

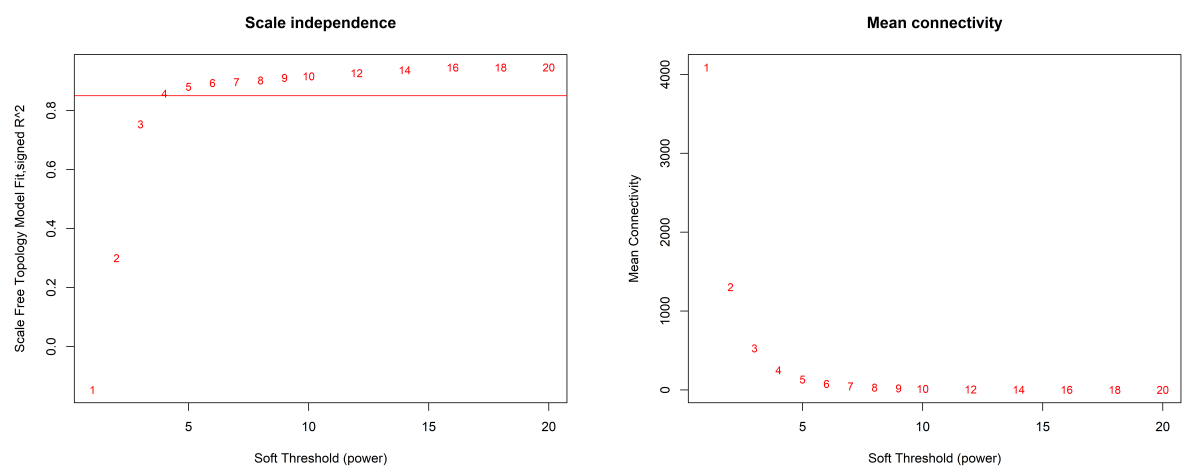
Supplementary

Number of figures and tables: 2 figures and 1 table

- **Table S1:** The top 30 significant genes within the PPI network.
- **Figure S1:** Soft threshold screening of the GSE27262 dataset for lung adenocarcinoma involves: (a) selecting the soft threshold based on the analysis of scale independence; (b) evaluating mean connectivity.
- **Figure S2:** Enrichment analysis of the selected 30 genes includes: (a) Results of the GO enrichment analysis, categorized into Biological Processes (BP), Cellular Components (CC), and Molecular Functions (MF). The length of the bars indicates the number of involved genes, while the intensity of the color reflects the significance of the adjusted p-values. (b) Outcomes of the KEGG enrichment analysis, where each dot represents a specific biological pathway. The color of the dot indicates the significance of the adjusted p-value, and its size denotes the proportion of associated genes.

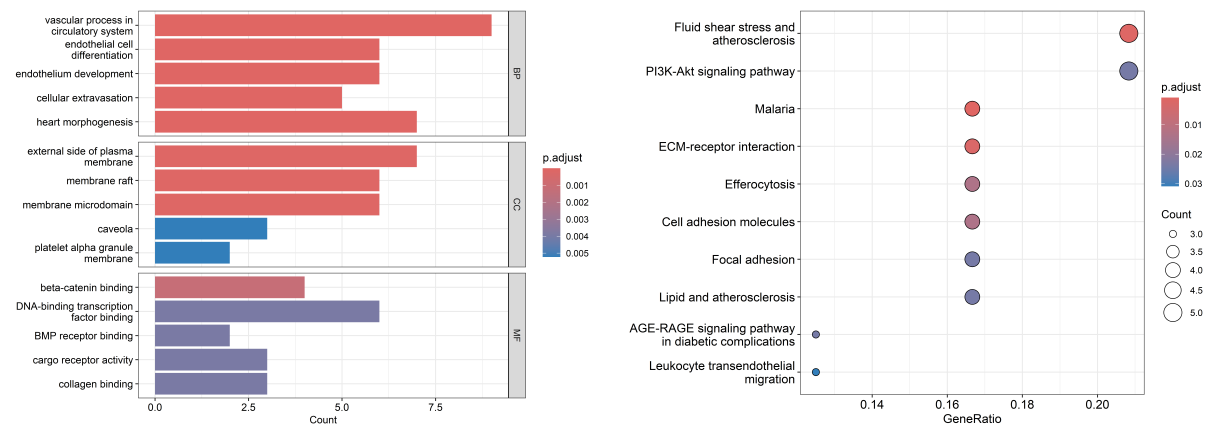
Table S1. The top 30 significant genes within the PPI network.

No.	Gene Name	Entry	Entry Name	Protein names
1	PECAM1	P16284	PECAM1_HUMAN	Platelet endothelial cell adhesion molecule
2	CDH5	P33151	CADH5_HUMAN	Cadherin-5
3	VWF	P04275	VWF_HUMAN	von Willebrand factor
4	TEK	Q02763	TIE2_HUMAN	Angiopoietin-1 receptor
5	CLDN5	O00501	CLD5_HUMAN	Claudin-5
6	EMCN	Q9ULC0	MUCEN_HUMAN	Endomucin
7	LYVE1	Q9Y5Y7	LYVE1_HUMAN	Lymphatic vessel endothelial hyaluronic acid receptor 1
8	CLEC14A	Q86T13	CLC14_HUMAN	C-type lectin domain family 14 member A
9	THBD	P07204	TRBM_HUMAN	Thrombomodulin
10	CD36	P16671	CD36_HUMAN	Platelet glycoprotein 4
11	SELE	P16581	LYAM2_HUMAN	E-selectin
12	CD93	Q9NPY3	C1QR1_HUMAN	Complement component C1q receptor
13	CAV1	Q03135	CAV1_HUMAN	Caveolin-1
14	EPAS1	Q99814	EPAS1_HUMAN	Endothelial PAS domain-containing protein 1
15	ITGA1	P56199	ITA11_HUMAN	Integrin alpha-11
16	SOX17	Q9H6I2	SOX17_HUMAN	Transcription factor SOX-17
17	KLF4	O43474	KLF4_HUMAN	Krueppel-like factor 4
18	MMRN2	Q9H8L6	MMRN2_HUMAN	Multimerin-2
19	SOX9	P48436	SOX9_HUMAN	Transcription factor SOX-9
20	BDNF	P23560	BDNF_HUMAN	Brain-derived neurotrophic factor
21	BMP2	P12643	BMP2_HUMAN	Bone morphogenetic protein 2
22	AGER	Q15109	RAGE_HUMAN	Advanced glycosylation end product-specific receptor
23	CDKN2A	P42771	ARF_HUMAN	Tumor suppressor ARF
24	S1PR1	P21453	S1PR1_HUMAN	Sphingosine 1-phosphate receptor 1
25	MMP1	P03956	MMP1_HUMAN	Interstitial collagenase
26	EDNRB	P24530	EDNRB_HUMAN	Endothelin receptor type B
27	COMP	P49747	COMP_HUMAN	Cartilage oligomeric matrix protein
28	ECSCR	Q19T08	ECSCR_HUMAN	Endothelial cell-specific chemotaxis regulator
29	TBX3	O15119	TBX3_HUMAN	T-box transcription factor TBX3
30	RASIP1	Q5U651	RAIN_HUMAN	Ras-interacting protein 1



(a) Selection of Soft Threshold: Illustrates the determination of the soft threshold based on scale independence analysis. (b) Depicts the assessment of mean connectivity within the dataset.

Fig. S1. Soft threshold screening of the GSE27262 dataset for lung adenocarcinoma involves.



(a) GO Analysis: Bar graph showing gene counts across Biological Processes (BP), Cellular Components (CC), and Molecular Functions (MF), with color intensity indicating significance levels of adjusted p-values. (b) KEGG Analysis: Scatter plot representing pathways affected by the genes, where dot color and size reflect p-value significance and gene proportion, respectively.

Fig. S2. The figure displays the enrichment analysis of the top 30 genes identified in the PPI network using the MCC algorithm: Panel (a) presents the results of the GO enrichment analysis, while Panel (b) shows the results of the KEGG pathway enrichment analysis.