

# Biomarker-driven clinical trials

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# Introduction

## What is a biomarker ? (National Cancer Institute)

- A biological molecule found in *blood, other body fluids, or tissues*
- that is a sign of a *normal or abnormal process, or of a condition or disease*
- Also called *molecular marker* and *signature molecule*

# Introduction

## Clinical utility of markers

- PROGNOSTIC

Biomarker associated with disease outcome *independent of any treatment*

- PREDICTIVE

Biomarker that *predicts for response or resistance to a specific treatment*

Prognostic  $\neq$  Predictive

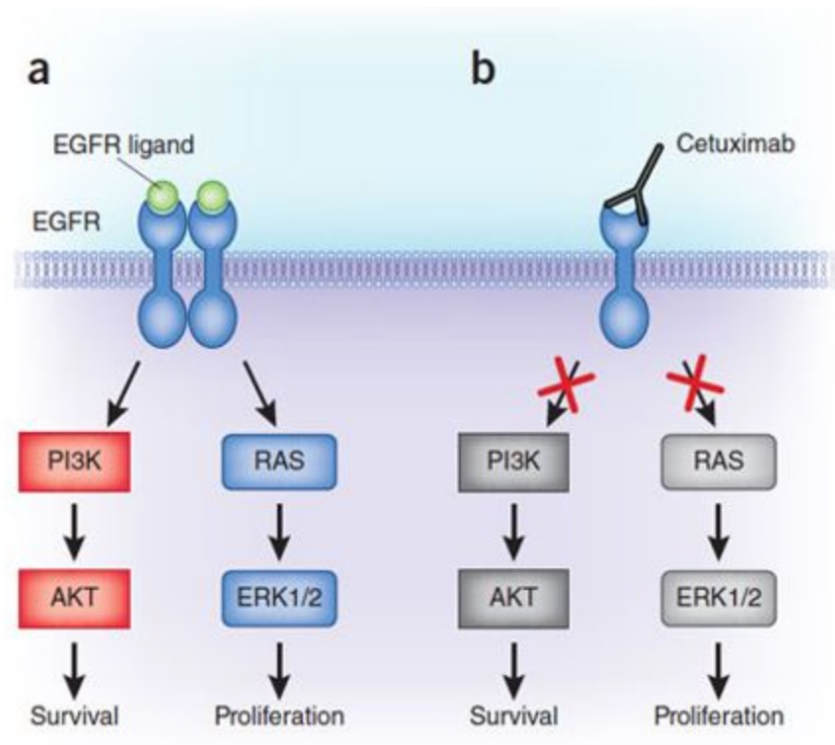
# Introduction

## CETUXIMAB

= monoclonal antibody against EGFR

- Only approved targeted therapy in head and neck cancer
- Response rate as single agent: 13%

**No biomarker predictive of response or resistance!**



# Introduction

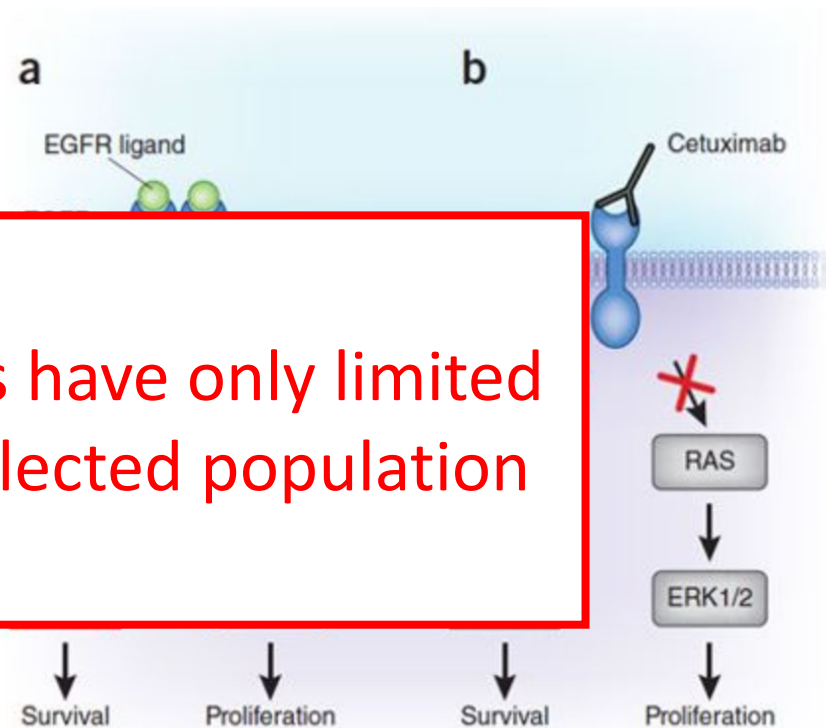
## CETUXIMAB

= monoclonal antibody against EGFR

- Only appropriate therapy in cancer
- Response rate to agent: 13%

Targeted agents have only limited activity in unselected population

No biomarker predictive of response or resistance!



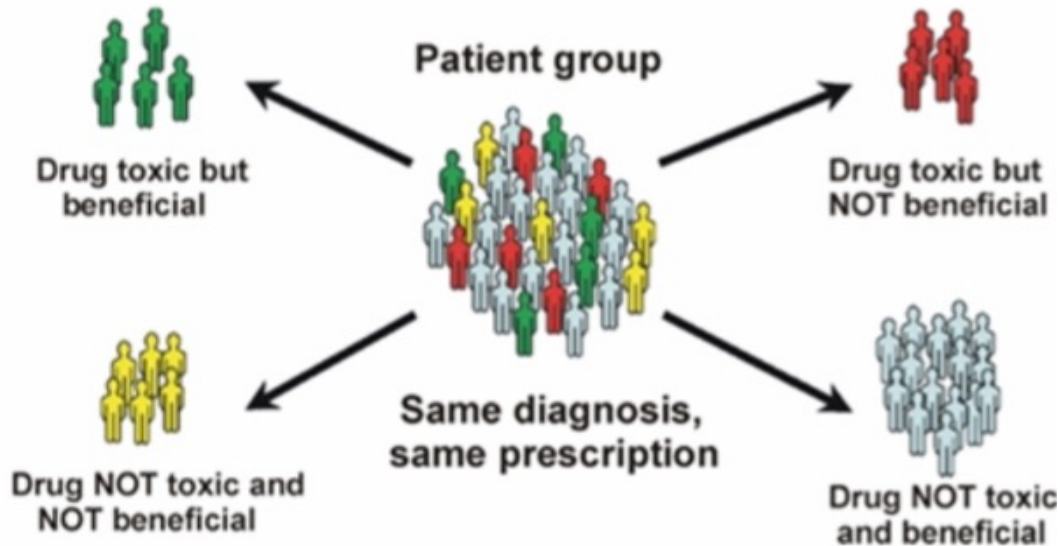
# Introduction

Can we select the population based on biomarker ?

Biomarker + patient



Targeted drug



**PRECISION  
ONCOLOGY**

**Give the right  
drug to the right  
patient !**

# Introduction

## **Biomarker-based treatment in clinical practice**

- *HER2* amplified breast cancer treated with HER2 targeting therapies
- *EGFR* mutated lung cancer treated with EGFR tyrosine kinase inhibitors

# Introduction

Treatment landscape in oncology is changing !

**« One treatment fits all »**

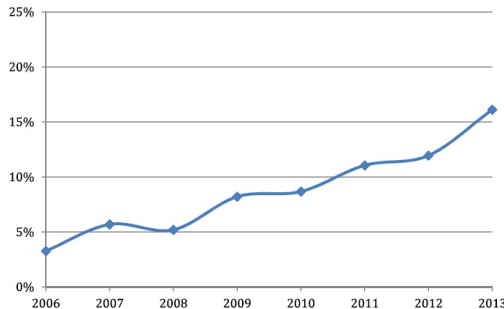


**« Precision Medicine » based on biomarkers**

Proper testing in clinical trials is indispensable to  
validate claims of efficacy and safety !



