Clin. Lab. 2025;71:XXX-XXX

ORIGINAL ARTICLE

The Role of TTC39A in Modulating the Immune Microenvironment and Its Impact on Cancer Prognosis

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SUMMARY

Background: **TTC39A (tetratricopeptide repeat domain protein 39A) belongs to the structural family of tetratricopeptide domain proteins. TTC39A had not been researched in cancers. The purpose of this study was to reveal the potential role of TTC39A in cancers.**

Methods: **In total, 33 cancers were included in this study. All the data came from the Cancer Genome Atlas (TCGA) database. The expression of TTC39A was explored in the 33 cancers. The relationship between the expression of TTC39A and prognosis, clinical characteristics, and immune infiltration was also explored. Paraffin-embedded cancer tissue microarrays (TMA) were used to detect the expression of TTC39A in LIHC (liver hepatocellular carcinoma) and LGG (brain lower grade glioma).**

Results: **The expression of TTC39A was higher in many cancers, compared with the corresponding normal tissues. For patients with LGG, LIHC, and SKCM (skin cutaneous melanoma), higher expression of TTC39A indicated worse OS. Survival analysis in clinical samples indicated that high expression of TTC39A was associated with shorter overall survival. The expression of TTC39A was related to the immune infiltration of some immune cells in LGG, LIHC, and SKCM. Also, the expression of TTC39A combined with the immune infiltration level of some immune cells could affect the OS of patients with these three cancers. Functional enrichment analysis and gene set enrichment analysis (GSEA) showed that TTC39A might play a role in many biological processes.**

Conclusions: **The expression of TTC39A was significantly higher in many cancers. TTC39A was associated with the prognosis of patients with LGG, LIHC, and SKCM, whether they were combined with the immune infiltration level of some immune cells or not. In these three cancers, TTC39A might play a role in some important biological processes.**

(Clin. Lab. 2025;71:xx-xx. DOI: 10.7754/Clin.Lab.2024.240923)

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Manuscript accepted October 29, 2024

