# THE UNIVERSITY OF TEXAS Cancer Center

Defining acquired mutations in healthy breast tissue and their association with breast cancer risk factors and breast cancer Raven Hollis<sup>1,2</sup>, Kevin Nead<sup>2,3</sup>, Christina Mcdowell<sup>2</sup> 1 Department of Biology, Prairie View A&M University, Prairie View, TX, USA 2 Department of Epidemiology The University of Texas at MD Anderson Cancer Center, Houston, TX, USA 3 Department of Radiation Oncology, The University of Texas at MD Anderson Cancer Center, Houston, TX, USA

Methods

## **The World Cancer Research Fund indicated that Breast Cancer in women is the most** common in women worldwide, and contributes to 25.4 % of the total number of new cases diagnosed in the year of 2018

Introduction

**Despite breast cancer being the** 

#### **Sectioning Plan for Samples**

- Need to be cut under DNase/RNase Free conditions
- After each section is sampled, discarded the blade used for sectioning
- Change collection brush with each sample to a disinfected brush
- **Clean stage with 100% Ethanol and UV sterilize** cryostat for 30 minutes
- Store unstained slides and OCT blocks at -80°C or on dry ice as much as possible.

#### **Steps for sectioning**

Take 1 x 4 µm section and make a cover slipped H&E Take 10 x 10 µm section could up to 12 µm section if it's easier to take with of unstained slides for dissection and DNA purification Take 1 x 4 µm section and make a coverslipped H&E Take 10 x 10 µm section of unstained slides for dissection and DNA purification Take 1 x 4 µm section and make a coverslipped H&E











most common cancer in women, our knowledge regarding acquired mutations in the breast tissue of women without breast cancer, and their association with known breast cancer risk factors and incident breast cancer risk



## Discussion

- Within our research, the breast biopsy sample is our abnormal test
- we are conducting research to determine if there are any drivers or biomarkers that later develop into cancer
- The patient blood sample is used as the standard as we search for mutations occurring over time
- TwinStrand sequencing is utilized in this research
- This method is an ultra-high accuracy sequencing method

# cancer

**Identification of mutational** 

signatures in healthy breast

tissue can be used to guide

personalized breast cancer

Objectives

- **To determine the frequency and** characteristics of acquired mutations in the healthy breast tissue of women without a history of breast cancer
- **To determine whether the presence** and burden of acquired mutations in the healthy breast tissue of women without breast cancer are associated with established breast cancer risk factors and incident breast cancer risk.

## Results

- The review has not been completed, and we are still analyzing the tissue and blood samples
- It is anticipated that our findings will demonstrate whether the presence and burden of acquired mutations in the healthy breast tissue of women without breast cancer are associated with established breast cancer risk factors and incident breast cancer
- We expect that If our hypothesis is correct, these findings will be used as a guide for personalized breast cancer prevention and prevent breast cancer

- TwinStrand overcomes the limitations of Next-Generation Sequencing in the process by independently tracking both strands of individual DNA molecules
- Then the paired sequences are compared to eliminate any errors

### References

Supported by a grant from The University of Texas MD **Anderson Cancer Center Duncan Family Institute for Cancer Prevention and Risk Assessment** Home. Leica Biosystems. (n.d.). https://www.leicabiosystems.com/histologyequipment/cryostats/leica-cm1950/. **Images provided by Christina McDowell** *TwinStrand Duplex Sequencing*<sup>™</sup> *Technology*. TwinStrand Biosciences. (n.d.). https://twinstrandbio.com/technology/. Worldwide cancer data: World Cancer Research Fund International. WCRF International. (2021, May 25). https://www.wcrf.org/dietandcancer/worldwide-cancerdata/.

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