# Single-cell analysis of endometriosis reveals a coordinated transcriptional programme driving immunotolerance and angiogenesis across eutopic and ectopic tissues

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## Abstract

Endometriosis is characterized by the growth of endometrial-like tissue outside the uterus. It affects many women during their reproductive age, causing years of pelvic pain and potential infertility. Its pathophysiology remains largely unknown, which limits early diagnosis and treatment. We characterized peritoneal and ovarian lesions at single-cell transcriptome resolution and compared them to matched eutopic endometrium, unaffected endometrium and organoids derived from these tissues, generating data on over 122,000 cells across 14 individuals. We spatially localized many of the cell types using imaging mass cytometry. We identify a perivascular mural cell specific to the peritoneal lesions, with dual roles in angiogenesis promotion and immune cell trafficking. We define an immunotolerant peritoneal niche, fundamental differences in eutopic endometrium and between lesion microenvironments and an unreported progenitor-like epithelial cell subpopulation. Altogether, this study provides a holistic view of the endometriosis microenvironment that represents a comprehensive cell atlas of the disease in individuals undergoing hormonal treatment, providing essential information for future therapeutics and diagnostics.