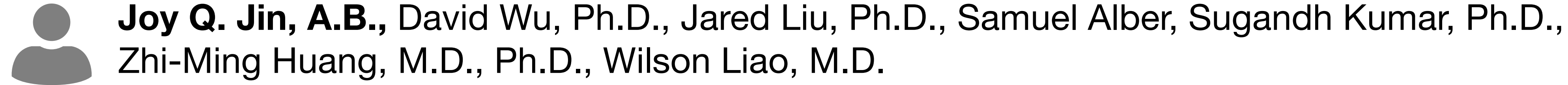
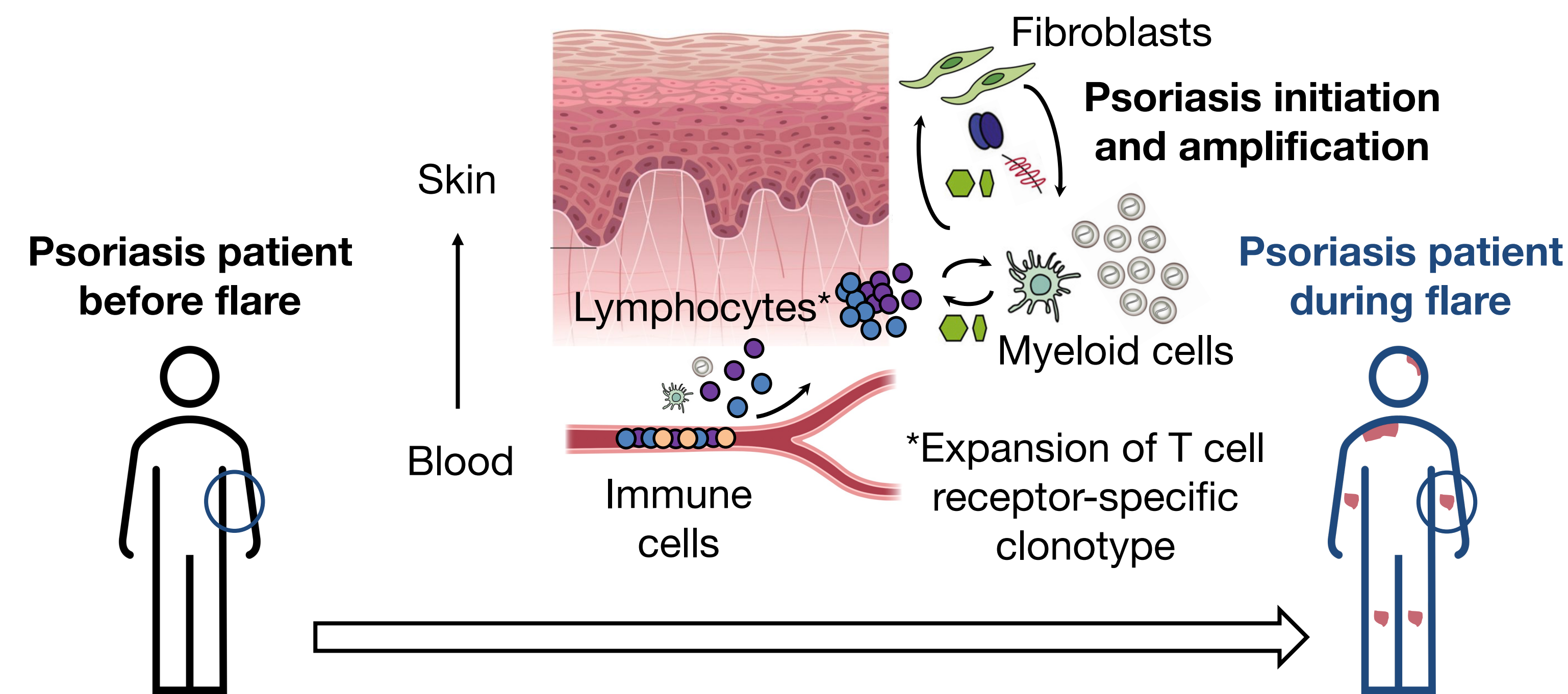


