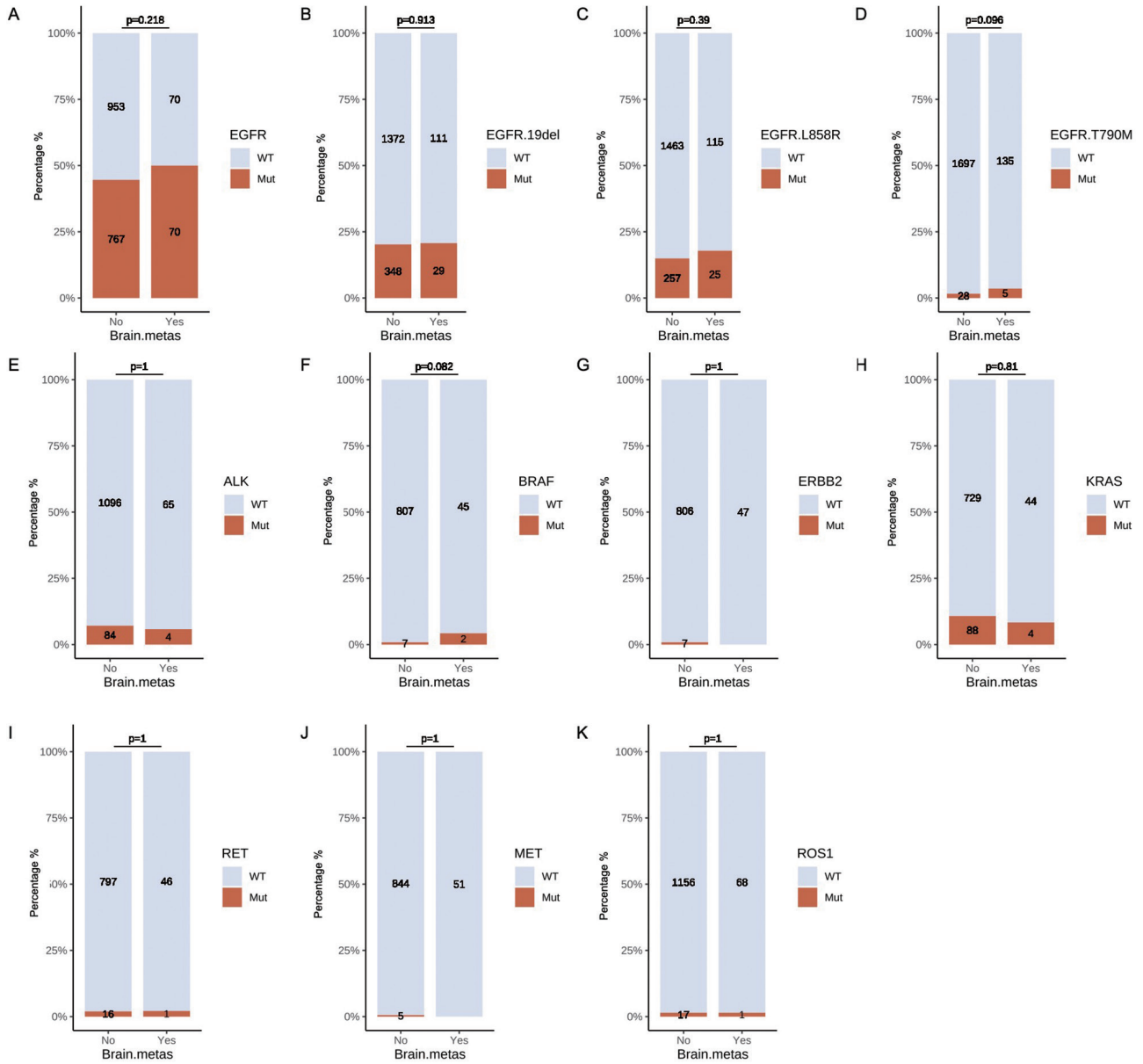
