

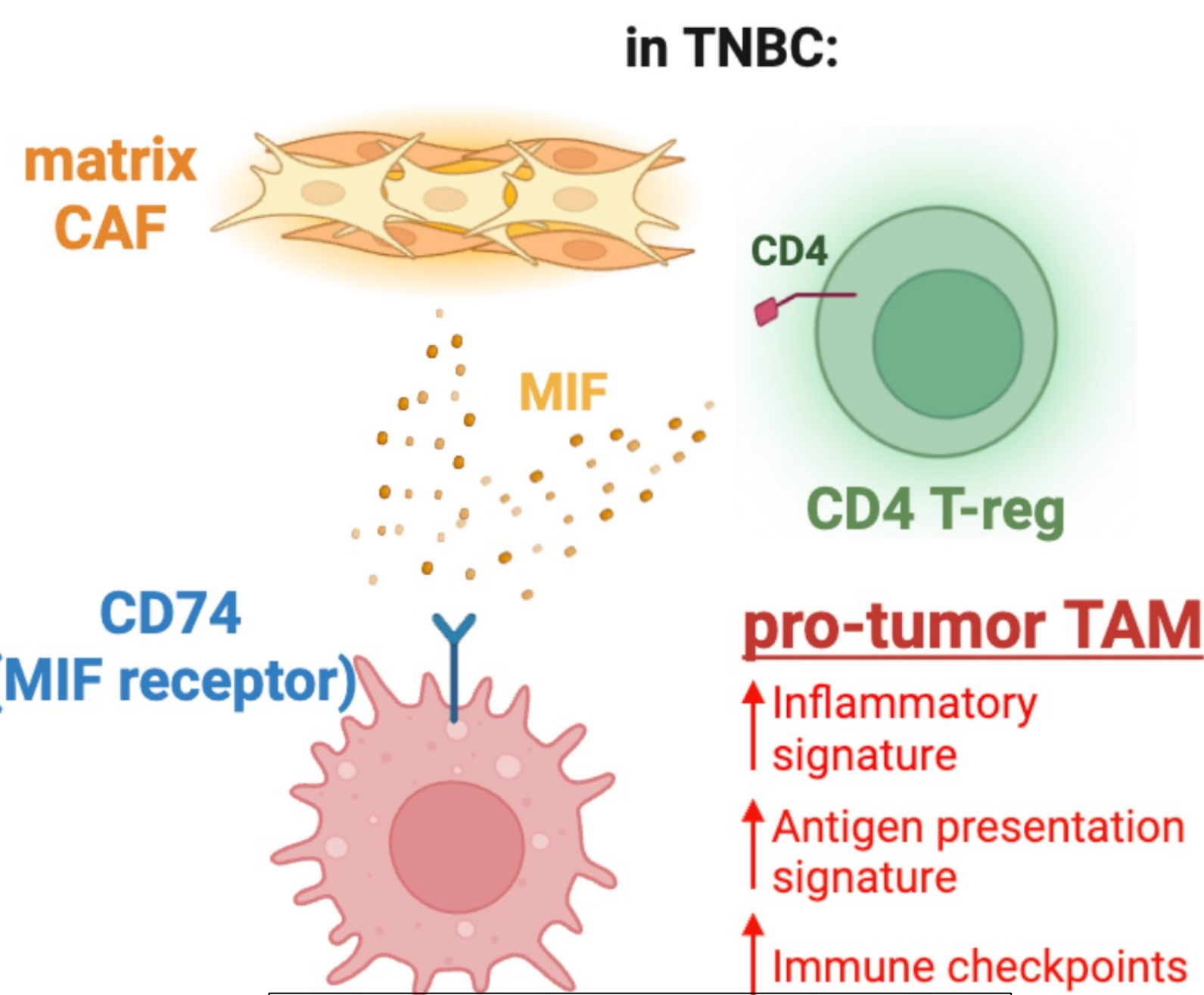
Tumor immune microenvironment (TIME) is associated with the survival outcome and progression in triple negative breast cancer

