Childhood Cancer Data Initiative Virtual Symposium Series

Logan Spector and Yi Xing

NIH NATIONAL CANCER INSTITUTE

April 8, 2026

Today's Speakers

Logan G. Spector, Ph.D., University of Minnesota

- Professor, Division Director, Division of Pediatric Epidemiology & Clinical Research
- Faculty, Department of Pediatrics and Brain Tumor Program
- Suzanne Holmes Hodder Chair in Pediatric Cancer Research, Children's Cancer Research Fund

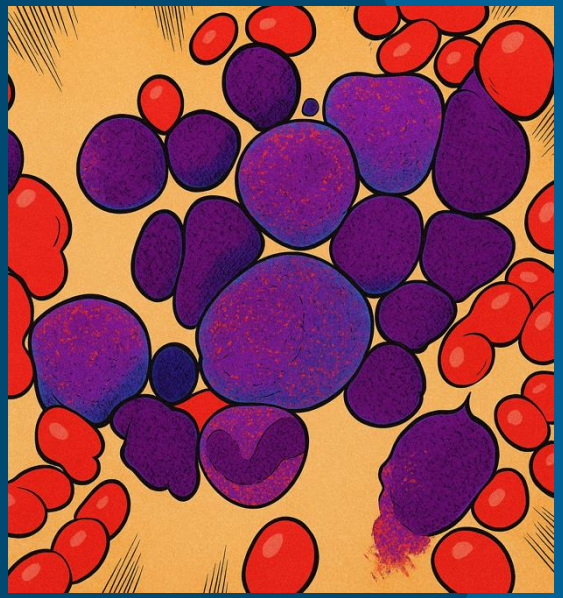
Yi Xing, Ph.D., Children's Hospital of Philadelphia

- Associate Chief Scientific Officer for Omics, Technology & Engineering
- Executive Director, Department of Biomedical and Health Informatics
- Director, Center for Computational and Genomic Medicine

Agenda

1. *The Emerging Genetic Architecture of B-Cell Acute Lymphoblastic Leukemia in African-American Children*
   - *Q&A*
2. *Illuminating Dark Antigens for Childhood Cancer Immunotherapy*
   - *Q&A*

Childhood Cancer Data Initiative Virtual Symposium Series



The Emerging Genetic Architecture of B-Cell Acute Lymphoblastic Leukemia in African-American Children

Logan G. Spector, Ph.D.

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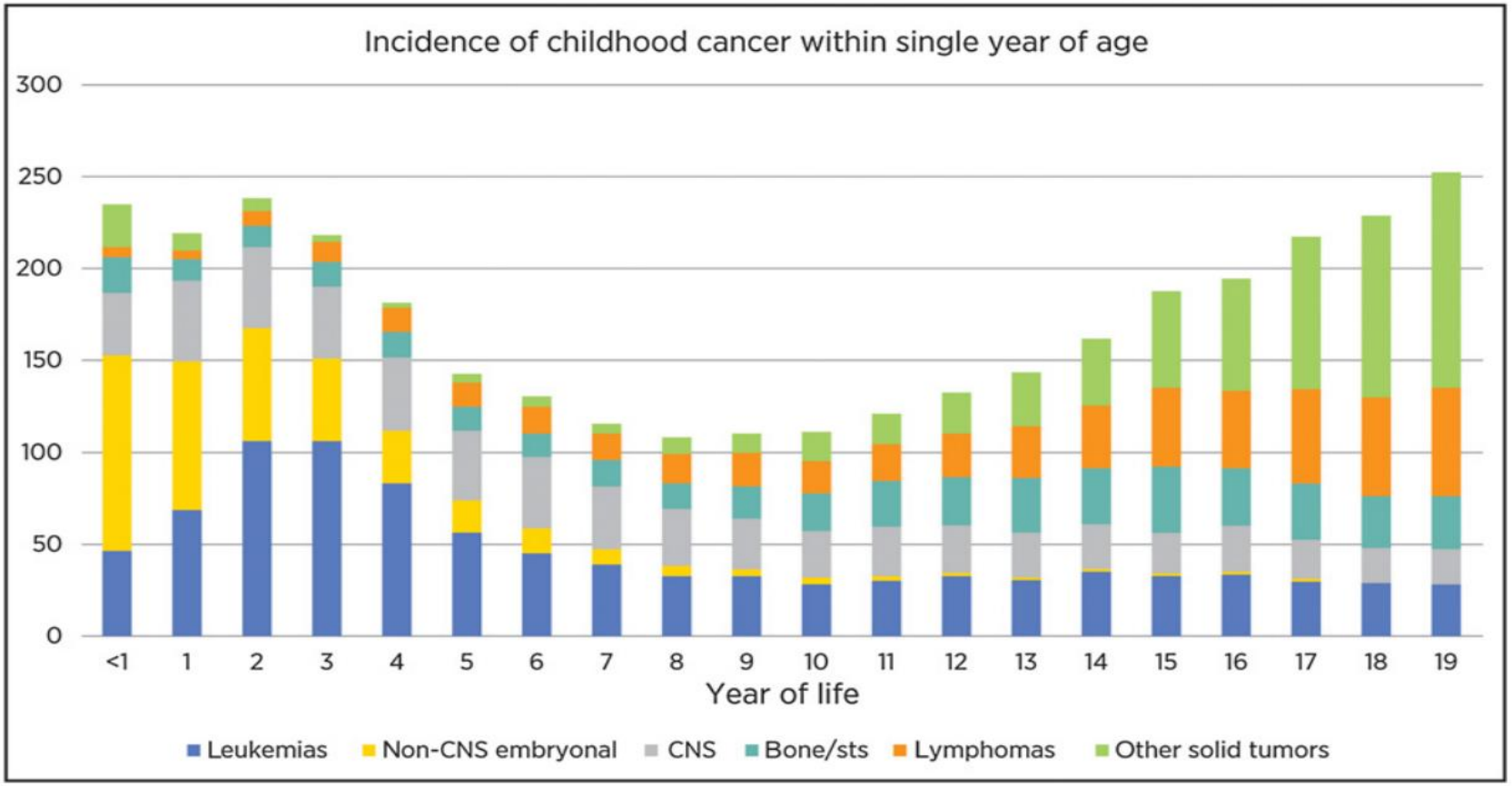
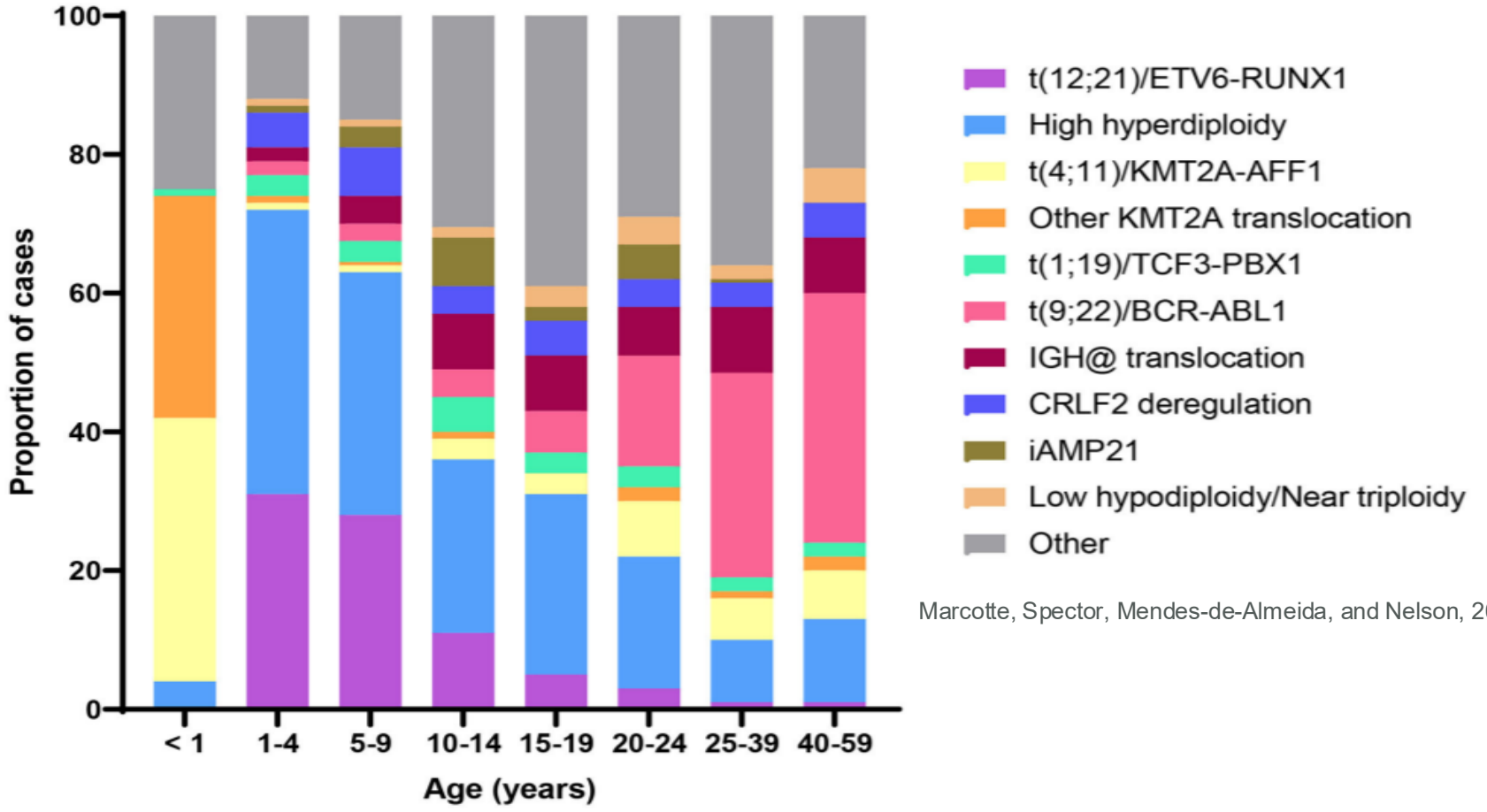


Spector and Lupo, 2020

Figure 2.
Distribution of tumors across the pediatric age spectrum.

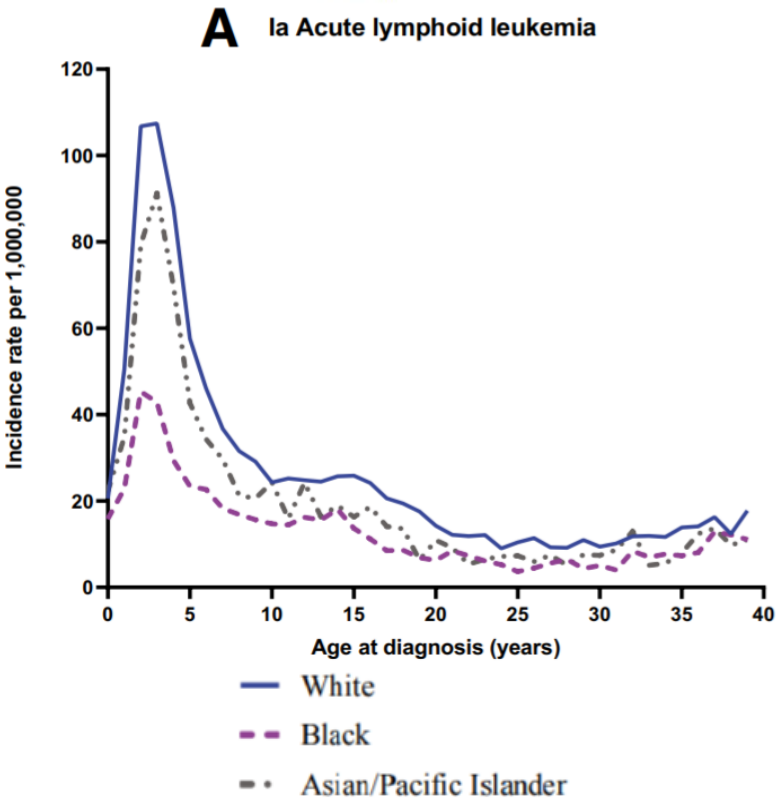


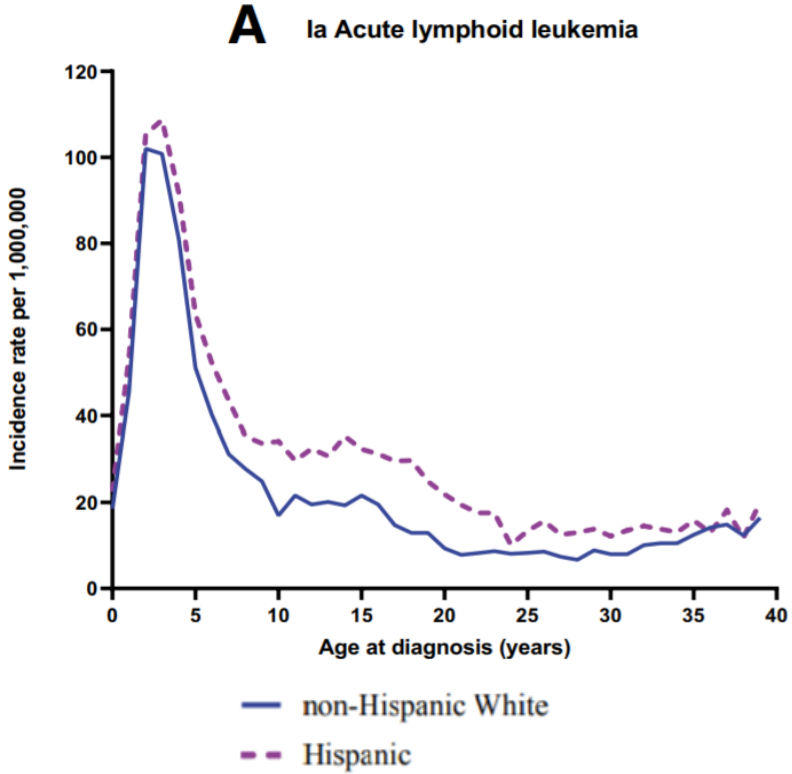
Marcotte, Spector, Mendes-de-Almeida, and Nelson, 2021

FIGURE 2 | Distribution of B-cell acute lymphoblastic leukemia (ALL) cytogenetic subtypes by age at diagnosis. Data adapted from (6).

Racial and Ethnic Disparities in Pediatric Cancer Incidence Among Children and Young Adults in the United States by Single Year of Age

Erin L. Marcotte, PhD [1,2]; Allison M. Domingues, MS[1]; Jeannette M. Sample, MPH [1]; Michaela R. Richardson, MPH[1]; and Logan G. Spector, PhD[1,2]

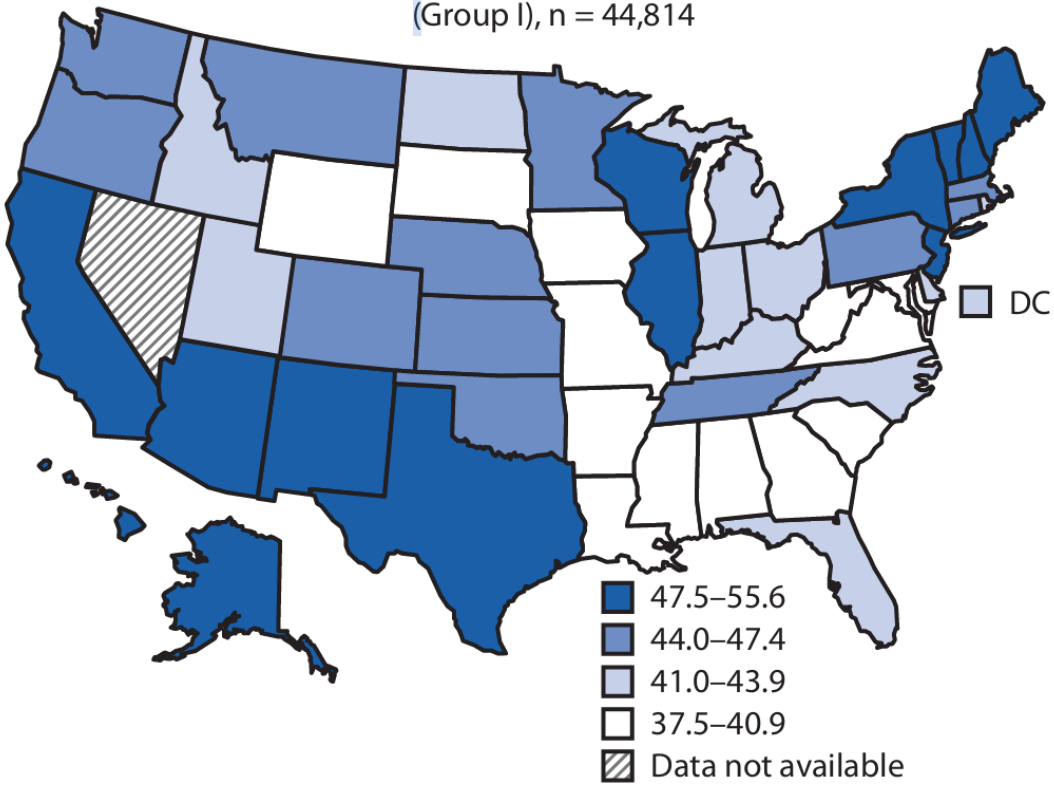




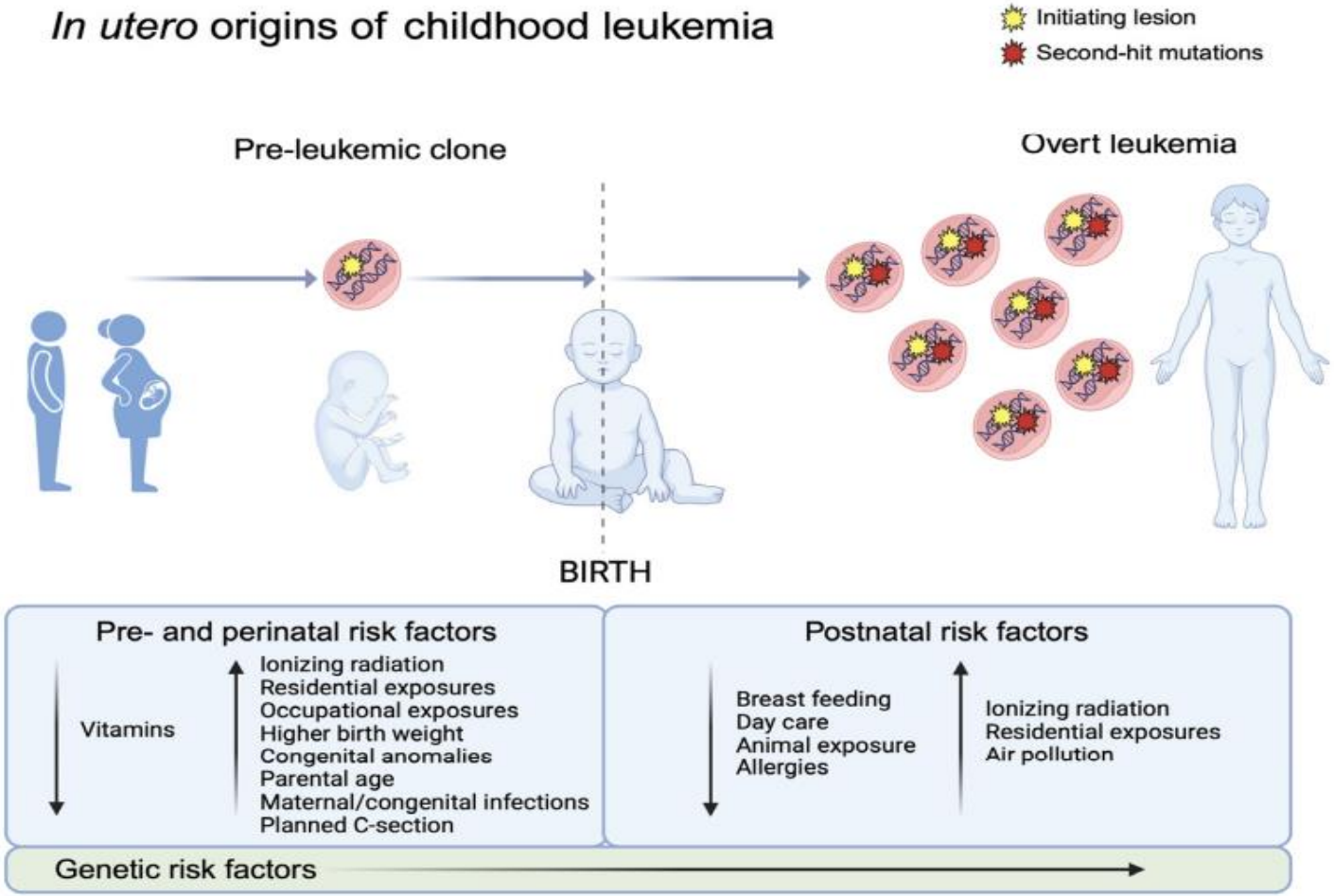
Geographic Variation in Pediatric Cancer Incidence — United States, 2003–2014

