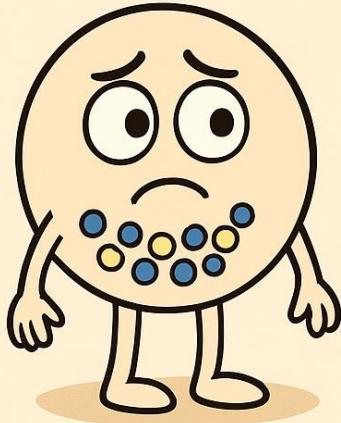


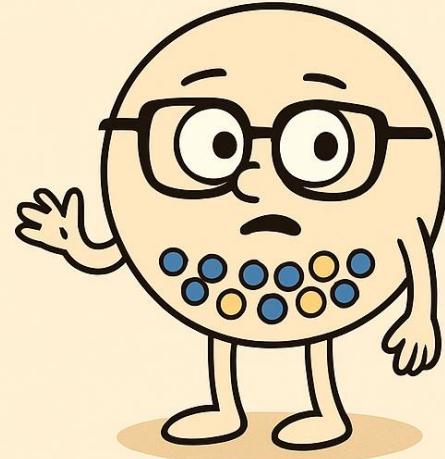
Characterization of TLS maturation states by CODEX, scRNA-seq dataset and clinical data

