

# M20: AN INTEGRATED OMIC MODEL TO PREDICT SPONTANEOUS PRETERM BIRTH RISK

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## BACKGROUND

### WHAT IS MISSING IN PTB RESEARCH?

Biomarkers for PTB risk before 20 weeks gestation and low risk pregnancies to help in the management of these pregnancies

### Previous work from our lab:

A logistic regression model has been previously developed for biomarker discovery of **cell-free RNA (cfRNA)** transcripts (1).

A list of **25 genes** of predictive potential were identified

### AIM OF THIS WORK :

Understand the predictive potential of **inflammatory proteomic markers** for sPTB risk

## CONCLUSION

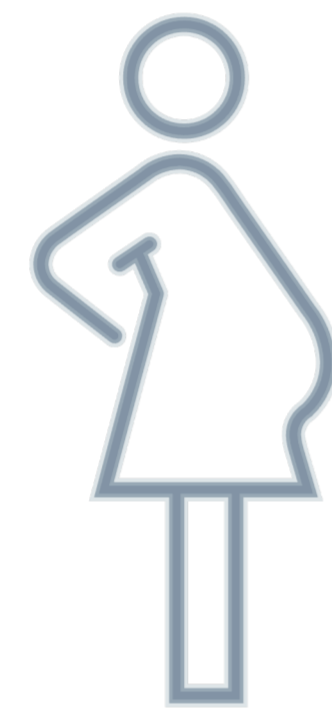
- Protein and cfRNA markers provide a non-invasive opportunity to understand biological mechanisms and have the potential to predict risk of PTB during the second trimester of pregnancy
- While inflammatory protein signatures alone show a lesser accuracy in the prediction of sPTB, integration with cfRNA profiles provide a better accuracy in predicting the risk of sPTB.

1. Camunas-Soler J et al. Predictive RNA profiles for early and very early spontaneous preterm birth. Am J Obstet Gynecol.2022Jul;227(1):72.e1-72.e16.

## METHODS

### STUDY DESIGN

141 maternal blood samples at 12-24 weeks gestation from women of the **INSIGHT** cohort



