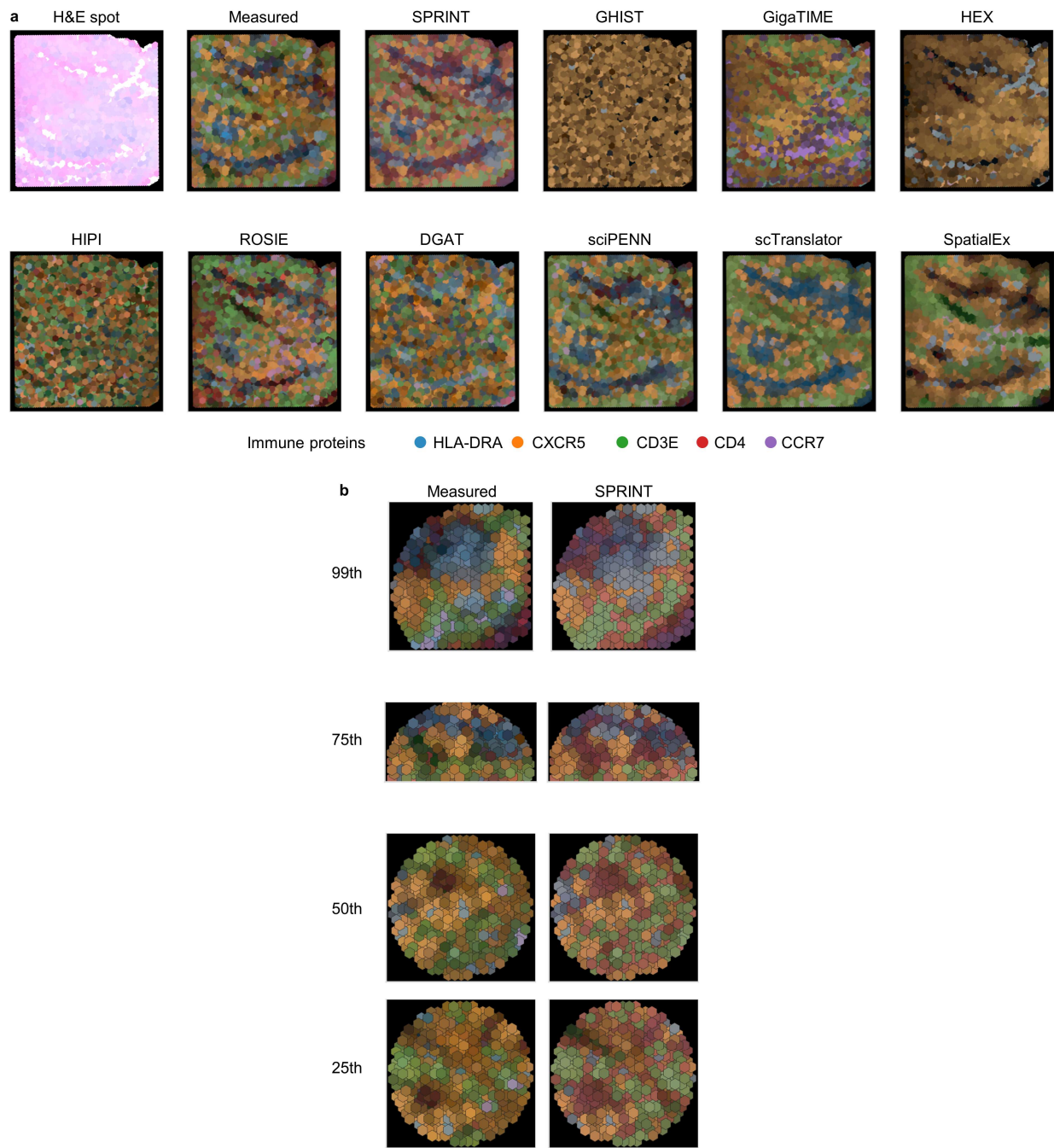


SPRINT enables spatial proteomic profile reconstruction through multimodal fusion of histology and transcriptomics

