

# Connecting clinical and genetic data on the St. Jude Survivorship Portal

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**CCSS**

Childhood Cancer  
Survivor Study

- Inter-departmental collaboration in 2019
  - Dr. Les Robison (Epidemiology and Cancer Control, SJLIFE)
  - Dr. Jinghui Zhang (Computational Biology)
- Built by the Comp Bio data visualization team led by Xin Zhou
  - 2019.10 ASHG → SJLIFE
  - 2020.7 AACR → SJLIFE and CCSS
  - Portal is under active development
- Design goals:
  - Curate and share clinical and genetic data from pediatric cancer survivors
  - Supports interactive real-time data analysis to promote genetic and epidemiology research

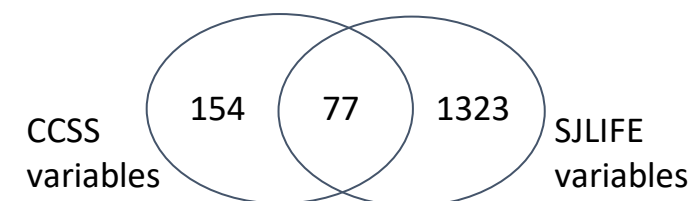
# Clinical and genetic data

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Clinical data

1531 variables about baseline assessments

- Cancer-related Variables
- Demographic Variables
- Self-reported Behavior and Outcome Variables
- Clinically-assessed Variables



7169 participants with clinical data

- CCSS n=2641, SJLIFE n=4528

Germline SNVs from  
whole-genome  
sequencing

90 million single nucleotide variations in total

5773 participants with WGS data

- CCSS n=2641, SJLIFE n=3132

# The Survivorship Portal

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<https://survivorship.stjude.cloud/>



## About the Project

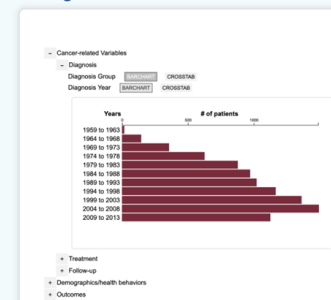
The Survivorship Portal shares high quality genomic, clinical, and patient-reported data from survivors of pediatric cancer. To accelerate the rate of discovery in survivorship research we have developed this SJLIFE Survivorship Portal, a data-sharing platform for genomic and clinical data from the St. Jude Lifetime Cohort hosted on the St. Jude Cloud. The Portal features the Clinical Data Browser, GenomePaint, a genetic variant browser, for browsing, visualizing and analyzing clinical and genetic data integratively. Additionally, the Survivorship Portal will serve as a site for an expanding portfolio of risk-prediction tools developed using the SJLIFE cohort, including the recently developed Cumulative Burden Risk-Prediction Tool.

[Methylation beta value matrix for 513 CpGs](#). Reference: Epigenetic Age Acceleration and Chronic Health Conditions among Adult Survivors of Childhood Cancer. JNCI 2020

### Beta Release

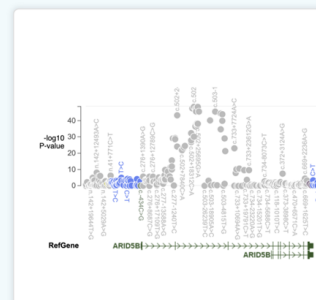
This initial version of the portal is read-only but future updates will allow authenticated users to create customized downloading of source data. For more information or help, please [contact us](#).

