

Publication List

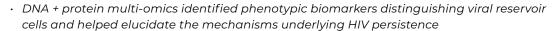


2023



Weiwei Sun et al. Nature (2023)

Phenotypic signatures of immune selection in HIV-1 reservoir cells





2022



J. Brett Heimlich et al. BioRxiv preprint (2022)

Mutated cells mediate distinct inflammatory responses in clonal hematopoiesis

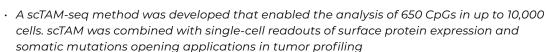


 Using mitochondrial lineage tracing, gene expression between mutated and non-mutated cells within individual clonal hematopoiesis patients was compared. It was found that mutated CH monocytes, but not non-mutated monocytes are pro-inflammatory, explaining why patients with larger CH clones have increased cardiovascular disease risk.



Bianchi A et al. Genome Biology (2022)

scTAM-seq enables targeted high-confidence analysis of DNA methylation in single cells









TaeHyung Kim et al. British Society of Haematology (2022)

Single cell proteogenomic sequencing identifies a relapse-fated AML subclone carrying FLT3-ITD with CN-LOH at chrl3q



· ScPGseq not only enabled the early detection of rare relapse-fated subclone showing immature myeloid signature but also highlighted the presence of homozygous 21 bp FLT3-ITDs in the clone at presentation.





Troy T. Robinson et al. et al., BioRxiv preprint

Single cell genotypic and phenotypic analysis of measurable residual disease in acute myeloid leukemia



· Developed a scMRD assay with a sensitivity of 10-4 (10 times better than current flow MRD), resolved clonal architecture, and provides clone-specific immunophenotype.





Felix Sahm et al. Acta Neuropathologica (2022)

Single-cell DNA sequencing reveals order of mutational acquisition in TRAF7/AKT1 and TRAF7/KLF4 mutant meningiomas



· Uncovered the order of mutational acquisition in TRAF7/AKT1 and TRAF7/KLF4 mutant meningiomas which bulk failed to resolve





Moritz Binder et al. BioRxiv preprint

Enhancer deregulation in TET2 Mutant Clonal Hematopoiesis is associated with increased COVID-19 related inflammation severity and mortality



· Sc-proteogenomic analysis revealed that mutations in TET2 promote amplification of proinflammatory classical and intermediate monocyte subsets.





Samuel W. Brady et al. Nature Genetics (2022)

The genomic landscape of pediatric acute lymphoblastic leukemia



· Characterized the clonal architecture and evolution in acute lymphoblastic leukemia









Ferran Nadeu et al. Nature Medicine (2022)

Detection of early seeding of Richter transformation in chronic lymphocytic leukemia



· Sc-DNA seq detected rare sublones at time of CLL diagnosis which were dormant for 6-19 years until rapid expansion at transformation





Bowman RL et al., BioRxiv preprint

Modeling clonal evolution and oncogenic dependency in vivo in the context of hematopoietic transformation



· Used DNA + protein multi-omics to gain insights into the mutant-specific alterations involved in leukemic transformation from premalignant clonal hematopoiesis to AML





Guess, T. et al., Blood Cancer Discovery

Distinct patterns of clonal evolution drive myelodysplastic syndrome progression to secondary acute myeloid leukemia



· Used DNA + protein multi-omics to characterize the clonal architecture and evolution in MDS patients who progress to sAML.





Droskea, L. et al., BioRxiv preprint

High-throughput single-cell sequencing for retroviral reservoir characterization



· Described a scDNA-seg method optimized for sequencing of proviral and host DNA for retroviral reservoir characterization.





Bianchi, A. et al., BioRxiv preprint

scTAM-seq enables targeted high-confidence analysis of DNA methylation in single cells



· Developed scTAM-seq, a targeted bisulfite-free method for analyzing DNA methylation at single-CpG resolution across thousands of single cells.







Maslah, N. et al., Blood Advances

Single-cell analysis reveals selection of TP53-mutated clones after MDM2 inhibition



· Demonstrated that MDM2 treatment can directly favor the emergence of TP53-mutated subclones in chronic myeloproliferative neoplasms (MPN).







Meyers, S. et al., HemaSphere

Monitoring of Leukemia Clones in B-cell Acute Lymphoblastic Leukemia at Diagnosis and During Treatment by Single-cell DNA Amplicon Sequencing



· Characterized the mutational heterogeneity and evolution in B-ALL, both at diagnosis and during treatment.







