Figure S1 Workflow of this study. TMB, tumor mutation burden. TMBPI, TMB prognostic index.
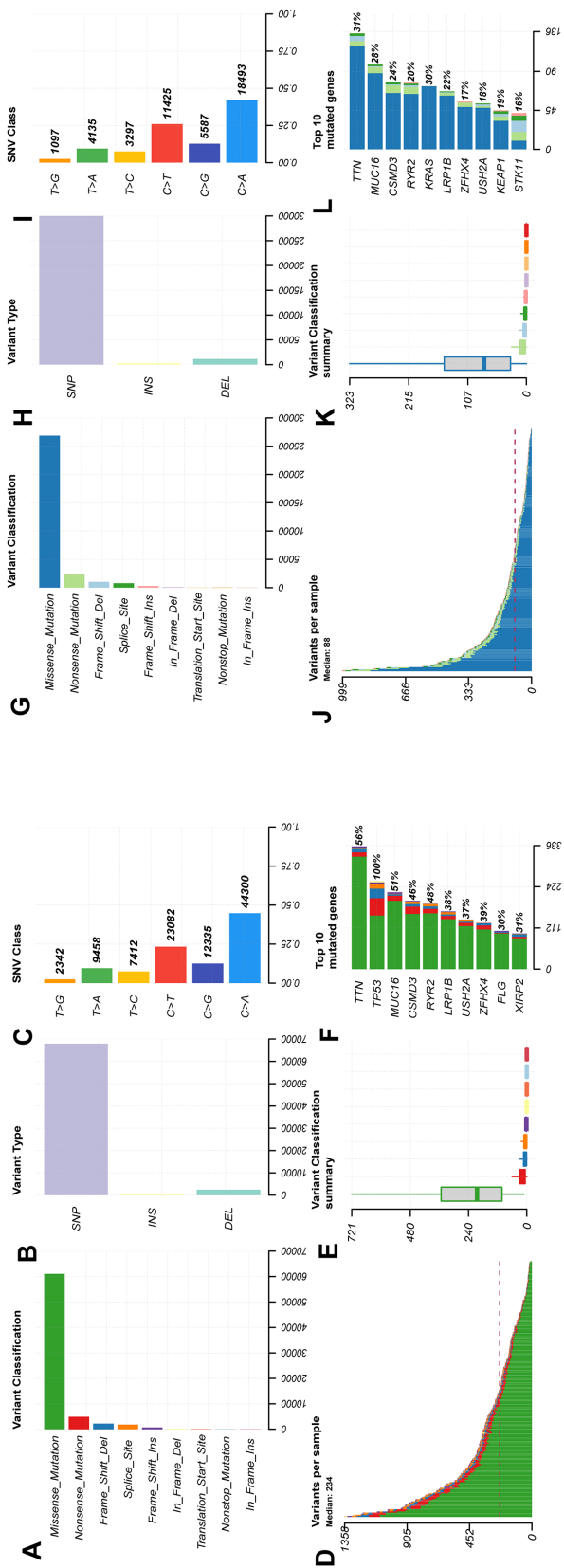
Figure S2 he general information of the mutations in *TP53*ᵐᵘᵗ (A-F) and *TP53*ʷᵗ (G-L) LUAD. (A-C; G-I) Statistical analysis of somatic mutation types according to category. The bar plots show the cumulative number of variants identified in the samples. (D-E; J-K) Assessment of tumor mutation burden with the number variants per sample. (F; L) The top 10 most frequently mutated genes in the samples. Colored bars represent variant classification. LUAD, lung adenocarcinoma; *TP53*ᵐᵘᵗ, *TP53* mutation; INS, insertion; DEL, deletion.
