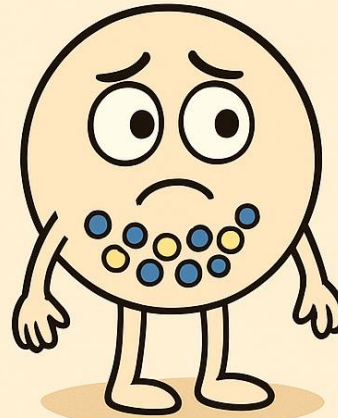


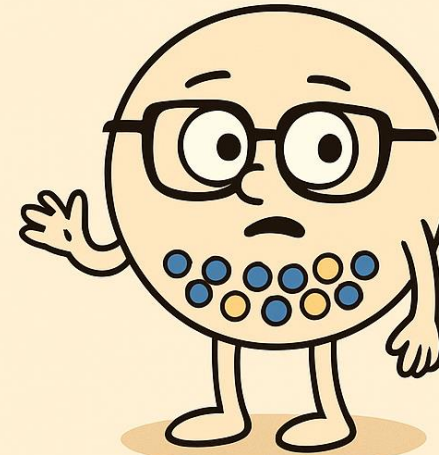
Characterization of TLS maturation states by **CODEX,** **scRNA-seq dataset and** **clinical data**

Team: TLS and the Gang
Team lead: Afrooz Jahedi

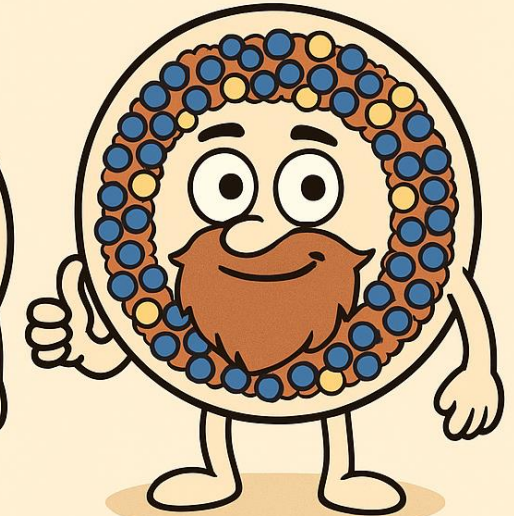
Stages of TLS Maturation



Early TLS



Intermediate
TLS

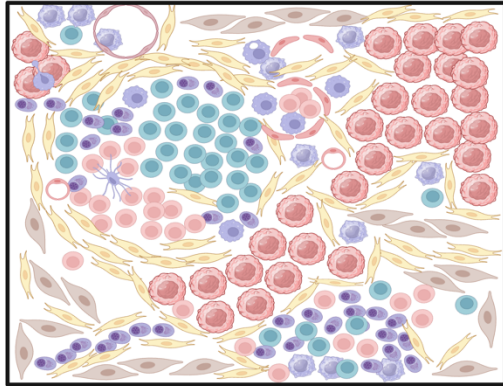


Mature TLS

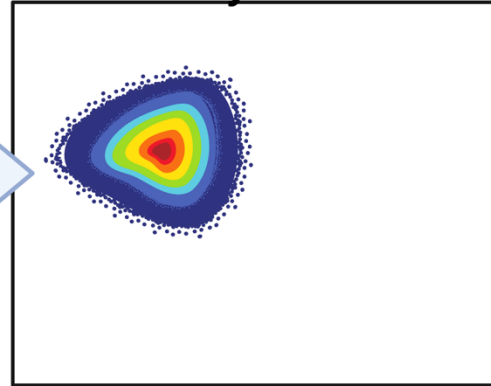
Principle for identification & classification of TLSs

