INTRODUCTION

- Axillary lymph node (ALN) metastasis often guides breast cancer treatment and prognostication
- To date, there have been few studies examining the genomics of SLN metastasis in triple negative breast cancer (TNBC)

OBJECTIVE

- The aim of this study is to characterize and compare gene expression patterns of primary breast cancers and paired ALN metastases.

METHODS

- Patients with stage 2-3 ER/PR negative, HER2 negative TNBC with macrometastasis to an ALN and no neoadjuvant therapy were selected
- The tumor-specific area was isolated from breast and ALN, including sentinel lymph node (SLN), paraffin embedded tissue sections
- Gene expression of a panel of 2,567 cancer-associated genes was analyzed with the HTG EdgeSeq system coupled with the Illumina Next Generation Sequencing (NGS) platform

RESULTS

- The most striking feature is the downregulation of genes known to regulate cell microenvironment interaction (MMP2, MMP 3, MMP 7, MMP 11, MMP14, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COL6A6, COL11A1, COL17A1)

CONCLUSION

- There was an upregulation of anti-apoptosis and survival signaling genes (i.e. BIRC3) in SLN metastasis
- There was also an upregulation of chemotaxis genes (CCL19, CCL21, CXCL13, TNFSF11)

Email: Marissa.Srour@cshs.org