Table SI. Post hoc power analysis for the primary PFS and secondary OS endpoints.

Parameter	PFS endpoint	OS endpoint
HR[a]	0.189	0.416
Proportion in high IHC-MPEP group, π_1	24/50 (0.48)	15/31 (0.48)
Proportion in low IHC-MPEP group, π_2	26/50 (0.52)	16/31 (0.52)
Observed events	50/50	31/31
Total sample size	50	31
Power, 1-β	1.000 (100.0%)	0.685 (68.5%)
β error probability	<0.001	0.315
Conclusion	Adequate power (>80%)	Insufficient power (<80%)

[a]HR was obtained from univariate Cox proportional hazards regression analysis (IHC-MPEP high group vs. low group). PFS HR=0.189 (95% CI: 0.094-0.381); OS HR=0.416 (95% CI: 0.196-0.884). PFS, progression-free survival; OS, overall survival; HR, hazard ratio; CI, confidence interval; IHC-MPEP, immunohistochemistry-quantified EGFR mutant protein expression percentage. The widely accepted 80% threshold was used to define adequate statistical power.

Table SII. Bland-Altman analysis for consistency between immunohistochemistry-detected EGFR mutational percentage and next-generation sequencing-derived mutational abundance (n=24).

Parameter	Value
Mean (CI)	14.949 (4.247-25.651)
P-value	P<0.001[a]
95% Upper limit of the LoA (CI)	67.377 (47.800-86.955)
95% Lower limit of the LoA (CI)	-37.480 (-57.058--17.902)
Repetition coefficient	59.099

[a]P<0.01. CI, confidence interval; LoA, limits of agreement.

Table SIII. Rank consistency assessment of three EGFR mutation metrics using Kendall's W test.

Variable	Rank average	Median	Kendall's W coefficient	χ^2	P-value
IHC mutation percentage	2.833	38.26			
Next-generation sequencing mutation abundance	2.083	24.02	0.771	37	P<0.001[a]
IHC staining expression score	1.083	2.00			

[a]P<0.01. IHC, immunohistochemistry.

Table SIV. Shapiro-Wilk normality test for continuous variables.

Variable	n	Deviation degree	Kurtosis degree	Shapiro-Wilk	P-value
Next-generation sequencing mutational abundance	24	-0.243	-0.688	0.937	P=0.137
Immunohistochemical mutational percentage	50	0.496	-0.762	0.974	P=0.329
Progression-free survival, months	50	1.900	3.881	0.802	P<0.001[a]
Overall survival, months	31	1.506	3.787	0.886	P=0.003[b]
EGFR exon 19 deletion	33	-0.396	-0.653	0.982	P=0.286
EGFR leucine-to-arginine substitution at codon 858	17	0.147	-1.341	0.932	P=0.232

[a]P<0.001, [b]P<0.01. P>0.05 indicated that the normal distribution assumption was met, and P<0.05 rejected the null hypothesis that the normal distribution assumption was not met.

Table SV. Independent samples Student's t-test of immunohistochemistry-detected EGFR mutation percentage between Del19 and L858R mutation subgroups.

Mutation subtype	n	Mean mutation, %	Standard deviation	95% confidence interval	T-value	Degrees of freedom	P-value
Del19	33	47.95	20.09	40.82-55.08			
L858R	17	55.50	17.70	46.40-64.60			
Between-group					-1.257	48	0.215

Between-group comparison of normally distributed continuous data was performed using the independent samples Student's t-test. Del19, exon 19 deletion; L858R, leucine-to-arginine substitution at codon 858.

Table SVI. Univariate Cox proportional hazards regression analysis of prognostic factors for PFS and OS.

	PFS (n=50)		OS (n=31)	
Variable	HR (95% CI)	P-value	HR (95% CI)	P-value
IHC-MPEP, high vs. low	0.19 (0.09-0.38)	<0.001[a]	0.420 (0.200-0.880)	0.023[b]
Smoking status, ever vs. never	1.205 (0.610-2.383)	0.591	0.759 (0.321-1.794)	0.530
Brain metastases, yes vs. no	0.734 (0.368-1.462)	0.379	0.749 (0.295-1.901)	0.543
EGFR mutation subtype, leucine-to-arginine substitution at codon 858 vs. exon 19 deletion	1.077 (0.551-2.103)	0.828	1.091 (0.440-2.702)	0.851

[a]P<0.001, [b]P<0.05. HR, hazard ratio; CI, confidence interval; PFS, progression-free survival; OS, overall survival; IHC-MPEP, immunohistochemistry-quantified EGFR mutant protein expression percentage.

Table SVII. Differential analysis of immunohistochemistry-quantified EGFR mutant protein expression percentage and EGFR tyrosine kinase inhibitor efficacy in the PR and SD subgroups.

Response subgroup	Mean value	Standard deviation	Mean difference	95% confidence interval	T-value	Degrees of freedom	P-value
SD	44.01	22.45					
PR	56.76	14.29	-12.76	-23.50-2.005	-2.397	40.704	0.021[a]
Total	50.39	19.71					

[a]P<0.05. PR, partial response; SD, stable disease.