

## Plasma MicroRNAs as Novel Biomarkers for Endometriosis and Endometriosis-Associated Ovarian Cancer

Swati Suryawanshi<sup>1</sup>, Anda M. Vlad<sup>1,2</sup>, Hui-Min Lin<sup>3</sup>, Gina Mantia-Smaldone<sup>5</sup>, Robin Laskey<sup>4</sup>, MinJae Lee<sup>6</sup>, Yan Lin<sup>3</sup>, Nicole Donnellan<sup>4</sup>, Marcia Klein-Patel<sup>4</sup>, Ted Lee<sup>4</sup>, Suketu Mansuria<sup>5</sup>, Esther Elishaev<sup>4</sup>, Raluca Budiu<sup>1</sup>, Robert P. Edwards<sup>2,4</sup>, and Xin Huang<sup>1,2</sup>

### Abstract

**Purpose:** Endometriosis, a largely benign, chronic inflammatory disease, is an independent risk factor for endometrioid and clear cell epithelial ovarian tumors. We aimed to identify plasma miRNAs that can be used to differentiate patients with endometriosis and ovarian cancer from healthy individuals.

**Experimental Design:** We conducted a two-stage exploratory study to investigate the use of plasma miRNA profiling to differentiate between patients with endometriosis, patients with endometriosis-associated ovarian cancer (EAOC), and healthy individuals. In the first stage, using global profiling of more than 1,000 miRNAs via reverse transcriptase quantitative PCR (RT-qPCR) in a 20-patient initial screening cohort, we identified 23 candidate miRNAs, which are differentially expressed between healthy controls ( $n = 6$ ), patients with endometriosis ( $n = 7$ ), and patients with EAOC ( $n = 7$ ) based on the fold changes. In the second stage, the 23 miRNAs were further tested in an expanded cohort ( $n = 88$ ) of healthy individuals ( $n = 20$ ), endometriosis ( $n = 33$ ), EAOC ( $n = 14$ ), and serous ovarian cancer cases (SOC;  $n = 21$ , included as controls).

**Results:** We identified three distinct miRNA signatures with reliable differential expression between healthy individuals, patients with endometriosis, and patients with EAOC. When profiled against the control SOC category, our results revealed different miRNAs, suggesting that the identified signatures are reflective of disease-specific pathogenic mechanisms. This was further supported by the fact that the majority of miRNAs differentially expressed in human EAOCs were mirrored in a double transgenic mouse EAOC model.

**Conclusion:** Our study reports for the first time that distinct plasma miRNA expression patterns may serve as highly specific and sensitive diagnostic biomarkers to discriminate between healthy, endometriosis, and EAOC cases. *Clin Cancer Res*; 19(5); 1213–24. ©2013 AACR.

### Introduction

Epithelial ovarian cancer (EOC) is the fifth leading cause of cancer death in women in the United States (1). It is often

called a "silent killer" due to advanced stage at presentation when the disease has spread beyond the pelvis (stage III or IV; ref. 2). Women with stage I disease have a 5-year survival rate of approximately 95%, which is in stark contrast to the considerably lower survival of only 33% associated with advanced-stage disease (3). Thus, the key to increase the overall survival of women with ovarian cancer lies in early detection and screening, especially in patients with precursor lesions.

Currently, 2 major screening approaches have been used for early detection of EOCs: transvaginal sonography (TVS) and serum protein biomarker testing (2). Both approaches have been found to have low sensitivity and specificity for early EOC screening and are therefore not recommended for screening the general population with average risk (2). CA125 is the most widely used serum biomarker in EOCs (4). However, less than 50% of patients with early-stage EOC have augmented CA125 levels, and elevated circulating CA125 levels can result from many other medical/physiologic conditions (2). As a result, CA125 has been mostly used for monitoring EOC progression (5).

**Authors' Affiliations:** <sup>1</sup>Magee-Womens Research Institute, Department of Obstetrics, Gynecology and Reproductive Sciences, University of Pittsburgh School of Medicine; <sup>2</sup>Women's Cancer Research Center, <sup>3</sup>Department of Biostatistics, Graduate School of Public Health, University of Pittsburgh and Biostatistics Facility, University of Pittsburgh Cancer Institute; <sup>4</sup>Magee-Womens Hospital, University of Pittsburgh Medical Center, Pittsburgh; <sup>5</sup>Division of Gynecologic Oncology; Hospital of the University of Pennsylvania, Philadelphia, Pennsylvania; and <sup>6</sup>Biostatistics/Epidemiology/Research Design (BERD) Core, Center for Clinical and Translational Sciences, The University of Texas Health Science Center, Houston, Texas

**Note:** Supplementary data for this article are available at Clinical Cancer Research Online (<http://clincancerres.aacrjournals.org/>).

S. Suryawanshi and A.M. Vlad contributed equally to this work.

**Corresponding Author:** Xin Huang, Magee-Womens Research Institute, 204 Craft Ave., B407, Pittsburgh, PA 15213. Phone: 412-641-3803; Fax: 412-641-6156; E-mail: [huangx2@upmc.edu](mailto:huangx2@upmc.edu)

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### Translational Relevance

Patients with epithelial ovarian cancer (EOC) typically have a poor prognosis because most cases are not diagnosed until they have reached advanced stages. The key to increasing the overall survival of women with EOC lies in early detection and screening, especially of patients with precursor lesions. In this study, we show that plasma miRNA expression signatures can be used as biomarkers to distinguish endometriosis, a precursor of endometrioid and clear cell adenocarcinoma of the ovary, and different histotypes of EOCs from healthy controls. Importantly, the plasma miRNA signatures we identified can be mirrored in an EOC mouse model, suggesting that they are reflective of EOC pathogenesis. Taken together, the plasma miRNAs identified in this study are promising biomarkers of endometriosis-to-EOC progression, which may ultimately be used to improve the clinical outcome of patients with ovarian cancer.

MicroRNAs (miRNA) are single-stranded, noncoding, small RNA molecules that regulate gene expression by inhibiting mRNA translation or by facilitating cleavage of the target mRNA (6). Past studies have shown that miRNAs are frequently dysregulated in human cancers, including EOCs (7, 8). Tumor-specific miRNA expression signatures have been reported in numerous malignancies and have been used to classify normal and malignant tissues as well as cancer subtypes (9). When used to classify poorly differentiated tumors, miRNA expression profiling outperformed mRNA expression profiling (10), suggesting that the former may be a superior approach in classifying human malignancies. Although tissue miRNA expression signatures have shown great promise as a new class of biomarkers, they cannot be used to address the current challenge of early detection of EOCs because tissue samples at or postdiagnosis are required.

Recent discoveries shown that miRNAs are exceptionally stable and can be readily and reliably detected in the systematic circulation (11, 12), raising the possibility of using blood-based miRNA assays to develop novel biomarkers for cancer detection, diagnosis, and prognosis (13, 14). In addition, blood-based miRNA expression profiling has several crucial advantages, such as easy accessibility using a minimally invasive method, and the potential of developing a test for population screening.

