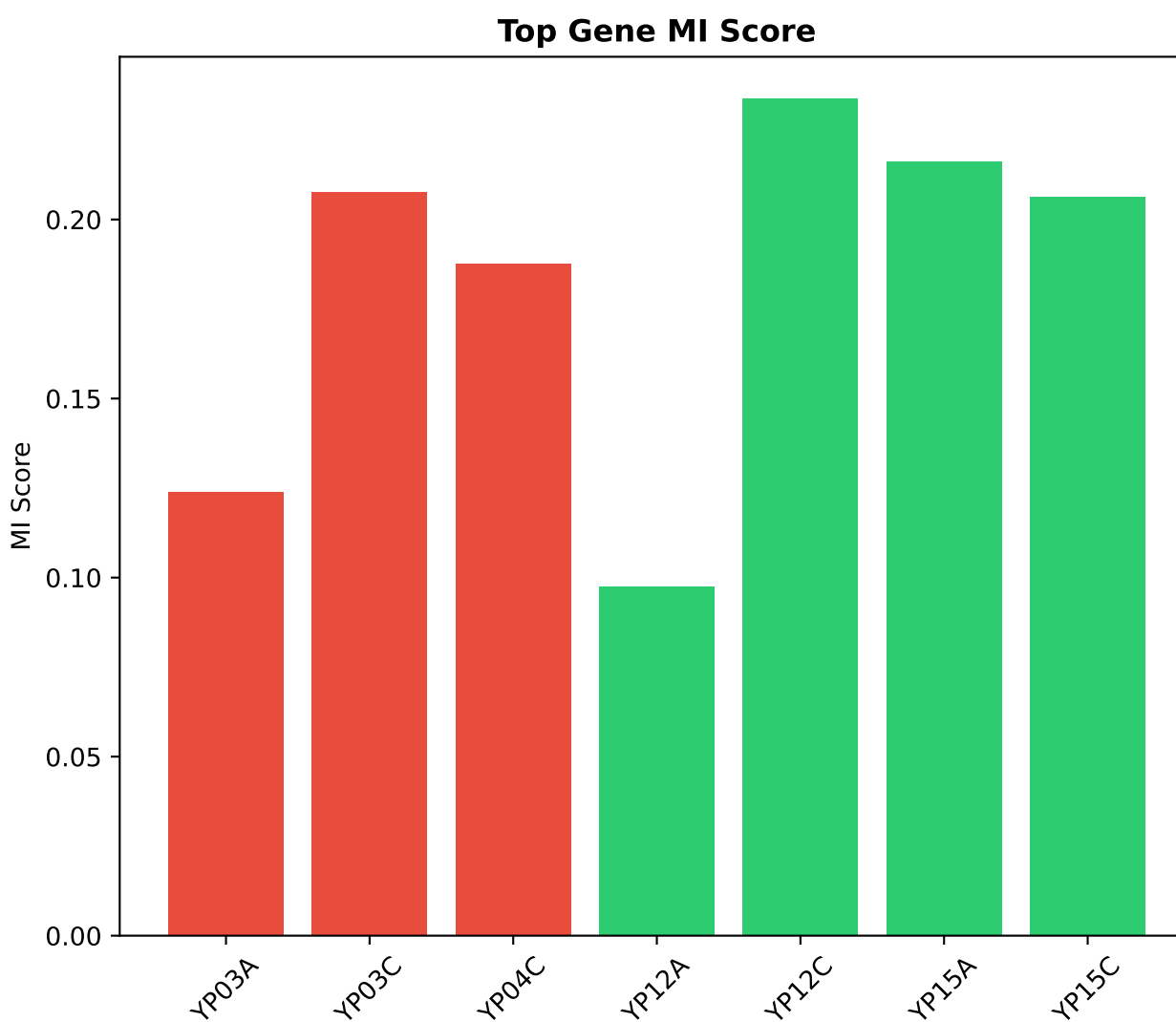
