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Summary

COMPARATIVE MULTI-OMICS ANALYSIS IN PERIPHERAL BLOOD IDENTIFIES UNIQUE AND SHARED CORE MOLECULAR SIGNATURES IN IBD, PSORIASIS, RHEUMATOID ARTHRITIS AND SLE

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IBD

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A cross-sectional study of 650 patients with chronic inflammatory diseases identified both shared molecular signatures across conditions and disease-specific pathways through RNA sequencing and methylation profiling.

KEY POINTS

- IBD shared the most differential gene expression and methylation signatures with rheumatoid arthritis, while systemic lupus erythematosus had the least overlap with other chronic inflammatory diseases
- Core transcriptomic changes persisted even during inactive disease across different conditions and were correlated with DNA methylation changes
- Commonly upregulated genes across all chronic inflammatory diseases were enriched in pathways related to inflammatory response, cytokine signaling, neutrophil chemotaxis, and humoral immune response
- Disease-specific pathways included interferon-beta production in systemic lupus erythematosus, metabolic processes in psoriasis, and complement activation in ulcerative colitis
- The study enrolled patients with Crohn's disease, ulcerative colitis, rheumatoid arthritis, psoriatic arthritis, psoriasis, and systemic lupus erythematosus from University Hospital Kiel with up to 5 years of follow-up

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