Team: TLS and the Gang
Team lead: Afrooz Jahedi

Stages of TLS Maturation



Early TLS



Intermediate
TLS

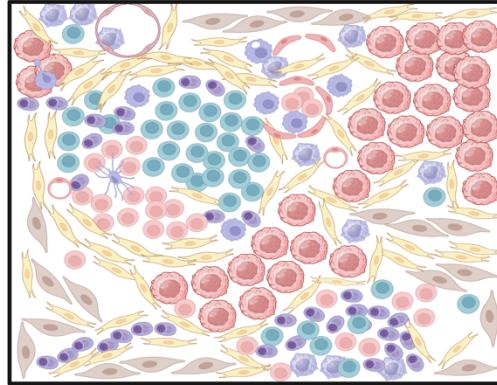


Mature TLS

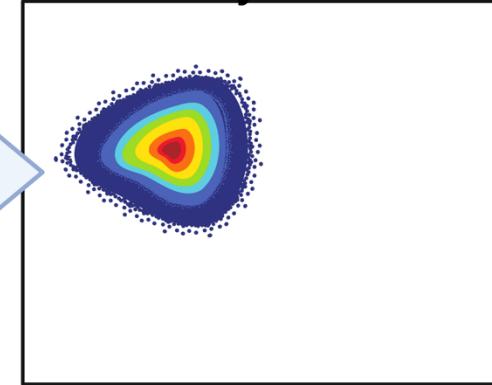
Identification classification

Principle for identification & classification of TLSs

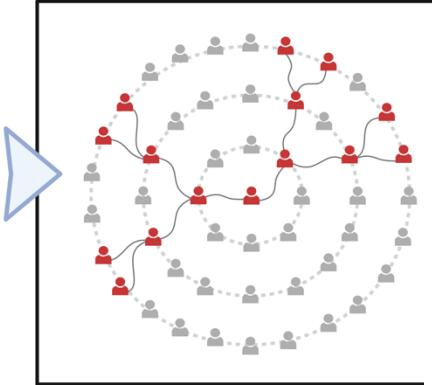
Tissue section



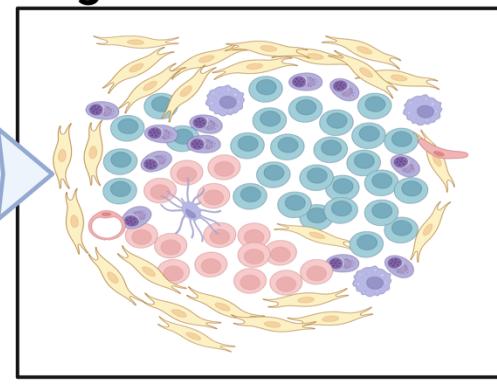
Screening B cell density



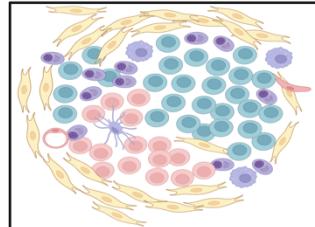
Neighbor extending for B centroid



TLS region segmentation

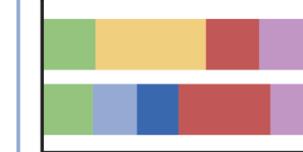


Extracted TLSs

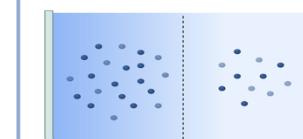


Spatial feature

Cell composition

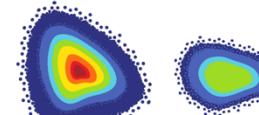


Cell aggregation

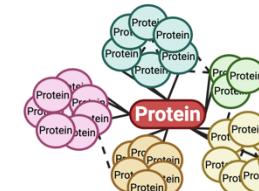


High → Low

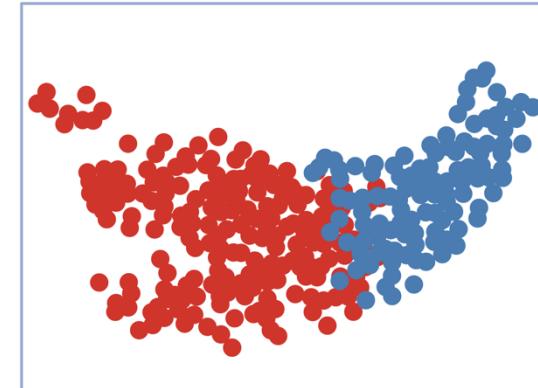
Cell density



Cell interactome

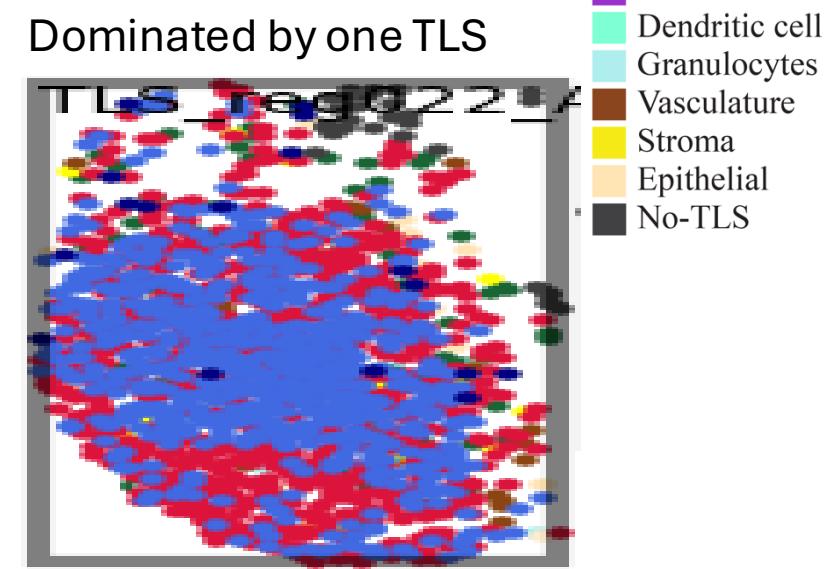
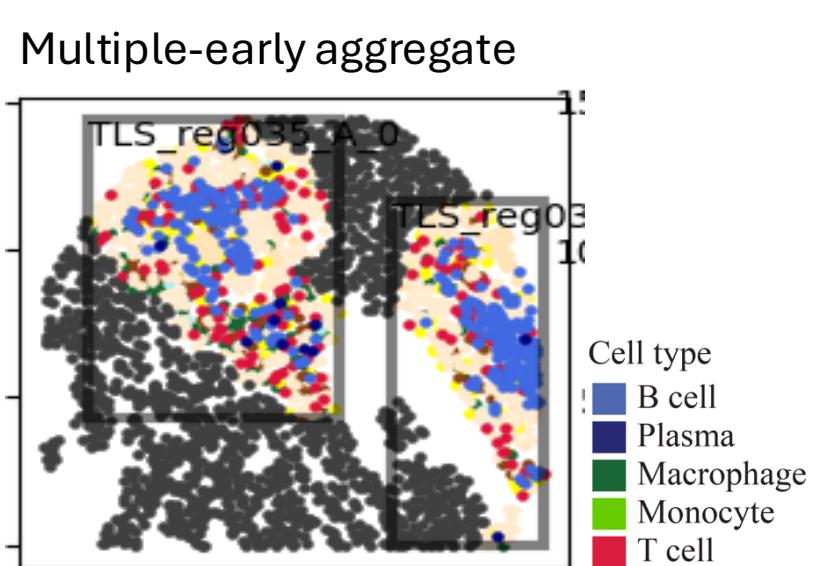
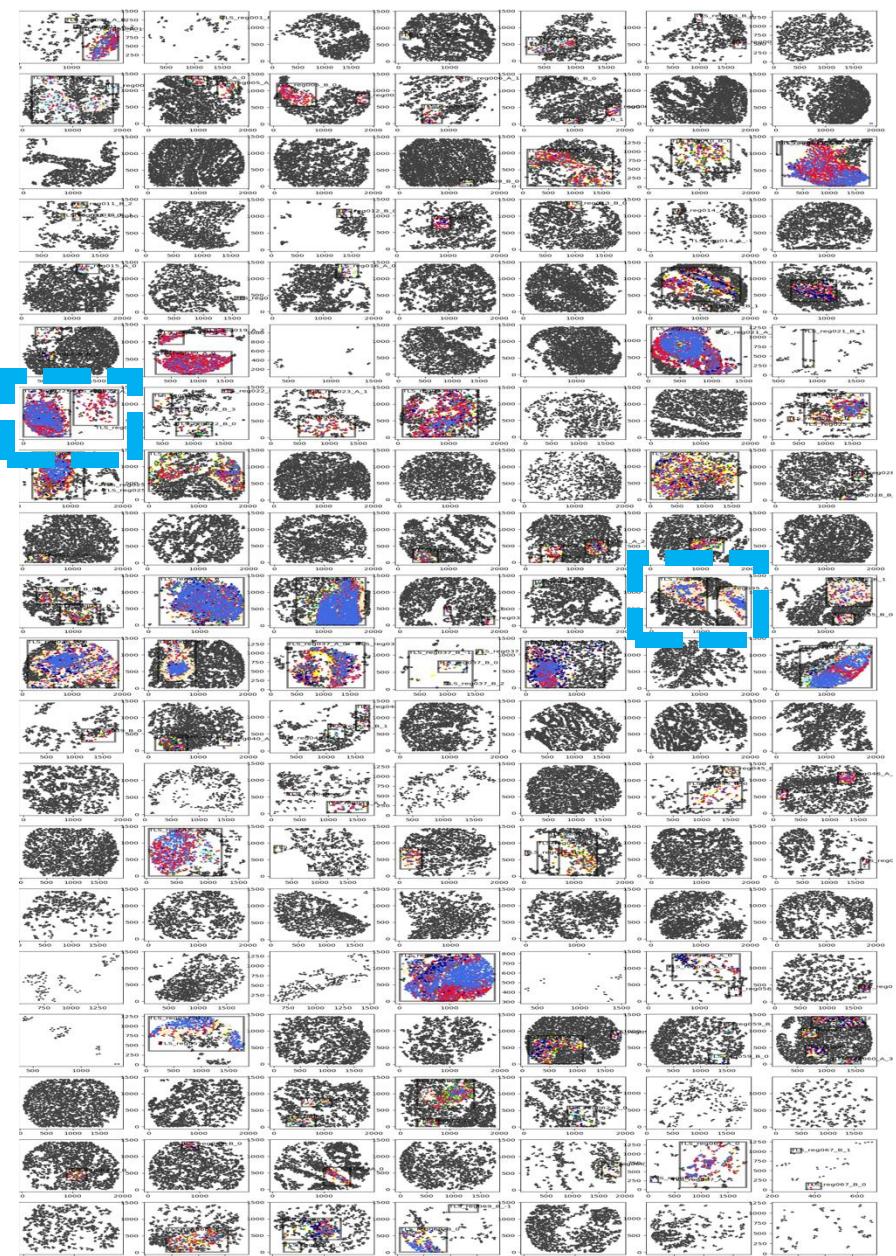


TLS subtypes

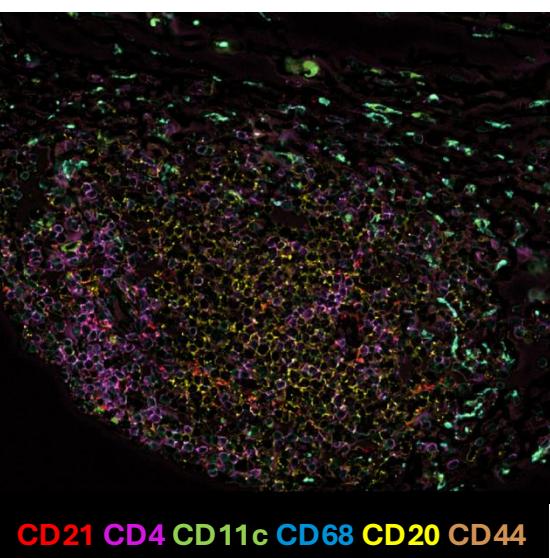
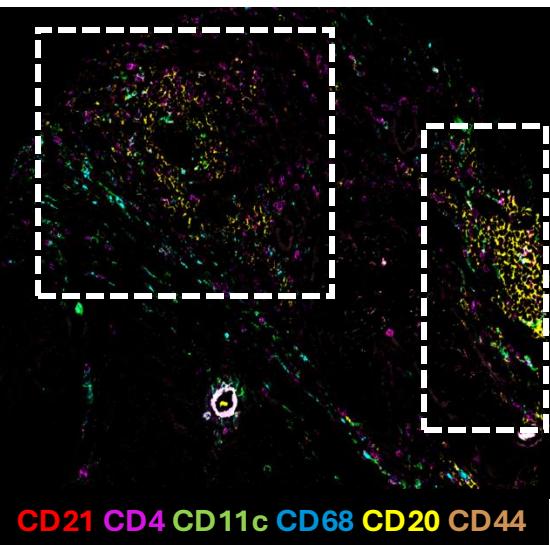


