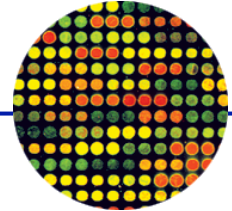


How to take Genetic Data to Clinical Practice in Oncology



Peter Lichter

German Cancer Research Center, DKFZ



dkfz.

GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION

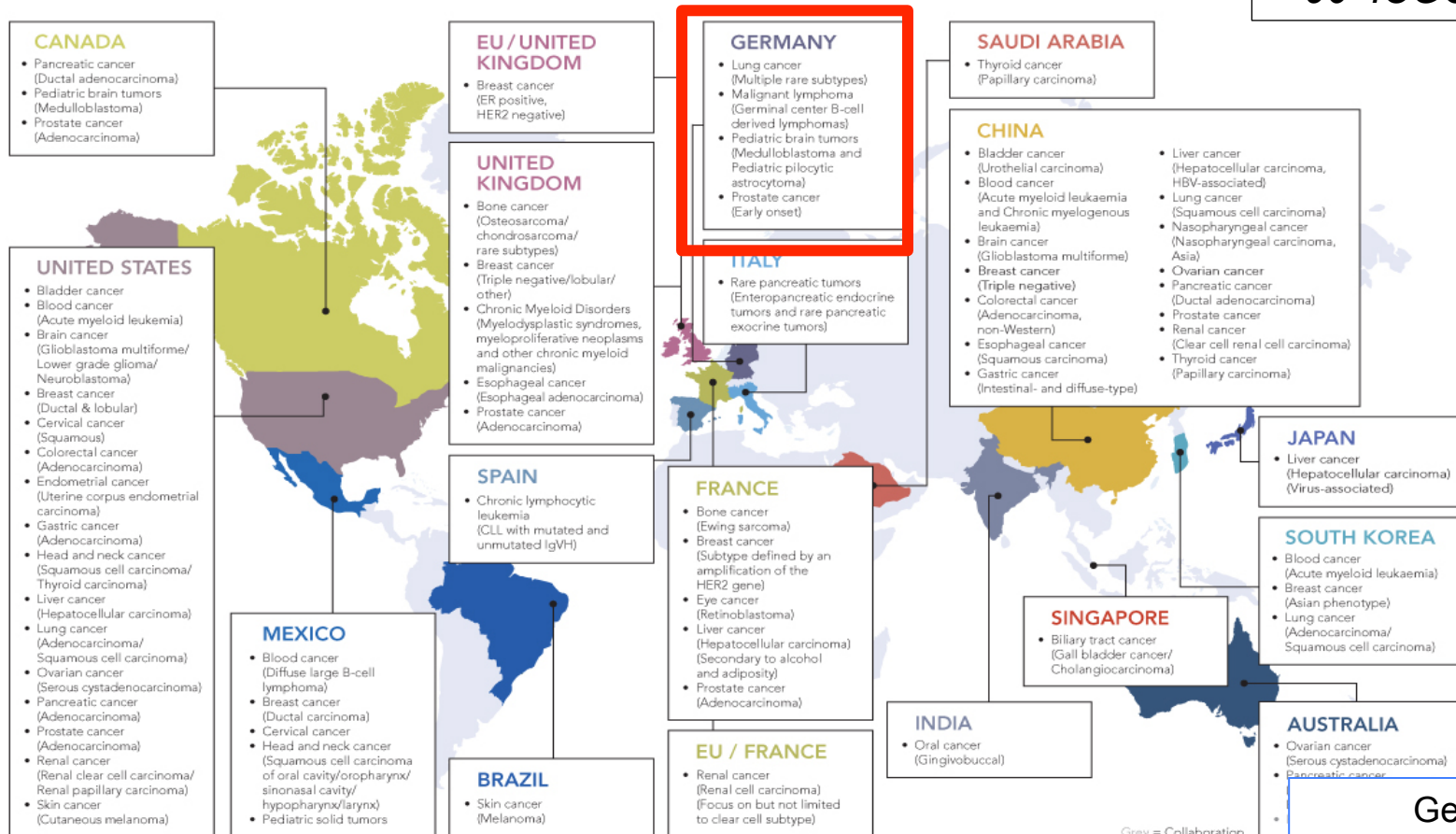


50 Years – Research for
A Life Without Cancer

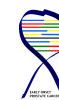
International Cancer Genome Consortium



> 90 ICGC Projects



- PedBrain Tumor (Pediatric Brain Tumors)
- Prostate Cancer (“Early Onset”)
- MML Seq (Molecular Mechanisms in Malignant Lymphoma)



Genome
Transcriptome
Methylome
Clinical Annotation

Tom Hudson et al.
Nature 464
993-998 (2010)



Low-grade Astrocytoma

Medulloblastoma

Glioblastoma

Ependymoma

> 600



ICGC-PedBrainTumor

dkfz.

Scientific Advisory Board

WP1: Coordination (Lichter)

WP11: Data Management (Eils)

WP2: Banking (Korshunov, Witt, Pfister)

WP3: Ref. Pathology and QC (Reifenberger)

WP4: Isolation of Analytes (von Kalle)

WP5: Genomic Sequencing (Pfister, Lichter)

WP6:
Paired-End
Mapping
(Korbel)

WP7:
Methylome
(Radlwimmer,
Korn)

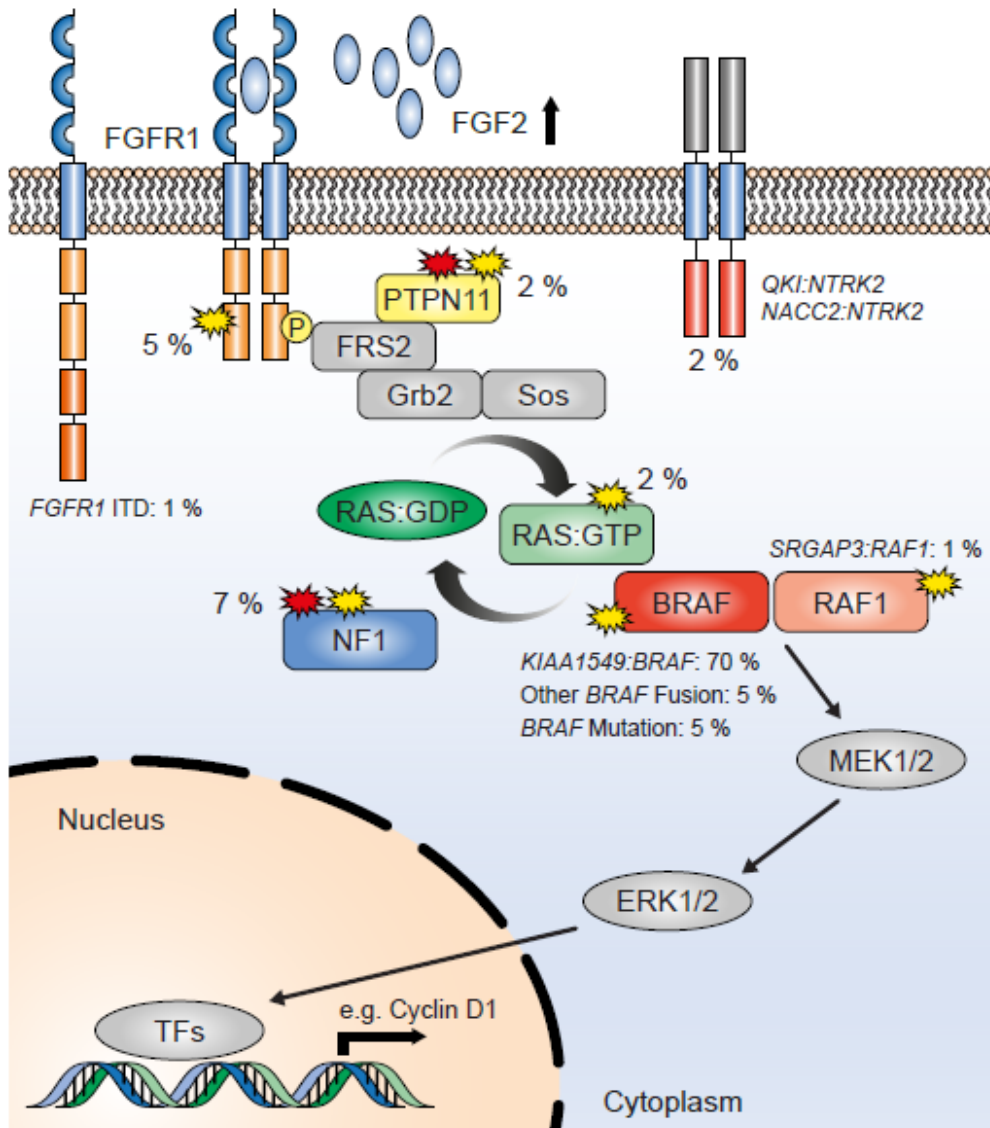
WP8:
Trans-
criptome
(Yaspo, Lehrach)

WP9:
small RNAs
(Landgraf, Bork-
hardt, Reifen-
berger)

WP10: Bioinformatics (Brors, Eils)

German Cancer Research Center – DKFZ
National Center for Tumor Diseases – NCT
University Hospital Heidelberg
European Molecular Biology Laboratory – EMBL
University Düsseldorf
Max-Planck-Institute for Molecular Genetics – MPI-MG

Pilocytic Astrocytoma

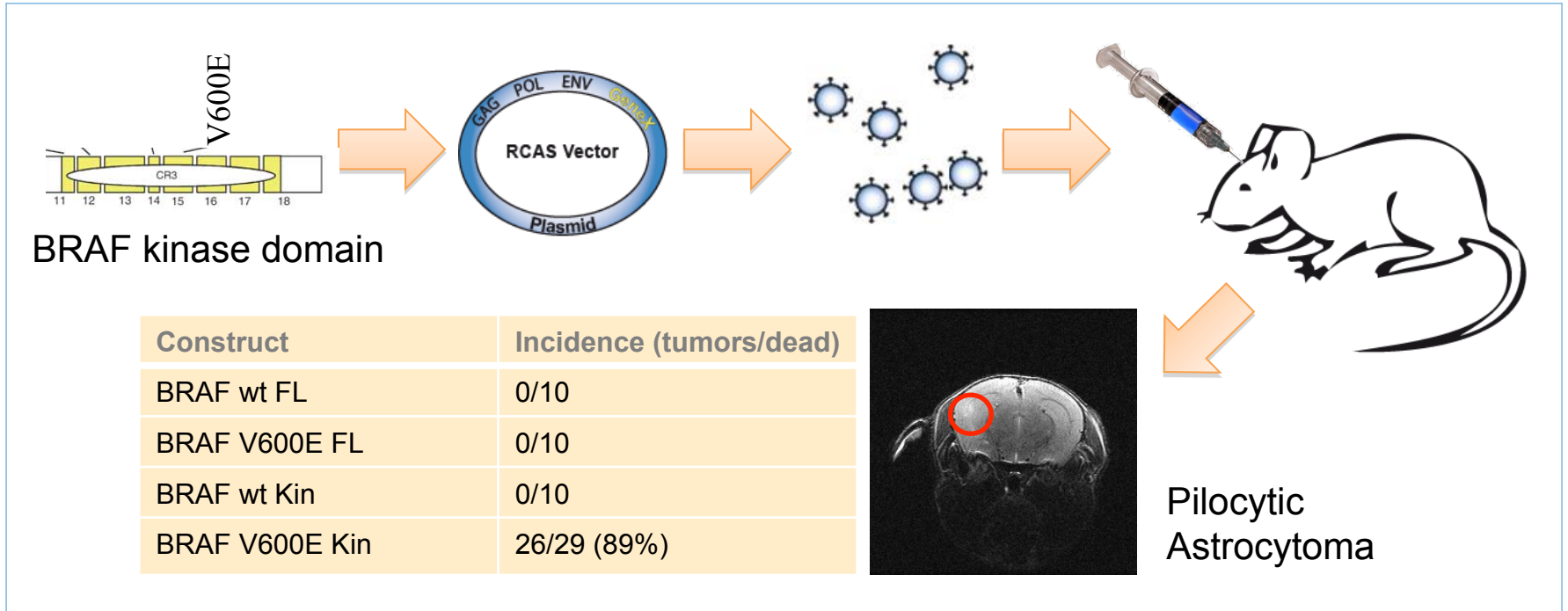


n = 96

- Novel “actionable” targets
 - Alterations in one pathway in 100% of cases
 - Pilocytic Astrocytoma: a “single pathway” disease!
- => „Druggable“ mutations
- => Therapy options



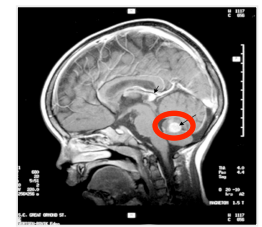
Preclinical model



Gronych et al., J Clin Invest, 2011

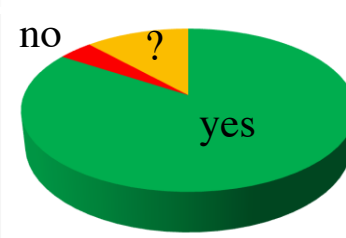
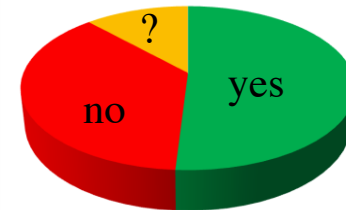
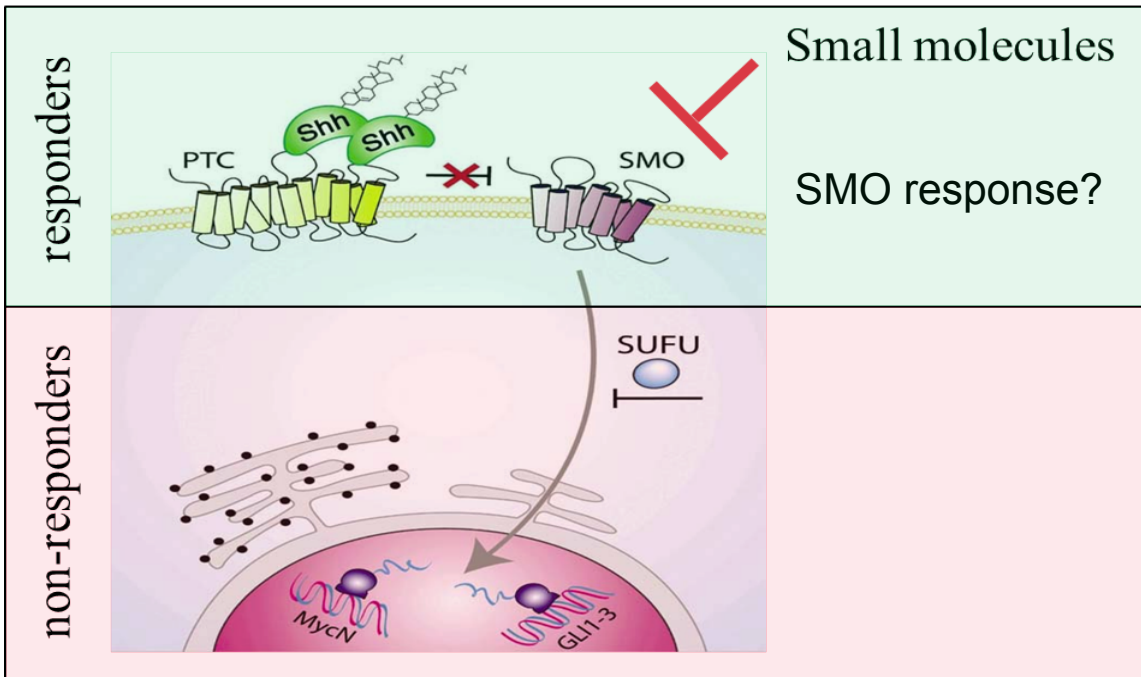
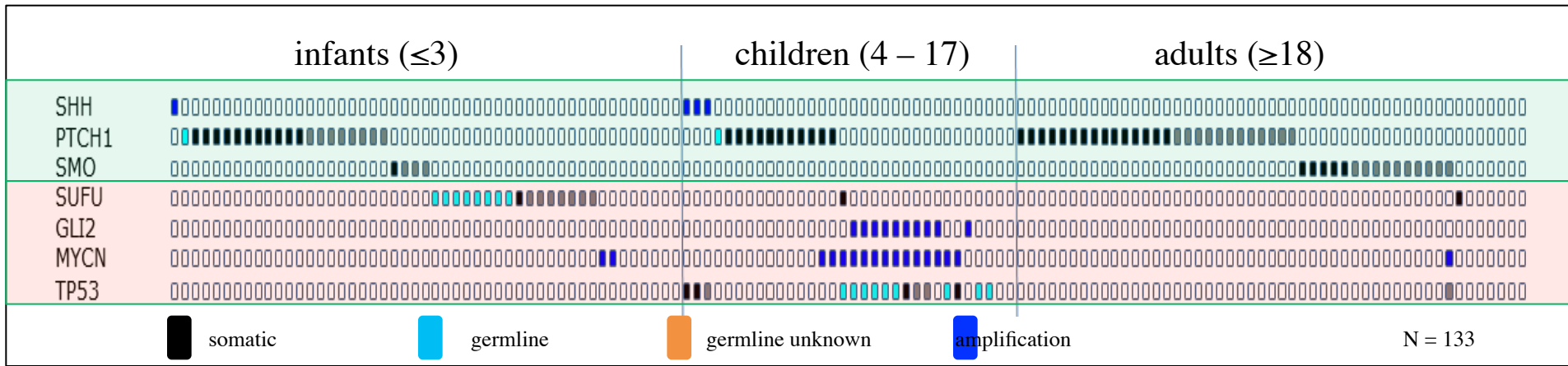
⇒ Currently used to test inhibitors of BRAF and other MAP kinase pathway factors

Medulloblastoma: Molecular Classification



Subgroup	WNT	SHH	Group 3	Group 4
Gender ratio				
Age distribution				
Histology	Classic; very rare LCA	Classic > Nodular > LCA > MBEN	Classic > LCA	Classic; rarely LCA
Metastasis @ Dx	~5-10%	~15-20%	~40-45%	~35-40%
Patient Survival	~95% OS	~75% OS	~50% OS	~75% OS
Proposed Cell of origin	Lower rhombic lip progenitor cells	CGNPs of the EGL and cochlear nucleus; neural stem cells of SVZ	Prominin1(+), lineage(-) neural stem cells; CGNPs of the EGL	Unknown

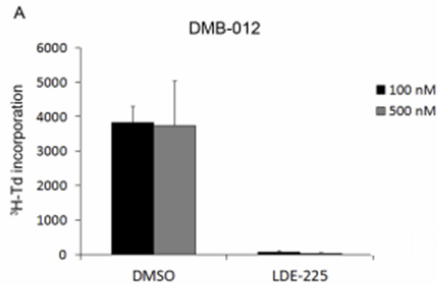
Infants, children & adult SHH-MBs: different mutations in pathway



