context. Among DEMs, differences were considered significant between patients and controls when proteins showed a fold change of ±1.5.

**Results** 17 records fulfilled inclusion criteria: a total of 550 patients and 403 controls were analysed. Among upregulated miRNAs, the ones with the widest delta between endometrial cancer patients and controls were: hsa-circ-0109046; hsa-circ-0002577; APOA1 (apolipoprotein A-I); HBB (haemoglobin subunit beta); CA1 (carbonic anhydrase 1); HBD (haemoglobin subunit delta); LPA (apolipoprotein A); SAA4 (serum amyloid A-4 protein); PF4V1 (platelet factor 4 variant); APOE (apolipoprotein E). Those can be found in serum through liquid biopsy. In parallel, the most downregulated miRNA in endometrial cancer patients compared to healthy subjects is miR-320a, to be found in endometrial specimens. Results are summarized in table 1.

**Conclusion** Although epigenetic regulation is unclear, upregulated miRNAs are feasible biomarkers to early detect endometrial cancer. MiRNAs modulation should be clarified during therapies or relapse, to plan targeted management.

**Disclosures** None declared.

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**Abstract #111**

**INDIVIDUALISING TREATMENT WITH MINIMALLY INVASIVE MOLECULAR MARKERS IN ENDOMETRIAL CANCER**

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**Introduction/Background** Integration of molecular markers has initiated more individualised approaches to treatment of endometrial cancer (EC). These are determined on tissue samples procured during diagnostic procedures or after surgical treatment, contributing to long turnaround times. Hence, their clinical utilisation is challenging. To overcome this we have developed, and are in the process of validating samples of microRNA (miRNA) determined from circulating free RNA. The aim of this study was to identify markers of epithelial-mesenchymal transition (EMT) to supplement current diagnostic assessment of women with EC.

**Methodology** The expression of EMT markers E- and N-cadherin in tumour tissue was evaluated by immunohistochemistry (IHC). Plasma levels of circulating cell free miR-148a-3p, miR-183–5p, miR-194–5p, miR-195–5p, miR-215–5p and miR-326 were quantified by RT-qPCR. Pretreatment assessment was classified as high risk for EC requiring escalated treatment and low risk EC. Correlations were performed using the Spearman rank test, continuous data was compared using the Mann-Whitney U test. Ongoing studies are evaluating the needed cfRNA characteristics and the validity of initial data.

**Results** Fifty women were included in this study. Median age was 69 years (min 35 - max 84 years). Median BMI was 31 (min 19 - max 41). IHC markers of E-cadherin and N-cadherin were not correlated with miRNA markers or clinico-pathological characteristics of EC. The age of patients was correlated with miRNA194 (rs=-.445, p<0.006), miRNA215 (rs=-.498, p<0.002), miRNA326 (rs=-.339, p<0.043). Furthermore, levels of miRNA194 (U=35.000; p<0.013) and miRNA215 (U=33.000; p<0.010) were correlated with menopausal status. Levels of miRNA326 (U=106.000; p<0.033), miRNA215 (U=106.000; p<0.033), miRNA194 (U=104.000; p<0.028), miRNA183 (U=101.000; p<0.023) was independently correlated with high risk EC. The levels of miRNA194 (U=85.000; p<0.005) and miRNA215 (U=101.000; p<0.021) were also correlated with myometrial invasion.

**Conclusion** Evaluation of miRNA levels should be explored with adjustment for age in order to develop appropriate minimally invasive prediction models for pre-treatment risk assessment.

**Disclosures** The authors have nothing to disclose.