Project Presentation

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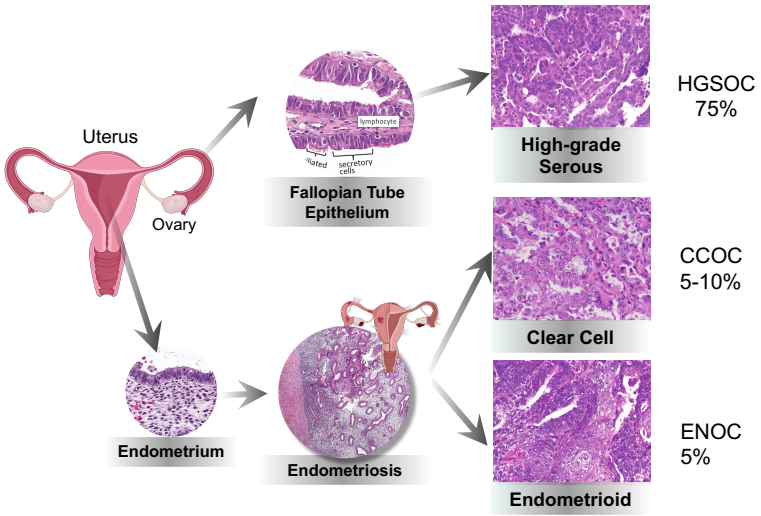
Background

Introduction

- **Group Name**: Packing the Bits
- **Group Members**: Jacob Morrison
- **Project Title**: Investigating Tissue Differences in the Human Fallopian Tube across Ovarian Cancer Subtypes

Ovarian Cancer Overview

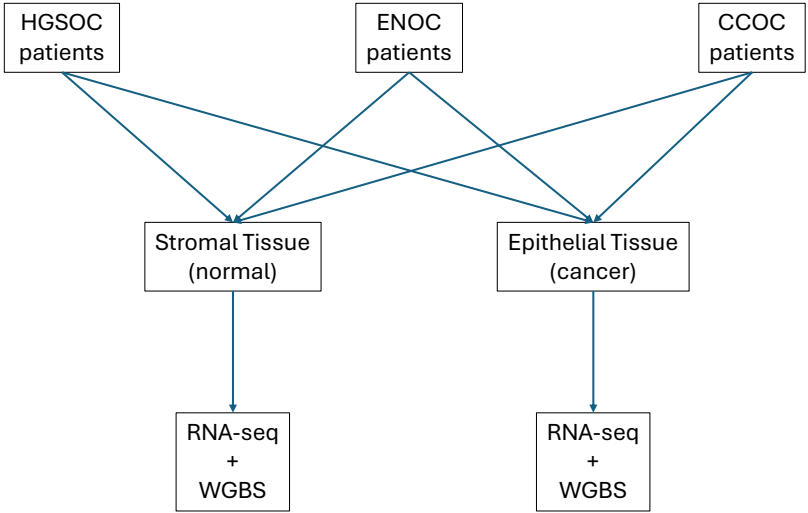


HGSOC=High grade serous ovarian carcinoma | ENOC=Endometrioid Ovarian Carcinoma | CCOC=Clear Cell Ovarian Carcinoma // Photo credit: Paige Matusiak

Related Work

- Previous results in the lab showed that differences between ENOC and CCOC are driven by cell state rather than cell type
- But, this was done with bulk tumor samples
  - This makes it hard to distinguish between normal cells and cancer cells
- To better understand differences, new tumor samples were collected and laser capture microdissection was performed
  - Allows for precise separation of normal and tumor samples
- Initial analysis showed that differences in the normal tissue was not driven by the type of cancer, but rather by another set of factors

