systemic involvement. Primary and localized ovarian involvement is uncommon and occurs in less than 10% of cases. In this study, a rare case of primary ovarian non-Hodgkin’s lymphoma is presented.

Methodology The patient was a 64-year-old woman with a history of hysterectomy and postmenopausal bleeding that referred to the academic hospital of Mashhad University of Medical Sciences. On ultrasound and CT scans, solid cystic foci were found between the bladder and rectum, consistent with the location of the cervix and uterus. Subsequent evaluations confirmed histological and immunohistochemical diagnosis of ovarian non-Hodgkin’s lymphoma.

Results Ovarian lymphoma is one of the differential diagnoses that should be considered in the pelvic masses.

Conclusion Ovarian lymphoma is one of the differential diagnoses that should be considered in the pelvic masses.

Introduction/Background The epithelial-mesenchymal transition (EMT) promotes alterations in cell signaling and morphology, favoring metastatic progression. Exosomes are extracellular vesicles, produced by cells under variable conditions, containing proteins involved in cell-cell communication. Our aim was to evaluate the proteome of exosomes secreted after EMT induction to identify potential biomarkers for ovarian cancer classification.

Methodology EMT was induced in the ovarian cancer cell line CAOV3 using 10 ng/mL EGF for 96 h after 24 h of serum deprivation. Exosomes were isolated from the supernatant using the exoEasyMaxi kit (Qiagen) after decellularization and then characterized. The exosome proteins were extracted, identified, and quantified by Label-Free-Quantification (LFQ) using LC-MS/MS. The proteomic data and mRNA expression TCGA database were integrated to identify potential biomarkers of mesenchymal subtype of high-grade ovarian serous carcinoma.

Results The CAOV3-exosomes obtained during EMT had ~150 nm in diameter and morphology similar to exosomes from nonstimulated CAOV3. The proteomic analysis highlighted 157 proteins differentially detected between EMT induced and nonstimulated CAOV3, 100 up and 57 down accumulated. Integrative analysis of up accumulated proteins with TCGA transcriptomic signature identified PLAU, LAMB1, COL6A1, and TGFBI as potential biomarkers of mesenchymal HGSOC subtype.

Conclusion The combination of EMT induction, exosome isolation, and large-scale proteomic analysis identified potential biomarkers of ovarian cancer aggressiveness. Our data warrant further investigation of the role of PLAU, LAMB1, COL6A1, and TGFBI in ovarian cancer outcomes.