### Transcriptomics

- Untargeted - cfRNA using the Mirvie RNA platform

### Proteomics

- Targeted - Olink Explore - 384 Inflammation panel

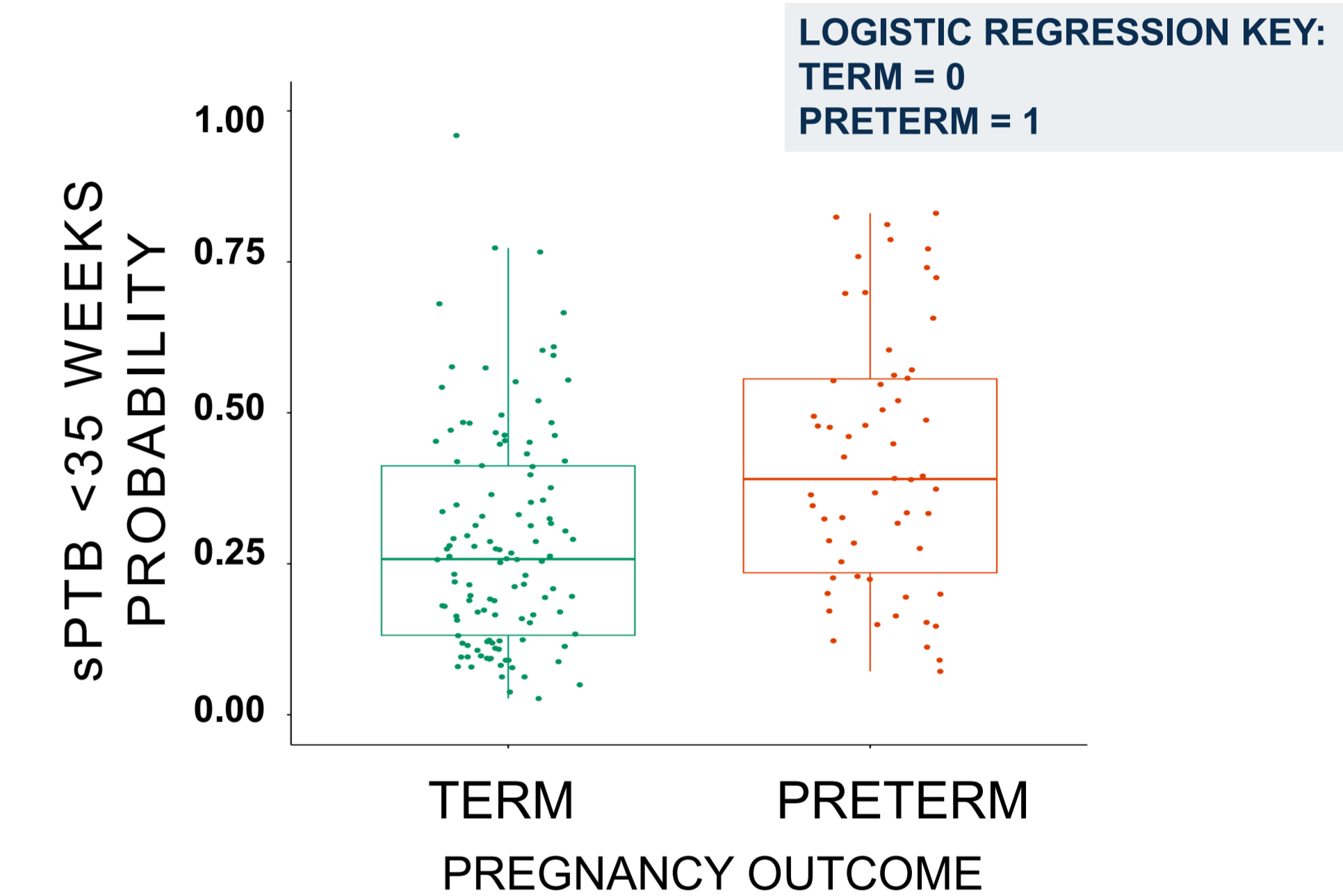
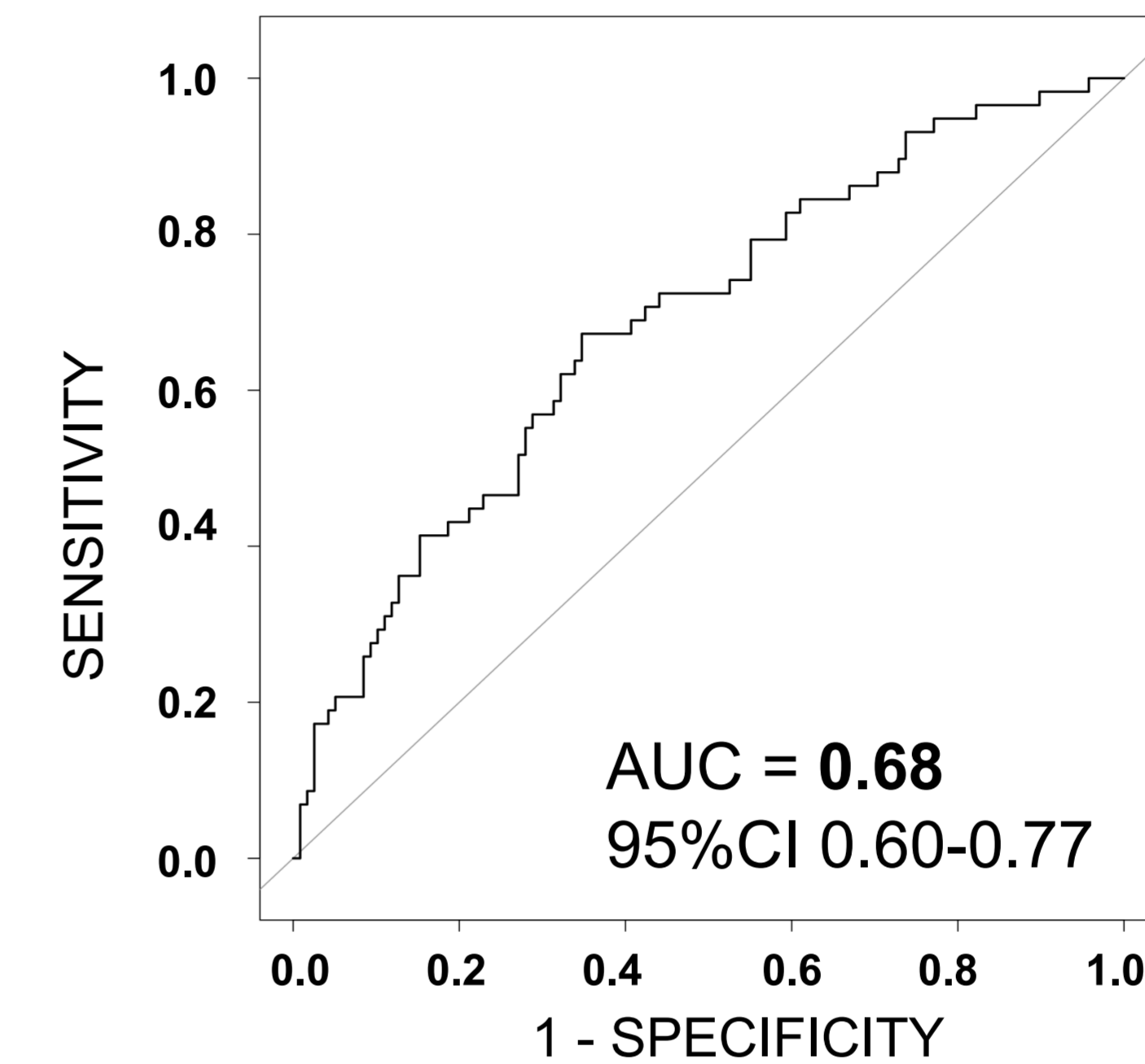
### PREDICTIVE MODEL DEVELOPMENT FOR SPTB (<35 WEEKS)

