# **Manuscript Title**

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In Brief	
Highlights	
Summary	
Keywords	
Introduction	
Results	
Discussion	
Acknowledgments	
Author Contributions	
Author	Contributions
Author John Doe	Contributions

# **Declarations of Interest**

### **Figure Titles and Legends**

## **Table Titles and Legends**

#### STAR METHODS

#### **RESOURCE AVAILABILITY**

#### Lead contact

Requests for access to OpenPedCan raw data and/or specimens may be directed to, and will be fulfilled by Jo Lynne Rokita (rokita@chop.edu).

**Materials availability** 

Data and code availability

**METHOD DETAILS** 

**Biospecimen Collection** 

Nucleic acids extraction and library preparation

**Data generation** 

**DNA WGS Alignment** 

**Quality Control of Sequencing Data** 

**Germline Variant Calling** 

SNP calling for B-allele Frequency (BAF) generation

**Somatic Mutation Calling** 

SNV and indel calling

VCF annotation and MAF creation

**Gather SNV and INDEL Hotspots** 

**Consensus SNV Calling** 

**Somatic Copy Number Variant Calling (WGS samples only)** 

**Consensus CNV Calling** 

Somatic Structural Variant Calling (WGS samples only)

**Gene Expression** 

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**Gene Expression Matrices with Unique HUGO Symbols** 

Gene fusion detection

### **QUANTIFICATION AND STATISTICAL ANALYSIS**

**Focal Copy Number Calling (focal-cn-file-preparation analysis module)** 

**Gene Set Variation Analysis (gene-set-enrichment-analysis analysis module)** 

Fusion prioritization (fusion\_filtering analysis module)

Mutational Signatures (mutational-signatures analysis module)

Tumor Mutation Burden (snv-callers analysis module)

**Clinical Data Harmonization** 

**WHO Classification of Disease Types** 

**Molecular Subtyping** 

TP53 Alteration Annotation (tp53\_nf1\_score analysis module)

Prediction of participants' genetic sex

Selection of independent samples (independent-samples analysis module)

**KEY RESOURCES TABLE** 

**Supplemental Information Titles and Legends** 

### Consortia

# References