A. Flowchart:

483 LUAD patients with RNA-seq and clinical data from TCGA

Differential expression analysis
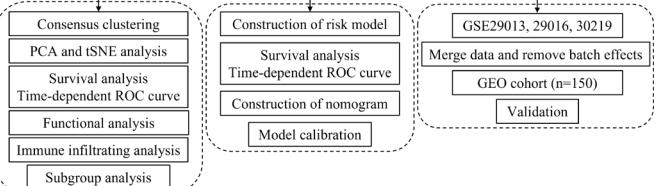$P < 0.05$, $|\log_2 FC| > 1.5$

99 DEGs between LUAD and Adjacent Tissue
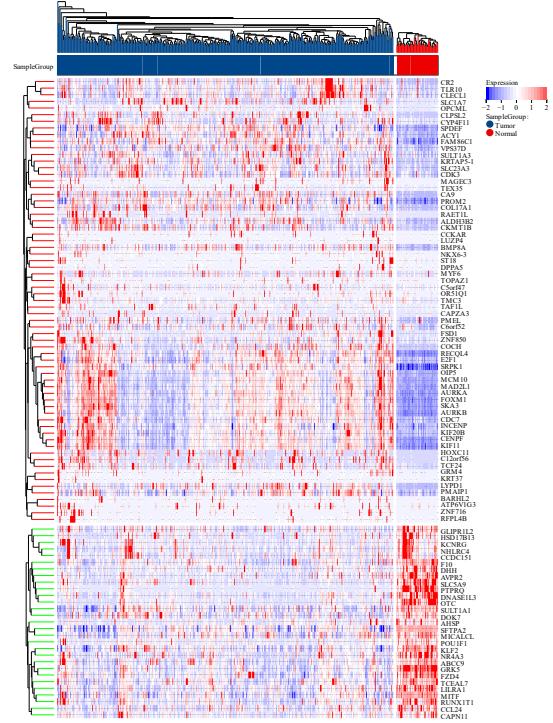
Univariate Cox regression analysis
$P < 0.05$

26 DEGs correlated with OS

LASSO regression analysis
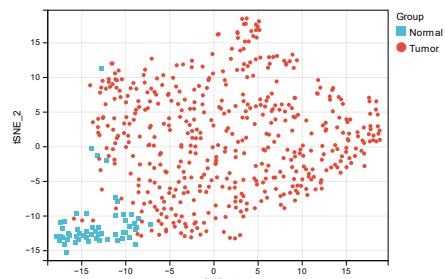Optimal score threshold = 0.057
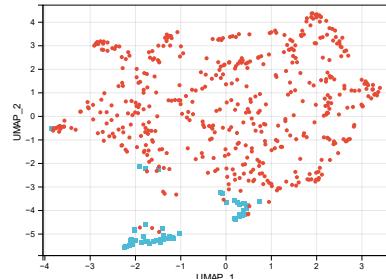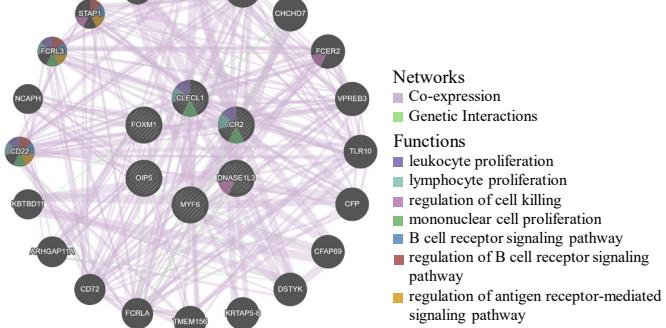
6 DEGs with the greatest prognostic value

Consensus clustering
PCA and tSNE analysis
Survival analysis
Time-dependent ROC curve
Functional analysis
Immune infiltrating analysis
Subgroup analysis

Construction of risk model
Survival analysis
Time-dependent ROC curve
Construction of nomogram
Model calibration

GSE29013, 29016, 30219
Merge data and remove batch effects
GEO cohort (n=150)
Validation

B, C, D, E panels as shown.