

Immune profiling of the tumor microenvironment in classic Hodgkin's lymphoma using high-complexity mass cytometry

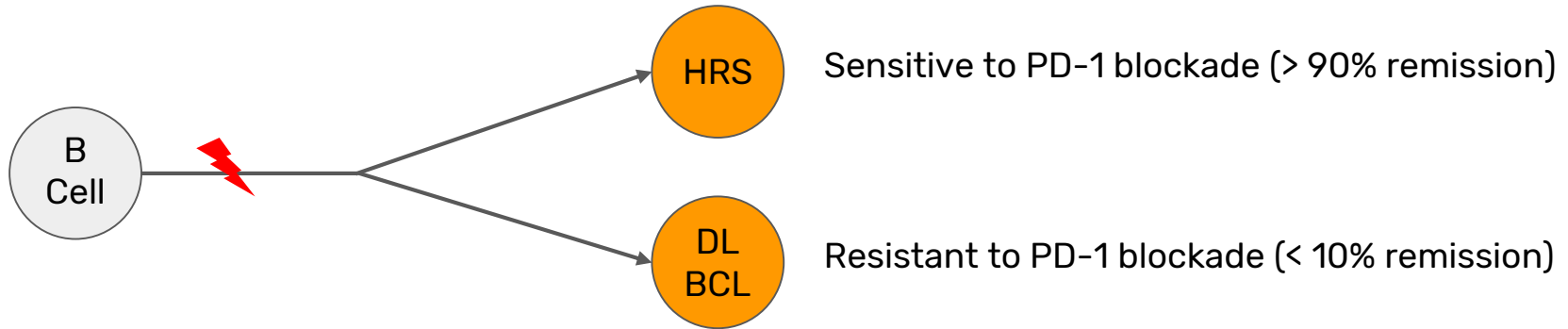
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² Astrolabe Diagnostics, Inc.

Classic Hodgkin's Lymphoma (cHL)

- Cancer cells are Hodgkin Reed-Sternberg (HRS) cells
 - Abnormal B lymphocytes
 - Commonly overexpress PD-1 ligands



- Few malignant HRS cells surrounded by a rich immune infiltrate
- High numbers of CD8+ T cells is associated with better outcome

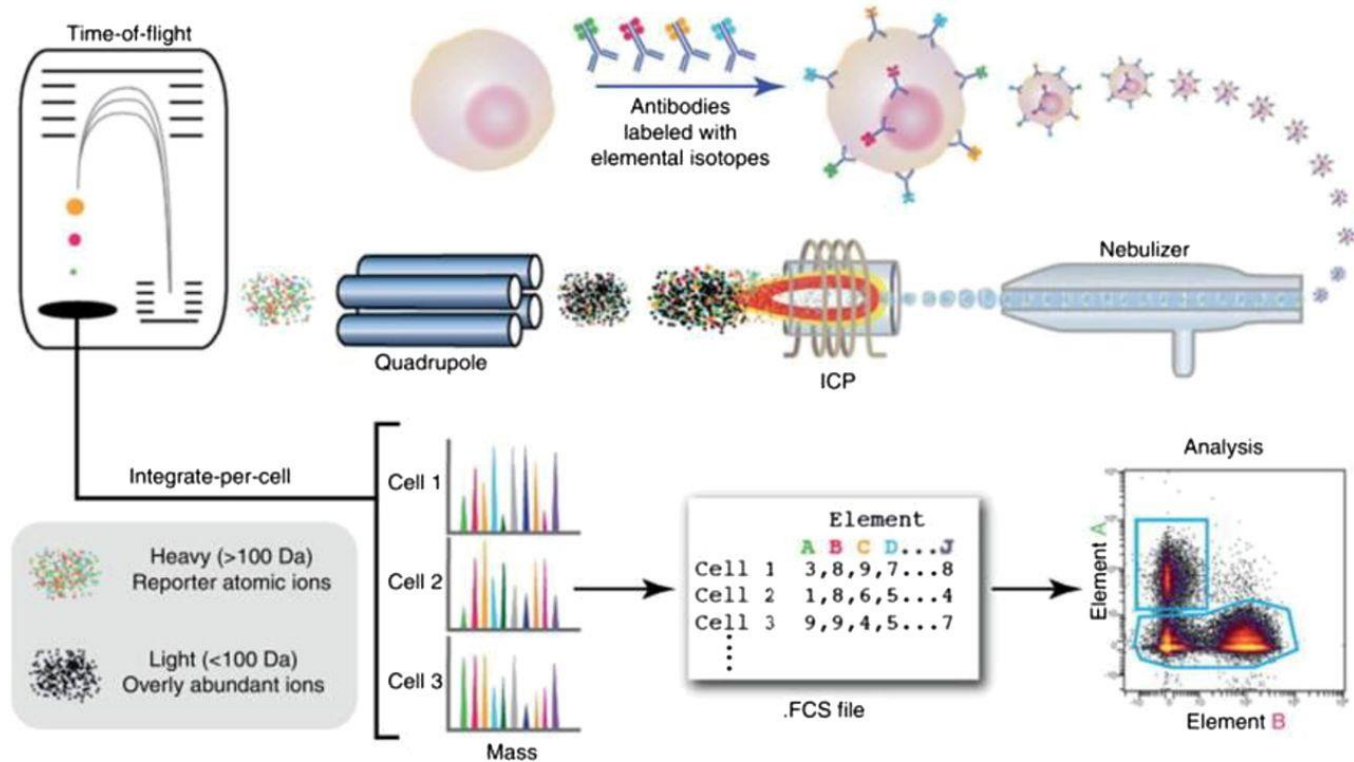
Understanding the immune system is critical
for better treatment of cHL

- Biomarker with prognostic value
- Clinical significance as a therapeutic target

Immune Profiling

- Identifying and quantifying immune populations according to their phenotypic and functional features
- Complex and heterogeneous biological system
 - 50+ known immune subsets (just in circulating blood!)
 - Our knowledge of biological complexity of different populations continues to grow

Mass Cytometry (CyTOF)

