

Auria: Biomarker Discovery Study

The goal of this study was two fold 1) determine what proteins could be detected in tears of diagnosed breast cancer patients and 2) determine what proteins could be used as a tool to differentiate between breast cancer and control samples. For Step 1, Proteome wide trypsin digestion was utilized to explore and identify any biomarkers present in detectable levels in tear fluid that may be indicative of breast cancer. Step 2 was carried out by analyzing selected biomarkers on an additional data set by ELISA. Tables below provide a brief overview of sample set demographics.

Table 1: Samples for LC MS/MS

Category	LC MS/MS (n=102)
Normal	51
Breast Cancer	51

Table 3: Samples for ELISA

Category	ELISA (n=171)
Normal	96
Breast Cancer	75

Table 2: Breast Cancer Subtypes for LC MS/MS

Breast Cancer Subtype	
IDC	28
ILC	4
DCIS	13
IDC/DCIS	3
Other	1
NR	2

Table 4: Breast Cancer Subtypes for ELISA

Breast Cancer Subtype	
IDC	44
ILC	5
DCIS	18
IDC/DCIS	4
Other	1
NR	3

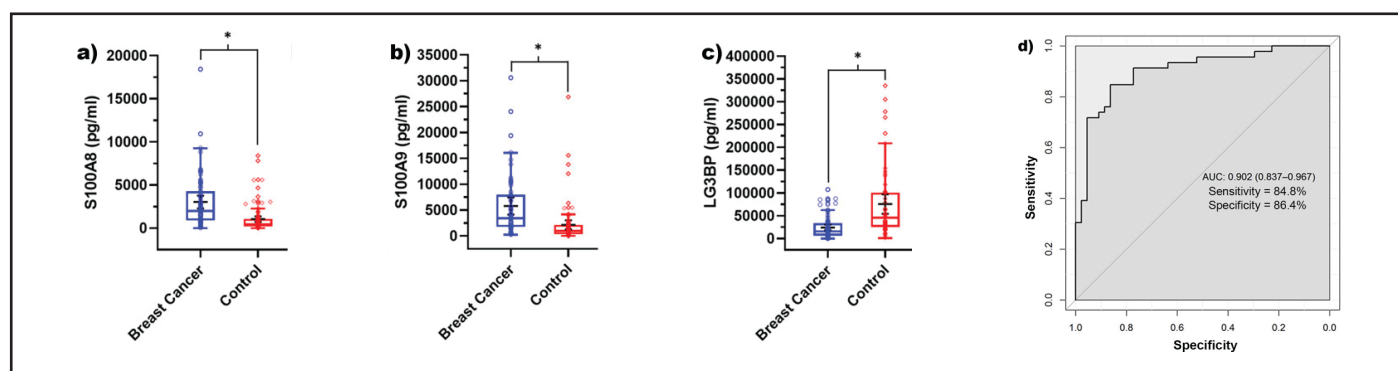


Figure 1: Box plot of S100A8, S100A9, and LG3BP concentrations by ELISA. Receiver operator characteristics curve (ROC) for protein expression of potential breast cancer markers.

In summary, the LC-MS/MS produced a promising data set of 14 biomarkers for potential further analysis. ELISA characterization on the top three biomarkers produced the following diagnostic Parameters: Sensitivity 84% Specificity 86%; providing enough validation to move forward with a larger data set.