

Spatial immune cell mapping for next-generation pathology

Single-cell genomics technologies are now applicable at scale, high-throughput and using standardized procedures for high-quality results. We expect single-cell transcriptomics technologies soon to advance the precision of patient diagnosis and stratification for therapy. Spatial transcriptomics techniques and particularly Single Molecule Imaging (SMI) methods go even beyond, promising to provide an unbiased snapshot of tissue complexity *in situ*, thereby adding valuable spatial information. We interrogated the tissue immune environments as a biomarker for precision medicine and therapy target nomination. Therefore, we generated a compendium of resident immune cells in healthy and diseased tissues to pinpoint causative and predictive cellular states and their spatial localization. Our single-cell reference atlases of secondary lymphoid organs, immune mediated diseases and tumor microenvironments provided the basis for the spatial *in situ* mapping of immune populations. Combining single-cell and SMI identified complex colocalization patterns of immune and stromal cells in inflamed tissues and cancer patients with potential diagnostic and therapeutic value. Hence, we expect spatial transcriptomics with SMI to critically expand our toolbox for precision medicine and to enable next-generation pathology.