



P3.104: CT-Derived Host Immuno-Metabolic Phenotyping Predicts Response to Neoadjuvant Chemoimmunotherapy in Resectable Locally Advanced NSCLC



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INTRODUCTION

Response to induction systemic therapy in locally advanced non-small cell lung cancer is variable, and established biomarkers are limited:

- Which patients will respond to immune checkpoint blockade?
- Do **CT-derived biomarkers** correlate with tumor molecular features in predicting pathologic complete response?

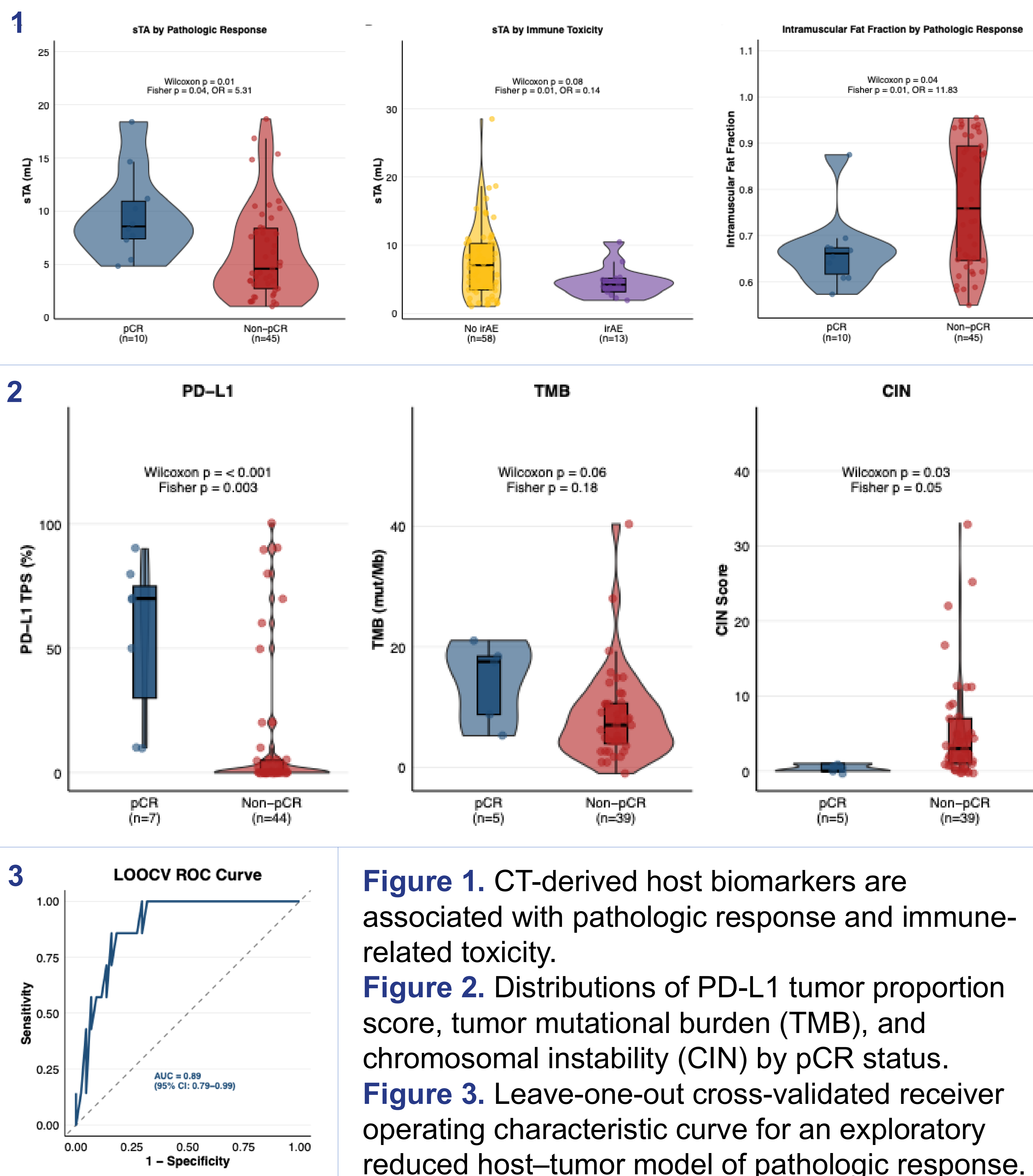
METHODS

- **Study Cohort:** resectable non-small cell lung cancer (NSCLC) treated with neoadjuvant platinum-doublet chemotherapy plus anti-PD-L1 immune checkpoint blockade at a single institution.
- **Spatially Informed Thymic Activity** and **Body Composition** were calculated from pretreatment computed tomography imaging.
- **Clinical, Pathologic, and Molecular Variables** were abstracted retrospectively from the electronic medical record and surgical pathology.
- **Statistical Analysis** was performed using R version 4.5.2 and Python version 3.11.15.

