Analyzing RNA splicing in single cell and spatial transcriptomics data with the SpliZ
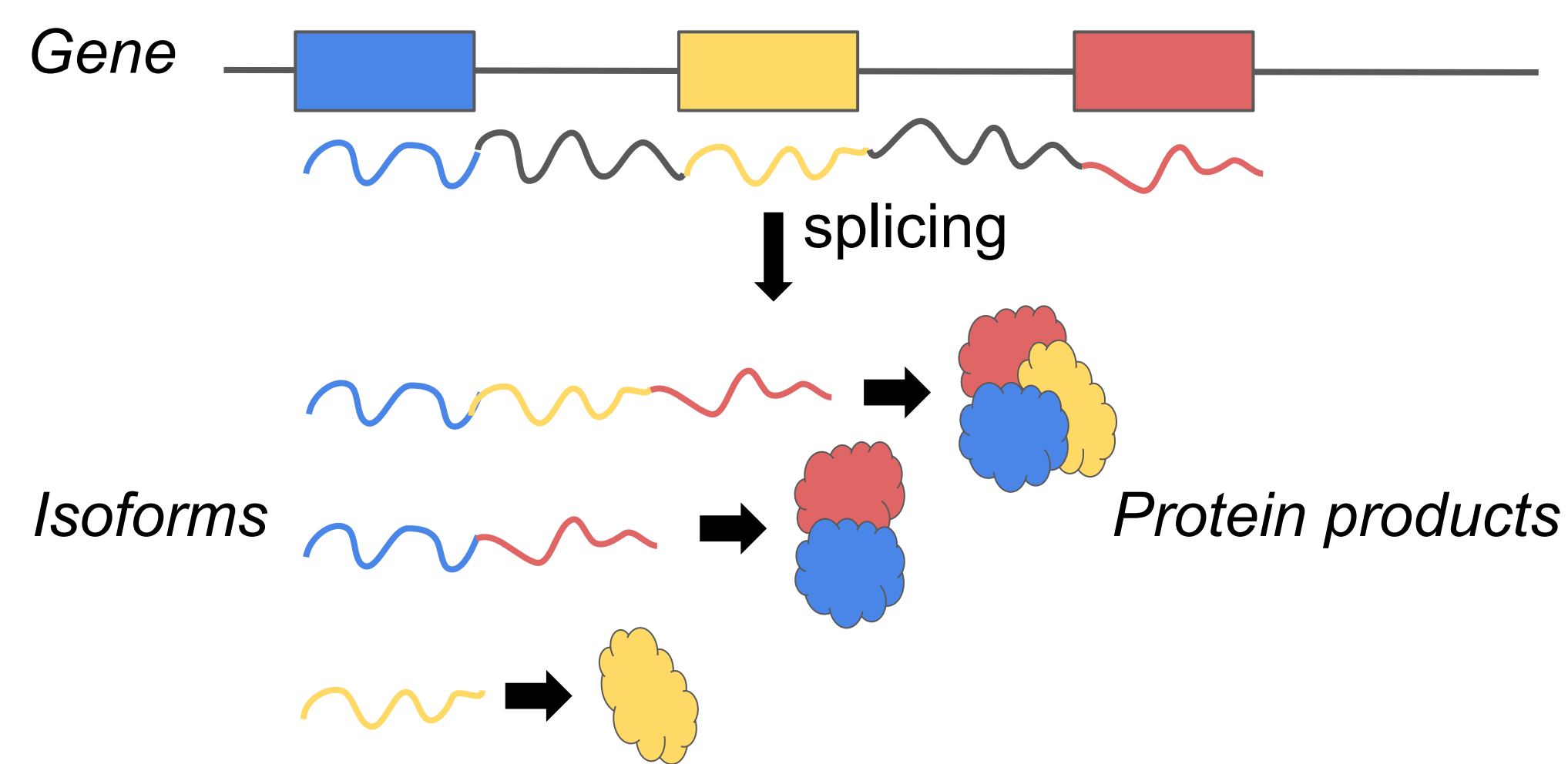
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What is RNA splicing?