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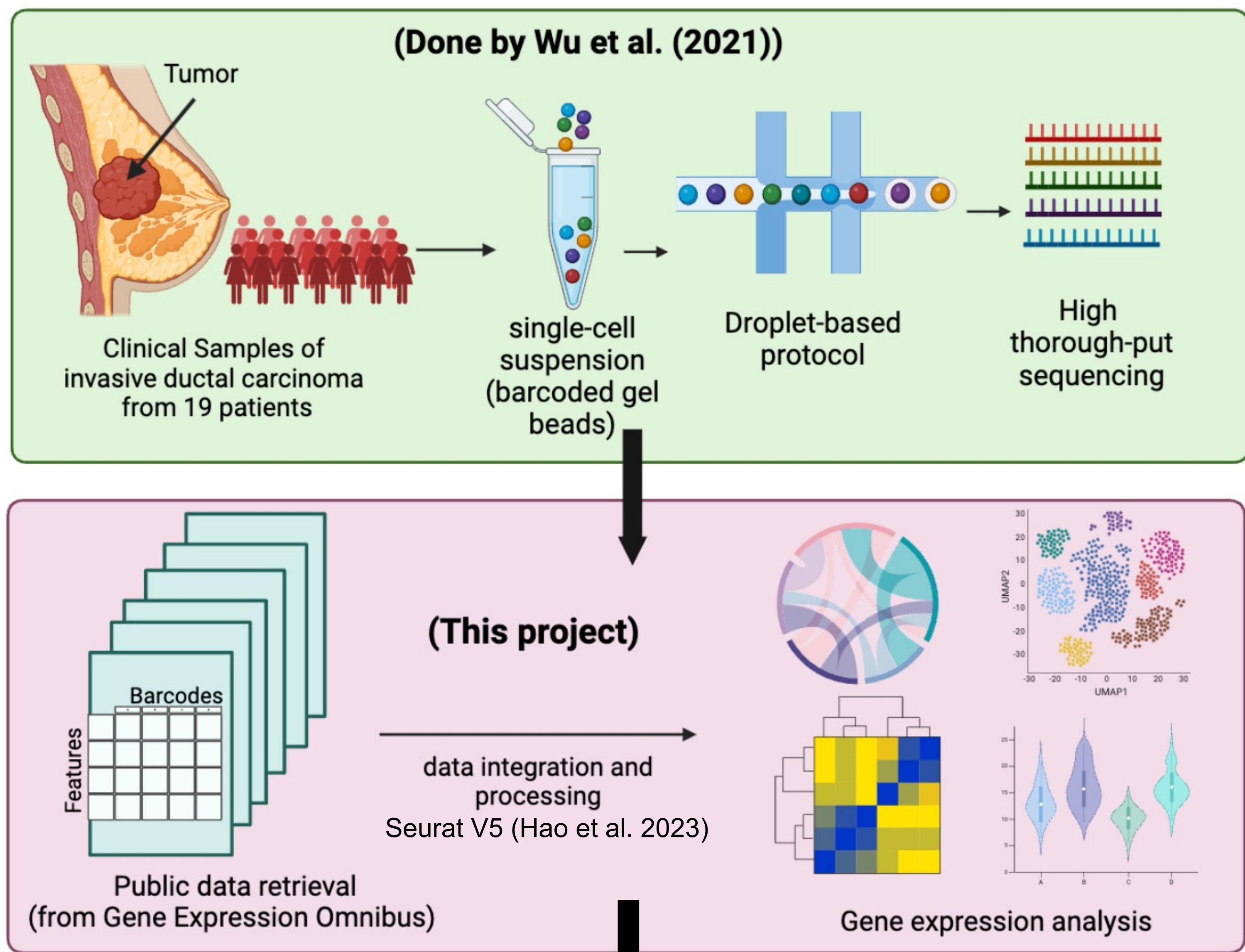
Abstract / summary



