

Update on Precision Medicine Trials & the ITCC Portfolio

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ITCC Introductory Course in Paediatric Drug Development

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Utrecht, NL



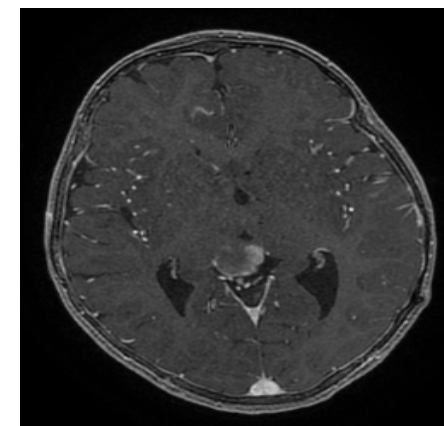
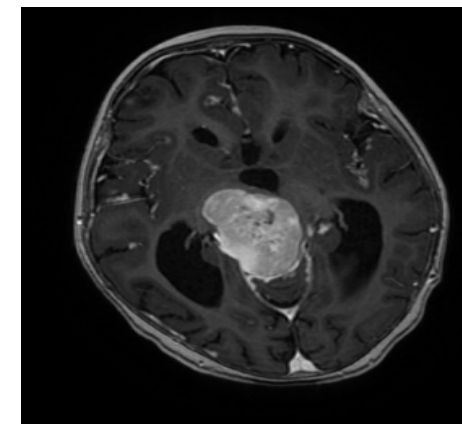
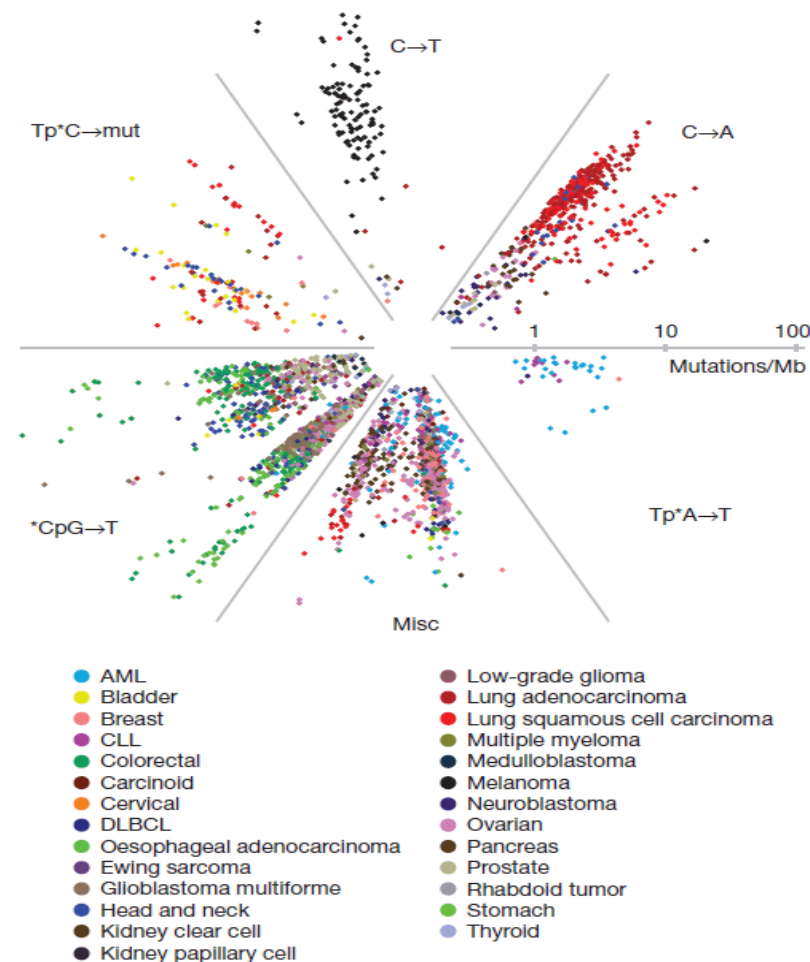
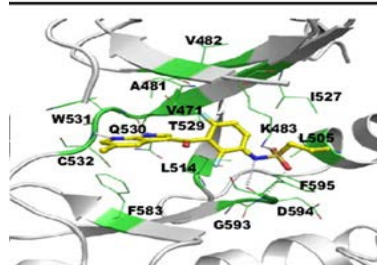
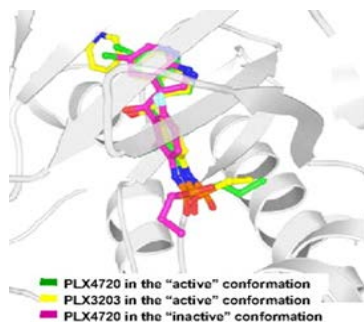
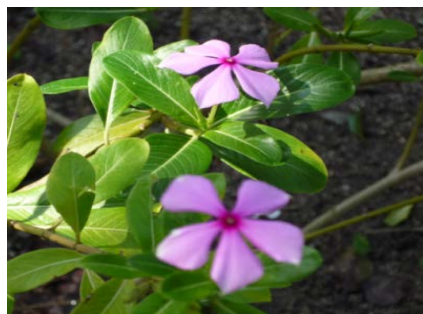
Change of Paradigm in Oncology Drug Development & Era of High-throughput Technologies

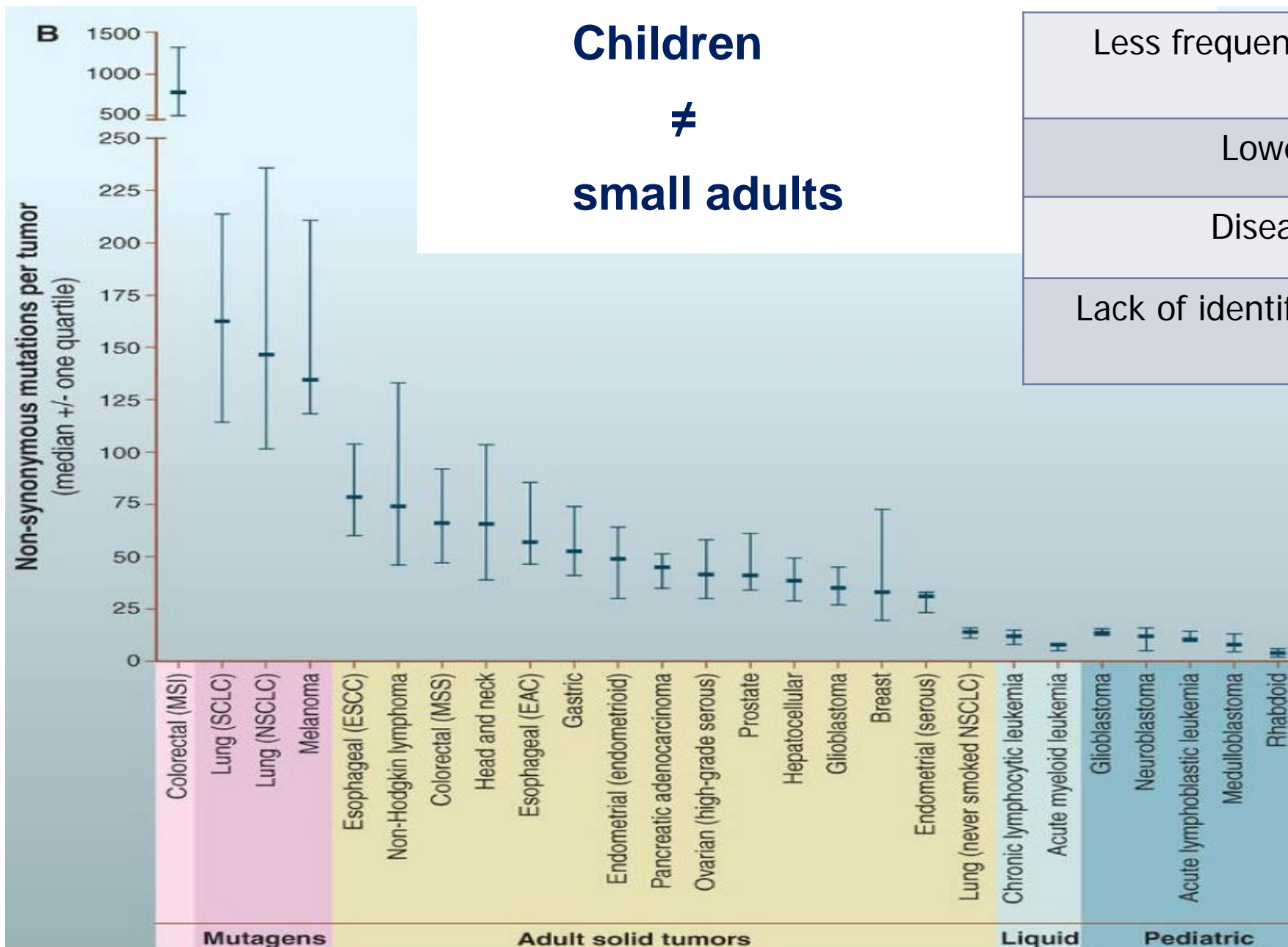
- When Biology Meets Clinics

~ 1000 Anticancer compounds yearly under development

Targeted anticancer compounds

- New mechanisms of action
- New profile of activity
- Distinct profile of toxicity
- Oral and prolonged administration





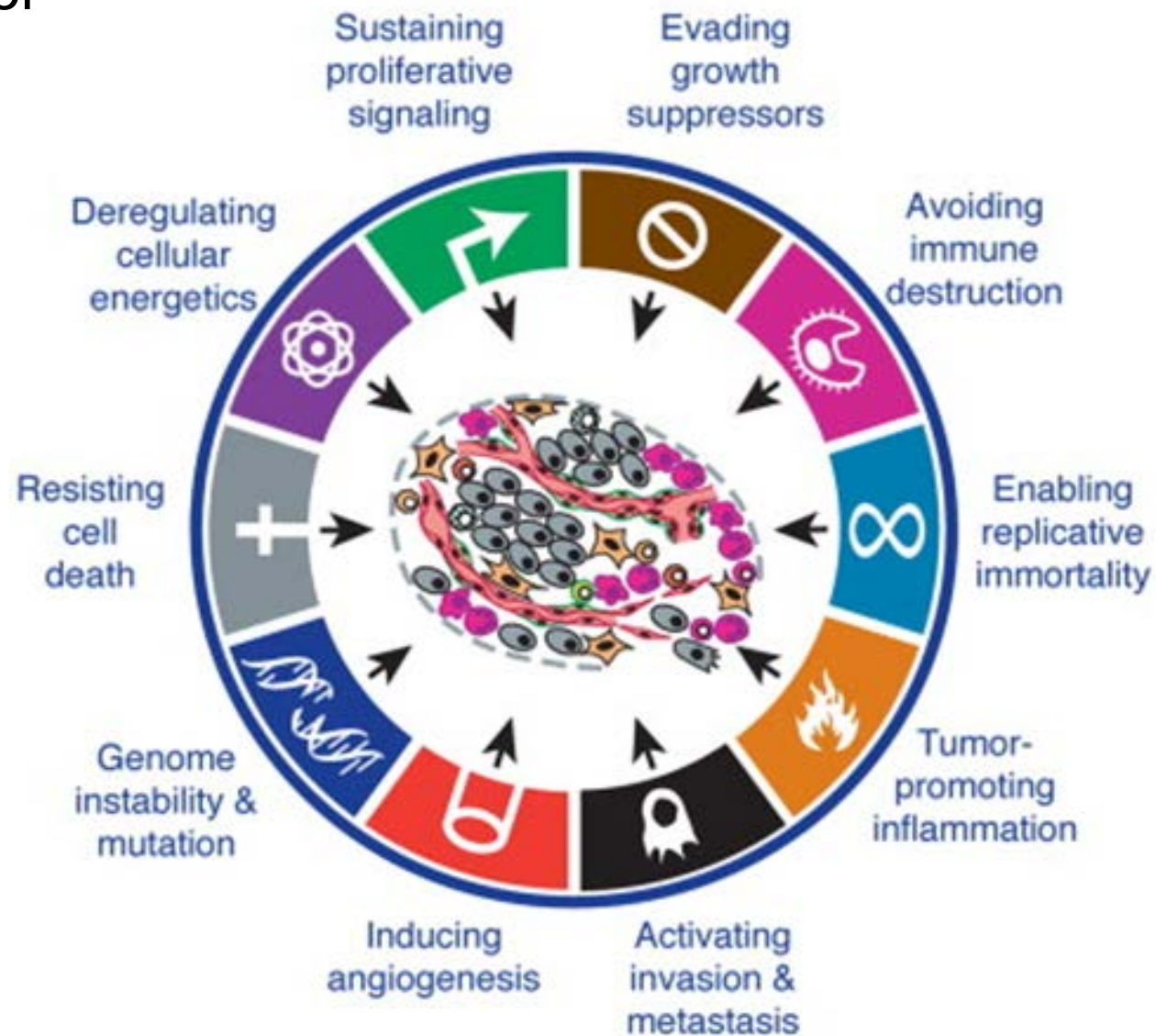
Less frequent / distinct gene alterations