Supplementary Data

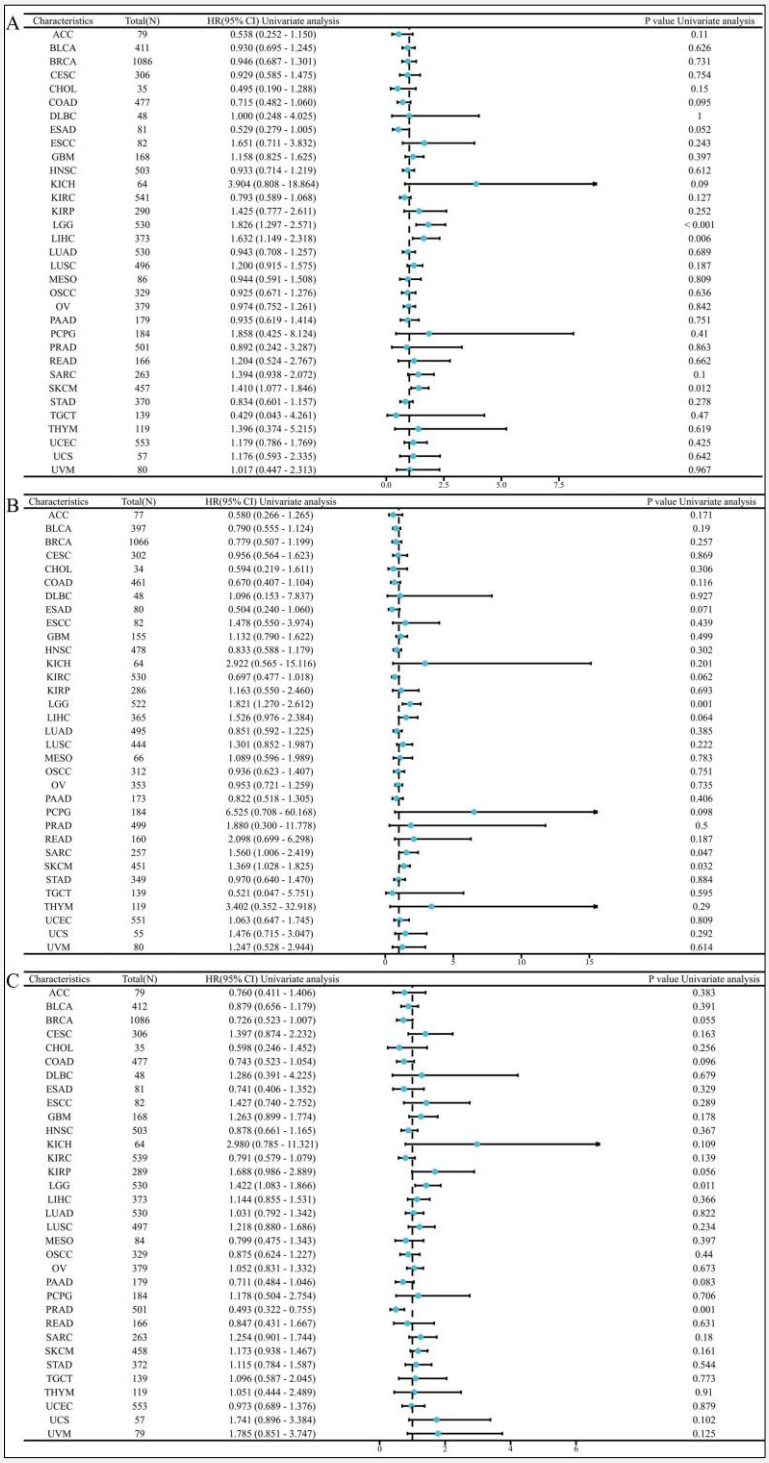

Figure S1. The relationship between TTC39A expression and OS, DSS, and PFI with the 33 kinds of cancers.

A) The forest map shows the relationship between the expression level of TTC39A and the OS of patients. B) The forest map shows the relationship between the expression level of TTC39A and the DSS of patients. C) The forest map shows the relationship between the expression level of TTC39A and the PFI of patients.

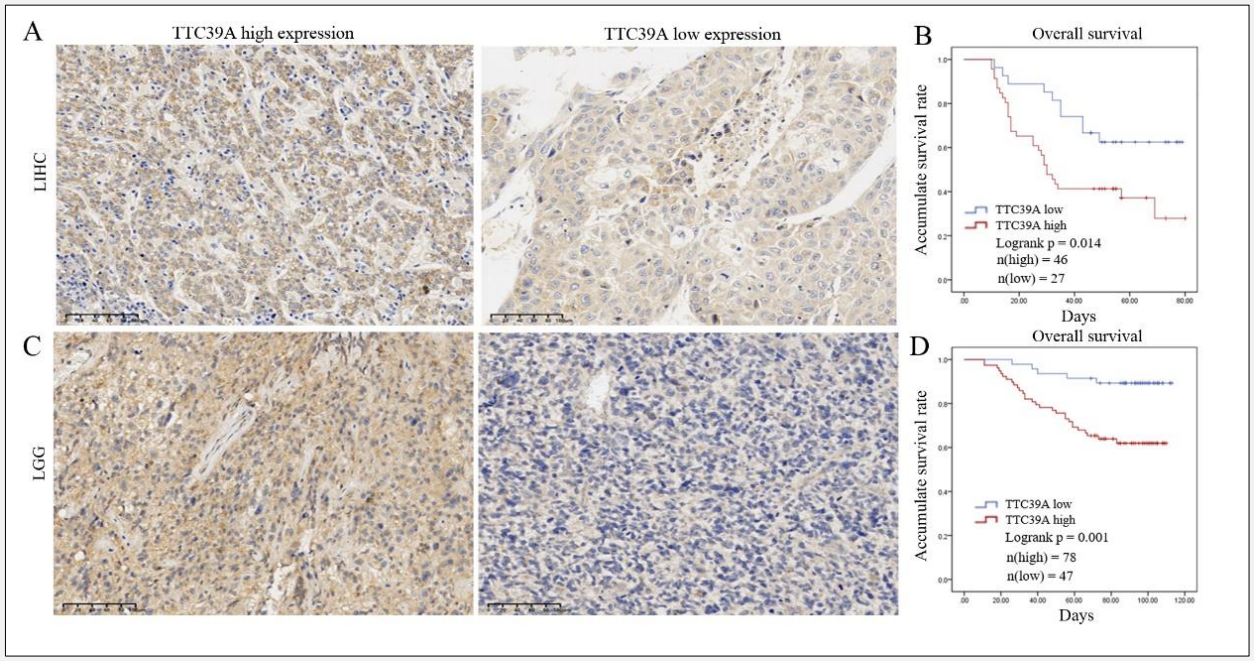

Figure S2. Expression of TTC39A protein in LIHC and LGG tissues.

