Figure S1 Quality control and enrichment score of FAO at the single-cell level. (A,B) Visualization after performing quality control. (C) Violin plots comparing the FAO 87-gene signature scores based on Percentage and ssGSEA methods between C0 and C1. ****, P<0.0001.
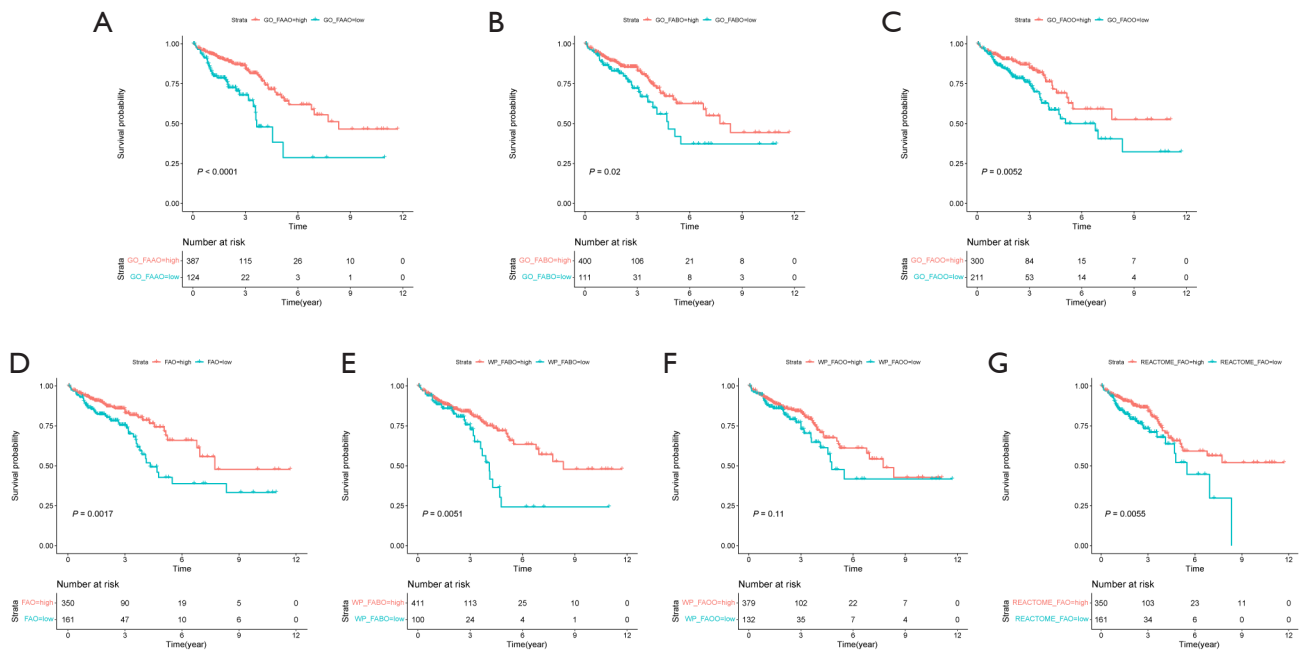
Figure S2 Survival analysis in seven gene sets related to FAO. (A-G) In the seven gene sets related to FAO, the K-M curves show that high-FAO patients tend to have favorable OS.