Lower patient numbers

Disease spectrum differs

Lack of identification of actionable targets

Hallmarks of Cancer



Microbiota

Epigenetic modulation

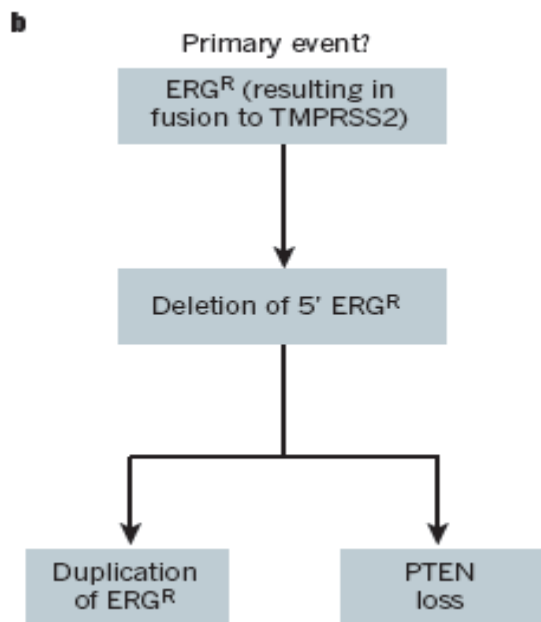
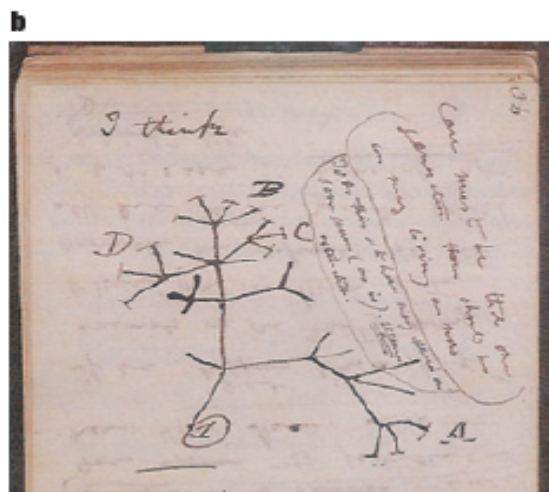
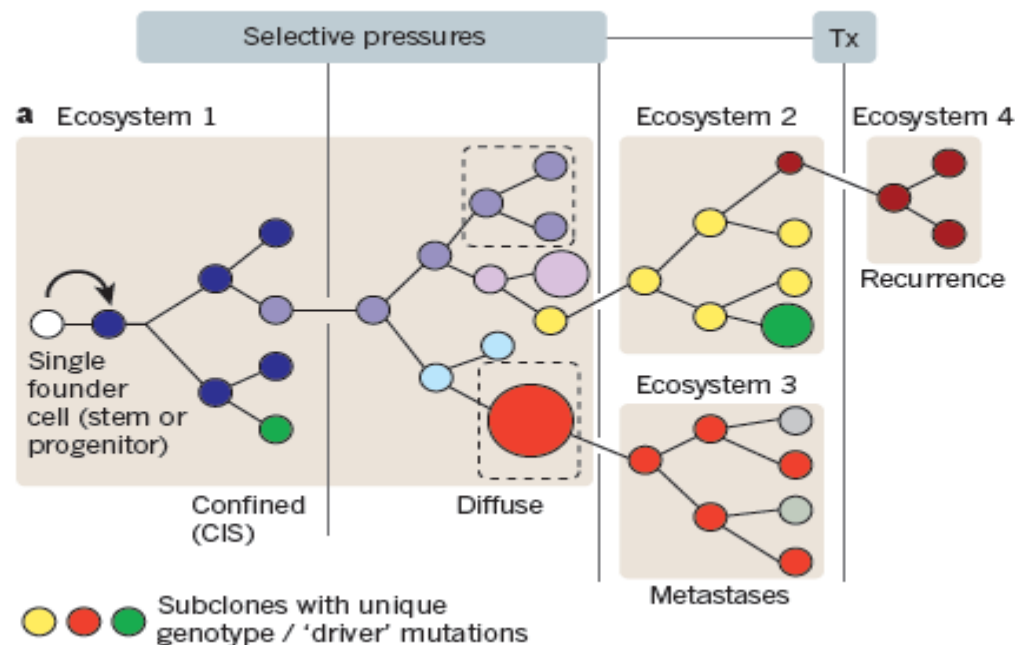
Douglas Hanahan^{1,2,*} and Robert A. Weinberg^{3,*}

Clonal evolution in cancer

Mel Greaves¹ & Carlo C. Maley²

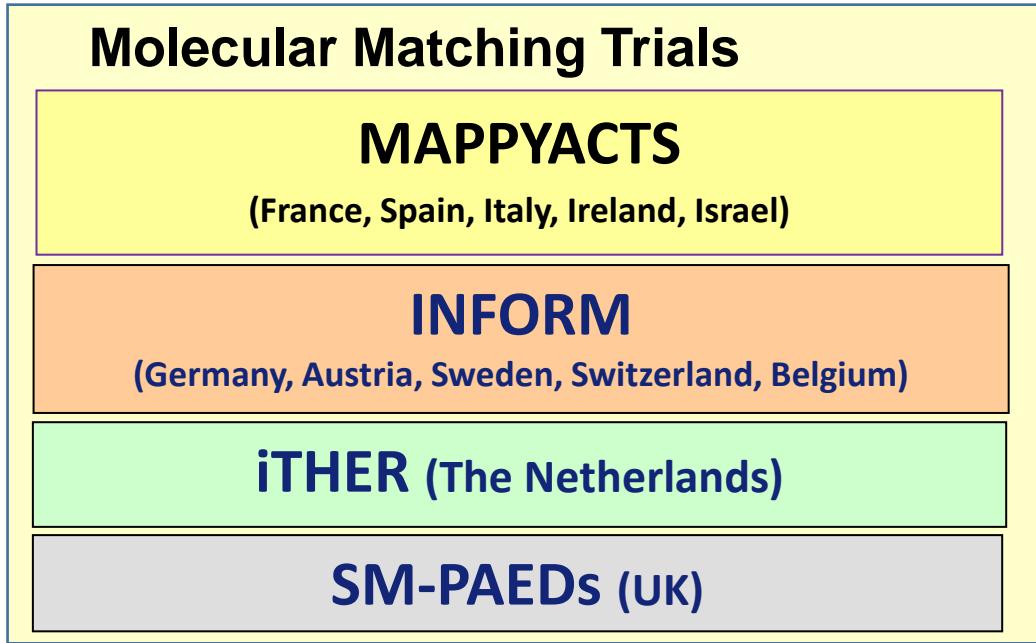
306 | NATURE | VOL 481 | 19 JANUARY 2012

Cancers evolve by a reiterative process of clonal expansion, genetic diversification and clonal selection within the adaptive landscapes of tissue ecosystems. The dynamics are complex, with highly variable patterns of genetic diversity and resulting clonal architecture. Therapeutic intervention may destroy cancer clones and erode their habitats, but it can also inadvertently provide a potent selective pressure for the expansion of resistant variants. The inherently Darwinian character of cancer is the primary reason for this therapeutic failure, but it may also hold the key to more effective control.



European Pediatric Precision Medicine Program in ITCC

1. Generate individual molecular information at relapse



MATCH

2. Match treatment and tumor profile

3. Evaluate activity of drugs and combinations

Phase 1 Trials (Industry and ISTs)

Phase 2 Trials (Industry and ISTs)

**Genentech Roche
Matrix Trial**

ESMART Multiarm trial

European Proof-of-Concept Therapeutic Stratification Trial of Molecular Anomalies in Relapsed or Refractory Tumors in children (ESMART)

INFORM2 trial series

SHARE



Project A

Project B

Project C

Project D

Project E

4. Generate new knowledge, new druggable pathways

Pediatric
New
Drug
Development

MAPPYACTS Design & Workflow

A multicentric, prospective proof-of-concept study **M**olecul**A**r **P**rofil**A**ng for **P**ediatric and **Y**oung **A**dult **C**ancer **T**reatment **S**tratification

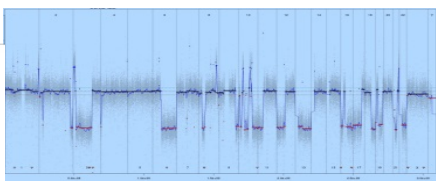
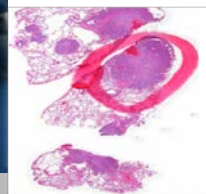
**Sample
collection**

