

**Figure S2.** Patient classification in the GEO cohort. (A) Consensus clustering results ( $K = 2$ ); (B) The consensus cumulative distribution function ( $K = 2$ ). (C) The delta area ( $K = 2$ ). (D) Distribution of cluster A and cluster B in t-SNE. (E) The expression levels of fatty acid metabolism genes between cluster A and cluster B. TPM = transcript per million. t-SNE = t-distributed stochastic neighbor embedding.

