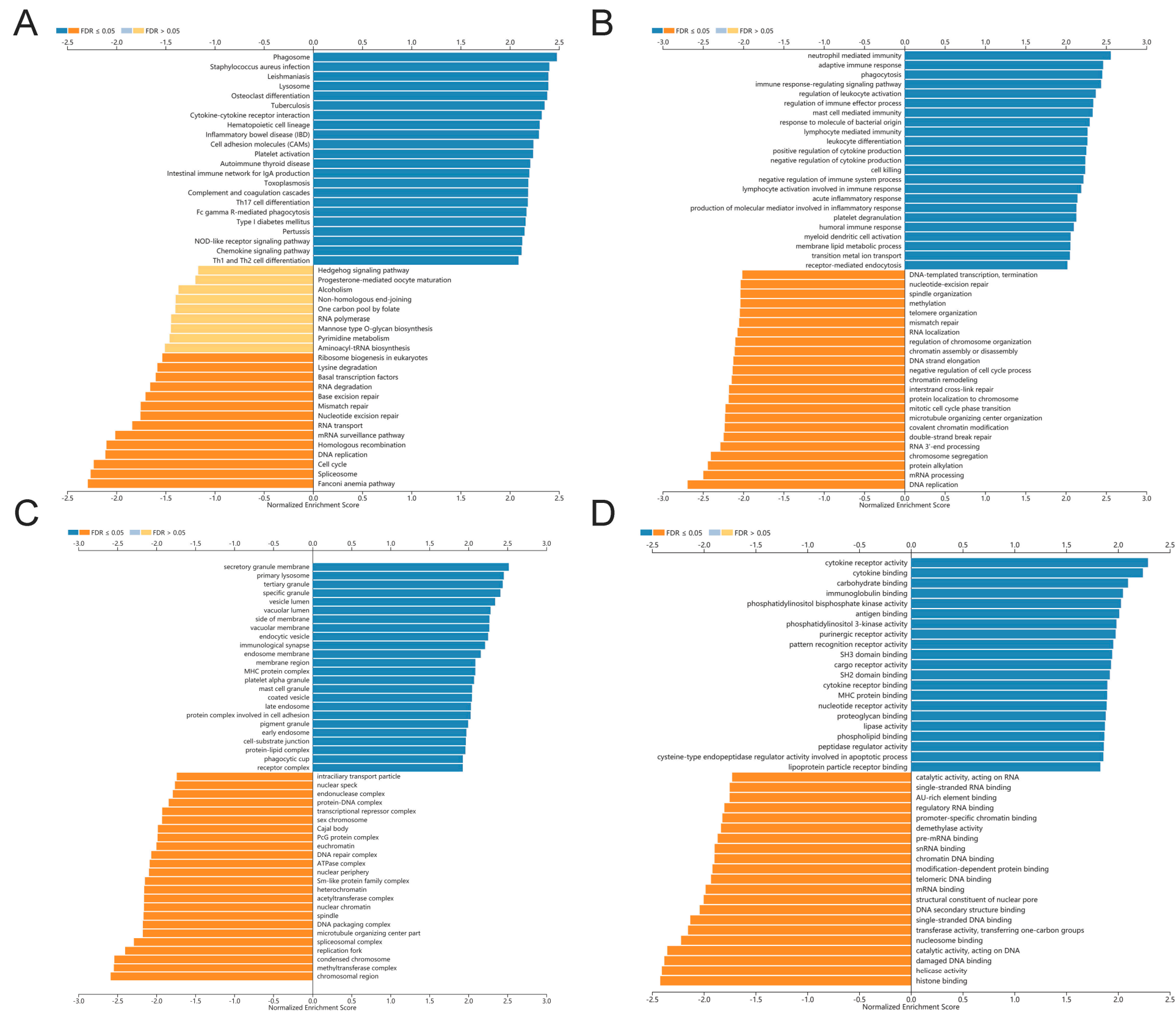
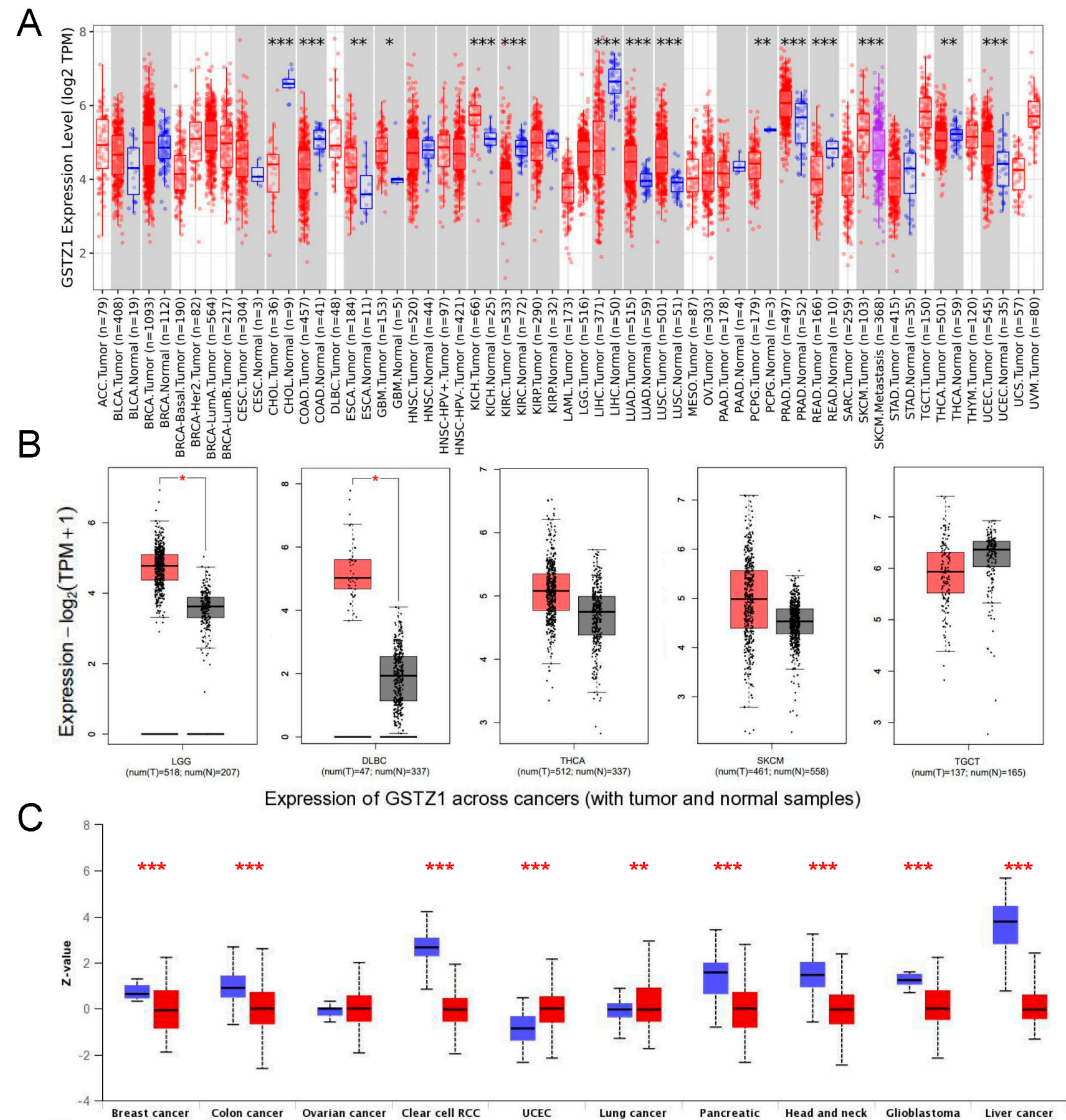