A) Representative images of TTC39A staining in LIHC tissues. B) Higher expression of TTC39A significantly correlated with poor OS in LIHC cohort. C) Representative images of TTC39A staining in LGG tissues. D) Higher expression of TTC39A significantly correlated with poor OS in LGG cohort.

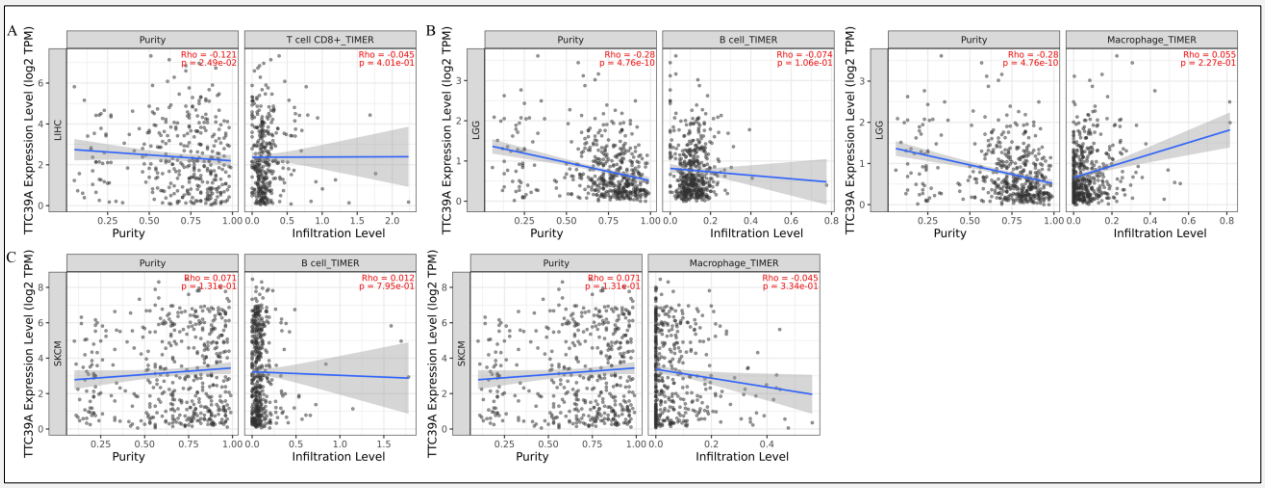

Figure S3. A) Correlation between the expression of the TTC39A and the infiltration of CD8+T cell in LIHC. B) Correlation between the expression of the TTC39A and the infiltration of B cell and macrophage in LGG. C) Correlation between the expression of the TTC39A and the infiltration of B cell and macrophage in SKCM.