Thang, H. et al., BioRxiv preprint

Application of high-throughput, high-depth, targeted single-nucleus DNA sequencing in pancreatic cancer



· Optimized a highly automated nuclei extraction workflow that achieved fast and reliable targeted single-nucleus DNA library preps from pancreatic adenocarcinoma (PDAC) patients

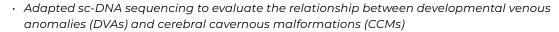




Snellings, D.A. et al., Nature Cardiovascular Research

Developmental Venous Anomalies are a Genetic Primer for Cerebral Cavernous Malformations









🔆 🎖 📩 Leighton, J. et al., BioRxiv preprint

Reconstructing mutational lineages in breast cancer by multi-patient targeted single cell DNA sequencing



· Developed a Multi-Patient-Targeted (MPT) scDNA-sequencing method to study tumor evolution in breast cancer







Kim, T. et al., British Society for Hematology

Single cell proteogenomic sequencing identifies a relapse-fated AML subclone carrying FLT3-ITD with CN-LOH at chrl3q



· Used DNA + protein multi-omics to detect a relapse-fated subclone at the time of initial diagnosis that was enriched with homozygous 21 bp FLT3-ITDs.







Blombery, P E. et al., Blood

Clonal hematopoiesis, myeloid disorders and BAX-mutated myelopoiesis in patients receiving venetoclax for CLL



· Sc-DNA sequencing revealed patterns of co-occuring BAX mutations in the myeloid compartments of CLL patients receiving venetoclax therapy







Wang, E. et al., The New England Journal of Medicine

Mechanisms of Resistance to Noncovalent Bruton's Tyrosine Kinase Inhibitors. The New England Journal of Medicine



· Identified clonal architecture of resistance mutations to a new class of non-covalent BTK inhibitors in CLL patients



2022 cont.





Zhang, Q. et al., Signal Transduction and Target Therapy

Activation of RAS/MAPK pathway confers MCL-1 mediated acquired resistance to BCL-2 inhibitor venetoclax in acute myeloid leukemia



· Identified the activation of RAS/MAPK pathway, leading to increased stability and higher levels of MCL-1 protein, as a major acquired mechanism of VEN resistance in AML.





Rodriguez, S. et al., Science Advances

Preneoplastic somatic mutations including MYD88 L265P in lymphoplasmacytic lymphoma



· DNA + protein multi-omics demonstrated that mutation in a gene relevant to B cell function, such as MYD88, represents a preneoplastic event that requires additional genetic alterations to drive lymphomagenesis

2021





Thompson E.R. et al., Blood Advances

Single-cell sequencing demonstrates complex resistance landscape in CLL and MCL treated with BTK and BCL2 inhibitors



· Identified clonal architecture of acquired genomic resistance to BTK and BCL2 inhibitors in CLL and MCL patients.





Zhao Y. et al., Nature

Diverse alterations associated with resistance to KRAS(G12C) inhibition



· Revealed a heterogeneous pattern of resistance involving many genes and multiple subclonal events emerging during KRAS (G12C) inhibitor treatment for lung and colorectal cancer.





Sharma R. et al., Blood

Gain-of-function mutations in RPA1 cause a syndrome with short telomeres and somatic genetic rescue



· Single-cell DNA+protein multi-omics revealed somatic genetic rescue events that evolved independently in HSPCs, myeloid cells, and B-cells in patients with telomere disorders.





Sahoo S.S. et al., Nature Medicine

Clinical evolution, genetic landscape, and trajectories of clonal hematopoiesis in SAMD9/SAMD9L syndromes



· Uncovered diversity of somatic genetic rescue events in pediatric instances of SAMD9/9L syndromes, some of which serve as "natural gene therapy."







Dillon L.W. et al., Blood Cancer Discovery

Personalized single-cell proteogenomics to distinguish acute myeloid leukemia from nonmalignant clonal hematopoiesis



· Distinguished malignant variants of AML from age-related clonal hematopoiesis by resolving immunophenotypic identity of clonal architecture.





Marin-Bejar, O. et al., Cancer Cell

Evolutionary predictability of genetic versus nongenetic resistance to anticancer drugs in melanoma



· An analysis of genetic and nongenetic mechanisms of therapy resistance in melanoma.





Thijssen, R. et al., Blood

Intact TP-53 function is essential for sustaining durable responses to BH3-mimetic drugs in leukemias



· Revealed the effect of TP-53 mutation status on treatment of AML with the BH3-mimetic drugs.





Wang, F. et al., Nature Communications

Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia



· Investigated clones that enabled relapse in AML patients who received IDH inhibitor treatment.





Ren, A. et al., Nature

PIK3CA and CCM mutations fuel cavernomas through a cancer-like mechanism



· Single-nuclei sequencing revealed patters of co-mutation that promote cerebral cavernous malformations (CCMs).







Lim, K.H. et al., Blood Advances

Clonal evolution and heterogeneity in advanced systemic mastocytosis revealed by single-cell DNA sequencing



· Investigation of resistance to the multikinase inhibitor, midostaurin, in patients with advanced systemic mastocytosis (advSM).









Demaree, B. et al., Nature Communications

Joint profiling of DNA and proteins in single cells to dissect genotype-phenotype associations in leukemia



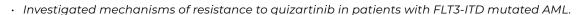
· Genotype & immunophenotype "decoupling" in leukemias samples was revealed using single-cell multi-omics.





