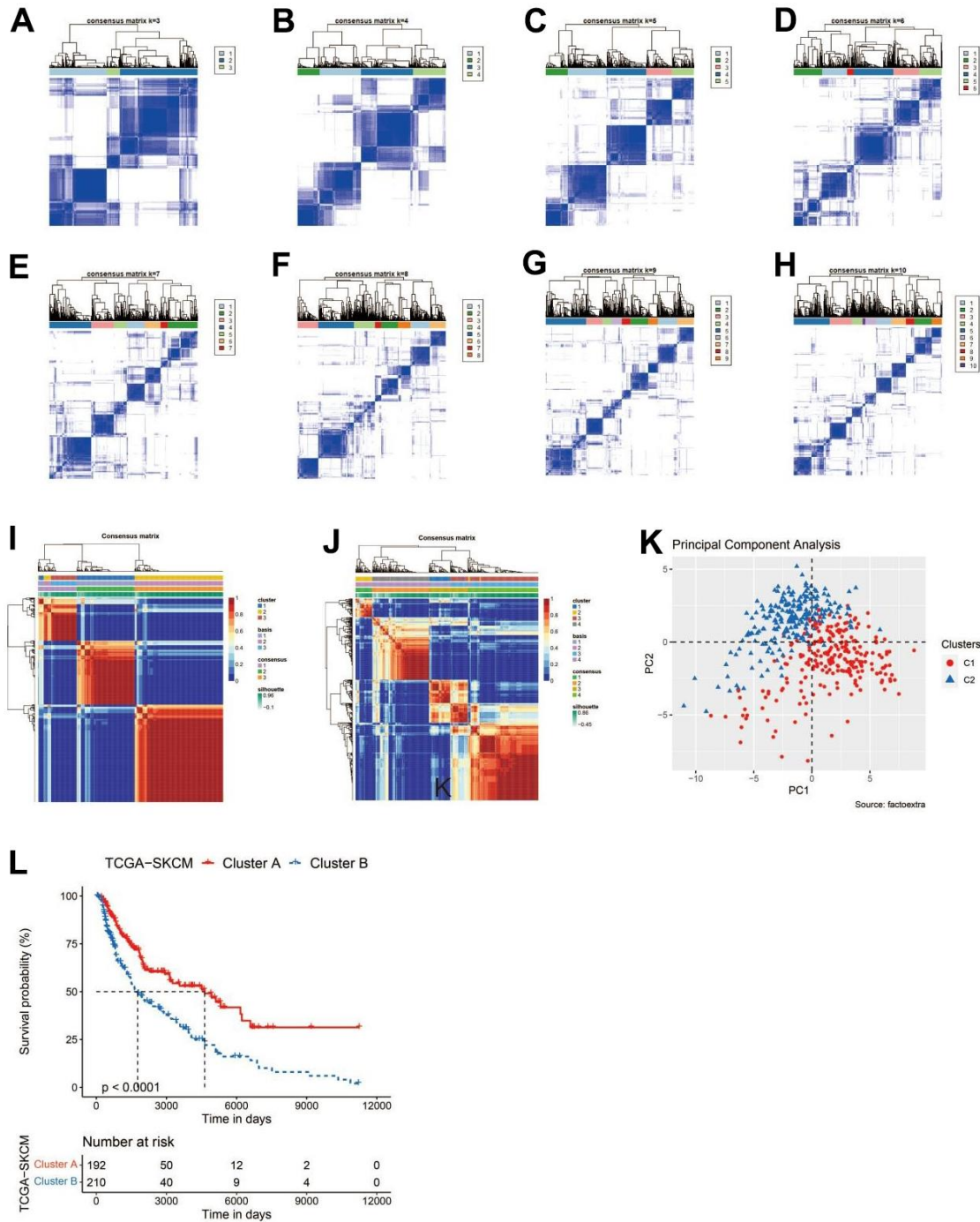
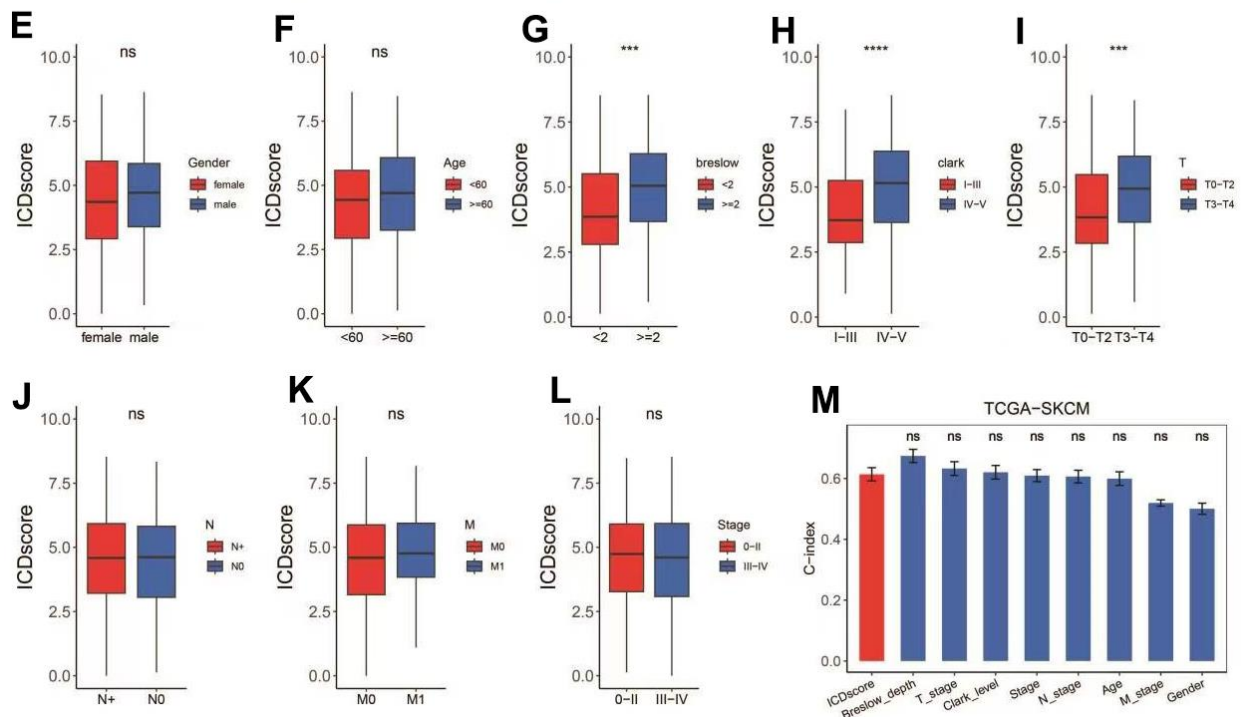
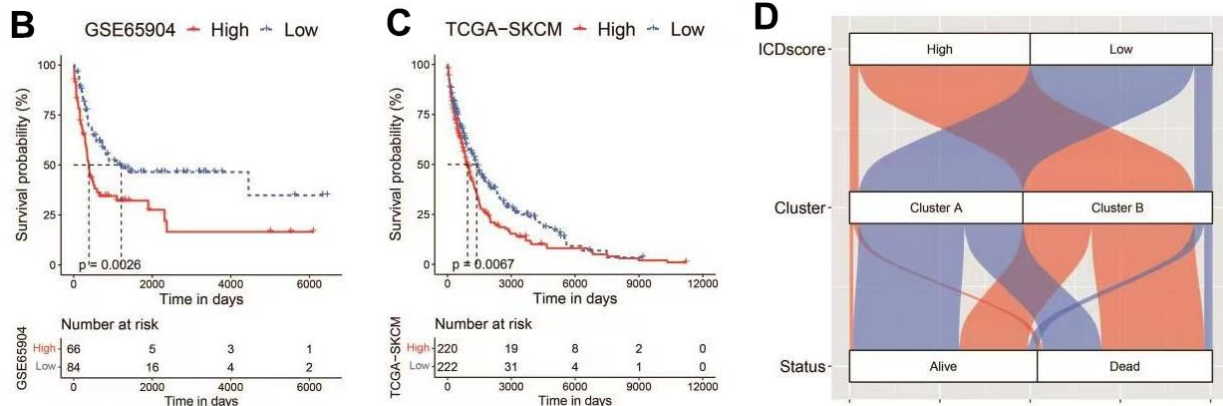
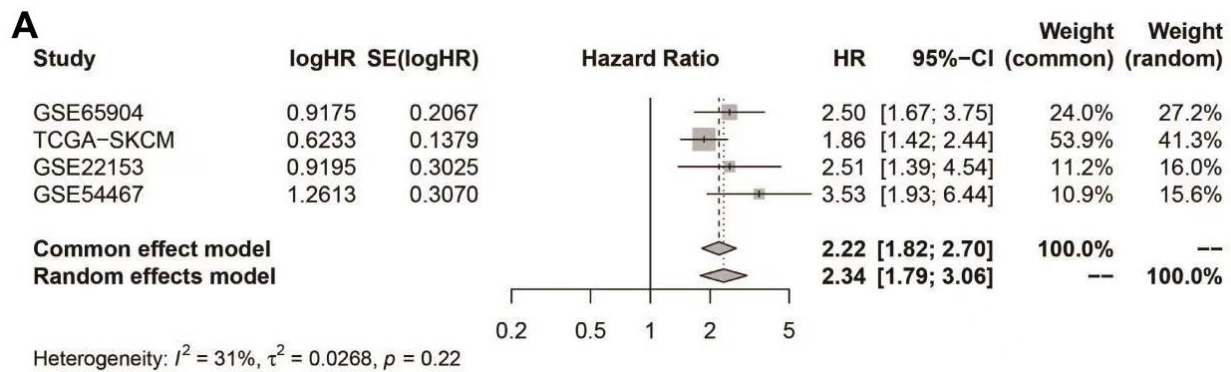


