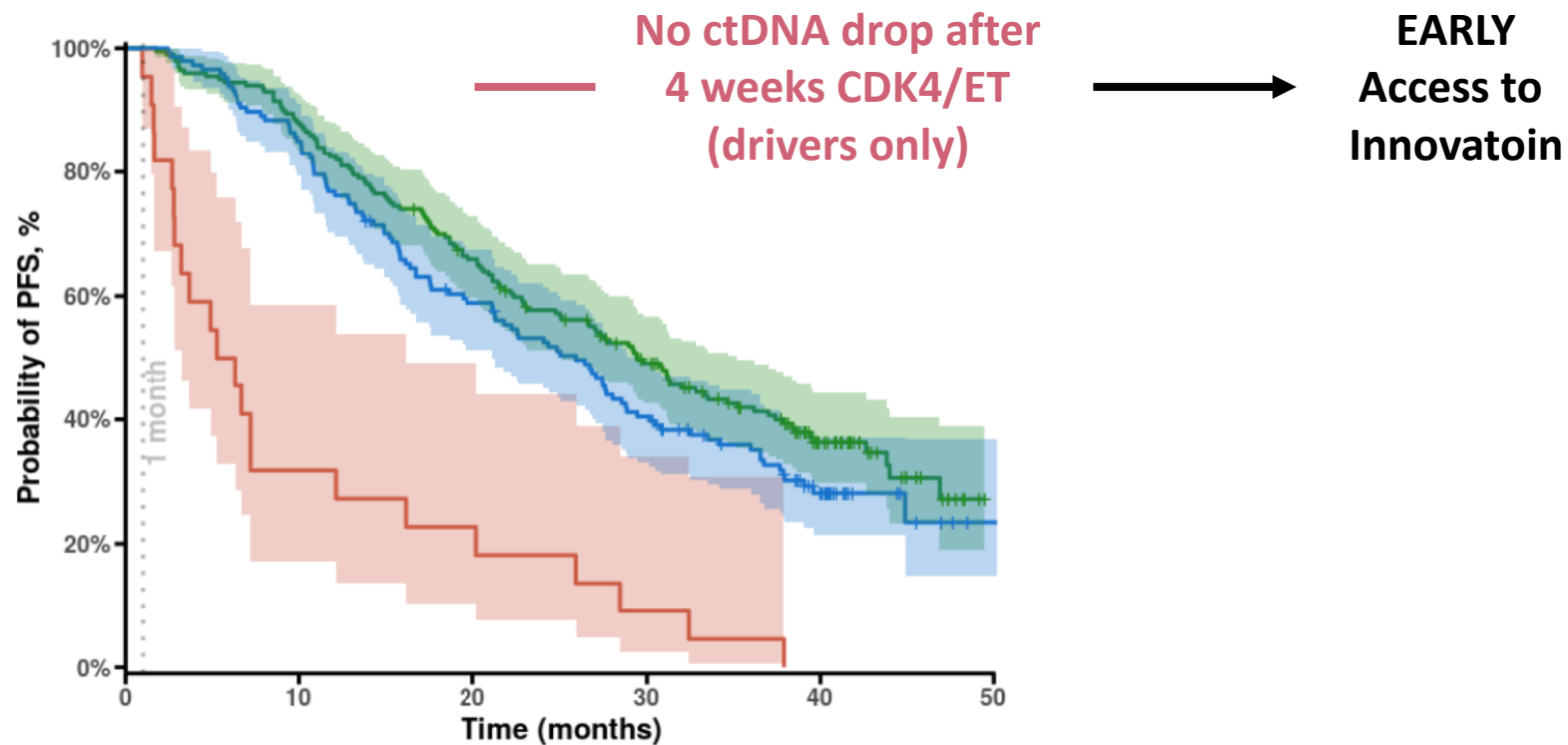
A digital pathology **marketplace**, accessible in **30+ centers** (incl. the full **Unicancer network**)

ctDNA to identify patients with high risk of cancer death or validated genomic alterations

Why does it decrease healthcare disparities ?

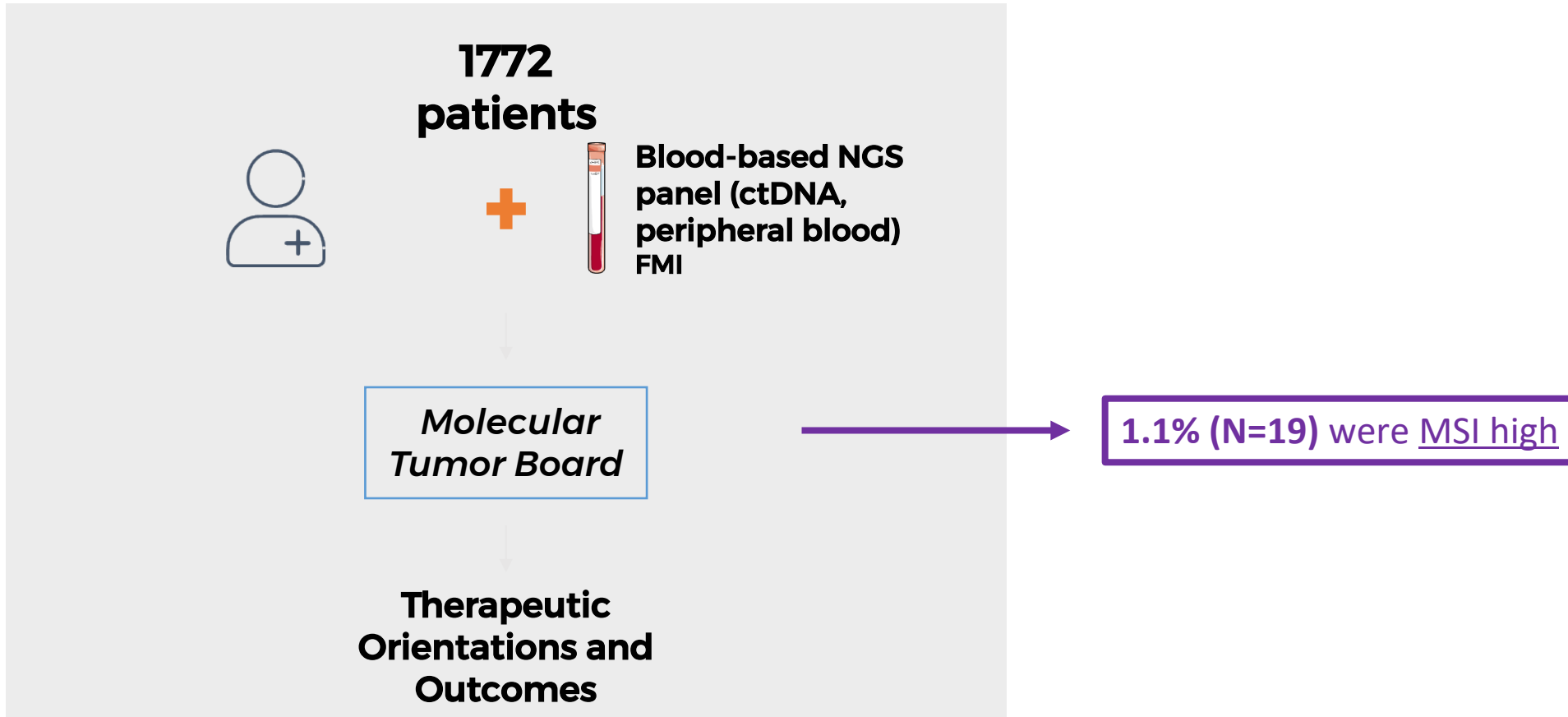
**Avoid the need for interventional radiology or specialized center
Assess the outcome and therefore drive patients to innovations**

Clinical utility of circulating tumor DNA sequencing with a large panel: Early detection of hard-to-treat cancers (SAFIR03)



PD17-02, Bailleux et al

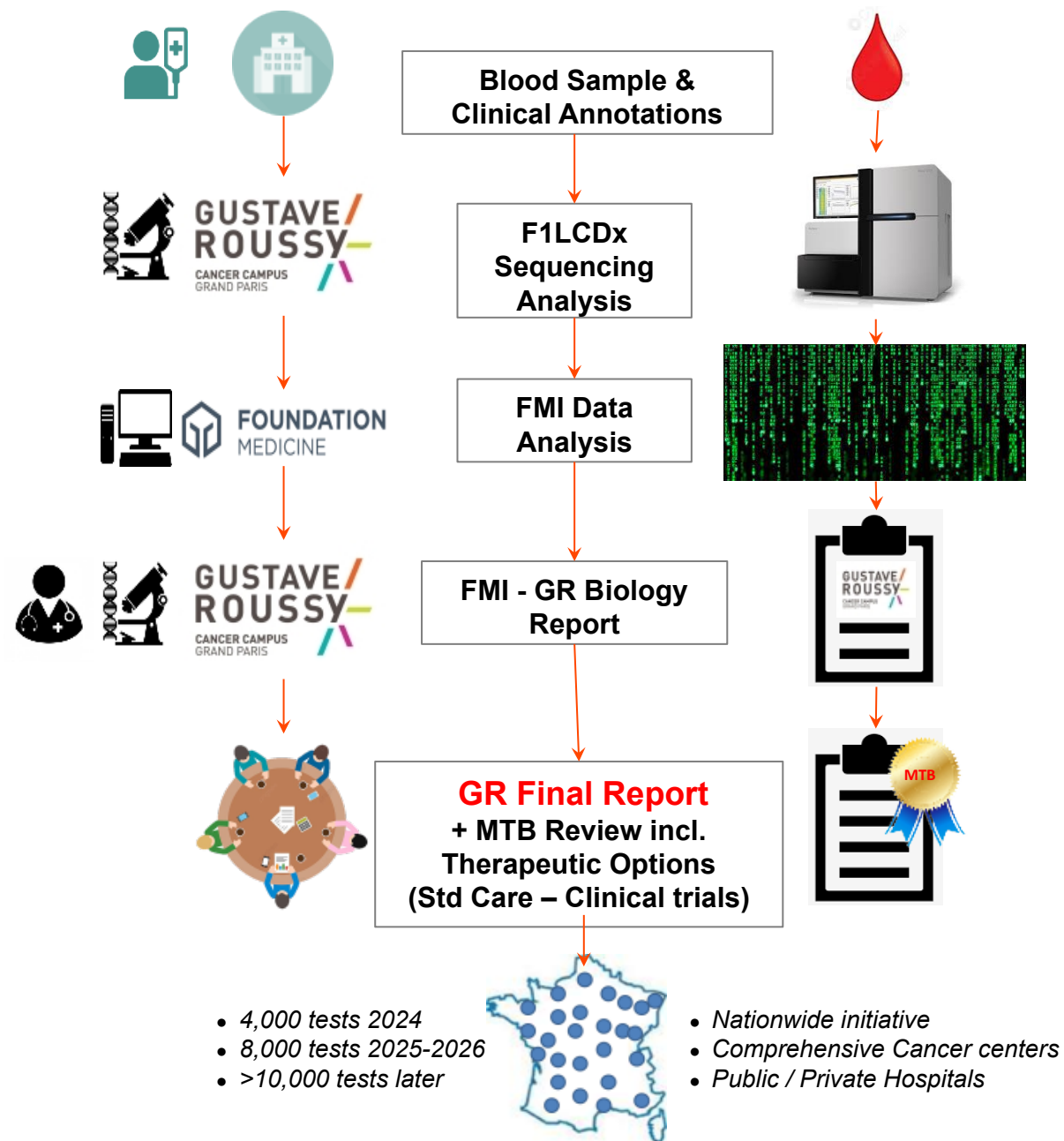
Clinical utility of circulating tumor DNA sequencing with a large panel: Targetable genomic alterations (STING)



Gustave Roussy - Roche – Foundation Medicine Partnership

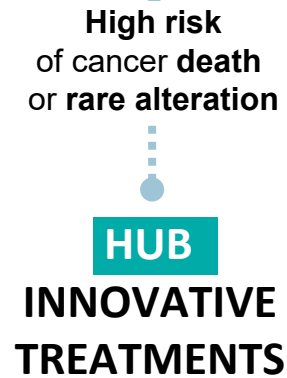
Our common ambition : extend french patients access to liquid-based comprehensive genomic profiling (CGP) beyond expert centers

- Promote precision medicine toward the oncology community
- Give opportunities and patients' ethical access to innovation (biomarker-driven clinical trials)
- Facilitate translational research programs by building very large clinically-annotated molecular databases
- Demonstrate and support value recognition by HTAs and national authorities
- Ambition: >10 000 patients per year