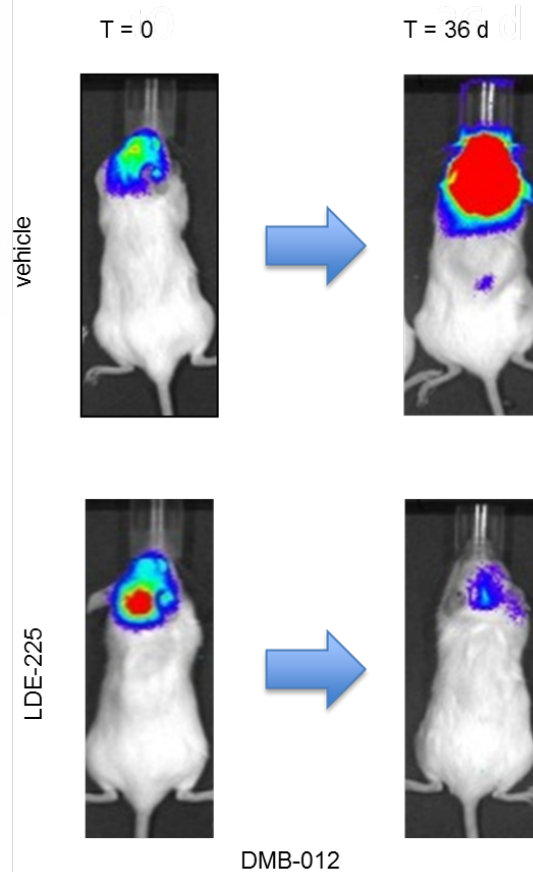
SMO inhibition in different SHH models

A

3 yr old female,
desmoplastic
PTCH1 mutation

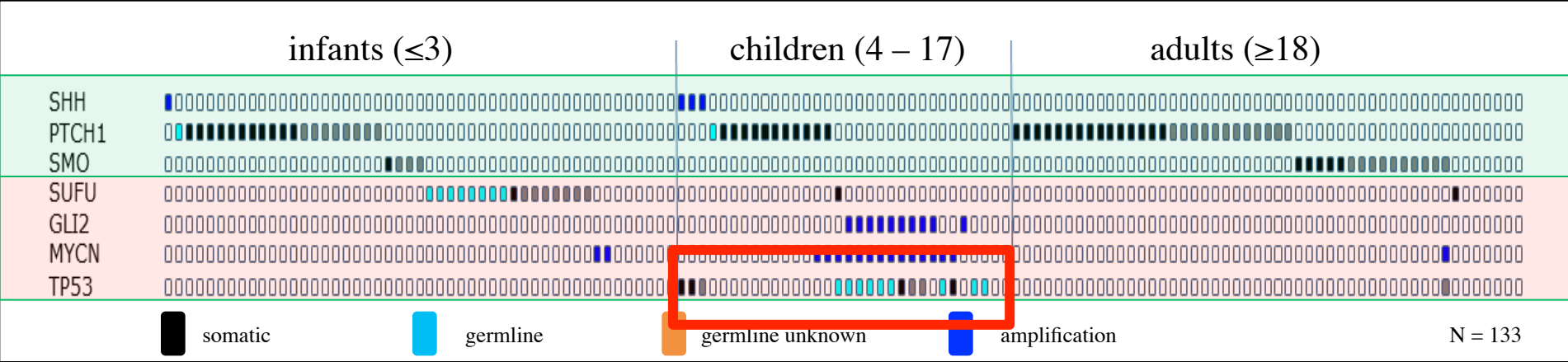


*LDE-225, a drug
already tested in
clinical trials*



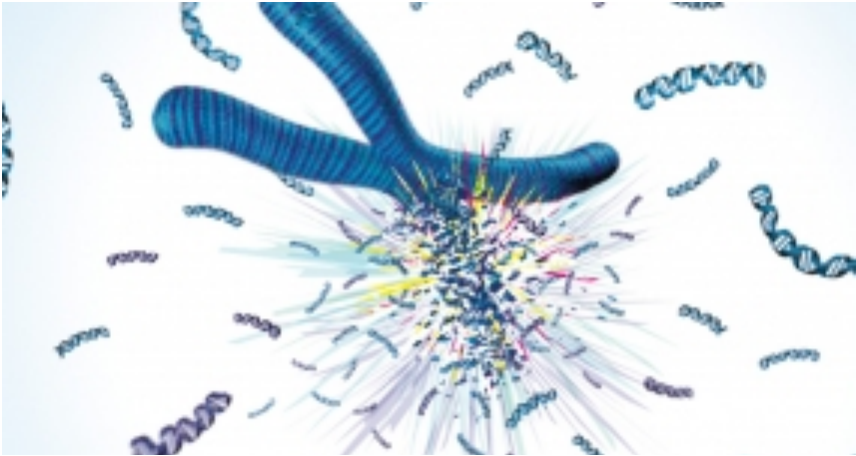
Rob Wechsler-
Reya

Infants, children & adult SHH-MBs: different mutations in pathway



Kool et al., Cancer Cell 2014

TP53 Mutations in SHH-Medulloblastoma are linked to chromothripsis and are germline mutations



Chromothripsis

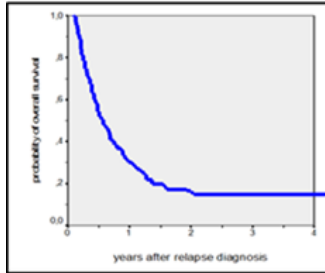
Clinical implications:

- ⇒ no SMO-inhibitors
- ⇒ minimize radiation
- ⇒ genetic counseling

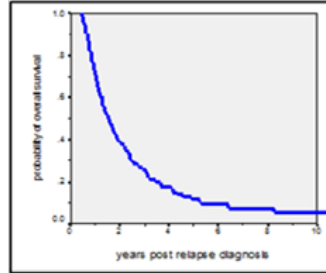
Rausch et. al, Cell 2012

Survival curves for relapsed pediatric patients

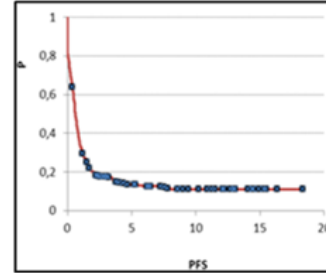
ALL-HR



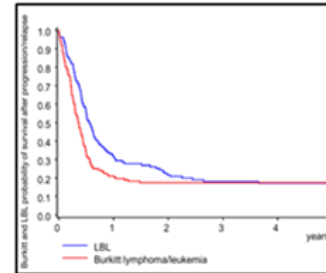
ALL post-SCT



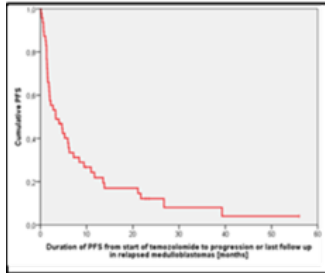
AML



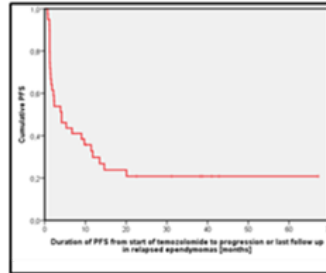
NHL



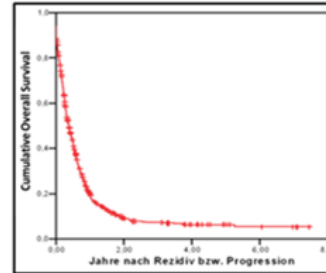
Medulloblastoma



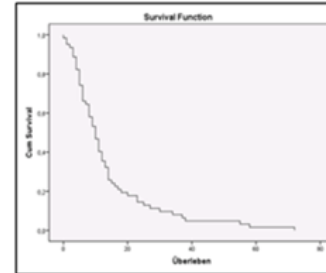
Ependymoma



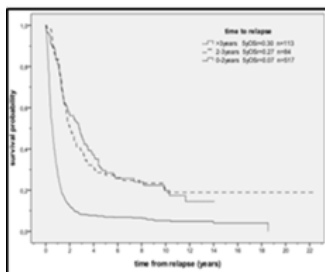
HGG (incl. DIPG)



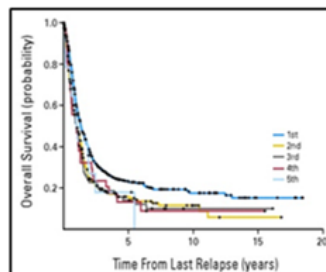
Rhabdoid Tumors



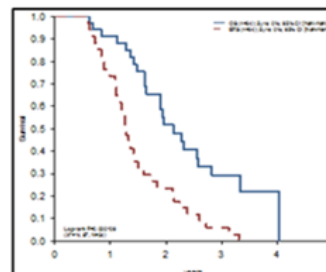
Ewing Sarcoma



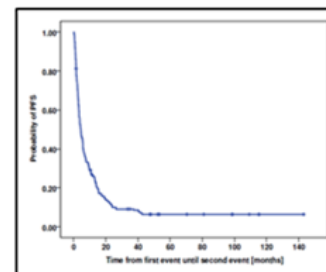
Osteosarcoma



Rhabdomyosarcoma



Neuroblastoma



INdividualized therapy FOR Relapsed Malignancies in childhood

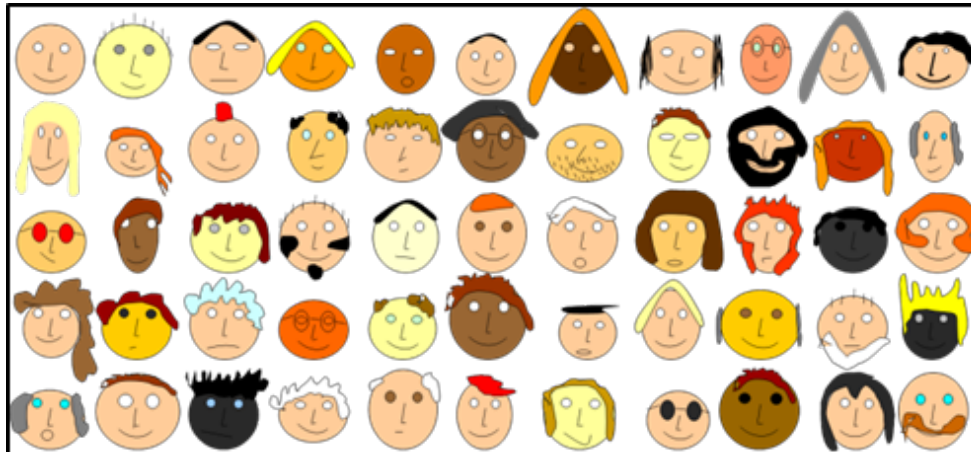
INFORM: next-generation diagnostics for children with progressive/relapsed malignancies



German Cancer Consortium



NATIONAL CENTER
FOR TUMOR DISEASES
HEIDELBERG



Stefan Pfister



Peter Lichter



Angelika Eggert



Olaf Witt

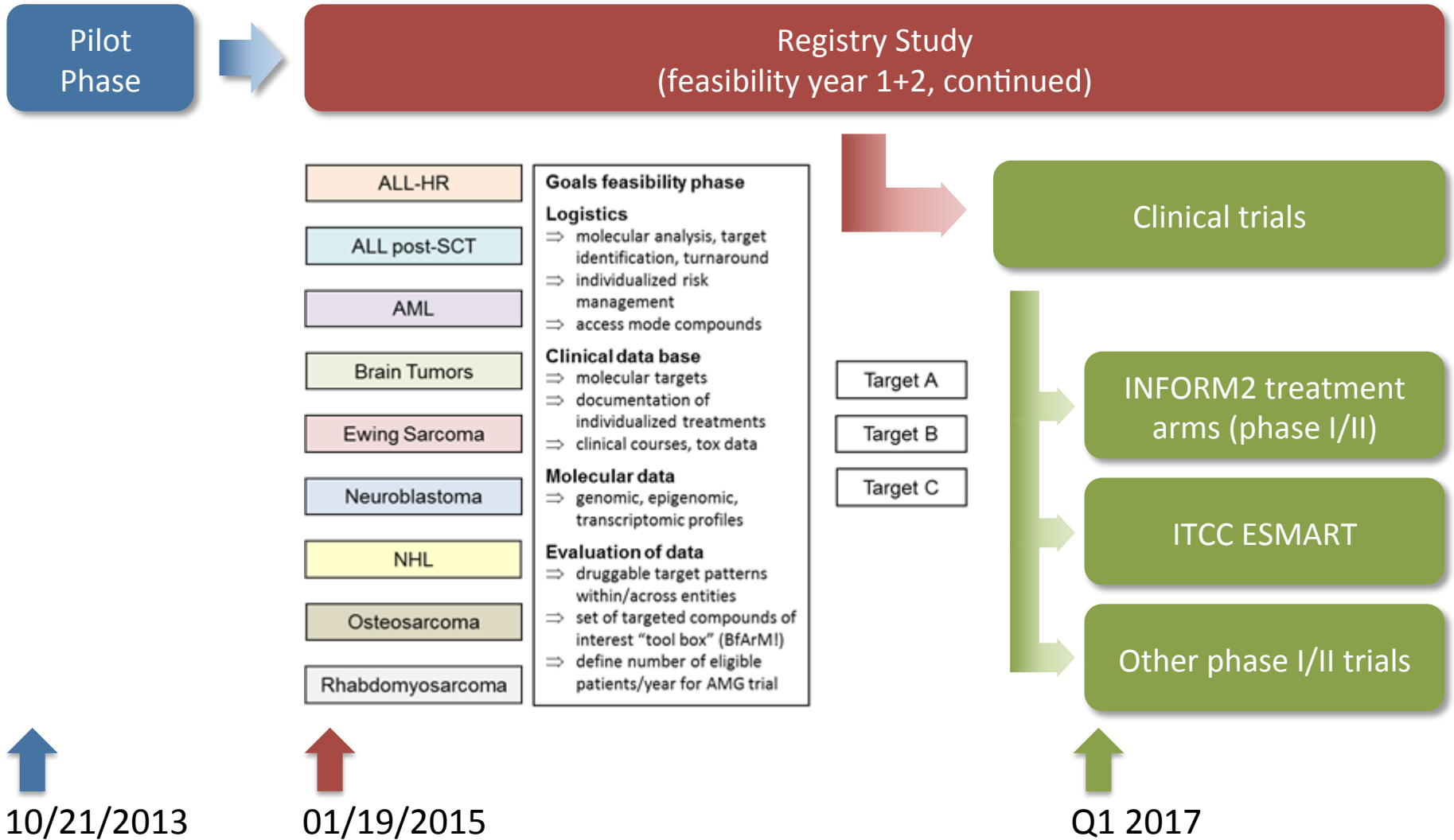


UniversityHospital Heidelberg



INFORM

Identification of actionable targets by NGS => molecular tumor board => targeted therapy approaches