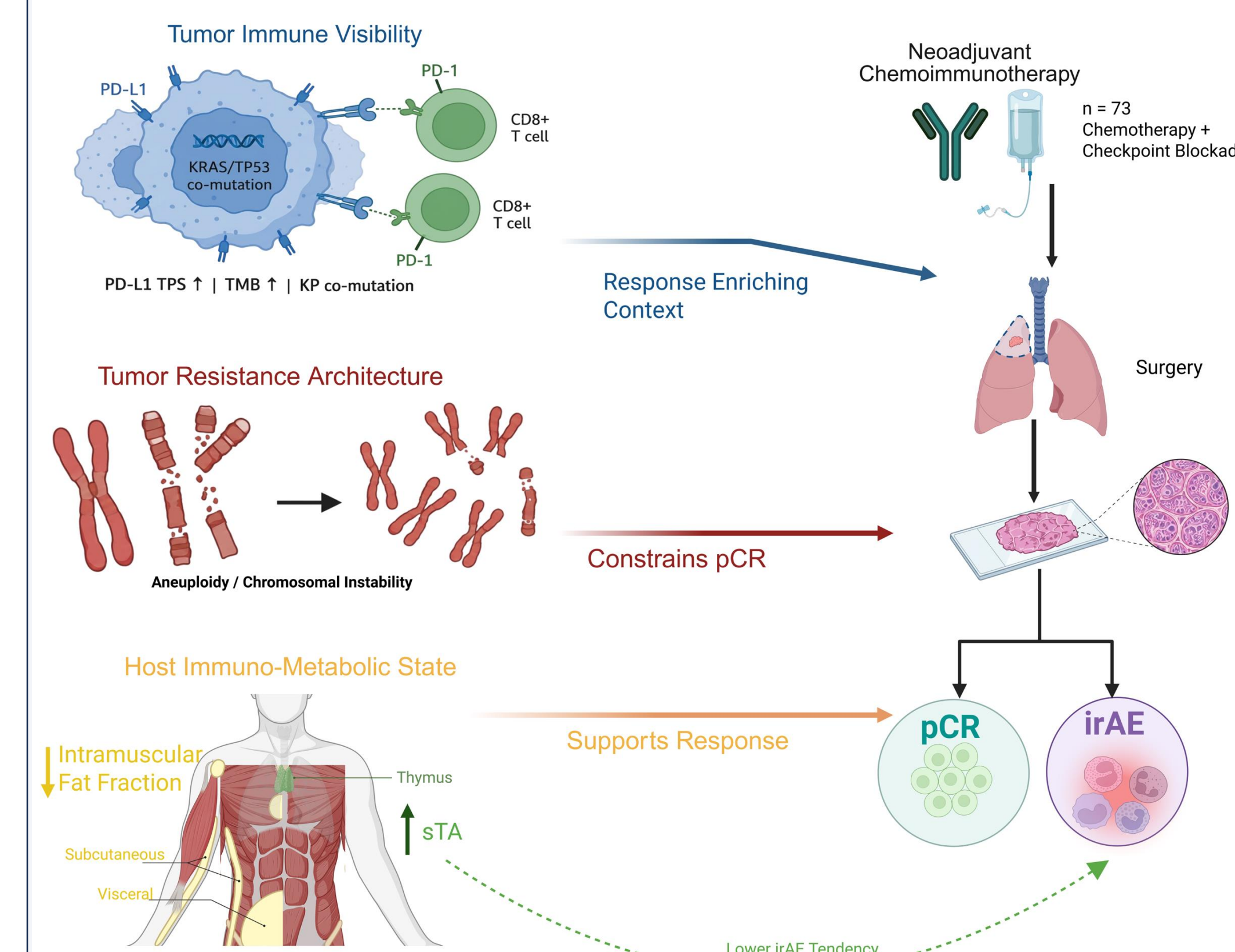
Code Available on GitHub:



RESULTS



DISCUSSION AND CONCLUSION



Therapeutic outcome reflects both tumor susceptibility and host immunometabolic condition

- Spatially informed thymic activity (sTA) and intramuscular fat fraction (ImFF), extracted from pretreatment CT, defined a host profile associated with pathologic complete response (pCR) and immune-related adverse event (irAE) occurrence.

Future applications of CT-derived host phenotyping

- One limitation of this investigation was the cohort size.
- We are working on applying an expanded host biology framework to predict treatment responses in additional patient cohorts.