

Table SV. Association between *MUC22* methylation and clinicopathologic features of the NSCLC patients

Characteristics	No. of cases	<i>MUC22</i> ^a		P-value
		Methylation n (%)	Unmethylation n (%)	
Total	47	30 (63.8)	17 (36.2)	
Sex				
Male	33	23 (69.7)	10 (30.3)	
Female	14	7 (50.0)	7 (50.0)	0.199
Age (years)				
≥60	25	15 (60.0)	10 (40.0)	
<60	22	15 (68.2)	7 (31.8)	0.560
Pathological type				
LUAD	23	7 (30.4)	16 (69.6)	
LUSC	24	23 (95.8)	1 (4.2)	3.1×10^{-5c}
Tumor invasive depth				
1	12	8 (66.7)	4 (33.3)	
2	30	19 (63.3)	11 (36.7)	0.839
3	5	3 (60.0)	2 (40.0)	0.793
Lymph node metastasis				
0	39	24 (61.5)	15 (38.5)	
1	8	6 (75.0)	2 (25.0)	0.470
Clinical stage				
I	3	3 (100.0)	0 (0.0)	
II	31	18 (58.1)	13 (41.9)	0.154
III	13	4 (30.8)	9 (69.2)	0.029 ^b
<i>MUC22</i> expression				
High	26	9 (34.6)	17 (65.4)	
Low	21	21 (100.0)	0 (0.0)	3.6×10^{-6c}

^aThe methylation status around transcription start site (TSS) of *MUC22* was analyzed by using methylation-specific PCR (MSP) (Figs. 2D and S1). ^bP<0.05, ^cP<0.001 (χ^2 test). *MUC22*, mucin 22; NSCLC, non-small cell lung carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma.