

# Single-Cell RNA Sequencing Reveals Transcriptomic Heterogeneity of Lymphocytes in Ulcerative Colitis

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Ulcerative colitis (UC) is an inflammatory bowel disease marked by inflammation or ulceration of the colon. While its exact cause is not fully understood, it is thought to involve a combination of environmental, genetic, and autoimmune factors. Given the incomplete understanding of the underlying mechanisms at the single-cell level, we conducted a meta-analysis of three single-cell RNA sequencing datasets from UC patients. Our analysis included 96,392 cells from 18 UC patients and 18 healthy individuals, revealing 9 distinct cell types. Notably, lymphocytes—such as plasma cells, B cells, and T cells—comprise the largest proportion of immune cells in the colon and exhibit significant transcriptomic changes. We also identified heterogeneity within these lymphocyte sub-clusters, which may influence UC development through altered gene expression patterns. Overall, our findings offer a comprehensive atlas of transcriptional changes in lymphocytes associated with UC.