Supplementary

Table S1 Comparison of T790M mutation between Exon 19 del and Exon 21 L858R

T790M mutation detected from rebiopsy	Exon 19 del	Exon 21 L858R	P value
No	11	14	0.569
Yes	21	20	

Table S2 Comparison of T790M mutation between first-line EGFR-TKIs applied

T790M mutation detected from rebiopsy	Gefitinib	Erlotinib	Afatinib	P value
No	11	13	1	1.000
Yes	17	22	2	

EGFR, epidermal growth factor receptor; TKI, tyrosine kinase inhibitor.

Table S3 Significantly enriched pathways in PD-L1-high samples of the NCCRI dataset

Pathway name	NES	NOM p-val	FDR q-val
HALLMARK_COMPLEMENT	2.048101	< 0.001	0.0292
HALLMARK_ALLOGRAFT_REJECTION	1.966872	0.002053	0.033883
HALLMARK_MITOTIC_SPINDLE	1.958839	0.002101	0.024289
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.851237	0.016227	0.044286
HALLMARK_INFLAMMATORY_RESPONSE	1.835194	0.005882	0.042558
HALLMARK_PI3K_AKT_MTOR_SIGNALING	1.784433	0.014433	0.051453
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	1.73737	0.024194	0.063726
HALLMARK_IL6_JAK_STAT3_SIGNALING	1.729845	0.010142	0.057661
HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.706928	0.031496	0.060933
HALLMARK_APOPTOSIS	1.558312	0.044	0.111092
HALLMARK_KRAS_SIGNALING_UP	1.541062	0.017857	0.111815
HALLMARK_IL2_STAT5_SIGNALING	1.52697	0.032	0.110468
HALLMARK_APICAL_SURFACE	1.519022	0.027833	0.100429
HALLMARK_COAGULATION	1.37665	0.04878	0.16847

NES, normalized enrichment score; NOM p-val, nominal p-value; FDR q-val, false discovery rate q-value.

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Table S4 Significantly enriched pathways in PD-L1-high samples of the TCGA dataset

Pathway Name	NES	NOM p-val	FDR q-val
HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.825302	< 0.001	0.233402
HALLMARK_MITOTIC_SPINDLE	1.76726	0.015209	0.194208
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.713135	0.012121	0.20482
HALLMARK_IL6_JAK_STAT3_SIGNALING	1.687761	0.010395	0.189793
HALLMARK_ALLOGRAFT_REJECTION	1.606663	0.012397	0.188941
HALLMARK_IL2_STAT5_SIGNALING	1.549698	0.020704	0.208801
HALLMARK_INFLAMMATORY_RESPONSE	1.544507	0.014644	0.193252
HALLMARK_APOPTOSIS	1.544013	0.049383	0.175785

NES, normalized enrichment score; NOM p-val, nominal p-value; FDR q-val, false discovery rate q-value.

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Table S5 Comparison of mutation profiles between PD-L1-high and PD-L1-low samples of the TCGA dataset

Gene	Fisher p-value	Number of mutated samples in PD-L1 high group (Incidence %)	Number of mutated samples in PD-L1 low group (Incidence %)
MUC16	0.034	11 (44.0)	12 (30.77)
TTN	0.043	12 (48.0)	17 (43.59)
CSMD1	0.031	5 (20.0)	9 (23.08)
ADAMTS20	0.045	1 (4.0)	3 (7.69)
CACNA1G	0.045	1 (4.0)	3 (7.69)
CACNG3	0.045	1 (4.0)	3 (7.69)
CHRNA4	0.045	1 (4.0)	3 (7.69)
CLEC16A	0.045	1 (4.0)	3 (7.69)
GABRA4	0.045	1 (4.0)	3 (7.69)
INSC	0.045	1 (4.0)	3 (7.69)
MED13	0.045	1 (4.0)	3 (7.69)
PGM2	0.045	1 (4.0)	3 (7.69)
PPP1R3A	0.045	1 (4.0)	3 (7.69)
SYTL4	0.045	1 (4.0)	3 (7.69)
TPO	0.045	1 (4.0)	3 (7.69)
ARHGAP6	0.013	0 (0.0)	3 (7.69)
BRINP1	0.013	0 (0.0)	3 (7.69)
COBL	0.013	0 (0.0)	3 (7.69)
PCDHA5	0.013	0 (0.0)	3 (7.69)
PCDHB2	0.013	0 (0.0)	3 (7.69)
PLA1A	0.013	0 (0.0)	3 (7.69)
POLQ	0.013	0 (0.0)	3 (7.69)
SEC14L5	0.013	0 (0.0)	3 (7.69)
TIE1	0.013	0 (0.0)	3 (7.69)
USP24	0.013	0 (0.0)	3 (7.69)
SIPA1L3	0.045	0 (0.0)	4 (10.26)

Only genes with significant differences are shown.

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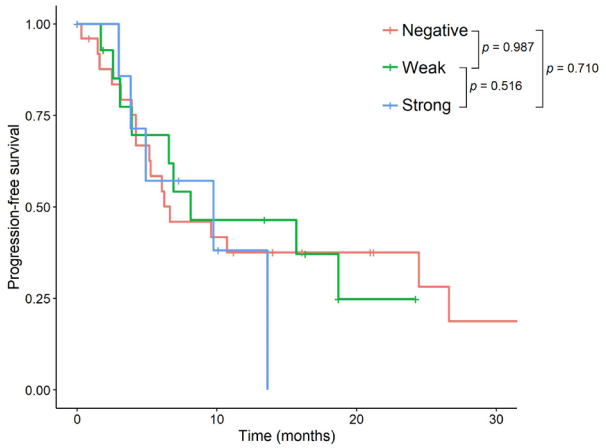

Figure S1 Kaplan-Meier curve of progression-free survival in patients receiving third-generation EGFR-TKI therapy. EGFR, epidermal growth factor receptor; TKI, tyrosine kinase inhibitor.

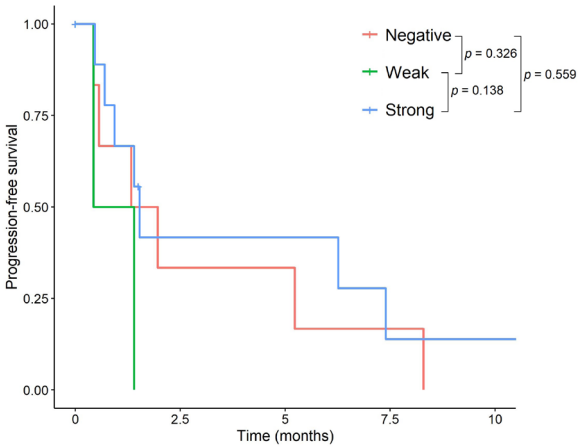

Figure S2 Kaplan-Meier curve of progression-free survival in patients receiving immune checkpoint inhibitor therapy.

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