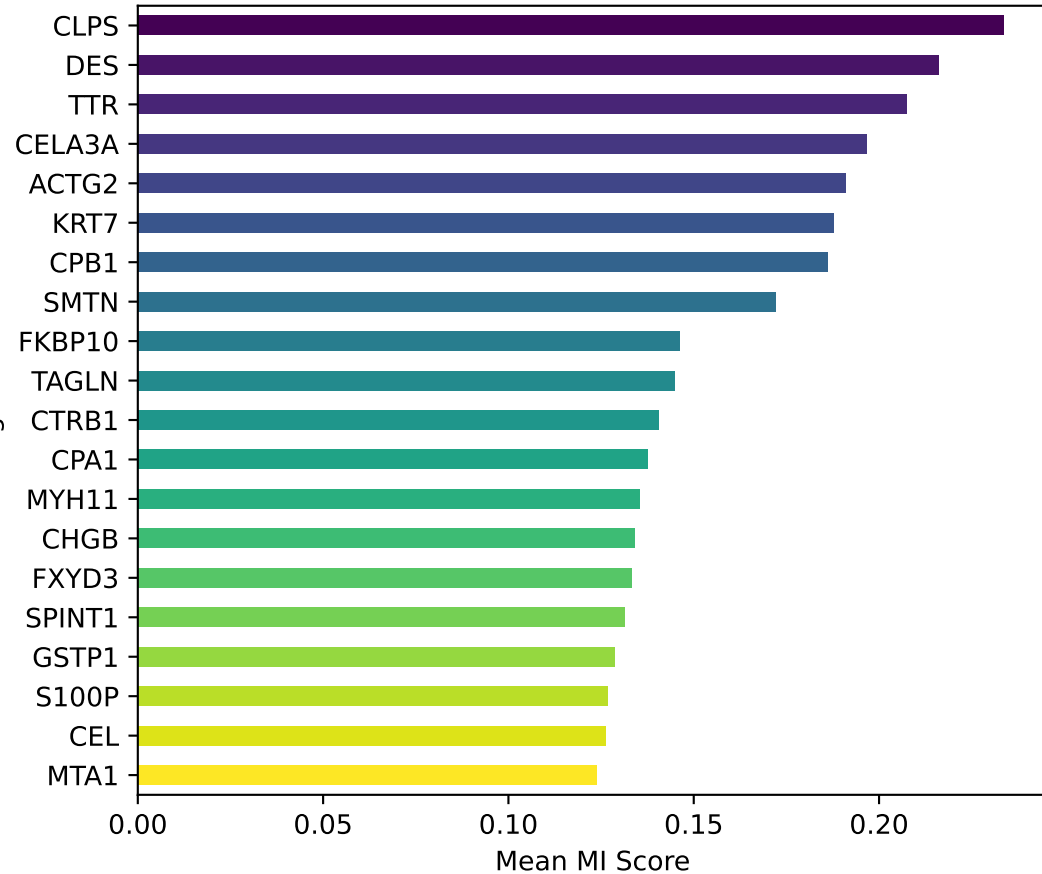
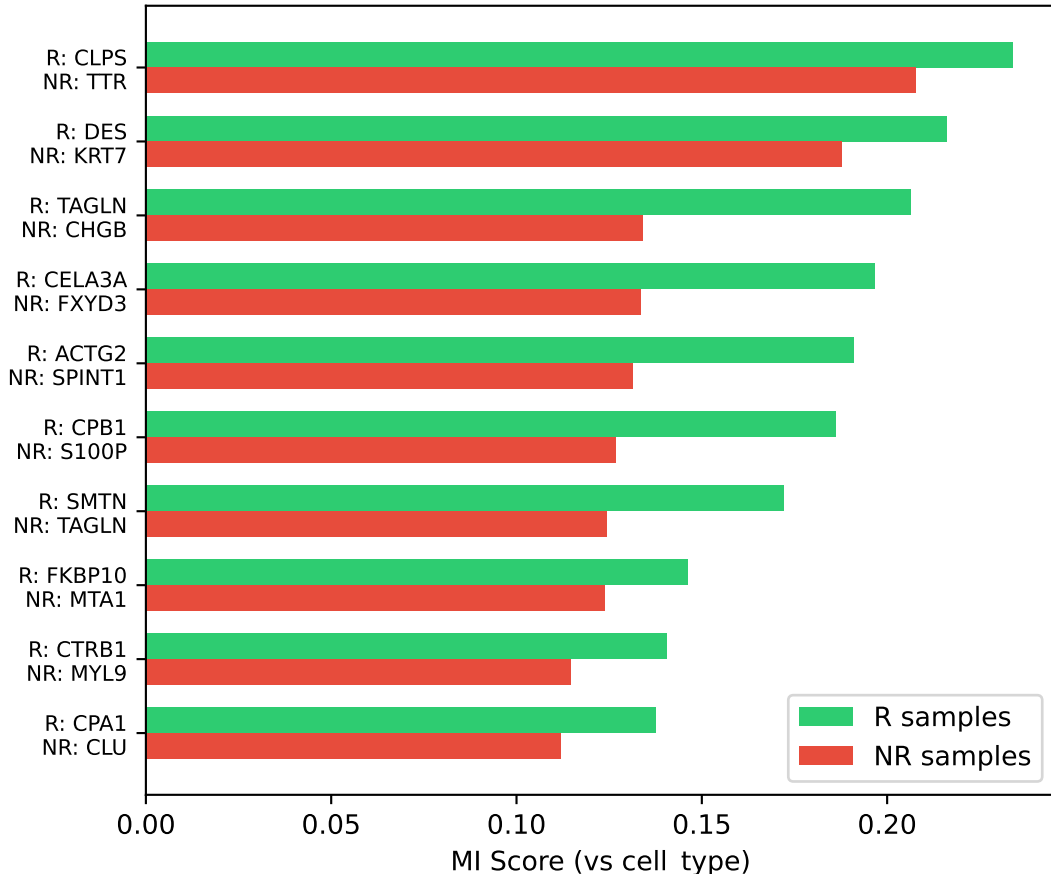


