

TRANSCRIPTOMICS AND SPATIAL PROTEOMICS FOR DISCOVERY  
AND VALIDATION OF MISSING PROTEINS IN HUMAN OVARY

*Loren Méar<sup>1,2,3</sup>, Xia Hao<sup>4</sup>, Feria Hikmet<sup>1</sup>, Pauliina Damdimopoulou<sup>2,3</sup>, Kenny A. Rodriguez-  
Wallberg<sup>3,4‡</sup>, Cecilia Lindskog<sup>1‡</sup> \**

‡These authors contributed equally

<sup>1</sup> Department of Immunology, Genetics and Pathology, Cancer Precision Medicine Research Program, Uppsala University, 751 85 Uppsala, Sweden

<sup>2</sup> Division of Obstetrics and Gynecology, Department of Clinical Science, Intervention and Technology, Karolinska Institutet, 14186 Stockholm, Sweden

<sup>3</sup> Department of Gynaecology and Reproductive Medicine, Karolinska University Hospital, 171 77 Stockholm, Sweden

<sup>4</sup> Department of Oncology-Pathology, Laboratory of Translational Fertility Preservation, Karolinska Institutet, BioClinicum, 171 64 Stockholm, Sweden

**\* Corresponding Author**

Cecilia Lindskog

Department of Immunology, Genetics and Pathology

Cancer Precision Medicine Research Program

Uppsala University

751 85 Uppsala, Sweden

Email: [cecilia.lindskog@igp.uu.se](mailto:cecilia.lindskog@igp.uu.se)

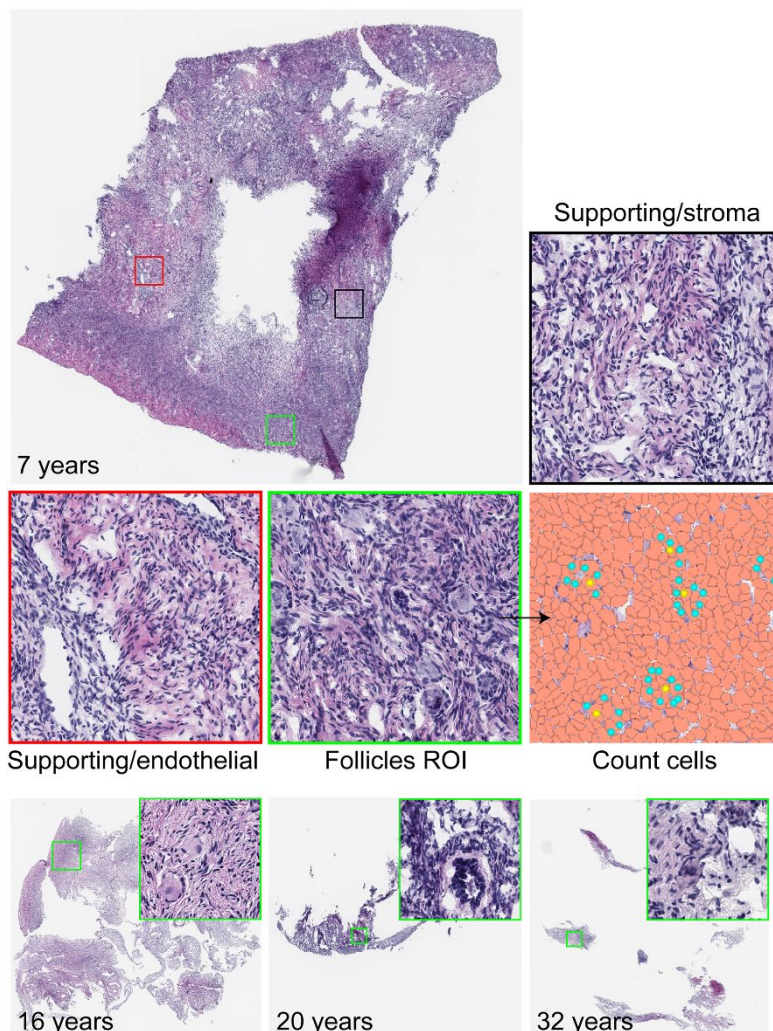
**Supporting Information**

S1

**Supplementary Figure 1: Cell-type estimation in fresh-frozen histology sections of human ovary**

From each fresh-frozen ovary tissue block (ages: 7, 16, 20 and 32), 5  $\mu\text{m}$  thick sections were cut and stained with H&E. Regions of interest (ROI) for follicle-rich, endothelial-rich, and ovarian stroma-rich areas were selected and cells of each type (oocyte, granulosa, endothelial, and ovarian stroma cells) were manually counted. The blow-ups show a magnified image of the

**Supplementary Figure 1.** Cell-type estimation in fresh-frozen histology sections of human ovary from each fresh-frozen ovary tissue block (ages: 7, 16, 20 and 32), 5  $\mu\text{m}$  thick sections were cut and stained with 2H&E. Regions of interest (ROI) for follicle-rich, endothelial-rich, and ovarian stroma-rich areas were selected and cells of each type (oocyte, granulosa, endothelial, and ovarian stroma cells) were manually counted. The blow-ups show a magnified image of the cell types indicated below each square and the Count-cells-square shows cells detected with image analysis and manually phenotyped in QuPath software.



cell types indicated below each square and the Count-cells-square shows cells detected with image analysis and manually phenotyped in QuPath software.

**Supplementary Table S1:** Description of the 61 MPs

**Supplementary Table S2:** Description of the 20 final candidates

**Supplementary Table S3:** IHC manual annotation results

**Supplementary Table S4:** Description of mIHC staining protocol and antibody details