Identification

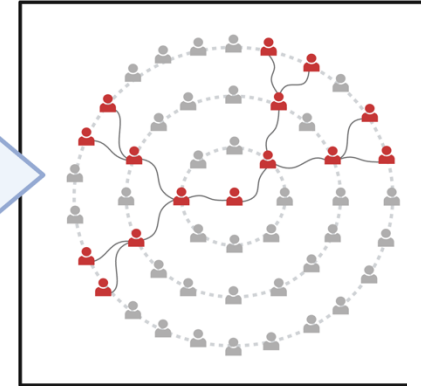
Tissue section



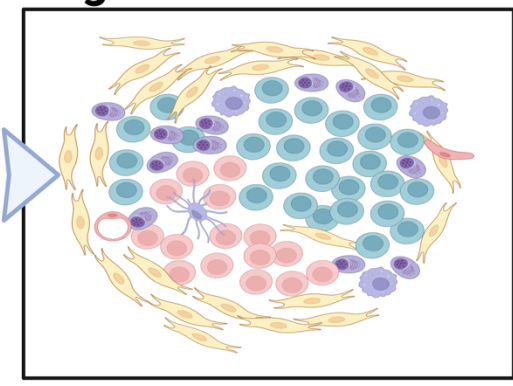
Screening B cell density



Neighbor extending for B centroid

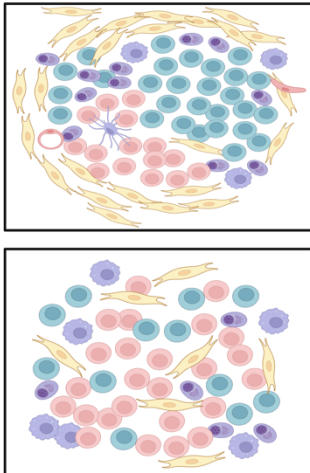


TLS region segmentation



classification

Extracted TLSs

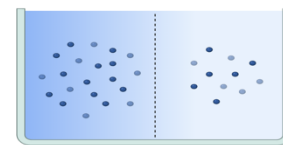


Spatial feature

Cell composition

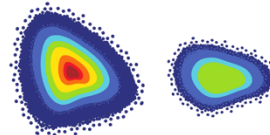


Cell aggregation

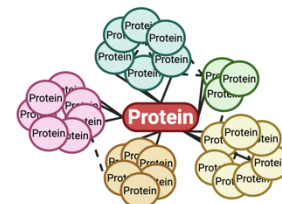


High → Low

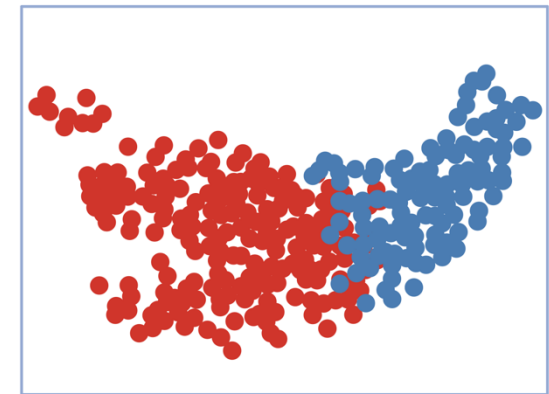
Cell density



Cell interactome

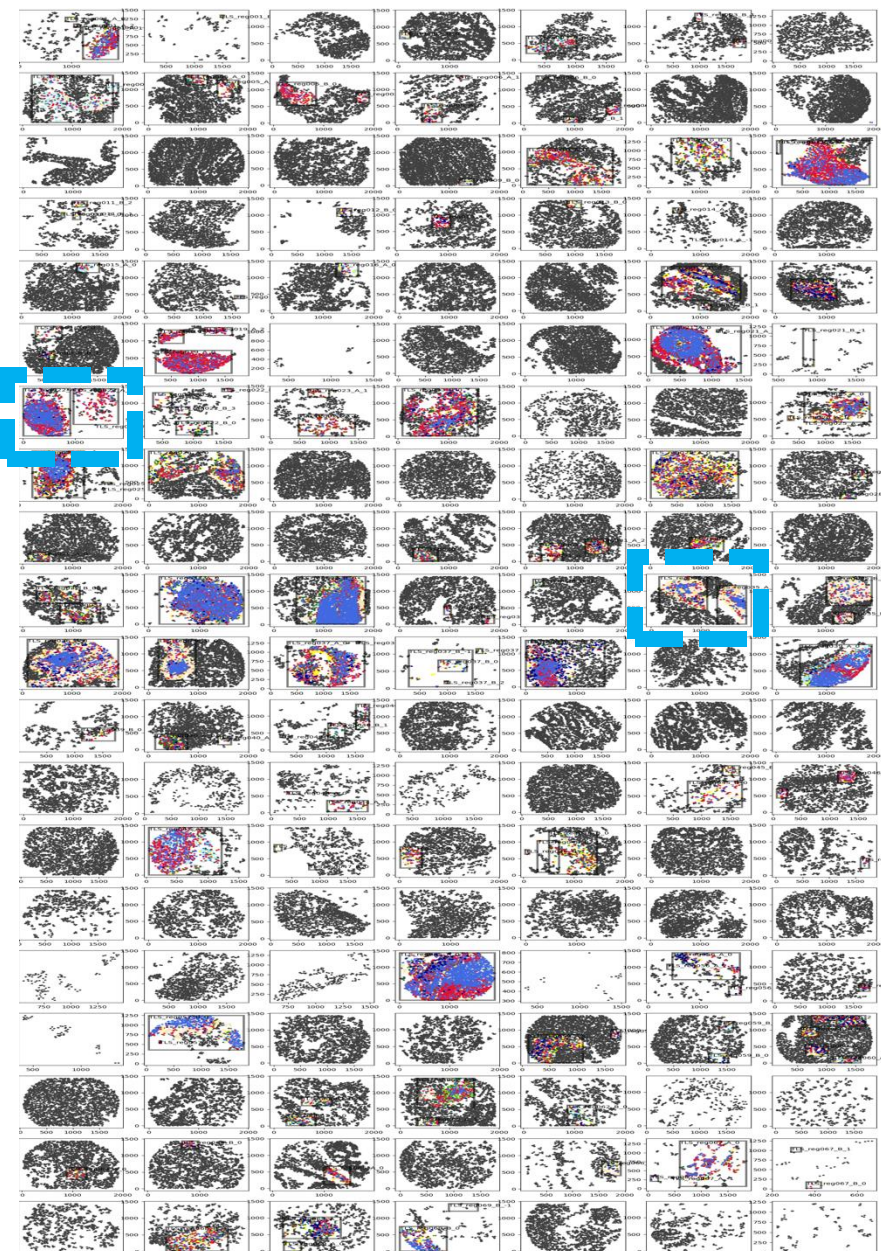


TLS subtypes

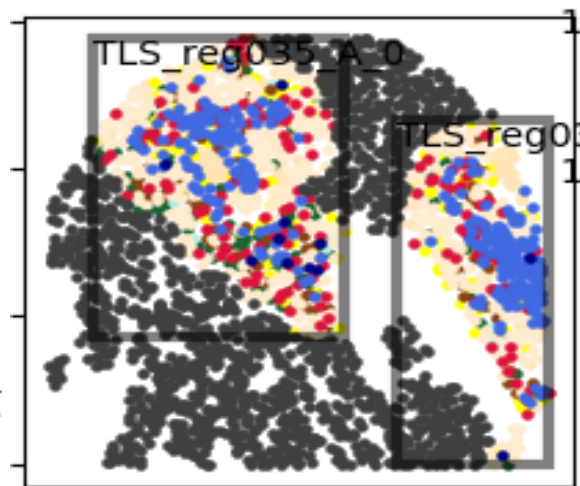


The landscape of TLSs identification

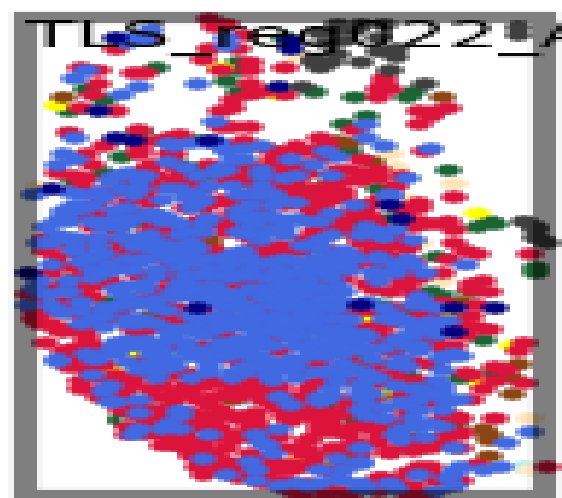
CODEX staining



Multiple-early aggregate

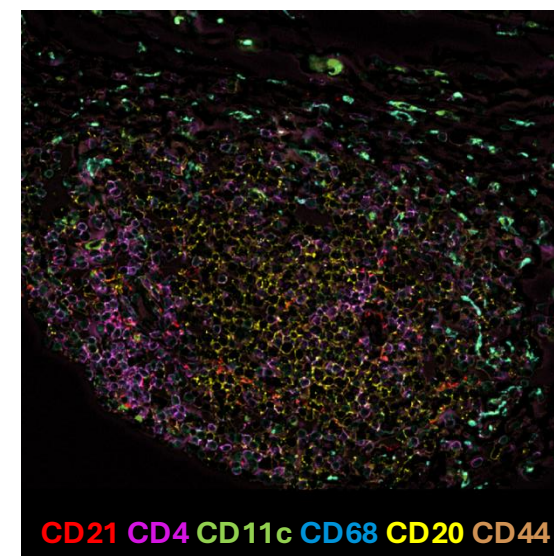
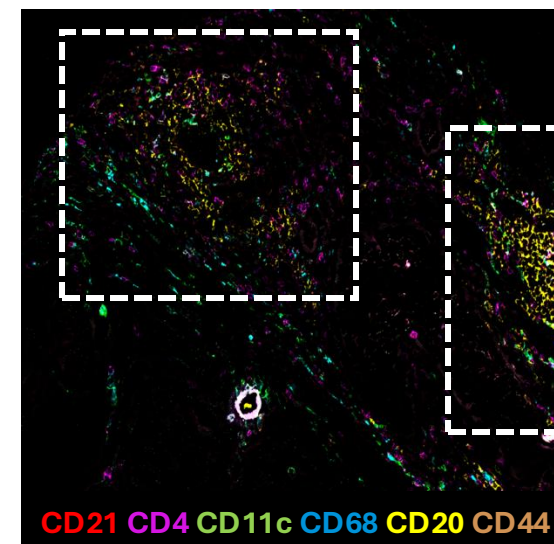


Dominated by one TLS

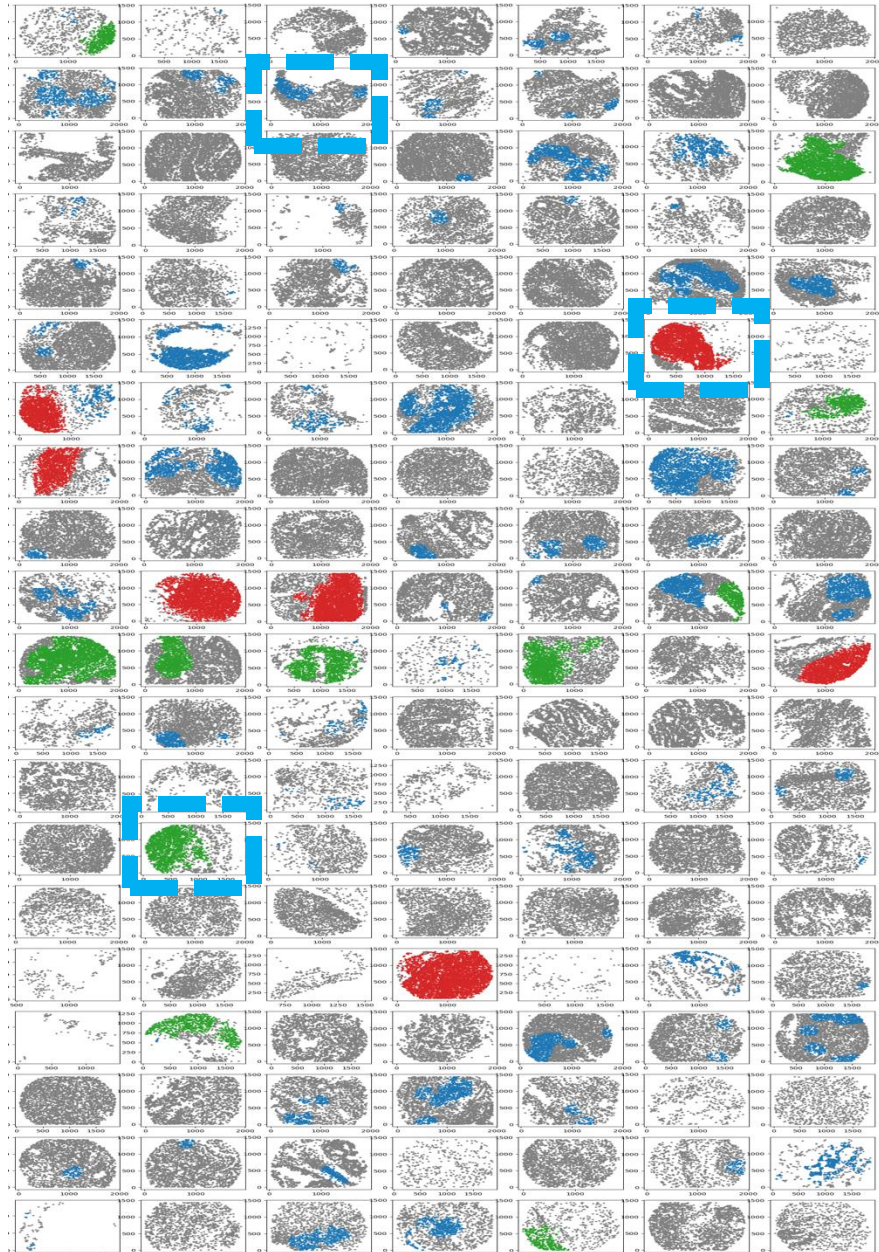


Cell type

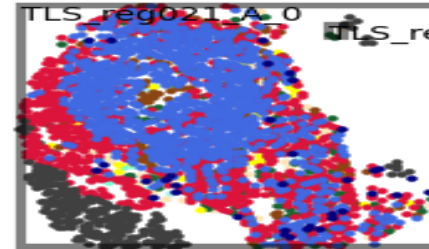
- B cell
- Plasma
- Macrophage
- Monocyte
- T cell
- NK cell
- Dendritic cell
- Granulocytes
- Vasculature
- Stroma
- Epithelial
- No-TLS



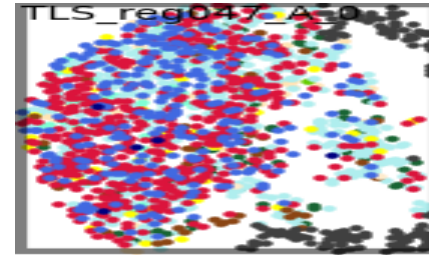
The landscape of TLSs classification



Mature TLS



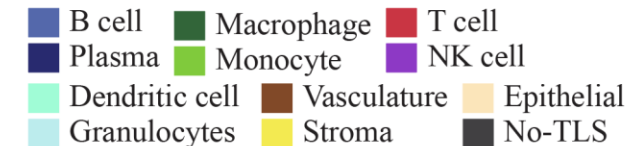
Intermediate TLS



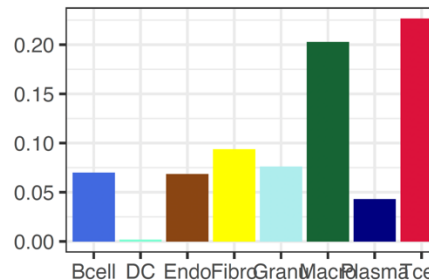
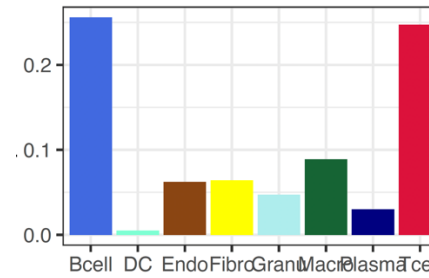
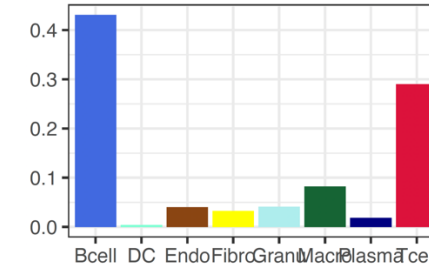
Nascent TLS



