Figure S1. mRNA expression patterns of (A) PYGB, (B) PYGL and (C) PYGM in different types of human cancer with tumor and normal samples analyzed at UALCAN. Dataset for pan-cancer from study accession phs000178.v11.p8 was used for the analysis. *P<0.05, **P<0.01, ***P<0.001. BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; GBM, glioblastoma multiforme; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LIHC(HCC), liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; PAAD, pancreatic adenocarcinoma; PRAD, prostate adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; READ, rectum adenocarcinoma; SARC, sarcoma; SKCM: skin cutaneous melanoma; THCA, thyroid carcinoma; THYM: thymoma; STAD: stomach adenocarcinoma; UCEC: uterine corpus endometrial carcinoma; PYGB, brain isoform of glycogen phosphorylase; PYGL, liver form of glycogen phosphorylase; PYGM, muscle form of glycogen phosphorylase.
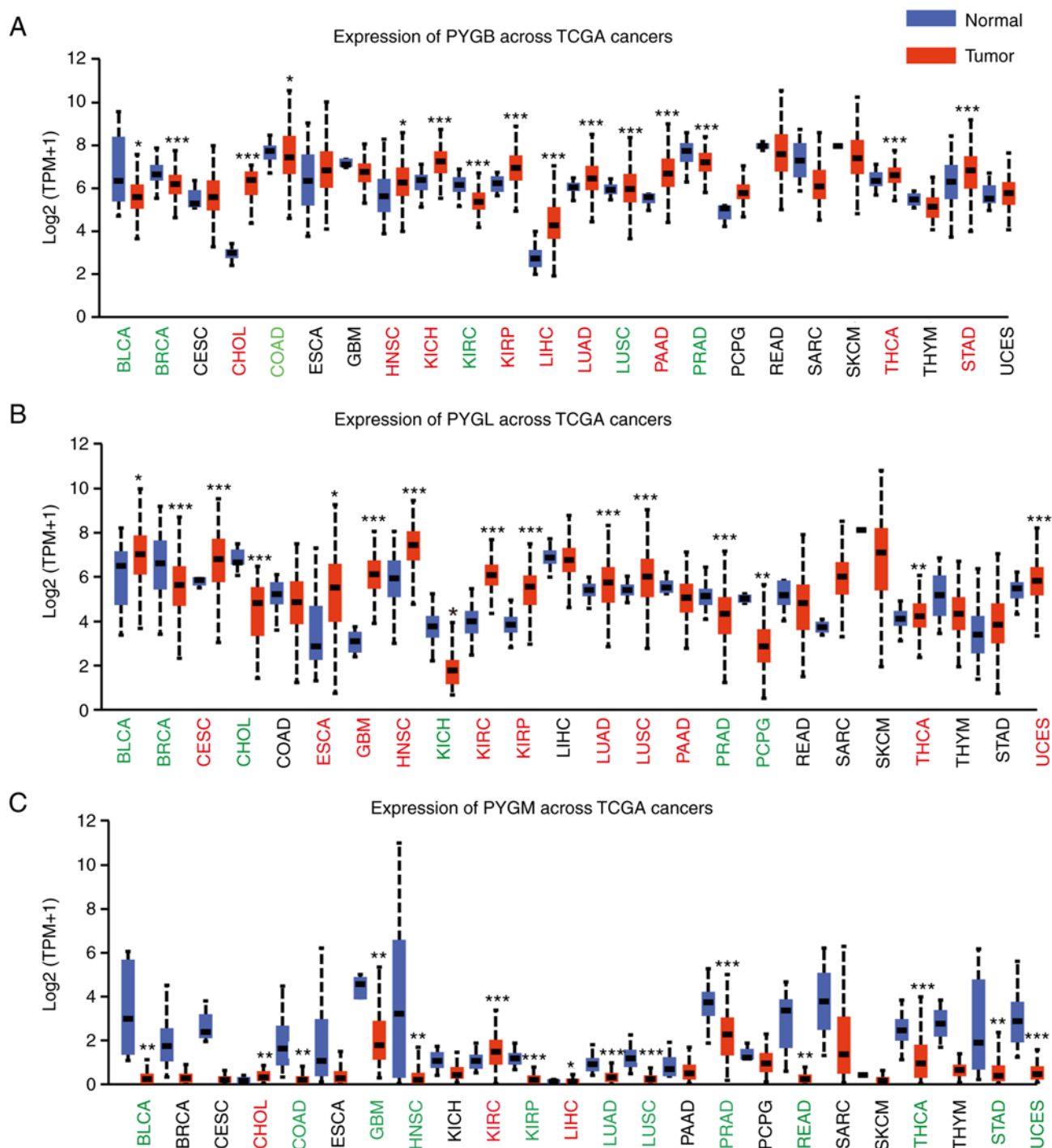
Figure S2. Alterations in PYGB, PYGL and PYGM in patients with HCC. (A) Protein structural of three GP subtypes. Data was collected from PDB database. The 4-digit codes of the deposited protein structures were the following: PYGB, 5IKP; PYGL, 1FA9; and PYGM, 1Z8D. (B) The mutations in PYGB, PYGL and PYGM in patients with HCC were analyzed in cBioPortal (https://www.cbioportal.org/). The data set PanCanAtlas (https://gdc.cancer.gov/about-data/publications/pancanatlas) was used for analysis. (C) Mutation sites of GPs in patients with HCC was analyzed in cBioPortal. The data set PanCanAtlas was used for analysis. PYGB, brain isoform of GP; PYGL, liver form of GP; PYGM, muscle form of GP; HCC, hepatocellular carcinoma; GP, glycogen phosphorylase.
