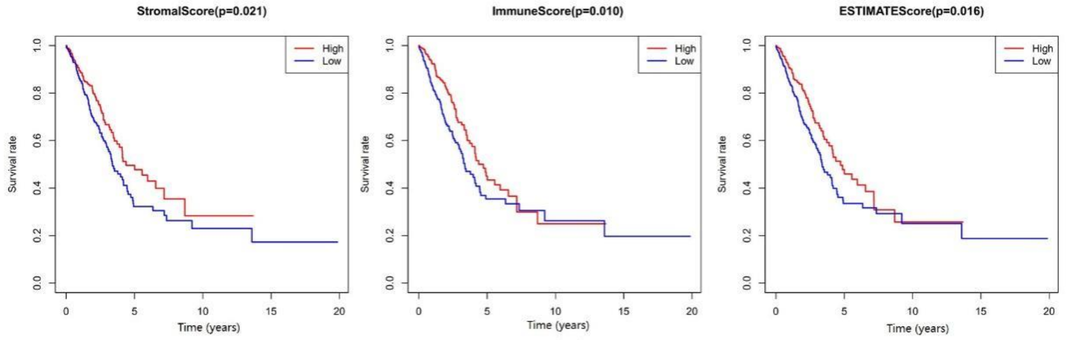
Supplementary figures



StromalScore(p=0.021)

ImmuneScore(p=0.010)

ESTIMATEScore(p=0.016)

Figure S1. **Association of stromal/immune/ESTIMATE scores with overall survival.** Elevated stromal/immune/ESTIMATE scores were associated with better overall survival in lung adenocarcinoma.

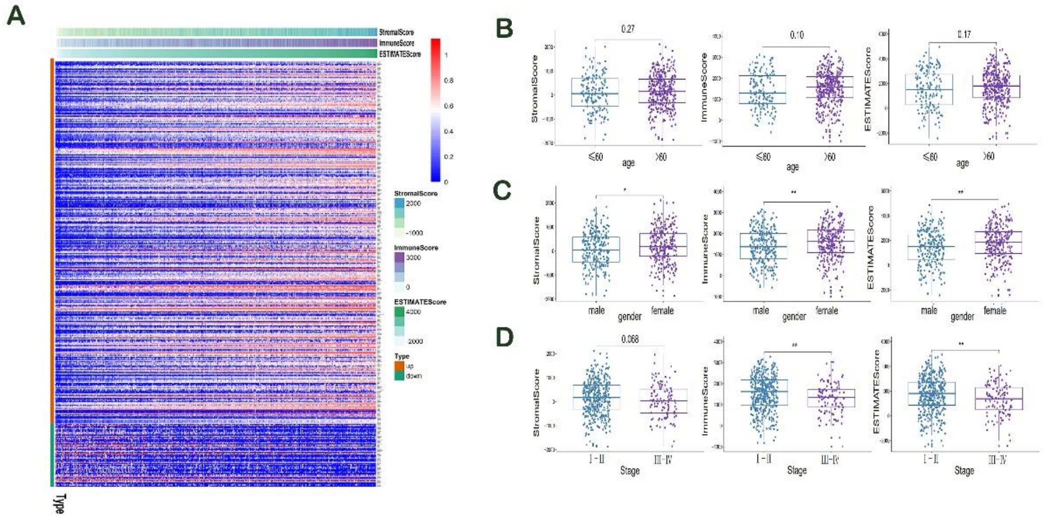


Figure S2. **Distribution of genetic characteristics and the clinicopathological parameters in LUAD patients with low- to high- ESTIMATE algorithm scores.** (**A**) The heatmap shows the expression pattern of stromal scores, immune scores, ESTIMATE scores and 396 overlapping genes. Samples ranked in ascending order by ESTIMATE scores. **(B)** No difference was found between patients over 60 years old and those less than 60 years old. **(C)** Female patients had higher stromal/immune/ESTIMATE scores. **(D)** Tumor stage was negatively associated with immune/ESTIMATE scores. LUAD, lung adenocarcinoma; **P*<0.05, ***P*<0.01, ****P*<0.001

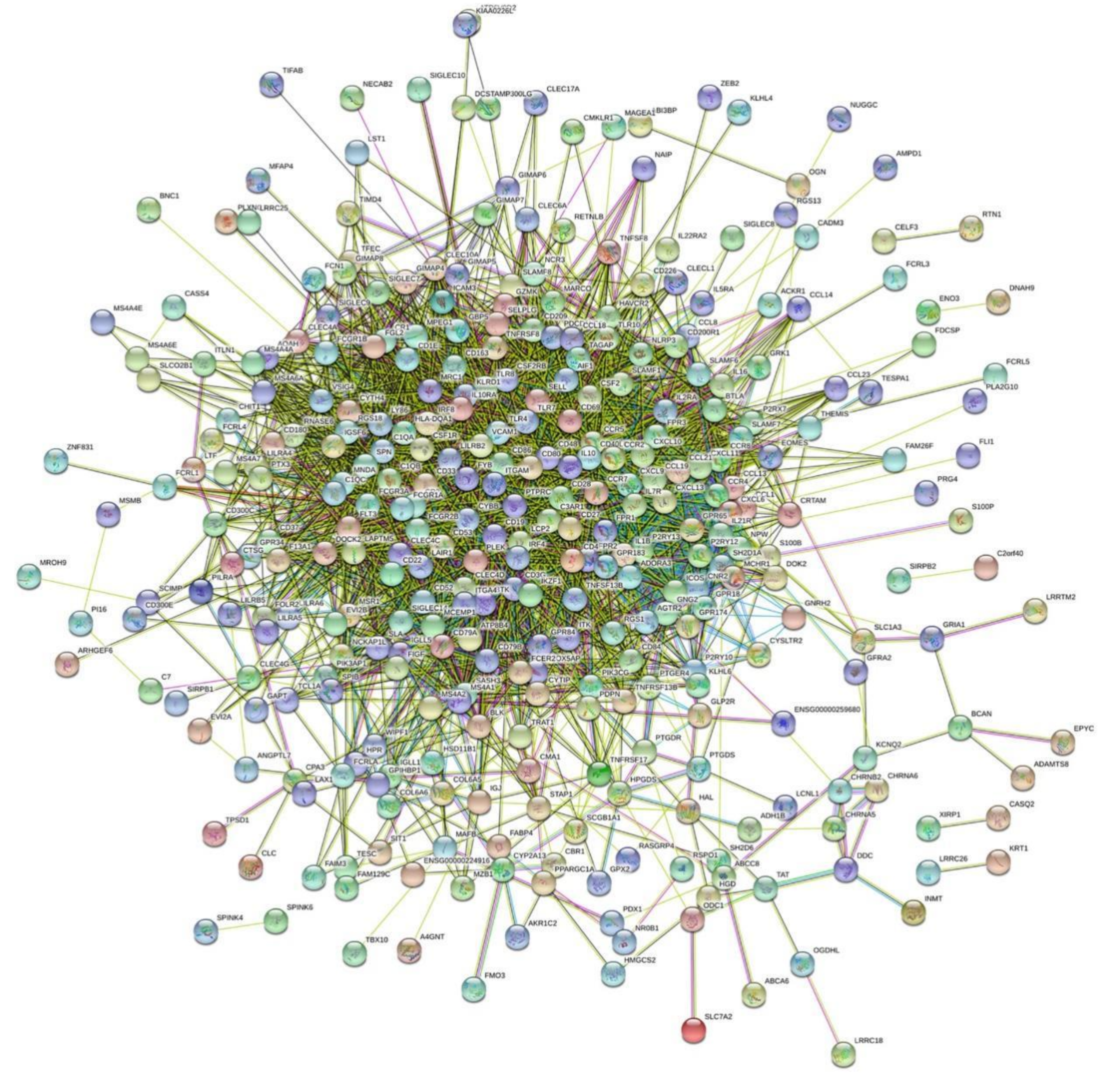


Figure S3. **PPI analysis of 396 genes based on STRING online tool (https://string-db.org/).** PPI, protein protein interaction; STRING, Search Tool for the Retrieval of Interacting Genes.