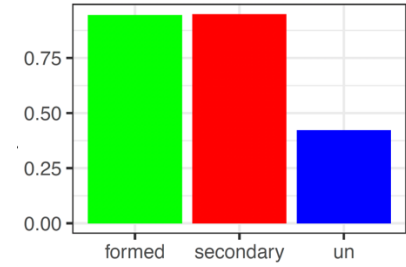
Cell type



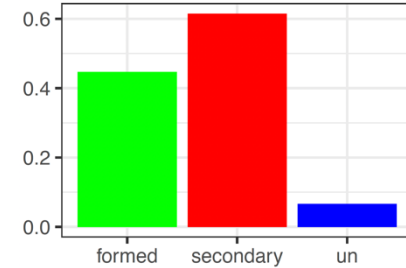
Maturation stage



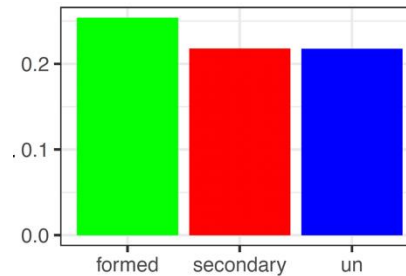
B aggregation



B-B interaction

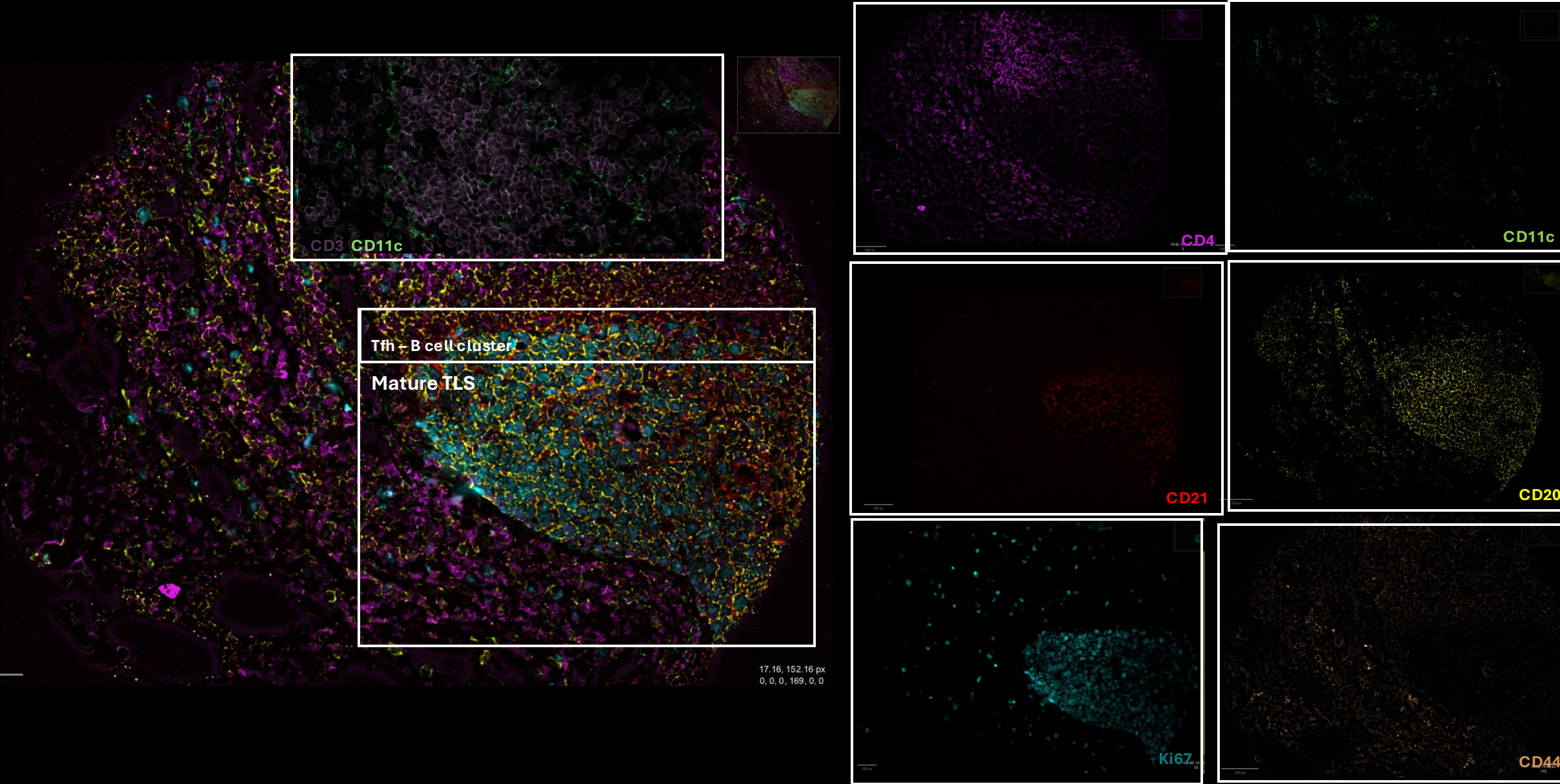


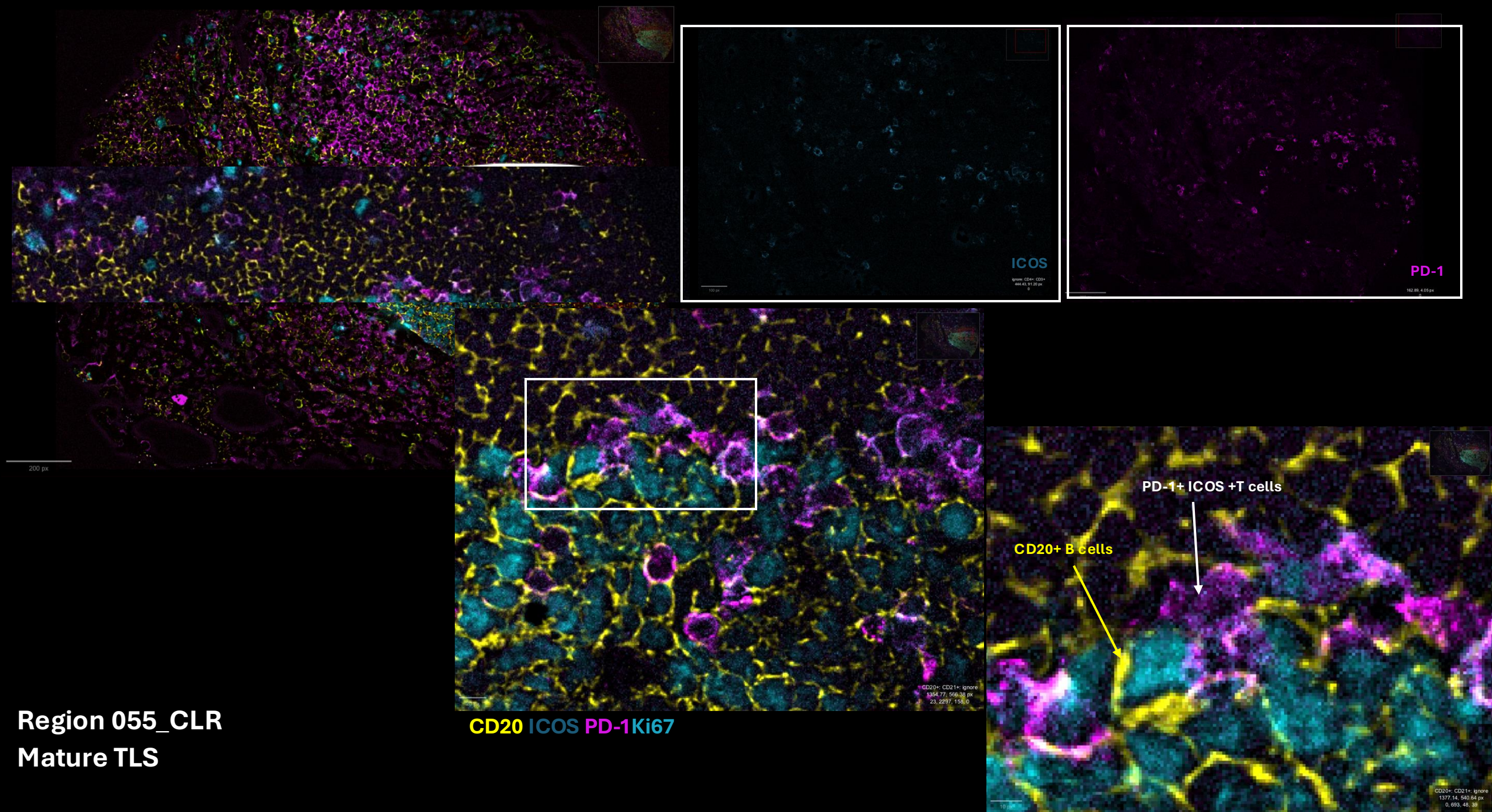
B-T interaction



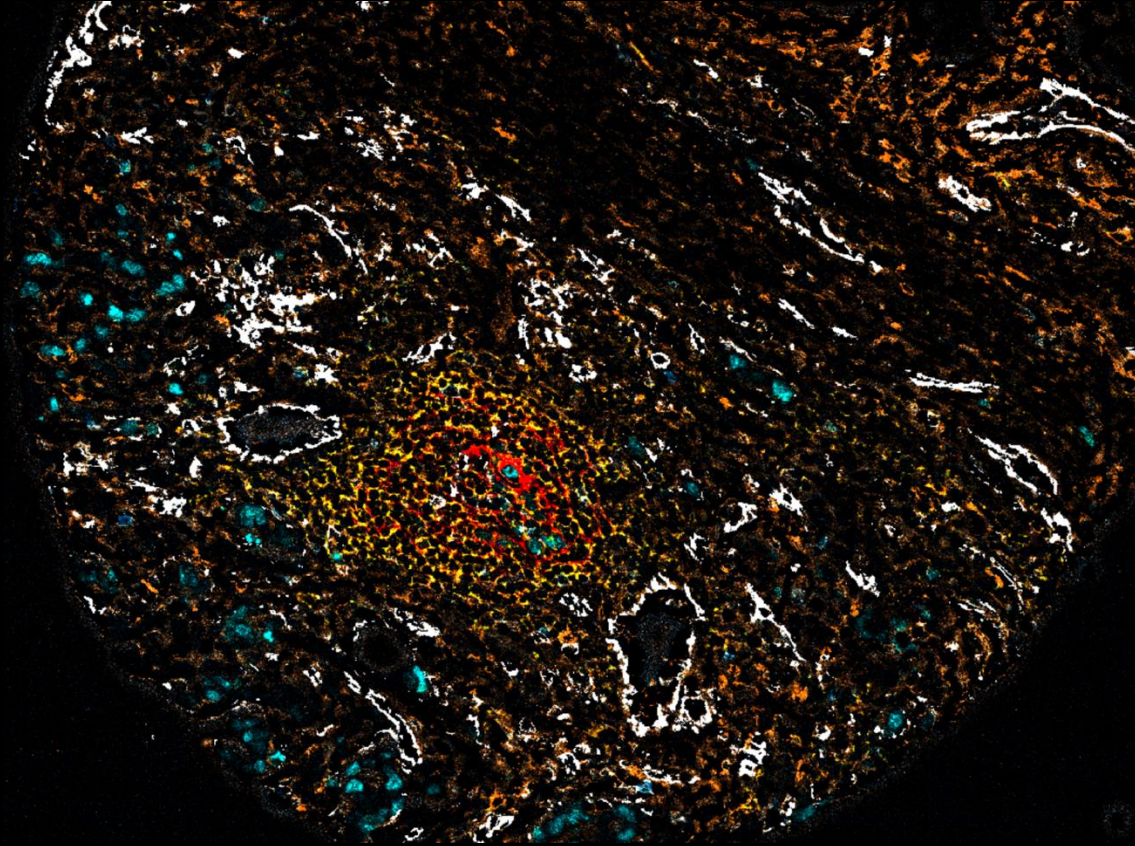
Intermediate
Mature
Nascent

Region 055_CLR

