

University of Massachusetts Medical School

eScholarship@UMMS

---

UMass Center for Clinical and Translational  
Science Research Retreat

2014 UMass Center for Clinical and  
Translational Science Research Retreat

---

May 20th, 12:30 PM

## Gene Expression Profiles Identify Features Common to Lobular and Ductal Premalignant Breast Lesions


Amy L. Roberts

*University of Massachusetts Amherst*

*Et al.*

Let us know how access to this document benefits you.

Follow this and additional works at: [https://escholarship.umassmed.edu/cts\\_retreat](https://escholarship.umassmed.edu/cts_retreat)

 Part of the [Cancer Biology Commons](#), [Genetic Structures Commons](#), [Investigative Techniques Commons](#), [Neoplasms Commons](#), and the [Translational Medical Research Commons](#)

---

Roberts AL, Jerry D, Gauger KJ, Schneider SS, Crisi GM, Makari-Judson G, Khan A, Simin K. (2014). Gene Expression Profiles Identify Features Common to Lobular and Ductal Premalignant Breast Lesions. UMass Center for Clinical and Translational Science Research Retreat. Retrieved from [https://escholarship.umassmed.edu/cts\\_retreat/2014/posters/129](https://escholarship.umassmed.edu/cts_retreat/2014/posters/129)

Creative Commons License



This work is licensed under a [Creative Commons Attribution-NonCommercial-Share Alike 3.0 License](#).

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in UMass Center for Clinical and Translational Science Research Retreat by an authorized administrator of eScholarship@UMMS. For more information, please contact [Lisa.Palmer@umassmed.edu](mailto:Lisa.Palmer@umassmed.edu).

## Gene Expression Profiles Identify Features Common to Lobular and Ductal Premalignant Breast Lesions.

Amy L. Roberts<sup>1</sup>, D. Joseph Jerry<sup>1,2</sup>, Kelly A. Gauger<sup>2</sup>, Sallie S. Schneider<sup>2</sup>, Giovanna M. Crisi<sup>3</sup>, Grace Makari-Judson<sup>3</sup>, Ashraf Khan<sup>4</sup>, Karl Simin<sup>4</sup>.

<sup>1</sup> University of Massachusetts Amherst, Amherst, MA; <sup>2</sup> Pioneer Valley Life Sciences Institute, Springfield, MA; <sup>3</sup> Baystate Medical Center, Springfield, MA; <sup>4</sup> University of Massachusetts Medical School, Worcester, MA.

### Abstract:

Premalignant lesions have been identified in both the ductal and lobular units of the breast epithelium. These lesions have a 4-fold increase in risk of progression to invasive breast cancer, but 80% will remain indolent. This may be due, in part, to the uncertainty of diagnoses as inter-observer reproducibility is poor. When treated with prophylactic hormone therapies blocking the estrogen receptor, up to 40% of women still develop tumors. Therefore the challenge is to develop diagnostic tests that identify the subset of high-risk lesions and provide appropriate prophylactic therapies.

We undertook genome-wide expression studies to define sets of genes that show reproducible alterations in atypical hyperplastic lesions. Patients with sporadic atypical hyperplasias and no evidence of breast cancer for at least 2 years following the initial biopsy were selected. RNA quality from formalin-fixed, paraffin-embedded (FFPE) was assessed using the ratio of 150 and 500 bp amplicons of B-actin determined by RT-qPCR. A total of 23 patients were included with diagnoses of pure flattened epithelial atypia (FEA, n=2), atypical lobular lesions (n=9), and atypical ductal lesions (n=12). The atypical lesions and histologically normal breast epithelium were microdissected separately from 6  $\mu$ m thick tissue sections from each patient. RNA was amplified linearly, labeled and hybridized to Affymetrix ST1.0 arrays. Genes differentially expressed by >2-fold between the lesion and normal epithelium *within* each patient were used to identify gene expression signatures of atypical hyperplasias. Hierarchical clustering of a 512 gene signature yielded 3 major groupings: Benign, Intermediate, Atypia. These results reveal that atypia of the lobular and ductal structures share common underlying transcriptional features. The gene profile provides markers that can improve the reproducibility of diagnoses of atypia. Expression profiling of individuals who subsequently progress to invasive carcinoma will provide biomarkers of high-risk premalignancies and assist selection of therapeutic choices.