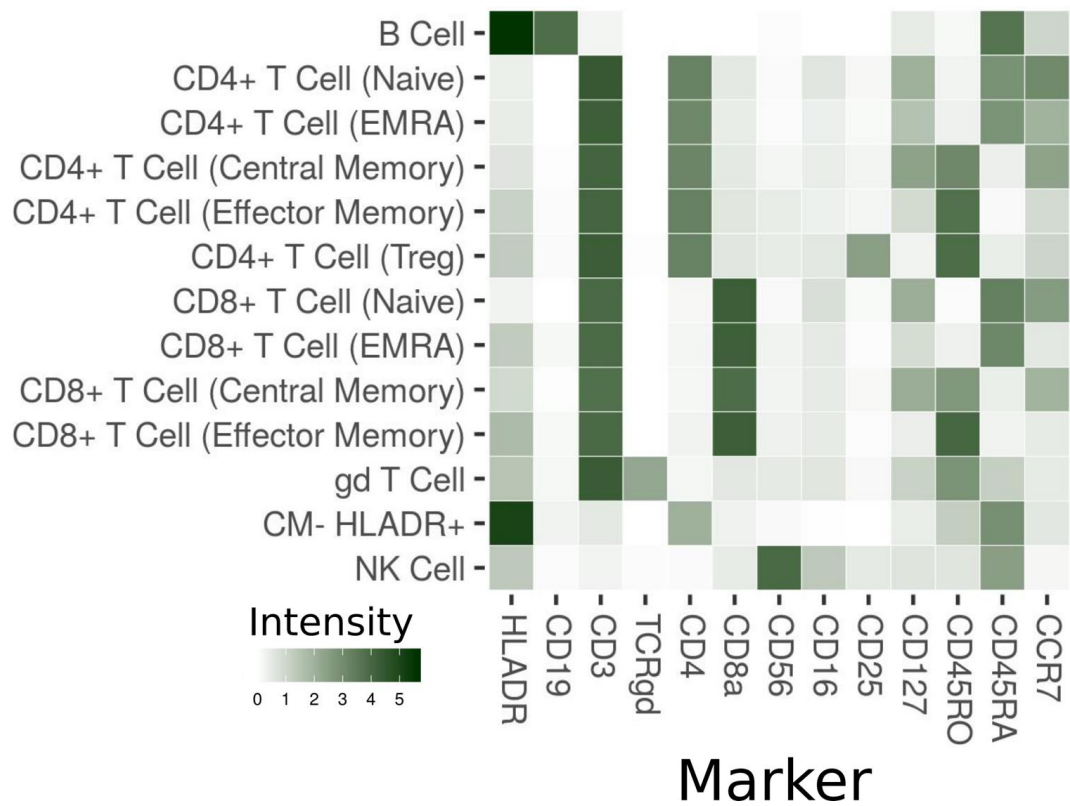


Qualitative/Exploratory Experiment Design

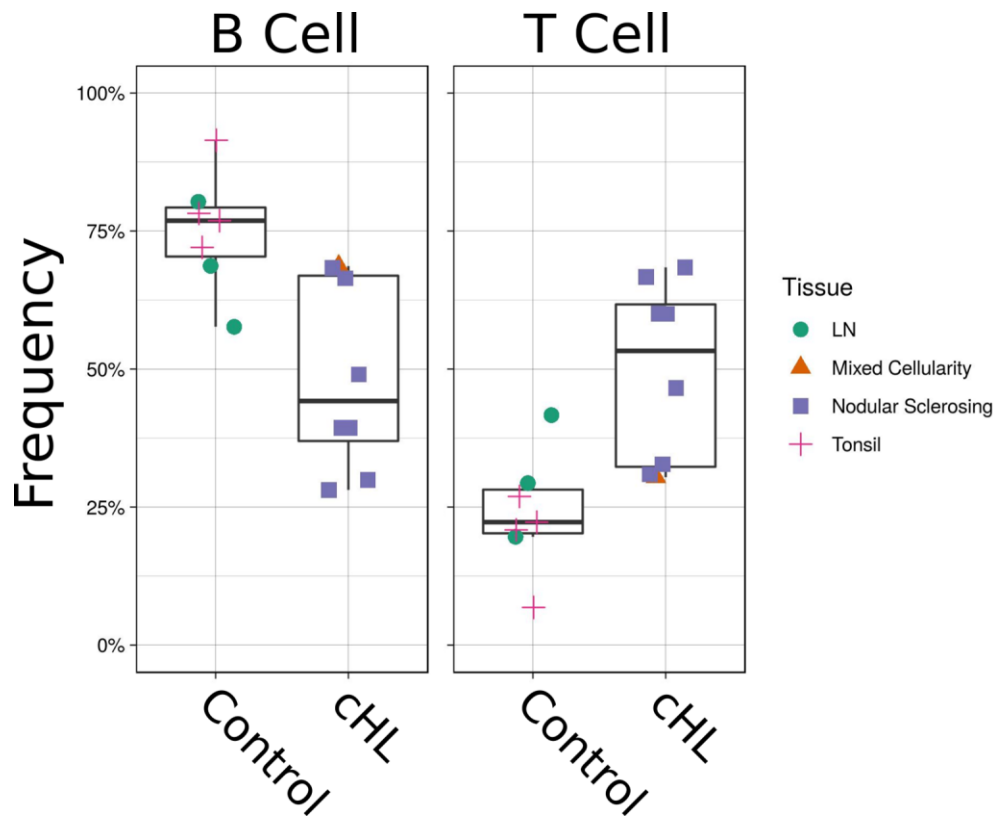
- 8 patient LN samples (7 nodular sclerosing, 1 mixed cellularity)
- 7 donor samples (3 LNs, 4 tonsil)
- Commercial analysis solution (Astrolabe Cytometry Platform)

<u>31 markers</u>			<u>15 major compartments</u>	<u>Additional resolution</u>
CCR4	CD27	ICOS	B Cell	Unsupervised clustering identified 43 unique clusters
CCR5	CD28	LAG3	CD4+ T Cell	
CCR6	CD44	PD1	CD8+ T Cell	
CCR7	CD45	TCRgd	NK Cell (CD56hi CD16-)	Manual exploration of PD1, ICOS, LAG3, and TIM3
CD3	CD45RA	TIM3	NK Cell (CD56mid CD16+)	
CD4	CD45RO		NKT Cell	
CD5	CD56		Lin- (Myeloids)	
CD7	CD69			
CD8a	CD127		<u>Within the T Cells</u>	
CD11a	CD161		CD4+ T Cell: Treg (memory/naive),	
CD16	CXCR3		Memory (Central/Effector), Naive,	
CD19	CXCR5		EMRA	
CD25	HLADR		CD8+ T Cell: Memory (Central/Effector),	
			Naive, EMRA	