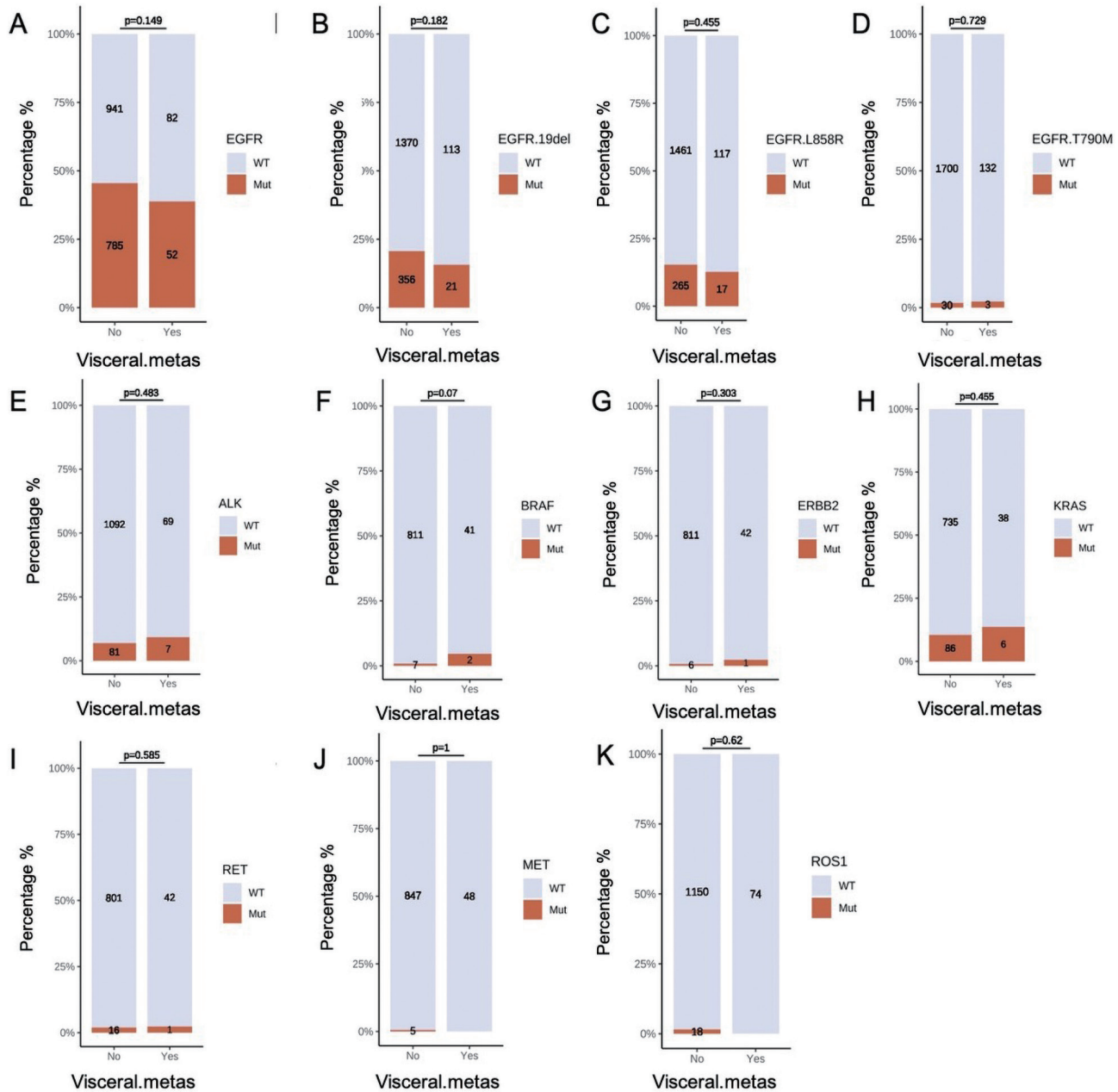