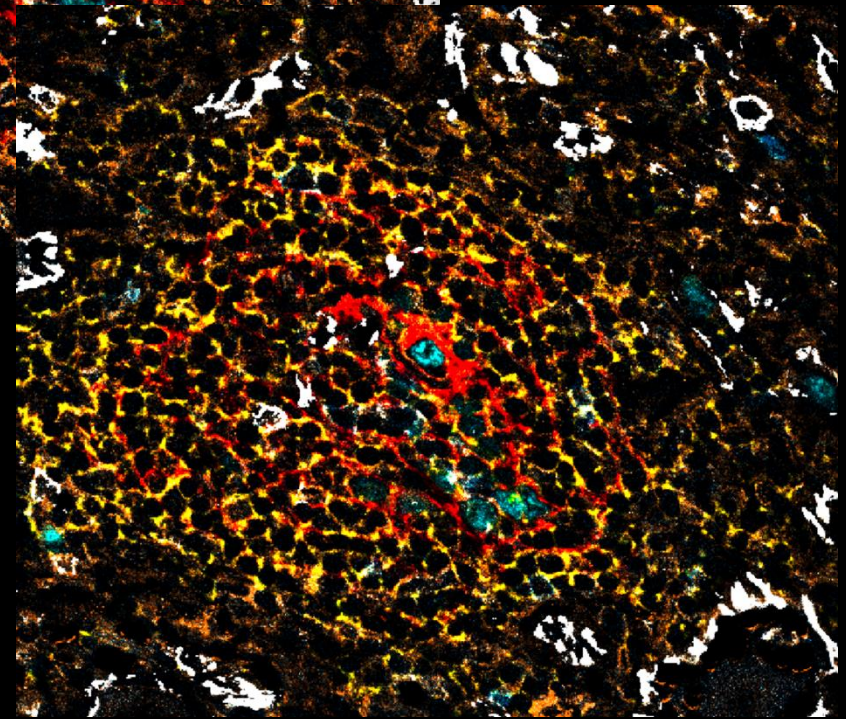
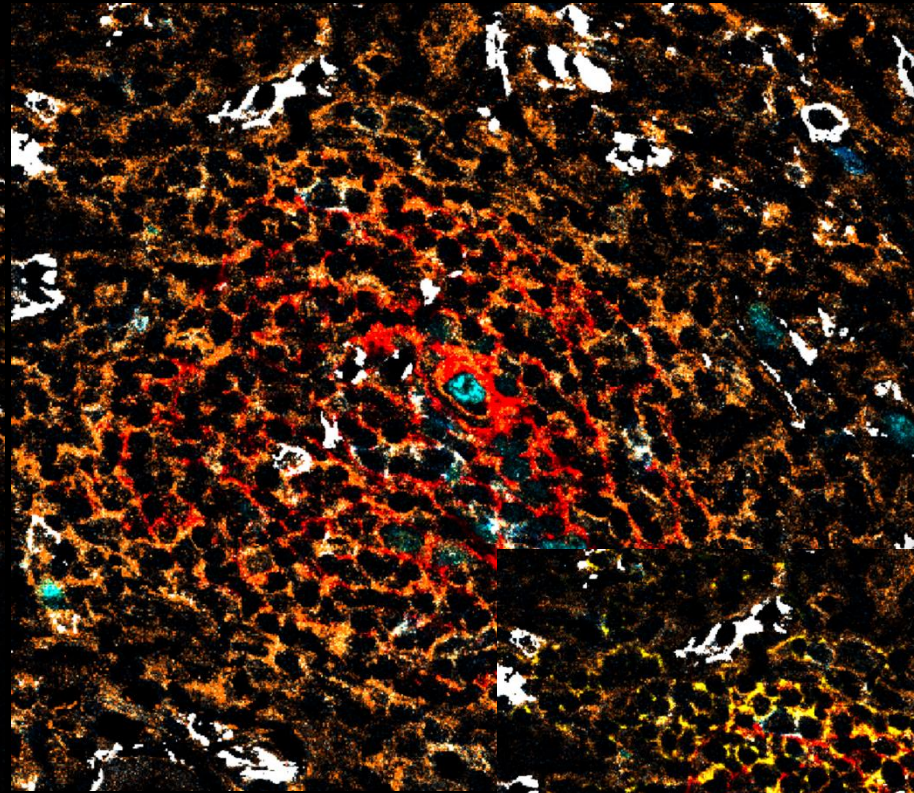




Region 35_DII

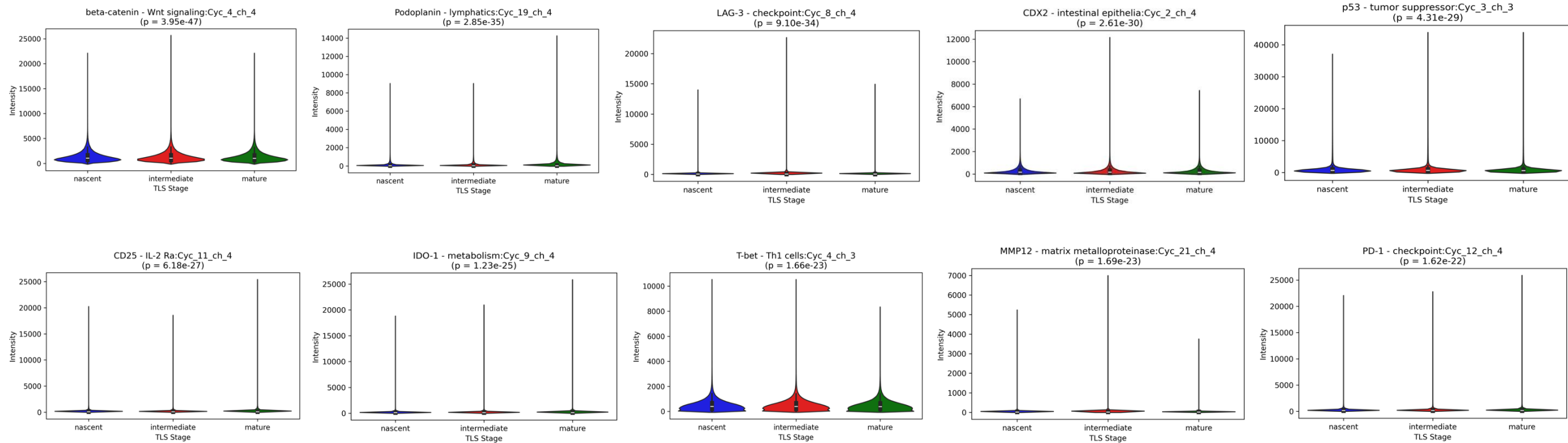


CD20 CD44 Ki67 CD31 CD21



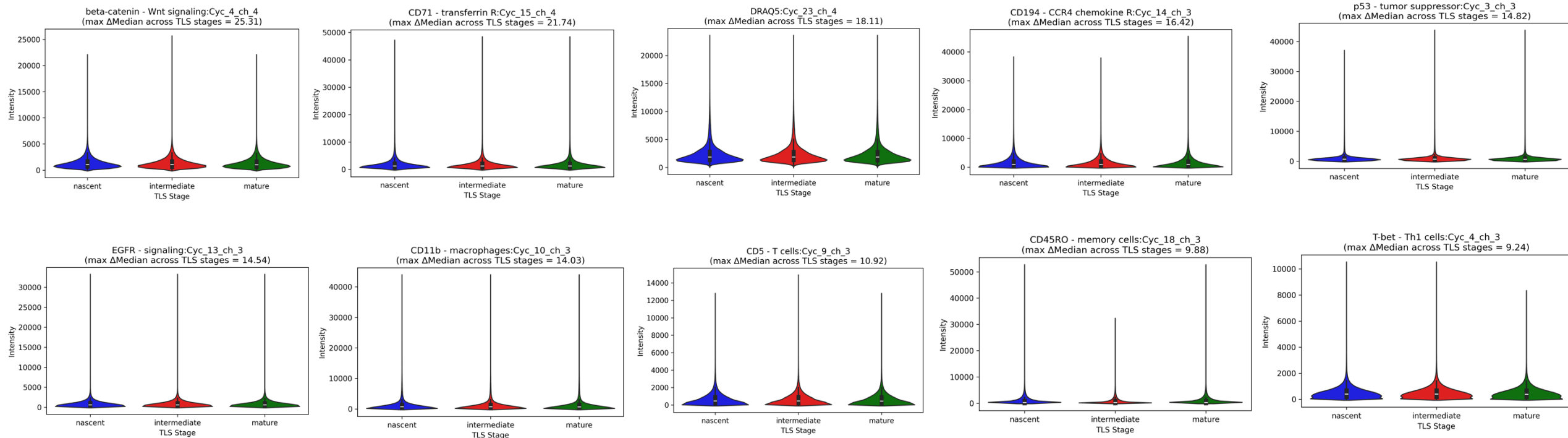
CD20 Ki67 CD31 CD21

Cell type composition 100 μ m around TLS structures sorted by intensity



Mesut Unal

Cell type composition change 100 μ m 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