# Introduction



Proportion of trials in USA requiring the presence/absence of a genomic alteration increased over 5-fold between 2006 and 2013

Cancer Treat Rev, 2015

In 2018, over one-third of trials were using biomarkers to stratify patients (IQVIA, Global trends in oncology 2018)

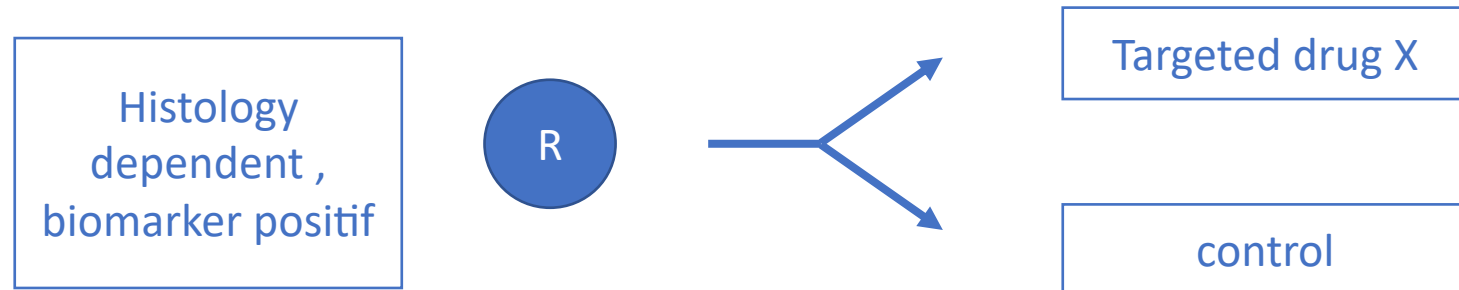
Number of U.S. Oncology Medicines with Required or Recommended Predictive Biomarker Testing



# Introduction

## Standard approach

Investigating one or two interventions in a single disease enriched for 1 biomarker

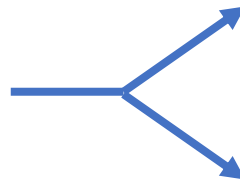


# Introduction

**Trastuzumab (Herceptin): Anti-HER2 Antibody, targets HER2 oncoprotein**

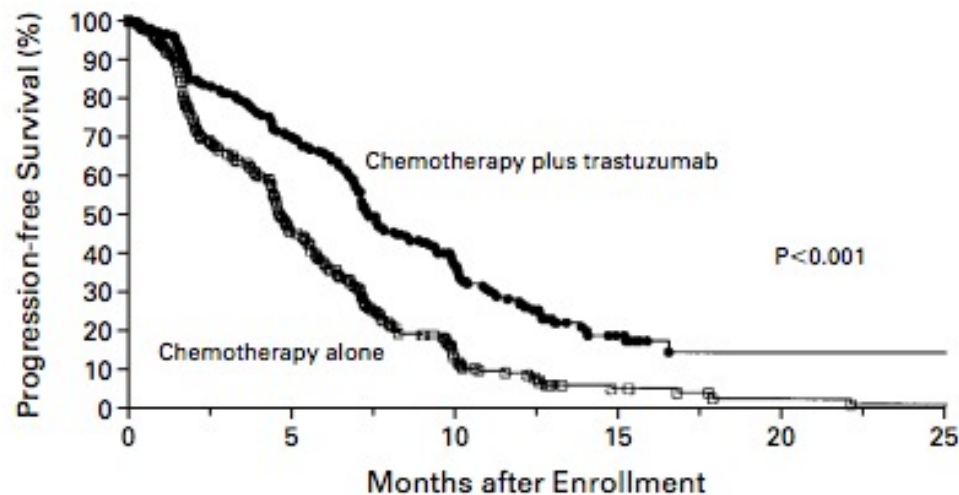
**25-30%  
of  
breast  
cancers**

Metastatic breast  
cancer  
overexpressing  
HER2



Chemotherapy +  
Trastuzumab

Chemotherapy



# Introduction

## Challenges

- Slow recruitment (low incidence biomarker)
- Expensive
- Time-consuming

# Next-generation clinical trials

- Master protocols
  - Basket trials
  - Umbrella trials
- Screening programs
- Strategy trials

# Master protocols

= Framework in which several (sub)studies that investigate multiple therapies are operated under one « overarching » master protocol

Regroups under the same protocol, sub-studies sharing key designs and operational aspects

# Master protocols

## Main aims

- Facilitate screening and patient accrual
- Answer more questions more efficiently and in less time
- Operational efficiency

# Master protocols

## Basket

histology  
independent

marker-  
specific  
cohorts



## Umbrella

Histology  
dependent  
many marker  
cohorts





# Basket Trials

**Histology-agnostic**



**Basket  
trial**

Disease or histologic feature 1    Disease or histologic feature 2    Disease or histologic feature 3

Screen for presence of target

Target-positive  
participants

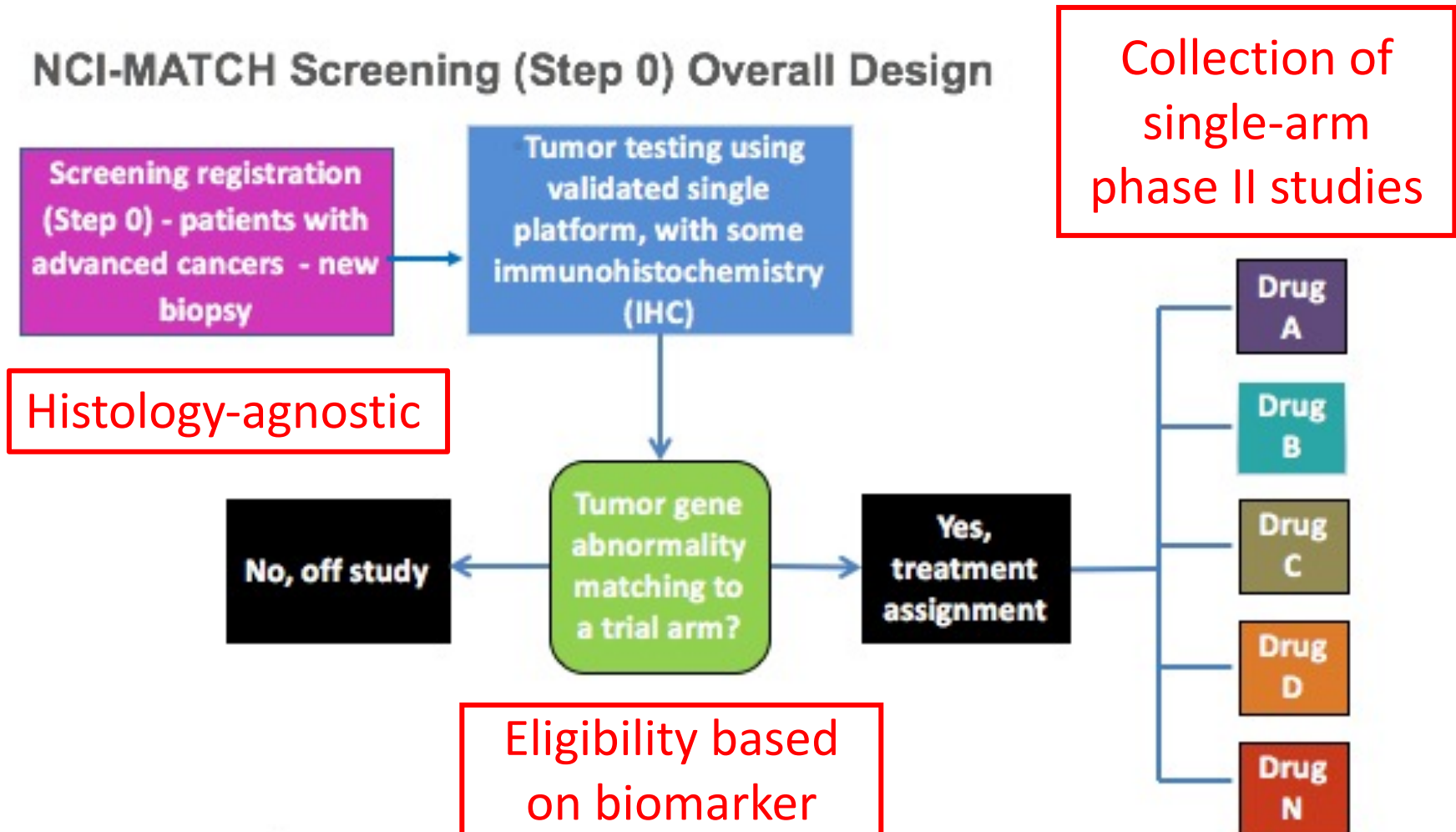
Trial of one targeted therapy  
(controlled or uncontrolled)

