

Supplementary data

Table S1. Distribution frequencies of interleukin (*IL*)-17A genotypes of patients with lung adenocarcinoma and multiple logistic regression analysis of epidermal growth factor receptor (EGFR) mutation associations.

Genotype SNP	Wild type (N = 109)	Mutated type (N = 168)	AOR (95% CI)	p value
rs8193036				
CC	63 (57.8%)	90 (53.6%)	1.00	
CT	39 (35.8%)	63 (37.5%)	1.077 (0.619~1.875)	0.792
TT	7 (6.4%)	15 (8.9%)	2.402 (0.850~6.793)	0.098
CT+TT	46 (42.2%)	78 (46.4%)	1.241 (0.736~2.093)	0.418
rs8193037				
GG	83 (76.1%)	136 (81.0%)	1.00	
GA	25 (22.9%)	31 (18.5%)	0.706 (0.370~1.348)	0.292
AA	1 (1.0%)	1 (0.5%)	0.619 (0.025~15.360)	0.770
GA+AA	26 (23.9%)	32 (19.0%)	0.703 (0.372~1.329)	0.278
rs2275913				
GG	32 (29.4%)	43 (25.6%)	1.00	
GA	48 (44.0%)	85 (50.6%)	1.115 (0.596~2.084)	0.734
AA	29 (26.6%)	40 (23.8%)	0.857 (0.417~1.761)	0.674
GA+AA	77 (70.6%)	125 (74.4%)	1.019 (0.568~1.830)	0.949
rs3748067				
CC	92 (84.4%)	135 (80.4%)	1.00	
CT	16 (14.7%)	32 (19.0%)	1.383 (0.684~2.799)	0.367
TT	1 (0.9%)	1 (0.6%)	0.729 (0.042~12.769)	0.829
CT+TT	17 (15.6%)	33 (19.6%)	1.341 (0.674~2.670)	0.403

Abbreviations: SNP, single-nucleotide polymorphism. The adjusted odds ratios (AORs) with their 95% confidence intervals (CIs) were estimated by multiple logistic regression models after controlling for age, gender, and the cigarette smoking status.

Table S2. Distribution frequencies of interleukin (*IL*)-17A genotypes of lung adenocarcinoma patients with the non-smoking status and multiple logistic regression analysis of epidermal growth factor receptor (EGFR) mutation associations.

Genotype SNP	Wild type (N = 49)	Mutated type (N = 130)	AOR (95% CI)	p value
rs8193036				
CC	27 (55.1%)	71 (54.6%)	1.00	

CT	21 (42.9%)	51 (39.2%)	0.991 (0.493~1.993)	0.979
TT	1 (2.0%)	8 (6.2%)	2.684 (0.316~22.806)	0.366
CT+TT	22 (44.9%)	59 (45.4%)	1.079 (0.545~2.137)	0.827
rs8193037				
GG	39 (79.6%)	101 (77.7%)	1.00	
GA	10 (20.4%)	28 (21.5%)	1.412 (0.586~3.402)	0.442
AA	0 (0.0%)	1 (0.8%)	---	---
GA+AA	10 (20.4%)	29 (22.3%)	1.443 (0.600~3.467)	0.412
rs2275913				
GG	9 (18.4%)	35 (26.9%)	1.00	
GA	25 (51.0%)	66 (50.8%)	0.537 (0.207~1.391)	0.200
AA	15 (30.6%)	29 (22.3%)	0.362 (0.128~1.025)	0.056
GA+AA	40 (81.6%)	95 (73.1%)	0.468 (0.189~1.159)	0.101
rs3748067				
CC	43 (87.8%)	103 (79.2%)	1.00	
CT	6 (12.2%)	26 (20.0%)	1.763 (0.657~4.733)	0.260
TT	0 (0.0%)	1 (0.8%)	---	---
CT+TT	6 (12.2%)	27 (20.8%)	1.827 (0.682~4.893)	0.231
rs763780				
TT	33 (67.3%)	87 (66.9%)	1.00	
TC	16 (32.7%)	39 (30.0%)	0.909 (0.442~1.871)	0.796
CC	0 (0.0%)	4 (3.1%)	---	---
TC+CC	16 (32.7%)	43 (33.1%)	0.998 (0.489~2.044)	0.986

Abbreviation: SNP, single-nucleotide polymorphism. The adjusted odds ratios (AORs) with their 95% confidence intervals (CIs) were estimated by multiple logistic regression models after controlling for age and gender.

Table S3. Clinicopathologic characteristics of lung adenocarcinoma patients with MT EGFR, stratified by polymorphic genotypes of interleukin (*IL*)-17A rs8193036.

Genotype SNP	CC (N = 90)	CT or TT (N = 78)	AOR (95% CI)	p value
Stage				
I or II	28 (31.1%)	19 (24.4%)	1.00	0.309
III or IV	62 (68.9%)	59 (75.6%)	1.440 (0.714~2.905)	
Tumor T status				
T1 or T2	57 (63.3%)	50 (64.1%)	1.00	0.854
T3 or T4	33 (36.7%)	28 (35.9%)	0.940 (0.485~1.822)	

Lymph node metastasis				
Negative	28 (31.1%)	25 (32.1%)	1.00	0.813
Positive	62 (68.9%)	53 (67.9%)	0.922 (0.471~1.805)	
Distant metastasis				
Negative	39 (43.3%)	41 (52.6%)	1.00	0.316
Positive	51 (56.7%)	37 (47.4%)	0.723 (0.384~1.362)	
Cell differentiation				
Good/Moderate	83 (92.2%)	75 (96.2%)	1.00	0.459
Poor	7 (7.8%)	3 (3.8%)	0.577 (0.134~2.476)	

Abbreviations: SNP, single-nucleotide polymorphism. The adjusted odds ratios (AORs) with their 95% confidence intervals (CIs) were estimated by multiple logistic regression models after controlling for age, gender, and the cigarette smoking status.