

Figure S1. Subgroup analysis in the training set and validation set. Kaplan–Meier survival for the OS in subgroups stratified by **A.** T 1, 2, **B.** T 3, 4, **C.** stage I, II, **D.** stage III IV, **E.** N 0, 1, **F.** N 2, 3, **G.** Age  $\leq 60$  and **H.** Age  $> 60$  in the training set, and **I.** Age  $< 60$ , **J.** Age  $> 60$ , **K.** Female and **L.** Male in the validation set.

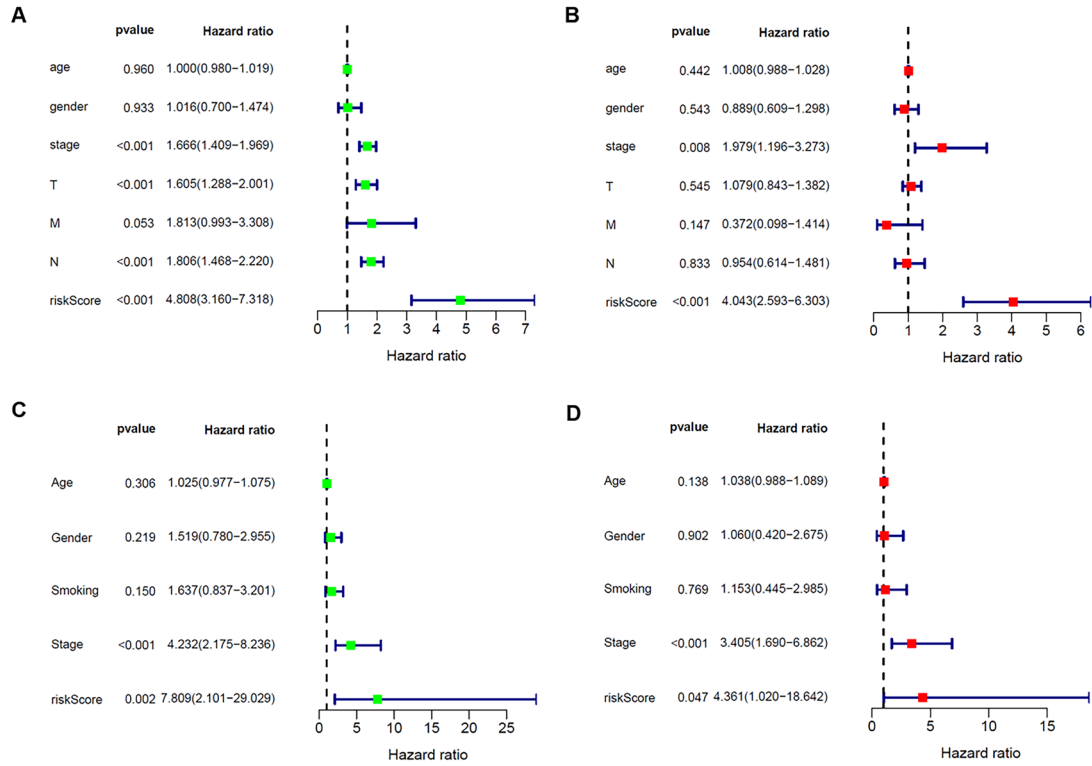
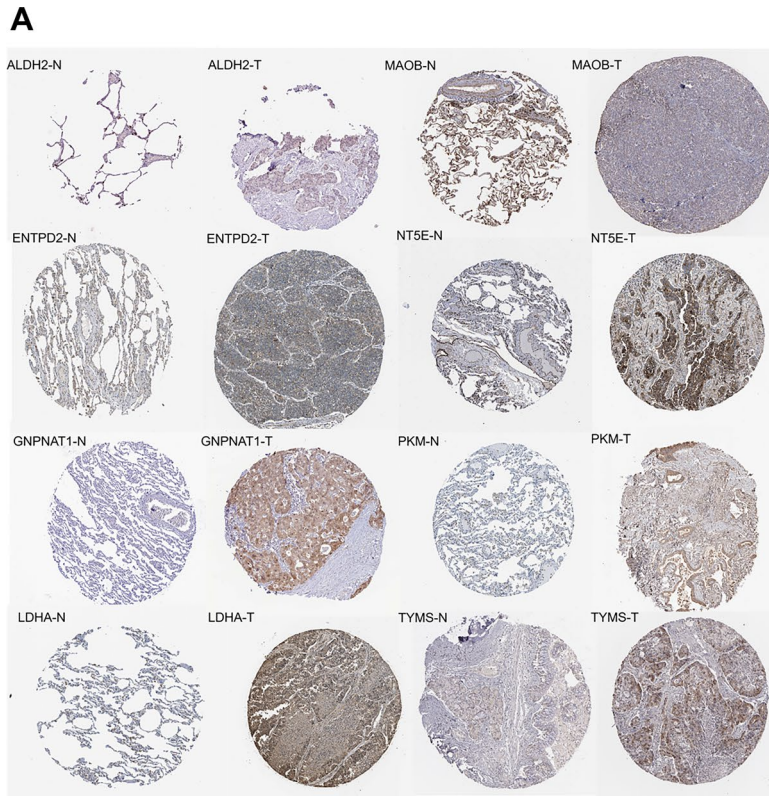


Figure S2. Independent prognostic analysis. **A.** Univariate and **B.** Multivariate COX regression analysis of LUAD in the training set. **C.** Univariate and **D.** Multivariate COX regression analysis of LUAD in the validation set.



**B**

Analysis Type by Cancer	Cancer vs. Normal														
	TYMS	ALDH2	PKM	GNPNAT1	LDHA	ENTPD2	NT5E	MAOB							
Bladder Cancer	4		4	2		1		4							
Brain and CNS Cancer	2	1	1		1		2								
Breast Cancer	12		11	3	1	2		6							
Cervical Cancer	3			1				3							
Colorectal Cancer	2		5	4		1	1	10							
Esophageal Cancer	2		1	1	2		2	1							
Gastric Cancer	2		1		2										
Head and Neck Cancer	1		1		1		3	6							
Kidney Cancer	4		3	8	1	9	2	2							
Leukemia	1	3	17	3		4	3								
Liver Cancer	3		3	3											
Lung Cancer	10		10	3		2	2	11							
Lymphoma	3	2	1	1	5		2								
Melanoma	2		1	1			2	2							
Myeloma					2										
Other Cancer	3	2	1	1	1		1	1							
Ovarian Cancer	1		2	4	1		2	8							
Pancreatic Cancer	1	1		3	2										
Prostate Cancer			1		1		1	3							
Sarcoma	11		7	4			1	8							
Significant Unique Analyses	66	7	3	62	39	5	12	1	28	5	1	13	14	1	64
Total Unique Analyses	458		419		410		305		461		383		445		409

Figure S3. Validation of the metabolic-related genes. **A.** Immunohistochemistry of the metabolism-related genes based on the Human Protein Atlas. The mRNA expression patterns of metabolism-related genes in overall cancers. **B.** The differences in mRNA expression between tumors and normal tissues were analyzed by the OncoPrint database.

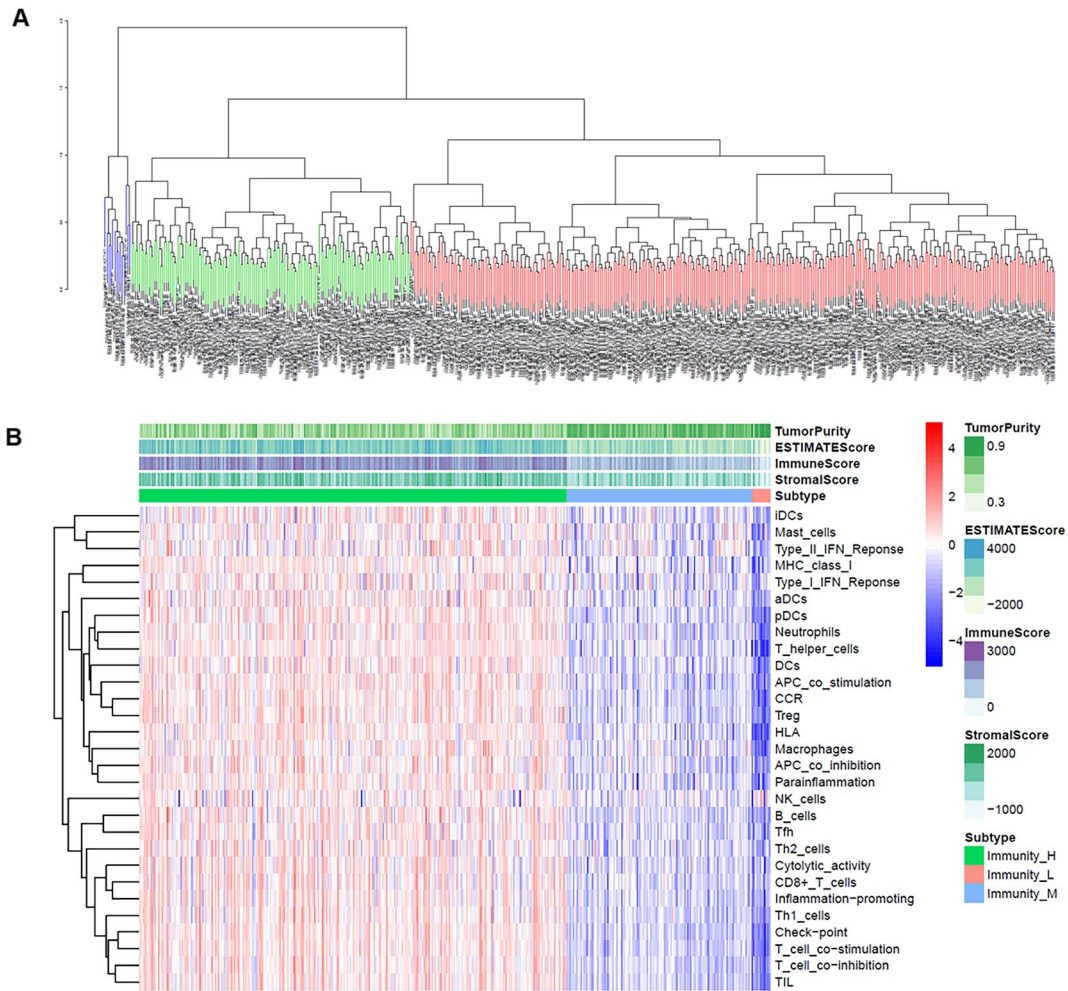


Figure S4. Single-sample Gene Set Enrichment Analysis (ssGSEA). **A.** Hierarchical clustering of LUAD based on the enrichment scores. **B.** Heatmap showing the correlation of transcriptome expression with diverse immune cell types, functions, and pathways.

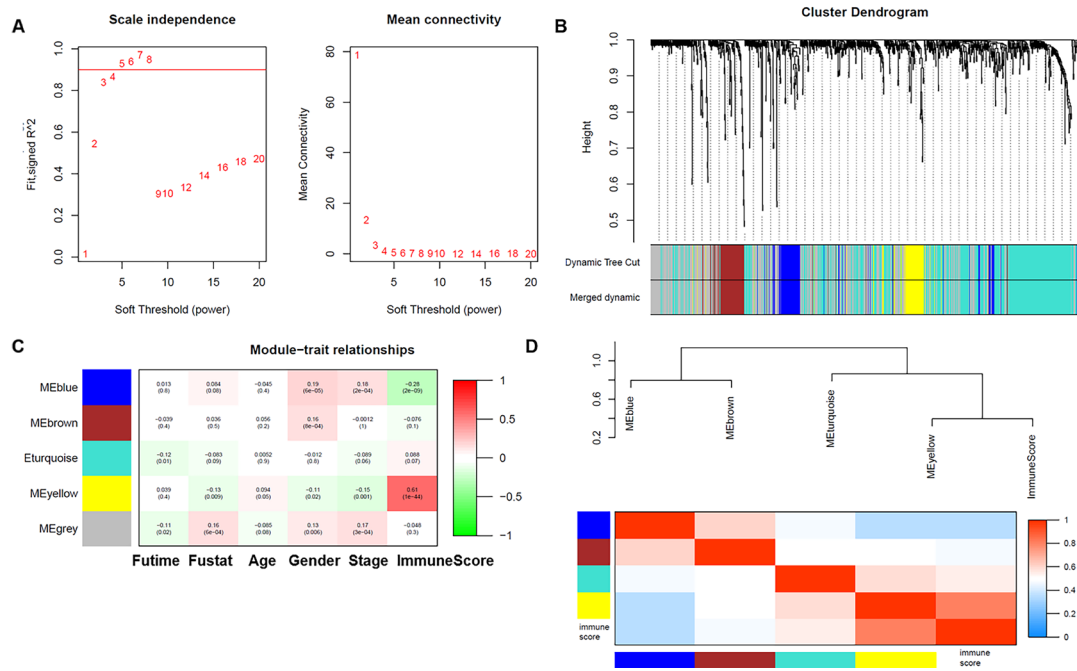


Figure S5. WGCNA analysis. **A.** Analysis of the scale-free fit index for various soft-thresholding powers ( $\beta$ ) and the mean connectivity for various soft-thresholding powers. Clustering dendrograms of metabolic-related genes. **B.** Each piece of the leaves on the cluster dendrogram corresponds to a gene. **C.** Correlation between the module eigengenes and clinical traits of lung adenocarcinoma. **D.** Hierarchical clustering and heatmap of the gene module.