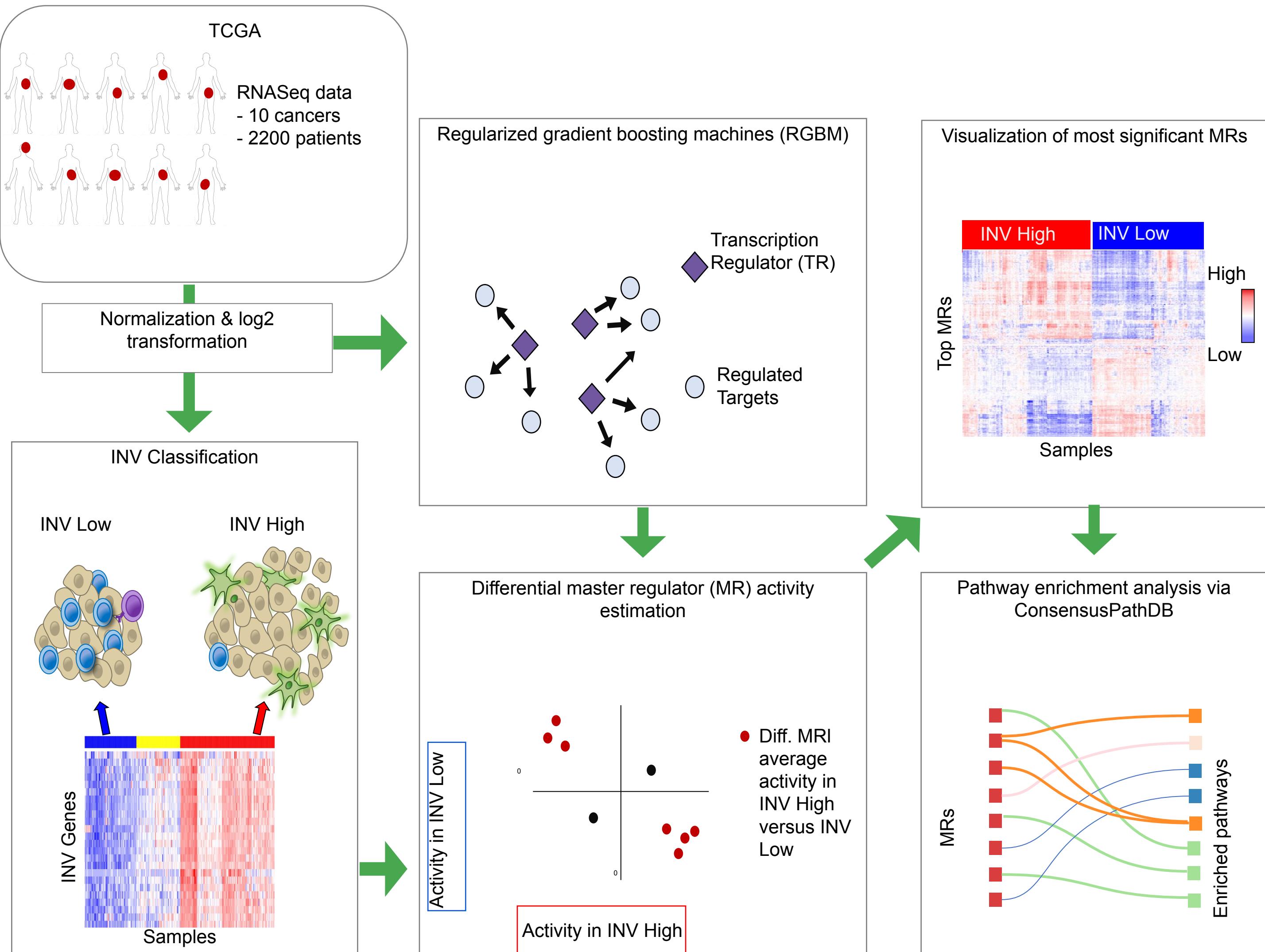


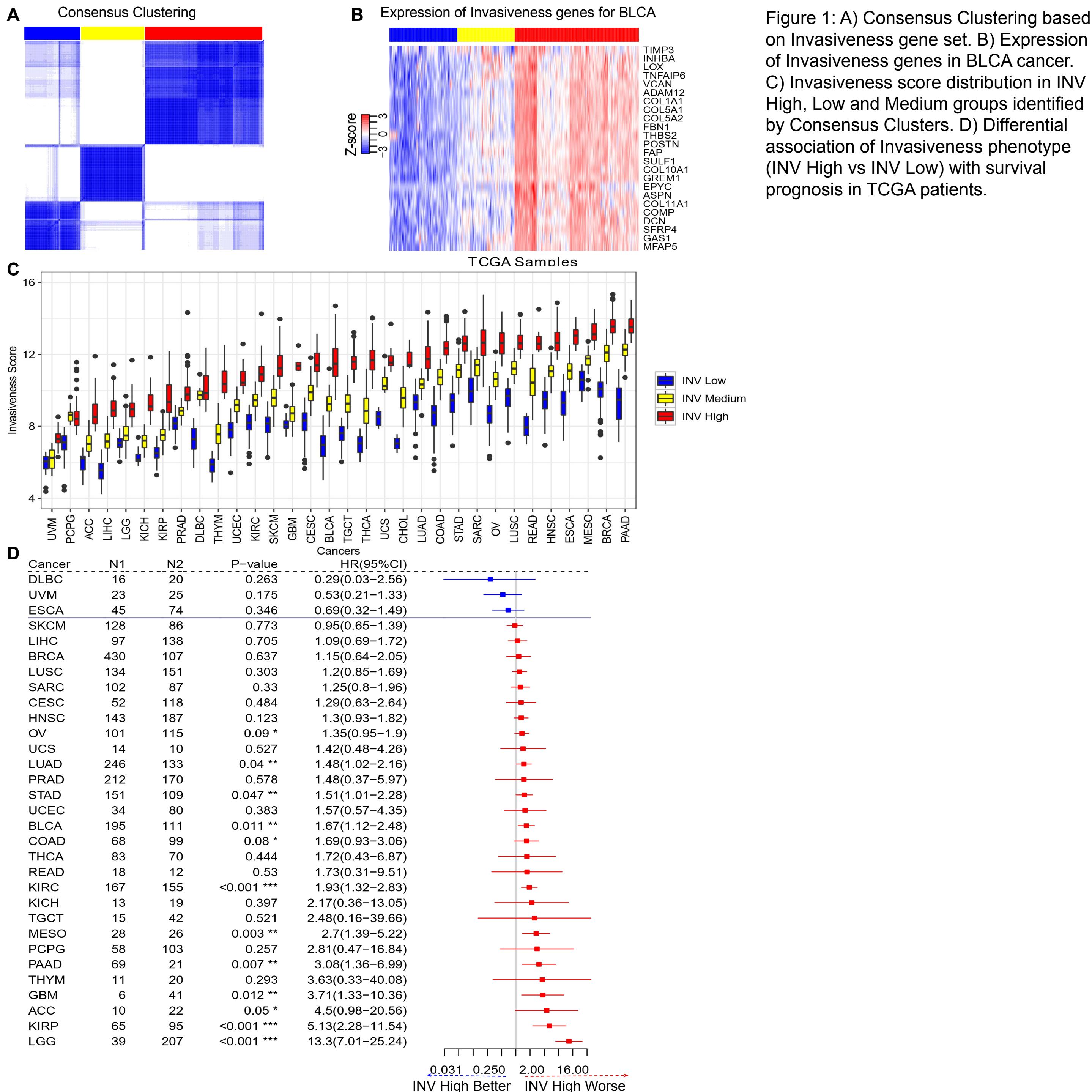
# Pancancer Network Analysis reveals key Master Regulators for a Cancer Invasiveness

Mahesh Jethalia (IIT KGP)  
Michele Ceccarelli (SCRC, Biogem)  
Raghvendra Mall (SJCRH, TII)

- Tumor invasiveness is infiltrating form of cancer, where it has developed and grown into surrounding healthy tissues.
- Tumor invasiveness reflects many biological changes associated with tumorigenesis, progression, metastasis, and drug resistance (Bi et al, JTRM, 2021).
- Bi et al, 2021 identified common invasiveness-associated dysregulated molecular features between high- and low-invasiveness groups across multiple cancers.
- Biological mechanisms underlying invasiveness and metastasis are largely an enigma.
- Invasiveness score defined based on 24 gene signature (Geeleher et al).
- Based on OS several TCGA cancers have prognostic association with invasiveness:
  - Invasiveness Phenotype - OV, LUAD, STAD, BLCA, COAD, KIRC, MESO, PAAD, KIRP, LGG  
Invasiveness High ↓ survival, Invasiveness Low ↑ survival
- Goal is to perform master regulator analysis and identify MRs specific to Invasiveness High and Low phenotypes & associated downstream targetable pathways.

# Graphical Abstract





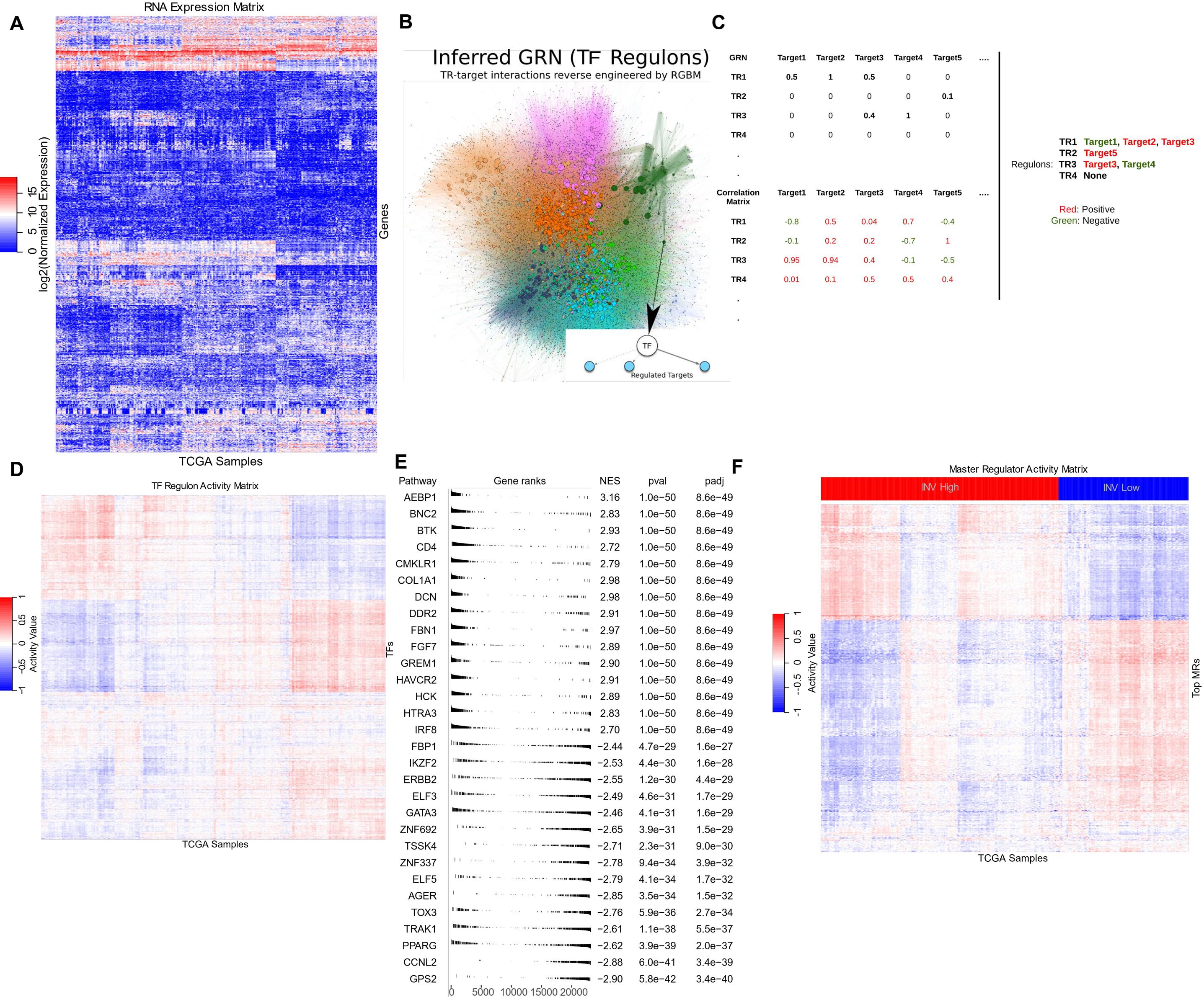


Figure 2: Master Regulator Analysis Pipeline for a Pancancer Invasiveness Phenotype

