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Summary

PREDICTIVE TRANSCRIPTIONAL SIGNATURES ASSOCIATED TO VEDOLIZUMAB THERAPY RESPONSE IN PATIENTS WITH ULCERATIVE COLITIS

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Transcriptomic analysis of peripheral blood cells identifies gene expression signatures that distinguish vedolizumab non-responders from responders in ulcerative colitis patients at baseline.

KEY POINTS

- Analysis of RNA-seq data from peripheral blood cells of ulcerative colitis patients found 20 gene sets positively enriched and 9 negatively enriched in vedolizumab non-responders versus responders at baseline.
- Comparative analysis with infliximab-treated patients showed approximately 50% overlap in enriched gene sets between the two biologics, suggesting both shared and treatment-specific transcriptional patterns.
- Peroxisome function, reactive oxygen function, and beta-catenin signalling were specifically enriched in vedolizumab non-responders, distinguishing them from infliximab non-responders.
- The authors conclude that these vedolizumab-specific transcriptional signatures in peripheral blood cells may provide a low-invasive approach to predict treatment response.
- This work addresses the current lack of reliable predictive tools for vedolizumab response in inflammatory bowel disease.

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