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Analysis of various ion channel transcripts in CD4+ T cell subsets using single-cell RNA sequencing.

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CD4+ T lymphocytes, a vital component of the immune system, play a pivotal role in various immune responses. Depending on their subsets, they are associated with the onset of diseases such as rheumatoid arthritis, autoimmune conditions, allergies, and more. These subsets, including TH1, TH2, TH9, TH17, TH22, T follicular helper cells (Tfh), and regulatory T cells (Treg), exhibit distinct immune responses. Notably, TH1 is linked to rheumatoid arthritis and autoimmune diseases, while TH2 is associated with allergies. Ion channels within immune cells are responsible for regulating diverse functions by controlling the movement of ions such as calcium, potassium, magnesium, chloride, and zinc. Among these, calcium ion channels, particularly the Calcium-Released Activated Calcium (CRAC) channel, represented by ORAI1, are crucial for immune cell activation. Potassium (K+) channels also play a role in enhancing calcium influx through calcium channels by regulating membrane potential. Other ion channels like Transient Receptor Potentials (TRP) channels, P2X receptors, and voltage-gated calcium channels are known. Despite the unique functions and immune responses of T cell subsets, research on the various ion channels in these cells is still insufficient. Recent research utilizing single-cell RNA sequencing (scRNA-seq) allows for a more detailed analysis of gene expression in individual cells, making it suitable for studying complex tissues and diverse cell populations. Our research aimed to explore functional differences in immune activity among T cell subsets by differentiating naive T cells into subsets (TH1, TH2, TH17, Treg) and analyzing their transcriptomes using scRNA-seq.