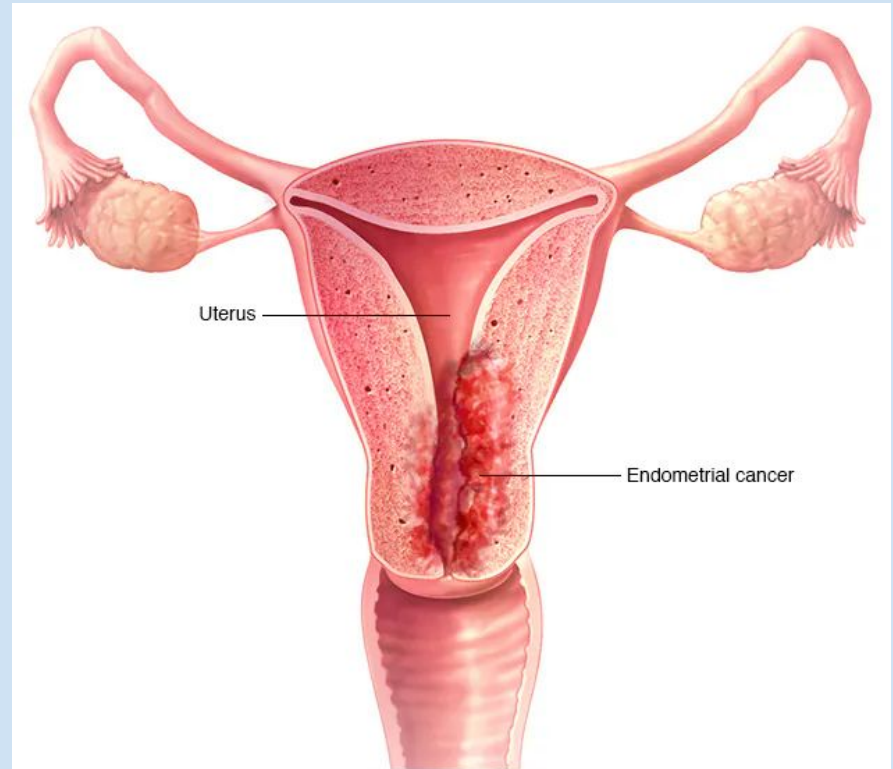


# **A Multi-Omic Analysis of Pregnancy Differences in Endometrial Carcinoma**

Erika Li, Tomás Manea, Nathan Yoon

# Background

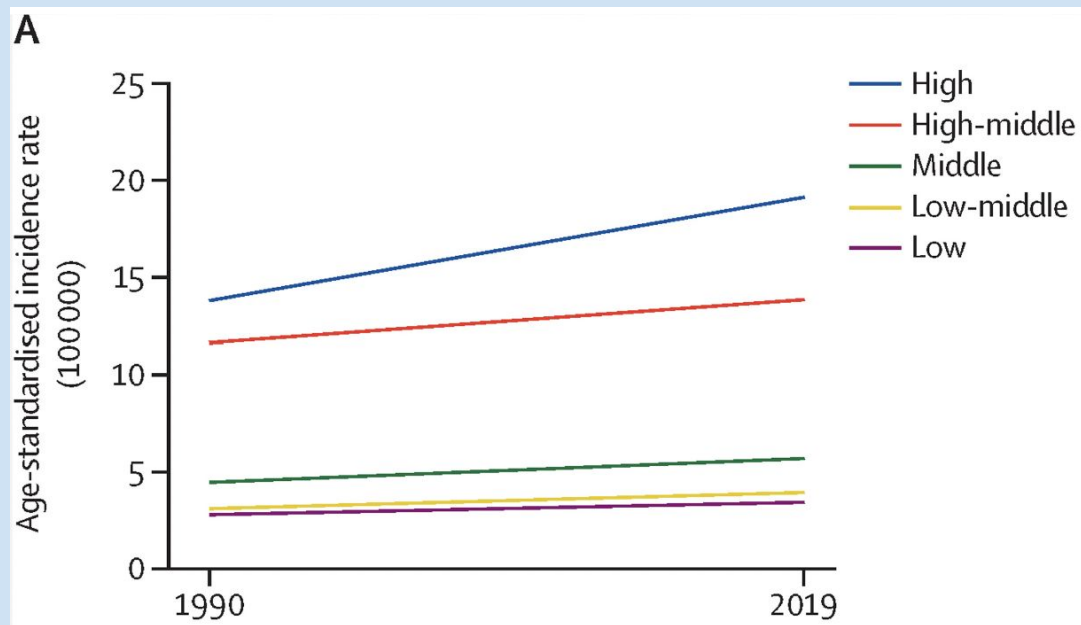
- Most common form of endometrial cancer
- Develops in uterine lining
- Symptomatology
- Treatment



Source: Mayo Clinic

# Background

- 84% 5-year survival rate
- Over 400,000 new cases reported in 2020
  - Increasing incidence rate



Source: Crosbie et. al (2022)

# Risk Factors

- Obesity
- Age
- Early menarche
- Late menopause
- Hormone treatment
- Nulliparity

<b>Table 1</b> <b>Risk Factors for Endometrial Carcinoma</b>	
<b>Characteristic</b>	<b>No. of Times Risk Increased</b>
Obesity	
30–49 lb	3.0
>50 lb	10.0
Nulliparity	2.0
Late menopause	2.4

