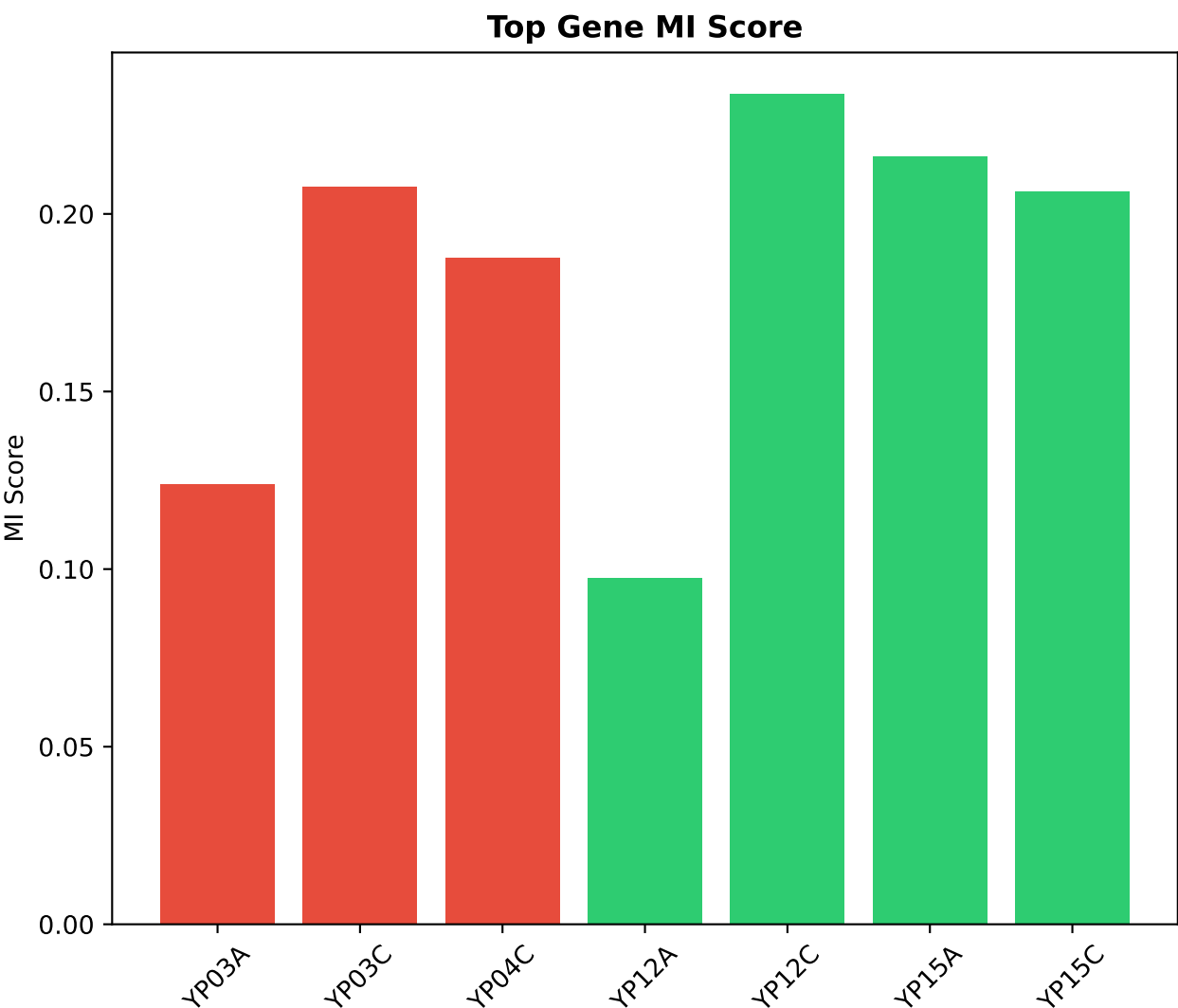
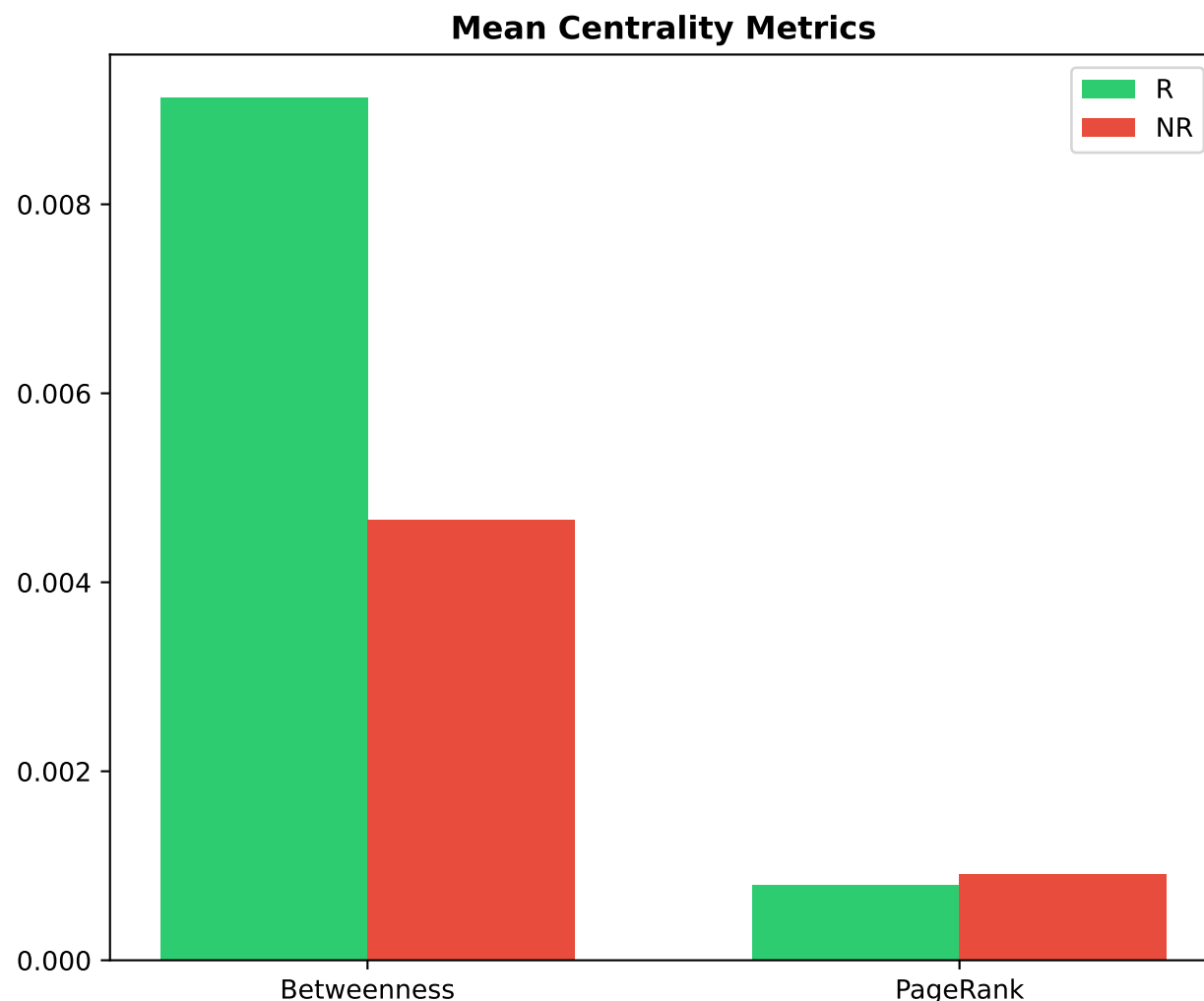
