

Figure S1 Flowchart of data processing of the TCGA dataset and the ICI-treated NSCLC cohort. TCGA, The Cancer Genome Atlas; ICI, immune checkpoint inhibitor; NSCLC, non-small cell lung cancer.

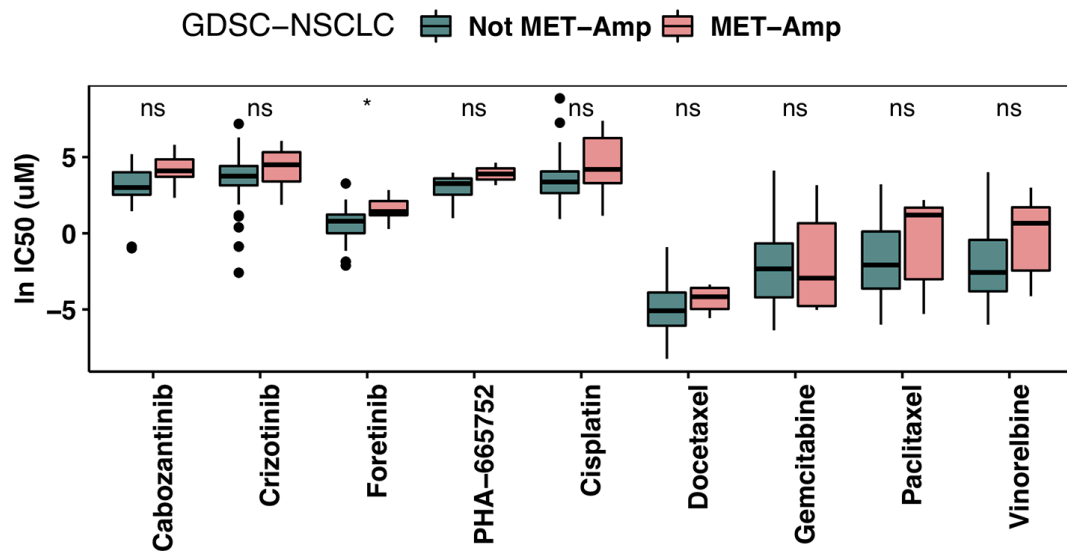


Figure S2 Comparison of the drug sensitivity of cell lines from the GDSC-NSCLC database between *MET*-Amp and non-*MET*-Amp cell lines. (Mann-Whitney U test; *, $P < 0.05$). GDSC, Genomics of Drug Sensitivity in Cancer; NSCLC, non-small cell lung cancer; MET, mesenchymal-epithelial transition; MET-Amp, MET-amplification.

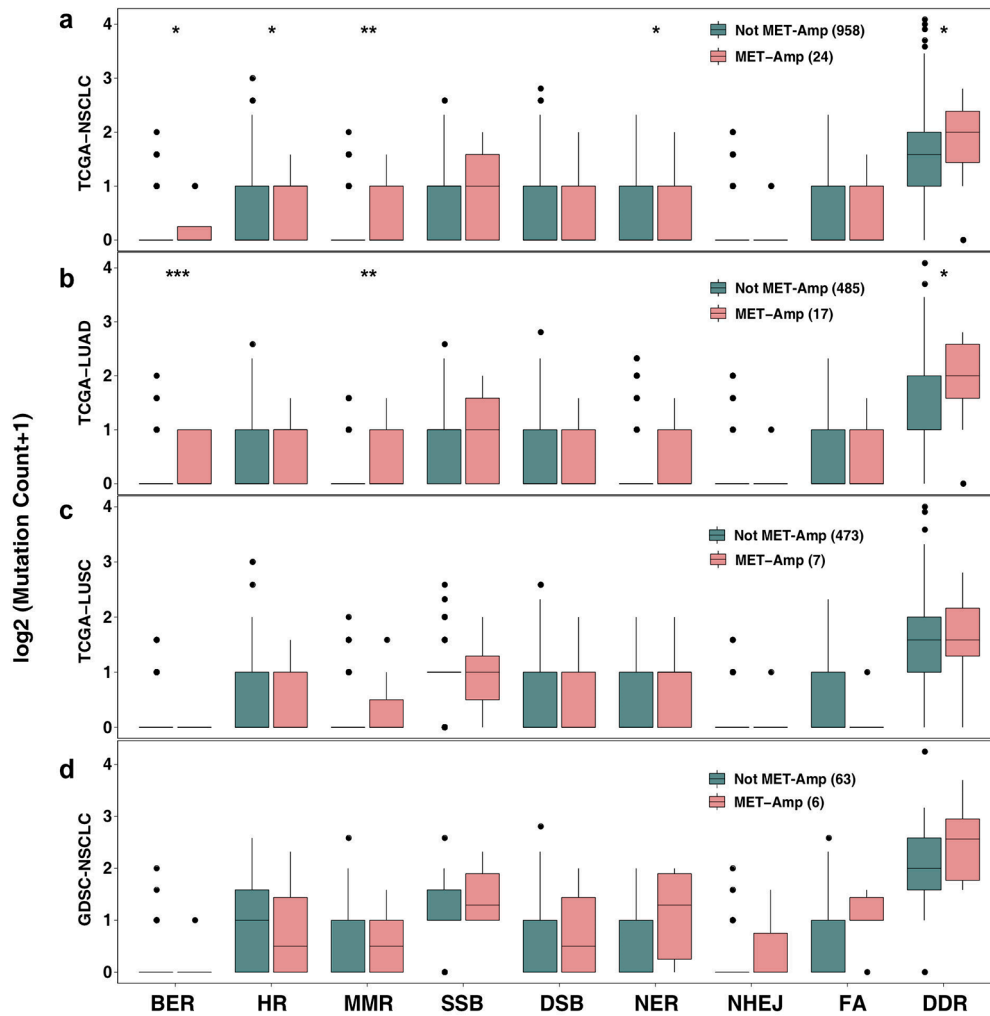


Figure S3 Comparison of DNA damage-related gene set alterations in cell lines from the TCGA-NSCLC (A), TCGA-LUAD (B), TCGA-LUSC (C), and GDSC-NSCLC (D) databases between the *MET*-Amp and non-*MET*-Amp groups. (Mann-Whitney U test; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$). TCGA, The Cancer Genome Atlas; NSCLC, non-small cell lung cancer; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; GDSC, Genomics of Drug Sensitivity in Cancer; MET, mesenchymal-epithelial transition; MET-Amp, MET-amplification.