**CLINICAL
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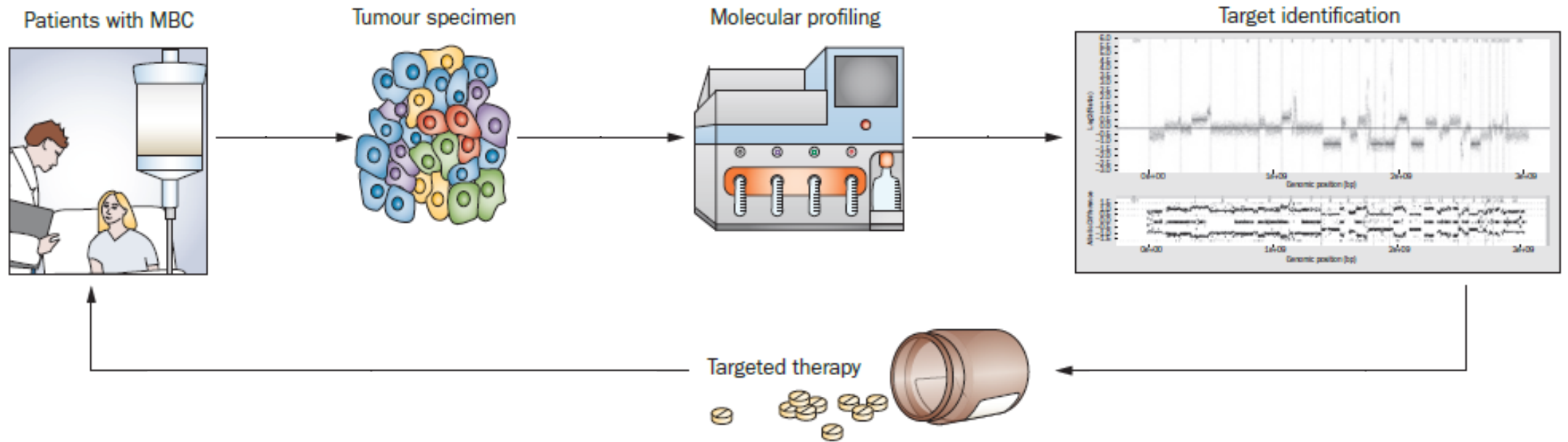
**= MODEL BIOLOGY
IN EACH PATIENT**



**Patients with cancer
(Nationwide)**

**RISK
ASSESSMENT
& VALIDATED
PREDICTIVE
ALTERATIONS**

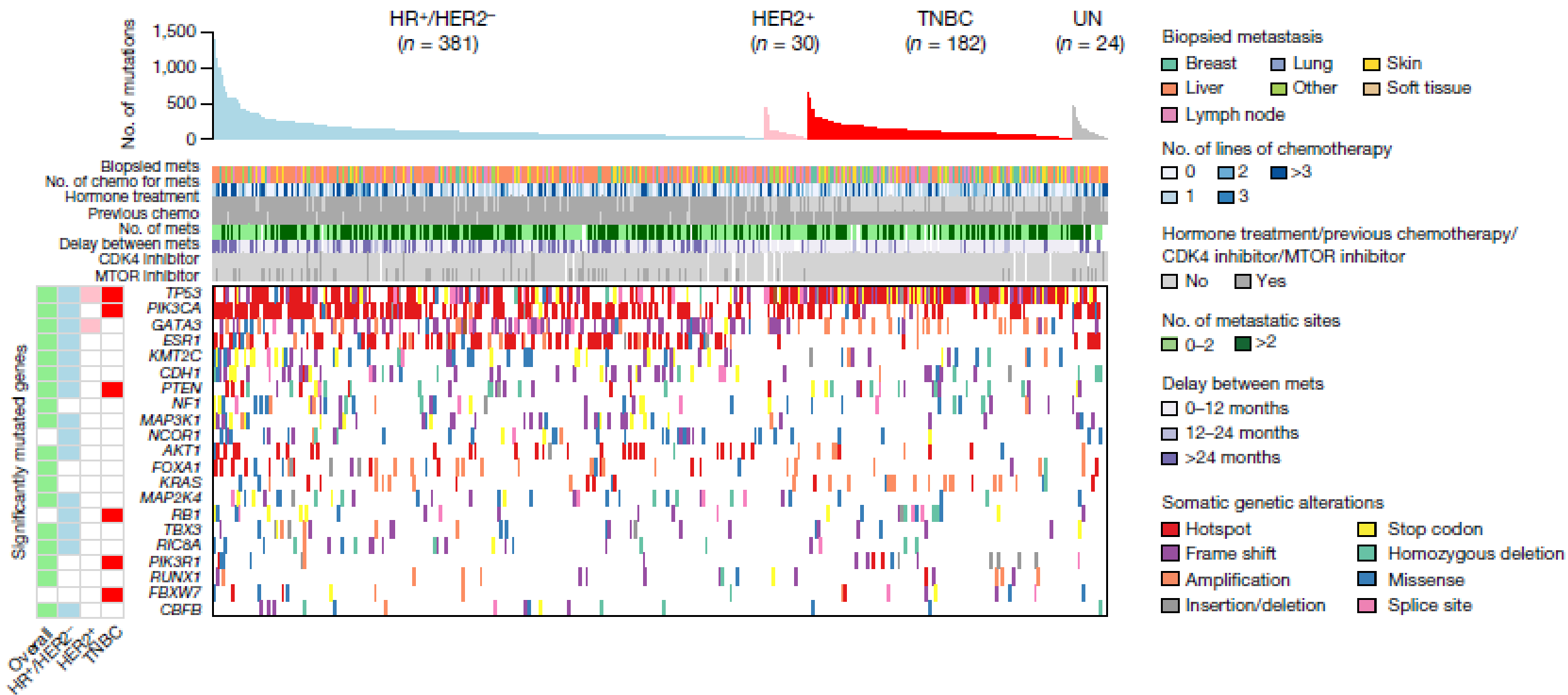
Hypothesis: if we identify the mechanisms of cancer progression or mechanism of drug sensitivity in each patient, it should improve PFS and OS



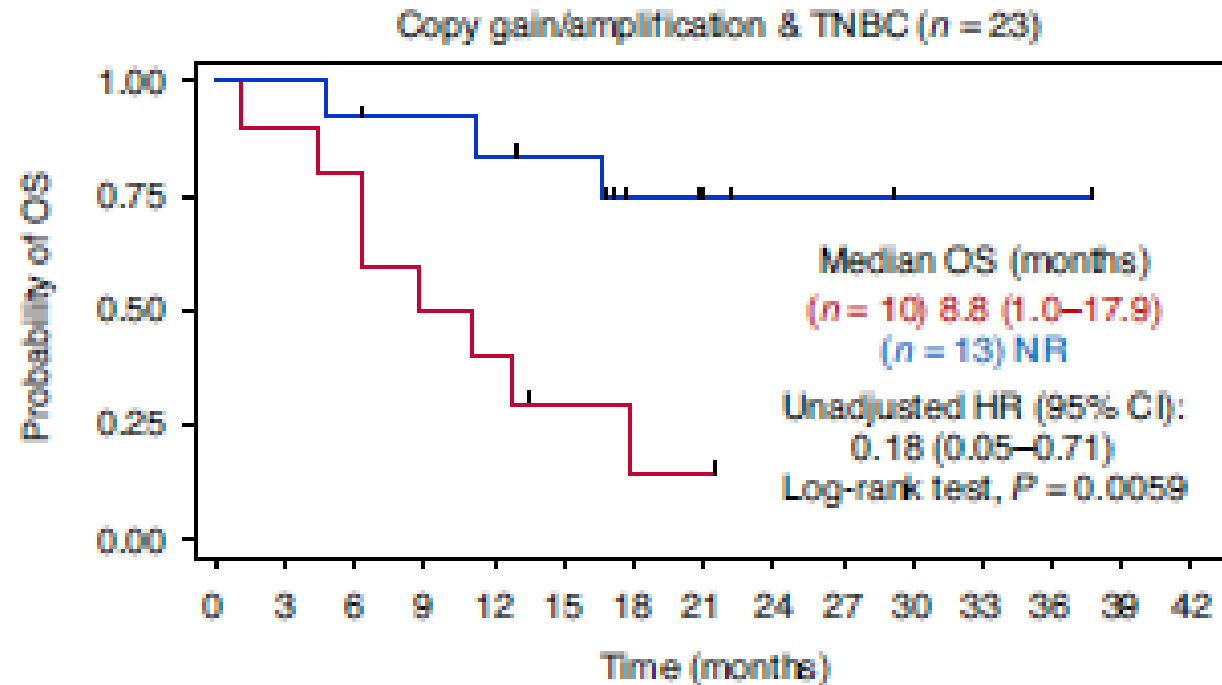
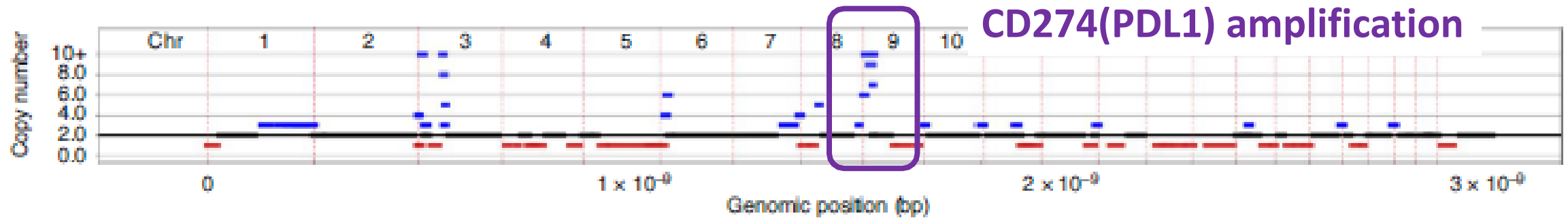
Cancer Modelling I :

Sequencing coding regions of DNA (= DNA sequencing)

Are they recurrent genomic drivers in metastatic breast cancers ?



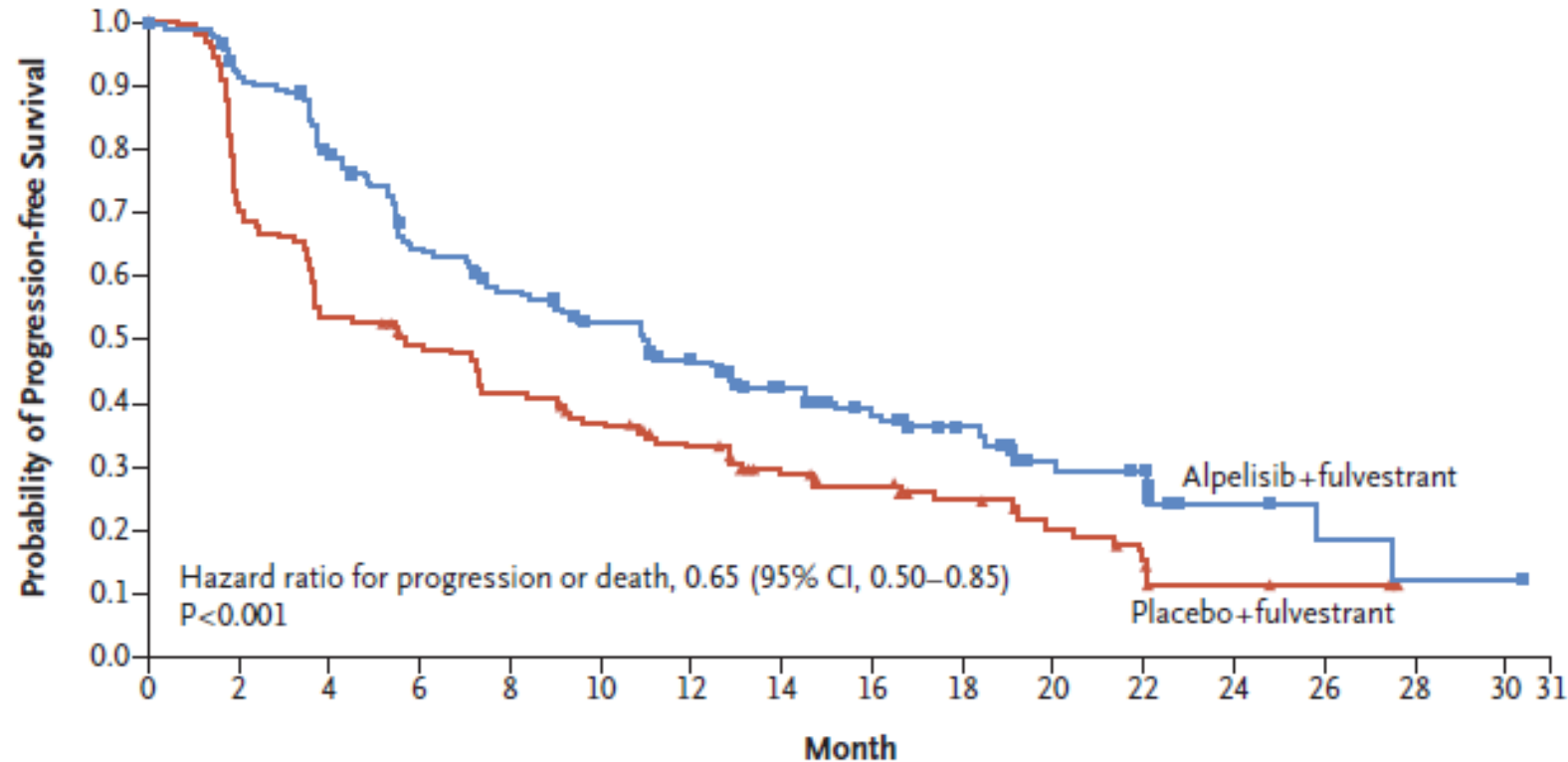
Are genomic alterations only involved in cancer cell biology ?