Yunhe Liu

The landscape of TLSs identification

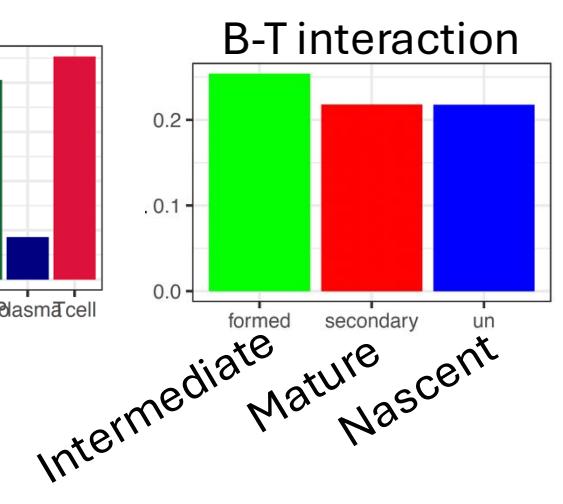
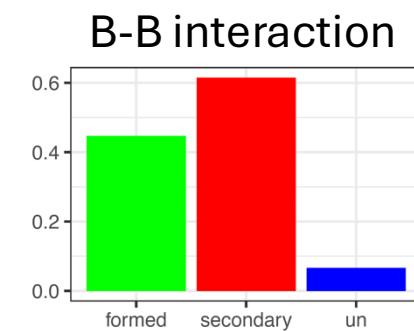
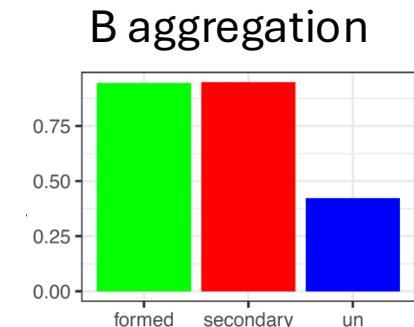
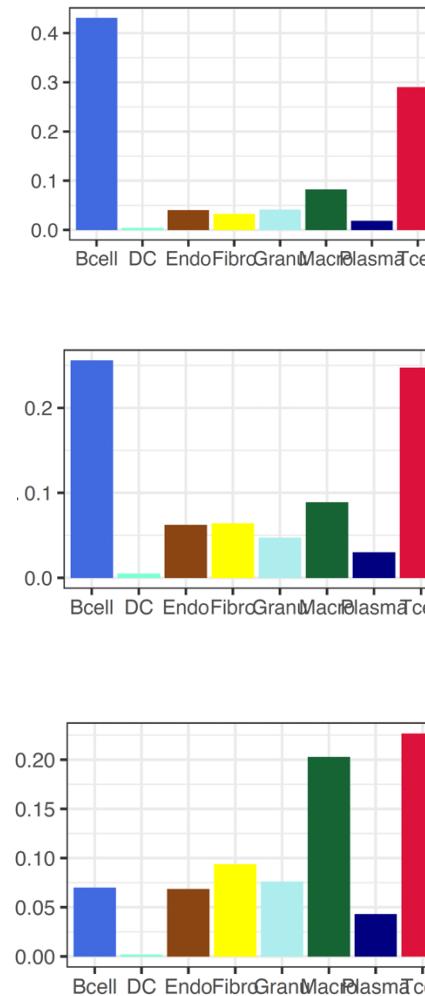
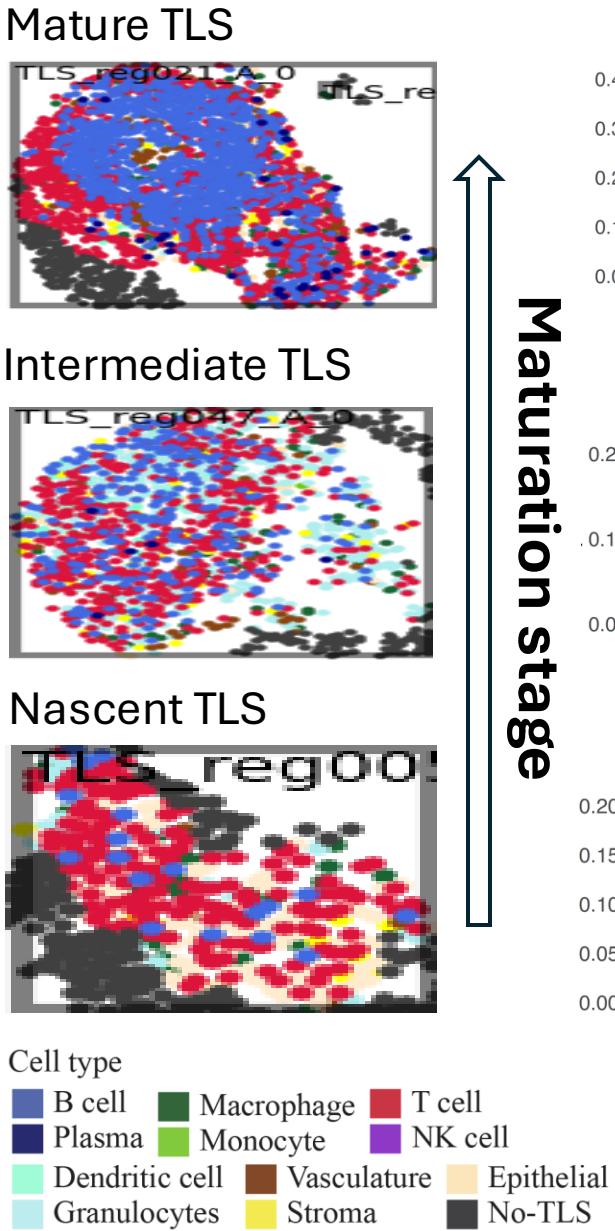
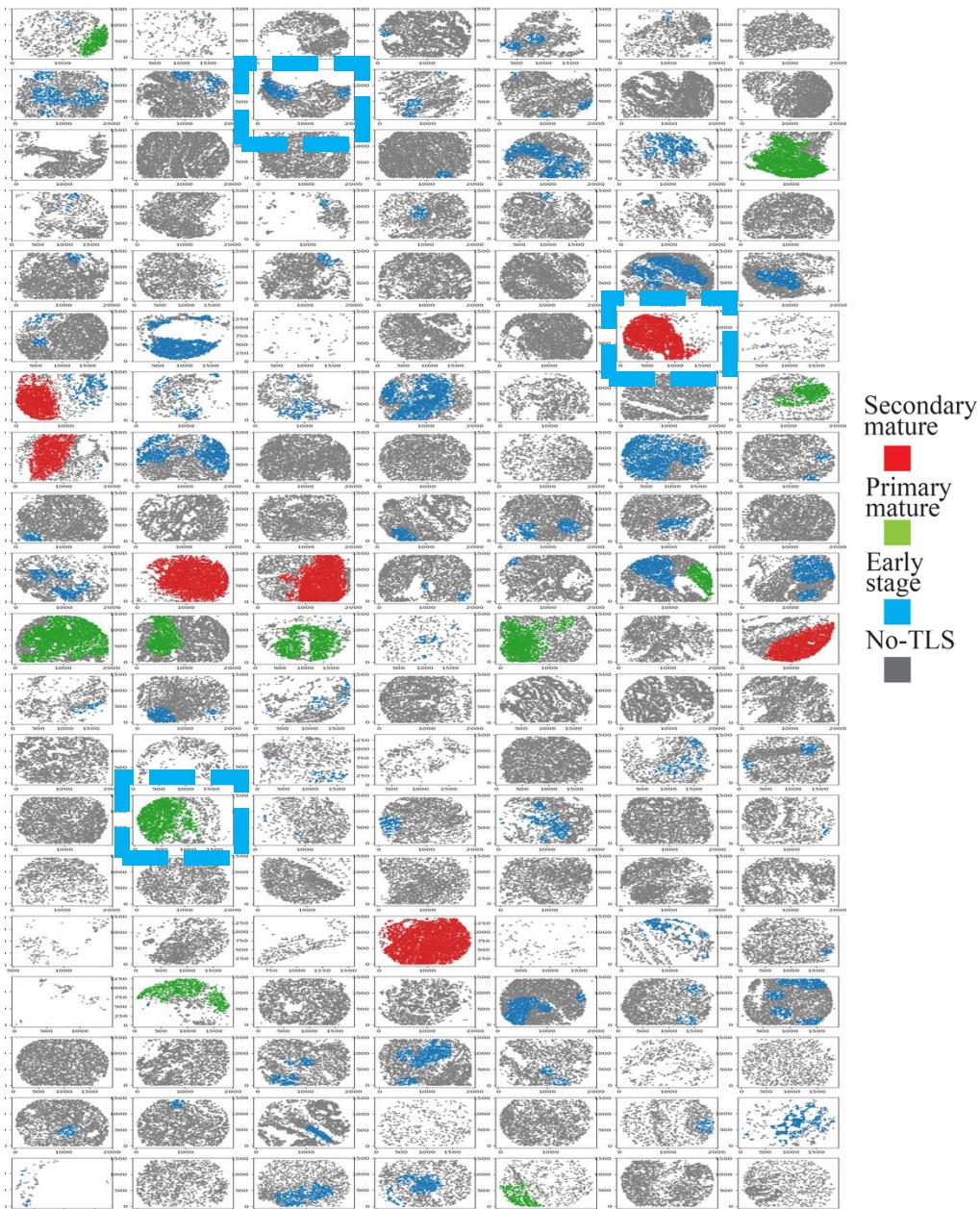