# Basket Trials

Study	Tumor	Biomarker testing	Methodology	Endpoint	Results
NCI-MATCH	All, <b>advanced solid tumors</b>	New biopsy, <b>sequencing on 143 genes</b>	Patients with <b>molecular alteration</b> are assigned in <b>1 of predefined treatment cohorts</b>	Objective response rate (ORR)	Reported per arm
My pathway	<b>Advanced refractory solid</b> tumor harboring <b>molecular alteration in HER2, EGFR, BRAF or Hedgehog pathway</b>	Molecular profiling was <b>not conducted as part of the trial</b>	Patients are assigned to <b>specific treatment cohorts</b> based on the presence of a relevant molecular alteration	ORR within each tumor-pathway cohort	ORR: 23% within different tumor types
SUMMIT	<b>Solid tumors</b> harboring <b>HER2 and HER3 mutations</b>	MP was <b>not conducted as part of the trial</b>	Pts wit HER2-mutations were enrolled into <b>disease-specific cohorts</b> and HER3 mutants into 1 cohort	ORR	HER2-mutant: primary endpoint only met for BC (ORR 32%) and not for lung, colorectal or bladder No responses in HER3 mutant cohort

# Basket trial – NCI MATCH

## NCI-MATCH Screening (Step 0) Overall Design



# Basket trial – NCI MATCH

## Objective

- To determine whether matching certain drugs or drug combinations in adults whose tumors have specific gene abnormalities will effectively treat their cancer, **regardless of the cancer type**
- **signal-finding trial**—treatments that show promise can advance to larger, more definitive trials

# Basket trial – NCI MATCH

- Open at US-based sites (nearly 1100 cancer centers)
- Master protocol with multiple phase II treatment arms (nearly 40 treatment arms)

Eligibility defined by molecular characteristics

- Single agents or combinations with recommended phase II dosage(s) known

FDA-approved for another indication or investigational

- Treatment arms open and close without affecting others

# Basket trial – NCI MATCH

- Successful laboratory testing for 93% of patients (5560/5962)
- Preplanned access to drugs within the trial (<-> screening programs)...however **only 12 %** (689/5560) were finally enrolled in the trial...

# Basket trial – NCI MATCH

## NCI-MATCH 30 Treatment Arms, By Prevalence Rate of Gene Abnormality

Arm	Variant	Prevalence Rate %	Drug	Arm	Variant	Prevalence Rate %	Drug
I	PIK3CA	3.47	Taselisib	Y	AKT	0.77	AZD5363
W	FGFR	2.86	AZD4547	H	BRAF V600 E/K	0.69	Tafinlar® Mekinist™
Z1I	BRCA1 or BRCA2	2.79	AZD1775	U	NF2 loss	0.69	Defactinib (VS-6063)
P	PTEN loss	1.93	GSK2636771	C2	MET exon 14	0.61	Xalkori®
Z1A	NRAS	1.90	Binimetinib	C1	MET amplif.	0.51	Xalkori®
S1	NF1	1.77	Mekinist™	T	SMO/PTCH1	0.42	Erivedge®
N	PTEN	1.75	GSK2636771	L	mTOR	0.31	TAK-228
Z1D	dMMR status	1.51	Opdivo®	S2	GNAQ/GNA11	0.16	Mekinist™
Q	HER2 amplif.	1.49	Kadcyla®	E	EGFR T790M	0.11	AZD9291
J	HER2 amplif.	1.49	Herceptin® Perjeta®	V	cKIT	0.11	Sutent®
Z1C	CDK4 or CDK6	1.36	Ibrance®	Z1E	NTRK	0.10	Larotrectinib
M	TSC1 or TSC2	1.11	TAK-228	G	ROS1	0.05	Xalkori®
B	HER2 activating	1.04	Gilotrif®	A	EGFR activating	0.05	Gilotrif®
Z1B	CCND1/2/3	0.84	Ibrance®	F	ALK	0.03	Xalkori®
R	BRAF fusions	0.80	Mekinist™	X	DDR2	0.00	Sprycel®

# Basket trial – NCI MATCH

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Z1I	BRCA1 or BRCA2	2.79	AZD1775	U	NF2 loss	0.69	Defactinib (VS-6063)
P	PTEN loss	2.68	Everolimus	CC	CCNE1	2.64	Ureli®
Z1A	NRAS	2.58	Ureli®	CC	CCNE1	2.64	Ureli®
S1	NF1	2.58	Ureli®	CC	CCNE1	2.64	Ureli®
N	PTEN	2.58	Ureli®	CC	CCNE1	2.64	Ureli®
Z1D	dMMR status	2.58	Ureli®	CC	CCNE1	2.64	Ureli®
Q	HER2 amplif.	2.58	Ureli®	CC	CCNE1	2.64	Ureli®
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**18% of screened tumors was found to have a genetic mutations that matched the patient to 1 of the 30 treatment arms: low prevalence of targeted variants**



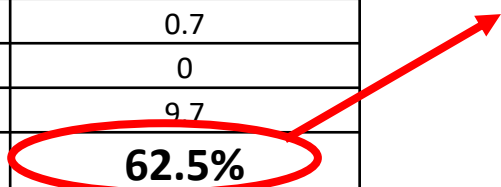
# Basket trial – NCI MATCH

Less Common Disease Type	% of Total Screened (N=5560)
Ovarian	9.5
Uterine	6.2
Pancreas	6.1
Sarcoma	4.6
Head and Neck	3.9
Neuroendocrine	3.3
Gastroesophageal	3.2
Cholangiocarcinoma	2.8
Liver and Hepatobiliary other than Cholangio.	1.9
Central Nervous System	1.7
Bladder/Urinary Tract	1.6
Cervical	1.6
Small Cell Lung	1.4
Melanoma	1.4
Kidney	1.2
Anal	0.8
Mesothelioma	0.8
Lymphoma	0.7
Myeloma	0
Other	9.7
<b>Less Common Cancers</b>	<b>62.5%</b>

Common Disease Type	% of Total Screened (N=5560)
Colorectal	15.3
Breast	12.4
Non-Small cell lung	7.3
Prostate	2.5
<b>Common Cancers</b>	<b>37.5%</b>

**Aim was to include 25% of « less common cancers »**

**Far exceeded !**



# Basket trial – NCI MATCH

**NCI MATCH: 11 of 35 Arms With Results  
3/11 Positive (27%)**

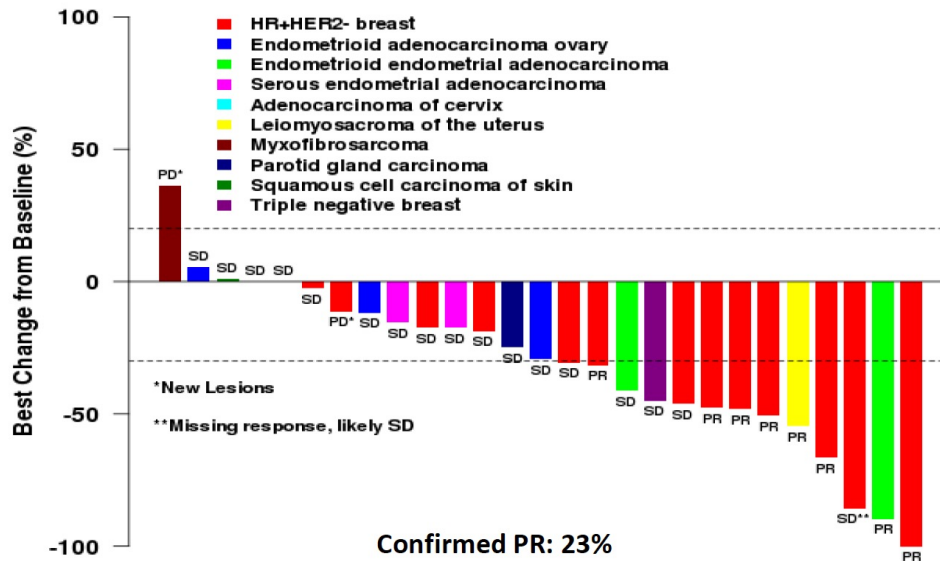
Subprotocol	Drug/molecular	Reported out	Result
Z1D	Nivolumab for MMRd	SITC 2017; manuscript pending	Positive
Y	Capivasertib/AKT mutations	Nov 2018	Positive
H	Trametinib/Dabrafenib/BRAFV600	June 2019	Positive
I	Taselisib/PIK3CA mutations	June 2018 (ASCO)	Neg
Q	Ado-trastuzumab emtansine/ERRB2 amplification	June 2018 (ASCO)	Neg (8% RR)
W	AZD4547/FGFR amplification, mutation, fusion	June 2018 (ASCO)	Neg (8% RR)
N/P	GSK2636771/PTEN mut or loss	October 2018 (ESMO)	Neg
B	Afatinib/ERRB2 activating mutations	April 2019 (AACR)	Neg (2.7%)
Z1-B	Palbociclib/CCND1, 2, or 3 amplifications	April 2019 (AACR)	Neg
Z1-I	AZD1775/BRCA 1 or BRCA2 mutations	April 2019 (AACR)	Neg (3.2%)