Defining Immune Cell Trajectories Between Blood and Skin in Psoriasis



BACKGROUND

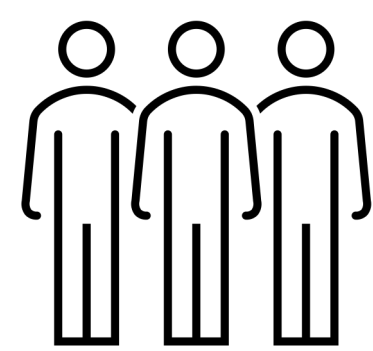
Psoriasis is a chronic, immune-mediated disease that affects approximately 3% of the U.S. The condition includes flares of skin plaques, frequent co-diagnosis of psoriatic arthritis, and increased risk for systemic comorbidities (e.g., cardiovascular disease, depression). While several biologic immunotherapies exist, with IL-17 being a key cytokine target, a sizeable subset of patients do not experience clinical relief with these treatments. Defining how immune cells in the blood and skin relate to each other to cause psoriasis is critical, as most prior studies have only profiled skin cells.



METHODS

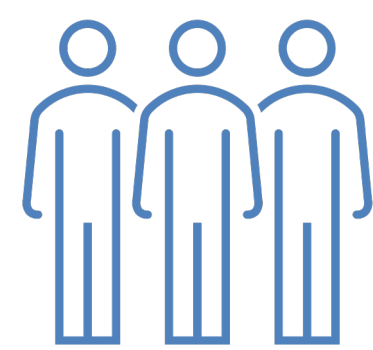
Obtain skin and blood samples

4 healthy controls



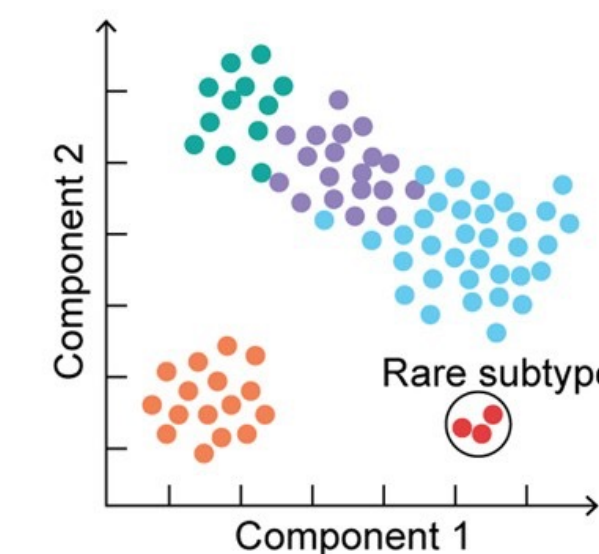
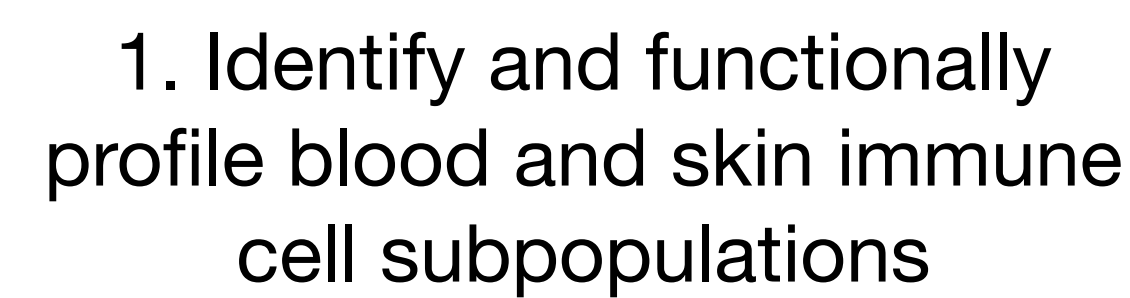
and

