

# Identification of novel genes/variants for pediatric cancer predisposition

## Professor Antonis Kattamis

Pediatric Hematology/Oncology Unit (POHemU)

1<sup>st</sup> Department of Pediatrics, University of Athens

Aghia Sophia Children's Hospital

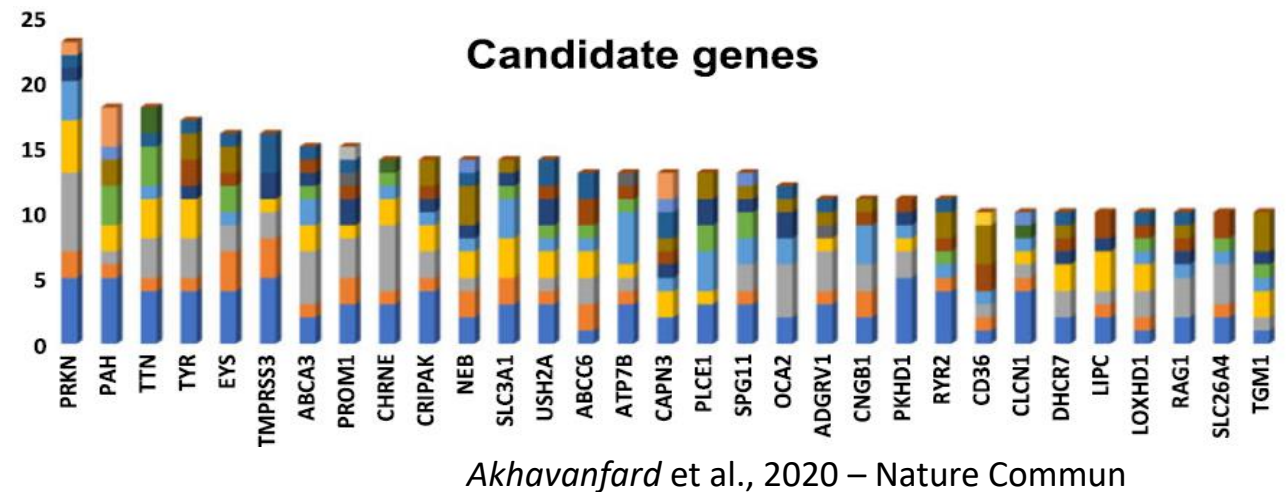
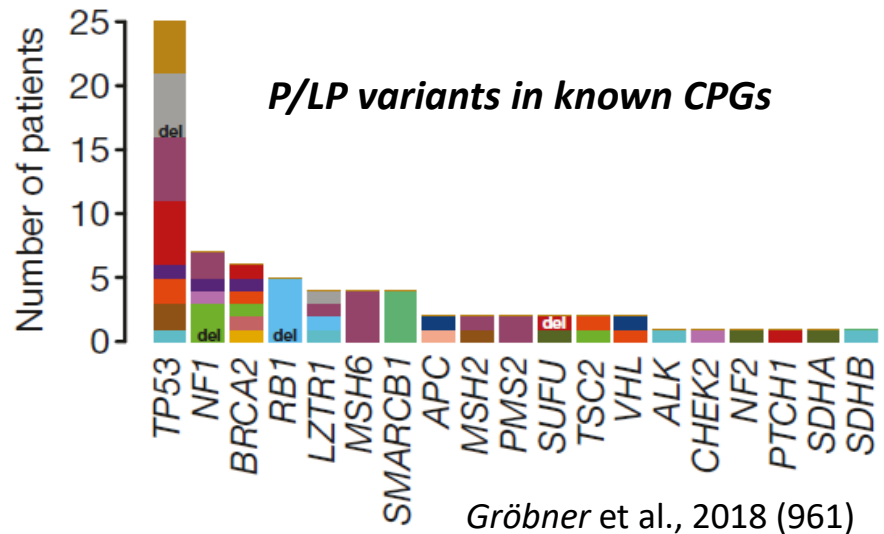
Athens, Greece



Children's Hospital  
"Agia Sofia"