Peter J. O'Dwyer, MD ECOG-ACRIN Cancer Research Group

# Basket trial – NCI MATCH

- Promising signals in some of the reported cohorts

## NCI MATCH, Capivasertib Arm Solid Tumors with AKT1 E17K Mutation (n =35)



AKT1 E17K mutation: 1.3% (70 of 5,548 patients)

ECOG-ACRIN K Kalinsky et al 2018 EORTC-NCI-AACR Symposium



# Master protocols

## ***BRAF<sup>V600E</sup> mutated cancers treated with BRAF inhibitor***

70% melanoma, 10% colorectal cancer, and 30-70% papillary thyroid carcinoma

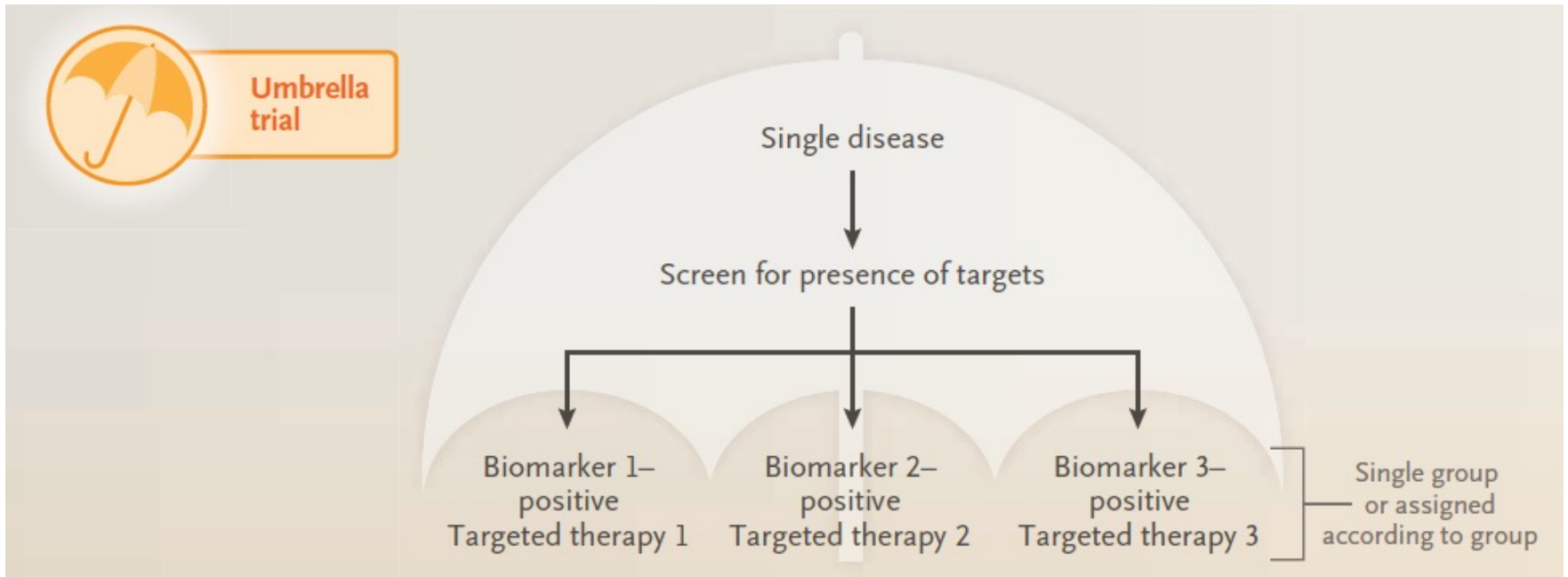
	Melanoma	Colorectal cancer
Response rate	80%	5%

Not always the case...

Tumors having the same oncogenic driver mutations can differ significantly in their responses to targeted cancer drugs.

# Umbrella trials

## Histology-specific



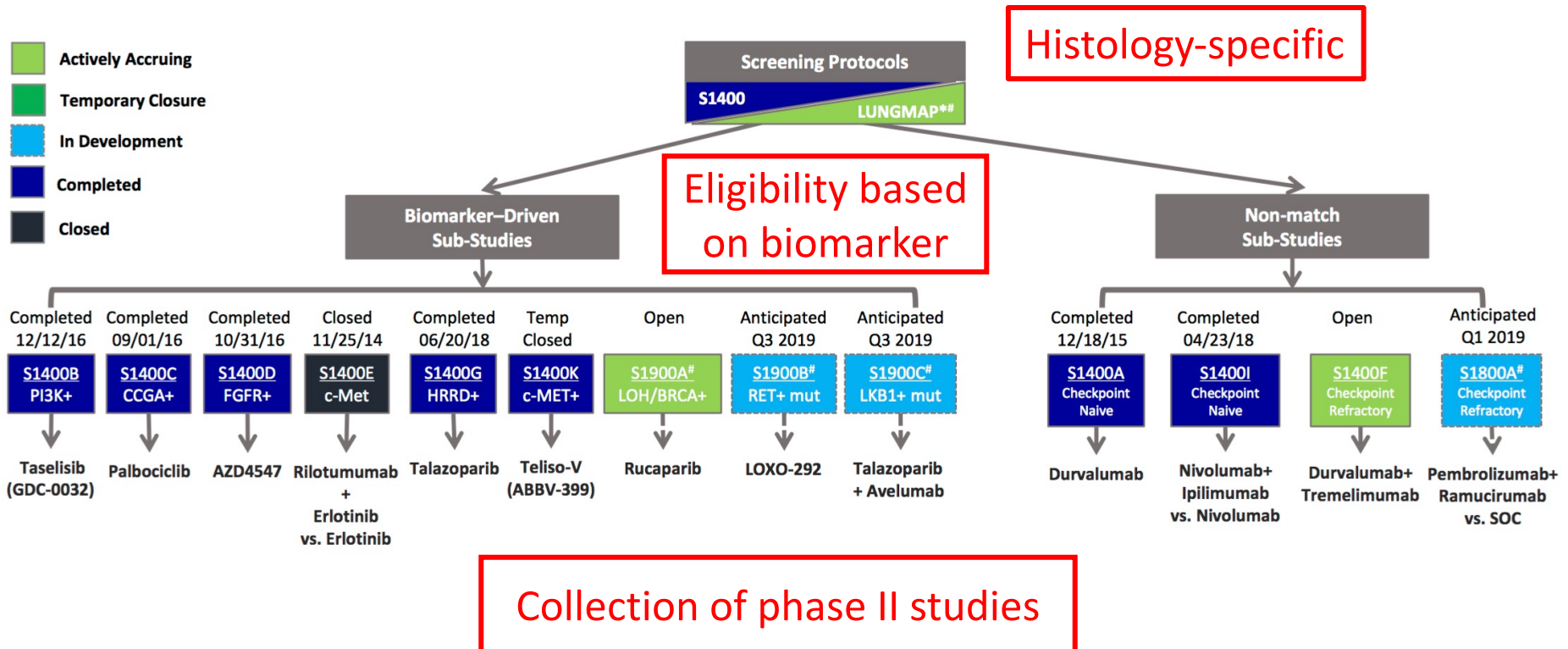
# Umbrella trials

Study	Tumor	Biomarker testing	Methodology	Endpoint	Results
<b>LUNG-MAP master protocol</b>	Advanced <b>lung SCC</b>	Archival or new biopsy  <b>FoundationOne NGS assay</b>	<b>Multiple arms:</b> based on the molecular profile, each patient is enrolled in substudy (matched or nonmatch)	Objective response rate (ORR)	Results for 3 biomarker-driven cohorts ORR 4-7%: closed for futility
<b>The National Lung Matrix</b>	Advanced <b>NSCLC</b>	Prescreening of tumor biopsy through the stratified Medicine Program (in // with 1st line): <b>adaptable 28-gene NGS sequencing platform</b>	<b>Multiple arms,</b> Patients are allocated to the appropriate targeted therapy according to the molecular genotype of their cancer	ORR or PFS	Some interim results per cohorts
<b>FOCUS 4</b>	Advanced <b>colorectal cancer</b>	FFPE before commenced of standard chemotherapy <b>Mutations of some preselected genes + some IHC</b>	<b>Multiple arms;</b> After induction chemotherapy, patients are enrolled in different cohorts on the basis on the MA	PFS	First results for 1 patient cohort (FOCUS4): Closed for futility

# Umbrella Trial – Lung-MAP

## Current Lung-MAP Schema

(January 2019 – Post LUNGMAP Activation)





# Umbrella Trial – Lung-MAP

## Objective

- To learn whether targeted cancer therapies that are matched to the genomic makeup of a patients' lung cancer tumors are more effective than the current standard therapies in halting or reversing the progress of the disease and in extending the patient's life.

