

# **RNA-seq and Tumor Infiltrating Lymphocytes as Markers of Tumor Microenvironment Changes after Cryoablation**



**Bioinformatics Analysis** 

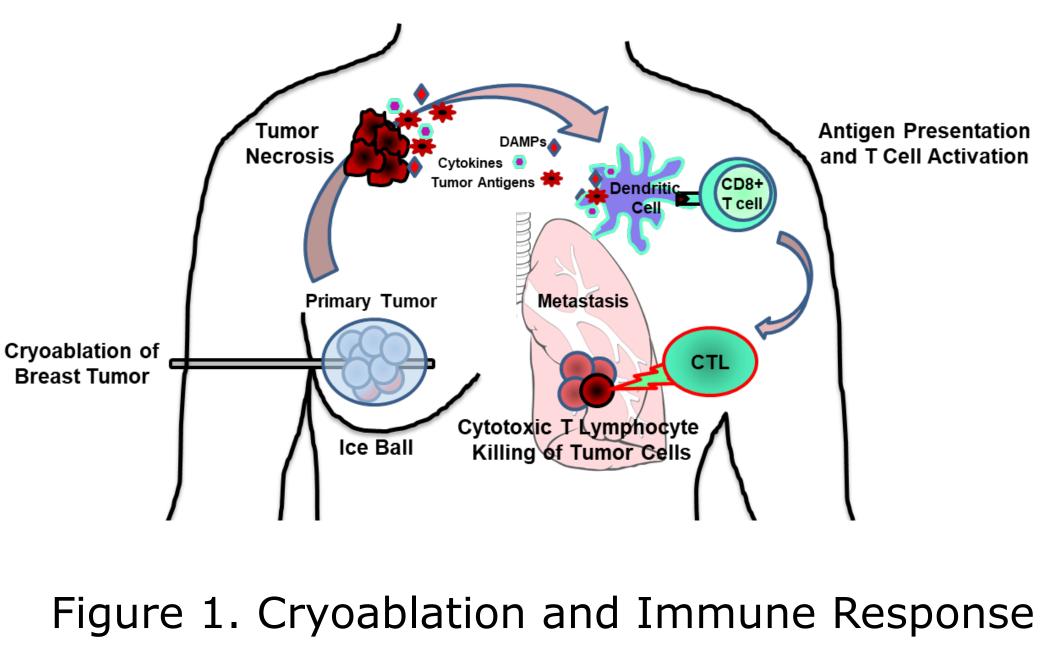
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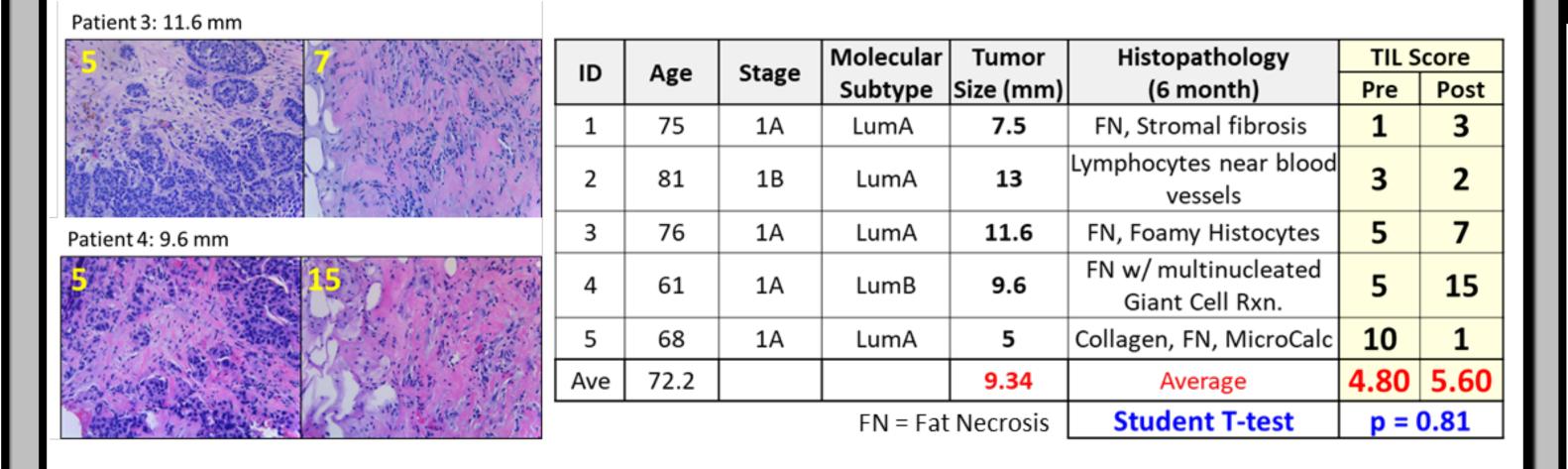
### Figure 2. Experimental Approach Introduction **TIL Scores Isolate RNA** Cryoablation is a minimally invasive procedure that **Biopsy Prepare Library** Reads Sequence induces target tissue necrosis through freeze/thaw non-cancerous area cycles, reaching less than $< -40^{\circ}$ C, while Tumor Periphery preserving surrounding tissue architecture. While the tumor is killed, potential cancer antigens are preserved. Since the ablated tumor remains in the FASTQ Files Histology Slides introduces the potential this for patient, Pre & Post Ingenuity Pathway Analysis Cryoablation augmentation of an immune response to tumor antigens still present which might target the cells that have already escaped for systemic disease

