



XIX CONGRESSO  
NAZIONALE  
SIES 2026

**L'ANALISI TRASCRIPTOMICA DELLE CELLULE CD34<sup>+</sup>  
NELLA MIELOFIBROSI EVIDENZIA IL LORO RUOLO  
NELLA DISREGOLAZIONE DELLA MATRICE  
EXTRACELLULARE E NELLA FIBROSI MIDOLLARE**

**Prof.ssa Simona Bernardi**

Firenze | 4-6 marzo 2026  
Palazzo degli Affari



## Disclosures of Simona Bernardi

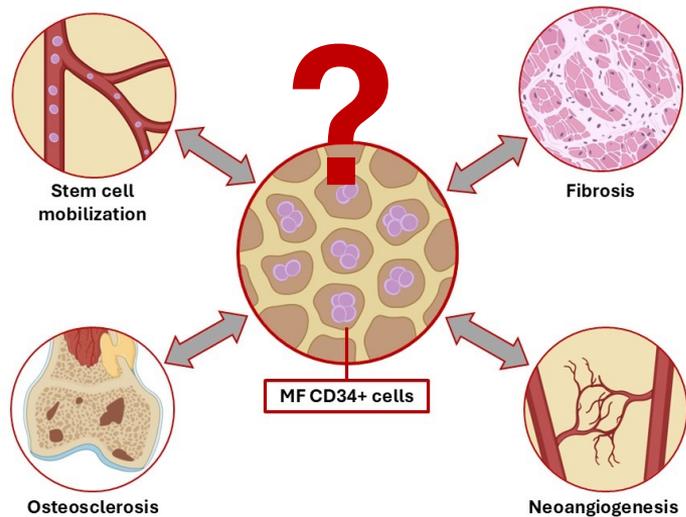
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# Background and Hypothesis

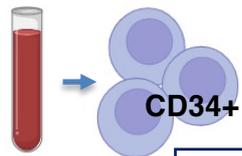
**Myelofibrosis:**

- Hematopoiesis altered partly by neoplastic transformation and partly by bone marrow fibrosis.
- Fibrosis is associated with proliferation of bone marrow fibroblasts.
- Alteration of both bone marrow and extramedullary microcirculation due to alterations in the vascular endothelium.



# Workflow

BM/PB of MF patients



CD34+

CD34+ cells of healthy donors served as controls

Total RNA



RNASeq



Bioinformatic/biostatistic analysis

(GeneOntology (GO) and KEGG)



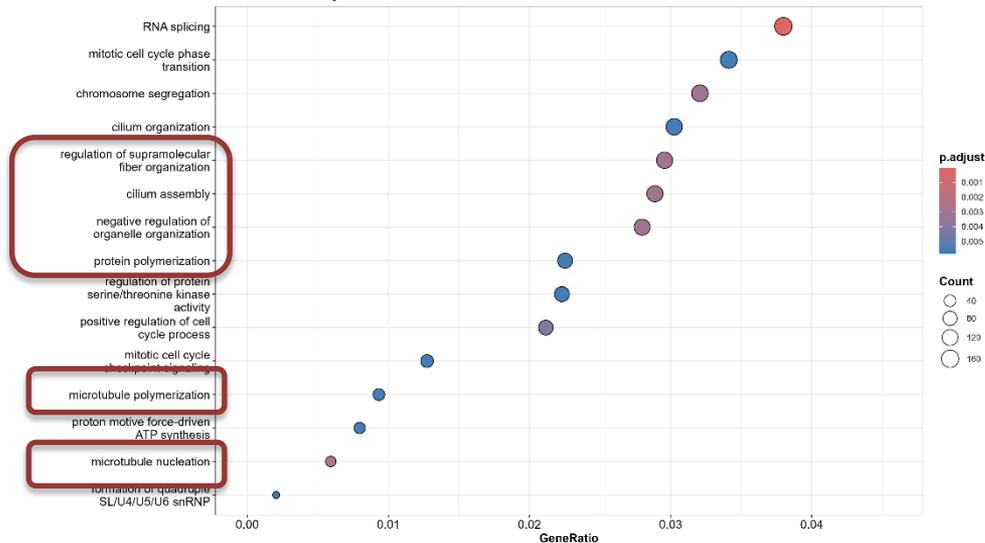
To identify the transcriptome differences according to:

- **degree of bone marrow fibrosis** ( $G \leq 1$  vs.  $G > 1$ )
- **disease subtype** (pre- PMF, overt-PMF, secondary-MF)
- **therapy with JAK-inhibitors** (therapy naïve, MF-TN vs. MF-JAKi)