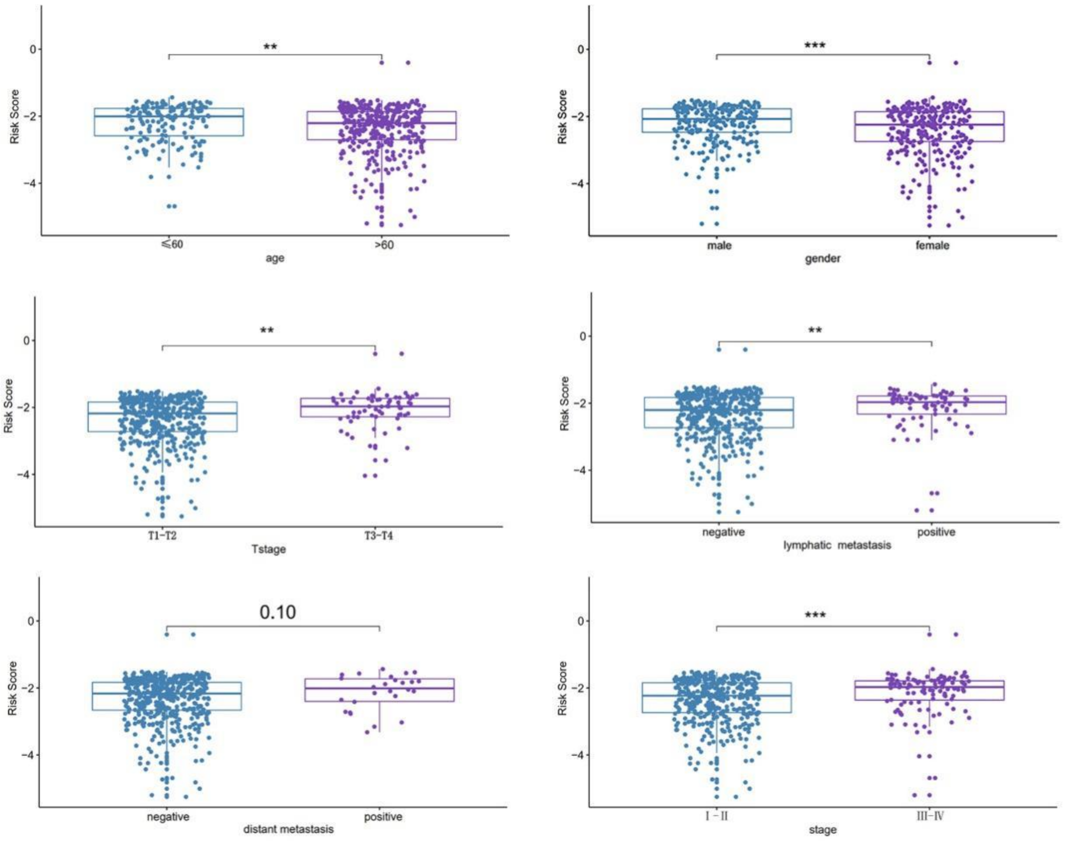


Figure S4. **Association with generated signature and clinicopathological characteristics.** *P<0.05, **P<0.01, ***P<0.001

