

MULTI-OMICS BIOMARKERS FOR PREDICTING THERAPEUTIC EFFICACY IN INFLAMMATORY BOWEL DISEASE: ADVANCING TOWARDS TAILORED TREATMENTS

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Poster

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A multi-omics study of 127 IBD patients identified transcriptomic, proteomic, metabolomic, and metagenomic biomarkers associated with response to biologics and JAK inhibitors at 14 weeks.

KEY POINTS

- Gene expression in intestinal tissue differed significantly between UC responders and non-responders to vedolizumab, and proteomic analysis of serum extracellular vesicles and tissue revealed differentially expressed proteins across study groups.
- Metabolomic analysis identified deregulation of 24 serum lipoproteins in CD patients responding to ustekinumab compared to non-responders, with pathway enrichment in ketone and butyrate metabolism, mitochondrial electron transport, carnitine synthesis, and fatty acid oxidation.
- Metagenomic analysis revealed microbial differences in UC responders to anti-TNF therapy compared to non-responders.
- The study analyzed serum, urine, extracellular vesicles, intestinal biopsies, and stool from 57 CD and 70 UC patients before and after 14 weeks of treatment, using endoscopic criteria to categorize response.
- The authors note that further studies are needed to confirm these findings and evaluate clinical relevance for predicting which patients will respond to specific therapies.

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