**Molecular
analysis**

**Molecular
Tumor Board**

**Clinical
Molecular
Tumor Board**

Treatment



On-purpose
image-guided biopsy
or
tumor resection

15-30 centers

**Whole Exome
& RNA Sequencing**
≥ 30% tumor cells

2 platforms

Biologists, bio-
informaticians,
physician-scientists

Weekly
discussion with
treating
physicians

Early phase clinical
trials
or
off-label or
compassionate use

**GUSTAVE
ROUSSY**
CANCER CAMPUS
GRAND PARIS

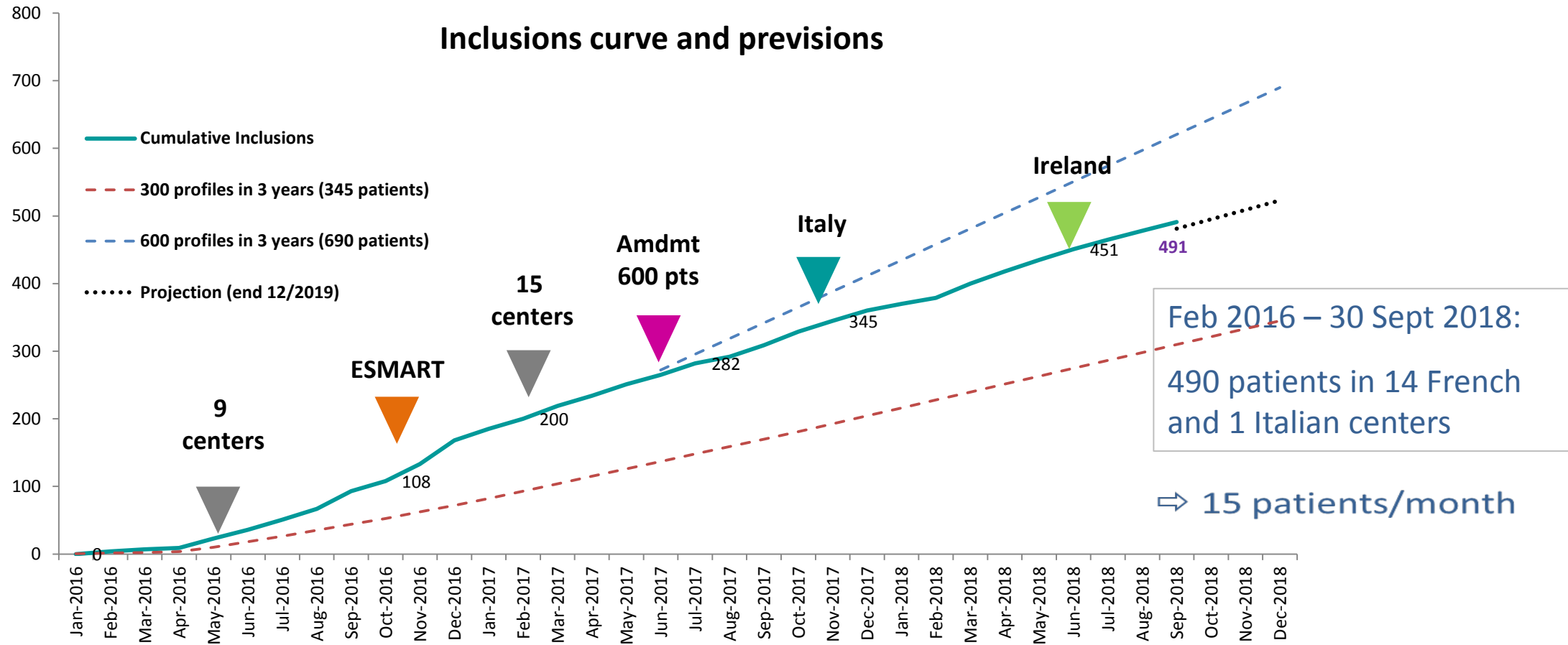
institut Curie
Together, let's beat cancer.

Aims:

- To screen relapsed or refractory pediatric patients
- To provide them with their individual molecular tumor profile
- Attribute them to matched innovative targeted treatments

Ancillary: cf DNA, Immune atlas, Patient-Derived Xenografts

MAPPYACTS - Inclusion

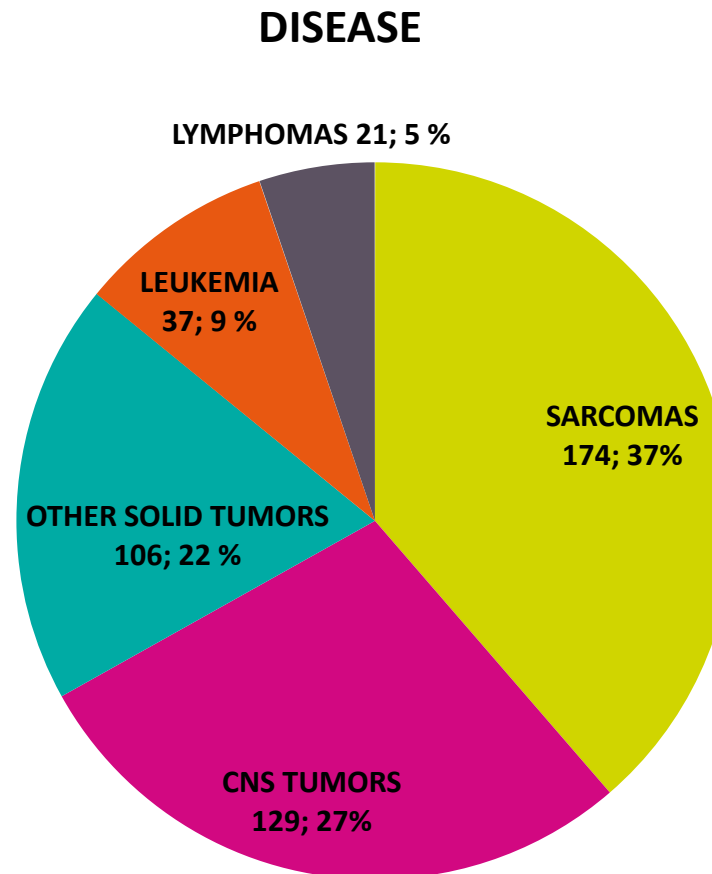


Main challenges:

- Critical is waiting time
 - Too advanced stage
- After biopsy other “standard” treatment
 - Proposition at earlier stage

MAPPYACTS - Study Population

- Median age: 12 years (range: 1- 33)
- Delay initial diagnosis to registration: 1.8 years (0.1 - 22.6)
- Gender: 291 male (62%)
- Diseases:



Molecular Analysis Whole Exome and RNA sequencing

- Tumor DNA/RNA and paired constitutional DNA (blood or bone marrow during MRD)
 - WES: mean depth of coverage: 100 – 120x in tumor samples, 80-100x in normal tissue, 95% at 20x
- Bioinformatics analysis of WES based on Illumina Pipeline and hg19 human genome:
 - Calling:
 - **SNV (mutations), SV**: following application of filters, modeling of potential functional impact and confrontation with RNAseq data (expression)
 - **CNA**: amplifications > 6 - 8 copies taking into account the ploidy background, and homozygous deletions, only focal events with a size under 1-2 Mb
- Bioinformatic analysis of RNAseq:
 - DeFuse, TopHat 2, Chimera Scan, Fusion Map, ...
 - Calling of:
 - Detection of fusion transcripts
 - Detection of splice variants
- Gene alterations were considered 'actionable' based on predicted function, taking into account of gain or loss of function and when targetable directly or their pathway upstream or downstream

MAPPYACTS CMTB Report

➡ Integrated Signatures

Exome Tumor and Germline
RNAseq

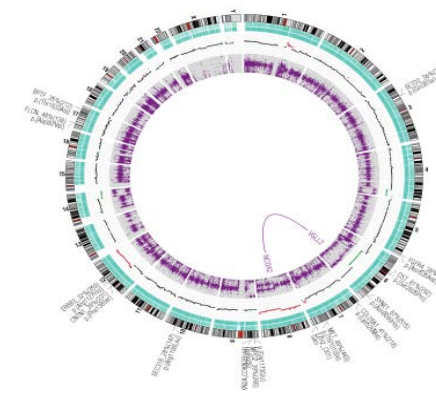
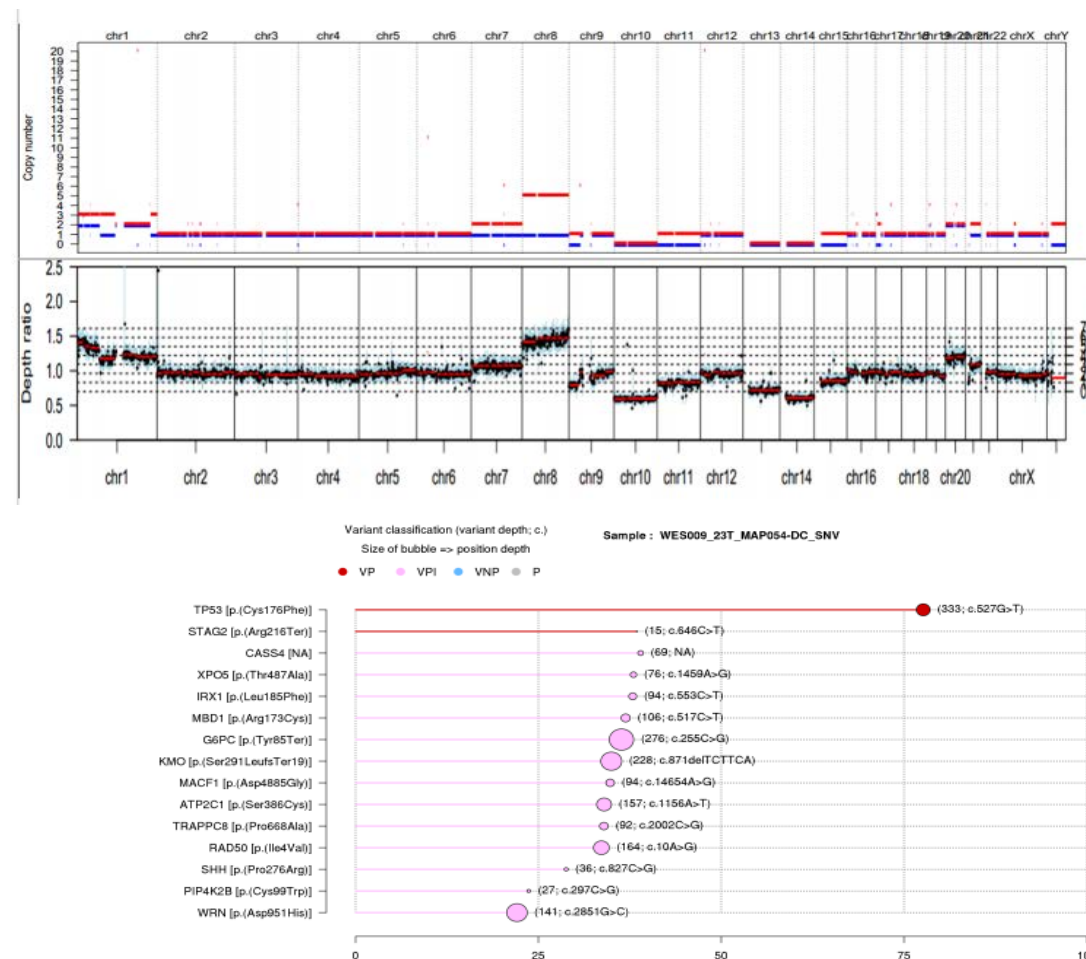
Copy number Profile