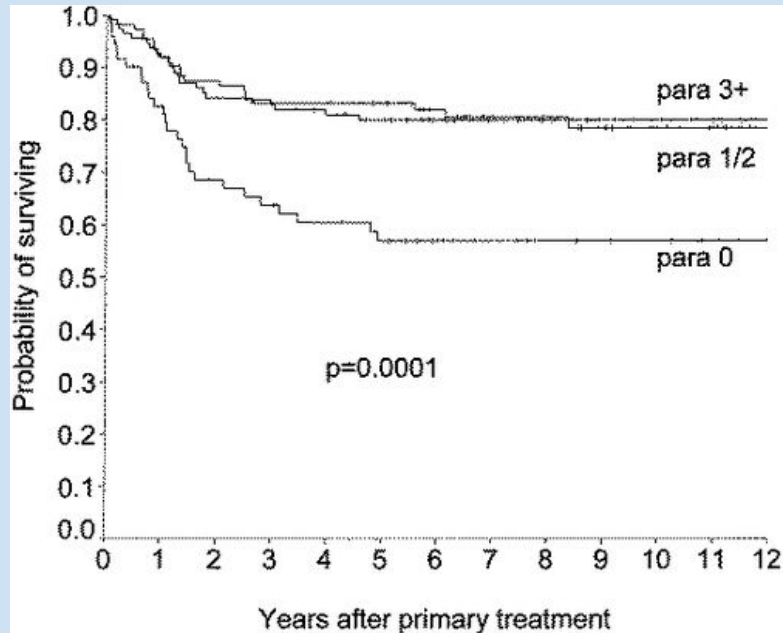
Source: Barakat et. al (1998)

# Protective effects of pregnancy

- **Jordan et. al (2020)**: each full-term pregnancy associated with a 15% reduction in cancer risk
- **D'Urso et. al (2022)**: **3 live births** compared to none attributed to 50% decrease in cancer risk

# Protective effects of pregnancy

- **Salvesen et. al (2000)**: nulliparous women had a poorer 5-year survival rate compared with patients who had had 1 or more deliveries
- **Hachisuga et. al (2002)**: highest survival in parity of **3 or more**



Aim to understand the variances between a **high pregnancy** group (three or more pregnancies) and a **low-medium pregnancy** group (less than three pregnancies), by exploring differences across **genomic**, **transcriptomic**, and **proteomic** landscapes in endometrial cancer.

# Introduction of Methods

- The Cancer Genome Atlas (**TCGA**)
  - $< 3$  pregnancies:  $n = 22$
  - $\geq 3$  pregnancies:  $n = 19$
- Clinical Proteomic Tumor Analysis Consortium (**CPTAC**)
  - $< 3$  pregnancies:  $n = 49$
  - $\geq 3$  pregnancies:  $n = 21$



# **TCGA - Genomic and Transcriptomic Data Analysis in RStudio**

# Welch Two Sample t-test

data: low\_preg\_pt\$tumor\_invasion\_percent and high\_preg\_pt\$tumor\_invasion\_percent

t = 1.3451, df = 35.48, p-value = 0.1871

alternative hypothesis: true difference in means is not equal to 0

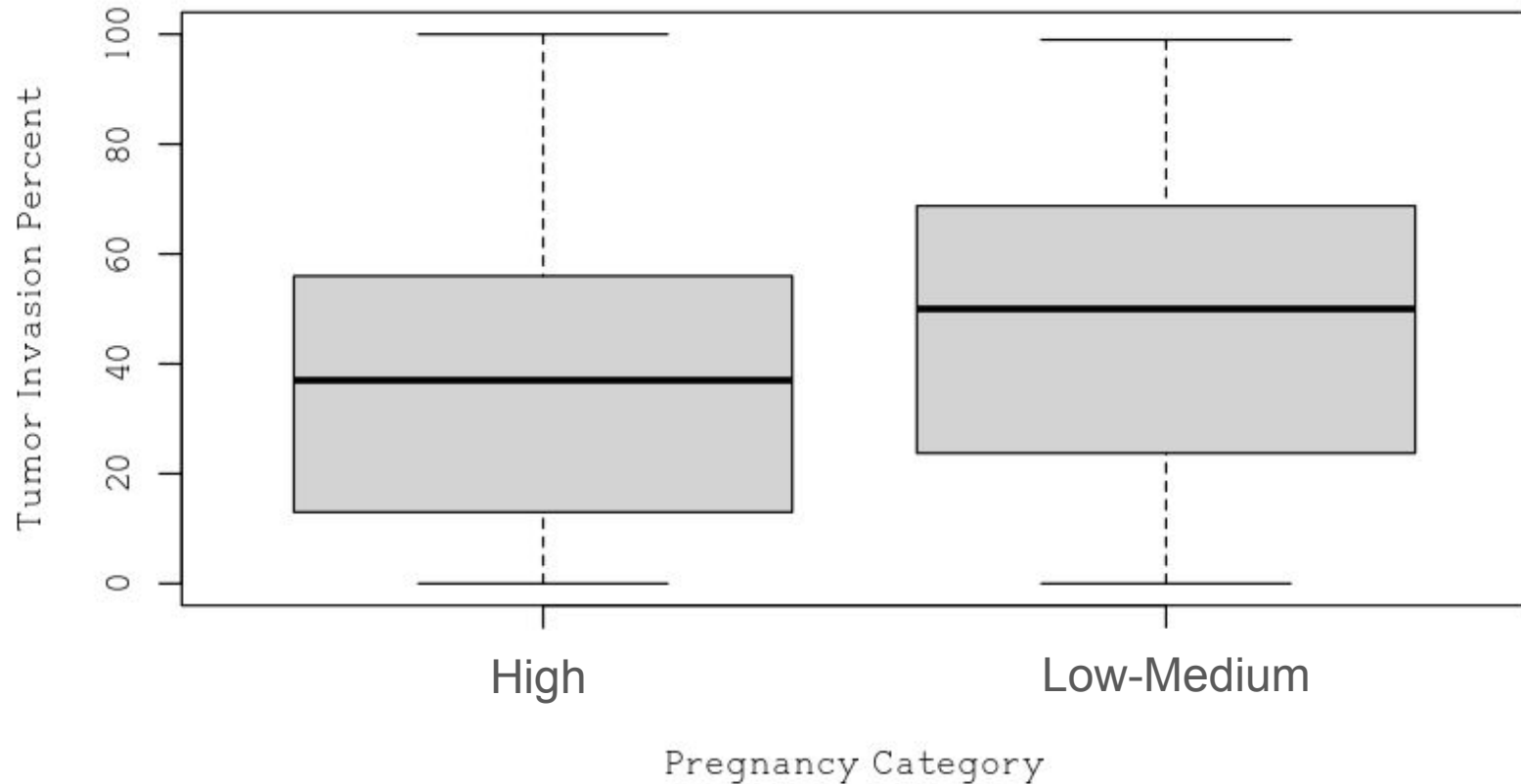
95 percent confidence interval:

-6.446363 31.796522

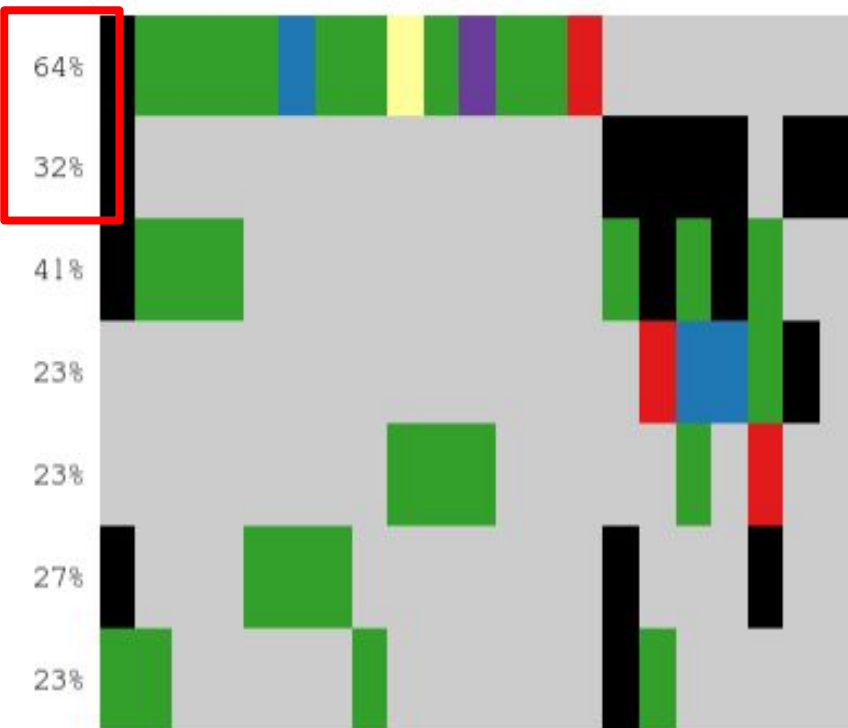
sample estimates:

mean of x mean of y

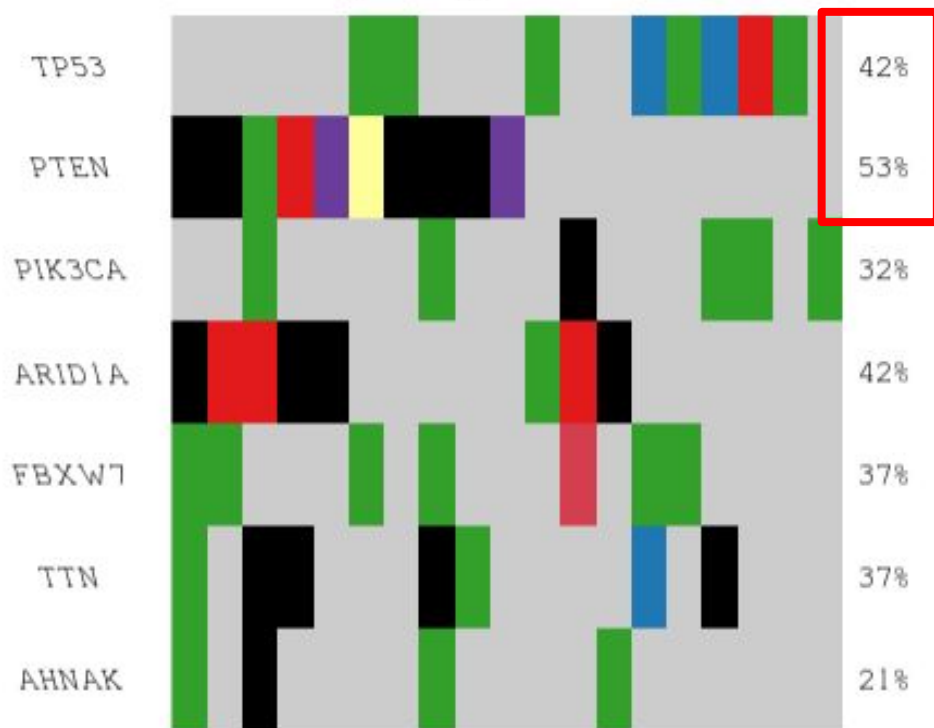
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<3 Pregnancy Patients (N = 22)

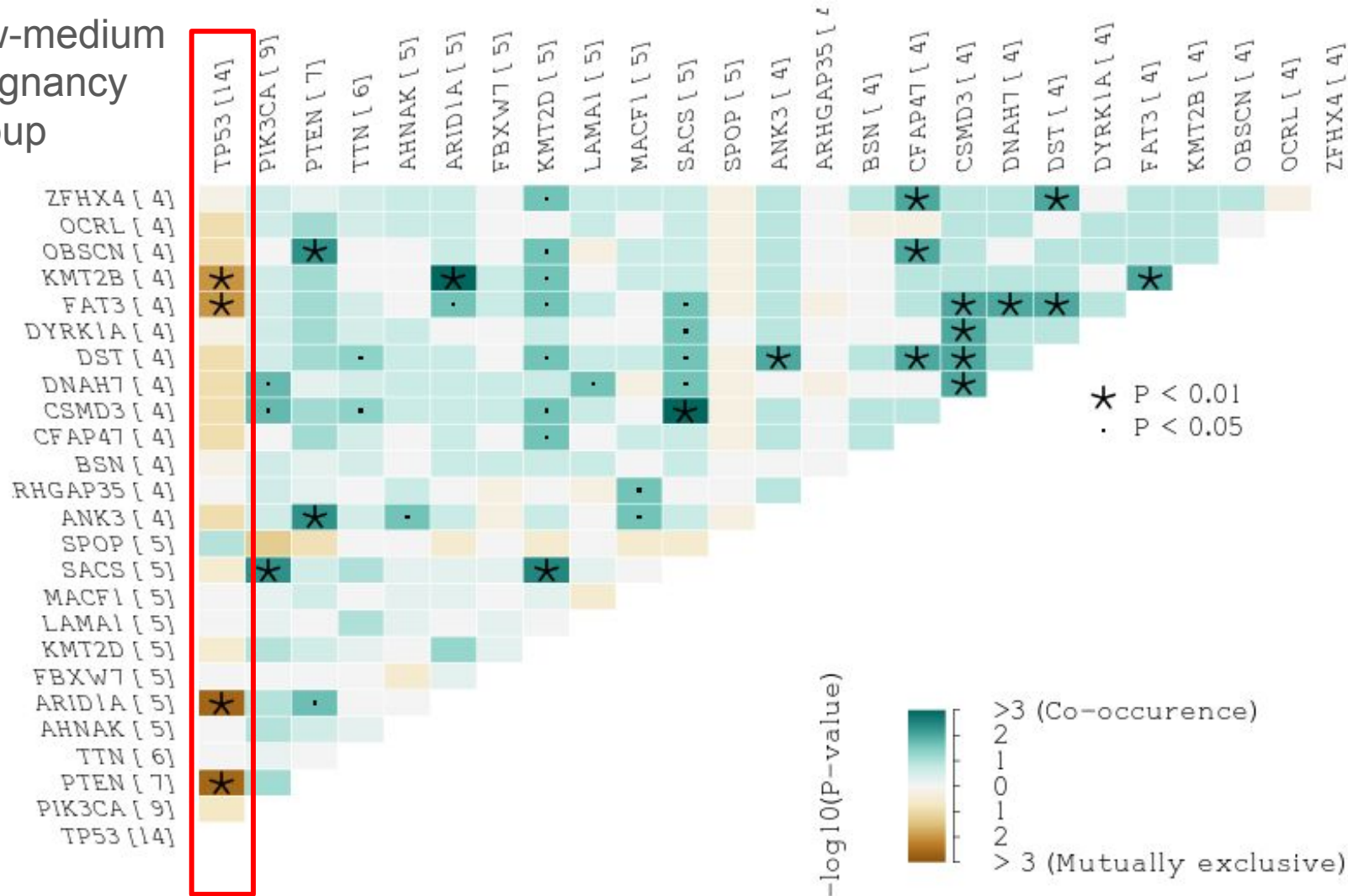


>= 3 Pregnancy Patients (N = 19)

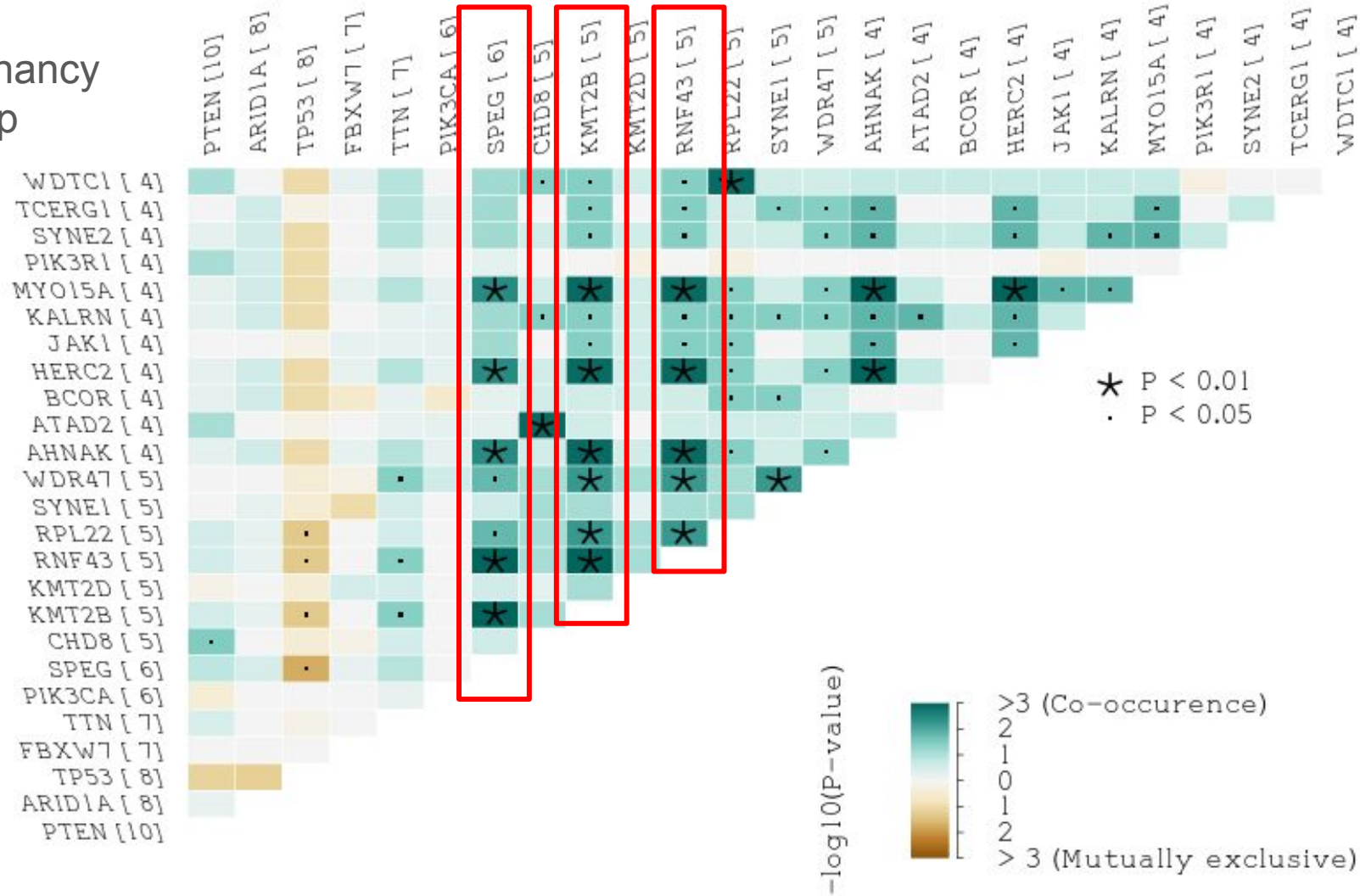


■ Frame\_Shift\_Del    ■ Splice\_Site  
■ Frame\_Shift\_Ins    ■ In\_Frame\_Del  
■ Missense\_Mutation    ■ Multi\_Hit  
■ Nonsense\_Mutation    ■ In\_Frame\_Ins