SUPPLEMENTARY FIGURES



Supplementary Figure 1. (A–H) Heatmap depicts consensus clustering solution for 34 ICD related genes in melanoma patients from the TCGA-SKCM dataset, when the $k = 3$ (A), 4 (B), 5 (C), 6 (D), 7 (E), 8 (F), 9 (G), and 10 (H). (I, J) Heatmap of NMF clustering results of melanoma patients from the TCGA-SKCM dataset, when the $k = 3$ (I) and 4 (J). (K) Principal component analysis (PCA) on the expression level of 34 ICD related genes in clusters classified by consensus clustering method. (L) Kaplan–Meier curves of OS in the Cluster A and B of melanoma patients.



Supplementary Figure 2. (A) Forest plot for the outcome of ICDscore in meta-analysis of melanoma patients using common or random model. (B, C) Kaplan–Meier curves of PFS in melanoma patients from ICDscore-high and ICDscore-low subgroups of GSE65904 (A) and TCGA-SKCM (B). (C) Sankey diagram showed the connection degree between ICD-based classification and Cluster A/B. (D) Sankey diagram showed the connection degree between ICDscore and patient clustering and survival status. (E–L) The distribution of ICDscore in melanoma patients divided by gender (E), age (F), Breslow depth (G), Clark level (H), T stage (I), N stage (J), M stage (K) and clinical stage (L). (M) The C-index of ICDscore and clinical features of melanoma patients.