David A. Siegel, MD[1,2]; Jun Li, MD, PhD[2]; S. Jane Henley, MSPH[2]; Reda J. Wilson, MPH[2]; Natasha Buchanan Lunsford, PhD[2]; Eric Tai, MD[2]; Elizabeth A. Van Dyne, MD[1,2]

Leukemias, myeloproliferative diseases, and myelodysplastic diseases (Group I), n = 44,814

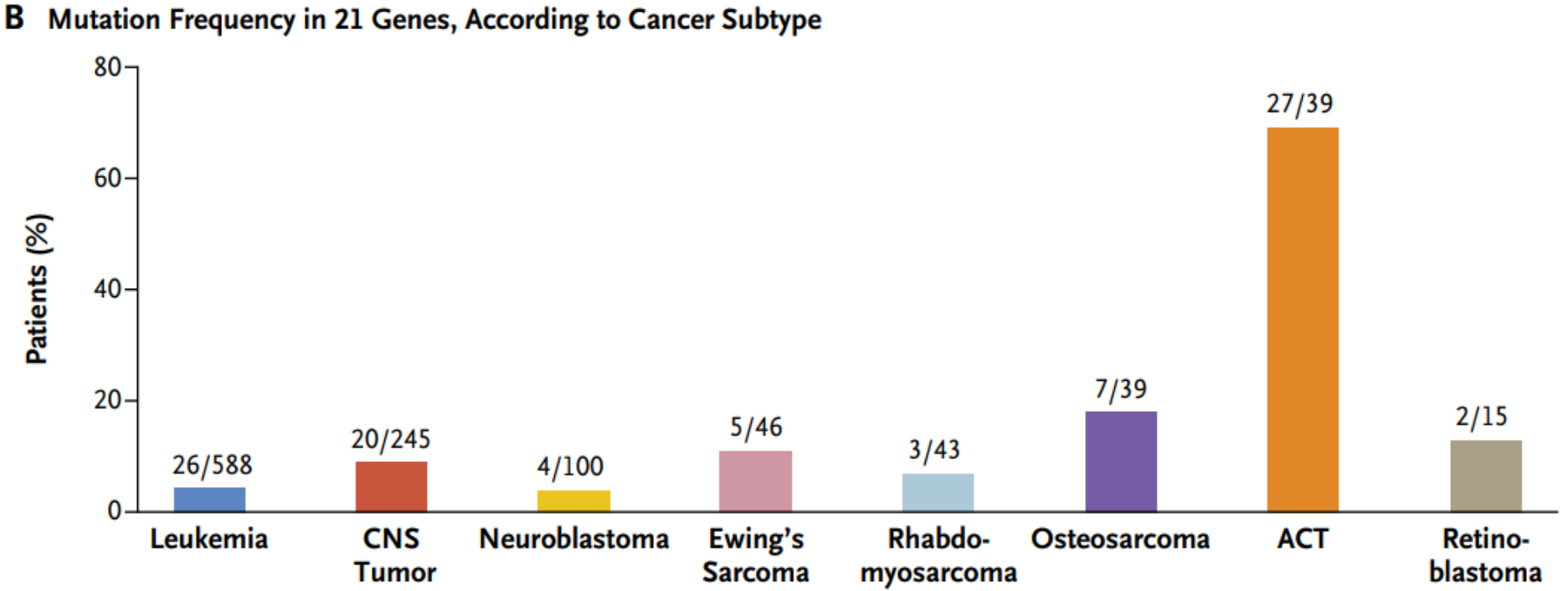


In utero origins of childhood leukemia

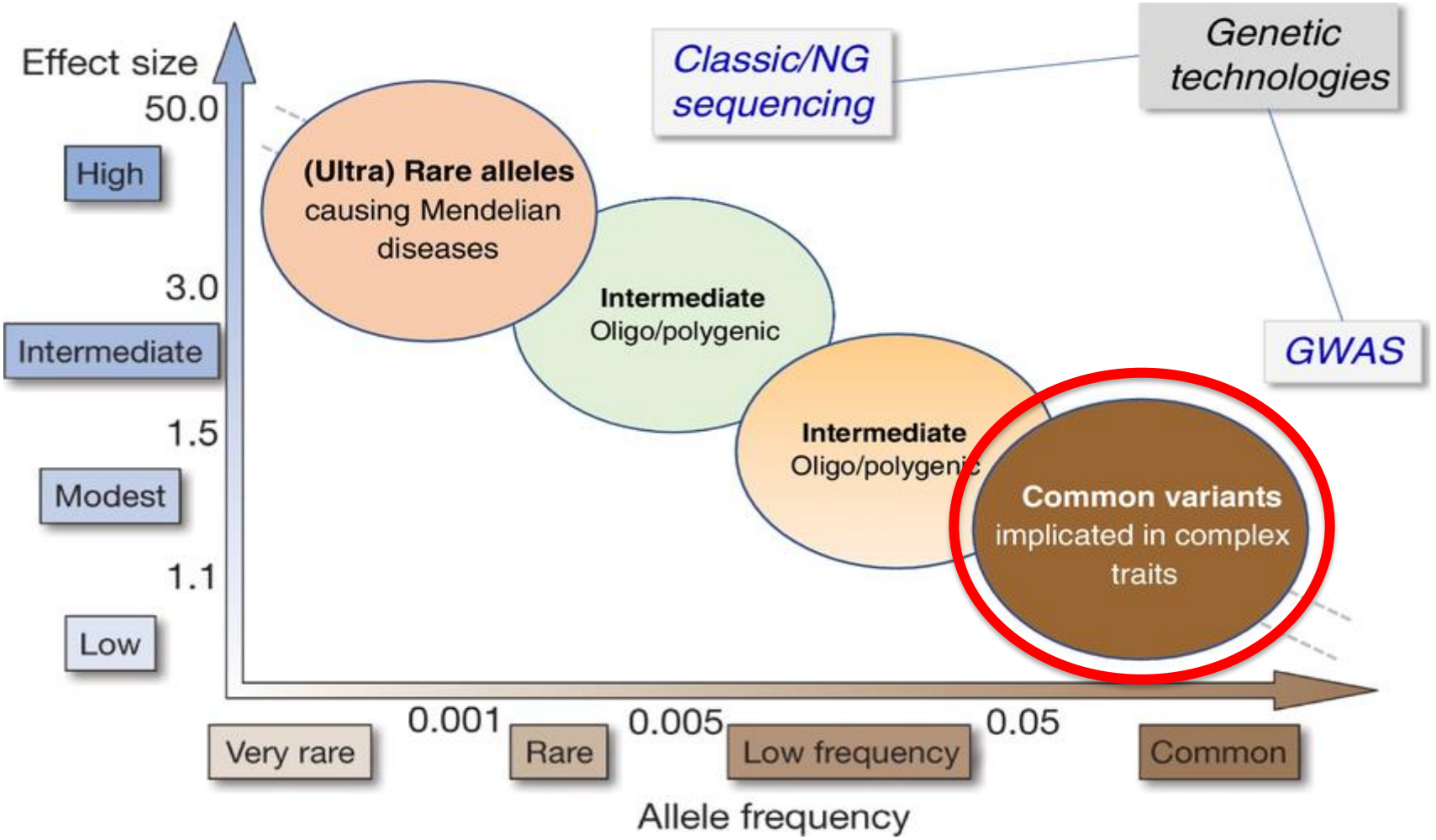


De Smith and Spector, 2024

Germline Mutations in Predisposition Genes in Pediatric Cancer

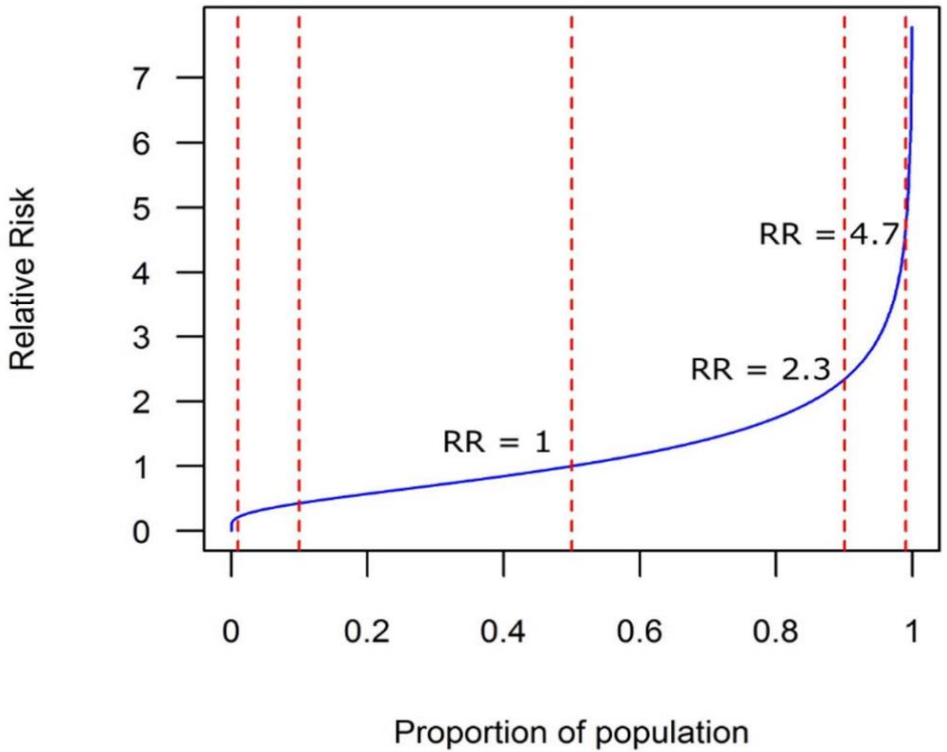


Zhang et al, 2015

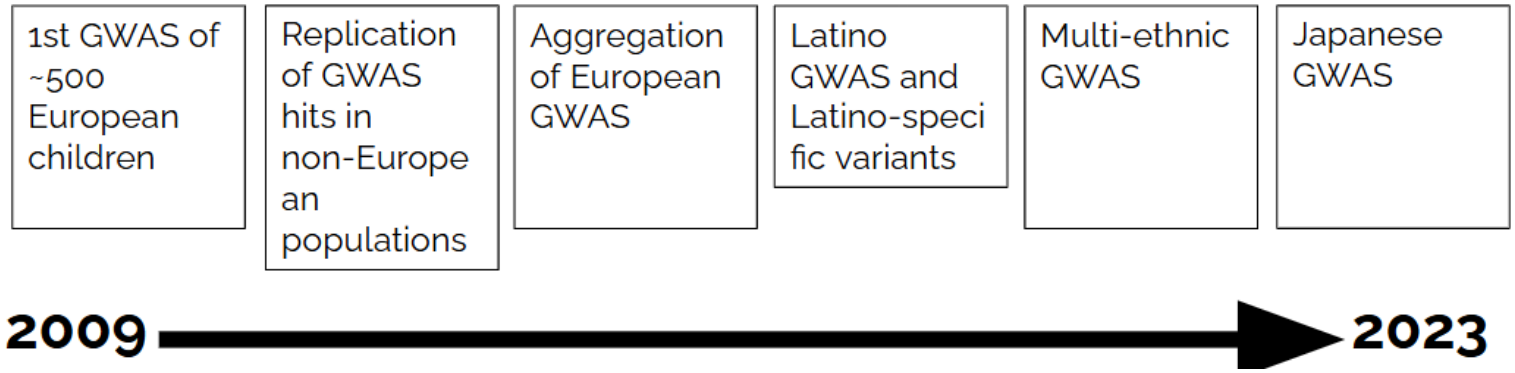

Effect size
50.0
High
3.0
Intermediate
1.5
Modest
1.1
Low
Classic/NG sequencing
Genetic technologies
(Ultra) Rare alleles causing Mendelian diseases
Intermediate Oligo/polygenic
Intermediate Oligo/polygenic
GWAS
Common variants implicated in complex traits
0.001
0.005
0.05
Very rare
Rare
Low frequency
Common
Allele frequency

Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk

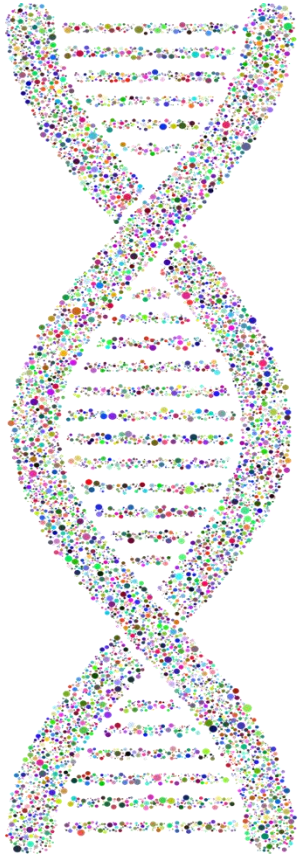
Jayaram Vijayakrishnan[1,19], Maoxiang Qian[2,3,19], James B. Studd[1], Wenjian Yang[2], Ben Kinnersley[1], Philip J. Law[1], Peter Broderick[1], Elizabeth A. Raetz[4], James Allan[5], Ching-Hon Pui[6,7], Ajay Vora[8], William E. Evans[2,7], Anthony Moorman[9], Allen Yeoh[10,11], Wentao Yang[2], Chunliang Li[12], Claus R. Bartram[13], Charles G. Mullighan[6,7,14], Martin Zimmerman[15], Stephen P. Hunger[16], Martin Schrappe[17], Mary V. Relling[2,7], Martin Stanulla[15], Mignon L. Loh[18], Richard S. Houlston[1*] & Jun J. Yang[2,6,7*]



History of GWAS in ALL



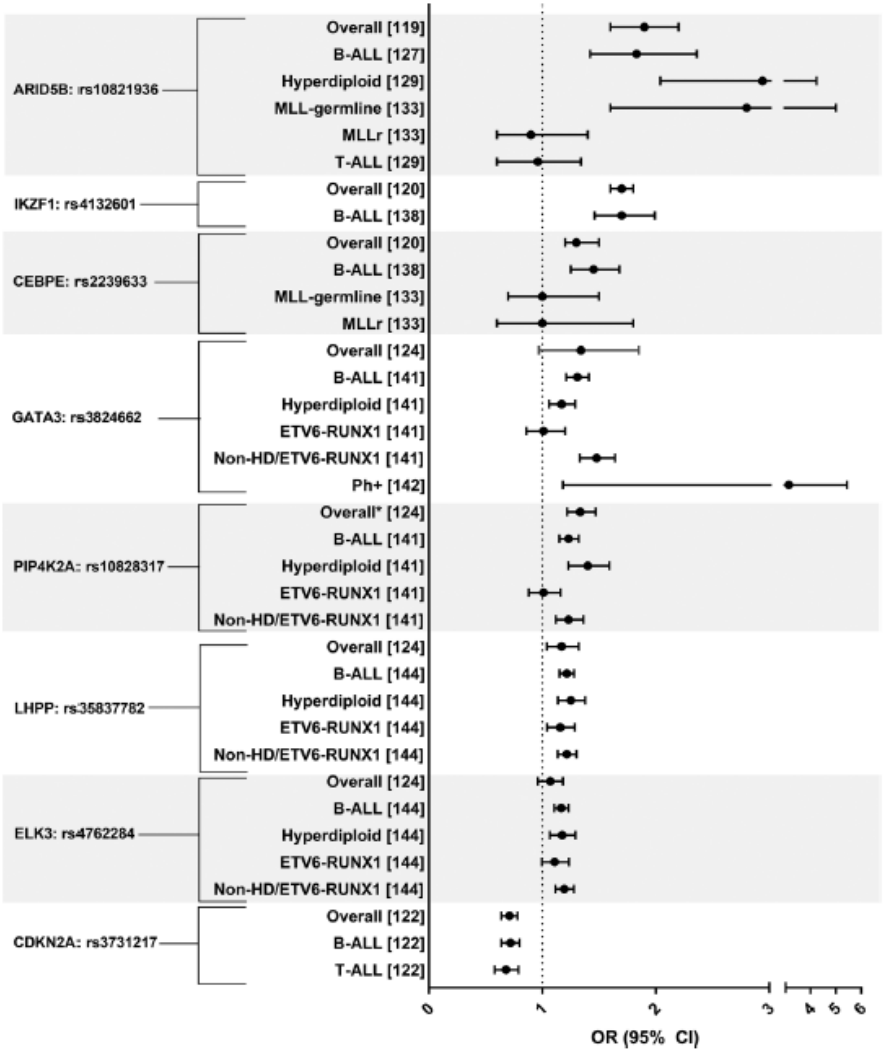
Themes in the Genetic Architecture of ALL



- Rare, high penetrance variation < 10% of patients
- Several moderately rare germline variants with OR's of 2-5 in genes of somatic interest (e.g. PAX5, ETV6)
- High common-SNP heritability (~24%)
- Strong per-allele OR's
- Most SNPs involved in lymphocyte development
- Most SNPs replicate transethnically with similar effect sizes despite differing allele frequencies
- Many variants have differing associations with molecularly-defined subtypes
- **<u>Population-specific variants have also emerged</u>**

Is There Etiologic Heterogeneity between Subtypes of Childhood Acute Lymphoblastic Leukemia? A Review of Variation in Risk by Subtype

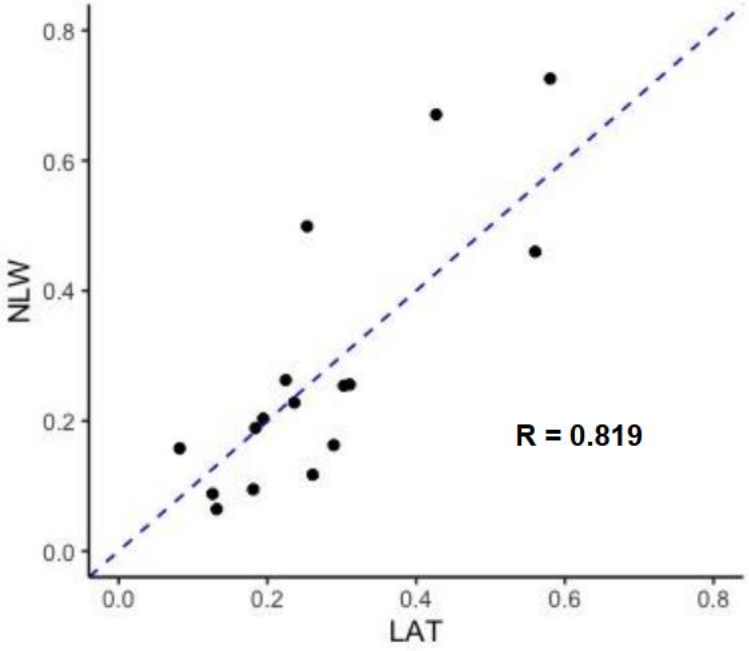
Lindsay A. Williams[1], Jun J. Yang[2,3], Betsy A. Hirsch[4,5], Erin L. Marcotte[1,5], and Logan G. Spector[1,5]