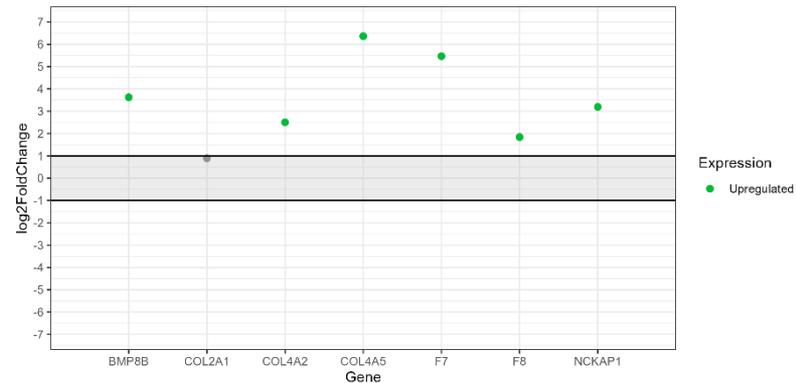
- Novogene total RNASeq solution on Illumina NextSeq 500/550 platform on a Mid-Output kit V2.5 (300 cycles).
- Genes were considered differentially expressed when presented at least  $>2$ - fold change and  $p$  value  $<0.05$ . To identify the most impactful pathways, a gene ratio cut-off of 0.02 was set as reference.

