

Table S5. Association between mRNA expression level and lung cancer clinicopathological parameters of four candidate genes in Asian ^a.

Characteristics	Total ^b n	<u>ARHGAP19</u>		<u>FRAT2</u>		<u>PAFAH1B1</u>		<u>ZNF322A</u>		
		overexpression ^c n (%)	Normal n (%)	overexpression ^c n (%)	Normal n (%)	overexpression ^c n (%)	Normal n (%)	overexpression ^c n (%)	Normal n (%)	
Overall	45	33 (73.3)	12 (26.7)	23 (51.1)	22 (48.9)	31 (68.9)	14 (31.1)	27 (60.0)	18 (40.0)	
<u>Clinicopathological parameters</u>										
Age	< 65	22	13 (59.1)	9 (40.9)	10 (45.5)	12 (54.5)	15 (68.2)	7 (31.1)	14 (63.6)	8 (36.4)
	≥ 65	23	20 (87.9) ^{0.035}	3 (13.1)	13 (56.5)	10 (43.5)	16 (69.6)	7 (30.4)	13 (56.5)	10 (43.5)
Sex	Male	36	29 (80.6) ^{0.028}	7 (19.4)	18 (50.0)	18 (50.0)	25 (69.4)	11 (30.6)	18 (50)	18 (50)
	Female	9	4 (44.4)	5 (55.6)	5 (55.6)	4 (44.4)	6 (66.7)	3 (33.3)	5 (55.6)	4 (44.4)
Smoker	Yes	18	15 (83.3) ^{0.019}	3 (16.7)	7 (38.8)	11 (61.2)	14 (77.8)	4 (22.2)	11 (61.1)	7 (38.9)
	No	8	3 (37.5)	5 (62.5)	5 (62.5)	3 (37.5)	5 (62.5)	3 (37.5)	6 (75.0)	2 (25.0)
<u>Tumor type</u>										
	ADC	28	16 (57.1)	12 (42.9)	10 (35.7)	18 (64.3)	18 (64.3)	10 (35.7)	15 (53.6)	13 (46.4)
	SCC	17	17 (100) ^{0.002}	0 (0)	13 (76.5) ^{0.008}	4 (23.5)	13 (76.5)	4 (23.5)	12 (70.6)	5 (29.4)
<u>Tumor stage</u>										
	I + II	21	16 (76.2)	5 (23.8)	10 (52.4)	11 (47.6)	13 (59.1)	9 (40.9)	14 (66.7)	7 (33.3)
	III + IV	23	16 (69.6)	7 (30.4)	12 (52.2)	11 (47.8)	18 (78.3)	5 (21.7)	12 (52.2)	11 (47.8)
<u>Correlation with protein</u>										
IHC	Over expression					14 (73.7) ^{0.041}	5 (26.3)	16 (84) ^{0.030}	3 (16)	
	Normal expression					3 (33.3)	6 (66.7)	4 (44.4)	5 (55.6)	

^a The *P* values with significance are shown as superscripts.

^b Total number of samples in some categories is less than the overall number analyzed because clinical data or molecular data was not available for these samples.

^c The mRNA overexpression of candidate genes was defined using the mean mRNA expression of normal lung tissue as a cutoff value to determine patients with mRNA overexpression.