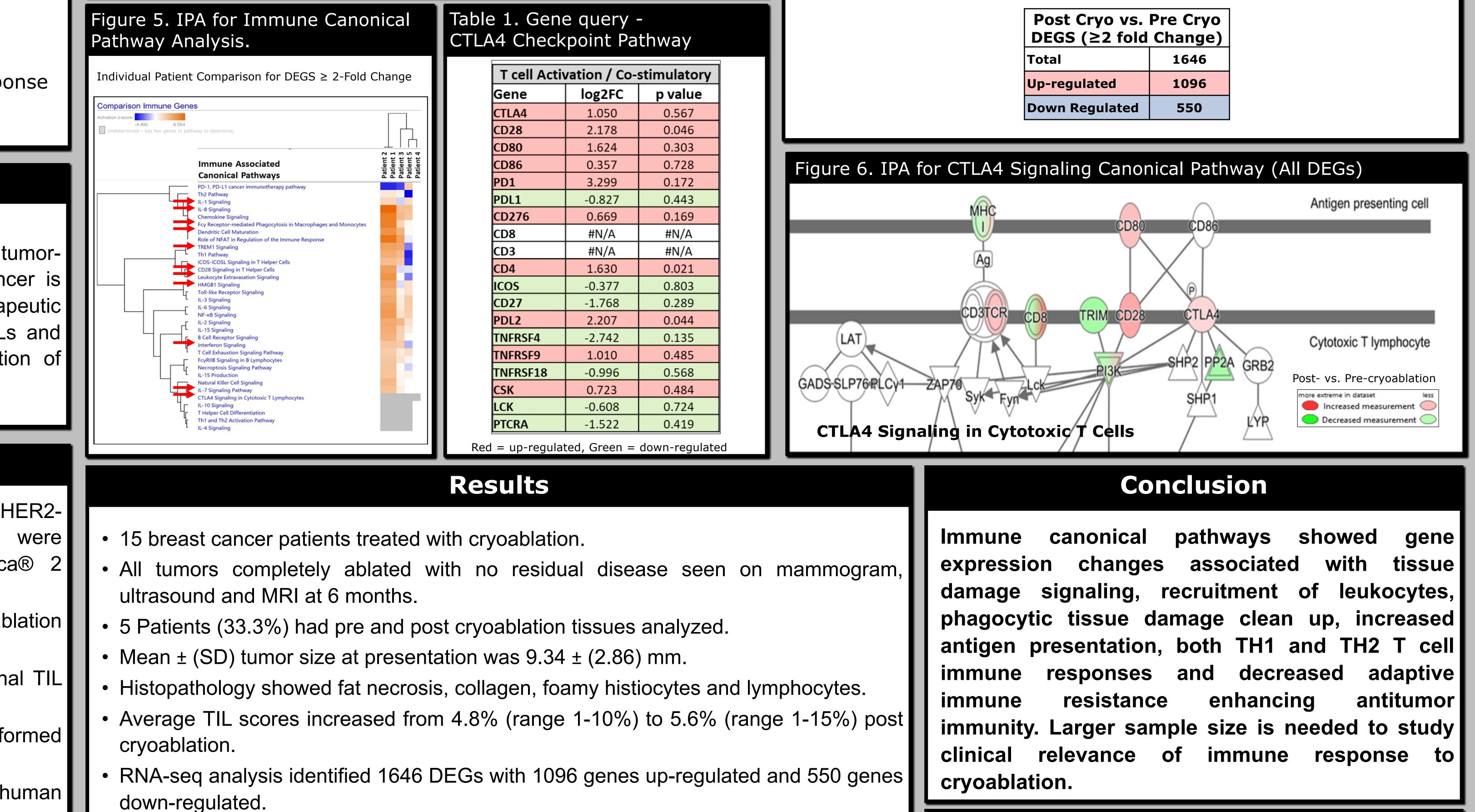


Immunological

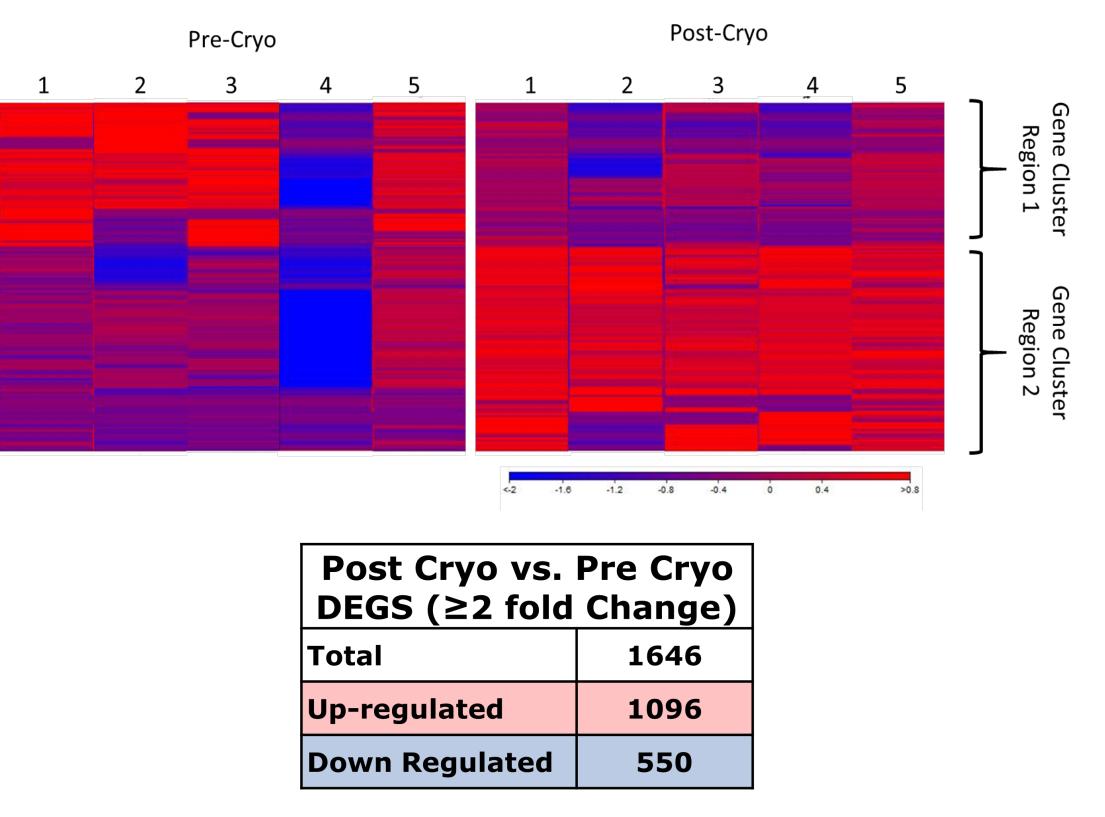


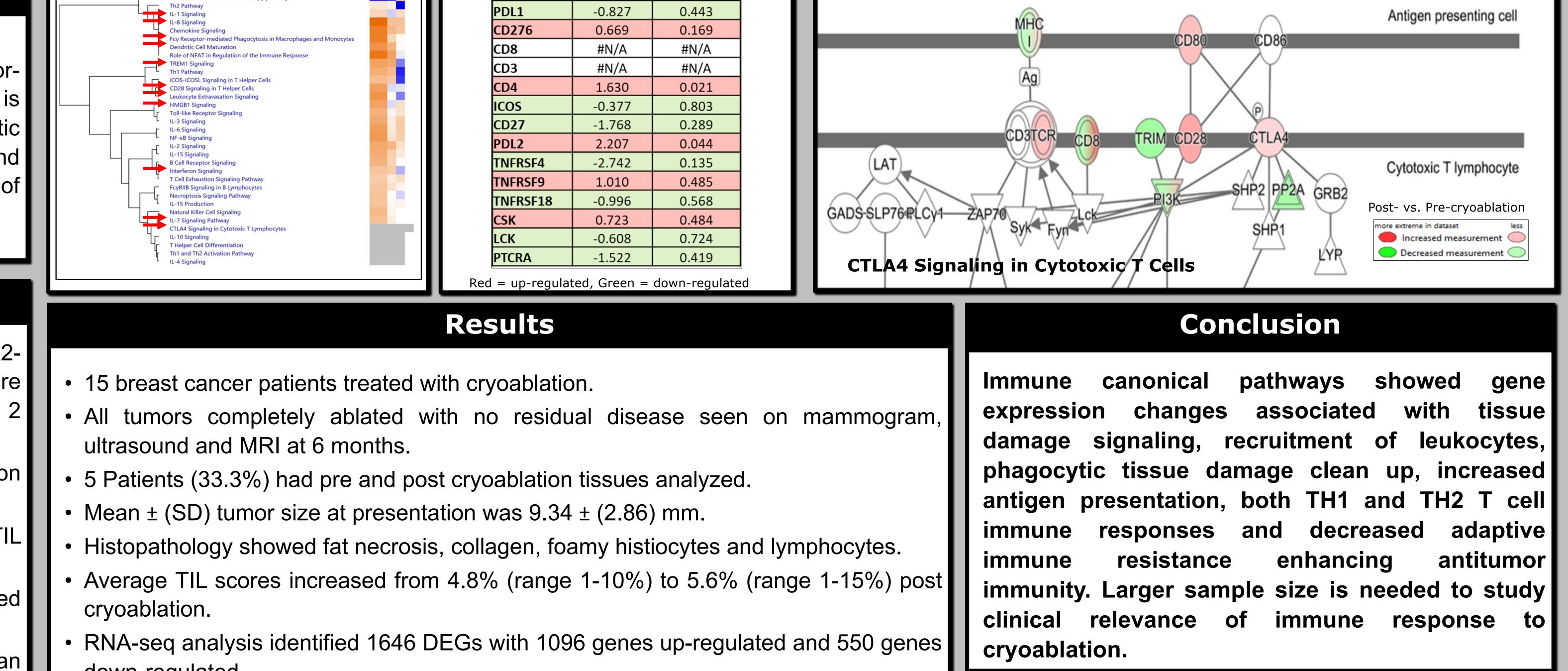












infiltrating lymphocytes (TILs) in breast cancer is becoming increasingly relevant as new therapeutic targets. This study explored changes in TILs and RNA-seq in breast cancers after cryoablation of low-risk tumors.

microenvironment

and

Objective

## **Materials and Methods**

- Women diagnosed with ER+, PR+, and HER2infiltrating ductal carcinomas  $\leq$  1.5 cm were treated with cryoablation using a Visica® 2 Treatment System
- Biopsy of tumor bed performed pre-cryoablation and at 6-month follow-up.