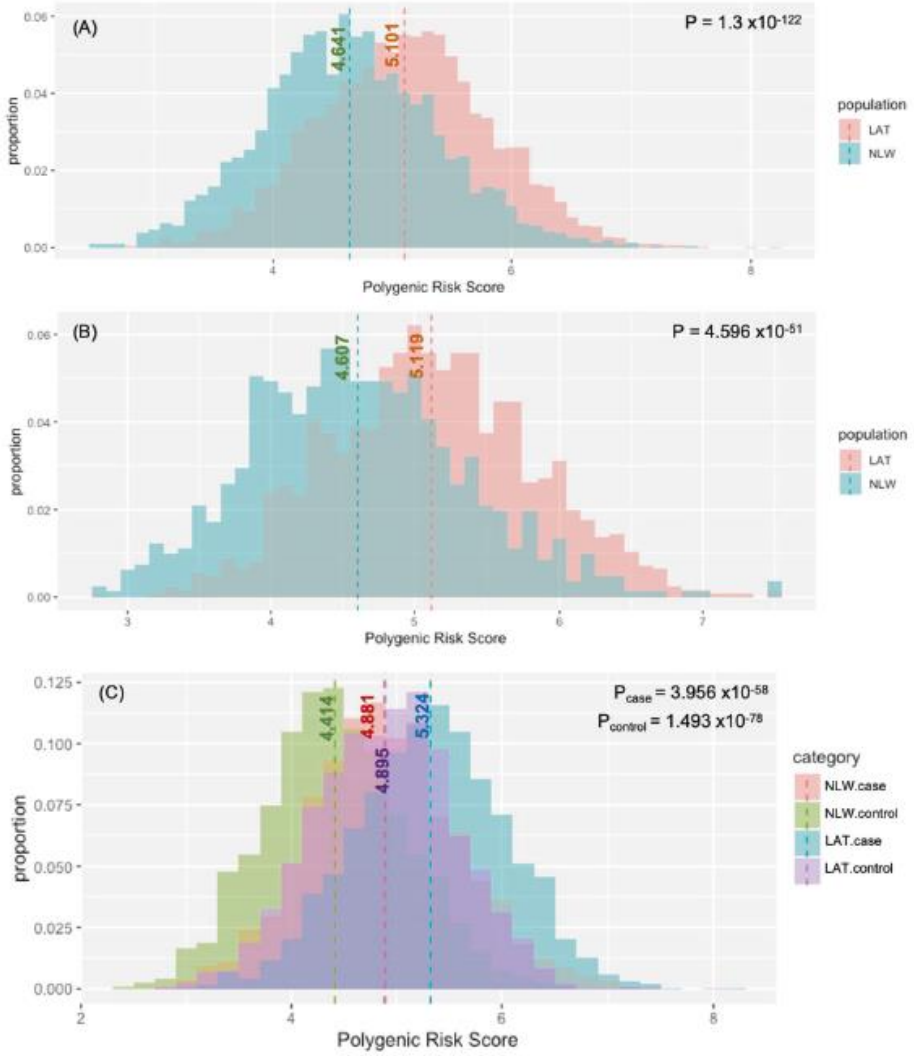
ACUTE LYMPHOBLASTIC LEUKEMIA

Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia

Soyoung Jeon[1,2], Adam J. de Smith[1], Shaobo Li[1,2], Minhui Chen[1], Tsz Fung Chan[1], Ivo S. Muskens[1], Libby M. Morimoto[3], Andrew T. DeWan[4,5], Nicholas Mancuso[1,6,7], Catherine Metayer[3], Xiaomei Ma[5], Joseph L. Wiemels[1] and Charleston W. K. Chiang[1,6]



Effect sizes for lead SNPs in each of the 16 known loci



A noncoding regulatory variant in *IKZF1* increases acute lymphoblastic leukemia risk in Hispanic/Latino children

Adam J. de Smith,[1,2,13,*] Lara Wahlster,[3,4,13] Soyoung Jeon,[1,2,13] Linda Kachuri,[5] Susan Black,[3,4] Jalen Langie,[1,2] Liam D. Cato,[3,4] Nathan Nakatsuka,[6] Tsz-Fung Chan,[1,2] Guangze Xia,[7] Soumyaa Mazumder,[3,4] Wenjian Yang,[8] Steven Gazal,[1,2] Celeste Eng,[9,10] Donglei Hu,[9] Esteban González Burchard,[9,10] Elad Ziv,[9] Catherine Metayer,[11] Nicholas Mancuso,[1,2] Jun J. Yang,[8] Xiaomei Ma,[12] Joseph L. Wiemels,[1,2] Fulong Yu,[3,4,7,14] Charleston W.K. Chiang,[1,2,14] and Vijay G. Sankaran[3,4,14,15,*]

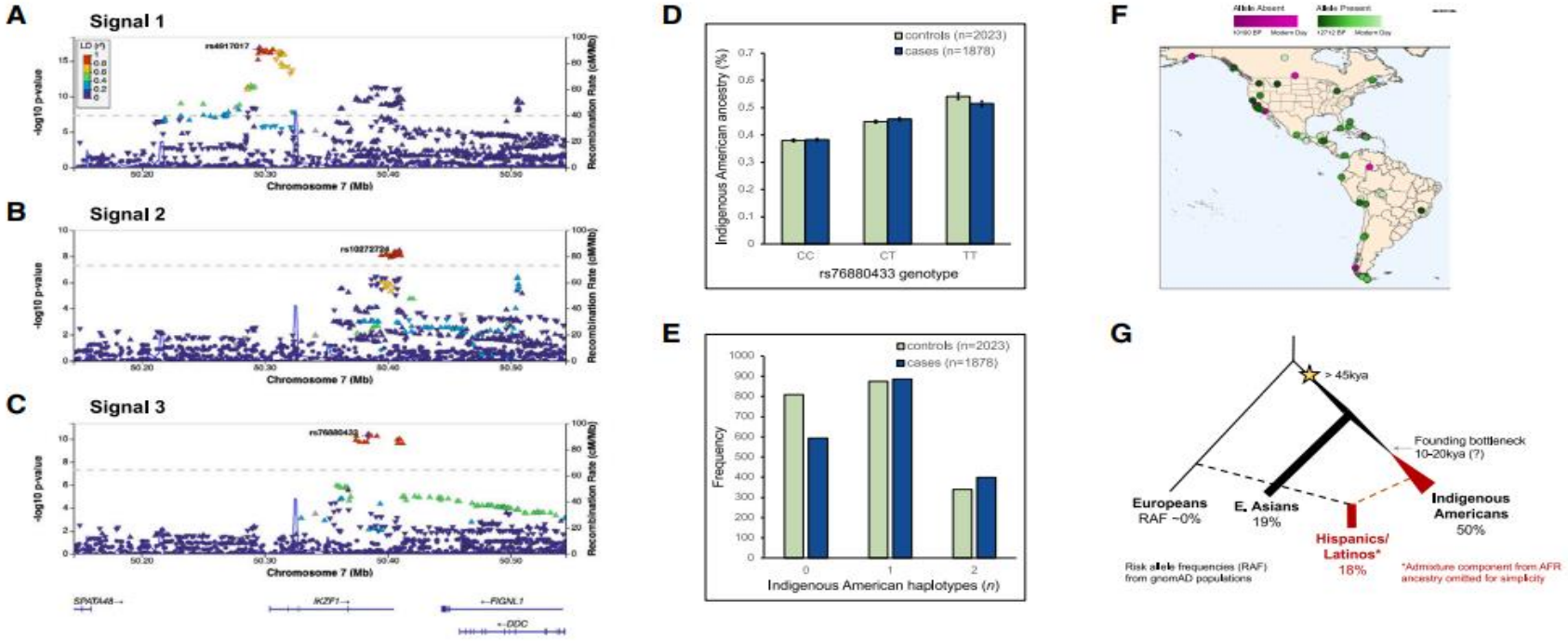
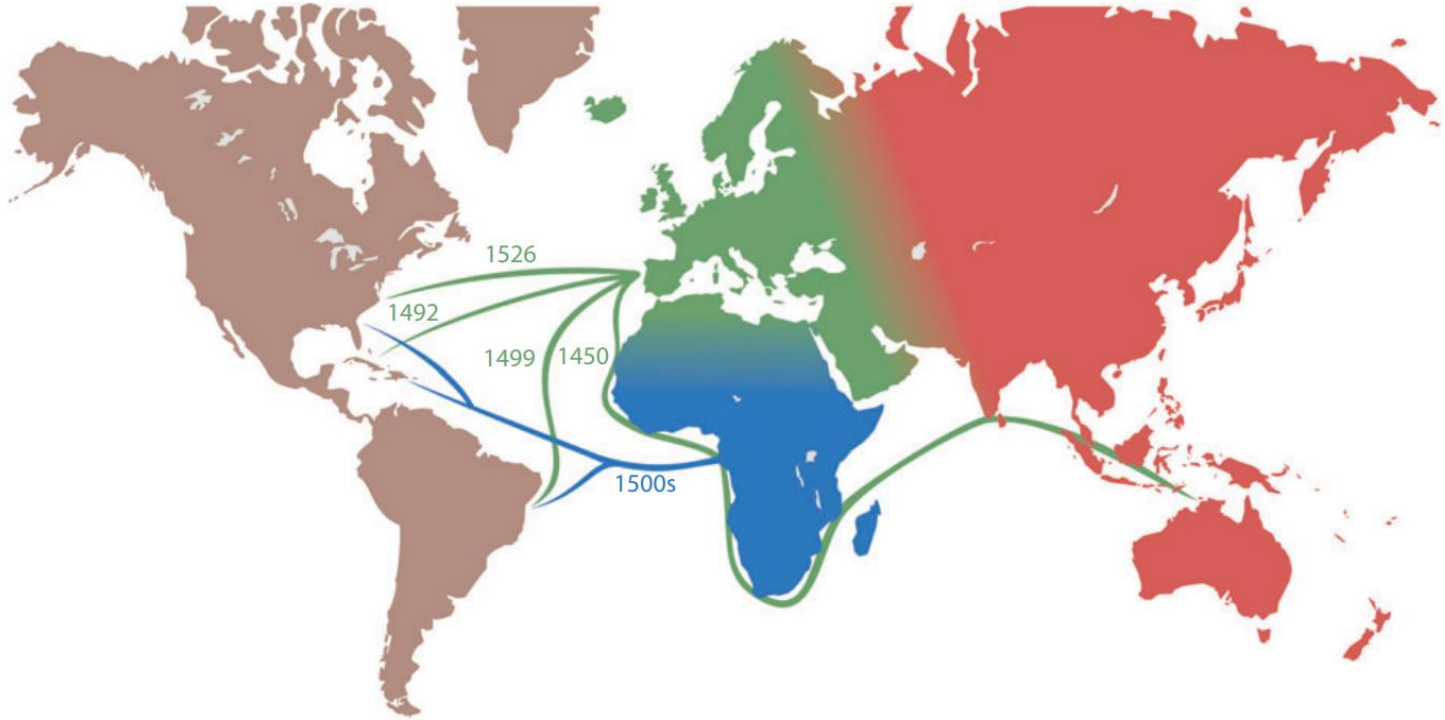


Figure 1. Novel childhood ALL risk locus at *IKZF1* is associated with Indigenous American ancestry and demonstrates ancient origins and positive selection in Hispanic/Latino populations

The ADMIRAL Study

Admixture analysis of acute lymphoblastic leukemia in African American children



The ADMIRAL Study

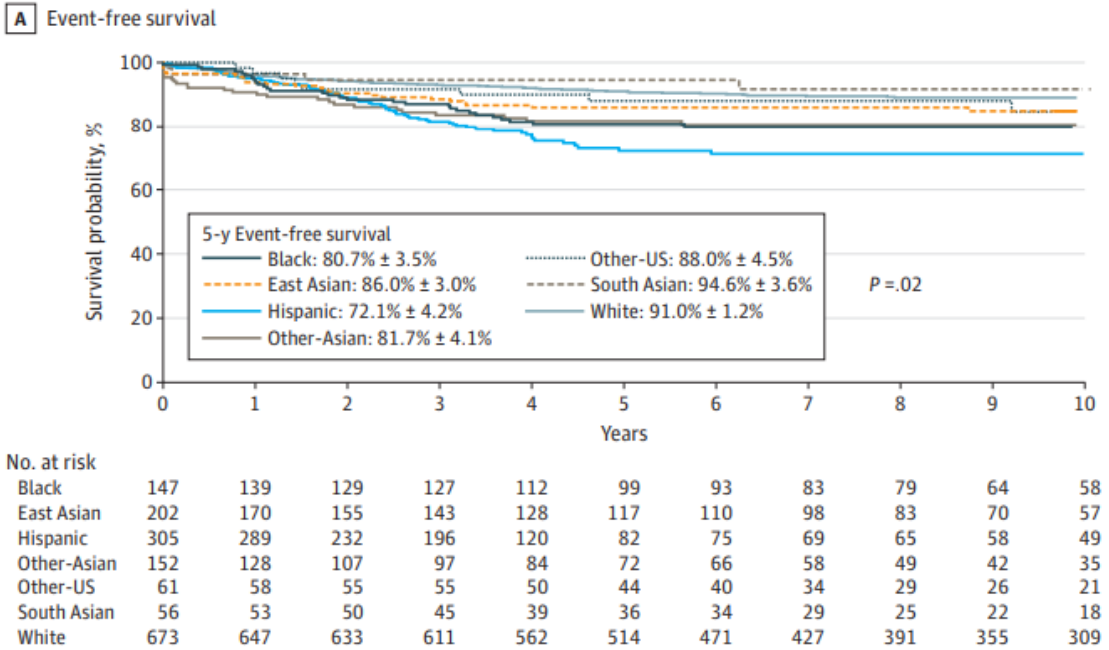
Admixture analysis of acute lymphoblastic leukemia in African American children

- Markedly lower risk in both sub-Saharan Africa and African diaspora
- Lower risk robust to control for SES and perinatal risk factors
- Burden of putative risk factors for ALL mostly fall more heavily on AA children
- Blood cell parameters differ widely in AA and have known genetic influences (e.g. Duffy allele)

JAMA Oncology | Original Investigation

Association of Genetic Ancestry With the Molecular Subtypes and Prognosis of Childhood Acute Lymphoblastic Leukemia

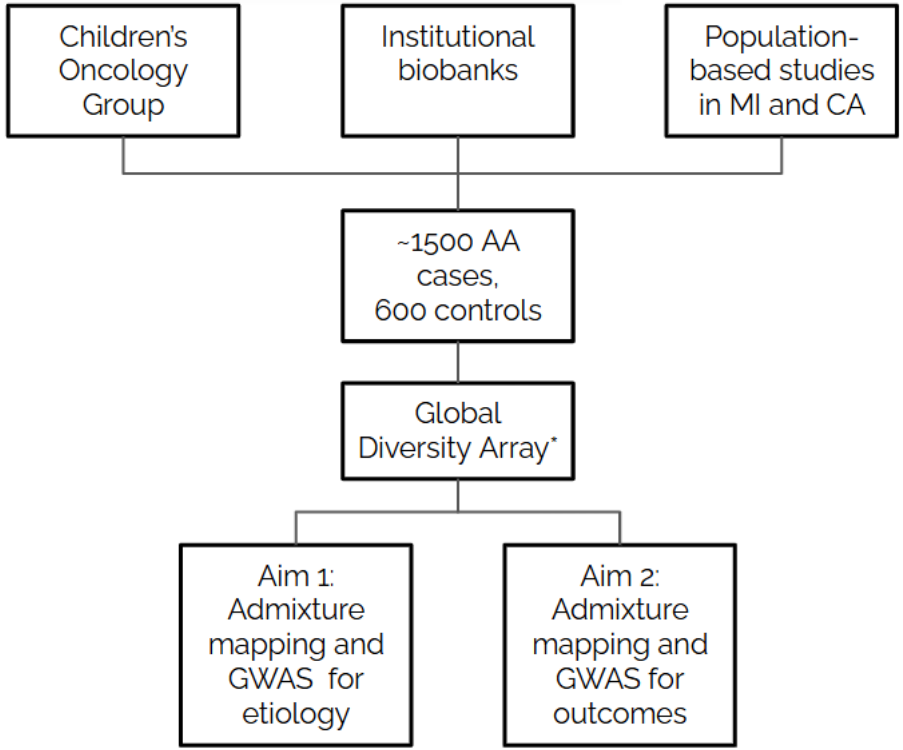
Shawn H. R. Lee, MBBS; Federico Antillon-Klussmann, MD; Deqing Pei, MS; Wenjian Yang, PhD; Kathryn G. Roberts, PhD; Zhenhua Li, PhD; Meenakshi Devidas, PhD; Wentao Yang, PhD; Cesar Najera, BS; Hai Peng Lin, MBBS; Ah Moy Tan, MBBS; Hany Ariffin, MBBS; Cheng Cheng, PhD; William E. Evans, PharmD; Stephen P. Hunger, MD; Sima Jeha, MD; Charles G. Mullighan, MD; Mignon L. Loh, MD; Allen E. J. Yeoh, MBBS; Ching-Hon Pui, MD; Jun J. Yang, PhD



Prognostic factor	Event-free survival HR (95% CI)	*P* value[a]
Age at diagnosis, y		
<1	2.4 (1.1-5.0)	
≥1 to <10	1 [Reference]	.06
≥10	1.2 (0.9-1.6)	
Leukocyte count at diagnosis, cells/μL		
<50 000	1 [Reference]	.006
≥50 000	1.5 (1.1-2.1)	
Biological subtypes[b]		
ETV6-RUNX1	1 [Reference]	<.001
DUX4	1.8 (0.7-4.4)	
Hyperdiploid	2.0 (1.0-3.8)	
ZNF384	2.9 (0.9-8.9)	
B other	3.4 (1.7-6.8)	
CRLF2	7.2 (3.4-15.0)	
ETV6-RUNX1-like	6.3 (2.7-14.9)	
KMT2A	6.5 (2.9-14.7)	
Low hypodiploid	10.0 (3.7-27.5)	
MEF2D	4.5 (1.3-15.8)	
Near haploid	12.2 (3.9-38.1)	
*PAX5*alt	3.5 (1.6-7.5)	
BCR-ABL1	7.4 (3.3-16.5)	
BCR-ABL1-like	6.9 (3.1-15.4)	
T-ALL	4.8 (2.5-9.0)	
TCF3-PBX1	2.3 (1.0-5.3)	
Percentage genetic ancestry[c]		
European	1 [Reference]	
African (every 25% increase)	1.2 (1.1-1.4)	.005
Native American (every 25% increase)	1.3 (1.01-1.6)	.04
East Asian (every 25% increase)	1.0 (0.7-1.4)	.87
South Asian (every 25% increase)	0.9 (0.7-1.3)	.70

The ADMIRAL Study

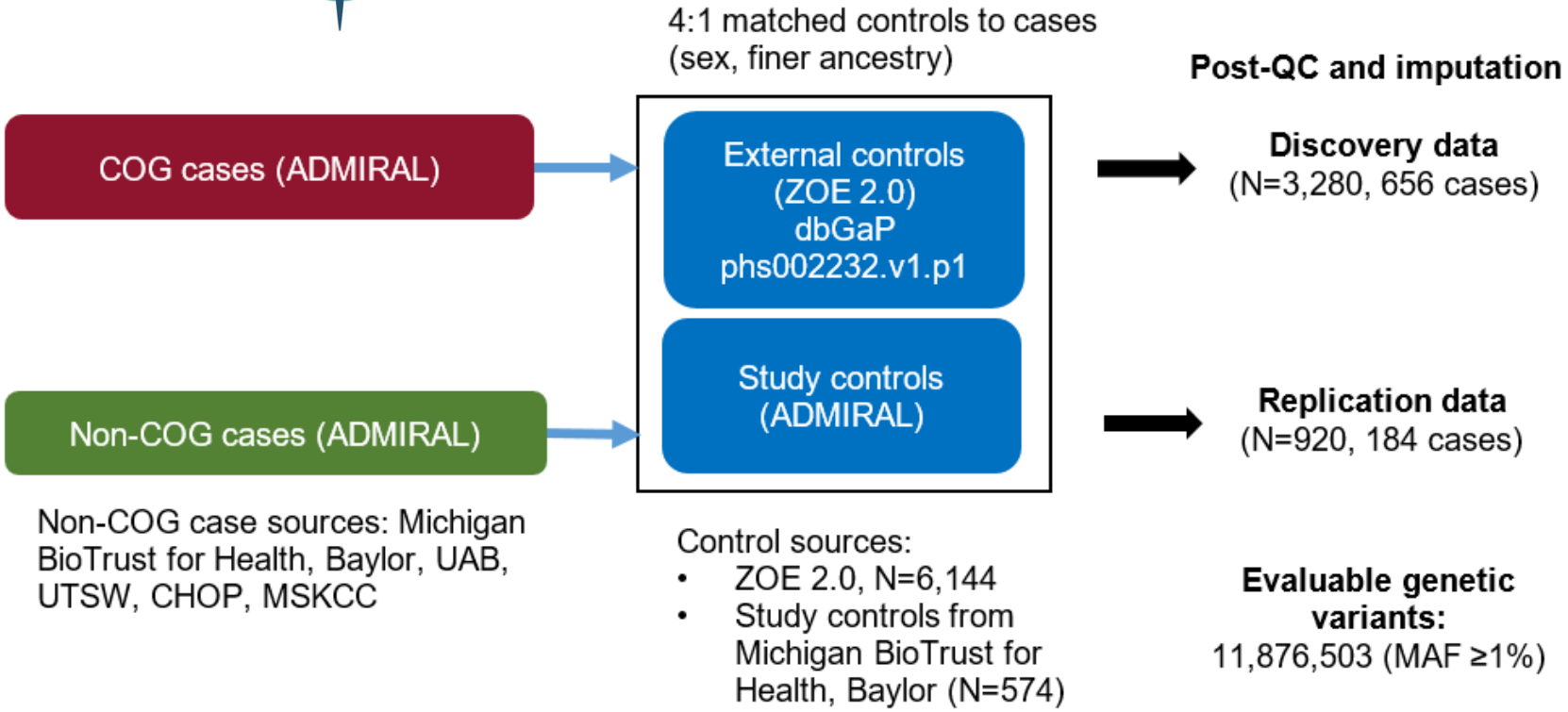
Admixture analysis of acute lymphoblastic leukemia in African American children