# Low-medium Pregnancy Group



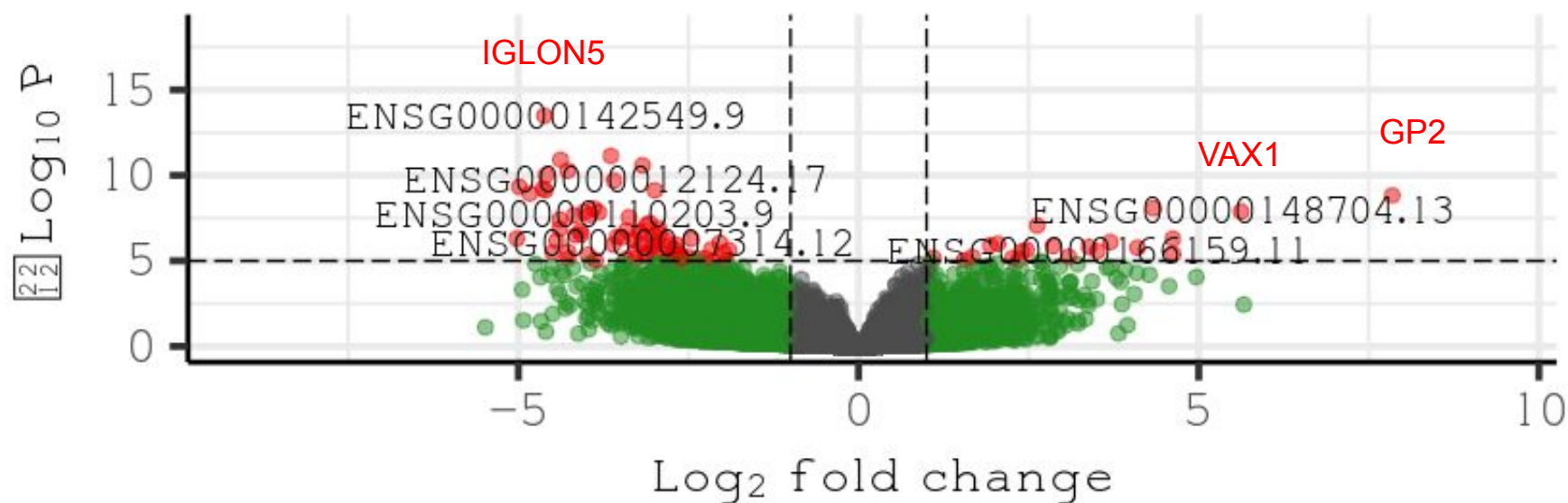
# High Pregnancy Group



Volcano plot

EnhancedVolcano

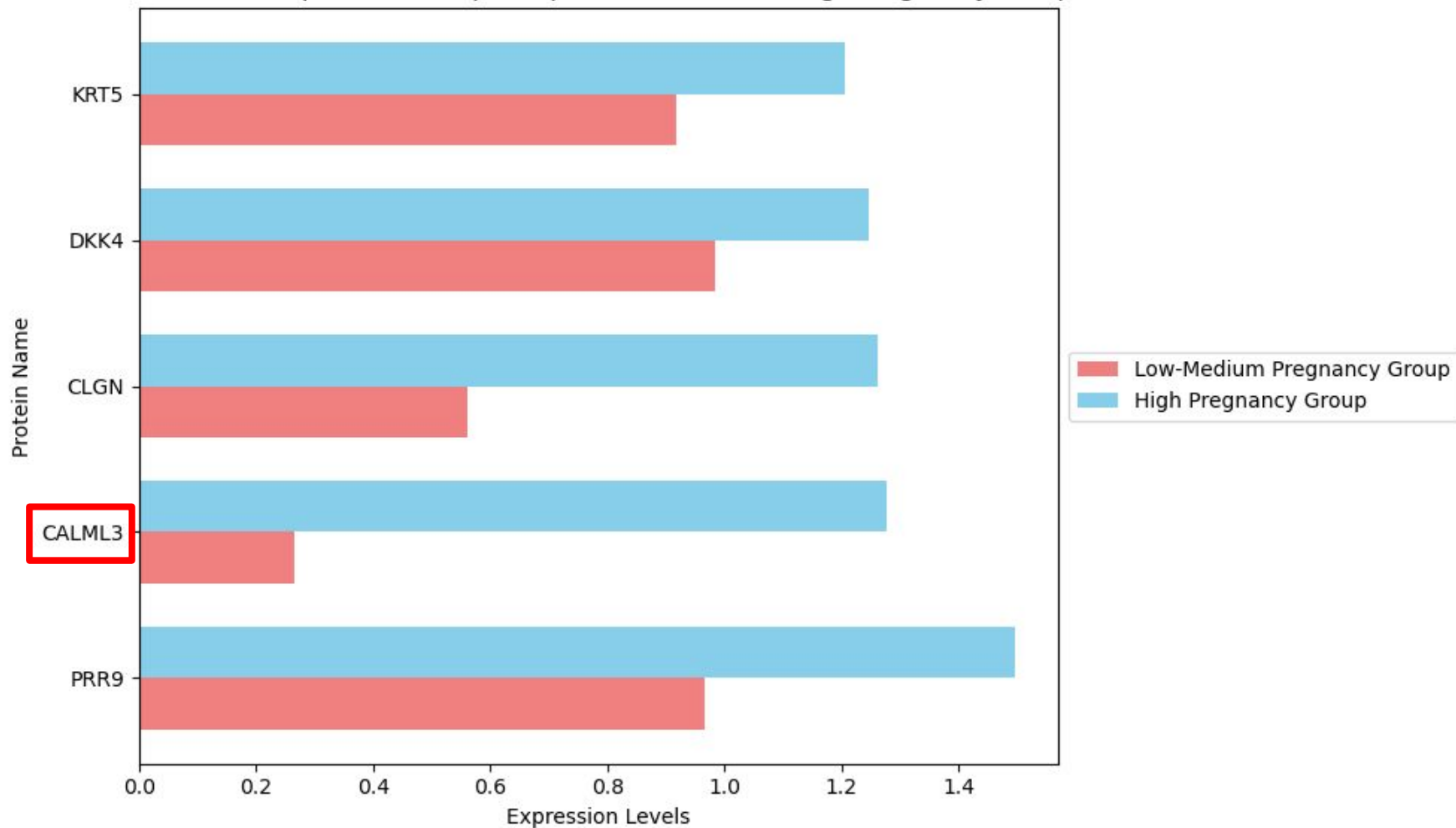
● NS ●  $\text{Log}_2 \text{FC}$  ●  $p$  value and  $\text{log}_2 \text{FC}$



total = 60660 variables

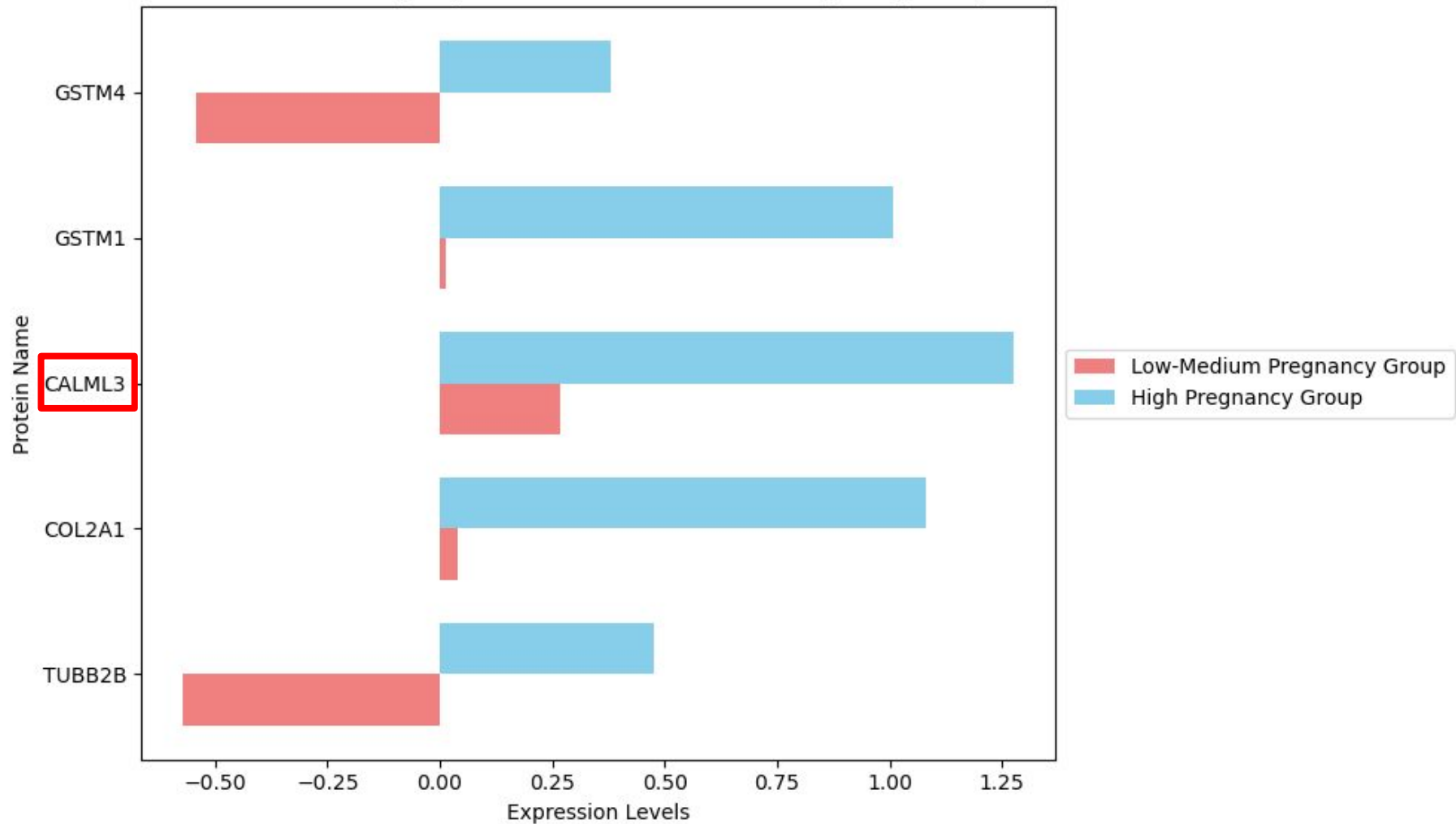
# **CPTAC - Proteomic Data Analysis in Python**

Differential Expression of Top 5 Expressed Proteins in High Pregnancy Group





Most Differentially Expressed Proteins Between Pregnancy Groups



## Discussion - TCGA

- **“High” pregnancy group**
- Genes, SPEG & RNF43, were ubiquitously co-occurrence
- Muscle Development - MYO15A & SPEG's relation

