

# #3523: PREDICTIVE MODELS OF RECURRENCE FROM TRANSCRIPTOMIC SIGNATURES OF THE TUMOR MICROENVIRONMENT AND CELL CYCLE IN STAGE III COLON CANCER FROM PETACC-8 AND IDEA-FRANCE TRIALS

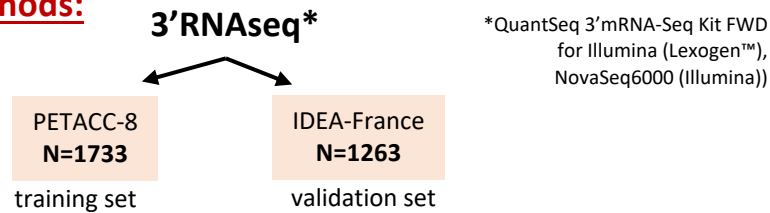
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## Objectives:

→to establish a **predictive model of the risk of recurrence in stage III colon cancer (CC)** based on transcriptomic signatures of the tumor microenvironment (TME) and cell cycle from the PETACC-8 and IDEA- France trials.

## Methods:



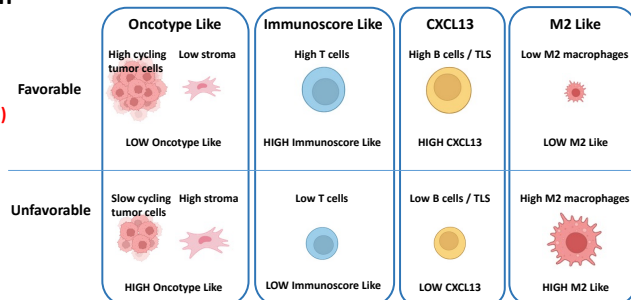
## 4 genomic signatures of TME and cell cycle

- **Immunoscore Like signature** (Marisa et al. JNCI 2018)
  - CD3E, CD3G, CD3D, CD8A and PTPRC
- **Oncotype Like score:** derived from the Oncotype DX® Colon Cancer RS (O'Connell et al. JCO 2010):
  - . stromal score = BGN, FAP and INHBA
  - . cell cycle score = MKI67, MYC and MYBL2

$$\text{Oncotype Like score} = 44 \times ((0.15 \times \text{stromal score} - 0.30 \times \text{cell cycle score} + 0.15 \times \text{gene expression of GADD45B}) + 0.82)$$

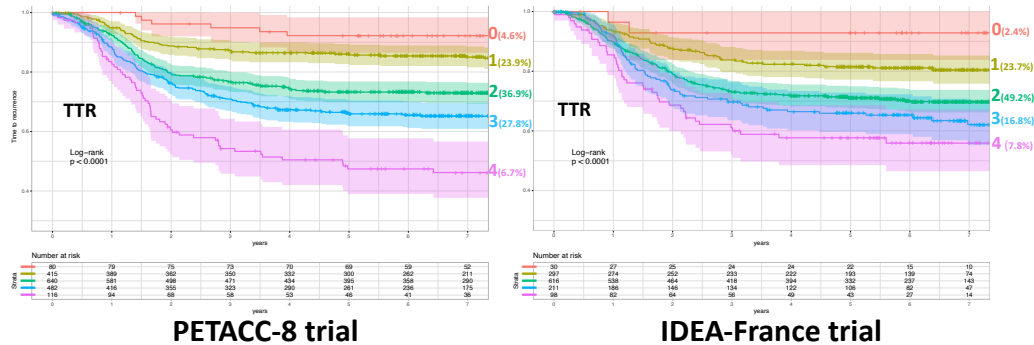
- **Macrophage M2 Like signature** (Combes et al. Cell 2022)
- **CXCL13 expression**

**IPS score**  
(Immune Proliferative Stromal)  
= number of unfavorable signatures (0 to 4)



In stage III colon cancer:  
3'RNAseq signatures related to:  
→ T cells  
→ B cells/TLS  
→ Macrophages M2  
→ Stroma  
→ Cell cycle  
provide important information for patient stratification on risk of recurrence

## Results



## Multivariate models

	PETACC-8		IDEA-France	
	adj HR	p	adj HR	p
T4	2.0	<0.01	1.6	<0.01
N2	2.2	<0.01	2.4	<0.01
IPS score				
1	1.8	0.2	2.3	0.2
2	3.4	<0.01	3.9	0.058
3	4.4	<0.01	4.6	0.03
4	6.7	<0.01	5.7	0.02
Dismal CMS combination	1.6	<0.01	1.1	0.5
Treatment duration: 3 months			1.5	<0.01

## Future Directions for Research:

Beyond T and N stage, for the decision of adjuvant chemotherapy in stage III CC, the combination of these different variables could be exploited in the future for personalized care (de-escalation, intensification), or stratification in therapeutic trials



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