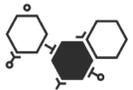


VII CONVEGNO NAZIONALE DELLA RETE ONCOLOGICA SIFaCT



Oltre il modello mutazionale e l'oncologia di precisione: la medicina personalizzata



ONCOFARMA

Milano 23-24 Giugno 2023



Focus on: Il presente della medicina di precisione e dell'immunoncologia:

I Risultati dei Trial Clinicamente Rilevanti

Gennaro Daniele, MD PhD

Conflicts of Interest

- Honoraria/Speaking/training fee: GSK; Gilead
- PI of Sponsored Trials by: Genetech/Hoffman-La-Roche; AstraZeneca; Pfizer; Bayer; Exelixis; Sotio biotech; Kinnate; Beigene; Takeda; SEAGEN; BMS;
- I am a member of Ministry of Health's consultation table on Clinical Trials
- Opinions expressed herein are my own.

The Issue: What is precision
Oncology model?

Comparison of Targeted to Untargeted Design

Simon R, Development and Validation of Biomarker Classifiers for Treatment Selection, JSPI

Treatment Hazard Ratio for <u>Marker Positive Patients</u>	Number of Events for Targeted Design	Number of Events for Traditional Design		
		Percent of Patients Marker Positive		
		50%	33%	20%
0.5	74	316	720	2040
0.67	200	820	1878	5200

“For many treatments (*Generally*), the variation in **prognosis** among patients exceeds the size of the treatment effect”

Una semplificazione...

Se un trial mostra risultati clinicamente rilevanti, il farmaco/intervento viene incorporato direttamente nella pratica clinica

Ma bisognerà pur fare una selezione...(esempi di rilevanza clinica)

1. Un nuovo Inizio

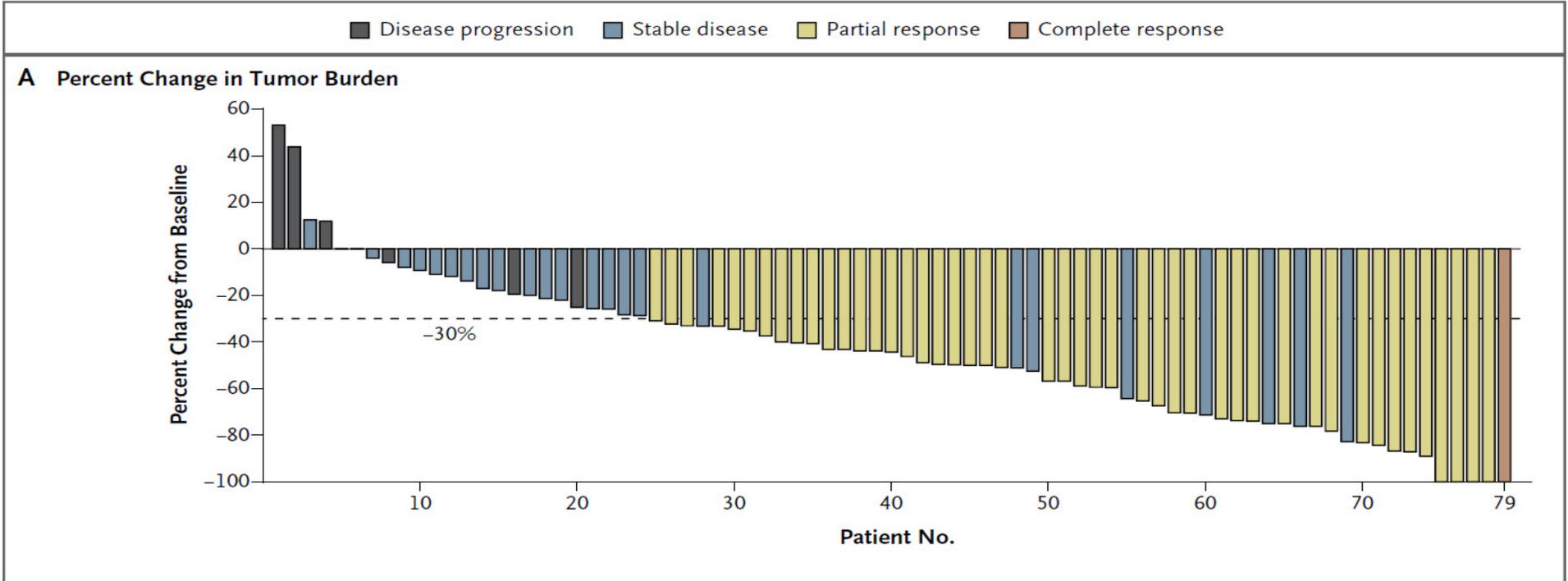
Anaplastic Lymphoma Kinase Inhibition in Non–Small-Cell
Lung Cancer

Study Design:

- Open-label, multicenter, two-part phase 1 trial
 - Crizotinib: oral ATP-competitive selective inhibitor of ALK and MET tyrosine kinases (inhibits tyrosine phosphorylation of activated ALK)
 - Maximum tolerated dose of 250mg po BID, one cycle was 28 days
- Patients were assessed for adverse events and response to therapy

Anaplastic Lymphoma Kinase Inhibition in Non–Small-Cell
Lung Cancer

- 2 patients with NSCLC with FISH positive for ALK rearrangement who were treated with crizotinib during dose escalation had dramatic improvement which prompted a large-scale prospective screening for NSCLC w ALK rearrangement
- 1500 patients were screened from 2008-2010; 82 patients had ALK rearrangement
 - 94% of patients had received at least one previous tx
 - 5 patients received crizotinib as first line