## Projects



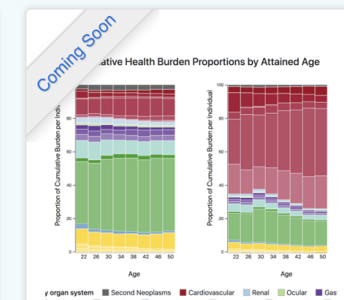
### Clinical Data Browser

The Clinical Data Browser enables interactive exploration of 1) Cancer-related variables such as diagnosis and treatment; 2) Demographic variables; and 3) Outcomes



### Genomic Data Browser

The GenomePaint displays germline SNV, indel, and copy number variants computed from WGS, allowing to display and filter variants based on a variety of functional



### Cumulative Health Burden

This web application visualizes estimated cumulative burden resulting from pediatric cancer and administered treatment. The estimates are generated using the statistical

# Browsing the clinical dictionary

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- + Genomic Profiling Status
- + Cancer-related Variables
- + Demographic Variables
- + Self-reported Behavior and Outcome Variables
- + Clinically-assessed Variables

- + Genomic Profiling Status
- Cancer-related Variables

- Diagnosis

Diagnosis Group

Diagnosis Code

VIEW

VIEW

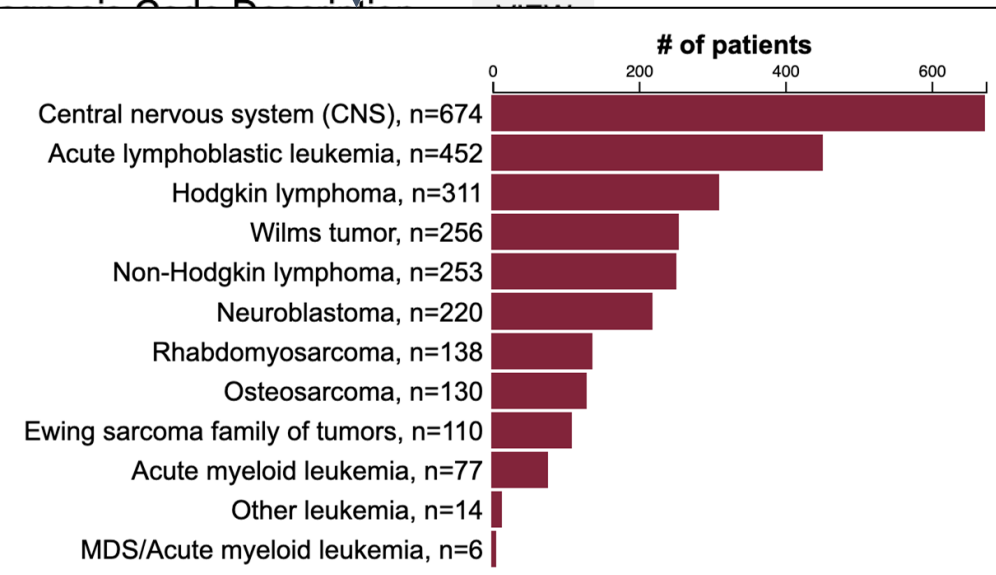
+ T

+ F

+ Demo

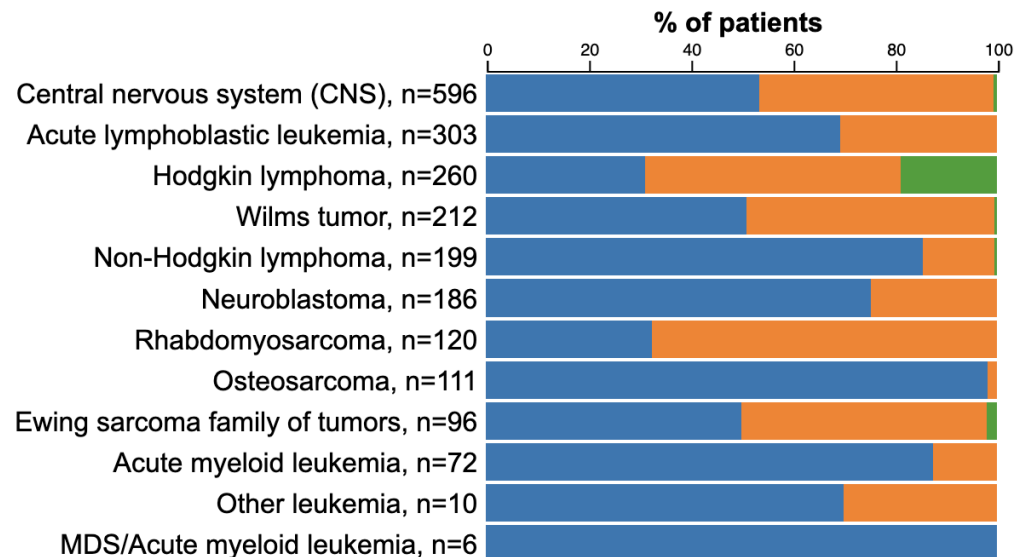
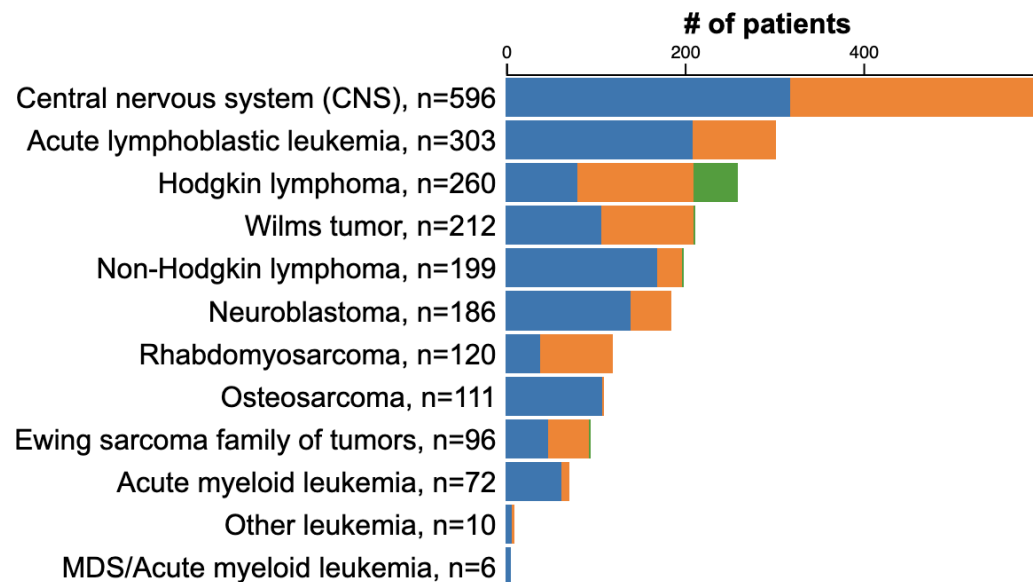
+ Self-re

+ Clinical



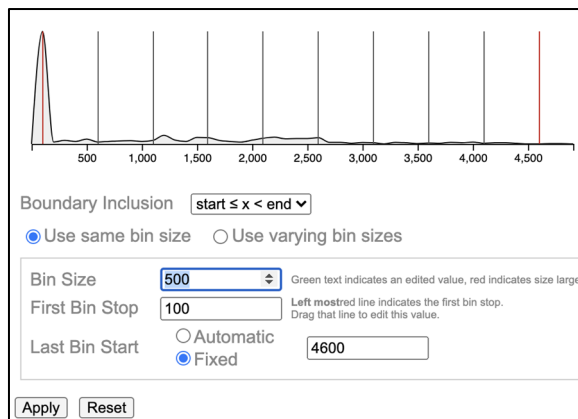
# Cross-tabulating two variables

ccss



Average dose to heart + TBI, cGy

- not treated, n=1300
- unknown exposure, n=464
- exposed, dose unknown, n=6
- ≤3000, n=814
- >3000, n=57



# Graded adverse events

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- Self-reported Behavior and Outcome Variables

