Inflammatory transcriptomic signatures and cell type compositions in inflamed and non-inflamed colonic mucosa of ulcerative colitis

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Ulcerative colitis (UC), a subtype of inflammatory bowel disease (IBD), arises from disrupted gut homeostasis, primarily due to an aberrant innate immune response to intestinal microbiota and an underlying genetic background. To uncover the underlying molecular mechanisms, we performed RNA Sequencing on colonic biopsies from UC patients, analyzing inflamed (UCA) and non-inflamed (UCI) regions and comparing them to normal controls (NC). We observed a significant increase in the number of differentially expressed genes (DEGs) in UCA, specifically linked to inflammatory pathways and immune cell activation. Cell type deconvolution revealed an elevation of inflammatory fibroblasts and monocytes in UCA, while Best4+ enterocytes showed a notable decrease. These findings were consistent across independent datasets from various ethnic groups. Additionally, this study enhances our understanding of UC pathogenesis and facilitates the identification of potential biomarkers and therapeutic targets for dealing persistent mucosal inflammation in UC patients.

keywords: Ulcerative colitis (UC), Transcriptomics, RNA sequencing, Inflammatory bowel disease (IBD), Cell type deconvolution