**Figure S1.** Functional enrichment analysis of HPGDS related genes in GBM. (A) Based on the TCGA database, we identified the genes with the highest correlation with HPGDS in GBM, and the genes with positive correlation and negative correlation are displayed in (B) and (C), respectively.

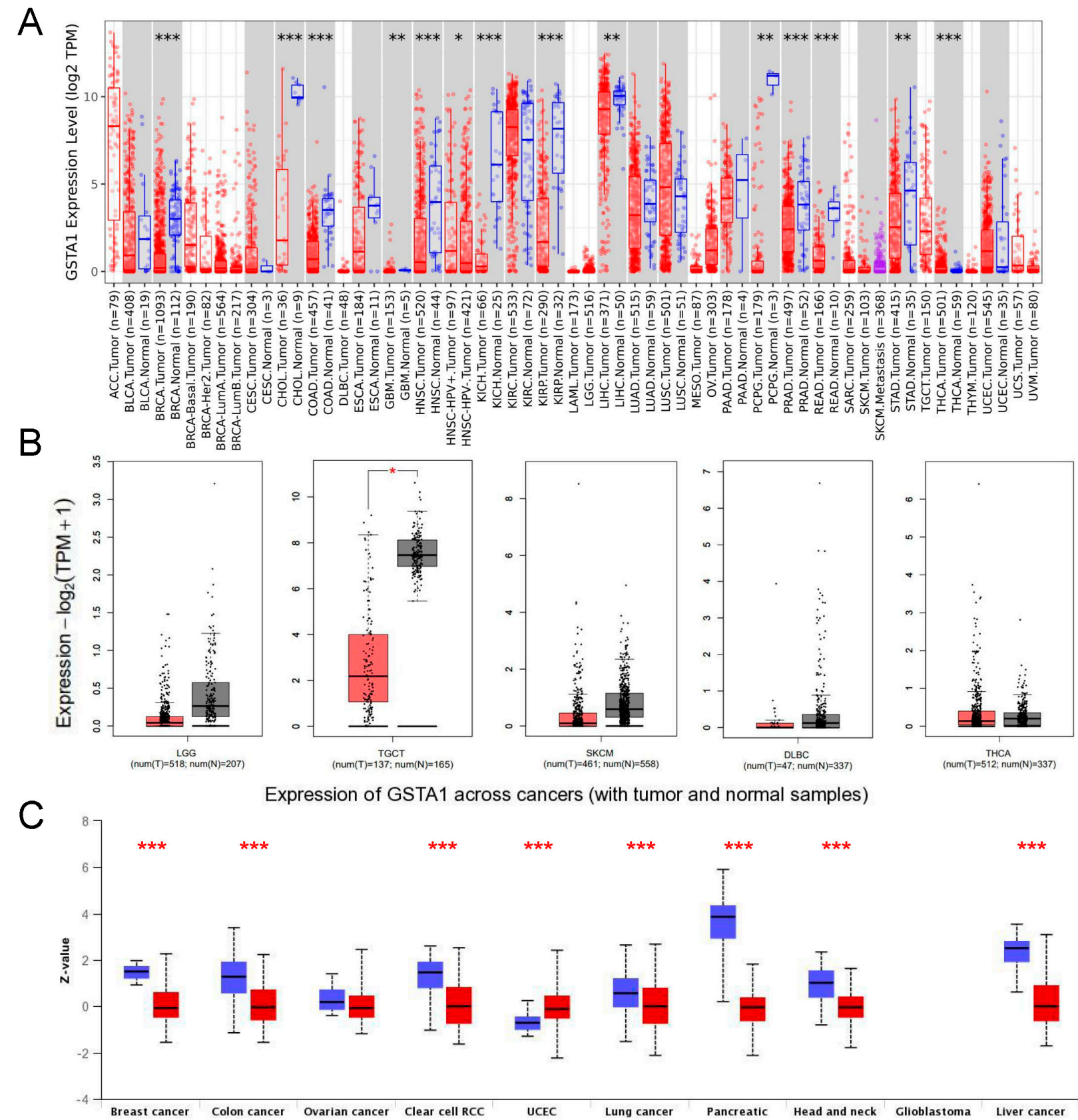


**Figure S2.** GSEA analysis of biological functions of HPGDS in GBM using LinkedOmics. **(A)** KEGG pathway analysis based on GSEA demonstrates the effect