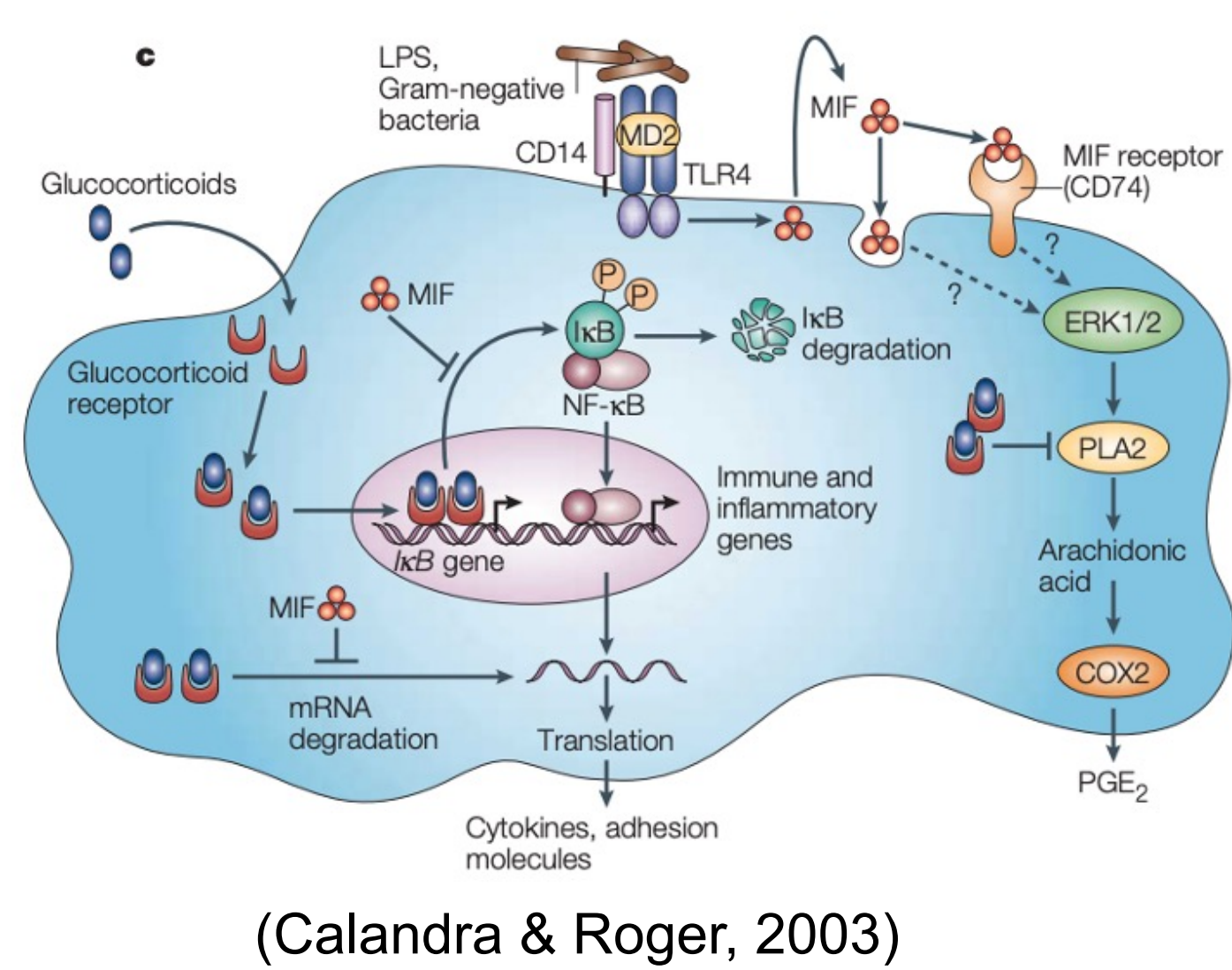
Introduction

- Severity: breast cancer is a chronic disease that **severely affect the world population** (2022: 2.3 million women with breast cancer) (World Health Organization, 2024)
- Breast cancer: broadly divided into different clinical subtypes, including **ER+, PR+, HER2+ breast cancer and TNBC**
- TNBC is the **most aggressive** and deadly subtype of breast cancer
- Tumor-immune micro-environment (TIME)** has been found to be crucial in determining the survival outcome of the patients
- Aim: characterize the crucial subtypes of tumor-associated cells that may potentially affect the **survival outcome** and **tumor progression in TNBC**

Materials and Methods



Discussion



Lipid associated macrophage (mac_FABP5 and mac_APOE) are under the regulation of mCAFs and CD4-Treg via MIF signaling.

Cell-cell communication analysis was conducted using *CellChat* (Jin et al., 2021)

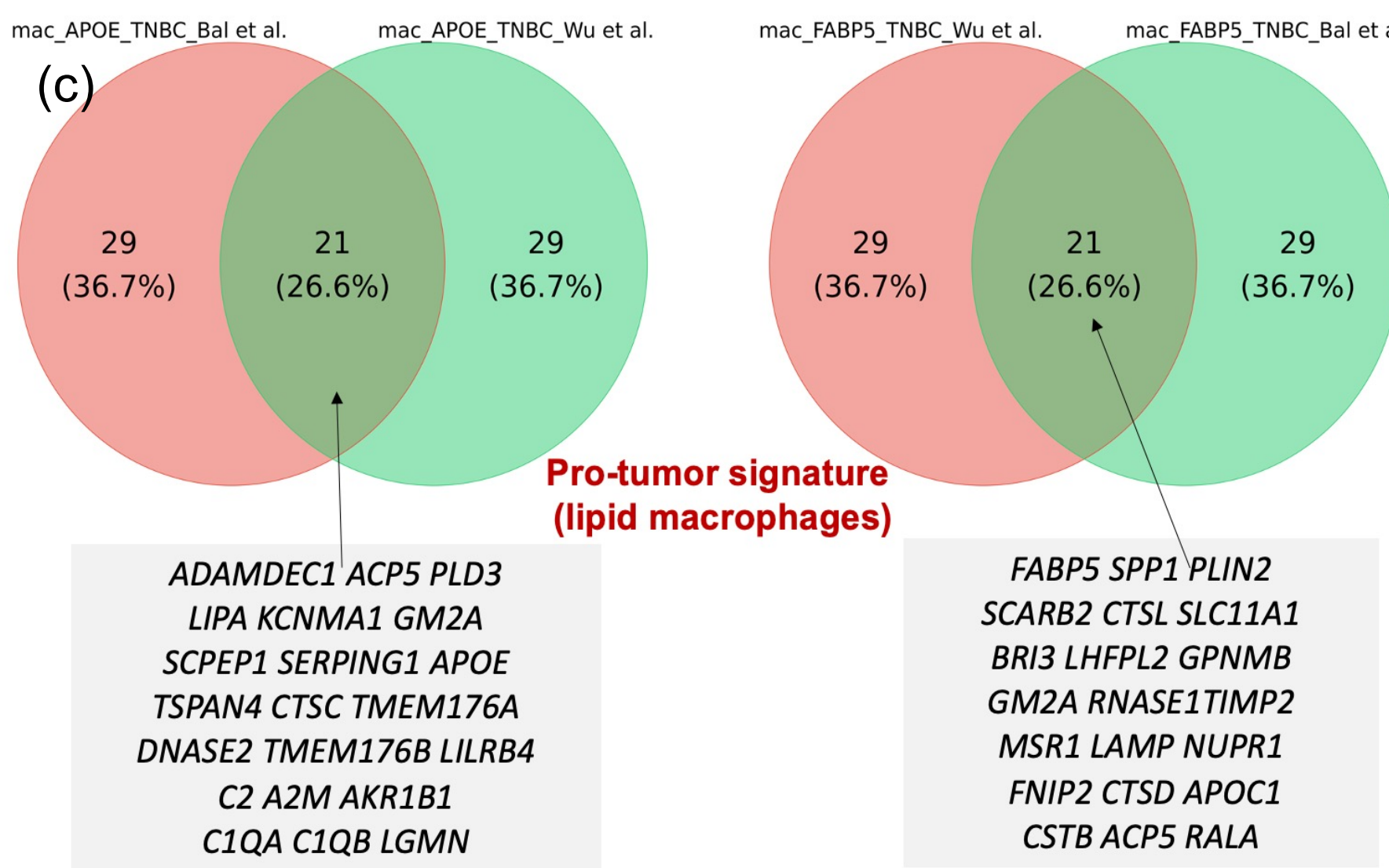
MIF signaling