# Umbrella Trial – Lung-MAP

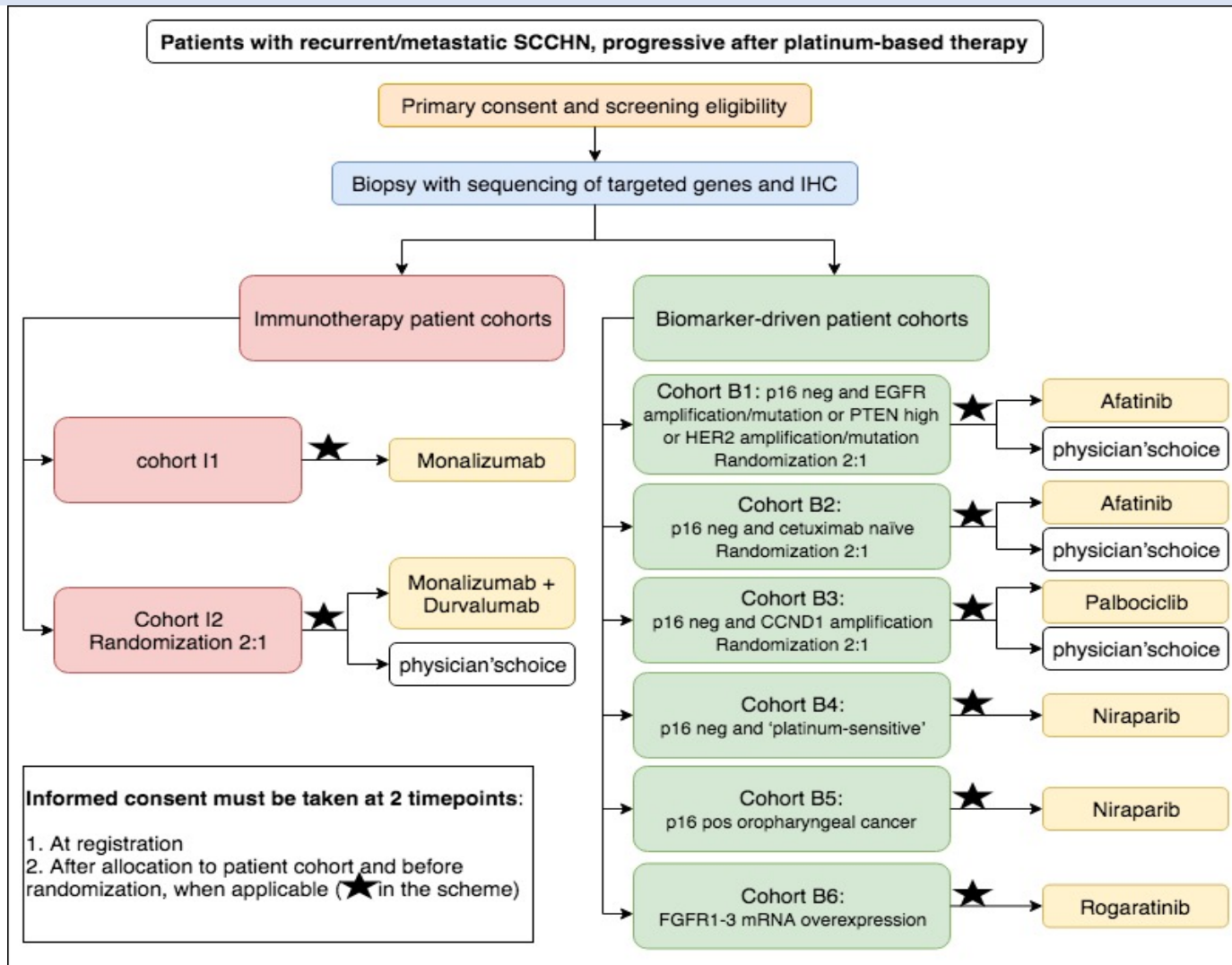
- Open at more than 700 sites in the US and Canada
- Master protocol with multiple phase II-III treatment arms
- “Umbrella” infrastructure allowed redesign with the major change of immunotherapy emergence
- “Umbrella” infrastructure & autonomy of each sub-study facilitates opening-closing of new sub- studies quickly (“Self-Sustaining”)

# Umbrella Trial – Lung-MAP

Update june 2018

- 1407 pts registered for screening , 1244 have biomarker results, 529 registered for a substudy (43%)
  - Results for 3 matched cohorts :
    - S1400B (PI3K inhibitor), S1400C (CDK4/6 inhibitor) and S1400D (FGFR inhibitor)
- Modest ORR 4-7%: closed due to futility at interim analysis**

# Umbrella Trial – Upstream trial



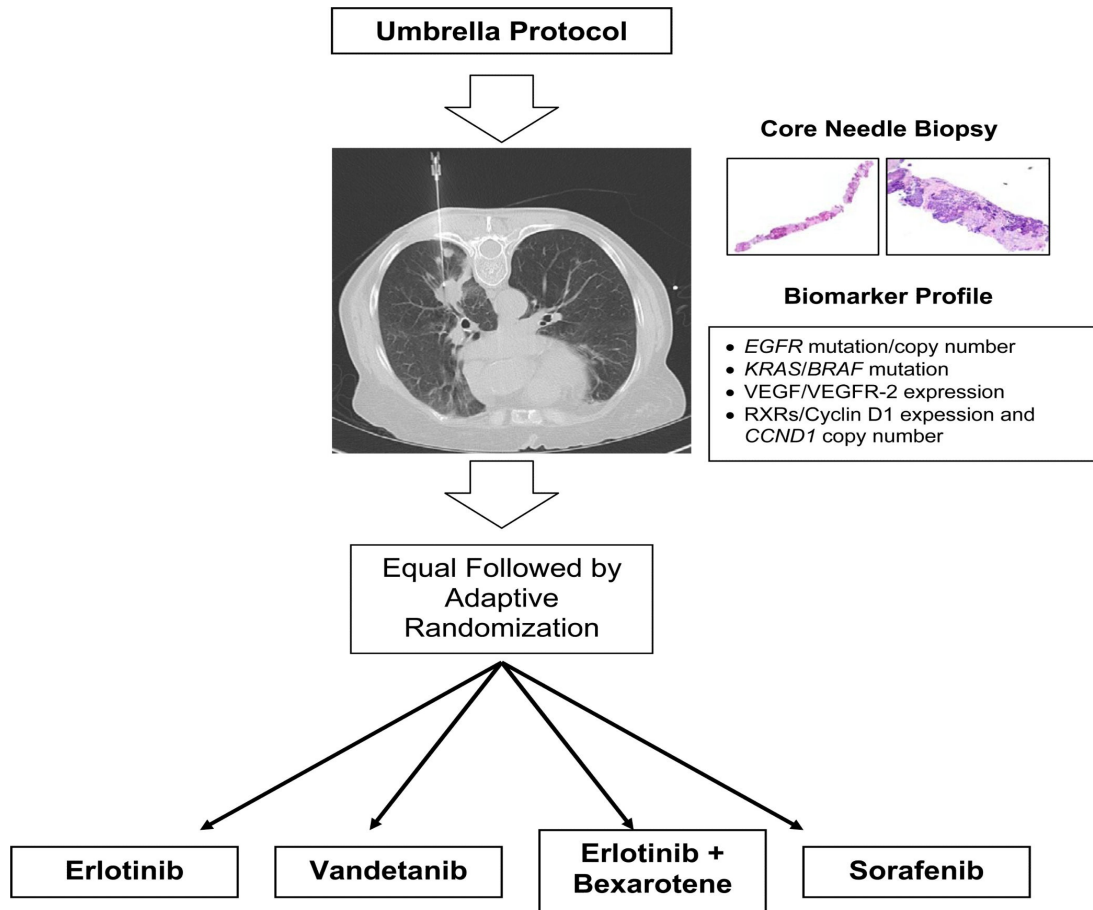
# Adaptive randomization

Adaptive randomization assigns more patients to the most promising therapies based on an appraisal of accumulated data

Aim:

Accelerate the identification of targeted therapies performing better within a biomarker-matched subgroup while avoiding unnecessary exposure of patients to therapies that are not beneficial to them.

