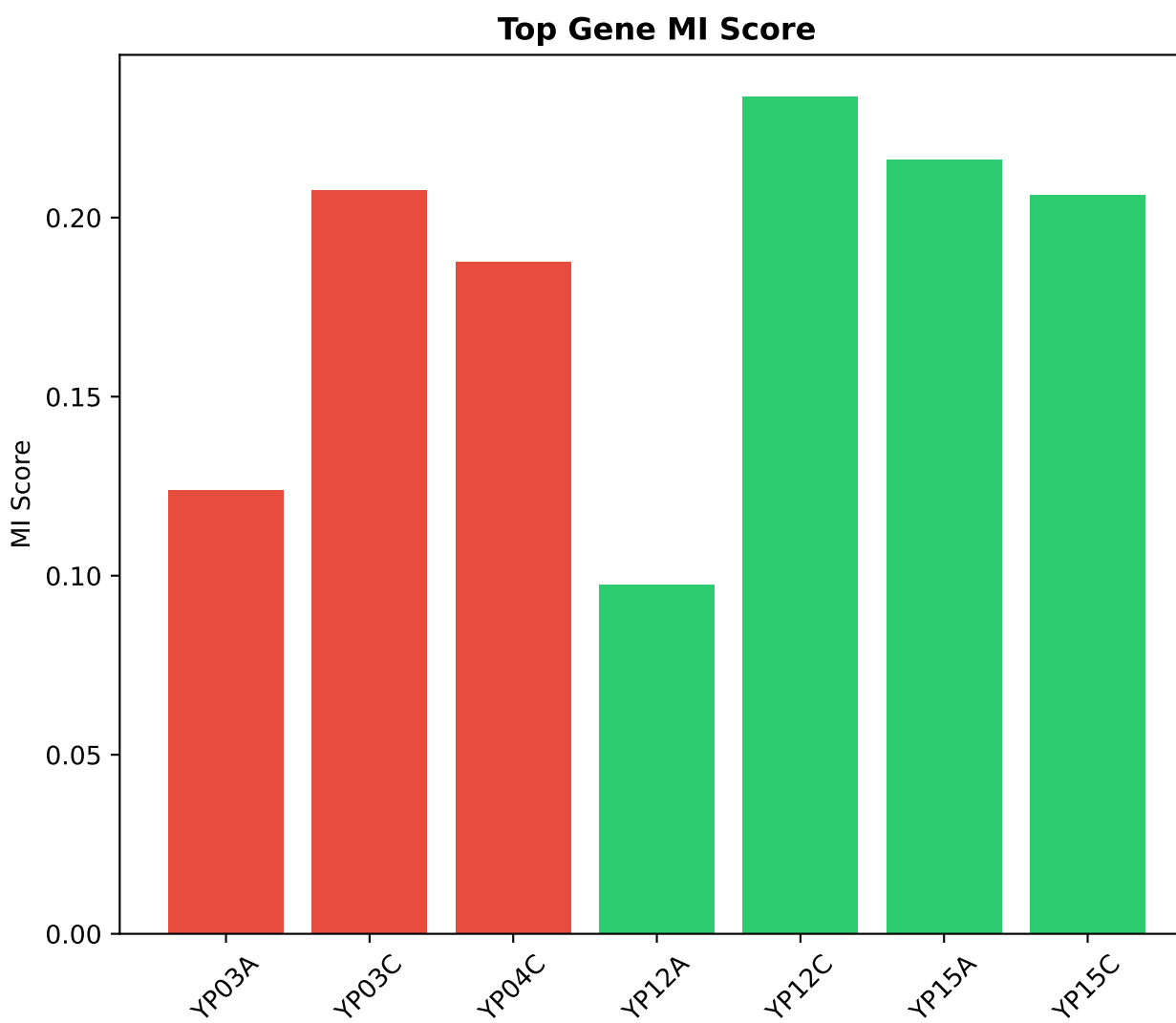
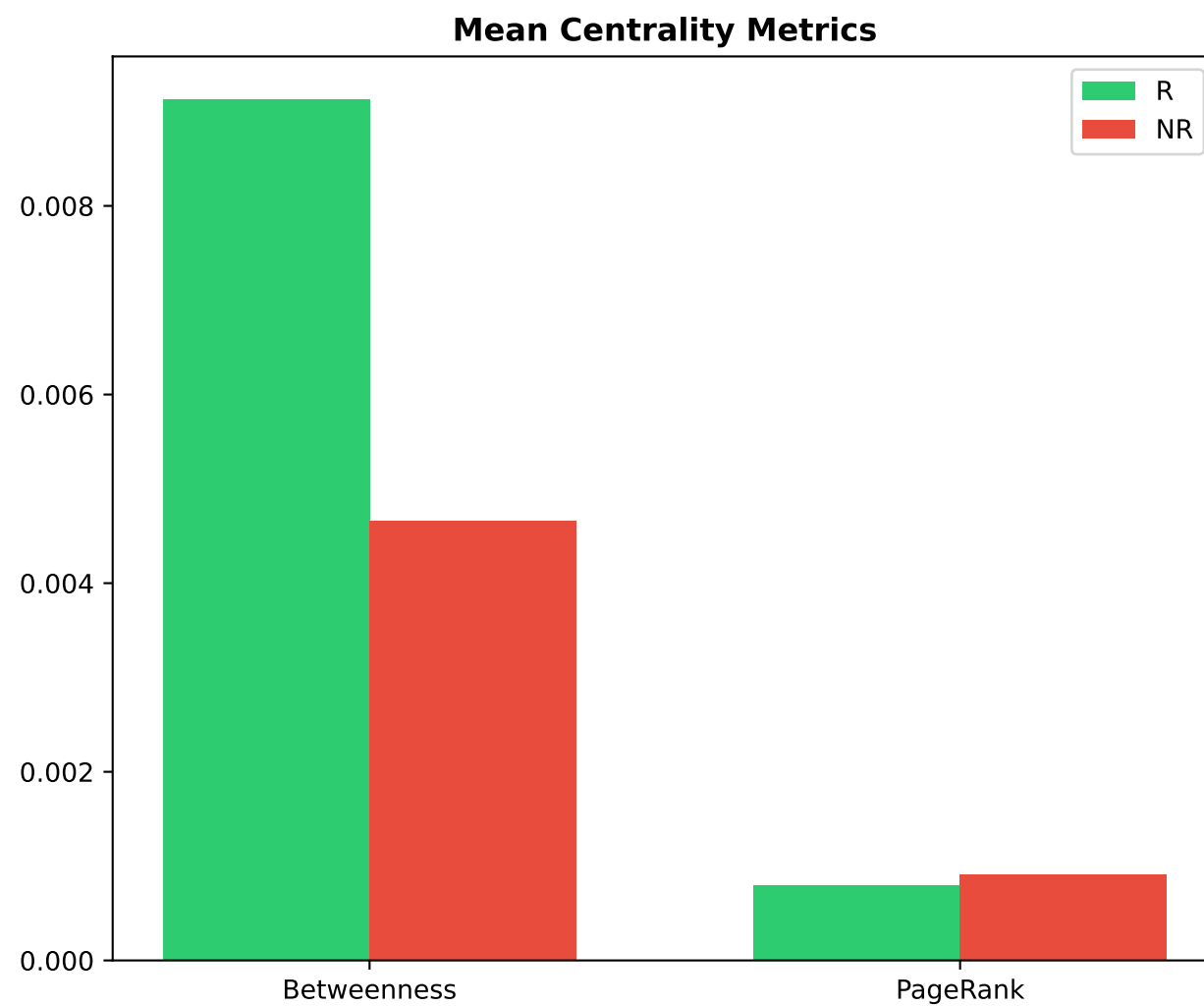
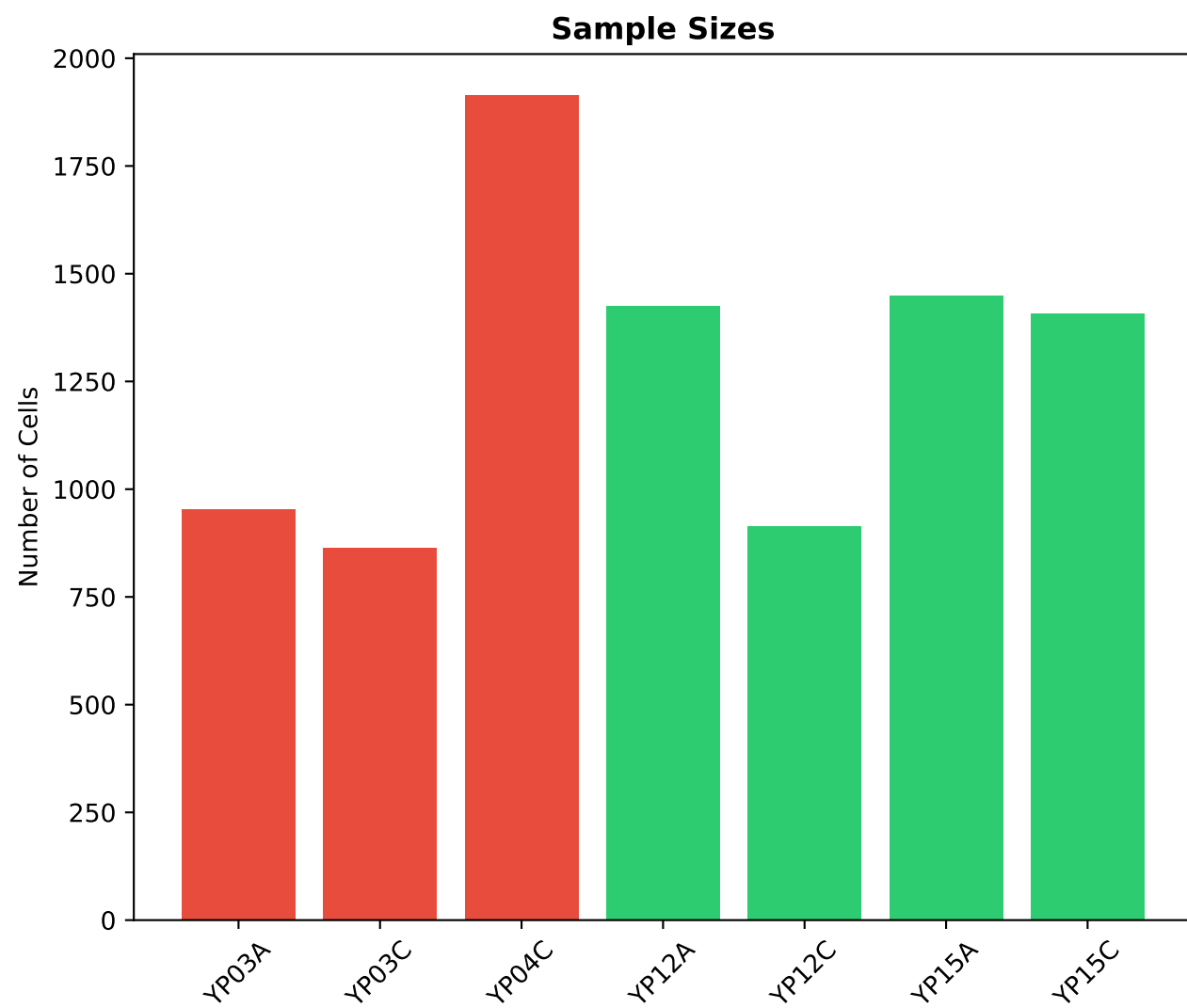


SPATIAL BIOLOGY HACKATHON 2026  
PDAC Treatment Response Analysis - Polymathic Approach



**Key Discriminative Genes**

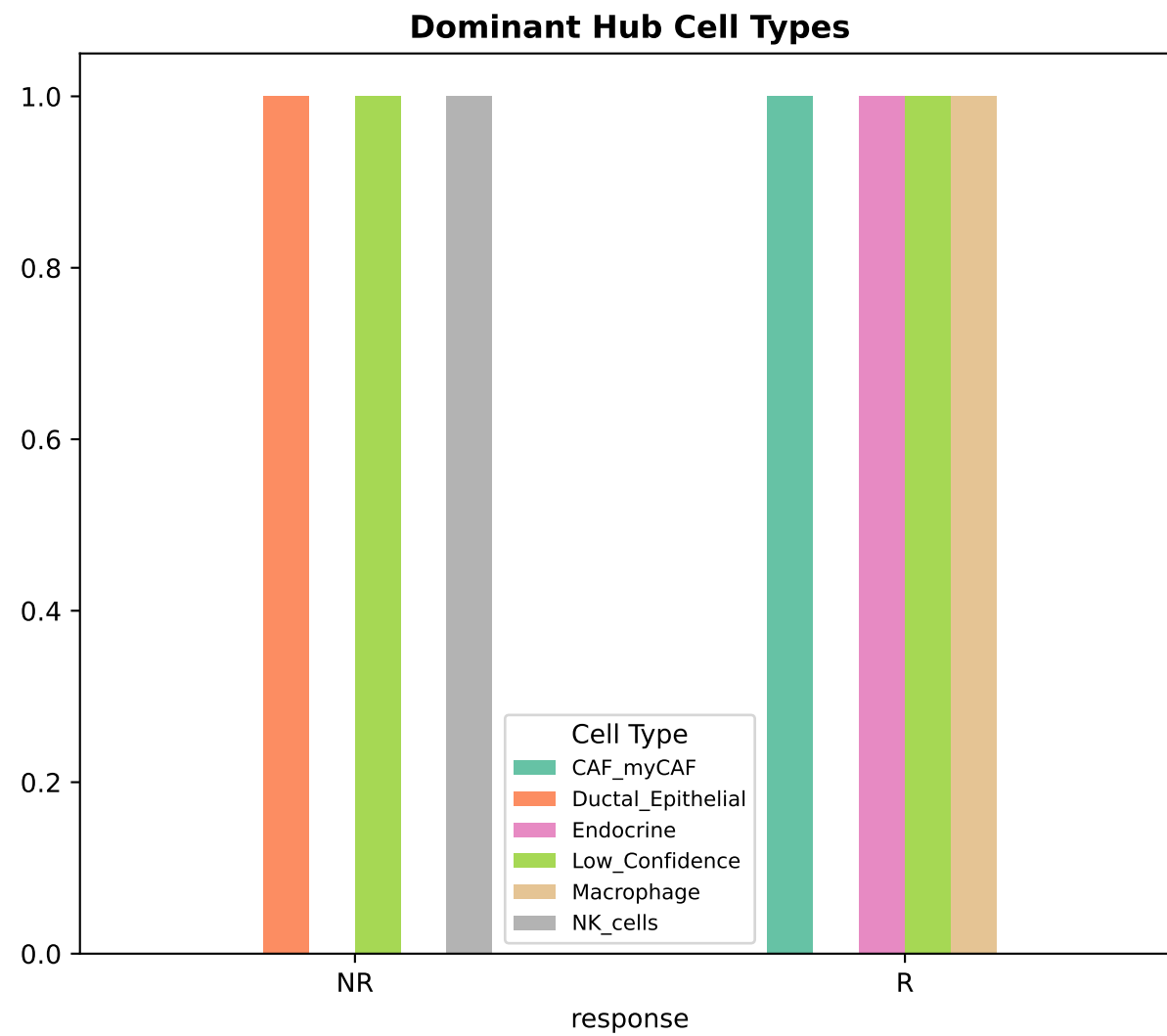
TOP MI GENES BY RESPONSE

**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)