Clin. Lab. 2025;71:1-7

ORIGINAL ARTICLE

Pan-Cancer Bioinformatics Analysis of Matrix Metalloproteinase-9 (MMP9)

Qianmei Zhan [2], Mengqiu Lan [2], Wenjie Huang [3], Yinxiu Chi [1], Dongliang Zhang [1]

[1] *Jiangsu Medical College, Yancheng, Jiangsu, China*
[2] *Liuzhou Municipal Liutie Central Hospital, Liuzhou, Guangxi, China*
[3] *Department of Reproductive Medicine, Liuzhou Maternity and Child Healthcare Hospital, Liuzhou, Guangxi, China*

SUMMARY

Background: **Matrix metalloproteinase-9 (MMP9) is a member of the matrix metalloproteinase family of proteases that have been linked to several major normal and pathologic processes. Although cell-based, animal-based, or clinical-based evidence supports the relationship between MMP9 and cancers, the role of MMP9 in pan-cancer is still not fully understood.**
Methods: **We explored the prognostic value and potential immunological roles of MMP9 in 33 cancer types using the Cancer Genome Atlas datasets.**
Results: **MMP9 is highly expressed at the RNA level in most cancers but is present at a low protein level in breast cancer, liver cancer, lung adenocarcinoma, and ovarian cancer. Furthermore, there are distinct associations between MMP9 expression and tumor patient prognosis. MMP9 expression was found to be associated with tumor mutational burden and microsatellite instability in eight cancer types, whereas it was associated with DNA methylation at multiple probes in 31 cancer types. Additionally, MMP9 expression was positively associated with the infiltration levels of most immune cells in 33 cancer types. Moreover, extracellular matrix organizing-related and collagen metabolism-related functions are involved in the functional mechanism of MMP9.**
Conclusions: **Our pan-cancer study offers a relatively comprehensive understanding of the role of MMP9 in tumorigenesis and tumor immunity in different tumors.**
(Clin. Lab. 2025;71:1-7. DOI: 10.7754/Clin.Lab.2025.241132)

Correspondence:
Dongliang Zhang
Jiangsu Medical College
Yancheng
Jiangsu, 224000
China
Email: dongliang20240524@163.com

Yinxiu Chi
Jiangsu Medical College
Yancheng
Jiangsu, 224000
China
Email: cyx18189345101@163.com

