

**iScience, Volume 25**

**Supplemental information**

**Spatially resolved transcriptomics of high-grade  
serous ovarian carcinoma**

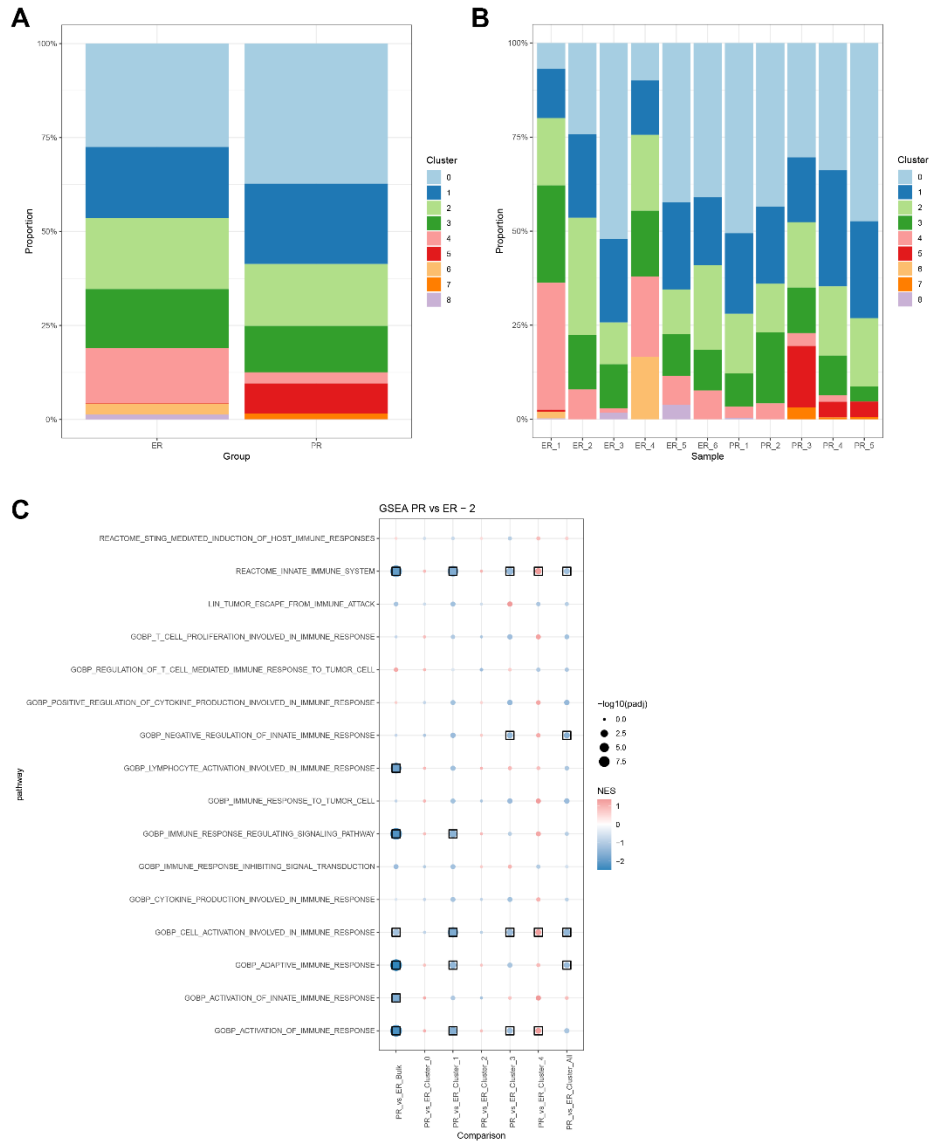
**Elaine Stur, Sara Corvigno, Mingchu Xu, Ken Chen, Yukun Tan, Sanghoon Lee, Jinsong Liu, Emily Ricco, Daniel Kraushaar, Patricia Castro, Jianhua Zhang, and Anil K. Sood**