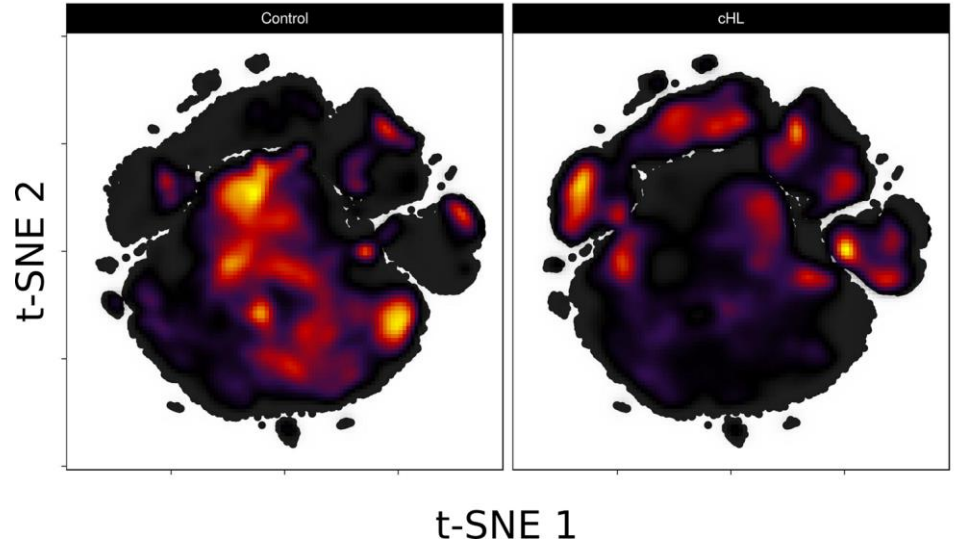
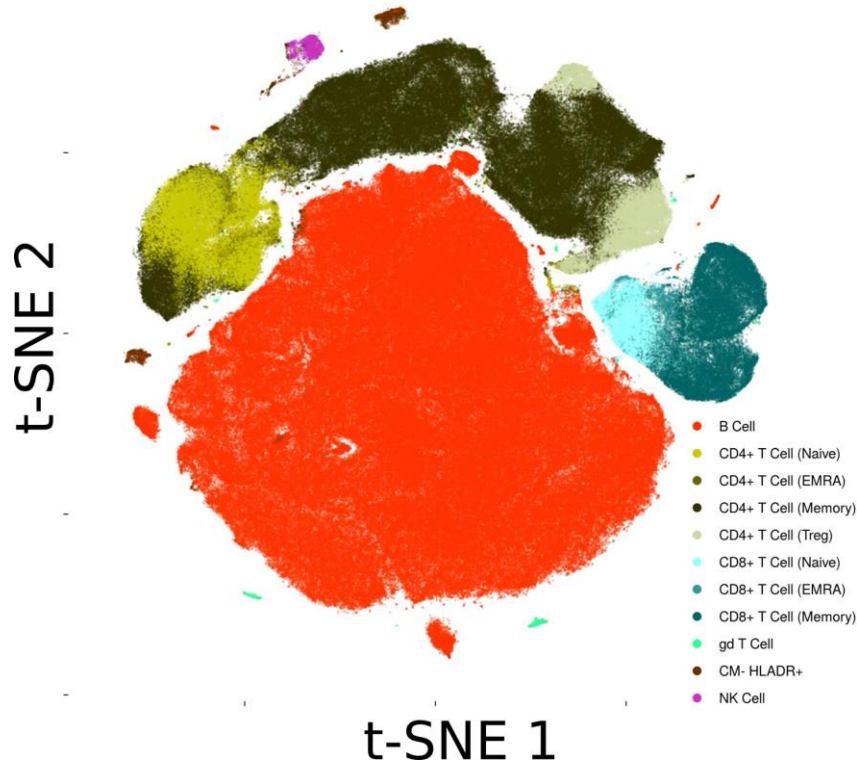
CyTOF Identifies Canonical Subsets