No. at risk	0	3	6	9	12	15	18	21	24	27	30	33	36	39	42
MC	10	9	8	5	4	2	1	1	0	0	0	0	0	0	0
D	13	13	12	11	10	9	5	3	2	2	1	1	1	1	0

What is the impact of targeting the protein encoded by a driver alteration in BC ?

Cohort with *PIK3CA*-Mutated Cancer



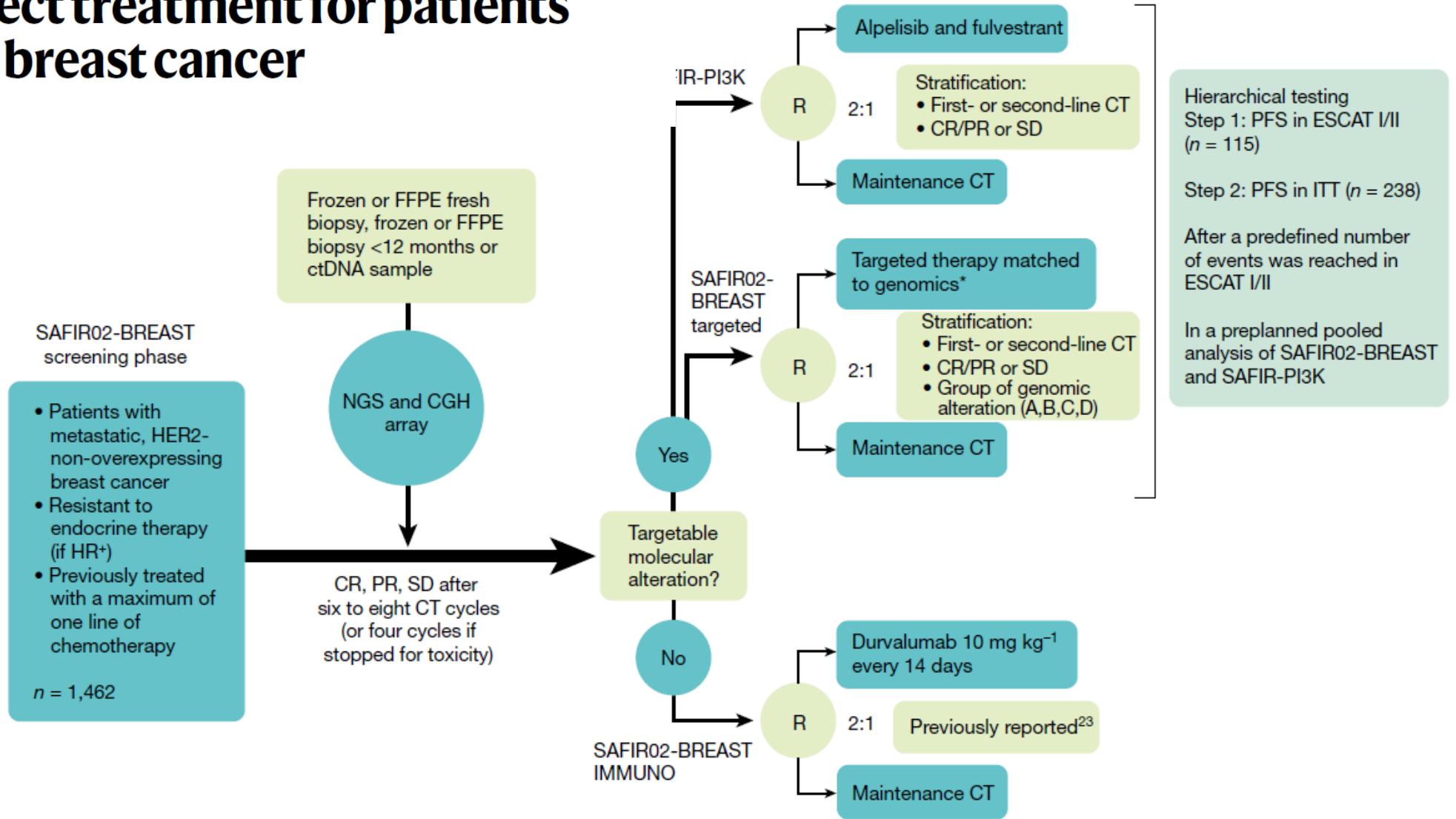
Andre F, NEJM, 2019

Targeting recurrent validated genomic drivers leads to tumor responses and improved PFS in patients presenting the alteration, but not in the population without the alteration

There is a need to perform genomic testing in patients with metastatic breast cancer

What is the benefit of multigene sequencing ?

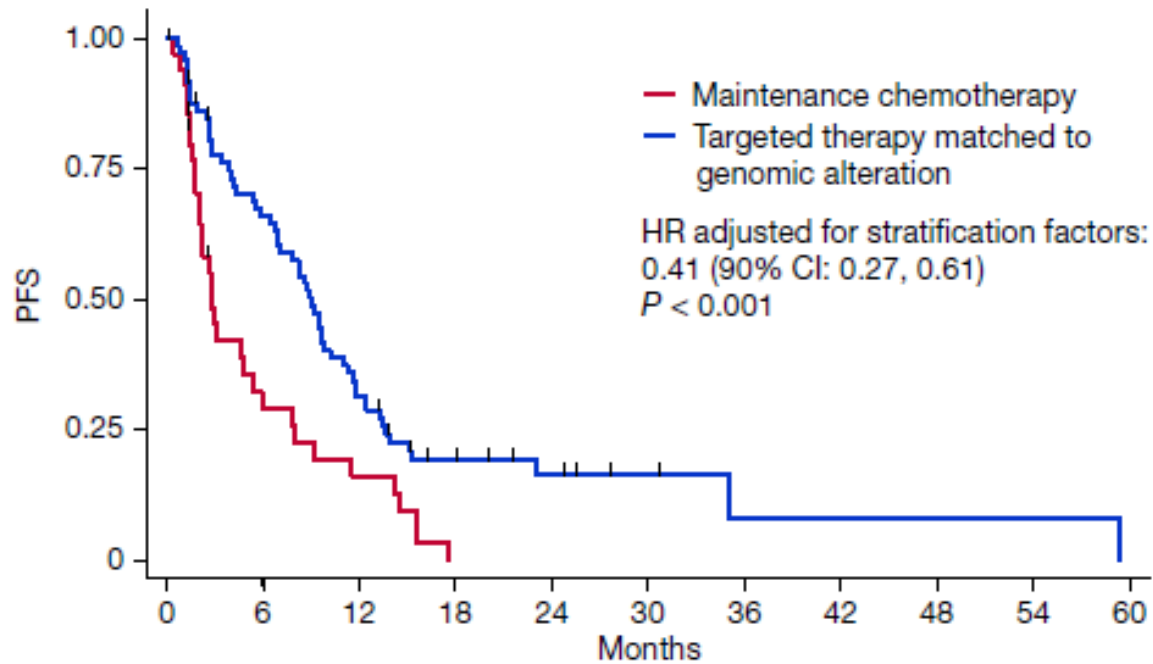
Genomics to select treatment for patients with metastatic breast cancer



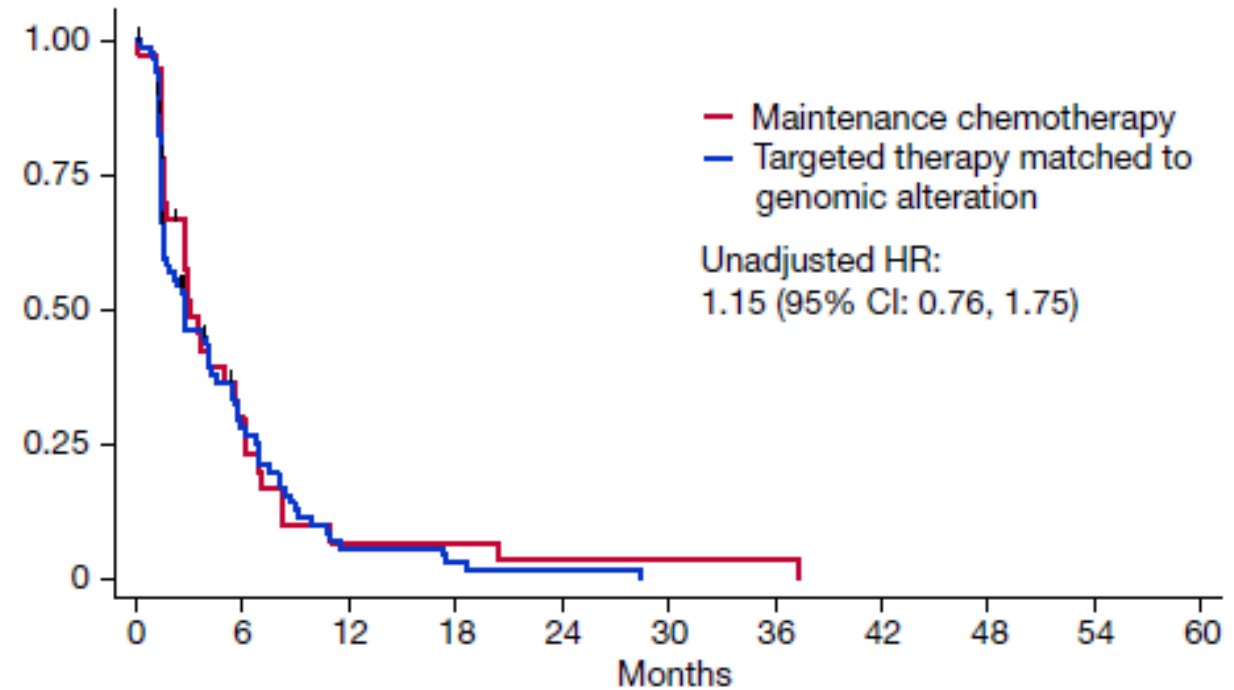
*olaparib, capivasertib, vistusertib, AZD8931, vandetanib, bicalutamide, AZD4547, selumetinib

Genomics to select treatment for patients with metastatic breast cancer

PFS in patients with ESCAT I/II genomic alterations ($n = 115$)



PFS in patients presenting genomic alteration beyond ESCAT I/II ($n = 123$)



It is useful to perform multigene sequencing IF analysed with the right framework of target classification

Summary

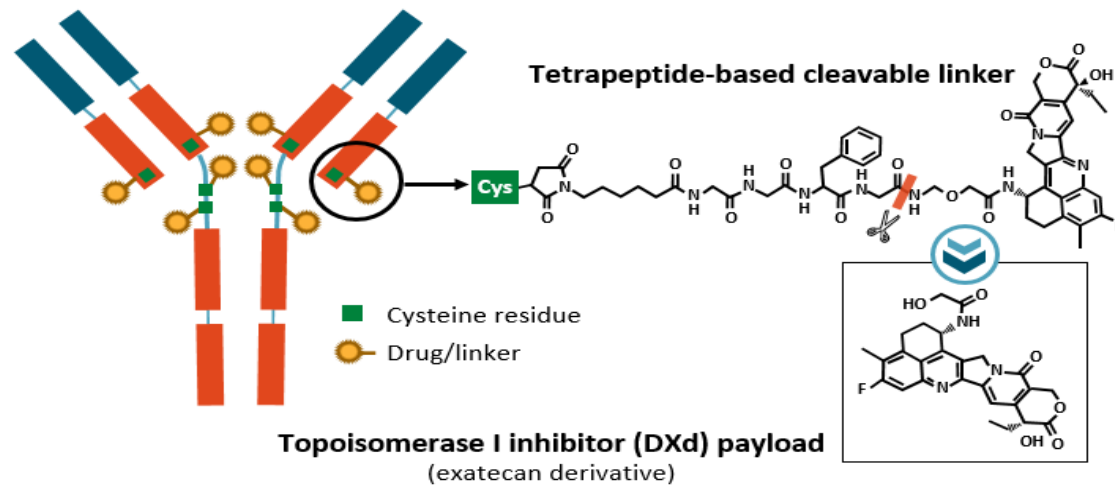
- Genomics is useful is around 10% of patients with metastatic cancer (maybe a little bit more in mBC because of PIK3CA)
- Genomics has reached a plateau
- What are the next technologies to model cancer biology and develop precision medicine ?

