Supplementary Figure 1. The flow diagram of the study.
Supplementary Figure 2. Edge-perturbation matrix construction and feature extraction. (A) Box-plot diagrams of randomly selected 1000 features in cancer and normal samples. (B) Scatter plots of randomly selected 1000 features in cancer and normal samples.

Supplementary Figure 3. (A–D) Comparative analysis results of edge perturbation feature subtypes. (A) Differences in tumor purity between cluster 1 and cluster 2: The abscissa axis represents the cluster group; the ordinate axis represents the percentage of tumor purity. (B) Differences in genome ploidy between cluster 1 and cluster 2: The abscissa axis represents the cluster group; the ordinate axis represents the percentage of tumor genome ploidy. (C) Differences in stemness indices of mRNA between cluster 1 and cluster 2: The abscissa axis represents the cluster group; the ordinate axis represents the percentage of stemness indices of mRNA. (D) Differences in epigenetic regulated stemness indices of mRNA between cluster 1 and cluster 2: The abscissa axis represents the cluster group; the ordinate axis represents the percentage of epigenetic regulated stemness indices of mRNA. (E–J) Comparison of clinical characteristics among different subtypes. (E) Comparison of the proportions of different stages (Stage I–IV) in different clusters: The abscissa axis represents different clusters; the ordinate axis represents the proportion of different stages. (F) Comparison of the proportions of different T stages (T1–T4) in different clusters: The abscissa axis represents different clusters; the ordinate axis represents the proportion of different T stages (T1–T4). (G) Comparison of the proportions of different N stages (N1–N3) in different clusters: The abscissa axis represents different clusters; the ordinate axis represents the proportion of different N stages (N1–N3). (H) Comparison of the proportions of different M stages (M0M1 or Mx) in different clusters: The abscissa axis represents different clusters; the ordinate axis represents the proportion of different M stages (M0M1 or Mx). (I) Comparison of the proportions of different smoking status in different clusters: The abscissa axis represents different clusters; the ordinate axis represents the proportion of different smoking status (little or often). (J) Comparison of the proportions of different age stages in different clusters: The abscissa axis represents different clusters; the ordinate axis represents the proportion of different age stages (younger, medium or older).
Supplementary Figure 4. Comparison of immune escape mechanism between the two clusters. (A) Comparison of homologous recombination deficiency scores between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the HRD score. (B) The level of chromosome instability between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the LST score. (C) The level of chromosome instability between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the TAI score. (D) The level of chromosome instability between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the LOH score. (E) The level of tumor mutation load between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the value of log10 (mutLoad nonsilent). (F) The level of tumor mutation load between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the value of log10 (mutLoad silent). (G) The level of tumor neoantigen load between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the value of log10 (SNV neoantigen). (H) The level of tumor neoantigen load between the two clusters: The abscissa axis represents different clusters; the ordinate axis represents the value of log10 (Indel neoantigen).
Supplementary Figure 5. (A) Pathway enrichment analysis results of the cluster 1. (B) Pathway enrichment analysis results of the cluster 2. (C) Identification results of differential methylation sites among characteristic subtypes: z-score heatmap of the top200 differential methylation sites. (D) Volcano map of differentially expressed genes. (E) Z-score heatmap of differentially expressed genes.