Manuscript accepted January 25, 2025

Supplementary Data

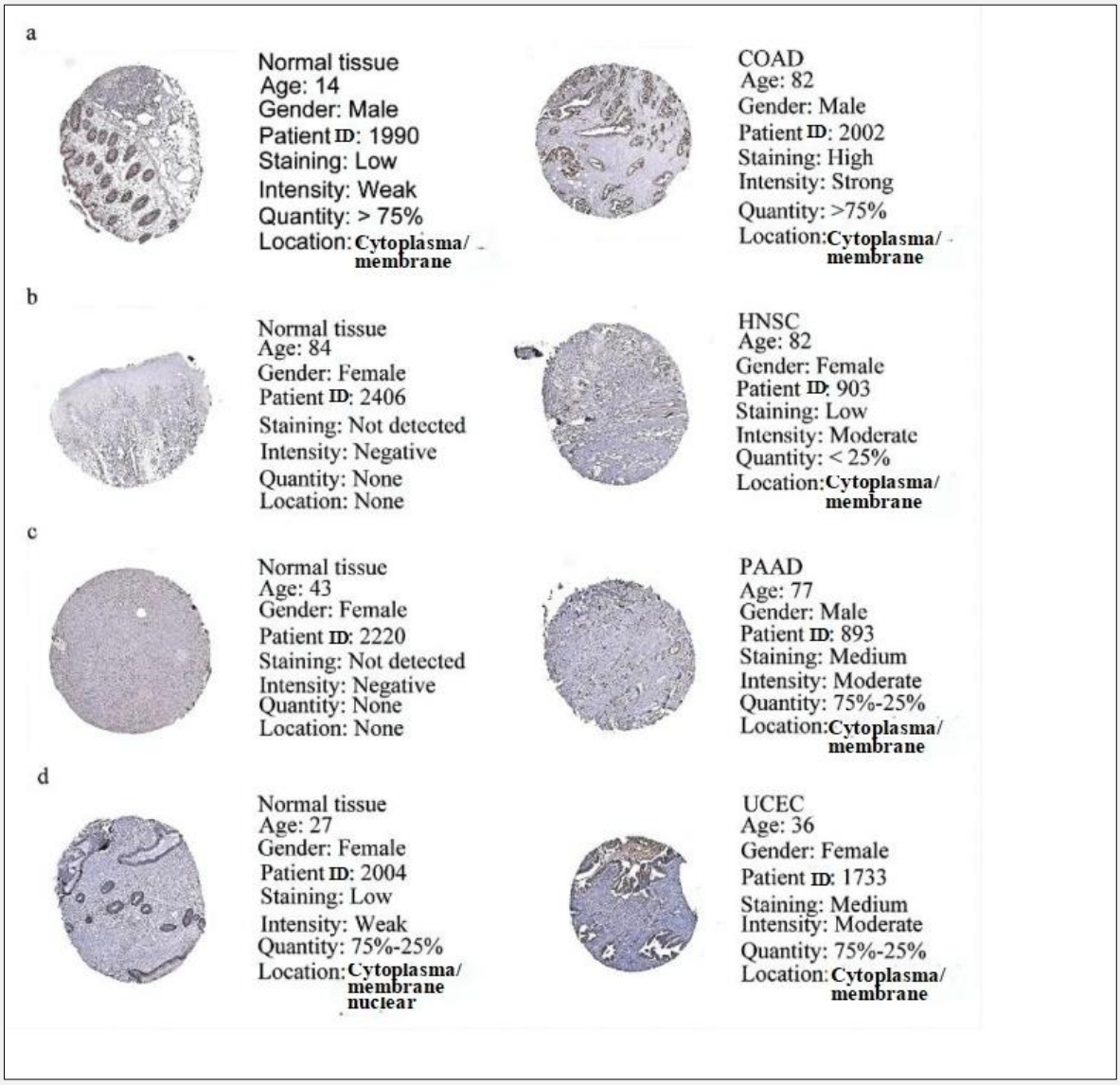

Figure S1. The immunohistochemistry images in normal and cancer tissues of COAD, HNSC, PAAD, and UCEC.

ns - no statistical significance, * - $p < 0.05$, ** - $p < 0.01$, * - $p < 0.001$.**