CODEX staining



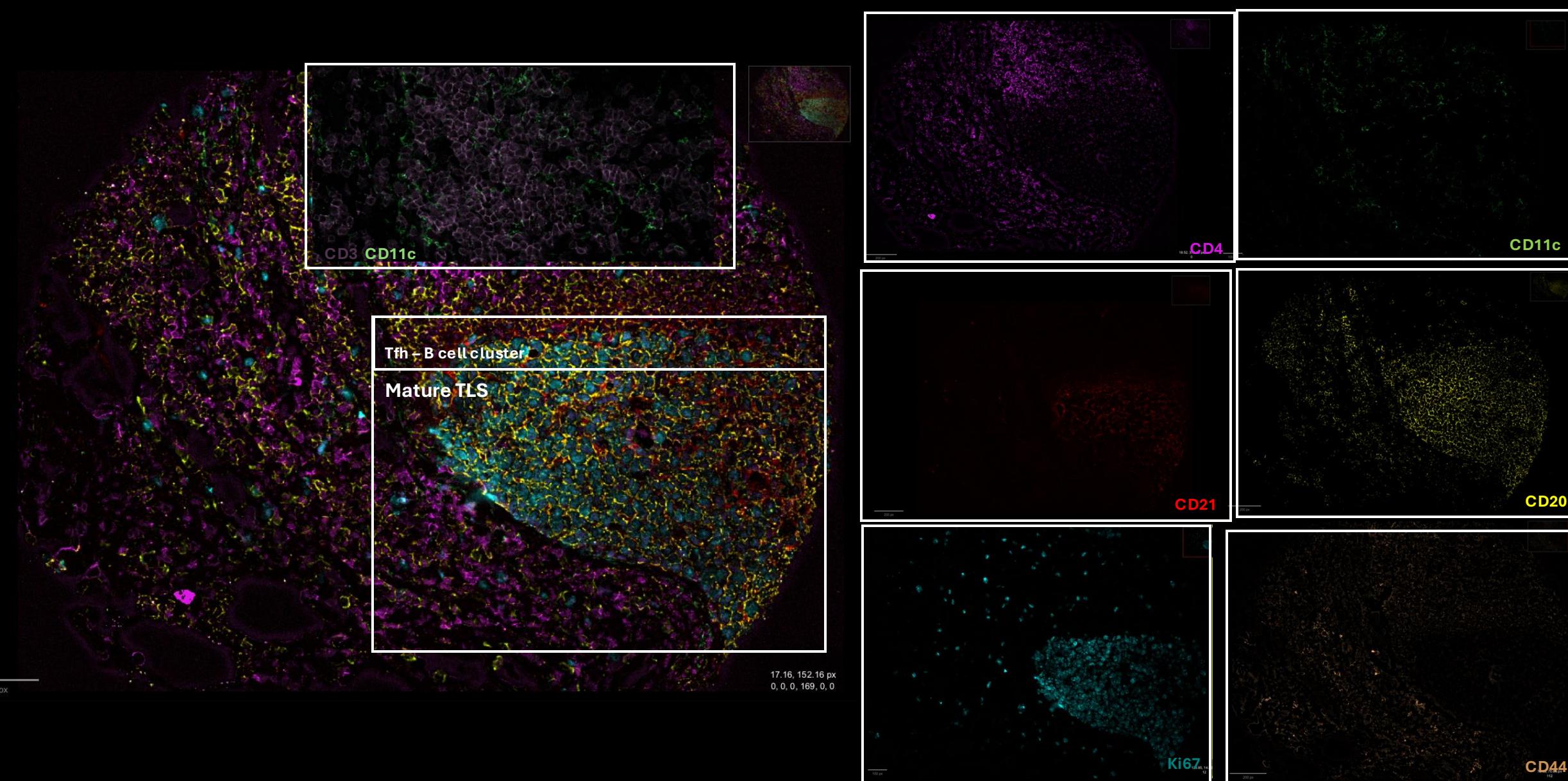
Yunhe Liu

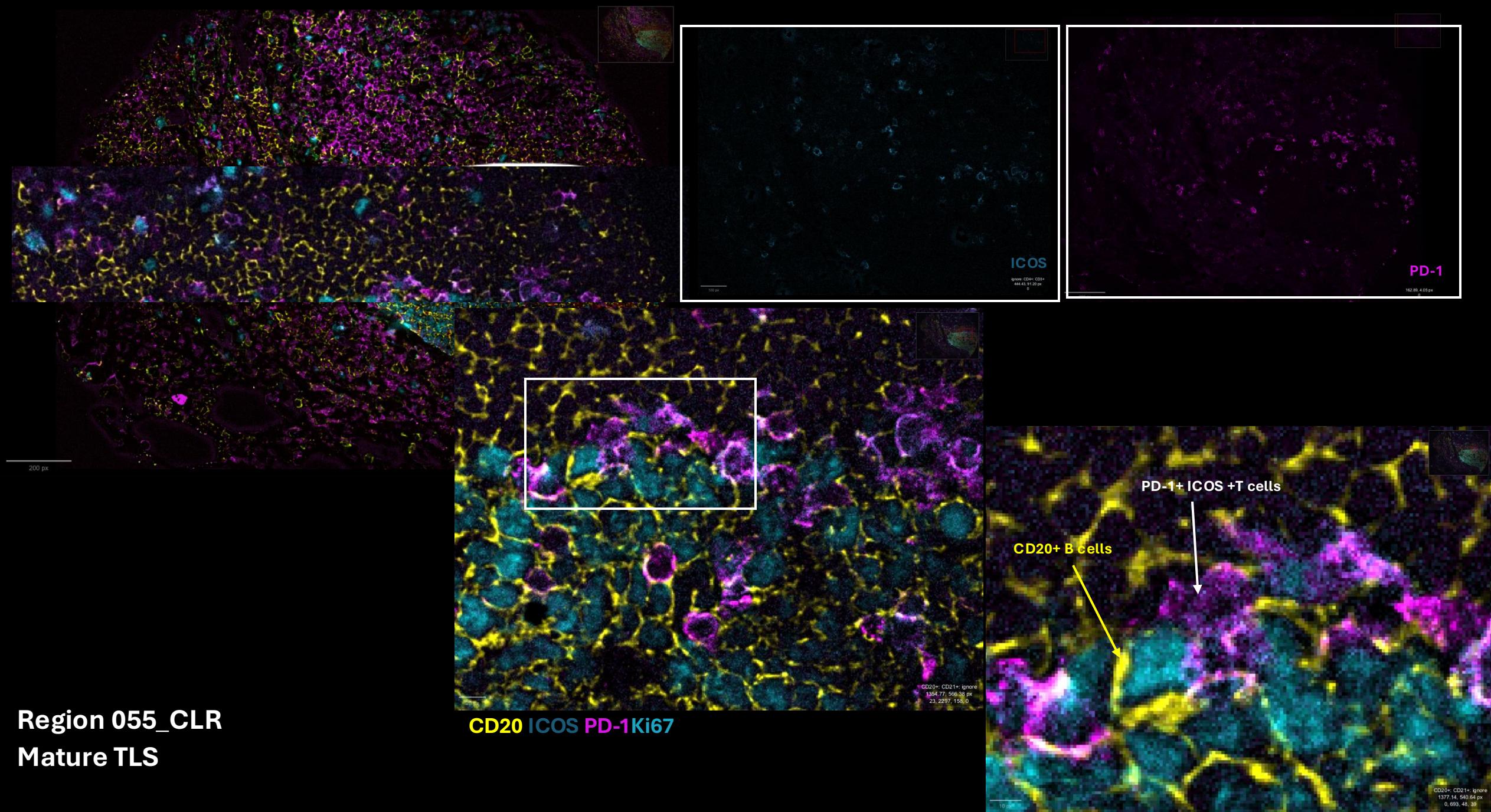
The landscape of TLSs classification



