Introduction/Background* Urine may offer an alternative sample type for gynecologic cancer detection1, which is easily accessible and allows self-sampling at home. DNA methylation is an emerging biomarker for early cancer detection, and the feasibility of endometrial cancer detection in urine using DNA methylation analysis has recently been reported2. This study aimed to determine the performance of DNA methylation analysis in urine for endometrial cancer detection, and to make a comparison to paired cervicovaginal self-samples and cervical scrapes.

Methodology From 110 women diagnosed with endometrial cancer, paired urine samples, cervicovaginal self-samples and cervical scrapes were collected as well as samples from age-matched healthy female controls. All samples were tested for six DNA methylation markers. Differences in DNA methylation levels between patients and controls were compared using the non-parametric Mann-Whitney U-test, and the performance was quantified by the area under the receiver operating characteristic (ROC) curve (AUCs) and logistic regression. Correlation of DNA methylation markers within paired sample types was determined using the Spearman correlation coefficients.

Result(s)* In urine, self-samples and cervical scrapes, all six DNA methylation markers showed increased methylation levels in patients as compared to controls. Analyses amongst the paired sample types showed a good correlation between the test results of the DNA methylation markers.

Conclusion* This study demonstrates that testing for DNA methylation markers in urine may provide an easy and accurate alternative method for the detection of endometrial cancer. Potential applications of this diagnostic approach include the screening of asymptomatic women, triaging women with (postmenopausal) bleeding symptoms, and monitoring women with increased endometrial cancer risk.

Introduction/Background* Endometrial cancer is the second most common carcinoma of the female genital tract globally, and its incidence is still increasing. Optimal treatment of EC depends on early diagnostics and pre-operative stratification to appropriately select the extent of surgery and to plan further therapeutic approach. Current diagnosis and treatment of EC patients is guided by histopathological and surgical findings since there are no accurate non-invasive diagnostic or prognostic methods available. The lack of non-invasive diagnostic and prognostic biomarkers of EC is addressed in the current clinical study titled ‘Biomarkers for Diagnosis and Prognosis of Endometrial Carcinoma’ (NCT03553589).

Methodology Patient recruitment takes place at six medical centers (University Medical Centre Ljubljana, Slovenia; University Medical Centre Maribor, Slovenia; Maastricht University Medical Centre, Maastricht, Netherlands; Department of Gynecology, Lublin University, Lublin, Poland; Institute of Computer Science, University of Tartu, Tartu, Estonia; Quintec Ltd., Tartu, Estonia; Scimics GmbH, Heidelberg, Germany; Institute for Diabetes and Cancer, Helmholtz Zentrum, Munich, Germany; Department of Gynecology and Obstetrics, University Hospital Brno, Brno, Czech Republic; Academic Unit of Obstetrics and Gynecology, IRCCS Ospedale Policlinico San Martino, Genoa, Italy; University Medical Centre Maribor, Division of Gynecology and Perinatology, Maribor, Slovenia).

Plasma samples from women with diagnosed EC and controls will be examined using non-targeted and targeted metabolomics and targeted proteomics approaches. Combined blood metabolome (>850 metabolites), proteome (>900 proteins), clinical and epidemiological data will be analyzed in order to construct diagnostic/prognostic algorithms for early diagnosis of EC and to identify patients with low/high risk for cancer progression and recurrence.

BioEndoCar consortium has defined inclusion/exclusion criteria and a strict standard operating procedure for sample collection, processing and storage that is followed in all medical centers.