EOC encompasses 4 major histotypes: serous, mucinous, clear cell, and endometrioid. Progressively accumulating evidence from epidemiological and molecular studies shows the role of endometriosis as a potential precursor of endometrioid and clear cell adenocarcinoma of the ovary, also known as endometriosis-associated ovarian cancer (EAOC; refs. 15, 16). Endometriosis, a common gynecologic disorder affecting up to 10% to 15% of women in the reproductive age group, consists of ectopic endome-

trial glands surrounded by stroma, found at locations outside uterine cavity (17). While largely benign, the lesions often show characteristics similar to those of malignancy such as cellular atypia, proliferation, invasion, tissue remodeling, and neovascularization (18). Around 60% to 80% of EAOCs occur in the presence of atypical ovarian endometriosis (19–21). Importantly, in about 25% of these cases, pathologists often describe direct continuity of the atypical ovarian endometriosis with ovarian cancer (20), suggesting a transition spectrum of nonatypical to atypical and malignant variants (21). The risk of direct malignant transformation of ovarian endometriosis has been estimated as 0.7% to 1.6% over an average of 8 years (22, 23).

As with early-stage EOCs, diagnosis of endometriosis is often difficult, with patients having to undergo invasive procedures via laparoscopy or laparotomy (17). Even in diagnosed patients, it remains a challenge to predict who is at risk to develop EAOCs later in life, showing a clear need for developing specific and minimally invasive biomarker assays for endometriosis and early-stage EAOCs.

In this study, we focused on plasma miRNAs as potential biomarkers that can be used to differentiate patients with endometriosis and EAOCs from healthy individuals. We conducted a global profiling of plasma miRNA expression by reverse transcriptase quantitative PCR (RT-qPCR), using plasma samples from patients diagnosed with EAOCs, patients with documented endometriosis, and healthy individuals. Our results reveal several distinct plasma miRNA expression patterns that may serve as specific and sensitive diagnostic biomarkers to discriminate between these different disease categories.

## Material and Methods

### Ethics statement

This research study protocol was approved by the institutional review board (IRB) at the University of Pittsburgh (Pittsburgh, PA), and informed consent was obtained from all study participants before blood collection.

### Patients

The clinical and demographic characteristics of patients with endometriosis ( $n = 33$ ), EAOC ( $n = 14$ , of which 6 were endometrioid, 7 were clear cell tumors, and 1 had mixed endometrioid/clear cell histology), and serous ovarian cancer (SOC;  $n = 21$ ) are shown in Supplementary Table S1. All patients with cancer were treated at Magee-Womens Hospital of the University of Pittsburgh Medical Center (UPMC) between 2006 and 2011. The inclusion criteria consisted of patients with primary ovarian tumors and confirmed histology of EAOCs or SOCs.

In the EAOC group, 5 patients had endometriosis on the final pathology. Of the 5, 2 had endometrioid, 2 had clear cell tumors, and 1 had mixed histology of clear cell and endometrioid type.

The patients with endometriosis were treated at Magee-Womens Hospital of UPMC between 2006 and 2011.

Samples from patients with confirmed histology of endometriosis were included in this study. The cases where endometriosis could not be histologically confirmed on surgically removed tissues were excluded from this study.

Plasma samples from healthy women (controls,  $n = 20$ ) were purchased from Innovative Research Labs (Seattle, WA). Women without any current clinical conditions and without family history of diseases, such as cancer, HIV, diabetes, and autoimmune diseases, were qualified as healthy individuals by Innovative Research Labs.

### Specimen characteristics

Peripheral blood was drawn in heparinized tubes (BD Biosciences) and processed at Magee-Womens Research Institute within 8 hours from collection. The tubes were centrifuged at 2,300 rpm for 20 minutes at room temperature. Plasma was collected in a sterile biohazard cabinet, aliquoted, and cryopreserved at  $-80^{\circ}\text{C}$  until ready to use. Processing of blood by Innovative Research Labs was similarly conducted.

### Study design

Of the total 88 retrospectively collected plasma samples, 20 were randomly selected for the initial discovery phase (healthy controls,  $n = 6$ ; endometriosis,  $n = 7$ ; EAOs,  $n = 7$ , of which 4 were endometrioid and 3 were clear cell tumors). We used all of the 88 samples for our validation analyses. Study design is illustrated in Supplementary Fig. S1. In the discovery phase, miRNAs extracted from 20 plasma samples were used to quantify a total of 1,113 miRNAs by RT-qPCR. Expression of 23 candidate miRNAs that are differentially expressed in these 3 categories of samples and expression of an endogenous control miRNA, miR-132, were confirmed by an independent RT-qPCR in these 20 samples. Finally, expression of the 24 miRNAs was further studied in the complete cohort of 88 plasma samples by RT-qPCR.

### miRNA isolation and RT-qPCR assay

RNA was isolated from 88 plasma samples using the mirVana miRNA Isolation Kit (Life Technologies). Concentrations of RNA were measured by a NanoDrop 2000 spectrophotometer (Thermo Scientific). Sixty nanograms of purified RNA was used for RT using the QuantiMir Kit (System Biosciences). One microliter of cDNA was then diluted 1:160 and 1.1  $\mu\text{L}$  of diluted cDNA was used in each qPCR reaction for a genome-wide expression profiling of 1113 miRNAs (Sanger miRBase Version 15) using the Human miRNome Profiler kit (System Biosciences). qPCR was carried out on an ABI7900HT Real-Time PCR System (Applied Biosystems) using the RT<sup>2</sup> SYBR Green ROX qPCR master mix (Qiagen) under the following conditions:  $50^{\circ}\text{C}$  for 2 minutes,  $95^{\circ}\text{C}$  for 10 minutes, 40 cycles of  $95^{\circ}\text{C}$  for 15 seconds followed by  $60^{\circ}\text{C}$  for 10 seconds, and a standard dissociation stage. The RT-qPCR data were analyzed according to the comparative  $C_T$  method (24).

### NanoString nCounter miRNA assay

The miRNeasy FFPE Kit (Qiagen) was used to isolate miRNAs from formalin-fixed, paraffin-embedded (FFPE) tissues for global miRNA profiling. The nCounter Human miRNA Panel v2 that evaluates 800 miRNAs was used (NanoString). miRNAs extracted from plasma and tissue samples were subjected to nCounter miRNA sample preparation according to the manufacturer's instructions. This was followed by ligation of 100 ng of miRNA and hybridization to probes at  $65^{\circ}\text{C}$  for 18 hours following the manufacturer's protocol. Next day, the hybridized probes were purified and counted on nCounter Prep Station and Digital Analyzer. The data obtained from Analyzer contained counts of individual fluorescent barcodes and thus a count of miRNAs present in the sample. The nCounter results were analyzed by the nSolver software according to the manufacturer's instructions.

### Plasma miRNA measurements in LSL-Kras<sup>G12D/+</sup>/Pten<sup>loxp/loxp</sup> mice with endometrioid ovarian cancer

All animal experiments were carried out according to a protocol approved by the University of Pittsburgh International Animal Care and Use Committee (IACUC). The mice were originally provided by Dr. Dinulescu (25), and the colony was maintained at the Magee-Womens Research Institute. Genotyping for the identification of LSL-Kras<sup>G12D/+</sup>/Pten<sup>loxp/loxp</sup> mice was conducted as previously described (25).

Survival surgery procedure and administration of recombinant adenovirus encoding for Cre recombinase [Ad5CMVCre (AdCre); University of Iowa Gene Transfer Vector Core] was conducted in synchronized animals as previously described by us and others (25, 26). Briefly, 7- to 9-week-old Kras<sup>G12D/+</sup>/Pten<sup>loxp/loxp</sup> virgin females were injected intraperitoneally (i.p.) with 5 U pregnant mare's serum gonadotropin (PMSG) followed by 5 U human chorionic gonadotropin (hCG) 48 hours later. Thirty-six hours later, mice received 5  $\mu\text{L}$  of  $2.5 \times 10^7$  plaque-forming units (p.f.u.) AdCre delivered to the ovary surface epithelium (OSE) of the left ovary only, via intrabursal injection. The contralateral ovary served as a control.