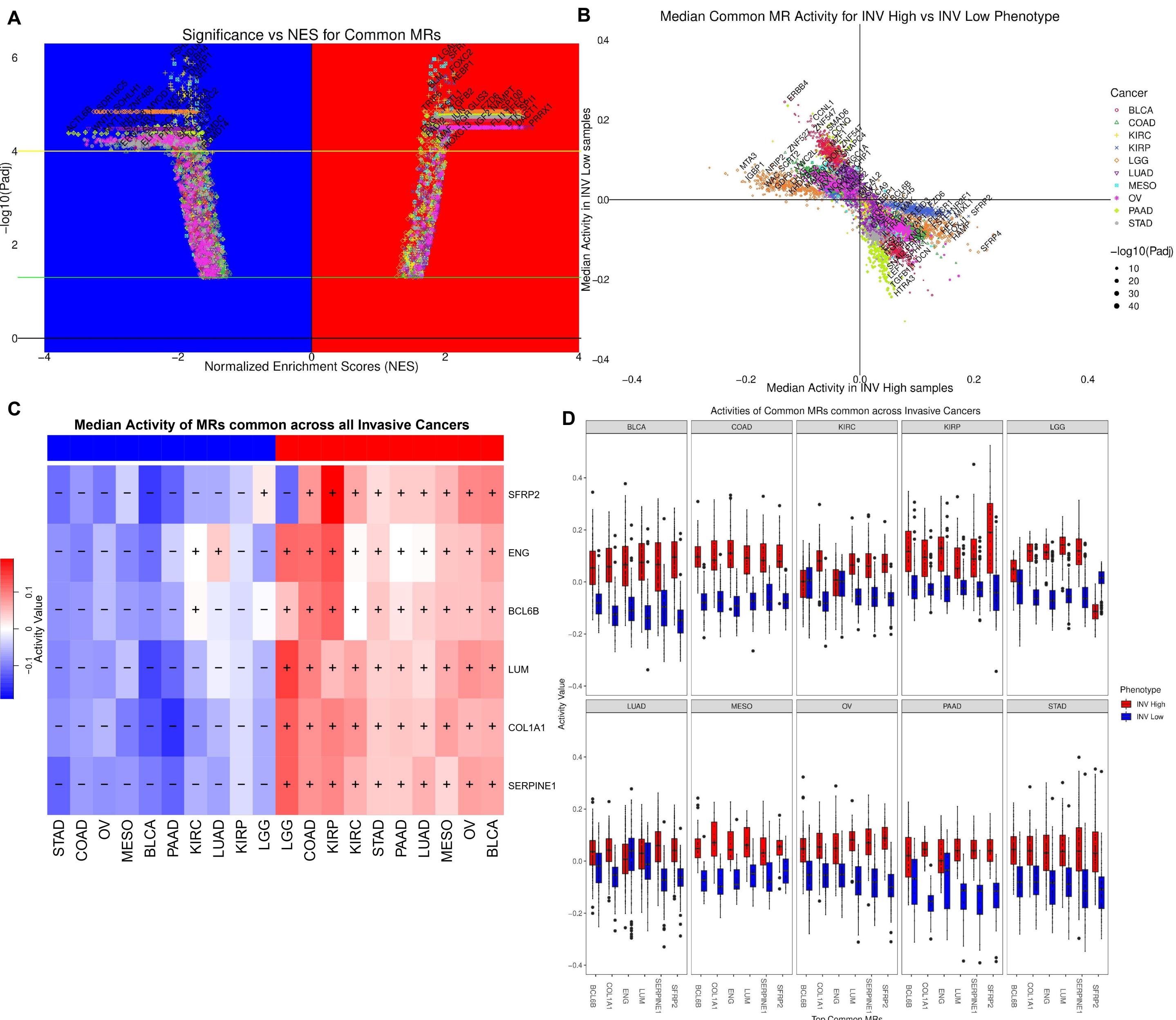


Figure 3: Top MRs common across all the 10 cancers where invasiveness has a significant prognostic impact