# Information-Theoretic Analysis: Cell-Type Markers vs Treatment Response Biomarkers

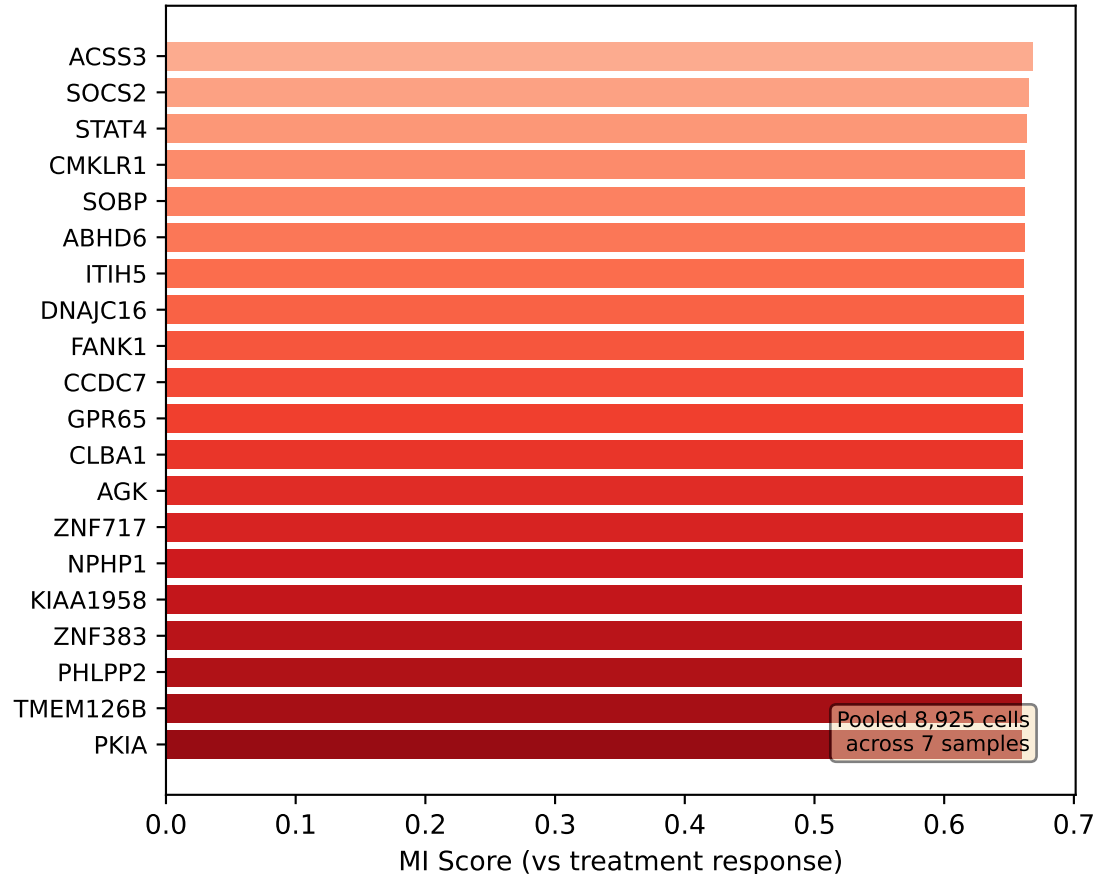
## Top 20 Cell-Type Marker Genes (MI vs cell\_type, averaged)



## Cell-Type Markers Stability Across Response Groups



## TRUE Response Biomarkers (MI vs R/NR across all cells)



## Understanding MI Analysis

### WHAT IS MUTUAL INFORMATION?

MI measures how much knowing one variable reduces uncertainty about another.

- $MI = 0$ : Variables are independent
- $MI > 0$ : Variables share information
- Higher MI = Stronger association

### TWO TYPES OF MI ANALYSIS:

1. MI vs CELL TYPE (Panels 1-2):  
"Which genes best distinguish cell types?"  
→ Useful for marker identification  
→ Applied per-sample
2. MI vs RESPONSE (Panel 3):  
"Which genes predict R vs NR?"  
→ TRUE treatment biomarkers  
→ Computed across all samples pooled

### KEY DIFFERENCE:

Panel 1-2: Same gene can be "top marker" in both R and NR - it just identifies cell types well regardless of response.

Panel 3: These genes specifically differ between responders and non-responders.

### TOP BIOMARKER CANDIDATES:

- ACSS3:  $MI=0.668$
- SOCS2:  $MI=0.665$
- STAT4:  $MI=0.664$
- CMKLR1:  $MI=0.662$
- SOBP:  $MI=0.662$