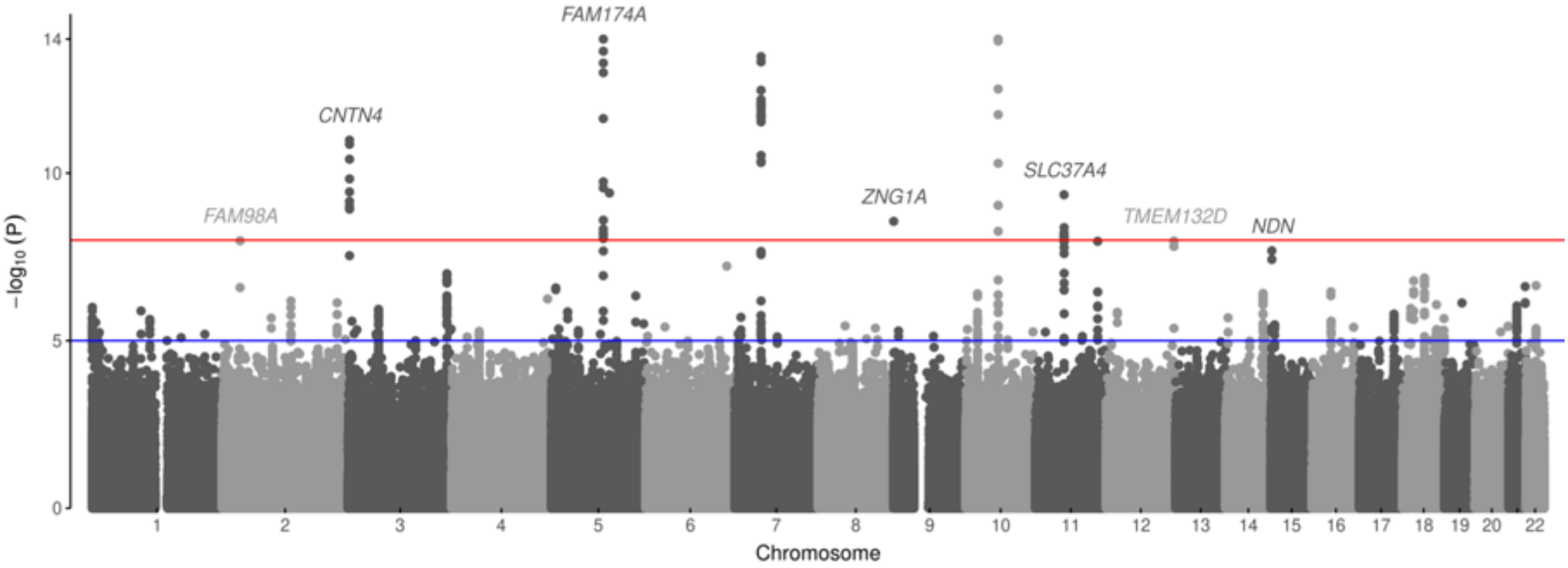
NIH R01 CA239701

*Affymetrix Axiom World Array in CA study

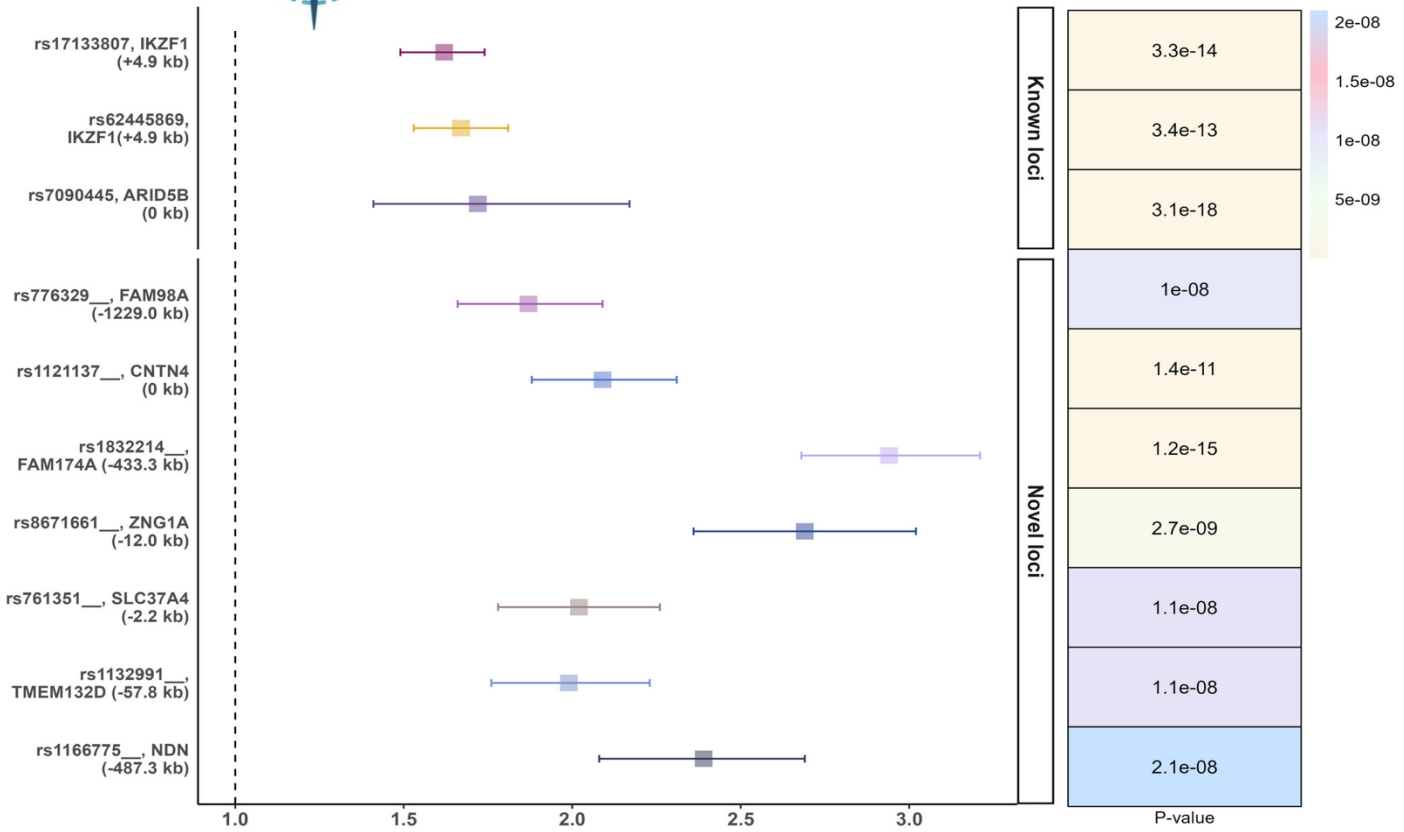
History of GWAS in ALL



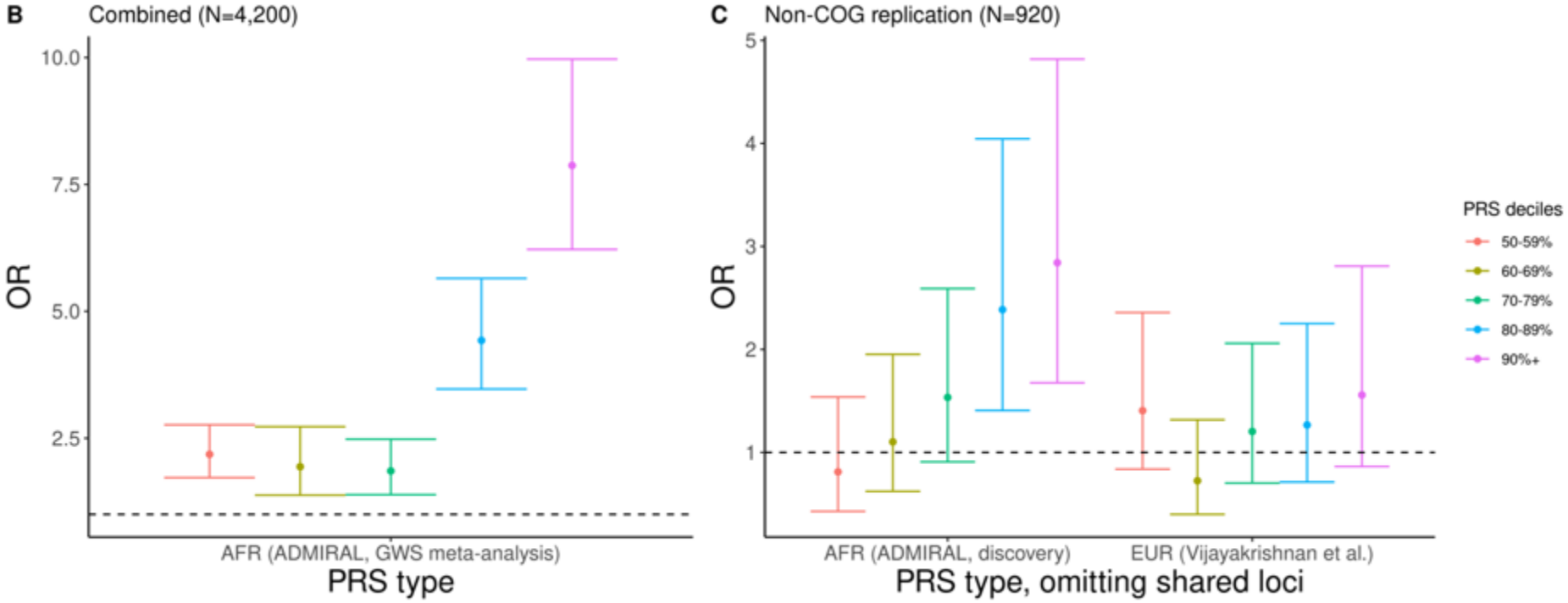
ADMIRAL GWAS



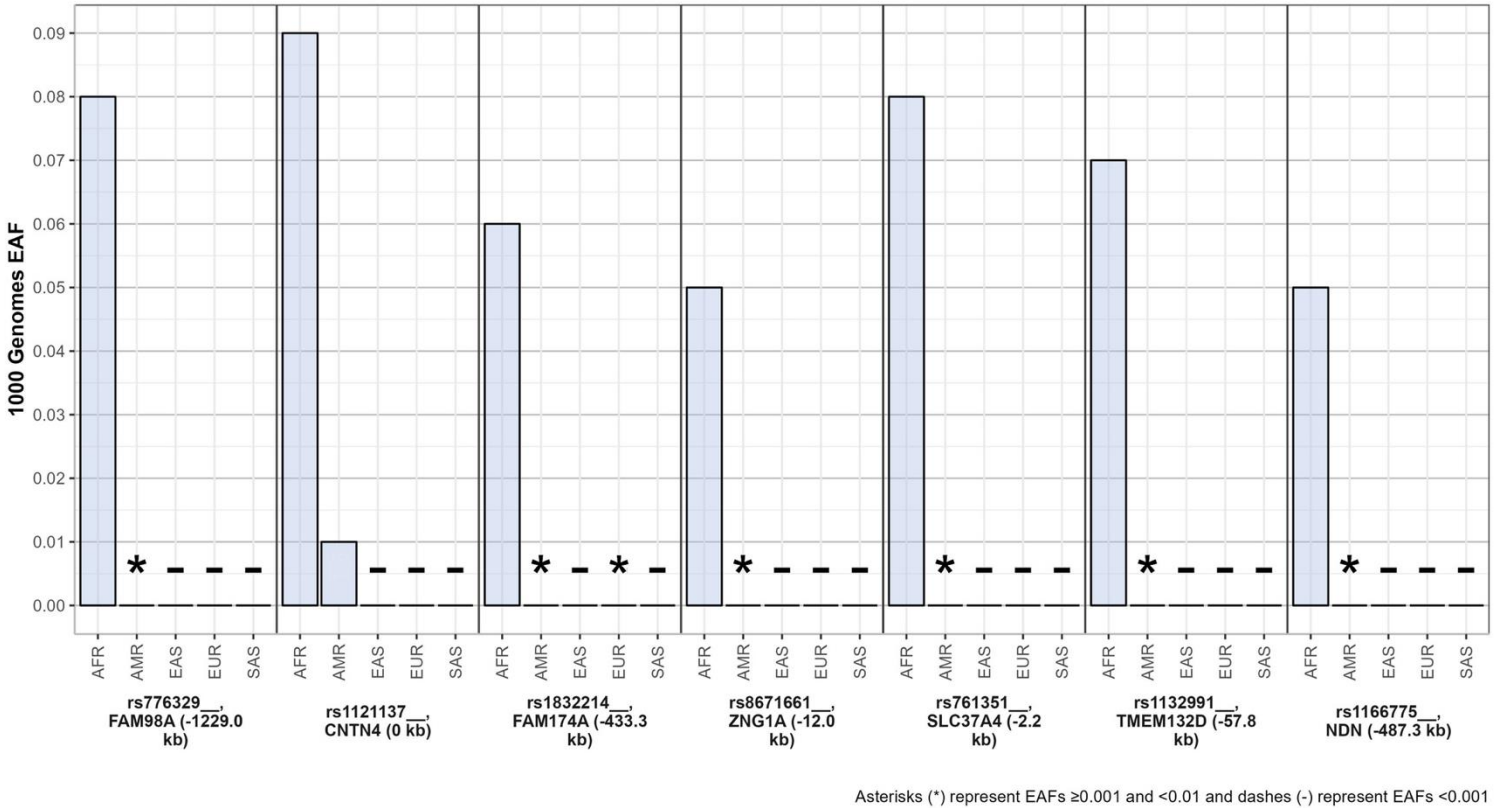
ADMIRAL GWAS



ADMIRAL Polygenic Risk Scores(s)

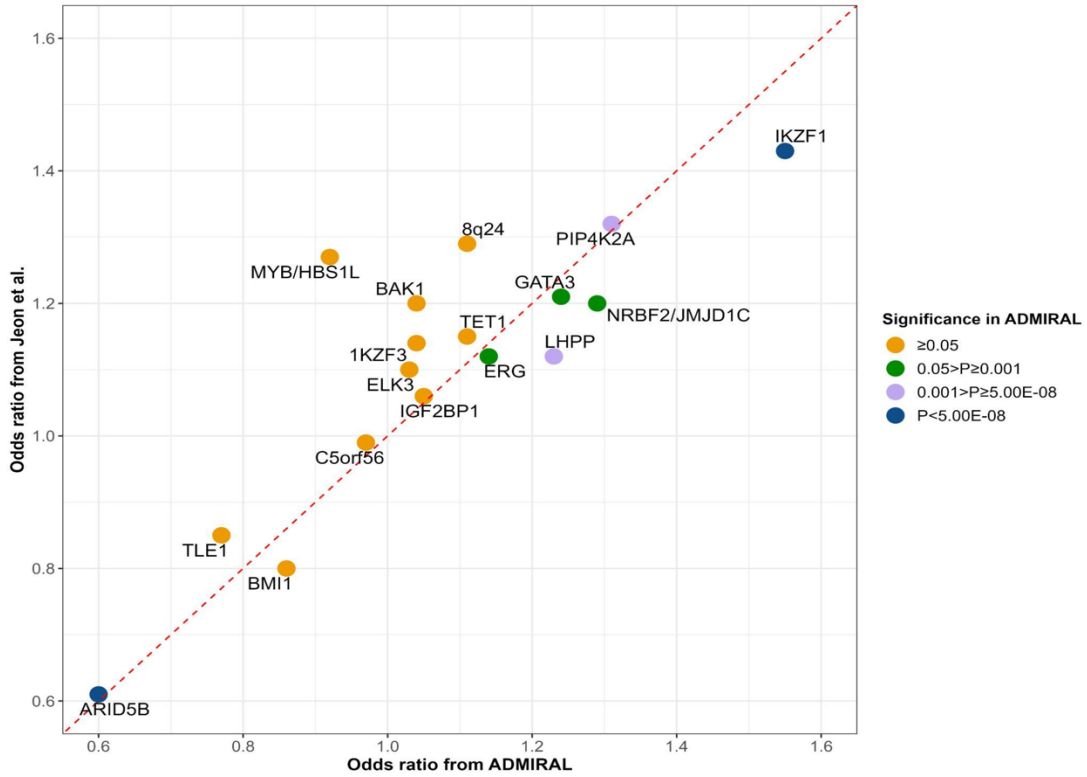


Effect Allele Frequency of Novel Loci in 1000 Genomes

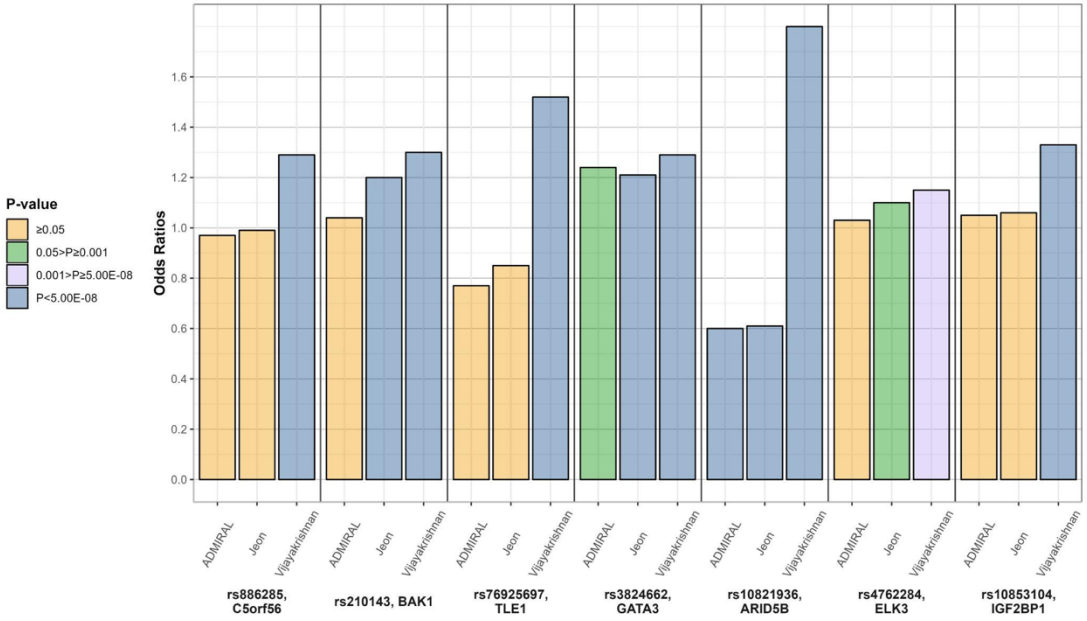


Asterisks (*) represent EAFs ≥0.001 and <0.01 and dashes (-) represent EAFs <0.001

Correlation of OR of Known Loci in Jeon et al with ADMIRAL



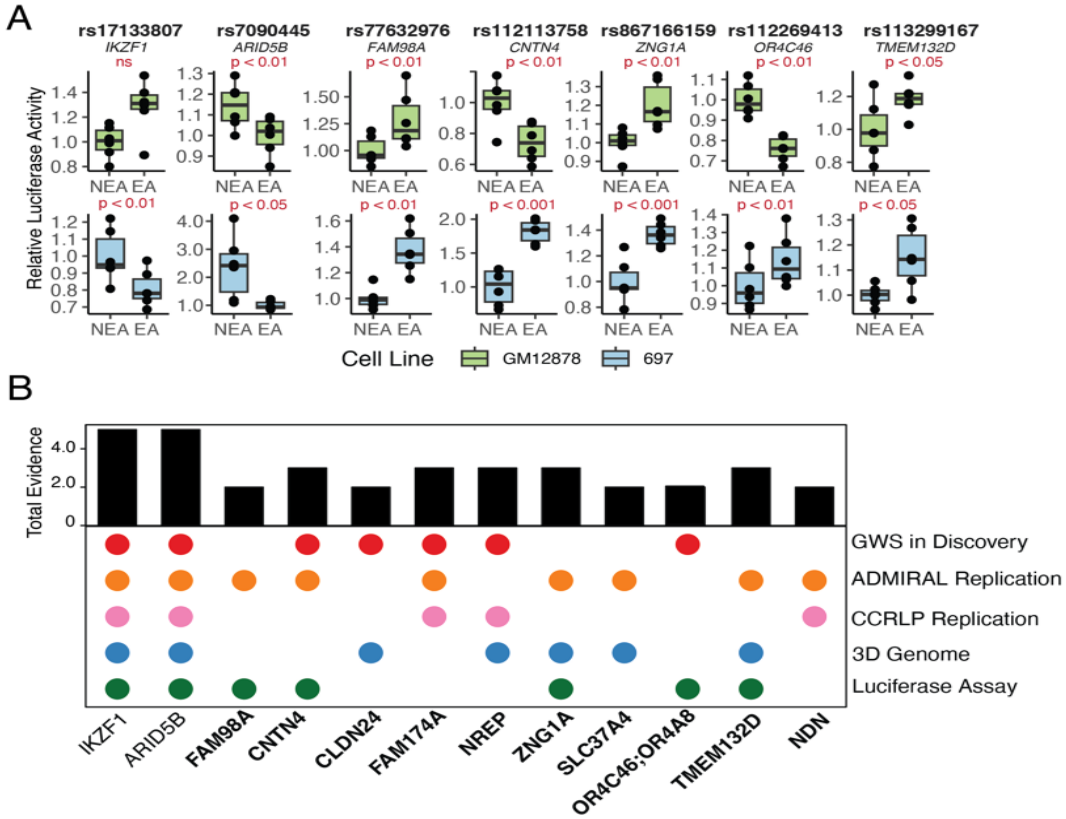
ORs in 3 GWAS and Effect Allele Frequencies in 1000 Genomes