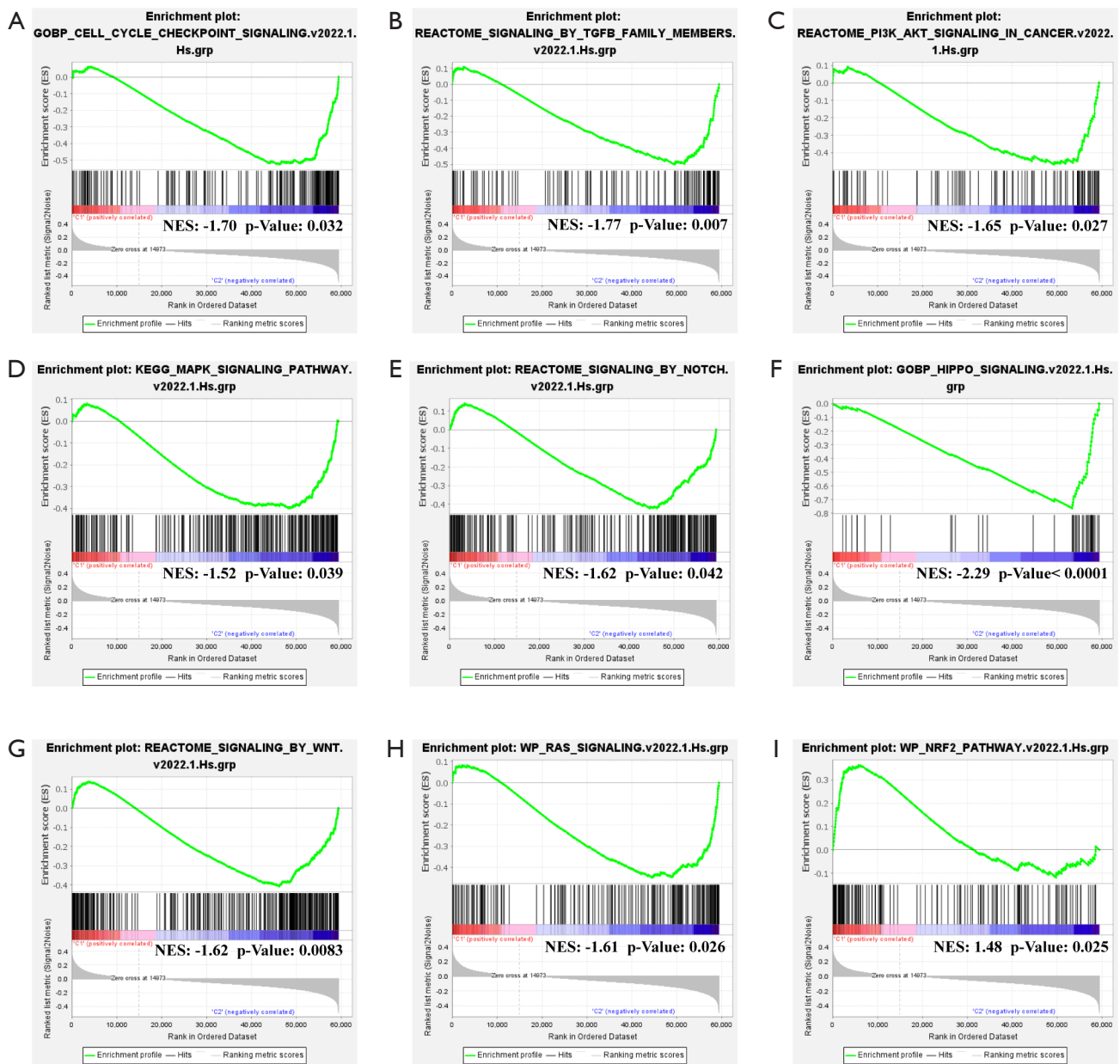
Figure S3 Enrichment analysis of carcinogenetic pathways in two clusters. (A-I) Gene set enrichment analysis (GSEA) of TCGA dataset in classical tumor pathways in Cluster 1 and Cluster 2.
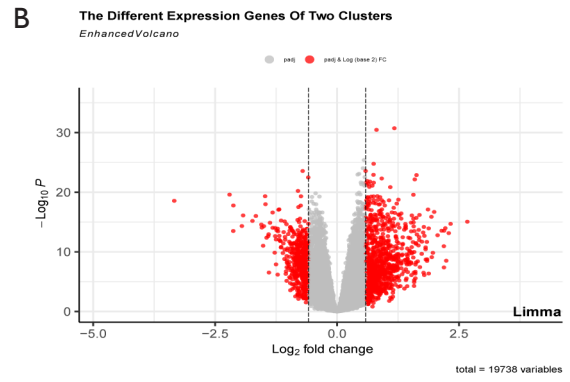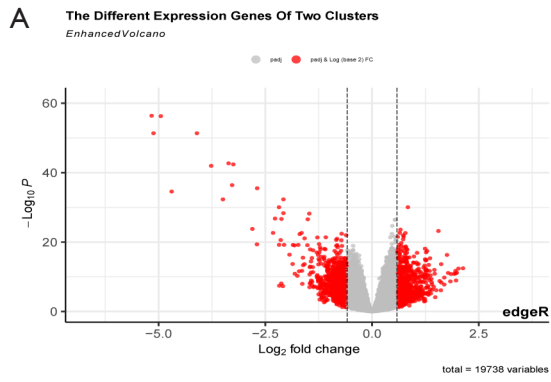
Figure S4 Differential gene expression analysis. (A,B) Volcano plots presenting the differential expression genes between Cluster 1 and Cluster 2 in TCGA based on *edgeR* and *limma* methods, red dots on the left side of the 0 axis represent downregulated genes, and the right-side red dots represent upregulated genes.