- Graded adverse events

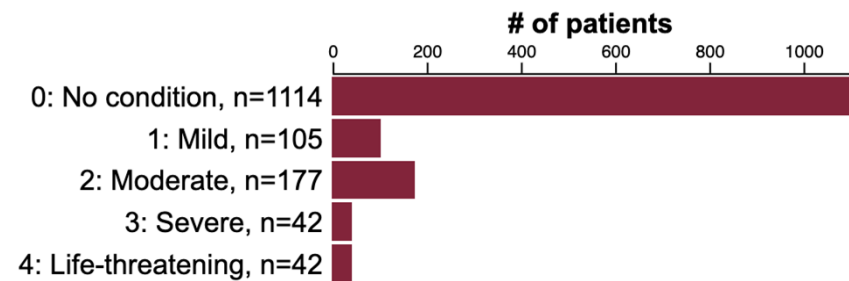
+ Auditory system

VIEW

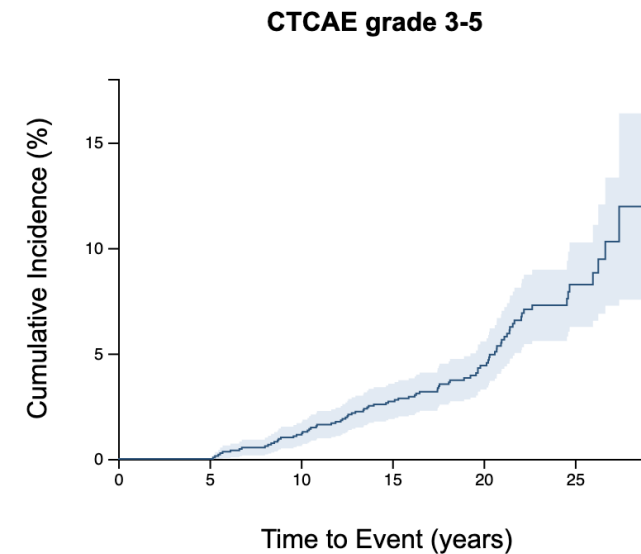
+ Cardiac system

VIEW

Maximum grade of each patient



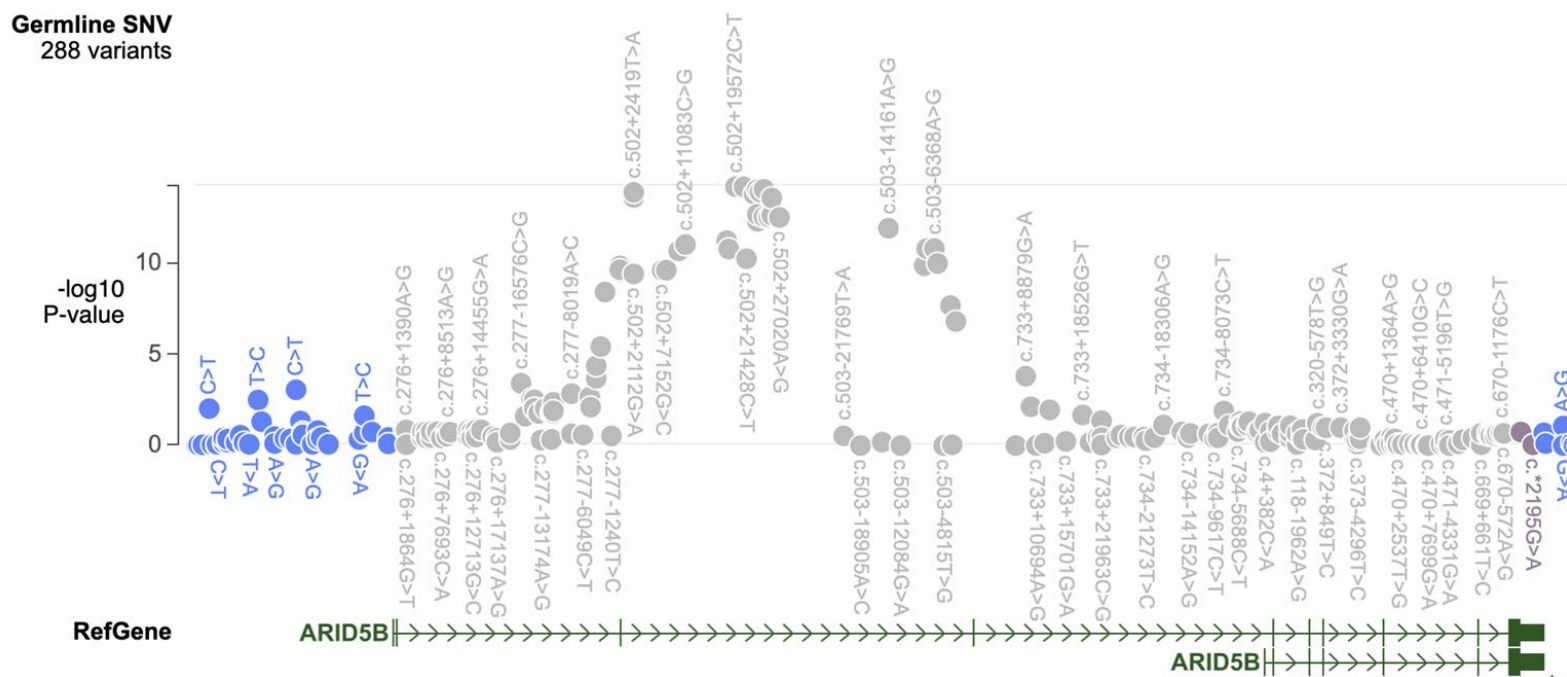
Cumulative incidence



# Genetic data browser

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## Locus-specific association study



GROUP 1 ALLELE FREQUENCY OF  AND DIAGNOSIS GROUP IS  n=376, view stats

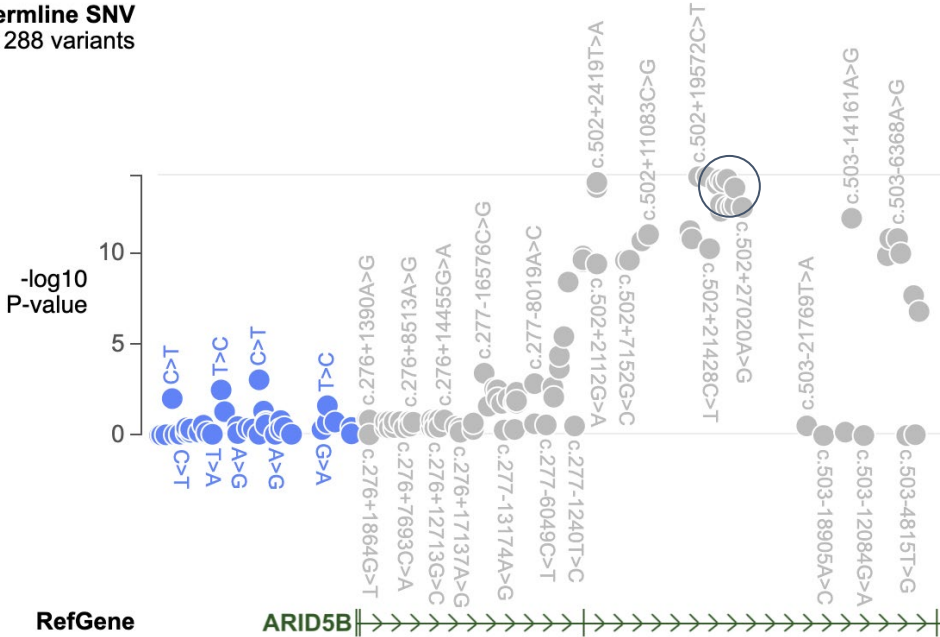
GROUP 2 ALLELE FREQUENCY OF  ☒ Adjust race background