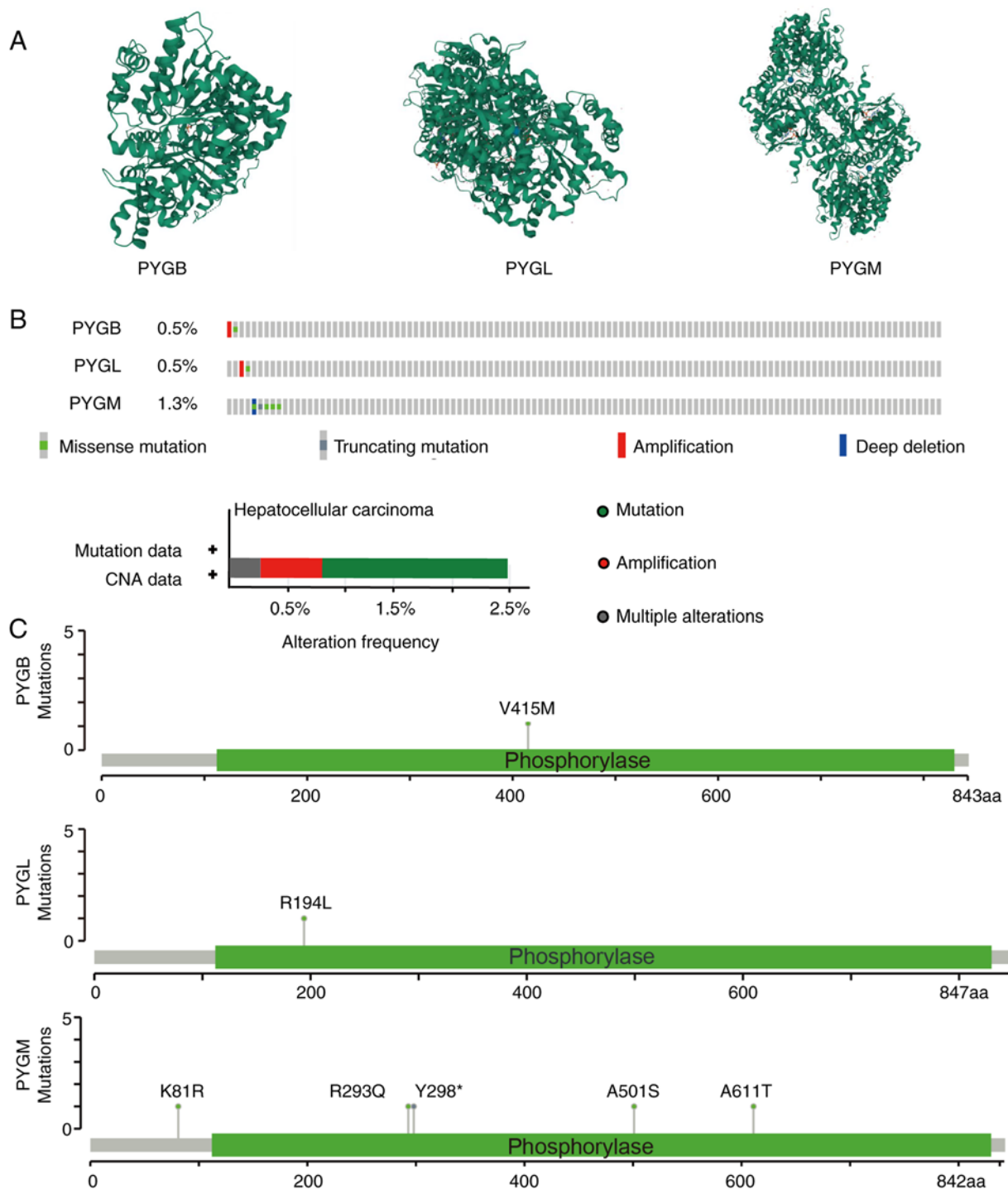
Figure S3. Association between clinicopathological factors and PYGB, PYGL and PYGM, respectively. The analysis was performed using the UALCAN. The dataset TCGA-LIHC from study accession phs000178.v11.p8 was used. (A) Age, (B) Sex and (C) tumor grade factors with HCC. *P<0.05, **P<0.01 and ***P<0.001. PYGB, brain isoform of glycogen phosphorylase; PYGL, liver form of glycogen phosphorylase; PYGM, muscle form of glycogen phosphorylase; HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas.