Supplementary Figure Legends

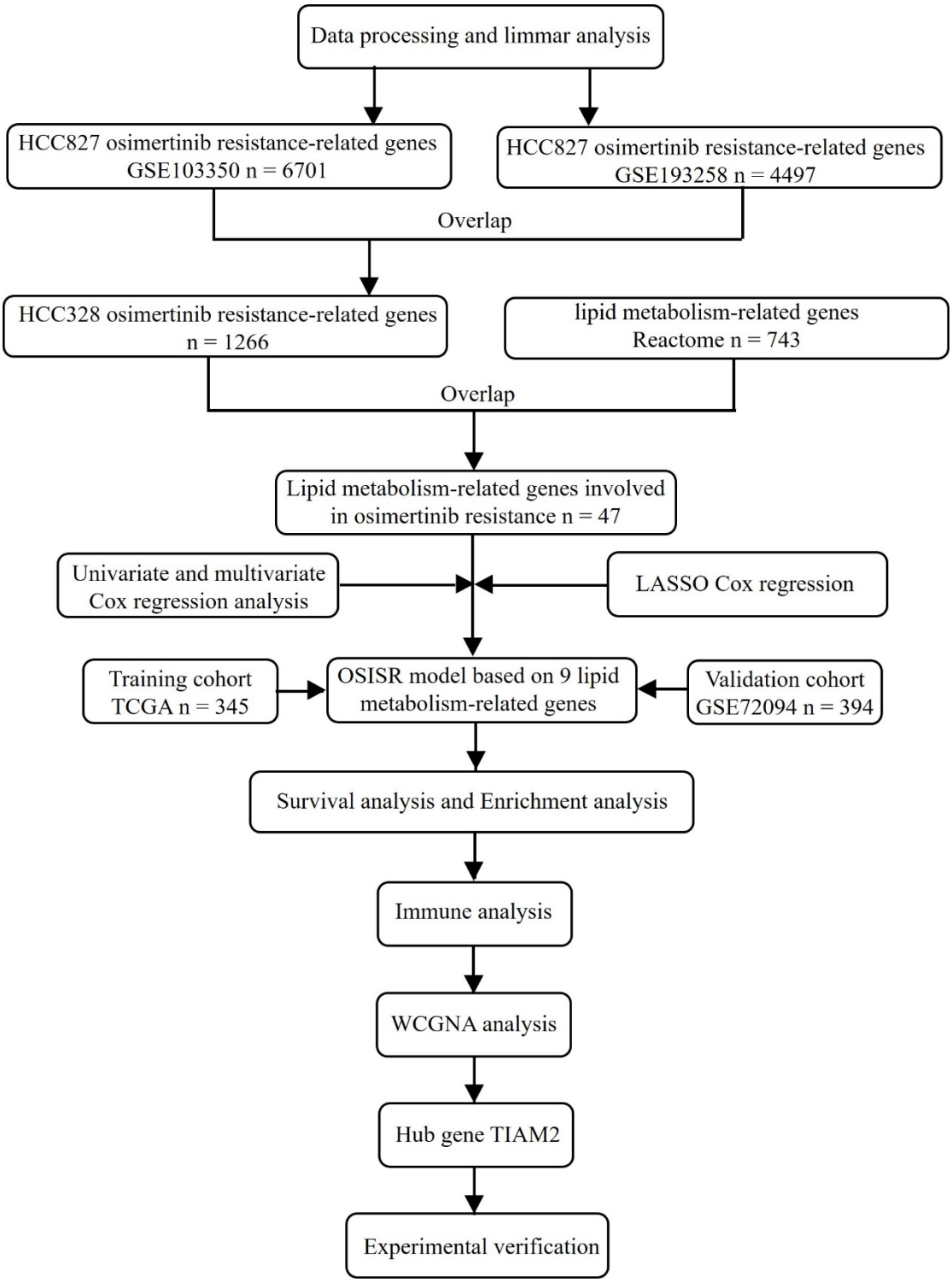


Figure S1 Study flow diagram.

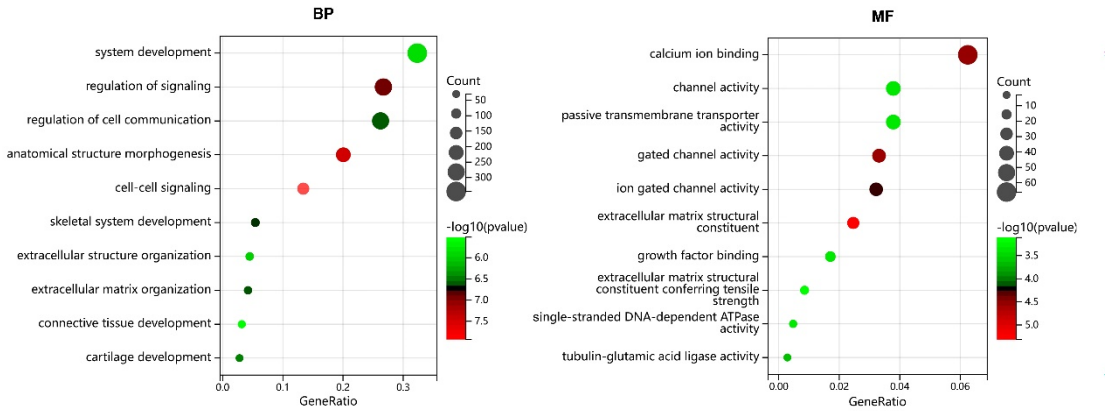


Figure S2 GO enrichment analysis showing the biological processes and molecular functions.