Mice were sacrificed when disease was clinically evident (tumor mass on the injected side and/or ascites accumulation) or when mice were moribund (hunched appearance, ruffled fur, unable to reach for food or water). Blood was collected by cardiac puncture at necropsy and serum cryopreserved until ready to use. Expression of mouse miRNAs, mmu-miR-15b, 16, 21, 191, and 195 was measured by RT-qPCR as described above.

### Statistical analysis and sample size justification

The candidate demographic variables analyzed were age, race, history of alcohol, and tobacco consumption. We also compared stage of disease in EAOs versus SOCs. For the baseline characteristics, we conducted univariate comparisons using  $\chi^2$  tests, ANOVA test, or their nonparametric equivalents, as appropriate. We determined the medians

and interquartile range as measures of central tendency for variables with highly skewed distribution (not normally distributed such as gravidity or parity). All analyses were conducted using SAS 9.3 (SAS Institute) assuming statistical significance at  $P < 0.05$ .

All qPCR  $C_T$  values were normalized to miR-132. The  $\Delta C_T$  of sample  $i$  marker  $j$  is defined as  $\Delta C_{T_{ij}} = C_{T_{ij}} - C_{T_{j\text{mir}132}}$ . Here  $\Delta C_{T_{ij}}$  and  $C_{T_{j\text{mir}132}}$  are  $C_T$  values of marker  $j$  and miR-132 for sample  $i$ , respectively. The fold change (FC) between 2 specific groups for a specific marker was calculated as  $FC = 2^{-\Delta\Delta C_T} = 2^{-(\overline{\Delta C_T}_{\text{group}1} - \overline{\Delta C_T}_{\text{group}2})}$ . To test the reliability of the assay, the 23 miRNAs of interest were tested twice on 20 randomly selected samples. The mixed-effect model-based method was used to calculate the coefficient of variation (CV) and intraclass correlation (ICC) on the  $\Delta C_T$  values of each marker (27). Only samples with detected values were used in the calculation. An average CV of 2.44% (range, 0.016%–12.6%) was observed across the markers, indicating good reproducibility of the assay. The ICC ranges from 8% to 99.9%, with a median value of 83%. ICC measures the percentage of variation contributing to the variation among individuals. This value is high when the variance component associated with individual samples greatly exceeds the variation of the assay. ICCs of 15 of the markers exceed 70% in our data.

For the discovery cohort, we used  $n = 20$  samples. We estimated that the mean for the CV of the assay was 2.44%. The calculation is based on the method described by Gail and colleagues (27). By the delta method, we could approximate the variance of the  $1/n(\Delta C_T)$  by the CV of the measurement. The effect size (ES) is defined as  $ES = \frac{\ln(\overline{\Delta T})_{\text{group}1} - \ln(\overline{\Delta T})_{\text{group}2}}{\text{std}(\Delta T)} = \frac{\ln(FC)}{\sqrt{CV}}$ , thus, the fold change can be calculated as  $\exp(ES \times \sqrt{CV})$ .

For the validation cohort, we used a total of  $n = 88$  cases. We applied the Bonferroni adjustment, with a  $P$  cutoff of  $0.05/23 = 0.002$  to control the overall family-wise error rate (FWER) at 0.05. A total of 23 markers passed the initial screening and were formally tested using all 88 samples. With 20 samples from the healthy individuals and at least 14 samples in the disease group, there is at least 90% power to detect an effect size of 1.72 at the log level with a 2-sided Wilcoxon rank-sum test ( $\alpha = 0.05/23 = 0.002$ ). This translates into an FC of 1.3.

Hierarchical clustering analysis was applied to the  $\Delta C_T$  values. Markers that were consistently detected across all groups in the expansion cohort (missing data rate < 30%) were used in the clustering analysis.

Wilcoxon rank-sum tests were used to search for differentially expressed miRNAs between 2 groups. Only markers that were consistently detected in both groups (total number of samples with nonmissing values > 5) were used in the differential gene analysis. The Benjamini and Hochberg method was used to control the false discovery rate (FDR) at 20% (28). Principle component analysis (PCA) was applied to the differentially expressed miRNAs to reduce the dimension and to visualize the clusters. Linear discrim-

inant analysis (LDA) was used to generate a 3-marker model to classify samples of different groups (29, 30). Area under the receiver-operating characteristic (AUROC) curve, sensitivity, and specificity were calculated for each model. We used leaved-one-out cross-validation (LOOCV) to avoid overfitting of the data.

## Results

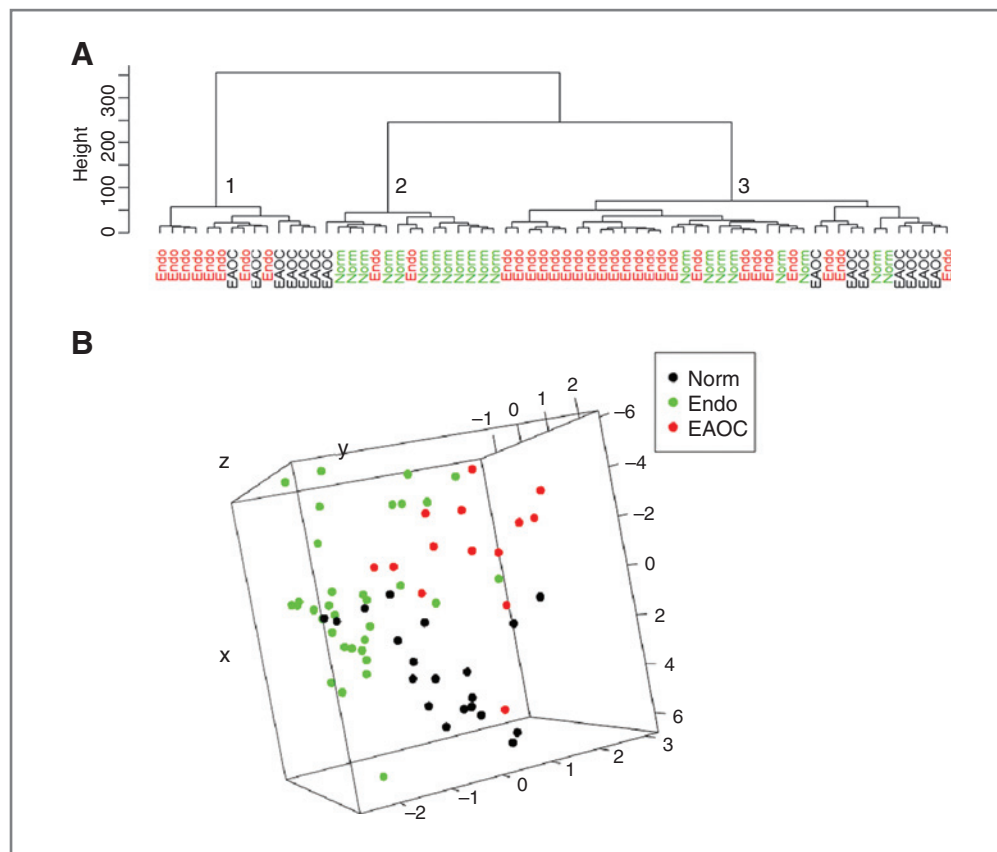
### Reproducibility and reliability of our approach

Our overall experimental design for miRNA profiling is outlined in Supplementary Fig. S1. First, we confirmed that our extracted plasma miRNAs accurately reflect the original plasma miRNA population by adding spike-ins of serially diluted, synthetic miR-210, into aliquots of a randomly selected plasma sample from a healthy subject. Following miRNA extraction, we consistently detected miR-210 in a linear fashion by RT-qPCR, validating our miRNA extraction method (Supplementary Fig. S2A). Next, we examined the reproducibility of our RT-qPCR protocol by 2 approaches. First, expression of 3 randomly selected miRNAs, miR-132, 362-5p, and 1974, was measured in 3 independent RT-qPCR assays using miRNAs extracted from 6 plasma samples. The  $C_T$  values of all 3 runs in each plasma sample for each of the 3 miRNAs were highly consistent among measurements (Supplementary Fig. S2B), showing that extracted plasma miRNAs can be reproducibly detected by our RT-qPCR approach. Second, we examined miR-132 expression in 3 consecutive plasma samples collected 1 month apart from each of 3 preoperative patients with EAOCs. Remarkably, consistent expression of miR-132 is detected in all 3 samples from each of these patients (Supplementary Fig. S2C).