29 psoriasis patients

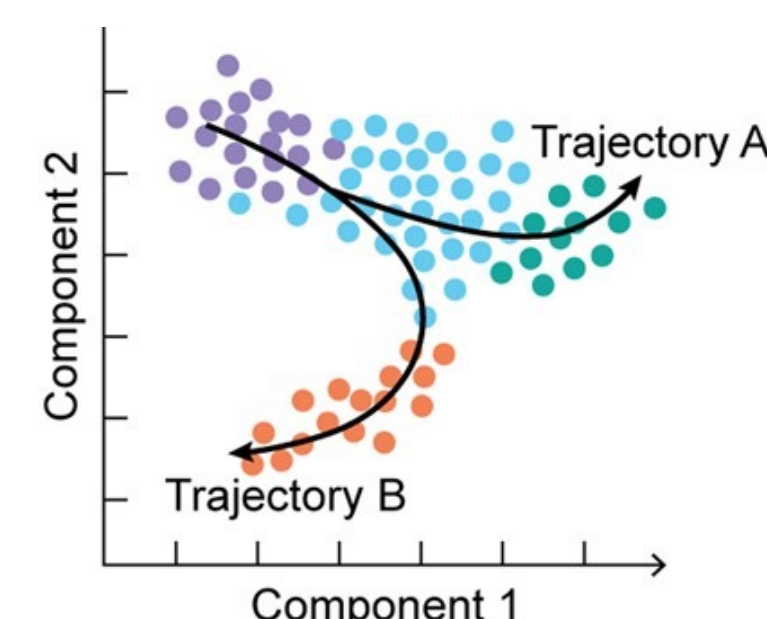
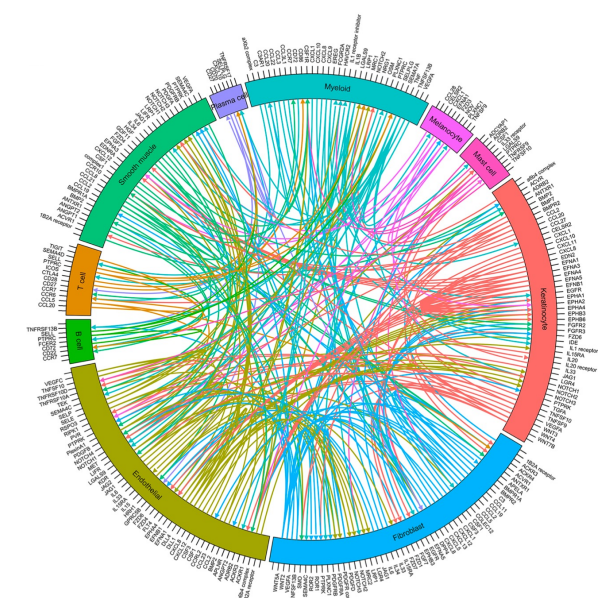


