



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

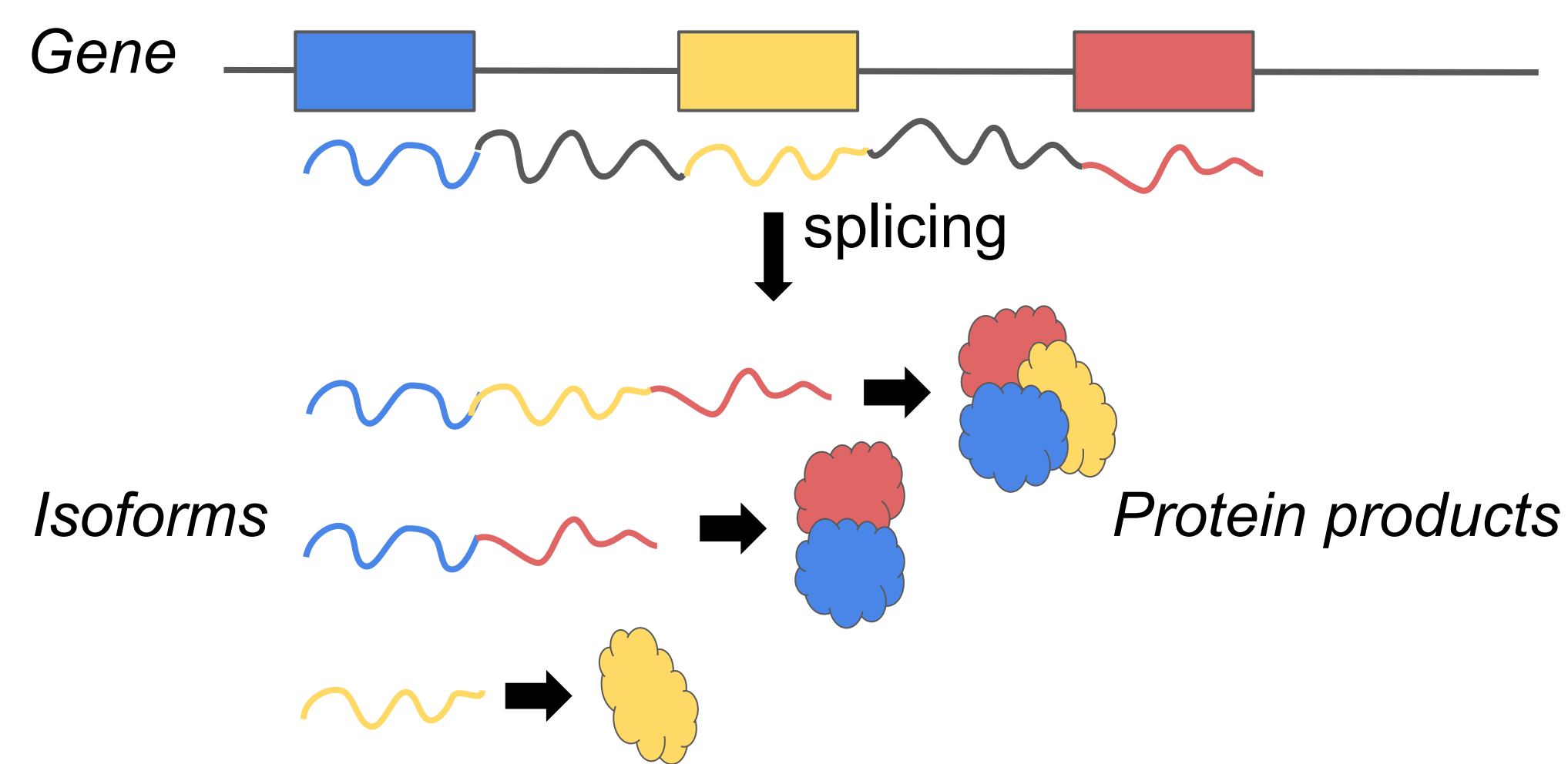


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What is RNA splicing?

