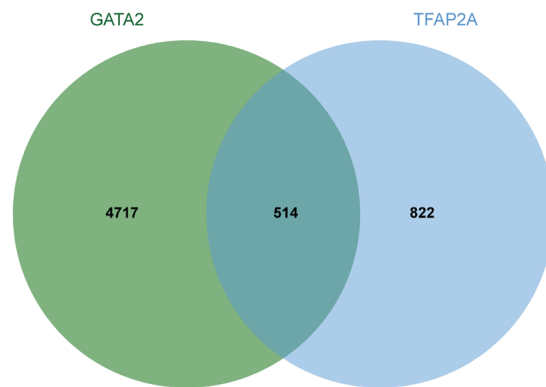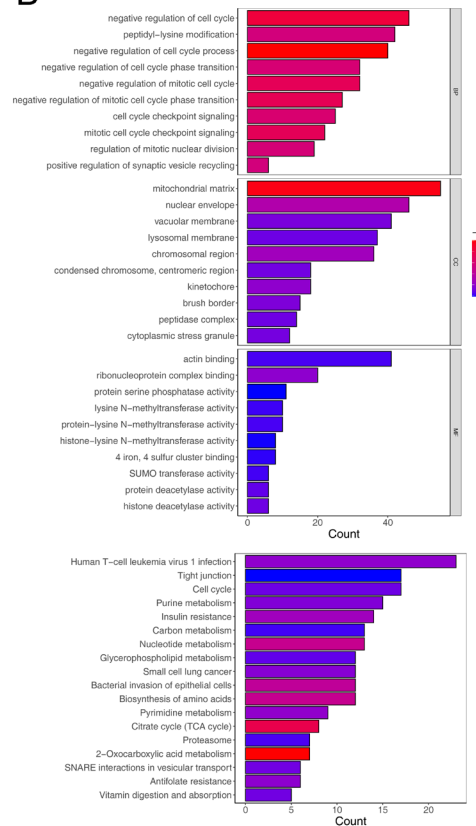**Figure S1** The analytical flow of this study. TCGA, The Cancer Genome Atlas; LUAD, lung adenocarcinoma; PPI, protein-protein interaction; LASSO, least absolute shrinkage and selection operator; ROC, receiver operating characteristic; K-M, Kaplan-Meier; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.
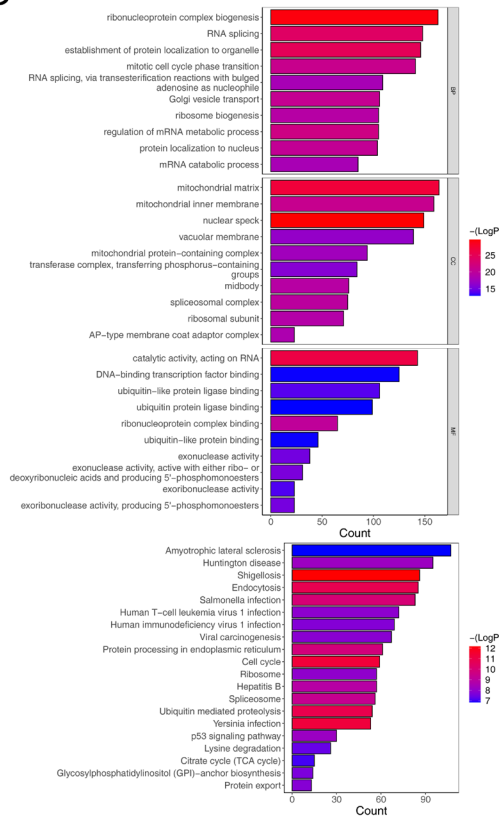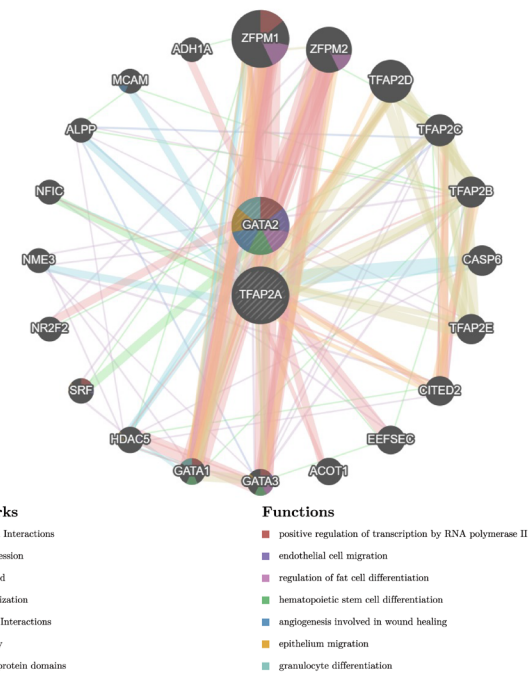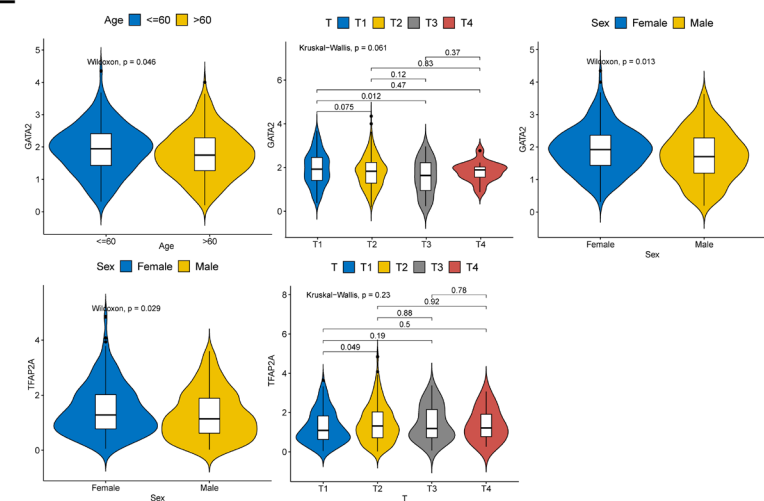