INFORM: Molecular Analysis



Low-cov. WGS

Copy-number changes



Exome Seq

SNVs/InDels

- somatic (drug targets, ADME)
- germline (tumor predisposition, ADME)



RNA Seq

- Fusion genes
- Expression of somatic SNVs
- Changes in gene expression



Gene expression

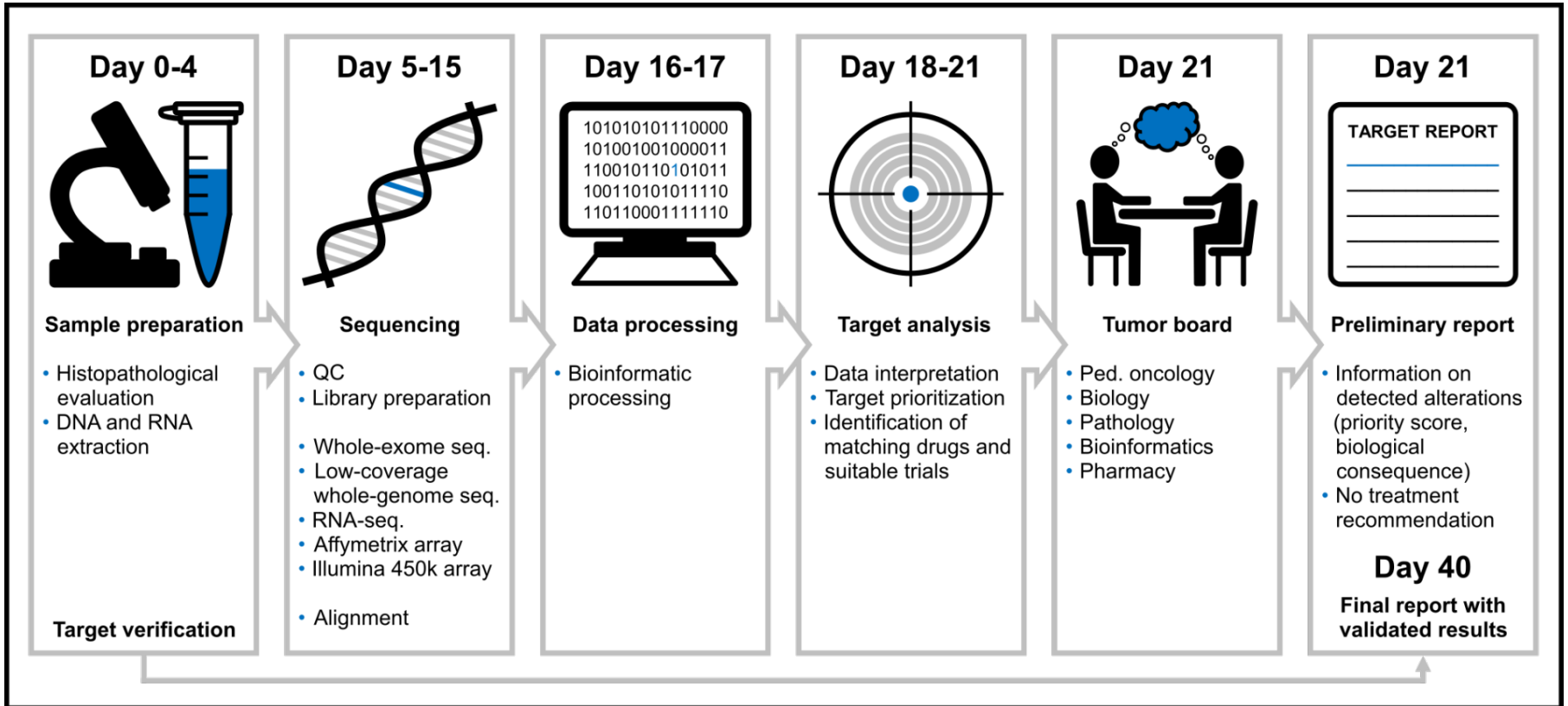
- Changes in gene expression
(comparison with entity specific reference cohorts)



450k methylation

- Classification (e.g. brain tumors)
- Gen-Silencing

INFORM – Workflow Heidelberg

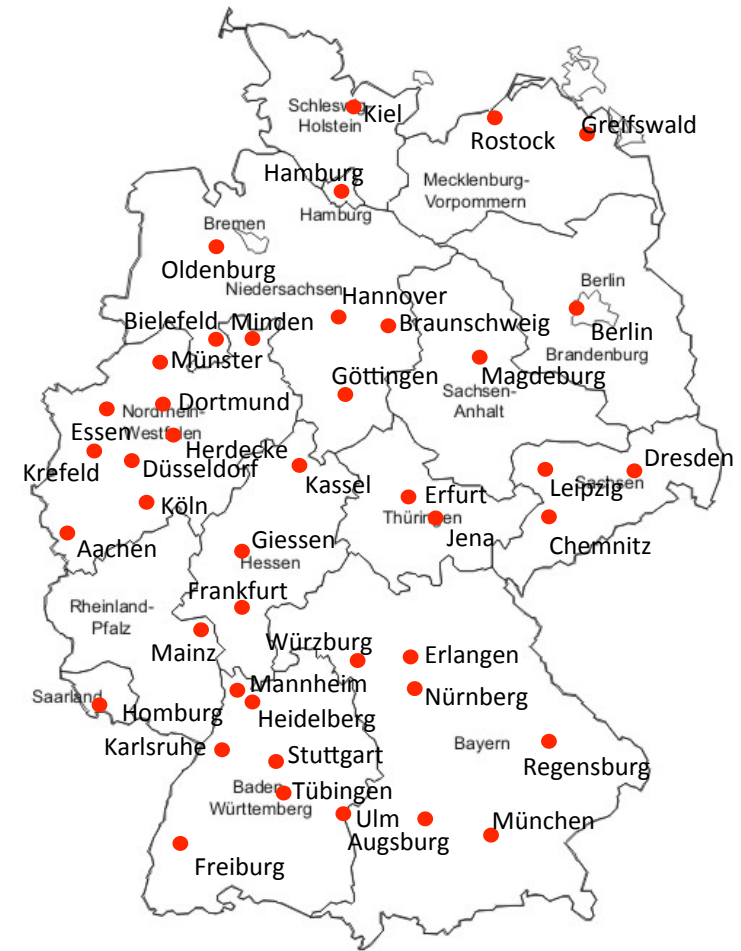
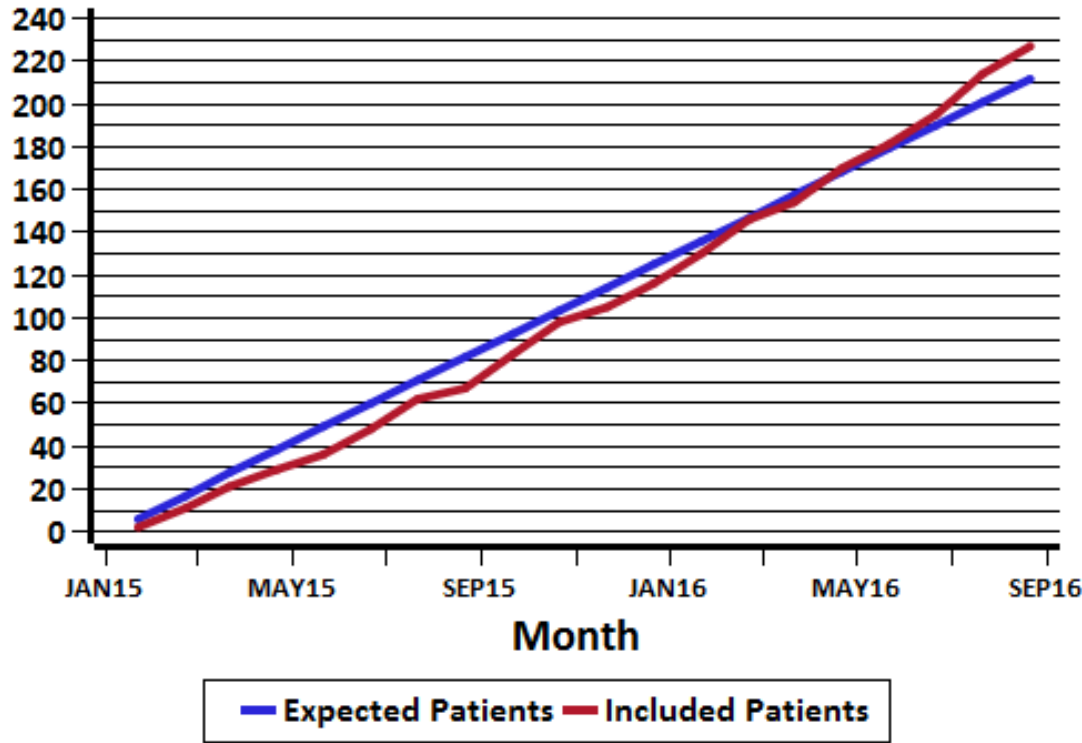


Worst et. al, Eur J Cancer, 2016



INFORM recruitment Germany (registry phase, 01/2015-09/2016)

Number of patients



INFORM Patients (pilot/registry phase, 10/2013-09/2016)

