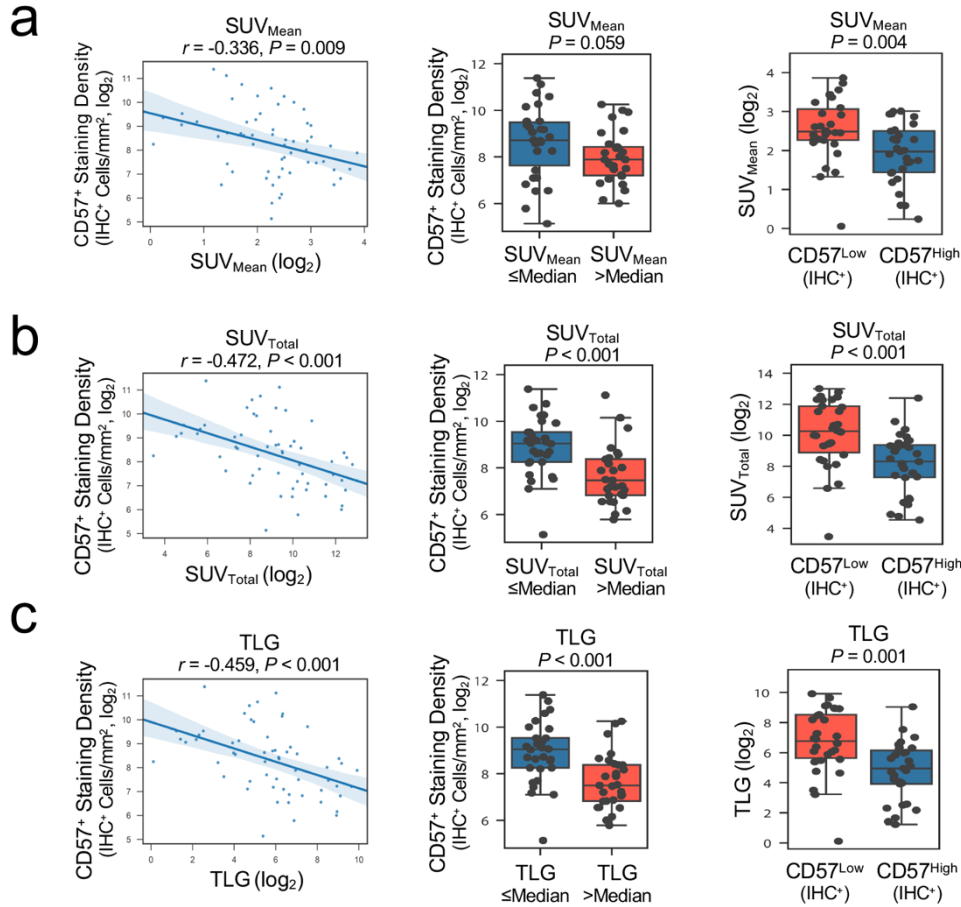
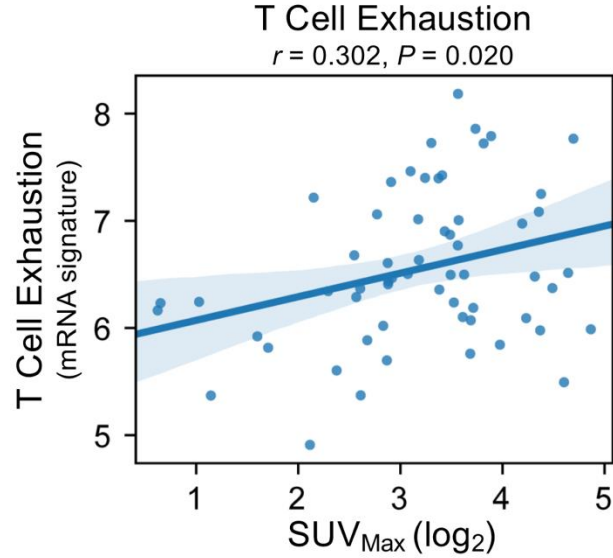