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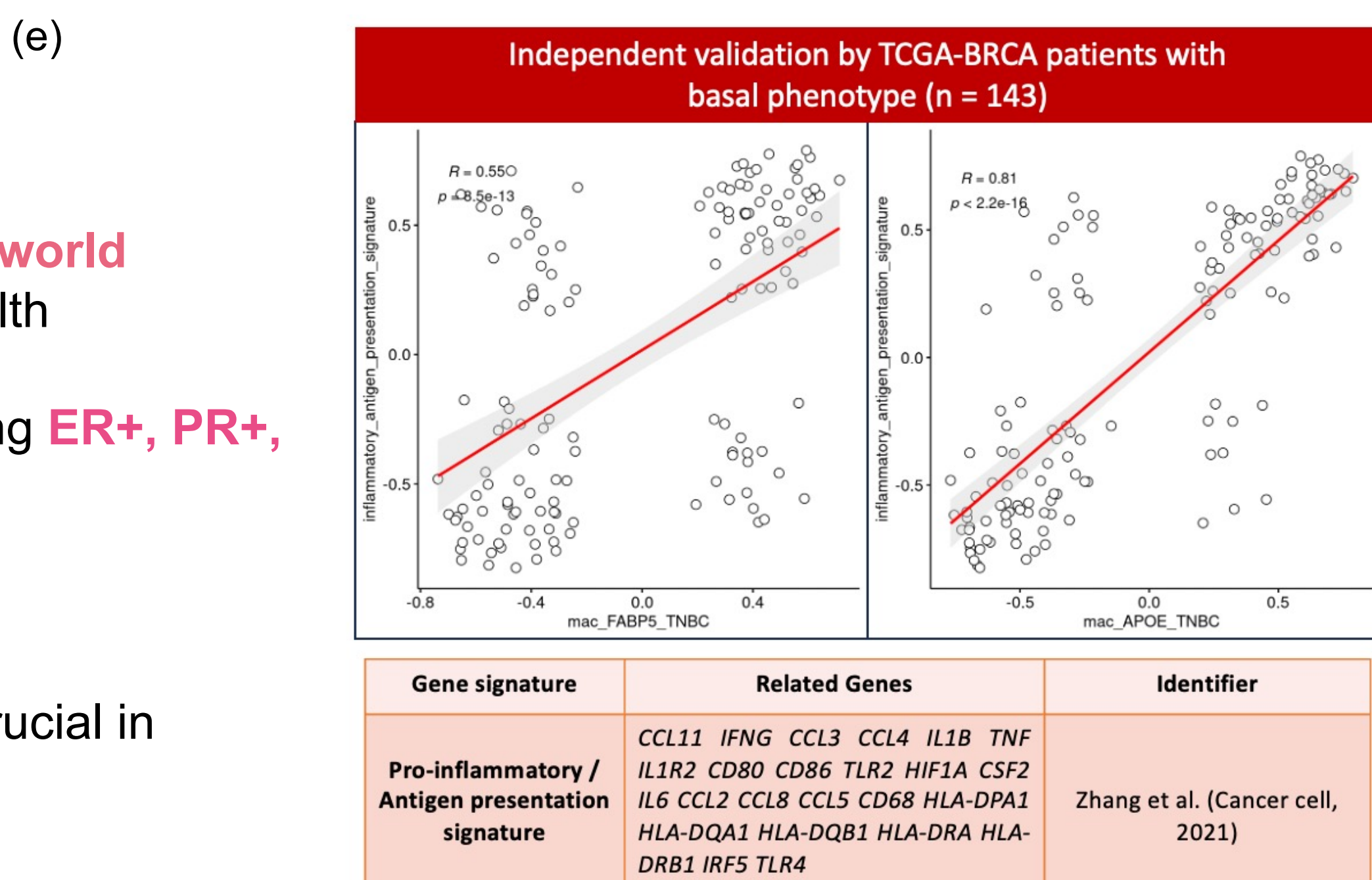
inflammatory phenotype in myeloid cells