ORR: 57% [95% CI 46-68] at a mean treatment duration of 6.4 months

46/82 (56%) of patients had confirmed PR

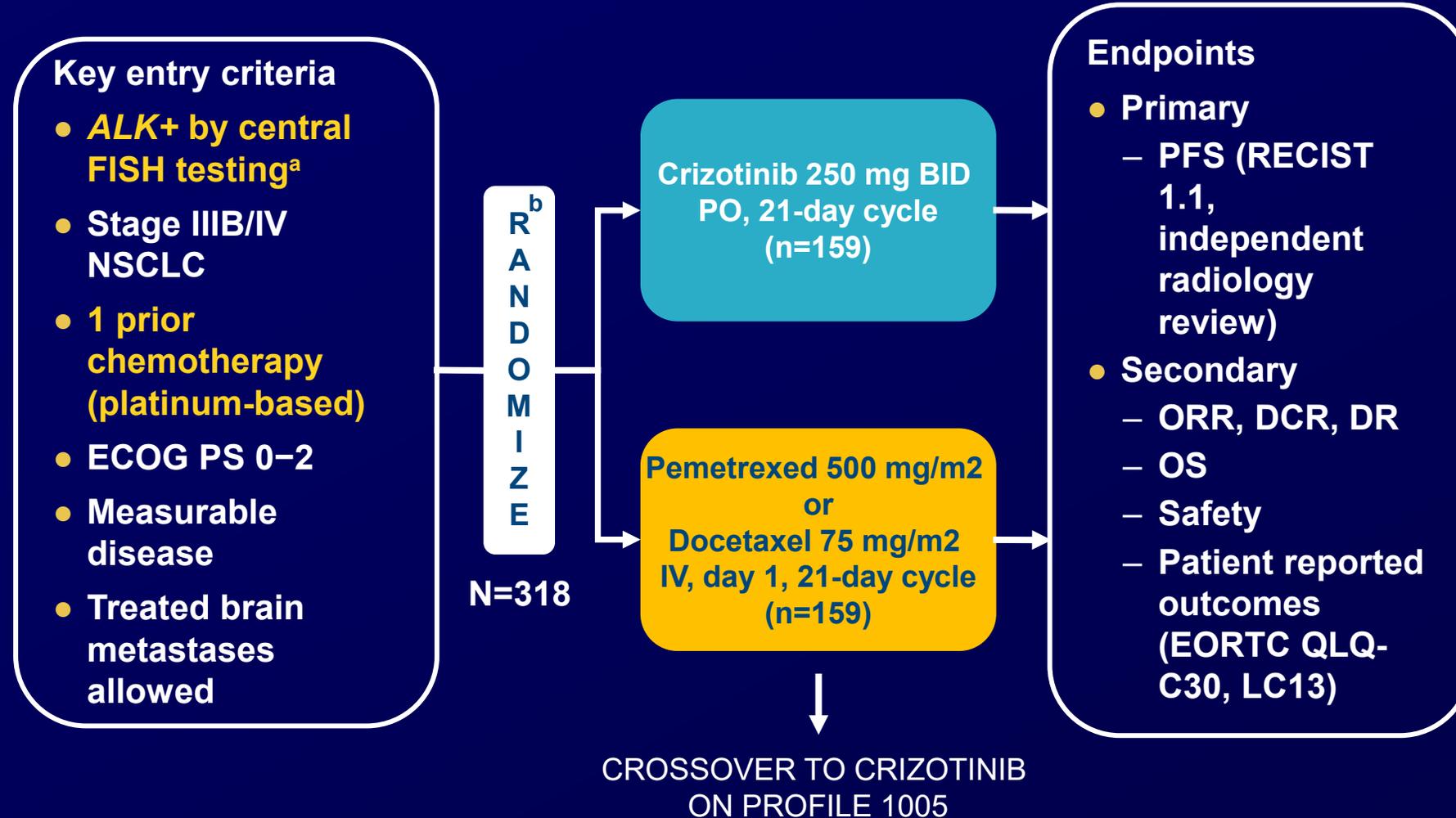
1/82 patients had CR

27/82 (33%) of patients had stable disease

Estimated probability of 6-month PFS was 72%

8/2011 FDA granted accelerated approval to crizotinib

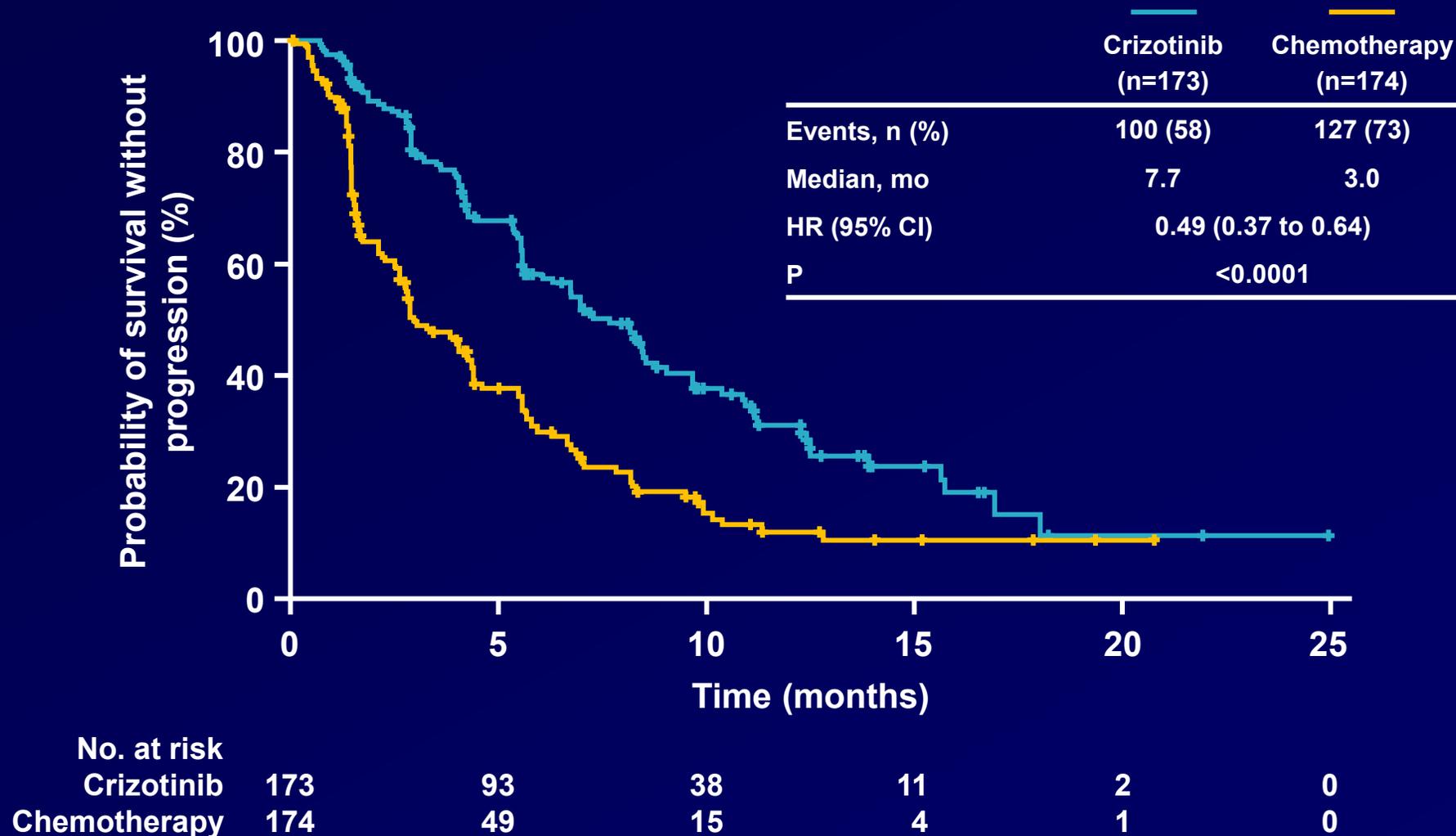
PROFILE 1007: Study Design



^aALK status determined using standard ALK break-apart FISH assay

^bStratification factors: ECOG PS (0/1 vs 2), brain metastases (present/absent), and prior EGFR TKI (yes/no)

Primary Endpoint: PFS by Independent Radiologic Review (ITT Population)



Presented at ESMO 2012

La rilevanza WOW
(IO+Precision)!!

