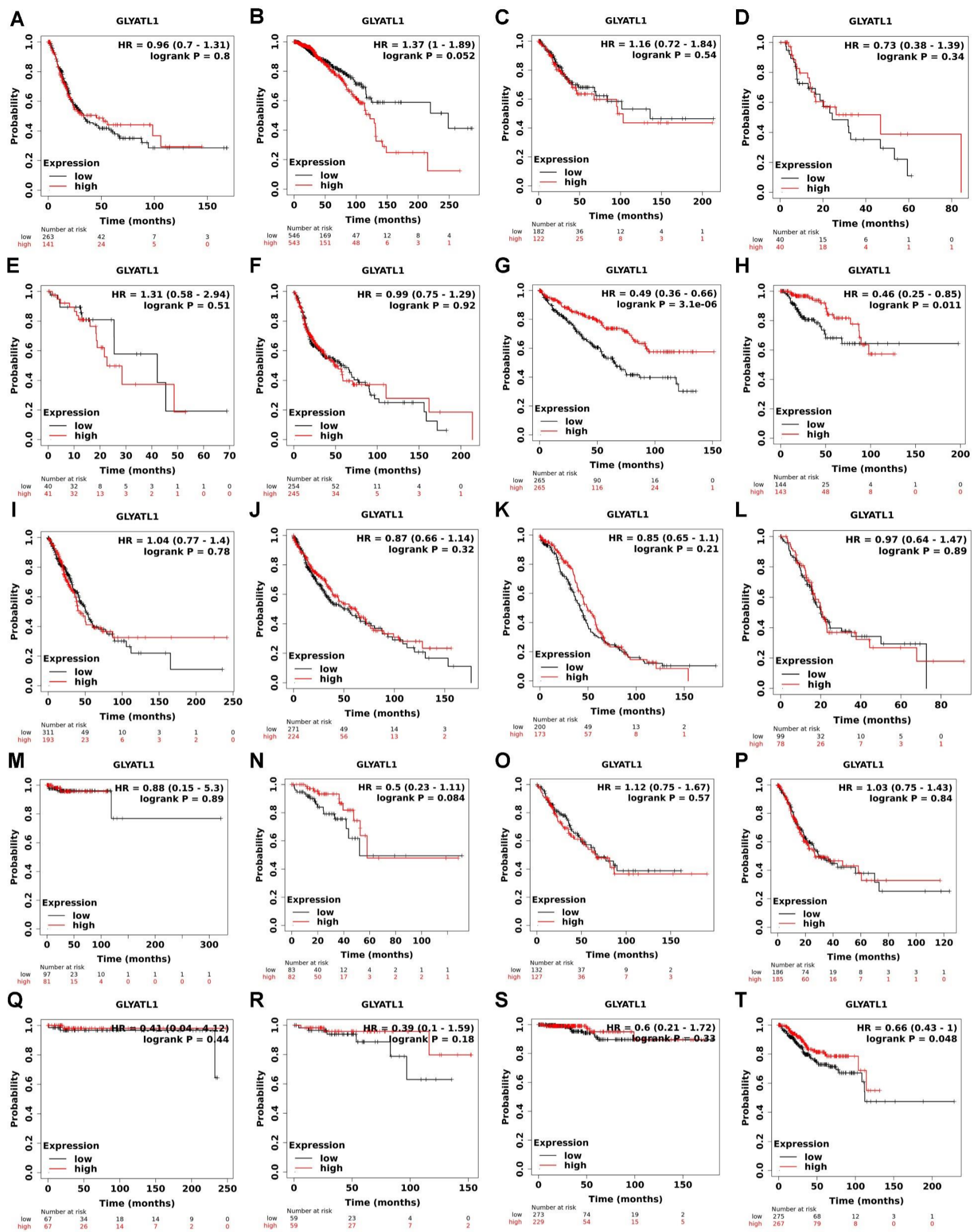
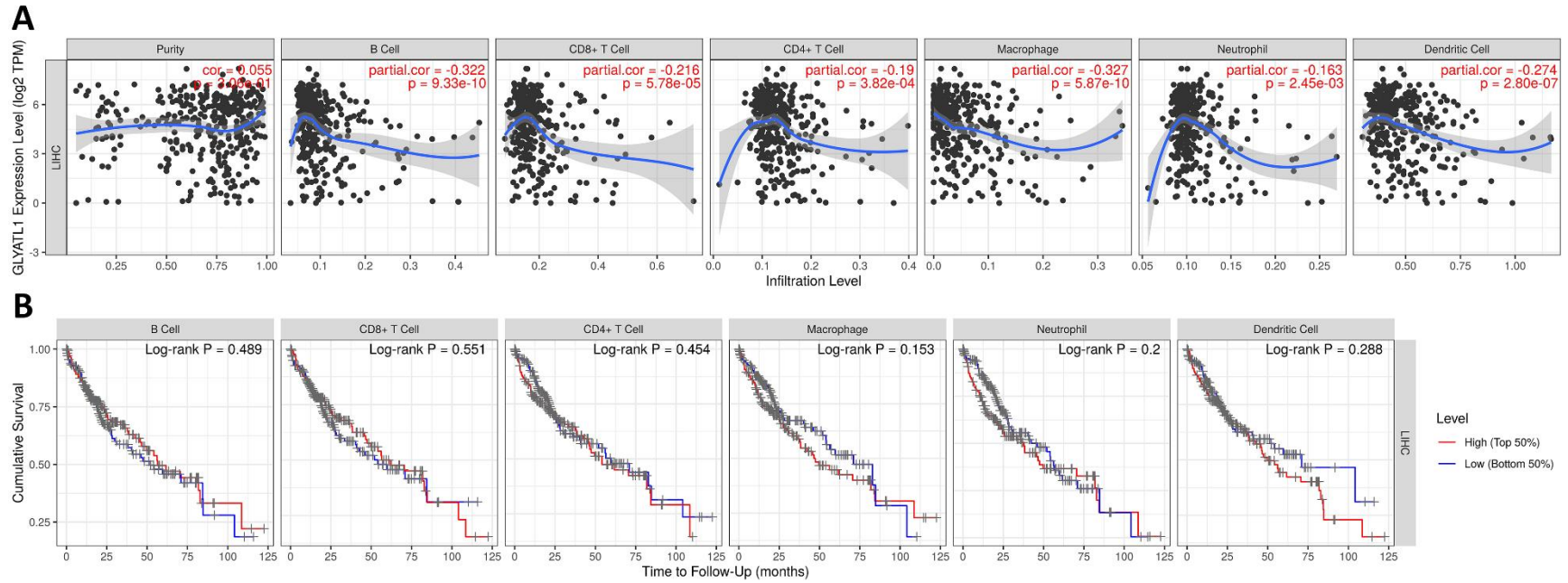