- mCAF and CD4-Treg: potential **source** of MIF signaling
- Association with **immuno-suppression** in myeloid cells
- Tuned down **anti-cancer immunity** by macrophage

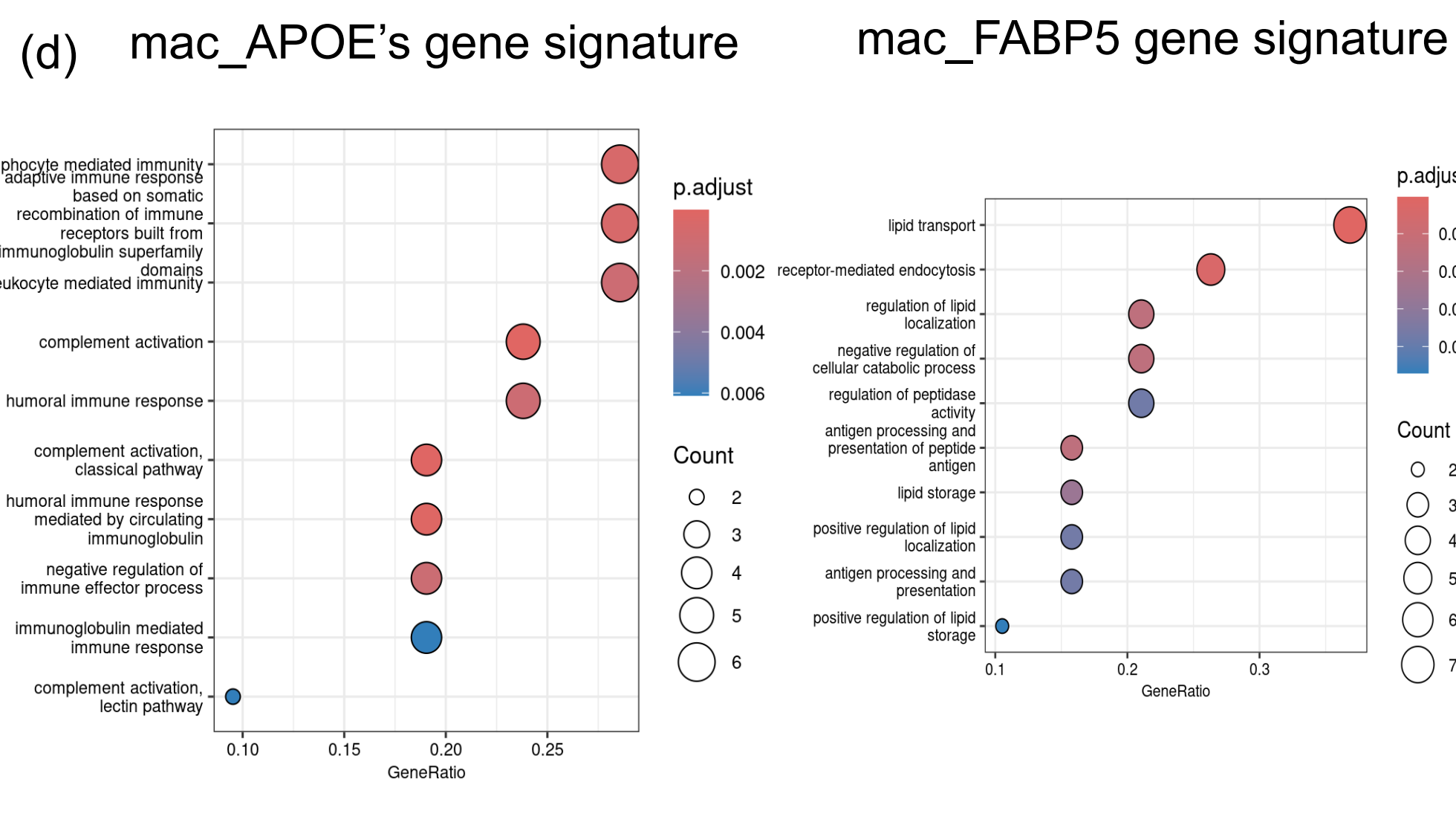
- **Future research directions:**
 - study the correlations between MIF signaling, lipid macrophage signature and other T cell signature (e.g. T-cell dysfunction in effector T cells)