TEST METHOD

RESTRICT TO

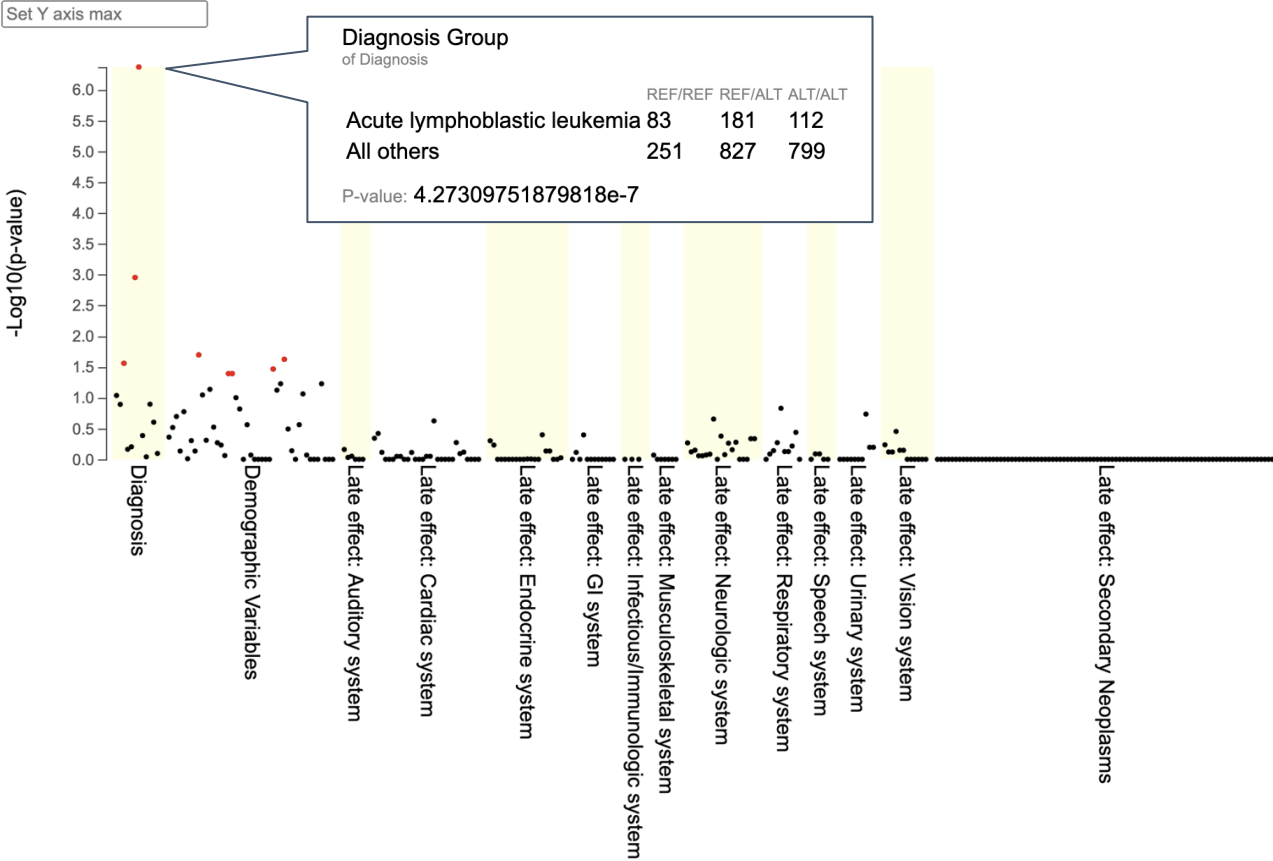


Germline SNV  
288 variants



FILTER  AND  IS  AND  IS  n=2253

281 attributes tested, 8 attributes with p-value <= 0.05, Max -log10(p-value) is 6.369257195787377



Enhance Opportunities for Research by Providing Access to CCSS Phenotype, Genotype and Outcomes Data Through Development of a Cloud-based Data Analysis Ecosystem

