

SPATIAL PROFILING OF HUMAN CELLS AND HOST-MICROBIOME INTERACTIONS IN CROHN'S DISEASE

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Poster

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Spatial transcriptomics study maps host-microbiome interactions in terminal ileum of Crohn's disease patients with and without post-surgical recurrence, identifying distinct bacterial localization patterns in inflamed tissue.

KEY POINTS

- Researchers analyzed 24 FFPE ileum samples from CD patients post-resection (8 remission, 16 recurrence) using 10x Genomics Xenium platform with 322-gene human colon panel plus 100 custom genes and 11 bacterial probes targeting 16S rRNA.
- Analysis successfully identified seven major cell types and detected microbial transcripts predominantly localized around the lumen, clearly distinguishable from human tissue regions.
- Two of six top spatially patterned genes were identified as bacteria, particularly in the epithelial layer, with differences in bacterial transcript abundance observed across samples.
- The study demonstrates feasibility of spatially profiling both host and microbial transcripts in FFPE samples and supports future investigation into how host-microbiome interactions may associate with CD progression and recurrence.
- Researchers suggest specific bacterial populations occupy defined locations in inflamed recurrent tissue and may interact with particular host cell types, potentially contributing to recurrence mechanisms.

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