

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    | <i>PDCD1, CTLA4, TIGIT, LAG3</i>                            | Canonical immune checkpoint signaling and T-cell exhaustion                                                                  |
| Suppressive immune signature | <i>PDCD1, CTLA4, TIGIT, LAG3, FOXP3, IL2RA, CD163, MRC1</i> | Integrated representation of checkpoint signaling, regulatory T-cell activity, and M2 macrophage-mediated immune suppression |

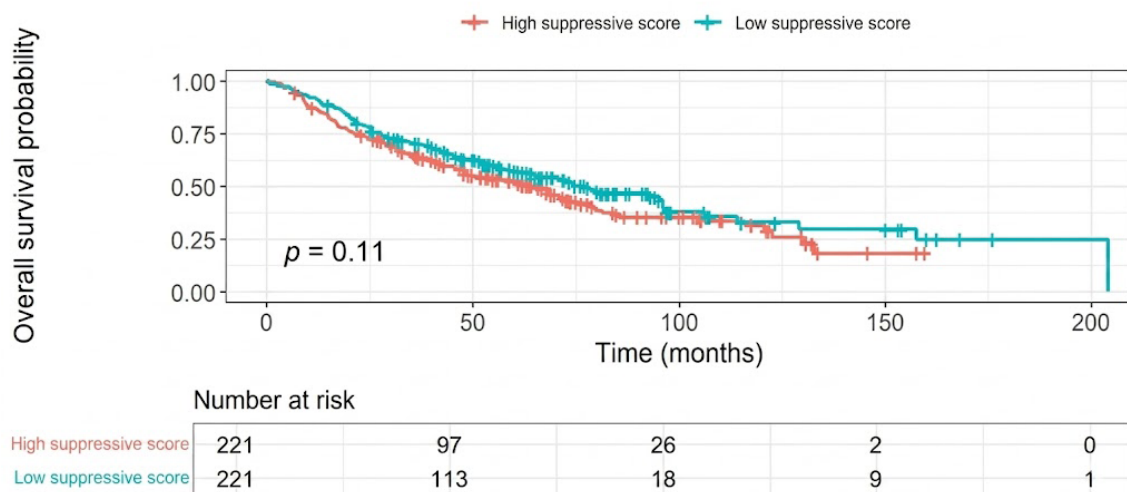


**Figure S1.** Exploratory external validation of the suppressive immune signature in the independent GSE68465 lung adenocarcinoma cohort

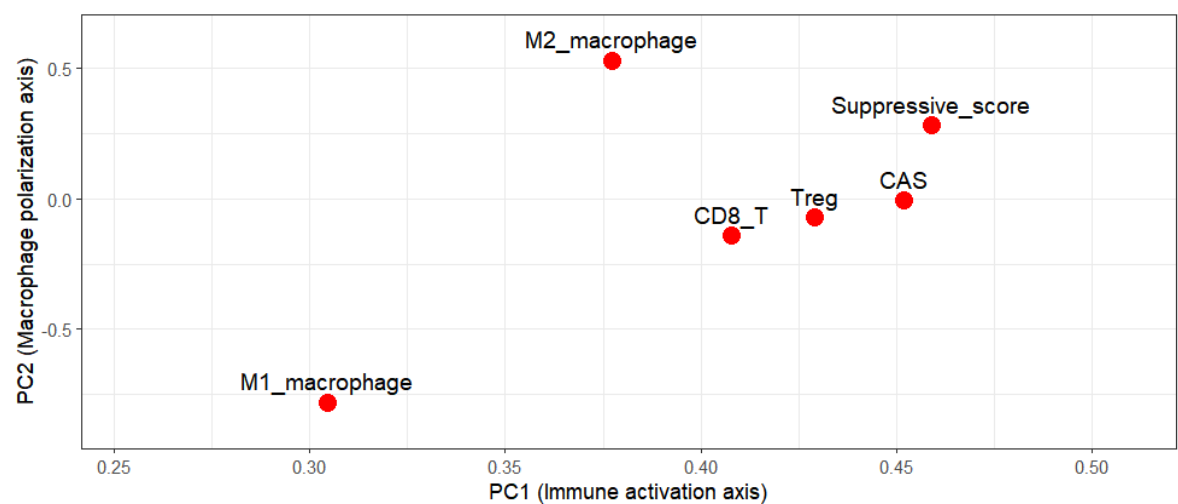


Figure S2. Principal component analysis of immune-related features reveals structured inter-tumor variability across the pan-cancer immune landscape