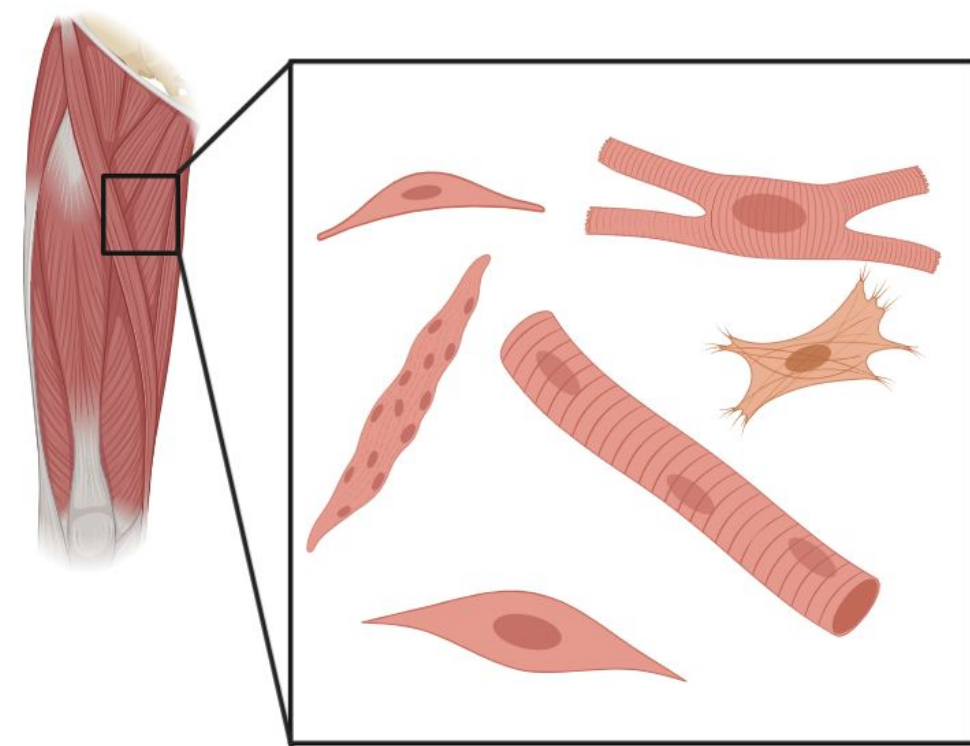
- **Alternative splicing:** a process by which different RNAs (isoforms) are created from the same gene



- > 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?