## **Supplemental Information**

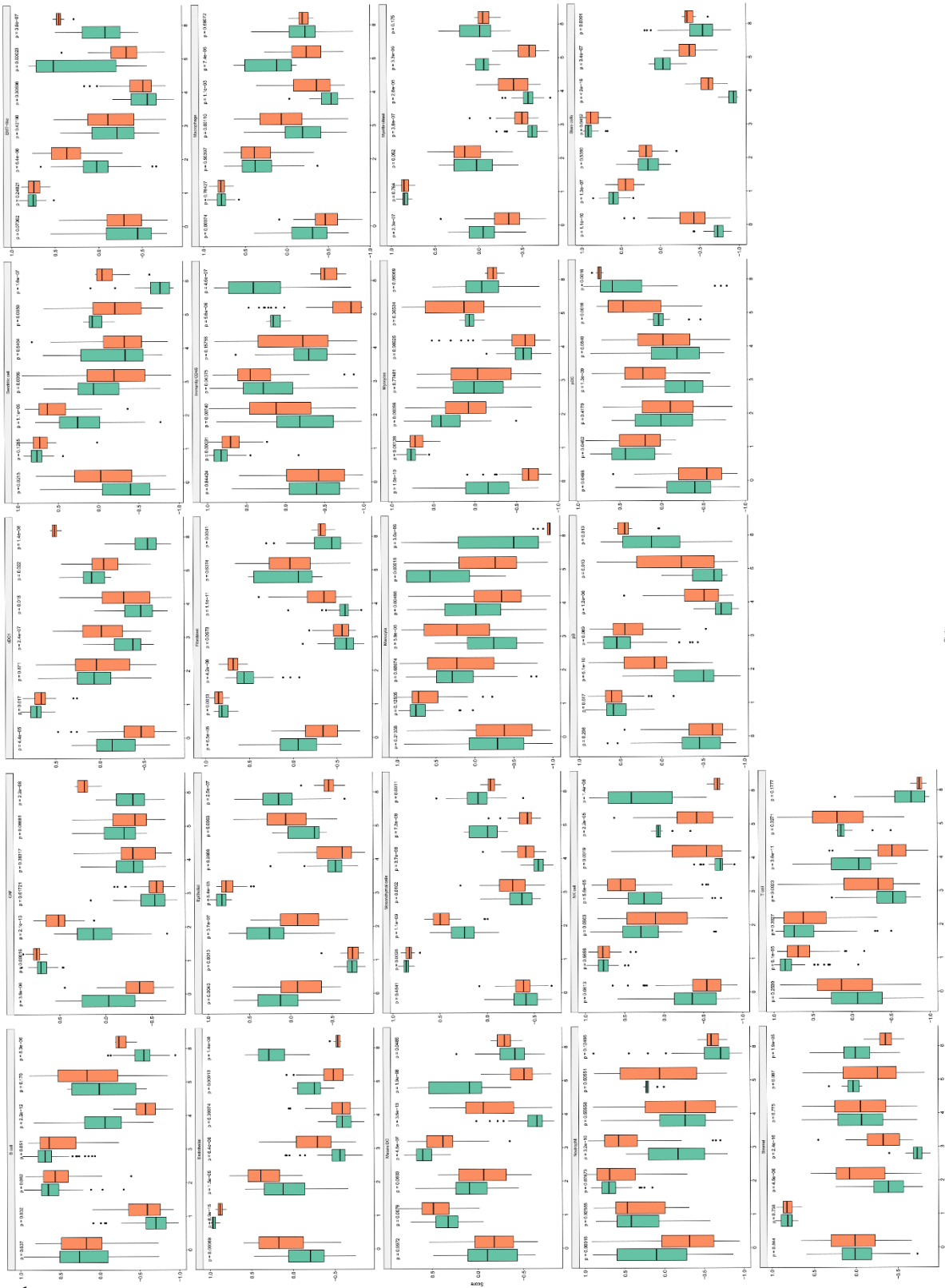
### **Spatially resolved transcriptomics of high-grade serous ovarian carcinoma**

Elaine Stur, Sara Corvigno, Mingchu Xu, Ken Chen, Yukun Tan, Sanghoon Lee, Jinsong Liu,

Emily Ricco, Daniel Kraushaar, Patricia Castro, Jianhua Zhang, Anil K. Sood.



**Fig. S1:** Quantitative representation of cluster proportions by **(A)** ER and PR groups and **(B)** samples. **(C)** Dot-plot of gene set enrichment analysis of immune pathways comparing bulk RNA sequencing and spatial transcriptomics of the main clusters (0-4). Black boxes are shown around the point where the gene set enrichment analysis adjusted p value is  $< 0.1$ . Related to Figure 1.



**Fig. S2:** Comparative bar plots of putative cell composition of each cluster of the excellent responder (ER) and poor responder (PR) groups. Related to Figure 1.