Mismatch Repair Deficient Colon Cancer

Approximately 10-15% of colon cancers are mismatch repair deficient (dMMR)

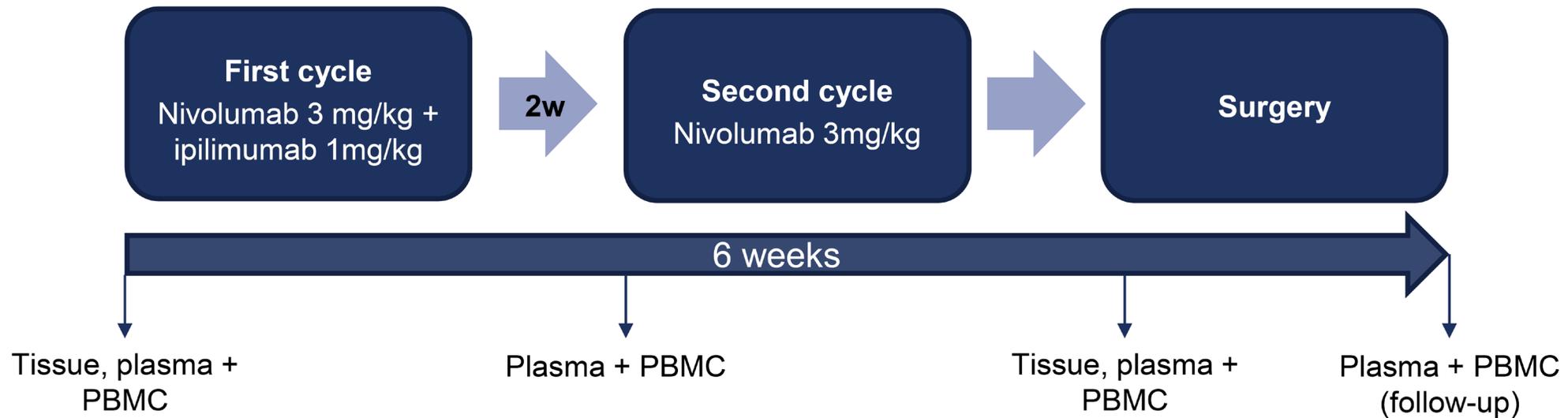
1/3 of dMMR colorectal cancers are associated with Lynch Syndrome

Recurrence rates of 20-40% for **stage III dMMR** tumors **despite** standard-of-care chemotherapy

- High-risk disease (T4 or N2) is highly associated with poor survival

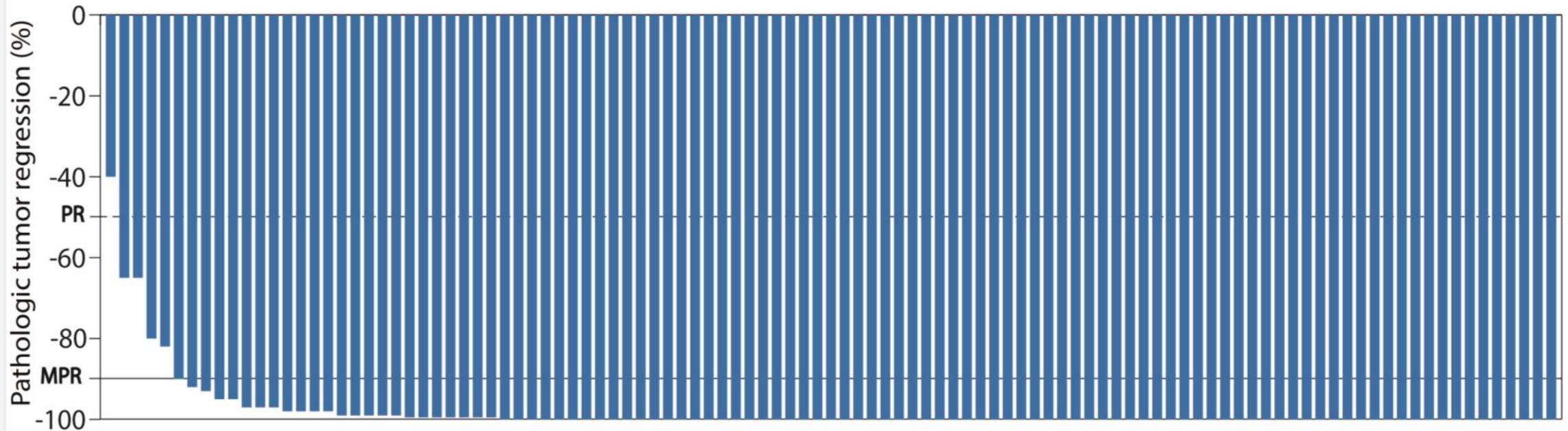
NICHE-2 study design

- Investigator-initiated, non-randomized multicenter* study



*6 participating hospitals in the Netherlands
PBMC = peripheral blood mononuclear cells

Major pathologic response in 95% of patients; 67% pCR



Una oasi (?) nel deserto!