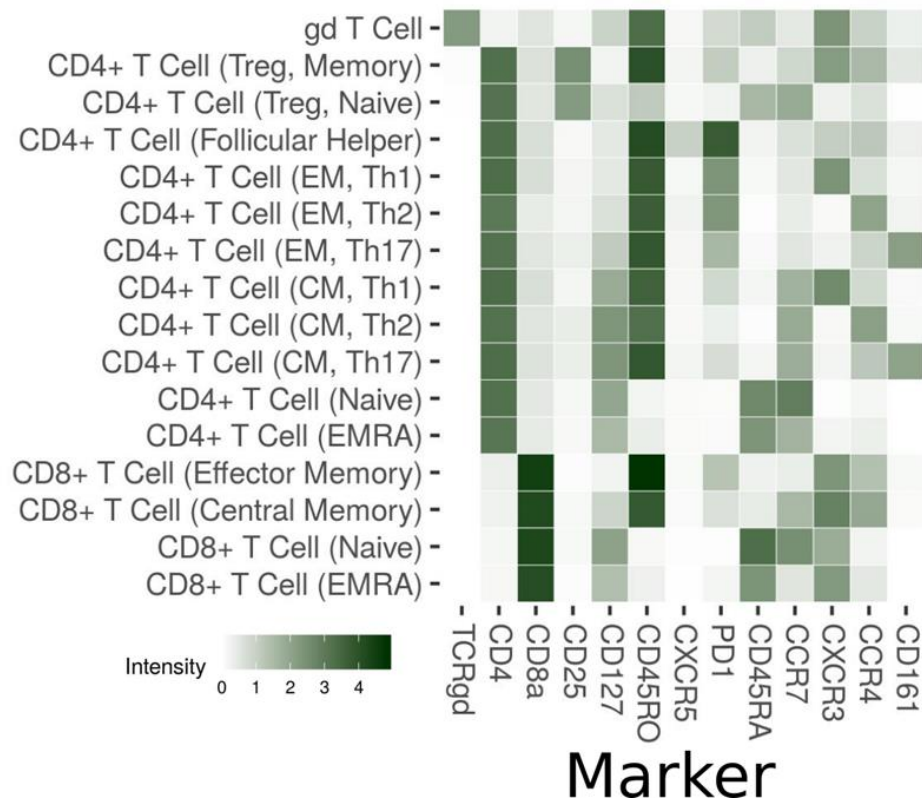
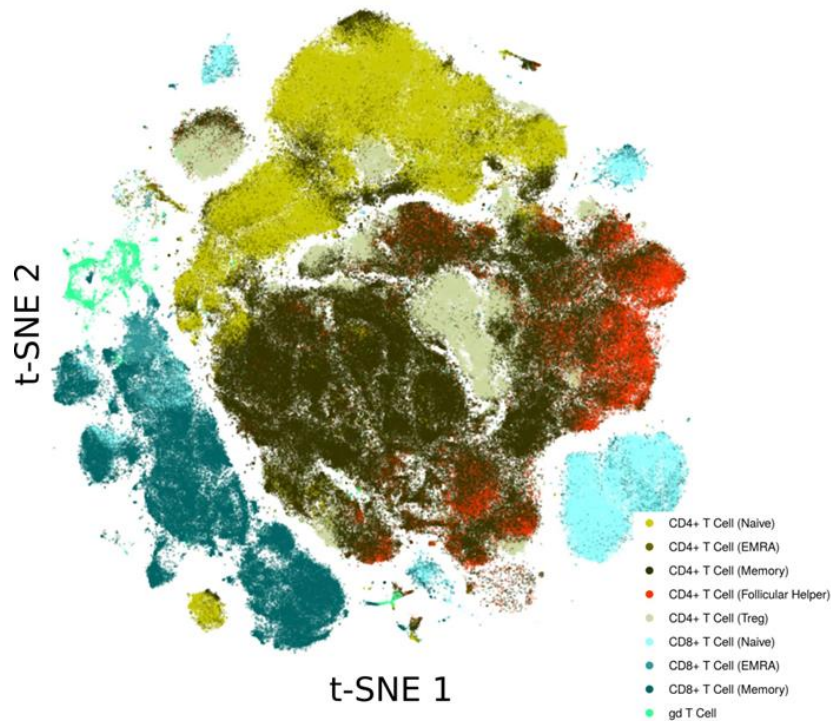
Recapitulation of Known B Cell and T Cell Trends



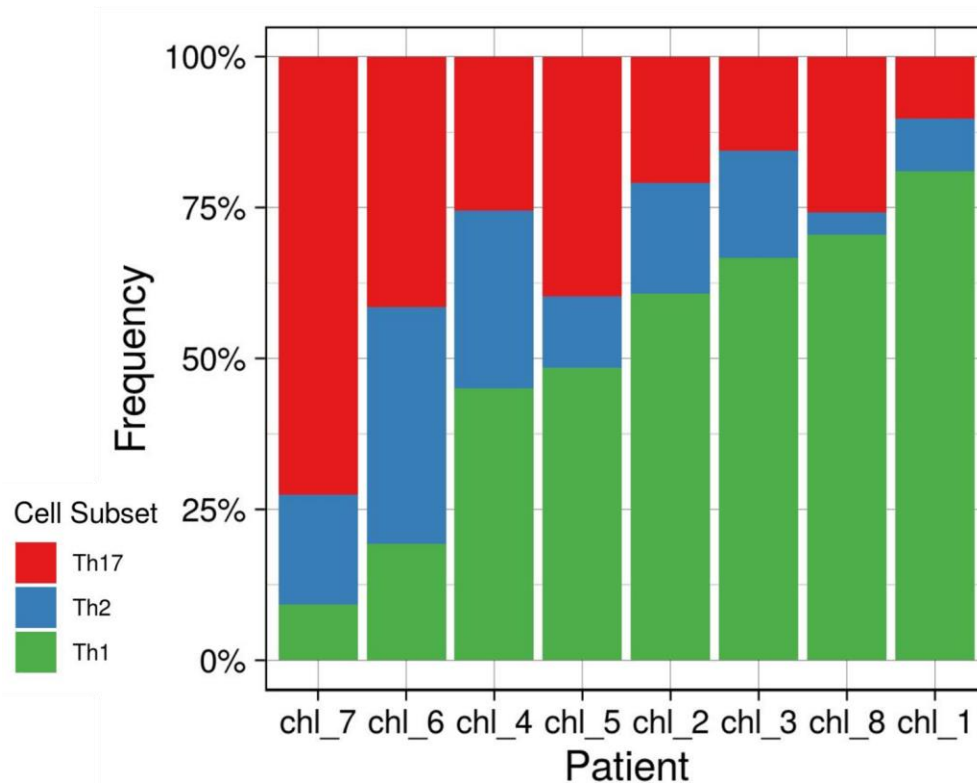
Dimensionality Reduction Reveals Further Structure