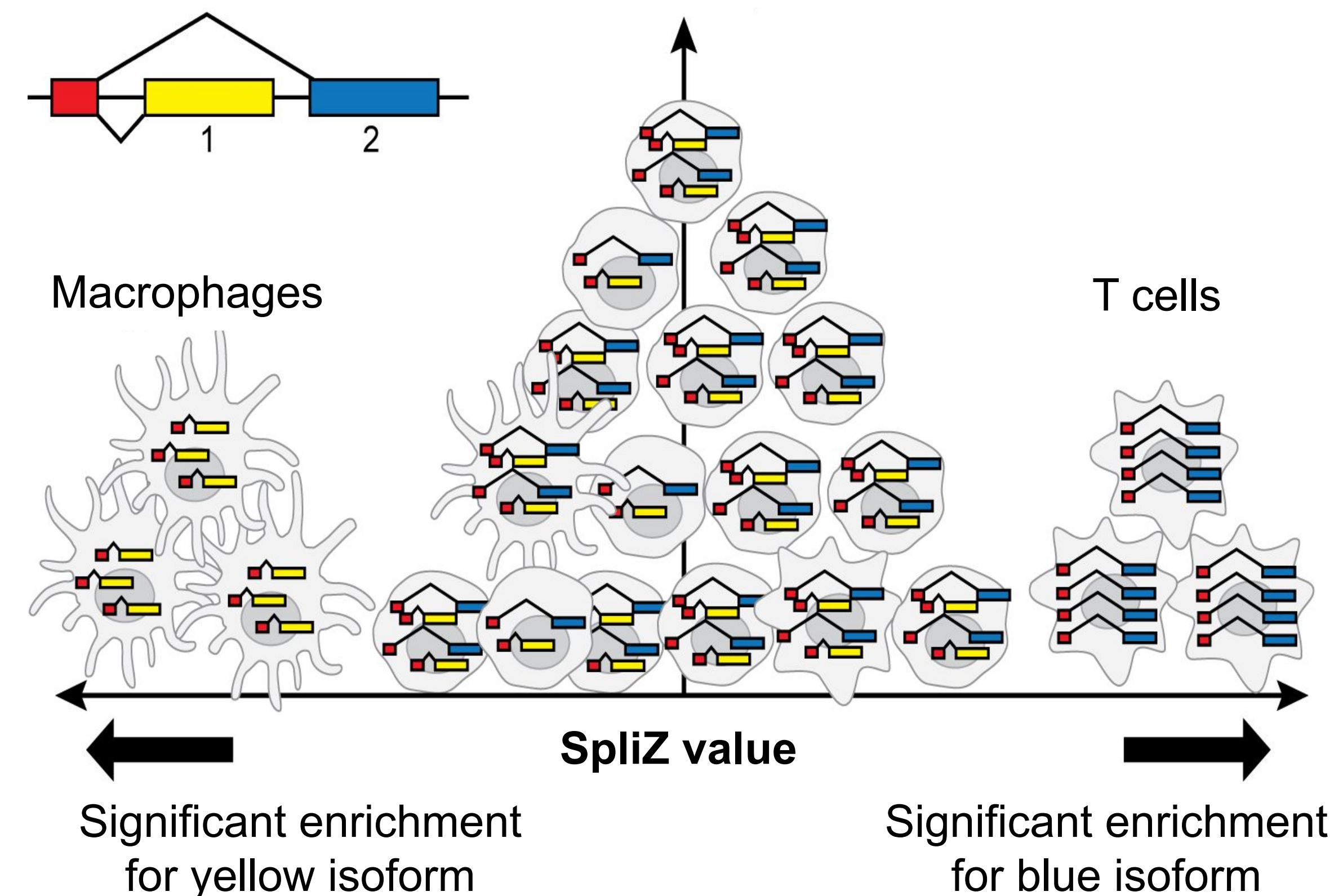


Cell type may be partially determined by isoform

Goal: Quantify alternative splicing in scRNA-seq data

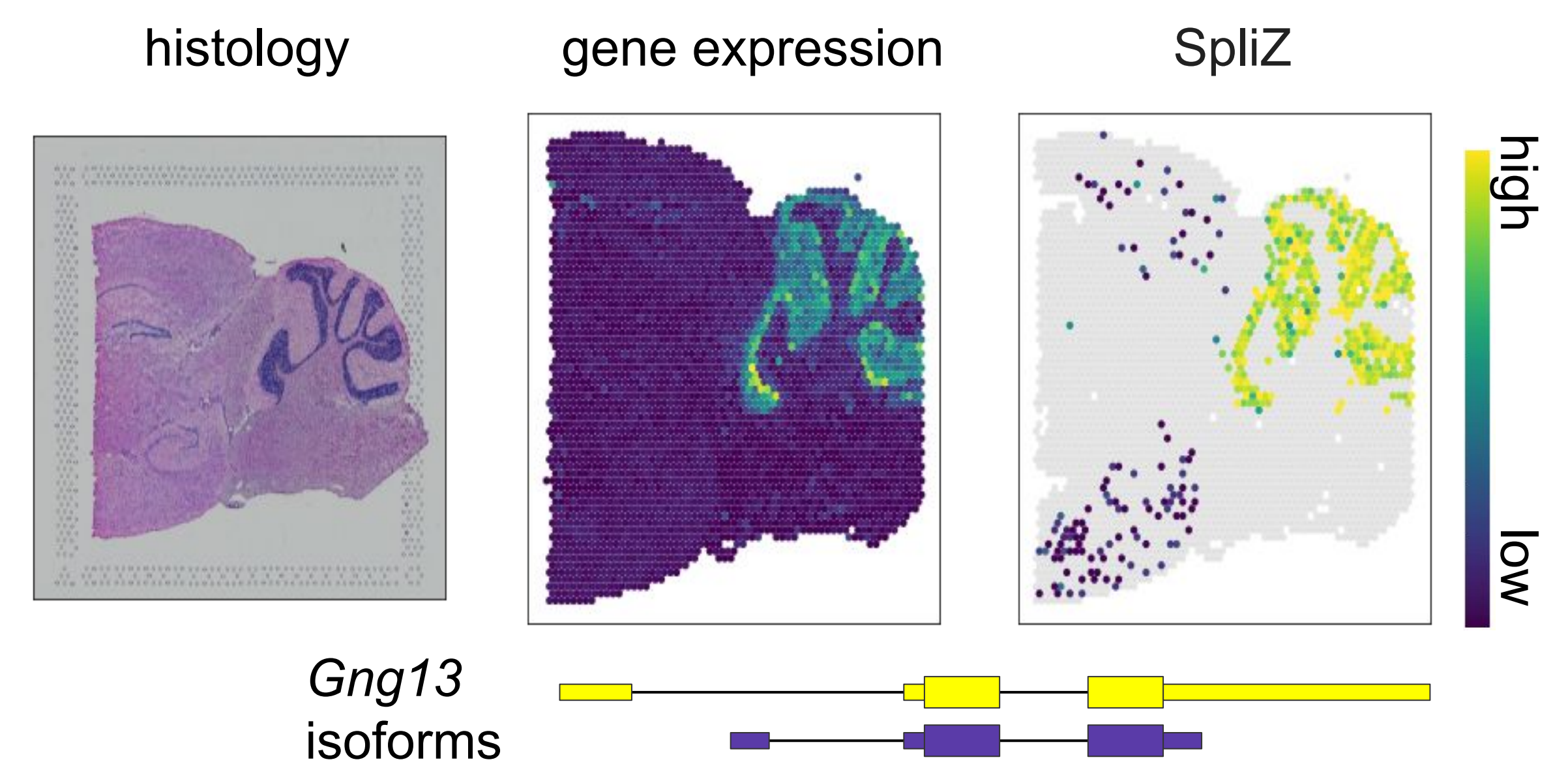
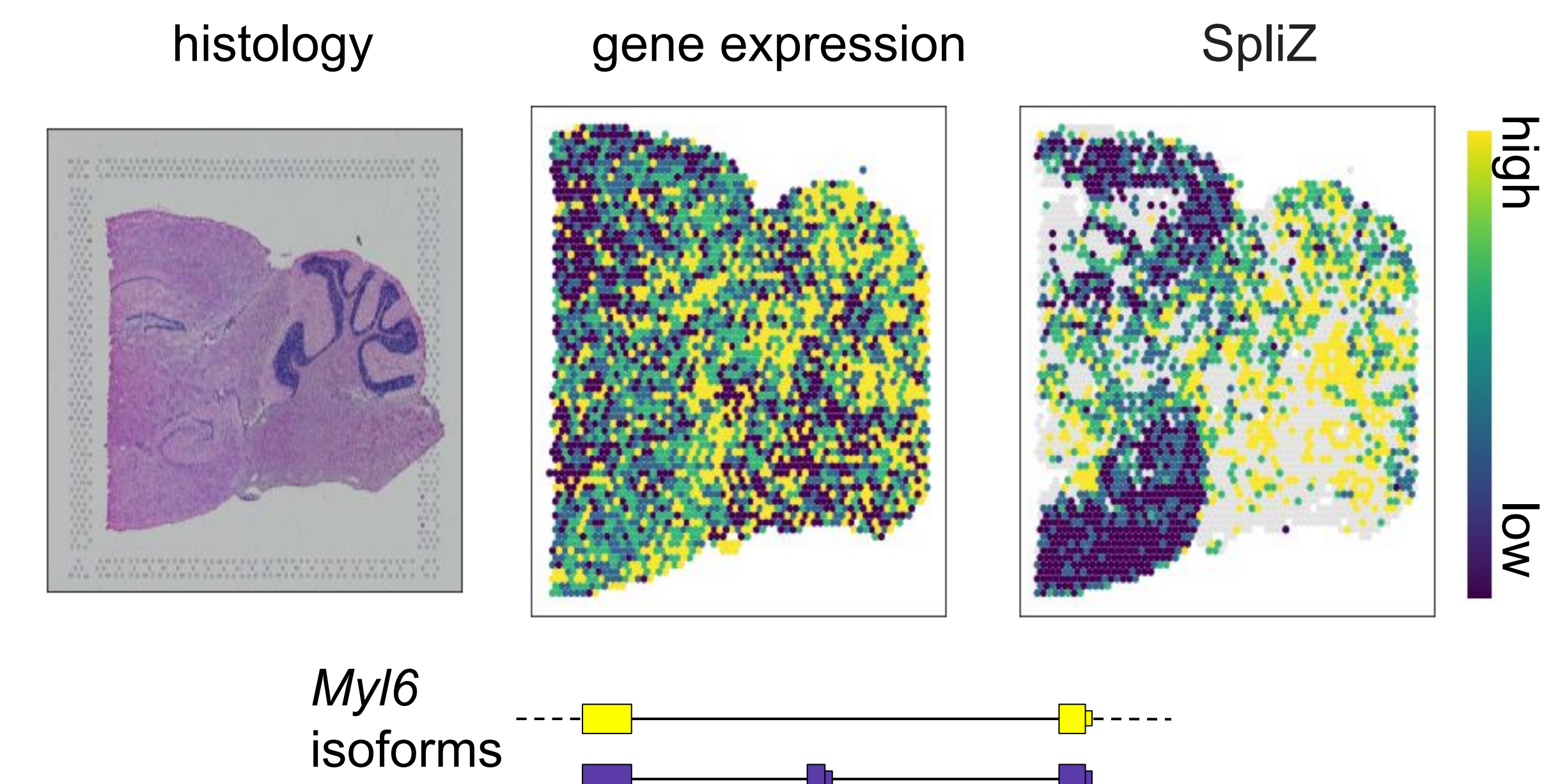
The SpliZ: splicing score per cell/gene