291 patients approached

sex:	female	130
	male	161
age:	average	13 years
	min	1 year
	max	40 years

34 ineligible

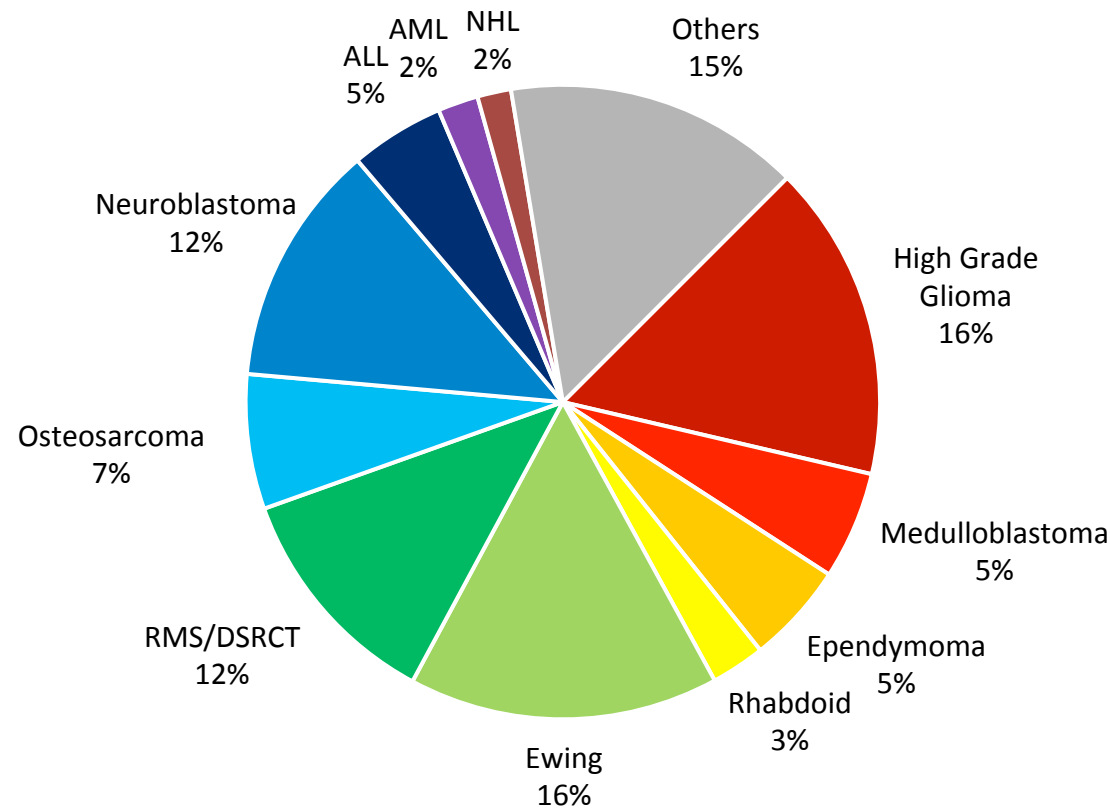
257 patients enrolled

7 insufficient/no tumor

237 patients sequenced

5 no tumor

232 patients analyzed (13 patients pending)

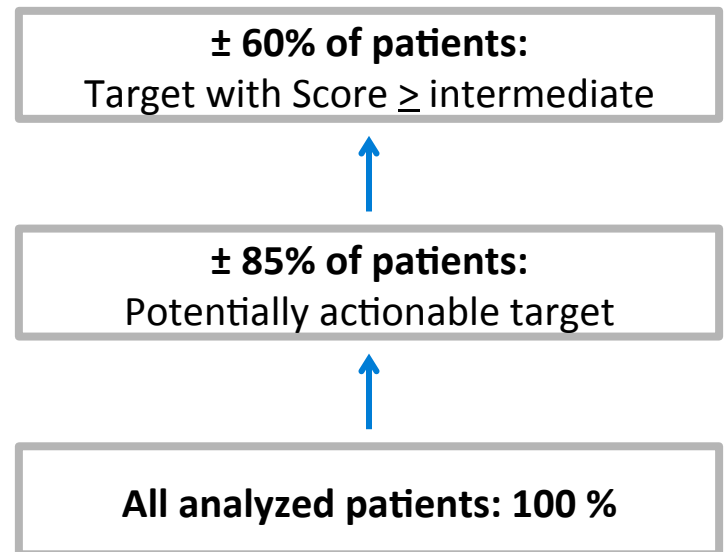


Target Prioritization – stratification for INFORM2

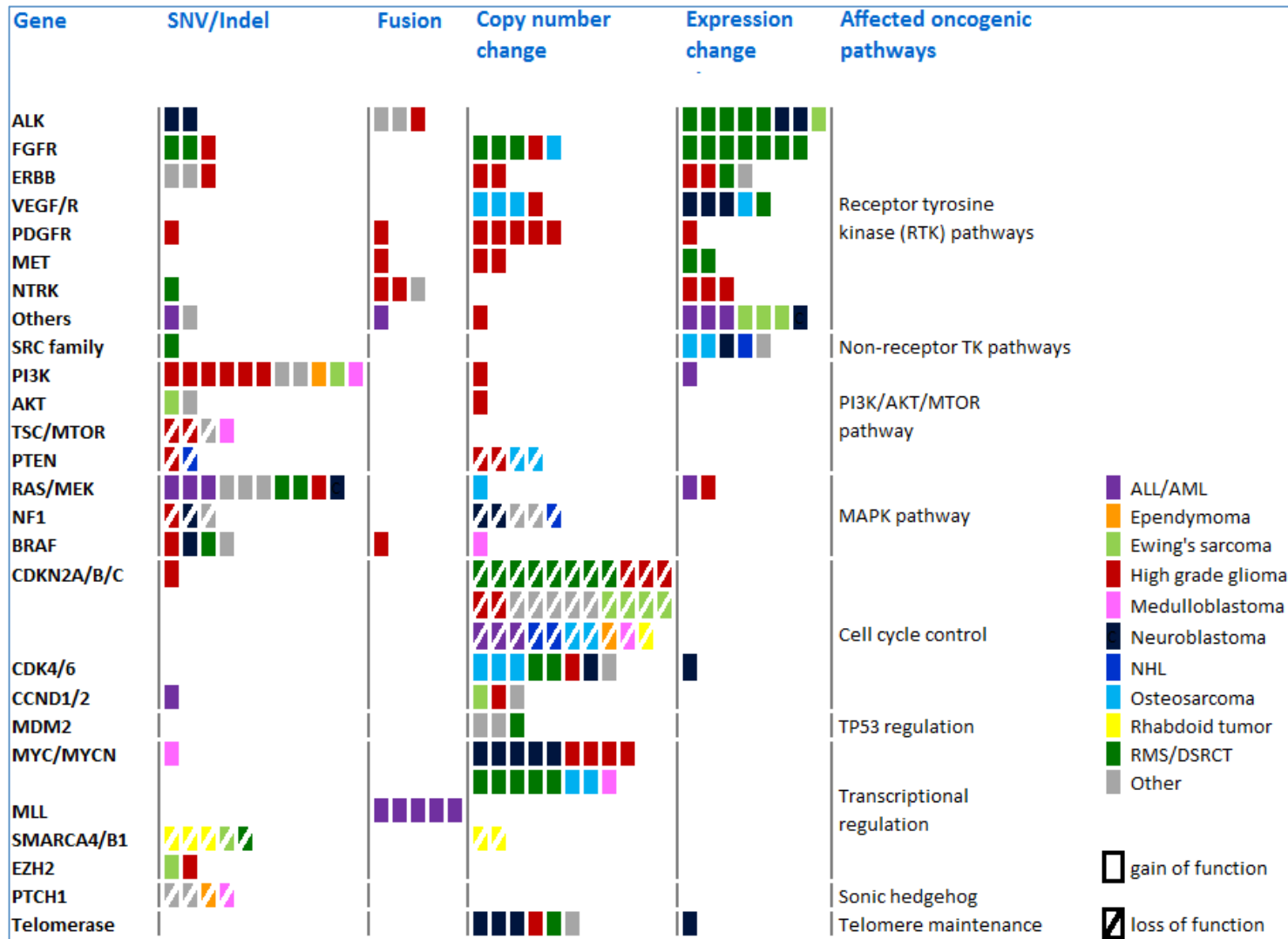
Priority	Target Type	Entity	Target Status
Very high	Confirmed driver	Specific	Genetic hit (mutation/rearrangement)
High	Confirmed driver	Any	Genetic hit (focal high-amplitude CNV)
	Confirmed driver	Other	Genetic hit (mutation/rearrangement)
	Confirmed pathway activation, genetic	Specific	Genetic hit (mutation/rearrangement)
Moderate	Presumed driver	Specific	Genetic hit (mutation/focal low-amplitude CNV)
	Presumed pathway activation, genetic	Specific	Genetic hit
	Confirmed pathway activation, genetic	Other	Genetic hit (mutation/rearrangement)
Intermediate	Presumed driver	Other	Genetic hit (mutation/focal low-amplitude CNV)
	Presumed pathway activation, genetic	Other	Genetic hit
	Synthetic lethal / Predictive marker, genetic	Any	Genetic hit
	Overexpressed driver	Specific	Protein/Expression Change
Borderline	Possible driver	Any	Genetic hit
	Overexpressed driver	Other	Protein/Expression Change
Low	Possible pathway activation, genetic	Any	Genetic hit
	Pathway activation, expression	Any	Protein/Expression Change
	Synthetic lethal / Predictive marker, expression	Any	Protein/Expression Change
Very low	Circumstantial evidence	Any	Genetic/Protein/Expression Change
NA	Biological interest	Any	Genetic hit

Algorithm to be tested in INFORM2

Can a higher score predict a better response/outcome?



Targets mit Score \geq intermediate (198 patients, 10/2013-06/2016)



Worst et. al, Eur J Cancer, 2016



INFORM2 plans – clinical trials

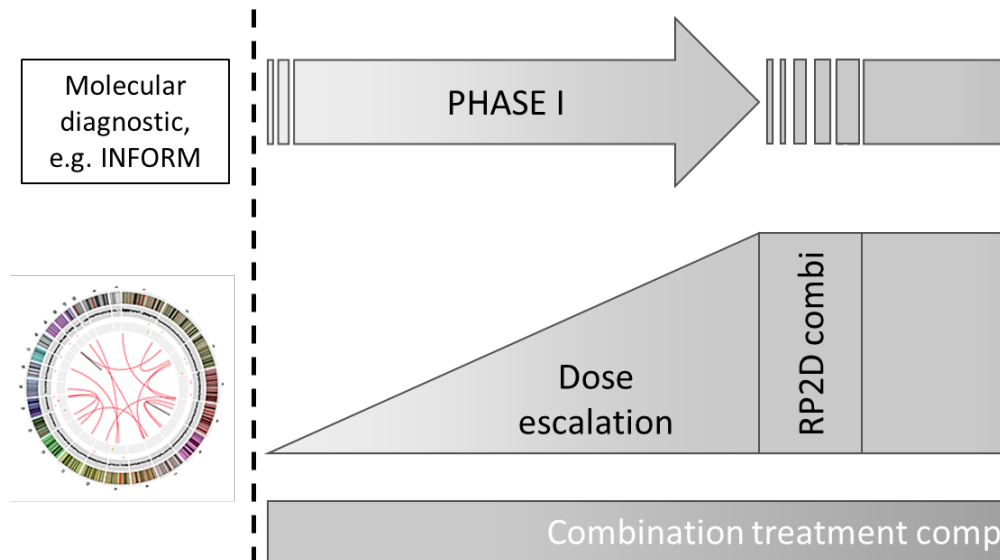
Design principles

- Entity versus **target** driven approach
 - limited number of recurrent actionable alterations
- Mono- versus **combination** therapy
 - but at least one drug with pediatric RP2D (recommended phase II dose)
- Phase I versus phase **I/II**
 - fast escalation phase I (assuming no interactions and known toxicity profile) to max. 100% pediatric RP2D
 - seamless phase II thereafter
- Multi-arm versus **multiple trials**
 - multiple trials in 1 mock-up protocol (medical regulatory body: BfArM)