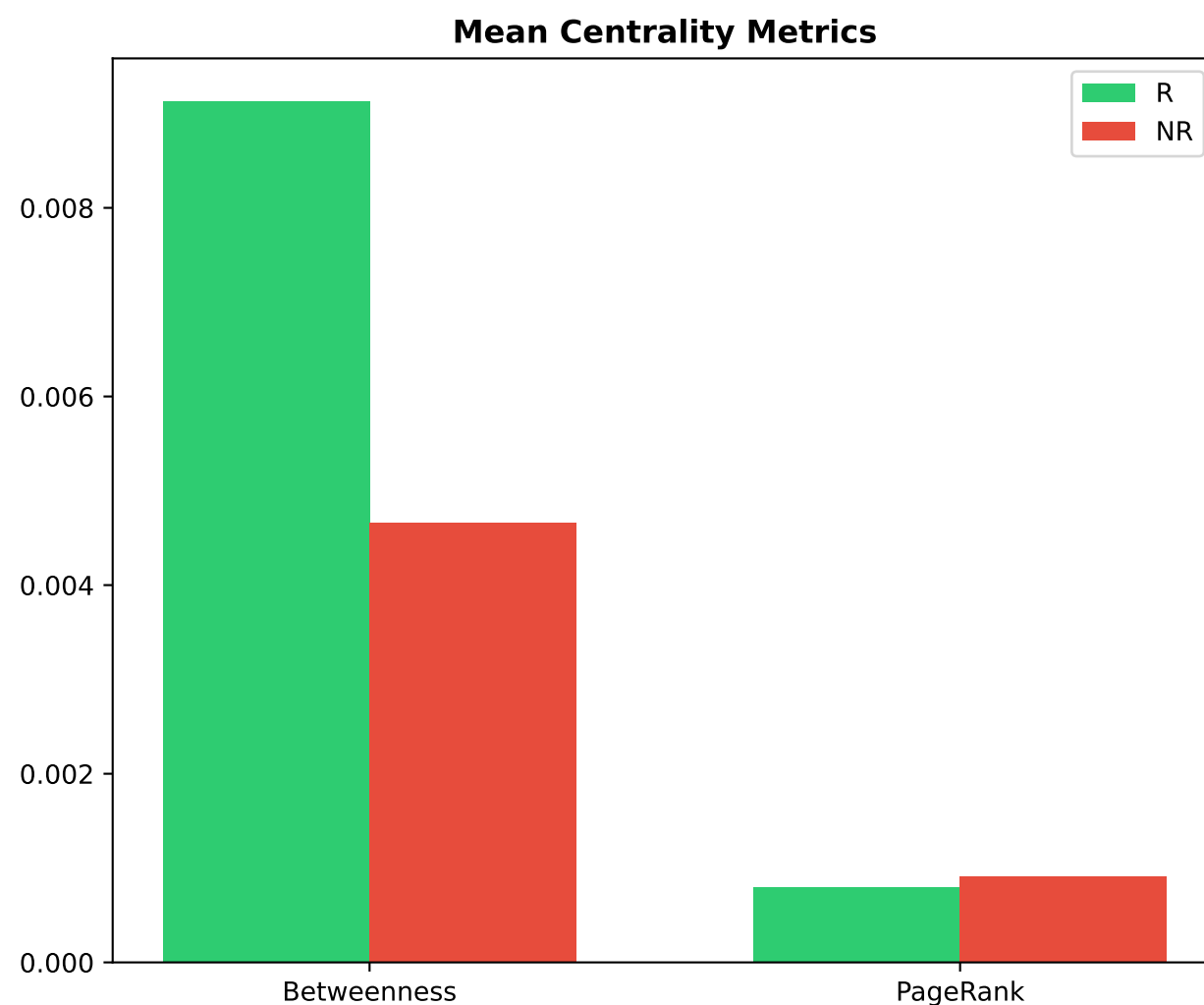