Lesional + contralateral
lesional + non-lesional skin
biopsies

Single-cell RNA + T cell receptor (TCR) sequencing



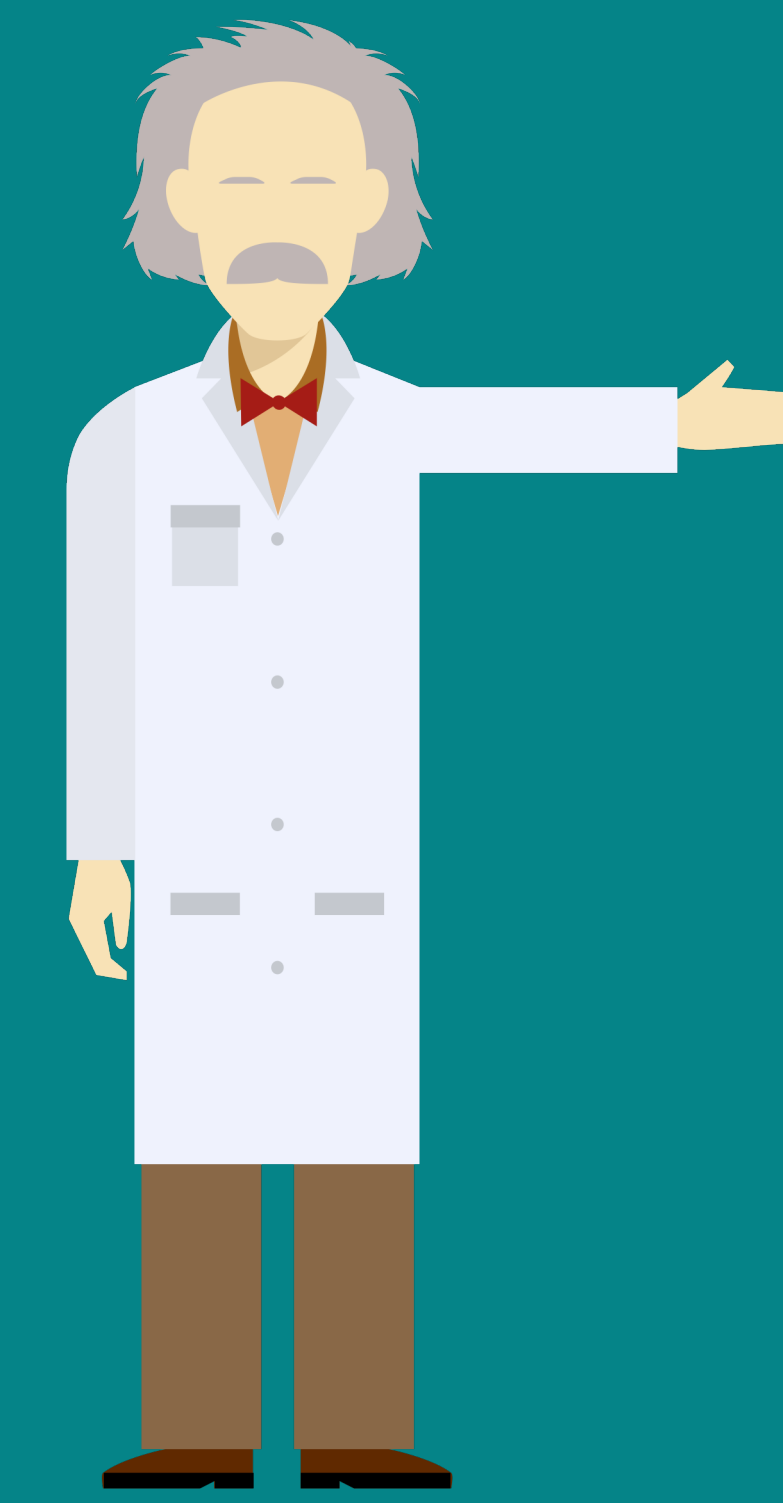
2. Analyze clonal sharing and perform cell trajectory analysis between blood and skin cells



