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Spatial transcriptomics provide additional insights into the tumor microenvironment and prognosis of high grade serous cancer

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High grade serous cancer (HGSC) is the most common and lethal subtype of epithelial ovarian cancer, characterized by late-stage diagnosis and a high rate of recurrence. Despite therapeutic advances, overall survival remains poor, underscoring the need to better understand the tumor microenvironment (TME), which plays a critical role in disease progression and treatment response. This study integrated single-cell transcriptomics and spatial transcriptomics in patients with HGSC to investigate the spatial organization of the TME associated with prognosis. From 31,812 cells, we identified 11 cell types and mapped them onto tissue coordinates to characterize cellular composition and distribution. Fibroblasts and monocytes were predominant across most HGSC samples, alongside tumor cells. Using graph-based clustering, we defined transcriptionally distinct spatial clusters, and through cell–cell interaction analysis (CellChat v2), we inferred ligand–receptor signaling pathways between clusters. Pathways associated with tumor growth and metastasis, as well as macrophage-related signaling axes, were broadly active across all cases. Patients with favorable prognosis showed low tumor burden, minimal or absent fibroblast infiltration, prominent anti-tumor signaling and spatial confinement of tumors to specific regions. In contrast, patients with poor prognosis showed complex intermixing of tumors and fibroblasts, poorly defined tumor–stroma boundaries, and loss of anti-tumor signaling axes. Importantly, spatial transcriptomics enabled direct visualization of tumor–stroma architecture and signaling interactions that are difficult

to capture with conventional transcriptomic approaches, providing additional insights for understanding the TME and indicating that spatial features can provide important evidence to guide therapy selection and prognosis.