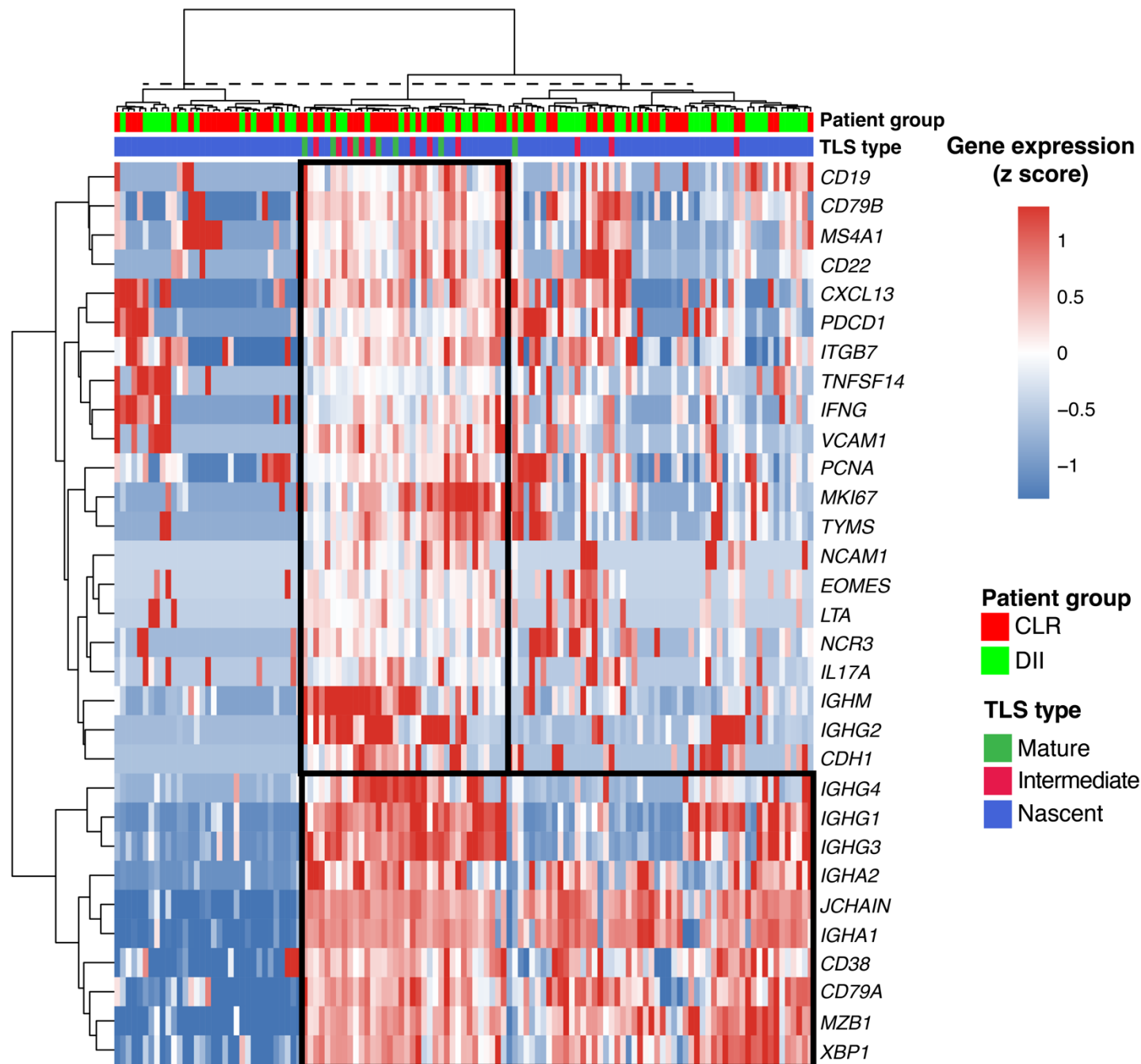


Construct pseudobulk
expression matrix for each
TLS region

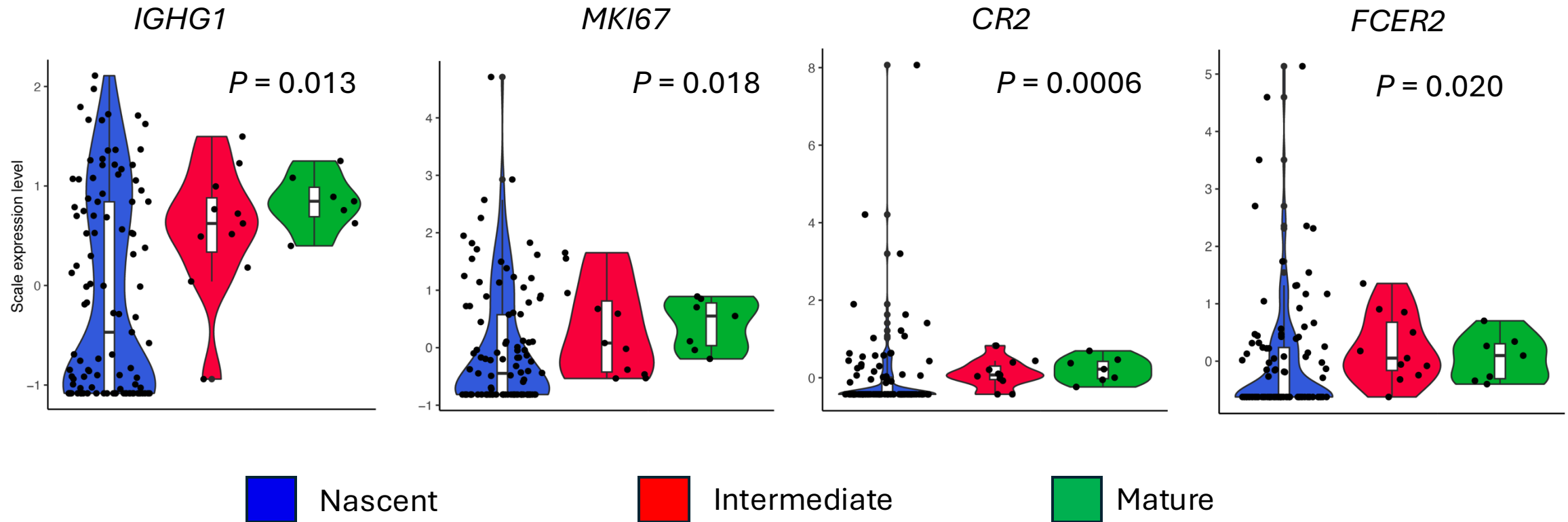


TLS phenotyping

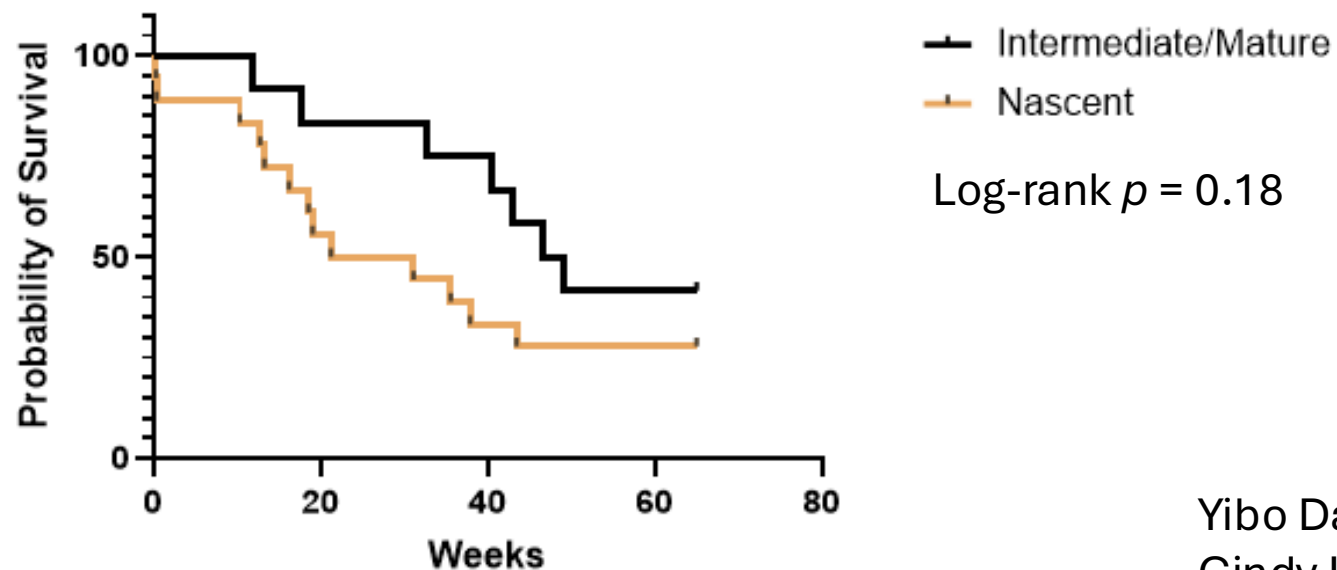
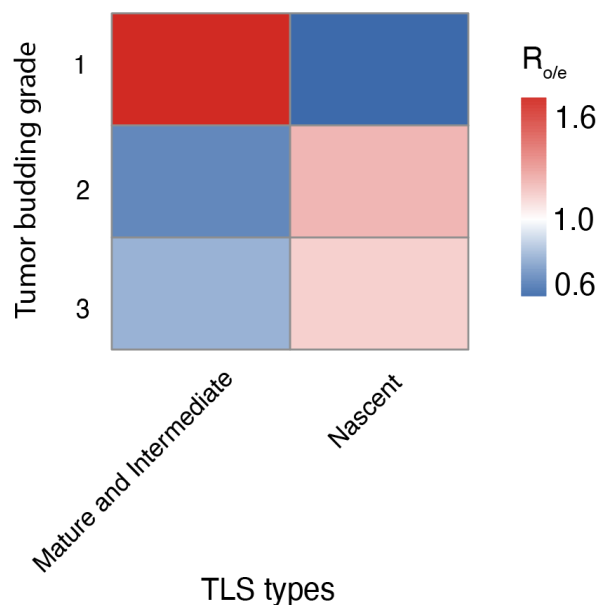
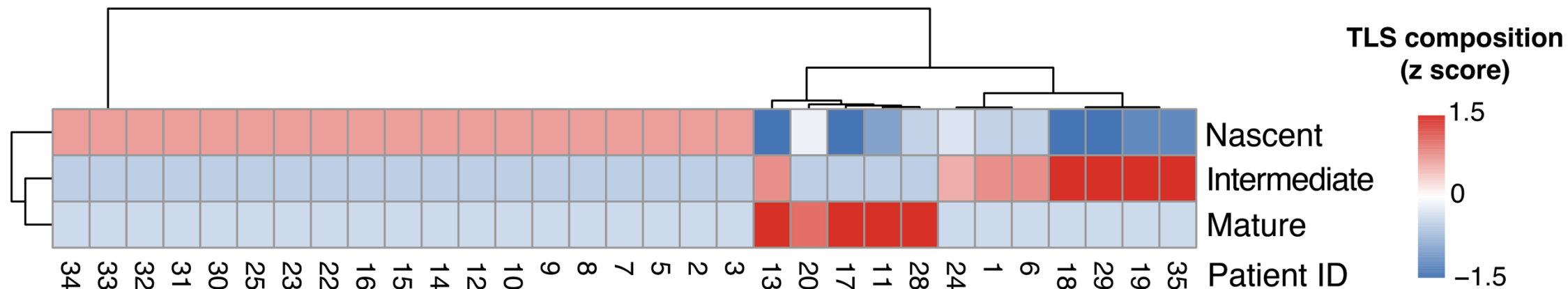
Yibo Dai