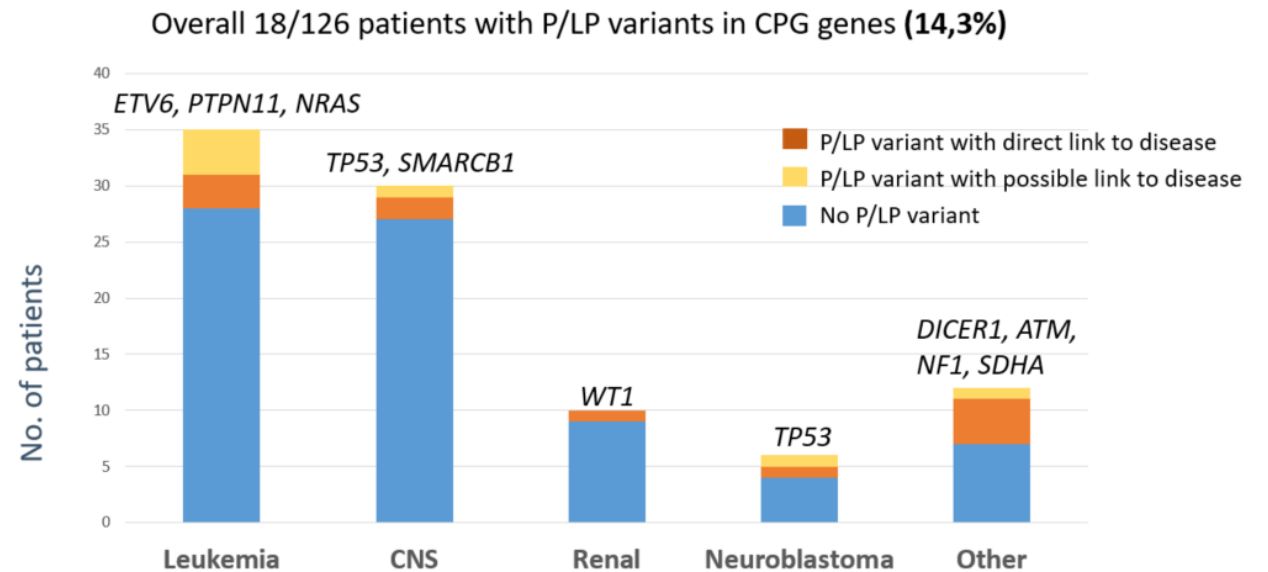
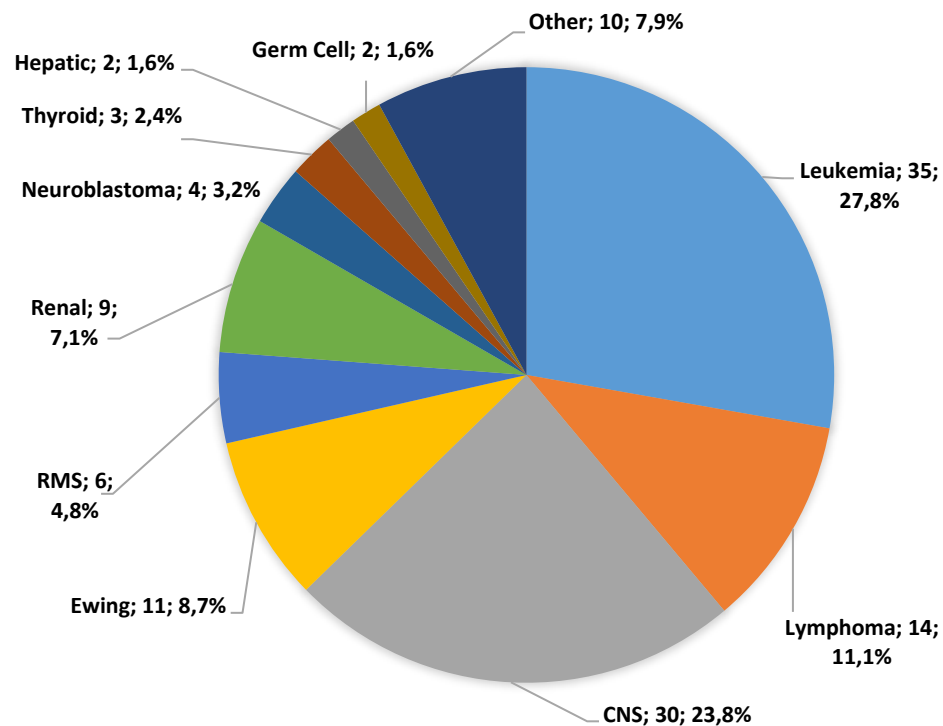
# Pediatric cancer (PedCan) predisposition

- In Europe one out of 300 newborns will develop cancer before turning 20.
- In Greece we expect ~300 new cases every year.
- ~10% pediatric cancer patients carry a Pathogenic/ Likely pathogenic (P/LP) variant in Cancer Predisposing Gene (CPG)
- Novel candidate genes/variants related to pediatric cancer predisposition are expected to be found