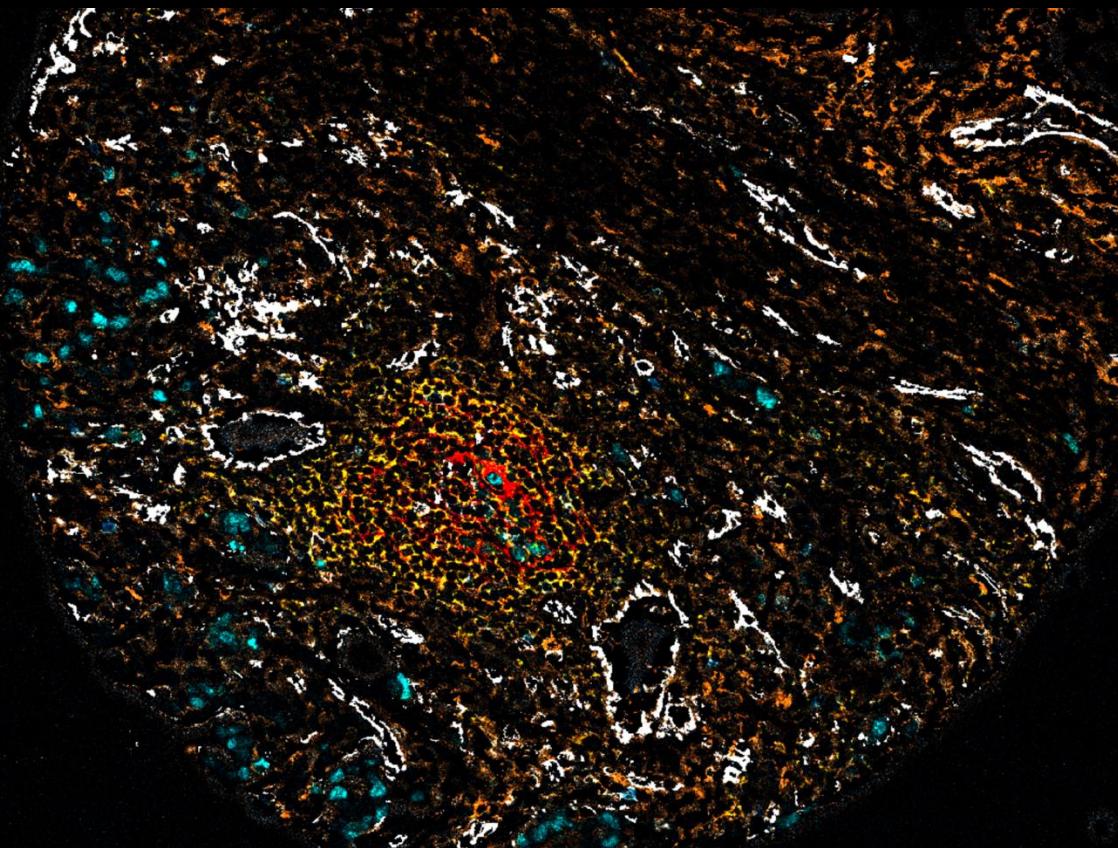
Yunhe Liu

Region 055_CLR

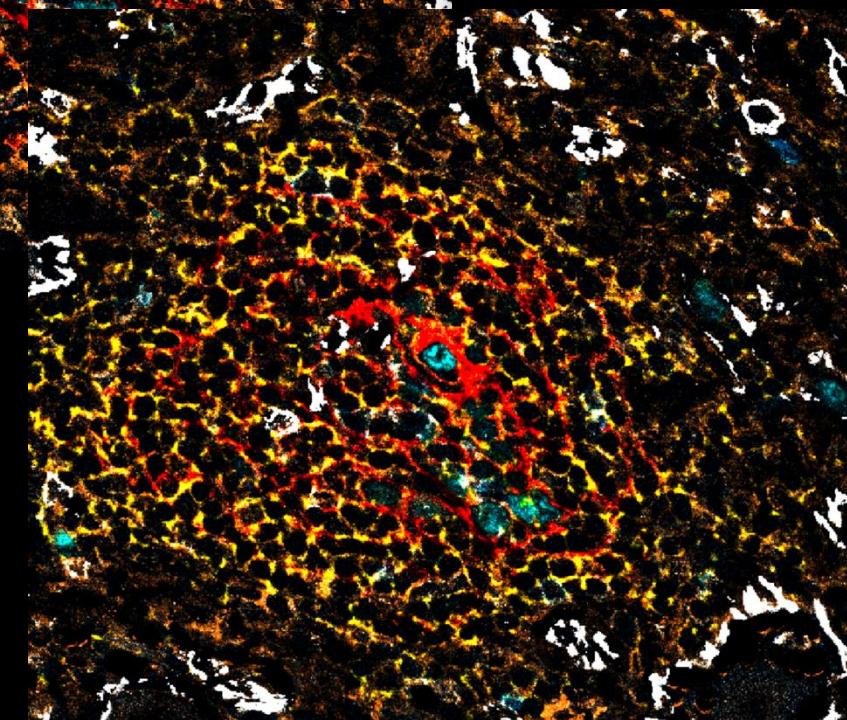
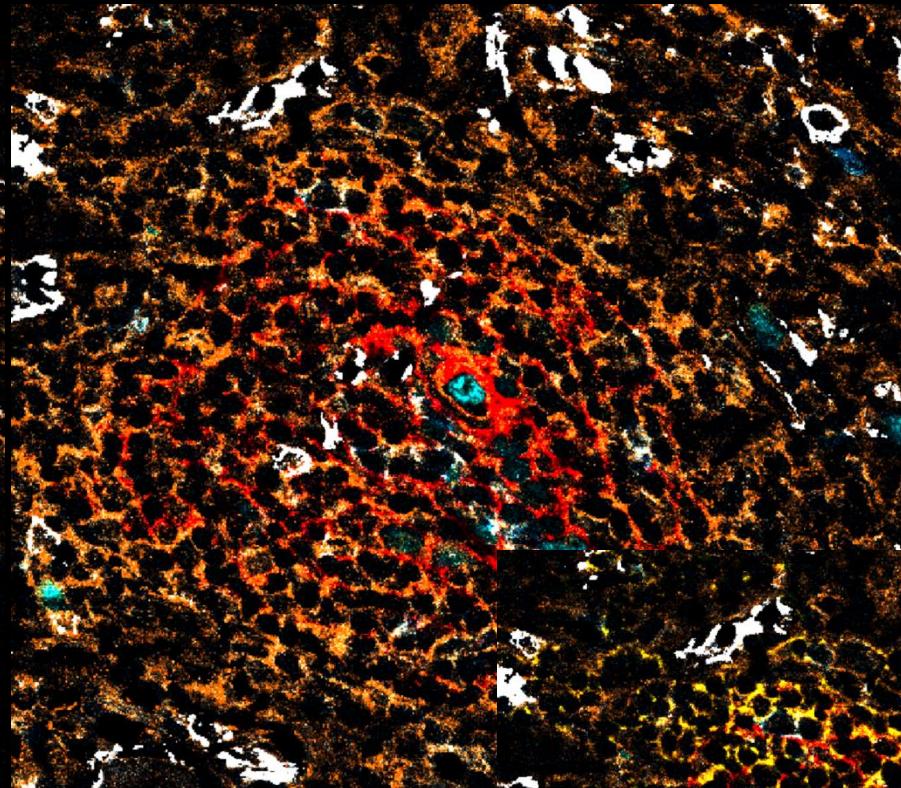