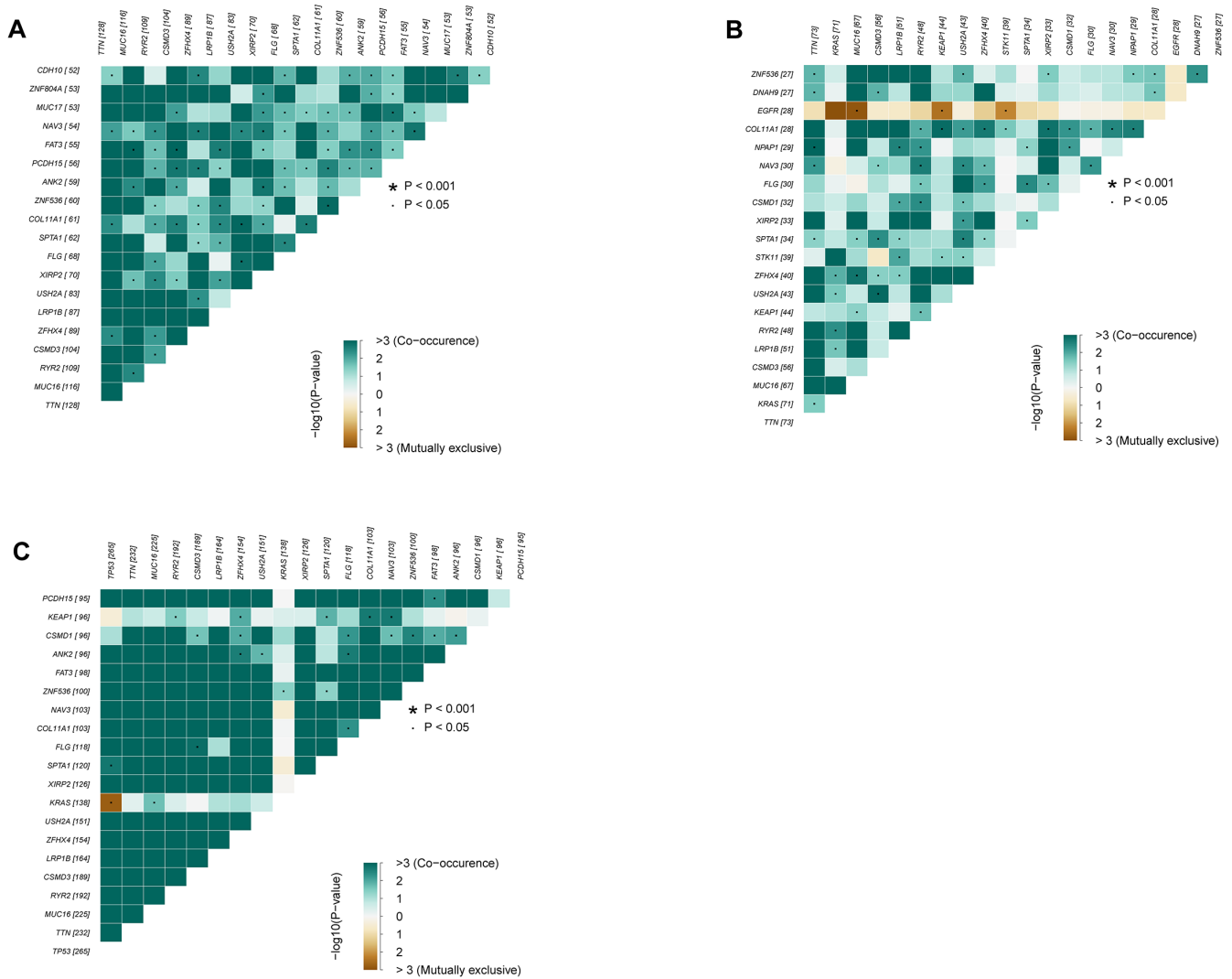
Figure S3 The coincident and exclusive associations across the mutated genes in $TP53^{mut}$ (A), $TP53^{wt}$ (B) and all (C) LUAD. Green represents co-occurrence and red represents mutually exclusive relationships (*P<0.001; •P<0.05). LUAD, lung adenocarcinoma; $TP53^{mut}$, $TP53$ mutation; $TP53^{wt}$, wild-type $TP53$.