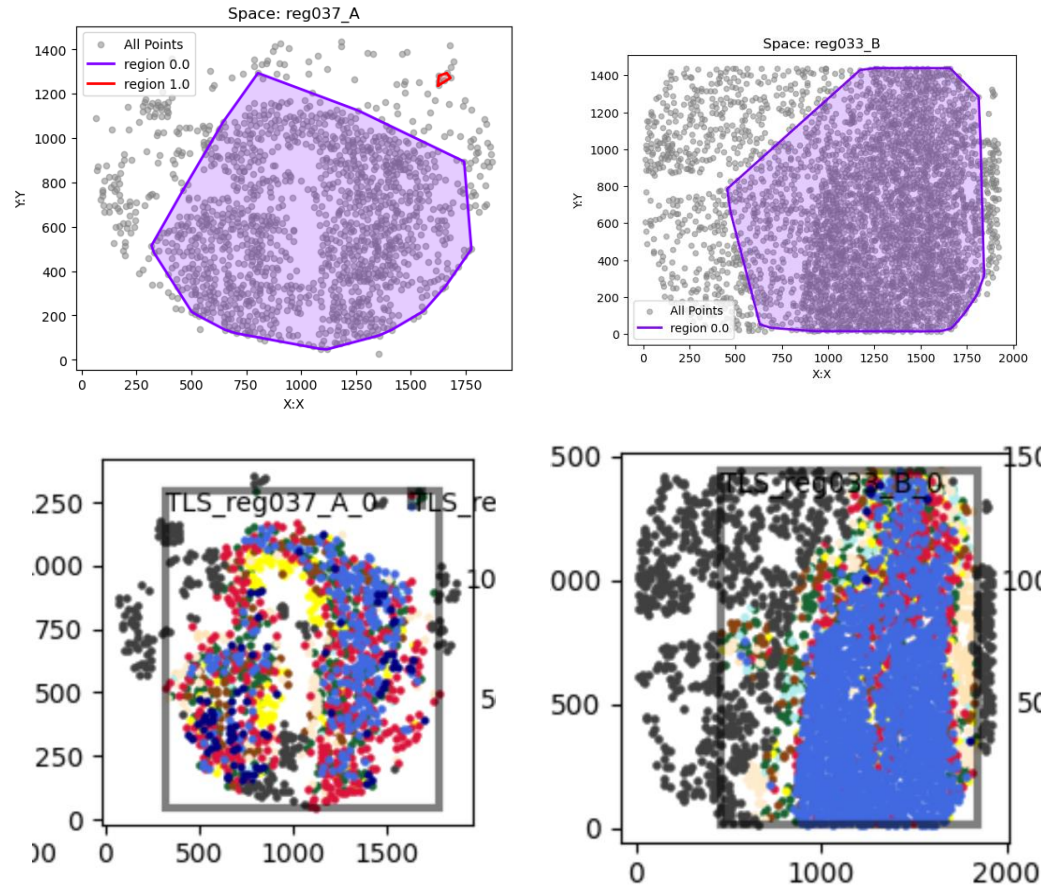
Validation of TLS classifications with single-cell RNA sequencing data



Correlation with clinical information



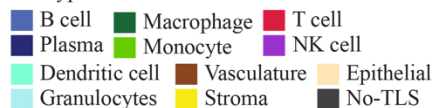
Cell Composition Analysis within TLS



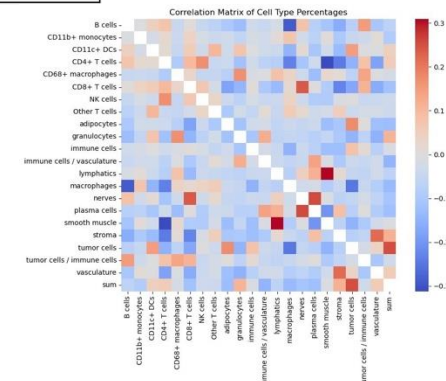
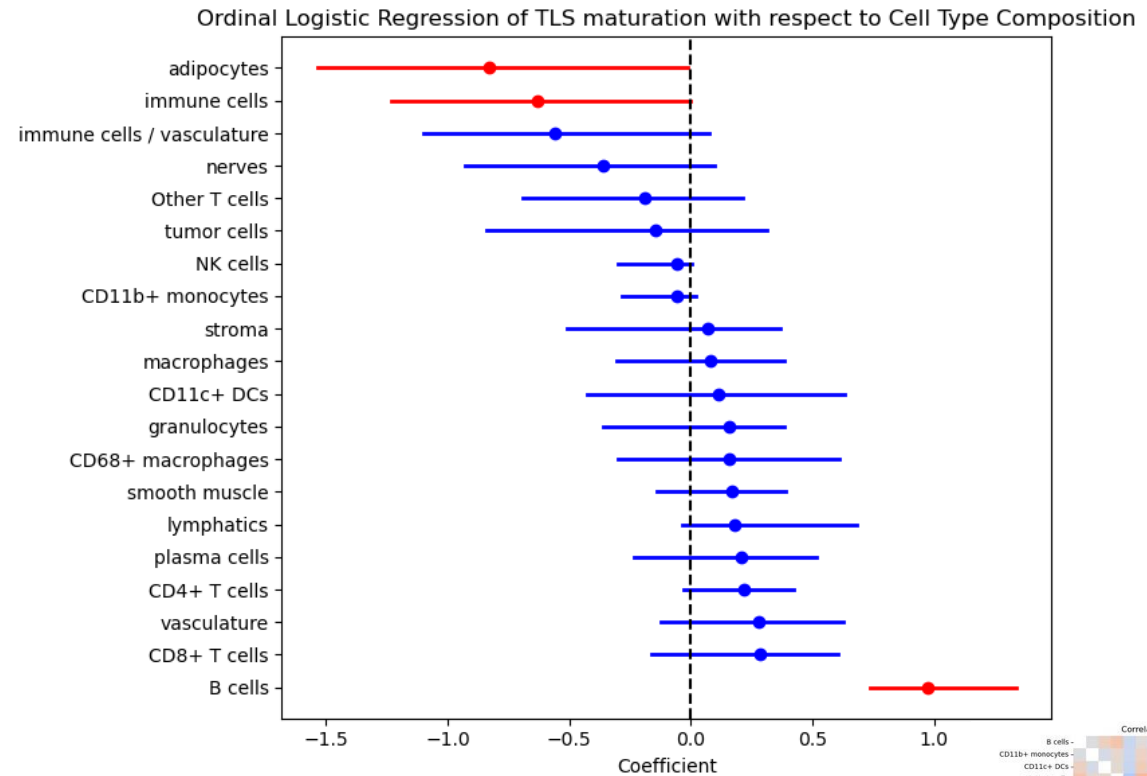
entropy: 2.59