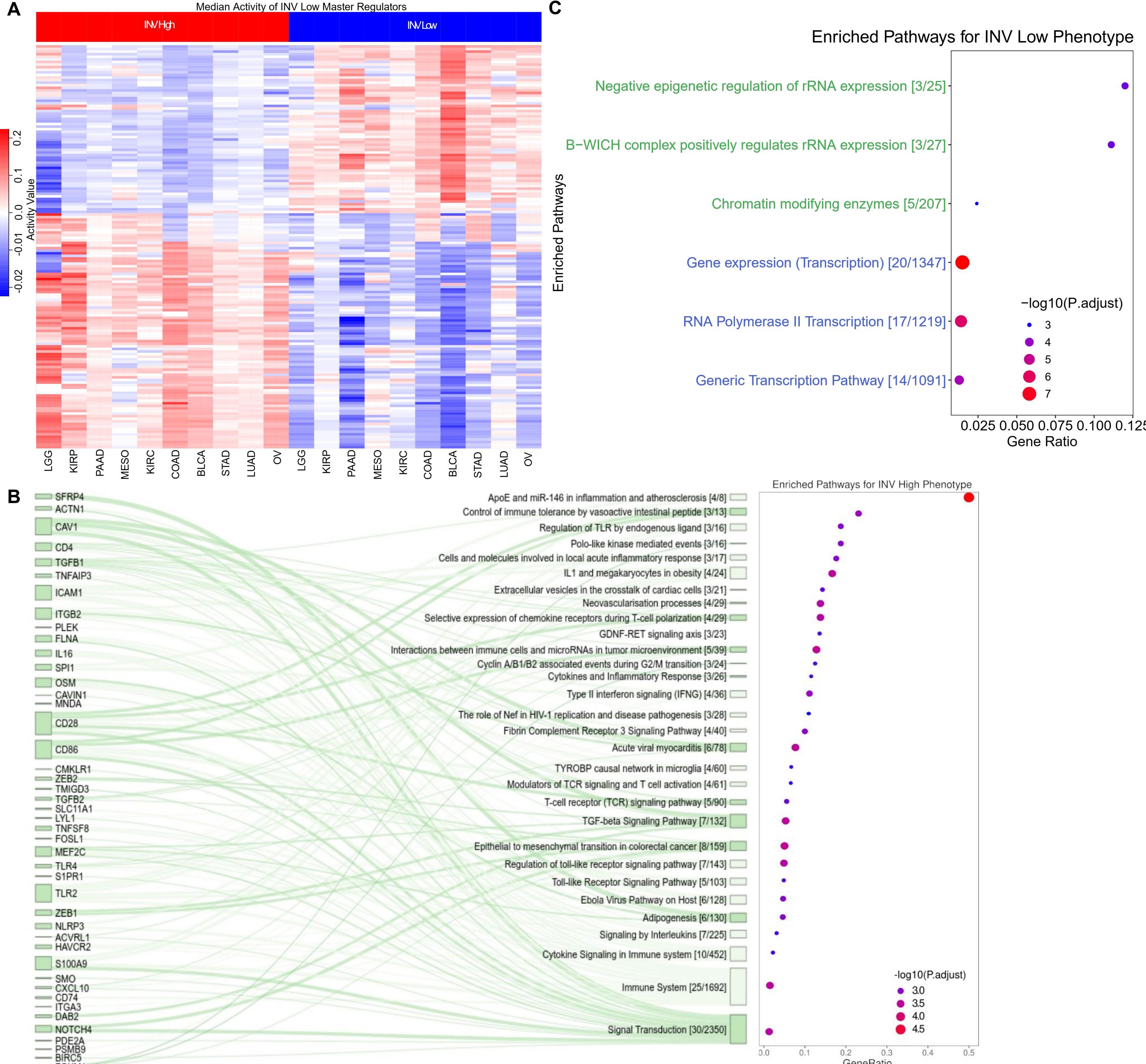
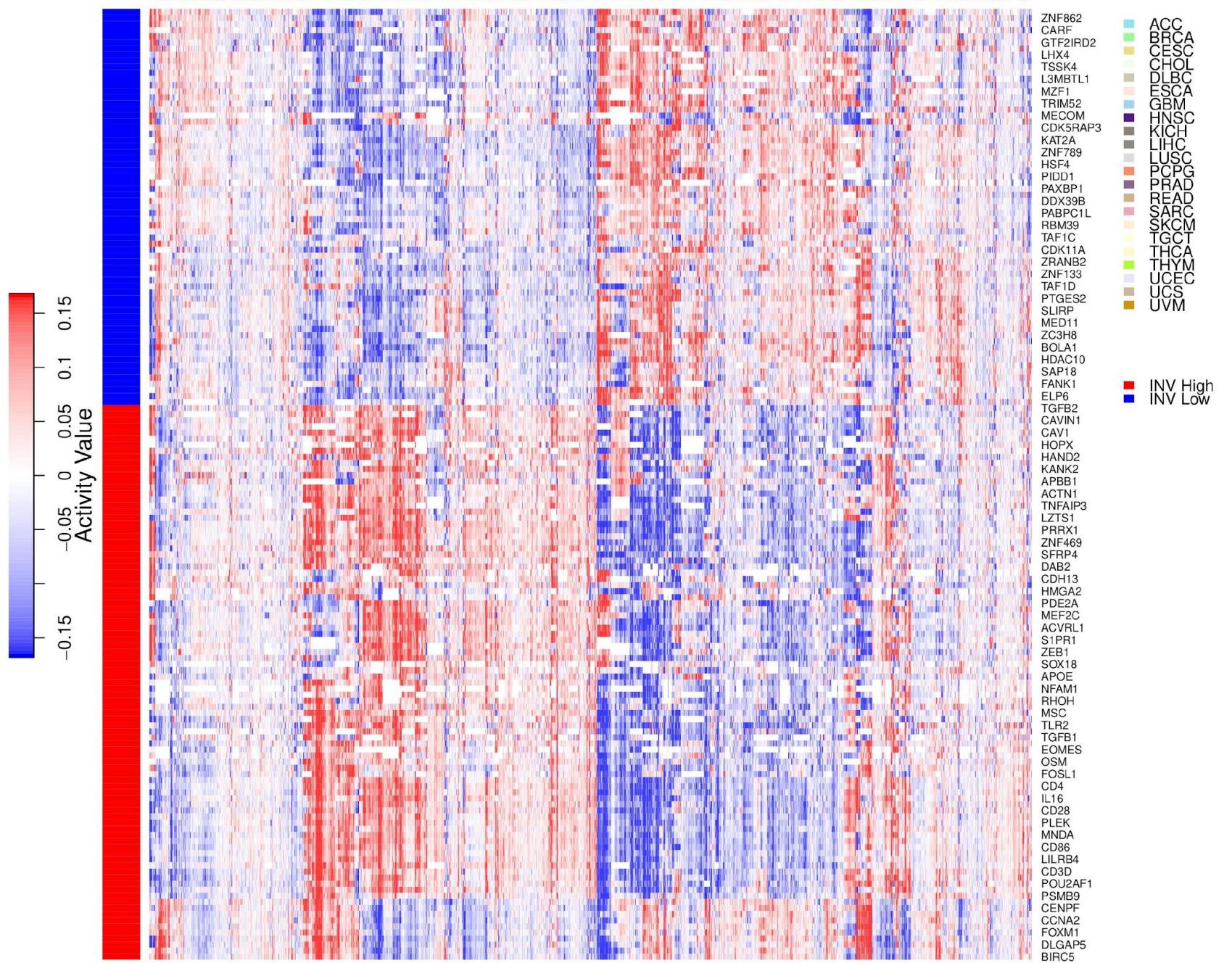


Figure 4: Top MRs specific to INV High/Low phenotype (MR in >5 out of 10 cancers). Pathways associated with INV Low and INV High specific MRs.

**A**

**Figure 5: Validation of INV High and INV Low specific MR activity in cancers where INV is not prognostic. Independent validation of INV High and Low specific MR activity in datasets obtained from PRECOG repository**

**B**