INFORM2 plans – potential subtrials

Compound class 1	Compound class 2
MET/ALK/ROS1 inhibitor	MEK1/2 inhibitor
RTK inhibitor (e.g. ABL, PDGFR, VEGFR2 Src, RET, FGFR, NTRK)	MEK1/2 inhibitor
PI3K inhibitor	HDAC inhibitor
anti-PD-1 antibody	-

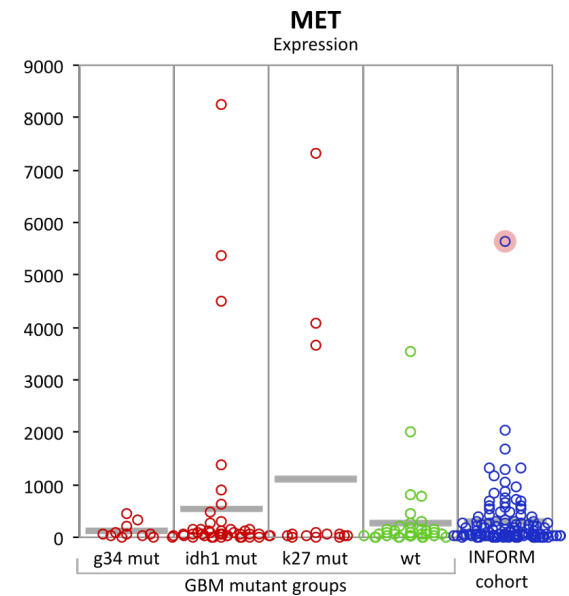
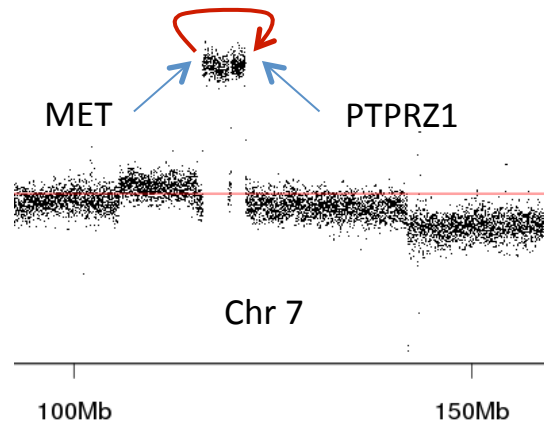
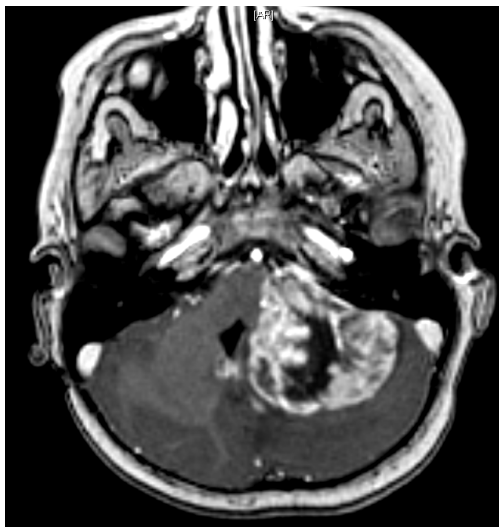


Examples:
Stratum A: panTKi + MEKi
Stratum B: „spec”TKi + MEKi
Stratum C: EZH2i + DNMTi
Stratum D: PI3Ki + MEKi
Stratum E: RAFi + MEKi
Stratum F(i): HDACi + BETi/AURKi
Stratum G: METi + MEKi
Stratum H: ALKi + MEKi
Stratum I: SMOi + PI3Ki
Stratum K: CDKi + MEKi
Stratum L: MDM2i + MEKi

Patient example I

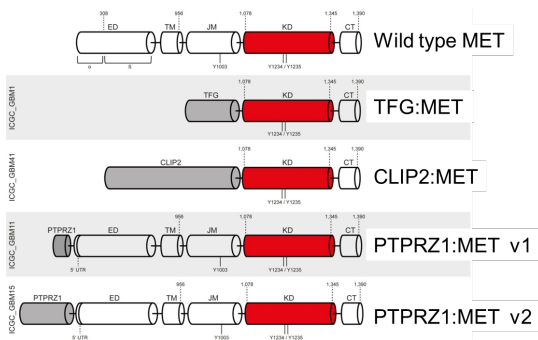
*2006, male

- 04/2011: initial diagnosis of a metastasized group 3 **Medulloblastoma** treatment according to the standard protocol (incl. craniospinal irradiation)
- 09/2014: massive tumor growth
- 10/2014: **INFORM** analysis: **PTPRZ1-MET fusion** with **amplification** and **overexpression** of **MET** + **TP53** mutation (most likely radiation-induced **Glioblastoma**)



Sequencing of 55 Pediatric Glioblastoma

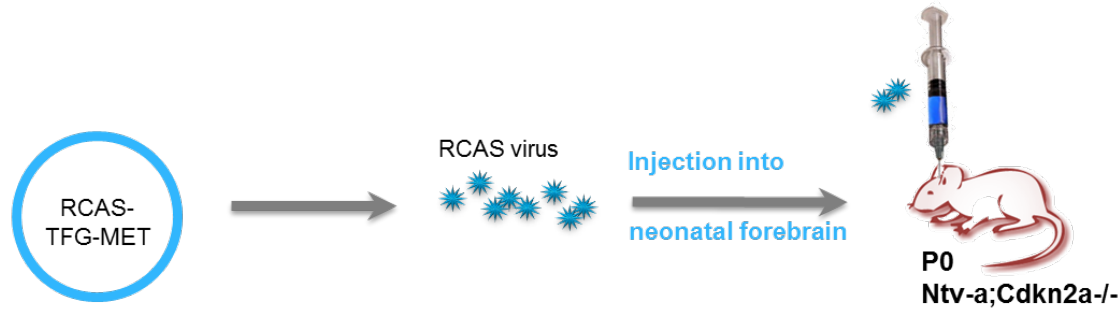
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Age [years]	24	16	13	18	7	11	x	8	27	5	NY	6	x	28	4	5	8	5	13	8	13	14	15	19	19	30	31	25	16	27	12	6	1	12	15	17	5	4	12	13	7	1	7	8	4	7	7	4	20	12	14	9	NY	7	19	16	14
Location	[Color-coded]																				[Color-coded]																																				
H3F3A	[Color-coded]																				[Color-coded]																																				
IDH1/2	[Color-coded]																				[Color-coded]																																				
ATRX	[Color-coded]																				[Color-coded]																																				
SETD1A	[Color-coded]																				[Color-coded]																																				
MYC/MYCN	[Color-coded]																				[Color-coded]																																				
BRAF	[Color-coded]																				[Color-coded]																																				
EGFR	[Color-coded]																				[Color-coded]																																				
FGFR1-4	[Color-coded]																				[Color-coded]																																				
KIT	[Color-coded]																				[Color-coded]																																				
MAPK1	[Color-coded]																				[Color-coded]																																				
MET	[Color-coded]																				[Color-coded]																																				
MTOR	[Color-coded]																				[Color-coded]																																				
NF1	[Color-coded]																				[Color-coded]																																				
NRAS/KRAS	[Color-coded]																				[Color-coded]																																				
NTRK1-3	[Color-coded]																				[Color-coded]																																				
PDGFRA	[Color-coded]																				[Color-coded]																																				
PIK3CA	[Color-coded]																				[Color-coded]																																				
PIK3R1/2	[Color-coded]																				[Color-coded]																																				
PTEN	[Color-coded]																				[Color-coded]																																				
MSH6	[Color-coded]																				[Color-coded]																																				
CDKN2A/B	[Color-coded]																				[Color-coded]																																				
TP53/PPM1D	[Color-coded]																				[Color-coded]																																				
RB1	[Color-coded]																				[Color-coded]																																				



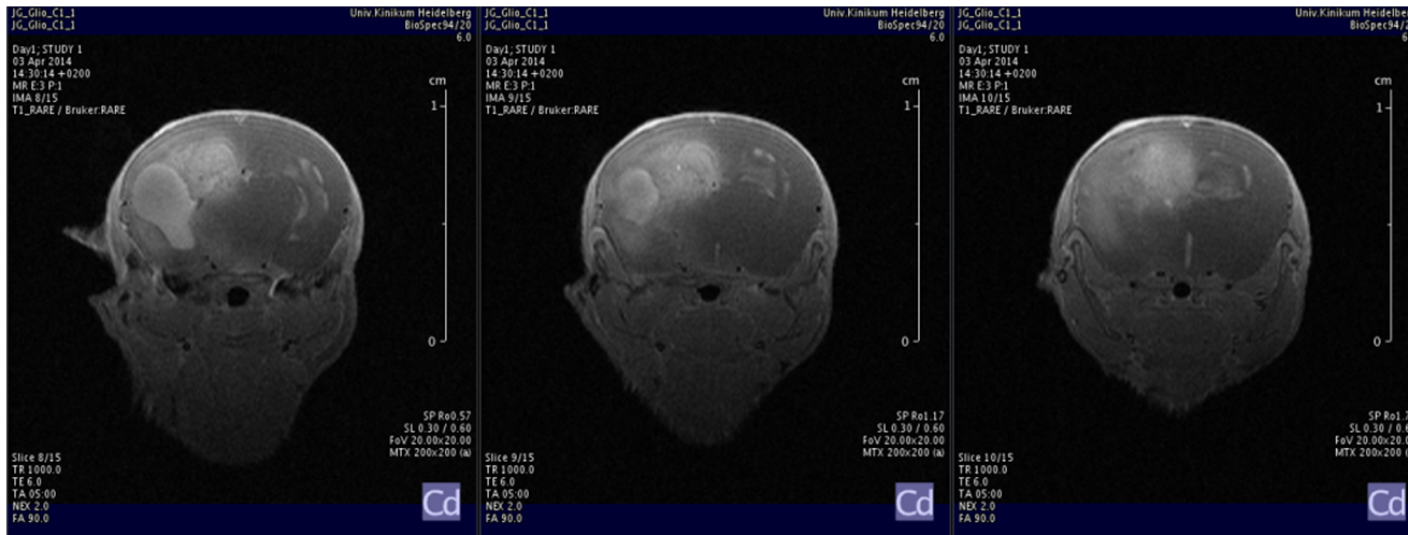
RNAseq showed recurrent fusions involving *MET*

ICGC PedBrain Paper:
Bender et al., *Nature Medicine* (Oct 17, 2016)

