

Figure S1 The mRNA level of PD-L1 and PD-1 based on the GEO database. (A,B,C,D) PD-L1 mRNA level of ADC and SCC in GEO database. (E,F,G,H) PD-1 mRNA level of ADC and SCC in GEO database. SCC, squamous cell carcinoma; ADC, lung adenocarcinoma. *, P<0.05.

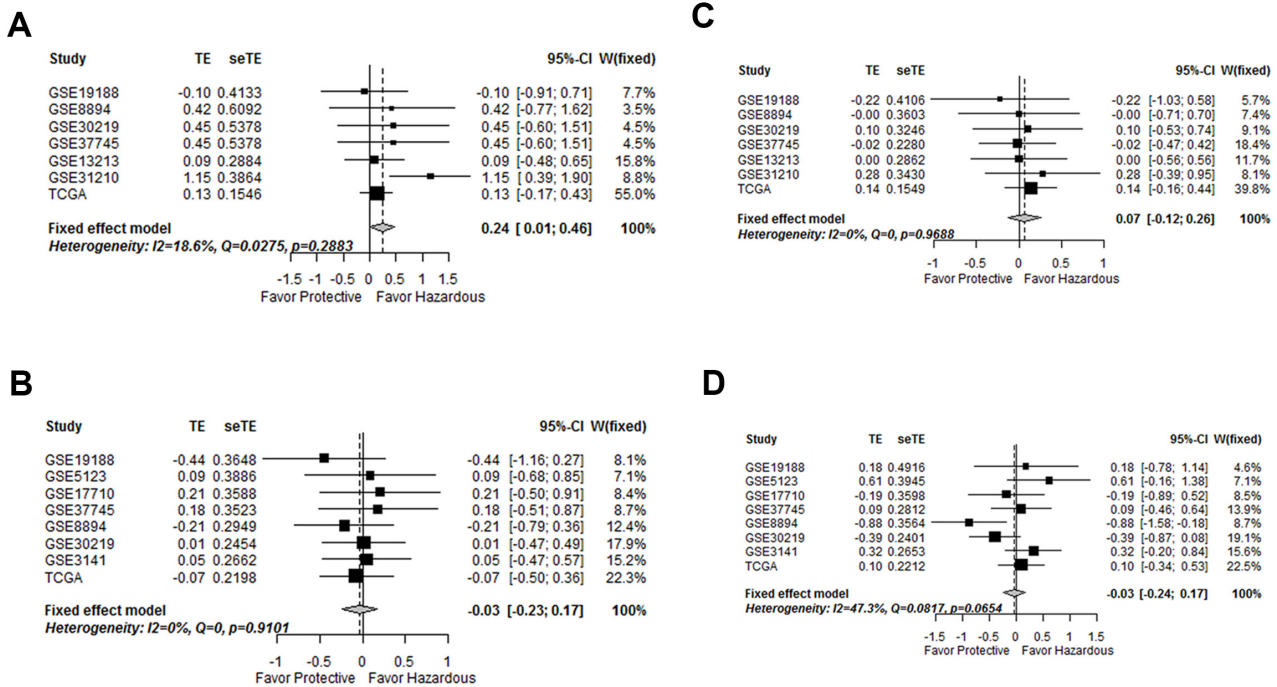


Figure S2 Meta-analysis of OS against PD-L1 and PD-1 levels. HR plot of OS against PD-L1 levels in ADC patients (A) and SCC patients (B). HR plot of OS against PD-1 levels in ADC patients (C) and SCC patients (D). OS, overall survival; HR, hazard ratio; SCC, squamous cell carcinoma; ADC, lung adenocarcinoma.

Table S1 Baseline characteristics of two cohorts

Characteristics	Cohort No.1 (N=118) %				Cohort No.2 (N=144) %			
	Total (N=118), N (%)	ADC (N=70), N (%)	SCC (N=48), N (%)	P	Total (N=144), N (%)	ADC (N=98), N (%)	SCC (N=64), N (%)	P
Age median (range)	59 (30-75)	58 (35-74)	60 (41-75)	0.708	59 (34-75)	58 (34-75)	60 (43-75)	0.213
<60	60 (50.8)	37 (61.7)	23 (38.3)		80 (55.6)	58 (72.5)	22 (27.5)	
≥60	58 (49.2)	33 (59.3)	25 (40.7)		64 (44.4)	40 (62.5)	24 (37.5)	
Gender				<0.001				<0.001
Male	76 (64.4)	33 (43.4)	43 (56.6)		82 (56.9)	41 (50.0)	41 (50.0)	
Female	42 (35.6)	37 (88.1)	5 (11.9)		62 (43.1)	57 (91.9)	5 (8.1)	
Smoking status				0.001				<0.001
Never-smoker	60 (50.8)	45 (75.0)	15 (25.0)		79 (54.9)	70 (88.6)	9 (11.4)	
Ever-smoker	58 (49.2)	25 (43.1)	33 (56.9)		65 (45.1)	28 (43.1)	37 (56.9)	
Tumor differentiation				0.008				0.008
Well	46 (39.0)	35 (76.1)	11 (23.9)		41 (28.5)	33 (80.5)	8 (19.5)	
Moderate-poor	72 (61.0)	36 (50.0)	36 (50.0)		74 (51.4)	41 (55.4)	33 (44.6)	
Unknown	0 (0)	0	0		29 (20.1)	24 (82.8)	5 (17.2)	
pT stage				0.038				<0.001
T1+2	93 (78.8)	60 (64.5)	33 (35.5)		41 (28.5)	37 (90.2)	4 (9.8)	
T3+4	25 (21.2)	10 (40.0)	15 (60.0)		103 (71.5)	61 (59.2)	42 (40.8)	
Lymphatic invasion				0.708				0.028
Negative	60 (50.8)	37 (61.7)	23 (38.3)		57 (39.6)	45 (78.9)	12 (21.1)	
Positive	58 (49.2)	33 (56.9)	25 (43.1)		87 (60.4)	53 (60.9)	34 (39.1)	
pTNM stage				0.053				0.072
I stage	48 (40.7)	34 (70.8)	14 (29.2)		47 (32.6)	38 (80.9)	9 (19.1)	
II stage	28 (23.7)	12 (42.9)	16 (57.1)		47 (32.6)	29 (61.7)	18 (38.3)	
III stage	42 (35.6)	24 (57.1)	18 (42.9)		50 (34.7)	31 (62.0)	19 (38.0)	
EGFR status				<0.001				<0.001
Mutant	51 (43.2)	47 (92.2)	4 (7.8)		64 (44.4)	56 (87.5)	8 (12.5)	
Wild type	67 (56.8)	23 (34.3)	44 (65.7)		47 (55.6)	42 (52.5)	38 (47.5)	

Table S2 Spearman's correlation analysis of PD-L1 mRNA level of ADC by TCGA database

Term	Count	%	P value	Benjamini
immune response	12	20.0	2.8E-5	1.7E-2
regulation of cell cycle process	5	8.3	7.6E-4	2.0E-1
regulation of cell cycle	7	11.7	1.2E-3	2.1E-1
cell cycle	10	16.7	1.7E-3	2.2E-1
response to wounding	8	13.3	2.8E-3	2.9E-1
negative regulation of T cell proliferation	3	5.0	4.3E-3	3.5E-1
negative regulation of leukocyte proliferation	3	5.0	5.9E-3	4.0E-1
negative regulation of mononuclear cell proliferation	3	5.0	5.9E-3	4.0E-1
negative regulation of lymphocyte proliferation	3	5.0	5.9E-3	4.0E-1
regulation of cell proliferation	9	15.0	6.8E-3	4.0E-1

Table S3 Spearman's correlations between PD-L1 and CD8⁺TILs of two cohorts

PD-L1 expression	Cohort No.1				Cohort No.2			
	CD8 ⁺ TILs in ADC		CD8 ⁺ TILs in SCC		CD8 ⁺ TILs in ADC		CD8 ⁺ TILs in SCC	
	Spearman's r	P value	Spearman's r	P value	Spearman's r	P value	Spearman's r	P value
IC	0.379	0.001	0.369	0.01	0.483	<0.001	0.401	0.006
TC	0.373	0.001	0.192	0.192	0.469	<0.001	0.035	0.818

Table S4 Characteristics of studies in meta-analysis for the overall survival in NSCLC

Study name	Type	N	PD-L1		PD-1	
			HR	95% CI	HR	95% CI
GSE8894	ADE	62	1.528	0.745-3.133	0.997	0.492-2.02
GSE19188	ADE	45	0.906	0.405-2.025	0.801	0.358-1.79
GSE30219	ADE	84	1.57	0.837-2.945	1.109	0.587-2.095
GSE37745	ADE	106	1.57	0.837-2.945	0.987	0.626-1.53
GSE31210	ADE	226	3.15	1.48-6.73	1.32	0.67-2.57
GSE13213	ADE	117	1.09	0.62-1.92	1.0	0.57-1.75
TCGA	ADE	475	1.14	0.84-1.54	1.15	0.85-1.56
GSE5123	SCC	51	1.09	0.51-2.34	1.84	0.85-3.99
GSE3141	SCC	109	1.05	0.62-1.76	1.38	0.82-2.32
GSE17710	SCC	56	1.23	0.61-2.49	0.83	0.41-1.68
TCGA	SCC	175	0.93	0.6-1.42	1.1	0.71-1.69
GSE8894	SCC	76	0.808	0.415-1.571	0.414	0.206-0.833
GSE19188	SCC	27	0.642	0.246-1.676	1.198	0.457-3.139
GSE30219	SCC	96	1.014	0.641-1.603	0.674	0.421-1.079
GSE37745	SCC	66	1.2	0.694-2.075	1.095	0.631-1.9

Table S5 Univariate and multivariate survival analysis in Cohort No. 2

Variables	Univariate analysis			Multivariate analysis		
	HR	95% CI	P	HR	95% CI	P
ADC						
Age	0.947	0.438-2.048	0.89			
Gender	0.985	0.445-2.131	0.969			
Smoking status	0.782	0.34-1.799	0.536			
Differentiation	3.285	1.379-7.827	0.007**			
TNM stage	2.657	1.634-4.32	0.000***	2.507	1.529-4.111	0.000***
EGFR status	0.871	0.388-1.954	0.737			
PD-L1	3.291	1.381-7.840	0.007**	2.658	1.110-6.364	0.028*
CD8 ⁺ PD-1	0.859	0.383-1.926	0.712			
SCC						
Age	1.481	0.632-3.473	0.366			
Gender	1.274	0.298-5.457	0.744			
Smoking status	1.29	0.505-3.299	0.594			
Differentiation	0.935	0.344-2.541	0.895			
TNM stage	2.512	1.355-4.657	0.003**	2.482	1.349-4.567	0.003**
EGFR status	0.042	0-15.277	0.291			
PD-L1	0.832	0.246-2.819	0.768			
CD8 ⁺ PD-1	2.285	0.985-5.299	0.054	2.304	0.988-5.371	0.053

*P<0.05, **P<0.01, ***P<0.001.