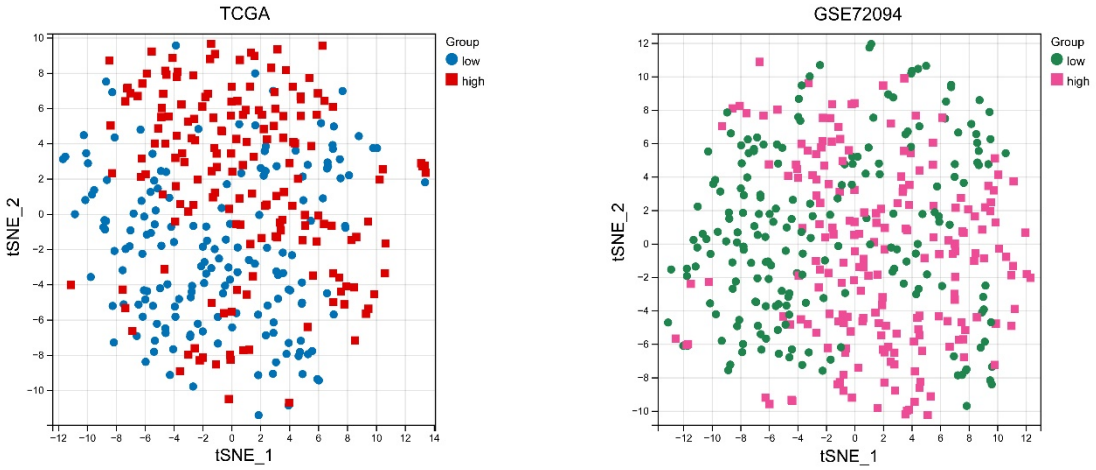


Figure S3 t-SNE analysis of grouped samples from the training and validation cohorts.

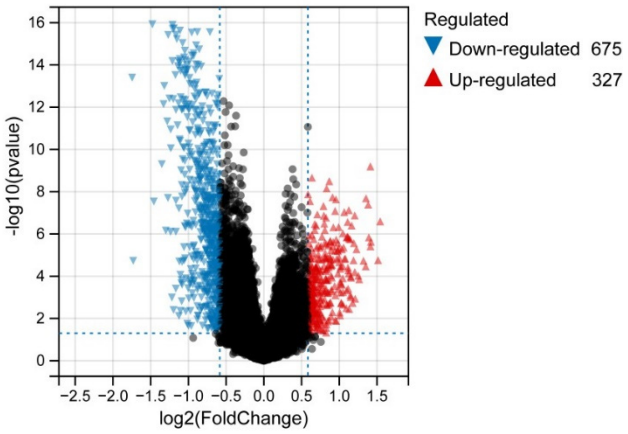


Figure S4 Volcano plot presenting the DEGs in the TCGA-LUAD cohort based on median M2/M1 ratios.

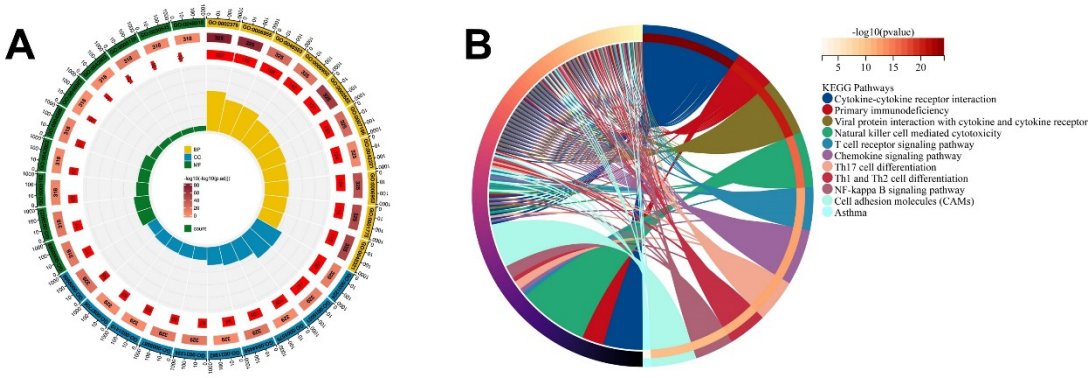


Figure S5 GO and KEGG analysis of DEGs in high and low M2/M1 ratio groups.