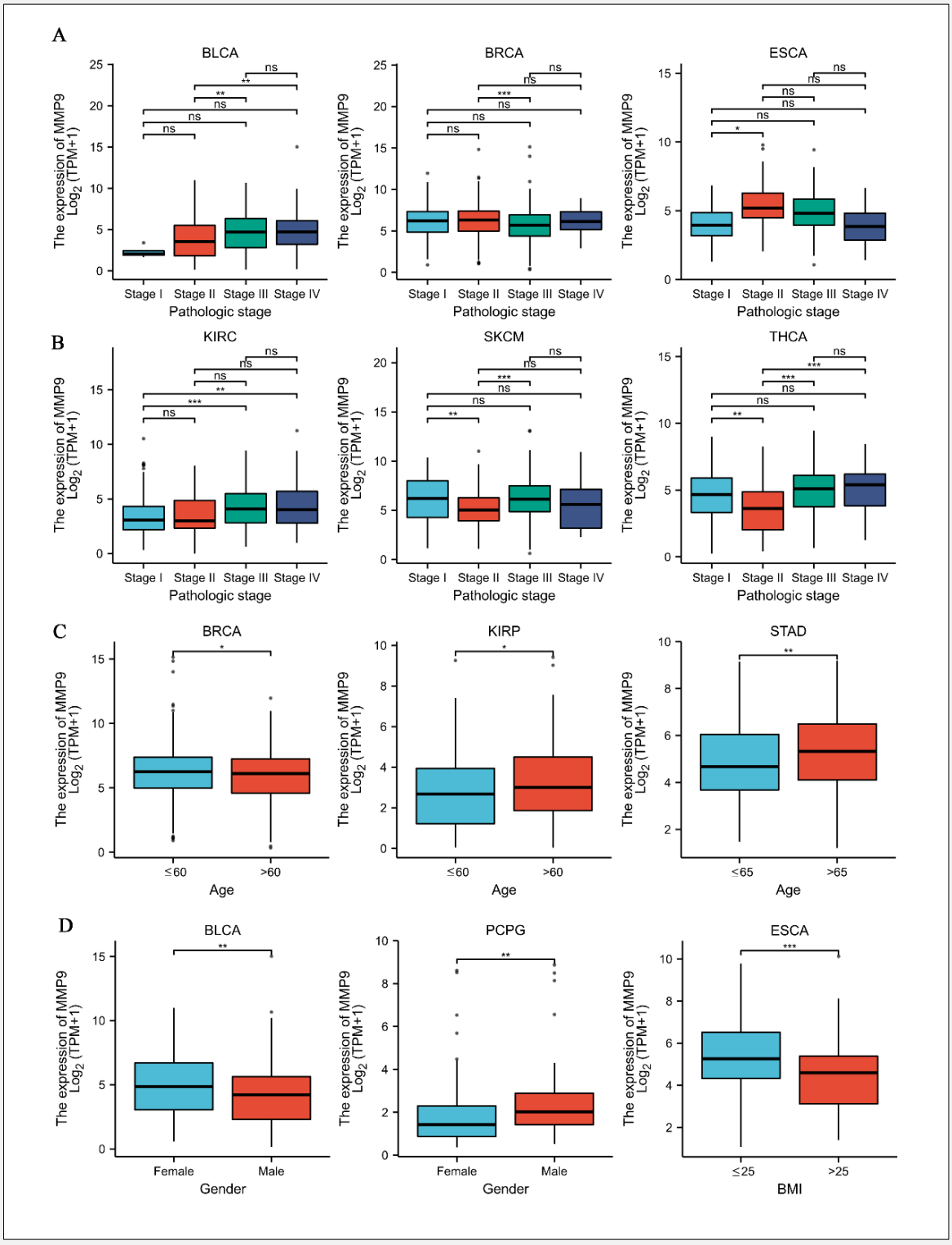

Figure S2. Expression level of MMP9 gene in different pathological stages.
A - Based on the TCGA data, the expression levels of the MMP9 gene were analyzed by the main pathological stages (stage I, stage II, stage III and stage IV) of BCLA, BRCA, ESCA, KIRC, SKCM and THCA. B - D - Association between demographic data (age, gender, and BMI) and MMP9 gene expression.

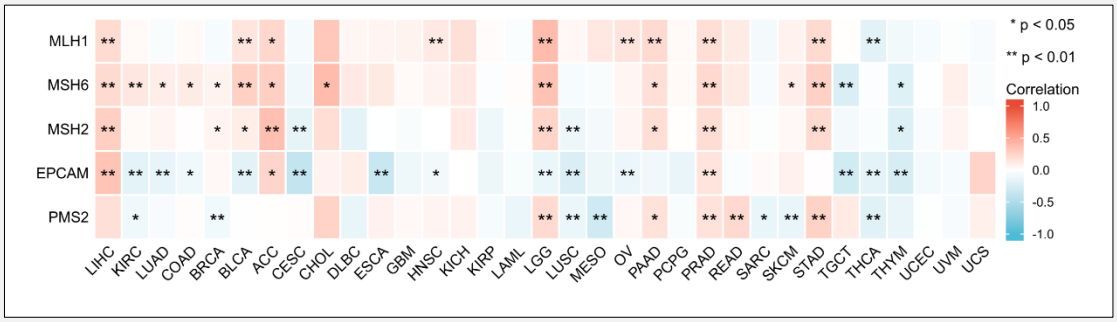

Figure S3. Heatmap illustrating the association between MMP9 expression and MMR genes.