of HPGDS expression on signaling pathways in GBM. **(B–D)** GO analysis based on GSEA demonstrates the effects of HPGDS expression on cellular components, biological processes and molecular functions in GBM.



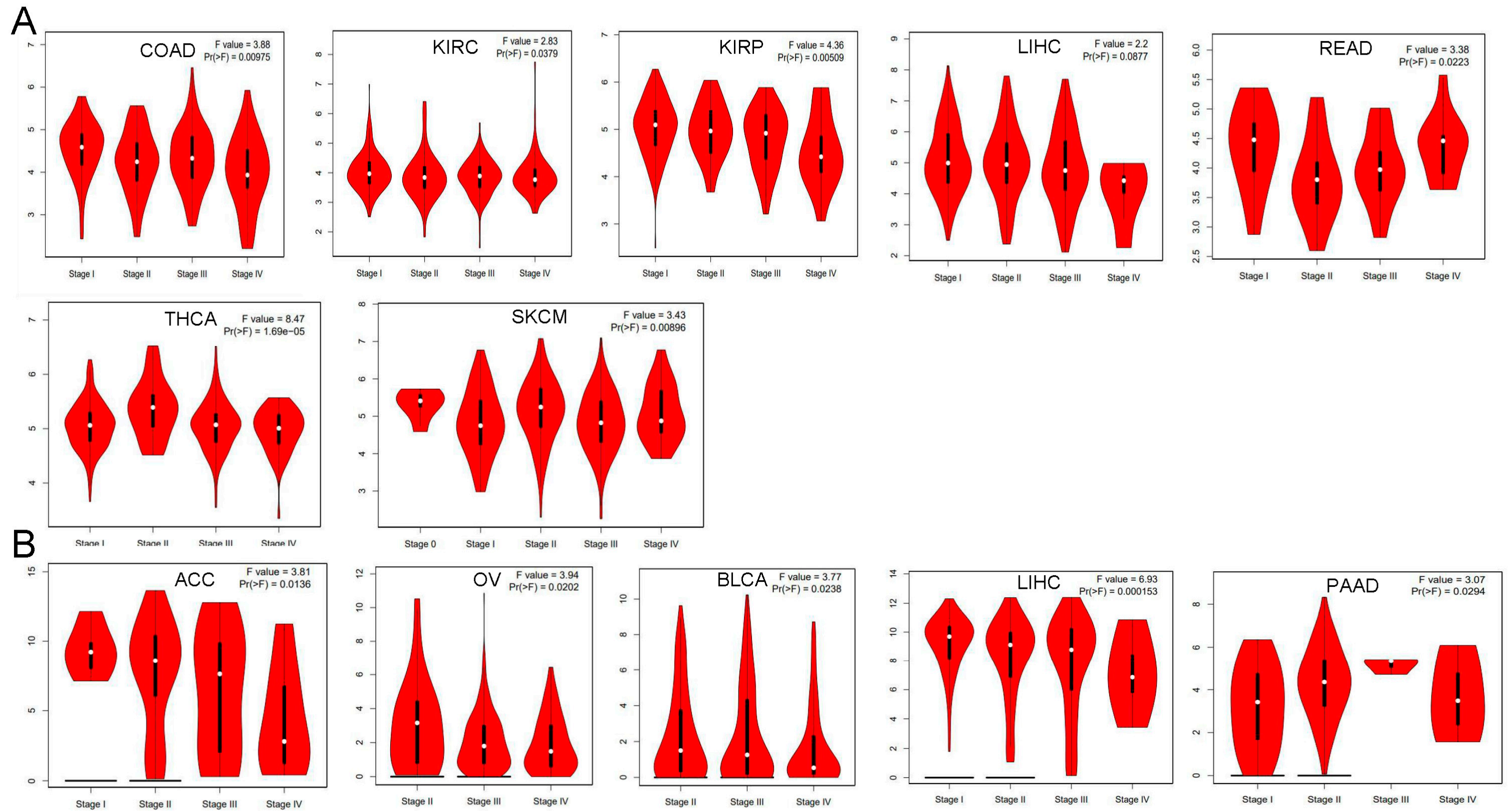


**Figure S3.** The levels of GSTZ1 mRNA and protein in different cancers. (A,B) The mRNA level of GSTZ1 in different cancers was analyzed with TIMER2. (C) The protein level of GSTZ1 in different cancer types was analyzed with UALCAN.