# Adaptive randomization– Battle



## Adaptive randomized umbrella trial in advanced NSCL

Pts were assigned in 4 biomarker-positive subgroups and 1 biomarker negative subgroup

Within each subgroup, pts were randomized to 4 different targeted therapies

# Screening programs

Molecular screening program to **facilitate the access to precision medicine trials**

Can be

- histology agnostic (IMPACT, MOSCATO 01)
- histology specific (SAFIR 01)

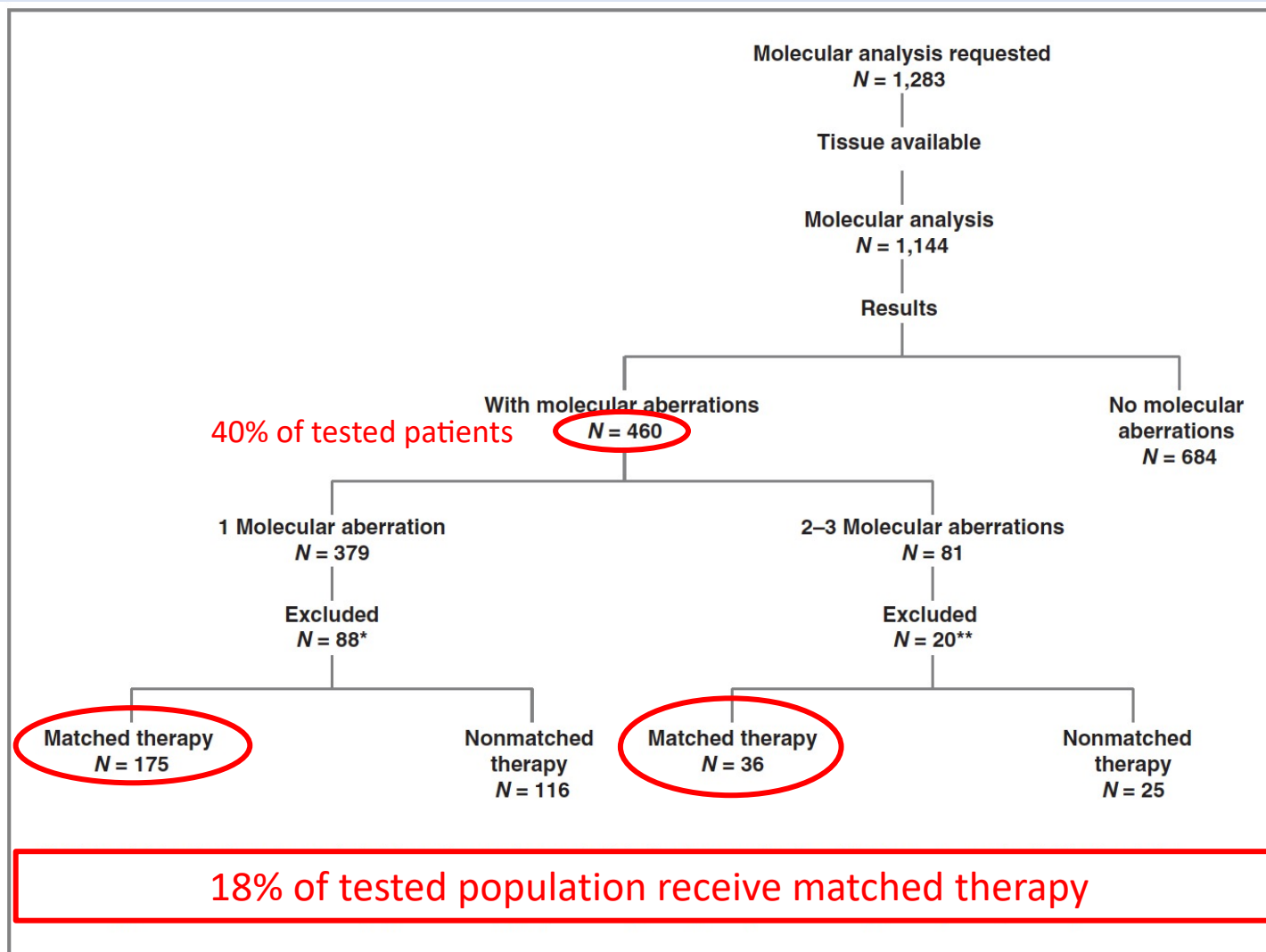
# Screening programs - IMPACT

IMPACT trial = Initiative for Molecular Profiling and Advanced Cancer Therapy

- personalized medicine program for patients who were referred to the phase I clinical trials program at MD Anderson Cancer Center
- **Assignment to phase I clinical trials** based on identification of a molecular alteration



# Screening programs - IMPACT



# Screening programs

Number of patients finally treated with matched therapy in different screening programs: **13%-19%**

→ Why a low enrolment rate ?

- Tumor tissue issues
- Decline of performance status
- Rapidly progressing disease
- Absence of targetable event
- Acces to matched clinical trials or drugs

# Screening programs - IMPACT

Endpoint:

clinical outcome of pts with MA treated with matched therapy versus pts not treated with matched therapy

	Matched therapy (n=381)	Non-matched therapy (n=238)	HR (95% CI)	p
ORR	43 (11%)	12 (5%)		.0099
SD $\geq$ 6mo + CR + PR	111 (29%)	56 (24%)		.13
FFS (months)	3.4	2.9	0.81 (0.69 to 0.96)	0.015
OS (months)	8.4	7.3	0.84 (0.71 to 0.99)	0.041

JCO, 2017

Only 8% of the of the whole population finally experienced a clinical benefit (111/1436 pts)

# Screening programs

→ Why limited clinical benefit ?

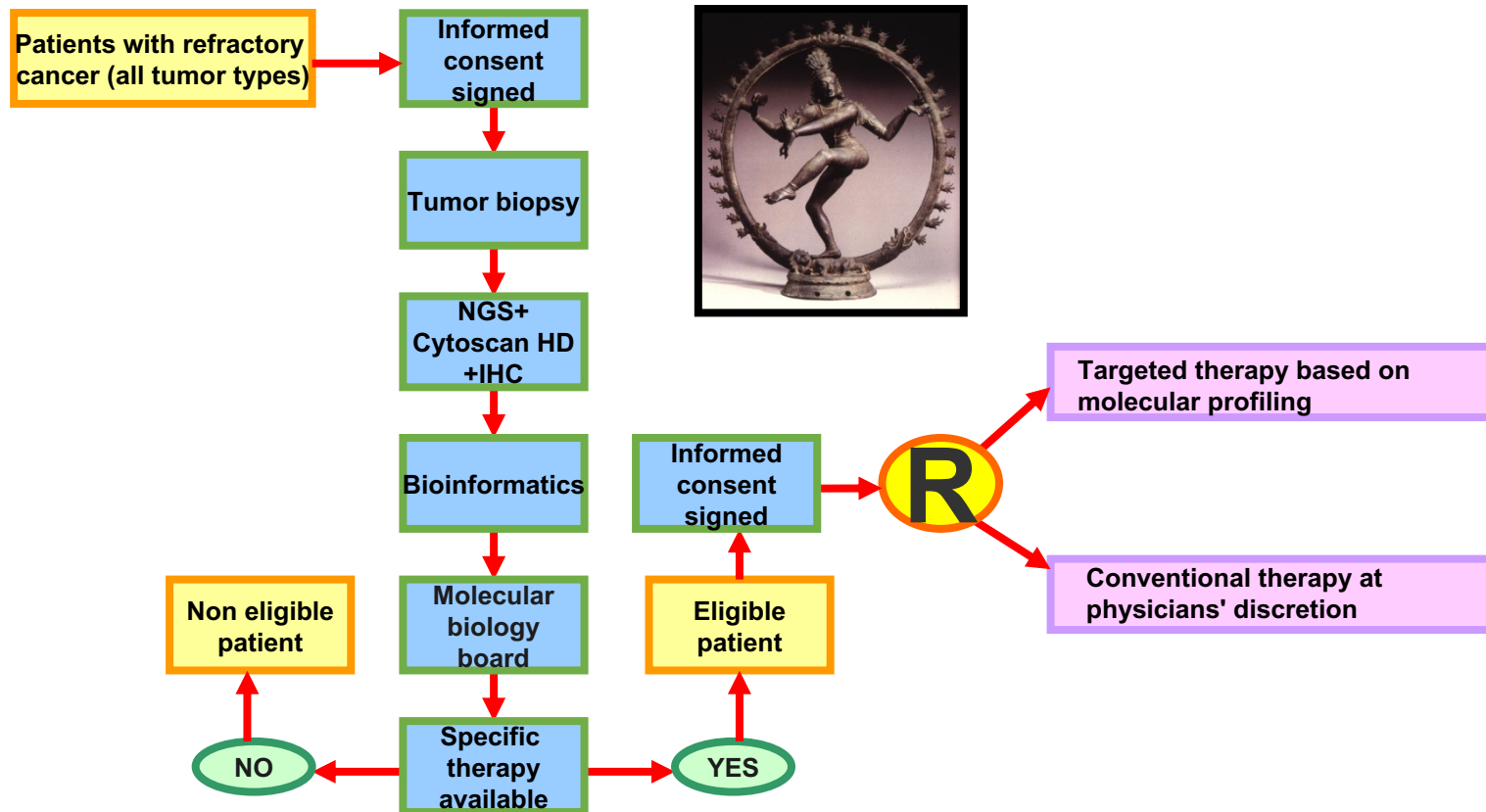
- Non-optimal targeted drugs in phase I trials
- Suboptimal dosages in phase I trials
- Level of evidence concerning the investigated biomarker