entropy: 7.50

Cell type



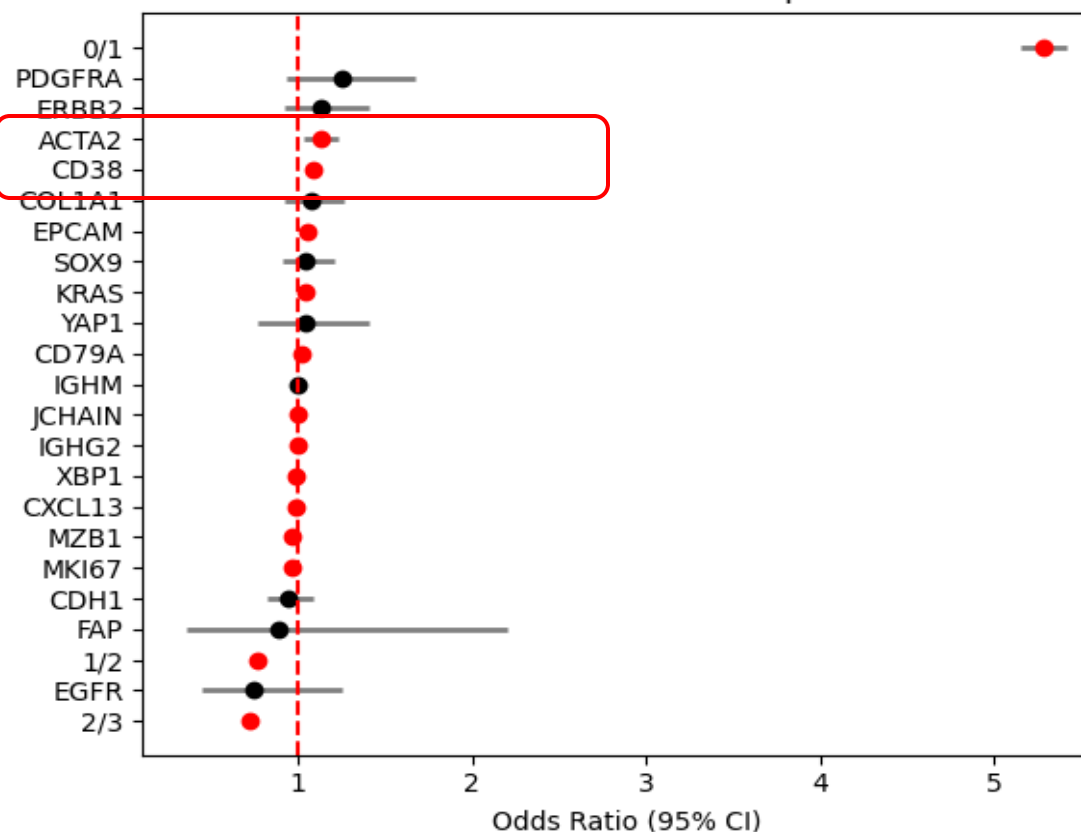
β (entropy)^{***}: 1.62



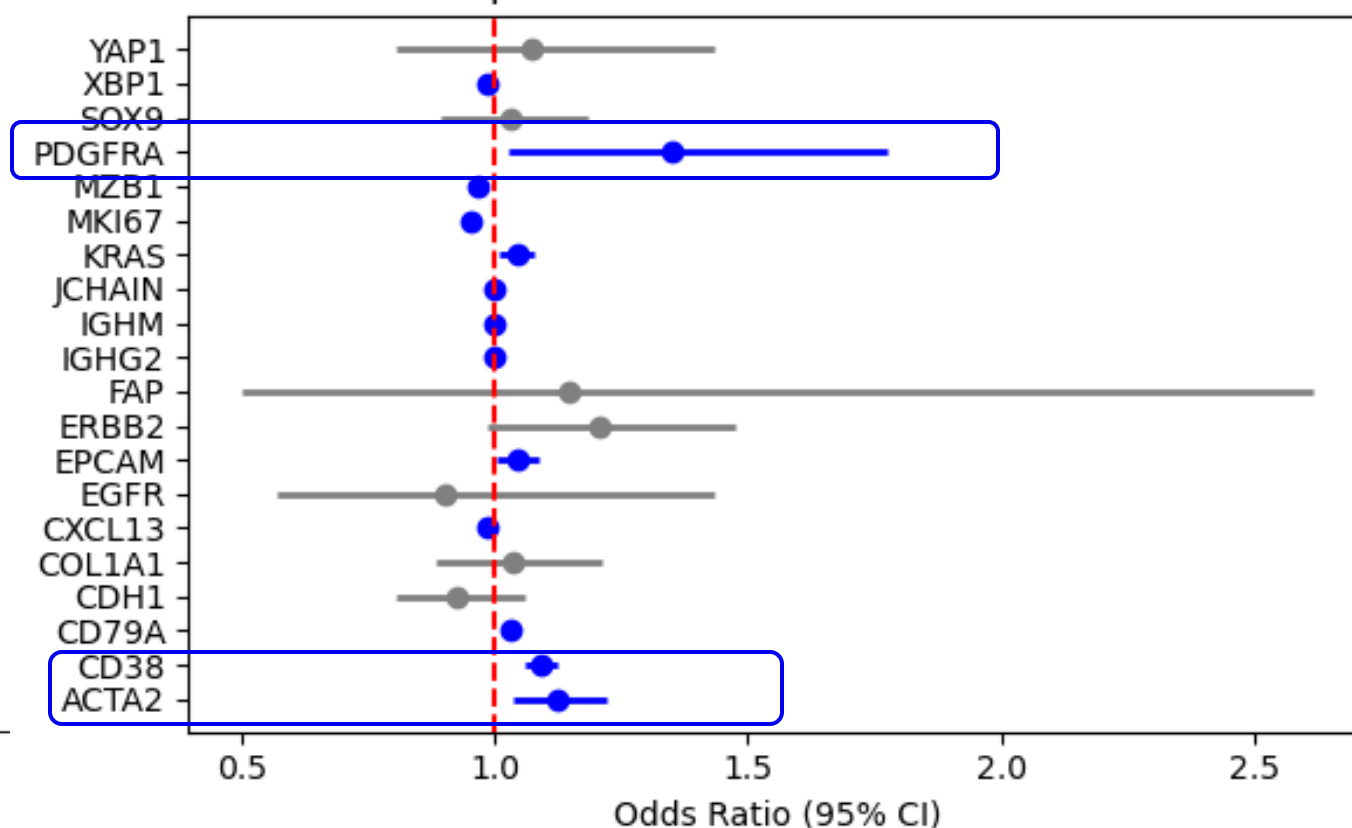
Yu Ding

Gene Expression Profile in/out TLS

TLS Maturation v.s. Gene Expression

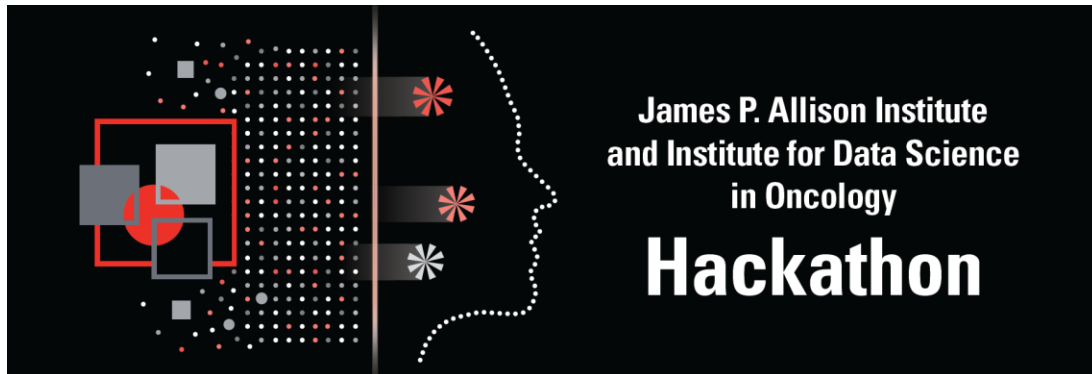


Gene expression difference in TLS vs. non-TLS



Acknowledgement

Dr. James Allison
Dr. Padmanee Sharma
Dr. Jaffray David
Dr. Garry Nolan
Dr. Linghua Wang
Dr. Yury Gultsev
Dr. Yuqi Tan
Dr. Bokai Zhu
Dr. James Mancuso
Andrea Hawkins
Adolph Trudeau
John Wood



Schematic of workflow