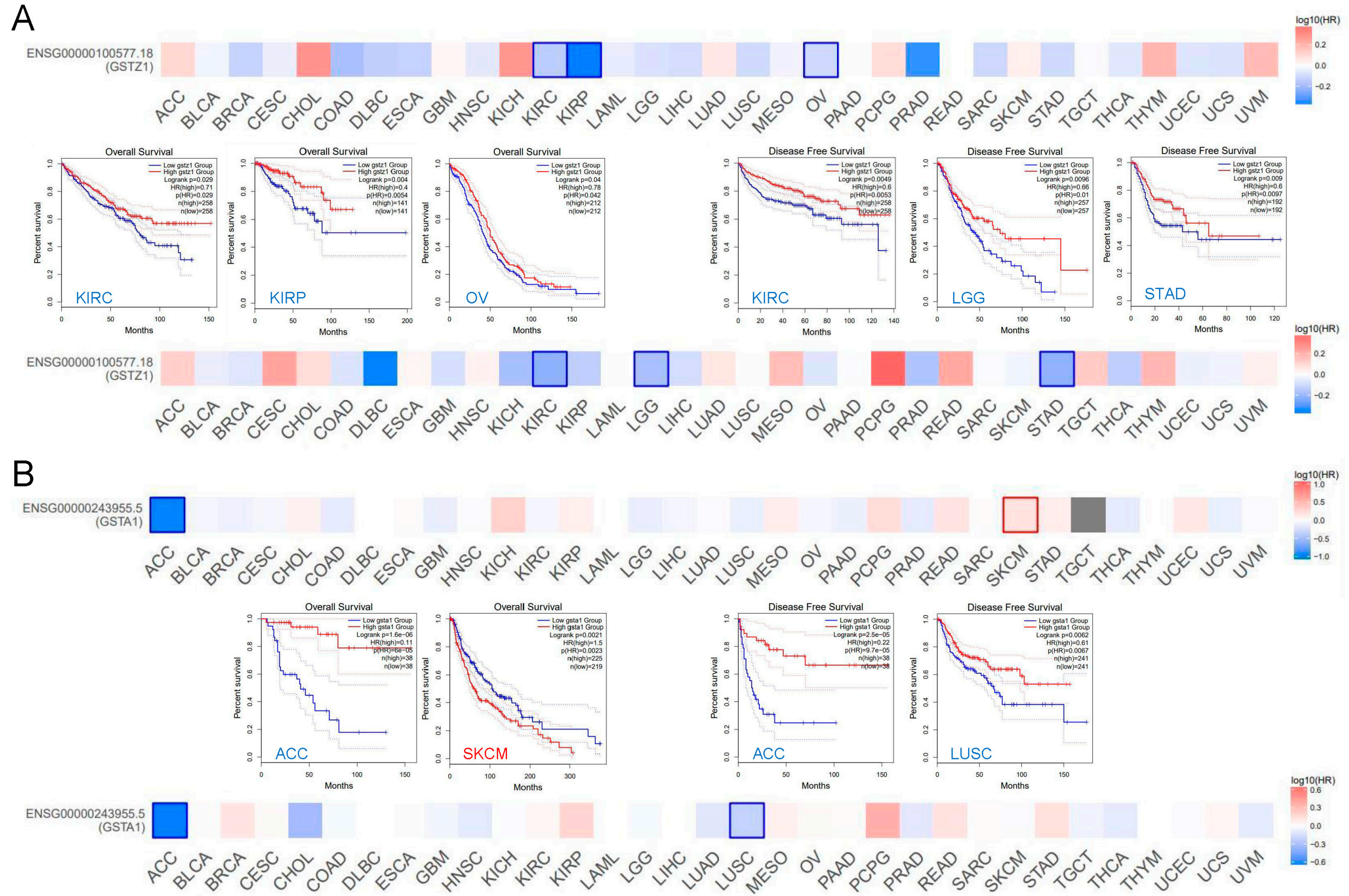
**Figure S4.** The levels of GSTA1 mRNA and protein in different cancers. (A,B) The mRNA level of GSTA1 in different cancers was analyzed with TIMER2. (C) The protein level of GSTA1 in different cancer types was analyzed with UALCAN.





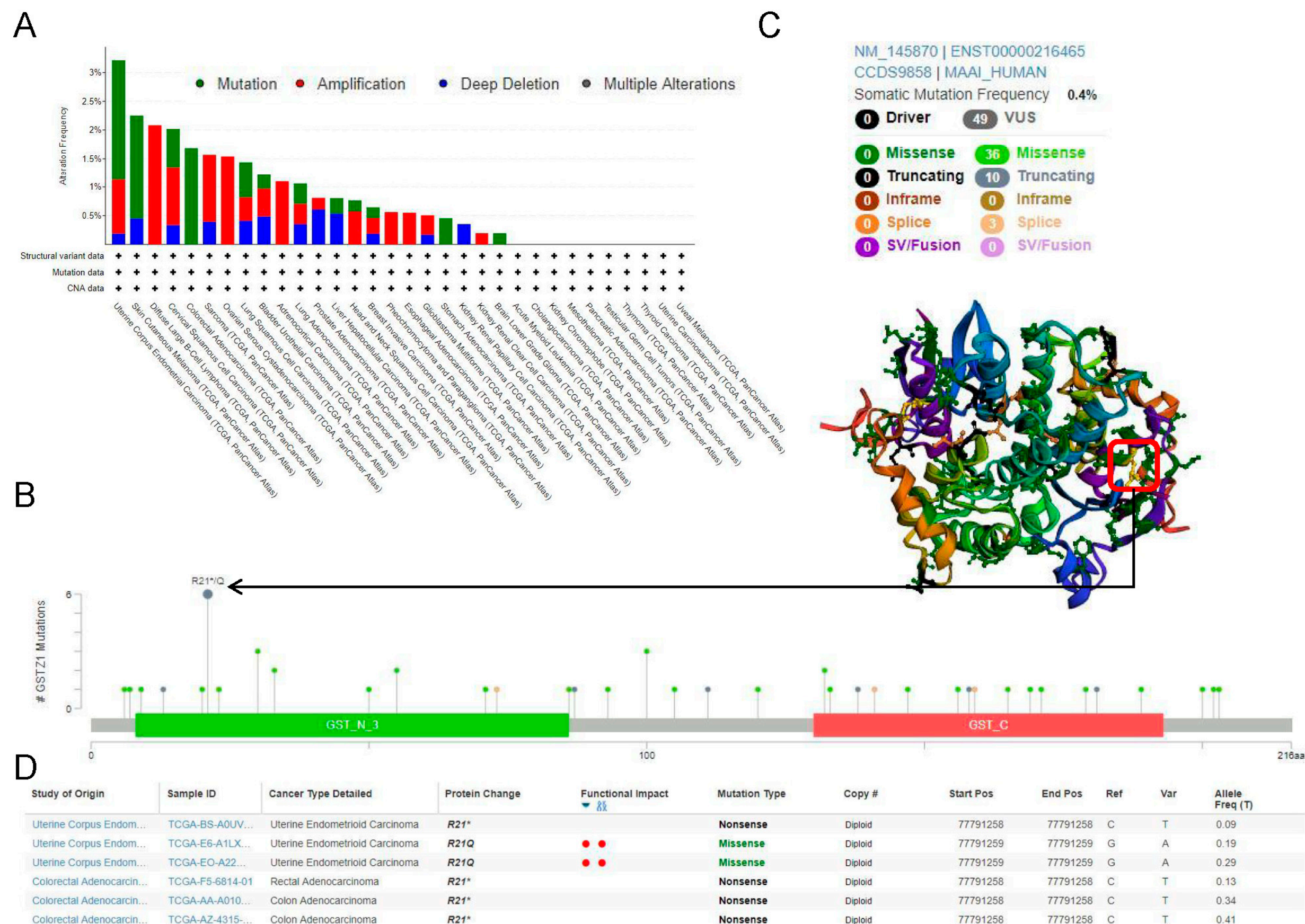
**Figure S5.** Analysis of the TCGA database to investigate correlations between expression of GSTs and cancer prognoses. Based on the TCGA data, the expression levels of the genes encoding GSTZ1 (**A**), and GSTA1 (**B**) were analyzed according to the main pathological stages (stage I, stage II, stage III, and stage IV) of different cancers. The equation  $\text{Log}_2(\text{TPM} + 1)$  was applied for the log-scale.





**Figure S6.** Correlation between GSTs expression and cancer prognosis according to the TCGA database. The OS and DFS of different cancers in the TCGA were compared with GSTZ1 expression (A) and GSTA1 expression (B). The survival map and Kaplan-Meier curves with positive results are given.