The NEW ENGLAND JOURNAL *of* MEDICINE

ORIGINAL ARTICLE

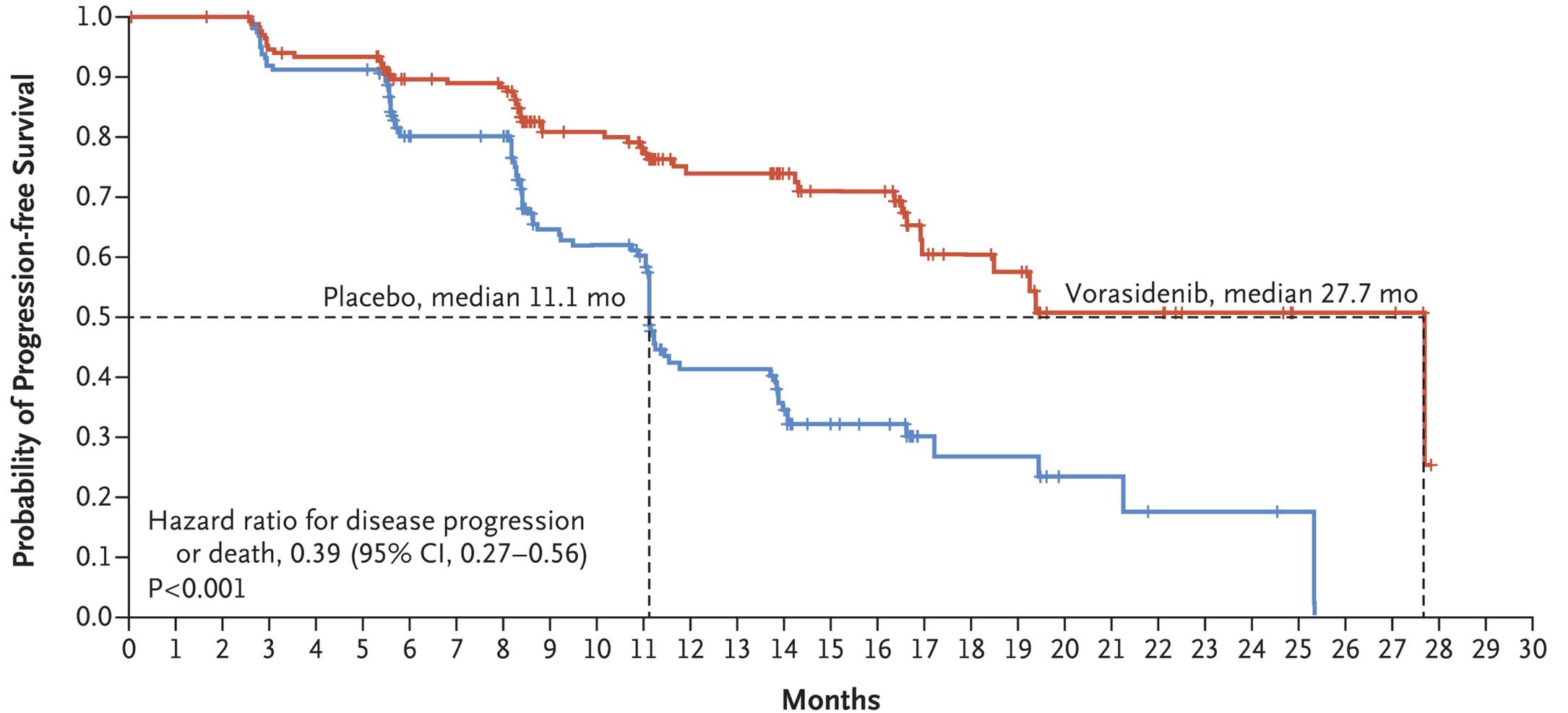
Vorasidenib in IDH1- or IDH2-Mutant Low-Grade Glioma

I.K. Mellinghoff, M.J. van den Bent, D.T. Blumenthal, M. Touat, K.B. Peters, J. Clarke, J. Mendez, S. Yust-Katz, L. Welsh, W.P. Mason, F. Ducray, Y. Umemura, B. Nabors, M. Holdhoff, A.F. Hottinger, Y. Arakawa, J.M. Sepulveda, W. Wick, R. Soffietti, J.R. Perry, P. Giglio, M. de la Fuente, E.A. Maher, S. Schoenfeld, D. Zhao, S.S. Pandya, L. Steelman, I. Hassan, P.Y. Wen, and T.F. Cloughesy

The Indigo Trial

- Phase 3 randomised trial (1:1)
- Double blind/Placebo controlled
- Patients 12y.o. or older with
- Grade 2 glioma (WHO 2016)
- IDH1/IDH2 mutated (Oncomine Dx assessed centrally)
- Primary endpoint: Progression Free Survival
- EXP-RX: Vorasidenib 40mg (qd) q28
- CTRL-RX: placebo (Crossover whether PD at BICR)

A Progression-free Survival



No. at Risk

Vorasidenib	168	166	166	157	154	154	133	131	129	93	91	81	63	63	52	45	45	25	22	20	11	11	11	7	7	4	4	4	0
Placebo	163	162	161	146	145	145	117	116	114	73	70	65	38	38	29	21	19	9	8	8	4	4	2	2	2	1	0		

Quali sono gli spunti di riflessione
nel 2023?

“For many treatments, the variation in **prognosis** among patients exceeds the **size of the treatment effect**”

- Il paradigma della medicina di precisione non può prescindere dalla «qualità» dei farmaci
- Quale metodologia per produrre dati «rilevanti»

In un mondo ideale...

- Il successo della strategia di precisione dipende dalla sommatoria di 2 fattori cruciali (indipendenti):
 - Valore prognostico del biomarker (importanza del target per il tumore)
 - Valore del farmaco nella popolazione selezionata (attività farmacologica)

Nel mondo reale...

- Il valore del biomarker è misurato sulla base del suo ruolo di «target» per l'inibizione farmacologica (valore predittivo).
- Ci si è concentrati molto spesso sul valore predittivo ignorando quello prognostico

ESCAT: ESMO Scale of Clinical Actionability for molecular Targets

	ESCAT evidence tier		Required level of evidence	Clinical implication
Ready for routine use	I Alteration-drug match is associated with improved outcome in clinical trials	I-A	Prospective, randomised clinical trials show the alteration-drug match in a specific tumour type results in a clinically meaningful improvement of a survival end point	Access to the treatment should be considered standard of care
		I-B	Prospective, non-randomised clinical trials show that the alteration-drug match in a specific tumour type, results in clinically meaningful benefit as defined by ESMO MCBS 1.1	
		I-C	Clinical trials across tumour types or basket clinical trials show clinical benefit associated with the alteration-drug match, with similar benefit observed across tumour types	
Investigational	II Alteration-drug match is associated with antitumour activity, but magnitude of benefit is unknown	II-A	Retrospective studies show patients with the specific alteration in a specific tumour type experience clinically meaningful benefit with matched drug compared with alteration-negative patients	Treatment to be considered “preferable” in the context of evidence collection either as a prospective registry or as a prospective clinical trial
		II-B	Prospective clinical trial(s) show the alteration-drug match in a specific tumour type results in increased responsiveness when treated with a matched drug, however, no data currently available on survival end points	
Hypothetical target	III Alteration-drug match suspected to improve outcome based on clinical trial data in other tumour type(s) or with similar molecular alteration	III-A	Clinical benefit demonstrated in patients with the specific alteration (as tiers I and II above) but in a different tumour type. Limited/absence of clinical evidence available for the patient-specific cancer type or broadly across cancer types	Clinical trials to be discussed with patients
		III-B	An alteration that has a similar predicted functional impact as an already studied tier I abnormality in the same gene or pathway, but does not have associated supportive clinical data	
	IV Pre-clinical evidence of actionability	IV-A	Evidence that the alteration or a functionally similar alteration influences drug sensitivity in pre-clinical <i>in vitro</i> or <i>in vivo</i> models	Treatment should “only be considered” in the context of early clinical trials. Lack of clinical data should be stressed to patients
		IV-B	Actionability predicted <i>in silico</i>	
Combination development	V Alteration-drug match is associated with objective response, but without clinically meaningful benefit		Prospective studies show that targeted therapy is associated with objective responses, but this does not lead to improved outcome	Clinical trials assessing drug combination strategies could be considered
Lack of Evidence	X Lack of evidence for actionability		No evidence that the genomic alteration is therapeutically actionable	The finding should not be taken into account for clinical decision