# TN-MF vs Healthy controls

Therapy-naïve MF vs Control  
Enriched GO Pathways

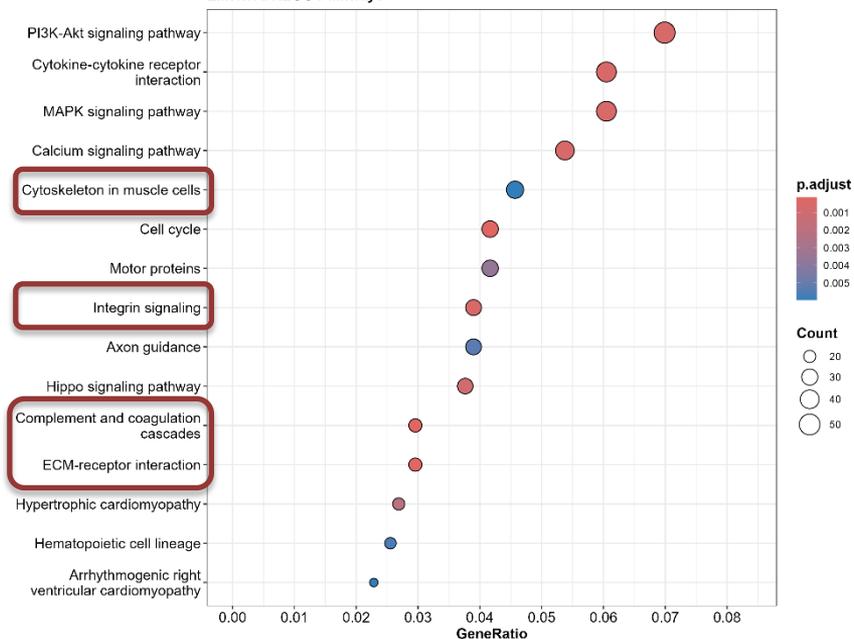


Differentially expressed genes between Therapy-naïve MF vs Control

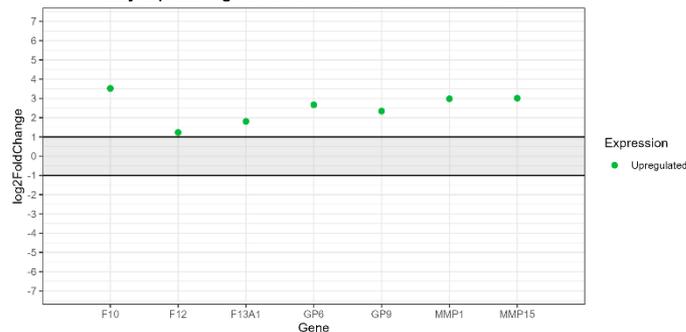


# Fibrosis grade: $G > 1$ vs $G \leq 1$

Fibrosis  $G > 1$  vs Fibrosis  $G \leq 1$   
Enriched KEGG Pathways

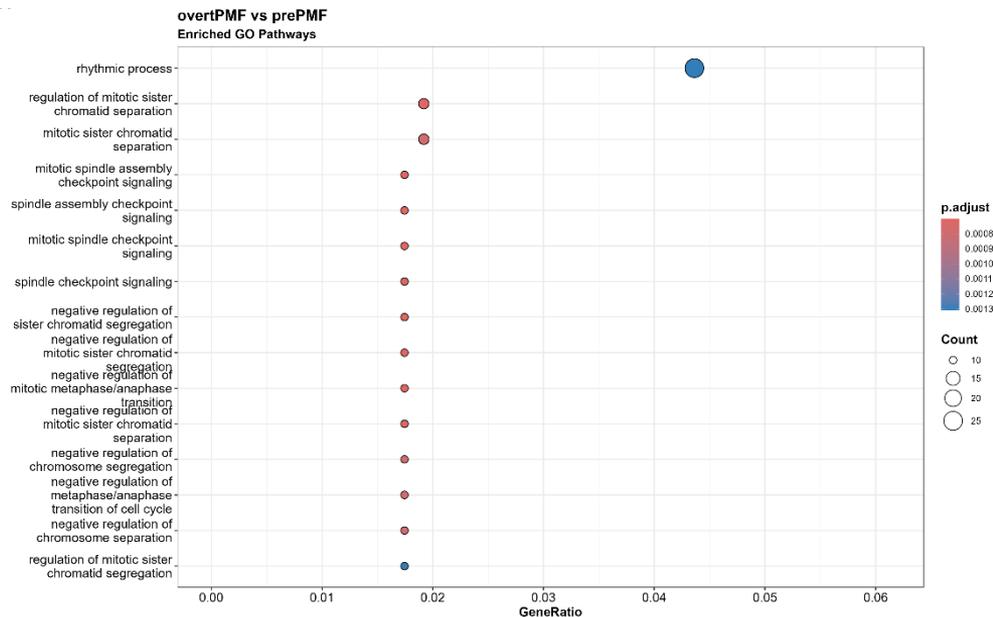


Differentially expressed genes between Fibrosis  $G > 1$  vs Fibrosis  $G \leq 1$

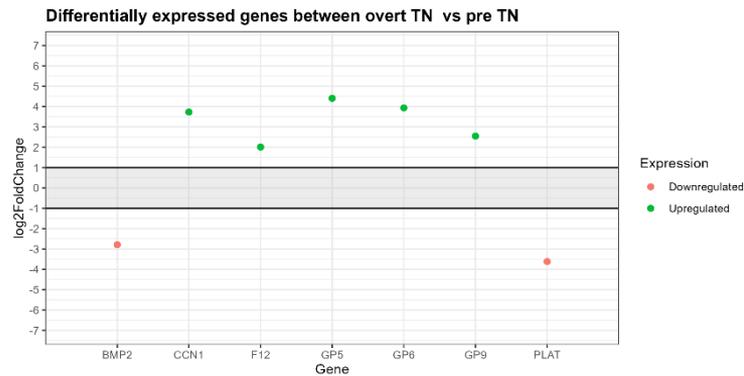
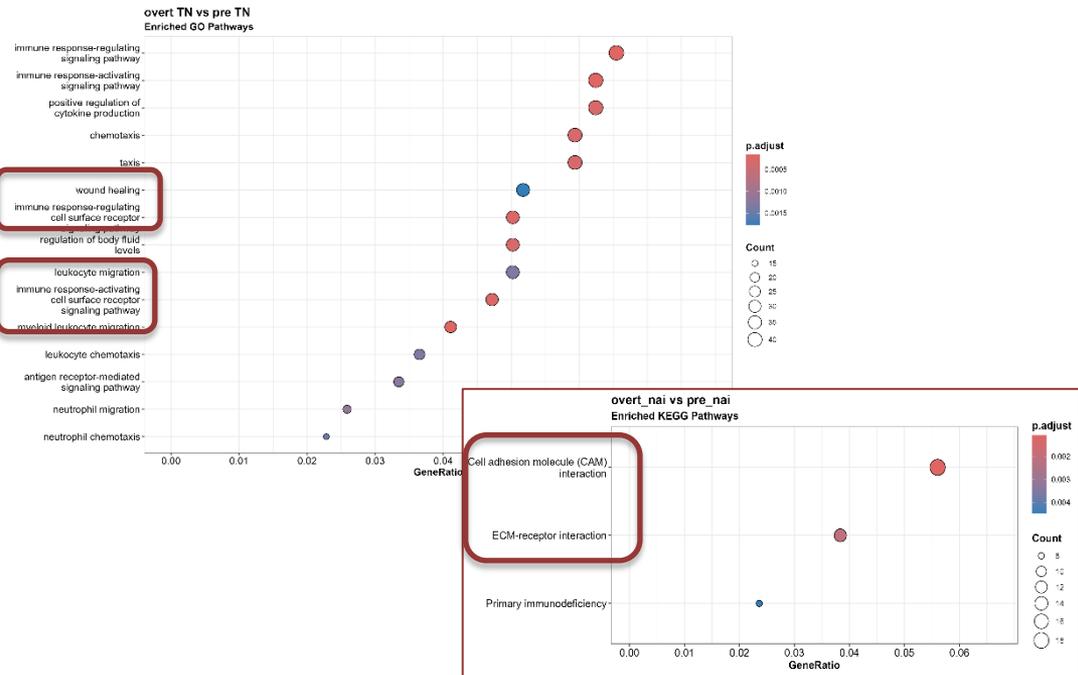