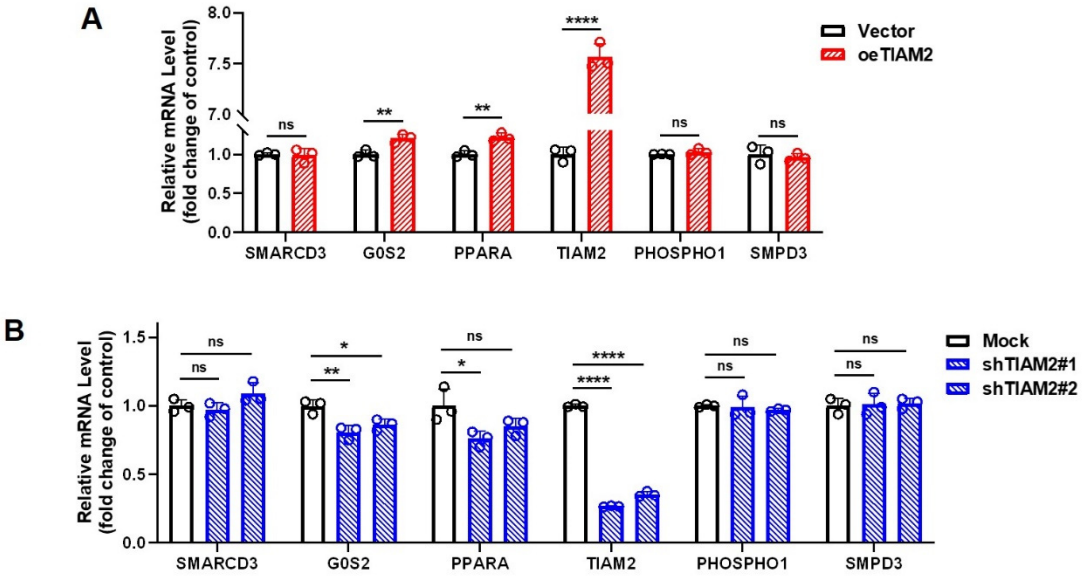


Figure S6 The mRNA levels of 6 lipid metabolism-related genes were detected by RT-qPCR in cell lines overexpressing or knockdown *TIAM2*.

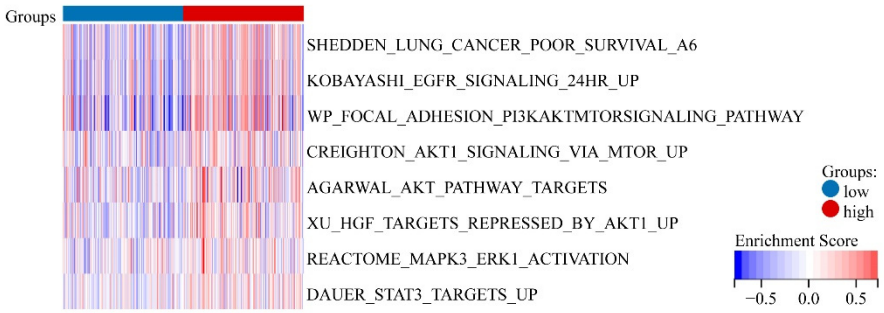


Figure S7 GSVA analysis on samples from high-risk and low-risk groups of TCGA.

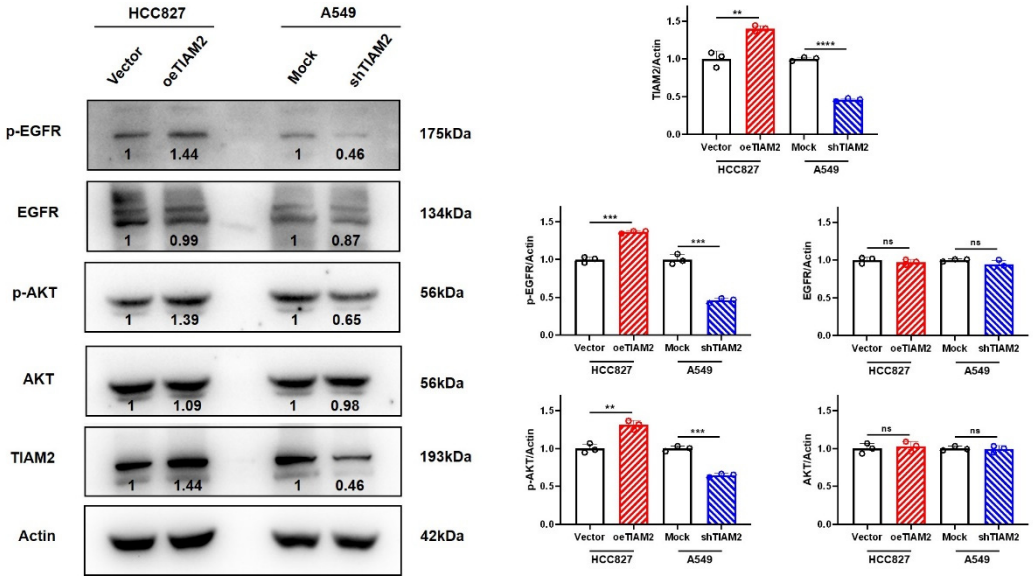


Figure S8 Left, protein expression levels of p-EGFR, EGFR, p-AKT and AKT in overexpressing or knockdown cell lines were detected by WB. Right, amounts of p-EGFR, EGFR, p-AKT, AKT and TIAM2 were quantified from experiment.