Assessing new dimensions of the biology for treatment selection

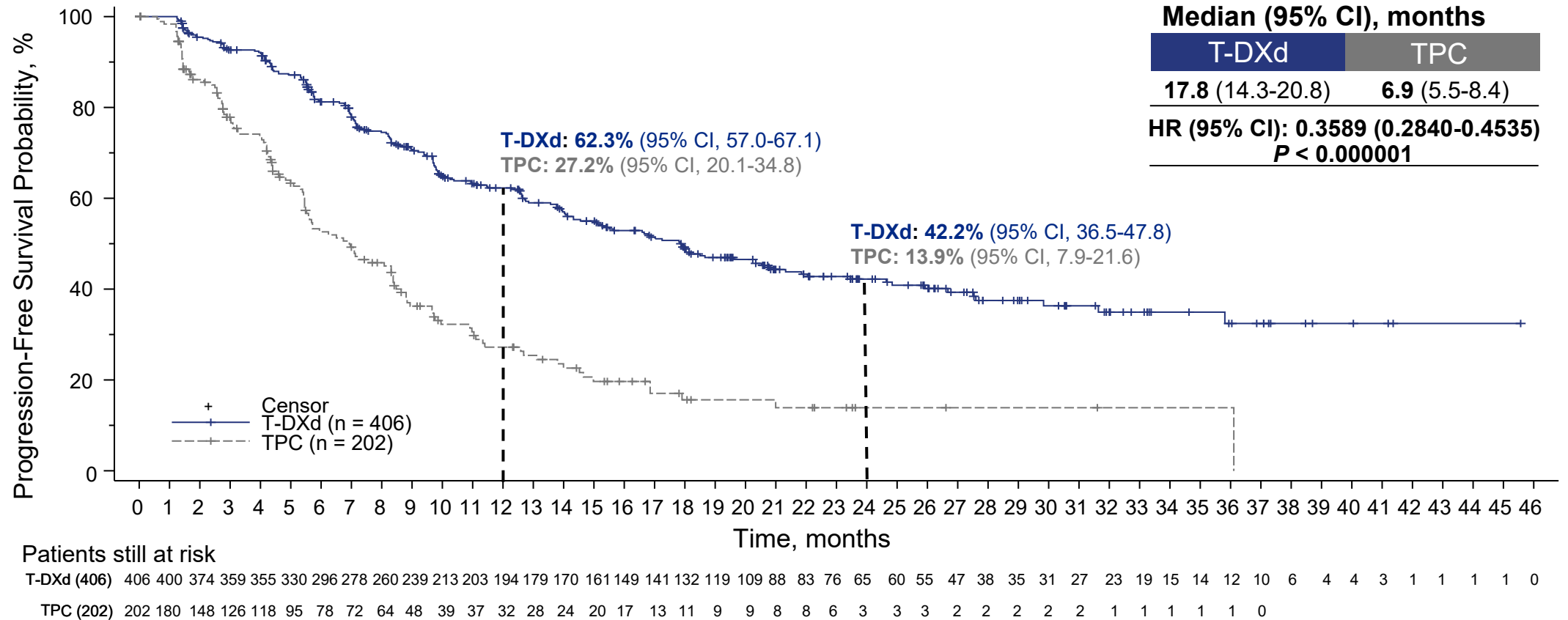
- Linking ATAC seq / CHIP seq with epigenetic reprogramming
- **Predicting sensitivity to biotechnological therapeutics by spatial biology**
- Monitoring cancer adaptation to new therapies by CTCs
- Organoids
 - Cancer cells
 - Cytotoxic T cells

Illustration I: T-DXd

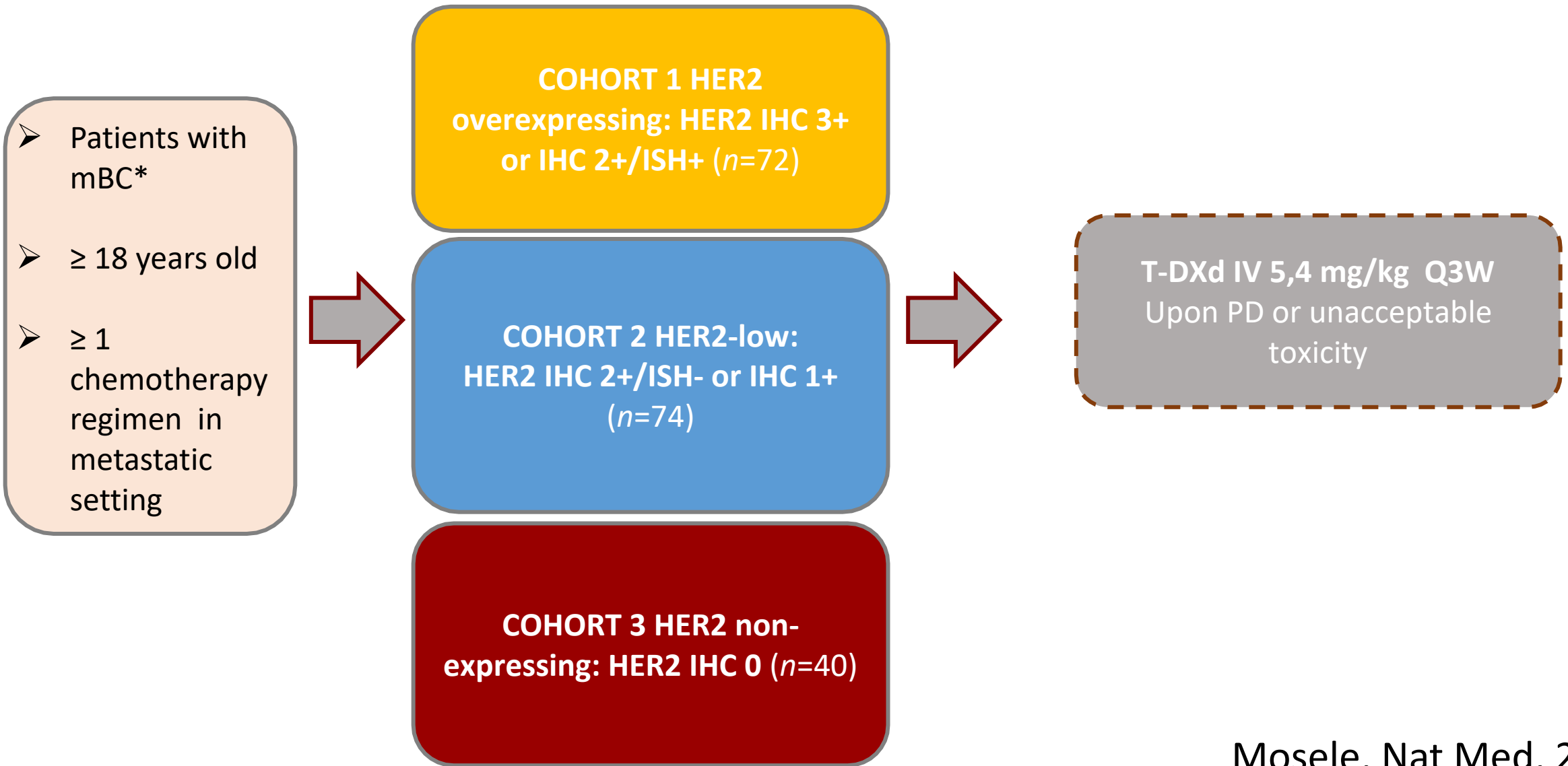
- **Antibody:** Monoclonal humanized anti-Her2 IgG1
- **Linker:** Cleavable linker (Gly-Gly-Phe-Gly)
- **Payload:** Topoisomerase I inhibitor
- **DAR:** ~8:1



