CLINICAL SYMPTOM TRAJECTORIES ARE SUPPORTED BY DIFFERENTIAL REGULATION OF MUCOSAL TRANSCRIPTOMES IN PATIENTS WITH ULCERATIVE COLITIS TREATED WITH FILGOTINIB: A POST HOC ANALYSIS OF THE SELECTION STUDY

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Post hoc RNA sequencing analysis of the SELECTION trial identified transcriptional differences between symptom trajectory groups in ulcerative colitis patients treated with filgotinib, with higher numbers of differentially expressed genes associated with greater symptomatic improvement.

KEY POINTS

- Filgotinib responders from the SELECTION trial were clustered into five trajectory groups based on partial Mayo Clinic Score changes from baseline to week 58, with colon biopsies analyzed at baseline and week 10.
- Minimal transcriptional differences were found between trajectory groups at baseline, but the number of differentially expressed genes from baseline to week 10 varied substantially between groups.
- Trajectory groups with greater symptomatic improvement beyond week 10 showed higher numbers of differentially expressed genes, ranging from 1306 (2.47%) in Group C to 14,690 (27.76%) in Group D and 14,677 (27.73%) in Group E.
- Authors suggest preliminary results support potential for personalized medicine in ulcerative colitis and may help identify blood biomarkers predicting treatment outcomes with filgotinib.

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