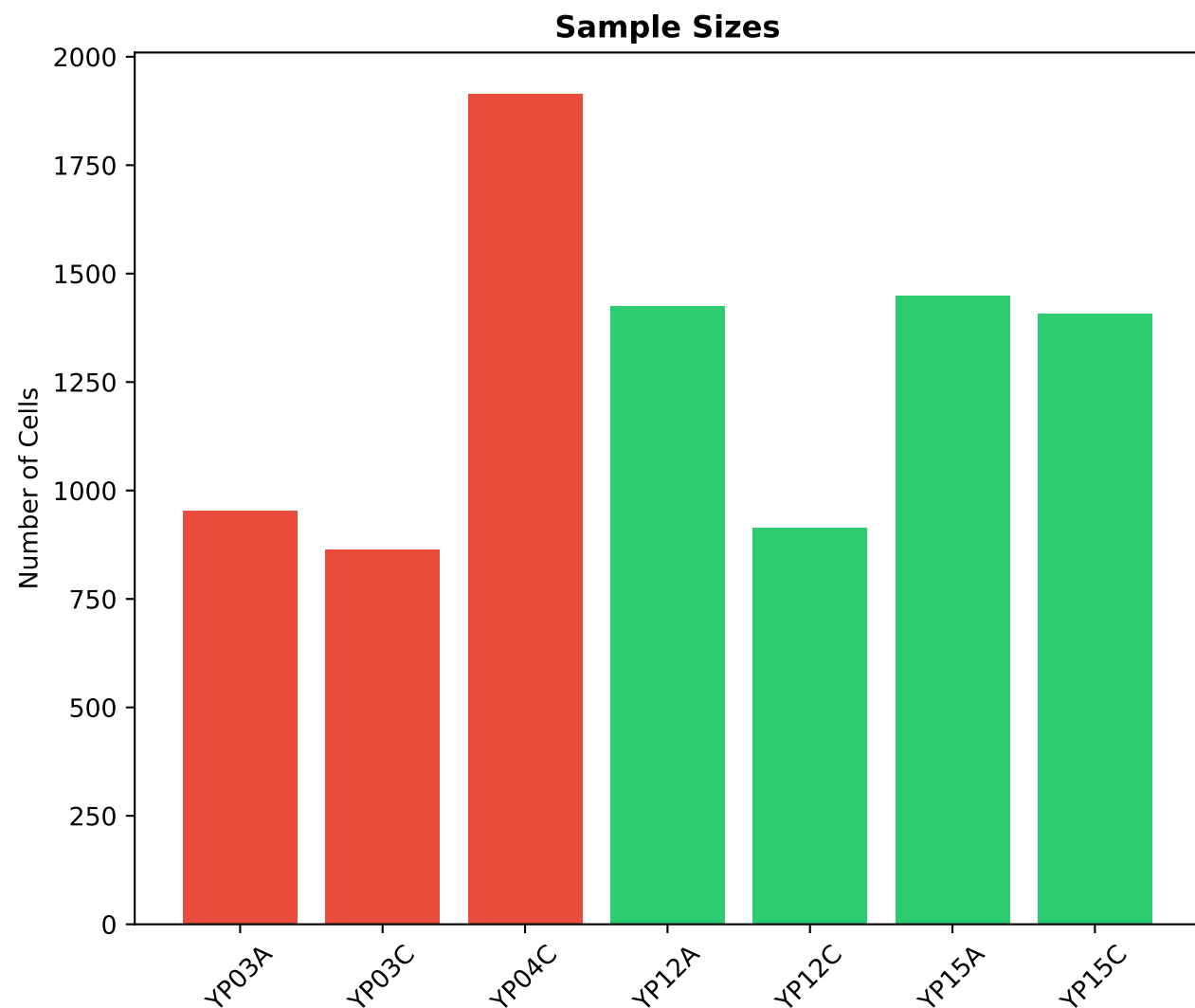


SPATIAL BIOLOGY HACKATHON 2026
PDAC Treatment Response