Supplementary Table 1. Clinical and pathological variables and the expression of FUT4 in lung cancer patients (Tissue Cohort).

Clinical factors	**n**	**FUT4 Low expression**	**FUT4 High expression**	**P-value***
Age (years)				**P = 0.021**
<65	11	4	7	
≥65	8	3	5	
Tumor size (cm)				**P = 0.008**
<3	9	6	3	
≥3	10	1	9	
Gender				**P = 0.015**
Male	11	2	9	
Female	8	5	3	
Clinical stage				**P = 0.006**
I	6	5	1	
II	4	1	3	
III	9	1	8	
Lymph node metastasis				**P < 0.001**
Absent	8	6	2	
Present	11	1	10	

FUT4, fucosyltransferase 4. Lung cancer patients (n=19) were divided into FUT4 low and FUT4 high expression groups according to the median cutoff value. P-values were calculated using Fisher's exact test for categorical variables due to the small sample size. Exact P values are reported. $P < 0.05$ was considered statistically significant. The tissue cohort included patients with stage I–III NSCLC only; no stage IV patients were included.

Supplementary Table 2. Clinical serum variables and the expression of FUT4 and MALAT1 in lung cancer patients (Serum Cohort).

Clinical factors	**n**	**FUT4 Low expression**	**FUT4 High expression**	**P-value (FUT4)***	**MALAT1 Low expression**	**MALAT1 High expression**	**P-value (MALAT1)***
Gender	50			**P = 0.003**			**P = 0.002**
Male	27	10	17		9	18	
Female	23	14	9		15	8	
Clinical stage	50			**P < 0.001**			**P < 0.001**
I	13	7	6		7	6	
II	12	5	7		5	7	
III	13	4	9		4	9	
IV	12	2	10		2	10	

FUT4, fucosyltransferase 4; MALAT1, metastasis-associated lung adenocarcinoma transcript 1. Serum samples from patients and healthy controls (n=50) were classified according to each biomarker's cutoff value (median expression). P-values were calculated using the chi-square test for trend across stage categories and Fisher's exact test for gender comparisons. Exact P values are reported. $P < 0.05$ was considered statistically significant. The serum cohort included 15 healthy controls, 20 treatment-naïve NSCLC patients (stages I–IV), and 15 post-chemotherapy patients.

Supplementary Table 3. Primer sequences used for quantitative real-time PCR (RT-qPCR).

Gene	Forward Primer (5′→3′)	Reverse Primer (5′→3′)	Amplicon (bp)	Accession Number
MALAT1	AAAGGAACACAGGACAGCAC	CTAGAAGGTGGAAGAGCAGC	~150	NR_002819.4
FUT4	GACCATTTCCGAGCCACTTT	AGCATCGCTTCACTGTGTTC	~140	NM_002033.4
GAPDH	GAAGGTGAAGGTCGGAGTC	GAAGATGGTGATGGGATTTC	~120	NM_002046.7
β-actin	CATGTACGTTGCTATCCAGGC	CTCCTTAATGTCACGGACGAT	~100	NM_001101.5

MALAT1, metastasis-associated lung adenocarcinoma transcript 1; FUT4, fucosyltransferase 4; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; RT-qPCR, reverse transcription-quantitative polymerase chain reaction. Primer specificity was confirmed by BLAST analysis and melt curve analysis showing single peaks. Amplification efficiencies for all primer pairs were between 90–105% as determined by standard curve analysis.

Supplementary Table 4. Antibodies used for Western blot analysis.

Antibody Target	Vendor	Catalog Number	Dilution	RRID
FUT4	Proteintech	13039-1-AP	1:1000	AB_10597591
p-PI3K	Cell Signaling Technology	4228	1:1000	AB_659940
PI3K	Cell Signaling Technology	4257	1:1000	AB_659941
p-Akt (Ser473)	Cell Signaling Technology	4060	1:2000	AB_2315049
Akt	Cell Signaling Technology	4691	1:1000	AB_915783
p-PDK	Cell Signaling Technology	5666	1:1000	AB_10695545
PDK	Cell Signaling Technology	5662	1:1000	AB_10694072
β-actin	Cell Signaling Technology	3700	1:5000	AB_2242334
HRP-anti-rabbit IgG	Cell Signaling Technology	7074	1:5000	AB_2099233
HRP-anti-mouse IgG	Cell Signaling Technology	7076	1:5000	AB_330924

HRP, horseradish peroxidase; IgG, immunoglobulin G; RRID, Research Resource Identifier (for antibody authentication and reproducibility). All Western blot assays were conducted using three independent biological replicates. Antibody validation information is available from the manufacturers' websites using the provided catalog numbers.