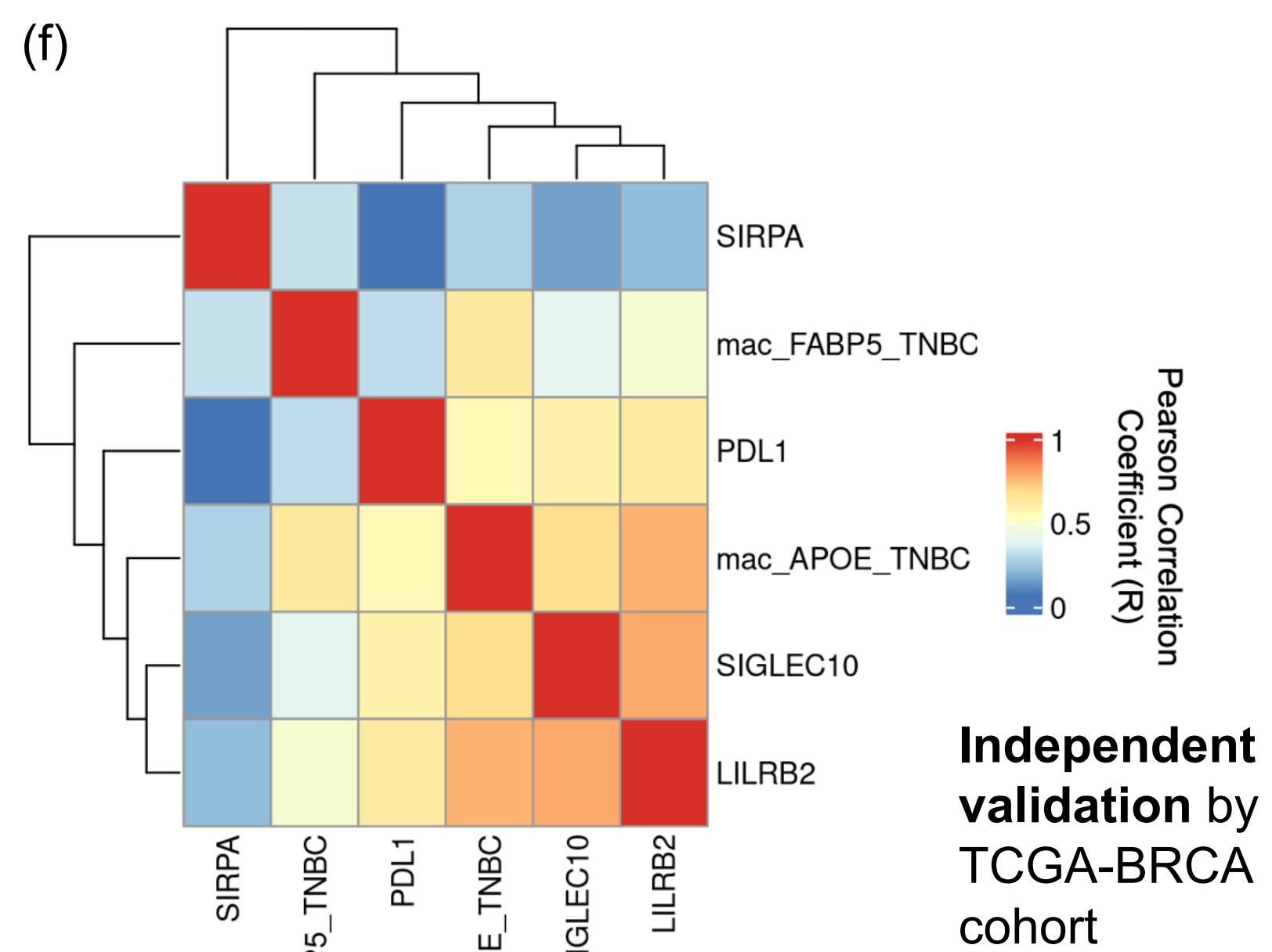
Independent validation of lipid macrophage signature using another set of **single-cell RNA seq** data from Bal et al. (2021)