A **Logistic regression** model using leave-one-out cross-validation (LOOCV).

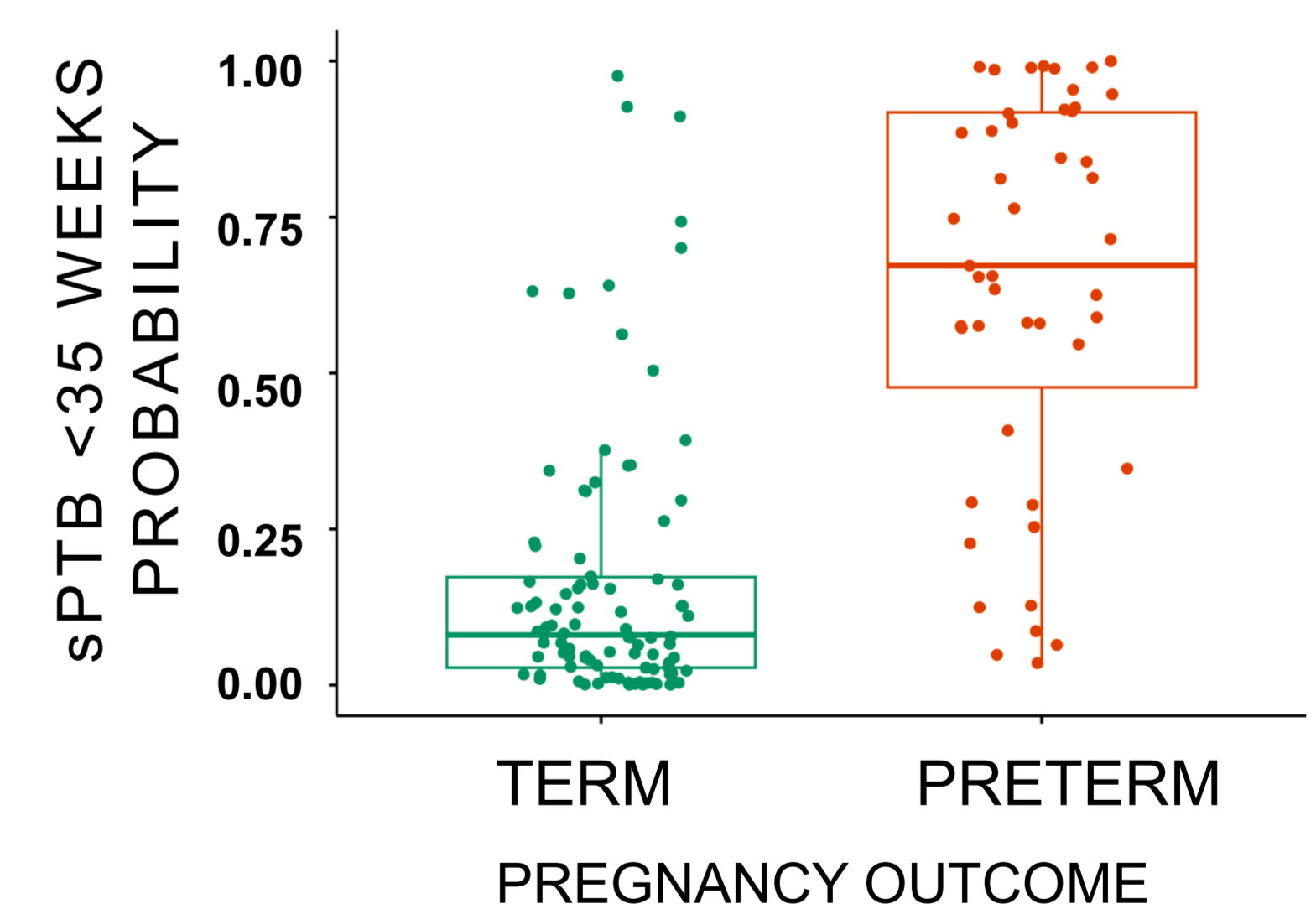
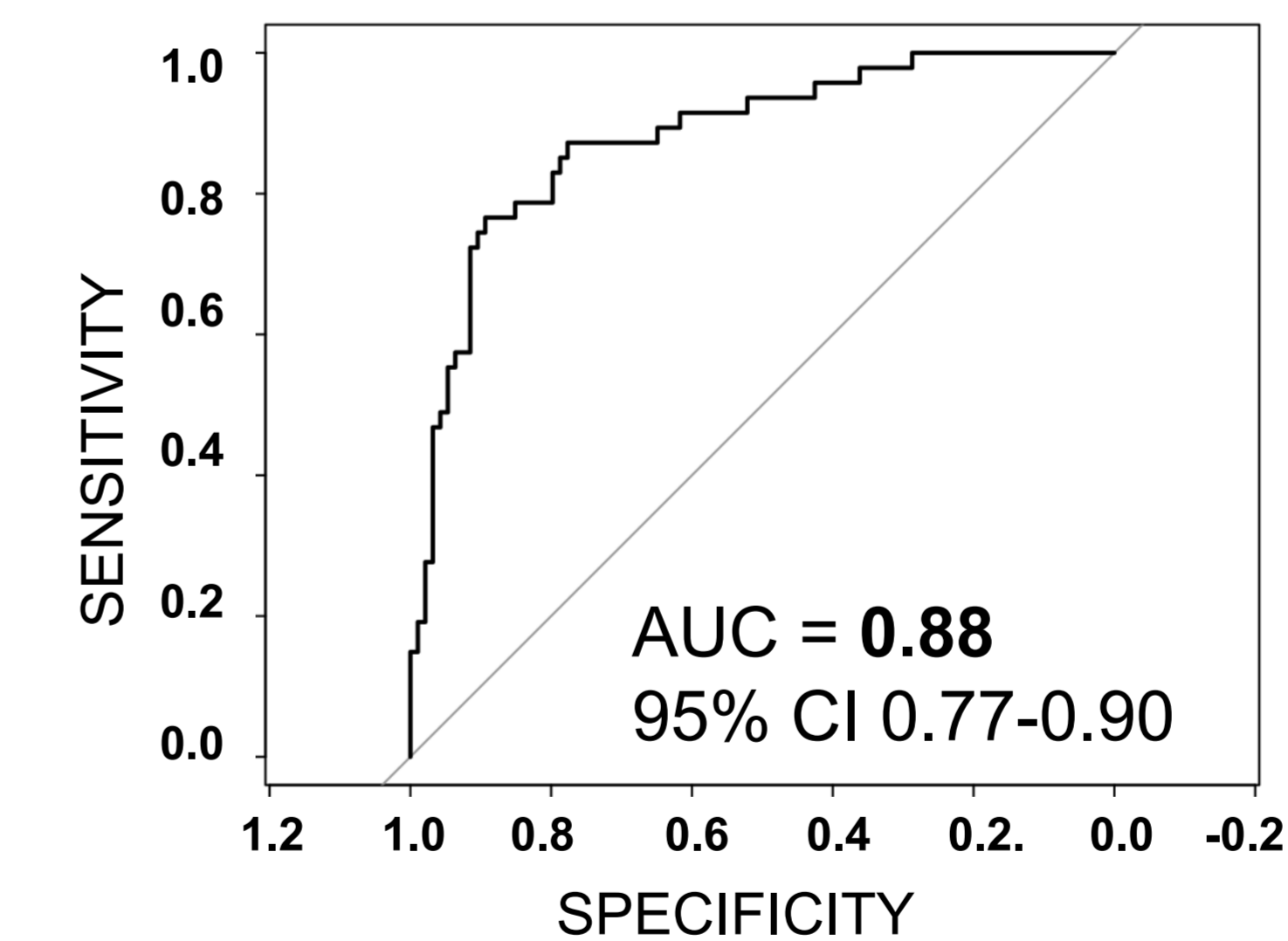
1. Proteomic markers only (34)
2. Proteomic (34) + cfRNA markers (25) – 59 omic markers

## RESULTS

### INFLAMMATORY PROTEOMIC MARKERS ALONE TO PREDICT SPTB (<35 WEEKS)



### INTEGRATION OF PROTEOMIC AND CFRNA MARKERS TO PREDICT SPTB (<35 WEEKS)



Generating of list of 25 genes and 10 proteins that contributed to predicting sPTB risk