ACCSCIENCE PUBLISHING

Tumor Discovery

ORIGINAL RESEARCH ARTICLE

Computational identification of immune-suppressive gene signatures associated with tumor progression and immunotherapy resistance

Supplementary Files

Table S1. Immune-related gene sets used for scoring analyses

Signature	Genes	Functional rationale
Checkpoint activity score	*PDCD1*, *CTLA4*, *TIGIT*, *LAG3*	Canonical immune checkpoint signaling and T-cell exhaustion
Suppressive immune signature	*PDCD1*, *CTLA4*, *TIGIT*, *LAG3*, *FOXP3*, *IL2RA*, *CD163*, *MRC1*	Integrated representation of checkpoint signaling, regulatory T-cell activity, and M2 macrophage-mediated immune suppression

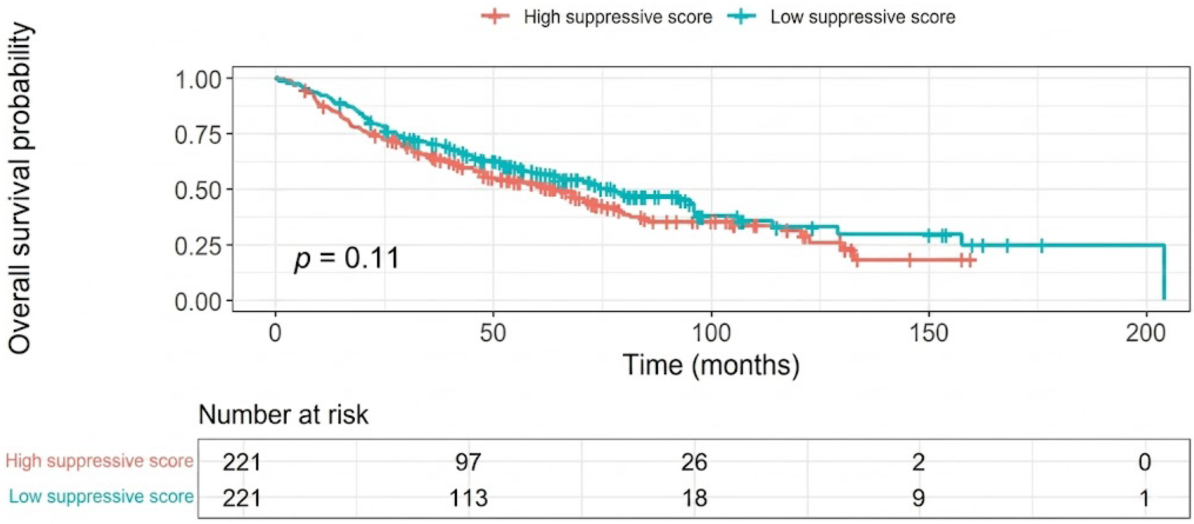

Figure S1. Exploratory external validation of the suppressive immune signature in the independent GSE68465 lung adenocarcinoma cohort

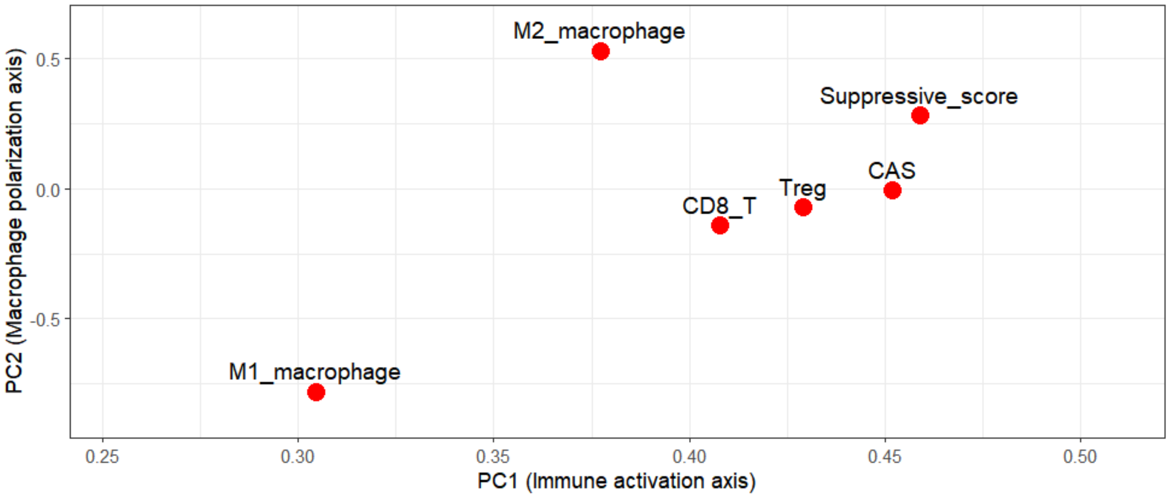

Figure S2. Principal component analysis of immune-related features reveals structured inter-tumor variability across the pan-cancer immune landscape