# POHemU work on PedCan predisposition analysis

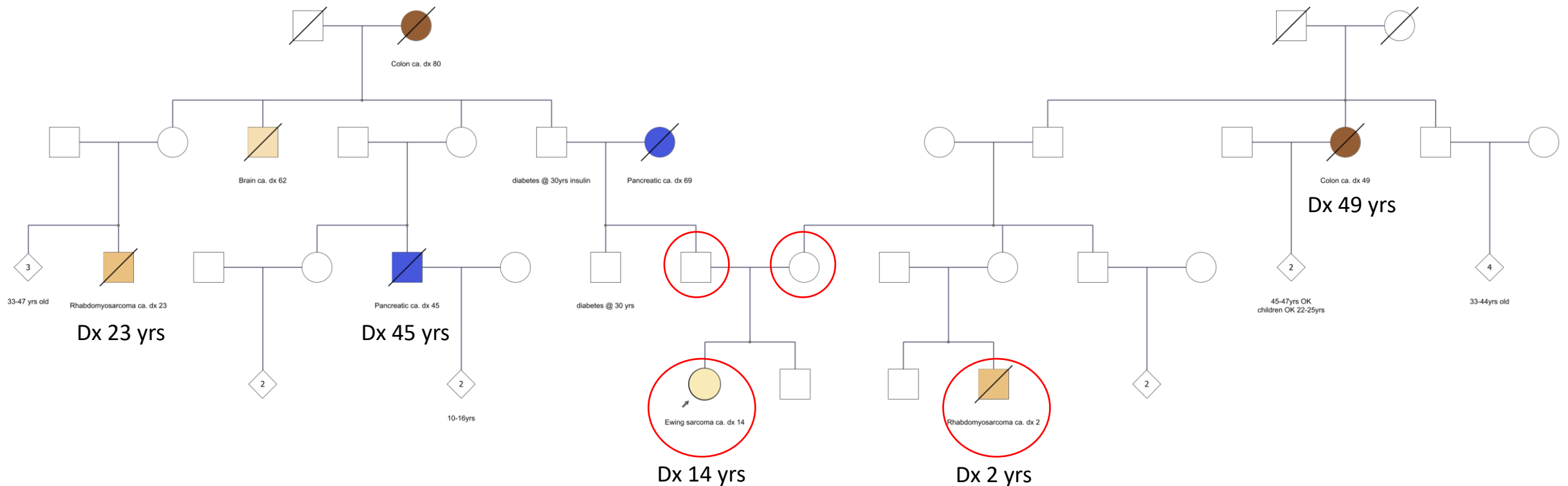
- POHemU laboratory has developed an NGS-based CPG Panel that targets ~200 genes and so far we have screened 126 PedCan patients with average age at diagnosis 9 years (0-16 years old)
- Patient inclusion criteria: cancer family history, rare tumor type or site, relapse or refractory disease



**108 patients with negative results**

# Aim of the project

- Our aim was to perform extensive genetic analysis in families with  $\geq 2$  PedCan patients in order to identify new candidate causal genes/variants



# Project's outline

PedCan patients who fulfill specific criteria



Negative for pathogenic (P) variants



Additional family samples collection and informed consent



Multiple analyses strategy

- ✓ Rare variants shared in family patients
- ✓ Digenic inheritance
- ✓ De novo variants
- ✓ Integration of data with larger studies

QC, Bioinformatic analysis

```
AGGTCGTTACGTACGCTAC  
GACCTACATCAGTACATAG  
GCATGACAAAGCTAGGTGT
```

Mapping, alignment,  
variant calling

Whole exome sequencing



# Whole Exome Sequencing (WES) prioritization analysis

Proband WES detected variants: 54,575

Screen for variants shared with patient

Shared variants with relative patient: 21,212

i) Screen against internal WES database

ii) Screen against large genetic databases  
(1000Genomes, Gnomad, MAF  $\leq$  0,01%)

Number of rare variants: 120

Screen for variants with functional impact

Number of Candidate variants: 27

ex. *GEN1* frameshift

Screen for variants for Digenic inheritance



ORVAL: Oligogenic  
Resource for Variant  
AnaLysis

8 Gene-pair combinations



# Acknowledgments

**Prof Kattamis Antonis**

Avgerinou Georgia

Binenbaum Ilona

Fillipidou Maria

Glentis Stavros

Katsibardi Katerina

Perari Panagiota

Rigatou Efthimia

Roka Kleoniki

Solomou Elena

Vlachou Antonia



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