

Figure S1 KEGG pathways and Gene Ontology terms analyses for Stromal score and Immune score separately.

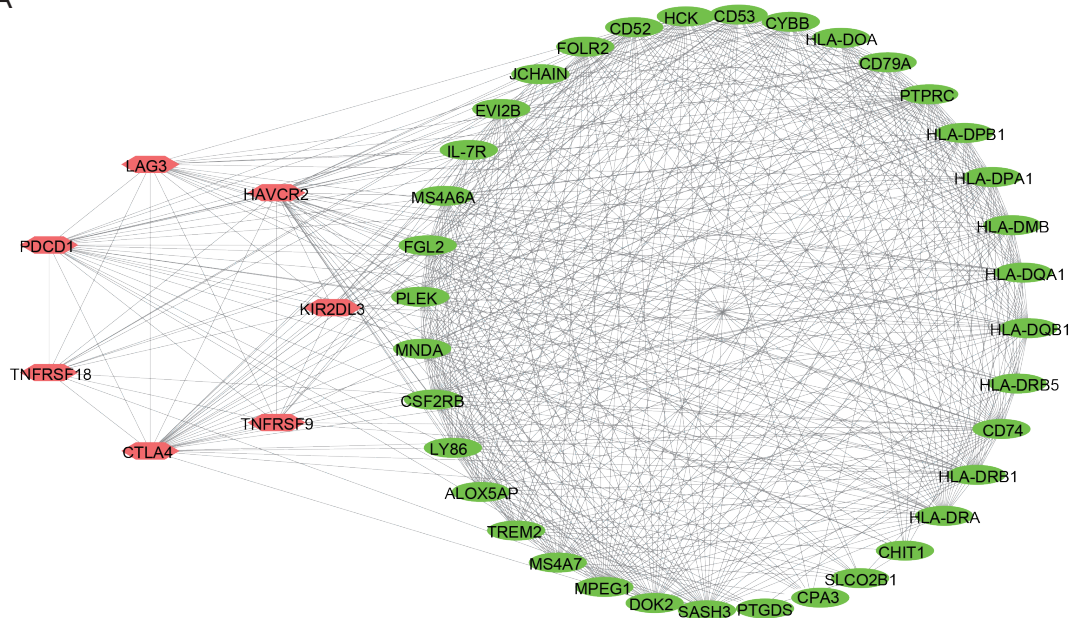
A. Top 9 KEGG pathways enriched by the Stromal score-related DEGs.

B. Top 10 KEGG pathways enriched by the Immune score-related DEGs.

C. Top 10 Gene Ontology terms enriched by the Stromal score-related DEGs.

D. Top 10 Gene Ontology terms enriched by the Immune score-related DEGs.

A



B

Shared Gene	ID	Interaction degree	Function	Ref
PTPRC	GC01P198607	39	An essential regulator of T- and B-cell antigen receptor signaling, and a member of the protein tyrosine phosphatase (PTP) family. Comprises proteins activated in tumors.	48
FGL2	GC07M077193	38	Positively correlated with infiltration of immune cells. Promote tumor progress by activating fibroblasts. High expression was correlated with better prognostic outcomes.	49
CD74	GC05M150378	38	Release clip and facilitate the binding of antigenic peptides to the MHC-II. Essential for B cell survival and represent a genomic signature of early oncogenesis.	40
HLA-DRB1	GC06M032578	36	Presenting peptides derived from extracellular proteins, strongly associated with the risk of lung cancer.	50
CD52	GC01P026317	35	Anti-adhesion, allowing cells to freely move around. Inhibit T-cell activation by impairing phosphorylation of T-cell receptor associated kinases Lck and Zap70	51
CSF2RB	GC22P036913	34	Associated with ineffective clearance of surfactant by pulmonary alveolar macrophages resulting in PAP (protein alveolar proteinosis)	Sup. 1
LY86	GC06P006588	33	Associated with prognosis in lung adenocarcinoma. Interacts with the Toll-like receptor and mediate the immune response to bacterial LPS (lipopolysaccharide).	Sup. 2
PLEK	GC02P068365	33	Block neoplastic transformation. Low expression was associated with poor survival rates in lung cancer patients.	Sup. 3
HLA-DPA1	GC06M033064	33	Mainly expressed on tumor-infiltrating macrophages and DCs which was related to a better prognosis. And contribute to the human breast cancer lung metastasis	Sup. 4
HLA-DQB1	GC06M032660	33	Promote activation of the IgA+ B lymphocyte, present antigenic peptides to T lymphocyte, and elicit immune response trough cytotoxic cell	50

Figure S2 PPI network of 44 DEGs

A. 7 clinically applied immune checkpoint inhibitors target genes (red circles) and 36 selected prognostic genes (green circles) from TCGA have complicate interactions in the PPI network analysis.

B. Top 10 potential immunotherapy target genes and brief function introductions.