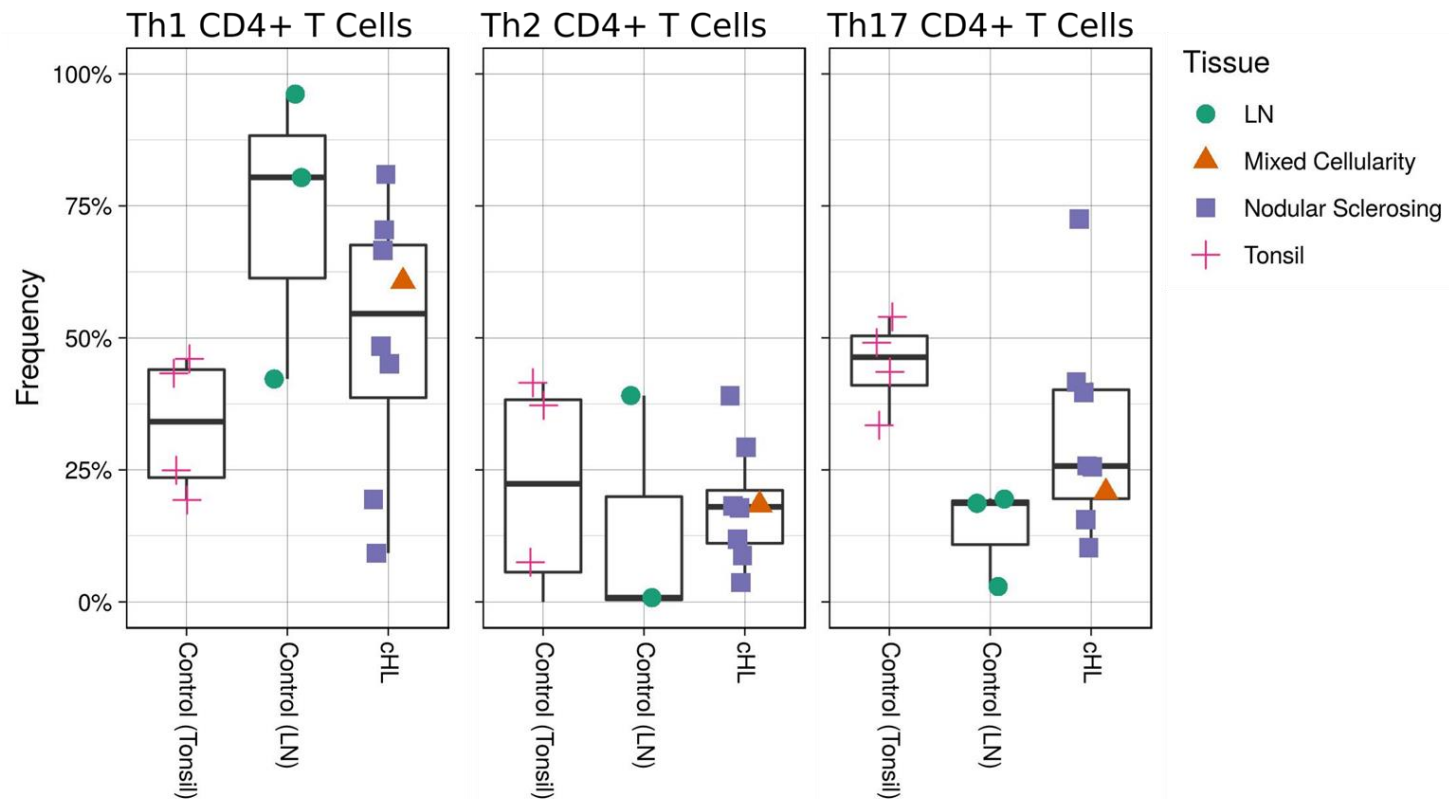
Immunophenotyping of T Cell Compartment



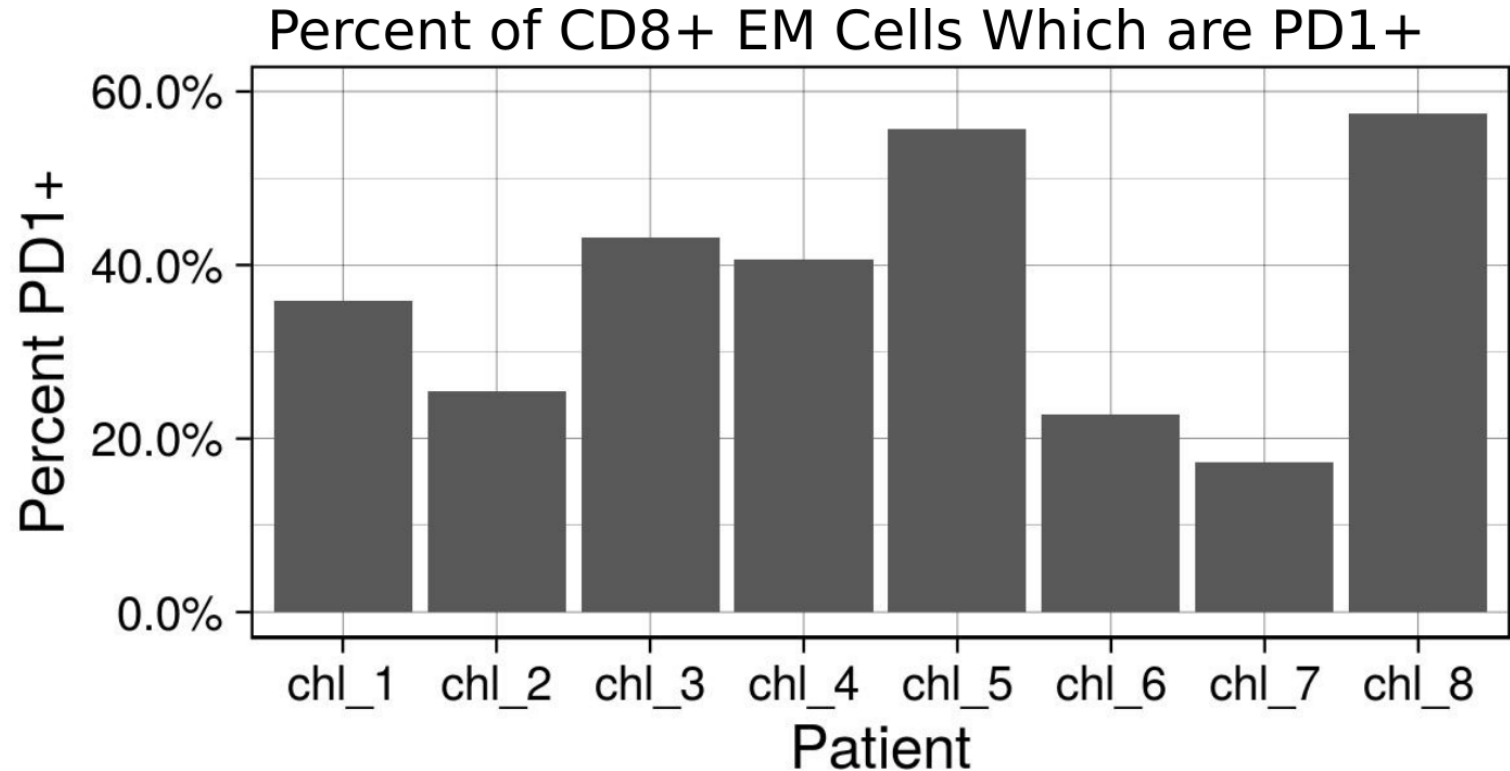
T_h Frequencies Vary Between Patients



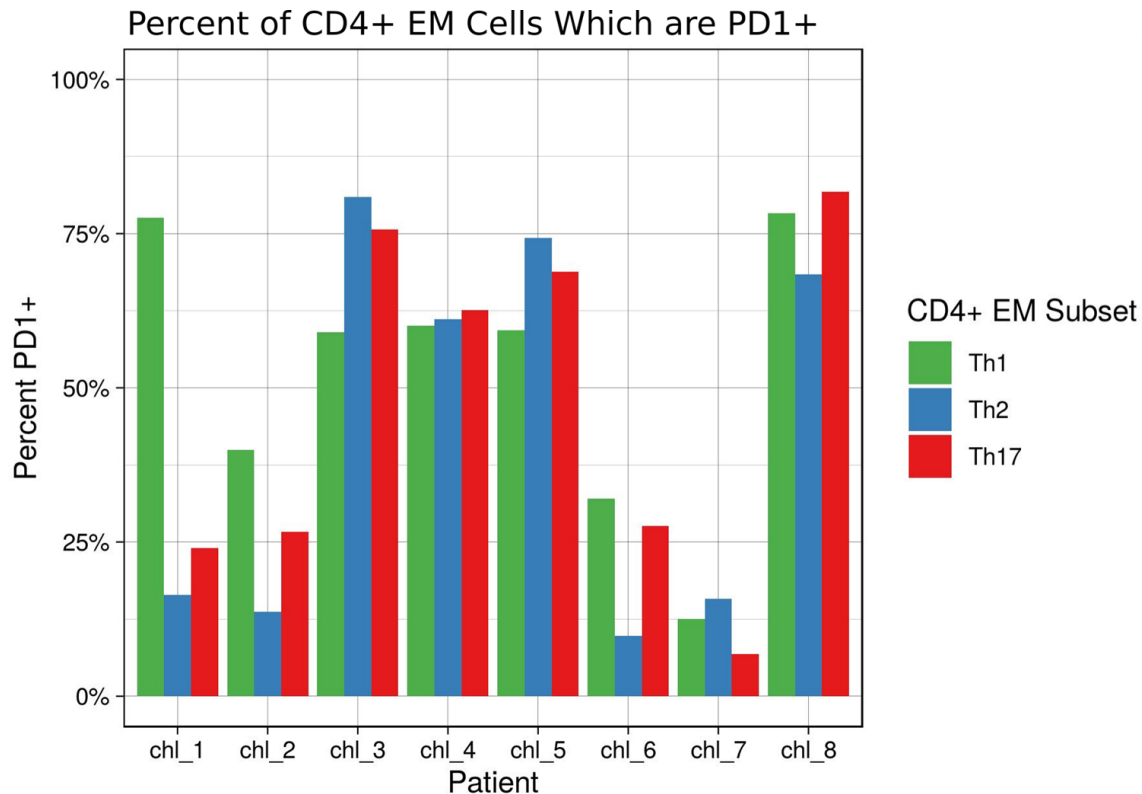
T_h Frequencies Vary Between Patients



CD8+ T Cell PD-1 Level is Heterogeneous Between Patients



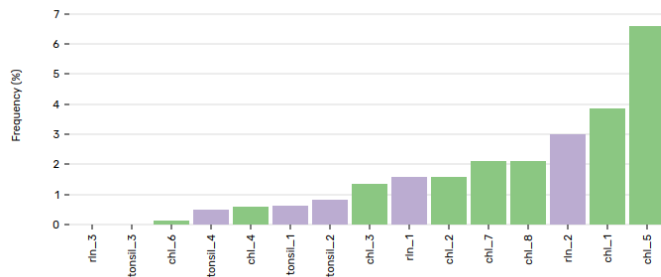
CD4+ T Cell PD-1 Level is Also Heterogeneous



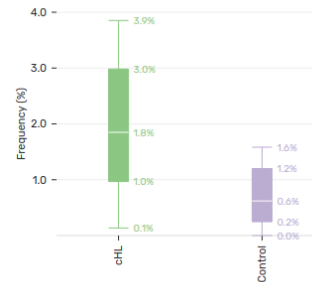
