# Supplementary Method 4

By integrating data from the Genotype-Tissue Expression (GTEx) database and The Cancer Genome Atlas (TCGA), we systematically analyzed the expression differences of these molecular biomarkers between primary tumor tissues (particularly LIHC) and normal tissues. Subsequently, we employed the Cox proportional hazards regression model to explore the associations between the expression levels of these molecular biomarkers and overall survival (OS) prognosis across various cancer types, with a specific emphasis on LIHC. Furthermore, to gain deeper insights into the potential mechanisms of action of key proteins in the tumor microenvironment, we examined the correlations between the expression levels of molecular biomarkers and the infiltration degrees of different immune cells by integrating immune infiltration-related matrix data. The outcomes of the correlation analysis were visualized using heatmaps, thereby uncovering the potential pathways through which they may regulate the tumor immune microenvironment.