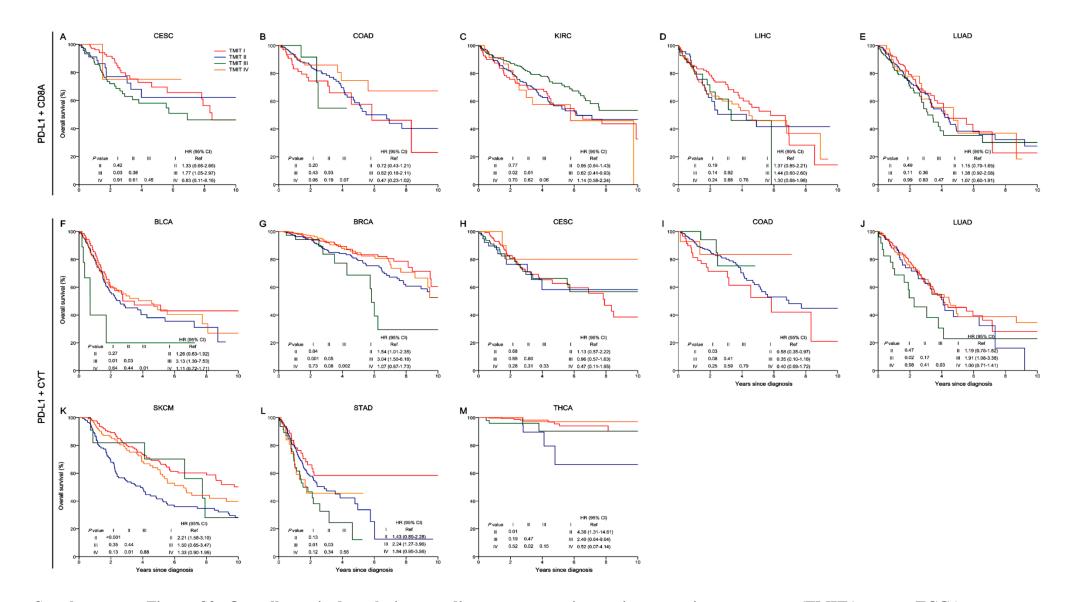


Supplementary Figure S1. Correlation between mutation burden and neoantigen number. The number of somatic mutations is significantly correlated with that of neoantigens across all TCGA cancer types. R^2 and P values are calculated by the Spearman correlation test.



Supplementary Figure S2. Overall survival analysis according to tumor microenvironment immune types (TMITs) across TCGA cancer types. Kaplan-Meier plot of overall survival according to TMIT as defined by PD-L1 and CD8A expression in CESC, COAD, KIRC, LIHC, LUAD (A–E), and by PD-L1 and CYT expression in BLCA, BRCA, CESC, COAD, LUAD, SKCM, STAD, and THCA. *P* values are calculated by log-rank test. Hazard ratios (HRs) and corresponding confidence intervals (CIs) of different TMIT types as compared to type I are calculated by Cox proportional hazards model.