Figure S2 Analysis of TFAP2A and GATA2. (A) Venn diagram of the 514 common target genes of TFAP2A and GATA2. (B) GO and KEGG enrichment results for TFAP2A. (C) GO and KEGG enrichment results for GATA2. (D) The PPI network of TFAP2A, GATA2, and their interacting genes. (E) The fluctuations in TFAP2A and GATA2 among different subtypes of age, sex, and T stage. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein-protein interaction.
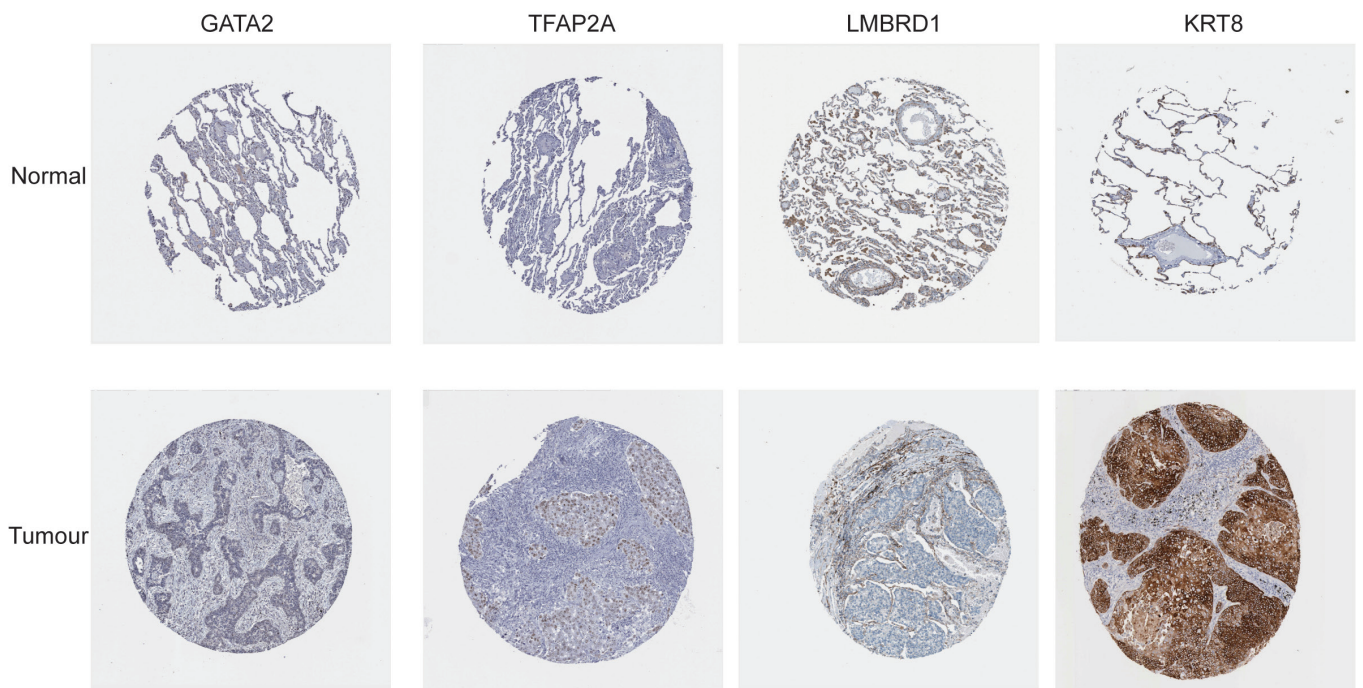
Figure S3 IHC for *GATA2*, *TFAP2A*, *LMBRD1*, and *KRT8* expression in LUAD and normal lung tissues retrieved from HPA database. IHC, immunohistochemistry; LUAD, lung adenocarcinoma; HPA, human protein atlas.