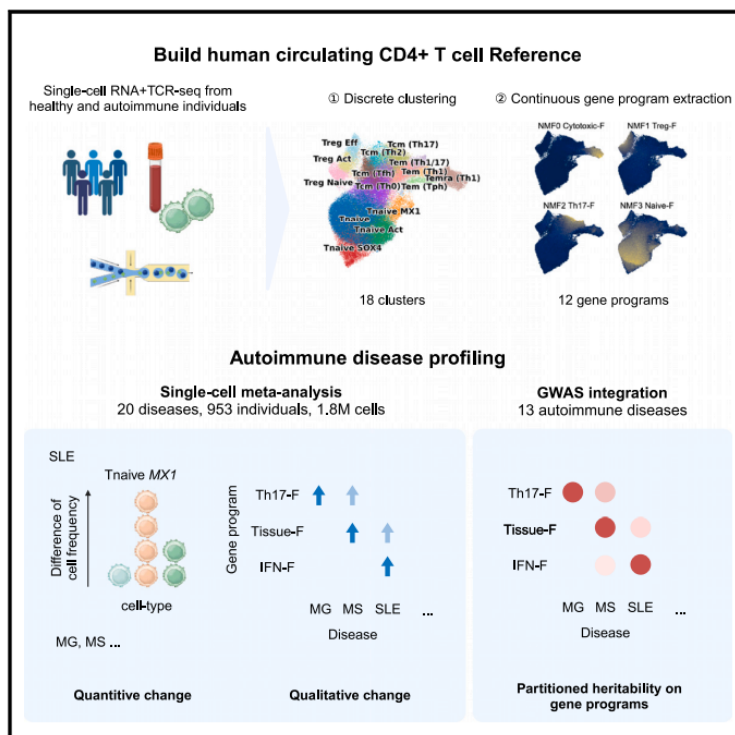


Single-cell transcriptome landscape of circulating CD4⁺ T cell populations in autoimmune diseases

Keywords: autoimmune disease, CD4⁺ T cell, single cell RNA-seq

Points

- The authors identified 18 cell types and 12 gene programs from CD4⁺ T cells in peripheral blood.
- They performed a meta-analysis using 1,809,668 CD4⁺ cells from 20 diseases and 953 people, and identified autoimmune disease-specific CD4⁺ T cell mutations.
- They revealed the accumulation of genetic factors in the CD4⁺ T cell gene program.



Sample collection strategy and UMAP plots

License: CC BY 4.0

Journal: *Cell Genomics* (Jan. 4, 2024 online)

Title: "Single-cell transcriptome landscape of circulating CD4⁺ T cell populations in autoimmune diseases"

Authors: Yoshiaki Yasumizu, Daiki Takeuchi, Reo Morimoto, Yusuke Takeshima, Tatsusada Okuno, Makoto Kinoshita, Takayoshi Morita, Yasuhiro Kato, Min Wang, Daisuke Motooka, Daisuke Okuzaki, Yamami Nakamura, Norihisa Mikami, Masaya Arai, Xuan Zhang, Atsushi Kumanogoh, Hideki Mochizuki, Naganari Ohkura*, Shimon Sakaguchi* (*correspondence)

DOI: <https://doi.org/10.1016/j.xgen.2023.100473>