Mutational Overview

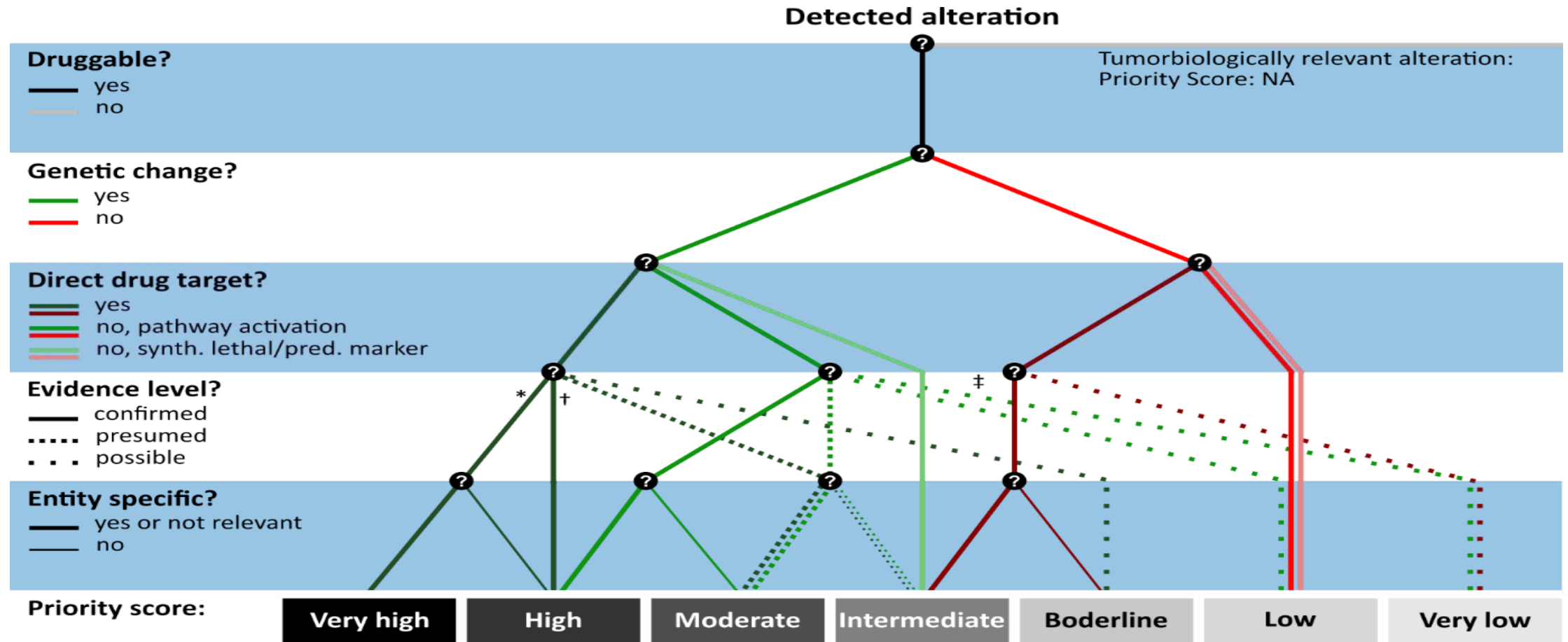
Translocation identification

Signature assessment

- ➡ A single molecular report for clinical use including
 - ➡ Patient's disease history
 - ➡ Targeted therapy orientation
 - ➡ Germline event: Genetic Counseling Parent/Family



Target prioritization – how to translate “gut feeling” into a score!?



Drug availability is currently not a criterium in the pediatric setting
(otherwise almost all targets would get a low score)

Target prioritization – stratification

Prioritization table v4

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

Individualized therapy **F**OR **R**elapsed
Malignancies in childhood

INFORM



73 patients (61 %)
target with score \geq intermediate

89 patients (74 %)
target with score \geq borderline

103 patients (86 %):
actionable alteration

120 patients analyzed
(5 patients pending)

MAPPYACTS CMTB report

LEVEL OF EVIDENCE
Ready for routine use
Investigational
Hypothetical target
Mutation associated to resistance to targeted treatment
Oncogenic without a level of evidence
Oncogenic not targetable

ECCO / PCM recommendation

In 318 contributive samples:

Ready for routine use: 16 (5%)

NPM1/ALK , KIAA1549-BRAF, ETV6-NTRK3, KANK2/NTRK2, CCDC6-RET fusions; BRAF p.V600E, PTCH1, NF1 mutations

Investigational: ~40%

CDK4 ampli, CDKN2A/B del, PI3KCA, PTEN loss, FGFR ampli/mut, MYC ampli, ATR, ATM mut, SMARCA1...

Hypothetical target: ~ 20%

Histone mut, CNA gains, TP53 mut?

Resistance mutations:

SMO p.I408V, NTRK3 p.G623R

Oncogenic without level of evidence:

TP53 mut?, VUS, subclonal events

Oncogenic not targetable:

EWS/FLI1, PAX/FOXO1

Clinical Molecular Tumor Board (CMTB)

Date CMTB: 27/09/2018

Les perspectives thérapeutiques proposées ci-dessous sont fondées sur des hypothèses précliniques ou cliniques qui n'ont pas systématiquement de preuve évidente d'activité ou d'efficacité.

1. Potential phase I/II clinical trials and treatment recommendations based on genetic alterations identified in the tumor

LEVEL OF EVIDENCE
Ready for routine use
Investigational
Hypothetical target
Mutation associated to resistance to targeted treatment
Oncogenic without a level of evidence
Oncogenic not targetable

Somatic genetic alteration :	Potential treatment :	Level of evidence :
CDKN2A/B focal homozygotic deletion	CDK4/6 inhibiteur : Ribociclib + TOTEM (bras A ESMART ; no slot)	Investigational
ESWR1-FLI-1 fusion	Confirms dg of Ewing	Oncogenic not targetable

2. Potential phase I/II clinical trials based on tumor type available
 - Ewing sarcome avec transcrit de fusion ESWR1-FLI-1 = Regobone (slot disponible)
 - PARP inhibiteur : Olaparib + Irinotecan (ESMART bras D)

Hiérarchie recommandations: Regobone > ESMART Bras D > ESMART Bras A

Clinical Molecular Tumor Board (CMTB)

Date CMTB: 27/09/18

Les perspectives thérapeutiques proposées ci-dessous sont fondées sur des hypothèses précliniques ou cliniques qui n'ont pas systématiquement de preuve évidente d'activité ou d'efficacité.

1. Potential phase I/II clinical trials and treatment recommendations based on genetic alterations identified in the tumor

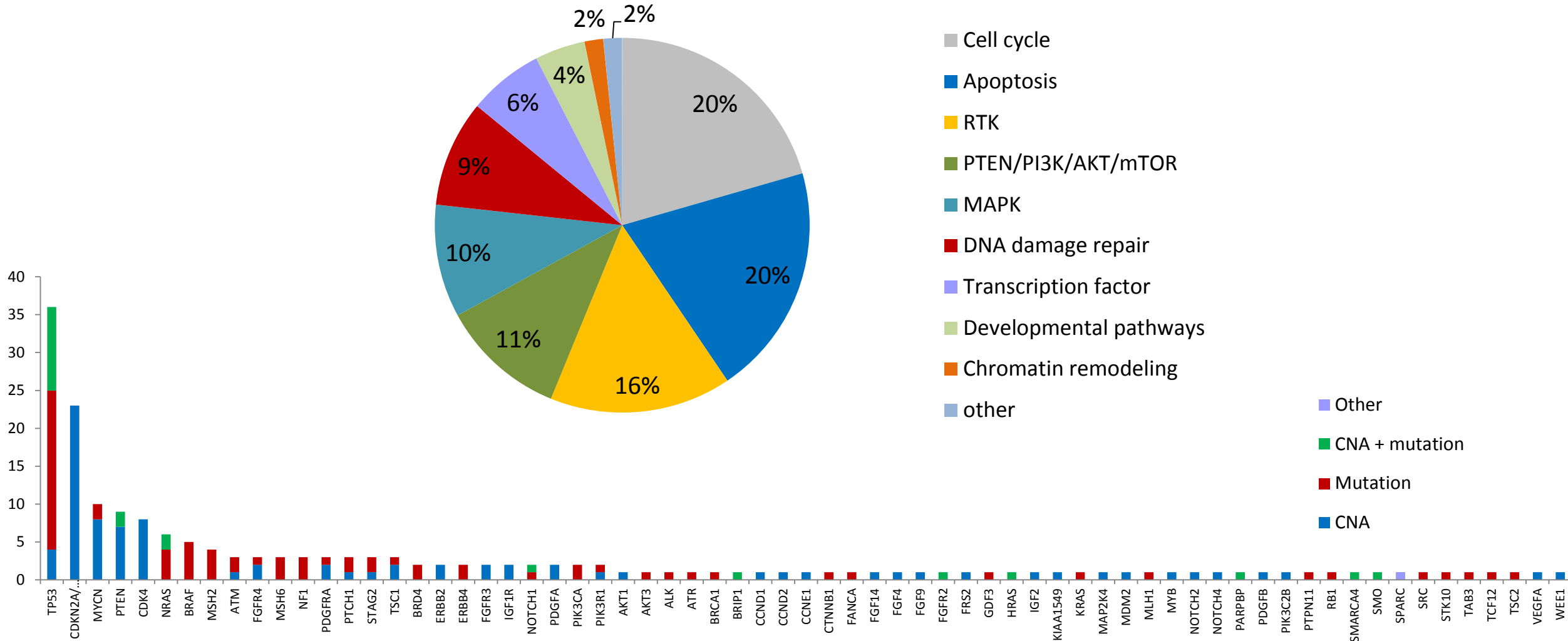
LEVEL OF EVIDENCE
Ready for routine use
Investigational
Hypothetical target
Mutation associated to resistance to targeted treatment
Oncogenic without a level of evidence
Oncogenic not targetable

Somatic genetic alteration :	Potential treatment :	Level of evidence
PBRM1 p.(Asp632Glu/Ter11) VP homozygote (LOH) (95,35%)	Epigenetic modulator: EZH2 or HDAC inhibiteurs or depakine (no inclusion criteria for EZH-102 ; off label/ATU)	Hypothetical target
C11orf95/RELA fusion	Confirms dg of supratentorial ependymoma	Oncogenic not targetable

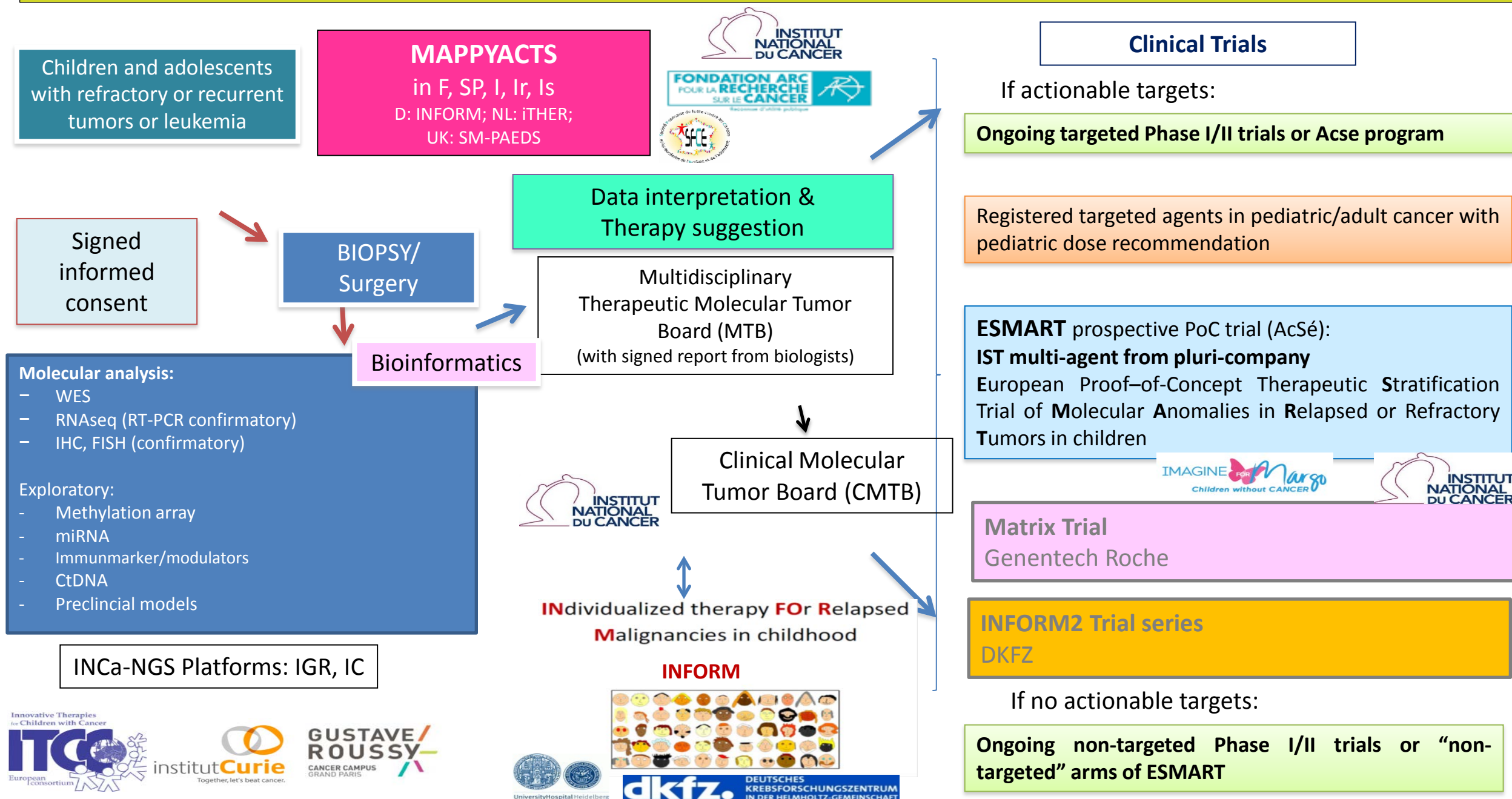
2. Potential phase I/II clinical trials based on tumor type available
Aucune