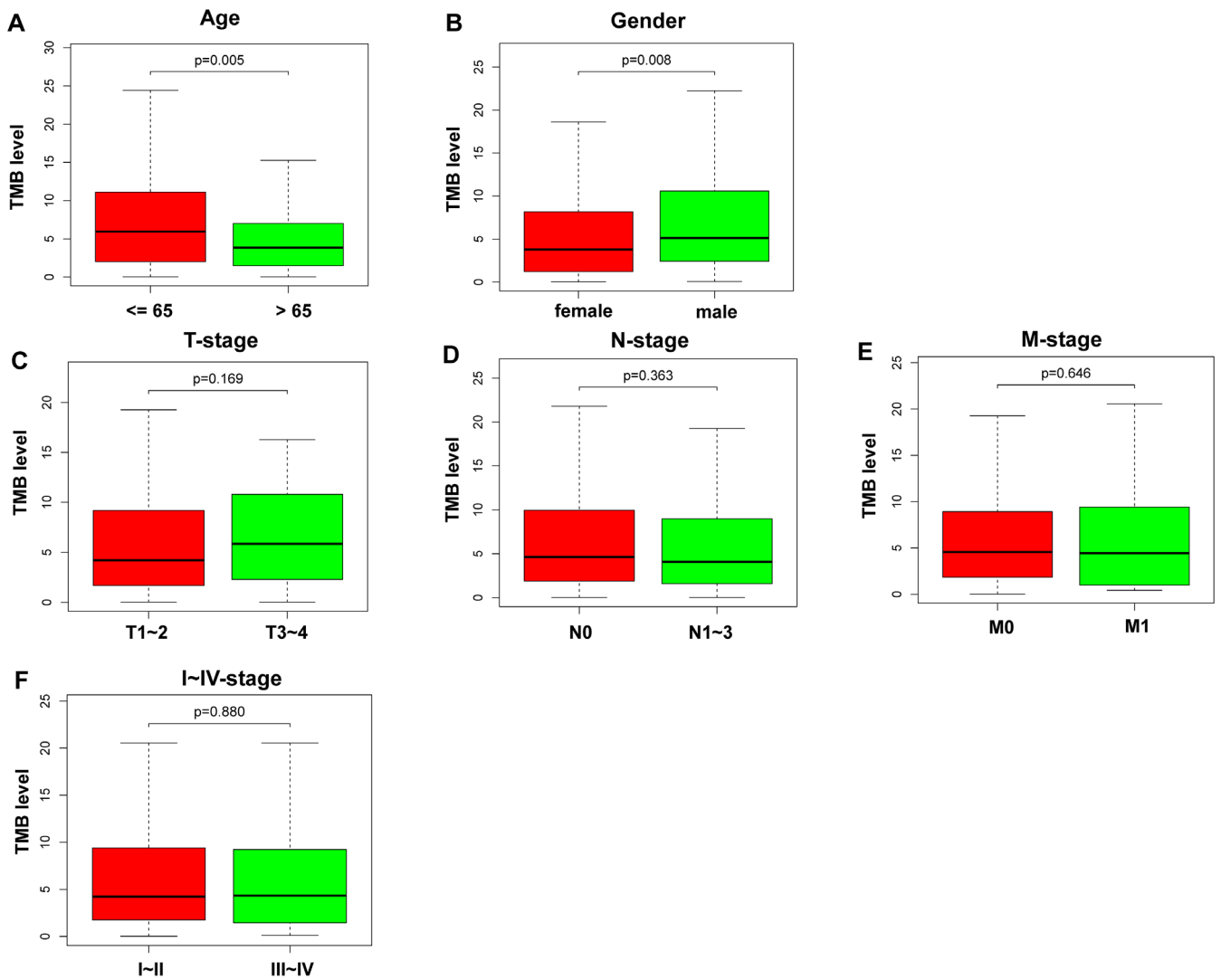
Figure S4 Correlation of TMB levels with clinical features. (A, B) Higher TMB levels related significantly to the ≤65-year age group (P=0.005) and male gender (P=0.003). (C-F) No significant difference of TMB levels was observed for AJCC-T stage, AJCC-N stage, AJCC-M stage, and AJCC-I~IV stage. Red and green represent the different groups in each box plot. TMB, tumor mutation burden.