Peretz, C.A. et al., Blood Advances

Single cell DNA sequencing reveals complex mechanisms of resistance to quizartinib









Ilacobucci, I. et al., Blood

Modeling and targeting of erythroleukemia by hematopoietic genome editing

· Used scDNA-seq analyze CRISPR-edited cells in preclinical models of acute erythroid leukemia (AEL).







Kennedy, A.L. et al., Nature Communications

Distinct genetic pathways define pre-malignant versus compensatory clonal hematopoiesis in Shwachman-Diamond syndrome



· Zygosity and CN-LOH are reliably measured with high sensitivity (0.1%) and predict progression to leukemia in patients with Shwachman-Diamond syndrome.







Alberti-Servera, L. et al., Blood

Single-cell DNA amplicon sequencing reveals clonal heterogeneity and evolution in T-cell acute lymphoblastic leukemia



· First study to assess the clonality and order of mutation acquisition of T-cell acute lymphoblastic leukemia (T-ALL) patient samples.





Patel, B.A. et al., Haematologica

Detectable mutations precede late myeloid neoplasmia in aplastic anemia



· Identified evolution of mutations in a rare case where an severe aplastic anemia (SAA) patient who received immunosuppressive therapy developed MDS/AML with normal cytogenetics.





Thompson E.R. et al., Haematologica

Clonal independence of JAK2 and CALR or MPL mutations in comutated myeloproliferative neoplasms demonstrated by single cell DNA sequencing



· First publication in T-cell acute lymphoblastic leukemia (T-ALL) that highlights SNVs/indels and MRD detection.





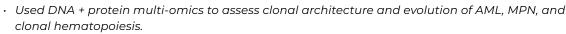






Miles, L.A. et al., Nature

Single-cell mutation analysis of clonal evolution in myeloid malignancies



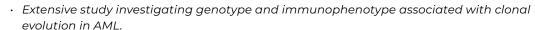






● Morita, K. et al., Nature Communications

Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics











Ten Hacken, E. et al., Genome Biology

High throughput single-cell detection of multiplex CRISPR-edited gene modifications

· Analyzed single and multiplexed CRISPR edits in individual cells in models of chronic lymphocytic leukemia (CLL).







Xiao, W. et al., Blood Advances

A JAK2/IDH1-mutant MPN clone unmasked by ivosidenib in an AML patient without antecedent MPN



· Clonal architecture of a relapsed AML patient, in which treatment with an IDH1 inhibitor promoted outgrowth of a minor myeloid neoplasm (MPN) clone.





Taylor, J. et al., Blood

Single-cell genomics reveals the genetic and molecular bases for escape from mutational epistasis in myeloid neoplasms



· Studied a rare phenomenon in biology where 2 splicing mutations co-occur in the patient sample.





Maia, C. et al., Blood

Biological and clinical significance of dysplastic hematopoiesis in patients with newly-diagnosed multiple myeloma



 Identified biomarkers from multiple myeloma samples that develop into MDS using multidimensional flow cytometry and single-cell DNA-seq.





Choe, S. et al., Blood Advances

Molecular mechanisms mediating relapse following ivosidenib monotherapy in IDH1-mutant relapsed or refractory AML



· Biopharma study that showed molecular resistance mechanisms in 174 patients following ivosidenib monotherapy for R/R AML.







2020 cont.





DiNardo, C.D. et al., Blood

Molecular patterns of response and treatment failure after frontline venetoclax combinations in older patients with AML



· Molecular basis for treatment resistance or durable remission in older patients with AML given venetoclax combination therapy.





Ediriwickrema, A. et al., Blood Advances

Single-cell mutational profiling enhances the clinical evaluation of AML MRD



· MRD detection identified clones at remission that expanded into the dominant clone at relapse in patients with AML.

2019





Xu, L. et al., Scientific Reports

Clonal evolution and changes in two AML patients detected with a novel single-cell DNA sequencing platform



· Clonal remodeling in patients with AML after bone marrow transplant revealed donor chimerism and unique clones.





Gao, Y. et al., Cancer Discovery

V211D mutation in MEK1 causes resistance to MEK inhibitors in colon cancer



· Treatment resistance mechanism revealed in colon cancer PDX model after treatment with MEK inhibitor binimetinib and EGFR antibody panitumumab.







McMahon, C. et al., Cancer Discovery

Clonal selection with Ras pathway activation mediates secondary clinical resistance to selective FLT3 inhibition in acute myeloid leukemia



· Treatment resistance mechanism revealed in AML with co-occurring FLT3 and RAS mutations after treatment with the FLT3-inhibitor gilteritin in patients with AML.

2018







Pellegrino, M. et al., Genome Research

High-throughput single-cell DNA sequencing of acute myeloid leukemia tumors with droplet microfluidics



· First publication that showcased single-cell DNA sequencing of thousands of cells using droplets in longitudinal AML sample.