Hiérarchie recommandations: Traitement standard > EZH2 ou HDACi (ATU) or depakine

'Actionable' Molecular Alterations



European Precision Medicine Program: Pediatric Oncology-Hematology 2018



Ongoing Early Clinical Trials, France October 2018

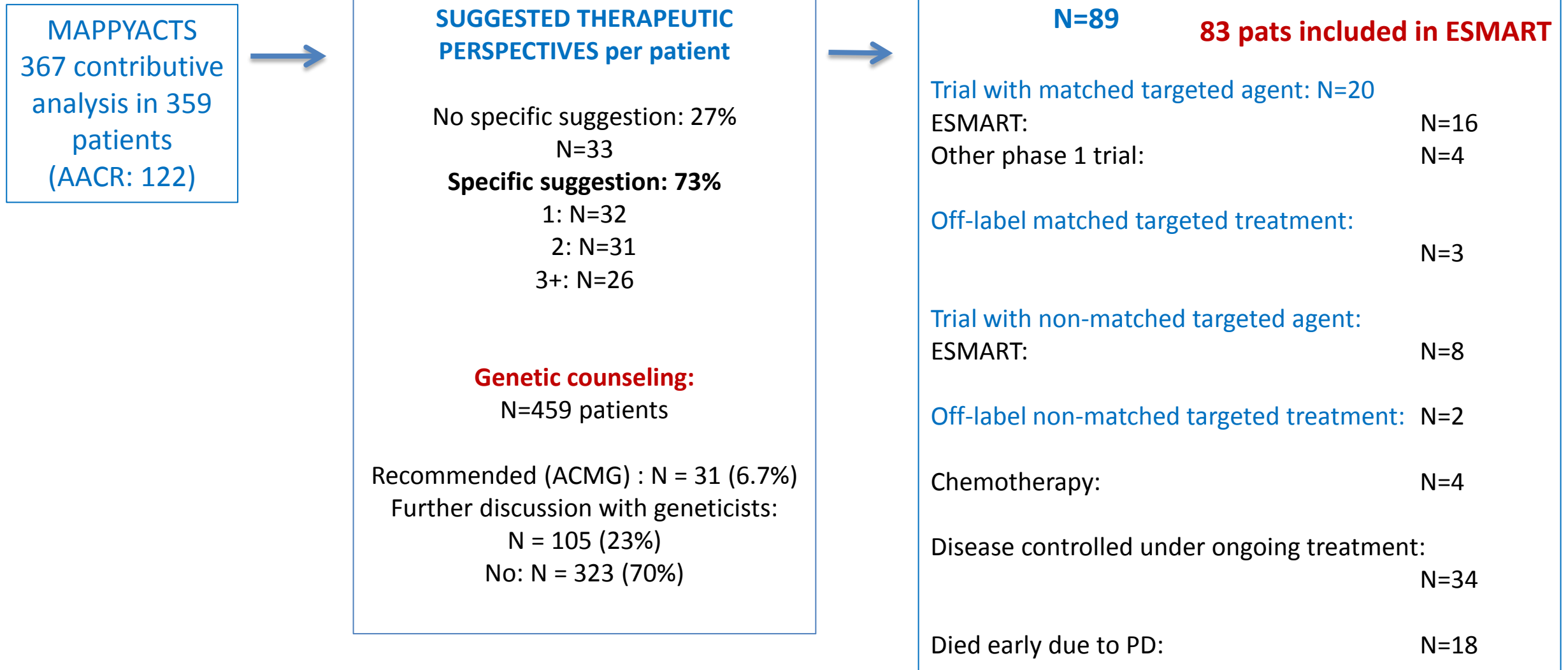
Phase 1:

- **Leukemia:**
 - [ITCC-015 VIDAZA](#) *pending*
 - [ITCC-052](#) Carfilzomib + R3
 - [ITCC-054](#) Bosutinib
 - [ITCC-059](#) Inotuzumab Ozogamycin
 - ITCC-070 Daratumumab CD-38
 - ITCC-067 AC-220 quizartinib Flt-3
- **Leukemia + solid:**
 - [ITCC-057](#) AcSe-ESMART A-J
 - ITCC-062 Arginase BCT-100 (Leuk + solid)
 - ITCC-068 Venetoclax BCL2
- **Solid:**
 - [Talimogene Laherparepvec](#)
 - [ITCC-037](#) Dabrafenib (BRAFv600) (Phase 2)
 - [ITCC-047](#) Regorafenib + VI
 - [Trametinib](#) (MEK) +/- dabrafenib (Phase 2)
 - [ITCC-049](#) Afatinib (Expansion)
 - [Pembrolizumab](#) (HD, MSI)
 - [ITCC-061](#) EPZ 6438 Tamezetostat (pending)
 - [ITCC-055](#) Cobimetinib
 - [Fluvabrex](#) 12-08
 - [ITCC-066](#) LOXO-101
 - LOXO-195
- **Molecular Profiling:**
 - [MAPPYACTS](#)
- > 18 years one may also consider adult phase I/II trials in adult centers

Phase 2:

- **Leukemia/Lymphoma:**
 - [RIALTO](#) 20130320
 - [Nivolumab](#)-brentuximab CA209744
 - [ITCC-065](#) Ibrutinib + Rice
 - ITCC-063 Selumetinib +dexa (Dec 2018)
- **Multiple:**
 - [Tamezetostat](#): Rhaboid and INI-neg >16 yr
 - ITCC-053 CRISP (Nov 2018)
- **Sarcoma:**
 - [ITCC-050](#). [Lenvatinib](#) + ifo-VP-16 osteo
 - [Regobone](#): [Ewing](#) > 10yrs
 - [Pembrosarc](#) >18yrs
 - [Cabone](#) > 12 yrs
 - [Metzolimos](#)
 - [Pazopanib](#) GW786034
- **Neuroblastoma:**
 - [ITCC-032](#) BEACON
 - ITCC-077 3F8 (anti-GD2)Naxitamab
 - Lorlatinib NANT (Nov 2018)
- **Brain Tumors:**
 - [ITCC-022](#) VINILO Ph2 Randomization
 - [ITCC-051](#) BIOMEDE
 - [Ipilumab-Nivolumab CNS](#)
 - Pomalidomide ([CC-4047](#))
 - [ITCC-064](#) ABT-414 >12yrs




Therapeutic Suggestions and Treatments



Main Inclusion Criteria:







- Patients < 18 years with a relapsed or refractory malignancy (solid tumor or leukemia)
- Evaluable disease
- Lansky/Karnofsky $\geq 70\%$
- No toxicity $\geq G2$
- Deep tumor molecular analysis available is mandatory

WAVE 1 of Treatments

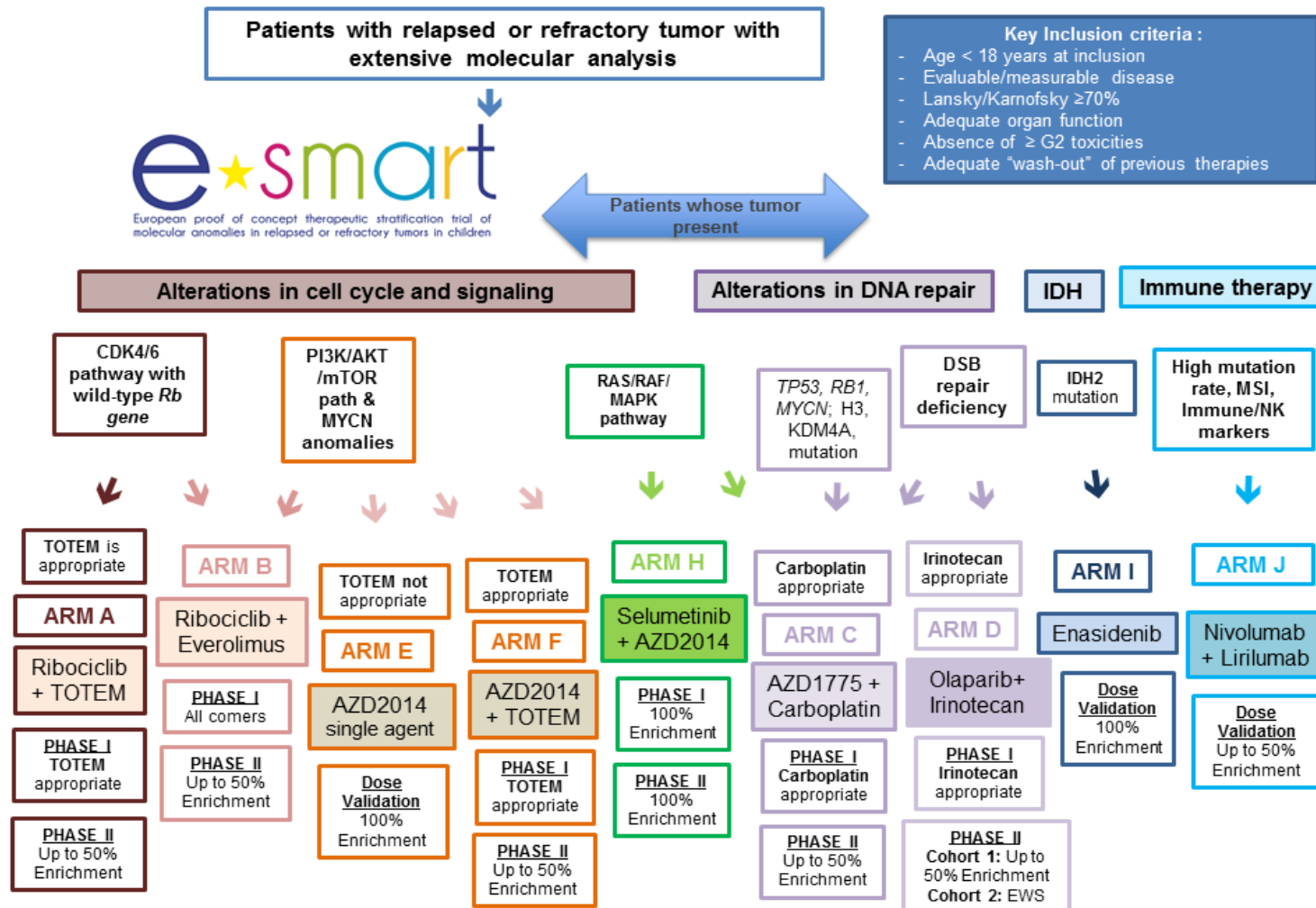
ARM	Pathway	Target	Treatment	Enrichment	Pharma
Arm A	Cell Cycle	CDK4/6	Ribociclib + TOTEM*	50%	
Arm B			Ribociclib + Everolimus	50%	
Arm C	DNA repair	WEE1	AZD1775 + Carboplatin	50%	
Arm D		PARP	Olaparib + Irinotecan	50%	
Arm E	PI3K/AKT/mTOR	mTORC1/ TORC2	AZD2014	100%	
Arm F			AZD2014 + TOTEM*	50%	
Arm G	Immune checkpoints	PD1	Nivolumab + CyclophoP** +/-RT***	NA	
* topotecan + temozolomide; ** cyclophosphamide; ***radiotherapy					