**Figure S1** mRNA level of GLYATL1 in different tumor types from the TCGA and GTEx project in the GEPIA cancer database. The red boxes represent cancer tissues, and the gray boxes represent normal tissues. \*,  $P < 0.05$ . BRCA, breast invasive carcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; KICH, kidney chromophobe carcinoma; KIRP, kidney renal papillary cell carcinoma; LIHC, liver hepatocellular carcinoma; PRAD, prostate adenocarcinoma; READ, rectal adenocarcinoma; SARC, sarcoma.



**Figure S2** Kaplan-Meier survival curves comparing high and low GLYATL1 mRNA expression across 21 cancers in the TCGA database. (A) Bladder carcinoma; (B) breast cancer; (C) cervical squamous cell carcinoma; (D) esophageal adenocarcinoma; (E) esophageal squamous cell carcinoma; (F) head-neck squamous cell carcinoma; (G) clear cell renal cell carcinoma; (H) kidney renal papillary cell carcinoma; (I) lung adenocarcinoma; (J) lung squamous cell carcinoma; (K) ovarian cancer; (L) pancreatic ductal adenocarcinoma; (M) pheochromocytoma and paraganglioma; (N) rectum adenocarcinoma; (O) sarcoma; (P) stomach adenocarcinoma; (Q) testicular germ cell tumor; (R) thymoma; (S) Thyroid carcinoma; (T) uterine endometrial carcinoma.



**Figure S3** The correlations among immune cell infiltration, GLYATL1 expression and cumulative survival. (A) Correlations between GLYATL1 expression and six immune cell types: B cells, CD4+ T cells, CD8+ T cells, neutrophils, macrophages and dendritic cells. (B) Kaplan-Meier plots comparing high and low immune infiltrates in liver cancer tissues from the TCGA database.

**Table S1** Significant associations between GLYATL1 expression and overall survival across different cancers in Prognoscan

Dataset	Cancer type	Cut-point	N	Cox P value	HR (95% CI)
GSE17537	Colorectal cancer	0.109	55	0.001	0.01 (0.00–0.15)
GSE1456-GPL97	Breast cancer	0.629	159	0.004	1.73 (1.19–2.52)
GSE17536	Colorectal cancer	0.345	177	0.016	0.47 (0.25–0.87)
GSE17536	Colorectal cancer	0.429	177	0.023	0.26 (0.08–0.83)
GSE31210	Lung adenocarcinoma	0.152	204	0.034	0.56 (0.32–0.96)
GSE19234	Skin melanoma	0.737	38	0.036	2.51 (1.06–5.94)
E-DKFZ-1	Renal cell carcinoma	0.475	59	0.040	0.20 (0.04–0.93)

**Table S2** Survival differences based on immune cell infiltration in patients with liver cancer from the GSE116174 dataset

Parameters	Hazard ratio	95% CI	P value
CD8A (high/low)	1.298	0.607–2.773	0.501
CD19 (high/low)	1.414	0.655–3.049	0.377
IRF5 (high/low)	0.642	0.298–1.384	0.258
CD163 (high/low)	1.541	0.715–3.323	0.27
NRP1 (high/low)	1.341	0.627–2.865	0.449
ITGAM (high/low)	1.318	0.535–2.421	0.78

Markers include CD8A (CD8+ T cells), CD19 (B cells), IRF5 (M1 macrophages), CD163 (M2 macrophages), NRP1 (dendritic cells), and ITGAM (neutrophils). IRF5, interferon regulatory factor 5; NRP1, neuropilin 1; ITGAM, integrin, alpha M.