# Welch Two Sample t-test

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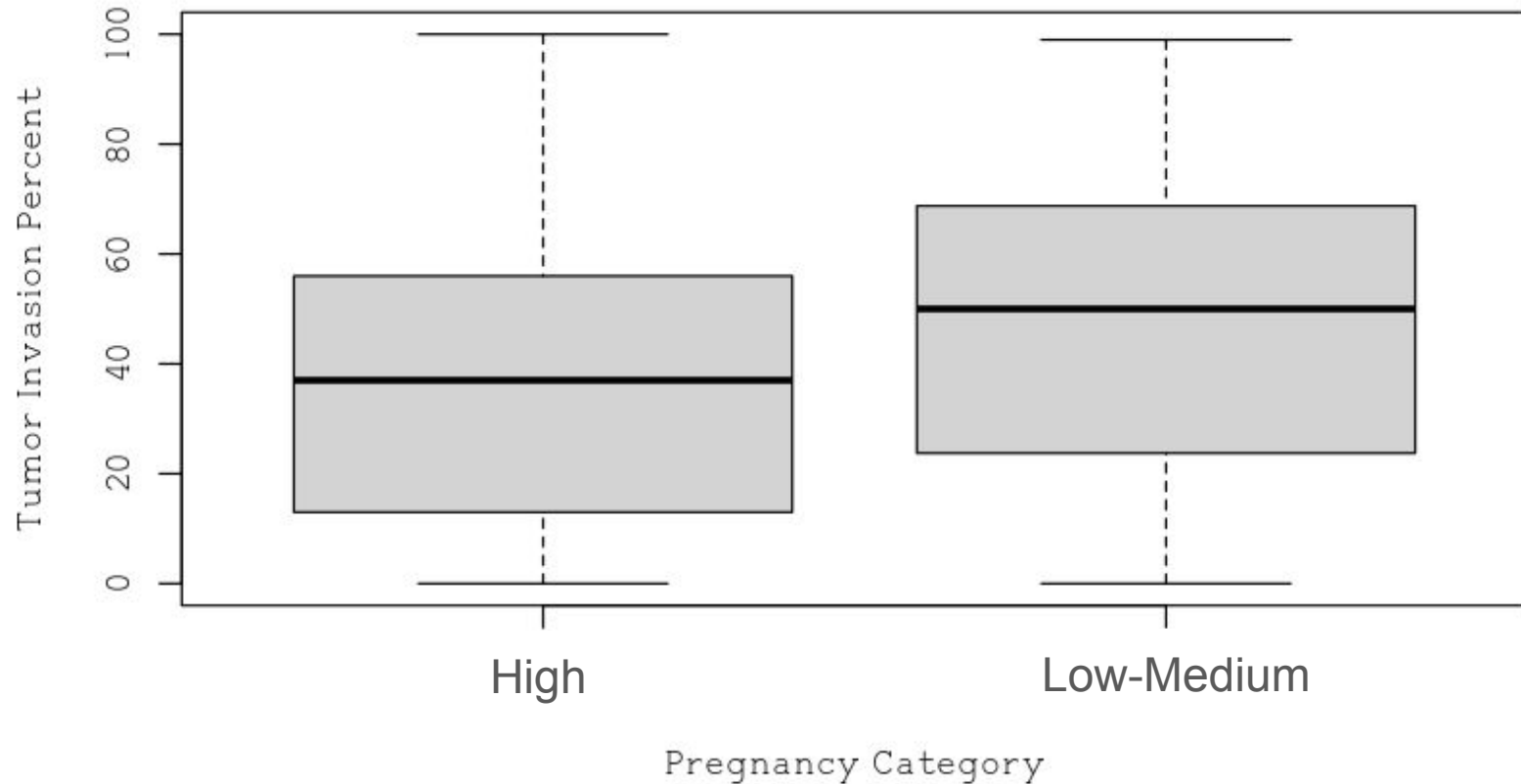
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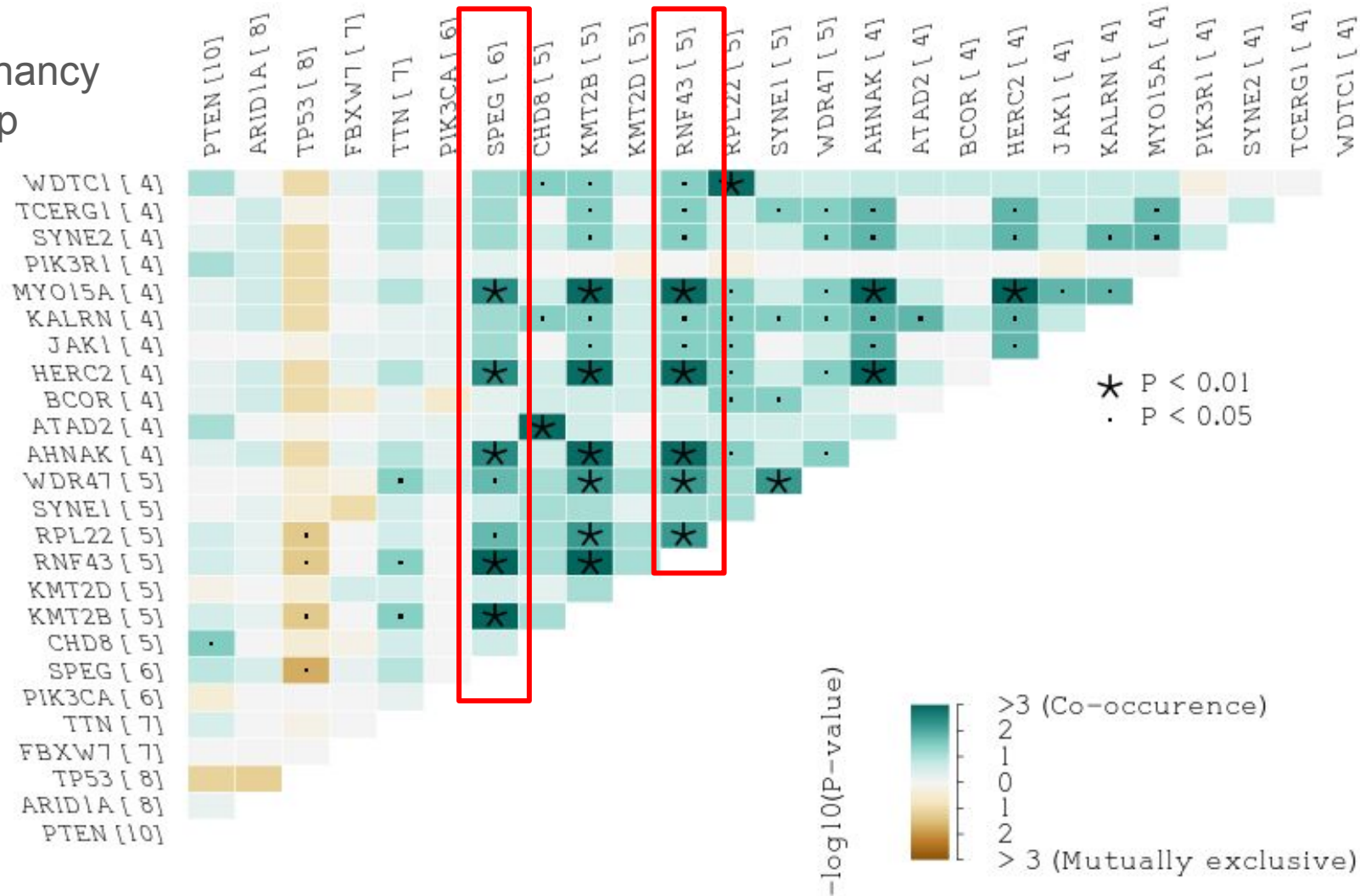
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## Discussion - TCGA