# Strategy trials

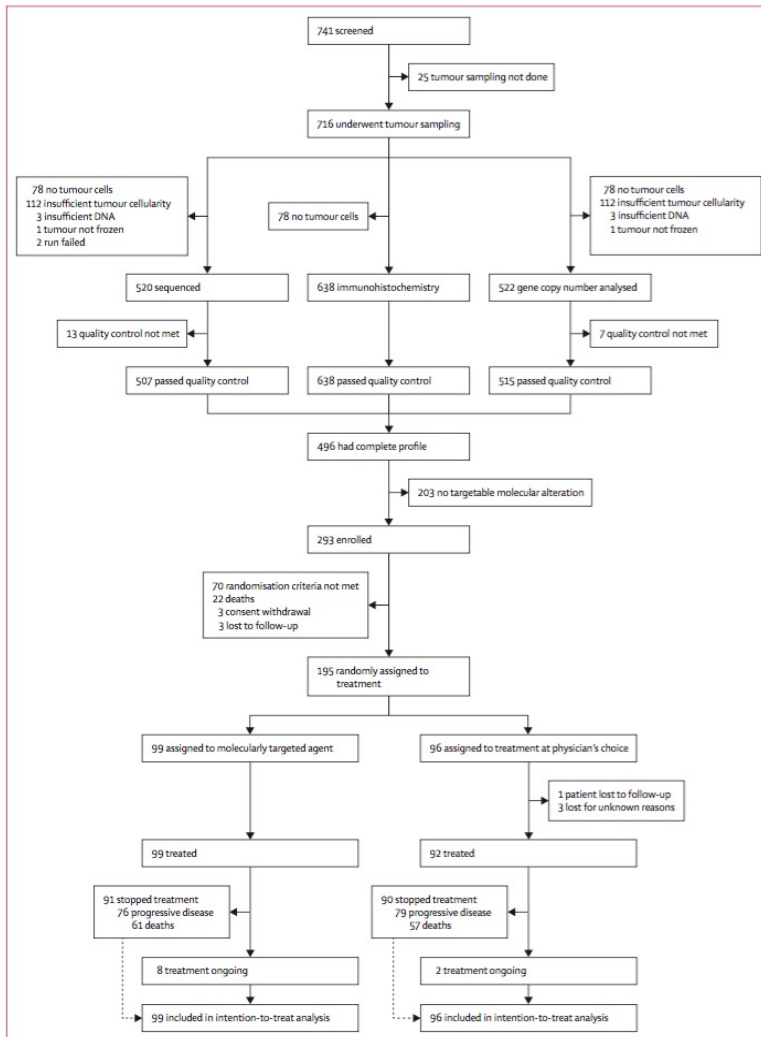
## **Testing the strategy of precision medicine**

Investigates if selecting the treatment based on molecular alterations (independently of the disease, the studied biomarker and the targeted drug) results in superior outcome compared with standard therapy

# Strategy trials: SHIVA



# Strategy trials: SHIVA



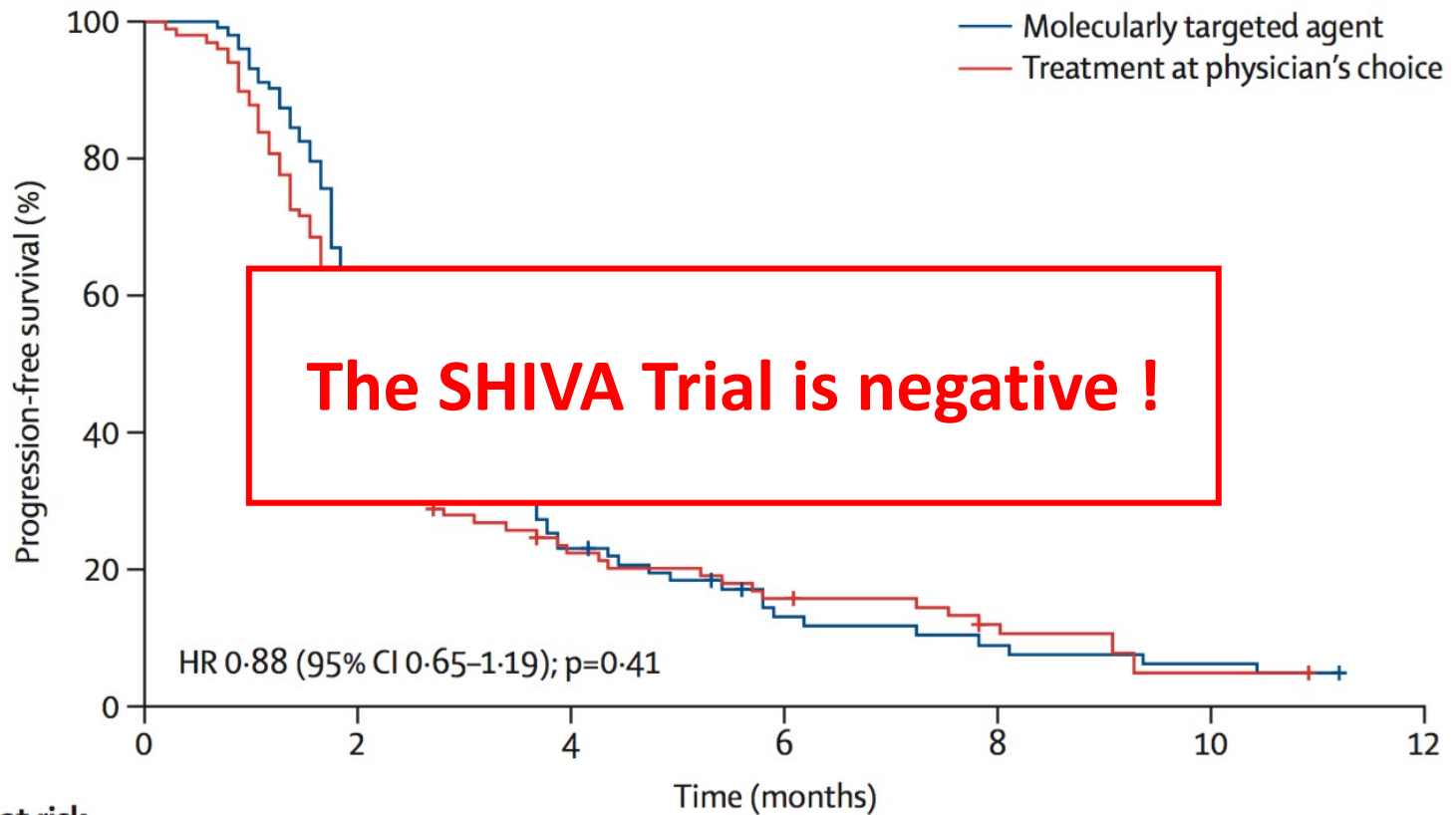
- Oct 2012– July 2014:  
Screening of 741 patients (any tumour type)

293 (40%) had at least one molecular alteration matching one of the 11 available regimens

195 (26%) randomly assigned, 99 in experimental group and 96 in control group

- Primary endpoint: progression-free survival

# Strategy trials: SHIVA



Number at risk	0	2	4	6	8	10	12
Molecularly targeted agent	99	62	20	10	5	2	0
Treatment at physician's choice	95*	50	19	12	8	1	0



# Strategy trials: SHIVA

→ Why ?

- Drugs marketed in France at that time...old molecules (eg everolimus instead of double mTor inhibitor)
- Heterogeneous experimental arm with various drugs and various tumor types: can blind the benefit of some drugs in some specific cancers
- Unidimensional treatment algorithm: single molecular alteration to predict efficacy: us multidimensional treatment algorithm including information from several genes ?

