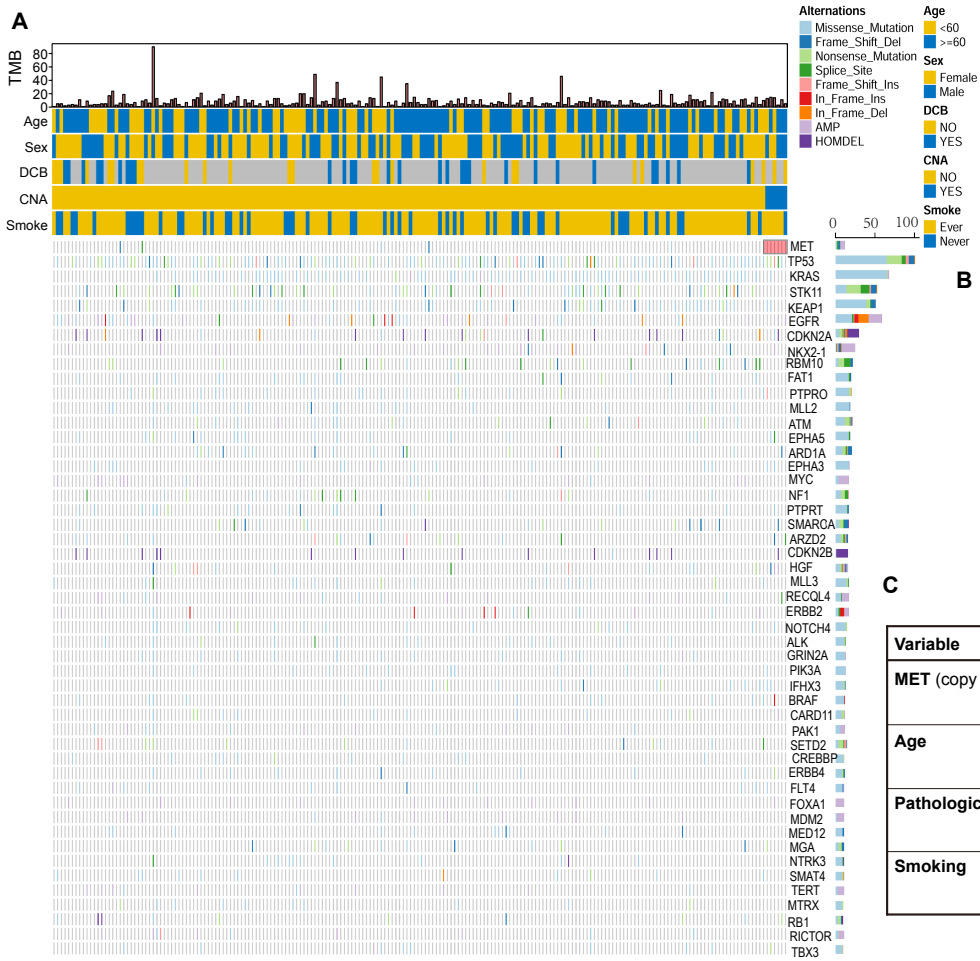
Supplementary Figure S2

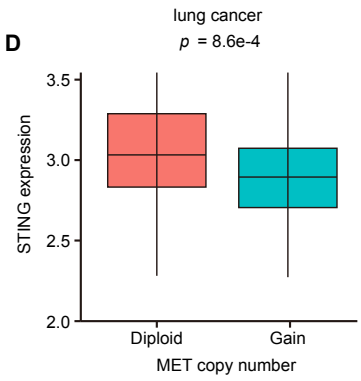


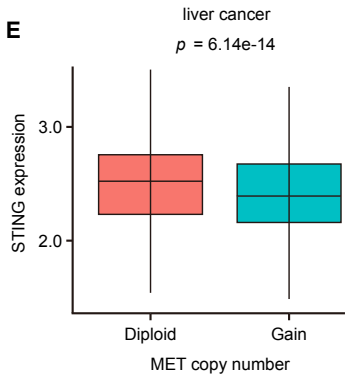
B

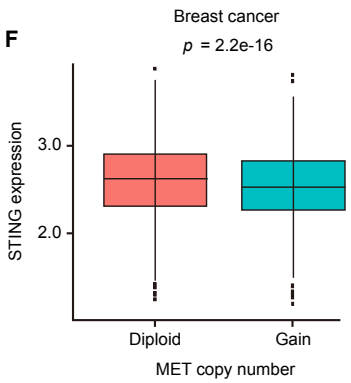
Characteristics (n = 193)	95%HR .CI	*p* Value
Age (≥ 60 *vs* < 60)	1.05 (0.72-1.55)	0.79
Sex (male *vs* female)	1.17 (0.81-1.68)	0.42
Smoker (never *vs* ever)	1 (0.65-1.55)	0.99
TMB (> median *vs* < median)	0.96 (0.66-1.39)	0.83
MET (AMP *vs* WT)	2.06 (1.11-5.05)	0.06

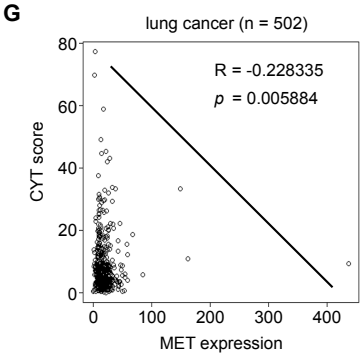
C

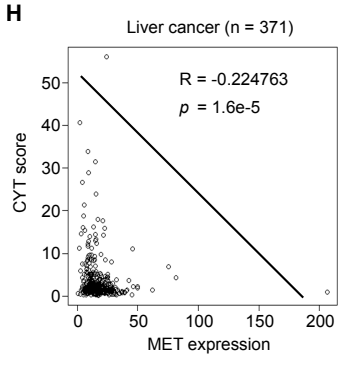
Variable		N	Hazard ratio		*p* Value
MET (copy number)	< 5	70		Reference	
	≥ 5	11		3.70 (1.77, 7.76)	< 0.001
Age	< 60	39		Reference	
	≥ 60	42		1.16 (0.64, 2.10)	0.3
Pathological	SCC	12		Reference	
	AC	69		1.63 (0.67, 3.95)	0.6
Smoking	Never	14		Reference	
	Ever	67		1.10 (0.49, 2.44)	0.8











Supplementary Figure S2. MET amplification is associated with poor response to ICB

A, MET amplification is associated with poor response to ICB in NSCLC. Stacked plots show mutational burden (histogram, top), mutations or CNA (copy number alternation) in *MET*, *TP53*, *STK11*, *KRAS*, *KEAP1*, *EGFR*, *FAT1*, *MLL2*, *MYC* (more than 5% of the mutated genes were present), their mutational rates in patients having achieved DCB (durable clinical response) or progressive disease. Multivariable analysis of DCB to gene mutations or CNA, age, TMB, smoke, and sex. Mutational marks (bottom), mutational rates (histogram, right), MET AMP group (n = 6) marked as red box.

B, Multivariate Cox regression to identify independent predictor in MSKCC cohort (n = 193).

C, Multivariable analysis of PFS in NSCLC patients underwent anti-PD1 therapy in Hubei cancer hospital cohort (n = 81).

D-F, The correlation of MET amplification and STING expression in TCGA data.

G-H, Immune cytolytic (CYT) score across 2 human cancers derived from TCGA sequencing data stratified by MET high and MET low status.