**Supplementary Table 1:** Clinicopathological parameters of 522 LUAD patients from TCGA.

|  |  |  |
| --- | --- | --- |
| **Characteristics** | **Number of cases** | **%** |
| Age (years) |  |  |
| <65 | 223 | 42.7 |
| ≥65 | 180 | 53.6 |
| NR | 19 | 3.6 |
| Gender |  |  |
| Female | 280 | 53.6 |
| Male | 242 | 46.4 |
| T stage |  |  |
| T1 | 172 | 33.0 |
| T2 | 281 | 53.8 |
| T3 | 47 | 9.0 |
| T4 | 19 | 3.6 |
| TX | 3 | 0.6 |
| N stage |  |  |
| N0 | 335 | 64.2 |
| N1 | 98 | 18.8 |
| N2 | 75 | 14.4 |
| N3 | 2 | 0.4 |
| NX | 11 | 2.0 |
| NR | 1 | 0.2 |
| M stage |  |  |
| M0 | 353 | 67.6 |
| M1 | 25 | 4.8 |
| MX | 140 | 26.8 |
| NR | 4 | 0.8 |
| TNM stage |  |  |
| I | 279 | 53.4 |
| II | 124 | 23.8 |
| III | 85 | 16.3 |
| IV | 26 | 4.9 |
| NR | 8 | 1.5 |

MX: M stage not recognized; NR: Not reported; NX: N stage not recognized; TX: T stage not recognized.

**Supplementary Figure 1:** Identification of DEGs based on immune and stromal scores. **(A)** Heatmap of the DEGs associated with immune scores based on the median immune score. Genes with higher expression are shown in red, and genes with lower expression are shown in green. **(B)** Heatmap of the DEGs associated with stromal scores based on the median stromal score. **(C, D)** Venn plot showing the number of commonly upregulated or downregulated DEGs in immune and stromal score groups. **(E, F)** GO terms and KEGG enrichment analysis of common DEGs revealed significant BP, CC, MF, and pathways. BP: Biological processes; CC: Cellular component; DEGs: Differentially expressed genes; GO: Gene ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes; MF: Molecular function.

Figure S1.tif

**Supplementary Figure 2:** Correlation between the expression of individual DEGs and LUAD patients overall survival in the TCGA database. **(A–H)** K–M survival curves of representative genes showed that the high (red) expression of these genes was significantly related to a better prognosis. **(A)** ABI3BP, **(B)** BLK, **(C)** CCL14, **(D)** CSF2RB, **(E)** JAML, **(F)** LILRA6, **(G)** LY86, and **(H)** SLAMF1. DEGs: Differentially expressed genes; K–M: Kaplan–Meier; LUAD: lung adenocarcinoma; TCGA: The Cancer Genome Atlas.

Figure S2.tif

**Supplementary Figure S3:** GO terms and KEGG pathway analysis of DEGs with prognostic value. DEGs: Differentially expressed genes; GO: Gene ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes.

Figure S3.tif

**Supplementary Figure 4:** Verification of DEGs with prognostic value in the GEO database. Kaplan–Meier survival curves of **(A)** ABI3BP, **(B)** ATP6V0D2, **(C)** CSF2RB, **(D)** KBTBD8, **(E)** PKHD1L1, and **(F)** SCML4. DEGs: Differentially expressed genes; K–M: Kaplan–Meier; GEO: Gene Expression Omnibus.

Figure S4.tif

**Supplementary Figure S5:** GSEA centered on CSF2RB. **(A–E)** Five pathways are most significantly related to CSF2RB. **(A)** TCR pathway, **(B)** IL2RB pathway, **(C)** FCER1 pathway, **(D)** FMLP pathway, and **(E)** CTCF pathway. GSEA: gene set enrichment analysis.

Figure S5.tif

**Supplementary Figure 6:** GSEA centered on PKHD1L1. **(A–E)** Five pathways are most significantly related to PKHD1L1. **(A)** TOB1 pathway, **(B)** CTLA4 pathway, **(C)** GH pathway, **(D)** IL7 pathway, and **(E)** FCER1 pathway. GSEA: gene set enrichment analysis.

Figure S6.tif

**Supplementary Figure S7:** GSEA centered on KBTBD8. **(A–E)** Five pathways are most significantly related to KBTBD8. **(A)** CTLA4 pathway, **(B)** NO2IL12 pathway, **(C)** NKT pathway, **(D)** IL12 pathway, and **(E)** TH1TH2 pathway. GSEA: gene set enrichment analysis.

Figure S7.tif

**Supplementary Figure 8:** GSEA centered on ABI3BP. **(A–E)** Five pathways are most significantly related to ABI3BP. **(A)** CTLA4 pathway, **(B)** NO2IL12 pathway, **(C)** IL12 pathway, **(D)** NKT pathway, and **(E)** TH1TH2 pathway. GSEA: gene set enrichment analysis.

Figure S8.tif

**Supplementary Figure 9:** GSEA centered on SCML4. **(A–E)** Five pathways are most significantly related to SCML4. **(A)** IL12 pathway, **(B)** NO2IL12 pathway, **(C)** CTLA4 pathway, **(D)** TH1TH2 pathway, and **(E)** NKT pathway. GSEA: gene set enrichment analysis.

Figure S9.tif