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Spatial Transcriptomics Analysis of Mouse Spleen Tissue Seq-scope Data Using SSAM

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Spatial transcriptomics has emerged as a pivotal technique to spatially assess single-cell gene expression, offering novel insights into the intricate spatial interactions underpinning life phenomena. Within this domain, sequencing-based spatial transcription analysis methods are garnering attention due to their independence from complex optical devices and resilience to self-fluorescence, enhancing accessibility. The present study employs Seq-Scope, a leading-edge sequencing-based spatial transcription barcode technology, boasting a resolution parallel to optical microscopes. We present the inaugural analysis of mouse spleen data generated via the Seq-Scope method, utilizing the segmentation-free cell type analysis tool, SSAM. Our investigation aims to elucidate intricate gene expression patterns in spleen tissue and discern the interplay of cell types influencing immune function therein. Ultimately, this research endeavors to elucidate the mechanistic intricacies of spleen immune responses, providing foundational knowledge for advancing our understanding of immune reactions, disease etiologies, and the conceptualization of targeted therapeutic strategies.