Region 35_DII

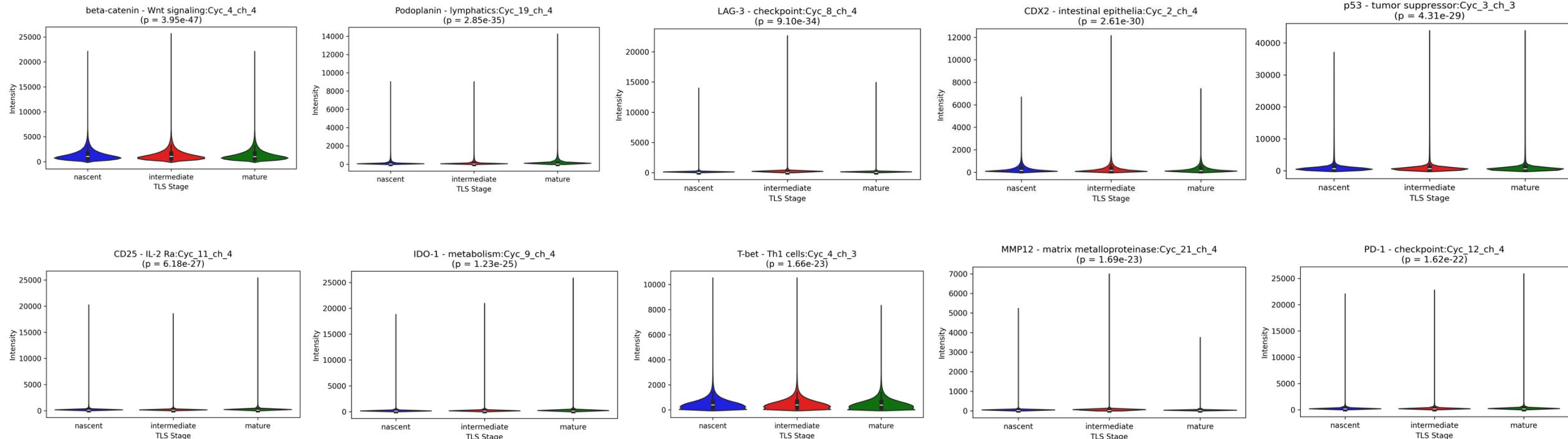


CD20 CD44 Ki67 CD31 CD21



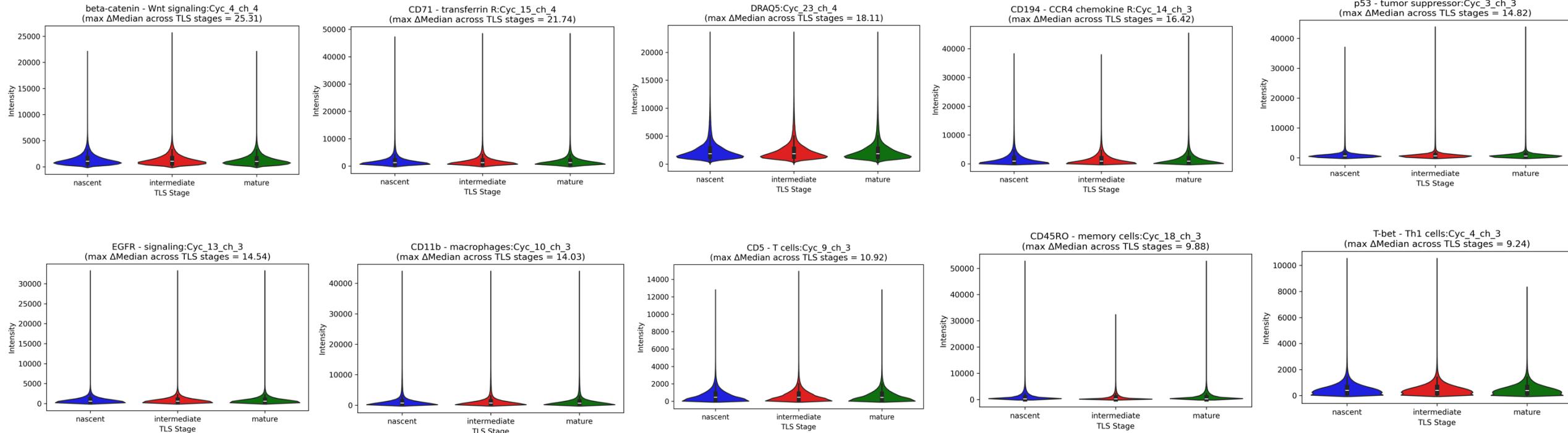
CD20 Ki67 CD31 CD21

Cell type composition 100 μm around TLS structures sorted by intensity



Mesut Unal

Cell type composition change 100 µm around TLS structures



Mesut Unal

Validation of TLS classifications with single-cell RNA sequencing data