Color scales represent the correlation and range from red (1) to blue (-1).
*** - p < 0.05, ** - p < 0.01, *** - p < 0.001.**

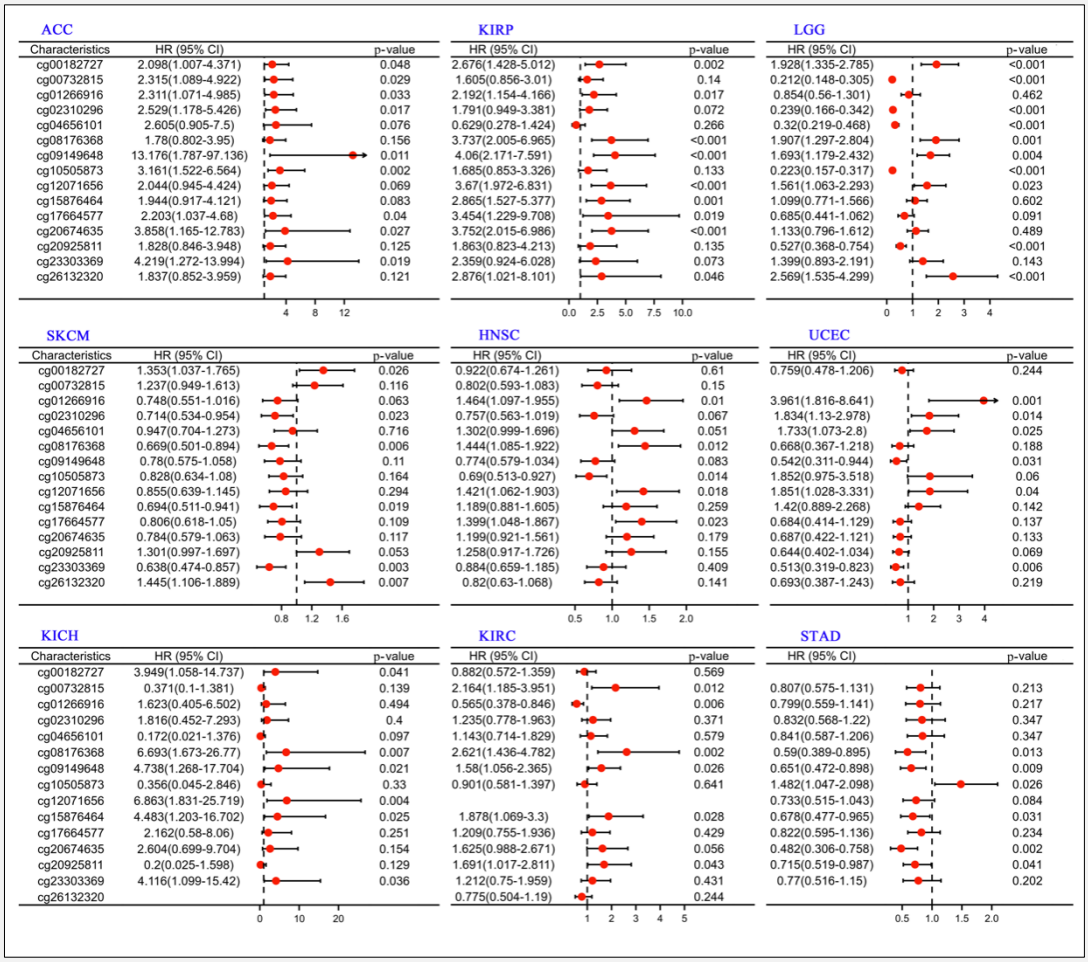

Figure S4. Forest plot of survival analysis of MMP9 methylation of multiple probes in different types of cancer, including ACC, KIRP, LGG, SKCM, HNSC, UCEC, KICH, KIRC, and STAD.

