[BIOINFO 2023]

Integrative Analysis of Bulk RNAseq and single cell RNAseq revealed distinct cell types associated with Ulcerative Colitis

Zehra Ramsha[1], Jahanzeb Saqib[1], and Junil Kim[1,*]

[1]*School of Systems Biomedical Science, Soongsil University, 369 Sangdo-Ro, Dongjak-Gu, Seoul 06978, Republic of Korea*
**Corresponding author: junilkim@ssu.ac.kr*

Ulcerative colitis (UC) is a chronic inflammatory disorder in the lining of the colon and rectum. Despite extensive research, the exact cause of UC remains unknown. Here, we investigated transcriptomic signature of UC using RNA sequencing obtained from 15 active (inflamed), 15 inactive (non-inflamed) samples of UC, and 15 healthy controls. The transcriptomics profiling revealed that inflammatory transcriptome signature was significantly enriched in the active samples. Nevertheless, the cell type information which is crucial in such a persistent inflammation cannot be obtained from this bulk RNAseq. To overcome this limitation, we utilized the power of single cell RNAseq. Deconvolution of bulk RNAseq based on single cell RNAseq estimated active UC-enriched cell types, such as inflammatory monocytes and fibroblasts. This integrative approach using bulk and single cell transcriptomics provide not target genes but also target cell types of UC therapeutic purpose.