CXCR3-Dependent Differences Between Tregs

CD4+ T Cell (Treg, Memory) CD69hi CXCR3hi CD161lo, $-\log_{10}(\text{FDR}) = 0.102$

[Download Bar Chart...](#)



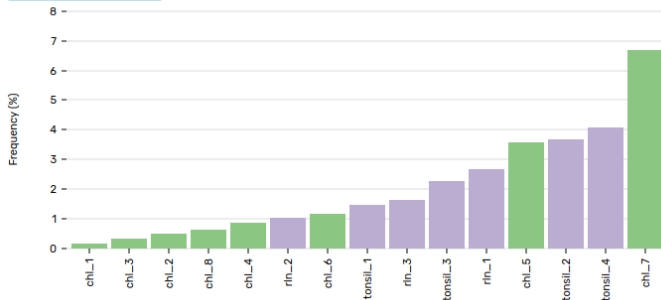
[Download Box Plot...](#)



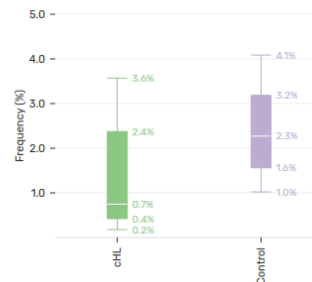
3x fold **increase** in cHL

CD4+ T Cell (Treg, Memory) CD69hi CXCR3lo CD161lo, $-\log_{10}(\text{FDR}) = 0.102$

[Download Bar Chart...](#)

