



Figure S1 Serum inflammation factors in metastatic NSCLC and non-metastatic NSCLC in the modeling cohort. (A) The mean of monocyte count in the metastasis group was higher than that in the no-metastasis group [(0.73 ± 0.09) vs. $(0.37 \pm 0.01) \times 10^9$, $P=0.094$]. (B) The mean of lymphocyte count in the metastasis group was lower than that in the no-metastasis group [(1.61 ± 0.52) vs. $(1.74 \pm 0.56) \times 10^9$, $P=0.092$]. (C) The mean of MLR in the metastasis group was higher than that in the no-metastasis group (0.45 ± 0.10 vs. 0.23 ± 0.08 , $P=0.063$). NSCLC, non-small cell lung cancer.

Table S1 Characteristics of the 243 patients with NSCLC enrolled in this study

Characteristics	Value (total)	Value (modeling cohort)	Value (validation cohort)	P-value
Patient number	243	182	61	
SUVmean1.0				0.94
Range	0.60–8.37	0.60–7.86	1.20–8.37	
Median	3.62	3.71	3.25	
Mean±SD	3.77±1.48	3.77±1.31	3.75±1.91	
SUVmean1.5				0.93
Range	0.38–8.95	0.38–7.86	1.20–8.95	
Median	3.92	4.01	3.62	
Mean±SD	4.16±1.50	4.17±1.31	4.14±1.98	
SUVmean2.0				0.92
Range	1.20–9.74	2.11–8.31	1.20–9.74	
Median	4.33	4.415	4.12	
Mean±SD	4.58±1.54	4.59±1.33	4.5±2.07	
SUVmean2.5				0.96
Range	1.20–10.04	2.11–9.07	1.20–10.04	
Median	4.71	4.790	4.45	
Mean±SD	4.97±1.63	4.98±1.41	4.96±2.19	
MTV1.0				0.88
Range	0.39–64.97	0.46–64.97	0.39–29.26	
Median	6.16	5.94	6.43	
Mean±SD	7.69±6.43	7.73±6.63	7.58±5.85	
MTV1.5				0.99
Range	0.05–60.95	0.32–60.95	0.05–28.91	
Median	5.05	5.04	5.69	
Mean±SD	6.53±6.00	6.54±6.15	6.53±5.58	
MTV2.0				0.87
Range	0.01–49.09	0.19–49.09	0.01–27.87	
Median	4.21	4.12	5.23	
Mean±SD	5.56±5.25	5.53±5.29	5.66±5.20	
MTV2.5				0.90
Range	0.01–48.09	0.09–48.09	0.01–20.17	
Median	3.56	3.50	4.24	
Mean±SD	4.81±4.87	4.79±4.99	4.88±4.54	
TLG1.0				0.75
Range	0.31–419.71	0.31–419.706	0.48–204.53	
Median	21.61	21.58	22.12	
Mean±SD	33.37±40.12	32.90±40.38	34.79±39.64	
TLG1.5				0.70
Range	0.08–427.26	0.144–427.260	0.08–202.95	
Median	21.02	20.81	21.91	
Mean±SD	31.80±40.20	31.22±40.55	33.53±39.40	
TLG2.0				0.58
Range	0.02–381.92	0.478–381.920	0.02–212.37	
Median	19.06	18.98	19.08	
Mean±SD	30.04±38.21	29.24±37.75	32.44±39.77	
TLG2.5				0.57
Range	0.02–386.16	0.26–386.16	0.02–184.86	
Median	17.77	17.82	16.71	
Mean±SD	28.50±37.69	27.70±37.69	30.89±37.92	
COV1.0				0.27
Range	0.06–3.43	0.06–3.43	0.11–0.93	
Median	0.54	0.550	0.52	
Mean±SD	0.56±0.24	0.57±0.25	0.53±0.18	
COV1.5				0.99
Range	0.03–1.31	0.30–0.83	0.03–1.31	
Median	0.46	0.46	0.45	
Mean±SD	0.47±0.16	0.47±0.13	0.47±0.21	
COV2.5				0.17
Range	0.01–0.97	0.01–0.98	0.10–0.32	
Median	0.34	0.350	0.32	
Mean±SD	0.35±0.15	0.35±0.14	0.32±0.17	
White cell count (10 ⁹ /L)				0.89
Range	2.90–24.20	2.90–24.20	3.70–16.60	
Median	6.40	6.50	6.20	
Mean±SD	6.87±2.49	6.95±2.58	6.63±2.18	
Neutrophil count (10 ⁹ /L)				0.50
Range	1.80–19.0	1.80–19.00	1.80–14.00	
Median	4.20	4.20	4.00	
Mean±SD	4.61±2.11	4.69±2.58	4.38±1.86	
Monocyte count (10 ⁹ /L)				0.30
Range	0.10–19.00	0.10–19.00	0.20–0.80	
Median	0.40	0.40	0.40	
Mean±SD	0.50±0.24	0.54±0.44	0.40±0.15	
Platelet count (10 ⁹ /L)				0.34
Range	101.00–416.00	101.00–416.00	104.00–380.00	
Median	220.00	217.50	221.00	
Mean±SD	227.99±63.12	229.05±64.90	224.82 ±5 8.87	
Lymphocyte count (10 ⁹ /L)				0.98
Range	0.50–4.10	0.5–3.1	0.80–4.10	
Median	1.60	1.60	1.70	
Mean±SD	1.67±0.56	1.68±0.54	1.66±0.62	
Fibrinogen(g/L)				0.54
Range	0.93–6.41	1.23–6.41	0.93–5.25	
Median	2.90	2.94	2.76	
Mean±SD	3.06±0.92	3.12±0.92	2.86±0.90	
NLR				0.53
Range	1.04–15.30	1.04–15.30	1.05–7.78	
Median	2.55	2.58	2.45	
Mean±SD	3.06±0.15	3.11±2.83	2.93±1.49	
PLR				0.58
Range	42.27–421.25	62.69–421.25	42.27–298.75	
Median	133.53	134.88	130.00	
Mean±SD	148.61±56.70	147.45±54.28	152.06±63.74	
MLR				0.47
Range	0.07–10.56	0.07–10.56	0.11–0.89	
Median	0.23	0.23	0.24	
Mean±SD	0.33±0.79	0.26±0.12	0.32±0.26	

SUVmean, standardized uptake value; MTV, metabolic tumor volume; TLG, total lesion glycolysis; COV, coefficient of variation; neutrophil-to-lymphocyte ratio; platelet-to-lymphocyte ratio; MLR monocyte-to-lymphocyte ratio; SD, standard deviation,

Table S2 Univariate analysis for the association of PD-L1 levels with patient characteristics in 243 patients

Characteristics	Number	pPDL1 levels			P-value
		Negative	Moderate	Strong	
Age (years)					0.469
<64	80	32	23	25	
≥64	88	33	25	30	
Gender					0.060
Female	71	33	19	19	
Male	97	48	26	23	
Smoking history					0.675
Smoker	82	35	20	27	
Non-smoker	86	30	26	30	
Pathologic subtype					0.904
ADC	148	65	40	43	
SQCC	20	18	2	0	
TNM stage					0.186
I	59	22	27	10	
IIIB	22	9	6	7	
IVA	35	14	12	9	
IVB	52	14	16	22	

TNM, tumor-node-metastasis; SQCC, squamous cell carcinoma; ADC, adenocarcinoma; PD-L1, programmed death ligand 1.

Table S3 Univariate analysis for the association of gene mutations with patient characteristics in 243 patients

Characteristics	EGFR Mutation (n)		ALK Rearrangement (n)		ROS1 Fusion (n)		KRAS Mutation (n)		BRAF Mutation (n)						
	Negative	Positive	P	Negative	Positive	P	Negative	Positive	P	Negative	Positive				
Age (years)			0.910			0.171			0.258			0.780			0.219
<64	50	39		73	16		79	10		82	7		88	1	
≥64	57	43		89	11		83	17		91	9		96	4	
Gender			0.011			0.122			0.766			0.947			0.625
Female	44	49		76	17		79	14		85	8		90	3	
Male	63	33		86	10		83	13		88	8		94	2	
Smoking history			0.099			0.050			0.905			0.422			0.748
Smoker	51	49		81	19		86	14		90	10		97	3	
Non-smoker	56	33		81	8		76	13		83	6		87	2	
Pathologic subtype			0.641			0.801			0.866			0.449			0.682
ADC	103	80		159	24		157	26		167	16		178	5	
SQCC	4	2		5	1		5	1		6	0		6	0	
TNM stage			0.812			0.077			0.278			0.736			0.459
I	49	31		72	8		71	9		72	8		79	1	
IIIB	16	7		17	6		17	6		21	2		23	0	
IVA	30	15		41	4		40	5		43	2		43	2	
IVB	28	13		32	9		34	7		37	4		39	2	

TNM, tumor-node-metastasis; SQCC, squamous cell carcinoma; ADC, adenocarcinoma.

Table S4 The association of gene mutations with COV2.0 and serum SII in 243 patients

Characteristics	n	COV2.0			SII		
		H-COV2.0	L-COV2.0	P value	H-SII	L-SII	P value
EGFR Mutation				0.853			0.723
Negative	107	77	30		47	70	
Positive	82	58	24		35	47	
ALK Rearrangement				0.293			0.453
Negative	162	118	44		56	96	
Positive	27	17	10		12	15	
ROS1 Fusion				0.077			0.784
Negative	172	126	46		65	107	
Positive	17	9	8		7	10	
KRAS Mutation				0.283			0.959
Negative	173	125	49		66	107	
Positive	16	10	6		6	10	
BRAF Mutation				0.572			0.929
Negative	184	132	52		70	114	
Positive	5	3	2		2	3	

COV, coefficient of variation; SII, systemic immune-inflammation index.

Table S5 Univariate and analysis multivariate logistic regression analysis of PD-L1 expression and gene mutations for metastasis in patients with NSCLC

Variables	Univariate analysis		Multivariate analysis	
	HR (95% CI)	P value	HR (95% CI)	P value
EGFR		0.451		0.275
ALK		0.705		0.385
ROS1		0.345		0.475
KRAS		0.075		0.205
BRAF		0.421		0.424
PD-L1		0.891		0.521

PD-L1, programmed death ligand 1; NSCLC, non-small cell lung cancer; HR, hazard ratio; CI, confidence interval.