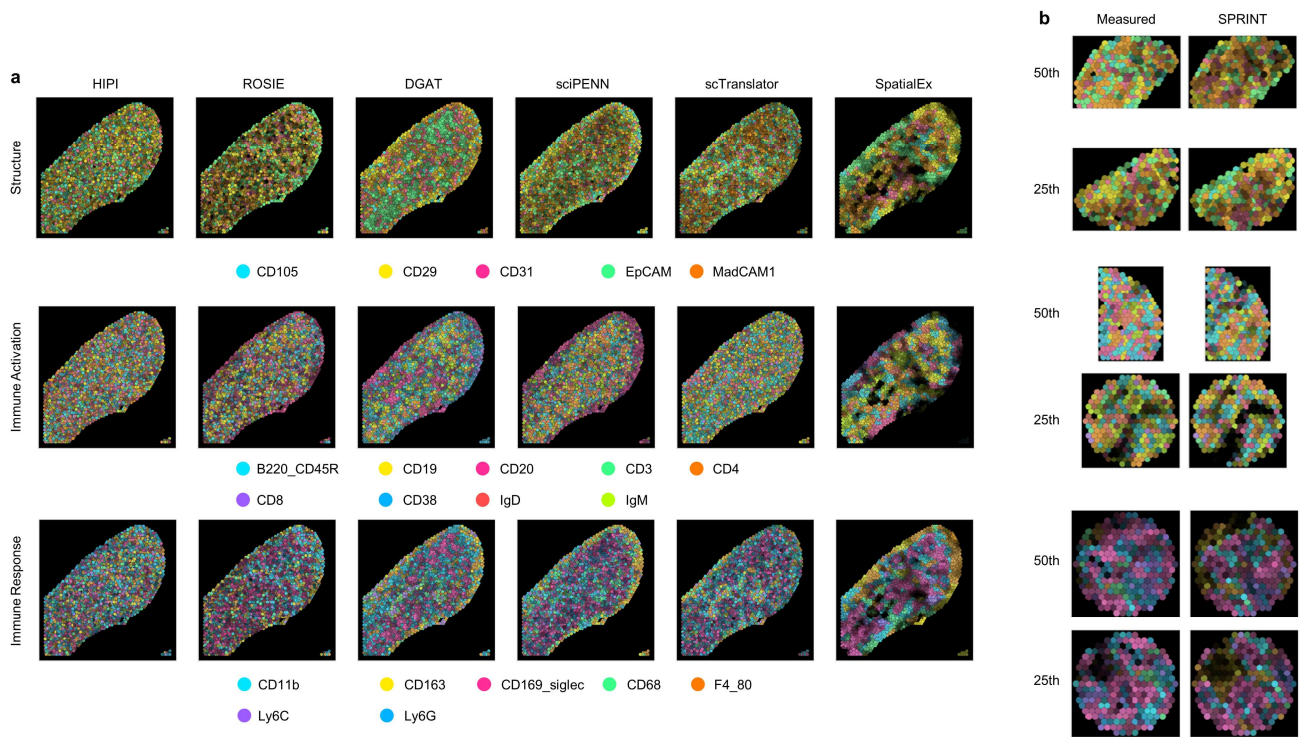
Yuzhi Sun¹, XianLiu¹, Tianyi Zhao^{2, 3, *}, Yadong Wang^{1, 2, *}