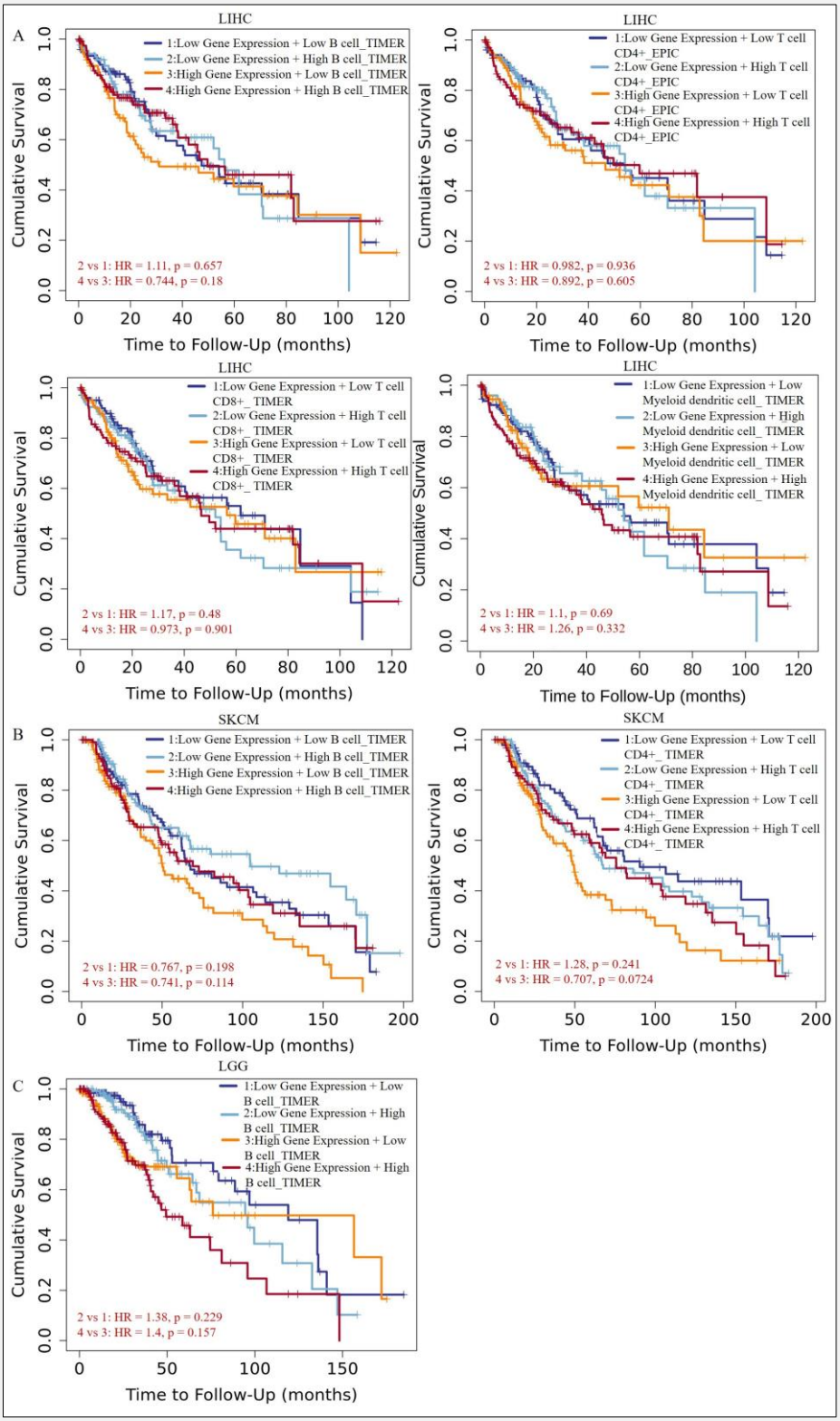

Figure S4. A) Regardless of TTC39A expression levels, OS in LIHC patients shown no significant correlation with B-cell, CD4+T cell, CD8+T cell and myeloid dendritic cell infiltration. B) Regardless of TTC39A expression levels, OS in SKCM patients shown no significant correlation with B-cell and CD4+T cell infiltration. C) Regardless of TTC39A expression levels, OS in LGG patients shown no significant correlation with B-cell infiltration.

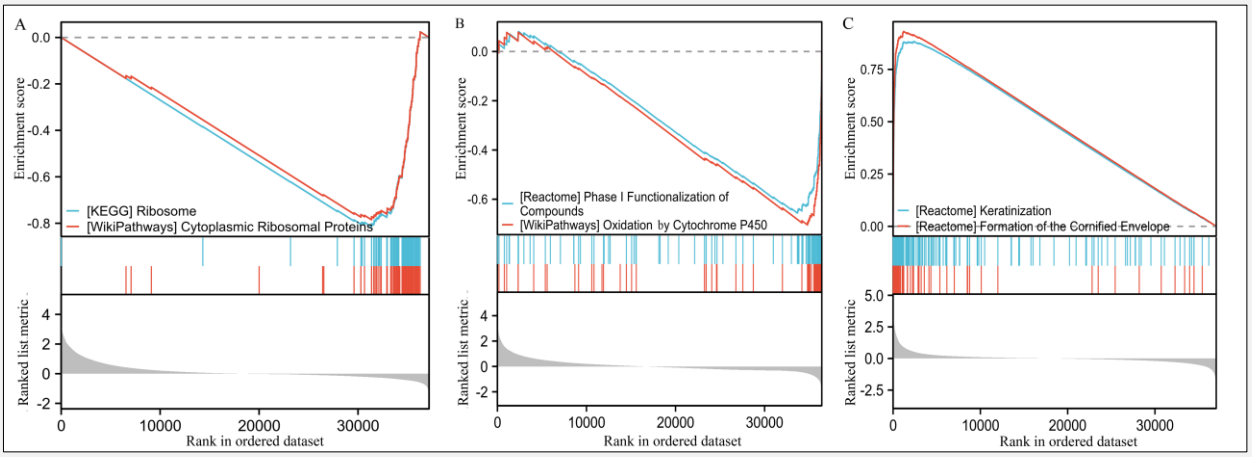

Figure S5. GSEA of TTC39A in LGG (A), LIHC (B), and SKCM (C).