Because the peripheral blood used in this study was drawn in heparinized tubes and heparin is a known inhibitor of RT-PCR reaction, the robustness of our RT-qPCR was tested by comparing the expression of miR-16, 21, and 195 in 3 plasma samples collected in heparinized tubes and in matched serum samples collected in tubes without anticoagulant from patients with EAOCs. Comparable expression levels of the 3 miRNAs between plasma and serum samples suggest that the influence of heparin on our RT-qPCR is minimal (Supplementary Fig. S3A). Despite similar blood collection protocols, our case and control plasma samples are from different institutions. Thus, we examined whether different sources of plasma samples may affect miRNA measurements in our study. Clearly, no difference was detected when miR-132 expression was examined by RT-qPCR between purchased healthy controls and endometriosis and EAOC samples collected at our institution (Supplementary Fig. S3B).

### Global miRNA profiling in patient plasma

The clinical demographics of all cases used in this study are summarized in Supplementary Table S1. The majority of patients in the EAOC, endometriosis, and SOC categories were Caucasian (100%, 88%, and 100%, respectively) whereas the control group contained individuals more



**Figure 1.** Plasma miRNA expression profiles can distinguish different disease categories. A, unsupervised hierarchical clustering was applied to miRNAs with <30% missing values in healthy controls, endometriosis, and EAOC samples ( $n = 20, 33,$  and  $14,$  respectively). Different distance measure and link were explored. Samples are classified into 3 clusters based on the expression signature of 23 plasma miRNAs. B, PCA was applied to markers with adjusted  $P < 0.2$  in either 1 of the 3 groups' pairwise comparisons. First 3 components were used for the 3-dimensional plot. Norm, healthy controls; Endo, endometriosis.

evenly distributed among the Caucasian, African-American, and Hispanic categories (45%, 35%, and 20%, respectively,  $P < 0.0001$ ). As expected, the patients with endometriosis were younger than those with cancer and had lower gravidity and parity scores. Sixty-four percent of the EAOC cases were stage I or II, whereas only 14% of the SOC cases were early stages, consistent with the more aggressive phenotype and late diagnosis seen in patients with SOCs (31). There were no significant associations with body mass index, tobacco, or alcohol use. Of the EAOC cases ( $n = 14$ ), 43% ( $n = 6$ ) were clear cell and 50% ( $n = 7$ ) were endometrioid tumors, whereas 7% ( $n = 1$ ) was with mixed clear cell/endometrioid histology. Presence of concurrent endometriosis at the time of cancer diagnosis was confirmed by pathology in 36% EAOC cases ( $n = 5$ ), of which 2 were endometrioid, 2 were clear cell, and 1 was mixed endometrioid/clear cell tumor.

Because the genome-wide circulating miRNA expression profile in endometriosis and EAOCs has not been established to date, we conducted global plasma miRNA expression profiling by RT-qPCR in the discovery phase of our study. Because the purpose of our study is to identify plasma miRNAs that can serve as biomarkers to distinguish endo-

metriosis and EAOC samples from healthy controls, expression of 1,113 human miRNAs was measured in 20 plasma samples from healthy individuals ( $n = 6$ ), patients with endometriosis ( $n = 7$ ), and patients with EAOC ( $n = 7$ ) to pick candidate miRNAs that are expressed in these sample categories and have potential to differentiate different groups of patients. Of the 1,113 miRNAs, miRNAs that were not expressed in any of the samples were eliminated first. Of the remaining 286 miRNAs, miRNAs that were not expressed in at least 4 samples in any sample category were further removed. Finally, 23 miRNAs with a minimal differential average  $C_T$  value of 2 ( $\Delta C_T \geq 2$ ) among EAOCs, endometriosis, and healthy controls, and miR-132, a potential endogenous control miRNA, were selected as candidate biomarkers for further study (Supplementary Table S2). Expression of these 24 miRNAs was confirmed in independent RT-qPCR runs using the 20 samples in the discovery cohort.

#### Unique plasma miRNA signatures can differentiate between patient categories

The 24 candidate miRNAs were next validated by RT-qPCR in a total of 67 samples (healthy,  $n = 20$ ;

endometriosis,  $n = 33$ ; EAO,  $n = 14$ ), including the 20 samples from the discovery phase. The SOC cases ( $n = 21$ ) were added as non-EAO controls (15). Currently, there is no consensus on housekeeping miRNAs used for plasma miRNA RT-qPCR data normalization. In our study, we found that miR-132 is the most consistently expressed miRNA across all samples from all categories (Supplementary Fig. S4). Thus, miR-132 was subsequently used as an endogenous control for plasma miRNA RT-qPCR data normalization.

The unsupervised clustering analysis using the expression of the candidate plasma miRNAs in healthy controls ( $n = 20$ ), endometriosis ( $n = 33$ ), and EAO ( $n = 14$ ) shows 3 distinct clusters: cluster 1 is enriched with endometriosis ( $n = 8$ ) and EAOs ( $n = 6$ ) samples; cluster 2 is enriched with normal samples with 2 endometriosis cases and 1 EAO case misclassified in this cluster; cluster 3 has 2 subclusters. One is enriched with endometriosis samples with 6 healthy controls misclassified in this subcluster; the other is enriched with EAO cases ( $n = 7$ ) but with misclassified endometriosis ( $n = 3$ ) and healthy controls ( $n = 2$ ; Fig. 1A). We also used PCA to aid the visualization of the data at lower dimension. Consistent with our clustering analysis, the plot of the first 3 principle components of the data also shows that the 3 groups form 3 distinct but not completely separated clouds (Fig. 1B). These results reveal the potential of using plasma miRNA expression patterns for classification of these diseases. When the unsupervised clustering analysis was conducted in all cases ( $n = 88$ , including SOC), the 21 SOC cases were found to be interspersed into the other 3 categories and cannot be separated from other categories of diseases (Supplementary Fig. S5A). Similarly, an unsupervised clustering in pairwise comparison of endometriosis/EAO or endometriosis/SOC (Supplementary Fig. S5B and S5C) showed that while the majority of endometriosis and EAO samples can be classified into relatively distinct clusters, the SOC samples are mixed with endometriosis samples. However, when EAO and SOC samples were compared, the 23-miRNA signature correctly classified the majority of them into 2 major clusters (93% and 81%, respectively; Supplementary Fig. S5D), and when unsupervised clustering was conducted between healthy controls and SOC or healthy controls and EAOs, the 23-miRNA signature can also correctly classify cancer samples from controls (Supplementary Fig. S5E and S5F). Overall, these results suggest that although the 23-miRNA signature is reflective of its originating clinical entity (endometriosis and EAOs from the discovery cohort), it also contains commonly dysregulated plasma miRNAs across different EOC histotypes. Thus, optimization of this list of candidate miRNAs may provide novel plasma biomarkers for detection and classification of endometriosis and EAOs.

We then compared the expression of the 23 miRNAs between all categories (healthy controls,  $n = 20$ ; endometriosis,  $n = 33$ ; EAO,  $n = 14$ ; and SOC,  $n = 21$ ) in the validation cohort to identify the top 10 differentially

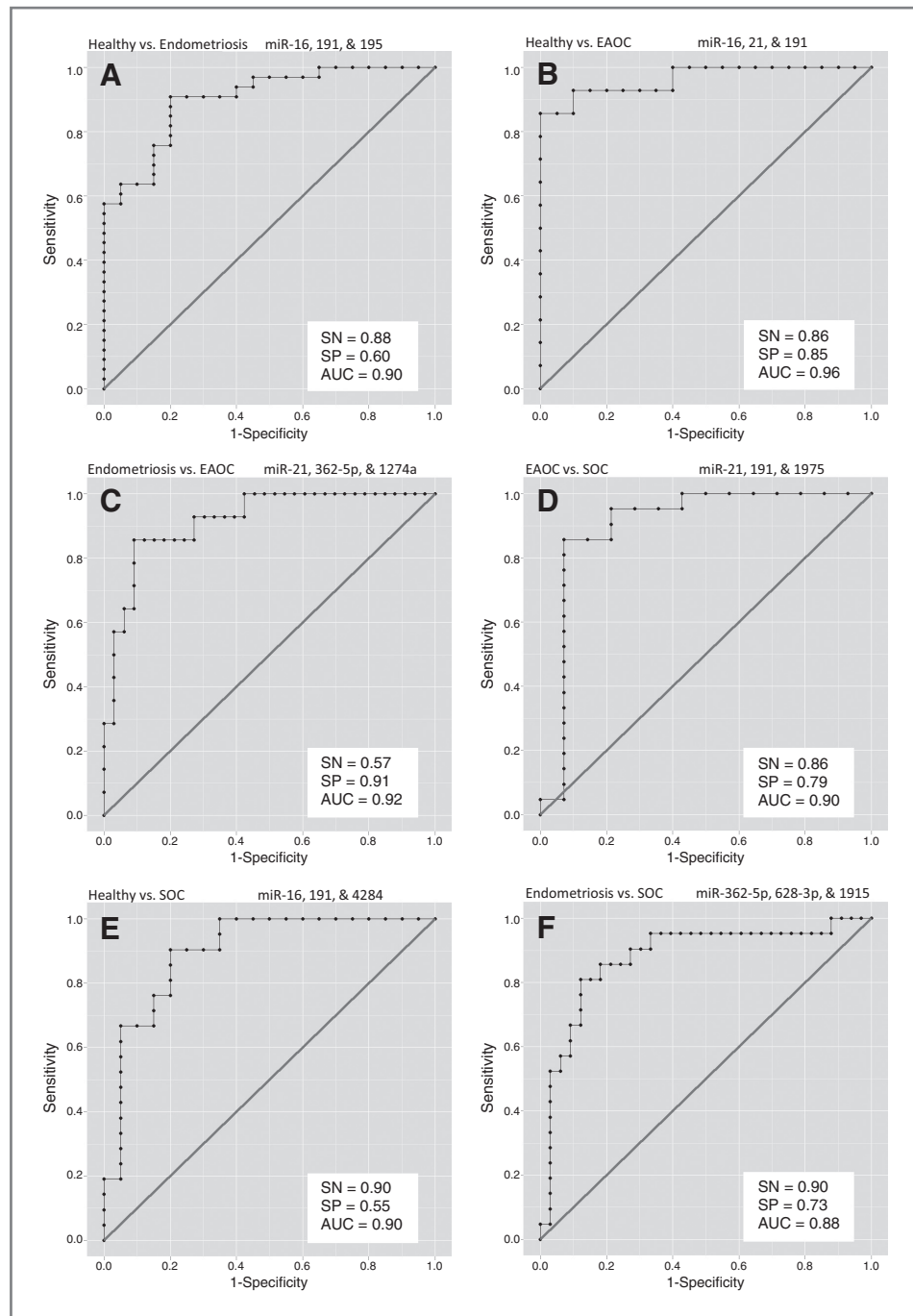
expressed miRNAs between any 2 categories by Wilcoxon rank-sum test (Table 1 and Supplementary Table S3). The top 3 candidate miRNAs for each of the pairwise comparisons are shown in Supplementary Fig. S6. While the majority of the top differentially expressed plasma miRNAs in both EAO and SOC samples are overexpressed compared with healthy controls, the level of expression in EAO samples is generally much higher than in SOC samples (Supplementary Fig. S6F). Next, we examined which combination of miRNAs among the candidate miRNAs could

**Table 1.** FCs of the 10 most differentially expressed plasma miRNAs in pairwise comparisons among healthy controls, endometriosis, and EAO samples

<b>Endometriosis (<math>n = 33</math>) vs. healthy controls (<math>n = 20</math>)</b>	<b><math>P^a</math></b>	<b><math>P^b</math></b>	<b>FC</b>
hsa-miR-16	0.00000	0.00001	396.62
hsa-miR-195	0.00001	0.00011	62.02
hsa-miR-191	0.00004	0.00028	79.05
hsa-miR-1974	0.00007	0.00034	15.43
hsa-miR-4284	0.00025	0.00101	16.79
hsa-miR-15b	0.00041	0.00124	26.27
hsa-miR-1978	0.00041	0.00124	51.29
hsa-miR-1979	0.00051	0.00135	30.54
hsa-miR-362-5p	0.00062	0.00149	3.41
hsa-miR-1973	0.00113	0.00259	16.69
<b>EAO (<math>n = 14</math>) vs. healthy controls (<math>n = 20</math>)</b>	<b><math>P^a</math></b>	<b><math>P^b</math></b>	<b>FC</b>
hsa-miR-21	0.00001	0.00014	147.40
hsa-miR-191	0.00001	0.00014	380.01
hsa-miR-16	0.00002	0.00015	1323.18
hsa-miR-15b	0.00005	0.00032	80.50
hsa-miR-1977	0.00029	0.00117	11.48
hsa-miR-1979	0.00029	0.00117	99.11
hsa-miR-1973	0.00038	0.00131	58.96
hsa-miR-1974	0.00057	0.00170	20.75
hsa-miR-4284	0.00073	0.00196	26.58
hsa-miR-195	0.00137	0.00273	48.02
<b>EAO (<math>n = 14</math>) vs. endometriosis (<math>n = 33</math>)</b>	<b><math>P^a</math></b>	<b><math>P^b</math></b>	<b>FC</b>
hsa-miR-362-5p	0.00014	0.00343	0.14
hsa-miR-1274a	0.01323	0.09634	0.13
hsa-miR-21	0.01606	0.09634	13.84
hsa-miR-766	0.02195	0.10534	15.11
hsa-miR-1975	0.03142	0.11204	7.75
hsa-miR-1308	0.03527	0.11204	0.13
hsa-miR-191	0.03735	0.11204	4.81
hsa-miR-744	0.05209	0.13192	4.89
hsa-miR-376a	0.05497	0.13192	6.38
hsa-miR-1246	0.06112	0.14058	1.36

<sup>a</sup>Wilcoxon  $P$  value.

<sup>b</sup>Adjusted Wilcoxon  $P$  value

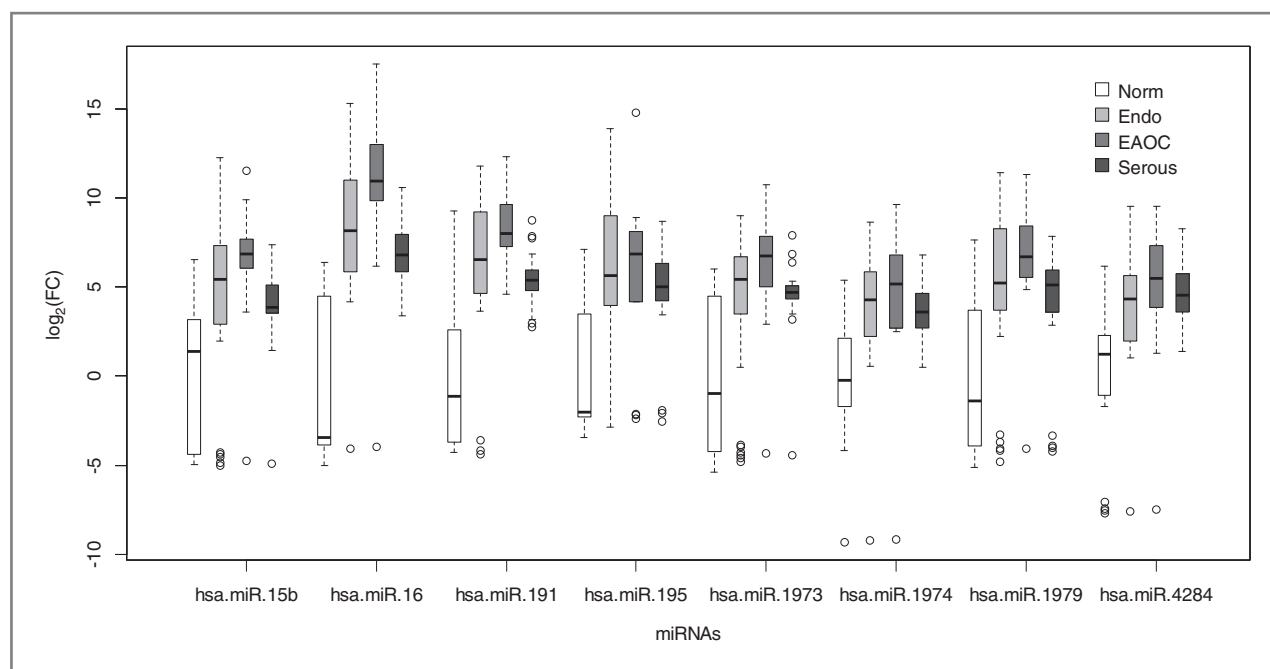


**Figure 2.** The LOCOV receiver-operating characteristic (ROC) curves of logistic regression model for 4 groups' pair-wise comparisons are plotted on the basis of the top 3 markers. AUC is also provided.

differentiate between the sample groups with the highest predictive power by linear discriminant analysis (LDA). LOOCV was used to avoid overfitting of the data. Application of LDA revealed 3 plasma miRNAs, miR-16, 191, and 195, all upregulated in endometriosis that could differentiate between healthy and endometriosis cases with 88% sensitivity (SN), 60% specificity (SP; Fig. 2A). A combination of miR-16, 21, and 191 can differentiate between healthy and EAOcs with 86% SN and 85% SP (Fig. 2B), whereas miR-21, 362-5p, and 1274a can differentiate

between endometriosis and EAOcs with 57% SN and 91% SP (Fig. 2C). miR-21, 191, and 1975 together could distinguish between EAOc and SOC with 86% SN and 79% SP (Fig. 2D). Expression signature of miR-16, 191, and 4284 could be used for discerning healthy individuals from patients with SOCs with 90% SN and 55% SP (Fig. 2E), whereas miR-362-5p, 628-3p, and 1915 can differentiate endometriosis and SOCs with 90% SN and 73% SP (Fig. 2F). Interestingly, we also noticed a general trend of elevated plasma miRNA expression from healthy controls

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**Figure 3.** Increased expression of plasma miRNAs along with the progression of diseases from endometriosis to EAOs, but not in SOC samples. The 8 miRNAs are derived from shared top 10 most differentially expressed miRNAs in both endometriosis and EAO samples compared with healthy controls. y-axis,  $\log_2$  of fold changes of plasma miRNA expression [ $\log_2(\text{FC})$ ]. Norm, healthy controls; serous, SOC; Endo, endometriosis.

to endometriosis to EAOs but not in SOC samples (Fig. 3), suggesting that these miRNAs may serve as novel biomarkers that reflect the pathologic progression from benign to precursor lesion to fully developed EAOs. Altogether, we have identified different panels of plasma miRNAs that may serve as novel biomarkers to discriminate between healthy, patients with endometriosis, EAOs, and SOCs.

#### Validation of human miRNA signature in a preclinical mouse model

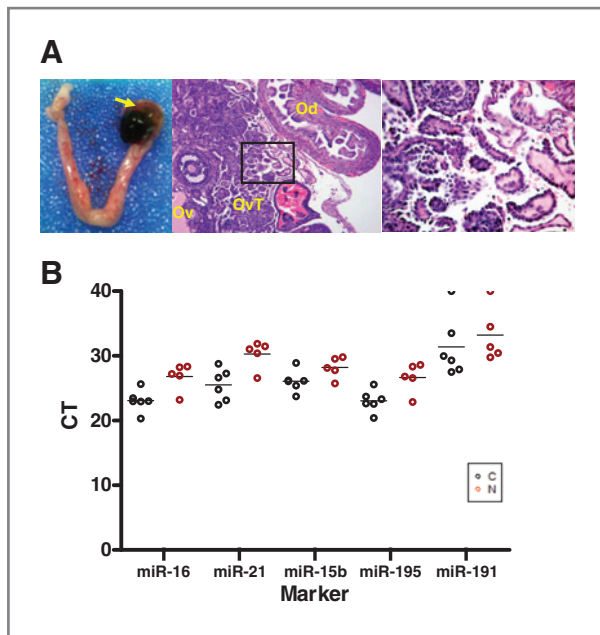
Mouse models of human diseases are powerful tools to study the mechanism of disease and test the efficacy of preclinical therapeutics. We next tested whether some of the most differentially expressed miRNAs between healthy controls and patients with EAOs (Table 1) are also differentially expressed between healthy mice and mice with endometrioid ovarian tumors. To achieve this, we used a previously described conditional mouse model for endometriosis-associated endometrioid ovarian cancer (25). The *LSL-Kras<sup>G12D/+</sup>/Pten<sup>loxp/loxp</sup>* conditional mice develop orthotopic tumors 12 weeks after AdCre injection under the ovarian bursa (Fig. 4A; ref. 25). We induced tumors in 6 female mice, sacrificed the mice when moribund, and collected serum at necropsy. Five healthy (noninjected), age-matched female mice were sacrificed as controls. Serum miRNAs were extracted and subjected to RT-qPCR analysis to measure expression of miR-15b, 16, 21, 191, and 195. Among the top 10 differentially expressed human miRNAs between healthy controls and patients with EAOs (Table 1), these 5 are the only miRNAs that have mouse orthologs.

Our results show that 4 of the 5 miRNAs can also delineate the EAO mice from healthy controls (Fig. 4B), suggesting a potential EAO-specific pathogenesis leading to the dysregulation of miR-15b, 16, 21, and 195, and further validating the biologic relevance of the plasma miRNA expression signature we have identified as biomarkers of human EAOs.

#### Ovarian tumor tissue and corresponding plasma have distinct miRNA expression profiles

Numerous miRNAs have been reported to be dysregulated in ovarian tumors (8, 32). Despite the great potential circulating miRNAs hold as novel biomarkers for classification and early diagnosis of EOC, it remains unclear whether miRNAs in patient plasma reflect miRNA expression occurring in corresponding diseased tissues. To address this question, we profiled miRNA expression in 6 pairs of endometriosis tissue or EAO primary tumors and corresponding plasma samples using the NanoString technology (33), which provides digital counting of miRNA copy numbers without the need for miRNA amplification. While we detected a very modest correlation of overall miRNA expression in paired tissue and plasma samples, we also observed distinct miRNA expression profiles, especially among the highly expressed miRNAs (Fig. 5). Specifically, while miR-16, 21, and 132 were consistently ranked as the top 3 most highly expressed plasma miRNAs, only miR-21 was consistently ranked among the top 5 most highly expressed tissue miRNAs. To further support our conclusion, we examined the expression of 10 miRNAs with mouse orthologs (miR-15b, 16, 21, 132, 191, 195, 362-5p, 652,





**Figure 4.** The plasma miRNA expression signature that differentiates healthy controls from patients with EAOs can be detected in a mouse endometrioid ovarian cancer model. **A**, left, ovarian tumor at the AdCre-injected site (arrow) but no tumor formation seen on noninjected left ovary. Middle, 10 $\times$  H&E staining of a cross-section of mouse ovarian tumor with ovary (Ov), oviduct (Od), and ovarian tumor (OvT). Right, magnified image of ovarian tumor with endometrioid histology ( $\times 40$ ). **B**, expression of orthologous miRNAs in healthy mice ( $n = 5$ ) and mice with EAOs ( $n = 6$ ). Four of the 5 miRNAs are significantly upregulated in most of the mice with EAO as compared with normals ( $P = 0.00009$ , 0.000433, 0.000209, and 0.00014 for miR-16, 21, 15b, and 195, respectively; Student  $t$  test), similar to the profiles in human EAO samples. miR-191 did not reach statistical significance, although there is also a trend that expression of plasma miR-191 is elevated in EAO mice compared with that of in normal mice. Equal amount of RNA extracted from mouse serum was used for RT and qPCR. The raw  $C_T$  values were plotted because currently there is no consensus on endogenous plasma miRNA in mouse that can be used for normalization. C, mice with EAO tumors; N, normal control mice.

744, and 1274a) from the 24 miRNAs identified from the discovery cohort (Supplementary Table S2) in 5 paired tumor and plasma samples from tumor-bearing LSL-*Kras*<sup>G12D/+</sup>/*Pten*<sup>loxp/loxp</sup> mice. No significant correlation was detected in the paired samples from all 5 mice (Supplementary Fig. S7), mirroring the findings in humans. Our data suggest that plasma and tissue samples have distinct miRNA expression profiles. Thus, differentially expressed miRNAs identified through comparing normal and tumor tissues as reported in numerous studies cannot be simply applied to study plasma/serum samples.

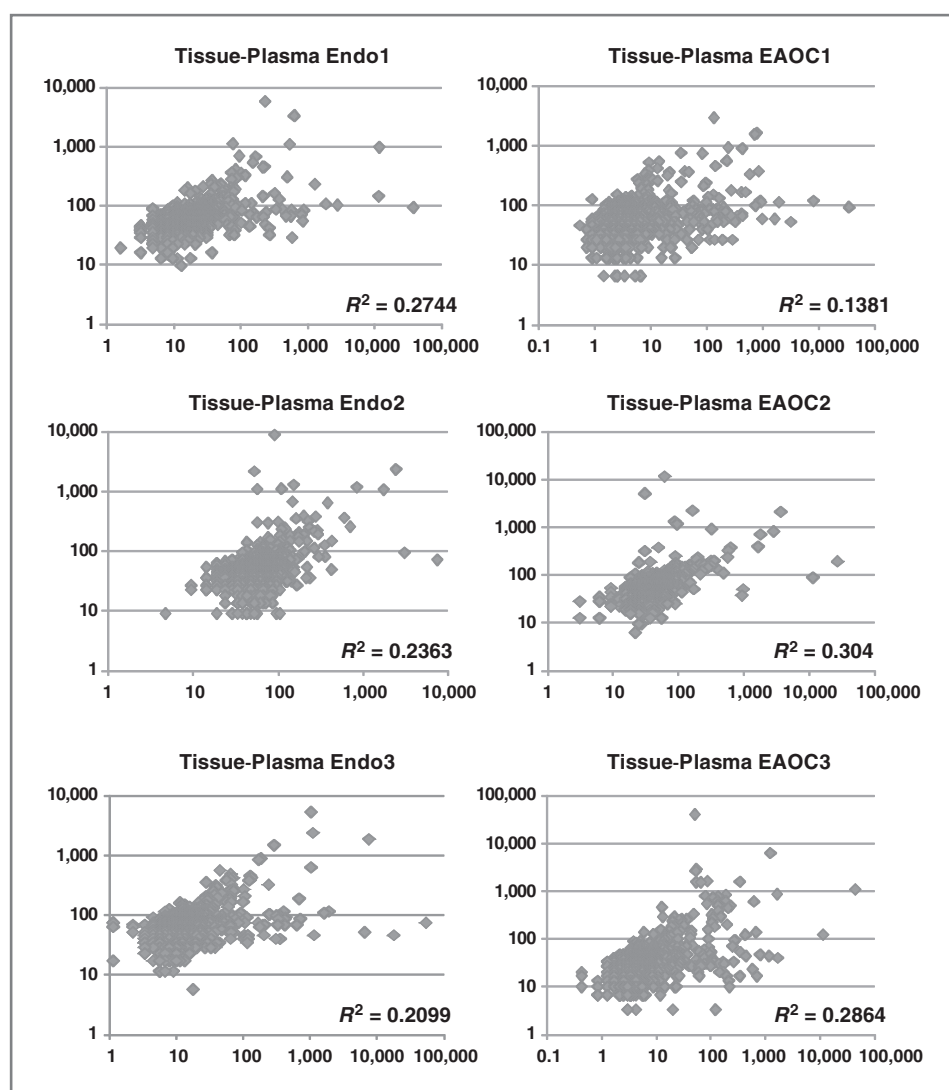
## Discussion

In this study, we conducted, to our knowledge, the first global profiling of circulating miRNAs in endometriosis and EAO samples. We have identified unique plasma miRNA expression signatures that distinguish patients with endometriosis and EAO from healthy controls, suggesting that circulating miRNAs may serve as promising biomarkers

with high sensitivity and specificity for early detection and diagnosis of endometriosis and EAOs. Remarkably, 4 of 5 miRNAs (miR-15b, 16, 21, and 195) we found differentially expressed in human EAOs from healthy controls show a similar expression pattern in a preclinical mouse model for EAOs, providing a strong support for the validity of our results and also suggesting that changes in these miRNA levels are likely due to disease-specific pathogenesis. This is also the first time that plasma miRNA biomarkers are validated in an ovarian cancer mouse model.