Trastuzumab deruxtecan in patients with Her2 3+ mBC

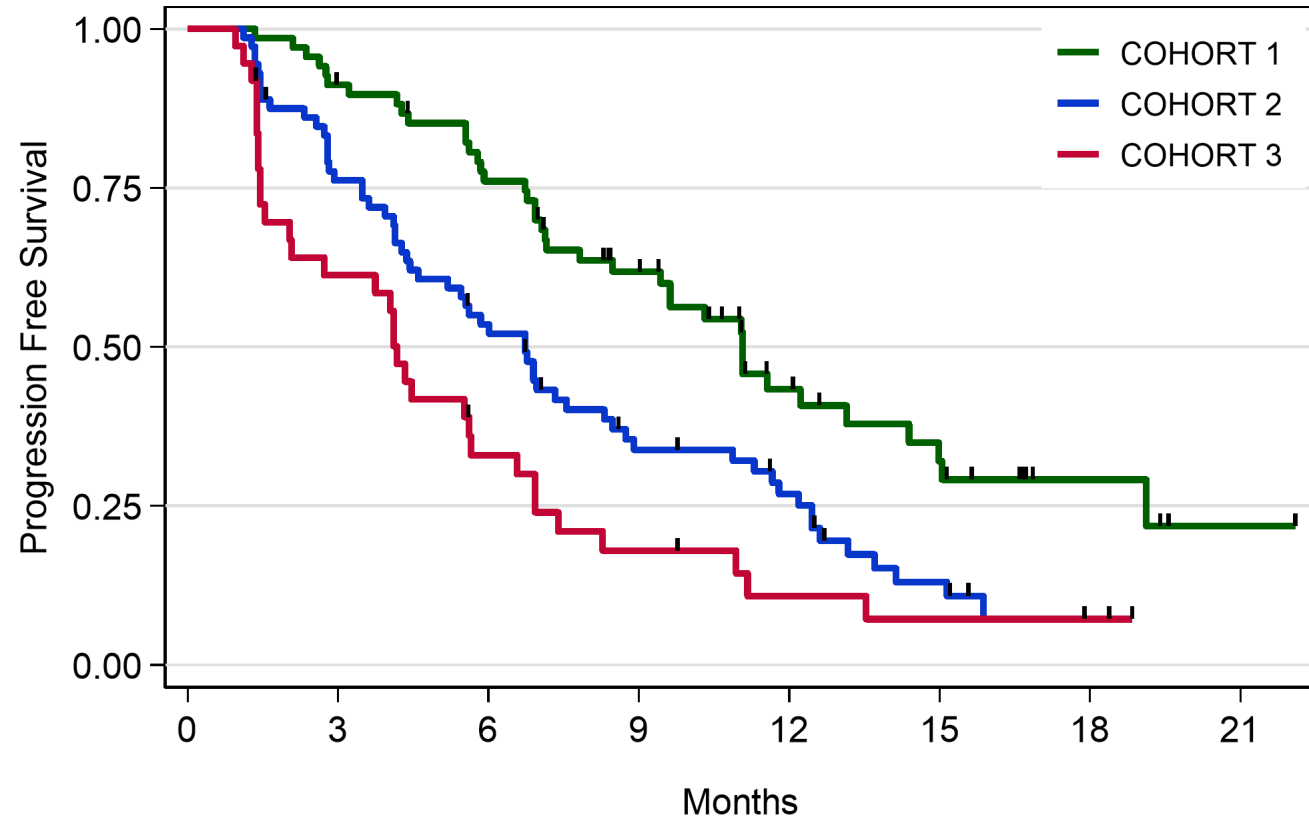


DAISY: Study Design



Drug efficacy is driven by Her2 expression

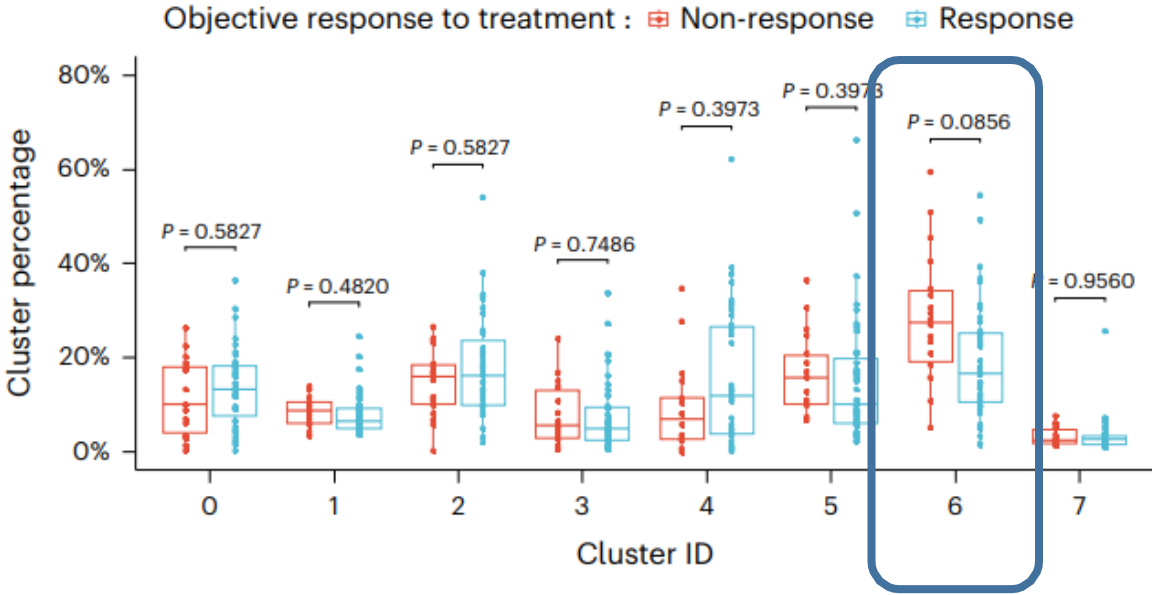
Data cut-off: Oct 19, 2021	Cohort 1 HER2 IHC 3+ or IHC 2+/ISH+ (n=68)	Cohort 2 HER2 IHC 2+/ISH- or IHC 1+ (n=72)	Cohort 3 HER2 IHC 0 (n=37)
Median PFS (mths) (95% CI)	11.1 (8.5–14.4)	6.7 (4.4-8.3)	4.2 (2-5.7)
HR (95% CI)	0.53 (0.34-0.84)	1.00	1.96 (1.21-3.15)
<i>p</i> -value	<i>p</i> < 0.0001		



COHORT 1	68	61	50	34	18	11	4	1
COHORT 2	72	54	37	21	15	6	2	0
COHORT 3	37	22	11	6	3	2	1	0

Mosele, Nat Med, 2023

Large Her2-null area is associated with lower response rates in patients with Her2-overexpressing cancers



Cluster 6 from a patient with non-objective response to T-DXd



Cluster 6 from a patient with objective response to T-DXd

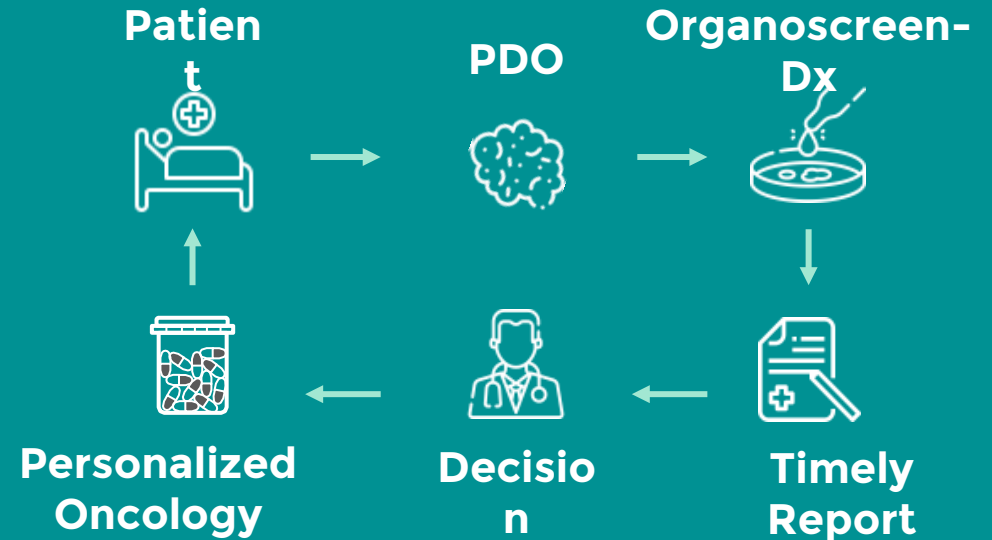
Assessing new dimensions of the biology for treatment selection

- Linking ATAC seq / CHIP seq with epigenetic reprogramming
- Predicting sensitivity to biotechnological therapeutics by spatial biology
- Monitoring cancer adaptation to new therapies by CTCs
- **Organoids**
 - **Cancer cells**
 - **Cytotoxic T cells**

ORGANOTREAT Clinical trial

	Phase :	Organ :	Patients
ORGANOTREAT-01	I/II	CRC	60 (GMI)
ORGANOTREAT-02R	III	PDAC	314
ORGANOTREAT-02R	III	CRC	582
ORGANOTREAT-02	II	Other	...

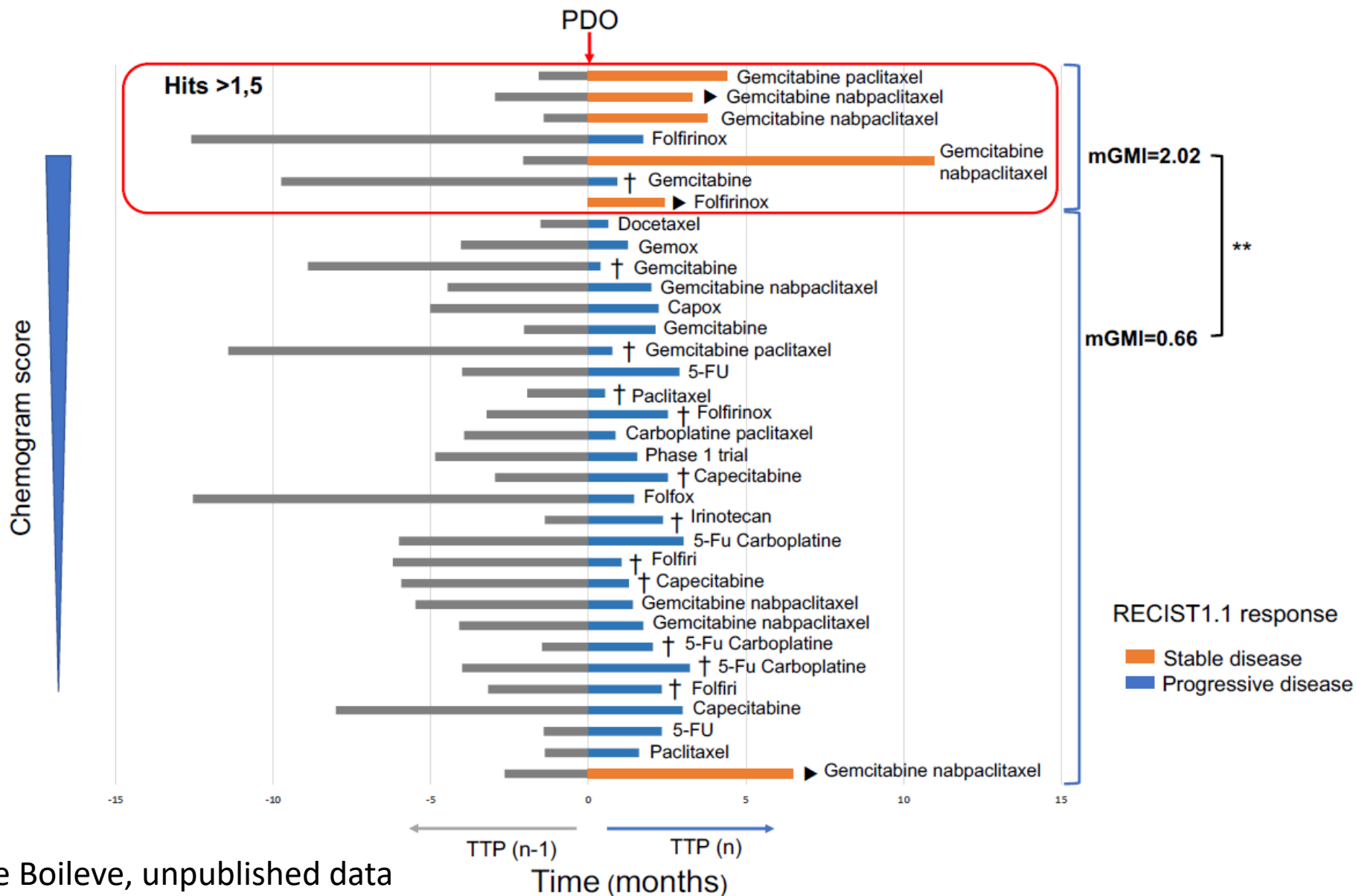
PI/Clinic: Pr Michel Ducreux
 PI/Scientific: F. Jaulin

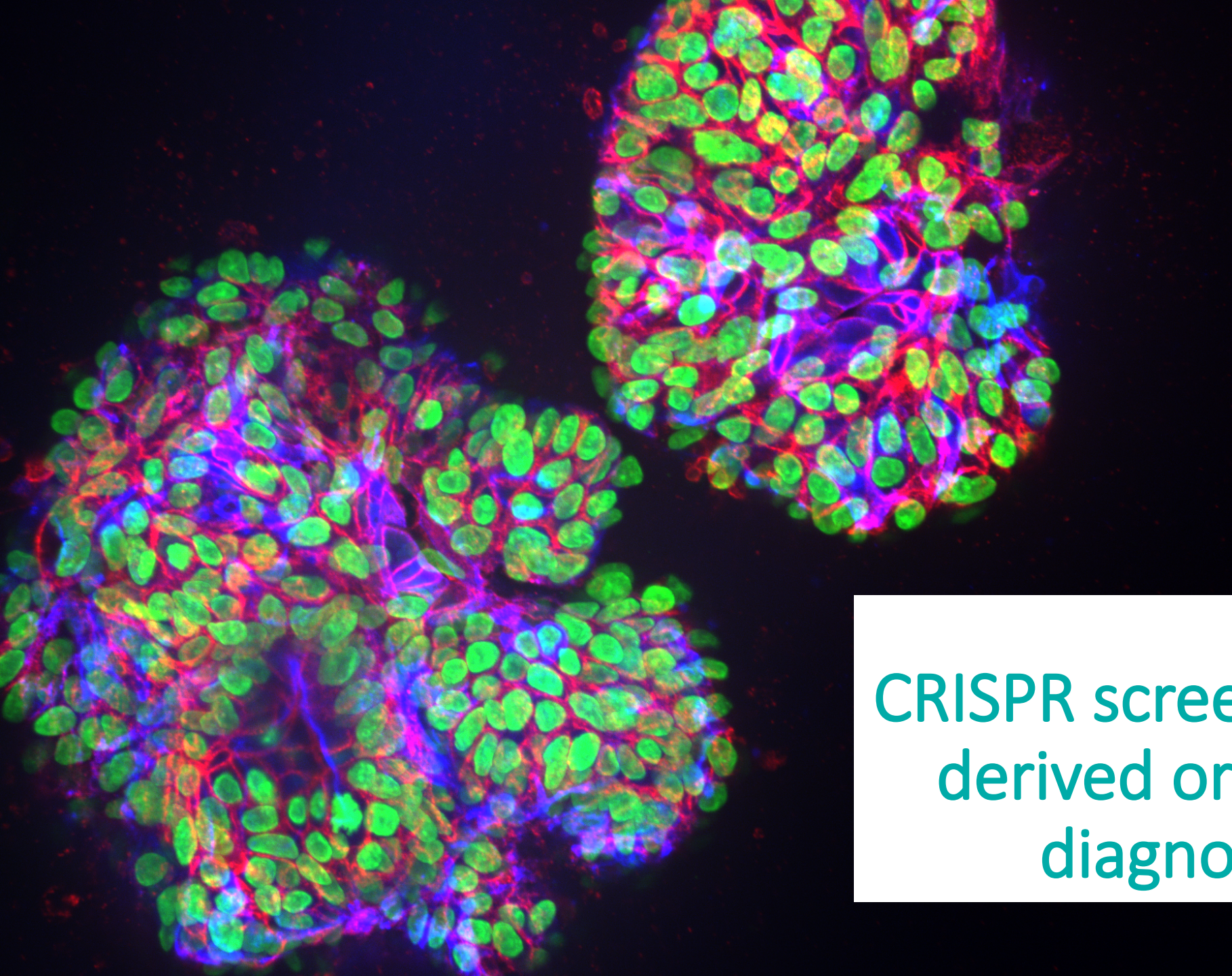


Interventional trial

ALL solid tumors, >1000 patients

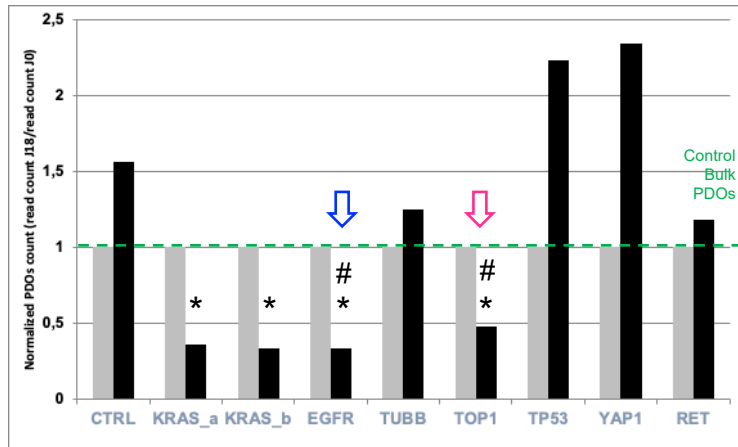
Treatment guided by organoids is associated with stable diseases in patient with pancreatic cancer and high chemogram score