Data integration by Maxfuse



Matching single-cell data with CODEX data

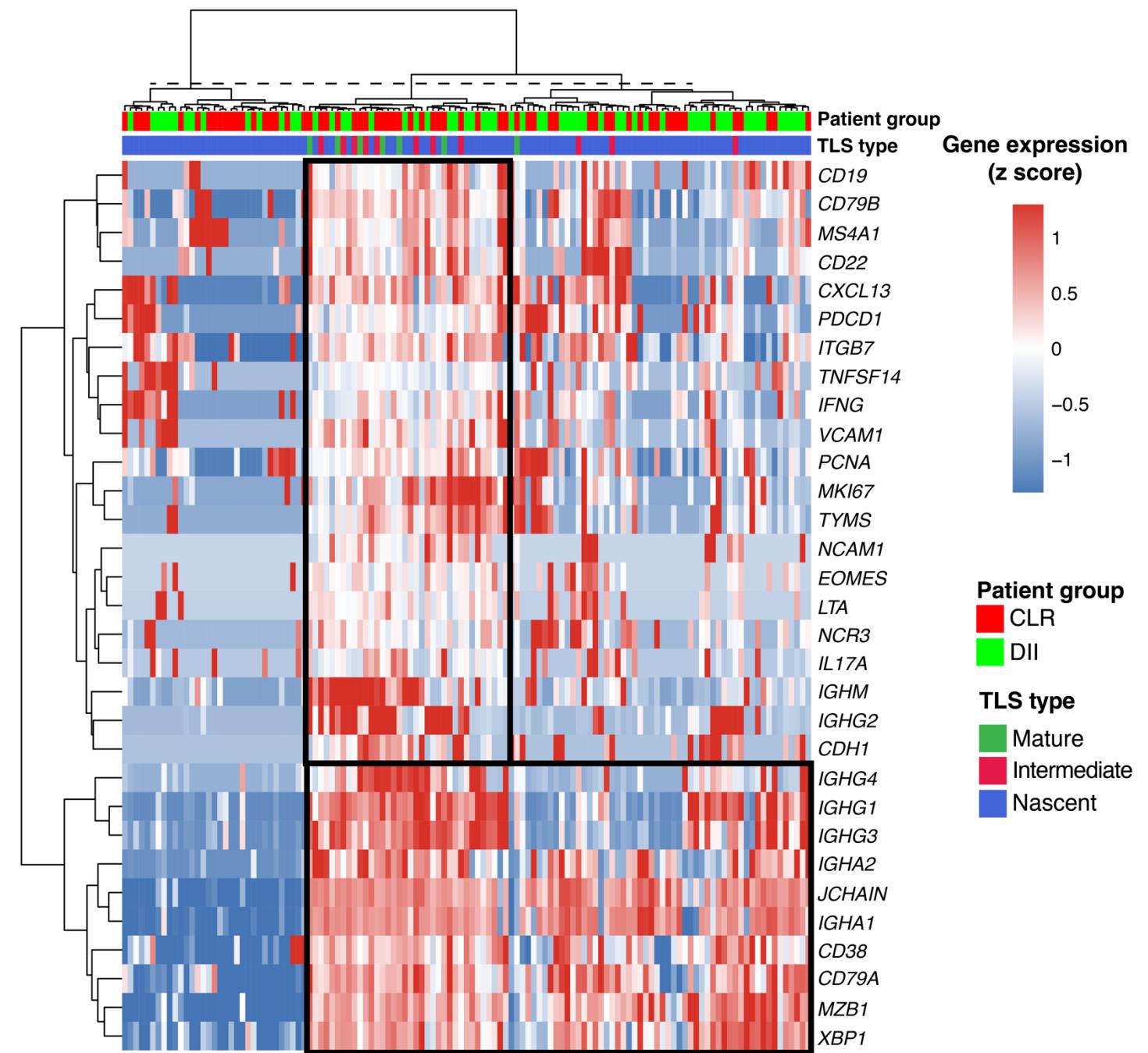


Construct pseudobulk expression matrix for each TLS region

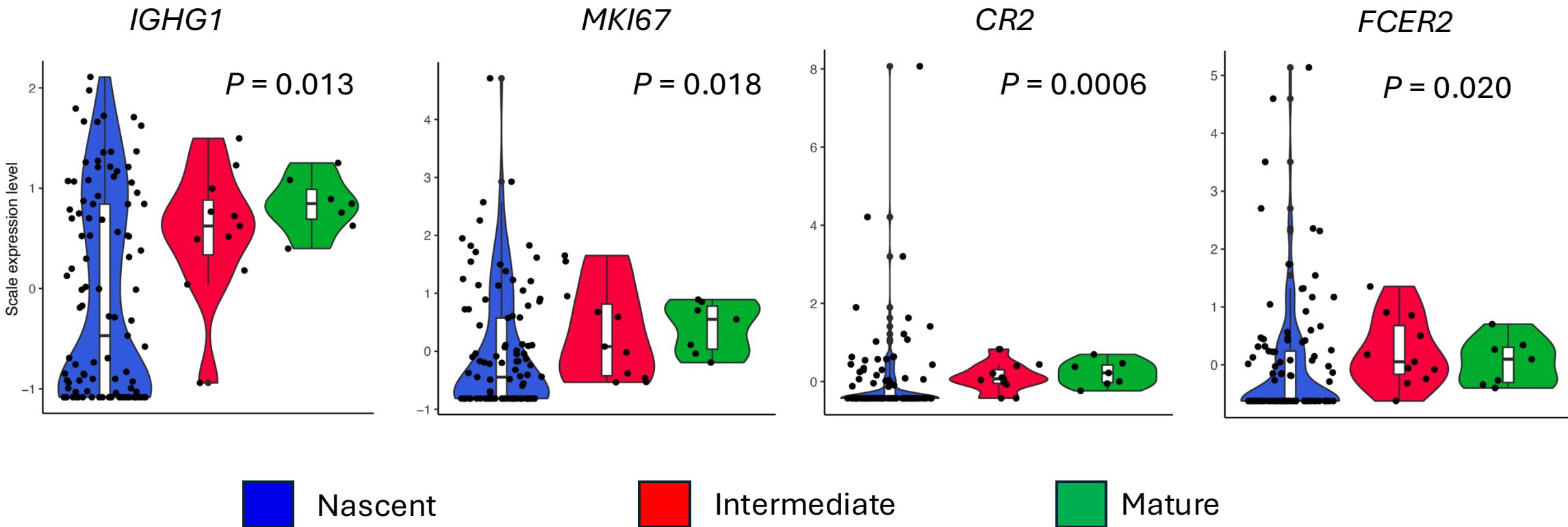


TLS phenotyping

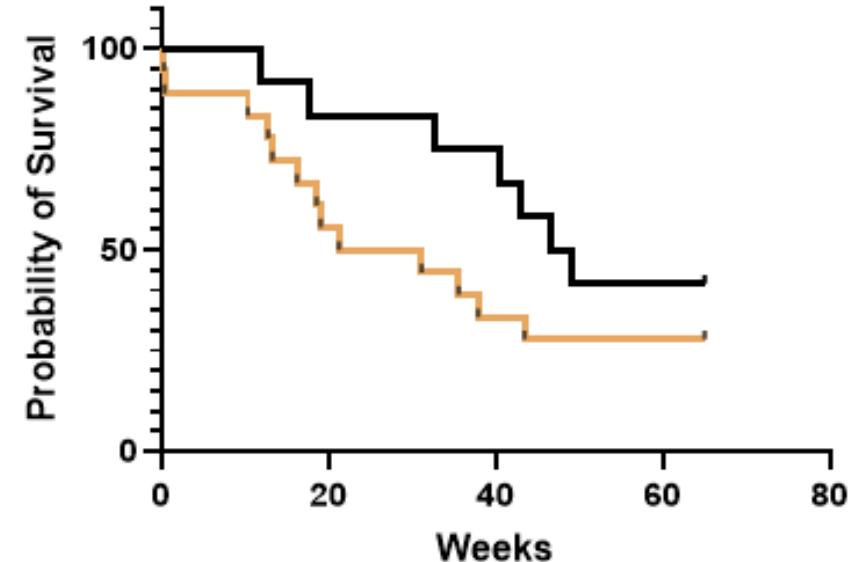
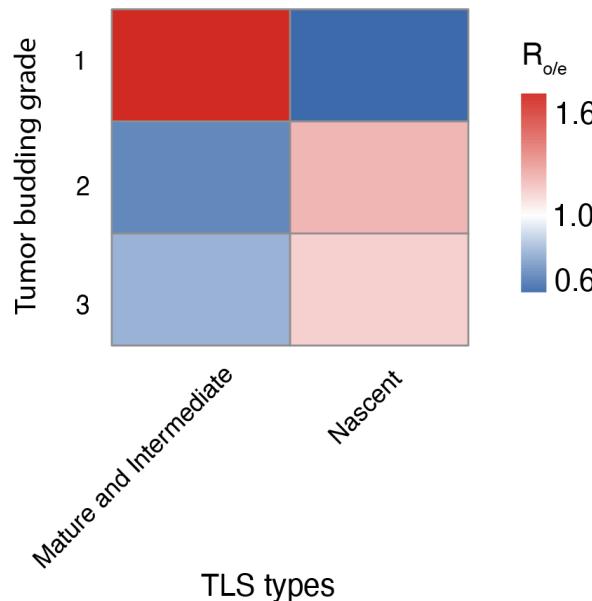
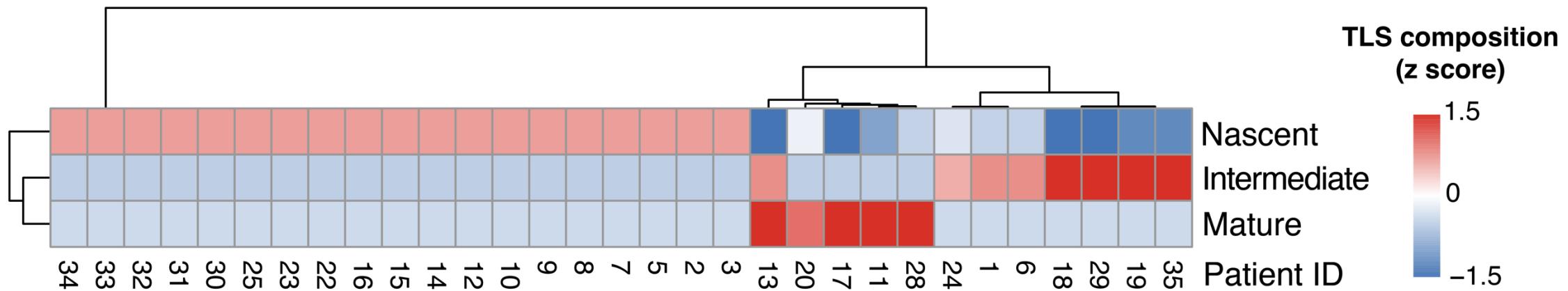
Yibo Dai