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



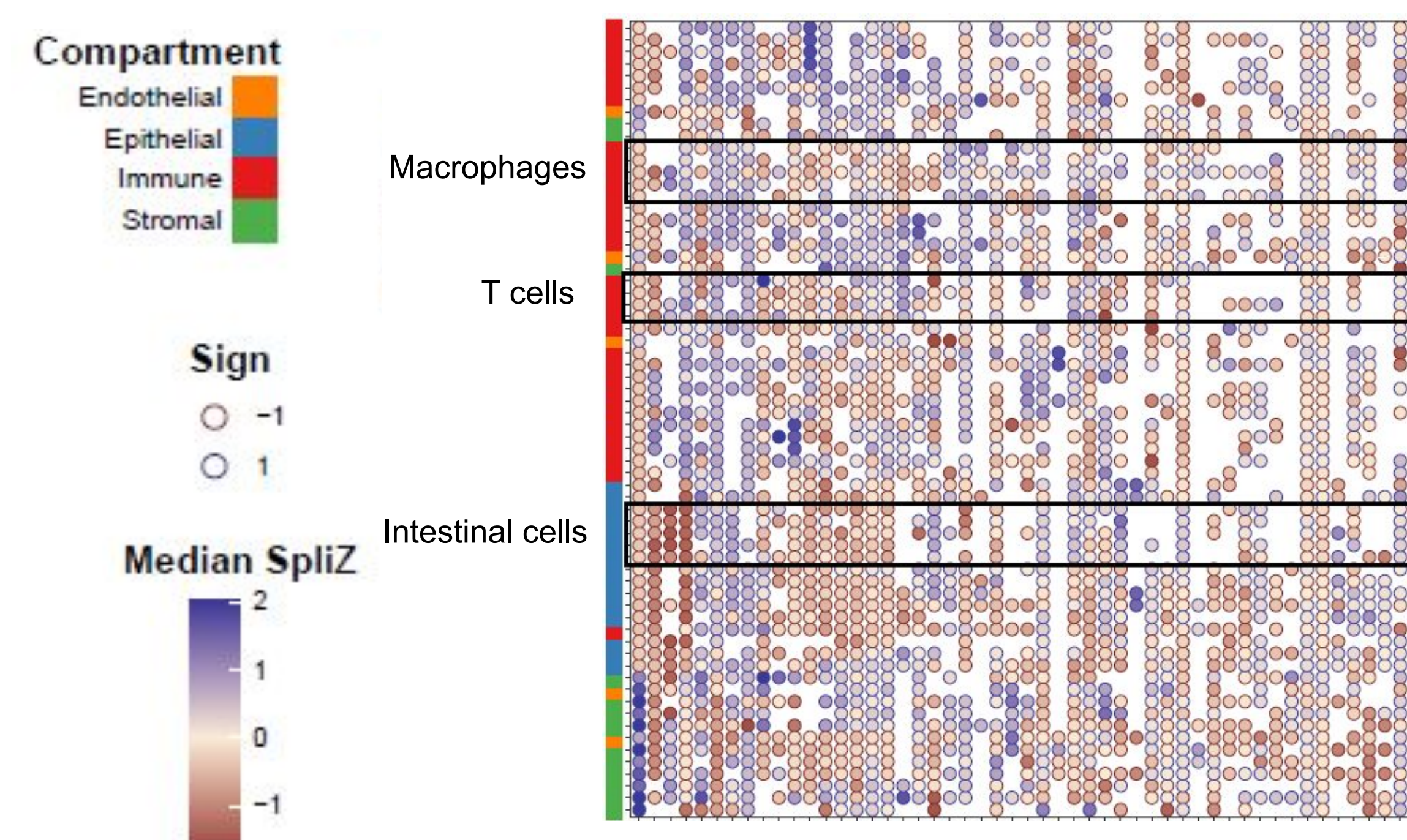
Application to spatial transcriptomics

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



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



Acknowledgements

The SpliZ software is available here: <https://github.com/salzmanlab/SpliZ>

Julia E Olivieri, Roozbeh Dehghannasiri, Julia Salzman. 2022. "The SpliZ generalizes" Percent Spliced In" to reveal regulated splicing at single-cell resolution." *Nature Methods* 19(3), 307-310. <https://doi.org/10.1038/s41592-022-01400-x>.

Julia E Olivieri, Roozbeh Dehghannasiri, Peter Wang, Antoine de Morree, Serena Tan, SoRi Jang, Timothy Wu, Julia Salzman. 2021. "RNA splicing programs define tissue compartments and cell types at single cell resolution." *eLife* 10:e70692. <https://doi.org/10.7554/eLife.70692>.

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