# Disappointments in Master protocols

- The tissue in which the cancer mutation occurs can determine treatment response (*BRAF<sup>v600e</sup>* : Melanoma versus colon)
- *KRAS* mutation is classified as « actionable » (MEK inhibitor) but MEK inhibitors have modest activity in this setting.
- *BRCA1/2* mutations confer sensitivity to PARP inhibitors. *BRCA1*-like tumors lacking *BRCA1* mutation are sensitive to PARP inhibitors

# Dissappointments in Master protocols

- Tumors having the same oncogenic driver mutations can differ significantly in their responses to targeted cancer drugs
- Tumors that lack a specific oncogenic driver mutation may nevertheless display very similar responses to therapy due to similarity in gene expression patterns

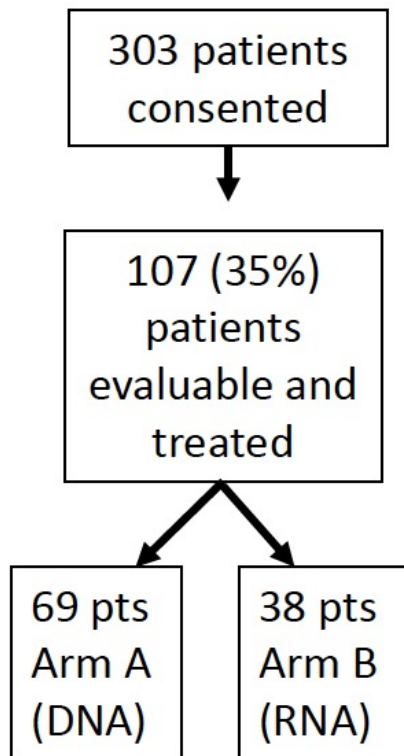
# Dissappointments in Master protocols

- Tumors having the same oncogenic driver mutations can differ significantly in their responses to treatment
- Tumors with similar driver mutations can have different responses to therapy due to similarity in gene expression patterns

These explain why biomarker-driven studies based on the genotype of the tumor only, are only moderately successful

# Testing beyond genomics

## WINTHER: genomic + transcriptomics (DNA + RNA)



**Table 1 | Outcome data including SD  $\geq$  6 months and PR/CR as well as PFS2/PFS1 in the WINTHER trial**

	Arm A (DNA) <sup>a</sup>	Arm B (RNA) <sup>a</sup>	All patients
SD $\geq$ 6 months/PR/CR <sup>b</sup>	16 (23.2%)	12 (31.6%)	28 (26.2%)
Response: CR/PR	9 (13.0%)	3 (7.9%)	12 (11.2%)
SD $\geq$ 6 months	7 (10.1%)	9 (23.7%)	16 (15.0%)
PD or SD < 6 months <sup>a</sup>	53 (76.8%)	26 (68.4%)	79 (73.8%)
Total	69 (100%)	38 (100%)	107 (100%)
Frequency (N (%)) <sup>c</sup>			
PFS2/PFS1 of >1.5			
Yes <sup>d</sup>	14 (20.3%)	10 (26.3%)	24 (22.4%)
No	55 (79.7%)	28 (73.7%)	83 (77.6%)
Total	69 (100%)	38 (100%)	107 (100%)

# Testing beyond genomics

## WINTHER: genomic + transcriptomics (DNA + RNA)

303 patients  
consented

Table 1 | Outcome data including SD  $\geq$  6 months and PR/CR as well as PFS2/PFS1 in the WINTHER trial

**Transcriptomic profiling expands precision medicine**

Transcriptomics enhanced the number of patients treated with a matched therapy from 23% to 35% of consented patients

69 pts  
Arm A  
(DNA)

38 pts  
Arm B  
(RNA)

No	55 (79.7%)	28 (73.7%)	83 (77.6%)
Total	69 (100%)	38 (100%)	107 (100%)

# Dissappointments in Master protocols

Biomarker-driven clinical trials use monotherapy targeted agents...

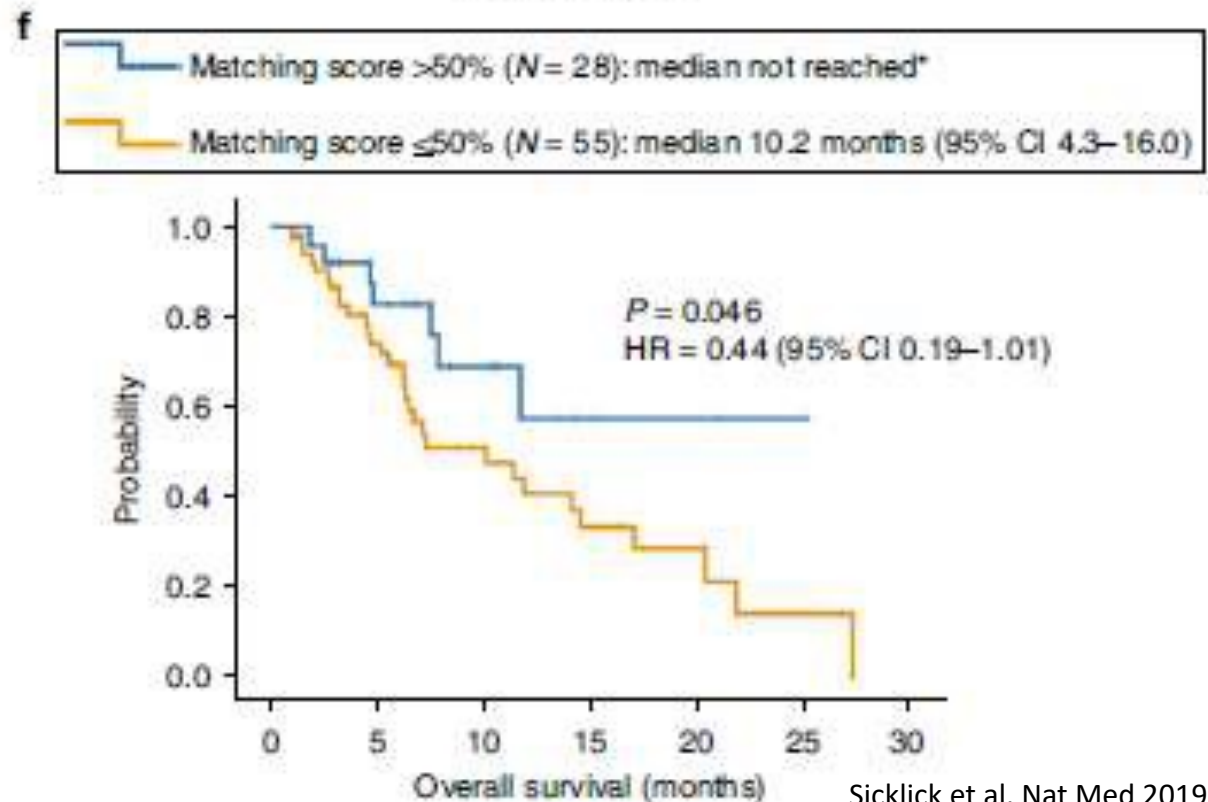
Does not address tumor heterogeneity that can cause treatment resistance

# Combination strategies

**I-PREDICT: personalized multidrug combinations to target the majority of genomic alterations in each patient's tumor**

## Matching score

= Total number of molecular alterations matched to the administered drugs divided by the total number of characterized genomic aberrations





# Combination strategies

**I-PREDICT: personalized multidrug combinations to target the majority of genomic alterations in each patient's tumor**

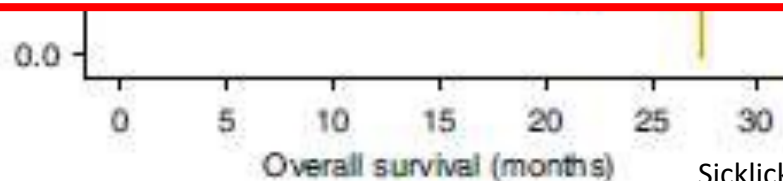
## Matching

= Total number of molecular alterations matched to administered therapies divided by number of characterized aberrations

Combination treatment can perform better than single agents

Biomarkers beyond a single genomic alteration

Personalization of combination therapies to each individual's tumor



# Conclusion

**Table 1. Advantages and pitfalls of 'biomarker-driven' clinical trial designs**

	<b>Advantages</b>	<b>Disadvantages</b>
<b>Master protocols</b>		
<b>Basket trials</b> Histology agnostic	Can include rare cancer types Can target low incidence actionable/targetable molecular alterations	Assumes that molecular biology can replace histology and that a specific genetic alteration has the same significance across different tumor types
<b>Umbrella trials</b> Histology specific	Targets molecular alterations in one cancer type and avoid heterogeneity due to multiple cancer histologies Enables to get more conclusive results for one tumor type	Feasibility limited for rare cancers
<b>Screening programs</b>	Have the potential to identify an actionable/targetable genetic alteration Can facilitate the access to early development clinical trials	If an actionable/targetable alteration is present, the specific drug is not always available with the risk that a low number of patients finally benefits from this program
<b>Strategy trials</b>	Have the potential to identify an actionable/targetable genetic alteration	Effect of the strategy can be diluted by less effective target-drug pairs

**Biomarker beyond genomics + combination therapies to be implemented in the future !**

Thank you !