- **Alternative splicing:** a process by which different RNAs (isoforms) are created from the same gene

- > 95% of human genes are alternatively spliced

- Some genes have thousands of isoforms

- Different isoforms can have opposite functions

Splicing detection in single cells

Single cell studies currently use gene expression levels to investigate cell types. Are there cell-specific splicing patterns as well?
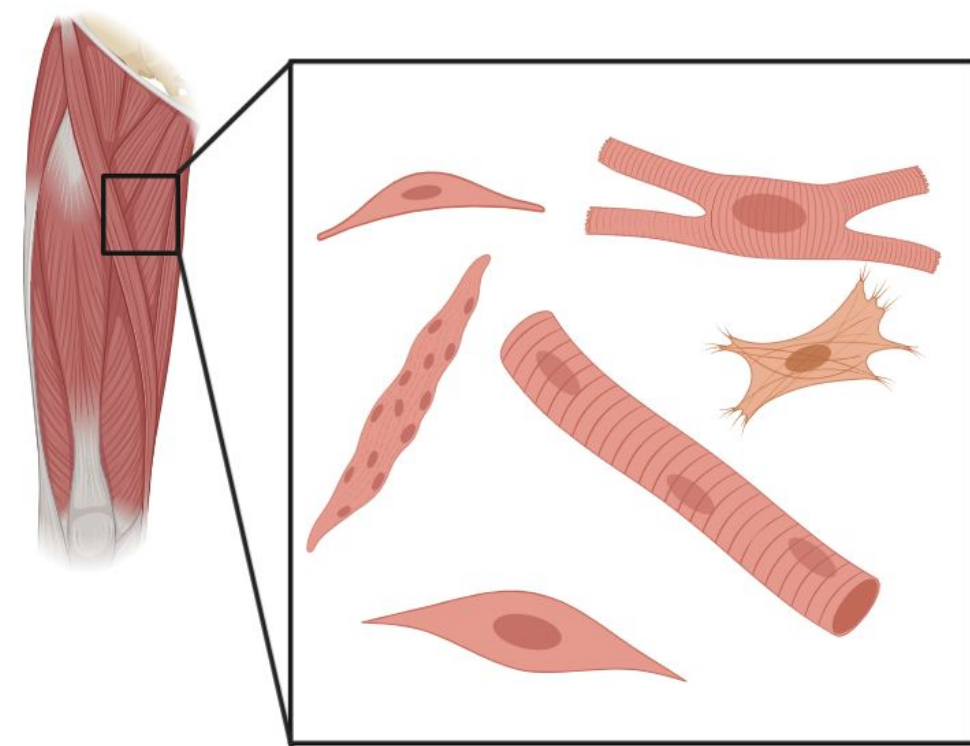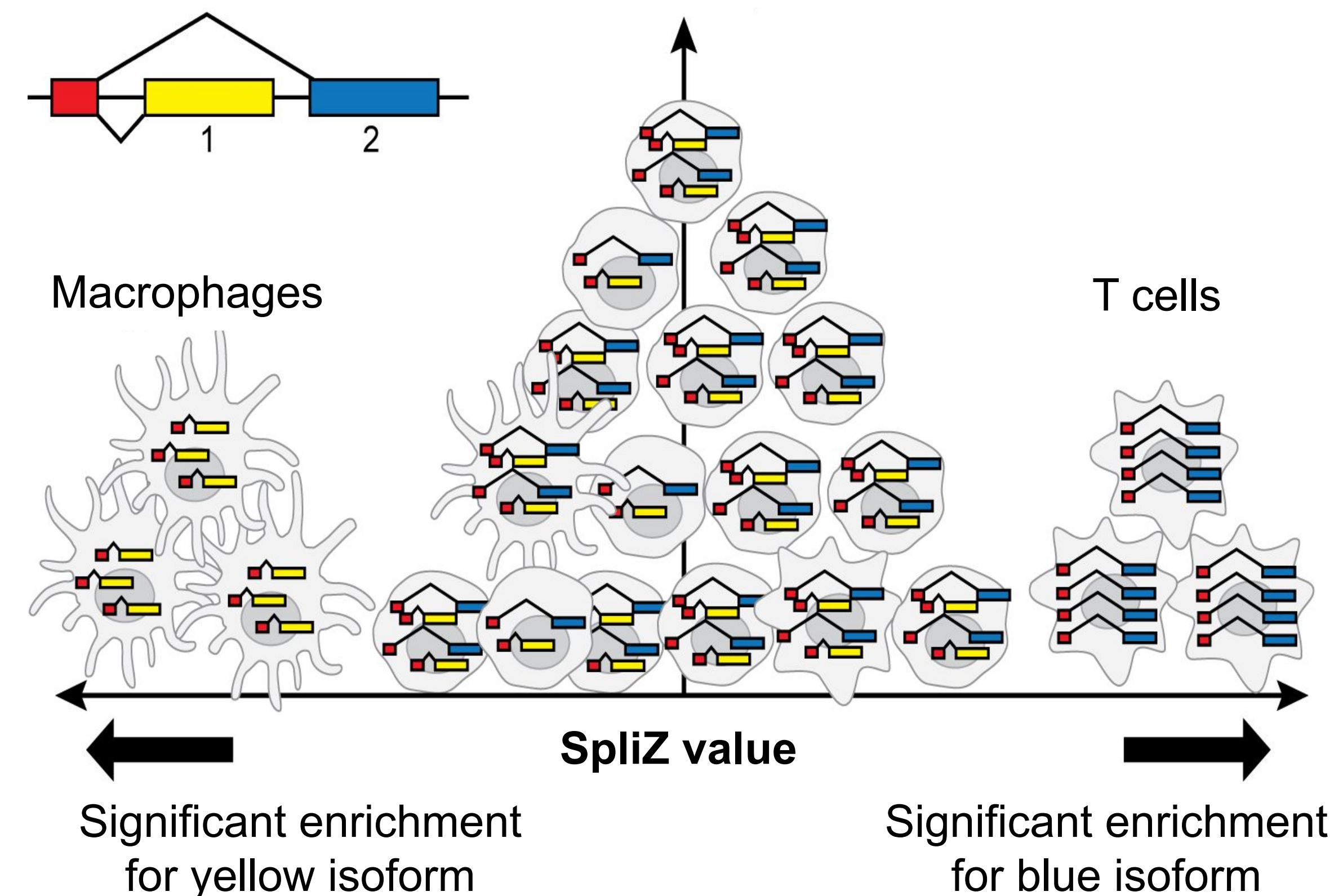

