

Figure S1 RNA-seq analysis and experimental validation results. (A) The work flow of RNA-seq. (B) Heatmap of the correlation between each sample according to Pearson correlation coefficient analyses. (C) PCA analysis of three pairs of LUAD samples. (D) Flow cytometry of the cell cycle assay in H1975 cells. (E) Knockdown efficiency of ΔcircSPECC1 on qRT-PCR. Data are the mean ± SD. *, $P < 0.05$ for the t -test. LUAD, lung adenocarcinoma; miRNA, microRNA; mRNA, messenger RNA; circRNA, circular RNA; ceRNA, competing endogenous RNA; UALCAN, University of Alberta Cancer Research; GO, Gene Ontology; NC, negative control; circSPECC1, SPECC1 circular RNA; PCA, principal component analysis; qRT-PCR, quantitative real-time polymerase chain reaction; SD, standard deviation.

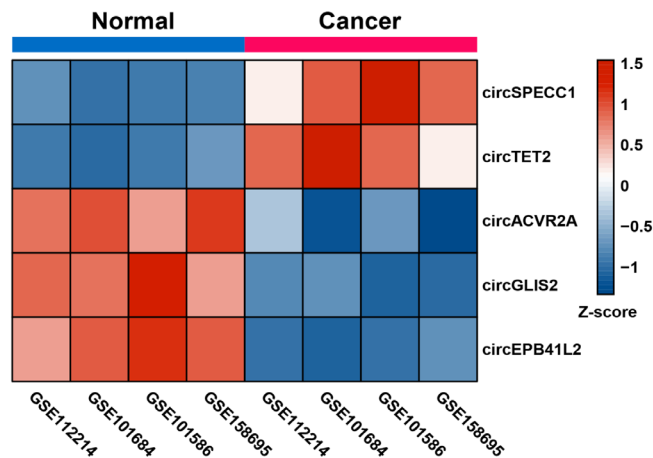


Figure S2 Heatmap display expression profiles of circRNA in the GEO data sets (GSE112214, GSE101684, GSE101586 and GSE158695). The junction reads were normalized to the z score. circSPECC1, SPECC1 circular RNA; circRNA, circular RNA; GEO, Gene Expression Omnibus.