In addition to causing pain and infertility, endometriosis is also considered a precursor of EAO, as supported by a growing number of epidemiologic and molecular studies (15, 34). Frequent mutations of a tumor suppressor gene, *ARID1A*, have not only been identified in clear cell and endometrioid ovarian tumors but have also been found in concurrent endometriosis and atypical endometriosis lesions (34), suggesting loss of *ARID1A* function to be an early step in the transformation of endometriosis to EAOs. Although the complete pathway remains unclear, these notable findings strongly support the molecular links between endometriosis and EAOs (35) and pave the way for developing new, reliable biomarkers that not only aid in the diagnosis of endometriosis and EAO but also identify patients with endometriosis at risk for developing EAOs. The plasma miRNA signatures reported in our study, focused on distinguishing endometriosis or EAO from healthy controls, is particularly valuable because these biomarkers may potentially be used in a well-defined high-risk population, such as patients with prolonged history of suspected or confirmed endometriosis and with other ovarian cancer predisposing risk factors such as age, reproductive history, or family history of ovarian cancer.

It is estimated that a screening test for ovarian cancer would require a sensitivity of at least 75% and a specificity of more than 99.6% to achieve a positive predictive value (PPV) of 10%, the minimum PPV required for a screening test. Despite extensive efforts to develop new protein biomarkers for early detection of ovarian cancer, CA125 still stands to be the most dependable of all biomarkers examined to date (36). However, even CA125 falls short of the requirement for sensitivity and specificity to be useful as a biomarker for ovarian cancer screening (36, 37). Ovarian cancer is a highly heterogeneous disease and the 4 main histologic subtypes of ovarian cancer are now considered different diseases, which may develop differently, respond differently to chemotherapy, and express different sets of biomarkers (38). However, in the majority of past biomarker development studies, ovarian cancer has been largely regarded as a single entity. This may at least partially account for the failed effort to develop biomarkers for early detection of ovarian cancer. Our results further support this concept by showing that EAOs and SOCs are different clinical entities and can be distinguished on the basis of plasma miRNA expression profiles (Supplementary Fig. S5D). Although the sensitivity and specificity values of the plasma miRNA signatures reported here are lower than required to be applied in clinical practice yet, our study



**Figure 5.** NanoString analysis reveals very low correlation of miRNA expression between matching tissue and plasma of patients with EOCs and endometriosis. Left, comparison of 3 matched endometriosis tissue and plasma samples; right, comparison of 3 matched EAO tissue and plasma samples. The NanoString data were normalized using the nSolver software. x-axis, copy number of miRNAs in tissue samples; y-axis, copy number of miRNAs in plasma samples. Endo, endometriosis.

nevertheless serves as a foundation for future follow-up studies with larger sample sizes. In addition, combining histotype-specific plasma miRNA expression signatures with CA125 may be a promising strategy to improve the sensitivity and specificity of ovarian cancer early detection.

The panel of plasma miRNAs we identified clearly shows that circulating miRNAs are promising novel biomarkers for early detection of EOCs. Surprisingly, when we compared the global miRNA expression in primary EOC tumors or endometriosis tissues to corresponding plasma samples, only a very modest correlation was observed (Fig. 5). Interestingly, neovascularization is important for pathogenesis of endometriosis and EOCs and the lesions of endometriosis and EOCs are highly vascular (39, 40). Despite no consensus on the cellular origin of circulating miRNAs at present (41), the lack of correlation between paired tissue-plasma miRNA expression profiles in both endometriosis and patients with EOCs and in EOC mouse model (Fig. 5 and Supplementary Fig. S7) strongly suggests that disease tissue or malignant tumor cells are not the sole source of

circulating miRNAs. Because locoregional inflammation plays an important role in endometriosis and EOC pathogenesis (42, 43), it is more likely that the miRNA signatures we detected in patient plasma actually reflect the output of a systematic response of host microenvironment to the disease. Currently, the majority of circulating miRNA biomarker studies is based on primary tumor miRNA expression profiles. In light of our results, by not conducting independent global miRNA profiling in plasma/serum samples, these studies may have missed many relevant biomarker candidates.

Numerous miRNAs have been reported to be dysregulated in EOCs (8, 44), among which miR-21 and members of the miR-200 family are the most consistently upregulated compared with normal controls. Because SOC accounts for a majority of EOC cases, few reports have focused on identifying miRNA expression signatures in other EOC histotypes. Upregulation of miR-21, miR-203, and miR-205 was found to be specific to the endometrioid histotype and miR-222 was downregulated in EAO samples (8). By

using next-generation sequencing, a different set of miRNAs that are specifically upregulated in endometrioid and clear cell histotypes have also been reported recently (44), of which miR-9, 96, 182, 183, 196a, 196b, 205, and 375 are specifically upregulated in endometrioid histotype, and miR-30a, 30a\*, and 486-5p are upregulated in clear cell histotype. Among the top 10 plasma miRNAs that are most differentially expressed between EAOs and healthy controls (Table 1), miR-21 is the only miRNA that overlaps with the EAO-specific miRNA signature derived from tumor tissues (8). This discrepancy further supports our conclusion that tumor cells are not a major source of circulating miRNAs. Interestingly, miR-21 has been reported as one of the most consistently overexpressed oncomiRs in almost all tumor types (45), raising the possibility that the highly elevated miR-21 expression in the plasma of patients with EAOs may reflect activation of a common oncogenic pathway that contributes to EAO pathogenesis, despite the source of circulating miR-21 remains unknown.

Circulating miRNAs hold great promise as biomarkers for cancer early detection, diagnosis, and prognosis. Plasma/serum miRNA signatures have been reported in almost all tumor types, such as in lung (13, 46), gastric (47), breast (48), pancreatic (14), and ovarian cancers (49, 50). Among the 3 miRNAs that comprise the signature that distinguishes EAOs from healthy controls (Fig. 2B), overexpression of plasma/serum miR-16 and miR-21 has been reported in many tumor types (14, 46, 47), including in ovarian cancer (49, 50). However, dysregulated circulating miR-191 expression has not been implicated in any cancers to date. Thus, the combination of miR-16, 21, and 191 may represent a unique signature to EAOs.

Despite our rigorous statistical methods for signature identification, we acknowledge the limited sample size of our studies and the need for further validation of findings in larger cohorts. In addition, inclusion of cases with atypical endometriosis, concurrent endometriosis–EAO cases, and of early-stage EAOs is warranted in future studies to further

validate our miRNA signatures. The plasma miRNAs identified in this study are promising biomarkers of endometriosis-to-EAO progression and, ultimately, will be extremely useful to improve the clinical outcome of patients with ovarian cancer.

#### Disclosure of Potential Conflicts of Interest

T. Lee is a Consultant/Advisory Board member of Ethicon Endosurgery. No potential conflicts of interest were disclosed by the other authors.

#### Authors' Contributions

**Conception and design:** S.M. Suryawanshi, A.M. Vlad, R.P. Edwards, X. Huang

**Development of methodology:** S.M. Suryawanshi, X. Huang

**Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.):** A.M. Vlad, G. Mantia-Smaldone, R. Laskey, N. Donnellan, M. Klein-Patel, S. Mansuria, E. Elishaev, R. Budiuh, R.P. Edwards, X. Huang

**Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis):** A.M. Vlad, H.-M. Lin, M. Lee, Y. Lin, R.P. Edwards, X. Huang

**Writing, review, and/or revision of the manuscript:** S.M. Suryawanshi, A.M. Vlad, G. Mantia-Smaldone, Y. Lin, N. Donnellan, E. Elishaev, R. Budiuh, R.P. Edwards, X. Huang

**Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases):** A.M. Vlad, T. Lee, R.P. Edwards

**Study supervision:** A.M. Vlad, R.P. Edwards, X. Huang

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