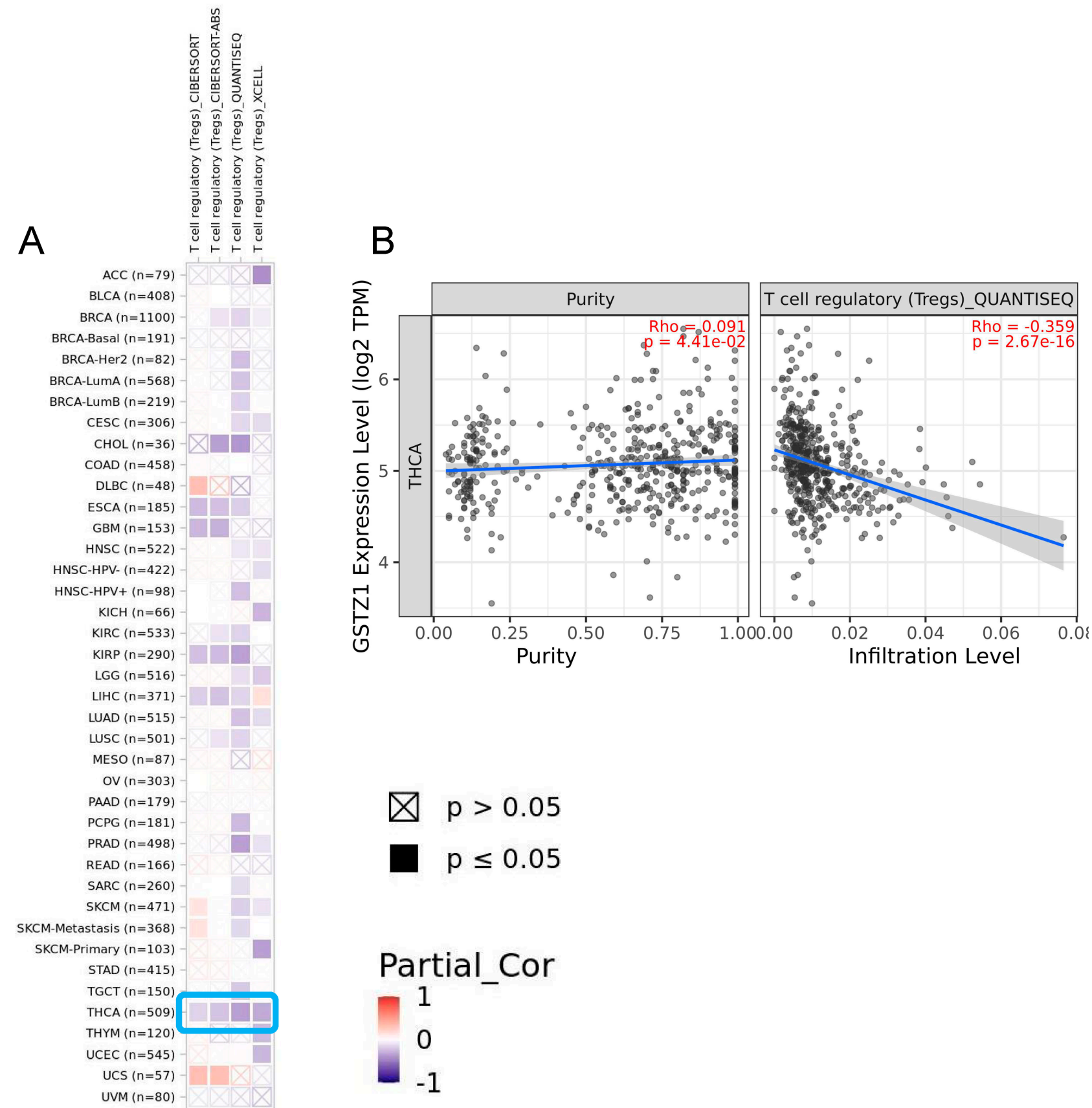


**Figure S7.** Mutation of GSTZ1 in different cancers via TCGA analyses. (A) The alteration frequency of GSTZ1 with mutation type in various cancers according to the TCGA. (B) The alteration frequency of GSTZ1 with mutation site in various cancers according to the TCGA. (C,D) Information regarding the mutation site with the highest alteration frequency (R21\*/Q). This site in the three-dimensional structure of GSTZ1 is shown in yellow.

