

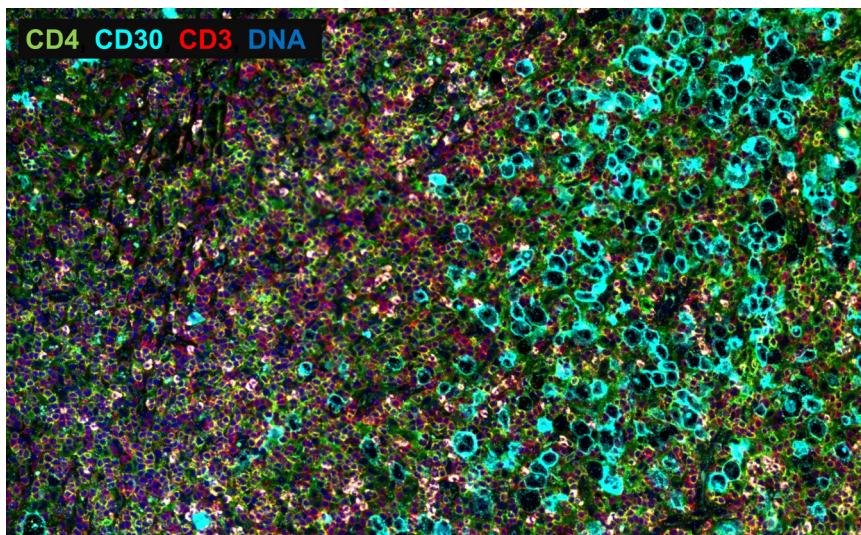
Lymph node Lymphoma

Study Purpose

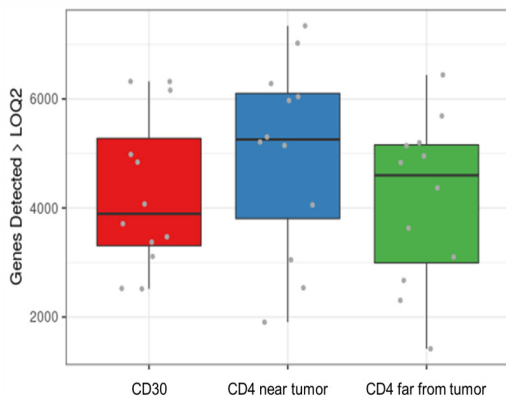
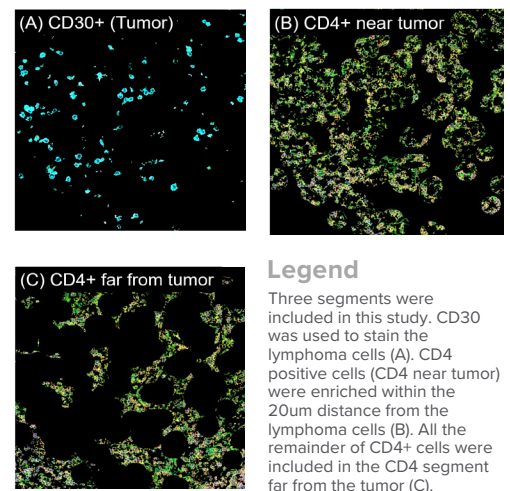
Classic Hodgkin's lymphoma (CHL) with different Epstein-Barr virus (EBV) status and Adult T-cell leukemia/lymphoma (ATLL) samples were studied in this experiment. CD30+ lymphoma cells and CD4+ T cells near and far from lymphoma cells were segmented and profiled using the GeoMx Human Whole Transcriptome Atlas. The differential gene expression profiles of CD4+ T cells between near and far from the tumor were explored and the gene expression changes of these cell types among the diseases were investigated.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Contour, Cell-type specific
Assay	Human Whole Transcriptome Atlas
Morphology Markers	CD4, CD30, CD3, DNA
Targets Detected	13,278 targets
Application	Pathway analysis



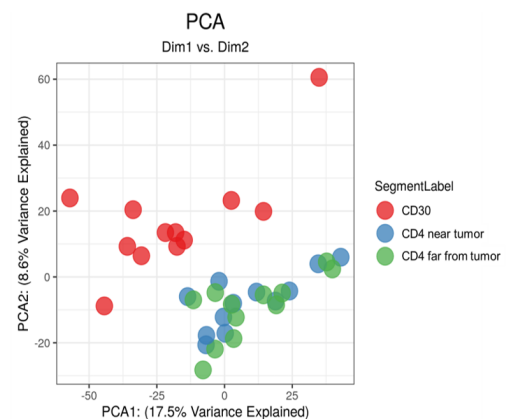
Segmentation Strategy



Legend

Left:
The number of targets detected above the background (LOQ2*) by AOI groups.

Right:
Principal component analysis (PCA) plot.



*AOI = Area of Illumination; LOQ=Limit of Quantitation

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For more information, please visit

<https://nanosttring.com/geomx-morphology-markers/>

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