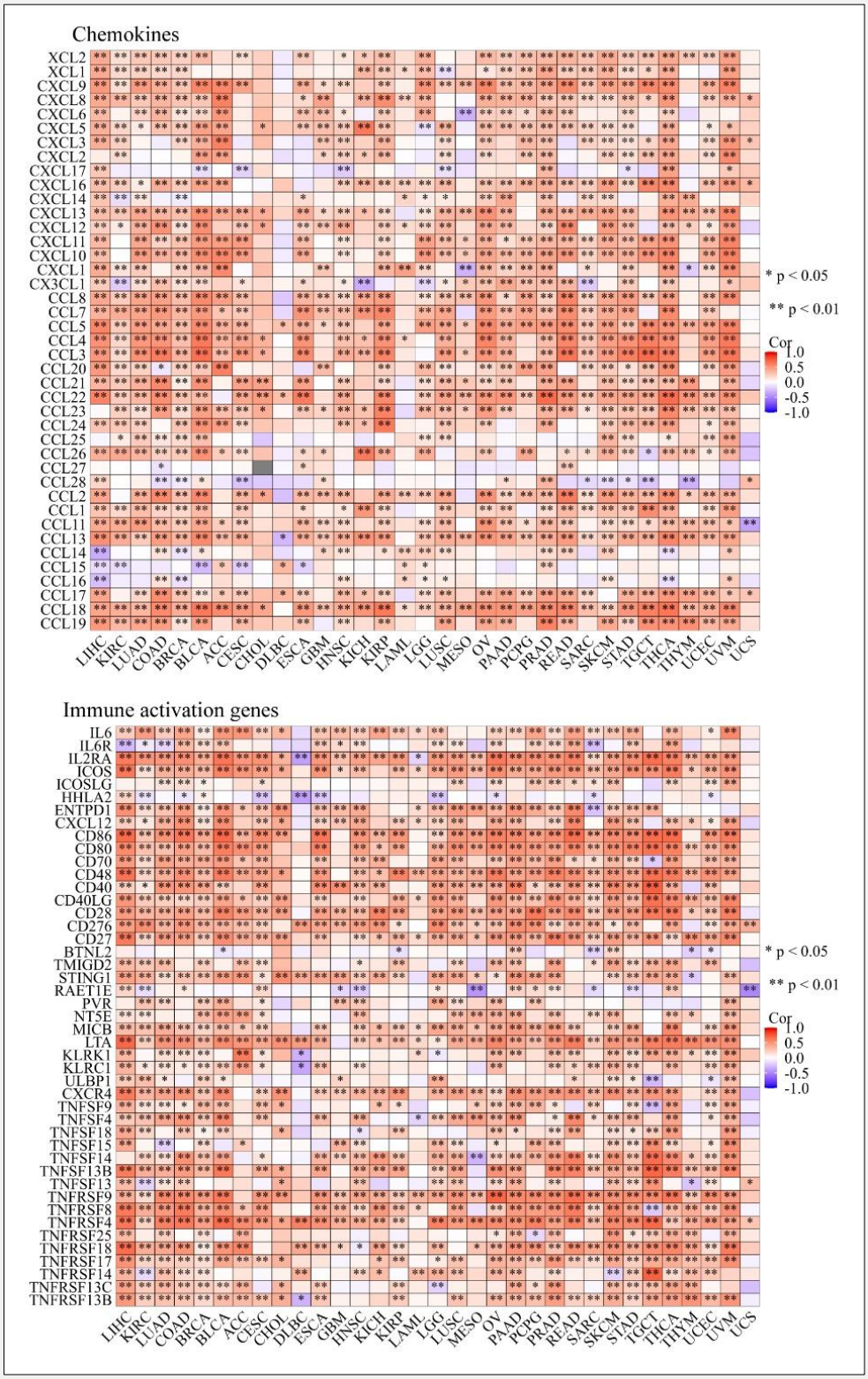

Figure S5. The correlation between MMP9 and chemokines and immune activation genes.