Nel mondo reale...

- Il valore del biomarker è misurato sulla base del suo ruolo di «target» per l'inibizione farmacologica (valore predittivo).
- Ci si è concentrati molto spesso sul valore predittivo ignorando quello prognostico

PFS, OS & RR in Precision Oncology Trials and

Trial	NTC number	PFS	OS	ORR	Attrition
CREATE	NCT01524926	9,00	NA	50,00	34%
PANGEA	NCT02213289	8,20	15,70	74,07	49%
Battle	NCT00409968	1,90	8,80	3,69	72%
I-PREDICT	NCT02534675	3,67	11,80	23,29	6%
NCI-MATCH (subprotocol H)	NCT02465060	11.4	28.6	37,93	1%
Tapur (breat-TMBh)	NCT02693535	2,65	7,65	21,00	
ROAR	NCT02034110	9,00	14,00	51,20	7%
NCI-MATCH (subprotocol Q)	NCT02465060	3,10	8,40	5,56	1%
Drug Rediscovery protocol	NCT02925234	3,00	10,00	15,35	33%
NCI-MATCH Subprotocol EAY131-Y	NCT02465060	5,5	14,5	28,00	
plasmaMATCH	NCT03182634	5,20	NA	13,10	12%
CUSTOM	NCT01306045	2,30	6,50	25,58	7%
NCI-MATCH (subprotocol Z1D)	NCT02465060	6.3	17.3	35,71	1%
National Lung Matrix Trial	NCT02664935	3,00	NA	10,00	5%

Nel mondo reale...

- Il valore del biomarker è misurato sulla base del suo ruolo di «target» per l'inibizione farmacologica (valore predittivo).
- Ci si è concentrati molto spesso sul valore predittivo ignorando quello prognostico
- Questo non ci consente di valutare correttamente il valore di un farmaco in una popolazione target e crea dei:
 - Dati scontati

