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Single-cell transcriptomics reveals tumor landscape in ovarian carcinosarcoma

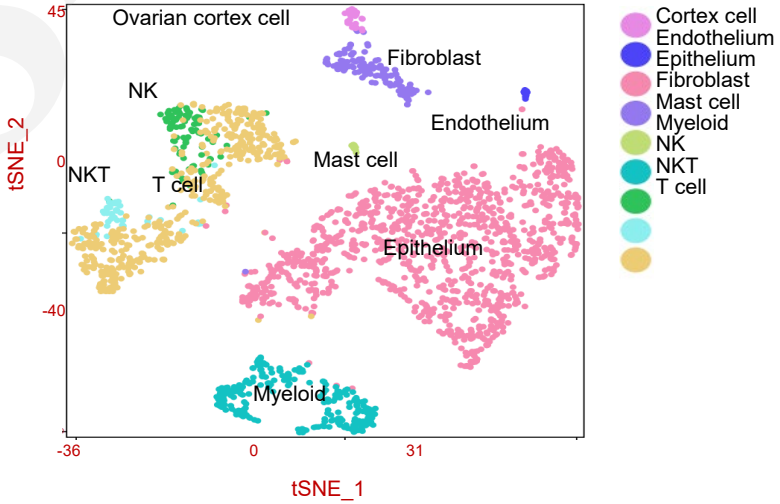
Key words: Ovarian carcinosarcoma; Single-cell RNA sequencing (scRNA-seq); Tumor heterogeneity

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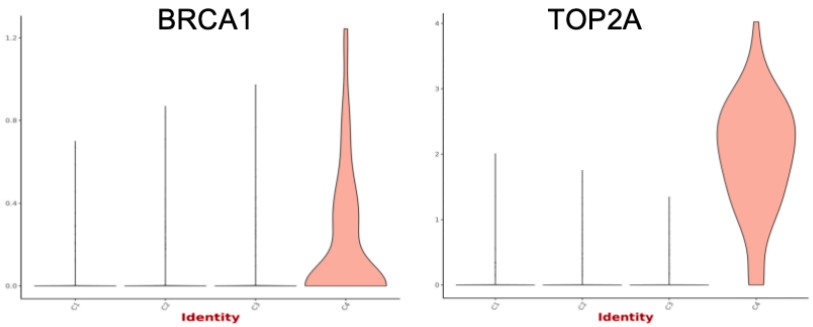
Research summary

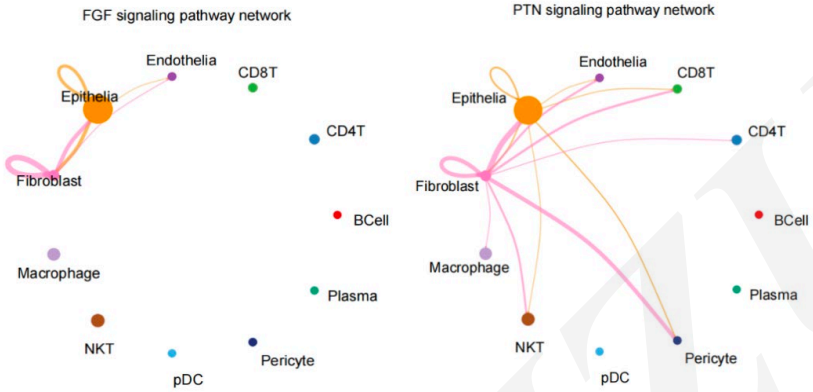
This article uses single-cell RNA sequencing (scRNA-seq) to characterize the cellular composition of ovarian carcinosarcoma (OCS) and to identify its molecular characteristics.

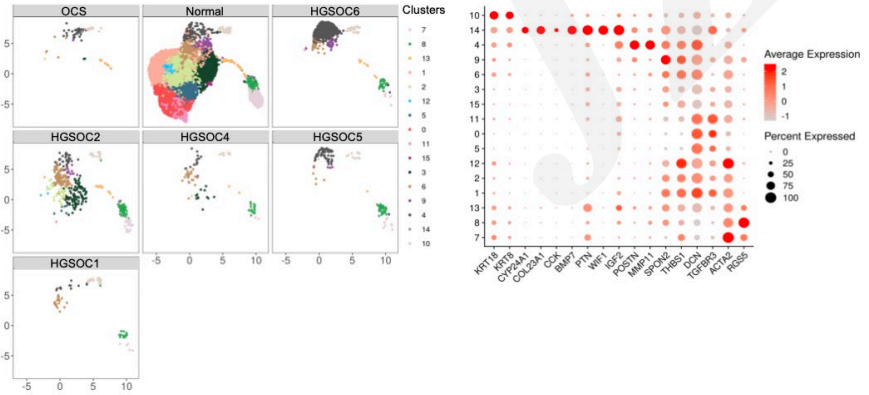
- Single-cell transcriptional atlas analysis and cell composition in OCS tissues.
- Clustering-based copy-number variation resolves the malignant elements from non-cancer cells.
- Transcriptional landscape intra-tumoral heterogeneity of OCS epithelial cells.
- Distinct mesenchymal cell subpopulations in the human OCS.
- The scRNA-seq data comparison between OCS and the published HGSOC tumors.
- The scRNA-seq data comparison between our OCS dataset and the previously published OCS tumor dataset as well as normal ovarian samples.



Innovation points







- Certain epithelial cell subclusters of the OCS tumor presented high levels of BRCA1 and TOP2A expression.
- FGF and PTN signaling pathways were the main pathways contributing to the epithelial cells and fibroblasts communication in the OCS.
- Certain mesenchymal subcluster exhibited specific expression patterns in the OCS tumor, characterized by elevated levels of CYP24A1, CYP23A1, CCK, BMP7, PTN, WIF1, and IGF2 expression.