*** - p < 0.05, ** - p < 0.01.**

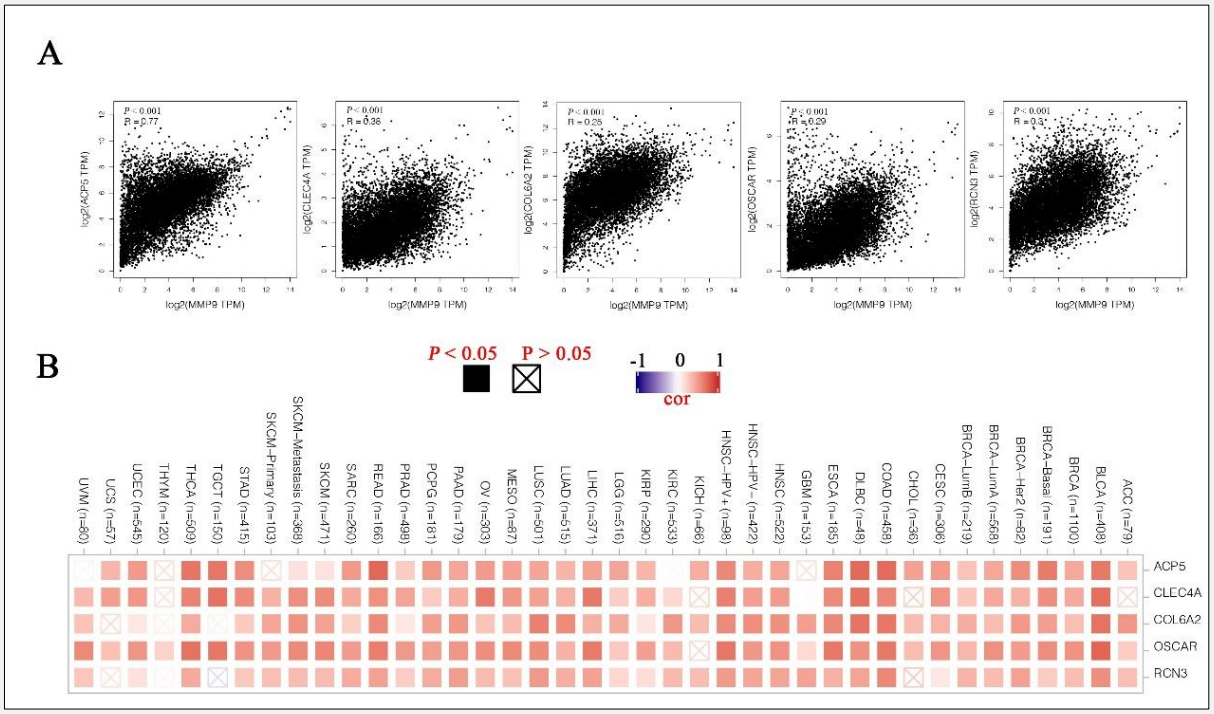

Figure 6. A - Using the GEPIA2 approach, we also obtained the top 200 MMP9-correlated genes in TCGA projects and analyzed the expression correlation between MMP9 and selected targeting genes, including ACP5, CLEC4A, COL6A2, OSCARs, and RCN3. B - The corresponding heatmap data in the detailed cancer types are displayed.

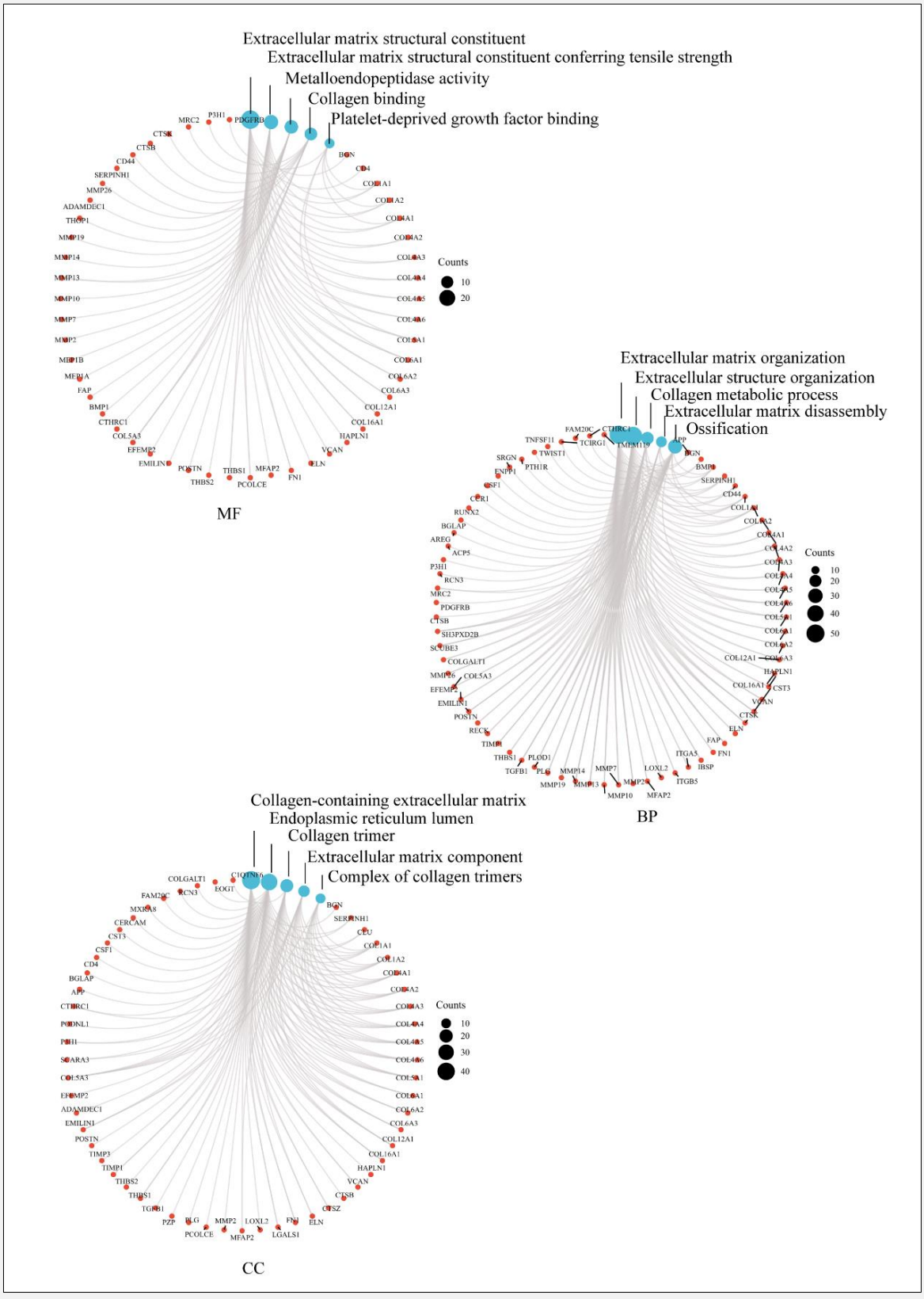

Figure S7. The cnetplots for the molecular function, biological process, and cellular component in GO analyses.