Genomics to select treatment for patients with metastatic breast cancer

<https://doi.org/10.1038/s41586-022-05068-3>

Received: 24 October 2021

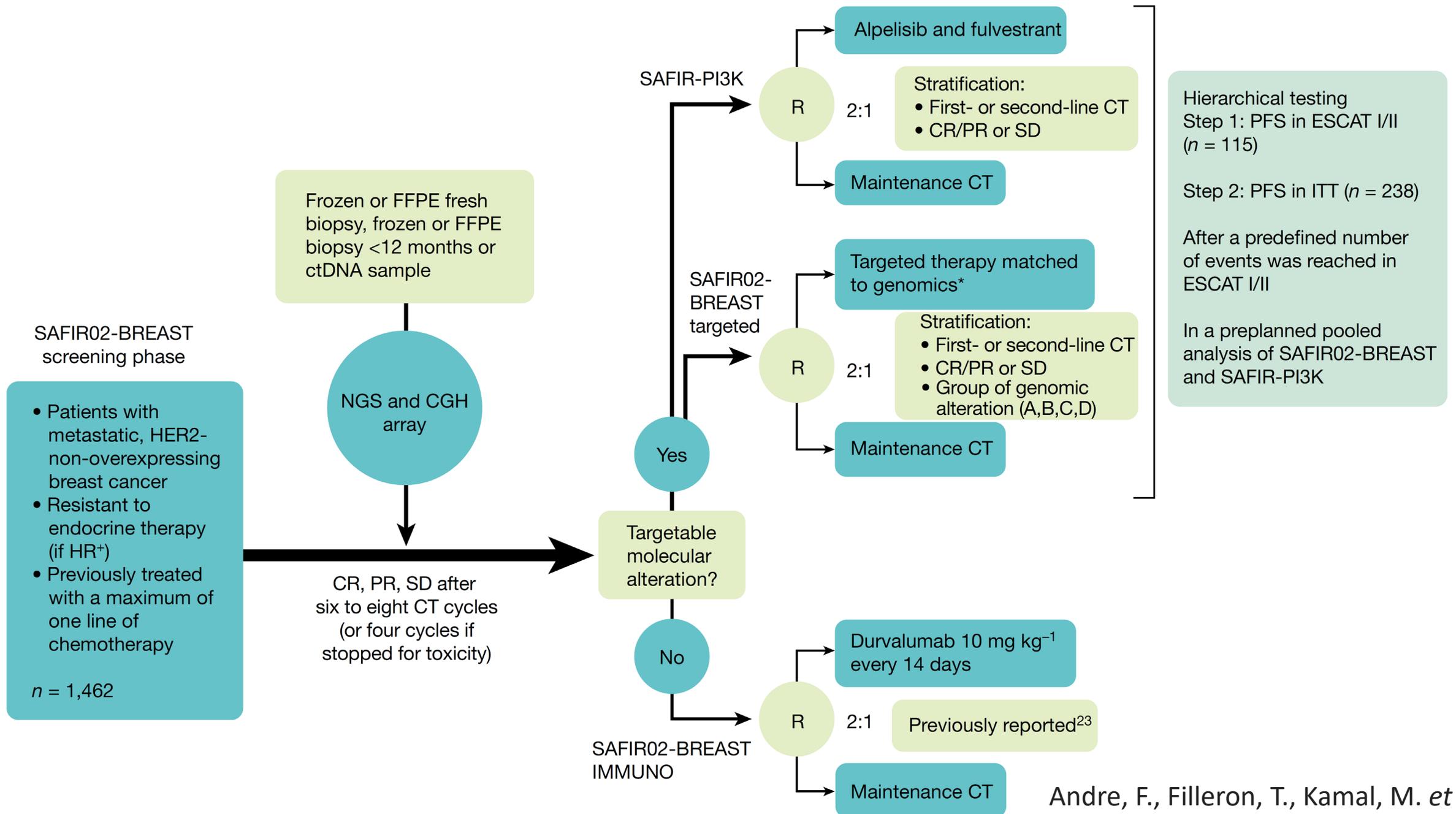
Accepted: 3 July 2022

Published online: 7 September 2022



Check for updates

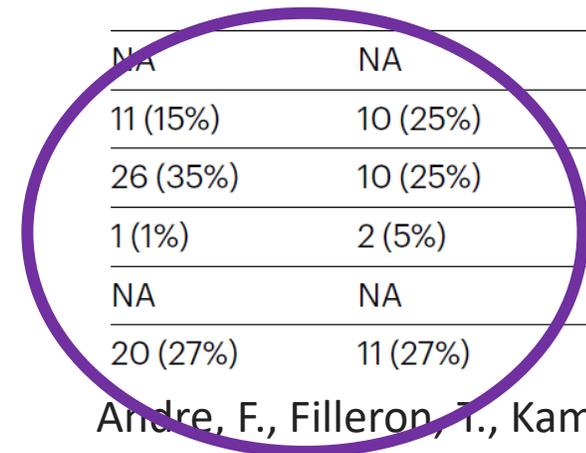
Fabrice Andre^{1,2,3,4,34}✉, Thomas Filleron^{5,34}, Maud Kamal^{6,34}, Fernanda Mosele², Monica Arnedos¹, Florence Dalenc⁷, Marie-Paule Sablin^{6,8}, Mario Campone⁹, Hervé Bonnefoi¹⁰, Claudia Lefeuvre-Plesse¹¹, William Jacot¹², Florence Coussy¹³, Jean-Marc Ferrero¹⁴, George Emile¹⁵, Marie-Ange Mouret-Reynier¹⁶, Jean-Christophe Thery¹⁷, Nicolas Isambert¹⁸, Alice Mege¹⁹, Philippe Barthelemy²⁰, Benoit You²¹, Nawale Hajjaji²², Ludovic Lacroix²³, Etienne Rouleau²³, Alicia Tran-Dien^{2,3,24}, Sandrine Boyault²⁵, Valery Attignon²⁵, Pierre Gestraud²⁶, Nicolas Servant²⁶, Christophe Le Tourneau⁶, Linda Larbi Cherif⁶, Isabelle Soubeyran²⁷, Filippo Montemurro²⁸, Alain Morel²⁹, Amelie Lusque⁵, Marta Jimenez³⁰, Alexandra Jacquet³⁰, Anthony Gonçalves^{31,35}, Thomas Bachelot^{32,35} & Ivan Bieche^{33,35}



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

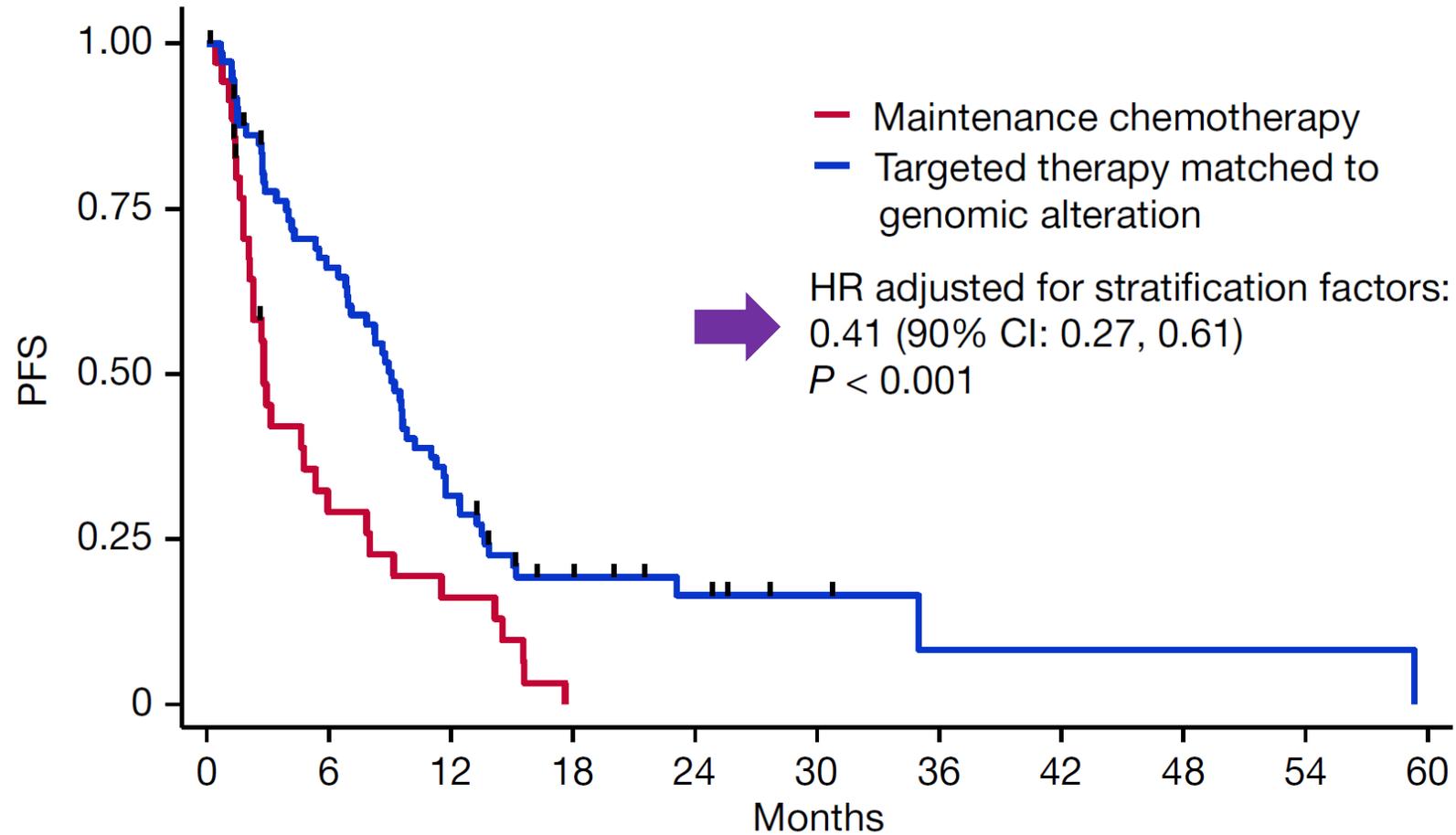
Matched genomic alteration/targeted therapy decision by MTB

