

SINGLE-CELL TRANSCRIPTOMIC ANALYSIS IDENTIFIES EARLY IMMUNE DISTURBANCES IN PRECLINICAL CROHN'S DISEASE

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Single-cell RNA sequencing of peripheral blood in two patients with incidentally-diagnosed preclinical Crohn's disease identified 49 differentially expressed genes and altered immunoregulatory pathways compared to healthy controls.

KEY POINTS

- The study analyzed peripheral blood mononuclear cells from two patients with Crohn's disease diagnosed incidentally during colorectal cancer screening and two healthy controls using single-cell RNA sequencing.
- Forty-nine differentially expressed genes were identified between preclinical Crohn's disease patients and controls across six cell types, with 30 genes differentially expressed in all cell types.
- Pathway analysis revealed significant enrichment of immunoregulatory interactions between lymphoid and non-lymphoid cells, and functional annotation identified gene products related to immunological defense.
- Significant transcriptomic alterations were found in genes previously associated with symptomatic inflammatory bowel disease or reported as potential biomarkers.
- CD8+ T-cells showed greater separation between patient groups in principal component analysis compared to other cell types.

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