# Disease type: overt-PMF vs pre-PMF

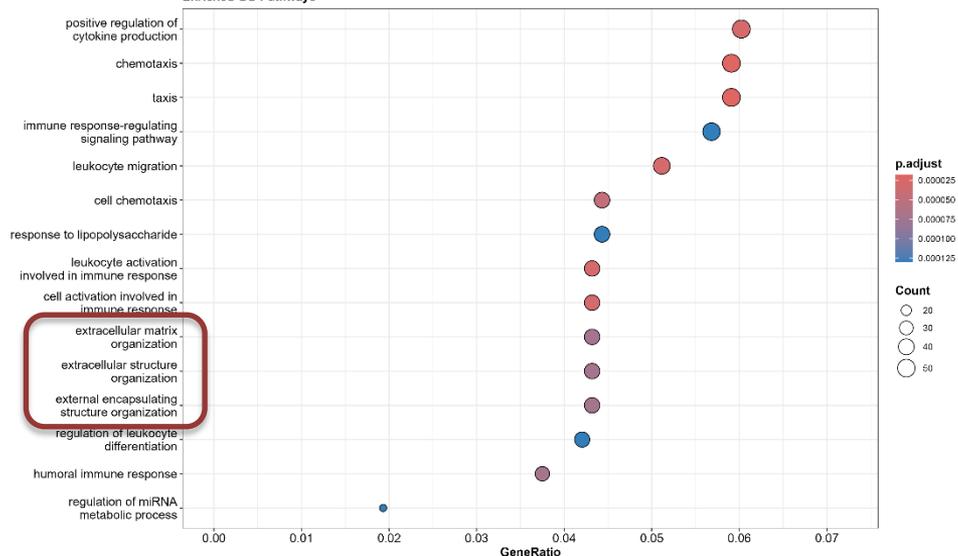


# Disease type without JAKi: overt-PMF TN vs pre-PMF TN

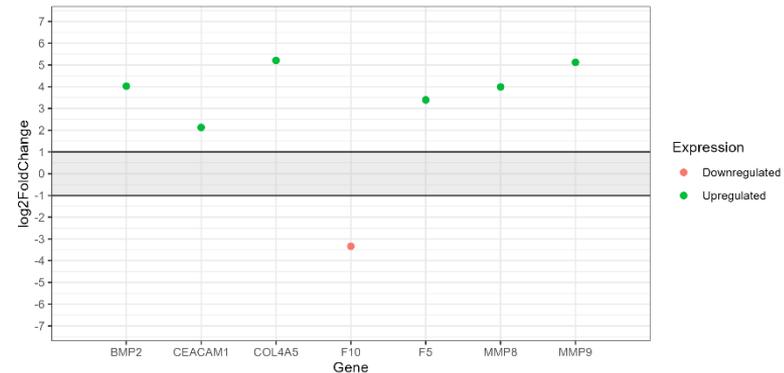


# Therapy: MF-TN vs MF-JAKi

Therapy-naive MF vs JAK2-i Therapy MF  
Enriched GO Pathways



Differentially expressed genes between Therapy-naive MF vs JAK2-i Therapy MF



## Conclusions

- For the first time, our analysis reveals that pathways associated with wound healing, collagen organization, osteo- and angiogenesis, and extracellular matrix remodeling are differentially expressed in malignant CD34<sup>+</sup> cells, correlating with the extent of bone marrow fibrosis.
- JAKi therapy modulates the expression of several of these genes involved in tissue remodeling and angiogenesis, suggesting a broader impact on disease biology beyond cytokine signaling suppression.



## Call PRIN 2022 – Ministry of University and Research (cod. 2022ZB3EYX)

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**We are grateful to all patients and their families for  
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