Analysis - Polymathic Approach



Key Discriminative Genes

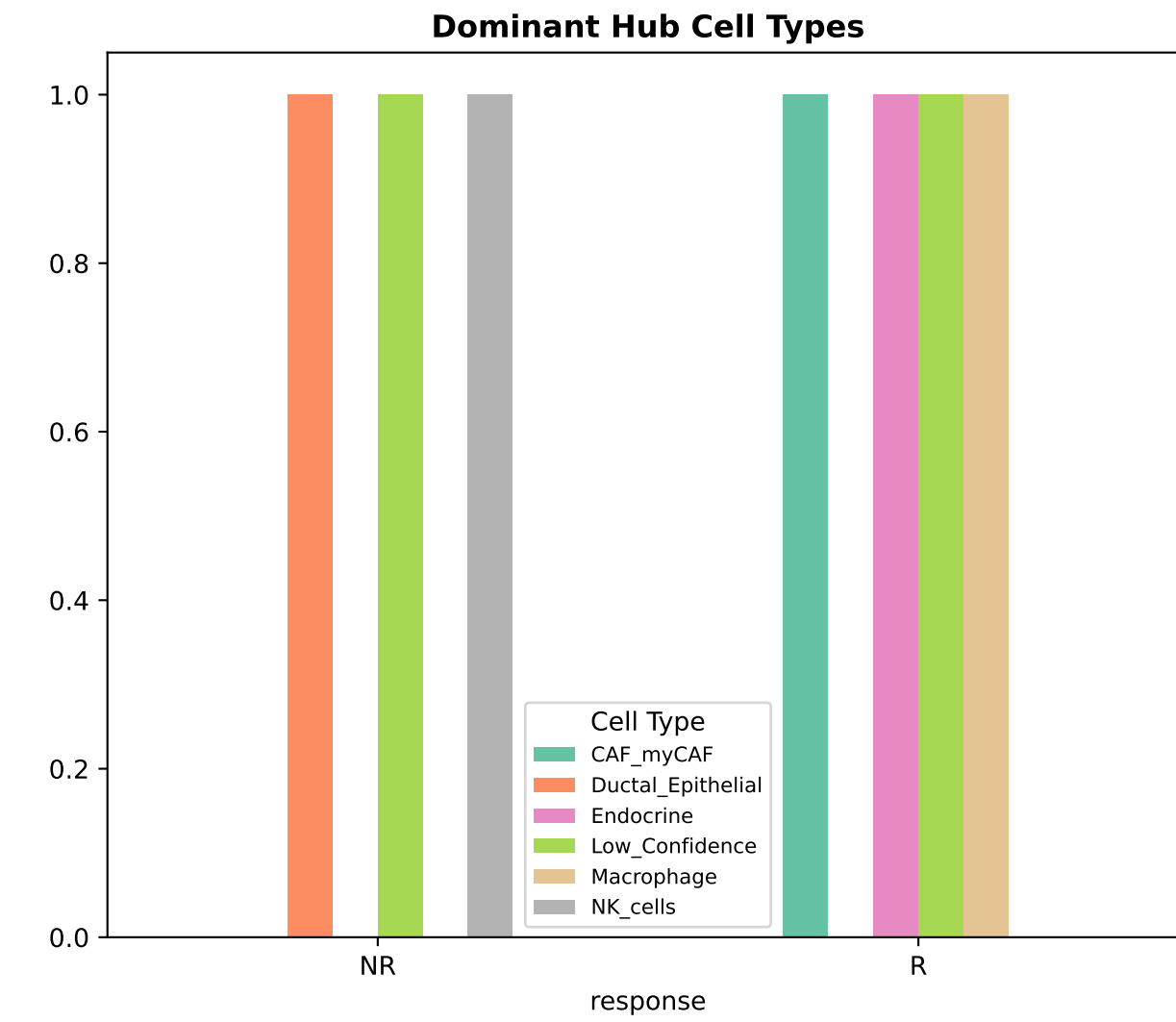
TOP MI GENES BY RESPONSE

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)