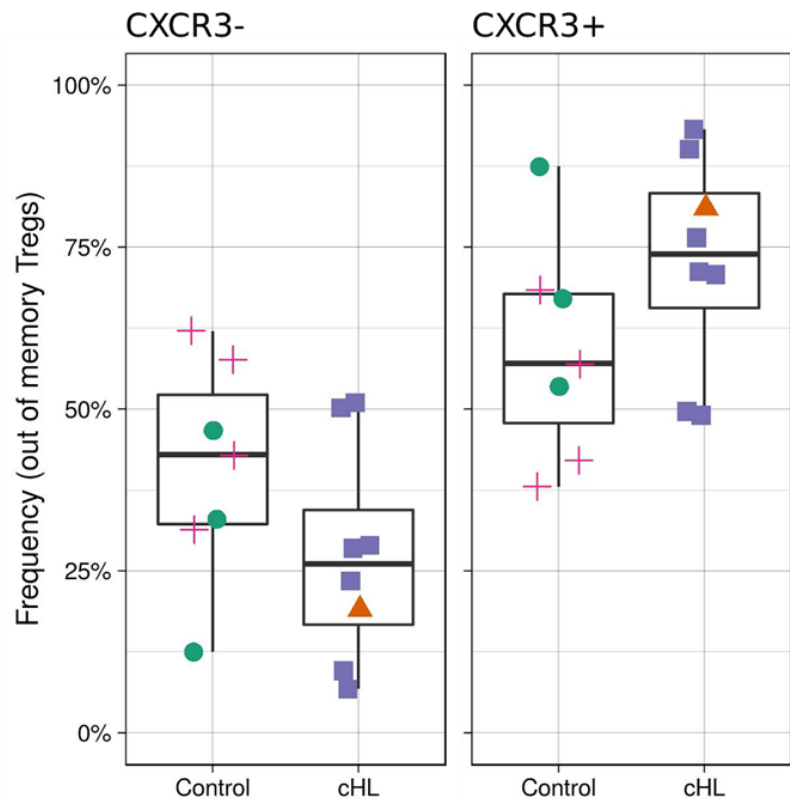


[Download Box Plot...](#)



3x fold **decrease** in cHL

CXCR3-Dependent Differences Between Tregs

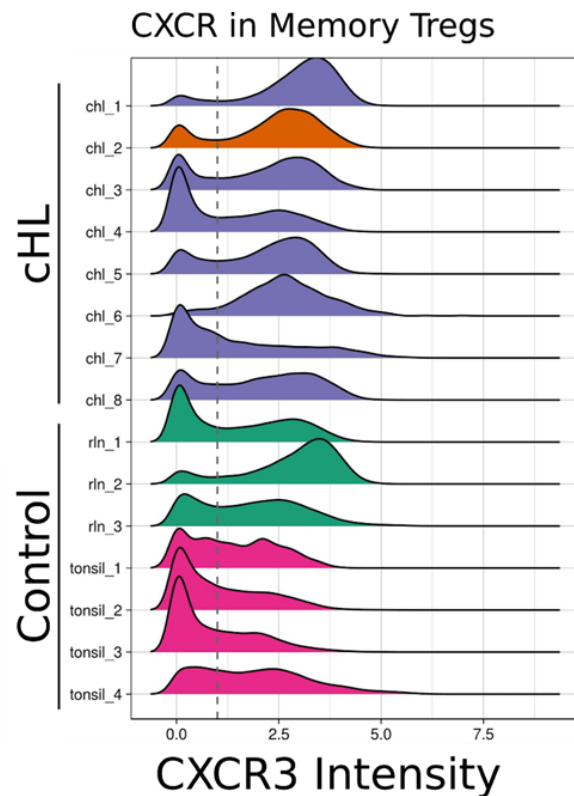


Tissue

- LN
- ▲ Mixed Cellularity
- Nodular Sclerosing
- + Tonsil

Tissue

- LN
- Mixed Cellularity
- Nodular Sclerosing
- Tonsil



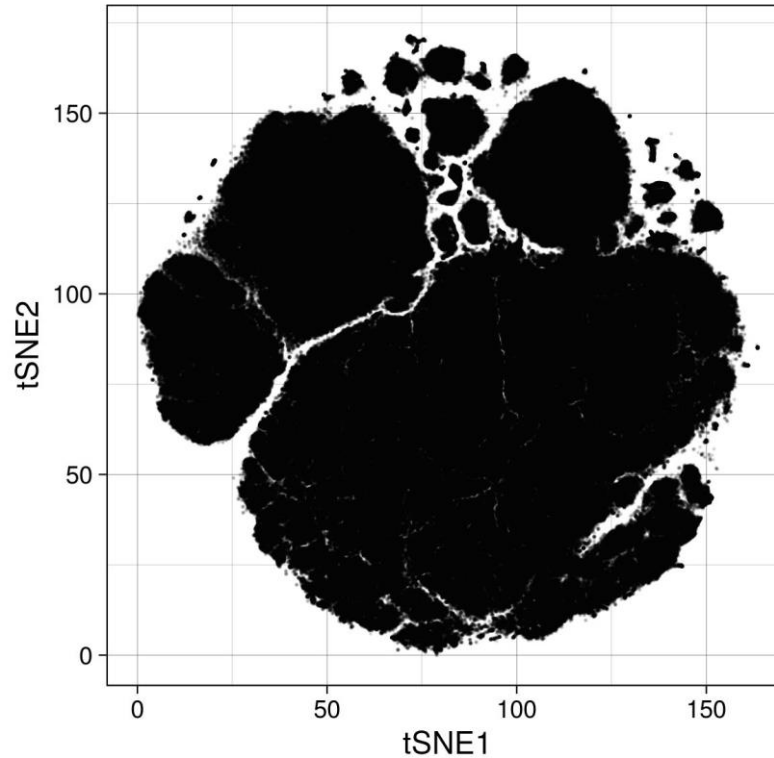
Detection of HRS Cells using CyTOF + Semi-Supervised DR