IGF1R amplification (n=3), TSC1/2 mutation (n=3), STK11 deletion (n=1), RPTOR amplification (n=1) and AZD2014	7 (4%)	1 (1%)	-	NA	NA	-
AKT1 mutation and AZD5363	12 (8%)	4 (5%)		12 (16%)	4 (10%)	
PTEN mutation and/or deletion and AZD5363	8 (5%)	2 (2%)		4 (5%)	1 (3%)	
PIK3CA (n=36), PIK3R1 (n=2); mutations/PIK3CB (n=1), AKT1 (n=1), AKT3 (n=1), PDPK1 (n=1); amplifications and AZD5363	30 (19%)	12 (15%)		NA	NA	
FGFR1 (n=19), FGFR2 (n=1), FGF4 (n=4), FGFR3 (n=1); amplifications/FGFR2 (n=1), FGFR4 (n=1); mutations and AZD4547	17 (11%)	10 (12%)		NA	NA	
ERBB2 mutation and AZD8931	1 (0.5%)	2 (2%)		1 (1%)	2 (5%)	
EGFR mutation/amplification (n=3) or ERBB3 mutation (n=2) and AZD8931	2 (1%)	3 (4%)		NA	NA	
FRS2 amplification (n=10), NF1 mutation (n=7), KRAS mutation (n=4), BRAF amplification (n=1), BRAF mutation (n=1) and selumetinib	17 (11%)	6 (7%)		NA	NA	
VEGFA amplification (n=3), RET mutation (n=1), EGFR amplification (n=1), KDR mutation (n=1) and vandetanib	3 (2%)	3 (4%)		NA	NA	
AR amplification and bicalutamide	0	1 (1%)		NA	NA	
BRCA1 mutation and olaparib	11 (7%)	10 (12%)		11 (15%)	10 (25%)	
BRCA2 mutation and olaparib	26 (16%)	10 (12%)		26 (35%)	10 (25%)	
PALB2 mutation and olaparib	1 (0.5%)	2 (2%)		1 (1%)	2 (5%)	
ATR/ATM mutation/deletion and olaparib	2 (1%)	4 (5%)		NA	NA	
PIK3CA mutation and alpelisib	20 (13%)	11 (14%)		20 (27%)	11 (27%)	



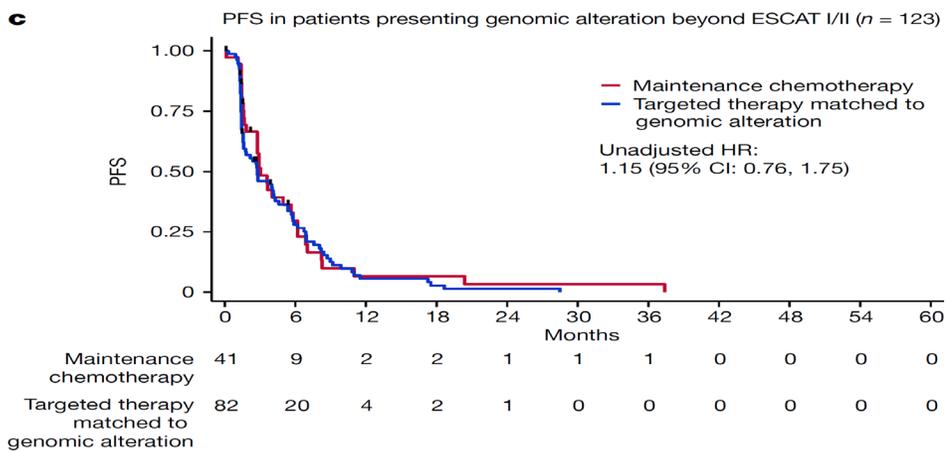
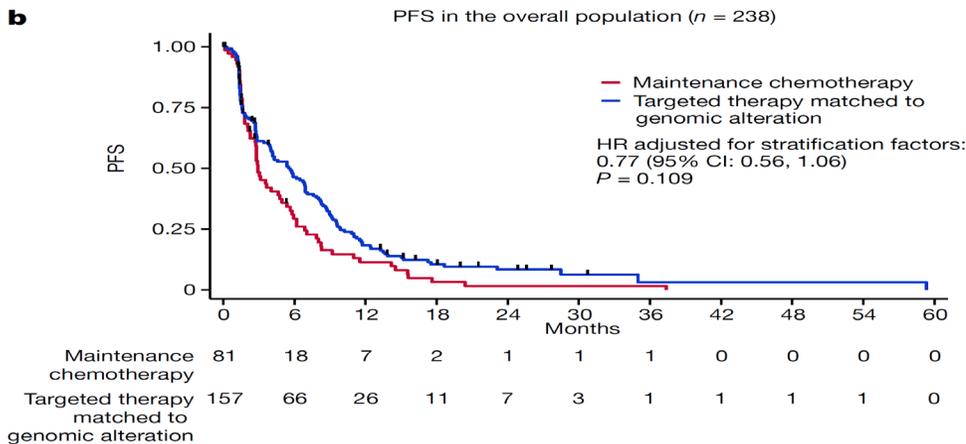
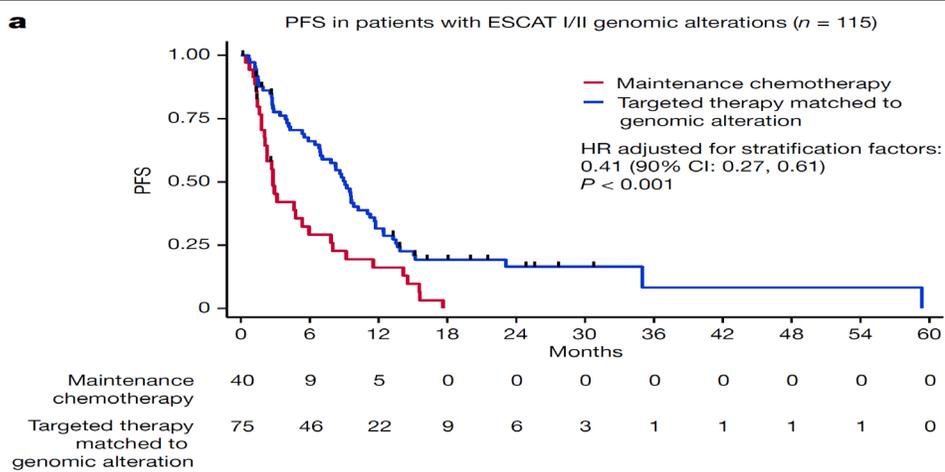
Andre, F., Filleron, T., Kamal, M. et al. *Nature* **610**, 343–348 (2022).

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



Maintenance chemotherapy	40	9	5	0	0	0	0	0	0	0
Targeted therapy matched to genomic alteration	75	46	22	9	6	3	1	1	1	0

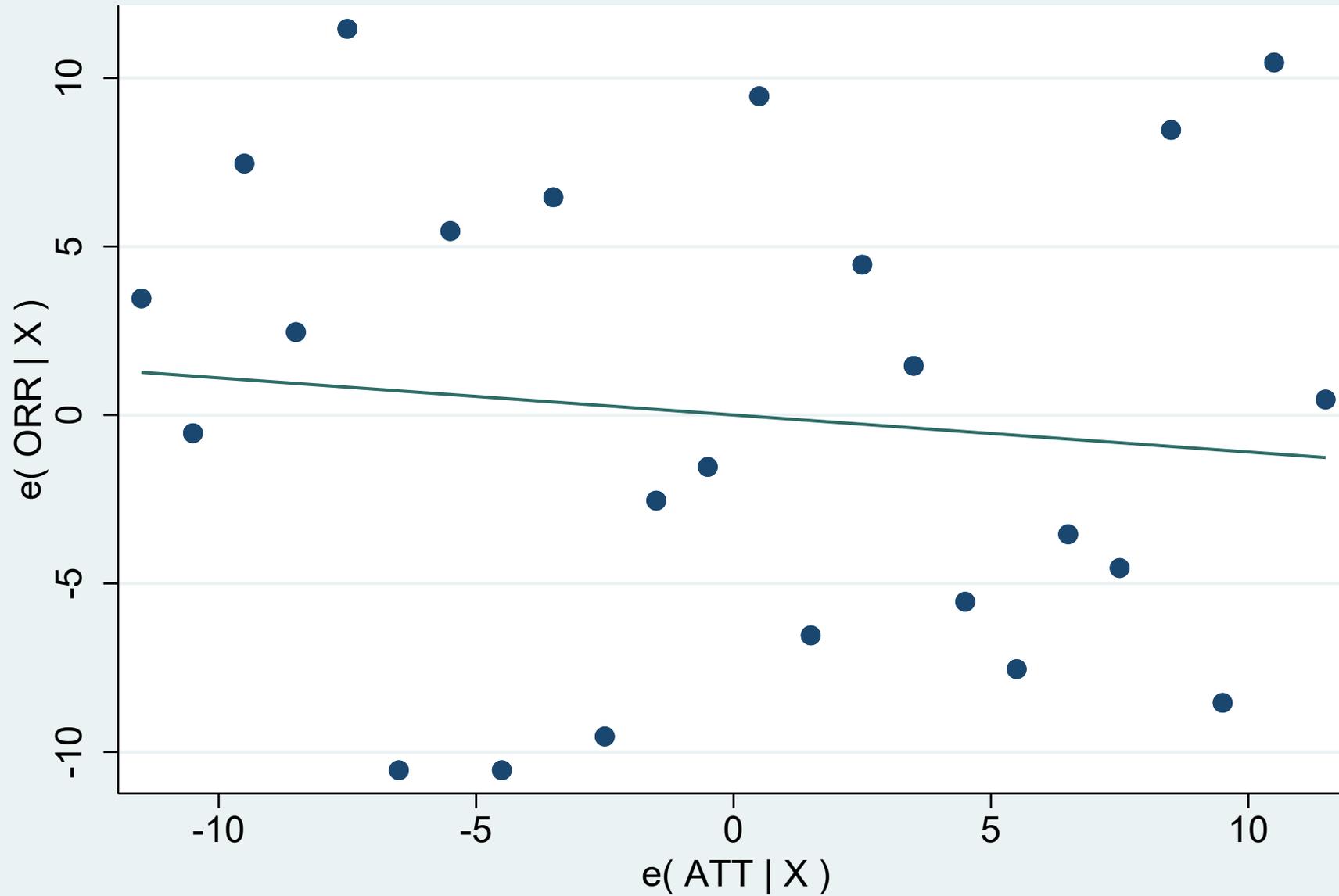
Andre, F., Filleron, T., Kamal, M. *et al.* *Nature* **610**, 343–348 (2022).



- Il vantaggio si ottiene esclusivamente nelle mutazioni ESCAT I/II
- E' molto debole e (non statisticamente significativo nella popolazione generale, test gerarchico)
- Nullo (dato forte) nella popolazione con mutazione ESCAT III-
- **Questo dato può essere considerato più una validazione dell'ESCAT come fattore predittivo nelle pazienti mBC HER2- che un'informazione aggiuntiva rispetto a quanto noto!!**

Nel mondo reale...

- Il valore del biomarker è misurato sulla base del suo ruolo di «target» per l'inibizione farmacologica (valore predittivo).
- Ci si è concentrati molto spesso sul valore predittivo ignorando quello prognostico
- Questo non ci consente di valutare correttamente il valore di un farmaco in una popolazione target e crea dei:
 - Dati scontati
 - Potenziali paradossi



coef = -.11, se = .20984121, t = -.52

- Il paradigma della medicina di precisione non prescinde dalla «qualità» dei farmaci
- **Quale metodologia per produrre dati «rilevanti»**

LETTERS TO THE EDITOR

Why will there never be a randomized trial for NTRK-rearranged tumors?



The optimal assessment of the risk-to-benefit ratio of a new treatment, particularly in oncology, has always been based on the results of prospective randomized trials, ideally carried out in a double-blind manner with a large sample size and overall survival as the primary endpoint. This is still the best level of evidence available and has been an indisputable metric for discussing approval and reimbursement with health authorities for decades. This remains true in clinical oncology. However, it is no longer an appropriate standard in personalized medicine, particularly when focusing on rare subtypes. Indeed, molecular screening can categorize common diseases into several ultra-rare pathologies, each grouping a limited number of patients. For example, patients with NTRK-rearranged tumors are textbook cases. They could be identified and receive personalized treatment; but, in some countries, access to treatment is suspended pending the results of randomized trials. However, the demand is insurmountable.

However, (RCT) is no longer appropriate for Precision Oncology...
...Rarity of the molecular alteration (ultra-rare tumors) and the absence of standard-of-care pose risk to EQUIPOISE!!

³Department of Medical Oncology, Centre Léon Bérard, Lyon;

⁴Medical Oncology Department, Université Claude Bernard, Lyon, France

(*E-mail: n-penel@o-lambret.fr).

Available online 15 April 2023

© 2023 European Society for Medical Oncology. Published by Elsevier Ltd. All rights reserved.

<https://doi.org/10.1016/j.annonc.2023.04.001>

E voi randomizzereste i pazienti
NTRK??

Take home message

**Bisogna fare ancora molta ricerca
sulla ricerca in oncologia di
precisione.**