CRISPR screen on patient-derived organoids for diagnostic use

CRISPR-based screen in patient-derived organoids



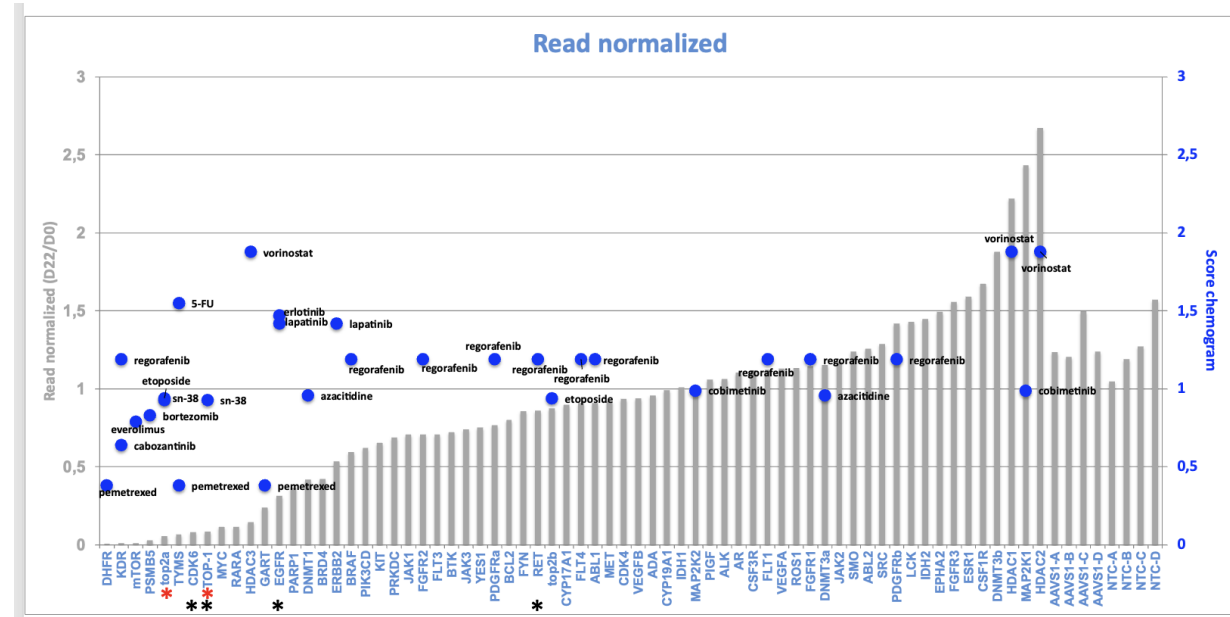
Targeted CRISPR screen on PDO from PDAC patient PGR-20

* hits => PDO growth is inhibited

could not be predicted based-on genomics

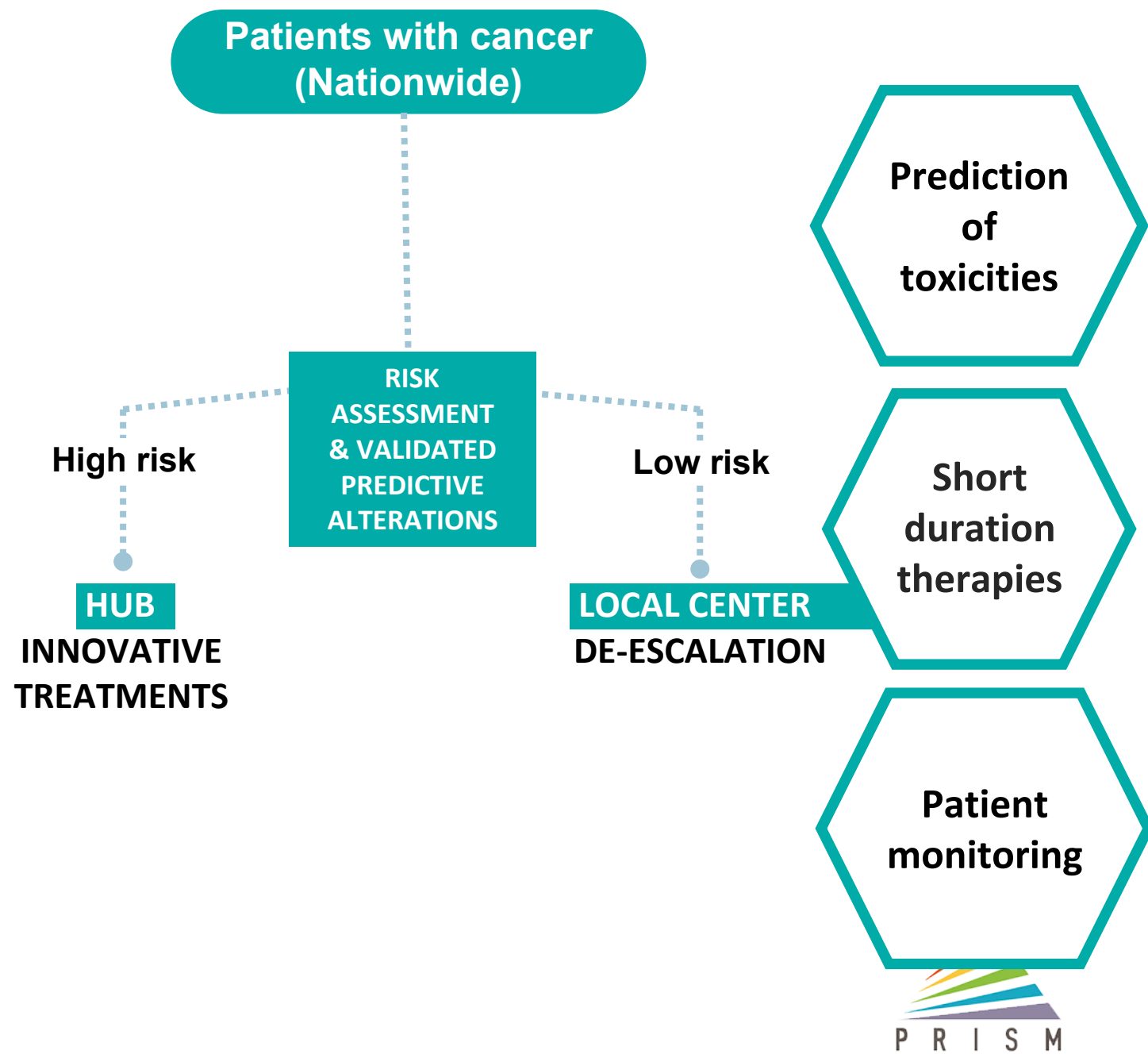
Sensitivity to EGFR confirmed by Erlotinib & Lapatinib

Sensitivity to TOP1 confirmed by Irinotecan

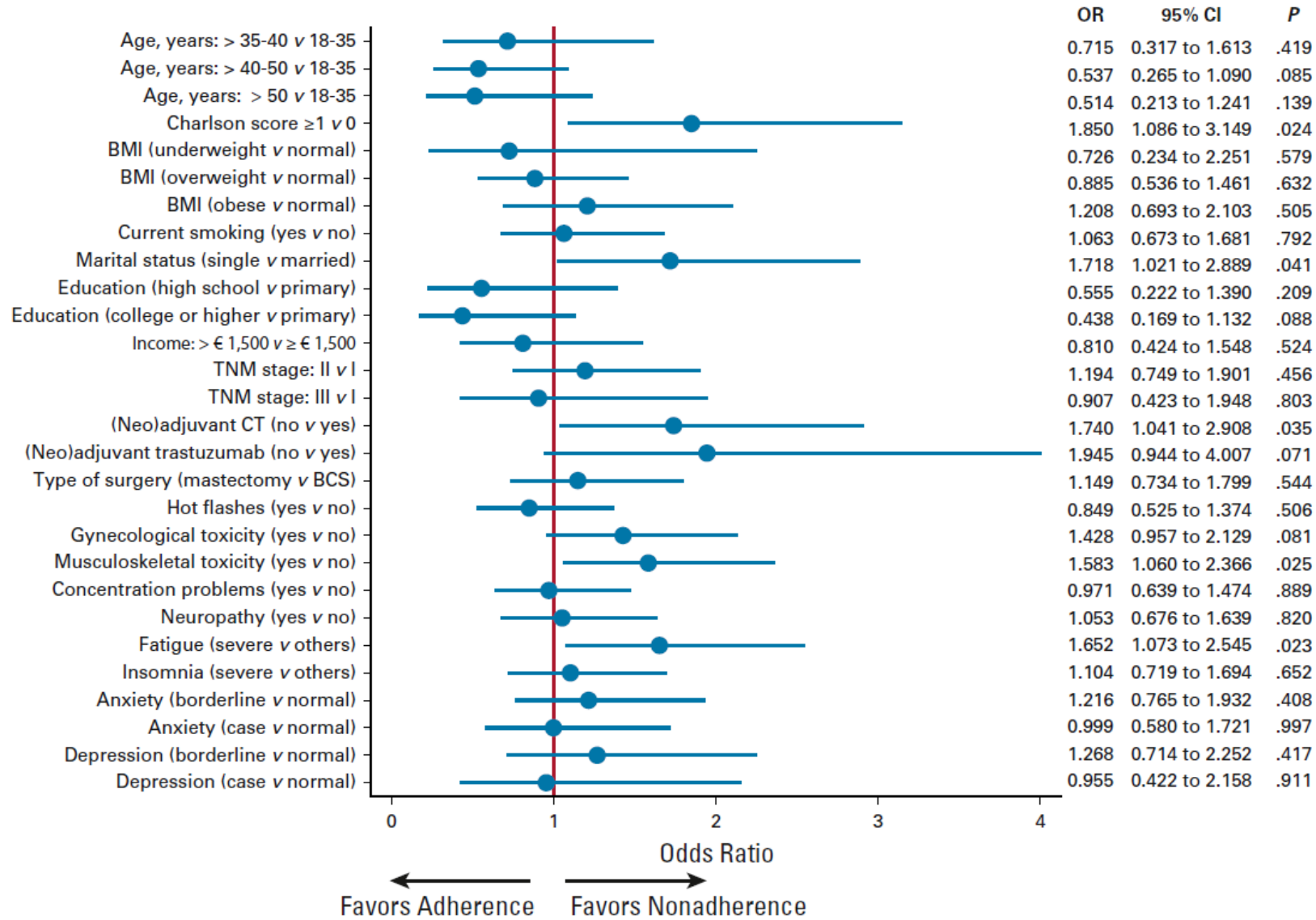
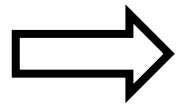
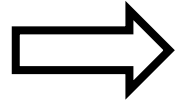


Here: PDAC PDO + “Druggable oncogenome” library (66 genes, [Hu et al Biomaterials. 2022](#)) Addgene#182133)

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Social determinants of health and toxicities are associated with lower adherence to therapy



Can shorter therapies cure patients ?