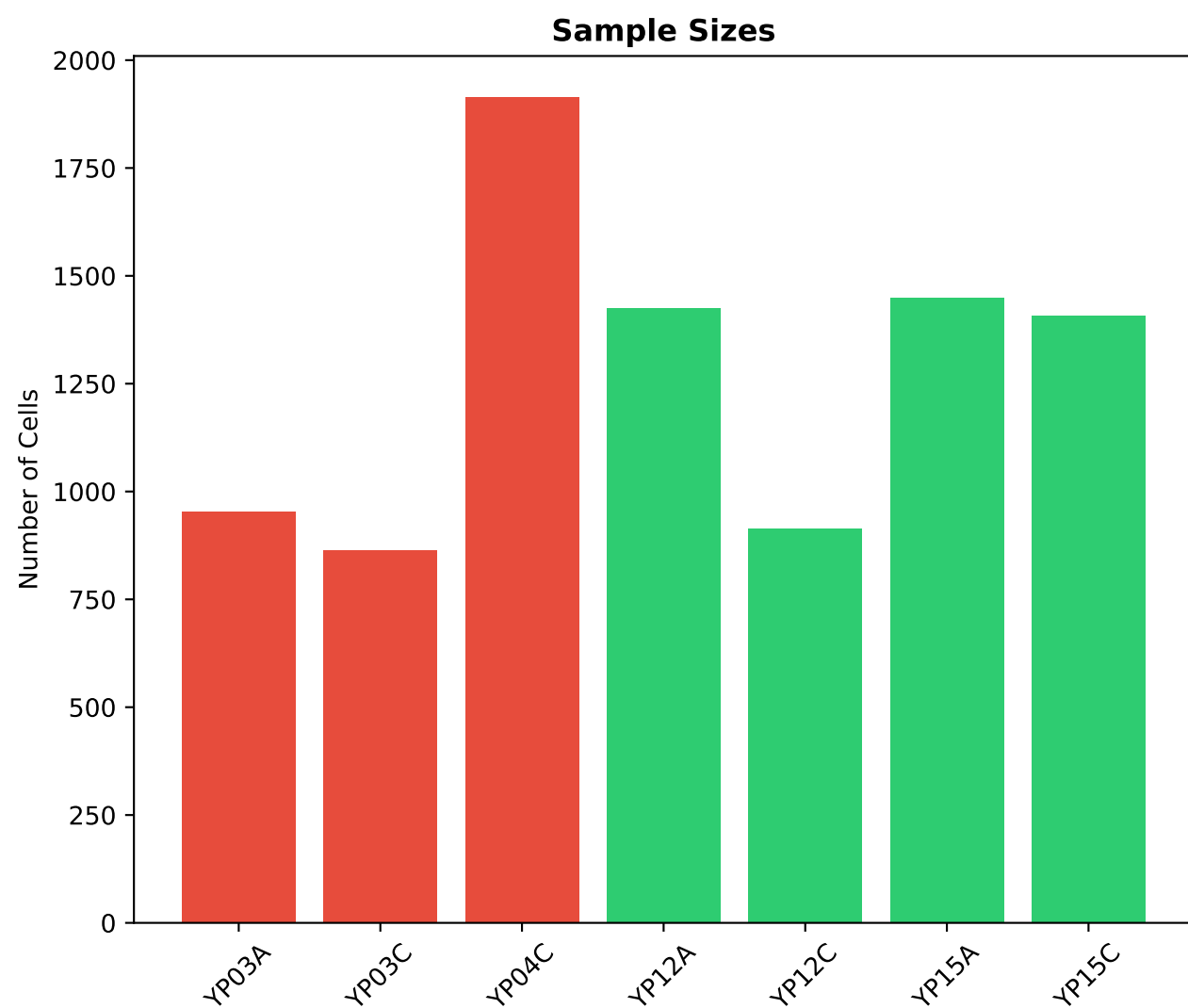