Validation of TLS classifications with single-cell RNA sequencing data

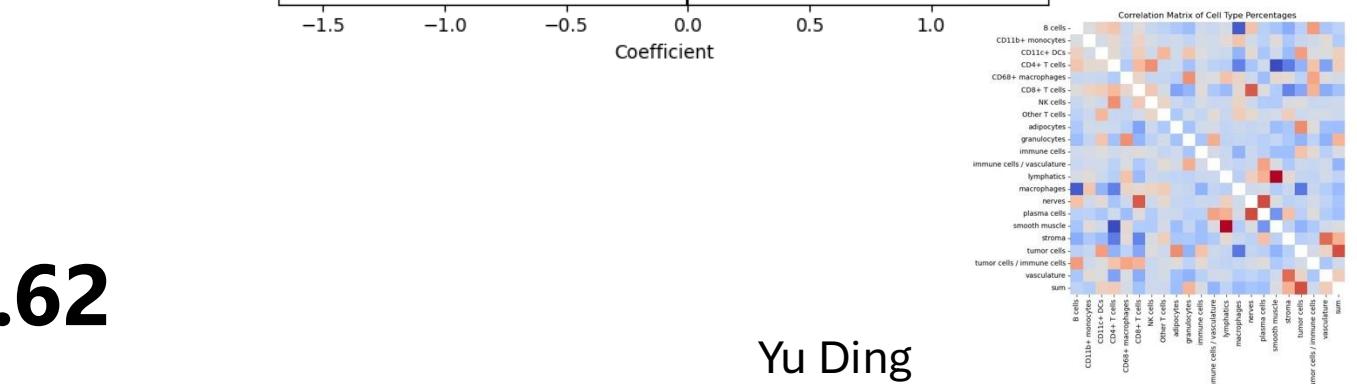
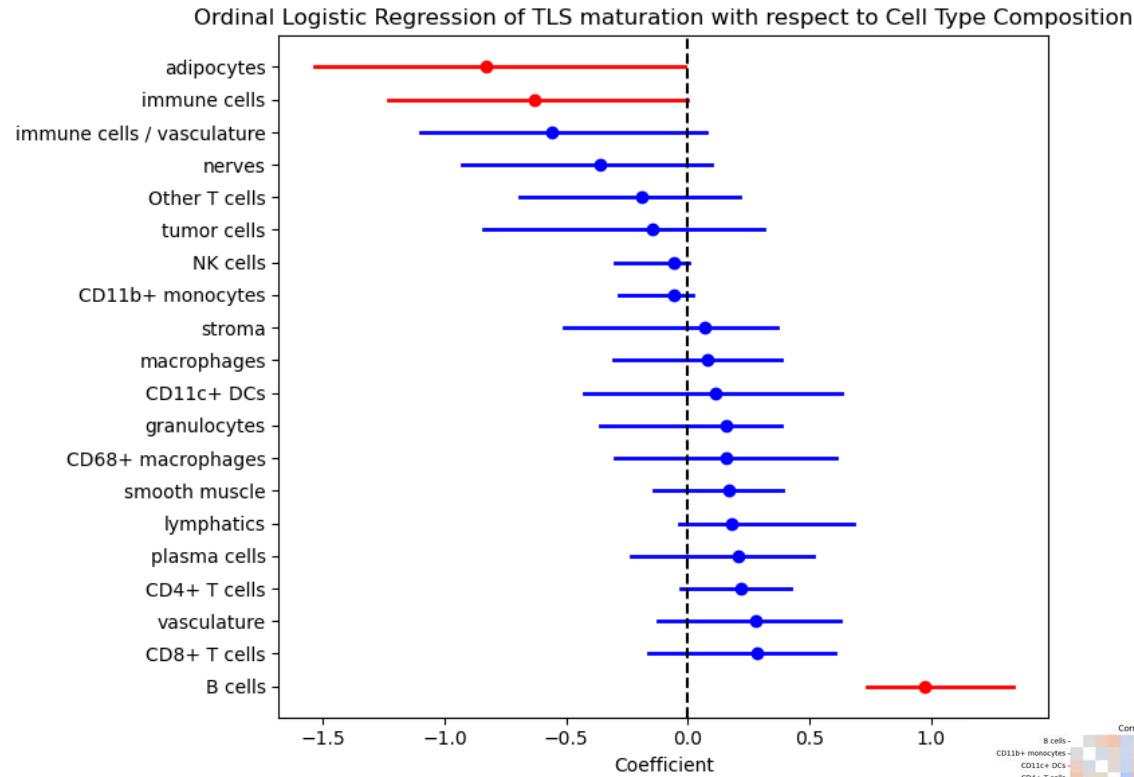
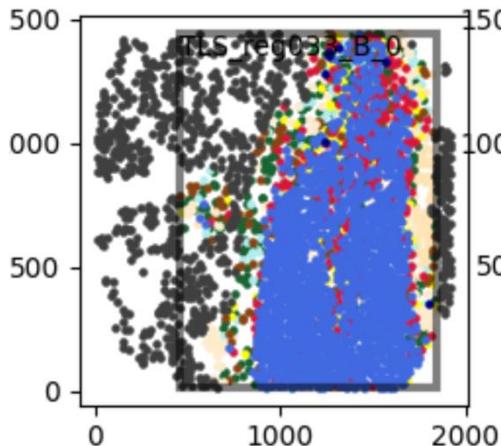
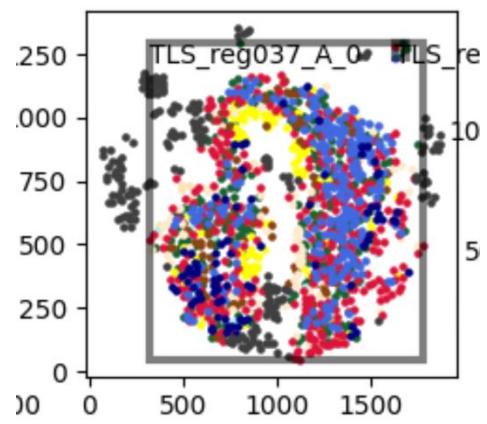
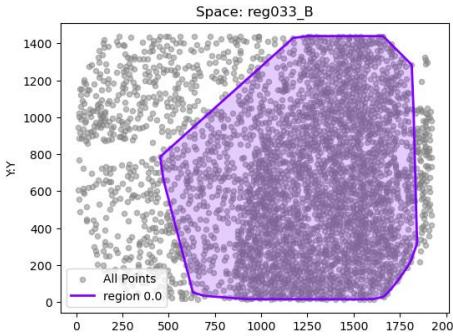
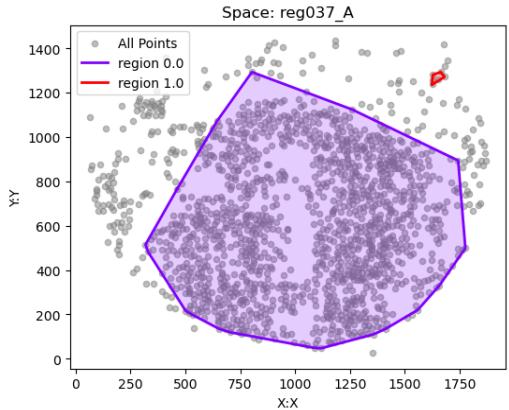


Correlation with clinical information



Yibo Dai
Cindy Liu

Cell Composition Analysis within TLS



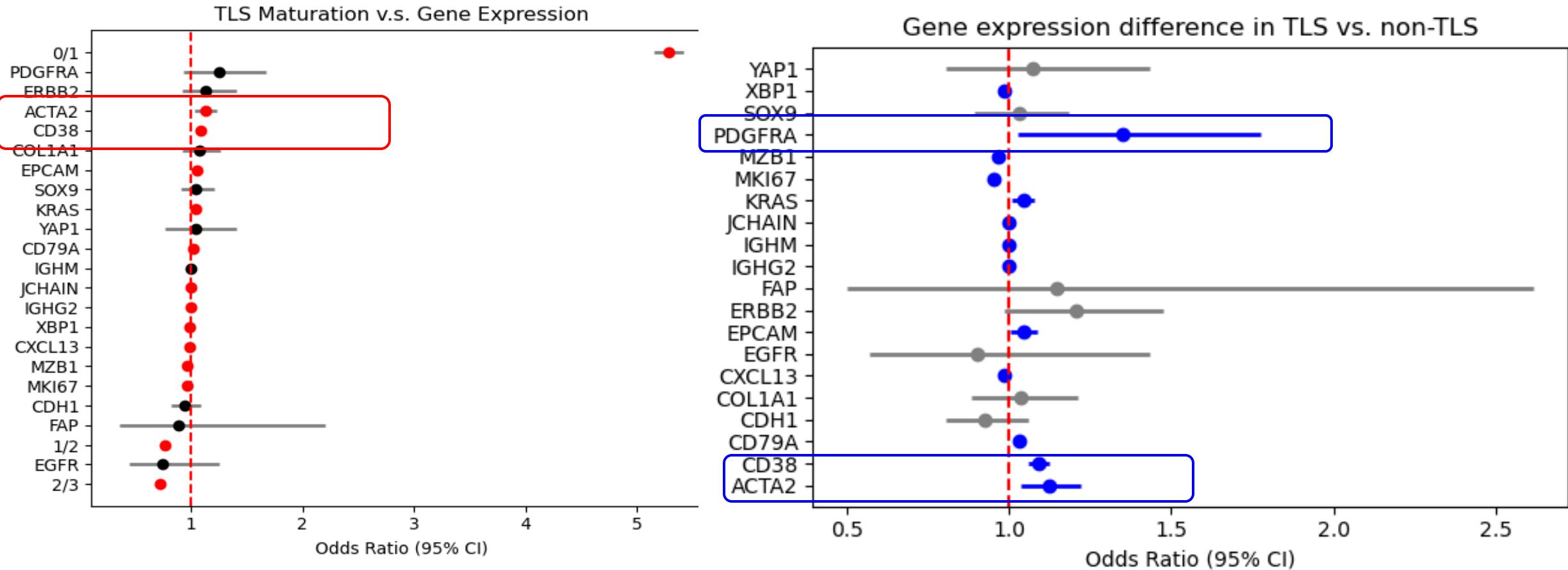
β (entropy)***: 1.62

Cell type

B cell	Macrophage	T cell
Plasma	Monocyte	NK cell
Dendritic cell	Vasculature	Epithelial
Granulocytes	Stroma	No-TLS

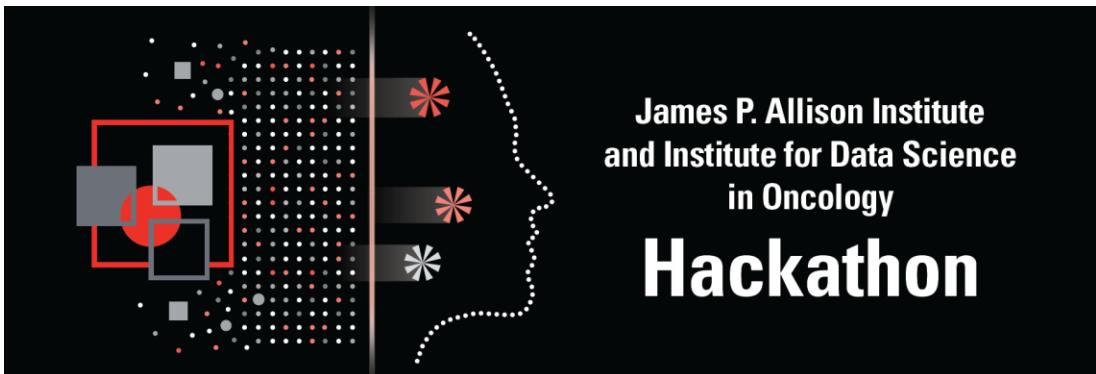
Yu Ding

Gene Expression Profile in/out TLS



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Adolph Trudeau
John Wood



Schematic of workflow