The Open Pediatric Cancer Project

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## In Brief

## Highlights

## Summary

## Keywords

## Introduction

## Results

## Discussion

## Acknowledgments

## Author Contributions

| Author | Contributions |
| --- | --- |
| Eric Wafula | Formal analysis, Software |
| Krutika S. Gaonkar | Data curation, Formal analysis, Investigation, Methodology, Software, Writing – Original draft, Writing - Review and editing |
| Run Jin | Data curation, Formal analysis, Visualization, Writing – Original draft, Writing - Review and editing |
| Komal S. Rathi | Formal analysis, Investigation, Methodology, Writing – Original draft |
| Yuankun Zhu | Data curation, Formal analysis, Investigation, Methodology, Supervision |
| Bailey K. Farrow | Data curation, Software |
| Daniel P. Miller | Formal analysis |
| Mariarita Santi | Investigation, Validation, Writing - Review and editing |
| Adam A. Kraya | Methodology |
| Xiaoyan Huang | Formal analysis |
| Bo Zhang | Data curation, Formal analysis |
| Brian M. Ennis | Data curation, Formal analysis |
| Ryan J. Corbett | Formal analysis |
| Sharon J. Diskin | Investigation, Supervision, Validation, Funding acquisition, Writing - Review and editing |
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| Noel Coleman | Data curation |
| Christopher Blackden | Resources |
| Jennifer L. Mason | Supervision |
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| Miguel A. Brown | Data curation, Methodology, Formal analysis |
| Alex Sickler | Methodology, Formal analysis |
| Adam C. Resnick | Conceptualization, Funding acquisition, Resources, Supervision |
| Jo Lynne Rokita^ | Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Software, Supervision, Writing – Original draft, Writing - Review and editing |
| Kelsey Keith | Software, Writing - original draft, API, Formal Analysis, Data Curation, Visualization |

## Declarations of Interest

## Figure Titles and Legends

## Table Titles and Legends

## OPENPEDCAN 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

This study did not create new, unique reagents.

#### Data and code availability

Merged summary files for OpenPedCan v12 are openly accessible in [CAVATICA](https://cavatica.sbgenomics.com/u/cavatica/opentarget) or via download script in the <https://github.com/PediatricOpenTargets/OpenPedCan-analysis> repository. Cancer group summary data are visible within the NCI’s pediatric [Molecular Targets Platform](https://moleculartargets.ccdi.cancer.gov/) and cohort, cancer group, and individual data are visible within [PedcBioPortal](https://pedcbioportal.kidsfirstdrc.org/study/summary?id=openpedcan_v12)

OpenPedCan analysis modules were developed within OpenPBTA [[1](#ref-5VXMHJ7N)], modified based on OpenPBTA, or newly created and can be found within the following publicly available repositories. OpenPBTA module analyses can be found at <https://github.com/AlexsLemonade/OpenPBTA-analysis>. OpenPedCan module analyses can be found at <https://github.com/PediatricOpenTargets/OpenPedCan-analysis>. OpenPedCan api code can be found at <https://github.com/PediatricOpenTargets/OpenPedCan-api>.

Software versions are documented in **Table XX**.

#### Data releases

### EXPERIMENTAL MODEL AND STUDY PARTICIPANT DETAILS

### METHOD DETAILS

#### Nucleic acids extraction and library preparation

#### Data generation

#### DNA WGS Alignment

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

#### Quality Control of Sequencing Data

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

##### SNP calling for B-allele Frequency (BAF) generation

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

#### Somatic Mutation Calling

##### SNV and indel calling

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

##### 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)

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

#### Methylation Analysis

#### Gene Expression

##### Abundance Estimation

##### Gene Expression Matrices with Unique HUGO Symbols

##### Gene fusion detection

### QUANTIFICATION AND STATISTICAL ANALYSIS

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

Please refer to the OpenPBTA manuscript for details on assignment of copy number status values to CNV segments, cytobands, and genes [[1](#ref-5VXMHJ7N)]. We applied criteria to resolve instances of multiple conflicting status calls for the same gene and sample, which are described in detail in the [focal-cn-file-preparation](https://github.com/PediatricOpenTargets/OpenPedCan-analysis/tree/dev/analyses/focal-cn-file-preparation) module. Briefly, we prioritized 1) non-neutral status calls, 2) calls made from dominant segments with respect to gene overlap, and 3) amplification and deep deletion status calls over gain and loss calls, respectively, when selecting a dominant status call per gene and sample. These methods resolved >99% of duplicated gene-level status calls.

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

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

##### 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

Here, we build upon the molecular subtyping performed in OpenPBTA [[1](#ref-5VXMHJ7N)].

High-grade gliomas..

Atypical teratoid rhabdoid tumors..

Neuroblastoma tumors…

###### Integration of brain tumor methylation classifications

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

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

#### Prediction of participants’ genetic sex

Please refer to the OpenPBTA manuscript for details [[1](#ref-5VXMHJ7N)].

#### Selection of independent samples (independent-samples analysis module)

For analyses that require all input biospecimens to be independent, we use the OpenPedCan-analysis [independent-samples](https://github.com/PediatricOpenTargets/OpenPedCan-analysis/tree/d397339d567ddeff17e7a8cdca892f6a9dd2a0ba/analyses/independent-samples) module to select only one biospecimen from each input participant. For each input participant of an analysis, the independent biospecimen is selected based on the analysis-specific filters and preferences for the biospecimen metadata, such as experimental strategy, cancer group, and tumor descriptor.

## Supplemental Information Titles and Legends

## Consortia

## References

1. **OpenPBTA: The Open Pediatric Brain Tumor Atlas** Joshua A Shapiro, Krutika S Gaonkar, Stephanie J Spielman, Candace L Savonen, Chante J Bethell, Run Jin, Komal S Rathi, Yuankun Zhu, Laura E Egolf, Bailey K Farrow, … Jaclyn N Taroni *Cell Genomics* (2023-05) <https://doi.org/gr92p6> DOI: [10.1016/j.xgen.2023.100340](https://doi.org/10.1016/j.xgen.2023.100340)