Supplementary Figures

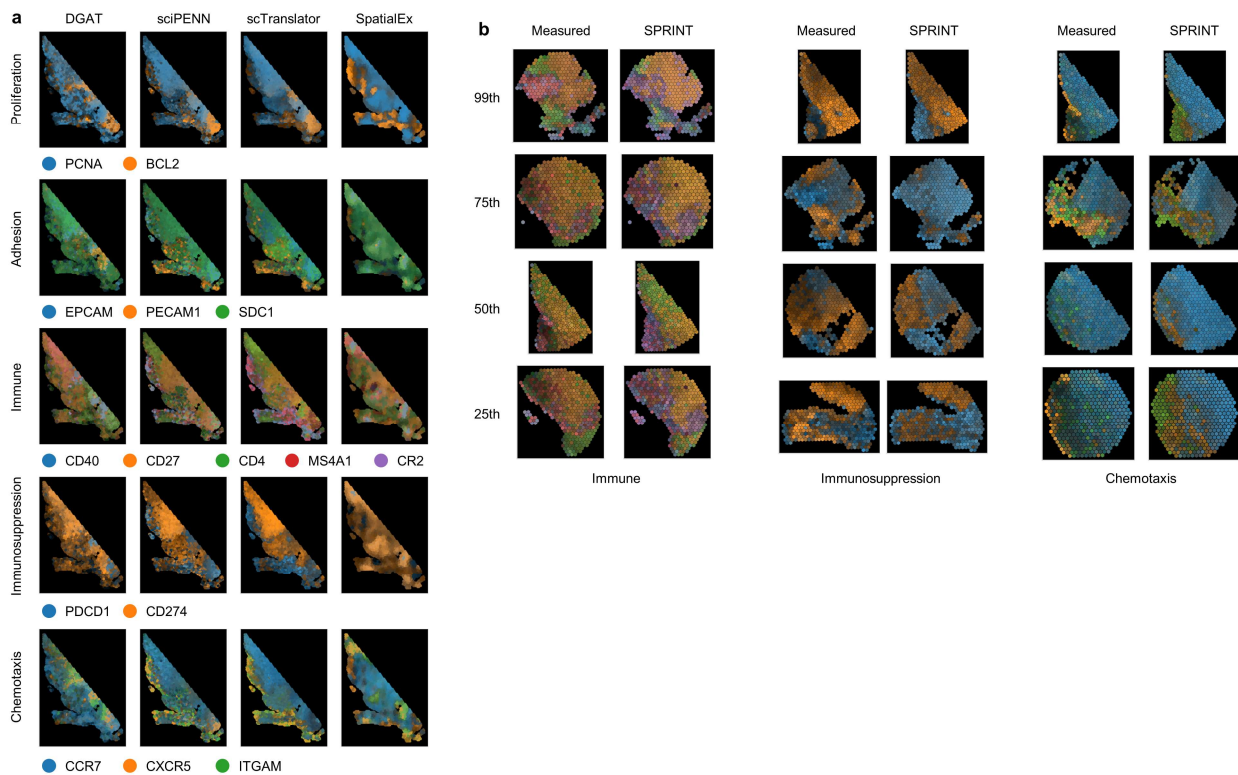


Supplementary Figure 1. a. In silico visualization of spatial protein expression in human tonsil tissue. The expression patterns of the immune markers are presented as an additive colour overlay. **b.** Examples of SPRINT spatial protein predictions at different prediction-accuracy percentiles.

* Corresponding authors: Tianyi Zhao (zty2009@hit.edu.cn), Yadong Wang (ydwang@hit.edu.cn).
 1 Faculty of Computing, Harbin Institute of Technology, Harbin, China.
 2 Harbin Institute of Technology Zhengzhou Research Institute, Zhengzhou, China.
 3 School of Medicine and Health, Harbin Institute of Technology, Harbin, China.



Supplementary Figure 2. a. In silico visualization of spatial protein expression in the test spleen section. **b.** Representative local neighbourhoods of measured and SPRINT-predicted protein expression.



Supplementary Figure 3. a. In silico visualization of spatial protein expression in the test region. **b.** Representative local neighbourhoods of measured and SPRINT-predicted protein expression for the Immune, Immunosuppression and Chemotaxis groups.