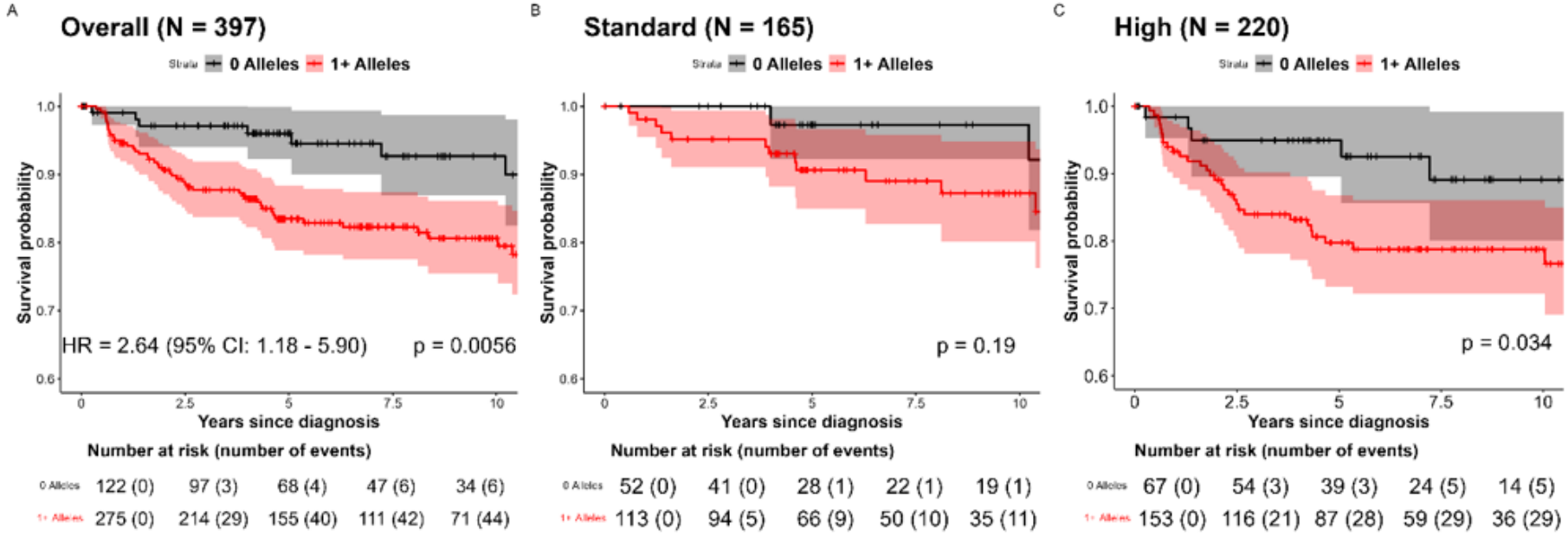
	rs886285, C5orf56	rs210143, BAK1	rs76925697, TLE1	rs3824662, GATA3	rs10821936, ARID5B	rs4762284, ELK3	rs10853104, IGF2BP1
AFR	0.28	0.76	0.03	0.08	0.80	0.45	0.69
AMR	0.70	0.76	0.03	0.37	0.53	0.49	0.42
EAS	0.35	0.83	0.00	0.27	0.64	0.60	0.12
EUR	0.66	0.73	0.04	0.19	0.67	0.30	0.47
SAS	0.48	0.87	0.02	0.17	0.49	0.31	0.40

0.0 0.2 0.4 0.6 0.8

Functional Evidence from Luciferase Reporter Assays (A), Statistical Replication (B), and 3D Genome Data (B)



Novel Alleles and Overall Survival for B-ALL in ADMIRAL



Hazard ratio (HR) adjusted for sex, genetic ancestry, and trial treatment risk stratification

ADMIRAL Conclusions

- **Known transethnic variants replicate in AA children**
  - Remarkably similar magnitudes of association
  - PRS less in AA children due to lower allele freqs
  - Partial explanation for lower risk in AA
- **Novel loci fit profile**
  - Low allele frequency (<10%)Spelling out all acronyms during the first instance
  - Large OR's
  - African-ancestry specific
  - High evidence of function
- **Novel variants appear associated with survival**

Thank you!

University of Minnesota
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Karen Rabin
Sarah Vargas

USC
Adam de Smith
Joe Wiemels

UC Berkeley
Catherine Metayer
Alice Kang

St Jude
Dan Savic
Jun Yang

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Blood Cancer United

CLIC

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St. Baldrick's FOUNDATION
Conquer Childhood Cancers

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Q&A

Childhood Cancer Data Initiative Virtual Symposium Series

Illuminating Dark Antigens for Childhood Cancer Immunotherapy

Yi Xing, Ph.D.

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Acknowledgments

Xing Lab

CHOP

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Penn

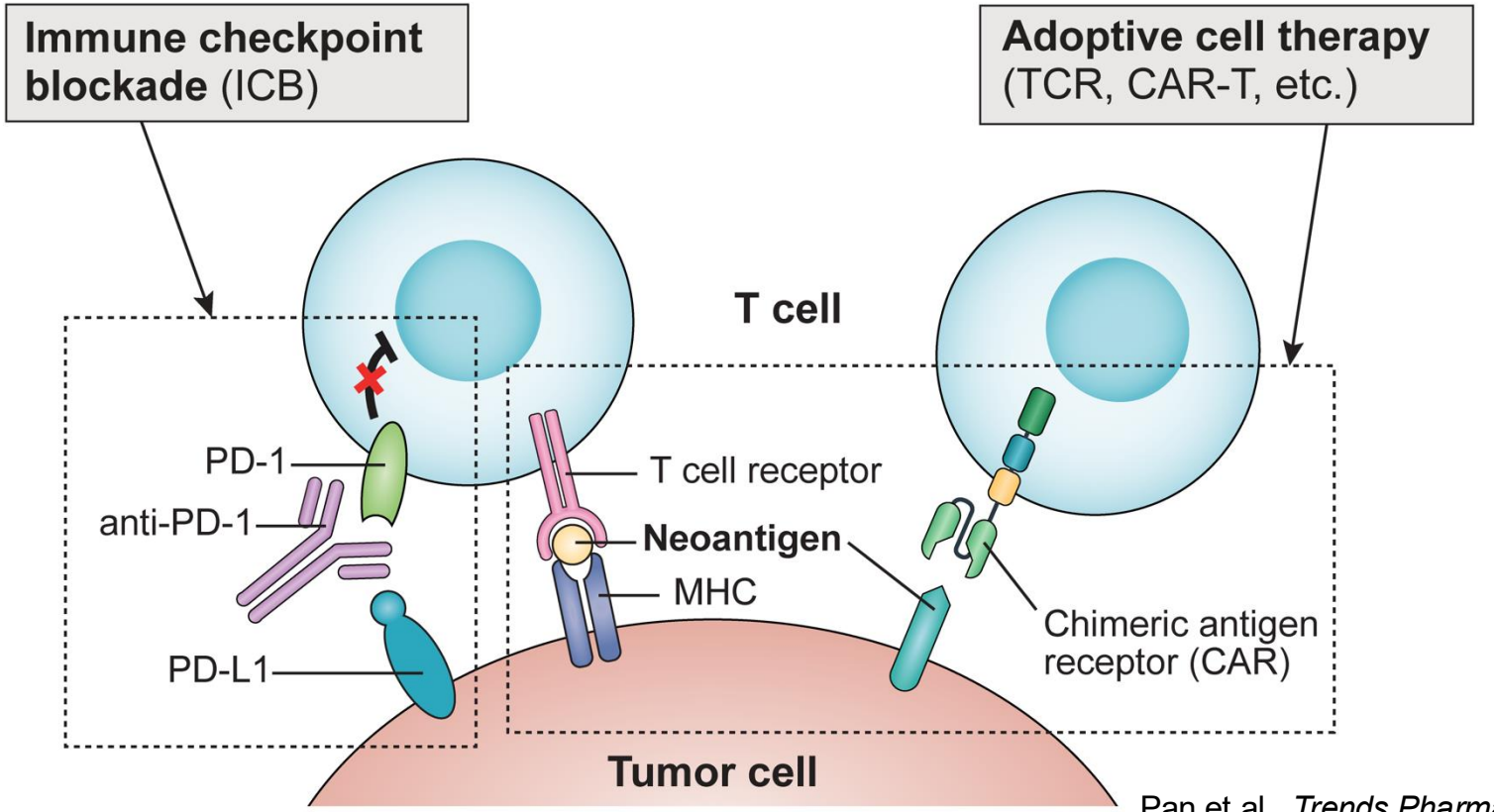
Carl June | Avery Posey

Roswell Park

Song Liu

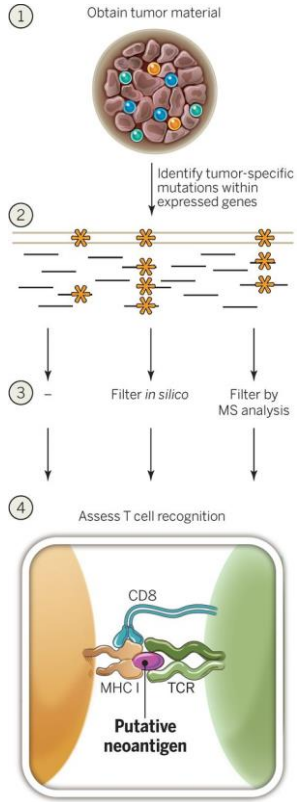
Antoni Ribas | Sanaz Memarzadeh | Anthony Wang

Targeting Tumor Antigens for Cancer Immunotherapies



Pan et al., *Trends Pharmacol Sci*, 2021

Immunotherapy & Tumor Antigen Discovery



Schumacher & Schreiber, *Science*, 2015

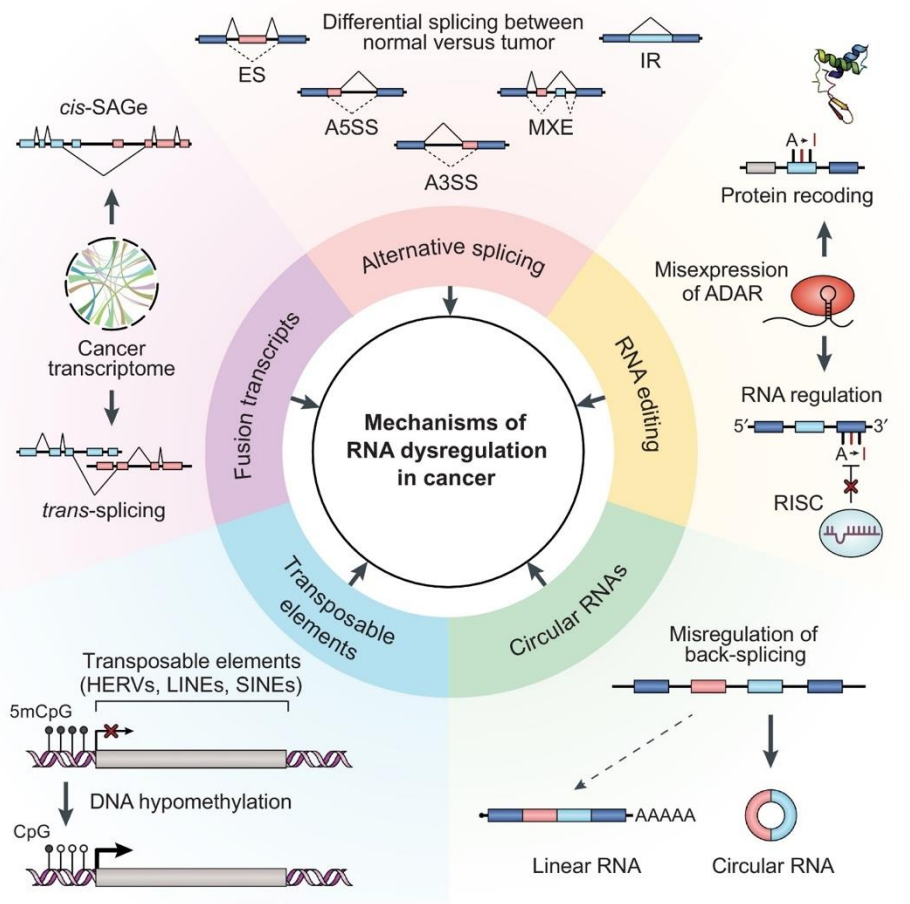
First-generation tumor antigen discovery tools

- Focus on somatic mutations
- Use RNA-seq and/or MS proteomics to confirm expression

Limitations

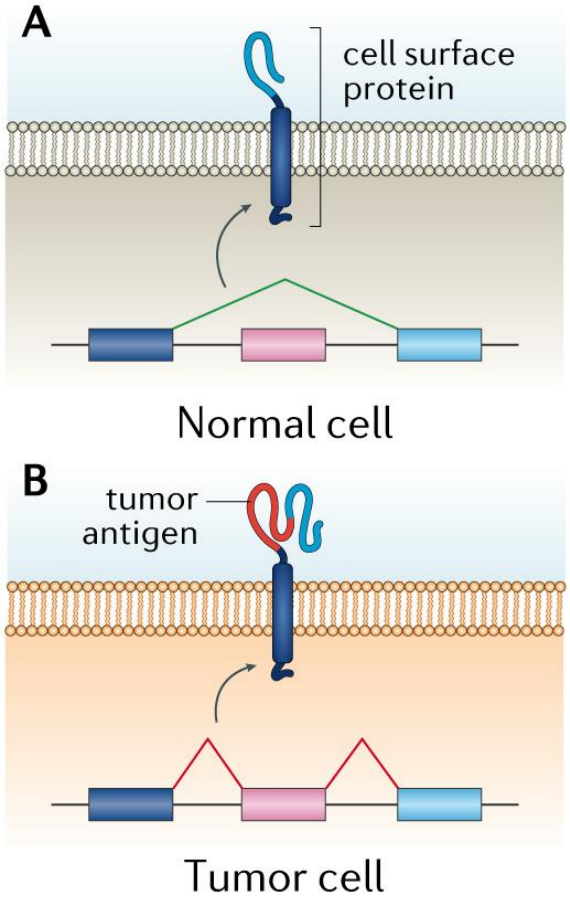
- Ignore other sources of transcriptomic and proteomic alterations in cancer cells (e.g., alternative splicing, RNA editing, fusion transcripts)

RNA Dysregulation in Cancer



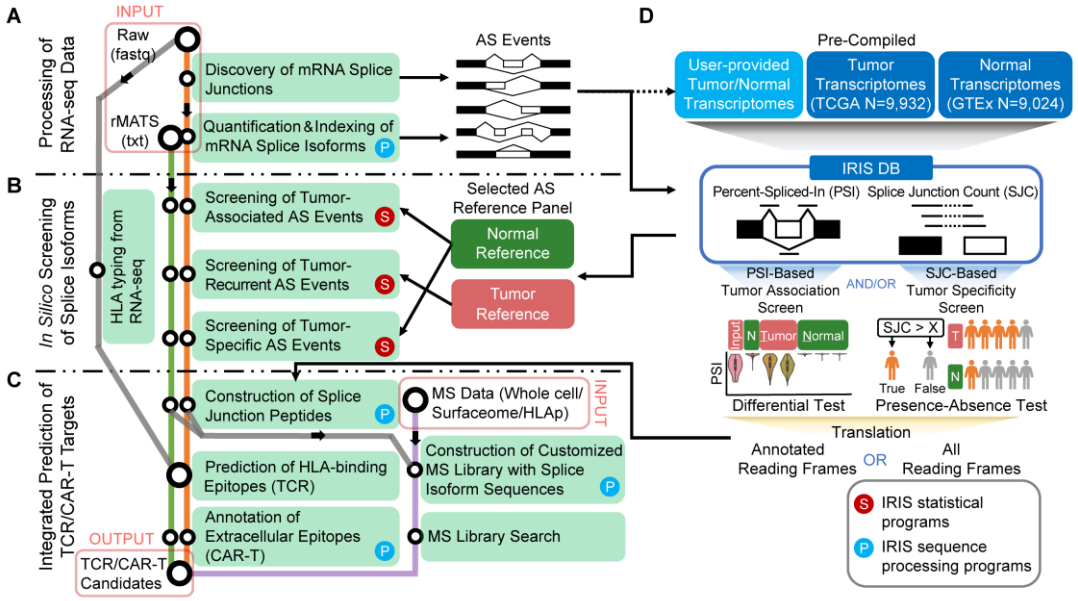
Pan et al., *Trends Pharmacol Sci*, 2021

RNA Dysregulation May Create Tumor Antigens



IRIS: Discovery of Splicing-Derived Immunotherapy Targets Using Short-Read RNA-seq Data

Isoform peptides from **R**NA splicing for **I**mmunotherapy target **S**creening



Targets for TCR-T/CAR-T

rMATS (Shen et al., PNAS, 2014)

↓

DARTS (Zhang et al., Nature Methods, 2019)

↓

IRIS (Yang et al., bioRxiv, 2019)

↓

IRIS 2.0 (Yang et al., PNAS, 2023)

PARKER INSTITUTE for CANCER IMMUNOTHERAPY

CANCER MOONSHOT

IOTN Immuno-Oncology Translational Network

Recruiting

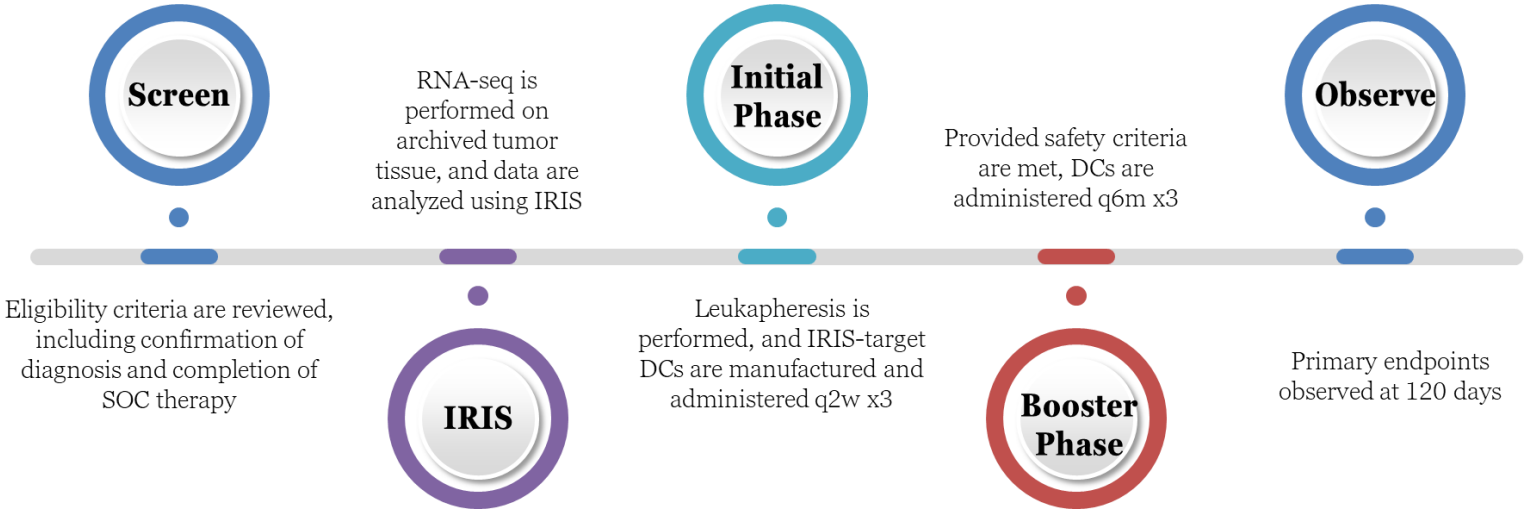
A Vaccine (Neoantigen-Targeted ppDC) for the Treatment of H3 G34-mutant Diffuse Hemispheric Glioma

ClinicalTrials.gov ID NCT06342908

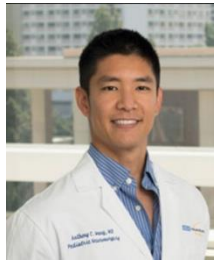
Sponsor Jonsson Comprehensive Cancer Center

Information provided by Jonsson Comprehensive Cancer Center (Responsible Party)

Last Update Posted 2024-12-09



UCLA



Anthony Wang, M.D.