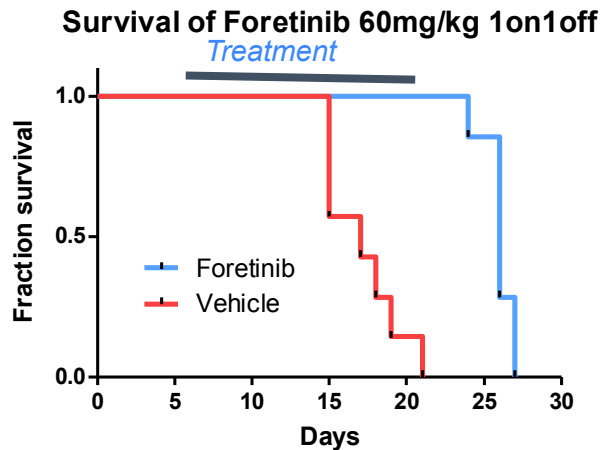
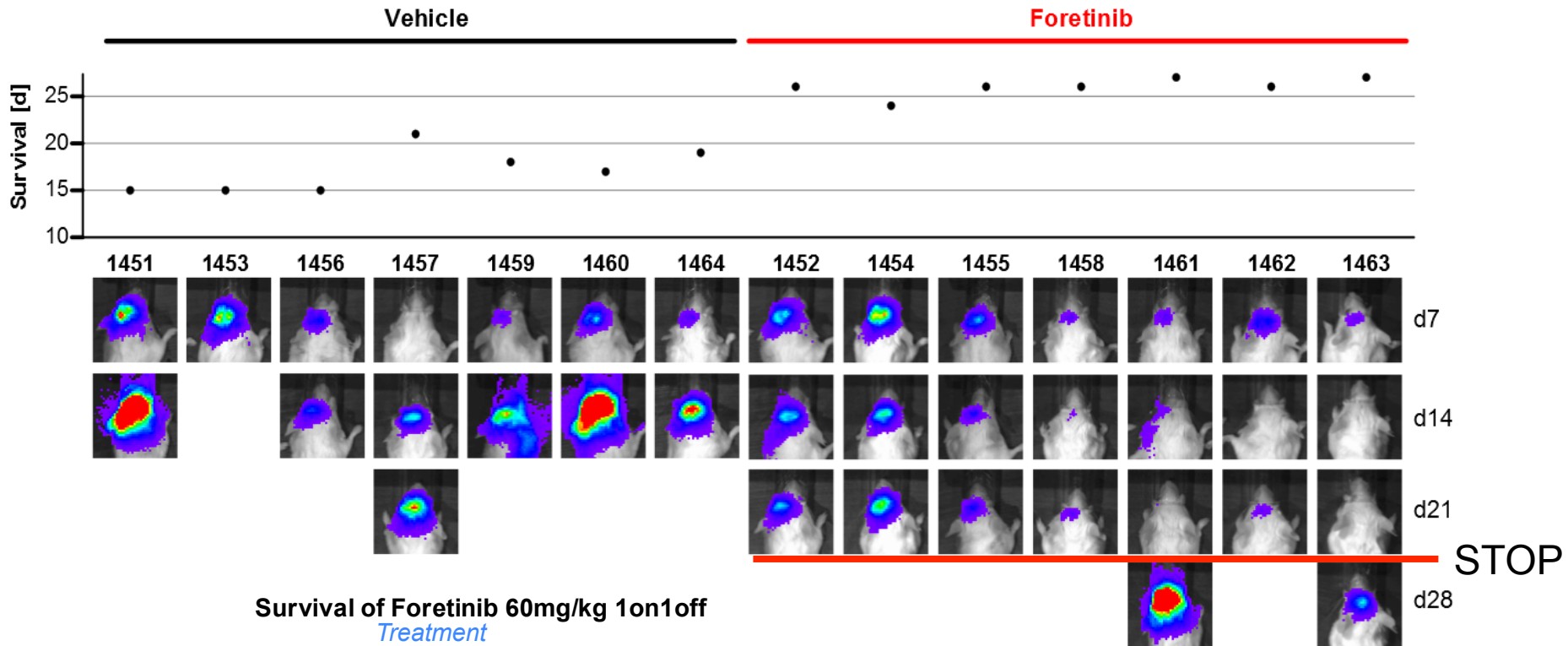
Mouse model: MET fusion causative for glioblastoma



Jan Gronych



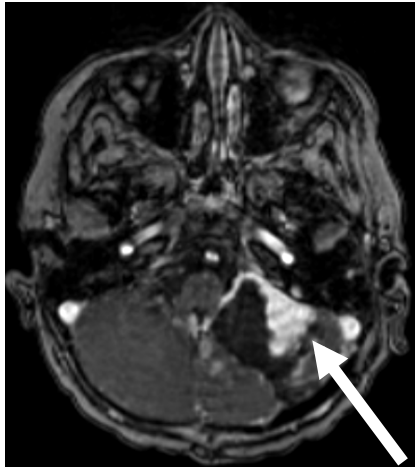
Preclinical testing of targeting inhibitors



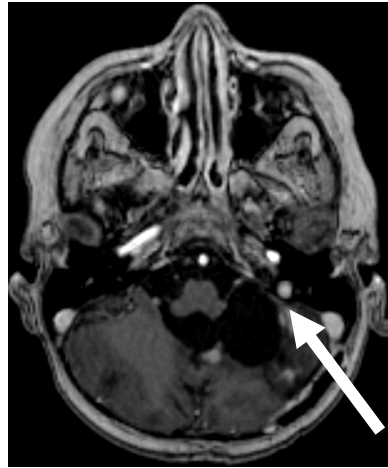
Patient example I: Treatment response and resistance?

Treatment with a **MET-inhibitor (Crizotinib)**

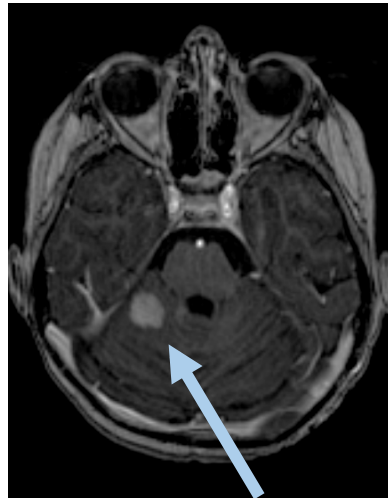
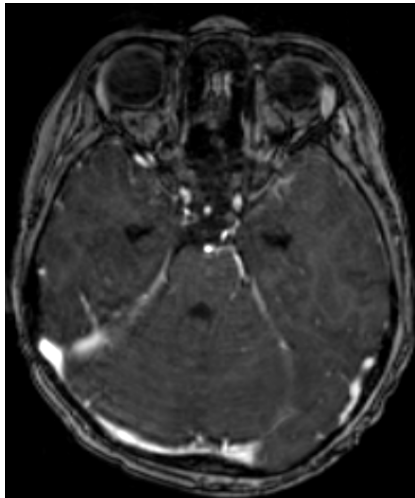
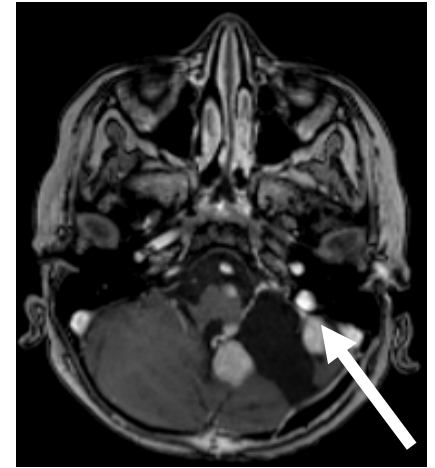
baseline post-OP



2 months Crizotinib



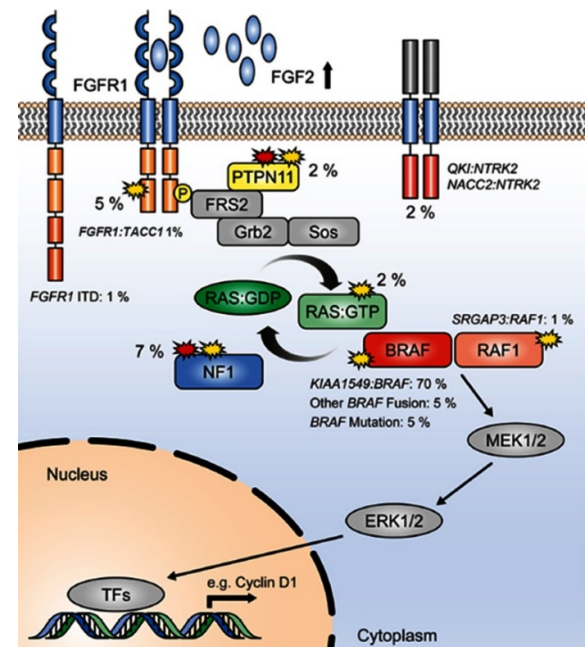
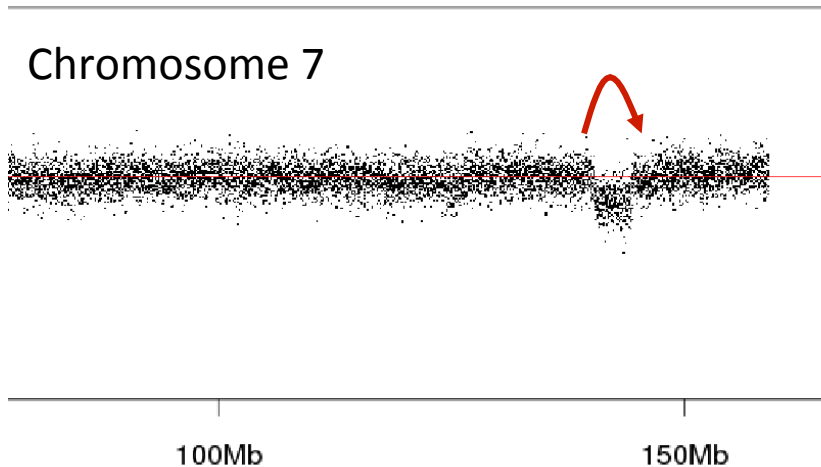
further 16 days Crizotinib



Patient example II

*2008, female

- initial diagnosis of an **Anaplastic Astrocytoma III°** in 11/2013
treatment according to the standard protocol (HIT-HGG, RTx and TMZ)
- Tumor progress in 11/2014
- 12/2014: **INFORM** analysis: **FAM131B:BRAF fusion** identified, typical for **Pilocytic Astrocytoma I°**
=> MAPK pathway activation
- Patient is now treated with a **MEK-inhibitor (Trametinib)**
+ valproate + low-dose cyclophosphamide + chloroquine
- 10/2015: **stable disease**