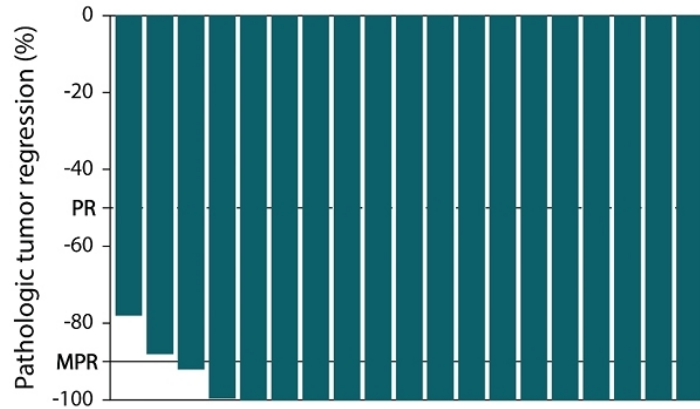
- Short duration therapies in patients with excellent outcome (LESS, UNICANCER, PI: E Deluche)
- Short duration therapies in patients with outlier response to new drug (POP-DURVA, PRISM, PI: J Ribeiro)
- Impacts:
 - Reduce compliance issues
 - Reallocate resources to patients with high unmet medical need

Can short duration IO cure some patients selected by biological markers ?

MMR-deficient colon cancers

Pathologic response in 100% of patients; 79% pCR

The primary endpoint was met in stage I with a pathologic response rate of 100%



Pathologic response (RVT)	Patients n = 19
Yes ($\leq 50\%$)	19 (100%)
Major ($\leq 50\%$)	17 (89%)
Complete (0%)	15 (79%)
Partial (10-50%)	2 (11%)
No ($>50\%$)	0

Adjuvant chemotherapy

All patients had ypN0 disease at resection and no patients received adjuvant chemotherapy

POP-Durva

Eligibility criteria

- TNBC
- TILs $\geq 5\%$

-30

D1

D15

D22

Surgery

Durvalumab Q2w x 2 cycles
10 mg/Kg

4 weeks

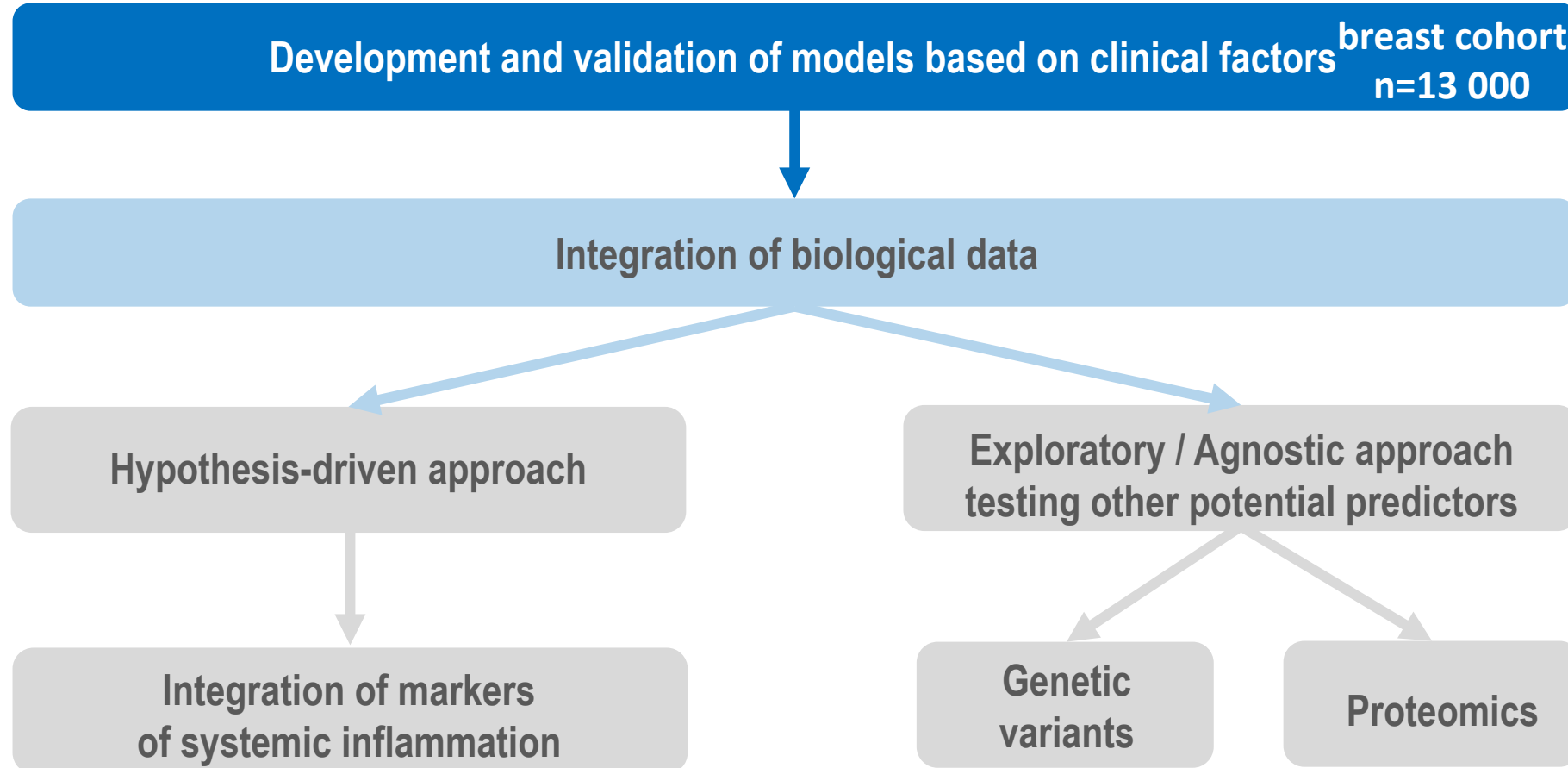


Can biology predict risk of toxicities ?

WHY ?????

To provide supportive care or to substitute with a less toxic drug in order to improve QOL and improve adherence

Building a bio-behavioral predictor of long-term cancer & treatment related fatigue among survivors



Building a bio-behavioral predictor of long-term cancer & treatment related fatigue among survivors: The triade Inflammation-biological aging-frailty

Systemic inflammation (n=1373, 16 markers + metabolic sd array)

Variable	Odds Ratio	95% CI		p
Severe fatigue at diagnosis, Yes vs. No	3.99	2.81	5.66	<.0001
Age, continuous	0.98	0.97	0.99	0.0021
Tobacco use behavior, Former vs. Never	0.96	0.68	1.35	0.7991
Tobacco use behavior, Current vs. Never	1.81	1.26	2.58	0.0012
Pain, continuous	1.01	1	1.02	0.0023
Insomnia, continuous	1.01	1	1.01	0.0002
IL-6, middle low vs. low	1.27	0.87	1.86	0.2234
IL-6, middle high vs. low	1.15	0.78	1.69	0.4957
IL-6, high vs. low	2.06	1.4	3.03	0.0002
Intercept	0.49	0.22	1.05	0.0672

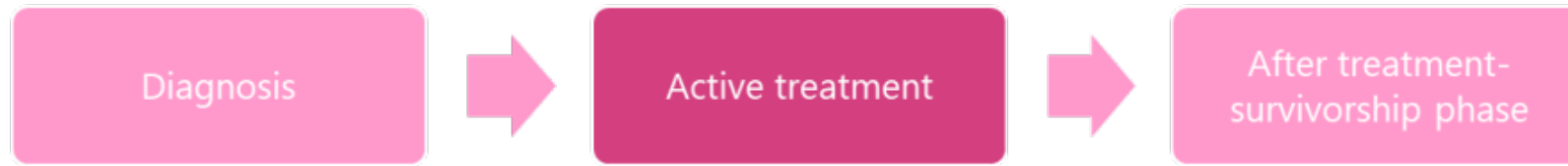
Clonal Haematopoiesis (n=1000 , 17 genes)

Predictive model of CRF at Y-4	Odds Ratio		95% CL	Pr > t
Menopausal status, Post- vs. Pre-	0.600	0.438	0.821	0.0014
Hormonotherapy, Yes vs. No	1.382	0.913	2.092	0.1258
Severe fatigue at diagnosis, Yes vs. No	3.025	2.071	4.418	<.0001
Anxiety, Doubtful case vs. Non-case	1.340	0.900	1.993	0.1490
Anxiety, Case vs. Non-case	1.717	1.175	2.509	0.0052
Insomnia, continuous	1.006	1.001	1.011	0.0184
Pain, continuous	1.017	1.009	1.024	<.0001
CH, VAF >= 2% vs <2%	1.643	1.077	2.509	0.0213

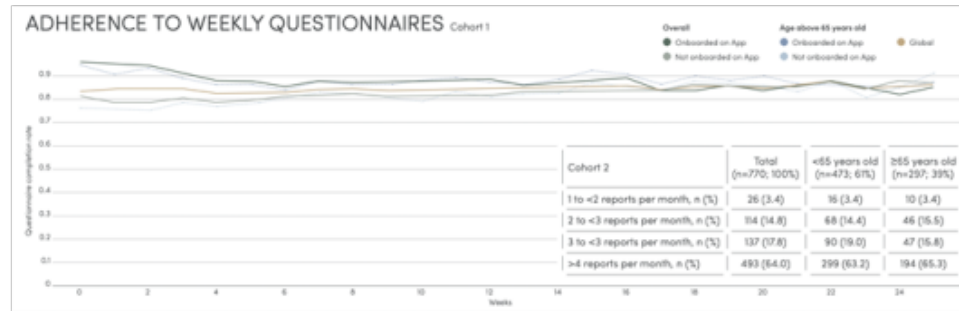
Efficacy of digital remote monitoring of patients under anticancer oral drugs

Relative Dose Intensity	Remote Digital monitoring	Control		
RDI (until study discontinuation)				
No. of patients	272	287	559	$t = 4.38$
Mean (s.d.)	0.9344 (0.2590)	0.8943 (0.1914)	0.9138 (0.2275)	$P = 0.0426$
95% CI	0.9035-0.9653	0.8720-0.9165	0.8949-0.9327	
Min-Max	0.20-2.00	0.00-1.51	0.00-2.00	
Median	1.00	1.00	1.00	
Q1-Q3	0.80-1.00	0.80-1.00	0.80-1.00	
RDI (until study discontinuation) adjusted for global adherence				
No. of patients	255	265	520	$t = 4.07$
Mean (s.d.)	0.8417 (0.2632)	0.7998 (0.2090)	0.8204 (0.2378)	$P = 0.0451$
95% CI	0.8093-0.8742	0.7745-0.8251	0.7999-0.8408	
Min-Max	0.0-2.0	0.0-1.3	0.0-2.0	
Median	0.9	0.8	0.9	
Q1-Q3	0.7-1.0	0.7-1.0	0.7-1.0	

Digital health as an opportunity: participatory care and behavioural interventions: routine care



Remote patient monitoring with ePROs + therapeutic education during active treatment phase



2055 patients across 26 highly diverse centers:

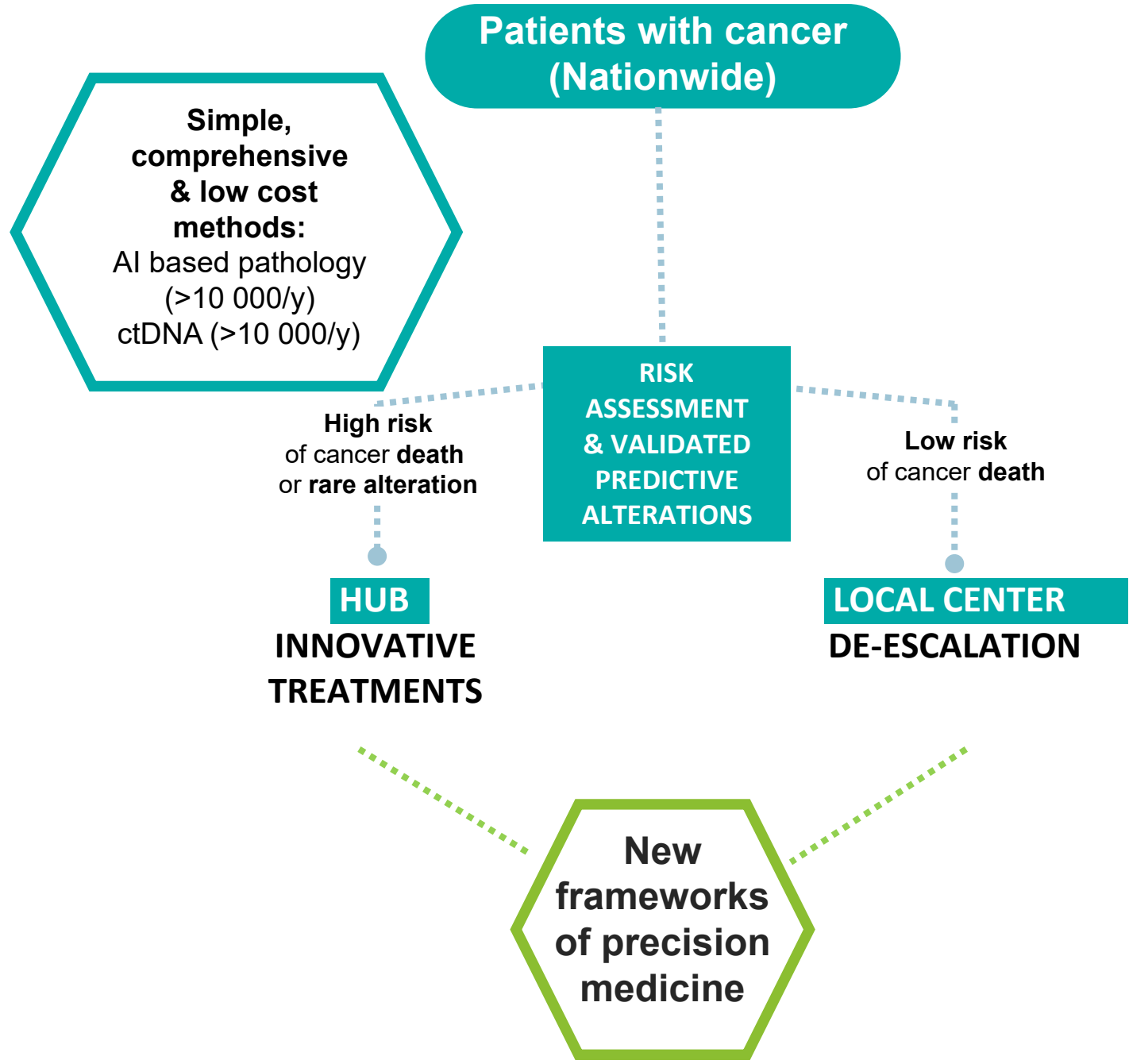
- 70% patients reporting via mobile app
- **Adherence to weekly ePRO reporting: 85% (overall); 81.1% (>65y)**

Digital therapeutics

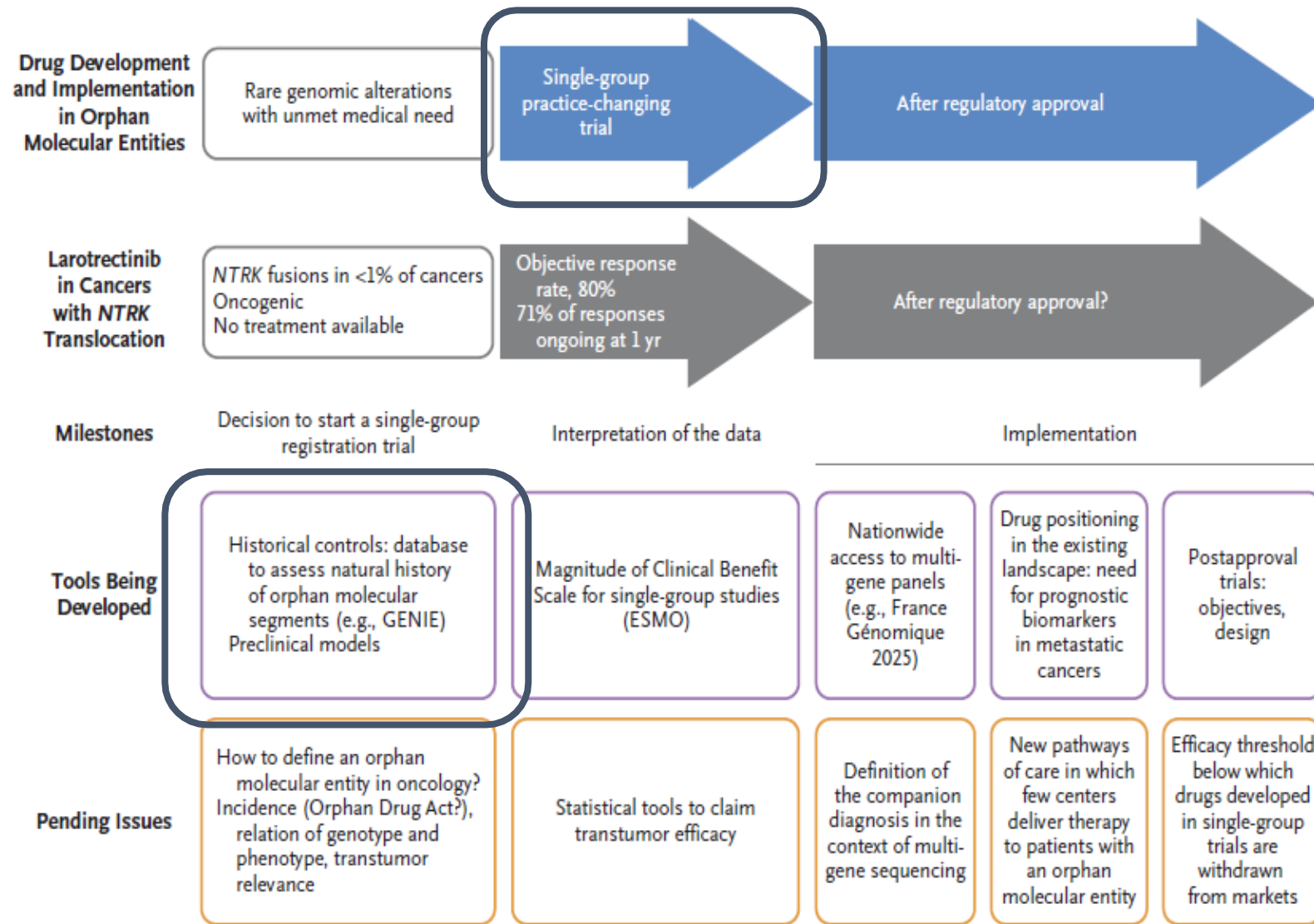


Qualitative studies during the co-design phase (n=35): elevated satisfaction and interest

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Drug development in rare genomic entities: Single arm trials for drug registration



Should we move organ-agnostic developments ?



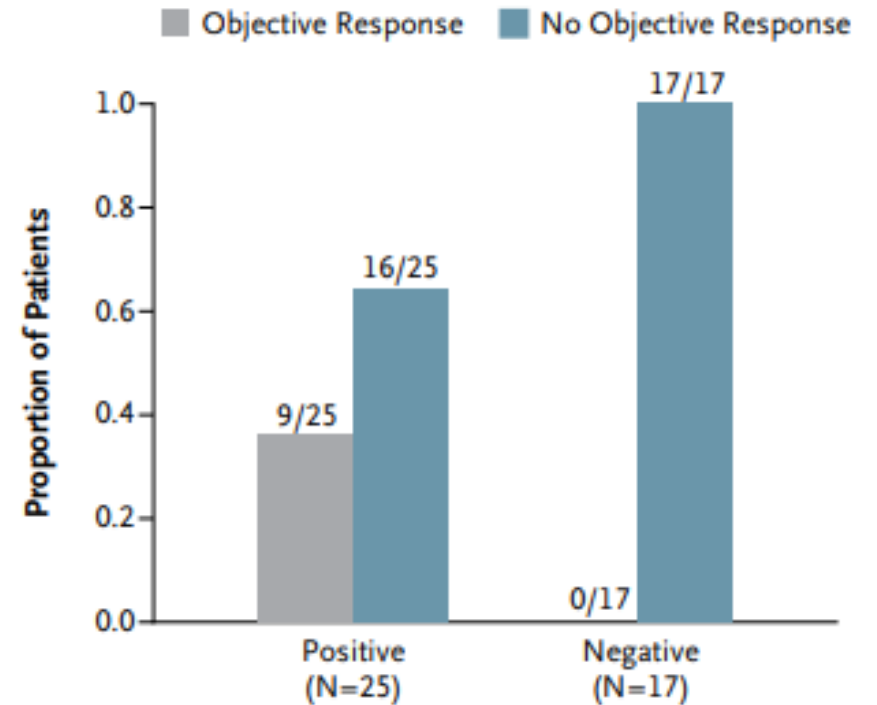
ESTABLISHED IN 1812

JUNE 28, 2012

VOL. 366 NO. 26

Safety, Activity, and Immune Correlates of Anti-PD-1 Antibody in Cancer

Suzanne L. Topalian, M.D., F. Stephen Hodi, M.D., Julie R. Brahmer, M.D., Scott N. Gettinger, M.D., David C. Smith, M.D., David F. McDermott, M.D., John D. Powderly, M.D., Richard D. Carvajal, M.D., Jeffrey A. Sosman, M.D., Michael B. Atkins, M.D., Philip D. Leming, M.D., David R. Spigel, M.D., Scott J. Antonia, M.D., Ph.D., Leora Horn, M.D., Charles G. Drake, M.D., Ph.D., Drew M. Pardoll, M.D., Ph.D., Lieping Chen, M.D., Ph.D., William H. Sharfman, M.D., Robert A. Anders, M.D., Ph.D., Janis M. Taube, M.D., Tracee L. McMiller, M.S., Haiying Xu, B.A., Alan J. Korman, Ph.D., Maria Jure-Kunkel, Ph.D., Shruti Agrawal, Ph.D., Daniel McDonald, M.B.A., Georgia D. Kollia, Ph.D., Ashok Gupta, M.D., Ph.D., Jon M. Wigginton, M.D., and Mario Sznol, M.D.



PD-L1 Status



TARGET

= key element of classification !

ORIGINAL ARTICLE

Atezolizumab and Nab-Paclitaxel in Advanced Triple-Negative Breast Cancer

P. Schmid, S. Adams, H.S. Rugo, A. Schneeweiss, C.H. Barrios, H. Iwata, V. Diéras, R. Hegg, S.-A. Im, G. Shaw Wright, V. Henschel, L. Molinero, S.Y. Chui, R. Funke, A. Husain, E.P. Winer, S. Loi, and L.A. Emens, for the IMpassion130 Trial Investigators*

This article was published on October 20, 2018, and updated on November 15, 2018, at NEJM.org.

N Engl J Med 2018;379:2108-21.

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**30%* 30% * 600 k * 6 years =
>300 000 more patients with TNBC
would have got access
to anti-PD1 if we classified cancers
by their targets
(under the hypothesis that drugs
are available everywhere...)**

Pancancer estimate : around 3 M patients
missed access to anti-PD1 because cancer
Classifications are not based on biology

Change disease representation

Patient perception of cancer driven by its complexity and including biology



- "I have a *HER2*-positive cancer located in the breast"
- "My tumor is hormone-receptor positive and has a specific mutation called *PIK3CA* and is primary located in the breast" "Both of our cancers are located in the breast but are different tumors!"
- "My cancer responds well to oral therapy; this is why I need to take them everyday and discuss side effects with the care team and seek for available strategies close to home to manage them"
- "I should not compare my history to other because each cancer is unique, and the complexity of each case is different"



- "My tumor has a specific mutation that does not respond well to usual care. The best treatment for me is a novel clinical trial in a complex cancer center"
- "Oh, I see... Mine although located in the same organ as you has all the characteristics that respond well to standard treatment, this is why I can be treated close to home"
- "I discussed with my doctor the pros and cons of the treatment options and which side effects would be acceptable for me in my daily life"



- "We knew that this could happen and allowed us to plan ahead"
- "Yes, and knowing all this allowed us to participate in advocacy and research initiatives, that can also help others facing a similar situation"



Consequences:

- Trust in the healthcare system and research
- Improved research participation and representation
- Rationale use of healthcare resources
- Better adherence to treatment plans
- Increased participation in their care (self-management, shared decision making, advocacy)

Conclusion

- There is a need to develop large scale screening of patients presenting a high risk of cancer death or toxicities in order to provide them early access to innovation
- Sequencing coding region of DNA as a screening tool has allowed acceleration of drug development but has now reached a plateau
- There is a need to develop new modalities of target screening for patients eligible to therapeutic trials
- Short treatment duration driven by molecular analyses could allow rationale use of resources and avoid compliance issues
- Digital monitoring could increase treatment compliance and patient follow-up
- Implementation of molecular oncology requires development of new frameworks for drug development, oncology practice and disease representation