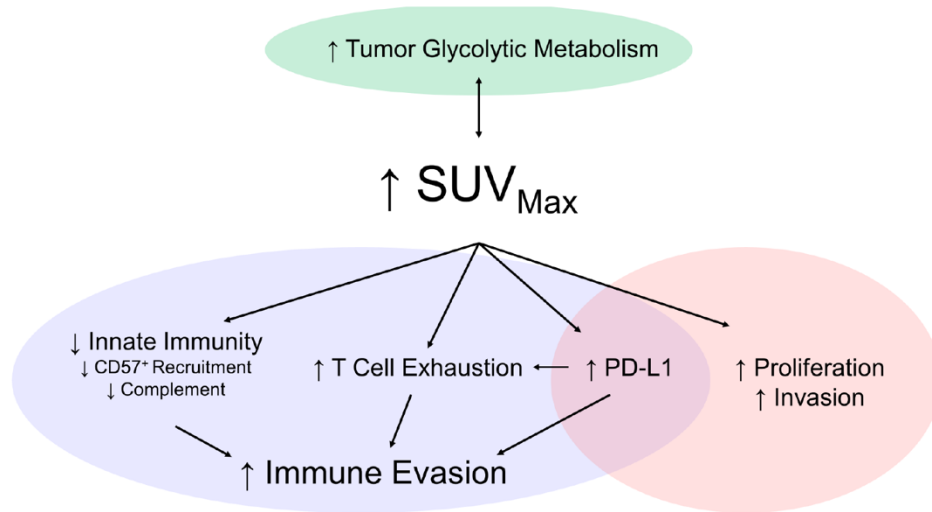
Supplementary Fig. 1 Consolidated Standards of Reporting Trials (CONSORT) diagram outlining the identification of eligible patients in the PROSPECT cohort.



Supplementary Fig. 2 Elevated preoperative ¹⁸F-FDG PET retention is associated with reduced intratumoral CD57⁺ immune cell infiltration ($n = 59$). **a-c**, associations between enhanced tumor ¹⁸F-FDG avidity according to (a) SUV_{Mean}, (b) SUV_{Total}, and (c) TLG and reduced intratumoral infiltration by immune cells expressing CD57. Values provided in **a-c** (left panels) are Pearson coefficients for pairwise correlations between log₂-transformed values; a two-tailed P value of 0.05 was used to determine statistical significance. In **a-c** (center and right panels), boxes depict median and interquartile range (IQR); bars represent minimum and maximum values excluding outliers (median \pm 1.5 IQR). P values in the center and right panels were calculated using unpaired t tests. The cohort was dichotomized according to the median of each parameter (center panels; SUV_{Mean}, 4.90; SUV_{Total}, 643.26; TLG, 64.72) and density of cells expressing CD57 (right panels, 330.4 cells/mm²).



Supplementary Fig. 3 Association between increased ¹⁸F-FDG retention as quantified by SUV_{Max} and expression of a gene signature indicative of T cell exhaustion in NSCLC patients ($n = 59$). The provided value is the Pearson coefficient for pairwise correlation between log₂-transformed values; a two-tailed P value of 0.05 was used to determine statistical significance. The T cell exhaustion signature was quantified as the mean overall expression level of *CTLA4*, *HAVCR2*, *LAG3*, *PDCD1*, and *TIGIT*. *CTLA4*, cytotoxic T-lymphocyte associated protein 4; *HAVCR2*, hepatitis A virus cellular receptor 2; *PDCD1*, programmed cell death 1.



Supplementary Fig. 4 Proposed model depicting the associations between SUV_{Max} with tumor immune and metabolic phenotypes in resected NSCLC.

Supplementary Table 1 Clinicopathologic and treatment characteristics of patients in the PROSPECT cohort (n = 59). ECOG, Eastern Cooperative Oncology Group; NH, non-Hispanic.

Variable	n (%)
Age ≥ 65 years	27 (46)
Sex	
Male	34 (58)
Female	25 (42)
ECOG Performance Status	
0	29 (49)
1	27 (46)
2	3 (5)
Race	
NH Black	5 (9)
NH White	49 (83)
Asian	1 (2)
Hispanic	4 (7)
Smoking Status	
Former/Current	52 (88)
Never	7 (12)
Histology	
Adenocarcinoma	43 (73)
Squamous Cell Carcinoma	16 (27)
Differentiation	
Well/Moderate	35 (59)
Poor	24 (41)
Clinical Stage	
I	34 (58)
II	14 (24)
III	11 (19)
Neoadjuvant Platinum-Based Chemotherapy	10 (17)
Pathologic Stage	
I	32 (54)
II	12 (20)
III	15 (25)
Adjuvant Therapy	
Systemic Therapy ^a	20 (34)
Radiotherapy	6 (10)

^aOf the 20 patients who received adjuvant systemic therapy, 18/20 (90.0%) received adjuvant platinum-based chemotherapy, and 2/20 (10.0%) received neoadjuvant platinum-based chemotherapy and adjuvant erlotinib.