Arms Summary protocol v2.0

Protocol v1.3
Protocol v2.0
Arm removed from the protocol

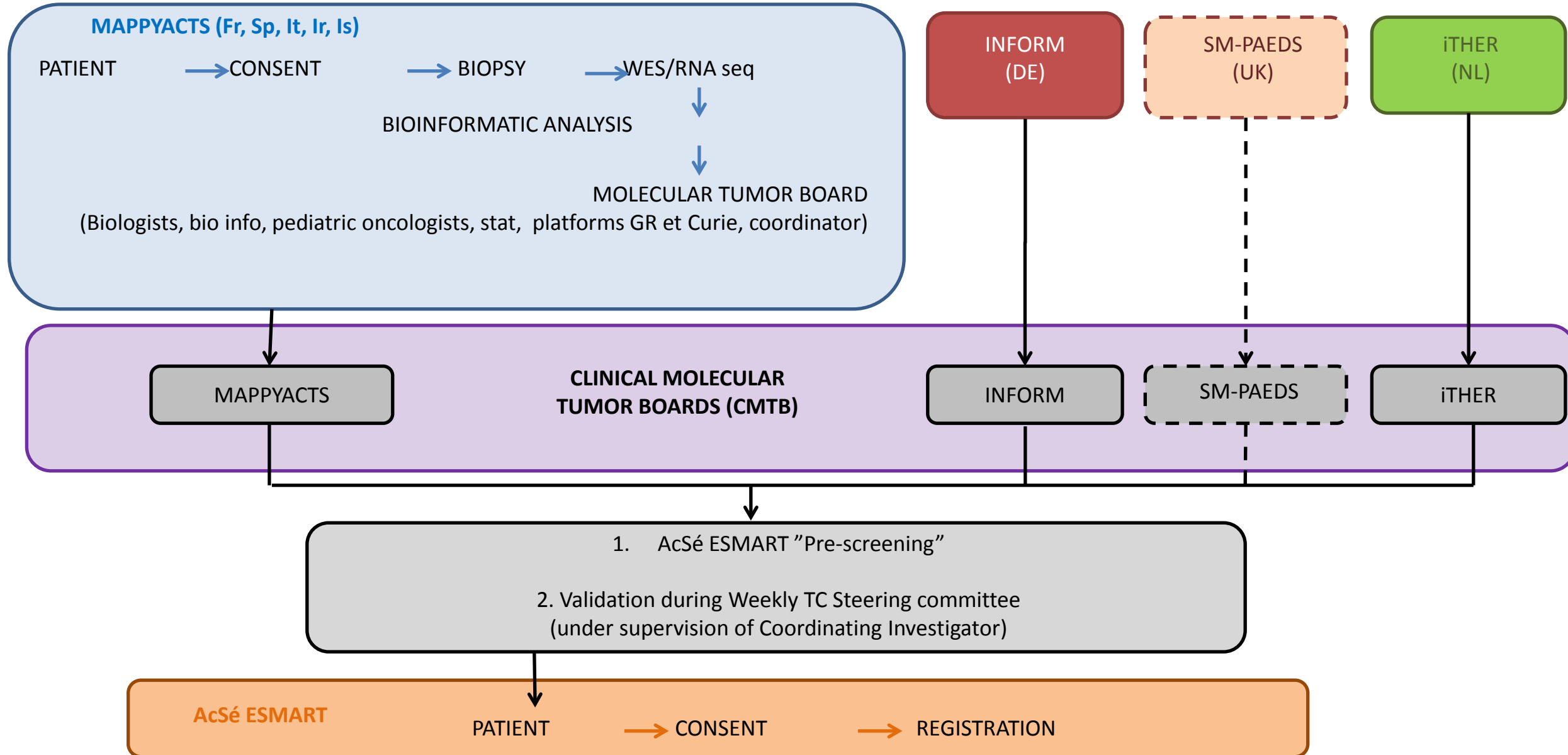
ARM	Pathway	Target	Treatment	Enrichment	Pharma	Investigator
Arm A	Cell Cycle	CDK4/6	Ribociclib + TOTEM*	50%		Francisco Bautista
Arm B			Ribociclib + Everolimus	50%		Francisco Bautista
Arm C	DNA repair	WEE1	AZD1775 + Carboplatin	50%		Francisco Bautista
Arm D		PARP	Olaparib + Irinotecan	50%		Susanne Gatz
Arm E	PI3K/AKT/mTOR	mTORC1/TORC2	Vistusertib	100%		Lynley Marshall
Arm F			Vistusertib + TOTEM*	50%		Lynley Marshall
Arm G	Immune checkpoints	PD1	Nivolumab + CyclophoP** +/-RT***	NA		Claudia Pasqualini
Arm H	PI3K/AKT/mTOR Ras-Raf-MEK-ERK	MEK + mTOR	Selumetinib + Vistusertib	100%		Pablo Berlanga
Arm I	Metabolic pathway	IDH2	AG-221 (Enasidenib)	100%		Stephane Ducassou
Arm J	Immune checkpoints	PD1 + KIR	Nivolumab + Lirilumab	NA		Nicolas Andre

Complexity of Hypothesis Driven Enrichment Strategy & Proof-of-Concept for the Clinical Roles of Molecular Alterations



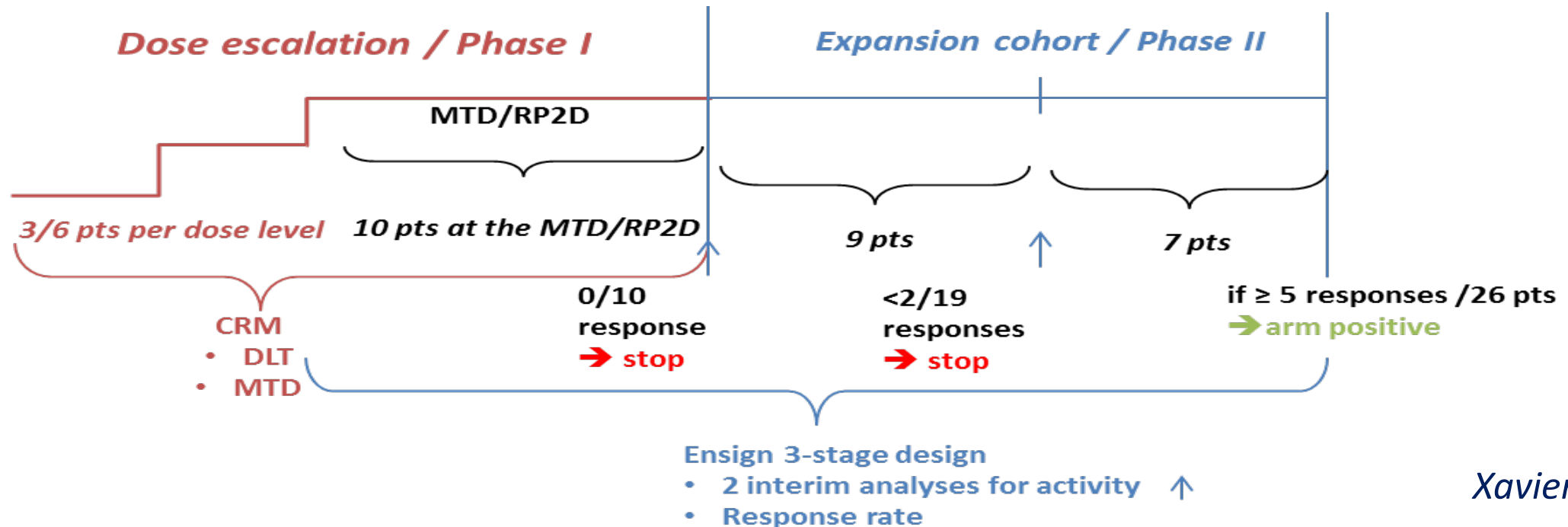
- Molecular alterations:
 - Variable level of biological evidence
 - Fusions – CNA – VP/VUS/VNP
 - Homozygotic vs heterozygotic events
 - Subclonal events
- ☐ Hierarchy of multiple alterations
- ☐ Lack of gene methylation, protein expression and functional data
- Profiles of patients in each arm are currently further explored

Interaction between European molecular profiling programs and inclusion in AcSé- ESMART



AcSé-ESMART Statistical Design

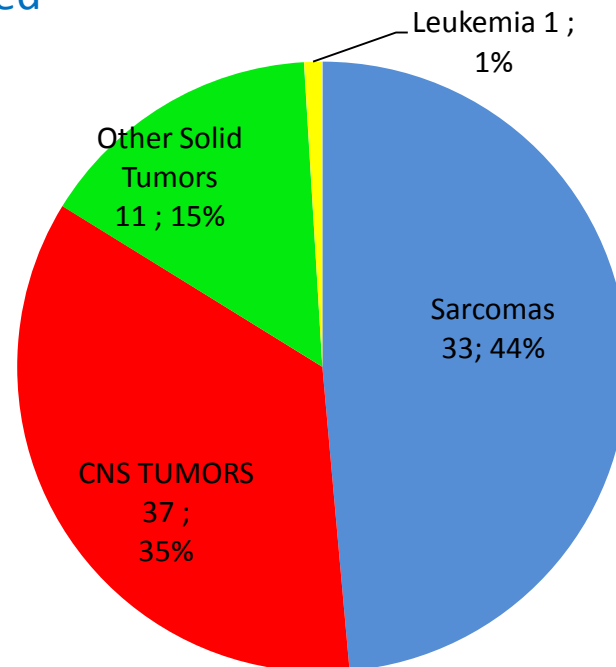
- Each arm is run independently (6-38 patients/arm)
- 2 parts : Phase I et Phase II
 - Evaluation of safety (DLT, MTD, RP2D) AND activity
 - 200 à 285 evaluable patients in 3 years
 - IDMC (1 pediatric oncologist, 1 medical oncologist, 1 pharmacovigilant, 1 statisticien)



ESMART Inclusions

August 2016 to 30 September 2018:

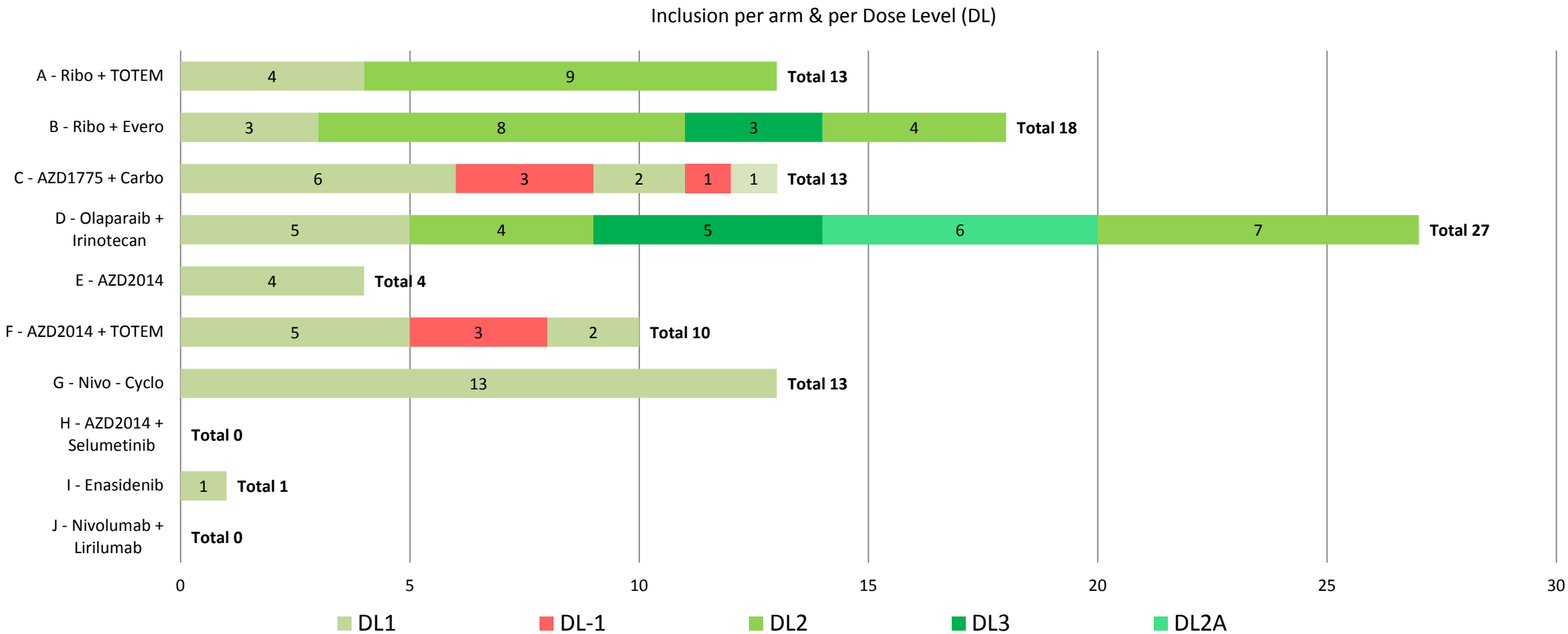
- 106 patients included (~4.2 per month)
- Median age: 14 years (1 – 23 years)
- 11 patients were enrolled in a second AcSé-ESMART arm
- More than 50% were 'enriched'



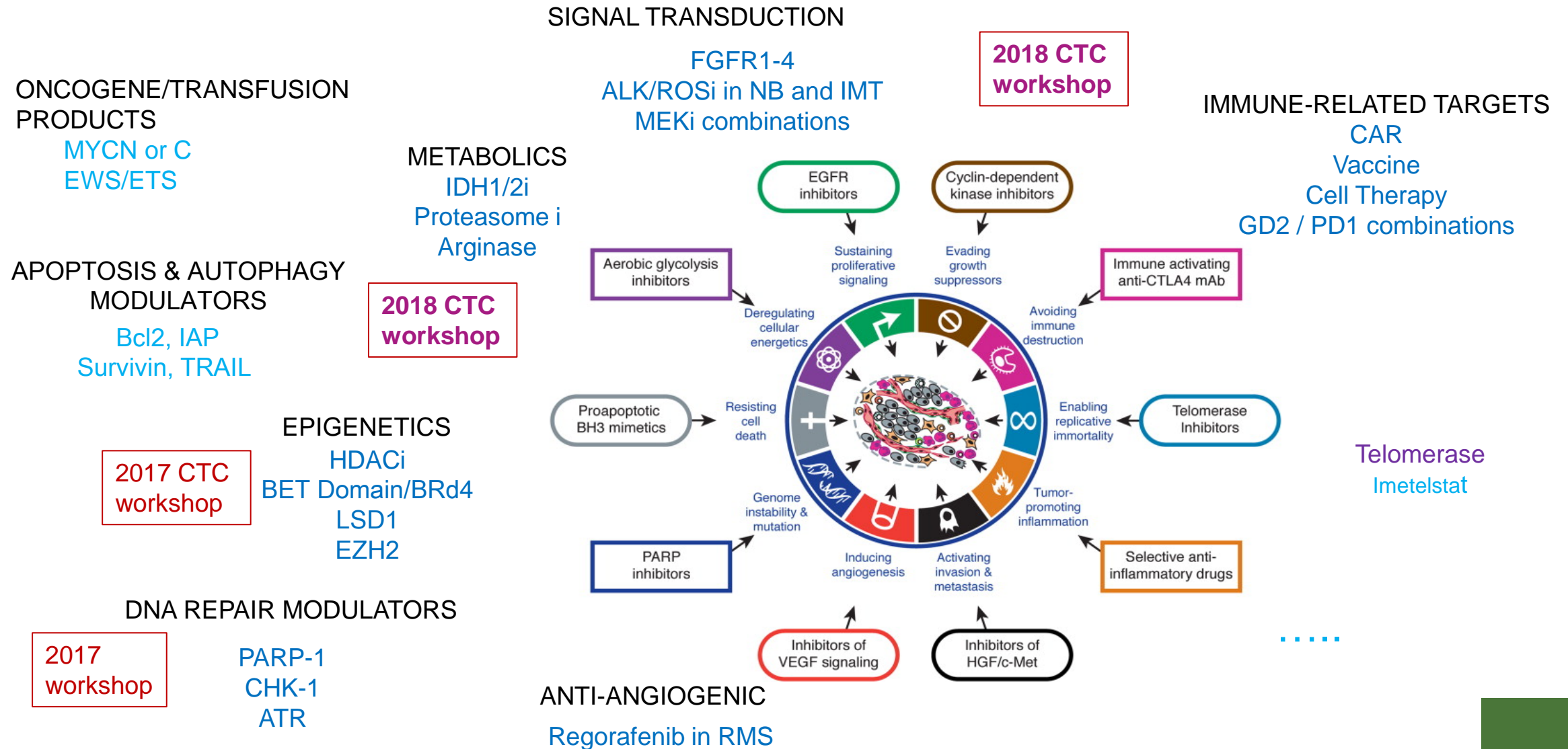
Advanced Molecular Profiling:

- MAPPYACTS: 83 inclusions
- MOSCATO-01 7
- BIOMEDE 5
- Other 11
 - IThER 4
 - Inform 2
 - Curie 2
 - Rare 1
 - Copenhagen 1
 - Sweden 1

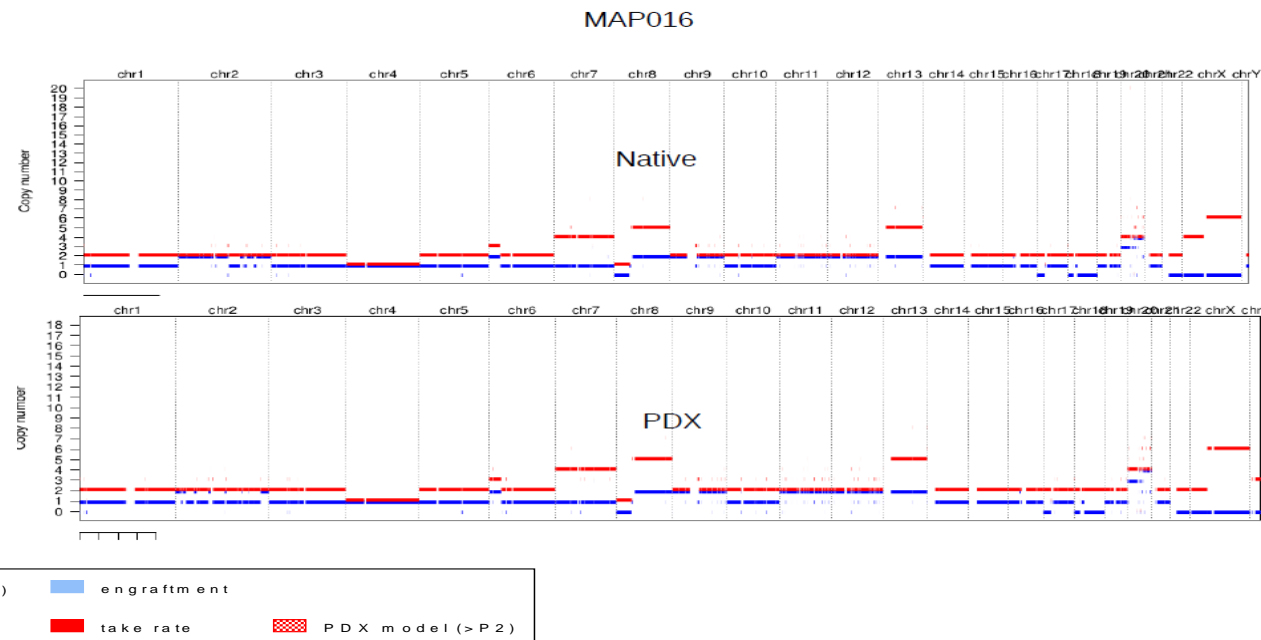
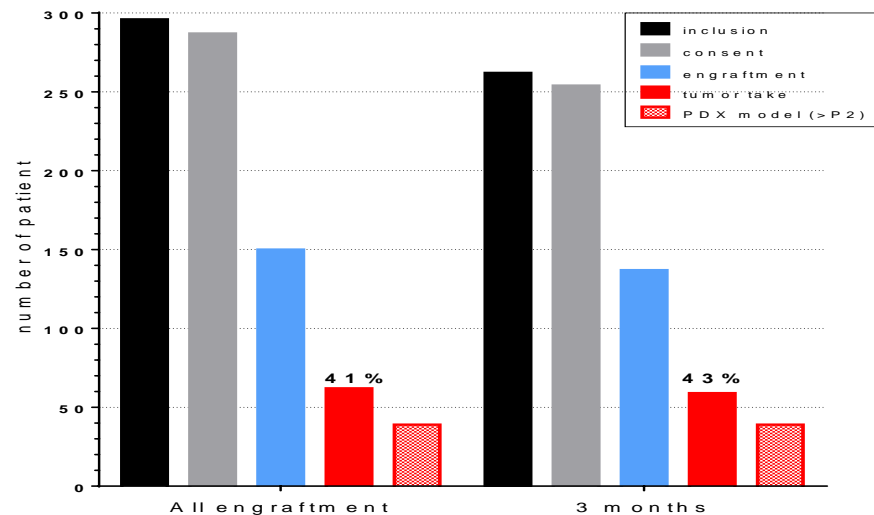
ESMART Inclusions per Treatment Arm



