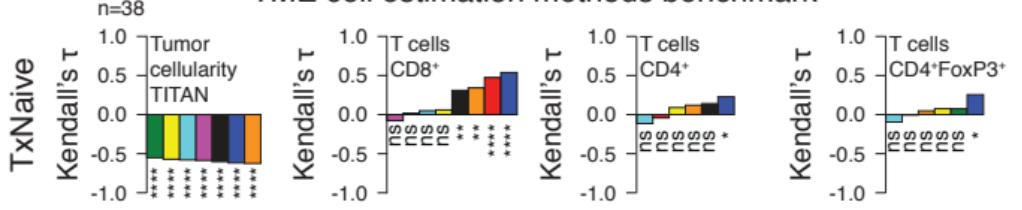


a

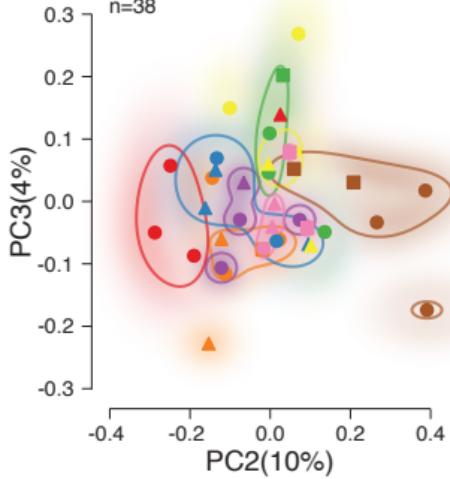
TME cell estimation methods benchmark

**b**

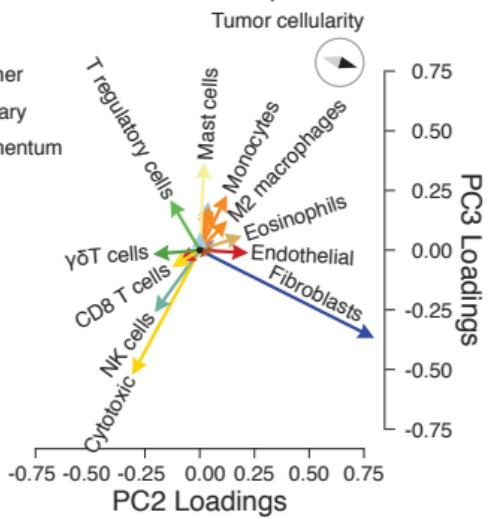
TME estimation methods

Performance: Worst → Best

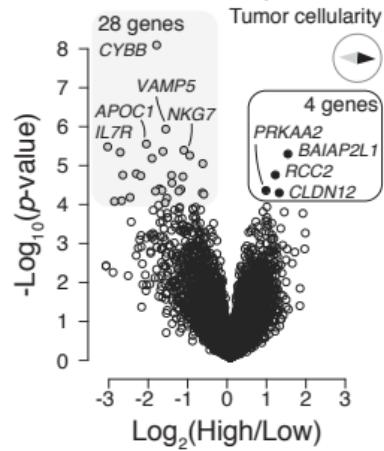
- Bindea
- CIBERSORT
- Consensus^{TME}
- Danaher
- Davoli
- MCP counter
- TIMER
- xCELL

cssGSEA
(Consensus^{TME} gene sets)**d**

Factors map

**e**

Differential expression

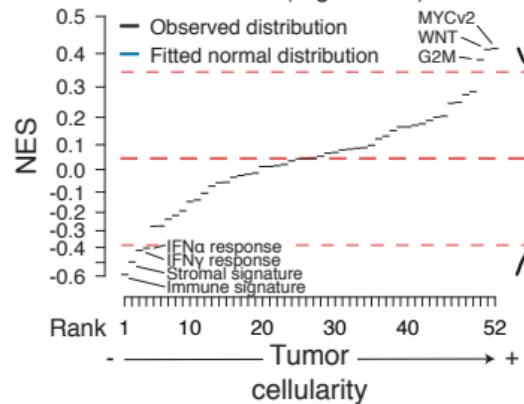
**f**

Gene ontology

(Low tumor cellularity 28 genes)

Fisher/FDR

****	Immune system process
**	Regulation of immune system process
*	Regulation of immune response
*	Immune effector process
***	Defense response
****	Immune response
***	Cell activation
*	Leukocyte mediated immunity
*	Cell activation in immune response
*	Leukocyte activation in immune response
***	Innate immune response
***	Myeloid leukocyte activation
*	Response to IFNγ
*	Humoral immune response

gHallmarks
(High vs low)**h**Consensus^{TME}
(High vs low)