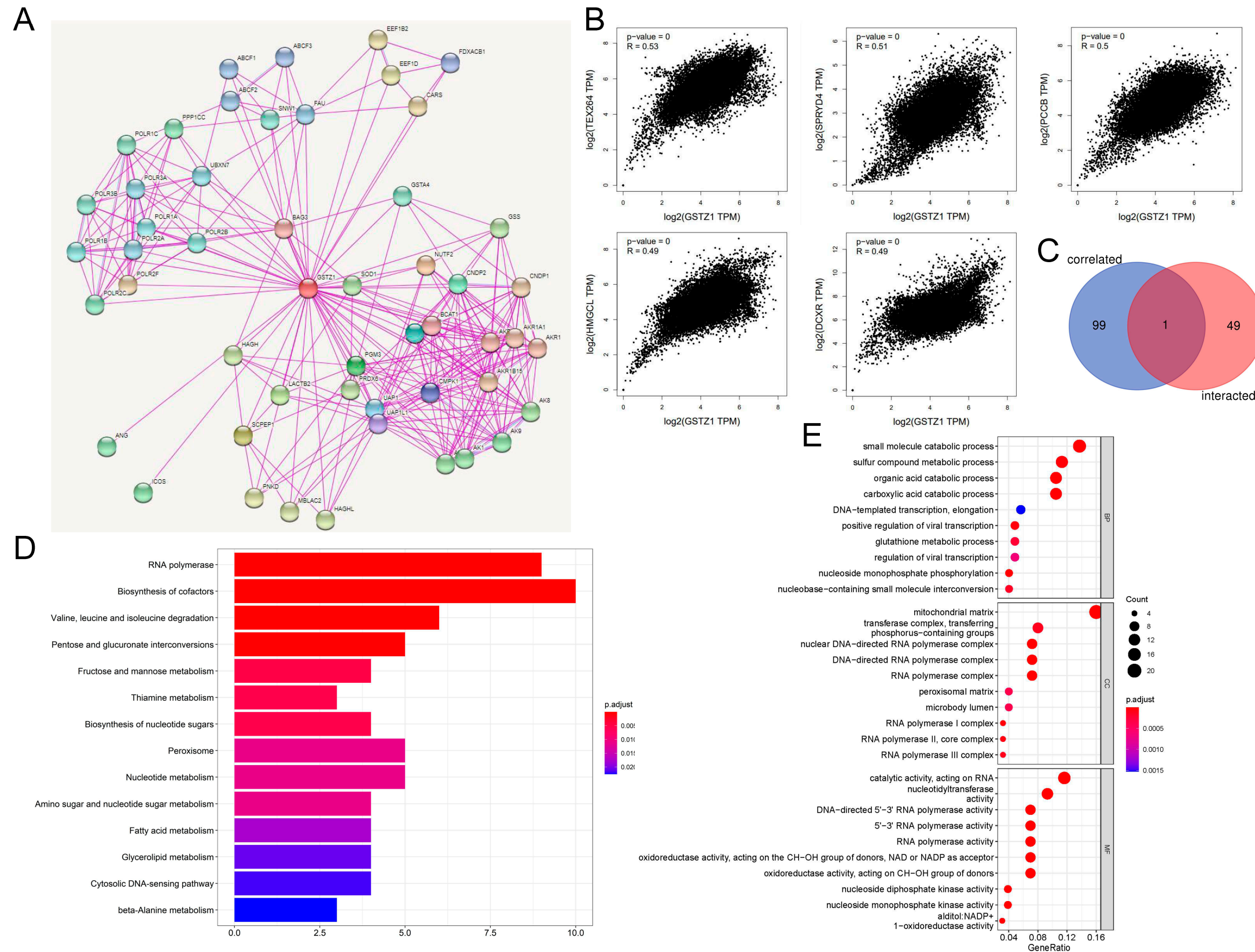






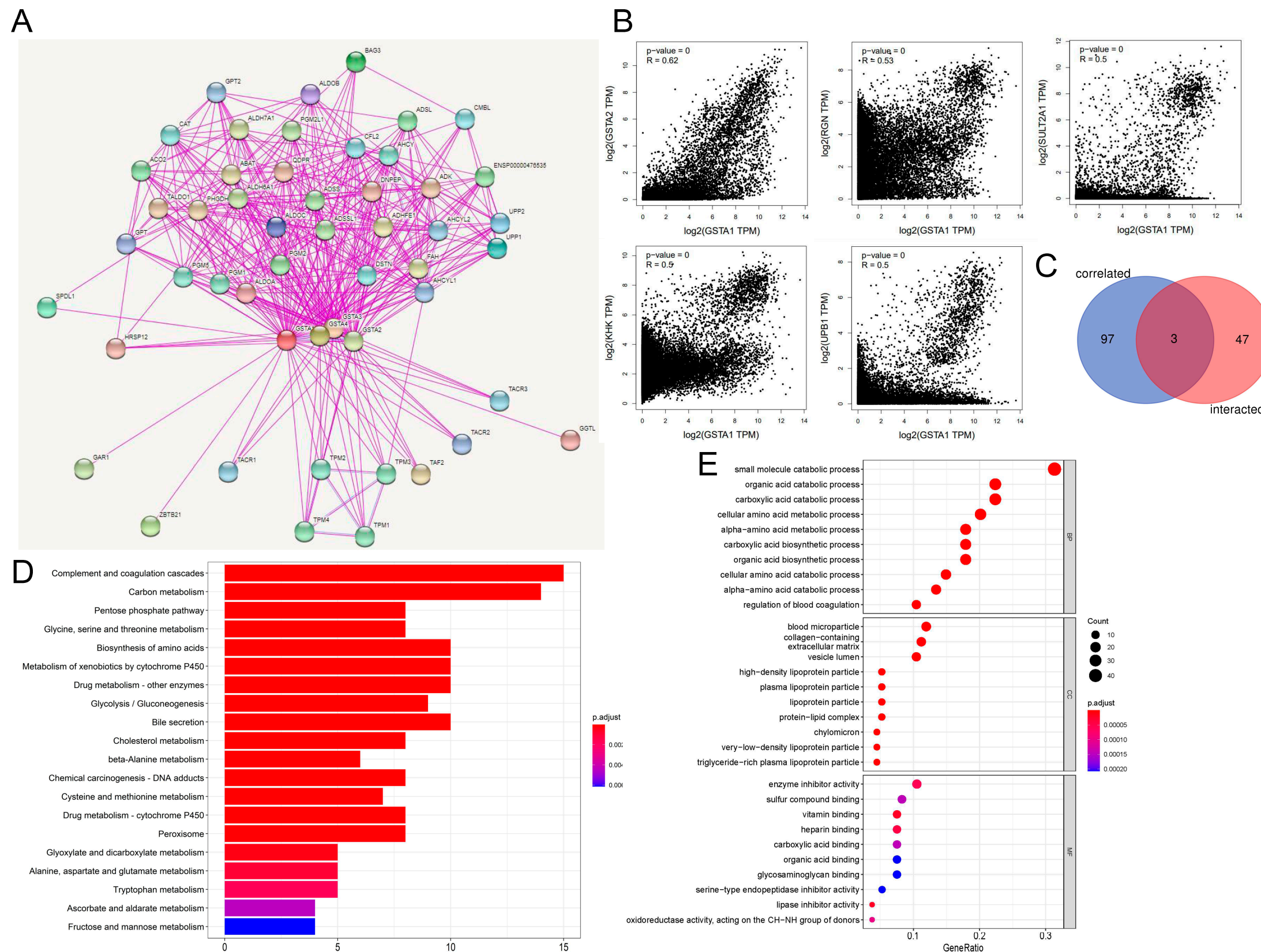


**Figure S9.** Analysis of correlations between GSTZ1 expression and infiltration of cancer-associated immune cells. **(A)** Multiple algorithms were used to explore potential correlations between the expression of GSTZ1 and the infiltration of cancer-associated Tregs across all types of cancer in TCGA. **(B)** The results with the highest correlation scores, which were verified by multiple algorithms, are shown.