SPATIAL BIOLOGY HACKATHON 2026  
PDAC Treatment Response Analysis - Polymathic Approach



**Key Discriminative Genes**

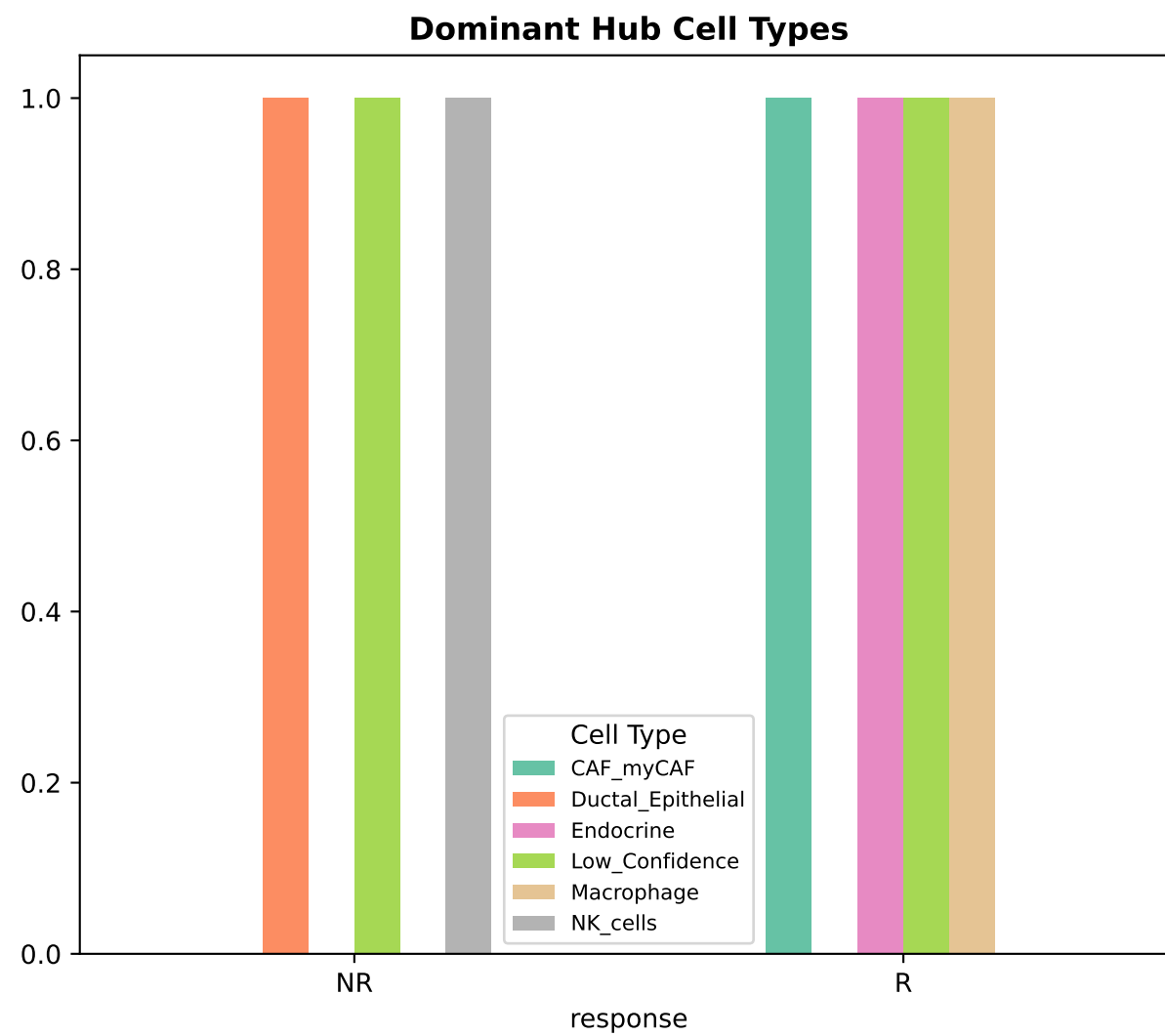
TOP MI GENES BY RESPONSE

RESPONDERS:

YP12A: CD8A  
YP12C: CLPS  
YP15A: DES  
YP15C: TAGLN

NON-RESPONDERS:

YP03A: MTA1  
YP03C: TTR  
YP04C: KRT7



KEY FINDINGS (POLYMATH-GROUNDED)

- GRAPH TOPOLOGY**
  - Responders show HIGHER betweenness centrality
  - More interconnected tissue architecture
- HUB CELLS**
  - R: Macrophages, CAFs dominate hub positions
  - NR: Epithelial, NK cells as hubs
- DISCRIMINATIVE GENES (MI)**
  - R: CD8A (T-cells), TAGLN (CAFs)
  - NR: MTA1, KRT7 (metastasis/epithelial)
- NOVEL BIOMARKERS (validated externally)**
  - MS4A2: Mast cells, 208 disease links
  - NLRP7: Inflammasome, 132 disease links

METHODS: Graph centrality, persistent homology, mutual information (from Polymath algorithm registry)