- TIL scores calculated using the International TIL Working Group guidelines.
- Whole transcriptome sequencing was performed on an Illumina NextSeq 500 instrument.
- Sequencing reads were mapped to the human

reference genome Hg38.

 Differentially Expressed Genes (DEGs) were identified between pre and post cryoablation as  $\geq$ two-fold changes and a correction p-value of  $\leq$ 0.05.

 DEGs analyzed with Ingenuity Pathway Analysis Software (IPA®, QIAGEN).

• Overall, gene expression associated with immune cell functions were increased.

 IPA gene analysis showed increased gene expression for immune canonical pathways: HMGB1 Signaling, IL-8 Signaling, CXCR4 Pathway, Leukocyte Extravasation, FCy Receptor Mediated Phagocytosis in Macrophages and Monocytes, Dendritic Cell Maturation, Natural Killer Cell Signaling, CD28 Signaling in T Helper Cells, IL-15 Production, and decreases in genes associated with the PD-1 PD-L1 Cancer Immunotherapy Pathway.

 Up-regulation of T cell costimulatory CD28 (> 2-fold) and inhibitory CTLA-4 (< 2-fold)</li> receptors.

Future

Clinical Study: Local Therapy Optimization by Grouping Immune-modulation with Cryoablation (LOGIC) for High-Risk Breast Cancers.

### Acknowledgements

We would like to thank TTUHSC School of Medicine, Department of Surgery, and ASCO provided financial support.

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