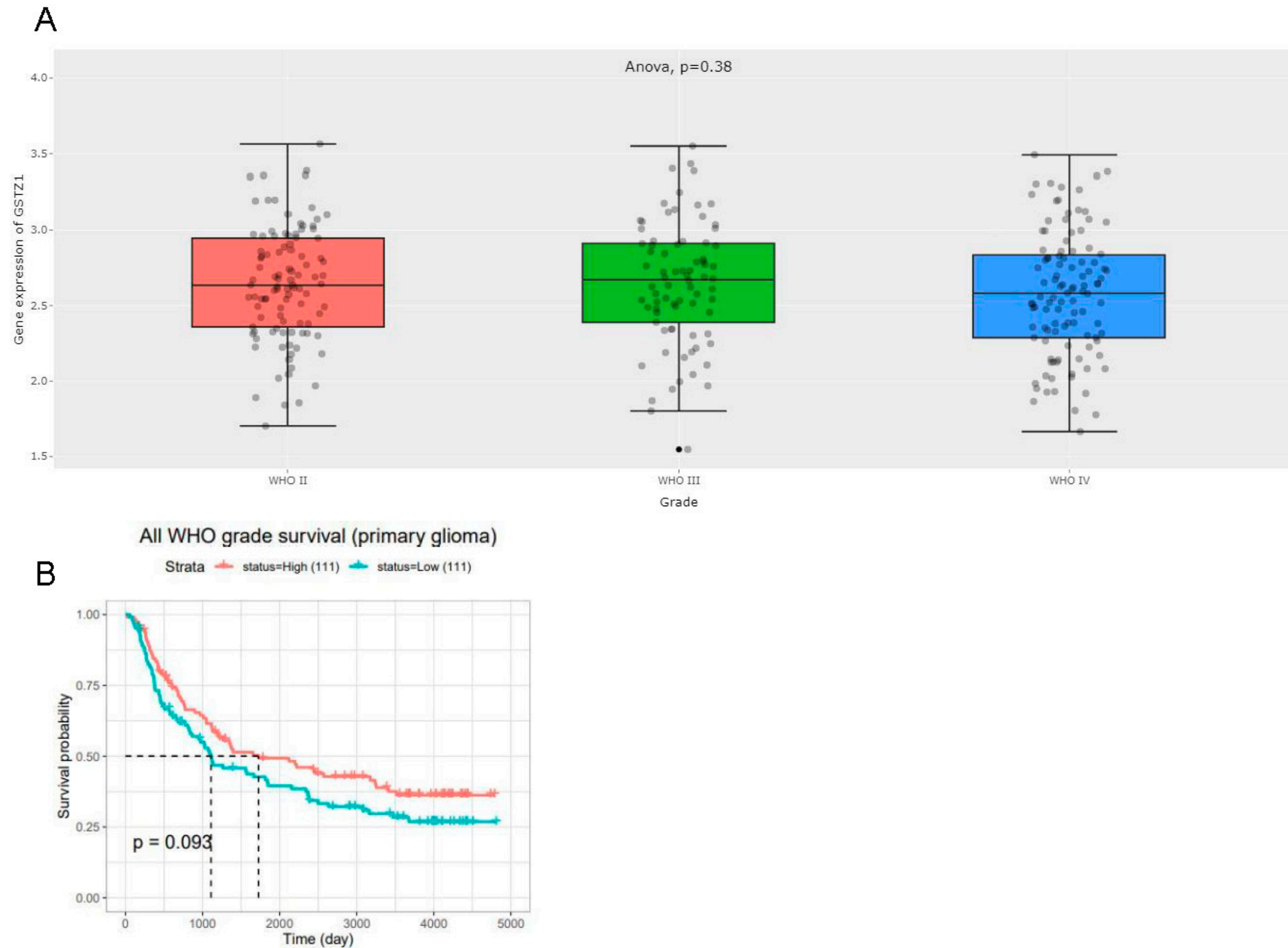
**Figure S10.** GSTZ1-related gene enrichment analysis. **(A)** Experimentally determined GSTZ1-binding proteins were identified using STRING. **(B)** The correlations of the expression of GSTZ1 and the five most related genes in cancers are shown. **(C)** An analysis of intersections of genes encoding GSTZ1-binding proteins and expression-correlated genes was conducted. **(D)** KEGG pathway analyses were performed on the genes encoding GSTZ1-binding proteins and expression-correlated genes. **(E)** GO analyses were also performed.





**Figure S11.** GSTA1-related gene enrichment analysis. **(A)** Experimentally determined GSTA1-binding proteins were identified using STRING. **(B)** The correlations of the expression of GSTA1 and the five most related genes in cancers are shown. **(C)** An analysis of intersections of genes encoding GSTA1-binding proteins and expression-correlated genes was conducted. **(D)** KEGG pathway analyses were performed on the genes encoding GSTA1-binding proteins and expression-correlated genes. **(E)** GO analyses were also performed.





**Figure S12.** Correlation analysis of GSTZ1 expression and patient prognosis based on the CGGA database. **(A)** The results of CGGA database analyses showed the level of GSTZ1 expression in glioma. **(B)** Differences in survival rates of patients according to GSTZ1 expression levels did not reach statistical significance in all glioma patients.



Abbreviation	Full name
ACC	Adrenocortical carcinoma
BLCA	Bladder Urothelial Carcinoma
BRCA	Breast invasive carcinoma
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma
CHOL	Cholangio carcinoma
COAD	Colon adenocarcinoma
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
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
LAML	Acute Myeloid Leukemia
LGG	Brain Lower Grade Glioma
LIHC	Liver hepatocellular carcinoma
LUAD	Lung adenocarcinoma
LUSC	Lung squamous cell carcinoma
MESO	Mesothelioma
OV	Ovarian serous cystadenocarcinoma
PAAD	Pancreatic adenocarcinoma
PCPG	Pheochromocytoma and Paraganglioma
PRAD	Prostate adenocarcinoma
READ	Rectum adenocarcinoma
SARC	Sarcoma
SKCM	Skin Cutaneous Melanoma
STAD	Stomach adenocarcinoma
TGCT	Testicular Germ Cell Tumors
THCA	Thyroid carcinoma
THYM	Thymoma
UCEC	Uterine Corpus Endometrial Carcinoma
UCS	Uterine Carcinosarcoma
UVM	Uveal Melanoma

**Figure S13.** Abbreviations and full names of each cancer mentioned in this manuscript.