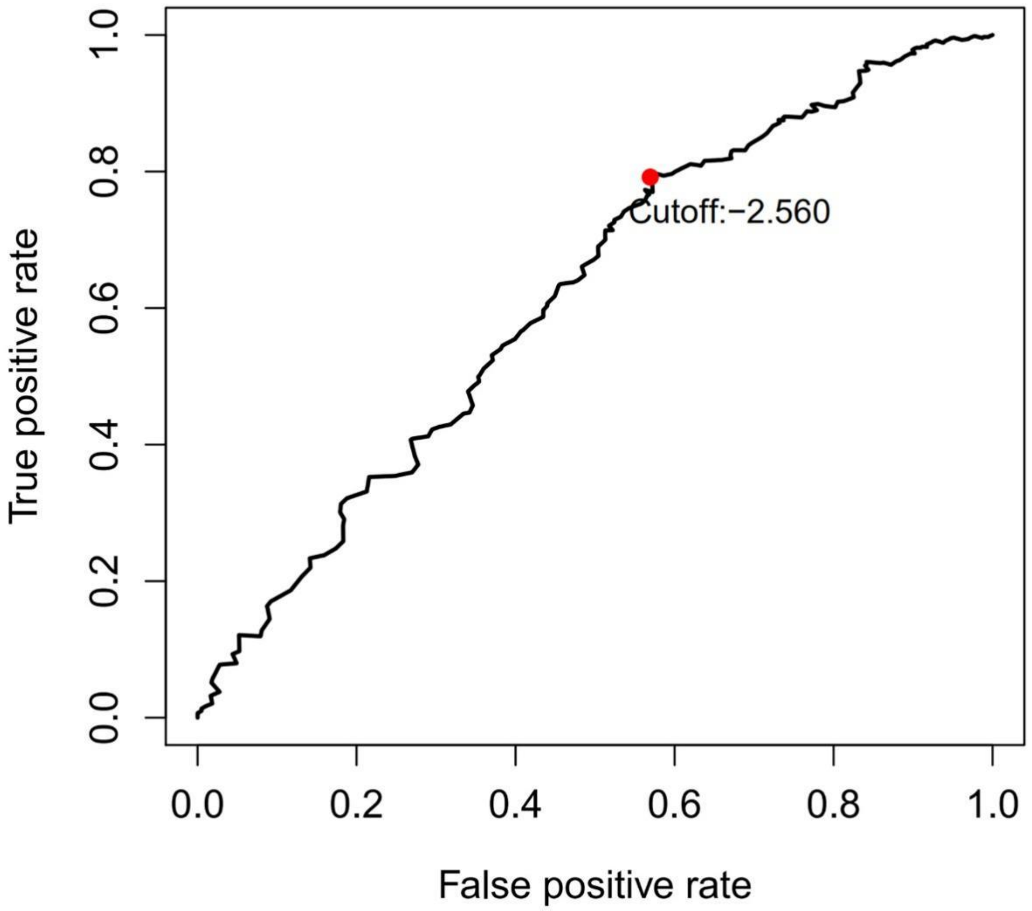


Figure S5. **Identification of the optimal cut-off point for "risk score" via ROC curves.** ROC, Receiver operating characteristic.

