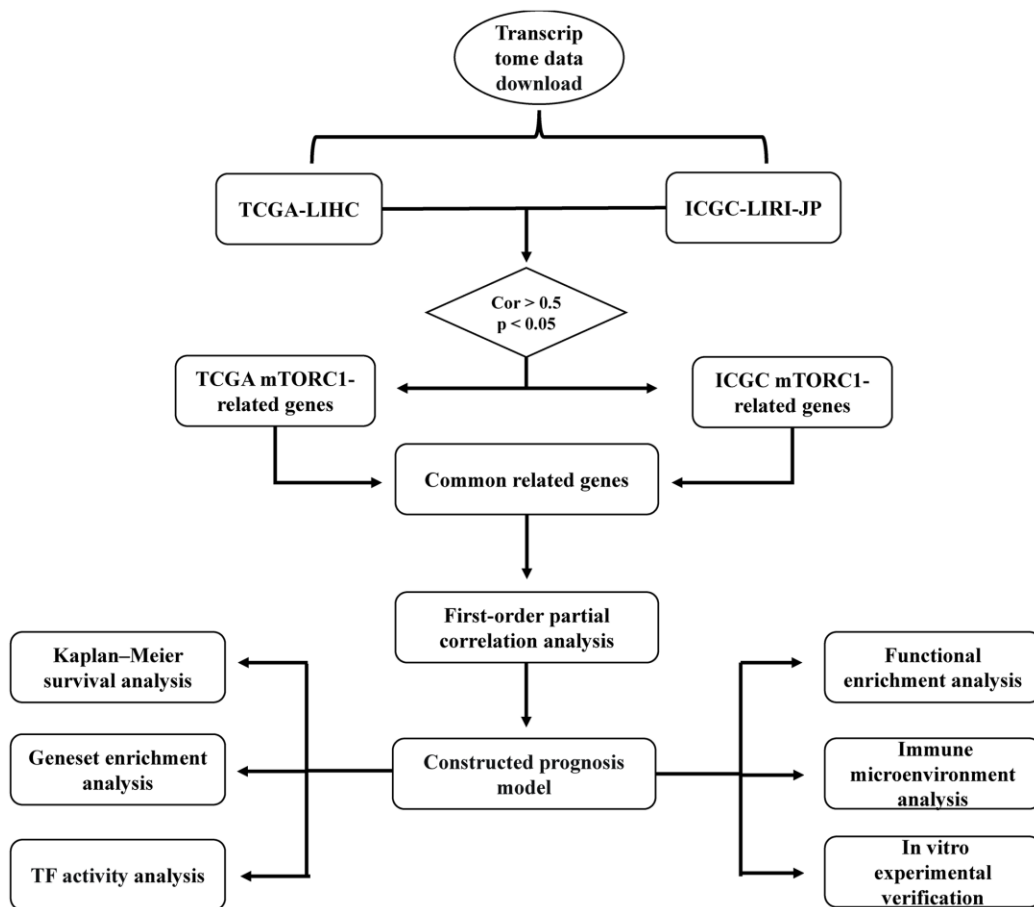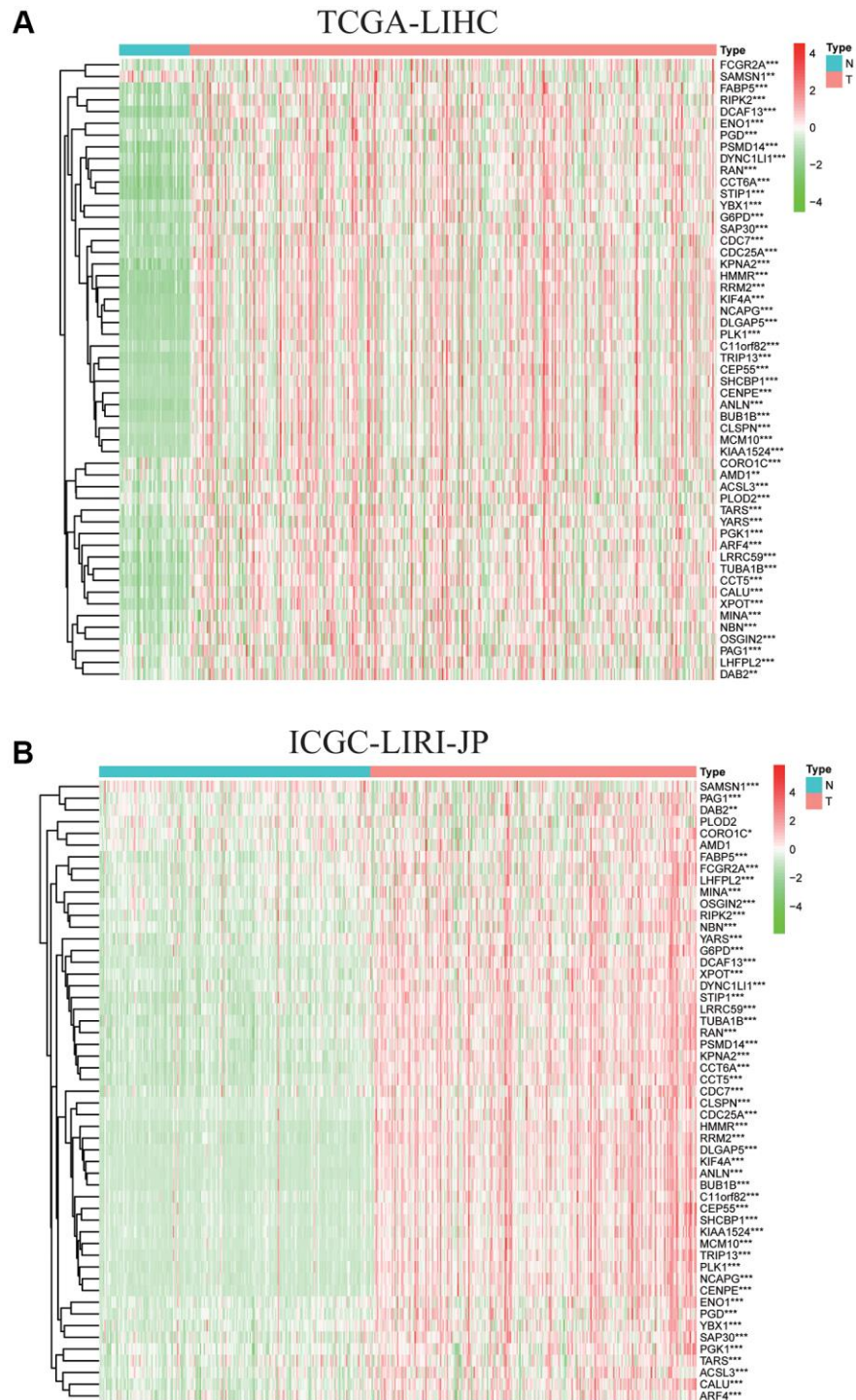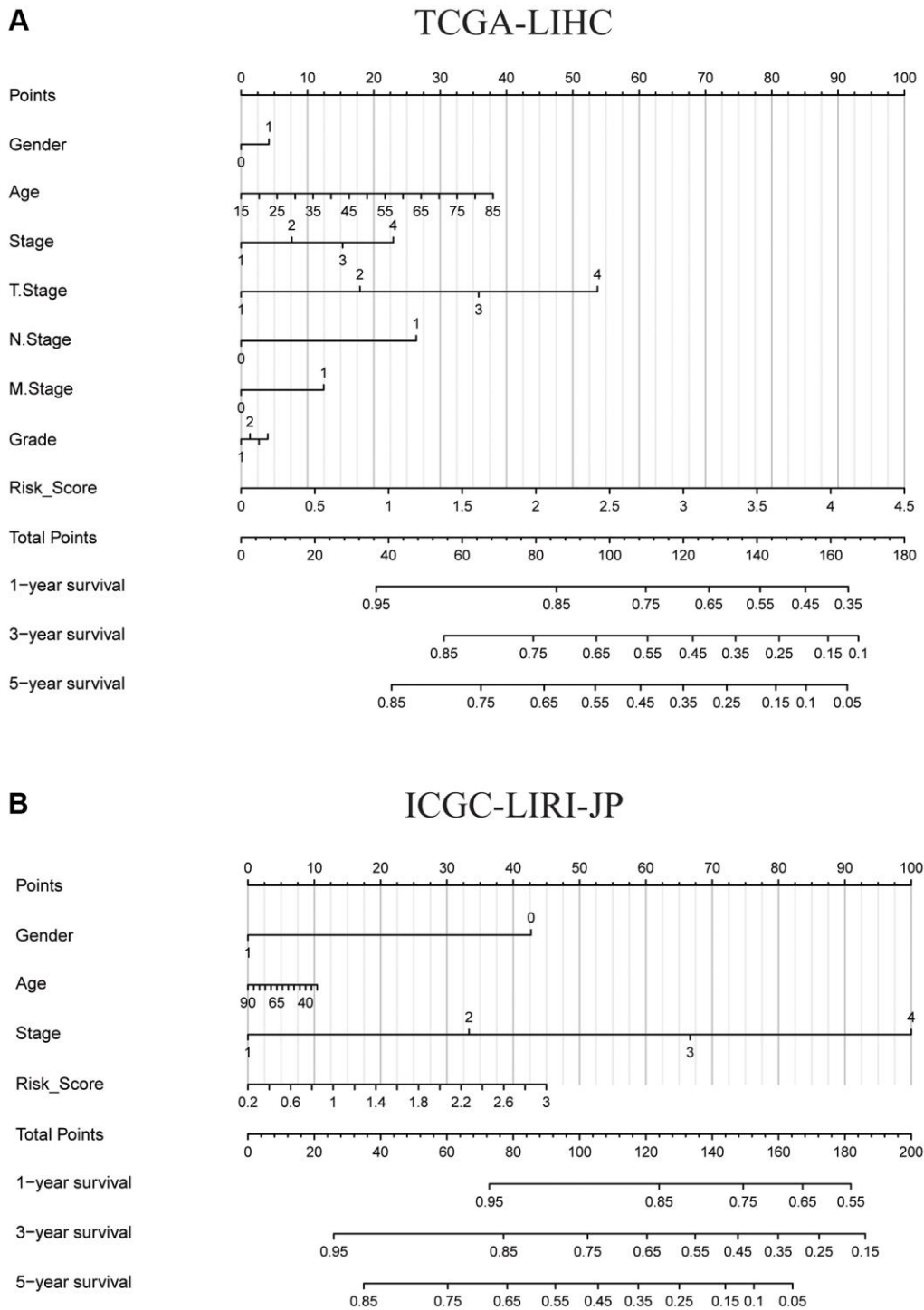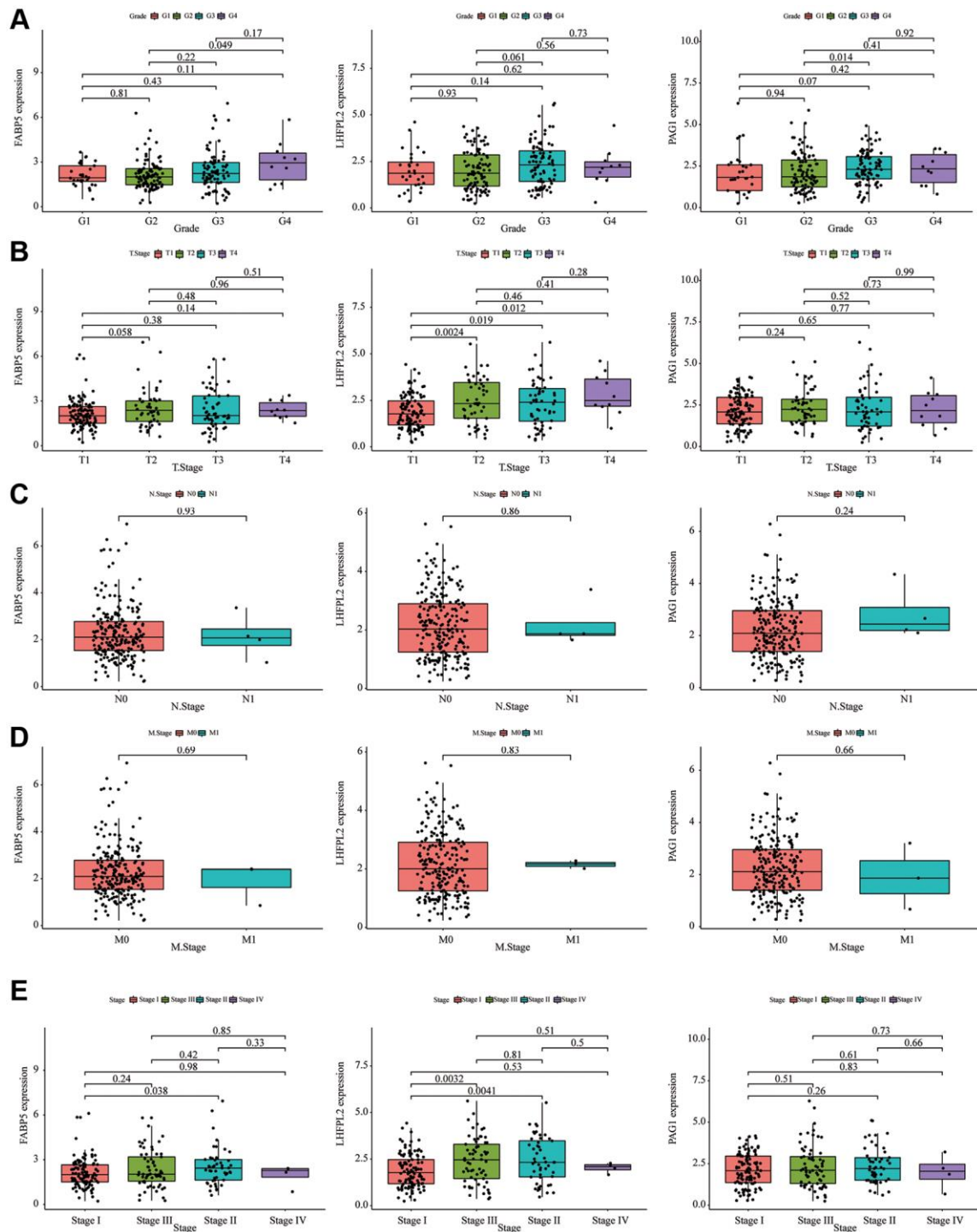# SUPPLEMENTARY FIGURES

Supplementary Figure 1. Flow diagram of the study.

Supplementary Figure 2. Heatmap of the mRNA expression levels of 53 genes in the two subtypes in (**A**) TCGA-LIHC and (**B**) ICGC-LIRI-JP datasets.

A

TCGA-LIHC

B

ICGC-LIRI-JP

Supplementary Figure 3. Construction of nomogram to assess the predictive efficiency of mTORC1-related signature in (**A**) TCGA-LIHC and (**B**) ICGC-LIRI-JP datasets.

Supplementary Figure 4. (**A**) The expression levels of three genes in different grades of cancers from TCGA database. (**B**) The expression levels of three genes in different T stages of cancers from TCGA database. (**C**) The expression levels of three genes in different *N* stages of cancers from TCGA database. (**D**) The expression levels of three genes in different M stages of cancers from TCGA database. (**E**) The expression levels of three genes in different tumor stages of cancers from TCGA database.