- **Strong positive correlation** between pro-inflammatory signature and gene signature of lipid macrophage signature



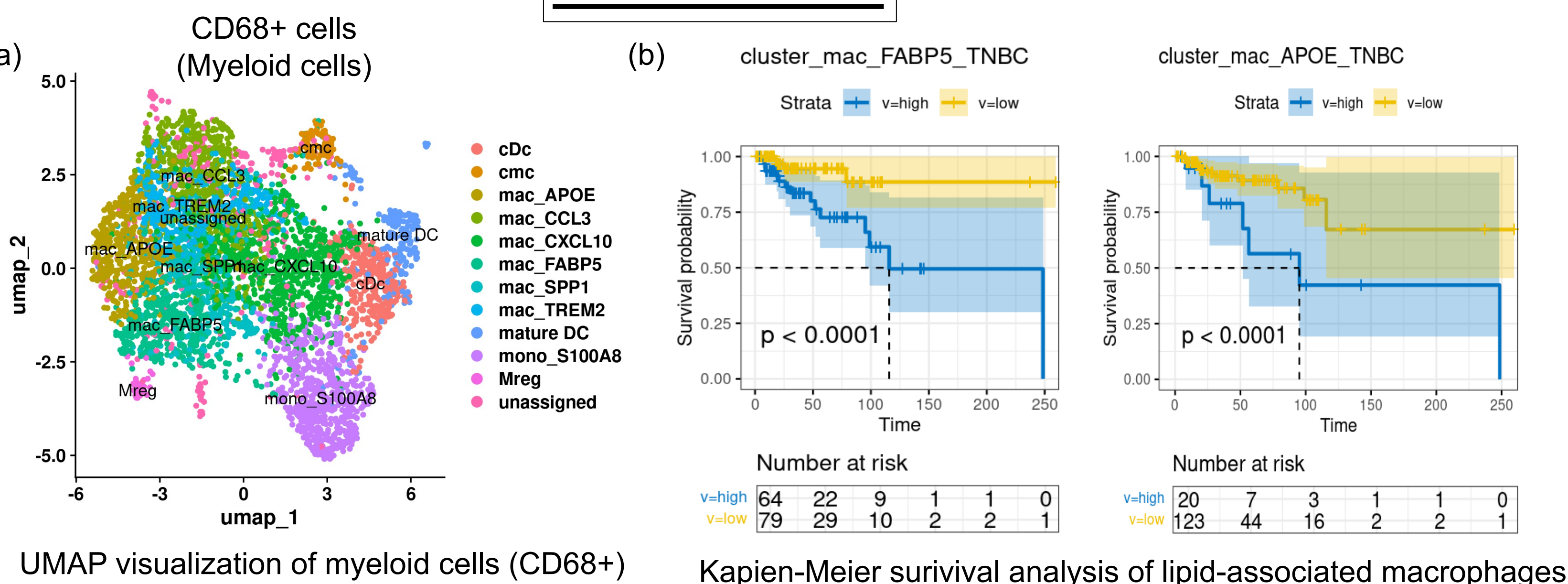
Gene ontology (GO) analysis of co-expressed lipid-mac signature



- **Strong positive correlation** between some well-known myeloid immune checkpoints and gene signature of lipid macrophage signature.

Independent Validation by bulk RNA seq data (TCGA-BRCA cohort)

Results



Reference:

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