Cell type may be partially determined by isoform

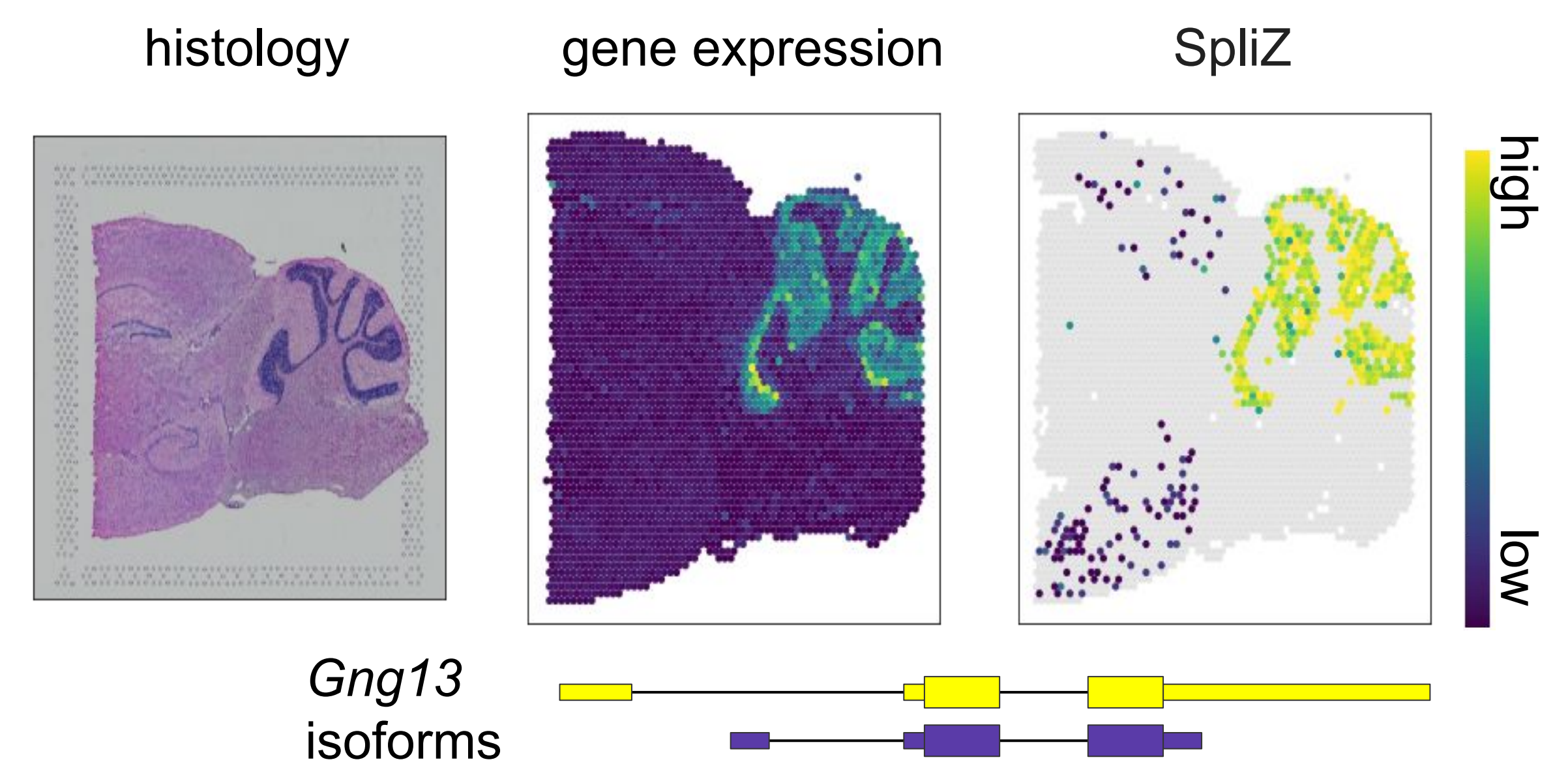