31 markers

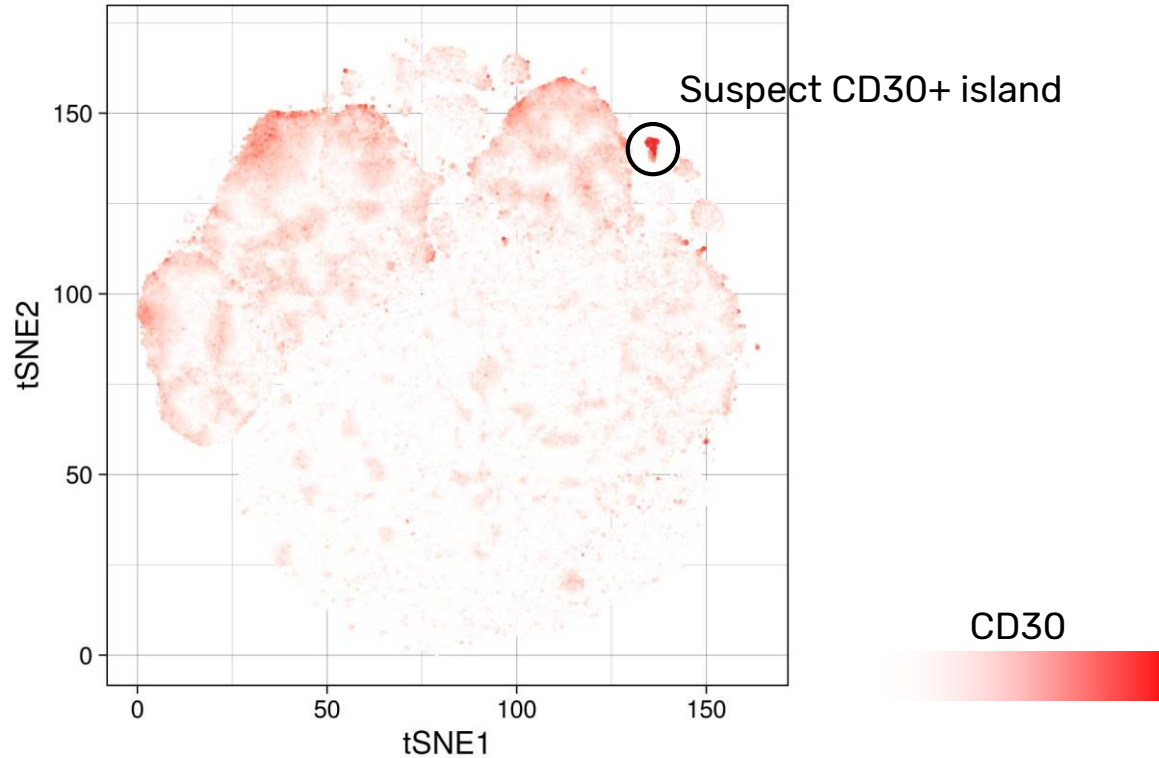
CCR4	CD27	ICOS
CCR5	CD28	LAG3
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CD5	CD56	
CD7	CD69	
CD8a	CD127	
CD11a	CD161	
CD16	CXCR3	
CD19	CXCR5	
CD25	HLADR	

... and CD30, PD-L1, and PD-L2

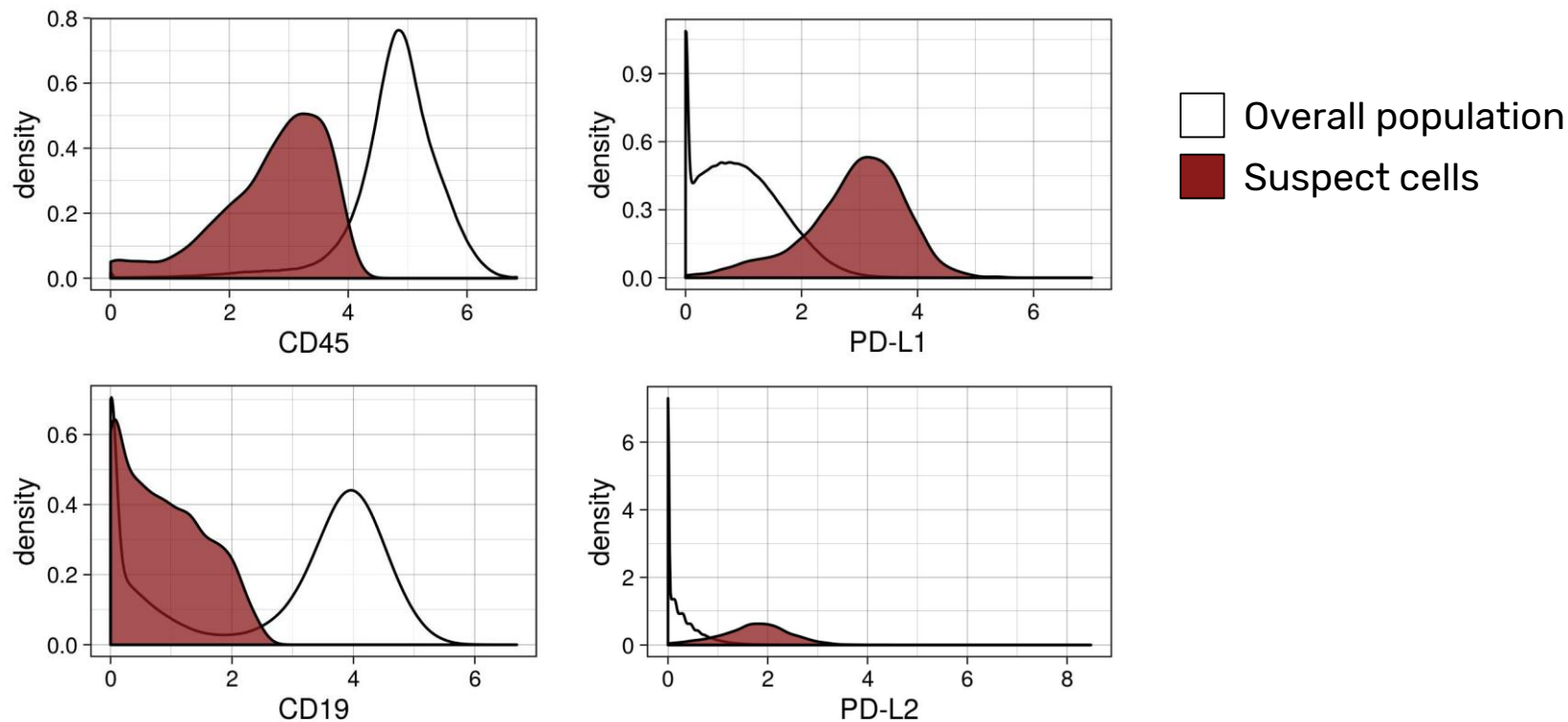
Detection of HRS Cells using CyTOF + Semi-Supervised DR



Detection of HRS Cells using CyTOF + Semi-Supervised DR



Further Investigation Confirms HRS Phenotype



Summary

- The combination of high-complexity cytometry and sophisticated analytics enables immune profiling of cHL
- PD-1 expression on cytotoxic T cells might be only part of the story, other subsets are potentially involved
- Semi-supervised analysis can identify HRS cells

Acknowledgements

The patients and their families

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