Supplementary Table 1

Comparison of the baseline characteristics between common and uncommon EGFR mutation

NSCLC

-					
Patient Characteristics Total		Total N	Common	Uncommon	<i>P</i> -value
			mutation	mutation	
		2,121	1,986	135	
Age					
_	<60 years	906 (42.7%)	859 (43.3%)	47 (34.8%)	0.06
	≥60 years	1215 (57.3%)	1127 (56.7%)	88 (65.2%)	
Sex	•	,			
	Male	780 (36.8%)	716 (36.1%)	64 (47.4%)	0.02
	Female	1341 (63.2%)	1270 (63.9%)	71 (52.6%)	
ECOG PS				,	
	0	442 (20.9%)	414 (20.8%)	28 (20.7%)	0.247
	1	1573 (74.2%)	1477 (74.4%)	96 (71.1%)	V,
	2	106 (5.0%)	95 (4.8%)	11 (8.1%)	
Smoking status				(-)	
	Never smoker	1484 (70.0%)	1409 (70.9%)	75 (55.2%)	0.003
	Ex-smoker	432 (20.4 %)	387 (19.5%)	45 (33.3%)	
	Current smoker	205 (9.7%)	190 (9.6%)	15 (11.1%)	
History of curative thoracic surgery		(>1,7.1)	220 (21011)	(
Yes		685 (32.3%)	659 (33.2%)	26 (19.2%)	0.55
No		1436 (67.7%)	1327 (66.8%)	109 (80.7%)	0.00
EGFR-TKI		- 10 0 (071771)	(((((((((((((((((((((==================================	
Gefitinib		1046 (49.3%)	999 (50.0%)	47 (38.5%)	0.043
Erlotinib		305 (14.4%)	284 (14.2%)	21 (17.2%)	0.0.15
Afatinib		770 (36.3%)	716 (35.8%)	54 (44.3%)	
Patients who experienced disease		1316	1,238	78	
progression		(62.0%)	(61.9%)	(63.9%)	0.70
Sequential treatment		(=====)	(021)11)	(001)11)	
Bequein		859	824	35	
	Rate of re-biopsy after failing	(65.3%,	(66.6%,	(44.9%,	< 0.001
	first-line EGFR-TKIs	,	` '	,	<0.001
		859/1316)	824/1238) 523	35/78) 10	
	Detection acts of T700M	533			<0.001
	Detection rate of T790M	(62.0%,	(63.5%,	(28.6%,	< 0.001
C		533/859)	523/824)	10/35)	
Sequential treatment		500(45.50()	500 (47 00()	17 (21 00/)	<0.001
Third-generation EGFR-TKIs		599(45.5%)	582 (47.0%)	17 (21.8%)	< 0.001
Cytotoxic chemotherapy		488 (37.1%)	447 (36.1%)	41 (52.6%)	
No sequential treatment		229 (17.4%)	209 (16.9%)	20 (25.6%)	

Supplementary Fig. 1. (A) Median progression-free survival (PFS) according to the type of epidermal growth factor receptor *(EGFR)* mutation (common versus uncommon). (B) Median overall survival (OS) according to the type of EGFR mutation (common versus uncommon)