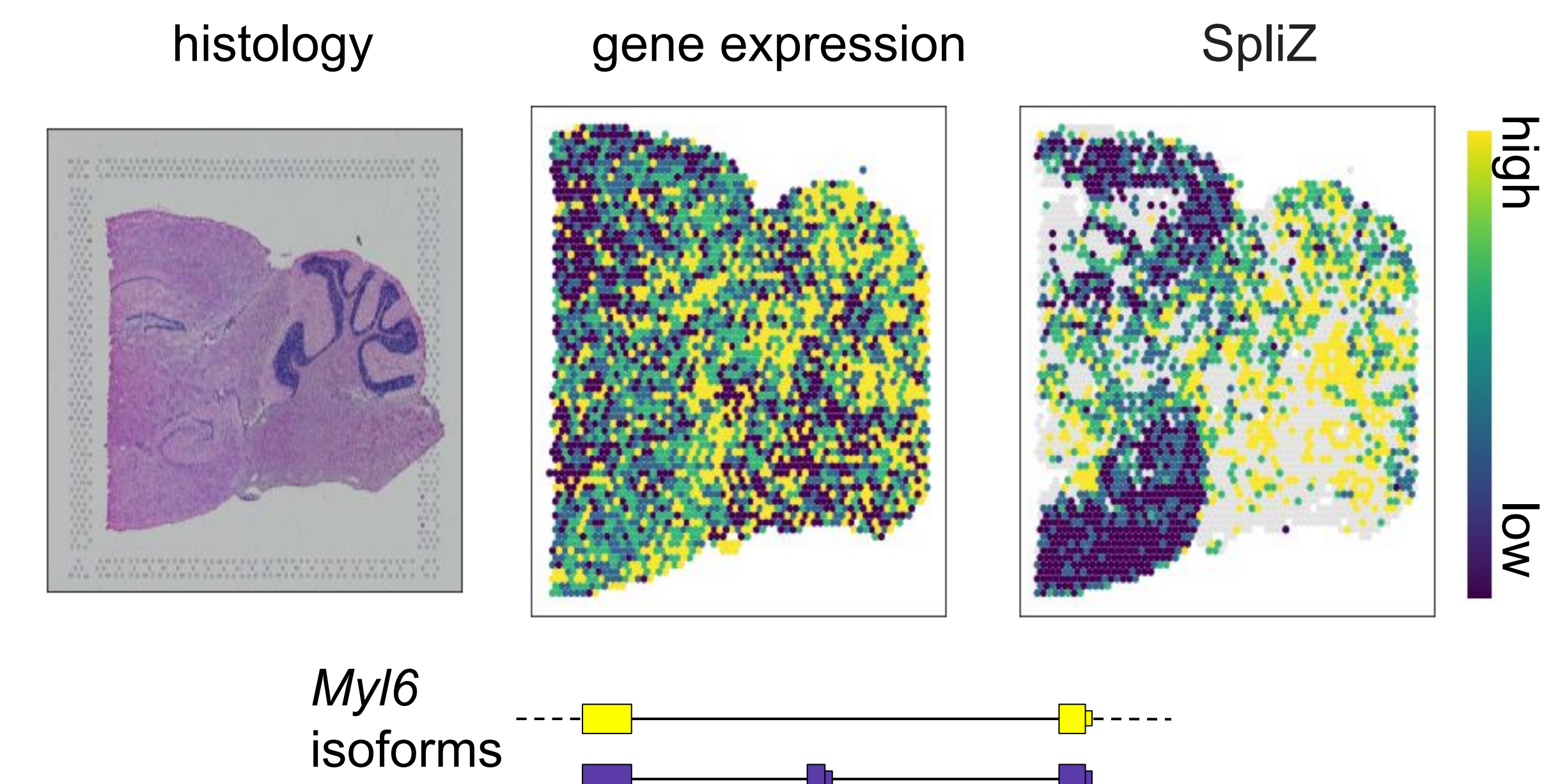*Goal: Quantify alternative splicing in scRNA-seq data*

The SpliZ: splicing score per cell/gene

For each gene, the SpliZ assigns cells with shorter introns lower SpliZ values

SpliZ value

Significant enrichment for yellow isoform

Significant enrichment for blue isoform

Application to 10x data from 12 tissues

Applying the SpliZ to **75,146 10x cells across 12 human tissues and 82 cell types** from the Tabula Sapiens dataset allows for the creation of the first single cell splicing atlas
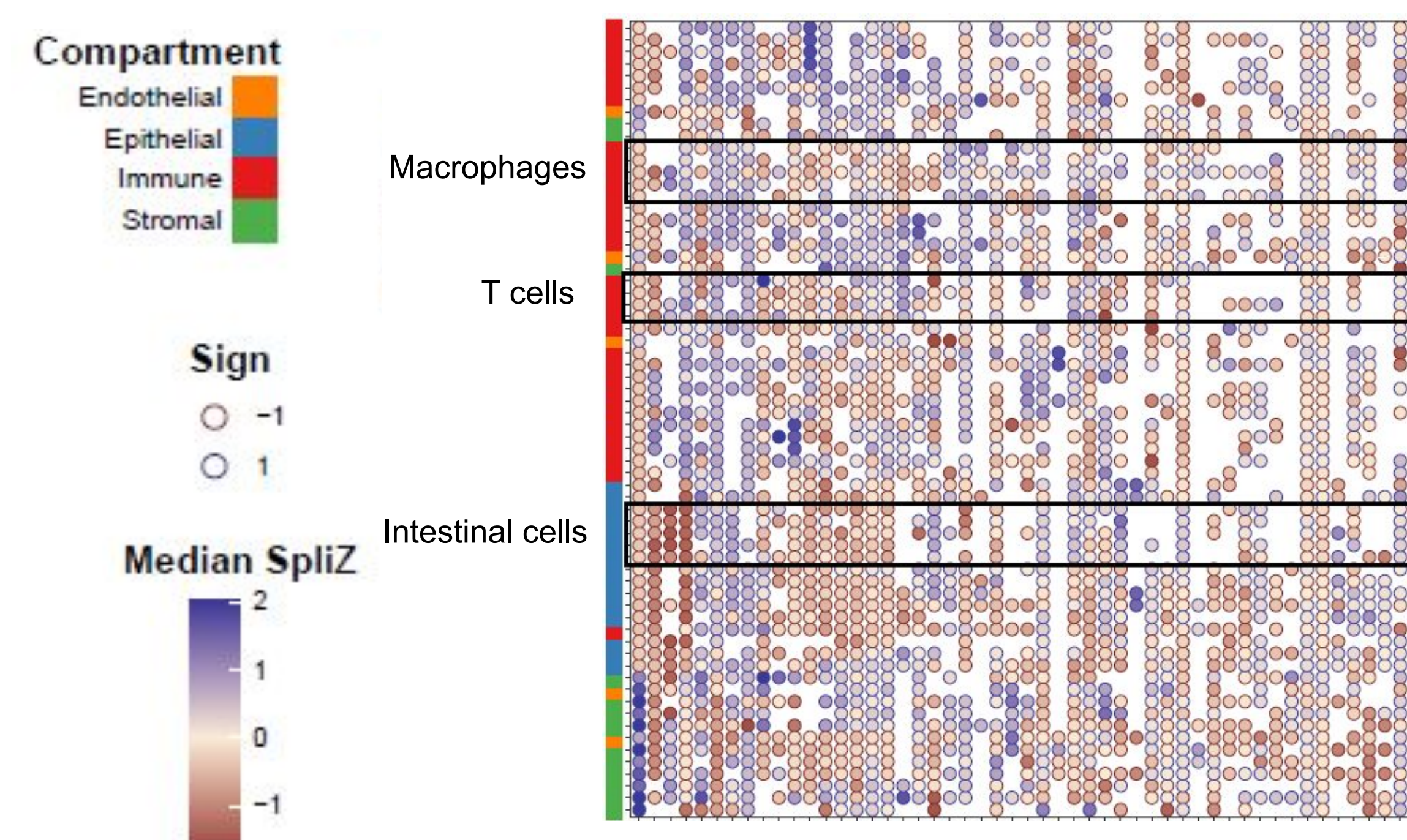

Application to spatial transcriptomics

Application of the SpliZ to **visium data** from the mouse brain reveals **spatial localization of splice isoforms** distinct from gene expression localization.

histology   gene expression   SpliZ

Myl6 isoforms

histology   gene expression   SpliZ

Gng13 isoforms

Acknowledgements