Introduction

- Ovarian Cancer 5 Year survival rate is <30%
- Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors (Elias et. al., 2016)
- PAX8 plays an important role in the transcriptional changes that distinguish healthy FTs from ovarian cancer cells.

Objective

Identify PAX8 binding sites in the genome that are unique to ovarian cancer cells compared to other PAX8 expressing tissues and cancer types.

Methods

- Laboratory research working with cells and nuclear lysates including the following techniques:
  - Cell Culture
  - Western Blotting
  - Universal Transcription Factor Binding Assays
- Weekly lab meetings to discuss results and plan for moving forward.

Results

Western Blots
- Confirming the presence of PAX8 in:
  - Ovarian Cancer Lines
  - Thyroid
  - Kidney
- Identification of proper controls, specifically, a nearly complete negative control.
- Identification of appropriate anti-PAX8 primary antibody.

Universal Transcription Factor Binding Assays
- Detect specific transcription factor DNA binding
- By measuring the luminescence of a sample we could quantify the relative affinity of PAX8 to a specific binding sequence of our design.

Discussion

- Originally predicted we would be able to identify a sequence of DNA (12-15 bp) which would bind to Ovarian Cancer PAX8 but not to other PAX8 expressing tissue types.
- We had successfully identified sequences for specific PAX8 binding but we did not see significant variation between the cell types.

Conclusion

- It now seems less likely that differential binding across cell types is due to modifications of the PAX8 protein itself.

Next Steps

- Study differences in the DNA across tissue types to see if the differential binding is due to an epigenetic factor.

References