Supplementary Table 2 Pairwise correlations between overall tumor glycolysis gene expression and expression of immune-related genes ($n = 59$). A false discovery rate-adjusted two-tailed P value of 0.05 was used to determine statistical significance. FDR, false discovery rate.

Gene	Pearson's r	FDR-adjusted P
<i>GPI</i>	0.833	0.000
<i>MIF</i>	0.668	0.000
<i>F12</i>	0.602	0.000
<i>MAP3K1</i>	-0.605	0.000
<i>A2M</i>	-0.589	0.000
<i>CDK1</i>	0.565	0.000
<i>SERPINB2</i>	0.565	0.000
<i>CD55</i>	-0.550	0.000
<i>PSMB7</i>	0.550	0.000
<i>IL1RAP</i>	0.543	0.001
<i>MEF2C</i>	-0.533	0.001
<i>C5</i>	-0.524	0.001
<i>ATG5</i>	-0.517	0.001
<i>CREB1</i>	-0.520	0.001
<i>LRRN3</i>	-0.518	0.001
<i>TFRC</i>	0.513	0.001
<i>C1QBP</i>	0.510	0.001
<i>RELA</i>	0.512	0.001
<i>IL1A</i>	0.508	0.001
<i>IFNAR2</i>	-0.505	0.002
<i>IL1B</i>	0.498	0.002
<i>IL10</i>	-0.496	0.002
<i>ATG10</i>	-0.489	0.003
<i>CXCL16</i>	-0.485	0.003
<i>CCL26</i>	0.483	0.003
<i>BIRC5</i>	0.479	0.003
<i>CEACAM6</i>	-0.479	0.003
<i>IL18</i>	-0.477	0.003
<i>CDH5</i>	-0.471	0.004
<i>NFKBIA</i>	-0.470	0.004
<i>STAT5B</i>	-0.458	0.006
<i>CCND3</i>	-0.457	0.006
<i>ELANE</i>	-0.452	0.007
<i>MAPK3</i>	-0.453	0.007
<i>PRKCD</i>	-0.445	0.008
<i>TXNIP</i>	-0.446	0.008

<i>DUSP6</i>	-0.444	0.008
<i>IL4R</i>	-0.441	0.009
<i>SPN</i>	-0.440	0.009
<i>TTK</i>	0.439	0.009
<i>PSMD7</i>	0.437	0.009
<i>TNFRSF18</i>	0.433	0.010
<i>C4BPA</i>	-0.429	0.011
<i>MAP2K1</i>	0.429	0.011
<i>CD34</i>	-0.426	0.012
<i>RELB</i>	0.426	0.012
<i>SYT17</i>	-0.422	0.013
<i>TNFSF15</i>	-0.422	0.013
<i>CCL11</i>	0.411	0.018
<i>CD274</i>	0.408	0.018
<i>IL17F</i>	-0.408	0.018
<i>BID</i>	0.406	0.019
<i>ATG12</i>	-0.405	0.020
<i>CCR6</i>	-0.404	0.020
<i>CD1C</i>	-0.403	0.020
<i>JAM3</i>	-0.402	0.020
<i>TNFRSF14</i>	-0.400	0.021
<i>NFATC3</i>	-0.399	0.022
<i>IFI16</i>	0.394	0.024
<i>ITGB4</i>	0.394	0.024
<i>CCL14</i>	-0.392	0.025
<i>EWSR1</i>	0.385	0.029
<i>IRAK1</i>	0.385	0.029
<i>CTSH</i>	-0.383	0.031
<i>DPP4</i>	-0.382	0.031
<i>IL17B</i>	-0.381	0.031
<i>PLAU</i>	0.381	0.031
<i>C6</i>	-0.379	0.032
<i>FOXJ1</i>	-0.371	0.038
<i>IFNAR1</i>	-0.371	0.038
<i>MAGEB2</i>	0.371	0.038
<i>RRAD</i>	-0.370	0.039
<i>CXCL2</i>	-0.368	0.040
<i>IL1R1</i>	-0.368	0.040
<i>C7</i>	-0.365	0.040
<i>NEFL</i>	0.365	0.040
<i>NUP107</i>	0.367	0.040
<i>PECAM1</i>	-0.366	0.040
<i>TLR5</i>	-0.366	0.040

<i>HLA-DMB</i>	-0.362	0.043
<i>PBK</i>	0.358	0.047
<i>ATF2</i>	0.355	0.049
<i>C4B</i>	-0.355	0.049
<i>EP300</i>	0.354	0.050

Supplementary Table 3 Pairwise correlations between preoperative SUV_{Max} and expression of immune-related genes (*n* = 59). A false discovery rate-adjusted two-tailed *P* value of 0.05

was used to determine statistical significance. FDR, false discovery rate.

Gene	Pearson's <i>r</i>	FDR-adjusted <i>P</i>
<i>PBK</i>	0.543	0.003
<i>PLA2G1B</i>	-0.548	0.003
<i>ICAM4</i>	-0.522	0.005
<i>TTK</i>	0.514	0.005
<i>BIRC5</i>	0.488	0.012
<i>CDK1</i>	0.474	0.018
<i>C5</i>	-0.457	0.019
<i>CCND3</i>	-0.453	0.019
<i>CD1C</i>	-0.452	0.019
<i>CD3EAP</i>	0.453	0.019
<i>IL2RA</i>	0.460	0.019
<i>KIT</i>	-0.453	0.019
<i>S100A8</i>	0.450	0.019
<i>CTSH</i>	-0.443	0.022
<i>TFRC</i>	0.434	0.028
<i>IL1A</i>	0.421	0.039
<i>PRKCE</i>	-0.417	0.042
<i>CD55</i>	-0.412	0.044
<i>RRAD</i>	-0.412	0.044
<i>PSEN1</i>	-0.410	0.044
<i>ICAM2</i>	-0.407	0.046

Supplementary Table 4 Pairwise correlations between preoperative SUV_{Mean} and expression of immune-related genes (*n* = 59). A false discovery rate-adjusted two-tailed *P* value of 0.05 was used to determine statistical significance. FDR, false discovery rate.

Gene	Pearson's <i>r</i>	FDR-adjusted <i>P</i>
<i>BIRC5</i>	0.519	0.004
<i>ICAM4</i>	-0.519	0.004
<i>PBK</i>	0.531	0.004
<i>PLA2G1B</i>	-0.535	0.004
<i>TTK</i>	0.499	0.008
<i>C5</i>	-0.469	0.021
<i>IL2RA</i>	0.460	0.025
<i>PRKCE</i>	-0.450	0.031
<i>CD3EAP</i>	0.435	0.031
<i>CDK1</i>	0.436	0.031
<i>CTSH</i>	-0.436	0.031
<i>KIT</i>	-0.443	0.031
<i>MUC1</i>	-0.441	0.031
<i>STAT6</i>	-0.432	0.032
<i>MAGEA1</i>	0.423	0.039

Supplementary Table 5 Pairwise correlations between preoperative SUV_{Total} and expression of immune-related genes ($n = 59$). A false discovery rate-adjusted two-tailed P value of 0.05 was used to determine statistical significance. FDR, false discovery rate.

Gene	Pearson's <i>r</i>	FDR-adjusted <i>P</i>
<i>ICAM4</i>	-0.520	0.011
<i>PLA2G1B</i>	-0.515	0.011
<i>CREBBP</i>	-0.492	0.018
<i>C5</i>	-0.453	0.045
<i>LRRN3</i>	-0.456	0.045
<i>CCND3</i>	-0.446	0.048

Supplementary Table 6 Pairwise correlations between preoperative TLG and expression of immune-related genes ($n = 59$). A false discovery rate-adjusted two-tailed P value of 0.05 was used to determine statistical significance. FDR, false discovery rate.

Gene	Pearson's <i>r</i>	FDR-adjusted <i>P</i>
<i>PLA2G1B</i>	-0.516	0.011
<i>ICAM4</i>	-0.514	0.011
<i>CREBBP</i>	-0.491	0.018

Supplementary Table 7 Dysregulated genes according to elevated overall tumor expression of glycolytic genes (dichotomized according to the median among the entire cohort; $n = 59$).

Genes were considered dysregulated if $|\log\text{-fold change}| > 1$ and two-tailed $P < 0.05$.

Gene	Log-fold change	<i>P</i>
<i>IL1A</i>	1.777	0.000
<i>S100A8</i>	1.389	0.004
<i>SERPINB2</i>	1.377	0.001
<i>F12</i>	1.325	0.000
<i>IL1B</i>	1.246	0.000
<i>DEFB1</i>	1.220	0.035
<i>CDK1</i>	1.198	0.000
<i>GPI</i>	1.126	0.000
<i>SPP1</i>	1.126	0.010
<i>MAGEA4</i>	1.124	0.049
<i>BIRC5</i>	1.116	0.002
<i>TTK</i>	1.106	0.000
<i>ITGB4</i>	1.093	0.002
<i>S100A7</i>	1.083	0.006
<i>PBK</i>	1.020	0.003
<i>C4BPA</i>	-2.305	0.000
<i>CEACAM6</i>	-2.176	0.000
<i>PLA2G1B</i>	-1.417	0.005
<i>A2M</i>	-1.378	0.000
<i>C5</i>	-1.231	0.000
<i>CCL14</i>	-1.189	0.002
<i>CDH5</i>	-1.091	0.000
<i>KIT</i>	-1.063	0.010
<i>C7</i>	-1.060	0.007
<i>DPP4</i>	-1.009	0.003

Supplementary Table 8 Dysregulated genes according to elevated preoperative SUV_{Max}

(dichotomized according to the median among the entire cohort, 10.36; $n = 59$). Genes were

considered dysregulated if $|\log\text{-fold change}| > 1$ and two-tailed $P < 0.05$.

Gene	Log-fold change	<i>P</i>
<i>SPP1</i>	1.340	0.002
<i>PBK</i>	1.246	0.000
<i>IL1A</i>	1.195	0.007
<i>S100A8</i>	1.126	0.019
<i>BIRC5</i>	1.018	0.005
<i>F12</i>	1.004	0.002
<i>PLA2G1B</i>	-1.712	0.001
<i>C4BPA</i>	-1.353	0.021
<i>KIT</i>	-1.146	0.005
<i>FCERIA</i>	-1.068	0.006
<i>RRAD</i>	-1.007	0.005

Supplementary Table 9 Classification of NSCLC tumors in the study cohort according to overall tumor expression of glycolytic genes and SUV_{Max} (*n* = 59). The cohort was dichotomized according to the median value of each parameter among the entire cohort.

		SUV _{Max}		Total
		High	Low	
Overall Tumor Glycolytic Gene Expression	High	20 (69.0)	9 (30.0)	29
	Low	9 (30.0)	21 (70.0)	30
Total		29	30	

Supplementary Table 10 Dysregulated genes according to elevated preoperative SUV_{Mean}, SUV_{Total}, and TLG (n = 59). The cohort was dichotomized according to the median value of each parameter among the entire cohort (SUV_{Mean}, 4.90; SUV_{Total}, 643.26; TLG, 64.72). Genes were considered dysregulated if $|\log\text{-fold change}| > 1$ and two-tailed $P < 0.05$. LFC, log-fold change.

SUV _{Mean}			SUV _{Total}			TLG		
Gene	LFC	P	Gene	LFC	P	Gene	LFC	P
<i>MAGEA4</i>	1.309	0.021	<i>ITGB4</i>	1.197	0.001	<i>PLA2G1B</i>	-1.387	0.006
<i>CXCL10</i>	1.275	0.003	<i>IL1A</i>	1.026	0.022			
<i>S100A8</i>	1.235	0.010	<i>MAGEA1</i>	1.005	0.005			
<i>CXCL9</i>	1.230	0.012	<i>PLA2G1B</i>	-1.229	0.015			
<i>CXCL13</i>	1.148	0.019	<i>LRRN3</i>	-1.081	0.000			
<i>PBK</i>	1.073	0.002						
<i>PLA2G1B</i>	-1.534	0.002						
<i>C4BPA</i>	-1.452	0.013						
<i>CEACAM6</i>	-1.256	0.048						
<i>C5</i>	-1.006	0.003						