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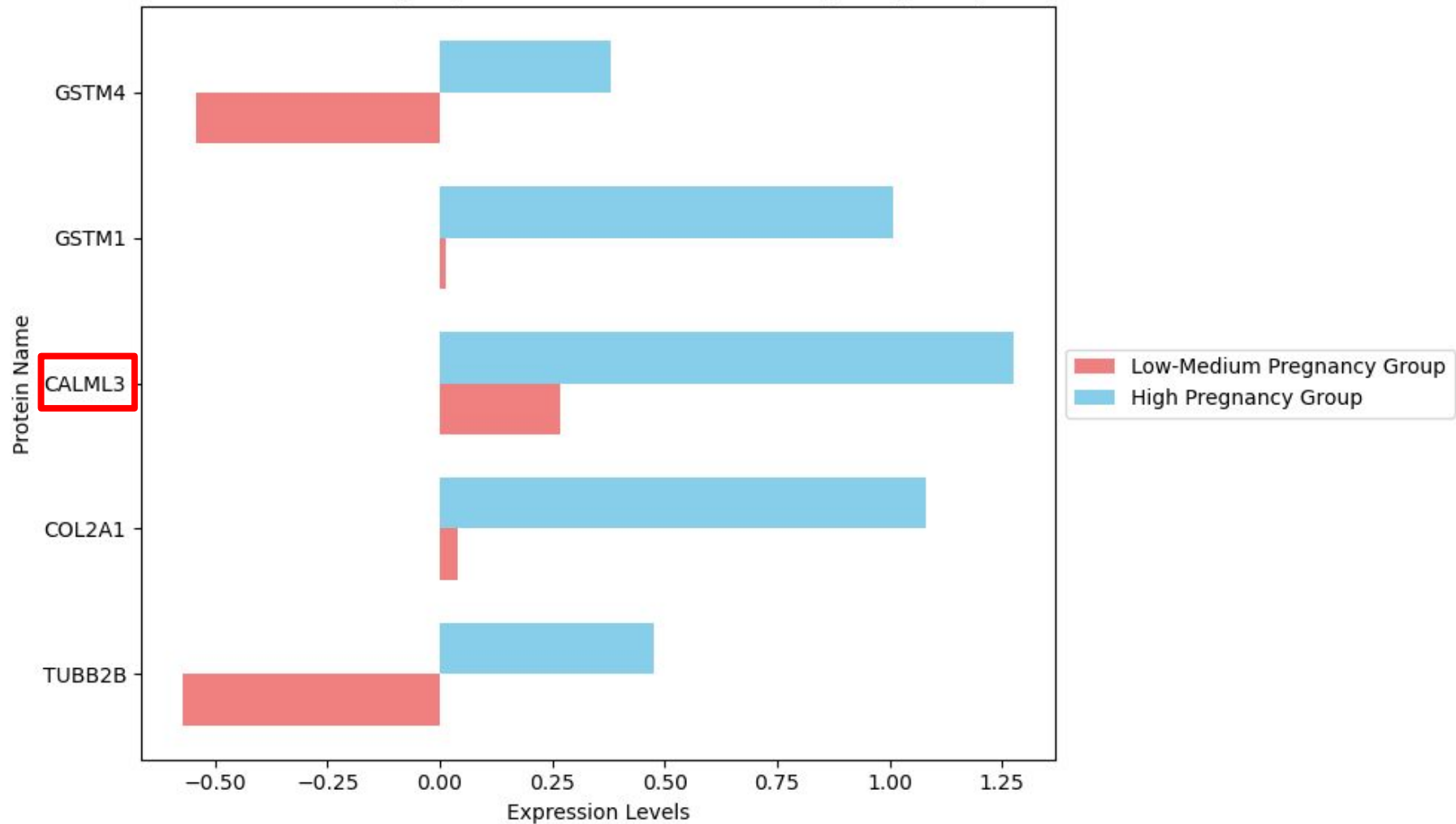
# High Pregnancy Group



## Discussion - CPTAC

- CALML3: Calcium ion binding activity
- Estrogen signaling & CALML3 upregulation

Most Differentially Expressed Proteins Between Pregnancy Groups



## Discussion - CPTAC

- CALML3: Calcium ion binding activity
- Estrogen signaling & CALML3 upregulation



## Limitations / Future Directions

- Stratifying parity through more factors
- Further contextualizing patient's data
- Honing in on myosin and estrogen-related protein pathways

**Thank you for listening!**  
**Questions?**

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