3. Nominate potential therapeutic targets: cell types, signaling pathways, specific genes



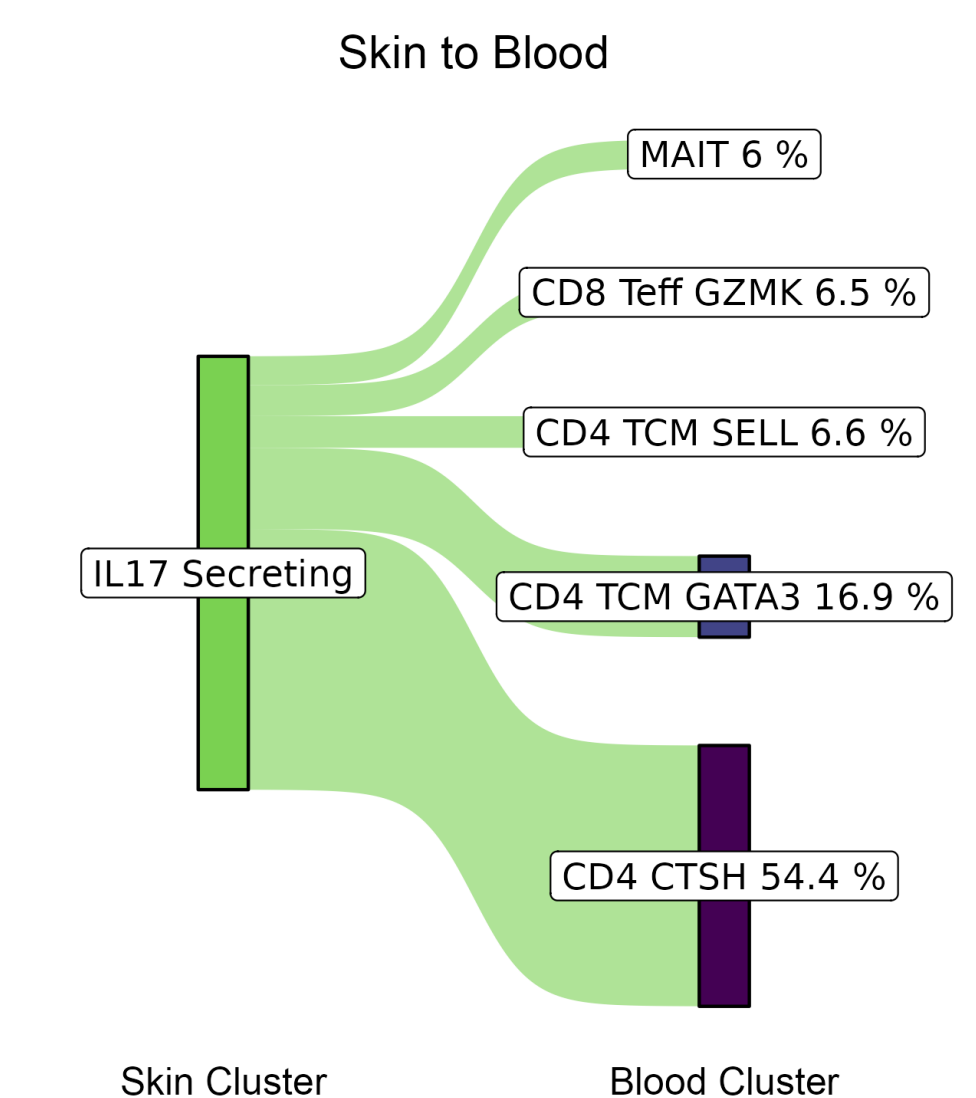
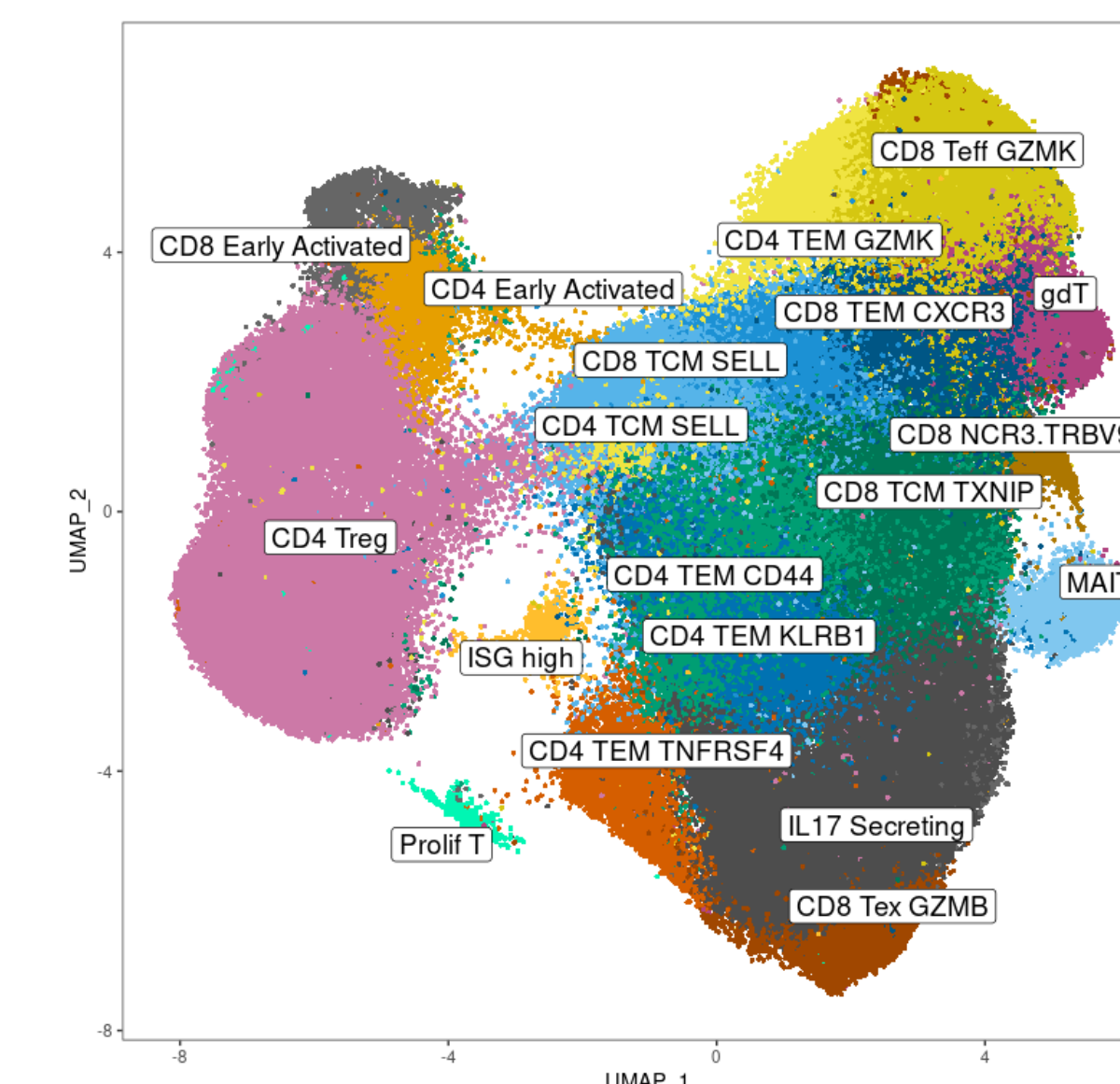
Scan to download our
published review of single-
cell studies in psoriasis!



We analyzed the RNA expression of over 500,000 individual cells in the blood and skin to learn about how psoriasis develops.

RESULTS

- 1 Defined 22 novel immune cell subpopulations, serving as a [reference atlas](#) for researchers.
- 2 Using TCR-seq, identified T cell clones shared between blood ([central memory T cells](#)) and skin ([IL-17 secreting populations](#)).



- 3 **OX40** was significantly elevated in **regulatory T cells** across psoriasis lesions, which persisted post-treatment.

DISCUSSION

These results reveal functional and developmental differences between circulating and resident skin tissue T cells, deepening our understanding of psoriatic pathogenesis. Regulatory T cells and the *OX40* gene were systematically nominated using single-cell techniques as potential therapeutic targets. However, as scRNA-seq was the primary method used to generate results, findings should be interpreted with caution given limitations of the technology (e.g., high dropout, low capture efficiency), and further investigation is needed via *in vitro* (e.g., spatial transcriptomics) and *in vivo* studies.

ACKNOWLEDGEMENTS

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