Cancer-Specific Alternative Splicing Creates Tumor Antigens

2023

PNAS RESEARCH ARTICLE | IMMUNOLOGY AND INFLAMMATION OPEN ACCESS

IRIS: Discovery of cancer immunotherapy targets arising from pre-mRNA alternative splicing

Yang Pan[a,b,1], John W. Phillips[c,1], Beatrice D. Zhang[b,1], Miyako Noguchi[c,1], Eric Kutschera[b], Jami McLaughlin[c], Pavlo A. Nesterenko[d], Zhiyuan Mao[a], Nathanael J. Bangayan[a], Robert Wang[b,f], Wendy Tran[c], Harry T. Yang[a], Yuanyuan Wang[a,b], Yang Xu[b,f], Matthew B. Obusan[c], Donghui Cheng[g], Alex H. Lee[e,h], Kathryn E. Kadash-Edmondson[b], Ameya Champhekar[i], Cristina Puig-Saus[i,j,k], Antoni Ribas[e,g,j,k,l,m], Robert M. Prins[e,h,j,k], Christopher S. Seet[e,g,j], Gay M. Crooks[g,j,n,o], Owen N. Witte[c,d,e,g,j,k,2], and Yi Xing[b,c,p,q,2]

2024

SCIENCE TRANSLATIONAL MEDICINE | RESEARCH ARTICLE

CANCER

Splicing neoantigen discovery with SNAF reveals shared targets for cancer immunotherapy

Guangyuan Li[1,2]*†, Shweta Mahajan[3]†, Siyuan Ma[3], Erin D. Jeffery[4], Xuan Zhang[3], Anukana Bhattacharjee[1], Meenakshi Venkatasubramanian[1,5], Matthew T. Weirauch[1,6,7,8], Emily R. Miraldi[1,3,8], H. Leighton Grimes[3,8], Gloria M. Sheynkman[4], Tamara Tilburgs[3,8]*, Nathan Salomonis[1,2,8]*

2024

nature communications

Article https://doi.org/10.1038/s41467-024-47649-y

Discovery of immunotherapy targets for pediatric solid and brain tumors by exon-level expression

Received: 13 November 2023

Accepted: 9 April 2024

Published online: 03 May 2024

Check for updates

Timothy I. Shaw[1,2,11], Jessica Wagner[3,11], Liqing Tian[1,3,11], Elizabeth Wickman[3,4], Suresh Poudel[5], Jian Wang[1], Robin Paul[1], Selene C. Koo[6], Meifen Lu[6], Heather Sheppard[6], Yiping Fan[7], Francis H. O'Neill[8], Ching C. Lau[8,9,10], Xin Zhou[1], Jinghui Zhang[1,12] & Stephen Gottschalk[3,12]

2025

Article

Tumour-wide RNA splicing aberrations generate actionable public neoantigens

https://doi.org/10.1038/s41586-024-08552-0

Received: 26 October 2023

Accepted: 19 December 2024

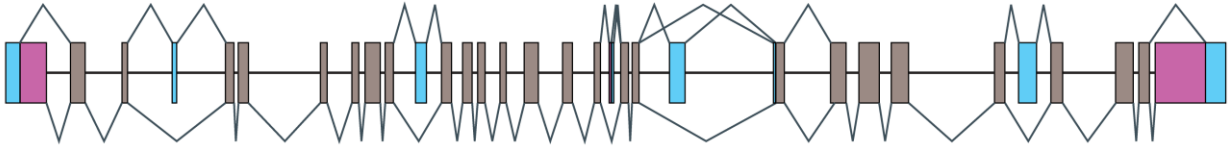
Published online: 19 February 2025

Open access

Darwin W. Kwok[1], Nicholas O. Stevers[1], Iñaki Etxeberria[2,3], Takahide Nejo[1], Maggie Colton Cove[1], Lee H. Chen[1], Jangham Jung[1], Kaori Okada[1], Senthilnath Lakshmanachetty[1], Marco Gallus[1,4], Abhilash Barpanda[5], Chibo Hong[1], Gary K. L. Chan[1], Jerry Liu[1], Samuel H. Wu[1], Emilio Ramos[5], Akane Yamamichi[1], Payal B. Watchmaker[1], Hirokazu Ogino[1], Atsuro Saijo[1], Aidan Du[1], Nadia R. Grishanina[1], James Woo[1], Aaron Diaz[1], Shawn L. Hervey-Jumper[1], Susan M. Chang[1], Joanna J. Phillips[1,6], Arun P. Wiita[5,7,8], Christopher A. Klebanoff[2,3,9], Joseph F. Costello[1] & Hideho Okada[1,10]

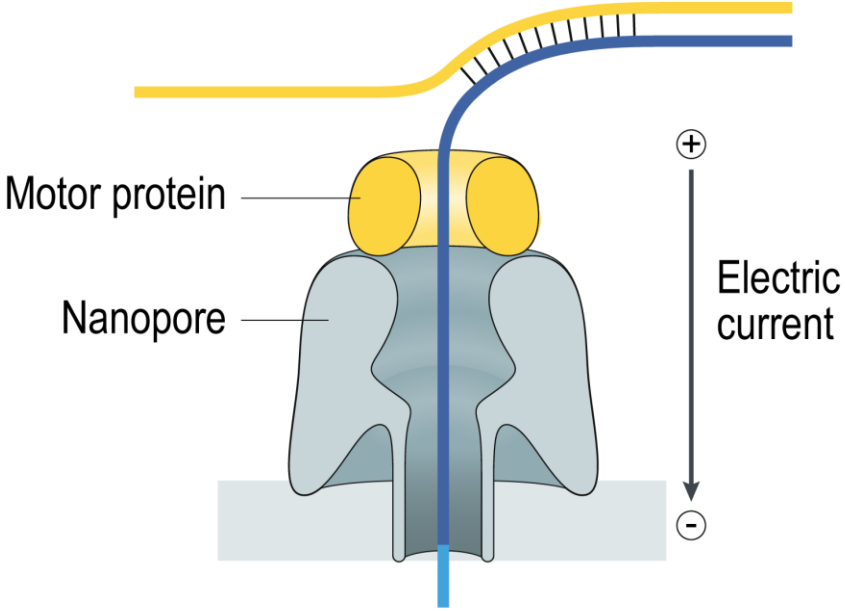
Traditional RNA Sequencing

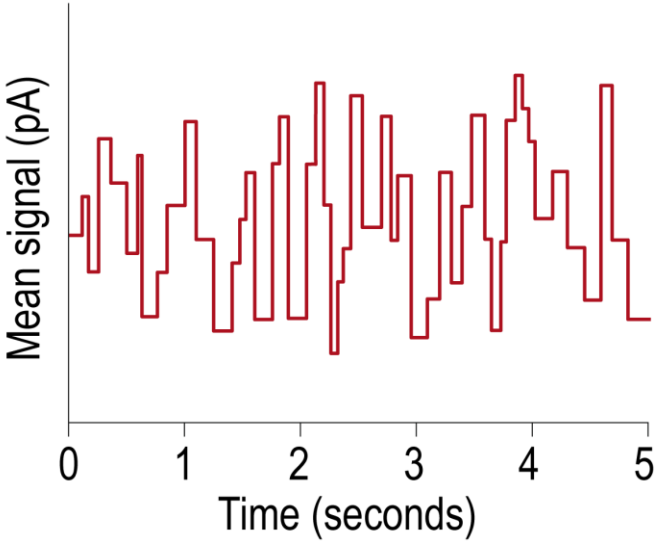
KCNMA1 pre-mRNA



Long-Read Sequencing: Seeing the Whole Picture

- Pacific Biosciences (PacBio)
- **Oxford Nanopore Technologies (ONT)**





- Generate reads > 10 kb
- Directly sequence entire transcript molecules

Logsdon et al., *Nat. Rev. Genet.* 2020

Robust and Low-Cost Technologies for Long-Read RNA-seq

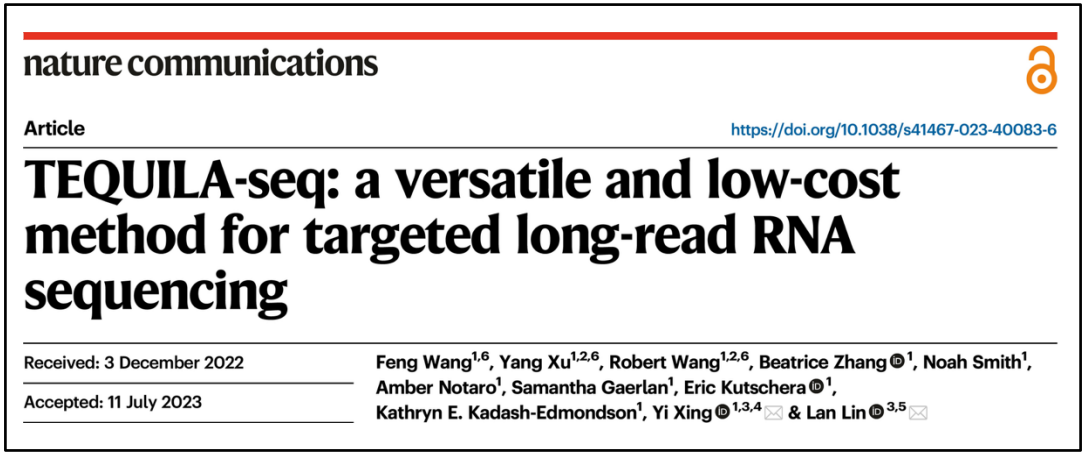
SCIENCE ADVANCES | RESEARCH ARTICLE

GENETICS

ESPRESSO: Robust discovery and quantification of transcript isoforms from error-prone long-read RNA-seq data

Yuan Gao[1*†‡], Feng Wang[1†], Robert Wang[1,2†], Eric Kutschera[1], Yang Xu[1,2], Stephan Xie[1], Yuanyuan Wang[1§], Kathryn E. Kadash-Edmondson[1], Lan Lin[3,4], Yi Xing[1,3,5*]

Gao et al.
Science Advances (2023)



nature communications

Article

https://doi.org/10.1038/s41467-023-40083-6

TEQUILA-seq: a versatile and low-cost method for targeted long-read RNA sequencing

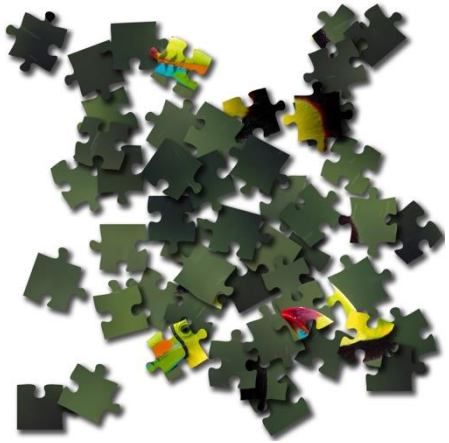
Received: 3 December 2022

Accepted: 11 July 2023

Feng Wang[1,6], Yang Xu[1,2,6], Robert Wang[1,2,6], Beatrice Zhang[1], Noah Smith[1], Amber Notaro[1], Samantha Gaerlan[1], Eric Kutschera[1], Kathryn E. Kadash-Edmondson[1], Yi Xing[1,3,4] & Lan Lin[3,5]

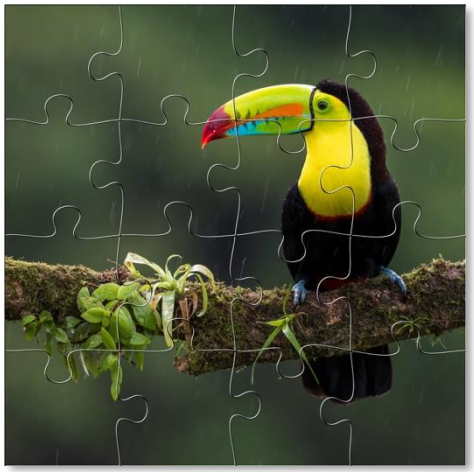
Wang et al.
Nature Communications (2023)

Short-read transcriptome

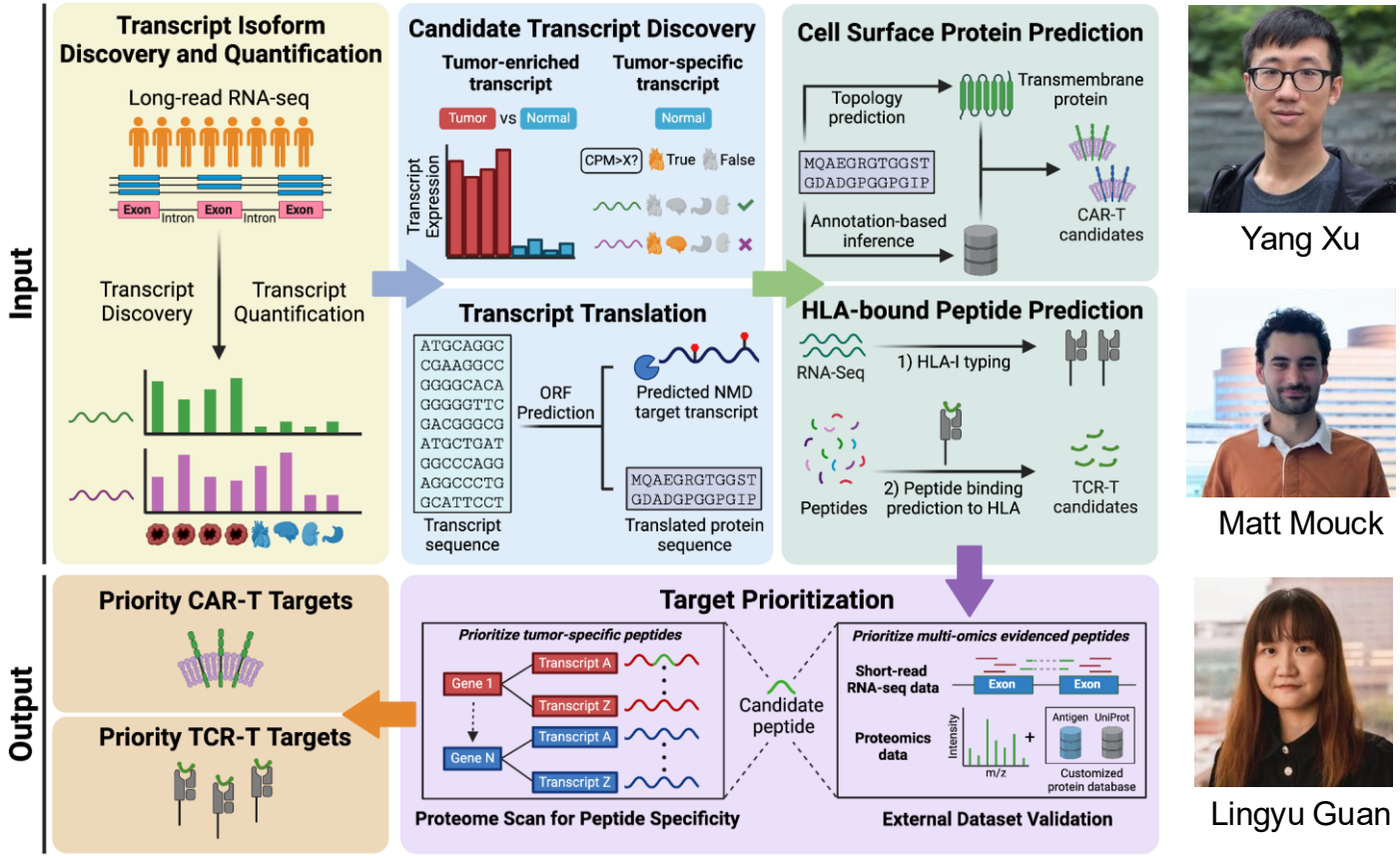


Long-read transcriptome

High-definition long-read transcriptome



IRIS-long: **I**soform peptides from **R**NA dysregulation for Immunotherapy target **S**creening – by **long**-read RNA-seq



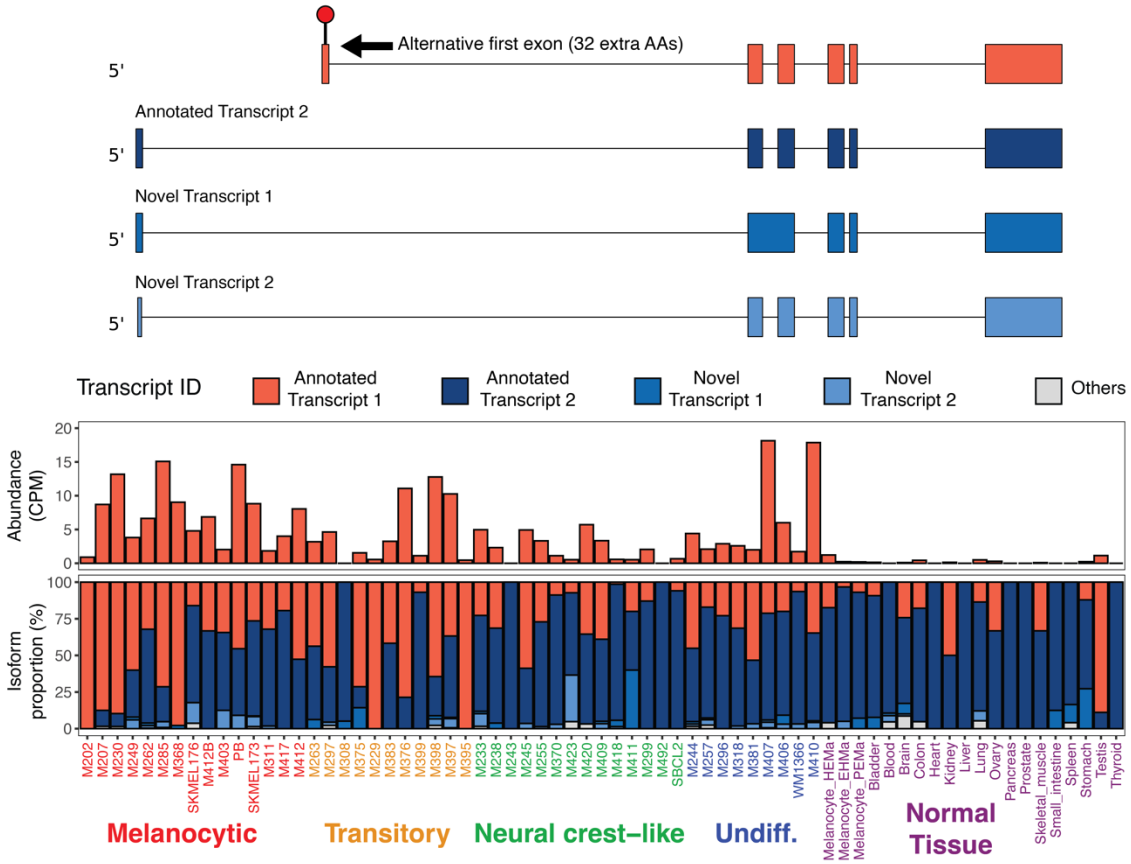
Yang Xu

Matt Mouck

Lingyu Guan

Manuscript in preparation

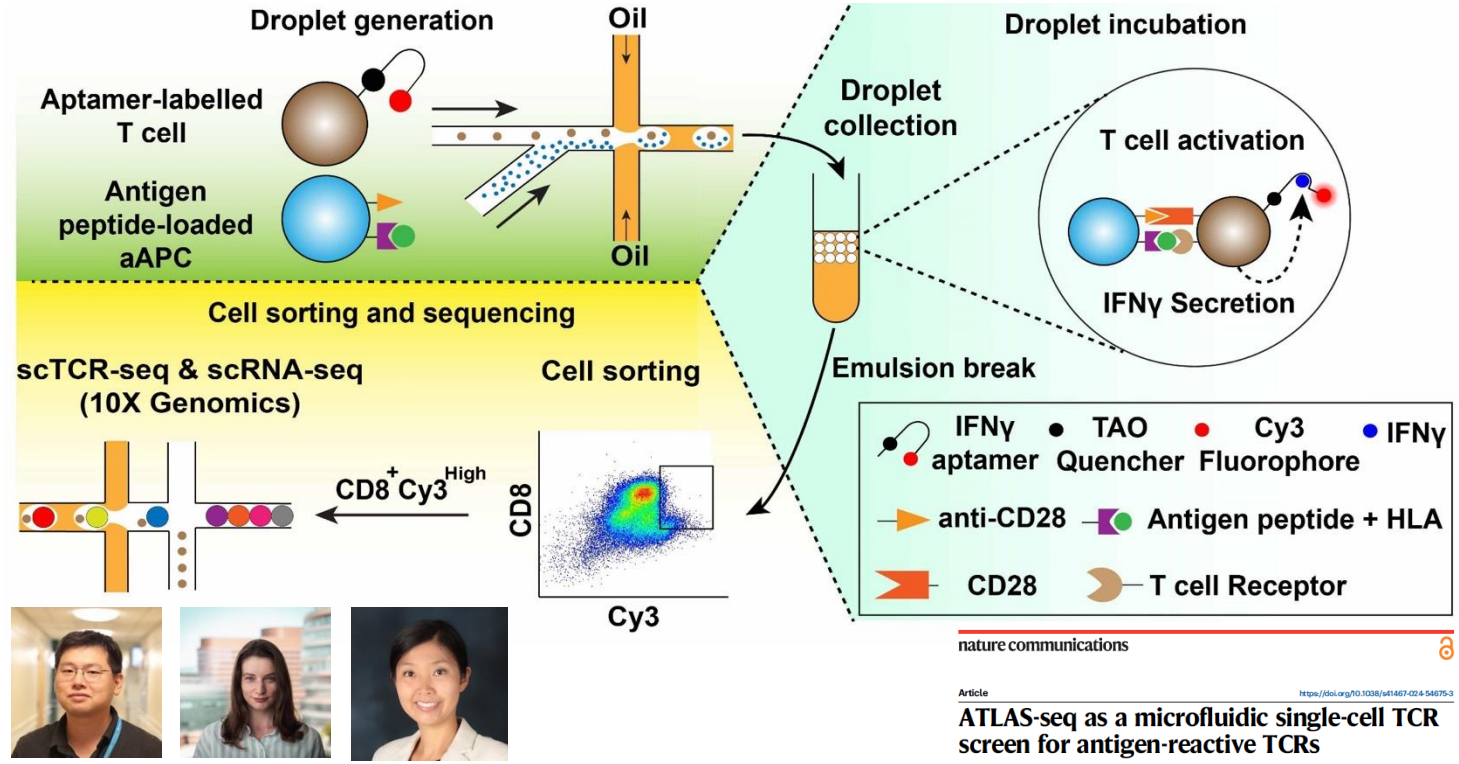
IRIS-long Predicts an MT1 Isoform as a Melanoma-Specific Antigen