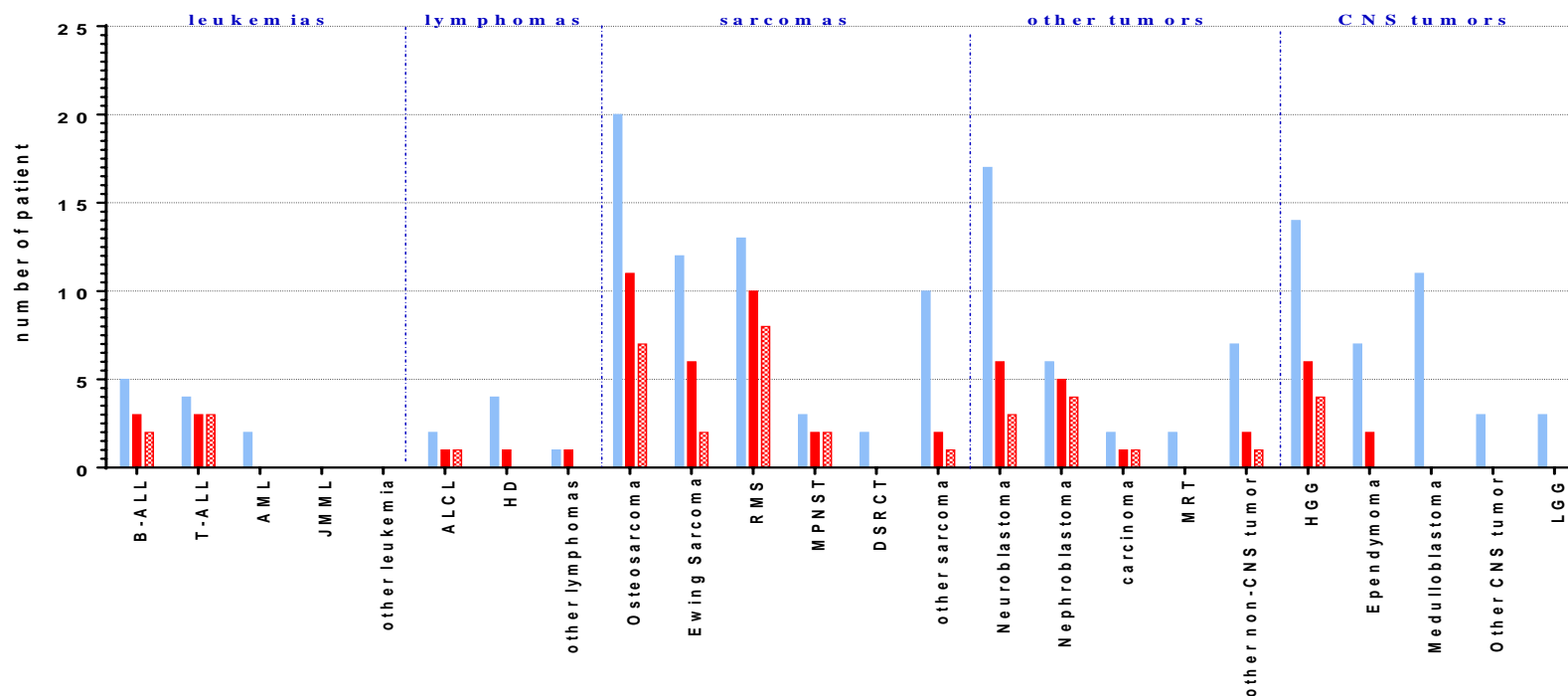
To define relevant pathways & combinations



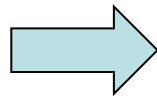
In ESMART – INFORM2 – Pharma – other ISTs



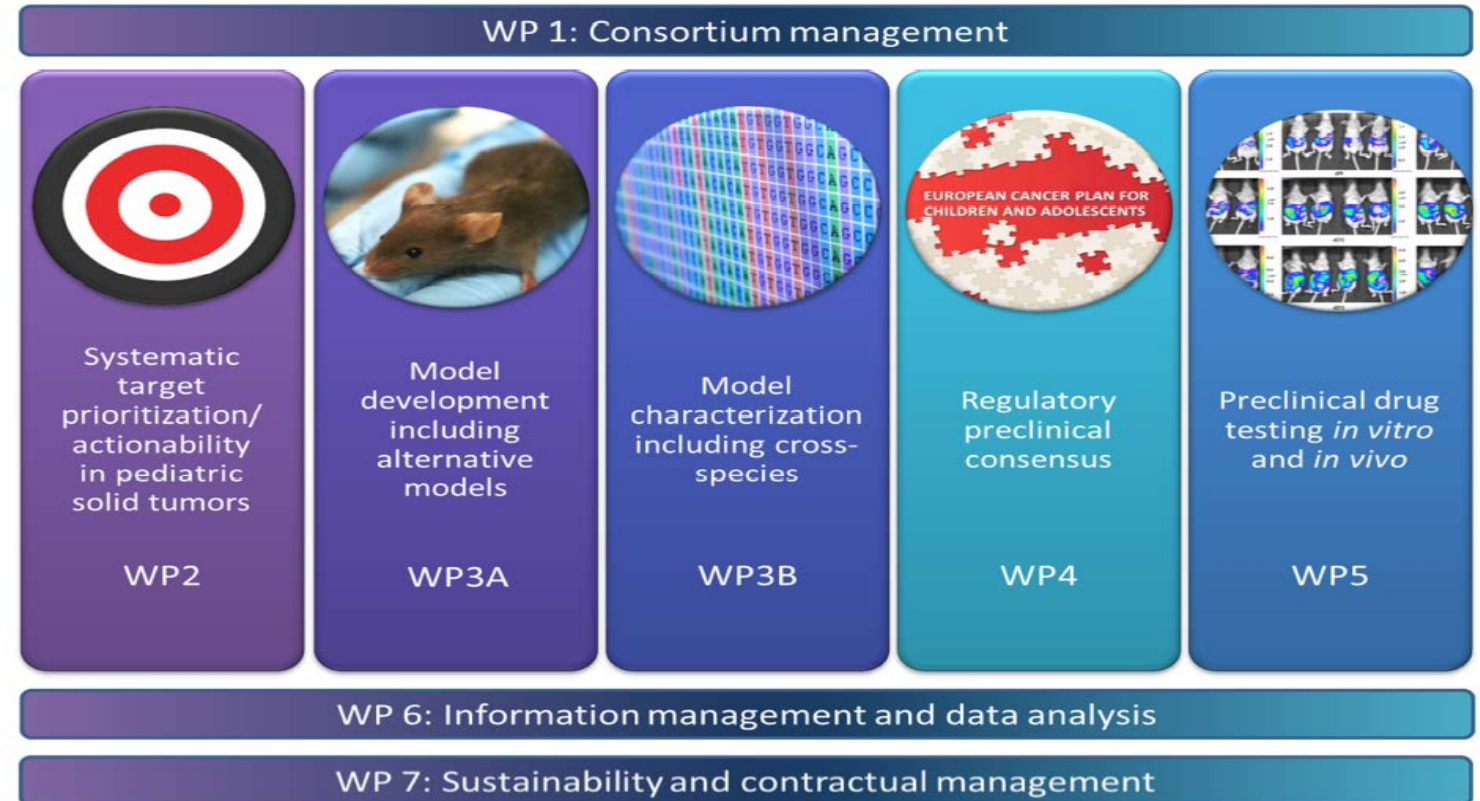
MAPPYACTS -
PDX
more than 65 growing



ITCC Pediatric Preclinical Proof-of-concept Platform (ITCC-P⁴)

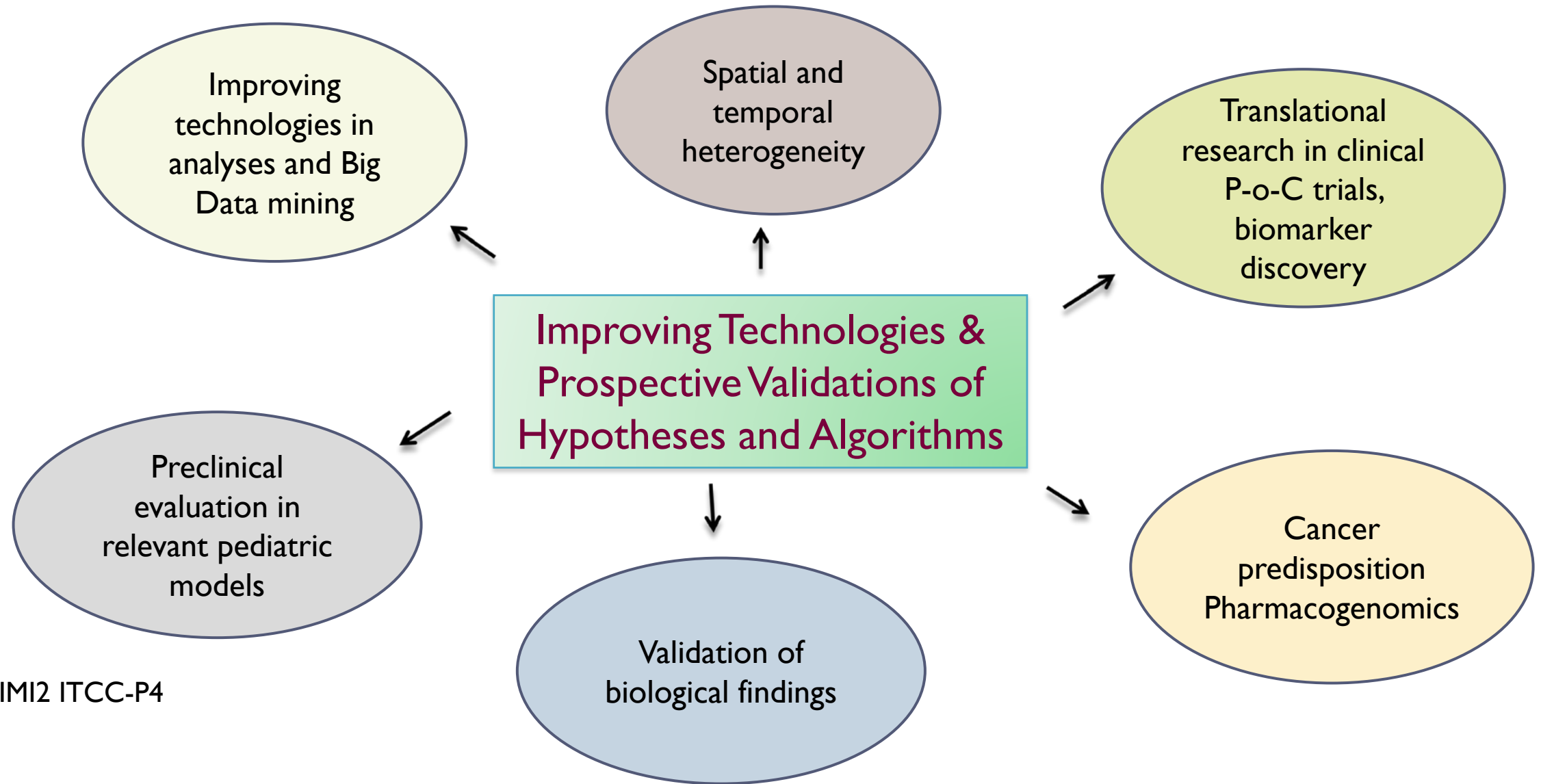


ITCC-P⁴ Workflow



- 400 PDX models/5 years, 2 GEMMs per entity
- 3 standard-of-care drugs and > 5 compounds
- Proof-of concept for immunotherapies in humanized models

2018/2019 - The End of the Beginning ...



Conclusions

- MAPPYACTS, INFORM, and iTHER show the feasibility of advanced molecular profiling at relapse in a multicentric setting
- Confirm that 'actionable' molecular alterations are frequently found in recurrent pediatric cancers
- Few tumors have unique and known targetable driver events
- Proof-of-concept trials are crucial to explore innovative strategies in an enriched setting
=> from Bedside back to Bench
- Multitude of ancillary research projects
- Only the End of the Beginning ...

Conclusions

Love of knowledge echoes in our hearts and nourishes great thoughts

Socrates

A new way of thinking is necessary if humanity is to survive

Albert Einstein

The Experimental Art of the Zeitgeist ...

Many thanks to
All patients and parents
Our teams
Pharmaceutical companies
Regulatory bodies
Funders