Sample Overview



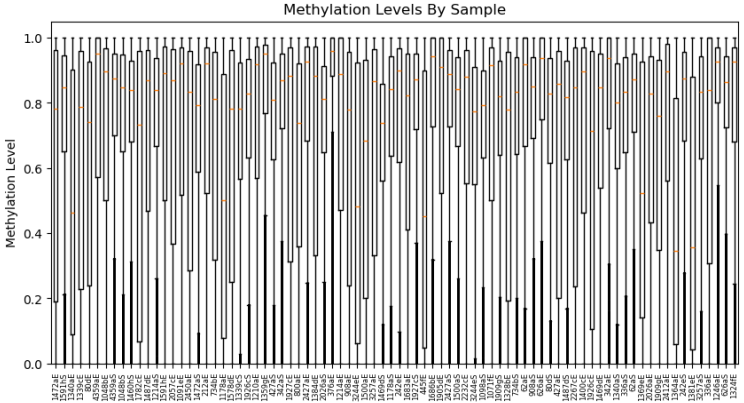
Methods

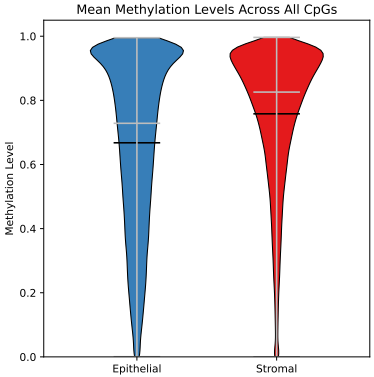
Methods

- Sample filtering
  - Started with 92 samples
  - Removed 10 samples due to contamination
- File processing
  - Data read in with `pandas`
  - Raw data points retained and logit-transformed values calculated
  - Data points removed that had coverage < 10 or were not on the canonical chromosomes (chr. 1-22, X, Y, or mitochondria)
  - Only positions found in all samples were retained to eliminate missing data
- Analysis notes
  - Dissimilarity metric used: $1 - \frac{\vec{x} \cdot \vec{y}}{||\vec{x}|| \times ||\vec{y}||}$, used the 10,000 most variable positions
  - PCA used the logit-transformed values and retained 2 dimensions ($\sim$30% of variance explained)

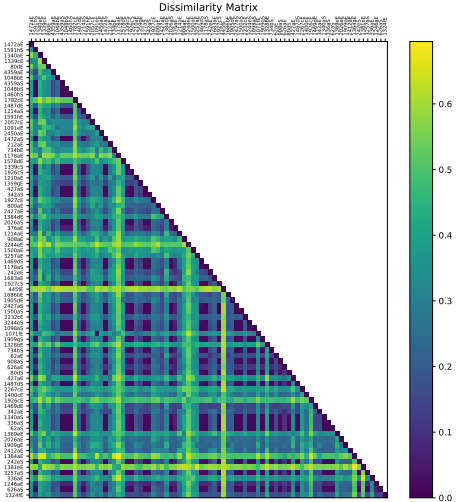
Results

Descriptive Statistics

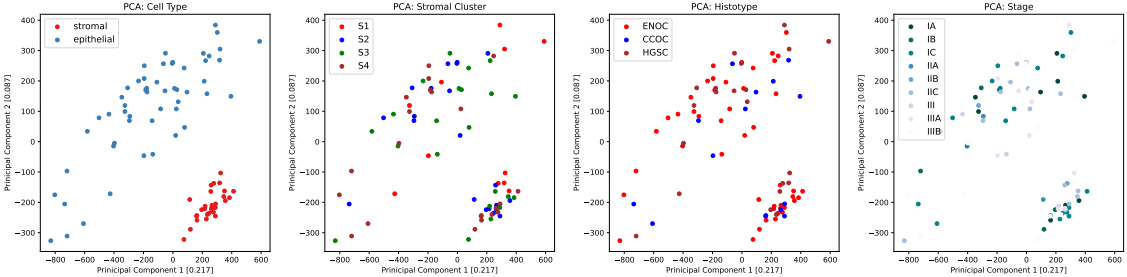




Dissimilarity



PCA


PCA: Cell Type
stromal
epithelial
PCA: Stromal Cluster
S1
S2
S3
S4
PCA: Histotype
ENOC
CCOC
HGSC
PCA: Stage
IA
IB
IC
IIA
IIB
IIC
III
IIIA
IIIB
Principal Component 1 [0.217]
Principal Component 2 [0.087]

Conclusion

Summary and Future Work

- Limitations and Future Work
  - Need to overcome differences of cancer versus normal samples $\rightarrow$ separate stromal and epithelial samples within PCA
  - All data compared across entire genome $\rightarrow$ look at biologically relevant regions of interest
- Summary
  - Broadly confirmatory of data quality rather than noteworthy results
  - Tumor samples differ from normal samples
  - Some samples do stand out as interesting to explore in more detail