Antoni Ribas (UCLA)

Unpublished/Confidential

ATLAS-seq: Aptamer-Based T Lymphocyte Activity Screening and Sequencing



Siwei Luo

Amber Notaro

Lan Lin

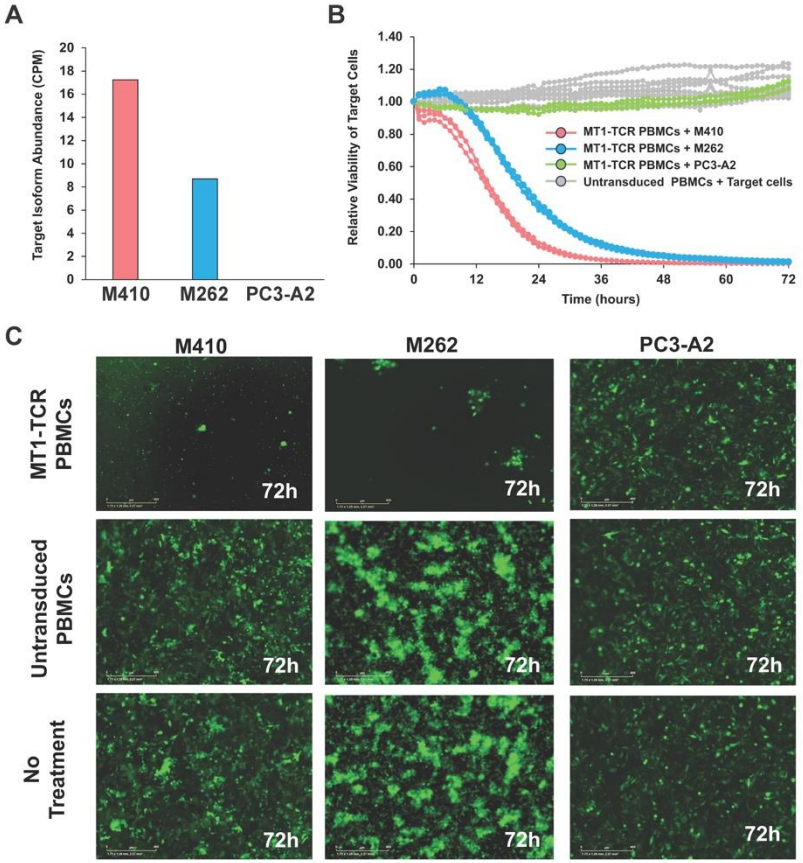
nature communications

Article https://doi.org/10.1038/s41467-024-54675-3

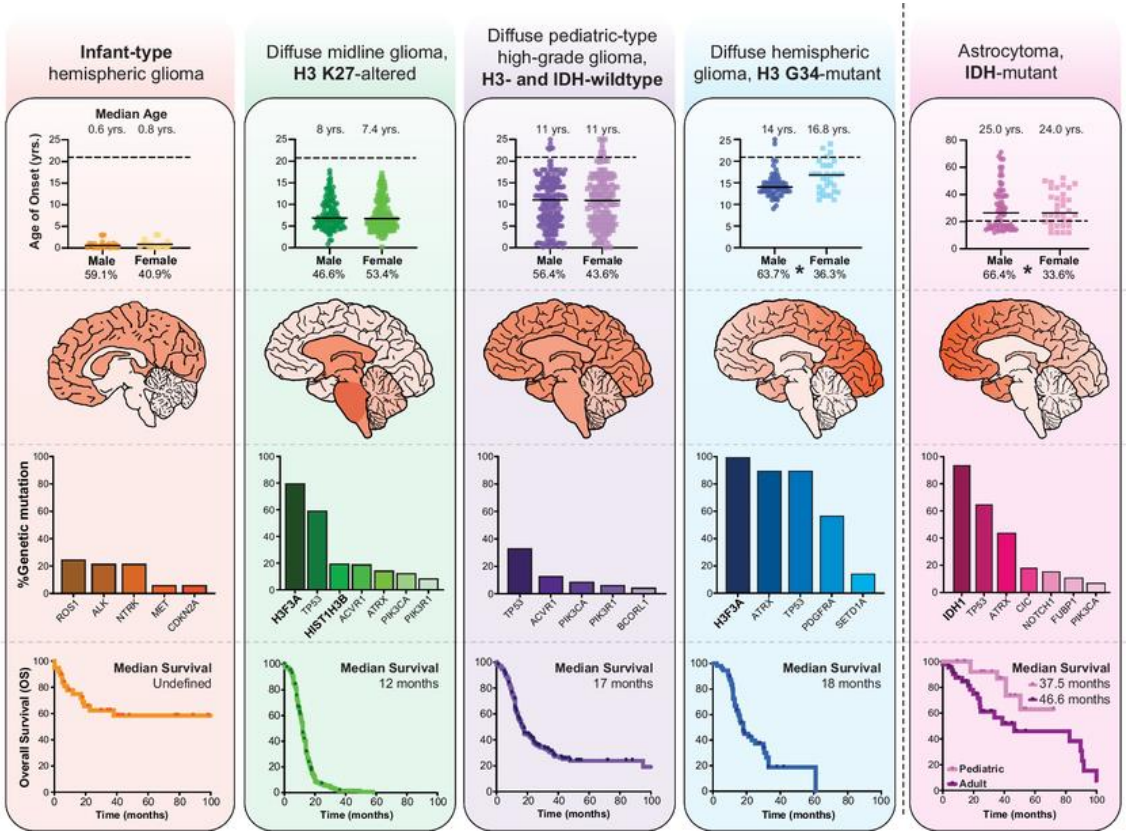
ATLAS-seq as a microfluidic single-cell TCR screen for antigen-reactive TCRs

Luo et al., *Nat. Commun*, 2025

MT1 Isoform Specific TCR Kills Melanoma Cells

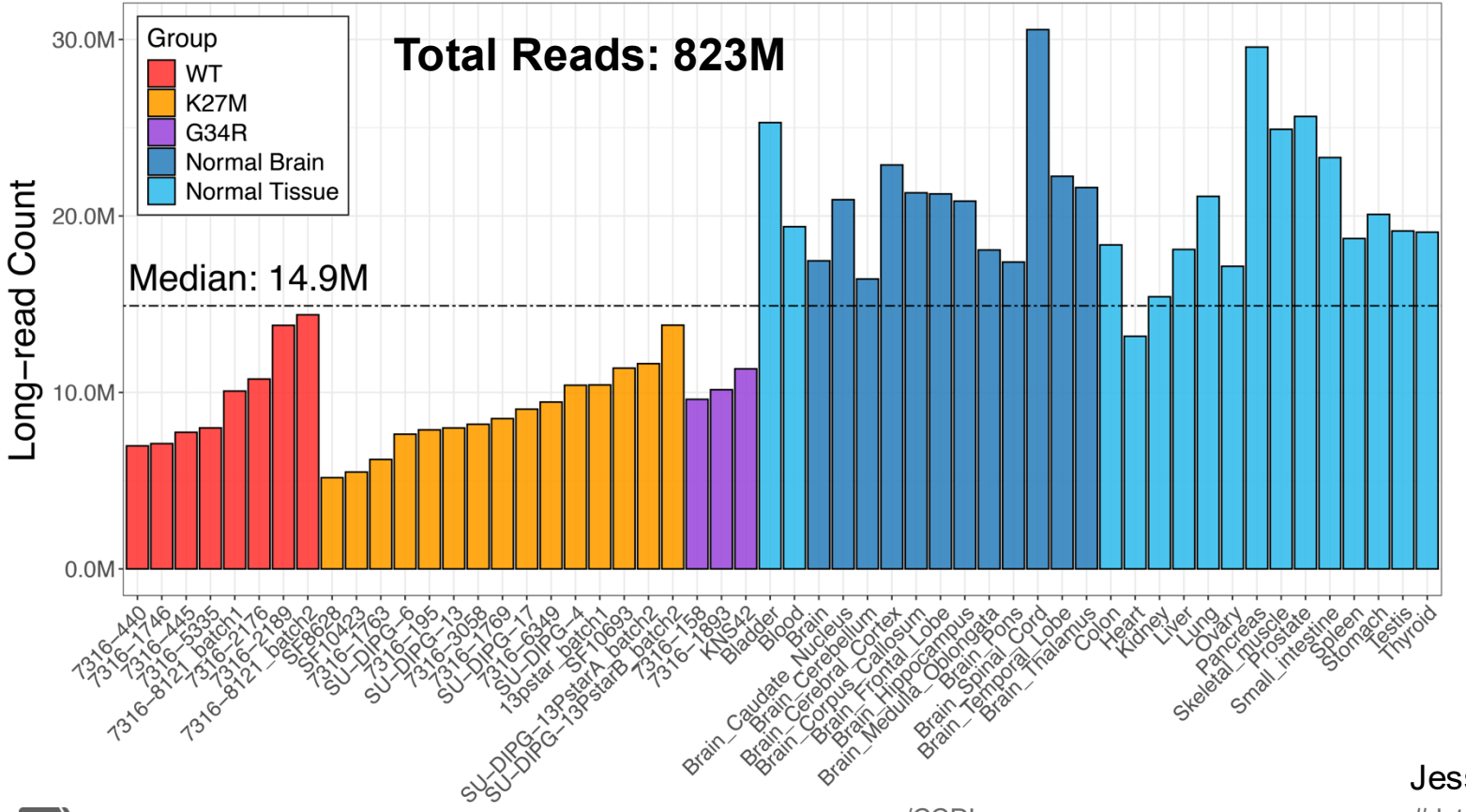


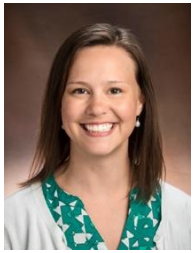
Pediatric High-Grade Gliomas Are Aggressive Brain and Spinal Cord Tumors



Ocasio, 2023

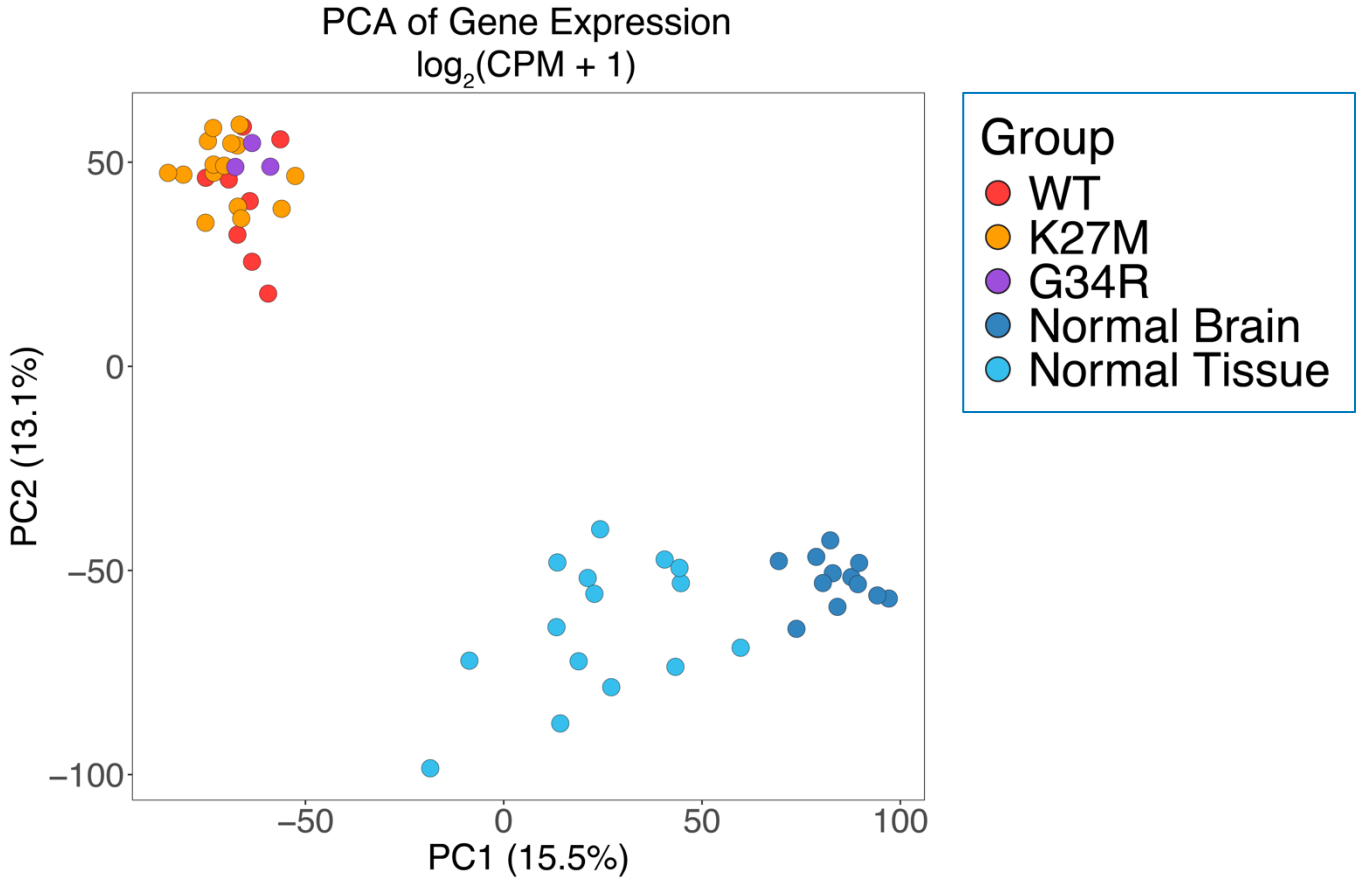
Long-Read RNA-seq of pHGG Subtypes and Diverse Normal Tissues



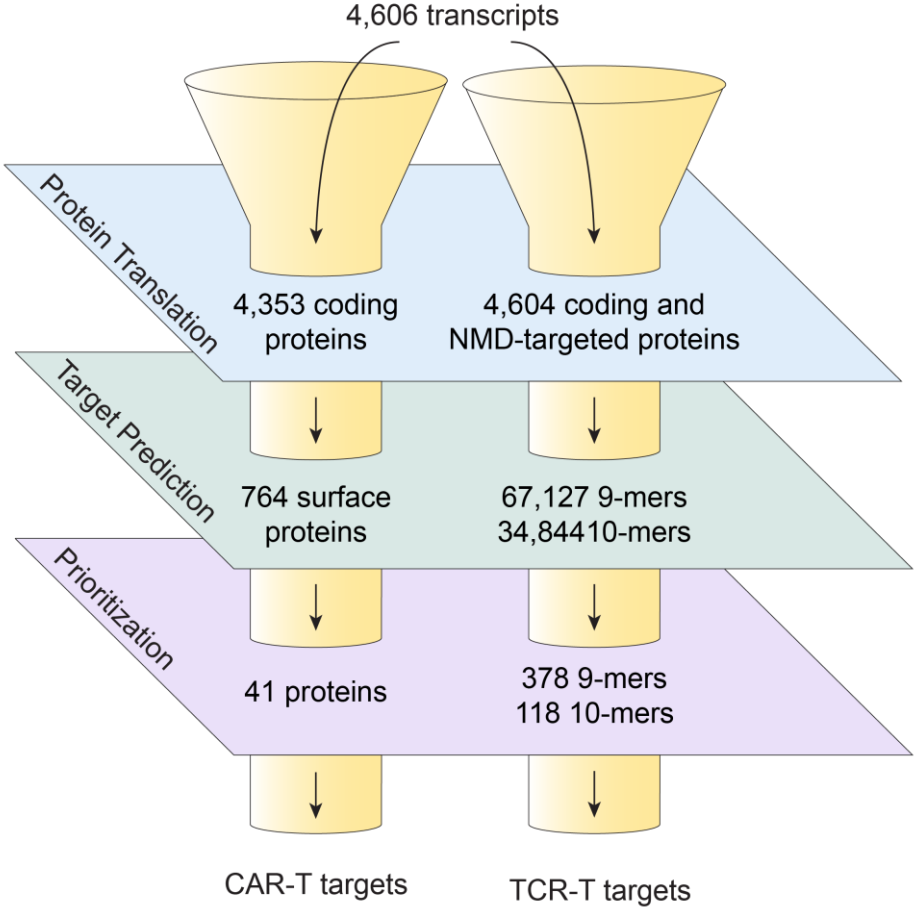


Jessica Foster (CHOP)

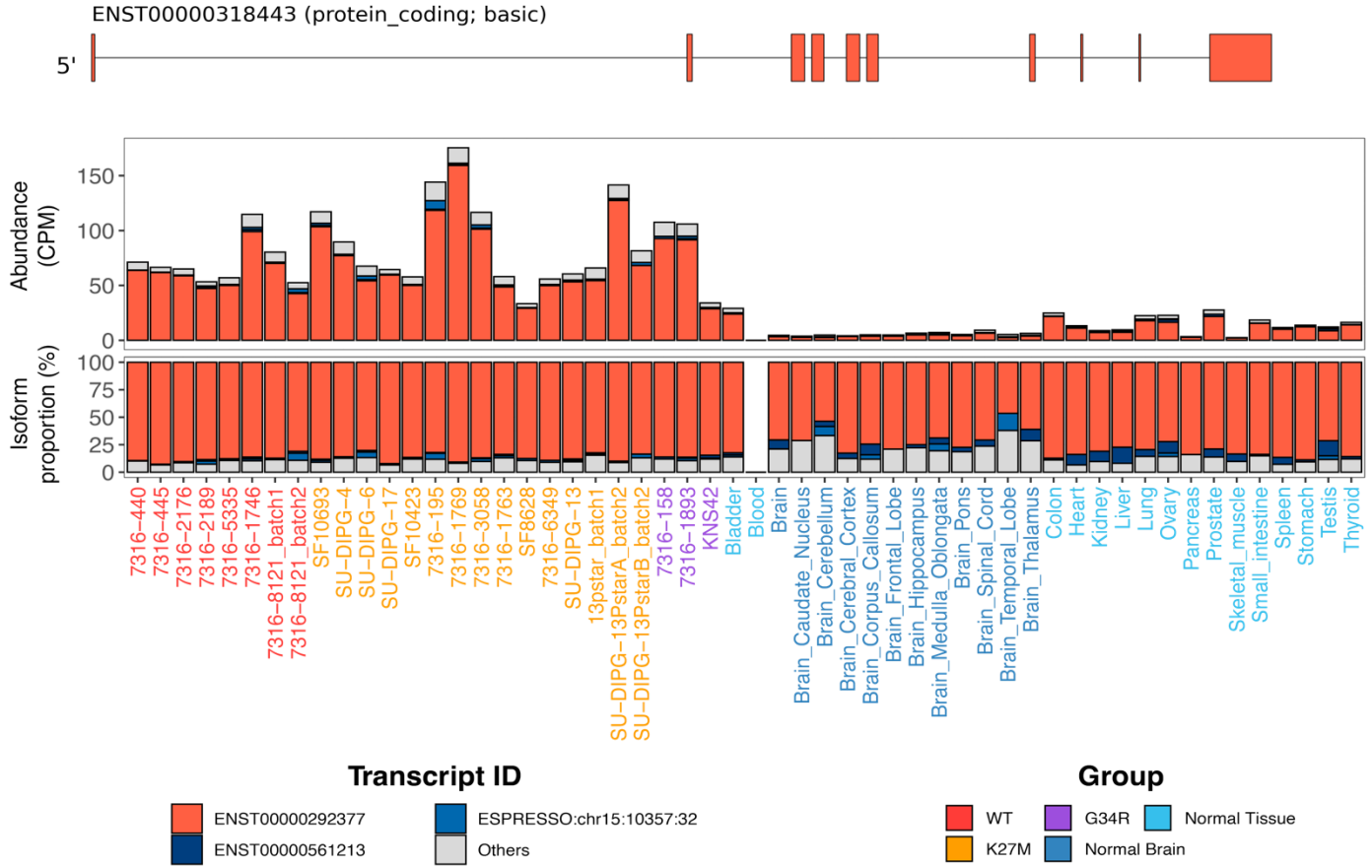
pHGG Samples Are Transcriptionally Distinct from Normal Tissues