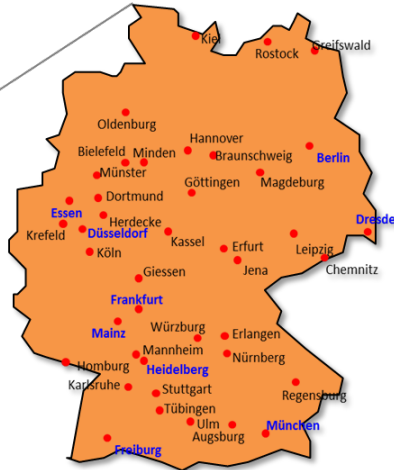
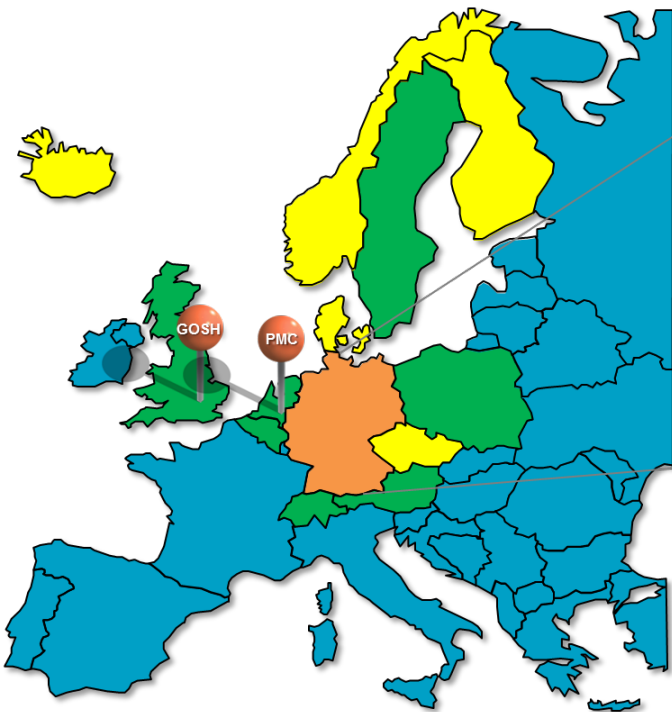
ICGC PedBrain Paper: Jones et al., *Nature Genet* 2013



INFORM registry international

European partners

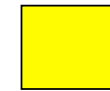
DKTK + partners



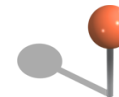
Australia & New Zealand



Countries that are currently preparing for participation (consent, ethics, logistics, national sponsors).



Countries that are currently considering participation

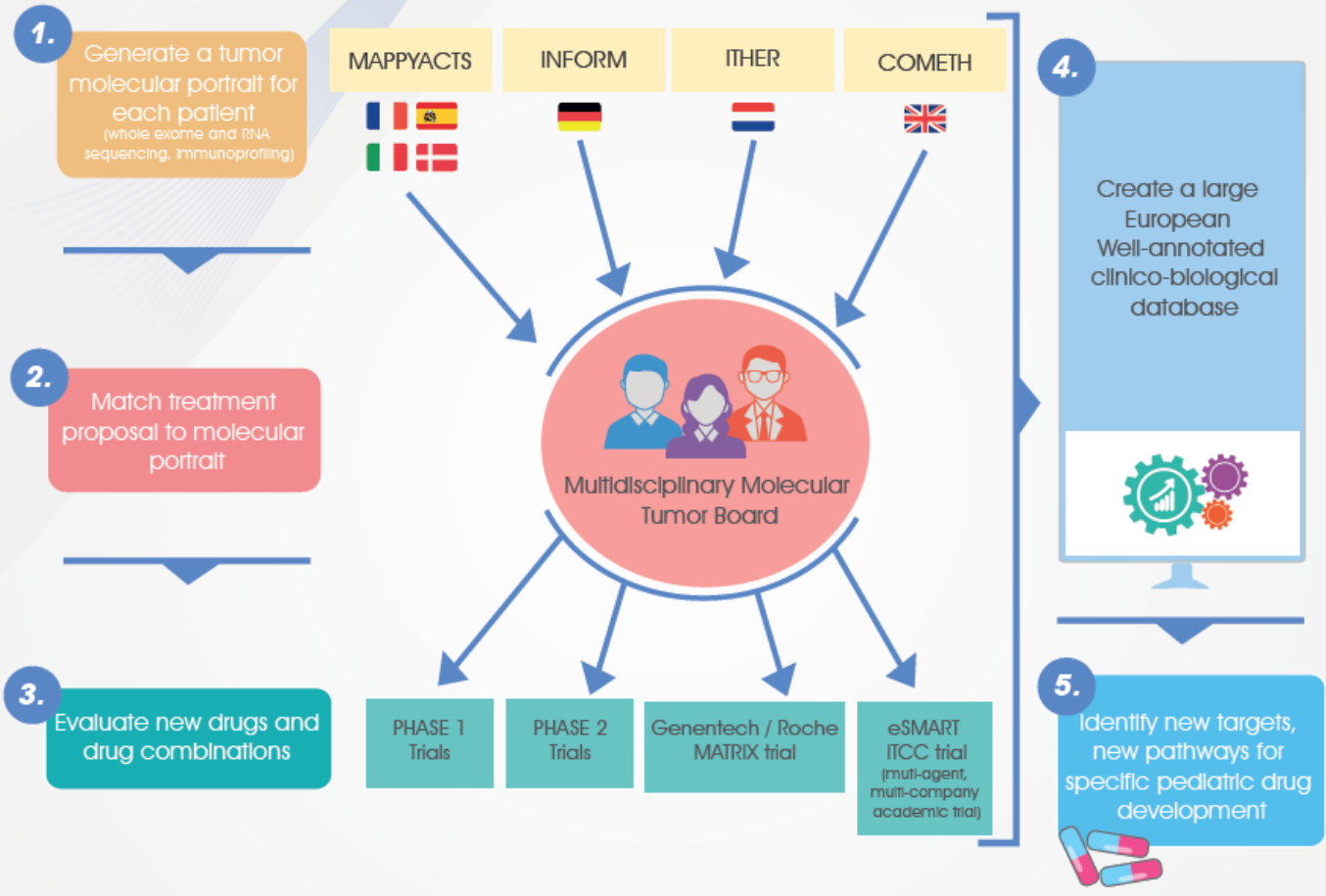


Strategic cooperation partners:
GOSH = Great Ormond Street Hospital London;
PMC = Prinsess Maxima Center Utrecht





Integration of national molecular matching trials



INFORM Team



Stefan Pfister



Peter Lichter



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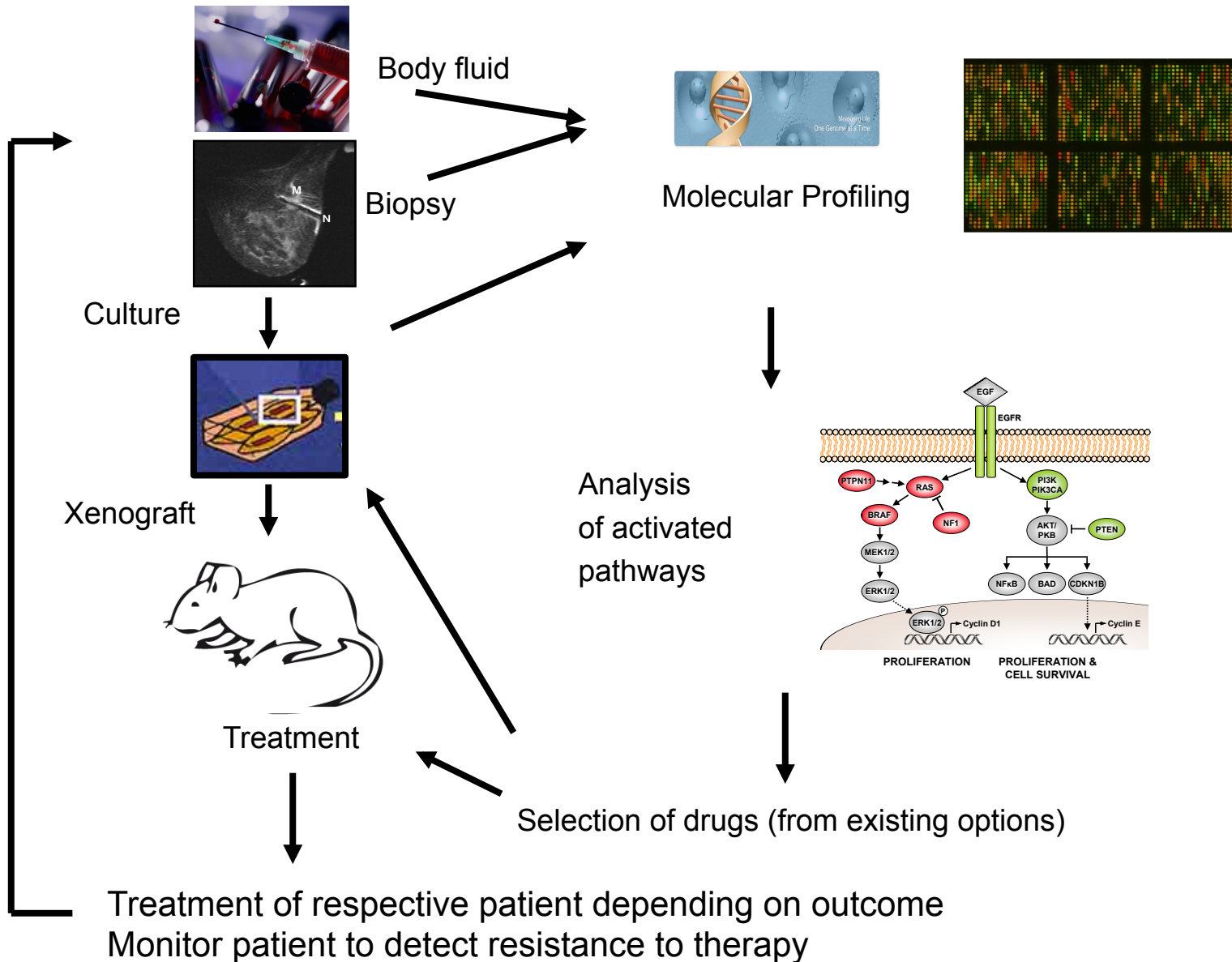
German Cancer Consortium



Worst et. al, Eur J Cancer, 2016



Outlook: Testing for therapy choice in cancer?





Goal: sequence samples from at least 200,000 cancer patients over the next decade

(One project: 4000 patients, e.g. over five years)

=> collection of adequate clinical information will be of utmost importance!

White paper: <http://icgcmed.org/>

The added value of ICGCmed:

Development of common databases containing information on

- **molecular alterations** that can be targeted by drugs
- the **prioritization of molecular targets**
- the impact of **rare molecular variants**
- the **availability of drugs** for respective applications
- **clinical response** that was observed
- the **tumor types**, in which **clinical response** could be expected
- the clinical consequences of **treatment combinations**
- the impact of **ethnic background** in this setting
- the association of **adverse drug effects** with patient's constitution
- the potential **familiar background** of cancer cases