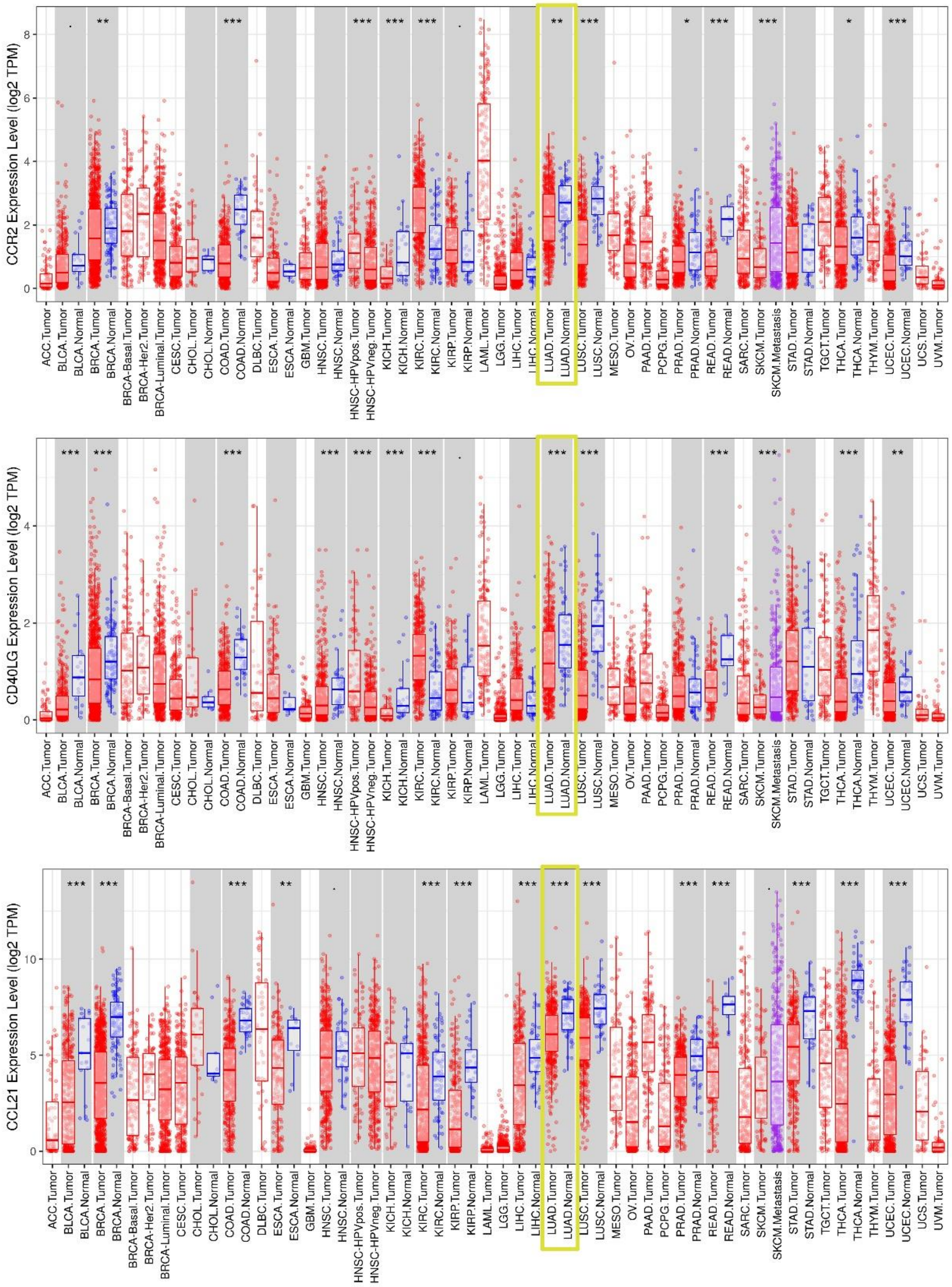


Figure S6. **Human *CCR2*, *CD40LG*, *CCL21* expression levels in different tumor types from TCGA database were determined by TIMER platform (https://cistrome.shinyapps.io/timer/).** TCGA, The Cancer Genome Atlas; TIMER, Tumor Immune Estimation Resource. *P < 0.05, **P <0.01, ***P < 0.001

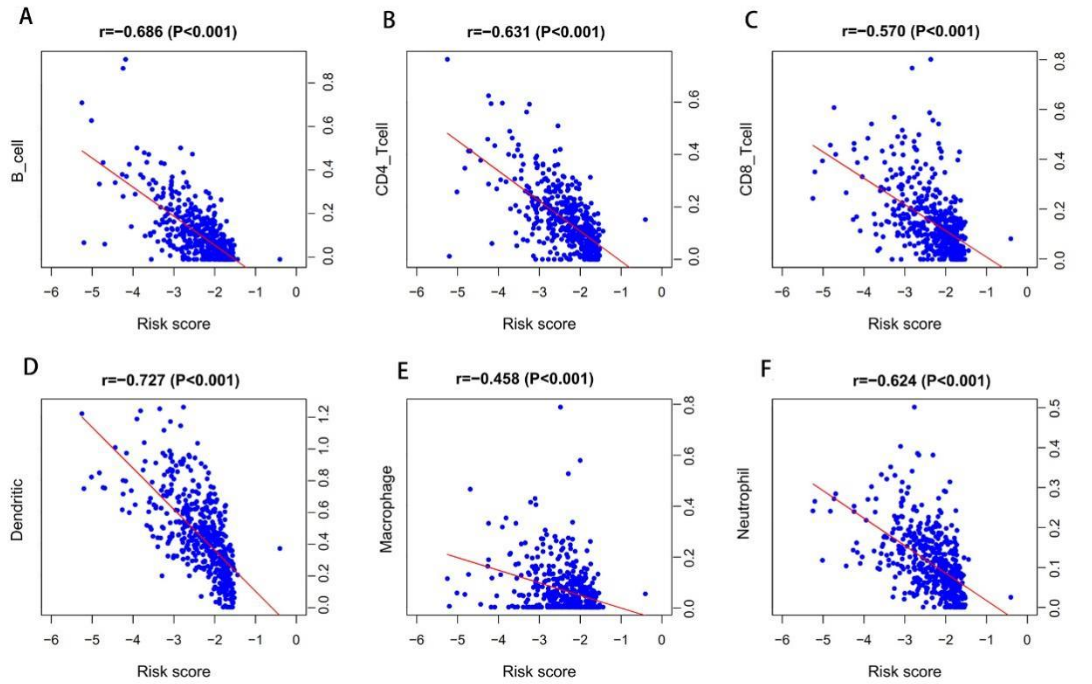


Figure S7. **Correlation analysis between "risk score" and immune cell infiltration.** (**A**) B cells; (**B**) CD4+ T cells; (**C**) CD8+ T cells; (**D**) Dendritic cells; (**E**) Macrophages; (F) Neutrophils.