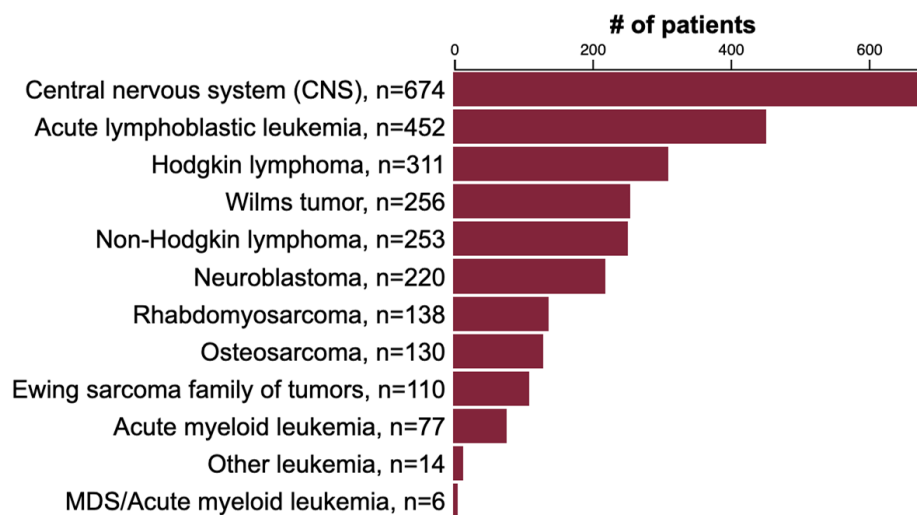
-Includes adding phenotype data for all 25,665 participants and genetic data on an addition 5,900 participants.

- Access to both raw and summary data supported by a searchable ontology-based data dictionary
  - Longitudinal follow-up and detailed lab results
- Conduct cloud-based computing to analyze genomic and clinical data using sophisticated computational/statistical pipelines in real time
  - Polygenic risk score
  - Adjust for covariates in association/regression analysis
- Download customized data sets through controlled access
- Access to a portfolio of intuitive, field-tested visualization tools to explore data and apply complex risk prediction modelling in a secure cloud environment

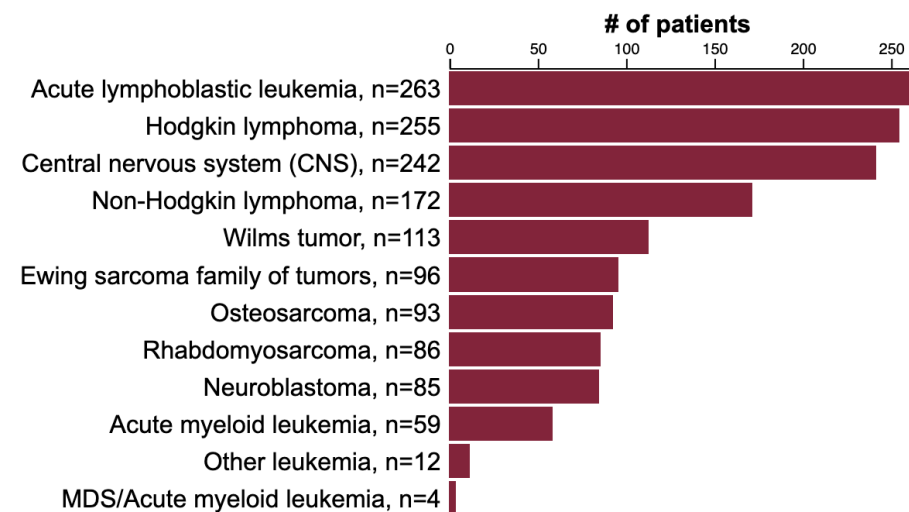
# Filtering

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GENETICALLY DEFINE... IS *European Ancestry* AND ( AVERAGE DOSE TO HEART + ... IS  $x \geq 0$  OR CUMULATIVE ANTHRACYCLINE... IS  $x \geq 0$  )



Apply filtering



- **Bring the complete CCSS cohort to St. Jude Survivorship portal**
- Clinical data
  - Longitudinal follow-up and detailed lab results
- Genetic data
  - WGS indel genotype calls, HLA typing, telomere length, haplotype
- Analysis features
  - Polygenic risk score
  - Adjust for covariates in association/regression analysis
  - Data download