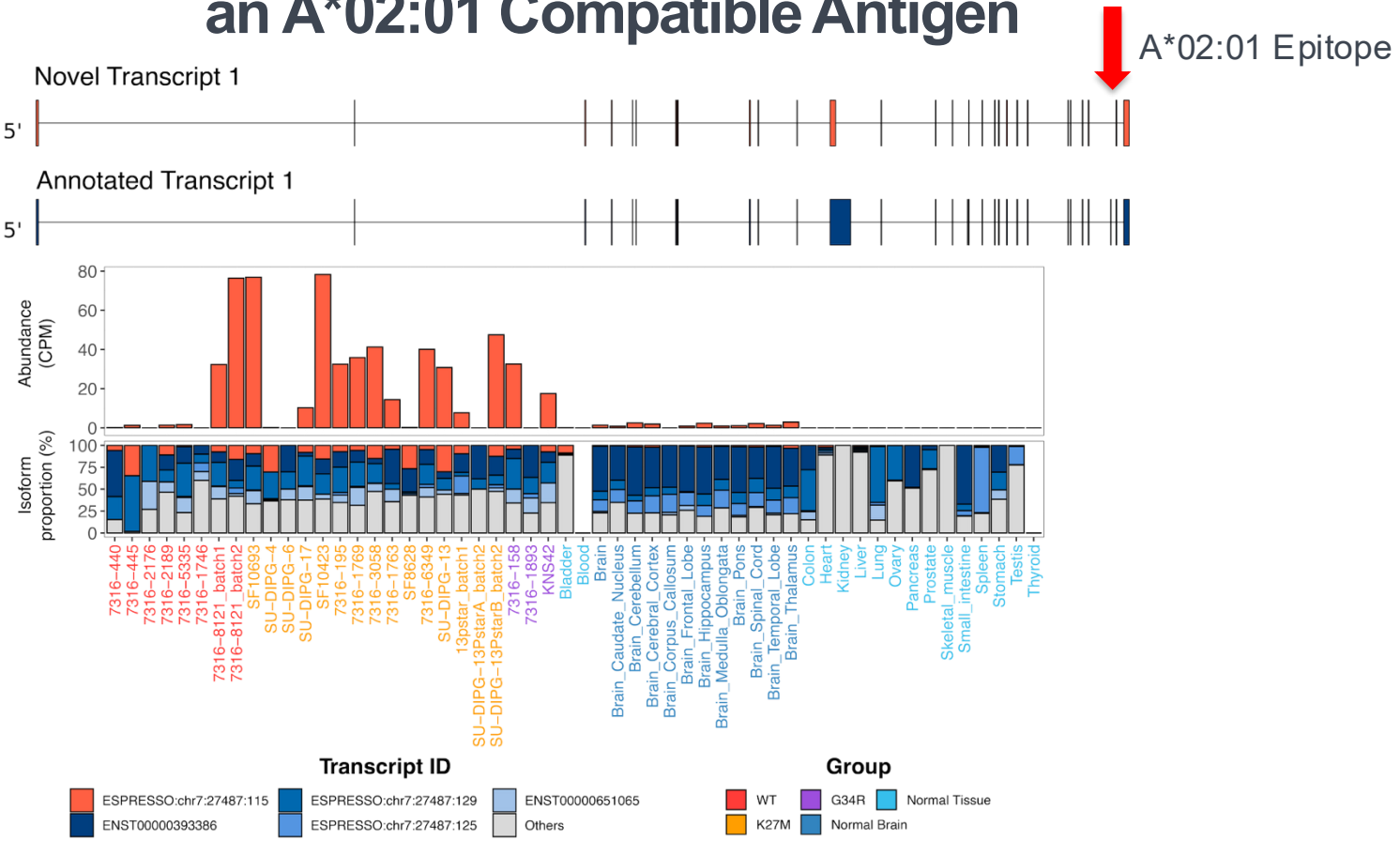
IRIS-long Identifies and Prioritizes pHGG CAR-T and TCR-T Targets



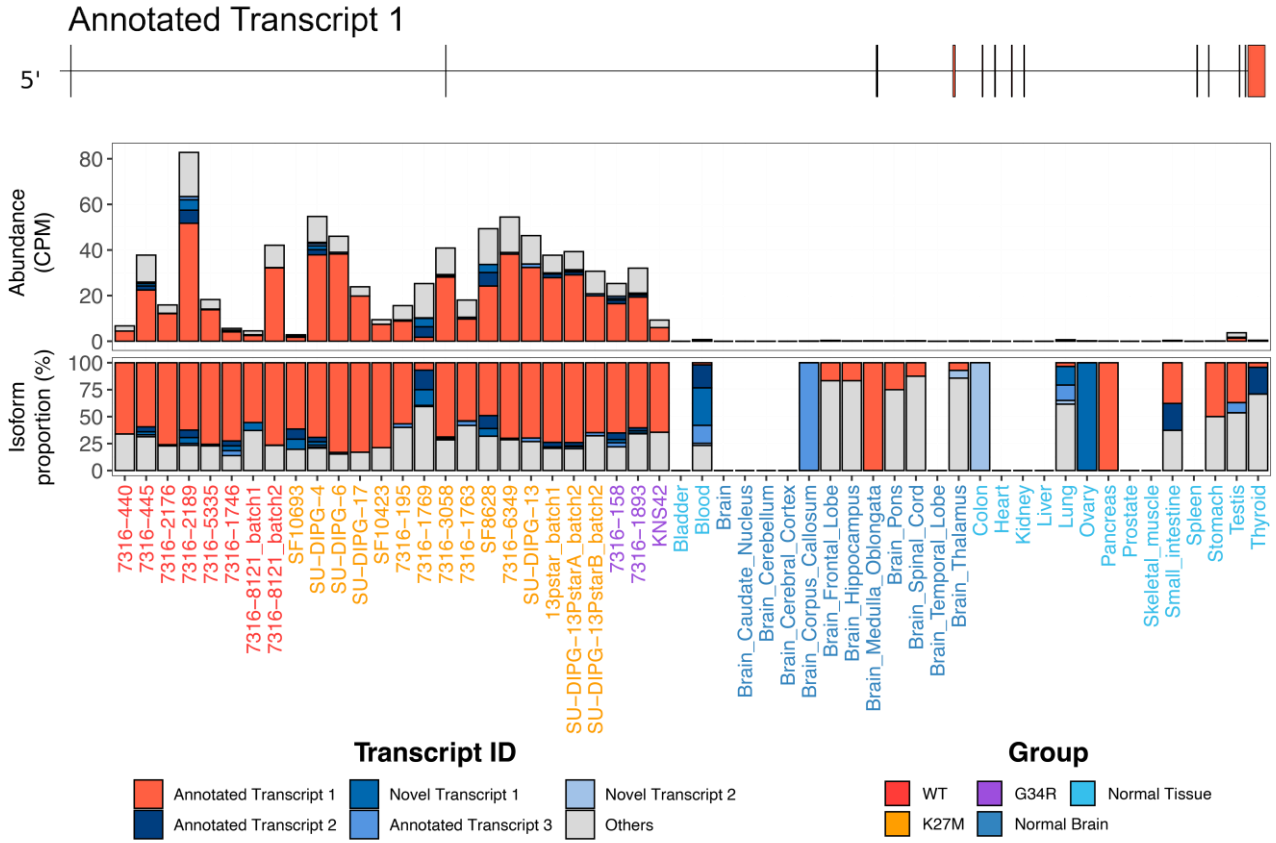
IRIS-long Recaptures B7-H3: A CAR-T Target in Clinical Trials



PGT1 Tumor-Specific Alternative Splicing Generates an A*02:01 Compatible Antigen

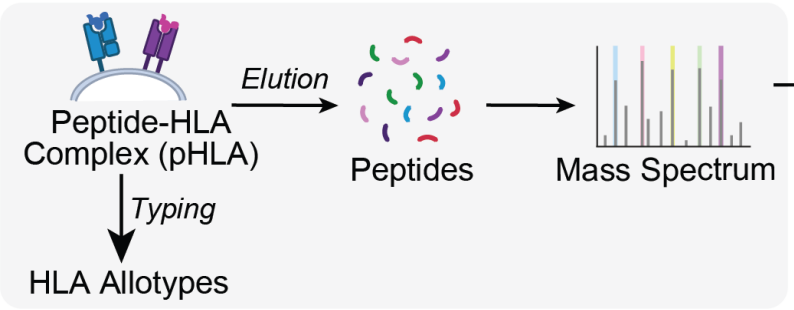


PGT2 Tumor-Specific Gene Expression Generates Multiple A*02:01 Compatible Antigens

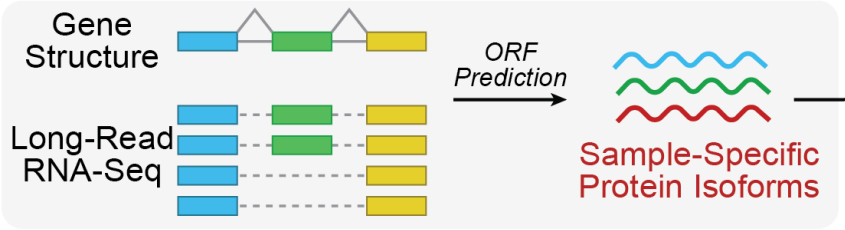


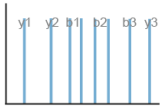
Long-Read RNA-seq Based Analysis of Immunopeptidomes

HLA Immunopeptidomics



Long-Read RNA-Seq Based Proteotranscriptomics Analysis





Match

Peptide Spectrum Matches (PSMs)

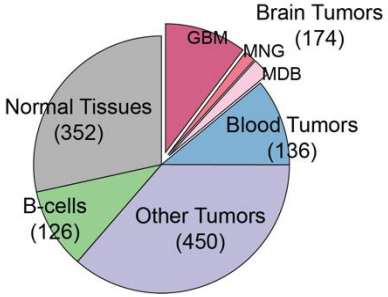
Post-Processing

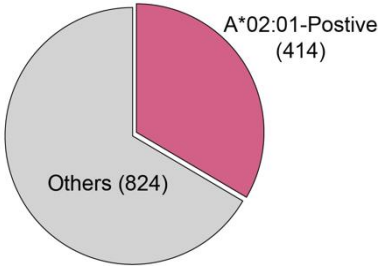
Peptides

Rigorous Filtering & Prioritization

Tumor Antigens (TAs)

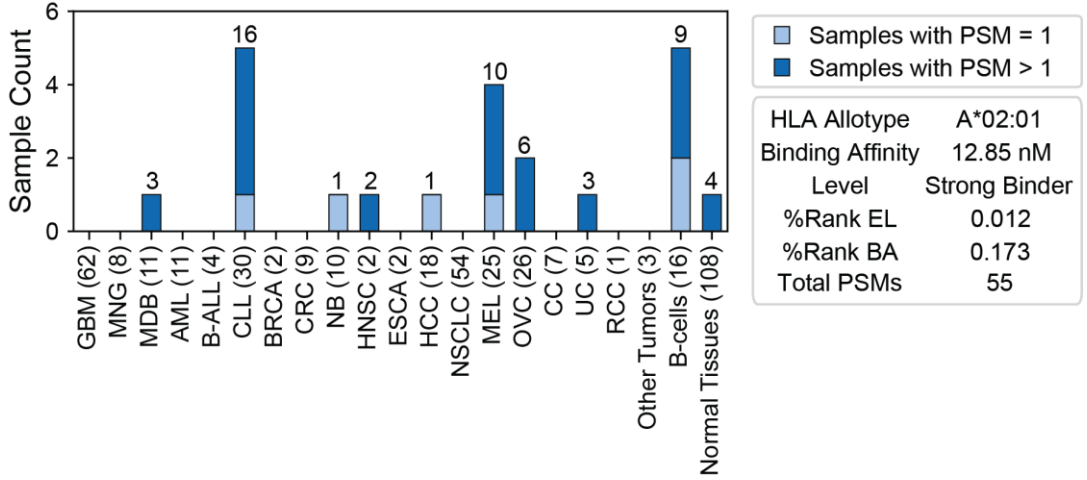
1,238 Samples
160.4 Million Mass Spectra



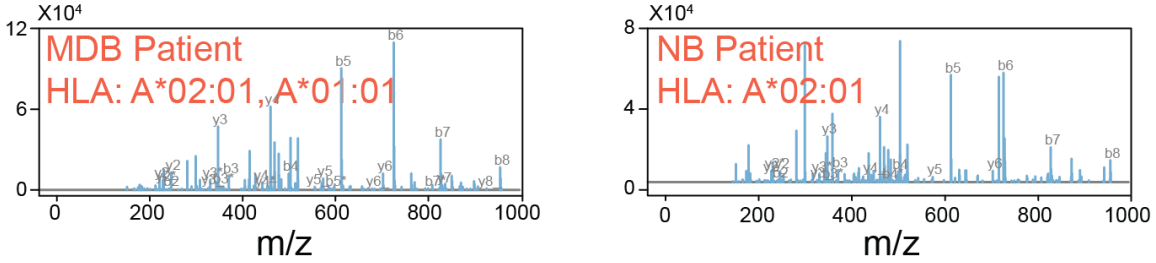


PGT2 A*02:01 Epitope Is Expressed Across Multiple Cancers

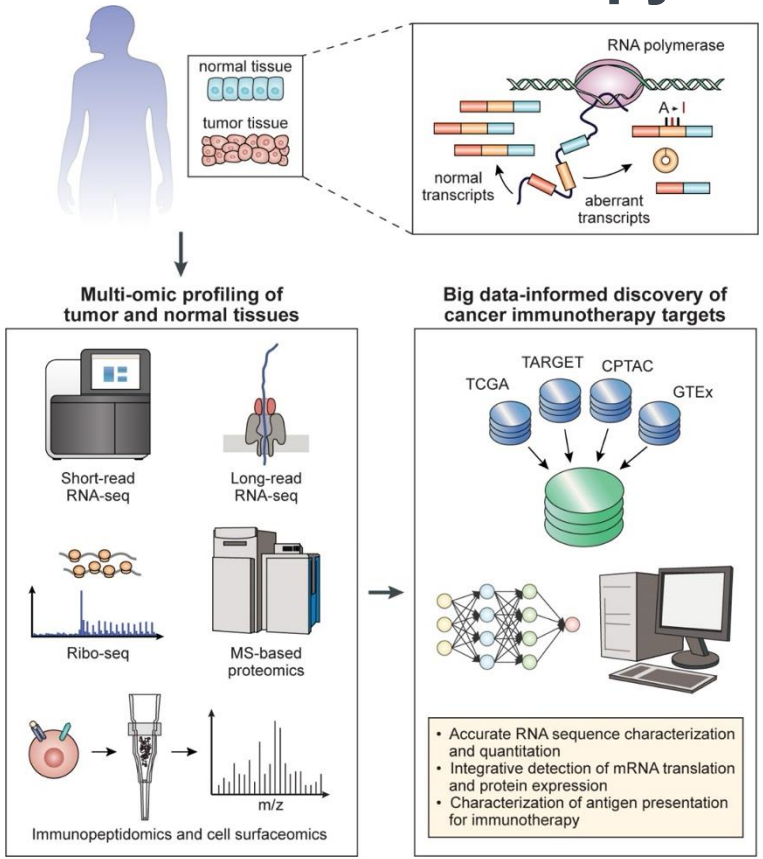
A*02:01 peptide of PGT2 in A*02:01-positive immunopeptidomes



Two experimental mass spectra matched to the A*02:01 peptide of PGT2



Multiomic and Big Data Strategies to Discover Immunotherapy Targets



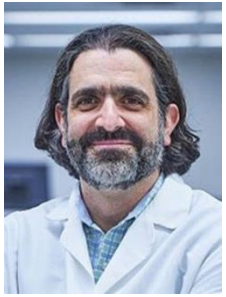
Pan et al., *Trends Pharmacol Sci*, 2021

Advanced Personalized Therapeutics and Precision Surgery Program for Childhood Cancers

Theodore Laetsch, M.D.

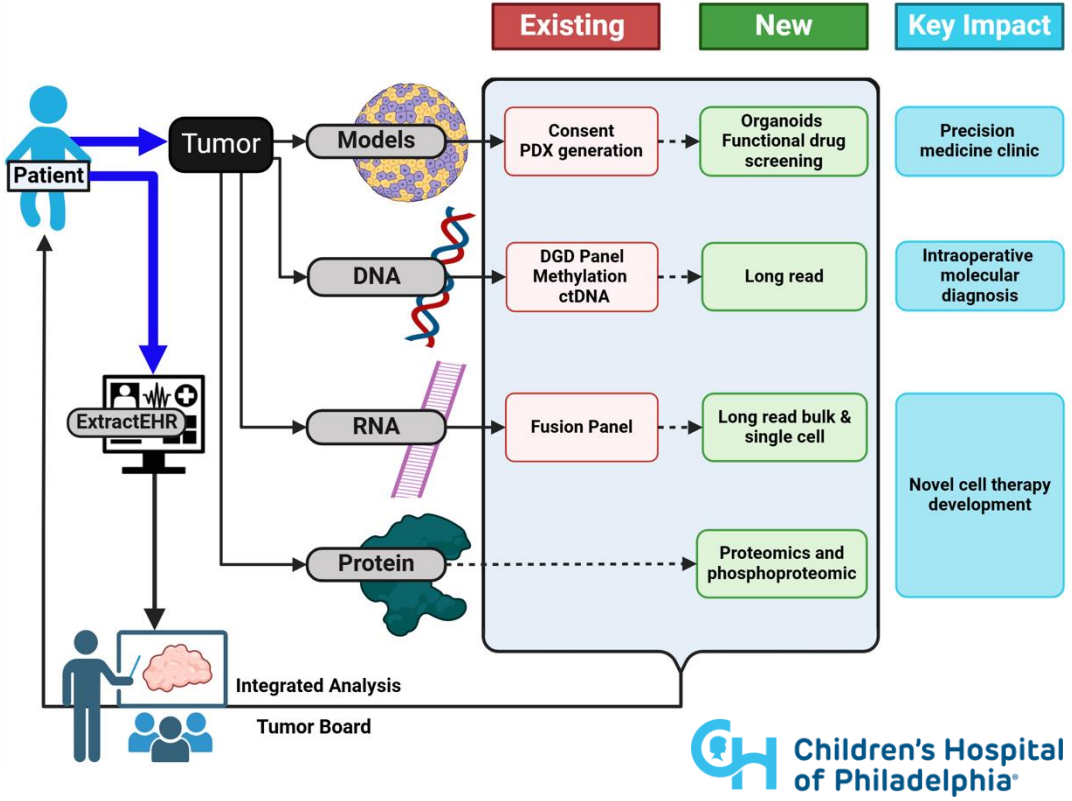
Marilyn Li, M.D., M.S.

Phillip Jay Storm, M.D.



Adam Resnick, Ph.D.

Yi Xing, Ph.D.



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Xing Lab

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Andrei Thomas-Tikhonenko
Theodore Laetsch
Song Liu
Carl June
Avery Posey
Owen Witte
Antoni Ribas
Sanaz Memarzadeh
Anthony Wang

Funding

CANCER MOONSHOT
IOTN Immuno-Oncology Translational Network
HuBMAP Human BioMolecular Atlas Program
National Cancer Institute
Prostate Cancer Foundation Curing Together.
CDMRP Department of Defense Congressionally Directed Medical Research Programs
CCDI Childhood Cancer Data Initiative
pennsylvania Department of Health

Q&A

Join Us For Our Upcoming Events!

Molecular Targeted Therapies Reveal Glioma Cell Plasticity Linked to Immune Evasion in BRAF-Mutant Brain Tumors

Tuesday, April 14 at 1:00–2:00 p.m. ET

CCDI Pediatric, Adolescent, and Young Adult Rare Cancer Study

Monday, April 27 at 12:00–1:00 p.m. ET

Learn more and register at **events.cancer.gov/ccdi/webinar**

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