Circulating miRNA Biomarkers in Early Breast Cancer Detection Following Mammography
Alexa Lean1, Jialu Lucy Yang2, Xiaohui Tan1, Christine B. Teal3, Rachel F. Brem2 and Sidney W. Fu 1 (Faculty Advisor)
1Department of Medicine, 2Department of Radiology, 3Department of Surgery, The George Washington University, Washington, DC

Introduction
The currently accepted stepwise model of breast tumorigenesis assumes a gradual transition from normal breast epithelial cells to atypical ductal hyperplasia (ADH), to ductal carcinoma in situ (DCIS), and then to invasive ductal carcinoma (IDC). Percutaneous core needle biopsy (CNB) is the standard technique following an abnormal mammographic finding. However, CNB is less reliable in differentiating simple ADH (sADH) from ADH component coexisted with advanced lesions such as DCIS and/or IDC (cADH). Therefore, to identify and validate novel reliable molecular biomarkers is essential in order to improve the efficiency of therapeutic recommendations, as well as to minimize anxiety and unnecessary procedures. Our lab has recently characterized two important miRNAs, miR-671-5p and miR-638, that are involved in breast cancer progression.

Materials & Methods
Microdissection and Total RNA isolation from FFPE samples. FFPE blocks were microdissected, with each sample containing normal, ADH, DCIS, and IDC tissue. Total RNA was isolated using the RecoverAll Total Nucleic Acid Isolation Kit. Collection of patients’ blood and Total RNA isolation before CNB procedure. Following IRB protocol, patients with lesions detected on mammography elected to donate a blood sample. miRNA was isolated using Purelink miRNA Isolation Kit. Examination of miRNA expression by qRT-PCR: qRT-PCR was performed to determine the gene expression of both the FFPE samples and the blood samples.

Results

Objective: Our data suggest that miRNAs, such as miR-671-5p and miR-638, may be potential circulating biomarkers for early breast cancer detection following mammography and CNB.