Supplementary

Table S1 Patient cohort used in this study

| Cohort | Number patients | NSCLC type | Source |
| :--- | :---: | :---: | :---: |
| E-MTAB-6149 | 5 | - | PMID: 29988129 |
| WCH | 44 | - | PMID: 35027529 |
| GSE154826 | 27 | LUAD used | PMID: 34767762 |
| GSE179994 | 8 | LUAD used | PMID: 35121991 |
| Bulk LUAD | 320 | LUAD used |  |
| TCGA-LUAD | 47 | LUAD used | PMID: 25079552 |
| SU2C-MARK |  |  | PMID: 37024582 |
| Others | 36 | - | PMID: 32381040 |
| GSE111907 | Variable | - | PMID: 34963056 |
| GSE184398 | - | PMID: 31242643 |  |
| Meta-12 cohorts |  |  |  |

NSCLC, non-small cell lung cancer; WCH, west China hospital; LUAD, lung adenocarcinoma; TCGA, The Cancer Genome Atlas; SU2CMARK, Stand Up to Cancer-Mark Foundation.


Figure S1 EPSTI1-related immunomodulators at TISIDB website. Pan-cancer based spearman correlation between EPSTII RNA expression and (A) immunoinhibitor, (B) immunostimulator, and (C) major histocompatibility complex molecule. The X-axis is the type of cancer and the Y-axis is the RNA expression of the immune signature. TISIDB, Tumor-Immune System Interactions and Drug Bank.


Figure S2 RNA expression of three-gene at GEPIA2 website. (A-C) RNA expression of CXCL13, EPSTI1, and CDK1 in TCGA and GTEx projects. Red represents cancer, while blue represents normal tissue. The horizontal axis is cancer type and the vertical axis is the expression in the form of TPM. TPM, transcripts per million; GEPIA2, Gene Expression Profiling Interactive Analysis; TCGA, The Cancer Genome Atlas; GTEx, genotype-tissue expression.


Figure S3 Three-gene quantified by the ssgsea method at GSE184398 cohort. (A-C) Box plot showing single sample score measured by CXCL13, EPSTI1, and CDK1 in the GSE 184398 cohort with $\mathrm{CD}^{+}$, $\mathrm{HLA}^{2} \mathrm{DR}^{+}$, and CD25 ${ }^{+} \mathrm{CD}^{+}$FACS. FACS, fluorescence-activated cell sorting.


Figure S4 Overlap of CXCL13 ${ }^{+}$EPSTI1 ${ }^{+}$CDK1 ${ }^{+}$subpopulation in four NSCLC cohorts. (A-D) Pie chart depicting the proportion of CXCL13 ${ }^{+}$EPSTI1 $^{+}$CDK1 ${ }^{+}$subpopulation belongs to the author-defined cell types in West China Hospital, E-MTAB-6149 T cells, GSE154826, and GSE179994 cohorts. In particular, GSE154826 and GSE179994 only included patients with LUAD. LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; NSCLC, non-small cell lung cancer.


Figure S5 Antibody information of three-gene at HPA website. (A) Protein levels and sublocalization of CXCL13 and EPSTI1 in the LUAD patient ID: 3003 at HPA website (https://www.proteinatlas.org/). (B) Quantification of anti-CXCL13 (HPA052613), antiEPSTI1 (HPA017362), and anti-CDK1 (CAB003799) in normal alveolar and macrophage cells. HPA, Human Protein Atlas; LUAD, lung adenocarcinoma.

Table S2 Cell count of CXCL13 ${ }^{+}$EPSTI1 $^{+} \mathrm{CDK1}^{+}$subpopulation in GSE179994

| CD8 ${ }^{+}$T cells |  | Total T cells |  |  |
| :---: | :---: | :---: | :---: | :---: |
| Sample | Cell_sum | Sample | Cell_sum | Timepoint |
| P1.post. 1 | 5 | P1.post. 1 | 29 | Post |
| P1.post. 2 | 8 | P1.post. 2 | 22 | Post |
| P1.post. 3 | 13 | P1.post. 3 | 27 | Post |
| P1.pre | 15 | P1.pre | 45 | Pre |
| P10.post. 1 | 3 | P10.post. 1 | 4 | Post |
| P10.pre | 61 | P10.pre | 81 | Pre |
| P13.post. 1 | 14 | P13.post. 1 | 80 | Post |
| P13.post. 2 | 4 | P13.post. 2 | 37 | Post |
| P19.pre | 210 | P13.pre | 1 | Pre |
| P29.post. 1 | 3 | P19.post. 1 | 3 | Post |
| P29.pre | 1 | P19.pre | 291 | Pre |
| P30.post. 1 | 5 | P29.post. 1 | 8 | Post |
| P30.pre | 26 | P29.pre | 5 | Pre |
| P33.post. 1 | 6 | P30.post. 1 | 16 | Post |
| P33.pre | 1 | P30.pre | 41 | Pre |
| P35.pre | 20 | P33.post. 1 | 18 | Post |
|  |  | P33.pre | 3 | Pre |
|  |  | P35.post. 1 | 0 | Post |
|  |  | P35.pre | 35 | Pre |