**Figure S1** Comparison of the prevalence of major driver mutations between patients with bone metastasis and patients without bone metastasis. (A-K) *EGFR*, *EGFR* 19 deletion, *EGFR* L858R, *EGFR* T790M, *ALK*, *BRAF*, *ERBB2*, *KRAS*, *RET*, *MET*, and *ROS1* mutation. WT, wild type; Mut, mutation.



**Figure S2** Comparison of the prevalence of major driver mutations between patients with brain metastasis and patients without brain metastasis. (A-K) *EGFR*, *EGFR* 19 deletion, *EGFR* L858R, *EGFR* T790M, *ALK*, *BRAF*, *ERBB2*, *KRAS*, *RET*, *MET*, and *ROS1* mutation. WT, wild type; Mut, mutation.



**Figure S3** Comparison of the prevalence of major driver mutations between patients with visceral metastasis and patients without visceral metastasis. (A-K) *EGFR*, *EGFR* 19 deletion, *EGFR* L858R, *EGFR* T790M, *ALK*, *BRAF*, *ERBB2*, *KRAS*, *RET*, *MET*, and *ROS1* mutation. WT, wild type; Mut, mutation.

**Table S1** The detection terms of the study population after PSM

Detection terms	ARMS	NGS
8 drivers	376	484
<i>EGFR</i>	618	NA
<i>EGFR</i> , <i>ALK</i> , <i>ROS1</i>	342	NA
<i>EGFR</i> , <i>ALK</i> , <i>ROS1</i> , <i>MET</i>	40	NA

PSM, propensity score matching; ARMS, amplification refractory mutation system; NGS, next-generation sequencing.

**Table S2** Baseline characteristics of lung cancer patients from ethnic groups in Yunnan

Characteristics	Han (n=3,664)	Yi (n=175)	Bai (n=100)	Hui (n=50)	Hani (n=48)	P value
Gender, n [%]						0.353
Female	1,745 [48]	73 [42]	45 [45]	23 [46]	18 [38]	
Male	1,919 [52]	102 [58]	55 [55]	27 [54]	30 [62]	
Age (years)						0.547
Mean $\pm$ SD	57.5 $\pm$ 10.4	56.7 $\pm$ 10.3	57.9 $\pm$ 11.0	55.4 $\pm$ 9.75	57.0 $\pm$ 11.6	
Median (min, max)	57.0 (17.0, 92.0)	56.0 (26.0, 81.0)	59.5 (28.0, 80.0)	54.0 (28.0, 82.0)	57.5 (31.0, 82.0)	
Smoking, n [%]						0.948
No	2,389 [65]	112 [64]	62 [62]	34 [68]	31 [65]	
Yes	1,275 [35]	63 [36]	38 [38]	16 [32]	17 [35]	
Brain metastasis, n [%]						0.645
No	3,288 [90]	159 [91]	90 [90]	48 [96]	44 [92]	
Yes	376 [10]	16 [9]	10 [10]	2 [4]	4 [8]	
Bone metastasis, n [%]						0.326
No	3,048 [83]	137 [78]	82 [82]	38 [76]	39 [81]	
Yes	616 [17]	38 [22]	18 [18]	12 [24]	9 [19]	
Visceral metastasis, n [%]						0.343
No	3,413 [93]	166 [95]	90 [90]	44 [88]	44 [92]	
Yes	251 [7]	9 [5]	10 [10]	6 [12]	4 [8]	
Stage, n [%]						0.262
I	824 [22]	37 [21]	17 [17]	14 [28]	8 [17]	
II	201 [5]	8 [5]	6 [6]	0 [0]	1 [2]	
III	629 [17]	29 [17]	16 [16]	3 [6]	6 [12]	
IV	2,010 [55]	101 [58]	61 [61]	33 [66]	33 [69]	
Histology, n [%]						0.817
LUAD	3,245 [89]	153 [87]	86 [86]	45 [90]	46 [96]	
LUSC	310 [8]	15 [9]	11 [11]	5 [10]	1 [2]	
NSCLC nos.	22 [1]	3 [2]	1 [1]	0 [0]	0 [0]	
ADSC	30 [1]	1 [1]	1 [1]	0 [0]	1 [2]	
LCLC	8 [0]	2 [1]	0 [0]	0 [0]	0 [0]	
Others	5 [0]	0 [0]	0 [0]	0 [0]	0 [0]	
SCLC	44 [1]	1 [1]	1 [1]	0 [0]	0 [0]	
Sample type, n [%]						0.637
PLA	1,307 [36]	57 [33]	37 [37]	16 [32]	13 [27]	
TIS	2,357 [64]	118 [67]	63 [63]	34 [68]	35 [73]	
Xuanwei, n [%]						<0.001
No	2,998 [82]	168 [96]	99 [99]	48 [96]	48 [100]	
Yes	666 [18]	7 [4]	1 [1]	2 [4]	0 [0]	

PSM, propensity score matching; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; NSCLC nos., non-small cell lung cancer not otherwise specified; ADSC, adipose-derived stem cell; LCLC, large-cell lung cancer; SCLC, small-cell lung cancer; PLA, plasma; TIS, tissue.